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Sheffield S10 3RA (GB). **STEAD, Ronald** [GB/CA]; 4
Glenelge Court, Bowmanville, Ontario L1C 4J1 (CA).

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(74) Agents: **BALDOCK, Sharon, Claire** et al.; BOULT
WADE TENNANT, Verulam Gardens, 70 Gray's Inn
Road, London WC1X 8BT (GB).

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(71) Applicants (*for all designated States except US*):
JANSSEN PHARMACEUTICA N.V. [BE/BE]; Turn-
houtseweg 30, B-2340 Beerse (BE). **HOLBURN THER-
APEUTICS INC.** [CA/CA]; 1100 Bennett Road, Bown-
manville, Ontario L1C 3K5 (CA).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **AERSSSENS,**
Jeroen Marcel Maria Rogers [BE/BE]; Kraaikant 22/c,
B-3221 Nieuwrode (BE). **PEETERS, Pieter Johan**
[BE/BE]; Dijkstraat 42, B-2480 Dessel (BE). **MEULE-**
MANS, Ann Louise Gabrielle [BE/BE]; Voortdijk 21,
B-2400 Mol (BE). **COULIE, Bernard** [BE/BE]; Grote
Molenweg 94, B-3020 Herent (BE). **HILLSLEY, Kirk**
[CA/CA]; 6 Anne Street, Millbrook, Ontario L0A 1G0
(CA). **GRUNDY, David** [GB/GB]; 21 Slayleigh Avenue,

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(54) Title: VAGAL AFFERENT NEURONS AS TARGETS FOR TREATMENT

(57) Abstract: A method of identifying a compound capable of reducing or preventing prolonged sensory neuron hyper-excitability comprising the steps of: (a) administering the compound to an experimental non-human animal having prolonged sensory neuron hyper-excitability; (b) generating an expression profile of the genes modulated in the Nodose Ganglia (NG) of the animal of step (a); (c) comparing the expression profile obtained in (b) with the expression profile of a corresponding panel of genes expressed in the NG of an experimental non-human animal having no prolonged sensory neuron hyper-excitability; wherein a positive correlation of the expression profiles is indicative that the compound is capable of reducing or preventing prolonged sensory neuron hyper-excitability in NG.

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VAGAL AFFERENT NEURONS AS TARGETS FOR TREATMENT

Field of Invention

The present invention relates to the treatment of sensory neuron hyper-excitability in
5 Nodose Ganglia (NG), methods for the identification of compounds suitable for this
application and pharmaceutical compositions comprising these compounds, as well as
their uses in the treatment of G.I tract disorders, depression and other stress related
disorders.

Background

10 *Vagal versus spinal visceral afferents*

The gastrointestinal (GI) tract receives dual extrinsic sensory innervation. Vagal afferents
have their cell bodies in the nodose ganglia (NG) and project centrally to make synaptic
connections in the brainstem, mainly at the level of the nucleus tractus solitarius; while
spinal afferents arise from the dorsal root ganglia (DRG) and project into the dorsal horn
15 of the spinal cord (Grundy D., Gut 2002; 51 Suppl 1:i2-i5). These two types of neurons
have different embryonic origins (epibranchial placode versus neural crest), different
dependencies upon neurotrophic factors for development and survival (BDNF/NT3
versus NGF/GDNF) and, in the adult form, phenotypically distinct subpopulations that
can be recognized by the presence or absence of certain peptides (particularly CGRP and
20 substance P) (Zhuo H, Ichikawa H, Helke CJ., 1997;52:79-107).

Vagal and spinal afferents supplying the GI tract also differ in the pattern of their
terminal innervation which, in part determines the stimulus-response properties of the
peripheral endings (Berthoud HR, Blackshaw LA, Brookes SJ, Grundy D., 2004;16 Suppl
1:28-33). Vagal afferents terminate close to the mucosal epithelium, where they are
25 exposed to chemicals (e.g. nutrients) absorbed from the lumen or mediators released from
enteroendocrine cells or immune cells in the lamina propria. These vagal afferents are
termed chemosensitive and can respond to a variety of different chemical stimuli. Vagal
afferents also form intramuscular arrays and intraganglionic laminar endings that are
thought to detect mechanical activity. Spinal afferents also innervate the mucosa,
30 submucosa and myenteric plexus. Additionally, projections of DRG neurons terminate in
the serosa and mesenteric attachments, often in association with blood vessels. These
endings are mechanosensitive but the basis of this mechanosensitivity at the molecular

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level is unknown. Both vagal and spinal afferents respond to distension and contraction but while vagal afferent endings respond to levels of distension that occur during the normal course of digestion, many spinal afferents have thresholds for activation that when applied in humans give rise to discomfort or pain (Gebhart GF., Gut 2000;47 Suppl 4:iv54-iv55).

These observations are the basis for the common view that vagal and spinal afferents have different functional roles: spinal afferents play a major role in nociception, while vagal afferents mediate physiological responses and behavioural regulation, particularly in a chemosensitive role, in relation to food intake, satiety, anorexia and emesis. However, there is some overlap, and vagal and spinal afferents share a number of features in common. Both have a large proportion of unmyelinated axons that can be ablated by the sensory neurotoxin, capsaicin; and both express the capsaicin receptor (TRPV1) that is often considered a hallmark of nociceptive neurons (Ward SM, Bayguinov J, Won KJ, Grundy D, Berthoud HR., J Comp Neurol 2003;465:121-135). In addition, chemosensitive vagal afferent neurons can also play a nociceptive role in acid signalling (Holzer, P., J Physiol Pharmacol 2003; 54(4), 43-53). Recently, both NG and DRG neurons have been shown to become sensitized following inflammatory insult, demonstrating plasticity in the mechanisms that regulate neuronal excitability which has implications for pain processing (Dang K, Bielefeldt K, Gebhart GF., Am J Physiol Gastrointest Liver Physiol 2004;286:G573-G579). As both NG and DRG neurons are altered following an inflammatory insult, it is possible that there is both altered chemosensitivity and altered mechanosensitivity in the post-inflammatory gut. Furthermore, there may be an interaction between changes in chemosensitive afferent pathways and changes in mechanosensitive afferent pathways.

Therefore, extrinsic afferent neurons supplying the gut are prime targets for new treatments of chronic visceral pain disorders such as IBS. The pathogenesis of IBS is heterogeneous but there are at least subpopulations of patients where emotional stress and/or enteric infection have been implicated.

Nippostrongylus brasiliensis infection as a model for IBS

Brain-gut interactions play a prominent role in the modulation of gut function in health and disease (Mayer EA, Naliboff BD, Chang L, Coutinho SV. V., Am J Physiol

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Gastrointest Liver Physiol 2001;280:G519-G524; Tache Y, Martinez V, Million M, Wang L., Am J Physiol Gastrointest Liver Physiol 2001;280:G173-G177). Therefore, every conceptual model of irritable bowel syndrome (IBS) should take into account that the central nervous system (CNS) and the GI-tract interact with each other under normal conditions and certainly during perturbations of homeostasis. Afferent signals from the gut to the brain (through splanchnic and vagal routes) are primarily involved in reflex regulation of gut function, but may also play an important role in such diverse functions as regulation of emotion, pain sensitivity and immune responses. Conversely, signals from the brain to the gut assure that digestive function is optimal for the overall state of the organism (e.g. stress vs relaxation, sleep vs awake). The fact that the presence of major life events around the time of gastroenteric infection is a risk factor for the development of PI-IBS symptoms underlines the importance of psycho-neuro-immune interactions.

By including a stress paradigm into an animal model we take into account this important aspect of IBS. As a trigger for the development of IBS a mild gastroenteric infection was induced using the nematode *Nippostrongylus brasiliensis*. The neural and cellular changes that occur following intestinal infection have been reasonably well documented. However, the physiological consequences of these changes are not well understood particularly in terms of the post-inflammatory changes which accompany intestinal recovery. Post-inflammatory jejunal hypersensitivity has been reported in the capsaicin-induced depressor response in rats previously infected (day 40-50) with *Nippostrongylus brasiliensis* (Mathison R, Davison JS, Naunyn Schmiedebergs Arch Pharmacol 1993;348:638-642). The afore mentioned study is pivotal as it shows that increased sensitivity can be observed in the absence of acute inflammation and this is relevant to and predictive of the pathophysiology of IBS. Indeed, the post-inflammatory changes which occur in the rat intestine post-infection with *N. brasiliensis* putatively parallel the pathophysiology of IBS (Camilleri M, Drug News Perspect 2001;14:268-278) and have been shown to include a variety of neuroimmune changes (Stead RH, Ann N Y Acad Sci 1992;664:443-455). In rats it has been shown that infection with *N. brasiliensis* leads to changes in intestinal mast cell number and peptidergic neurotransmission eventually leading to visceral hyperalgesia (McLean PG, Picard C, Garcia-Villar R, Ducos dL, More J, Fioramonti J, Bueno L, Neurogastroenterol Motil

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1998;10:499-508). Moreover these neuroimmune alterations lead to an increased intestinal motility response to CCK that involves a vagal pathway probably through CCK_A and CCK_B receptors (Gay J, Fioramonti J, Garcia-Villar R, Bueno L., Neurogastroenterol Motil 2001;13:155-162; Gay J, More J, Bueno L, Fioramonti J. ,
5 Brain Res 2002;942:124-127).

The present invention is based on the unexpected discovery by the inventors that after transient inflammation of the intestine induced by the nematode *Nippostrongylus brasiliensis* in mice combined with exposure to stress, gene expression profiles and electrophysiological properties of NG neurons projecting in to the gastrointestinal tract
10 are altered

The discovery is surprising because it has been previously shown that the activity of voltage sensitive sodium channels in DRG neurons in mice is increased after transient inflammation of the intestine with Nb, implicating DRG neurons in a variety of conditions resulting in chronic inflammatory and neuropathic pain.

15

Summary of the Invention

According to a first aspect of the present invention there is provided a method of identifying a compound capable of reducing or preventing prolonged sensory neuron
20 hyper-excitability comprising the steps of :

(a) administering the compound to an experimental non-human animal having prolonged sensory neuron hyper-excitability;

(b) generating an expression profile of the genes modulated in the Nodose Ganglia (NG) of the animal of step (a);

25 (c) comparing the expression profile obtained in (b) with the expression profile of a corresponding panel of genes expressed in the NG of an experimental non-human animal having no prolonged sensory neuron hyper-excitability;

wherein a positive correlation of the expression profiles is indicative that the compound is capable of reducing or preventing prolonged sensory neuron hyper-
30 excitability in NG.

It will be apparent that modulation of the expression of NG genes may be either up-regulation or down-regulation of expression. As used herein the term "expression

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profile” relates to methods that are able to outline the expression levels of various genes either at the transcript level or the protein level. Expression profiles can be obtained for example by Northern blot analysis, Western blot analysis, immunohistochemistry, in situ hybridization or other methods known in the art such as for example described in

5 Sambrook et al. (Molecular Cloning; A laboratory Manual, Second Edition, Cold Spring Harbour Laboratory Press, Cold Spring Harbour NY (1989)) or in Schena (Science 270 (1995) 467-470). Most preferably “expression profile” herein relates to methods using microarrays as e.g. described in the examples hereinafter.

10 Preferably, the modulation of genes expressed in the NG is compared at the nucleic acid level, in particular at the mRNA level.

It will be apparent to the skilled person that in order to obtain the NG for expression profiling the non human experimental animal is sacrificed.

15 It will be understood that the genes that are compared are genes whose expression is altered by at least 10%, more preferably the expression is altered by at least 25%, most preferably, the expression is altered by at least 50% in animals having prolonged sensory neuron hyper-excitability. As aforesaid, the expression may be up-regulated or down-regulated.

20 Preferably, the panel of prolonged sensory neuron hyper-excitability modulated genes are selected from the group consisting of those genes disclosed in Table 1 as shown at the end of the description.

25 Preferably, the prolonged sensory neuron hyper-excitability modulated signal compared comprises the expression level of at least one nucleic acid sequence encoding a receptor selected from the group consisting of the vanilloid receptor VR1 (*Trpv1*), cholecystokinin receptor A (*Cckar*), serotonin receptor 3A (*Htr3a*) and somatostatin 2 receptor (*Sstr2*). More preferably, the panel of prolonged sensory neuron hyper-excitability modulated signals compared comprises the expression level of at least nucleic acid molecules encoding the vanilloid receptor VR1 (*Trpv1*), cholecystokinin receptor A (*Cckar*), serotonin receptor 3A (*Htr3a*) and somatostatin 2 receptor (*Sstr2*). Most preferably, the method comprises comparing the expression of a panel of at least 40
30 nucleic acid sequences encoding genes having modulated expression in NG associated with having prolonged sensory neuron hyper-excitability. In a more particular embodiment, the method comprises comparing an expression panel of prolonged sensory

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neuron hyper-excitability modulated genes selected from the group consisting of those genes disclosed in Table 1. A particularly preferred panel of 51 genes whose expression is to be compared is shown in Table 2 below.

- 5 In a preferred embodiment of the invention the expression profile of prolonged sensory neuron hyper-excitability modulated genes is assessed at the mRNA level. It will be understood that the presence of the at least 1 nucleic acid molecule may be detected on the basis of a probe capable of hybridizing thereto which may be affixed to a solid support. A panel of probes capable of hybridizing to a panel of nucleic acids can be
10 affixed to a solid support in an arrayed form as described hereinafter.

- In a preferred embodiment of the invention, labelled mRNA is hybridized against a panel of different nucleic acids representing or comprising genes expressed in the NG. The term "labelled mRNA" herein refers to methods of labelling mRNA which for example can be performed by fluorescence-labelling using fluorescent dyes or by
15 autoradiographic labeling using e. g. ^{32}P or ^{33}P . Labelling methods are well known by those skilled in the art and are described (Sambrook et al., supra; Ausubel et al., supra, Eisen and Brown, Methods Enzymology 303 (1999), 179-205).

- The mRNA labelled as indicated above is hybridized against a panel of different "nucleic acids representing or comprising genes" expressed in the NG. The term "nucleic
20 acids representing or comprising genes" denotes for example oligonucleotides, cDNAs, PCR fragments amplified from ORFs, or any other polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides.

- In a preferred embodiment of the invention said panel of different nucleic acids is affixed to a solid support. The solid support herein can be for example represented by
25 polylysine-treated glass slides or activated slides that allow single strand covalent amino-mediated binding of cDNA, however, is not limited to those (Blohm and Guiseppi-Elie, Current Opinion Biotechnology 12 (2001), 41-47).

- In a preferred embodiment of the invention said panel of different nucleic acids is affixed to said solid support in arrayed form. The construction of microarrays is described
30 e. g. in the examples hereinafter or in Marton (Nature Medicine 4(1998), 1293-13).

Any non-human animal model of prolonged sensory neuron hyper-excitability is suitable for use in the screening methods of the present invention. Exemplified herein is a

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method in which a rodent is infected with *Nippostrongylus brasiliensis* and subjected to stress. Intestinal inflammation is induced by the infection but once the inflammation has subsided prolonged sensory neuron hyper-excitability remains. These post-inflammatory changes parallel the pathology of human irritable bowel syndrome (IBS). There are
5 however a number of other methods of modelling G. I. tract disorders in which intestinal inflammation can be induced with attendant prolonged sensory neuron hyper-excitability using a variety of infectious or non-infectious agents all of which would be suitable for use in the screening method of the invention and which may or may not be combined with the attendant application of stress.

10 For example, the relevant inflammatory response can be induced by other parasites, particularly Helminths such as *Heligmosomoides polygyrus*, *Trichuris muris* or *Leishmania major*. Other suitable parasitic Helminths are identified in the Table 3 below.

The prolonged sensory neuron hyper-excitability may begin and end at different times after the initial infection, depending upon the nature and life cycle of the infectious
15 agent and may be further enhanced by repeated or subsequent infections or other factors (physical and chemical stressors – see below).

TABLE 2

Probe Set ID	Gene Symbol	Title	Log2Ratio. Median.IS. over.SNS	GenBank ID	SwissProt ID
1421195_at	Cckar	cholecystokinin A receptor	0.80	BC020534	O08786
1437029_at	Tacr3	tachykinin receptor 3	1.65	AV328460	AAH66845 /// P47937
1443392_at	Trpv1	vanilloid receptor 1	1.10	BB346256	---
1418268_at	Htr3a	serotonin receptor 3A	-0.38	NM_013561	P23979 /// Q8K1F4
1459850_x_at	Girb	glycine receptor, beta subunit	0.66	BB345174	BAC38831 /// P48168
1417489_at	Npy2r	neuropeptide Y receptor Y2	1.23	NM_008731	P97295 /// Q8BWW1
1420799_at	Ntsr	neurotensin receptor	-0.71	NM_018766	O88319
1426204_a_at	Oprl	opioid receptor-like	0.63	AF043276	BAC30067 /// BAC37672 /// P35377 /// Q80WU7
1427331_at	Adora1	adenosine A1 receptor	0.85	BB518868	CAD88592 /// Q60612 /// Q8BGU7 /// Q8CAH1 /// Q8R0M5
1434172_at	Cnr1	cannabinoid receptor 1 (brain)	1.44	BQ177934	---
1433602_at	Gabra5	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 5	0.71	BQ175863	AAH62112 /// O88964 /// Q8BHJ7
1435021_at	Gabrb3	gamma-aminobutyric acid (GABA-A) receptor, subunit beta 3	0.74	BQ175666	BAC30230 /// P15433 /// Q8C446
1437968_at	Grin1	glutamate receptor, ionotropic, NMDA1 (zeta 1)	-1.17	AI385669	P35438 /// Q8BZ96 /// Q8CFS4
1421530_a_at	Grm8	glutamate receptor, metabotropic 8	0.60	NM_008174	P47743
1438613_at	Kcna4	potassium voltage-gated channel, shaker-related subfamily, member 4	0.72	BB131475	Q8CBF8
1439204_at	Scn3a	sodium channel, voltage-gated, type III, alpha polypeptide	0.85	BB096886	Q62204
1454768_at	Kcnfl	potassium voltage-gated channel, subfamily F, member 1	1.15	AV337635	Q7TSH7
1438093_x_at	Dbi	diazepam binding inhibitor	0.75	BB115327	BAB25730 /// BAB25755 /// BAB32175 /// BAC25658 /// P31786
1420596_at	Caeng2	calcium channel, voltage-dependent, gamma subunit 2	-1.18	NM_007583	O88602 /// Q8C8F5
1427418_a_at	Hif1a	hypoxia inducible factor 1, alpha subunit	1.37	X95580	Q61221
1449544_a_at	Kcnh2	potassium voltage-gated channel, subfamily H (eag-related), member 2	-0.77	NM_013569	AAQ82708 /// O35219 /// Q80WG1 /// Q80XE8
1439618_at	Pde10a	phosphodiesterase 10A	1.51	AI448308	Q8C8M0 /// Q8CA95 /// Q9WV11
1451707_s_at	Slc41a3	solute carrier family 41, member 3	-0.98	BC011108	Q921R8 /// Q9DC67

Probe Set ID	Gene Symbol	Title	Log2Ratio. Median.I.S. over.SNS	GenBank ID	SwissProt ID
1437864_at	Adipor2	adiponectin receptor 2	-0.70	BE632137	AAR08379 /// Q8BQS5
1437259_at	Slc9a2	solute carrier family 9 (sodium/hydrogen exchanger), member 2	0.80	AV274006	Q9WUJ4
1433536_at	Lrp11	low density lipoprotein receptor-related protein 11	1.65	BB435348	AAH59874 /// Q8CB67
1457164_at	Ank1m1	ANKTM1	1.10	BB309395	Q8BLA8
1420609_at	Axot	axotrophin	-0.38	NM_020575	Q9WV66
1451840_at	Calp	calsenilin-like protein	0.66	BG261945	AAH51130 /// Q8CAD0 /// Q8R4I2 /// Q9EQ01
1422659_at	Camk2d	calcium/calmodulin-dependent protein kinase II, delta	1.23	NM_023813	AAH52894 /// O70459 /// Q8C3F8 /// Q8C4I3 /// Q8C8X9 /// Q8CAC5 /// Q8CCM0 /// Q9CZEE
1434034_at	Cerk	ceramide kinase	-0.71	BI905090	BAC98226 /// Q8K4Q7
1449403_at	Pde9a	phosphodiesterase 9A	0.63	NM_008804	AAH61163 /// O70628 /// Q8BSU4 /// Q8CB29
1416013_at	Pld3	phospholipase D3	0.85	NM_011116	O35405
1437861_s_at	Prkce	protein kinase C, epsilon	1.44	BB335101	P16054
1416339_a_at	Prkcsb	protein kinase C substrate 80K-H	0.71	NM_008925	O08795 /// Q921X2
1416294_at	Scamp3	secretory carrier membrane protein 3	0.74	NM_011886	O35609
1418738_at	Scn1b	sodium channel, voltage-gated, type I, beta polypeptide	-1.17	BC009652	P97952
1420822_s_at	Sgpp1	sphingosine-1-phosphate phosphatase 1	0.60	NM_030750	Q9J199
1417622_at	Slc12a2	solute carrier family 12, member 2	0.72	BG069505	P55012
1417600_at	Slc15a2	solute carrier family 15 (H+/peptide transporter), member 2	0.85	NM_021301	Q80XC0 /// Q8VEK9 /// Q9CXC0 /// Q9JIM03
1448502_at	Slc16a7	solute carrier family 16 (monocarboxylic acid transporters), member 7	1.15	NM_011391	BAC36415 /// O70451
1418843_at	Slc30a4	solute carrier family 30 (zinc transporter), member 4	0.75	NM_011774	O35149
1419971_s_at	Slc35a5	solute carrier family 35, member A5	-1.18	C86506	Q921R7 /// Q9DC72
1453915_a_at	Slc37a3	solute carrier family 37 (glycerol-3-phosphate transporter), member 3	1.37	AK012071	Q8BVX2 /// Q99JR0
1454764_s_at	Slc38a1	solute carrier family 38, member 1	-0.77	BF165681	AAH66815 /// Q8BHI3 /// Q8BXE2 /// Q8K2P7 /// Q99PR1
1426432_a_at	Slc4a4	solute carrier family 4 (anion exchanger), member 4	1.51	BE655147	O88343 /// Q8QZR9 /// Q9R1C4
1438673_at	Slc4a7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	-0.98	AW555750	Q8BTY2 /// Q8BWZ4 /// Q9JL09

Probe Set ID	Gene Symbol	Title	Log2Ratio. Median.IS. over.SNS	GenBank ID	SwissProt ID
1428954_at	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 2	-0.70	AK004710	AAH65778 /// Q9JHL1
1428460_at	Syn2	synapsin II	0.76	AK013810	AAH66004 /// Q8CEI9 /// Q9QWV7
1415844_at	Syt4	synaptotagmin 4	0.78	AV336547	P40749
1440882_at	Lrp8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	1.11	BB750940	Q924X6

Table 3

Phylum	Class and order	Family	Genus and Species	Disease
Nematoda	Adenophorea; Enoplida	Trichinellidae (muscleworms)	Trichinella spiralis	Trichinosis
		Trichuridae (whipworms)	Trichuris trichiura	Trichuriasis
	Secernentea; Rhabditida	Strongyloididae (threadworms)	Strongyloides stercoralis	Strongyloidiasis
	Secernentea; Strongylida	Ancylostomatoidea (hookworms)	Ancylostoma duodenale	Hookworm disease
			Necator americanus	
	Secernentea; Ascaridida	Ascarididae (roundworms)	Ascaris lumbricoides	Ascariasis
		Onchocercidae (filarids)	Wuchereria bancrofti	Filariasis
			Brugia malayi	
Platyhelminthes	Trematoda; Strigeatoida (fluke worms)	Schistosomatidae	Schistosoma mansoni	Schistosomiasis
			Schistosoma japonicum	
			Schistosoma haematobium	
		Fasciolidea	Fasciola hepatica	Fascioliasis
	Cestoidea; Cyclophyllidea (tapeworms)	Taeniidae	Taenia solium	Cysticercosis
			Enchinococcus granulosus	Hydatid cyst

The immunopathology of various of these parasites is described in Gause et al,
 5 Trends in Immunology, Vol. 24, No. 5, May 2003.

Other infective agents suitable for inducing inflammatory conditions in the
 intestinal mucosa of a non-human animal include bacteria such as Campylobacter species,
 Helicobacter species and E.coli. Since the inflammation may be generated by antigenic
 determinants or toxins carried by the bacteria, the model may involve the administration
 10 of bacteria either dead or alive or the administration of individual inflammatory antigens,
 such as known bacterial toxins.

Other non-human animal models of prolonged sensory neuron hyper-excitability
 for use in the invention include those where an irritant material is administered to the
 intestine at some time prior to assessment of sensory neuron hyper-excitability. Suitable
 15 materials include a material selected from the group including: dinitrochlorobenzene ,
 trinitrobenzene sulphonic acid, dinitrobenzene sulphonic acid, acetic acid, mustard oil,

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dextran sodium sulphate, croton oil, carageenan, amylopectin sulphate, oxazalone and indomethacin.

The experimental non-human animal having prolonged sensory neuron hyper-excitability as used herein relates to other known non-human animal models of mucosal inflammation, such as those used to study the pathogenesis of inflammatory bowel disease, such as for example described in Strober et al. (Annu. Rev. Immunol. 2002 20:495-549) and the post-inflammatory states arising therefrom.

Further non-human animal models may also be used in the screening method of the invention where the non-human animal has a particular genetic background or carries a genetic defect or has been otherwise engineered (e.g. a transgenic animal) to exhibit intestinal inflammation and prolonged sensory neuron hyper-excitability.

Examples of genetic background differences in non-human animals include the different responses to various somatic and visceral painful stimuli exhibited by different strains of mice (Mogil et al., Pain 1999;80:67-82; Kamp et al., Am. J. Physiol., 2003;284:G434-G444); the heightened sensitivity to wrap restraint and water avoidance exhibited by Fischer rats when compared to Sprague Dawley and Lewis rats, respectively; and the well described depressive phenotype of Flinders rats (Yadid et al., Prog. Neurobiol. 2000;62:353-378) that results in enhanced visceromotor responses to colorectal distension (Eisenbruch et al., Neurogastroenterol. Mot. 2004;16:801-809).

Examples of genetic defect or engineered models are:

Tg₂₆ mice

TCR- α chain deficiency

TNF ^{$\Delta\Delta$ RE} mice (TNF- α overproduction)

WASP deficiency

C₃H/HeJBir mice

N-cadherin dominant-negative mice

Gi2 α -deficient mice

IL-2 deficient mice

Samp1/Yit mice

T-bet Tg mice

STAT4 Tg mice

TGF- β RII dominant-negative Tg mice

HLA-B27 Tg rats

Mdr1a-deficient mice

IL-7 Tg mice

5

The non-human animal may be a mouse, rat or other rodent, guinea pig, cat, dog, or non-human primate. The aforementioned models of mucosal inflammation may be operated with or without the concurrent application of stress to the animal. Alternatively, stress to the animal may in itself be sufficient to cause prolonged sensory neuron hyper-
10 excitability and accordingly useful in the methods of the invention. Stress may be applied in a number of ways, for example, over-crowded housing, poor handling, absence of tubes or gauze in a cage. Other stressors that may be employed are known in the art as described by Mayer et al.(supra) and Taché et al. (supra) and include: neonatal colonic irritation, maternal separation, foot shock, open field, loud noise, water avoidance, tail
15 shock, wrap restraint, cold water swim, exposure to cold or heat and other environmental stimuli. Such stressors may be employed alone, in combination with each other and / or in combination with inflammation.

In an alternative embodiment this invention provides the comparison of the expression profiles of the prolonged sensory neuron hyper-excitability modulated genes
20 in cell populations capable of expressing one or more of said genes disclosed in Table 1, preferably capable of expressing one or more of said genes disclosed in Table 2, more preferably in cell populations expressing at least one nucleic acid sequence encoding a receptor selected from the group consisting of the vanilloid receptor VR1 (*Trpv1*), cholecystokinin receptor A (*Cckar*), serotonin receptor 3A (*Htr3a*) and somatostatin 2
25 receptor (*Sstr2*). More preferably the invention involves comparing the expression profiles of at least nucleic acid molecules encoding the vanilloid receptor VR1 (*Trpv1*), cholecystokinin receptor A (*Cckar*), serotonin receptor 3A (*Htr3a*) and somatostatin 2 receptor (*Sstr2*). Most preferably the invention involves comparing the expression of a panel of at least 40 nucleic acid sequences encoding genes having modulated expression
30 in NG associated with having prolonged sensory neuron hyper-excitability. A particularly preferred panel of genes whose expression is to be compared is shown in Table 2 supra.

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In this alternative embodiment the expression profiles are compared between a test cell, i.e. a cell population known to have an expression profile as observed in the NG of the non-human animal having prolonged sensory neuron hyper-excitability with a reference cell population, i.e. a cell population known to have an expression profile as observed in the NG of the non-human animal not having prolonged sensory neuron hyper-excitability.

Accordingly in a second aspect the invention provides a method for identifying a compound capable of reducing or preventing prolonged sensory neuron hyper-excitability comprising the steps of:

- 10 (a) administering the compound to a test cell population;
- (b) generating an expression profile of the prolonged sensory neuron hyper-excitability modulated genes in the cell population of step (a);
- (c) comparing the expression profile obtained in (b) with the expression profile of the prolonged sensory neuron hyper-excitability modulated genes in a reference cell population;

15 wherein a positive correlation of the expression profiles is indicative that the compound is capable of reducing or preventing prolonged sensory neuron hyper-excitability in NG.

Preferably the test cell population is derived from the NG of an experimental non-human animal having prolonged sensory neuron hyper-excitability, and the reference cell population is derived from the NG of an experimental non-human animal not having prolonged sensory neuron hyper-excitability. More preferably the cell populations are derived from the NG of a rodent, in particular mice.

It is also an object of the present invention to provide the use of NG sensory neuron activity assays in a method to identify compounds capable of reducing or preventing prolonged sensory neuron hyper-excitability. Such assays are known in the art and typically involve measurement of ionic currents using either

- i) electrophysiological techniques such as for example using two-electrode voltage clamp recordings (Dascal N. (1987) Crit.Rev.Biochem **22**, 341-356), patch-clamp recordings (Zhou Z. *et al.*, (1998) Biophysical Journal **74**, 230-241), or measurement of action potentials using microelectrodes (Dall'Asta V. *et al.* (1997) Exp.Cell Research **231**, 260-268) or

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ii) fluorometric techniques wherein the ion currents, in particular calcium currents, are assessed using several ion-sensitive fluorescent dyes, including fura-2, fluo-3, fluo-4, fluo-5N, fura red, Sodium Green, SBFI and other similar probes from suppliers including Molecular Probes. The ionic currents, in particular calcium, can thus be determined in
5 real-time using fluorometric and fluorescence imaging techniques, including fluorescence microscopy with or without laser confocal methods combined with image analysis algorithms.

In a particular embodiment the NG sensory neuron activity assay consist of the patch clamp recordings as described in the examples hereinafter.

10 Accordingly in a third aspect the present invention provides a method for identifying a compound capable of reducing or preventing prolonged sensory neuron hyper-excitability comprising the steps of:

(a) administering the compound to NG having prolonged sensory neuron hyper-excitability; and

15 (b) determining the effect of said compound on the NG sensory neuron activity of said cells.

In a further embodiment of the aforementioned method the NG are derived from mouse previously infected with *Nippostrongylus brasiliensis*. In the aforementioned method the activity of the NG is assessed using any one of the assays described
20 hereinbefore, in particular the patch clamp recordings as described in the examples hereinafter. Alternatively, the capability of a compound to prevent or reduce prolonged sensory neuron hyper-excitability is assessed using whole animal nociceptive assays. In these assays quantifiable behaviour or physiological responses are used to compare pain perception in the non-human animal.

25 As described in Example 6 hereinafter, a particular assay to study prolonged sensory neuron hyper-excitability consists of the pressor-depressor model in which changes in arterial blood pressure, recorded during phasic distention of both the jejunum and the colon, is used to measure visceral hypersensitivity.

Further assays to study sensory neuron hyper-excitability are known in the art and
30 include;

i) the abdominal constriction, a.k.a. writhing test, wherein a noxious substance is injected into the peritoneal cavity to score the number of writhes – lengthwise stretches of the torso

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with a concomitant concave arching of the back- as a readout for hyper-excitability (Mogil J.S. et al., Pain 80 (1999) 67-82); or

ii) the colorectal distention test (CRD), wherein electromyographic (EMG) recording is used to determine the contraction of the abdominal musculature in response to phasic colorectal distention. This response is also known as the visceromotor response (Kamp E. et al., Am.J.Physiol.Gastrointest.Liver Physiol. 284 (2003) G434-G444.

It is accordingly a further object of this invention to provide the use of a nociceptive assay in a method to identify the capability of a compound to reduce or prevent prolonged sensory neuron hyper-excitability. It thus provides a method for identifying a compound capable of reducing or preventing prolonged sensory neuron hyper-excitability comprising the steps of:

(a) administering the compound to an experimental non-human animal having prolonged sensory neuron hyper-excitability; and

(b) determining the effect of said compound in a nociceptive assay.

In this method any non-human animal model of prolonged sensory neuron hyper-excitability as described hereinbefore can be used. In particular the experimental non-human animal having prolonged sensory neuron hyper-excitability is a rodent previously infected with *Nippostrongylus brasiliensis* and subjected to stress, even more particular a mouse previously infected with *Nippostrongylus brasiliensis* and subjected to stress. The nociceptive assay will typically consist of the pressor-depressor model as provided in example 6 hereinafter.

Further visceral and somatic nociceptive assays, reviewed for example in Mogil J. S *et al* (supra), which may be used in the current invention include, but are not limited to:- the autotomy following hindlimb denervation (AUT) test; the carrageenan hypersensitivity (CAR_{HT}) test; the formalin test (F_{early}/F_{late}); the hot-plate test (HP); the Hargreaves test of thermal nociception (HT); the Cheung peripheral nerve injury model(PNI_{HT}, PNI_{VF}); the tail withdrawal test (TW); and the Von Frey filament test of mechanical sensitivity (VF).

According to a fourth aspect of the current invention there is provided a method of treating a subject with a disease condition related to prolonged sensory neuron hyper-

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excitability, comprising administering to a subject an effective amount of an agent that modulates NG sensory neuron activity.

Preferably the agent is one which reduces or prevents prolonged sensory neuron hyper-excitability.

5 Preferably, the disease condition associated with prolonged sensory neuron hyper-excitability is a gastrointestinal (GI) tract disorder, particularly a bowel disorder, such as but not limited to, ulcerative colitis, Crohn's disease, ileitis, proctitis, celiac disease, enteropathy associated with arthropathies, microscopic or collagenous colitis, eosinophilic gastroenteritis, pouchitis resulting after proctocolectomy/post ileoanal
10 anastomosis, functional dyspepsia, functional vomiting, oesophagitis, gastric ulcer, duodenal ulcer or irritable bowel syndrome. In addition the disease or condition associated with prolonged sensory neuron hyper-sensitivity may be depression or other stress-related disorder.

 The agent may be one which modulates the expression or activity of one or more
15 of the genes listed in Table 1 or modulates the activity of any protein or polypeptide expressed from one or more of said genes. Preferably, the agents may be those which modulate the expression or activity of one or more receptors selected from the group consisting of Table 2

 Further, suitable agents are any compound identified as capable of reducing or
20 preventing prolonged sensory neuron hyper-excitability which are identified using any one of the compound screening methods described above.

 According to a fifth aspect of the present invention, there is provided a pharmaceutical composition for the treatment of a disease or disorder related to prolonged
25 sensory neuron hyper-excitability comprising any one or more of the compounds identified below, any other compound capable of modulating the expression or activity of one or more of the genes listed in Table 1 or any compound identified by the method of first aspect of the invention and at least one pharmaceutically acceptable diluent or excipient.

30 It will be understood that the pharmaceutical composition may be administered by any suitable means, such as, but not limited to oral or nasal administration, suppository, subcutaneous or intraperitoneal injection or intravenous administration.

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In the pharmaceutical composition of the invention, preferred compositions include pharmaceutically acceptable carriers including, for example, non-toxic salts, sterile water or the like. A suitable buffer may also be present allowing the compositions to be lyophilized and stored in sterile conditions prior to reconstitution by the addition of sterile water for subsequent administration. The carrier can also contain other pharmaceutically acceptable excipients for modifying other conditions such as pH, osmolarity, viscosity, sterility, lipophilicity, osmobility or the like. Pharmaceutical compositions which permit sustained or delayed release following administration may also be used.

Compounds which are identified are suitable for use in the methods of the current invention along with derivatives that retain substantially the same activity as the starting material, or more preferably exhibit improved activity, which may be produced according to standard principles of medicinal chemistry, which are well known in the art. Such derivatives may exhibit a lesser degree of activity than the starting material, so long as they retain sufficient activity to be therapeutically effective. Derivatives may exhibit improvements in other properties that are desirable in pharmaceutical active agents such as, for example, improved solubility, reduced toxicity, enhanced uptake, etc.

According to a sixth aspect of the present invention there is provided a method of making a pharmaceutical composition for the treatment of a disease or disorder related to prolonged sensory neuron hyper-excitability, comprising combining a compound identified according to the method of the first aspect of the invention or any of the compounds identified as suitable disclosed above together with a pharmaceutically acceptable diluent or excipient.

According to a seventh aspect of the current invention there is provided the use or one or more of the compounds recited below in the manufacture of a medicament for the treatment of a disease or disorder related to prolonged sensory neuron hyper-excitability.

Preferably, the prolonged sensory neuron hyper-excitability is NG sensory neuron hyper-excitability

Preferably, the disease or disorder related to prolonged sensory neuron hyper-excitability is a GI tract disorder. More preferably the GI tract disorder comprises a bowel disorder, such as but not limited to, ulcerative colitis, Crohn's disease, ileitis, proctitis, celiac disease, enteropathy associated with arthropathies, microscopic or

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collagenous colitis, eosinophilic gastroenteritis, pouchitis resulting after proctocolectomy and post ileoanal anastomosis, functional dyspepsia, functional vomiting, oesophagitis, gastric ulcer, duodenal ulcer or irritable bowel syndrome. In addition the disease or condition associated with prolonged sensory neuron hyper-sensitivity is depression or other stress-related disorder.

In a preferred embodiment the invention relates to uses of a modulator of serotonin receptor 3A (*Htr3a*) such as, for example, Ondansetron, Granisetron, Alosetron, Cilinsetron, or dolasetron in the manufacture of a medicament for the treatment of any one of the above GI tract disorders and in particular the treatment of irritable bowel syndrome.

All of the genes listed in Table 1 are potential pharmaceutical targets whose activity might be modulated to reduce or prevent prolonged sensory neuron hyper-excitability. Modulation of one or more of those genes is likely to be useful in the treatment of G.I. tract disorders or stress-related disorders such as ulcerative colitis, Crohn's disease, ileitis, proctitis, celiac disease, enteropathy associated with arthropathies, microscopic or collagenous colitis, eosinophilic gastroenteritis, pouchitis resulting after proctocolectomy and post ileoanal anastomosis, functional dyspepsia, functional vomiting, oesophagitis, gastric ulcer, duodenal ulcer, irritable bowel syndrome or depression.

Techniques which may be used to validate one or more of the genes of Table 1 as a pharmaceutical target in one or more of the above diseases are antisense technology or gene silencing using, for example, methylation of DNA or RNA interference (RNAi). "RNAi" is a process of sequence-specific down-regulation of gene expression RNAi may be performed using, for example, small interfering RNA (siRNA). This is a specific type of the well-known RNAi. technique. (also referred to as "RNA-mediated gene silencing") initiated by double-stranded RNA (dsRNA) that is complementary in sequence to a region of the target gene to be down-regulated (Fire, A. Trends Genet. Vol. 15, 358-363, 1999; Sharp, P.A. Genes Dev. Vol. 15, 485-490, 2001).

Over the last few years, down-regulation of target genes in multicellular organisms by means of RNA interference (RNAi) has become a well established technique. In general, RNAi comprises contacting the organism or cell with a double-stranded RNA fragment (generally either as two annealed complementary single-strands

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of RNA or as a hairpin construct) having a sequence that corresponds to at least part of a gene to be down-regulated (the "target gene"). Reference may be made to International application WO 99/32619 (Carnegie Institute of Washington), International application WO 99/53050 (Benitec), and to Fire et al., Nature, Vol. 391, pp.806-811, February 1998 for general description of the RNAi technique.

Elbashir *et al.* (Nature, 411, 494-498, 2001) demonstrated effective RNAi-mediated gene silencing in mammalian cells using dsRNA fragments of 21 nucleotides in length (also termed small interfering RNAs or siRNAs). These short siRNAs demonstrate effective and specific gene silencing, whilst avoiding the interferon-mediated non-specific reduction in gene expression which has been observed with the use of dsRNAs greater than 30bp in length in mammalian cells (Stark G.R. et al., Ann Rev Biochem. 1998, 67: 227-264; Manche, L et al., Mol Cell Biol., 1992, 12: 5238-5248). In practice these siRNAs may be between about 19 and about 23 nucleotides in length and can be introduced into the cell by standard transfection techniques or more appropriately be produced *in situ* using an expression vector for the production of siRNAs within cells. A particularly advantageous embodiment of the technique produces 50mer fragments in such a way that they form hairpin-like structures known as shRNAs. These are more stable than siRNA fragments. Commercial siRNA and shRNA kits are available such as one produced by Invivogen. (San Diego, USA)

In an eighth aspect the invention relates to the use of small interfering RNA (siRNA) to validate as pharmaceutical targets in the treatment of a G.I. tract disorder or stress-related disorder such as any of those already listed above, any one or more of the genes shown in Table 1. It will be appreciated that the silencing of any one of the genes will elucidate its role in the listed disorders thus, being an effective target validation mechanism.

Brief Description of the Drawings

The invention will be further understood with reference to the following experimental Examples and the accompanying figures in which:-

Figure 1A shows the numbers of labelled DRG neurons after injection of CTB488 label into the intestinal musculature (IM).

Figure 1B shows the numbers of labelled DRG neurons after injection of CTB549 label intraperitoneally (IP).

Figure 1C and D are panels showing that all neurons fluorescently labelled following IM injection of CTB488 were co-labelled by IP injection of CTB594.

5 Figure 2A shows the serum corticosterone stress enzyme levels in the groups of Nb infected and non infected mice after 5 weeks in a stressed or non stressed environment.

Figure 2B shows the average serum corticosterone levels in the stressed and non stressed mice after 5 weeks.

10 Figure 3A shows mean serum IgE levels in $\mu\text{g/ml}$ in infected and non infected stressed and non stressed mice.

Figure 3B shows the variation in IgE levels in Nb infected and non infected mice over time.

15 Figure 4 shows the variation in mast cell counts in Nb infected and non infected mice over time.

Figure 5 shows the histology of Nb infection in mouse, the panels showing the gut prior to infection, during acute inflammation and after acute inflammation has subsided.

Figure 6 shows the conductance of the DRG neurons from infected and non infected animals.

20 Figure 7 shows that in DRG neurons the Rheobase was lower in Nb infected mice compared to non infected mice.

Figure 8 shows that action potential number in DRG neurons following 500ms at 2x Rheobase was increased in Nb infected mice.

25 Figure 9 shows a comparison of the slow afterhyperpolarization (sAHP) in DRG neurons following action potentials in sham and Nb infected mice.

Figure 10 shows the resting conductance of NG neurons from infected and non infected animals, expressed as raw data and normalized to cell size (capacitance)

Figure 11 shows that action potential number in NG neurons following 500ms at 2x Rheobase was increased in Nb infected mice.

30 Figure 12 shows the change in antipeak amplitude, action potential half width and maximum decay slope in NG after Nb infection.

Figure 13 shows that in NG neurons the Rheobase was lower in Nb infected mice compared to non infected mice.

Figure 14 shows spectral map analysis and principal component plot of gene expression in DRG neurons isolated by laser capture from non infected / non stressed,
5 infected / non stressed, non infected / stressed, and infected / stressed groups of mice.

Figure 15 shows spectral map analysis of gene expression in NG neurons isolated by laser capture from non infected / non stressed, infected / non stressed, non infected / stressed, and infected / stressed groups of mice.

Figure 16 shows a Venn diagrammatic representation of the number of genes
10 identified by spectral map analysis (SPM), significance analysis (SAM) and fold difference filtering (FD). The selection of 1996 genes was based on the fulfilment of at least two of these three criteria.

Figure 17A shows the effect on expression of vanilloid receptor VR1 mRNA of Nb infection in DRG and NG neurons measured on an Affymatrix microarray.

15 Figure 17B show expression level of Trpv1 mRNA as assessed by quantitative PCR.

Figure 18A shows the effect on expression of 5-HT3 receptor of Nb infection in NG and DRG neurons.

Figure 18B shows the effect on expression of cholecystokinin receptor A of Nb
20 infection in NG neurons.

Figure 19A shows the effect on expression of somatostatin 2 receptor of Nb infection in NG neurons.

Figure 19B shows expression level of Sstr2 mRNA as assessed by quantitative PCR in DRG an NG neurons.

25 Figure 20A shows immunohistochemical staining of VR1 protein level in sham and Nb infected NG and DRG neuron sections.

Figure 20B shows a graphical representation of the level of VR1 protein staining seen in Figure 20B, showing that there is a significant increase in VR1 expression in Nb infected NG neurons.

30 Figure 21 shows the effect of jejunal phasic distension on pressor responses responses in Sham vs. Day 21 Post Nb infection animals.

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Figure 22 shows the effect of colonic phasic distension on pressor responses in Sham vs. Day 21 Post Nb infection animals.

Figure 23 shows the effect of 1 μ M of the the somatostatin antagonist octreotide on evoked action potential discharge in sham and infected NG neurons.

5 Figure 24 shows the mean effects of 1 μ M of the the somatostatin antagonist octreotide on evoked action potential discharge in sham and infected NG neurons.

Figure 25 shows in panel A the mean afferent nerve activity and in Panel B the IP response to intraluminal acid infusion in sham and Nb infected mice.

10 Figure 26 shows the acute and prolonged increase over baseline of nerve firing (Panel A) and IP (Panel B) in response to intraluminal acid infusion.

Materials and Methods

Retrograde labelling of sensory neurons

15 Female balb-c mice (20 ± 2 g, n=4) were anaesthetized with ketamine / xylazine / acepromazine (80 / 50 / 1 mg/kg, IP, respectively). Anaesthesia was subsequently maintained by top-up doses of 20 mg/kg ketamine (IP) as required. Following a midline laparotomy, a 5 cm section of the jejunum was exposed to enable intramuscular (IM) injections of fluorescently labelled cholera toxin subunit B (CTB488, Molecular Probes, Eugene, OR). A Hamilton syringe was used to inject 2-4 μ l of CTB488 into the intestinal
20 musculature at ten distinct sites along both sides of the jejunal segment. Following suturing of the abdominal incision and recovery from the surgery, mice were injected IP with a contrasting fluorophore (CTB594, 100 μ l, Molecular Probes). After a 4 day recovery period, animals were euthanized. NG and DRG from T1-L4 were removed.
25 Each ganglion was placed on a slide and a coverslip was used to cover and squash the ganglia to enable counts of CTB488- and CTB594-labelled neurons in the same ganglia, using a Leica fluorescence microscope equipped with TX2 (for CTB594) and L5 (for CTB488) filter blocks (Leica, Toronto, Canada). All procedures were approved by the institutional Animal Care Committee.

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Assessment of numbers of neurons in sensory ganglia

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CTB488 was administered IP (100µl) to mice and the animals were euthanized four days later. One of each pair of DRG from T10 to T13 were harvested and frozen, prior to sectioning on the cryostat at 10µm. The paired ganglia from the contra-lateral side were squashed on slides beneath cover slips, as described above. Photomicrographs of at least 10 cryostat sections per ganglion and the squash preparations were prepared using a Leica fluorescence microscope and filter block L5. The numbers of fluorescent cells were counted from the resultant photomicrographs. The cryostat sections were then stained with methylene blue and the total numbers of neurons (ganglion cells containing a recognizable nucleus) were counted. From these measurements it was possible to determine the percentage of fluorescent neurons in the cryostat sections (number of fluorescent cells x 100/total of number of neurons). This factor could then be applied to the squash preparation counts to determine the total numbers of neurons per ganglion (number of fluorescent neurons in squash preparations x 100/percentage fluorescent neurons).

15

Laser capture microdissection (LCM)

All ganglia harvested for microarray studies were removed 3-4 days after a single IP injection of CTB488 (100µl). Nodose and T10 to T13 dorsal root ganglia were procured from balb-c mice. Each labelled sensory ganglion was placed in tissue freezing medium (TFMTM, Triangle Biomedical Sciences, Durham, NC), frozen and stored at -80°C until the sample was used for RNA extraction or laser capture microdissection (LCM).

Cryostat sections (12µm) were attached to RNase-free PEN membrane-covered glass slides (P.A.L.M. Microlaser Technologies AG, Bernried, Germany), fixed with 100% ethanol and air dried prior to LCM. Microdissection was performed on a P.A.L.M. microbeam-equipped microscope (Axiovert 135, Zeiss, Göttingen, Germany). Fluorescent neuronal cells were detected and subsequently marked by cutting the contours of the cell with low laser energy. Marked cells were excised after Nissl staining (0.5% Cresyl violet Acetate [Sigma-Aldrich, St. Louis, MO]/0.1M SodiumAcetate [Fluka, Buchs, Switzerland]). Cells were catapulted in 75µl Rneasy lysis buffer (RLT, Qiagen GmbH, Hilden, Germany) containing 0.14M β-mercaptoethanol and 200ng polyinosinic acid (Sigma) and stored at -80°C.

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RNA isolation

Laser captured samples were incubated at 42°C for 20min and then chilled on ice. An equal volume of 70% ethanol was added to each sample and then transferred to RNeasy
5 MinElute Spin Columns (Qiagen). RNA was cleaned up according to manufacturer's instructions, eluted in 14µl of RNase free water and adjusted to 4µl by vacuum drying.

RNA Amplification

As “spike-in” controls, the GeneChip Poly-A RNA control kit (Affymetrix, Santa Clara,
10 CA) was used. Serial dilutions were made of the prokaryotic Poly-A control using the following dilution steps; 1:20, 1:50, 1:50, 1:20 and 1:10. This dilutions series was based on a estimated starting amount of 0.5 ng total RNA in the laser captured material. First strand cDNA was prepared as described by the Affymetrix two cycle cDNA synthesis protocol except for the use of Superscript III (Invitrogen, Carlsbad, CA) and incubation at
15 50°C for 30 minutes. Second strand master mix consisted of 1µl 10X *Bst* polymerase buffer (Epicentre, Madison, WI), 1µl of 10mM dNTP (Invitrogen), 0.5µl (1U) thermostable RnaseH (Invitrogen), 1µl (5U) *Bst* DNA polymerase (Epicentre) and water to 10µl. This master mix was added to the first strand cDNA reaction and incubated at 65°C for 10 min before heat inactivation at 80°C for 3min. Subsequently 2µl of
20 exonuclease mix was added containing *ExoI* and *ExoVII* and incubated at 37°C for 10min followed by heat inactivation at 80°C for 3min. Double-stranded cDNA was transcribed at 42°C for 3 hours using the AmpliScribe T7 High Yield Transcription Kit (Epicentre) in a total volume of 100 µl (final concentration of all reagents 0.2 x less than described in manufacturer's instructions). The resulting amplified RNA was incubated with DNase I
25 (4 Units/µl) at 37°C for 15 minutes. Amplified RNA was purified after adding 100 ng polyinosinic acid using RNeasy MinElute Cleanup Kit (Qiagen). RNA was eluted in 14 µl of RNase-free water and adjusted to 4 µl by vacuum drying. The second round of amplification was performed as described above except that 50ng of random hexamer primers was used to prime the reverse-transcription reaction and that the second strand
30 cDNA reaction was primed with 0.25ng T7 oligo.

RNA labelling and microarray hybridisation

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The third round amplification, including biotin labelling, was performed on 500ng of second round amplified RNA. First strand cDNA synthesis was performed as described above except that Superscript II was used and incubated at 37°C for 1 hour. Subsequently RNase H (1U) (Invitrogen) was added and incubated at 37°C for 20 min followed by
5 denaturation at 95°C for 2min. Second strand cDNA synthesis was performed using 1 µl T7 oligo dT24 (Affymetrix 100pmol/µl) annealed for 5 min at 70°C, and the reaction was then incubated at 42°C for 10 min. A master mix was prepared consisting of 10x second strand buffer, dNTPs (200mM final), *E. coli* RNase H (2U) and 10U *E. coli* DNA polymerase (Invitrogen) and added to the first strand reaction to obtain a 50 µl reaction
10 volume. Following incubation at 37°C for 10min, denaturation was done at 80°C for 3min. Cleanup of second strand cDNA synthesis was performed using Qiagen PCR purification kit according to manufacturer's instructions. For synthesis of biotin-labelled RNA the BioArray HighYield RNA transcript labelling Kit (Enzo Life Sciences, Farmingdale, NY) was used according to manufacturer's instructions. Clean-up of biotin
15 labelled RNA was performed using the RNeasy Mini Kit (Qiagen). Labelled RNA was hybridized to either mouse genome MG-U74v2 (12,000 transcripts) or MG-430_2.0 (39,000 transcripts) GeneChip arrays (Affymetrix). Hybridisation of microarrays was performed using 12.5µg biotin labelled RNA at 45°C for 16h under continuous rotation. Arrays were stained in Affymetrix Fluidics stations using Streptavidin/Phycoerythrin
20 (SAPE) followed by staining with anti-streptavidin antibody and a second SAPE staining. Subsequently arrays were scanned with a Agilent Laserscanner (Affymetrix) and data were analysed with the Microarray Suite Software 5.0 (Affymetrix). No scaling or normalization was performed at this stage.

25 **Data analysis and selection of genes**

Normalization: Genes that were called absent in all samples according to Affymetrix' MAS 5.0 software (p-value of >0.06) were removed from further analysis. Raw intensities from each chip were log₂ transformed and all data from the samples were quantile normalized per type of ganglion using the method described by Amaratunga and
30 Cabrera (Amaratunga D, Cabrera J., J Am Stat Assoc 2001;96:1161-1170). Following the group-wise quantile normalization, a second quantile normalization was carried out across the data of all DRG and NG derived samples. This alignment sets the range of

intensities of one array to the range measured across all arrays, compensating for array to array variations in hybridisation, washing and staining, ultimately allowing a reasonable comparison between arrays.

Spectral map analysis: Spectral map analysis is a recently introduced special type of
5 multivariate projection method that helps to reduce the complexity (dimensions) of highly dimensional data (n genes versus p samples) (Wouters L, Göhlmann HW, Bijmens L, Kass SU, Molenberghs G, Lewi PJ., Biometrics 2003;59:1133-1141). This unsupervised method allows the reduction of the complexity of large microarray datasets and provides a means to visually inspect and thereby identify clusters of genes and/or subjects in the
10 data without any bias from the observer. The aim of the technique is to retrieve the most predominant differences in the dataset, disregarding genes that do not contribute to the difference.

Significance analysis: Individual genes with different expression levels between groups (Sh/NS vs I/S) were identified using Significance Analysis of Microarray data (SAM)
15 (Tusher VG, Tibshirani R, Chu G., Proc Natl Acad Sci U S A 2001;98:5116-5121). SAM assigns a score to each gene based on the difference in gene expression level relative to the standard deviation of repeated measurements. SAM uses permutations of the repeated measurements to estimate the percentage of genes identified by chance; i.e. the false discovery rate (FDR). An extension of this FDR is the so-called *q*-value introduced by
20 Storey (Storey JD, Tibshirani R., Proc Natl Acad Sci U S A 2003;100:9440-9445). Whereas the *p*-value is commonly used for performing a single significance test, the *q*-value is useful for assigning a measure of significance to each of many tests performed simultaneously, as in microarray experiments. We applied a 10% threshold ($q = 0.1$) for our analysis (<http://faculty.washington.edu/~jstorey/qvalue/manual.pdf>;
25 [http://faculty.washington.edu/~jstorey/qvalue /manual.pdf](http://faculty.washington.edu/~jstorey/qvalue/manual.pdf) 2004).

Fold-difference filtering: A fold-difference filter was applied excluding all genes that exhibited a difference in expression below 50% (1.5 fold difference filter).

Effect of amplification and CTB488 injection on gene expression

30 *Effect of CTB488:* The effect of CTB488 labelling on gene expression profiles in sensory ganglia was assessed by comparing expression profiles of ganglia isolated from three vehicle treated animals to those of three combined intradermal and IP injected mice

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(resulting in labelling of almost all neurons). Although a clear difference in expression profile was observed between NG and DRG, no significant effect of the dye injection was noted.

Effect of amplification: In order to obtain sufficient material for microarray experiments, RNA isolated from laser captured neurons was amplified using a three round
5 amplification protocol. Efficiency and sensitivity of amplification were assessed by adding to the amplification reaction “spike-in” controls, consisting of four exogenous, pre-mixed, polyadenylated prokaryotic sequences. The resultant array signal intensities of the “spike-in” controls served as sensitive indicators of the amplification and labelling
10 efficiency, independent of starting sample quality. In agreement with previous reports, “spike-in” controls revealed a detection limit of 1 copy in 1,000,000 and a direct correlation between signal intensity and copy number.

Quantitative RT-PCR

15 Microarray data were confirmed using real time PCR analysis. First strand cDNA synthesis was performed on 50ng second round amplified RNA using random hexamer primers and Superscript II RT (Invitrogen). Quantitative PCR was performed on a ABIPrism 7900 cycler (Applied Biosystems, Foster City, CA) using a Taqman PCR kit (Applied Biosystems). Serial dilutions of cDNA were used to generate standard curves of
20 threshold cycles versus the logarithms of concentration for ATPase and the genes of interest (see Table 4 for sequences of primers (Eurogentec, Seraing, Belgium)).

Table 4

	CCKA	Forward	5'-CTGGGCAAGGGTGGTAACAT-3'
25	CCKA	probe	5'-Fam-CCCAAGGAAAAGTAGCATGTGGGACTCA-Tamra-3'
	CCKA	Reverse	5'-AGTTTTGGCATTCAAAGCTACTTATTAA-3'
	HTR3a	Forward	5'-TGTGCTCGCTTACAGCATCAC-3'
	HTR3a	probe	5'-Fam-CTGGTCACTCTCTGGTCCATTTGGCA-Tamra-
30	3'		
	HTR3a	Reverse	5'-GGCTGTGCCCCACTCAAGAAT-3'
	Trpv1	Forward	5'-GCTCCAGGCCCAAGAACTTG-3'

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	Trpv1	Probe	5'-fam-TTGGGACGCTCCTTCCTAGCT-Tamra-3'
	Trpv1	Reverse	5'-GGCAGTCTCTCCACCTCTCAGT-3'
	Sstr2	Forward	5'-TCCGGAGCGGAAGACATC-3'
	Sstr2	Probe	5'-fam-ACCAGGTCACACCCAGGCAA-Tamra-3'
5	Sstr2	Reverse	5'-GCCGGGCAGCTGTTTTTC-3'
	ATPSase	Forward	5'-GCACTGCAACTGATCTCTCCAT-3'
	ATPSase	Probe	5'-Fam-CAAGCGAGAGCTCAGGTTTCCTTC-Tamra-3'
	ATPSase	Reverse	5'-GCTCTTGTGTGGCCTGCAT-3'

10 **Murine environmental stressor**

Balb/c mice were housed under different environmental conditions to produce 'stressed' and 'non-stressed' animals (Table5). Non-stressed animals were housed 3 mice to a cage and cages were supplied with gauze to make bedding and tubing for environmental enrichment. These animals were assimilated to human handling. Stressed animals were housed 5 animals to a cage and were not supplied with gauze or tubing in their cages, and were not assimilated to human handling.

Table 5

Stressed	Non-stressed
5 per cage	3 per cage
No Tubes	Tubes
No Gauze	Gauze
Handle by tail only	Handle with support
Open access	Restricted access
Irregular handling	Habituation by repeated handling

20

Blood pressure-distension experiments

Balb/c mice were anaesthetized with isoflurane. The carotid artery was cannulated for monitoring blood pressure and heart rate. Following a mid line laparotomy, a 5cm

- 30 -

section of the mid jejunum was intubated to allow infusion of saline in order to distend the jejunum. A 5cm section of the proximal colon was also intubated to allow colonic distensions. The exposed and cannulated segments of gut were covered in gauze moistened with saline to prevent dehydration. Blood pressure was allowed to stabilize for at least 20 minutes prior to starting experimental stimuli. Phasic distensions were performed manually by attaching a syringe to the end of the intraluminal cannulae and injecting saline into the gut until the desired pressure is reached. This pressure was maintained manually for 30 secs before release and the intraluminal pressure returned to baseline (~0mmHg). The pressures attained were 12.5, 25, 50, 75, 100 mmHg, and there was a 10 minutes interval left between each stimulus. The volume injected during each distension was recorded. This series of phasic distensions from 12.5 – 100 mmHg were performed in the jejunum first, then after a 10 minute interval, in the proximal colon. The resultant deviations in the arterial blood pressure were recorded in response to each individual stimulus. With balb/c mice under isofluorane anaesthesia there was typically an increase in blood pressure (pressor response) followed by a decrease in blood pressure (depressor response). Each of these parameters was measured separately and dose response curves of the changes in blood pressures at increasing intraluminal pressures were plotted for both the jejunum and the colon.

20 Patch clamp experiments

Balb/c mice were injected intraperitoneally with the retrograde labelling agent cholera toxin B 488 3-7 days prior to experiments. Mice were then anaesthetized with ketamine/xylazine, the spinal cord removed and DRG neurons isolated (T10-T13) for electrophysiological recordings 18 – 24 hours after their dissociation and incubation, and mounted on the stage of an inverted microscope (Leica DMIRE2)) for both bright-field and fluorescence observation. Cholera toxin labelled neurons were identified by their green fluorescence under the N3 filter system (Leica). Whole cell currents and voltage clamp experiments were performed by using MultiClamp 7A amplifier and digitized with a DigiData 1322A converter (Axon Instruments). Stimulation and data acquisition were obtained by the pClamp 9 program (Axon Instruments). Signals were sampled at 10 kHz or 20 kHz, and low-pass filtered at 4 KHz. The series resistance was compensated.

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Neurons were excluded from analysis if the seal resistance or access resistance was unstable, or if they fired spontaneous action potentials.

Borosilicate glass (Harvard) was pulled with a P97 micropipette puller (Sutter, CA), and fire polished by a MF 200 microforge (World Precision Instrument) to a tip resistance of
5 5 – 10 M Ω . A silver-silver chloride pellet (World Precision Instrument) was placed in the recording dish as the reference electrode. The normal extracellular Krebs's solution contained (in mM): NaCl 118.0, KCl 4.7, NaH₂PO₄ 1.0, NaHCO₃ 25.0, MgSO₄ 1.2, CaCl₂ 2.5, D-Glucose 11.1, with pH adjusted to 7.3 by using NaOH. The normal intracellular solution contained (in mM): HEPES 10.0, KCl 130.0, MgCl₂ 1.0, CaCl₂ 1.0,
10 EGTA 2.0, K₂ATP 2, Na₃GTP 0.2, titrated with KOH to pH 7.25. The extracellular solution for isolating TTX-resistance Na currents composed of (in mM): NaCl 145.0, KCl 4.8, HEPES 10.0, MgCl₂ 1.0, CaCl₂ 2.5, D-glucose 11.1, TTX 0.0003, CdCl 0.5, 4-AP 1.0, TEA-Cl 5.0, CsCl 2.0, pH adjusted to 7.3 by using NaOH, and the corresponding intracellular solution was (in mM): HEPES 10.0, CsCl 130.0, MgCl₂ 1.0, CaCl₂ 1.0,
15 EGTA 2.0, K₂ATP 2.0, Na₃GTP 0.2, pH adjusted to 7.25 by using CsOH. All experiments were performed at temperature of 30°C – 33°C.

Data were analyzed by using pClamp 9 software (Axon Instruments). Neurons were recorded in both current-clamp and voltage-clamp configurations. Voltage clamp recordings were used to generate current-voltage relationships for cells. Current clamp
20 recordings were used to determine the rheobase for action potential firing of neurons. The number of action potentials elicited at 2x rheobase was subsequently assessed in current clamp mode.

Corticosterone Assay

25 Balb/c mice were anesthetized by ketamine/xylazine solution and blood was collected by a cardiac puncture to 3 ml vacutainer tubes containing EDTA (BD Scientific). Tubes were placed at 4°C for 2 hours and then plasma was separated by centrifugation at 15,000 RPMI for 15 minutes, transferred to an Eppendorff tubes and frozen at -20°C for up to 1 month prior to ELISA assay.

30 Corticosterone levels in mouse plasma were determined by OCTEIA EIA assay (ALPCO Diagnostics, Windham NH, USA). Briefly, plasma was diluted 1:10 with sample diluent in a glass tube (10x75 mm) and mixed on vortex. One hundred μ l of such

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diluted samples were loaded on pre-coated 96-well plates and 100 µl of enzyme conjugated solution was added to each well. Plates were incubated overnight at 4°C. Samples were run simultaneously with provided corticosterone calibrators. After incubation the contents of the plates were dumped and the plates were washed 3 times
5 with 250 µl of the washing buffer. TMB substrate (200 µl) was added to each well and incubation continued for additional 30 minutes at room temperature. Reaction was stopped by adding 100 µl of stop solution HCl and the plates were read at 450 nm in an automated ELISA reader ELx808. Data were analyzed using KCjunior software (Bio-Tek Instruments, Winooski VE, USA) and expressed in ng/ml.

10

Non-recovery surgical procedures

General anaesthesia in mice was induced with 3 % isoflurane and maintained with 2 % isoflurane. The right external jugular vein was cannulated to allow maintenance anaesthesia and the left external jugular vein was cannulated for systemic administration
15 of drugs. Body temperature was monitored with a rectal thermometer and maintained at around 37 °C by means of a heating blanket. A midline laparotomy was performed and the caecum was excised. A 5 cm loop of proximal jejunum was isolated and cannulated at the proximal end with a cannula connected to a syringe pump to allow infusion of intraluminal solutions. This inlet cannula was also connected to a pressure transducer to
20 allow monitoring of intraluminal pressure. The jejunal loop was cannulated at the distal end to allow drainage of intraluminal solutions to waste. The abdominal incision was sutured to a 20 mm diameter steel ring to form a well that was subsequently filled with pre-warmed (37 °C) light liquid paraffin.

25 Nerve preparation and afferent recording

A mesenteric arcade was placed on a black Perspex platform and a single nerve bundle was dissected from the surrounding tissue. This was severed distal from the wall of the jejunum (approximately 5-10 mm) to eliminate efferent nerve activity. It was then attached to one of a pair of platinum electrodes, with a strand of connective tissue
30 wrapped around the other to act as a differential. The electrodes were connected to a 1902 amplifier (Cambridge Electronic Design (CED), Cambridge, UK), filtered and

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differentially amplified with the resulting signal digitized via a 1401 plus interface (CED) and captured on a PC using Spike2 software (CED).

Quantitative Immunohistochemistry for VR1

- 5 To localize VR1-immunoreactivity, dorsal root ganglia and nodose ganglia were harvested from mice infected or sham-infected with Nb 21 days previously and sacrificed by an overdose of ketamine/xylazine (n=4 per group). Immediately after removal, the ganglia were immersed in 10% neutral buffered formalin (NBF) for 48 hours, before processing to paraffin. After embedding, sections were cut at 2 μ m and collected on
- 10 aminopropyltriethoxysilane-coated slides. Sections were dewaxed and endogenous peroxidase was blocked in 0.5% hydrogen peroxide in methanol. After rinsing in Tris buffered saline (TBS), sections were pre-treated with citrate buffer, pH6.0, for 30 minutes at 98°C and then incubated in 20% normal goat serum in TBS for 20 minutes, followed by anti-VR1 (PC420, Oncogene, now Calbiochem, San Diego, California, USA)
- 15 overnight at room temperature. Sites of primary antibody binding were detected using double-cycled, goat anti-rabbit Igs and streptavidin-peroxidase (Zymed Laboratories, South San Francisco, California). Colour was developed in aminoethylcarbazole and the nuclei were counterstained in haematoxylin. Sections were coverslipped in glycerine jelly. Quantitation was performed using Quantimet Image Analysis software (Version
- 20 2.7, Leica, Toronto, Canada). Integrated optical densities were determined at 20X objective magnification. The total integrated optical densities of the specific staining were used for comparison between animals and groups.

Chemosensitivity Experiments

- 25 Balb/c mice were injected subcutaneously with 500 L3 Nb larvae in PBS, or with PBS only (shams). Experiments were performed 3-4 weeks post-infection. Mesenteric afferent recordings were obtained from isoflurane anaesthetized mice using conventional extracellular recording techniques. A 5cm section of the jejunum was intubated to allow continuous intraluminal perfusion (0.15 ml/min) of either 0.9% saline or 50mM
- 30 hydrochloric acid (HCl). Jejunal afferent nerve activity and intraluminal pressure (IP) was recorded in response to a 2.5 min HCl application (at time 0s). Baseline activity (-100 to

0s), acute acid response (50 to 110 s) and prolonged acid response (410 to 560 s) were measured and compared between sham and Nb infected mice.

Examples

5

Example 1

Labelling of visceral sensory neurons

Intramuscular injection of abdominal tissues necessitates invasive surgery that is likely to alter the expression of a variety of genes. Initial experiments were thus performed to evaluate intraperitoneal (IP) injection of label as an alternative to injection into the intestinal musculature (IM), by comparing the retrograde labelling characteristics of DRG and NG after IM and IP injections of CTB488 and CTB594. Injection of CTB488 IM labelled DRG neurons from T2-L1, with 61% of neurons labelled between T10-T13 (Fig.1A). In comparison, IP injection of CTB594 labelled DRG neurons over a slightly larger range, from T1-L4, but with 50% of neurons labelled still located between T10-T13 (Fig.1B). Figs. 1C and 1D show that every neuron labelled following IM injection of CTB488 was co-labelled by IP injection of CTB594. Figs 1A and 1B also show that the total number of T10-T13 DRG neurons labelled following IM injection was 37 ± 12 ganglion cells, which was only 6.4 % of the neurons labelled following IP injection (580 ± 132 ganglion cells). There was also a similar percentage (8.2 %) of nodose neurons labelled with IM injection compared to IP injection (32 ± 18 vs. 398 ± 62 neurons respectively). There was no significant difference between the number of NG and DRG neurons labelled by IM injection ($p=0.55$). Similarly there was no significant difference between the number of NG and DRG neurons labelled by IP injection ($p=0.15$). Table 6 shows the numbers of fluorescent T10-T13 neurons counted in squash preparations labelled after IP injection, along with the percentage of fluorescent neurons as determined in cryostat sections. All four levels of dorsal root ganglia produced similar results, with $\leq 3\%$ of the neurons being labelled following IP injection. By extrapolation, the total numbers of neurons per ganglion were estimated to be in the region of 7,000 to 9,000.

In conclusion, since IM injections only cover a limited section of the GI tract and IP label injection may avoid any alterations in neuronal expression and/or function that may occur

following the surgery necessary for IM label injection, IP injection of CTB was used to label DRG and NG for subsequent microarray studies.

Full Legend for Figure 1

- 5 Figure 1: CTXB labelling of sensory neurons. A – Bar graph shows the mean number of neurons (n = 4-6 experiments) labelled by IM injection in DRGs, and nodose neurons. B – Bar graph showing the same data as A except following an IP injection. C&D - All neurons that are labelled by IP injection are co-labelled by IM injection. An example of a squash preparations of the same DRG illuminated through a FITC filter (C – IM injection with CTB Green 488) and a Cy3 filter (D – IP injection with CTB Red 594). More
10 neurons are labelled by IP injection than by IM injection. However, all of the fluorescent neurons that are labelled by IM injection (arrows) are also labelled by IP injection.

Table 6

<i>Parameter</i>	<i>T10</i>	<i>T11</i>	<i>T12</i>	<i>T13</i>
% Fluo. Cells	2.7±0.7	2.5±0.5	2.9±0.8	3.0±0.4
Mean # Fluo. Cells	194±34.4	225±30.9	233±27.4	252±15.9
# Neurons per Ganglion	7266	9066	8084	8508

15

Example 2

Mouse model of irritable bowel syndrome (IBS)

- A conceptual mouse model of IBS was set up by combining infection and exposure to stress. Transient jejunitis was induced in Balb/c mice by infection with *Nippostrongylus*
20 *brasiliensis* (Nb) larvae in PBS. Sham animals were injected with PBS only. Different levels of stress were obtained by combination of all of the following factors concerning housing of the animals; number of animals per cage, presence/absence of tubes and gauze, method of handling (Table 5). Combination of stress and infection resulted in four groups of animals including sham/non-stressed (Sh/NS), infected/non-stressed (I/NS),
25 sham/stressed (Sh/S) and infected/stressed (I/S) animals. Although considered as a mild stressor, Figs 2A and 2B shows that the differences in housing conditions resulted in pronounced differences in stress hormone levels after five weeks in different

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environments as indicated by plasma corticosterone levels. In agreement with observations in the rat, Figs 3B and 4 show that both serum IgE levels and mast cell counts were elevated in mice after Nb infection when compared to non infected mice. Fig 5 shows that three to six weeks after the infection all signs of acute inflammation disappeared: the epithelium is no longer regenerative; the lamina propria is no longer hypercellular nor oedematous; neutrophils are not evident; and the muscularis propria has returned to normal thickness. All further experiments were performed after day 21.

Full Figure Legends for Figures 2 to 5

10 Figures 2A and 2B: Mice were housed under stressed or non stressed conditions for 5 weeks. After two weeks animals were infected with *Nippostrongylus brasiliensis* or sham infected with vehicle. Plasma corticosterone levels were measured by ELISA. Data are expressed in ng/ml $\pm$ SEM. (A). Mean plasma corticosterone levels for each of the four experimental groups: SS – stressed sham; SI- stressed infected; NSS- non-stressed sham; 15 NSI- non-stressed infected. Using a general linear model (GLM), there was no significant difference between sham vs. infected, but there was an elevation on corticosterone levels in stressed vs. non-stressed animals. (B) Averaged data pooling the two stressed populations vs. the two non- stressed population. There was an increase in stressed vs. non-stressed animals.

20

Figure 3A Serum IgE levels in $\mu\text{g/ml}$ (mean $\pm$ SEM) in four different experimental groups as indicated. All animals were kept in the appropriate housing conditions for 5 weeks prior to measurements being taken. IgE levels were measured using ELISA 21 days after s.c. infection with either sham or 500 L3 Nb larvae. IgE levels were only 25 increased in Nb infected animals.

Figures 3B and 4: Serum IgE levels in $\mu\text{g/ml}$ (3) and mast cell counts (4) at different times post-infection. Mice were infected with *Nippostrongylus brasiliensis* (INF) or sham infected (CTRL). IgE levels were detectable 2 weeks after infection, peaked at 30 week 3-4 and remained elevated 12 weeks post-infection. Mast cell numbers increased at week 1; peaked at week 2 and returned to near normal levels at week 12 post-infection.

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Figure 5: Histological time course of mouse jejunum with Nb infection. Mice were infected sub-cutaneously on day 0 with 500 stage L3 larvae of *Nippostrongylus brasiliensis* after a two week assimilation period. Jejunum was collected on day 0, 7 and 21 days post infection. Tissue was fixed in formalin and stained with hematoxylin/eosin. Severity of inflammation was determined and expressed on different color intensity scale. Inflammation peaked at day 7 and returned to normal on day 21. Histological photographs of the representative time points are presented below the time scale.

Example 3

10 Persistent alterations in neuron excitability in mice infected with Nb

In order to study changes in electrophysiological properties, patch clamp recordings were performed on isolated NG and DRG neurons after stress exposure and Nb infection. NG were harvested on day 20-24 post infection, i.e., after histological and biochemical signs of acute gut inflammation are gone. Dispersed ganglion cells were plated on coverslips and incubated for 4-24 hr before mounting for patch clamp recording, using physiological extracellular saline and a K^+ -rich intracellular saline. Visceral DRG and NG neurons were identified by retrograde transport of a labelled cholera toxin subunit (Alexa Fluor-488-CTB), which had been injected IP, 3 to 8 days prior to sacrifice.

For DRG neurons recordings were made from small neurons (whole cell $C < 40$ pF, 91 neurons in total), which consistently showed a hump during spike repolarization. Spike shape and amplitude was not altered by Nb infection. Fig 6 shows that overall DRG neurons ($n=55$) derived from Nb infected animals had a lower resting conductance (88, 64 cf. 139, 132 pS/pF; median, IQR, $P < 0.001$) than those ($n=36$) derived from sham infected animals, but V_{rest} did not differ (-50 cf. -51 mV). Fig 7 shows that Rheobase was lower (1.1, 2.1 cf. 2.2, 4.5 pA/pF, $P < 0.001$) in Nb mice. Fig 8 shows that action potential number evoked during 500 ms at 2x rheobase was increased from 2, 2 to 5, 8, $P < 0.0001$) in Nb infected. Action potentials recorded from sham neurons were followed by a slow (0.2-1 s duration) afterhyperpolarization (sAHP) with maximal amplitude of 5, 3 mV. The sAHP amplitude was greatly reduced in neurons taken from Nb mice (0.2, 0.4 mV, $P < 0.001$) (Fig. 9).

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With respect to NG neurons, electrophysiological recordings were made from 31 neurons (17 sham vs. 14 infected) with a mean capacitance of 33.2 ± 3.8 pF. Resting conductance was also decreased with Nb infection as shown in Fig. 10, (sham 240.1 ± 42 , infected 141.3 ± 23.6 pS/pF, $p=0.058$) but there was no change in the resting membrane potential. Fig 11 shows that the number of action potentials evoked during a 500 ms pulse at 2x rheobase was increased from 1.8 ± 0.4 to 7.7 ± 1.7 ($p=0.004$) with Nb infection. Fig 12 shows that action potential half-width was decreased from 1.1 ± 0.1 to 0.7 ± 0.1 ms ($p=0.01$) in Nb infected neurons. Fig 13 shows that Rheobase was decreased in Nb neurons but was not significantly different (sham 5.2 ± 2.1 , infected 2.7 ± 1.2 pA/pF, $p=0.31$). Taken together these data clearly demonstrate that a mild, transient, intestinal inflammatory episode can lead to long term excitability (LTE) in both DRG and NG neurons, persisting for weeks after resolution of the gut inflammation.

Full Figure Legends for Figures 6 to 13

Figure 6: A scatterplot of the normalized resting conductance levels of sham and Nb infected DRG neuron populations. The conductance of each neuron under resting conditions at the beginning of each experiment is measured and divided by the capacitance of the cell in order to normalize the conductance level to cell size. Using a Mann-Whitney test, there is a significant reduction in the resting conductance of Nb infected neurons. Mean data is expressed as median $\pm$ interquartile range.

Figure 7: DRG neuron rheobase is decreased in Nb infected cells. The top half of this figure shows example traces of rheobase measurements in individual sham and Nb infected DRG neurons. The blue bars indicate increasing amounts of current injected into the cells, with the amount of current necessary to elicit an action potential (AP) highlighted. The green and red traces show the resulting membrane potential trace of sham and infected neurons respectively. In these particular examples, an AP was elicited at 44pA in the sham neuron and at 8pA in the infected neuron. The scatterplot below shows the entire population data normalized to cell capacitance. There is a significant decrease in the rheobase of Nb infected neurons.

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Figure 8: DRG excitability is increased in Nb infected neurons. The top half of this figure shows example traces of sham and Nb infected DRG neurons in response to a current injection equivalent to 2x rheobase. The blue bars indicate the amount of current injected into each cells, whilst the green and red traces show the resulting number of APs fired in sham and infected neurons respectively. In these particular examples, 2 APs were elicited in the sham neuron and 7 APs evoked in the infected neuron. The scatterplot below shows the entire population data. There is a significant increase in the number of APs evoked at 2x rheobase of Nb infected neurons.

10 Figure 9: sAHP amplitude is decreased in Nb infected neurons. The top half of this figure shows example traces of the sAHP elicited after a burst of APs in sham and Nb infected DRG neurons. The scatterplot below shows the entire population data. There is a significant decrease in the sAHP amplitude in Nb infected neurons.

15 Figure 10: Scatterplots of the resting conductance levels of sham and Nb infected nodose neurons. The conductance of each neuron under resting conditions at the beginning of each experiment is measured and plotted on the left. This data is then normalized by dividing by the capacitance of the cell as plotted on the right. Once normalized, the resting conductance of Nb infected neurons is shown to be decreased compared to sham, but this fall just outside of statistical significance.

Figure 11: Nodose neuron excitability is increased in Nb infected neurons. The top half of this figure shows example traces of sham and Nb infected DRG neurons in response to a current injection equivalent to 2x rheobase. In these particular examples, 2 APs were elicited in the sham neuron and 7 APs evoked in the infected neuron. The scatterplot below shows the entire population data. There is a significant increase in the number of APs evoked at 2x rheobase of Nb infected neurons.

Figure 12: Action potential shape parameters are altered in nodose neurons by Nb infection. These scatterplots demonstrate an increase (not statistically significant) in the antipeak amplitude of the AP (equivalent to the fast afterhyperpolarization), with a decrease in both the AP half-width and the AP maximum decay slope following Nb

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infection. The decreases in half width and decay slope are indicative of faster APs lacking a hump on the downward slope of the AP.

Figure 13: Nodose neuron rheobase is not significantly altered by Nb infection. The rheobase of each neuron is measured and plotted on the left. This data is then normalized by dividing by the capacitance of the cell as plotted on the right. Once normalized, although there is a slight decrease, there is no significant difference in the rheobase of Nb infected neurons.

10 **Example 4**

Gene expression profiling of nodose and dorsal root ganglia

Taking into account that only 3% of the neurons in DRG and NG project to the abdominal viscera, laser capture microdissection was applied to isolate these specific neurons out of the entire ganglion. In this way visceral afferent specific gene expression profiles in DRG and NG were identified in Sh/NS, I/NS, Sh/S and I/S mice.

(1) Gene expression profiles of visceral sensory neurons in dorsal root ganglia:

RNA extracted from laser captured DRG neurons was amplified and hybridised to MG-430V2.0 whole genome arrays interrogating expression levels of 39,000 gene transcripts simultaneously. Figure 14 shows a graphical exploration of microarray data using spectral map analysis (SPM). As can be seen from the overlapping nature of the quadrants this revealed no differences in gene expression between the four studies groups. In order to identify individual genes that could be differentially expressed, Significance Analysis of Microarray data (SAM, q -value < 0.1) and fold-difference filtering were applied (> 1.5 fold difference). However, in agreement with SPM results no significantly differentially expressed genes were identified.

(2) Gene expression profiles of visceral sensory neurons in nodose ganglia:

Laser captured material from NG was hybridised to MG-430V2.0 arrays. Spectral map analysis on the expression of 28,920 reliably detected genes as can be seen in Fig 15 showed a clear difference between Sh/NS and I/S, whereas overall expression profile of the Sh/S and the I/NS are in the transition zone between the two outer groups. Spectral map analysis revealed 2571 genes of which the expression profile contributes to the

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difference between Sh/NS vs I/S. Combining those with genes that are identified by SAM ($q < 0.1$) and fold-difference filtering (> 1.5 fold difference) lead to the identification of 1994 genes, as represented in Fig 16 that are significantly differently expressed after Nb infection, 1377 of which were increased and 617 were decreased. Altered NG genes
5 included 19 G-protein coupled receptors, 23 ion channel genes, 80 kinases, and 118 other receptor-related genes.

Unexpectedly these data indicate that changes in gene expression are observed in NG rather than DRG neurons in an animal model for IBS. This strongly suggests that molecular changes at the level of the vagus could underlie symptoms observed in IBS.

10

Full Figure Legends for Figures 14, 15 and 16

Figure 14 - DRG SPM

Panel A: First two principal components (PC) of the weighted Spectral map analysis (SPM) applied on normalized microarray data for gene expression profiles of DRG
15 neurons in all four animal groups (Sh/NS, I/NS, SH/S and IS). On the spectral map squares depict different samples whereas circles depict genes (size of circle correspond to intensity). Distances between squares are a measure for similarity between samples. A positive association of a gene with a given sample (i.e. an upregulation of that gene in that particular sample) results in the positioning of the gene and sample on a common line
20 through the centroid (depicted by a cross). Genes contributing significantly (measured by their distance from the centroid) to difference between samples are annotated with their Affymetrix identifier (www.affymetrix.com/analysis/netaffx). Only the first two principle components are plotted against each other, together explaining 27% of the variance in the data. As indicated by the coloured lines, no separation between the groups is observed
25 indicating no differences in overall gene expression pattern is presented at the level of visceral DRG neurons.

Panel B: Distribution of the samples over the different principal components in the spectral map analysis showing that none of the principal components differentiates the groups. The percentages of variance explained by each component are indicated at the
30 bottom of the graph.

Figure 15 - NG SPM: Spectral map biplot of gene expression profiles of DRG neurons in all four animal groups (Sh/NS, I/NS, SH/S and IS). Only the first two principle components are plotted against each other, together explaining 32% of the variance in the data. As indicated by the coloured lines and the dotted line, a clear separation between the Sh/NS and the I/S groups is observed indicating a clear differences in overall gene expression pattern is presented at the level of visceral NG neurons. Indicated by the shaded area are the 2571 genes contributing the most to this overall difference in expression profile.

Figure 16 - NG SPM-SAM-FC: Venn diagrams summarizing the number of genes identified by spectral map analysis (SPM), significance analysis (SAM) and fold difference filtering (FD). The selection of 1996 genes was based on the fulfilment of at least two of the three criteria mentioned above.

Example 5

Changes in VR₁, CCK_A, SST₂ and 5-HT_{3A}

Figs 17 to 20 show that both the vanilloid receptor VR₁ (*Trpv1*) and cholecystokinin receptor A (*Cckar*) were upregulated in Nb infected NG neurons, whilst serotonin receptor 3A (*Htr3a*) and somatostatin 2 receptor (*Sstr2*) were downregulated. It is also noted that the effect of Nb infection alone on expression level of these genes was enhanced in infected stress-exposed animals. Changes in mRNA levels measured on the arrays were confirmed using quantitative PCR. Fig 17B shows that expression of *Trpv1* mRNA was significantly increased in infected/stressed animals when compared to sham/non stressed. Fig 19B shows expression levels for SST₂ receptor in infected and non infected DRG and NG neurons from the same animal as assessed by quantitative PCR. It can be seen that there is no significant change in expression between infected and non infected neurons in DRG neurons, whereas, a significant decrease in expression is seen in NG neurons of infected / stressed animals when compared to non infected / non stressed animals.

In respect to the vanilloid receptor VR₁ (encoded by *Trpv1*) Fig 20A and B show that increased mRNA levels were confirmed at the protein level using

immunohistochemical staining of NG sections . In addition the lack of differences at the level of DRG neurons was confirmed with no difference in immunoreactivity in infected versus sham neurons.

5 **Full Figure Legends for Figures 17 to 20**

Figure 17 - NG TRPV1

Panel A: Signal intensities of Vanilloid Receptor 1 (Trpv1) mRNA levels as measured on the arrays. As indicated levels in DRG neurons did not differ whereas there was an obvious increase in expression level observed in NG neurons in infected stressed (I/S) animals compared to sham non stressed animals (Sh/NS).

Panel B: Expression levels for Trpv1 as assessed by quantitative PCR. A significant increase in Trpv1 mRNA levels was confirmed in infected stressed (I/S) animals compared to sham non stressed animals (Sh/NS).

15 Figure 18 - NG 5HT CCKA

Panel A: Signal intensities of the 5HT_{3A} receptor mRNA levels as measured on the arrays. Each dot represents expression level in a single animal. As indicated levels in DRG neurons did not differ whereas there was an obvious decrease in expression level observed in NG neurons in infected stressed (I/S) animals compared to sham non stressed animals (Sh/NS).

Panel B: Expression levels for CCK_A receptor. An increase in CCK_A receptor mRNA levels was observed in infected stressed (I/S) animals compared to sham non stressed animals (Sh/NS).

Figure 19 - NG SST2

25 **Panel A:** Signal intensities of SST₂ receptor (Sst2r) mRNA levels as measured on the arrays. As indicated there was an obvious decrease in expression level observed in NG neurons in infected stressed (I/S) animals compared to sham non stressed animals (Sh/NS).

30 **Panel B:** Expression levels for SST₂ receptor (Sst2r) mRNA as assessed by quantitative PCR. A significant decrease in SST₂ mRNA levels was confirmed in infected stressed (I/S) animals compared to sham non stressed animals (Sh/NS) whereas no difference could be detected in DRG neurons of the same animals.

Figure 20 - NG TRPV1 quantitative immunohistochemistry

Panel A: Representative images of Vanilloid Receptor 1 (VR1, Trpv1) immunoreactivity observed in sections of DRG and NG ganglia of infected and sham animals.

- 5 **Panel B:** Quantitation of VR1 immunoreactivity. A significant increase in immunoreactivity was observed in NG after infection, confirming array and quantitative PCR data.

Example 6

10 **Changes in pressor-depressor response in Nb infected mice**

- In order to measure visceral hypersensitivity in Nb infected mice changes in arterial blood pressure were recorded during phasic distention of both the jejunum and the colon. Figure 21 illustrates the increase in blood pressure (pressor response) to jejunal distension of sham non-stressed vs. infected stressed mice at 21 days post Nb infection. The pressor response is increased in infected animals when compared to sham: a 2-way ANOVA demonstrates that there is a significant increase in the overall response profile with infection ($p=0.0019$). Figure 22 illustrates the pressor response to colonic distension of sham non-stressed vs. infected stressed mice at 21 days post Nb infection. The pressor response is increased in infected animals when compared to sham: a 2-way ANOVA demonstrates that there is a significant increase in the overall response profile with infection ($p<0.0001$).

- It has been shown that a mild, transient, intestinal inflammatory episode inflicted by Nb can lead to long term excitability (LTE) in both DRG and NG neurons, persisting for weeks after resolution of the gut inflammation. However, at the molecular level, changes in mRNA and protein level were only observed in NG sensory neurons. Blood pressure recordings confirmed that LTE resulted in visceral hypersensitivity in mice post Nb infection. It is to be expected that these changes can be reversed by treating with modulators of molecules shown to be altered in vagal afferents. This data demonstrates a new and powerful model of sensory neuron plasticity that may be applied to the study of visceral pain. Moreover strong evidence is provided that vagal afferents are the major

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targets mediating visceral hypersensitivity and thus constitute an important target for the treatment of IBS.

Further work undertaken by the inventors on jejunal mechanosensitivity using balloon
5 ramp distension to 60mmHg has suggested that although there was a difference in initial studies, in repeated studies there was no difference. Therefore, any jejunal mechanosensitivity is inconsistent and a reason for this variability has yet to be elucidated

Full Figure Legends for Figures 21 and 22

10 Figure 21 -PR in jejunum: Effect of jejunal phasic distension on pressor responses in Sham vs. Day 21 Post Nb infection animals. Number of animals in each group is indicated between brackets.

Figure 22 -PR in colon: Effect of colonic phasic distension on pressor responses in Sham
15 vs. Day 21 Post Nb infection animals. Number of animals in each group is indicated between brackets.

Example 7

Compound Testing

20 The compound octreotide was tested in the non-human animal screen of the invention as follows:

Nodose neurons were dissociated and cultured in preparation for patch clamp experiments as has been described elsewhere. These nodose neurons were either obtained from Balb/c mice 21 days after infection with Nb or from sham mice, thus enabling a
25 comparison of the effects of octreotide on both sham and Nb-infected nodose neurons.

Octreotide (1 μ M) was applied to individual neurons via a fast perfusion system. Octreotide's effects were recorded on the cell's resting membrane potential (RMP) and the number of action potentials fired at 2x rheobase of each neuron.

Electrophysiological recordings were obtained in total from 30 sham neurons and
30 37 infected neurons. Of these, recordings were sustained during octreotide application in 27 sham neurons and 25 infected neurons. Octreotide had no significant effect on the

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RMP of either sham neurons (control: -57.6 ± 1.8 mV; octreotide: -54.7 ± 2.1 mV) or infected neurons (control: -51.6 ± 1.7 mV; octreotide: -51.7 ± 2.1 mV).

The number of action potentials evoked by a 2x rheobase current stimulus was significantly increased in infected neurons when compared to sham neurons. Octreotide reduced the number of action potentials at 2x rheobase in both sham and infected nodose neurons. Hence octreotide reduced neuronal excitability in both sham and infected neurons. These results suggest that the hyperexcitability observed in infected nodose neurons can be normalized by octreotide treatment.

The data confirming these results is shown in Figures 23 and 24.

Full Figure Legends for Figures 23 and 24

Figure 23 shows the effects of 1 μ M octreotide on evoked action potential discharge in sham and infected neurons. In control conditions in the presence of Krebs, a current that is 2x the rheobase of the neuron evokes 2 action potentials in a sham nodose neuron and 9 action potentials in an infected nodose neuron. After addition of 1 μ M octreotide, the number of action potentials evoked is reduced in both sham neurons (1 action potential) and infected (2 action potentials) neurons.

Figure 24 shows the mean effects of 1 μ M octreotide on evoked action potential discharge in sham and infected neurons. Infection significantly increases the number of action potentials evoked at 2x rheobase in nodose neurons. Addition of octreotide reduces the number of action potentials in both sham and infected neurons. There is no significant difference between the effect of octreotide on sham and infected neurons.

Example 8

Investigation of chemical hypersensitivity

In light of the conclusion that there is no consistent change in the mechanosensitivity of the jejunum following Nb infection, further work was undertaken to investigate if there is any change in the chemical sensitivity.

Balb/c mice were injected subcutaneously with 500 L3 Nb larvae in PBS, or with PBS only (shams). Experiments were performed 3-4 weeks post-infection. Mesenteric afferent

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recordings were obtained from isoflurane anaesthetized mice using conventional extracellular recording techniques. A 5cm section of the jejunum was intubated to allow continuous intraluminal perfusion (0.15 ml/min) of either 0.9% saline or 50mM hydrochloric acid (HCl). Jejunal afferent nerve activity and intraluminal pressure (IP) was recorded in response to a 2.5 min HCl application (at time 0s). Baseline activity (-100 to 0s), acute acid response (50 to 110 s) and prolonged acid response (410 to 560 s) were measured and compared between sham and Nb infected mice.

As shown in Figures 25 & 26, The experiments showed that in response to HCl perfusion there was an acute nerve response that peaked after 120 ± 14.9 s after the response onset, with no significant change in IP. As this response gradually decreased over ~10 mins, there was a concomitant increase in IP. Afferent nerve activity and IP never returned to pre-HCl exposure levels. There was no significant difference between baseline nerve activity in sham and Nb infected animals, but there was a significantly higher baseline IP in infected mice. The acute nerve response following HCl infusion was not significantly different between sham and infected mice. However, in the prolonged response period there was a significant increase in the nerve activity in infected animals. In addition there was a significantly greater prolonged increase in (IP) in Nb infected animals. Although it is possible that the increased IP may contribute to the increased prolonged nerve response in Nb infected mice, there was no significant direct correlation between the two measures.

The results indicate that Nb infection leads to an increased intestinal chemical sensitivity. Jejunal acidification elicits an acute nerve response which was similar in sham and infected groups and had no associated IP changes. This is followed by a prolonged nerve response that was significantly greater in infected groups than sham groups, and an uncorrelated prolonged IP response that was only clearly present in infected groups.

It is to be expected that these changes can be reversed by treating with modulators of molecules shown to be altered in vagal afferents. This data demonstrates a new and powerful model of sensory neuron plasticity that may be applied to the study of visceral

pain. Moreover strong evidence is provided that vagal afferents are the major targets mediating visceral hypersensitivity and thus constitute an important target for the treatment of IBS.

5 **Full Figure Legends for Figures 25 and 26**

- Figure 25 – Timecourse response to intraluminal administration of 50 mM HCl. A – Mesenteric afferent response to 50 mM HCl. Upon exposure of the nerves to acid (marked by ↑) there is a rapid increase in afferent activity that peaks after 120 ± 14.9 s and gradually decrease after this point, but never returns to spontaneous nerve activity levels. The afferent response in infected animals ($n = 28$) is larger (2-way ANOVA, $p < 0.001$) than that recorded in sham animals ($n=28$). B – Intraluminal pressure response to 50 mM HCl. Both the resting IP and the response to acid were greater (2-way ANOVA, $p < 0.001$) in infected animals ($n = 28$) than in sham animals ($n=28$).
- 15 Figure 26 – Response to intraluminal administration of 50 mM HCl. A – Increase over baseline in the acute (1-2 min post-acid) and prolonged (7-10 min post-acid) phases of the afferent response to acid. There was a significant increase in the prolonged afferent response to acid. B - Increase over baseline in the acute (1-2 min post-acid) and prolonged (7-10 min post-acid) phases of the IP response to acid. There was a significant
- 20 increase in the prolonged IP response to acid.

Probe Set ID	Gene Symbol	Description	Log2Ratio. Median.IS.o ver.SNS	GenBank ID	SwissProt ID
1456319_at	---	---	-2.84	BG065719	---
1460241_a_at	Stat9	siatyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-siatyltransferase)	-2.41	BB829192	O88829 /// Q9CZ65 /// Q9QWF8 /// Q9QWF9
1421508_at	Odz1	odd Ozfen-m homolog 1 (Drosophila)	-2.34	NM_011855	Q8CAT1 /// Q9WTS4
1430203_at	Usp16	ubiquitin specific protease 16	-2.12	BG067256	Q99KM0 /// Q99LG0
1437757_at	Mizf-pending	MBD2 (methyl-CpG-binding protein)-interacting zinc finger protein	-2.08	BB402190	Q8BWY0 /// Q8K1K9
1450252_at	Oneut1	one cut domain, family member 1	-2.07	NM_008262	O08755 /// Q8K1C8
1447359_at	---	Mus musculus transcribed sequence with weak similarity to protein sp:Q14587 (H.sapiens)	-2.05	A1326876	---
1449311_at	Bach1	Z268_HUMAN ZINC FINGER PROTEIN 268 (ZINC FINGER PROTEIN HZF3)	-2.00	NM_007520	P97302
1417548_at	Sart3	BTB and CNC homology 1	-1.94	BB546730	AAH57156 /// BAC97877 /// Q8BPK9 /// Q8C3B7 /// Q8CFU9 /// Q9JLI8
1419173_at	Acy1	squamous cell carcinoma antigen recognized by T-cells 3	-1.92	NM_025371	Q99JW2 /// Q9CR15
1423557_at	Ingir2	aminoacylase 1	-1.92	BF537076	Q63953 /// Q8C352
1447382_at	Pigt	interferon gamma receptor 2	-1.88	BB780056	Q8BXQ2
1453247_at	2810040O04Rik	phosphatidylinositol glycan, class T	-1.87	BE949501	Q9CZ99
1453886_a_at	Slc25a26	RIKEN cDNA 2810040O04 gene	-1.76	AK017037	Q8JZT2
1450332_s_at	Fmo5	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 26	-1.75	NM_010232	Q8R1W6
1427456_at	Wdfy3	flavin containing monooxygenase 5	-1.73	BF150771	AAH58274 /// Q8C8H7 /// Q8CHB9
1425556_at	Crk7	WD repeat and FYVE domain containing 3	-1.71	BG070845	BAC98047 /// Q8R457 /// Q9CVL4
1451676_at	Drap1	CDK2-related kinase 7	-1.71	BC002090	Q9D6N5
1422733_at	Fjx1	Dr1 associated protein 1 (negative cofactor 2 alpha)	-1.71	AV230815	Q8BQB4
1425050_at	2610034N03Rik	four jointed box 1 (Drosophila)	-1.66	AK010892	Q91V64 /// Q9D096
1453612_at	Nek1	RIKEN cDNA 2610034N03 gene	-1.62	AV254337	---
1455646_at	2010004M13Rik	NIMA (never in mitosis gene a)-related expressed kinase 1	-1.62	BI904583	---
1448472_at	Vars2	RIKEN cDNA 2010004M13 gene	-1.59	AF087680	Q7TPT7 /// Q9Z1Q9
1439365_at	Myt1	valyl-tRNA synthetase 2	-1.59	BB800584	AAH63252 /// O08995 /// Q8CFC2 /// Q8CFH1
1422455_s_at	Nsf	myelin transcription factor 1	-1.59	BB400581	P46460 /// Q8C3R2 /// Q8CCT9 /// Q8CEFO /// Q923C6
1449578_at	Supt16h	N-ethylmaleimide sensitive fusion protein	-1.58	AW536705	Q920B9 /// Q921H4
1427210_at	Baz2a	suppressor of Ty 16 homolog (S. cerevisiae)	-1.57	AW910654	AAH58241 /// Q80U42 /// Q80VL8 /// Q8BRP6 /// Q8CGH2 /// Q91YE5
1456281_at	Fbxl18	bromodomain adjacent to zinc finger domain, 2A	-1.57	BB401012	---
1416227_at	Apc1b	F-box and leucine-rich repeat protein 18	-1.56	BE979985	---
1447920_at	---	actin related protein 2/3 complex, subunit 1B	-1.55	BB420276	---
1437648_at	Pcytlb	Mus musculus transcribed sequences	-1.53	BB541022	Q80Y63 /// Q811Q8 /// Q811Q9 /// Q8BKD2 /// Q8C085
1422948_s_at	Hist1h3a	phosphate cytidylyltransferase 1, choline, beta isoform	-1.51	NM_013550	AAH58529 /// Q811M0
1455040_s_at	1110062M06Rik	histone 1, H3a	-1.49	BI965045	---
1444412_at	---	RIKEN cDNA 1110062M06 gene	-1.49	BM246867	---
1430173_x_at	Cyp4f16	Mus musculus transcribed sequences	-1.48	AK009445	Q99N17
1439615_at	Gan	cytochrome P450, family 4, subfamily f, polypeptide 16	-1.48	BB187898	Q8CA72
1432871_at	4932429P19Rik	giant axonal neuropathy	-1.47	AK016536	---
		RIKEN cDNA 4932429P19 gene			

1434588_x_at	Tbca	tubulin cofactor a	-1.46 A181686	BAB27228 /// P48428	
1421136_at	Edn3	endothelin 3	-1.46 NM_007903	BAC33211 /// BAC33915 /// BAC37561 /// P48299	/// Q9EQN7 ///
1422696_at	Ttyh1	twenty homolog 1 (Drosophila)	-1.45 NM_021324	Q9ESC3	
1442106_at	C730036B14Rik	RIKEN cDNA C730036B14 gene	-1.44 BB667730	Q8BGE5 /// Q8BKB7 /// Q8BUA8 /// Q8BYF4	
1453865_a_at	DXlnx46e	DNA segment, Chr X, Immunex 46, expressed	-1.44 AK010750	Q91YL5 /// Q9CV50 /// Q9JIG6	
1447250_a_at	2610301F02Rik	RIKEN cDNA 2610301F02 gene	-1.44 BB830098	Q8BLD3 /// Q8BLW1 /// Q8BUK9 /// Q9D003	
1417699_at	Gtf2f1	general transcription factor IIF, polypeptide 1	-1.43 AV325174	Q8BVJ2 /// Q8R5B7 /// Q9CSF1	
1439252_at	Incnp	inner centromere protein	-1.42 AV301185	Q7TN28 /// Q9WU62	
1428148_s_at	0610011B16Rik	RIKEN cDNA 0610011B16 gene	-1.42 BB203098	AAH61006 /// Q8C9V7 /// Q8CA54 /// Q9D2V7	
1443241_at	---	Mus musculus 13 days embryo stomach cDNA, RIKEN full-length enriched library, clone: D530023N15 product: unclassifiable, full insert sequence	-1.42 AW544264	---	
1452333_at	Smarca2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	-1.41 BM230202	Q35846 /// Q7TND4 /// Q8R1W7 /// Q99KH6 /// Q9CTU8 /// Q9D007	/// Q8C5L5 /// Q8CBM9 ///
1426361_at	5730454B08Rik	RIKEN cDNA 5730454B08 gene	-1.41 AV328883	Q99JN6	
1448531_at	Lmnb2	lamin B2	-1.40 NM_010722	P21619 /// P48680 /// Q8CGB1	
1422805_a_at	Ing3	inhibitor of growth family, member 3	-1.40 BB020556	Q8VEK6 /// Q99JS6 /// Q9ERB2	
1429070_at	4933440H19Rik	RIKEN cDNA 4933440H19 gene	-1.39 AK009216	AAH57613 /// Q8CEZ2	
1439021_at	Centb5	centaurin, beta 5	-1.39 B1412223	AAH67016 /// Q8C8T5	
1424054_at	Btdc2	BTB (POZ) domain containing 2	-1.38 BC016566	Q7TNF6 /// Q91YK4	
1416871_at	Adam8	a disintegrin and metalloprotease domain 8	-1.36 NM_007403	Q05910 /// Q8C269 /// Q8R3D3	
1436813_x_at	Khsrp	KH-type splicing regulatory protein	-1.36 BB332580	AAH64454 /// Q8CEN4	
1450450_at	Dscr12	Down syndrome critical region gene 1-like 2	-1.35 AF237888	Q9JKK0	
1435699_at	Ppm1f	protein phosphatase 1 (formerly 2C)-like	-1.35 BG074188	Q810H0 /// Q8BHN0 /// Q8C021 /// Q8C1D5 /// Q9Z0T1	
1432402_at	4930402F11Rik	RIKEN cDNA 4930402F11 gene	-1.35 AK015048	---	
1424142_at	Ikbpap	inhibitor of kappa light polypeptide enhancer in B-cells, kinase complex-associated protein	-1.34 AF367244	Q7TQH1 /// Q7TT37 /// Q8C6B3 /// Q8CB13 /// Q8CH82 /// Q8VHU5 /// Q8VHV9 /// Q9CT81	
1424486_a_at	Txnrd1	thioredoxin reductase 1	-1.33 BB284199	Q8CF34 /// Q8C131 /// Q99P49 /// Q9CSV5 /// Q9CVN8 /// Q9JMH6	
1426786_s_at	Dhx38	DEAH (Asp-Glu-Ala-His) box polypeptide 38	-1.32 BM195397	O89064 /// Q80X98 /// Q8R1J6	
1421013_at	Pitpnb	phosphatidylinositol transfer protein, beta	-1.32 NM_019640	BAC25830 /// P53811 /// Q8JZZ5	
1456800_a_at	D130029J02Rik	RIKEN cDNA D130029J02 gene	-1.32 BE685813	---	
1417379_at	Iqgap1	IQ motif containing GTPase activating protein 1	-1.32 NM_016721	BAC97854 /// Q07230 /// Q80UW7 /// Q8BPA6 /// Q8CC64 /// Q8CDT3 /// Q8CGH5 ///	
1460616_at	Sico4c1	solute carrier organic anion transporter family, member 4C1	-1.31 BB400146	Q9DA08 /// Q9JKF1	
1437107_at	D9Bwg0185e	DNA segment, Chr 9, Brigham & Women's Genetics	-1.30 AV220161	Q8BBD4	
1445813_at	0610012K18Rik	0185 expressed	-1.28 BB205459	AAH60618 /// BAC29230 /// P61294	
1418521_a_at	Mtx1	RIKEN cDNA 0610012K18 gene	-1.28 NM_013604	Q8C5V5 /// Q8CA00	
1417820_at	Tor1b	melaxin 1	-1.27 BB004887	P47802 /// Q8R5C0	
1416601_a_at	Dscr1	torsin family 1, member B	-1.26 AF282255	Q8CBP2 /// Q8VEI4 /// Q9ER41	
1447278_at	---	Down syndrome critical region homolog 1 (human)	-1.25 BB822306	BAC36729 /// Q7TNY3 /// Q9JHG6	
1449281_at	Ntrn	Mus musculus transcribed sequence with moderate similarity to protein ref: NP_055771.1 (H.sapiens)	-1.25 NM_008738	---	
1453261_at	2610035D17Rik	KIAA1052 protein [Homo sapiens]	-1.24 BB760848	P97463	
		neurturin	---	---	
		RIKEN cDNA 2610035D17 gene	---	---	

1433653_at	BC029169	cDNA sequence BC029169	-1.24 BG173581	Q8CID3 AAH57323 /// AAH64766 /// BAC30862 /// P51642 /// Q62509 /// Q8BPPY3 /// Q8C2B4 ///
1426326_at	Zfp91	zinc finger protein 91	-1.23 U05343	Q8CDZ3
1442775_at	---	Mus musculus transcribed sequences	-1.23 AI481700	---
1455622_at	Podx2	podocalyxin-like 2	-1.23 BB461988	Q8CAE9 /// Q8CFW3
1426432_a_at	Slc4a4	solute carrier family 4 (anion exchanger), member 4	-1.23 BE655147	Q88343 /// Q8QZR9 /// Q9R1C4
1447055_at	Dnaic1	DnaJ (Hsp40) homolog, subfamily C, member 11	-1.22 BB769600	Q8BP83 /// Q8C1Z4 /// Q8C6U5
1445854_at	C230004F18	hypothetical protein C230004F18	-1.22 BB380166	Q8C4I6
1433479_at	573041019Rik	RIKEN cDNA 573041019 gene	-1.22 AV030071	AAH58535 /// Q8BU04
1429034_at	Ene2	essential meiotic endonuclease 1 homolog 2 (S. pombe)	-1.21 AK012738	---
1421955_a_at	Nedd4	neural precursor cell expressed, developmentally down-regulated gene 4	-1.21 NM_010890	P46935 /// Q8BNU7
1432291_at	0610033M10Rik	RIKEN cDNA 0610033M10 gene	-1.21 AK002748	---
1431191_a_at	Sytl	synaptotagmin-1	-1.19 AK018163	P46096 /// Q8BRM4
1424151_at	Jiv1-pending	JTV1 gene	-1.19 BC026972	Q8R010 /// Q8R2Y6 /// Q8R3V2
1447065_at	9630041C05	hypothetical protein 9630041C05	-1.19 BB129691	---
1420596_at	Cacng2	calcium channel, voltage-dependent, gamma subunit 2	-1.18 NM_007583	Q88602 /// Q8C8F5
1454309_at	Bag5	BCL2-associated athanogene 5	-1.18 BB466622	Q8CDX7 /// Q9CQW7 /// Q9CVQ6
1445307_at	---	Mus musculus 12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:6720430F13	-1.18 BB051515	---
1437617_x_at	1110034G24Rik	product:unclassified, full insert sequence	-1.17 AB387677	Q9D112
1437968_at	Grin1	RIKEN cDNA 1110034G24 gene	-1.17 AB385669	P35438 /// Q8BZ96 /// Q8CFSA
1460704_at	Rng	glutamate receptor, ionotropic, NMDA1 (zebra 1)	-1.17 AK004573	AAH66023 /// O09009
1418414_at	Kcnh1	radical fringe gene homolog (Drosophila)	-1.16 NM_010600	Q60603
1419502_at	D11Lgp1e	potassium voltage-gated channel, subfamily H (eag-related), member 1	-1.16 NM_031871	Q99J23 /// Q99J92
1425163_at	LOC224833	DNA segment, Chr 11, Lothar Hennighausen 1, expressed	-1.16 BC006605	Q91Z58
1459881_at	---	hypothetical protein BC006605	-1.16 AI595406	Q80WS3
1432952_at	4930448E22Rik	Similar to fibrillarin (LOC237730), mRNA	-1.14 AK015416	---
1447612_x_at	---	RIKEN cDNA 4930448E22 gene	-1.14 BB494168	---
1445718_at	---	Mus musculus transcribed sequences	-1.14 BM237480	---
1439434_x_at	BC036961	Mus musculus transcribed sequences	-1.13 BB317673	---
1457280_at	---	cDNA sequence BC036961	-1.13 BB249354	Q80V87 /// Q9CZ86
1435481_at	E430039K05Rik	Mus musculus transcribed sequences	-1.13 BM194940	AAL66764 /// Q8BHR7 /// Q8CJ02
1424112_at	Igf2r	RIKEN cDNA E430039K05 gene	-1.12 BC092290	AAA16037 /// Q07113 /// Q7TMR1 /// Q80VF2 /// Q8C2F9 /// Q8C6V9 /// Q8K0J1
1424359_at	Oplah	insulin-like growth factor 2 receptor	-1.12 BC025120	Q8K010 /// Q8R3K2
1459536_at	Calcr1	5-oxoprolinase (ATP-hydrolysing)	-1.12 BB223961	Q9R1W5
1442277_at	Chka	calcitonin receptor-like choline kinase alpha	-1.12 BB546429	O54804 /// Q99KD4
1436167_at	---	MRNA similar to SHB (Src homology 2 domain containing) adaptor protein B (cDNA clone MGC:30399 IMAGE:4488005), complete cds	-1.11 BB798279	Q8CG80
1455474_at	D6Wsu116e	IMAGE:4488005), complete cds	-1.10 BM197316	AAH56942 /// Q80TW8 /// Q80UQ4 /// Q8BRP9 /// Q8CAPO /// Q9CT54
1427079_at	Mapre3	DNA segment, Chr 6, Wayne State University 116, expressed	-1.10 U51204	AAH57918 /// Q61167
		microtubule-associated protein, RPIEB family, member 3		

1433635_at	Wdr18	WD repeat domain 18	-1.10 BG073188	Q8BHQ0 /// Q8K265
1434794_at	Ahrf	ras homolog gene family, member f (in filopodia)	-1.10 BM241811	Q8BYP3
1418284_at	Tcf1	transcription factor-like 1	-1.10 NM_009336	Q62481 /// Q810A9 /// Q99K81
1457597_at	---	Mus musculus transcribed sequences	-1.09 AW121529	---
1441962_at	---	Mus musculus cDNA clone MGC:58861	-1.09 BB079625	Q810M3
1425383_a_at	Pbx1	IMAGE:6774557, complete cds	-1.08 L27453	AA871192 /// P41778 /// Q8BFR8 /// Q99LS8 /// Q9D621
1424277_at	1110020L19Rik	RIKEN cDNA 1110020L19 gene	-1.08 AV029337	Q8BKT8 /// Q924Z7
1460304_a_at	Ubf1	upstream binding transcription factor, RNA polymerase I	-1.08 BB832806	P25976 /// Q9DBH1
1449150_at	A930040G15Rik	RIKEN cDNA A930040G15 gene	-1.08 NM_133922	AAH66816 /// Q9JUG3
1417619_at	Gadd45gjp1	growth arrest and DNA-damage-inducible, gamma interacting protein 1	-1.08 BE368753	AAH61069 /// Q8BT05 /// Q9CR59
1427510_at	Gnai1	guanine nucleotide binding protein, alpha inhibiting 1	-1.08 U38501	Q61018
1428516_a_at	2310045B01Rik	RIKEN cDNA 2310045B01 gene	-1.07 BI903628	Q8K1H3 /// Q9CY41 /// Q9D6Z0 /// Q9D942
1443816_s_at	---	Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:9830142N16	-1.07 BB240086	Q8K323
1431885_a_at	Mus81	product:unclassified, full insert sequence	-1.07 AK004647	Q91ZJ0
1426514_at	4631426J05Rik	MUS81 endonuclease homolog (yeast)	-1.07 AK019474	Q80TW4 /// Q8BLQ5 /// Q91XQ5 /// Q9D2N6
1427635_at	Klf5a	RIKEN cDNA 4631426J05 gene	-1.07 AU067277	AAH67051 /// P28738 /// Q8CHF1
1451278_a_at	2610205E22Rik	kinesin family member 5A	-1.06 BC027220	Q8R2U4
1459865_x_at	---	RIKEN cDNA 2610205E22 gene	-1.06 AV278384	---
1429416_at	2900074C18Rik	---	-1.05 AK013779	Q9D6E4
1426249_at	Adrbk1	RIKEN cDNA 2900074C18 gene	-1.05 AF333028	Q7TS64 /// Q99MK8
1425558_at	Klc3	adrenergic receptor kinase, beta 1	-1.05 BC017147	Q91W40
1441456_at	Mmp24	kinesin light chain 3	-1.04 BB335489	---
1456571_at	1700001E16Rik	matrix metalloproteinase 24	-1.04 AV072149	Q8C517 /// Q9DAR7
1446947_at	---	RIKEN cDNA 1700001E16 gene	-1.04 BG072149	---
1442100_at	Inpp5f	inositol polyphosphate-5-phosphatase F	-1.04 BB619843	AAH67200 /// BAC98059 /// Q8C8G7 /// Q8CBW2 /// Q8CDA1
1451621_at	5830417C01Rik	RIKEN cDNA 5830417C01 gene	-1.04 BC002200	Q8BIB9 /// Q9D291
1438410_at	A230098A12Rik	RIKEN cDNA A230098A12 gene	-1.04 BB295128	Q8BJK6 /// Q8BYL5
1459430_at	Gpr158	G protein-coupled receptor 158	-1.04 BB429778	Q8BSU1 /// Q8C3D0 /// Q8C419 /// Q8CHB0
1444702_at	---	Adult male epididymis cDNA, RIKEN full-length enriched library, clone:9230116A06 product:unknown	-1.04 AV381472	---
1458193_at	Fabp9	EST, full insert sequence	-1.03 AV278565	---
1421846_at	Wsb2-pending	fatty acid binding protein 9, testis	-1.03 BM730566	AAH55100 /// O54929
1440817_x_at	G630024C07Rik	WD-40-repeat-containing protein with a SOCS box 2	-1.03 BB242445	AAH62882 /// Q8BJ90
1451286_s_at	Fus	RIKEN cDNA G630024C07 gene	-1.02 AF224264	AAH58247 /// P56959 /// Q8CFQ9 /// Q91VQ2
1425875_a_at	Lepr	fusion, derived from t(12;16) malignant liposarcoma (human)	-1.01 U58862	P48356
1433496_at	2810024B22Rik	leptin receptor	-1.01 AV123321	AAH56951 /// Q8K297
1441263_a_at	A930005H10Rik	RIKEN cDNA 2810024B22 gene	-1.00 AV009179	Q8CEK0
1423416_at	Smarrc1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	-1.00 BI558117	P97496 /// Q7TS80 /// Q7TT29
1435135_at	B230106124Rik	RIKEN cDNA B230106124 gene	-1.00 AV369935	Q8BLF1 /// Q8BYQ0 /// Q8BZK3
1428954_at	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 2	-1.00 AK004710	AAH65778 /// Q9JHL1

1437545_at	5730409011	hypothetical protein 5730409011	-0.99 BM194994	Q8BK28 /// Q8CFE3 /// Q8CHI2
1459705_at	---	Mus musculus transcribed sequences	---	---
1437524_x_at	0610011B16Rik	RIKEN cDNA 0610011B16 gene	-0.99 BE980857	AAH61006 /// Q8C9V7 /// Q8CA54 /// Q9D2V7
1425311_at	4930432F04Rik	RIKEN cDNA 4930432F04 gene	-0.99 BB534801	Q9D216
1456725_x_at	Vil2	villin 2	-0.99 BC016220	P26040 /// Q8CBU4
1434946_at	C330021A05Rik	RIKEN cDNA C330021A05 gene	-0.99 BB114808	Q8BX00 /// Q8CFP6 /// Q92310
1451707_s_at	Slc41a3	solute carrier family 41, member 3	-0.98 BC030415	Q921R8 /// Q9DC67
1416845_at	Hspa5bp1	heat shock 70kDa protein 5 binding protein 1	-0.98 NM_133804	Q8BX93 /// Q922P8
1447766_x_at	0610025L06Rik	RIKEN cDNA 0610025L06 gene	-0.98 AV003249	AAH68130 /// Q8BGB5
1459230_at	Plo2	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	-0.98 BB525112	Q8BIK8 /// Q9R0B9
1438489_at	Snn	survival motor neuron	-0.98 BM068889	P97801
1426790_at	Ssrp1	structure specific recognition protein 1	-0.98 BC024835	Q8CGA6
1422320_x_at	---	---	-0.98 NM_008836	---
1422977_at	Gp1bb	glycoprotein Ib, beta polypeptide	-0.98 NM_010327	---
1451778_at	BC011210	cDNA sequence BC011210	-0.97 BC011210	Q91X84
1435083_at	Cxn	cortixin	-0.97 B155559	Q8K129
1427334_s_at	2810474O19Rik	RIKEN cDNA 2810474O19 gene	-0.97 BE196832	Q8CCW3 /// Q8CCZ9 /// Q8CFR7 /// Q8CFA5 /// Q9CU82
1436576_x_at	2810454L23Rik	RIKEN cDNA 2810454L23 gene	-0.96 BG143413	---
1440255_at	Mizf-pending	MBD2 (methyl-CpG-binding protein)-interacting zinc finger protein	-0.96 BB826899	Q8BWO0 /// Q8K1K9
1416122_at	Cond2	cyclin D2	-0.96 NM_009829	P30280 /// Q9D8L9
1453349_at	2410019P08Rik	RIKEN cDNA 2410019P08 gene	-0.96 AK010559	Q9CWL2
1424657_at	MGC29021	hypothetical protein MGC29021	-0.96 BB151477	Q8JXZ2 /// Q8VE26 /// Q91VG7 /// Q9D3K9
1458623_at	---	Mus musculus transcribed sequences	-0.95 A413154	---
1431035_at	Daam1	Mus musculus associated activator of morphogenesis 1	-0.95 AV988556	AAAR05118 /// BAC97995 /// Q8BPM0 /// Q8BTF1
1447902_at	1810013A23Rik	RIKEN cDNA 1810013A23 gene	-0.95 AV050195	---
1415784_at	Vps35	vacuolar protein sorting 35	-0.95 B1654068	Q9EQH3
1451433_at	2310010G13Rik	RIKEN cDNA 2310010G13 gene	-0.94 BC019171	Q8VED1 /// Q9D7F8
1424077_at	2610020H15Rik	RIKEN cDNA 2610020H15 gene	-0.94 AK016023	Q9CRY7 /// Q9CT14 /// Q9D4X7
1429686_at	Pof3f	polymerase (RNA) III (DNA directed) polypeptide F	-0.94 BG070811	BAC29327 /// BAC36385 /// Q8C108 /// Q921X6
1449082_at	Mfap5	microfibrillar associated protein 5	-0.94 NM_015776	Q9QZJ6
1436909_at	B430110G05Rik	RIKEN cDNA B430110G05 gene	-0.94 AW542746	Q7TSU9 /// Q8BGF9
1424675_at	Slc39a6	solute carrier family 39 (metal ion transporter), member 6	-0.94 BB825002	Q7TPP9 /// Q7TQE0 /// Q8C145 /// Q8R518
1436468_at	Zdhc8	zinc finger, DHHC domain containing 8	-0.93 BB553914	Q7TNF7 /// Q8CCU8 /// Q99KF7
1456054_a_at	Pum1	pumilio 1 (Drosophila)	-0.93 BB314559	Q8OU78
1439214_a_at	Api5	apoptosis inhibitor 5	-0.93 AV118744	O35841 /// Q922L2
1456663_x_at	2410018G23Rik	RIKEN cDNA 2410018G23 gene	-0.93 BB718785	Q8BLJ1 /// Q8R014 /// Q9CWL9
1437607_at	Gcnt2	glucosaminyltransferase, l-branching enzyme	-0.93 BB357165	Q9D2A8
1429023_at	2900042E01Rik	RIKEN cDNA 2900042E01 gene	-0.92 AK013637	BAC38147
1436343_at	Chd4	chromodomain helicase DNA binding protein 4	-0.92 BM502696	AAH58578 /// Q8BM83 /// Q99JM0 /// Q9CTT2
1453172_at	Stch	stress 70 protein chaperone, microsome-associated, human homolog	-0.92 BE533039	Q8BM72 /// Q9D1X5
1460255_at	Tnfrsf13b	tumor necrosis factor (ligand) superfamily, member 13b	-0.92 NM_033622	Q7TQ58 /// Q8BVA3 /// Q8BWP2 /// Q8BZM8 /// Q9WU72
1434351_at	MGC37347	hypothetical protein MGC37347	-0.92 BF021398	Q8OU93 /// Q8CHS9
1438422_at	Lrrc20	leucine rich repeat containing 20	-0.92 BB143476	---
1427421_at	Tcp10	t-complex protein-10 complex	-0.91 AV257292	AAH61173 /// Q82184 /// Q80YU2 /// Q8C5S9 /// Q8C641
1439628_x_at	Rab38	Rab38, member of RAS oncogene family	-0.91 AV364767	Q8QZZ8

1446910_at	---	Mus musculus transcribed sequences	-0.91 BG073901
1421499_a_at	Ptpn14	protein tyrosine phosphatase, non-receptor type 14	-0.91 NM_008976
1449423_at	Mast1	microtubule associated serine/threonine kinase 1	-0.91 NM_019945
1427143_at	Jarid1b	jumoni, AT rich interactive domain 1B (Rbp2 like)	-0.91 BC019446
1456343_at	Slc35f1	solute carrier family 35, member F1	-0.91 BB540579
1421056_at	Dnase1l3	deoxyribonuclease 1-like 3	-0.91 BC012671
1451386_at	Blvrb	biliverdin reductase B (flavin reductase (NADPH))	-0.90 BC027279
1438416_at	Thrap5	thyroid hormone receptor associated protein 5	-0.90 BM238407
1418738_at	Scn1b	sodium channel, voltage-gated, type I, beta polypeptide fusion, derived from t(12;16) malignant liposarcoma (human)	-0.90 BC009652
1451285_at	Fus	thimet oligopeptidase 1	-0.90 AF224264
1448907_at	Thop1	RIKEN cDNA 3010027G13 gene	-0.90 NM_022653
1453111_a_at	3010027G13Rik	serine hydroxymethyl transferase 2 (mitochondrial)	-0.89 AK019396
1455084_x_at	Shmt2	methylated alanine rich protein kinase C substrate	-0.89 BB758291
1437034_x_at	Marcks	myristoylated alanine rich protein kinase C substrate	-0.89 BB332426
1430221_at	9130008F23Rik	RIKEN cDNA 9130008F23 gene	-0.89 BB763680
1449258_at	D11Wsu99e	DNA segment, Chr 11, Wayne State University 99, expressed	-0.89 AV225714
1456911_at	Clasp2	CLIP associating protein 2	-0.89 BB831639
1423117_at	Pum1	pumilio 1 (Drosophila)	-0.89 BB837171
1420397_a_at	Mint-pending	Msx2 interacting nuclear target protein	-0.89 NM_019763
1438112_at	---	Mus musculus transcribed sequence	-0.89 AA546727
1449685_s_at	4933425A18Rik	RIKEN cDNA 4933425A18 gene	-0.89 C80494
1451134_a_at	2410018G23Rik	RIKEN cDNA 2410018G23 gene	-0.88 BC026789
142718_a_at	Mdm2	transformed mouse 3T3 cell double minute 2	-0.88 X58876
1417144_at	Tubg1	tubulin, gamma 1	-0.88 NM_134024
1418003_at	1190002H23Rik	RIKEN cDNA 1190002H23 gene	-0.88 NM_025427
1429440_at	1810041L15Rik	RIKEN cDNA 1810041L15 gene	-0.88 B1734299
1450145_at	Dpht1	DNA binding protein with his-thr domain	-0.87 NM_019416
1439630_x_at	Sbsn	suprabasin	-0.87 A844734
1417236_at	Ehd3	EH-domain containing 3	-0.87 BM234719
1419379_x_at	Fxyd2	FXYD domain-containing ion transport regulator 2	-0.87 NM_052823
1436341_at	F830020C16Rik	RIKEN cDNA F830020C16 gene	-0.87 NM_052823
1433713_at	Gcn1l1	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	-0.87 BM125559
1454775_at	Hdac10	histone deacetylase 10	-0.87 BB794873
1451484_a_at	Syn1	synapsin I	-0.87 AW548891
1435560_at	Igal	integrin alpha L	-0.87 BC022954
1449615_s_at	Hdlbp	high density lipoprotein (HDL) binding protein	-0.87 B1554446
1419747_at	Asgr2	asialoglycoprotein receptor 2	-0.87 C77256
1460639_a_at	Atox1	ATX1 (antioxidant protein 1) homolog 1 (yeast)	-0.87 NM_007493
1423250_a_at	Tgfb2	transforming growth factor, beta 2	-0.86 NM_009720
1436014_a_at	Rusc1	RUN and SH3 domain containing 1	-0.86 BF144658
1421016_at	Ighmbp2	immunoglobulin mu binding protein 2	-0.86 BB806780
1430058_at	---	Mus musculus transcribed sequence with strong similarity to protein p12207 (M.musculus) S12207	-0.86 AW259474
1436320_at	---	hypothetical protein (B2 element) - mouse	---
1444022_at	---	Mus musculus, clone IMAGE:4206343, mRNA	---
1444022_at	---	Mus musculus transcribed sequences	-0.86 BF782342
142130_at	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
Q62130	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
Q77Q97	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
AAH57318	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
AAH59075	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
O55070	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
Q923D2	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
AAH57056	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
P97952	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
AAH58247	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
Q8C1A5	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
Q9D8K8	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
Q99K87	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
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Q9DZ26	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
AAH60965	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
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Q80UJ8	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
Q62504	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
Q8BT43	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
Q9D404	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
Q8BJJ1	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
P23804	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
P83887	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
Q9DU00	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
AAH62953	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
Q64150	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
Q8K590	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
BAC24982	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
Q80WC2	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
AAH56933	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
AAH64018	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
O88935	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
P24063	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
Q8VDJ3	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
P24721	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
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P27090	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
AAH56360	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
P40694	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
AK016826	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
WA5978	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---
BF782342	---	Q8C3A0 /// Q8CAV9 /// Q8CE88 /// Q8JLJ6 /// Q8JLJ7 /// Q8JLJ8 /// Q8JLJ9	---

1447938_at	---	Mus musculus cDNA clone MGC:69869	-0.86 BB379724	Q8BQ57 /// Q8C3Q3 /// Q8C5T7 /// Q8C8H0
1436022_at	Endog11	IMAGE:6822098, complete cds endonuclease G-like 1	-0.86 BB089035	Q8C163
1442590_at	Tnfrsf22	tumor necrosis factor receptor superfamily, member 22	-0.86 BB366863	Q8BFV5 /// Q9ER62
1424052_at	Thap4	THAP domain containing 4	-0.86 BC013538	AAH57963 /// AAH63758 /// AAH66042 /// Q91WR2 /// Q9CVE5 /// Q9CVG3
1451421_a_at	Lzf	leucine zipper domain protein	-0.86 BC008914	Q8BL37 /// Q922N4 /// Q923H8
1435888_at	9030024J15Rik	RIKEN cDNA 9030024J15 gene	-0.86 AV369812	---
1424749_at	Wdly1	WD40 and FYVE domain containing 1	-0.86 BC025226	Q8R315 /// Q9DAD3
1445218_at	---	Mus musculus transcribed sequences	-0.86 BE955408	---
1440801_s_at	---	Mus musculus transcribed sequences	-0.85 BB391602	Q8BVT9 /// Q8BX71
1436868_at	Rtn4r1	reticulin 4 receptor-like 1	-0.85 BM508396	AAP82835 /// Q8K0S5
1419299_at	2010012005Rik	RIKEN cDNA 2010012005 gene	-0.85 NM_025563	Q9CRC6
1447739_x_at	Klhdca4	kelch domain containing 4	-0.85 AV294746	AAH58359 /// Q8CIK0 /// Q92112
1417475_at	Apl13a	ATPase type 13A	-0.85 NM_133224	Q81OK8 /// Q9EPE9
1446374_at	Cln8	ceroid-lipofuscinosis, neuronal 8	-0.85 BB480605	AAH59212 /// AAH66074 /// AAO89218 /// BAC33570 /// BAC40944 /// Q80VH8
1460378_a_at	Tes	testis derived transcript	-0.85 BC010465	/// Q8BJ42 /// Q8BNW2 /// Q8BW76 /// Q8C033 /// Q922S7 /// Q9QUK3
1438858_x_at	H2-Aa	histocompatibility 2, class II antigen A, alpha	-0.85 AV018723	P47226 /// Q921B1 /// Q921W7 /// Q99L61
1435549_at	Trpm4	transient receptor potential cation channel, subfamily M, member 4	-0.85 BI685685	AAH58632 /// BAC81769 /// BAC81770 /// Q7TN37 /// Q80Y94 /// Q80YB3 /// Q811E2 ///
1415732_at	Bat5	HLA-B associated transcript 5	-0.85 BG071718	Q8BLM7
1422369_at	V1ra6	vomerol nasal 1 receptor, A6	-0.85 NM_053221	Q9Z1Q2
1434594_at	B230373P09Rik	RIKEN cDNA B230373P09 gene	-0.85 BB497449	Q8BWG2
1442103_at	C79399	expressed sequence C79399	-0.85 AV554925	---
1429272_s_at	Gcnf52	general control of amino acid synthesis-like 2 (yeast)	-0.84 NM_020004	AAH63752 /// Q99KW4 /// Q8JHD2
1436618_at	Sxn5	sideroflexin 5	-0.84 BB379739	Q8BRQ9 /// Q925N0
1423875_at	A1450540	expressed sequence A1450540	-0.84 BB321867	AAH62949 /// Q80TB5 /// Q80V13 /// Q8BKS4 /// Q8C8M2 /// Q8CDM8 /// Q8R1V3
1446973_at	---	Mus musculus transcribed sequences	-0.84 BG076107	---
1424755_at	Hip1	huntingtin interacting protein 1	-0.84 BB320674	Q8C303 /// Q8VD75 /// Q9D1Z6
1459863_x_at	Gga1	golgi associated, gamma adaptin ear containing, ARF binding protein 1	-0.84 BB006096	Q8R0H9
1429631_at	Sirt6	sirtuin 6 (silent mating type information regulation 2, homolog) 6 (S. cerevisiae)	-0.84 AK013316	P59941
1426095_a_at	Tnfrsf22	tumor necrosis factor receptor superfamily, member 22	-0.84 AY046551	Q8BFY5 /// Q9ER62
1445460_at	Bach2	BTB and CNC homology 2	-0.84 BE457827	---
1447074_at	---	Mus musculus transcribed sequences	-0.84 BG068627	---
1426920_x_at	Itgb1	integrin beta 1 (fibronectin receptor beta)	-0.83 BM120341	P09055 /// Q60993 /// Q8BTU0 /// Q8BUD1 /// Q8BVU1 /// Q8BY44
1423981_x_at	Slc25a29	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29	-0.83 BC006711	Q8BL03
1445564_at	---	Mus musculus transcribed sequences	-0.83 BE888513	---
1456271_at	---	suprabasin	-0.83 BB039066	Q8OV96
1459897_a_at	Sbsn-pending	DNA fragmentation factor, alpha subunit	-0.83 A1507307	AAR20795 /// Q80WB4 /// Q8C7L5 /// Q8CIT9 /// Q8K2V9
1457564_at	Dffa	plectin 1	-0.83 BB194910	AAH58213 /// Q54786 /// Q8BQC7 /// Q8C535 /// Q8CA98
1434610_at	Plec1	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 2	-0.83 BM210485	Q923J2 /// Q9QXS1
1417289_at	Plekha2	---	-0.83 NM_031257	Q9ERS5

1428147_at	0610011B16Rik	RIKEN cDNA 0610011B16 gene	-0.82 BB203098	AAH61006 /// Q8C9V7 /// Q8CA54 /// Q9D2V7
1427128_at	Ptpn23	protein tyrosine phosphatase, non-receptor type 23	-0.82 BM195862	AAH59902 /// Q8R1Z5 /// Q9Z3E6
1451452_a_at	Rgs16	regulator of G-protein signaling 16	-0.82 U72881	BAC37678 /// P97428 /// Q7TNU9 /// Q80V16
1417959_at	Pdlim7	PDZ and LIM domain 7	-0.82 NM_026131	Q80ZY6 /// Q810S3 /// Q8BVJ7 /// Q8C1S4 /// Q9CRA1
1423068_at	lft172	intracellular transport 172	-0.82 AK006007	AAH60948 /// AAH66096 /// AAR05390 /// Q80T14 /// Q80W19 /// Q9DAB0
1419038_a_at	Csnk2a1	casein kinase II, alpha 1 polypeptide	-0.82 BB283759	AAH60742 /// Q60737 /// Q61177 /// Q8CD20 /// Q8R0X4 /// Q9D0E8
1416360_at	Snag1	sorting nexin associated golgi protein 1	-0.82 AV344473	Q8C788 /// Q91ZR2
1460743_at	Tigd5	tigger transposable element derived 5	-0.82 BB553398	Q8BQA1 /// Q8C381 /// Q8CBD5
1452835_a_at	Polmt	polymerase (RNA) mitochondrial (DNA directed)	-0.82 AK003792	Q8BJE0 /// Q8BKF1 /// Q9D196
1439216_at	---	Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530095A18	-0.82 BB211804	Q8BRV0
1435680_a_at	Dpp7	product:hypothetical protein, full insert sequence dipeptidylpeptidase 7	-0.82 BG067113	Q8R082 /// Q9ET22
1426777_a_at	Wasl	Wiskott-Aldrich syndrome-like (human)	-0.81 BF466143	AAH58642 /// Q7TPN5 /// Q80VV6 /// Q91YD9 /// Q9CXO9
1435681_s_at	Homer3	homer homolog 3 (Drosophila)	-0.81 AI647511	---
1459568_at	---	Mus musculus transcribed sequence with weak similarity to protein p1r:158401 (M.musculus) f58401	-0.81 BB785334	P49718 /// Q8BQ03 /// Q8C219
1429345_at	D2Erd435e	protein-tyrosine kinase (EC 2.7.1.112) JAK3 - mouse DNA segment, Chr 2, ERATO D01 435, expressed	-0.81 AK016563	BAC32303 /// Q8BKL6 /// Q8BYN2 /// Q9D4F8
1435105_at	111006IN23Rik	RIKEN cDNA 111006IN23 gene	-0.81 BG066986	Q8BTC4 /// Q8K0W3
1453427_at	Csnk2a1	casein kinase II, alpha 1 polypeptide	-0.81 AK011501	AAH60742 /// Q60737 /// Q61177 /// Q8CD20 /// Q8R0X4 /// Q9D0E8
1424460_s_at	BC005662	cDNA sequence BC005662	-0.81 BG068664	AAH66809 /// Q8BG23 /// Q8BJT4 /// Q8BUX7 /// Q99JU6
1451083_s_at	Aars	alanyl-tRNA synthetase	-0.81 BC026611	AAH58620 /// AAP57355 /// Q8BGQ7 /// Q8R346
1415750_at	Tbl3	transducin (beta)-like 3	-0.81 BC019504	Q8CAJ7 /// Q8CE86 /// Q8VE90
1455394_at	Plasg-pending	protein inhibitor of activated STAT gamma solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29	-0.81 BI472631	Q9JM05
1438188_x_at	Slc25a29	RIKEN cDNA 2310015A05 gene	-0.81 BB832209	Q8BL03
1436106_x_at	2310015A05Rik	crystallin, lambda 1	-0.81 BI689456	---
1447112_s_at	Cry11	glutamic pyruvic transaminase 1, soluble	-0.81 C85932	BAC31583 /// BAC37964 /// Q8R4W7 /// Q99KP3
1426502_s_at	Gpt1	glutamate-cysteine ligase, modifier subunit	-0.80 AK008086	Q8QZR5
1418627_at	Gclm	RIKEN cDNA 2010209O12 gene	-0.80 NM_008129	BAC25831 /// O09172
1452170_at	2010209O12Rik	RIKEN cDNA 9930033D15 gene	-0.80 BC019714	Q80TE1 /// Q80VD4 /// Q8C228 /// Q8VCJ5
1444775_at	9930033D15Rik	expressed sequence BB219290	-0.80 BB660772	---
1419907_s_at	BB219290	plexin A2	-0.80 BB219290	AAH64708 /// Q8K3J9 /// Q8VHP5 /// Q920A9
1429772_at	Plxn2	heat shock protein 1	-0.80 BB085537	AAH56475 /// AAH68155 /// P70207 /// Q80TZT /// Q80XE5 /// Q8R114
1425964_x_at	Hspb1	Mus musculus, clone IMAGE:1246018, mRNA	-0.80 U03561	BAB22579 /// BAB27099 /// P14602 /// Q9Z2L2 /// Q9Z2L3
1434263_at	---	Mus musculus transcribed sequence with weak similarity to protein p1r:158401 (M.musculus) f58401	-0.80 AV307274	---
1459578_at	---	protein-tyrosine kinase (EC 2.7.1.112) JAK3 - mouse	-0.80 BG063140	---
1425429_s_at	Hif3a	hypoxia inducible factor 3, alpha subunit	-0.80 AF416641	Q8VHR1 /// Q9Z2I5
1448844_at	1810044O22Rik	RIKEN cDNA 1810044O22 gene	-0.80 NM_025558	AAH58812 /// AAH62980 /// Q9CQX2 /// Q9D1M6 /// Q9D8R3
1449738_s_at	P38ip-pending	transcription factor (p38 interacting protein)	-0.80 C80158	AAR87814 /// Q7TT00 /// Q8BG53 /// Q9JLS9
1439833_at	3110018K01Rik	RIKEN cDNA 3110018K01 gene	-0.80 BQ176645	---
1451769_s_at	Pcdha11	protocadherin alpha 11	---	AAH60211 /// BAC97930 /// Q88190 /// Q88191 /// Q88192 /// Q88193 /// Q88194 /// Q88195 /// Q88689 /// Q88690 /// Q88691 /// Q88692 /// Q88693 /// Q88694 /// Q88695 /// Q88696 /// Q88697 /// Q88698 /// Q88699 /// Q88700 /// Q88701 /// Q88702 /// Q88703 /// Q88704 /// Q88705 /// Q88706 /// Q88707 /// Q88708 /// Q88709 /// Q88710 /// Q88711 /// Q88712 /// Q88713 /// Q88714 /// Q88715 /// Q88716 /// Q88717 /// Q88718 /// Q88719 /// Q88720 /// Q88721

1439812_at	4930402H24Rik	RIKEN cDNA 4930402H24 gene	-0.79 BQ173880	AAH30418 /// Q8BIK2 /// Q8BIT3 /// Q9D5P8
1425525_a_at	P2rx4	purinergic receptor P2X, ligand-gated ion channel 4	-0.79 AF089751	Q9JJX3 /// Q9JJX4 /// Q9JJX5 /// Q9JJX6 /// Q9WUN9 /// Q9Z256 /// Q9Z257
1424922_a_at	Brd4	bromodomain containing 4	-0.79 BC008532	Q35692 /// Q8BS78 /// Q8VHF7 /// Q8VHF8 /// Q9ESU6
1445303_at	---	Mus musculus transcribed sequences	-0.79 BG066334	---
1441750_x_at	---	Mus musculus transcribed sequences	-0.79 BB796499	---
1421859_at	Adam17	a disintegrin and metalloproteinase domain 17	-0.78 C76813	Q9Z0F8
1428180_at	2810422J05Rik	RIKEN cDNA 2810422J05 gene	-0.78 AK013135	Q80XH1
1423944_at	Hpxn	hemopexin	-0.78 BC011246	Q91X72
1449362_a_at	Map4k6-pending 6	mitogen-activated protein kinase kinase kinase	-0.78 NM_016713	Q61155 /// Q7TT13 /// Q9JM52
1441190_at	---	Mus musculus transcribed sequence with moderate similarity to protein p1r:S12207 (M.musculus) S12207 hypothetical protein (B2 element) - mouse	-0.78 AV381444	Q9D898
1427825_at	Sico1b2	1b2	-0.78 AB037192	Q9JUL3
1426866_at	D4st1	dermatan 4 sulfotransferase 1	-0.78 AK011230	Q8OV53 /// Q8R304 /// Q9D0P2
1418089_at	Sbx8	synthaxin 8	-0.78 NM_018768	AAH61118 /// Q88983 /// Q8BS59
1437146_x_at	0610011B16Rik	RIKEN cDNA 0610011B16 gene	-0.78 AV025980	AAH61006 /// Q8C9V7 /// Q8CA54 /// Q9D2V7
1426699_at	AU040320	expressed sequence AU040320	-0.77 BG071197	Q8BHR5 /// Q8BHUT /// Q8BHZ3 /// Q8K135 /// Q8VBZ9
1449544_a_at	Kcnh2	potassium voltage-gated channel, subfamily H (eag-related), member 2	-0.77 NM_013569	AAQ82708 /// Q35219 /// Q80WG1 /// Q80XE8
1420221_at	---	Mus musculus, Similar to putative regulation protein GS3, clone IMAGE:538333, mRNA	-0.77 BB192718	---
1429552_at	1700019F09Rik	RIKEN cDNA 1700019F09 gene	-0.77 AK006118	Q9DA32 /// Q9DA68
1427193_at	Brd8	bromodomain containing 8	-0.77 BM219644	Q8C049 /// Q8R3B7 /// Q8R583 /// Q8VDPO /// Q9CXF6
1440312_at	Elov17	EL OVL family member 7, elongation of long chain fatty acids (yeast)	-0.77 BQ174957	Q8BX38 /// Q8BYY8 /// Q9D2Y9
1447476_at	---	Mus musculus transcribed sequences	-0.77 BB079952	---
1439429_x_at	Dxb2	dellex 2 homolog (Drosophila)	-0.77 BB518874	Q8R3P2
1427286_at	---	Mus musculus cDNA clone MGC:62856 IMAGE:6494361, complete cds	-0.77 BB130195	Q7TQ14 /// Q8VI61
1422853_at	Shc1	src homology 2 domain-containing transforming protein C1	-0.77 BB753533	P98083
1427699_a_at	Pton11	protein tyrosine phosphatase, non-receptor type 11	-0.77 L08663	AAH57398 /// AAH59278 /// P35235 /// Q63848 /// Q64509 /// Q99KW7 /// Q9CT18
1450214_at	Adora2b	adenosine A2b receptor	-0.77 NM_007413	Q60614 /// Q8BK41 /// Q8BX12
1444433_at	---	Mus musculus transcribed sequences	-0.77 BM246582	---
1417209_at	Sertad2	SERTA domain containing 2	-0.77 NM_021372	BAC97869 /// Q91VV6 /// Q9JJG5
1454370_at	4930557B21Rik	RIKEN cDNA 4930557B21 gene	-0.77 BB015975	---
1424429_s_at	Doc2a	double C2, alpha	-0.77 BG065288	Q7TMJ7 /// Q8R359
1425958_at	Il1f9	interleukin 1 family, member 9	-0.76 AY071843	Q8R460
1432515_at	2410124H12Rik	RIKEN cDNA 2410124H12 gene	-0.76 AK010774	Q9CWF8
1428708_x_at	2610009E16Rik	RIKEN cDNA 2610009E16 gene	-0.76 AK011360	Q80WS9 /// Q8VDD2 /// Q9D0J8
1418423_s_at	Serpinb9f	serine (or cysteine) proteinase inhibitor, clade B, member 9f	-0.76 AF425083	AAH64758 /// AAH64759 /// Q8VHQ1 /// Q9DAZ7
1451634_at	2810051F02Rik	RIKEN cDNA 2810051F02 gene	-0.76 BC009123	Q8BGE0 /// Q91VT2 /// Q9CZ68
1437219_at	---	Mus musculus transcribed sequences	-0.76 AW553541	---
1431251_at	1300011L04Rik	RIKEN cDNA 1300011L04 gene	-0.76 A4451838	---
1436622_at	---	Similar to KIAA0522 protein (LOC245666), mRNA	-0.76 AW492241	---
1451761_at	Hoxb4	homeo box B4	-0.76 AV307188	P10284
1427480_at	Leap2	liver-expressed antimicrobial peptide 2	-0.76 AA571276	Q91V13

1436695_x_at	Rbed1	RNA binding motif and ELMO domain 1	-0.76 BB557382	Q91YP6
1433464_at	Ipo13	importin 13	-0.76 BB475675	BAC98010 /// Q8K0C1
1430875_a_at	Pak1p1	PAK1 interacting protein 1	-0.76 AK017959	Q80UT4 /// Q8C5N6 /// Q923K2 /// Q9DCE5
1418298_s_at	Dpysl4	dihydropyrimidinase-like 4	-0.76 NM_011993	O35098
1455992_at	Vgll4	vestigial like 4 (Drosophila)	-0.75 BG967636	AAH60305 /// Q80V24 /// Q8BGS8
1439799_at	---	Mus musculus transcribed sequences	-0.75 BE953350	---
1421210_at	C2la	class II transactivator	-0.75 AF042158	P79621 /// Q8HW99
1452745_at	RIKEN cDNA 1810044A24	RIKEN cDNA 1810044A24 gene	-0.75 AK007766	Q8CD01 /// Q8CFV8 /// Q9D6K1 /// Q9D8R6
1430188_at	RIKEN cDNA 1700037C18	RIKEN cDNA 1700037C18 gene	-0.75 AK012792	Q8BT88 /// Q9D9P5
1422521_at	Dcdn1	dynactin 1	-0.75 NM_007835	AAH66061 /// Q08788
1437554_at	Plec1	plectin 1	-0.75 BM232239	Q923J2 /// Q9QXS1
1445517_at	---	Mus musculus transcribed sequence with weak similarity to protein refNP_Q81764.1 (M.musculus)	-0.75 BB144876	---
1446448_at	Pias1	protein inhibitor of activated STAT 1	-0.75 AW547576	---
1449403_at	Pde9a	phosphodiesterase 9A	-0.75 NM_008804	AAH61163 /// O70628 /// Q8BSU4 /// Q8CB29
1437861_s_at	Pkce	protein kinase C, epsilon	-0.75 BB335101	P16054
1417967_at	Mms19l	MMS19 (MET18 S. cerevisiae)-like	-0.75 NM_028152	Q925N8 /// Q9D071
1452110_at	Mtr	5-methyltetrahydrofolate-homocysteine methyltransferase	-0.75 BB757908	Q8C1A3 /// Q8R0Y3
1424428_at	A854876	expressed sequence A854876	-0.75 BG055288	Q7TMJ7 /// Q8R359
1422687_at	Nras	neuroblastoma ras oncogene	-0.74 BB018528	AAH58755 /// P08556 /// Q9D091
1428977_at	Chst8	sulfotransferase 8	-0.74 AK005217	BAC87753 /// Q80XD4 /// Q8BQ86
1422944_a_at	Diap3	diaphanous homolog 3 (Drosophila)	-0.74 NM_019670	Q8K331 /// Q9Z207
1416900_s_at	Lass1	longevity assurance homolog 1 (S. cerevisiae)	-0.74 NM_138647	P20863 /// P27545
1430081_at	Pnf15	PHD finger protein 15	-0.74 AK004823	BAC97907 /// Q8C7J4
1416294_at	Scamp3	secretory carrier membrane protein 3	-0.74 NM_011886	O35609
1417248_at	Ralp1	ralA binding protein 1	-0.74 NM_009087	AAH67073 /// Q62172
1451703_s_at	Apt	adenine phosphoribosyl transferase	-0.74 M11310	AAH05667 /// P08030 /// Q9DCY3
1444120_at	Bin1	bridging integrator 1	-0.74 BG293813	AAH65160 /// O08539 /// Q8C5M9 /// Q8C9N3
1416991_at	Mto1	mitochondrial translation optimization 1 homolog (S. cerevisiae)	-0.74 NM_026658	AAH63256 /// Q8C6J8 /// Q923Z3 /// Q9CYK7 /// Q9D2Q5
1416965_at	Pcsk1n	proprotein convertase subtilisin/kexin type 1 inhibitor	-0.74 AF181560	Q91W26 /// Q9ESU4 /// Q9QXV0
1420419_a_at	Otof	otoferlin	-0.73 NM_031875	Q8CCE7 /// Q9ESF1
1424255_at	Supt5h	suppressor of Ty 5 homolog (S. cerevisiae)	-0.73 BC007132	AAH57449 /// AAH58598 /// AAH59849 /// O55201
1439234_a_at	2410018G23Rik	RIKEN cDNA 2410018G23 gene	-0.73 BE200117	Q8B1J1 /// Q8R0I4 /// Q9CWL9
1417628_at	Supt6h	suppressor of Ty 6 homolog (S. cerevisiae)	-0.73 NM_009297	BAC97879 /// Q62383 /// Q8BQY6
1423396_at	Agt	angiotensinogen	-0.73 AK018763	Q8VCN0
1427762_x_at	Hist1h2bp	histone 1, H2bp	-0.73 M25487	AAH61044 /// Q64477 /// Q8C622
1440253_at	Psm11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	-0.73 AV136581	Q7TMD0 /// Q8BG32 /// Q8BK73 /// Q8C0Z6 /// Q8K2N7
1444974_at	---	Mus musculus transcribed sequences	-0.73 BG068713	---
1448330_at	Gstm1	glutathione S-transferase, mu 1	-0.73 NM_010358	P10649
1455801_x_at	Tbcd	tubulin-specific chaperone d	-0.73 BC392080	AAH59843 /// Q8BYA0 /// Q8CHC0 /// Q8R199
1448810_at	Gne	glucosamine	-0.73 BC015277	Q91W68
1449853_at	Sixn2	sideroflexin 2	-0.73 NM_053196	Q925N2
1447877_x_at	Dnm11	DNA methyltransferase (cytosine-5) 1	-0.73 BB116018	P13864 /// Q7TSJ0
1451395_at	D5Bwg0834e	DNA segment, Chr 5, Brigham & Women's Genetics 0834 expressed	-0.73 BC021492	Q8VDN4

1453146_at	4432404J10Rik	RIKEN cDNA 4432404J10 gene	-0.73 BM123170	AAH57164 /// AAH60123 /// BAC98191 /// Q80V37 /// Q80ZK4 /// Q8BTS5 /// Q9CRS2 ///
145888_at	B230217C06Rik	RIKEN cDNA B230217C06 gene	-0.73 BB125202	Q9CTT1
1424728_at	BC011248	cDNA sequence BC011248	-0.73 BC011248	Q8BLC0 /// Q8BZD4
1438154_x_at	2610002J02Rik	RIKEN cDNA 2610002J02 gene	-0.72 AV218922	Q91X71
1450505_a_at	1810015C04Rik	RIKEN cDNA 1810015C04 gene	-0.72 NM_025459	Q7TMY5 /// Q8VE91 /// Q9CUJ4 /// Q9D8Z5
1430561_at	5730496F10Rik	RIKEN cDNA 5730496F10 gene	-0.72 BE952491	---
1452650_at	6330414G21Rik	RIKEN cDNA 6330414G21 gene	-0.72 AK018173	Q80V85
1434006_at	Fksg24	hypothetical protein Fksg24	-0.72 BQ030992	Q80UR1 /// Q8VIK2
1424073_at	5430437P03Rik	RIKEN cDNA 5430437P03 gene	-0.72 BC005692	Q8C5Q8 /// Q99JU2 /// Q9CTJ4
1417725_a_at	Ssca1	Siogen's syndrome/scleroderma autoantigen 1 homolog (human)	-0.72 BC021593	BAA87050 /// BAB23917 /// BAB28340 /// P56873 /// Q9CZE1 /// Q9D002
1448054_at	---	Mus musculus transcribed sequences	-0.72 BE854760	Q8C0D7 /// Q8C1S7 /// Q8K3Q5 /// Q8K3Q6 /// Q8K3Q7 /// Q9D7F9
1460018_at	---	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932704A10	---	---
1440161_at	---	product:unclassified, full insert sequence	-0.72 AV278039	Q8BVK6 /// Q8CI06
1415886_at	Sh2d3c	Mus musculus transcribed sequences	-0.71 BB378819	---
1442280_at	D2Erd750e	SH2 domain containing 3C	-0.71 AB043953	Q9JME1 /// Q9QZS8
1416602_a_at	Rad52	DNA segment, Chr 2, ERATO Doi 750, expressed RAD52 homolog (S. cerevisiae)	-0.71 BM251033	Q8K2D9 /// Q9CYZ4 /// Q9D9Z1
1446683_at	Eps15-rs	epidermal growth factor receptor pathway substrate 15, related sequence	-0.71 NM_011236	P43352 /// Q8VEE2
1417467_a_at	Tada3l	transcriptional adaptor 3 (NGG1 homolog, yeast)-like	-0.71 BB098038	Q60902 /// Q8CB60 /// Q8CB70 /// Q91WH8
1451689_a_at	Sox10	SRY-box containing gene 10	-0.71 AK003405	Q8R0L9
1423825_at	Dhx16	DEAH (Asp-Glu-Ala-His) box polypeptide 16	-0.71 BC018551	AAH23356 /// Q88418 /// Q04888 /// Q80V12 /// Q8C916
1451847_s_at	Arid4b	AT rich interactive domain 4B (Rbp1 like)	-0.71 BC009147	Q80TX4 /// Q921Y1 /// Q9CRI3
1448567_at	Pl6-pending	PL6 protein	-0.71 BC024724	Q8BM18 /// Q8BV50 /// Q8BXV6 /// Q8BYA5 /// Q8BYB0 /// Q8R1E4
1423685_at	Aars	alanyl-tRNA synthetase	-0.71 NM_019704	BAC31672 /// Q9WUJ1
1423690_s_at	Gpsm1	G-protein signalling modulator 1 (AGS3-like, C. elegans)	-0.71 BC026611	AAH58620 /// AAP57355 /// Q8BGQ7 /// Q8R346
1416975_at	Stam2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	-0.71 BC026486	Q61366 /// Q8BUIK4 /// Q8BX78 /// Q8R0E6 /// Q8R0R9
1420799_at	Ntsr	neurotensin receptor	-0.71 BB125321	O88811 /// Q8C8Y4
1459223_at	B930095G15Rik	RIKEN cDNA B930095G15 gene	-0.71 NM_018766	O88319
1418261_at	Syk	spleen tyrosine kinase	-0.71 BB376007	Q8C3S9
1434652_at	Cdc42pbp	Cdc42 binding protein kinase beta	-0.70 AW907526	AAH65121 /// P48025
1419456_at	Dcxr	dicarbonyl L-xylulose reductase	-0.70 BF154551	Q7TT50 /// Q80W33
1434154_at	Kcid13	potassium channel tetramerisation domain containing 13	-0.70 BC012247	Q91X52 /// Q9D129 /// Q9D8W1
1434611_at	Rnf123	ring finger protein 123	-0.70 BQ177107	Q8BGV7
1453874_at	4933401B06Rik	RIKEN cDNA 4933401B06 gene	-0.70 BB765679	AAH57082
1443452_at	---	Mus musculus transcribed sequences	-0.70 AV278276	---
1437864_at	Adipor2	adiponectin receptor 2	-0.70 BM212484	---
1430986_at	Farsl	phenylalanine-tRNA synthetase-like	-0.70 BE632137	AAR08379 /// Q8BQ55
1435183_at	3110043L15Rik	RIKEN cDNA 3110043L15 gene	-0.70 AK012154	Q8C644 /// Q9CWNZ8 /// Q9CZU5 /// Q9WUJ2
1458826_at	---	Mus musculus transcribed sequences	-0.70 AV050349	AAH57590
1422943_a_at	Hspb1	heat shock protein 1	-0.70 BG066316	---
1439546_at	4933417O08Rik	RIKEN cDNA 4933417O08 gene	-0.70 NM_013560	BAB22579 /// BAB27099 /// P14602 /// Q9Z2L2 /// Q9Z2L3
1452258_at	6820402O20Rik	RIKEN cDNA 6820402O20 gene	-0.70 BB807546	Q9D428
1447607_at	---	---	-0.70 BB308157	AAH60121 /// Q8BLG0 /// Q8BZ14
			-0.69 AV045102	---

142637_a_at	1810037G04Rik	RIKEN cDNA 1810037G04 gene	-0.69 BC027558	Q9D8S9	
1436923_at	Rao2b	RAB2B, member RAS oncogene family	-0.69 BF466486	AAH61513 /// P59279 /// Q7TQF6 /// Q9DB48	
1458594_at	Shprh	SNF2 histone linker PHD RING helicase	-0.69 BB539406	Q7TPQ3 /// Q7TQ27 /// Q7TQ28 /// Q7TQ29 /// Q8BK2 /// Q8BUW0 /// Q8BXM1 /// Q922Q3	
1426136_x_at	Kira8	killer cell lectin-like receptor, subfamily A, member 8	-0.69 AF288380	Q64329 /// Q9JHN9	
1451284_at	D17Wsu94e	DNA segment, Chr 17, Wayne State University 94, expressed	-0.69 BC019384	Q8C998 /// Q8K5D1 /// Q8VCS2	
1417811_at	Slc24a6	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	-0.69 NM_133221	Q80XM7 /// Q925Q3	
1424432_at	Ubt1	ubiquitin domain containing 1	-0.69 BC016129	Q91WB7	
1436053_at	BC045600	cDNA sequence BC045600	-0.69 BB272520	AAH60066 /// Q80VE5	
1435809_at	---	CDNA clone MGC:56962 IMAGE:6391322, complete cds	-0.69 BE947974	Q7TST1	
1443569_at	4930430E16Rik	RIKEN cDNA 4930430E16 gene	-0.69 BB214806	Q8QZV6 /// Q9CUP0	
1441398_at	---	Mus musculus transcribed sequence with moderate similarity to protein ref.NP_003263.1 (H.sapiens) transmembrane 7 superfamily member 1 (upregulated in kidney); transmembrane 7 superfamily member 1 (upregulated in [Homo sapiens])	-0.69 BG068080	---	
1426805_at	Smarca4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	-0.69 AW701251	AAH60229 /// AAH61214 /// Q35845 /// Q7TQL1 /// Q8BQ54 /// Q8CGJ5 /// Q8R0K1 /// Q8R569	
1438105_at	---	Mus musculus transcribed sequences	-0.69 BB667172	---	
1445027_at	D030068L24	hypothetical protein D030068L24	-0.69 BG073163	---	
1428707_at	2610009E16Rik	RIKEN cDNA 2610009E16 gene	-0.69 AK011360	Q80WS9 /// Q8VDO2 /// Q9D0J8	
1434128_a_at	Zfp574	zinc finger protein 574	-0.69 BB131266	AAH59044 /// Q8BKB5 /// Q8BY46	
1430777_a_at	Golph3	golgi phosphoprotein 3	-0.69 AK014644	Q99KY1 /// Q9CRA5	
1422715_s_at	Acp1	acid phosphatase 1, soluble	-0.69 AW554436	Q9D358	
1454018_at	Tik2	tousled-like kinase 2 (Arabidopsis)	-0.69 AK014829	AAH66198 /// O55047 /// P70320 /// Q9D9L6	
1442600_at	---	Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130047J24 product:inferred: ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH {Rattus norvegicus, full insert sequence	-0.69 BB456595	---	
1457313_at	9530014D17Rik	RIKEN cDNA 9530014D17 gene	-0.68 BG074373	AAH68146 /// Q7TPR1 /// Q80XM6 /// Q8BXC9 /// Q8BXT3	
1423769_at	Ptcd2	pentatricopeptide repeat domain 2	-0.68 BC025110	Q8R3K3 /// Q91VG3 /// Q9D0S7	
1456313_x_at	Mrp28	mitochondrial ribosomal protein L28	-0.68 BB257397	Q9D1B9	
1428445_at	9430029K10Rik	RIKEN cDNA 9430029K10 gene	-0.68 AK020444	Q9CX30	
1449381_a_at	Pacsin1	protein kinase C and casein kinase substrate in neurons 1	-0.68 BI731319	BAC31717 /// Q61644	
1454732_at	6430517J16Rik	RIKEN cDNA 6430517J16 gene	-0.68 AV340862	Q7TMW8 /// Q8C052	
1421309_at	Mgmt	O-6-methylguanine-DNA methyltransferase	-0.68 NM_008598	BAC16763 /// BAC16764 /// P26187	
1438760_x_at	Adam15	a disintegrin and metalloproteinase domain 15 (metargidin)	-0.68 BB392633	AAH57909 /// O88839 /// Q8CA82	
1426783_at	Gcn5l2	GCN5 general control of amino acid synthesis-like 2 (yeast)	-0.68 AW212720	AAH63752 /// Q99KW4 /// Q9JHD2	
1454599_at	4930425F17Rik	RIKEN cDNA 4930425F17 gene	-0.68 AK019583	Q9CTX4	
1440860_at	Mab211	mab-21-like 1 (C. elegans)	-0.68 BB126987	O70299	

1417001_a_at	D4Wsu53e	DNA segment, Chr 4, Wayne State University 53, expressed	-0.68 BE447520	AAH56986 /// Q80Y97 /// Q9CSN6 /// Q9D194 /// Q9JJF1
1448803_at	Golga4	golgi autoantigen, golgin subfamily a, 4	-0.68 NM_018748	Q8COA4 /// Q91VW5
1415987_at	Hdlbp	high density lipoprotein (HDL) binding protein	-0.68 BG065877	Q8VDJ3
1426297_at	Tcf2a	transcription factor E2a	-0.68 AF352579	P15806 /// Q8CAH9 /// Q8VCY4 /// Q922S2 /// Q99MB8 /// Q9CRT1 /// Q9CYJ4
1426943_at	RIKEN cDNA 1110015K06Rik	RIKEN cDNA 1110015K06 gene	-0.68 AK003728	Q8OUQ7 /// Q91ZD1 /// Q9CTF7
1455271_at	1500011J06Rik	RIKEN cDNA 1500011J06 gene	-0.68 BB560177	Q8K1E6
1429051_s_at	6230403H02Rik	RIKEN cDNA 6230403H02 gene	---	---
1417978_at	1300018P11Rik	RIKEN cDNA 1300018P11 gene	-0.67 BC027014	Q9D983 /// Q9DBB5
1460118_at	---	Mus musculus transcribed sequences	-0.67 BF455409	---
1436132_at	D430036N24Rik	RIKEN cDNA D430036N24 gene	-0.67 BB486539	---
1432622_a_at	4930507D05Rik	RIKEN cDNA 4930507D05 gene	-0.67 BB467733	---
1456078_x_at	4930542G03Rik	RIKEN cDNA 4930542G03 gene	-0.67 BB012080	AAH61039 /// Q9D4K5 /// Q9DCR1
1440740_at	---	---	-0.67 AV006603	---
1444355_at	Atp8a1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	-0.67 AW125445	P70704 /// Q8BR88 /// Q8CA15
1453476_at	1700060J05Rik	RIKEN cDNA 1700060J05 gene	-0.67 AK006643	---
1452372_at	1110063F24Rik	RIKEN cDNA 1110063F24 gene	-0.67 BF729638	Q80Y55 /// Q8BI04 /// Q8VDP1
1455049_at	Igsf2	immunoglobulin superfamily, member 2	-0.67 BA484576	BAC32470 /// BAC35000 /// BAC97961 /// Q7TPV3
1443877_a_at	C030018K18Rik	RIKEN cDNA C030018K18 gene	-0.67 BB306768	Q8BLC8 /// Q8BX14
1456530_x_at	Elovl1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	-0.67 BB748075	Q9JLJ5 /// Q9WU14
1448880_at	Ube2l3	ubiquitin-conjugating enzyme E2L 3	-0.67 BG066549	P51966
1422404_x_at	---	---	-0.67 NM_008334	Q8OSS5
1433802_at	AW125688	expressed sequence AW125688	-0.67 BM114677	---
1423689_a_at	Gpsm1	G-protein signalling modulator 1 (AGS3-like, C. elegans)	-0.67 BC026486	Q61366 /// Q8BUK4 /// Q8BX78 /// Q8R0E6 /// Q8R0R9
1459808_at	Fkbp4	FK506 binding protein 4	-0.66 BB087569	BAC39057 /// P30416 /// Q8CBS1
1428998_at	2810468K17Rik	RIKEN cDNA 2810468K17 gene	-0.66 AK013387	AAH58717 /// Q80UP6 /// Q9CYS2
1417348_at	2310039H08Rik	RIKEN cDNA 2310039H08 gene	-0.66 NM_025966	---
1418665_at	Zfp385	zinc finger protein 385	-0.66 NM_013866	Q8VD12 /// Q9QY68
1429328_at	Nsf1c	NSFL1 (p97) cofactor (p47)	-0.66 BG522397	Q9CZ44
1426257_a_at	Sars1	seryl-aminoacyl-tRNA synthetase 1	-0.66 BC008612	BAC35990 /// P26638 /// Q8C483 /// Q8CEH3
1452338_s_at	Itsn	intersectin (SH3 domain protein 1A)	AAH66105 /// Q80WF1 /// Q8C4B5 /// Q8CGU2 /// Q8CGU5 /// Q8CJ43 /// Q8CJ54 ///	Q8CJ55 /// Q8CJ62 /// Q8R358 /// Q9Z0R4
1435685_x_at	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	-0.66 AA172344	---
1421843_at	Il1rap	interleukin 1 receptor accessory protein	-0.66 AV150520	AAH61132 /// Q8CFP9 /// Q9JL43 /// Q9R1X5
1430004_s_at	Wdr20	WD repeat domain 20	-0.66 BE285634	Q61730
1437311_at	A930034L06Rik	RIKEN cDNA A930034L06 gene	-0.66 AK015014	Q80X67 /// Q9D5R2
1447247_at	---	Mus musculus transcribed sequences	-0.65 BB281971	Q8BV32
1448187_at	Pold1	polymerase (DNA directed), delta 1, catalytic subunit	-0.65 BE957311	---
1436674_at	Rap2ip	Rap2 interacting protein	-0.65 BC009128	P52431 /// Q8C2N0 /// Q91VT0
1417079_s_at	Lgalst2	lectin, galactose-binding, soluble 2	-0.65 AW489945	O08576 /// Q80Y95
1444299_at	A430093F15Rik	RIKEN cDNA A430093F15 gene	-0.65 NM_025622	Q8K111 /// Q9CQW5
1447107_at	Ddx55	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55	-0.65 BB209605	Q8C505
1453662_at	B230205O20Rik	RIKEN cDNA B230205O20 gene	-0.65 BB756348	BAC98212 /// Q810A4 /// Q8BK20 /// Q8BZR1 /// Q9CS87 /// Q9CS10
1440497_at	1110021J02Rik	RIKEN cDNA 1110021J02 gene	-0.65 AK020987	---
1454857_at	Rnf122	ring finger protein 122	-0.65 BE956898	Q8C7V0 /// Q9DBC3
			-0.65 AW551457	Q80VA7 /// Q8BGD3 /// Q8BP31

1426301_at	Alcam	activated leukocyte cell adhesion molecule	-0.65 U95030	Q61490	
1453014_a_at	Sec3111	SEC31-like 1 (S. cerevisiae)	-0.65 BM222383	Q7TQJ7 /// Q811J4 /// Q9CVL3	
1428443_a_at	Rap1ga1	Rap1, GTPase-activating protein 1	-0.65 AK005063	Q80VZ8 /// Q8K2L6	
1433757_a_at	Nisch	nischairin	-0.64 BB025231	Q80TM9 /// Q8C354 /// Q8C4X9 /// Q8CBH0 /// Q8CF63 /// Q91XW6 /// Q99LG6 /// Q9EPW8 /// Q9WUJ6	
1444228_s_at	Herc2	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 2	-0.64 BB333568	Q88473 /// Q7TPR5 /// Q80VV7	
1448378_at	Fscn1	fascin homolog 1, actin bundling protein	-0.64 NM_007984	Q61553 /// Q7TN32 /// Q80V75	
1420524_a_at	Masp2	(Strongylocentrotus) purpuratus) mannan-binding lectin serine protease 2	-0.64 NM_010767	Q91WP0 /// Q9QXA4 /// Q9QXD2 /// Q9QXD5 /// Q9Z338	
1428955_x_at	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 2	-0.64 AK004710	AAH65778 /// Q9JHL1	
1451680_at	Npr3	neoplastic progression 3	-0.64 BC011325	Q62368 /// Q9D975	
1428665_at	Katnb1	katanin p80 (WD40-containing) subunit B 1	-0.64 AK010364	Q8BG40 /// Q8CD18 /// Q8R1J0 /// Q9CWW2	
1439219_at	A730082K24Rik	RIKEN cDNA A730082K24 gene	-0.64 BB258061	---	
1441371_at	9330117B14	hypothetical protein 9330117B14	-0.64 BQ174019	---	
1423834_s_at	Gga1	golgi associated, gamma adaptin ear containing, ARF binding protein 1	-0.64 BC026802	Q8R0H9	
1453101_at	2810402K13Rik	RIKEN cDNA 2810402K13 gene	-0.64 AK012967	Q8K1D5 /// Q9CZ64	
1429135_at	1110059M19Rik	RIKEN cDNA 1110059M19 gene	-0.64 AV015858	Q9D0W7	
1422028_a_at	Els1	E26 avian leukemia oncogene 1, 5' domain	-0.64 BC010588	AAAR00342 /// P27577 /// Q8BVW8 /// Q8K3Q9 /// Q921D8	
1417316_at	Them2	thioesterase superfamily member 2	-0.64 NM_025790	Q9CQR4	
1457816_at	Casp9	caspase 9	-0.64 BB781510	AAH56372 /// AAH56447 /// Q8C3Q0 /// Q8C3Q9 /// Q9R0S9 /// Q9R0T0	
1451019_at	Ctsf	cathepsin F	-0.64 AK017474	BAC36013 /// Q99KQ9 /// Q9ES93 /// Q9R0T3	
1457272_at	---	Mus musculus transcribed sequences	-0.64 BB284000	---	
1424061_at	Manbal	mannosidase, beta A, lysosomal-like	-0.64 BC013803	Q9D8X0	
1448262_at	Psmb2	proteasome (prosome, macropain) subunit, beta type 2	-0.64 NM_011970	Q8BJX0 /// Q9R1P3	
1427928_s_at	BC028278	cDNA sequence BC028278	-0.64 AW538039	Q8K358	
1460109_at	D8Erd325e	DNA segment, Chr 8, ERATO Doi 325, expressed	-0.63 AV253069	Q80TL2 /// Q80ZX3 /// Q8BR80 /// Q8C200 /// Q8C2M3 /// Q8C6B4 /// Q8R3L2 /// Q9CUW0	
1454237_at	1700030K01Rik	RIKEN cDNA 1700030K01 gene	-0.63 AK016416	Q9D4M8 /// Q9D9R3	
1427617_at	Fut10	fucosyltransferase 10	-0.63 BC022579	AAH62113 /// Q8C457 /// Q8K0S3 /// Q8R247	
1428465_at	Dlgap4	discs, large homolog-associated protein 4 (Drosophila)	-0.63 BG066219	AAH58948 /// AAO89220 /// Q80TN3 /// Q8R3U9	
1437004_at	1700096K11Rik	RIKEN cDNA 1700096K11 gene	-0.63 BG069841	---	
1421018_at	1110018J18Rik	RIKEN cDNA 1110018J18 gene	-0.63 NM_025370	Q9D1A0	
1423146_at	Hes5	hairy and enhancer of split 5 (Drosophila)	-0.63 AV337579	BAC39904 /// P70120	
1457232_at	Fbxl21	F-box and leucine-rich repeat protein 21	-0.62 BE946365	Q8BFZ4	
1428520_at	1110032A13Rik	RIKEN cDNA 1110032A13 gene	-0.62 AK004019	AAH64066	
1459638_at	---	Mus musculus transcribed sequences	-0.62 BE852843	---	
1457032_at	Ak5	adenylate kinase 5	-0.62 BB546359	Q920P5	
1442652_at	---	Mus musculus transcribed sequences	-0.62 BM935317	---	
1434322_at	A930021H16Rik	RIKEN cDNA A930021H16 gene	-0.61 BB513585	Q80UK4	
1423937_at	Kctd5	potassium channel tetramerisation domain containing 5	-0.61 BF577853	BAC97887 /// Q8VC57 /// Q9CSZ1	
1416013_at	Pld3	phospholipase D3	-0.61 NM_011116	Q35405	
1416766_at	2810484M10Rik	RIKEN cDNA 2810484M10 gene	-0.61 NM_133684	Q8C5F6 /// Q922Q1	

1418786_at	Mapk8ip2	mitogen-activated protein kinase 8 interacting protein 2	-0.61 AF220195	AAH29704 /// AAL50331 /// O35287 /// Q924X2 /// Q9CUY3 /// Q9ERE9 /// Q9QYP4
1430978_at	Rps25	ribosomal protein S25	-0.61 BM729504	AAH27208 /// BAC36806 /// P25111
1447663_at	---	---	-0.61 BB044824	---
1443104_at	---	Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130112O04	---	---
1455157_a_at	23100061F22Rik	product:unknown EST, full insert sequence	-0.61 AV173117	BAC97905 /// Q7TQL5 /// Q80XT7 /// Q811I7 /// Q8BTG9 /// Q8C6I68
1417460_at	lftm3l	RIKEN cDNA 2310061F22 gene	-0.61 NM_030694	Q99J93
1457819_at	---	interferon induced transmembrane protein 3-like	---	---
1417104_at	Emp3	Mus musculus transcribed sequence with strong similarity to protein pir:S54771 (H.sapiens) S54771	-0.61 A1549833	---
1415991_a_at	Klhd3	sodium channel alpha subunit - human	-0.61 BC001999	O35912
1416335_at	Mif	epithelial membrane protein 3	-0.61 NM_027910	Q8VEM9 /// Q91XU6 /// Q99JH9 /// Q9DBG8
1448479_at	Psmc3	kelch domain containing 3	-0.61 NM_010798	BAB25980 /// BAB27123 /// BAB28792 /// P34884
1449028_at	Rhou	macrophage migration inhibitory factor	-0.61 NM_009439	P14685 /// Q8BK46
1423889_at	Rbm7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	-0.61 AF378088	Q9D778 /// Q9EQT3
1442944_at	---	ras homolog gene family, member U	-0.61 BC011344	Q7TQE3 /// Q91VN2 /// Q9CQT2
1420844_at	Ubqln2	RNA binding motif protein 7	-0.61 BG085699	---
1418454_at	Mfap5	ubiquitin 2	-0.60 AV171029	Q9QZM0
1421918_at	Anp32a	microtubillar associated protein 5	-0.60 NM_015776	Q9QZJ6
1437322_at	Rbm14	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	-0.60 AF022957	AAH62899 /// O35381
1424187_at	2610001E17Rik	RNA binding motif protein 14	-0.60 BM218282	O8752 /// Q8BN66 /// Q8C2Q3 /// Q8C7Q4 /// Q91TZ1 /// Q9DBI6
1436732_s_at	Fbxw8	RIKEN cDNA 2610001E17 gene	-0.60 BG074158	AAH58751 /// Q8C043 /// Q8C8E1 /// Q8R2G6 /// Q9CRM1 /// Q9CT39 /// Q9D6Z4
1437118_at	Usp7	F-box and WD-40 domain protein 8	AAH57302 /// P70678 /// Q8BHA5 /// Q8BIA4 /// Q8BTH9 /// Q8BIX9 /// Q8C658 /// Q8CHC6	/// Q8VDH1 /// Q9D5H7
1458464_at	Nedl2	ubiquitin specific protease 7	-0.60 C77542	Q8BW01
1422155_at	Hist2h3c2	NEDD4-related E3 ubiquitin ligase NEDL2	-0.60 BB445169	Q8BQD5
1418136_at	Tgfb1l1	histone 2, H3c2	-0.60 BC015270	---
1434575_at	Epb4.111	transforming growth factor beta 1 induced transcript 1	-0.60 NM_009365	AAH56362 /// Q62219
1418570_at	Ncstn	erythrocyte protein band 4.1-like 1	-0.60 BB794965	Q8OU34 /// Q8C8P2 /// Q8K204 /// Q9Z2H5
1428383_a_at	2310021P13Rik	nicastrin	-0.59 BC019998	BAC97912 /// P57716
1452221_a_at	Cxxc1	RIKEN cDNA 2310021P13 gene	-0.59 BC026504	AAH58666 /// AAH59058 /// Q80Y41 /// Q8CE12 /// Q8CHC3 /// Q9D789
1425511_at	Mark1	CXXC finger 1 (PHD domain)	-0.59 BB447351	AAH28246 /// BAC38986 /// Q9CWW7
1451745_a_at	Znhit1	MAP/microtubule affinity-regulating kinase 1	-0.59 BM213279	Q8VHJ5
1425054_a_at	2510006D16Rik	zinc finger, HIT domain containing 1	-0.59 BC026751	Q8R331
1460405_at	2810441C07Rik	RIKEN cDNA 2510006D16 gene	-0.59 BC024696	Q8CEZ5 /// Q8R1E7 /// Q9D484
1425304_s_at	Prima1	RIKEN cDNA 2810441C07 gene	-0.59 AV238183	AAH59220 /// BAC98218 /// Q8C1A1 /// Q8VDH5 /// Q922V5
1417038_at	---	proline rich membrane anchor 1	-0.59 AY043275	Q810F0 /// Q9D1X7
1427142_s_at	Jarid1b	septin 9	-0.59 NM_017380	Q8OUJ5 /// Q9QYX9
1436377_at	---	jumonji, AT rich interactive domain 1B (Rbp2 like)	-0.59 BC019446	AAH57318 /// Q80Y84 /// Q8BLU1 /// Q8C1P6 /// Q8JZL8 /// Q8VCQ4
1426393_a_at	Sdf4	Mus musculus mRNA similar to chromosome 11	---	---
1450432_s_at	Mus81	hypothetical protein ORF4 (cDNA clone MGC:56861 IMAGE:6308873), complete cds	-0.59 BI410102	Q8OUB6 /// Q8OZU9
1451409_at	2210021J22Rik	stromal cell derived factor 4	-0.59 BM198177	AAH68152 /// Q61112
		MUS81 endonuclease homolog (yeast)	-0.59 AF425647	Q91ZJ0
		RIKEN cDNA 2210021J22 gene	-0.59 BC025858	Q8CEZ9 /// Q8R3A2

1423940_at	Yif1	Yip1 interacting factor homolog (S. cerevisiae)	-0.59 BC011117	Q91XB7 /// Q9CWB2
1431412_at	2810455B08Rik	RIKEN cDNA 2810455B08 gene	-0.59 B1692111	---
1419628_at	Chx10	C. elegans ceh-10 homeo domain containing homolog	-0.59 NM_007701	AAH58806 /// Q61412 /// Q80WF9
1420585_a_at	Nx2	nuclear RNA export factor 2	-0.59 NM_031259	Q99JG4 /// Q99MW6 /// Q99N10
1426886_s_at	Map3k3	mitogen activated protein kinase kinase 3	-0.59 BG175594	Q61084
1445333_at	---	---	-0.59 BG066013	---
1441878_s_at	1810049H13Rik	RIKEN cDNA 1810049H13 gene	-0.59 BB401085	Q9CR10
1455764_at	Lrpap1	low density lipoprotein receptor-related protein associated protein 1	-0.59 AV309553	AAH46641 /// AAH57979 /// AAH59887 /// BAA00500 /// CAG25840 /// Q8C252 /// Q8K295
1452257_at	Bdh	3-hydroxybutyrate dehydrogenase (heart, mitochondrial)	-0.59 BF322712	Q80XN0 /// Q8BK53 /// Q8R0C8
1440792_x_at	Opr1	opioid receptor, sigma 1	-0.59 BB405850	O55242 /// Q9JKU9
1446838_at	---	Mus musculus transcribed sequences	-0.59 BG063210	---
1452370_s_at	B230208H17Rik	RIKEN cDNA B230208H17 gene	-0.59 BG449608	AAH58585 /// Q8BFS4 /// Q8CGJ9
1425784_a_at	Olfm1	olfactomedin 1	-0.59 D78264	O88998 /// Q8R357
1456040_at	Sf3b2	splicing factor 3b, subunit 2	-0.59 BB473131	Q80W39 /// Q8BL33 /// Q9CS24
1432848_at	4930466F19Rik	RIKEN cDNA 4930466F19 gene	-0.59 AV044111	Q9D5C1
1443707_at	2900046B09Rik	RIKEN cDNA 2900046B09 gene	-0.59 BB16172	---
1425081_at	Zfp286	zinc finger protein 286	-0.58 BE651907	Q8C0E6 /// Q8R0E0
1437957_at	7030407O06Rik	RIKEN cDNA 7030407O06 gene	-0.58 AW536719	---
1422876_at	Capn9	calpain 9 (nCL-4)	-0.58 NM_023709	AAH58748 /// Q9D805
1428824_at	2310003C23Rik	RIKEN cDNA 2310003C23 gene	-0.58 AK009106	Q9D7M1
1437300_at	2210408E11Rik	RIKEN cDNA 2210408E11 gene	-0.58 BG067616	---
1416339_a_at	PrkcsH	protein kinase C substrate 80K-H	-0.58 NM_008925	O08795 /// Q921X2
1460334_at	Dnbl	drebrin-like	-0.58 AV328035	Q62418 /// Q80WP1 /// Q8BH56
1434417_at	Solh	small optic lobes homolog (Drosophila)	-0.58 BB022975	AAH58094 /// Q8R200
1418268_at	Htr3a	5-hydroxytryptamine (serotonin) receptor-3A	-0.38 NM_013561	P23979 /// Q8K1F4
1422256_at	Sstr2	somatostatin receptor 2	-0.34 NM_009217	P30875
1438921_at	---	Mus musculus transcribed sequence with moderate similarity to protein prf:2211433A (H.sapiens)	0.00 BM197239	---
1434423_at	Gulp1	2211433A FRP1 protein [Homo sapiens]	0.01 BB138485	Q8K2A1 /// Q9CRV4 /// Q9CYD2
1418849_x_at	Aqp7	GULP, engulfment adaptor PTB domain containing 1 aquaporin 7	0.10 AB056091	BAB68537 /// O54794
1459606_at	---	Mus musculus transcribed sequences	0.17 BB752953	---
1417704_a_at	Athgap6	Rho GTPase activating protein 6	0.17 NM_009707	O54834 /// Q8BG83 /// Q8C842 /// Q8C8B2
1459856_at	---	Mus musculus transcribed sequences	0.19 BB444619	---
1419171_at	2310044D20Rik	RIKEN cDNA 2310044D20 gene	0.20 BB667295	Q8CC46 /// Q8VDR1 /// Q9D238 /// Q9D3L0 /// Q9D6W5 /// Q9D6Z3
1453807_at	6330563C09Rik	RIKEN cDNA 6330563C09 gene	0.21 B1730484	---
1417753_at	Pkd2	polycystic kidney disease 2	0.32 AF014010	AAH62969 /// O35245 /// Q7TS17 /// Q8BPR6
1447173_at	---	---	0.34 BB704012	---
1421882_a_at	Elavl2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Htu antigen B)	0.34 BB105998	AAH58393 /// AAK74154 /// Q60899 /// Q80UJ0 /// Q80Y51 /// Q91X18 /// Q91X19
1437250_at	---	Mus musculus transcribed sequence with weak similarity to protein ref:NP_060470.1 (H.sapiens)	0.34 AV298358	AAH68125
1418318_at	Rnf128	hypothetical protein FLJ10716 [Homo sapiens]	0.36 AK004847	Q9CVG1 /// Q9D304 /// Q9DBN3 /// Q9J1UF8
1449007_at	Btg3	ring finger protein 128	0.37 NM_009770	P50615
1458504_at	6330583J20Rik	B-cell translocation gene 3	0.38 BM248637	AAH63066 /// Q8CCU4
1442019_at	B230343A10Rik	RIKEN cDNA B230343A10 gene	0.38 BB627097	---

1419207_at	Zfp37	zinc finger protein 37	0.38 NM_009554	AAH63757 /// P17141 /// Q8CCM5 /// Q8R1B1
1460707_at	Pip4a2	protein tyrosine phosphatase 4a2	0.40 AV049645	O70274
1454826_at	---	Mus musculus cDNA clone IMAGE:6485438, partial cds	0.41 BM195115	Q8BXA4 /// Q8BZQ5
1436841_at	B230380D07Rik	RIKEN cDNA B230380D07 gene	0.42 AV229336	AAH58683 /// Q7TML6 /// Q8BK25 /// Q8BL22 /// Q8BL47 /// Q8BZC1
1460017_at	9930105H17Rik	RIKEN cDNA 9930105H17 gene	0.42 BB371300	---
1416612_at	Cyp1b1	cytochrome P450, family 1, subfamily b, polypeptide 1	0.43 B1251808	Q64429 /// Q80V82 /// Q8BRY0 /// Q8C685 /// Q9CUA1
1438133_a_at	Cyr61	cysteine rich protein 61	0.43 BM202770	AAH66019 /// P18406
1428907_at	2600011C06Rik	RIKEN cDNA 2600011C06 gene	0.43 BG228787	AAH66150 /// AAH67400 /// Q8BU35 /// Q8BVT8 /// Q9CT49
1427934_at	2610208E05Rik	RIKEN cDNA 2610208E05 gene	0.43 AA250510	Q8R033
1436330_x_at	---	hypothetical protein 6720451E15	0.44 BG244780	Q8BIQ6
1448141_at	1110014J01Rik	RIKEN cDNA 1110014J01 gene	0.45 NM_029101	---
1417221_at	Ppm1a	protein phosphatase 1A, magnesium dependent, alpha isoform	0.45 BC008595	P49443 /// Q8R477 /// Q9EQE2 /// Q9EQE3
1434034_at	Cerk	ceramide kinase	0.46 B1905090	BAC98226 /// Q8K4Q7
1450064_at	Fmn2	formin 2	0.46 BM228488	Q9JL04
1433991_x_at	Dbi	diazepam binding inhibitor	0.46 AV007315	BAB25730 /// BAB25755 /// BAB32175 /// BAC25658 /// P31786
1454741_s_at	---	Mus musculus cDNA clone MGC:67308	0.46 BG064061	AAH56470 /// Q8C237 /// Q8C4K1
1428512_at	2700087I09Rik	IMAGE:5706838, complete cds	0.47 AK012577	AAH59871
1443052_at	C330019L16	RIKEN cDNA 2700087I09 gene	0.47 BB400711	---
1428468_at	3110043O21Rik	hypothetical protein C330019L16	0.48 AK014175	Q8K3B2
1422653_at	C030018L16Rik	RIKEN cDNA 3110043O21 gene	0.48 NM_023873	Q9CRL9 /// Q9CTS4 /// Q9JIC1
1448743_at	Ssx2lp	RIKEN cDNA C030018L16 gene	0.48 NM_138744	Q8BG59 /// Q8CTX0 /// Q8K2F7 /// Q8VC66
1416422_a_at	Ssb	synovial sarcoma, X breakpoint 2 interacting protein	0.48 BG796845	BAC28092 /// BAC40478 /// P32067 /// Q8BTU4 /// Q8BTY4 /// Q9CYB9
1434307_at	9630015D15Rik	Sjogren syndrome antigen B	0.49 AV489972	AAND5738 /// Q8CBJ4 /// Q8K2Q6
1436794_at	C330026N02Rik	RIKEN cDNA 9630015D15 gene	0.49 BG069844	Q8BWZ1
1415964_at	Scd1	RIKEN cDNA C330026N02 gene	0.49 NM_009127	AAM34744 /// AAM34747 /// P13516
1426270_at	Smc5l1	stearyl-Coenzyme A desaturase 1	0.49 AV257384	Q80TW7 /// Q8BKX5 /// Q8CG46 /// Q8CHX5 /// Q922K3
1416195_at	Pps	SMC5 structural maintenance of chromosomes 5-like 1 (yeast)	0.49 NM_008916	AAH66112 /// Q8C5L6
1428233_at	Cpsf6	putative phosphatase	0.50 BB425379	AAH68133
1425486_s_at	Mtmr6	cleavage and polyadenylation specific factor 6	0.50 BC020019	Q8VE11
1425484_at	Tox	myotubularin related protein 6	0.51 BB547854	Q8BKH9 /// Q8BYQ5 /// Q8R4H0
1435235_at	Txn1	thymocyte selection-associated HMG box gene	0.51 B1662855	AAH61123 /// O70379 /// Q8CDN6
1428075_at	Ndufb4	thioredoxin-like	0.51 BG968046	Q9CQC7 /// Q9DBH2
1416179_a_at	Rdx	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4	0.52 NM_009041	AAR87801 /// P26043 /// Q7TS66 /// Q8C2N4
1452675_at	Rbm22	radixin	0.52 BB758922	Q8BHS3 /// Q9CXA0
1448558_a_at	Pla2g4a	RNA binding motif protein 22	0.53 NM_008869	P47713 /// Q9DBX5
1416705_at	Rpe	phospholipase A2, group IVA (cytosolic, calcium-dependent)	0.53 BG916066	Q62505 /// Q8VEE0 /// Q91VZ4
1435123_at	mKIAA0953	ribulose-5-phosphate-3-epimerase	0.54 BB795377	BAC98057
1448269_a_at	Khlh13	mKIAA0953 protein	0.54 NM_026167	Q80TF4 /// Q8BKJ6 /// Q8BLH8 /// Q9CSA7
1448358_s_at	Snrp9	kelch-like 13 (Drosophila)	0.55 NM_026506	AAH51470 /// Q15357
1427376_a_at	Map4k5	small nuclear ribonucleoprotein polypeptide G	0.55 BC002309	AAH57930 /// Q8BPM2 /// Q8BRE4
1433446_at	Hmgcs1	mitogen-activated protein kinase kinase kinase kinase 5	0.55 BB705380	Q8C5F4 /// Q8JZK9 /// Q8K0I5
1452061_s_at	Spr	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	0.55 AK006314	AAQ88431 /// Q62262 /// Q8BFT4 /// Q8C5B7 /// Q91WM1 /// Q9CVM0
		spermatid perinuclear RNA binding protein		

1460432_a_at Eif3s6	eukaryotic translation initiation factor 3, subunit 6	0.56 AK002576	AAC53346 /// P60229 /// Q8BNE6 /// Q9CT23
1425828_a_at Gtf2i	general transcription factor II i	0.57 AF043220	Q9ESZ8
1448195_at Taf5l	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor	0.57 NM_133966	Q91WQ5
1415973_at Marcks	myristoylated alanine rich protein kinase C substrate	0.57 AW546141	P26845
1448236_at Rdx	radixin	0.58 NM_009041	AAH87801 /// P26043 /// Q7TSG6 /// Q8C2N4
1426083_a_at Btg1	B-cell translocation gene 1, anti-proliferative	0.58 L16846	P31607
1436139_at ---	Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330445K22	0.58 AV328974	---
1453180_at 6530404N21Rik	product:unknown EST, full insert sequence	0.58 AK018322	Q80W75
1434842_s_at Upf3b	UPF3 regulator of nonsense transcripts homolog B (yeast)	0.58 AV294165	Q80UJ8 /// Q9CS15
1427129_a_at Hnrpr	heterogeneous nuclear ribonucleoprotein R	0.58 AW701147	Q8BL32 /// Q8VHM5 /// Q99KG1 /// Q9CT37
1433825_at Ntrk3	neurotrophic tyrosine kinase, receptor, type 3	0.58 BM245880	AAP94280 /// Q9Z2P9 /// Q9Z2Q0
1454632_at 6330442E10Rik	RIKEN cDNA 6330442E10 gene	0.58 AV328515	AAH60607 /// Q8BFQ2 /// Q8CCD3
1433648_at Spag9	sperm associated antigen 9	0.58 BM938614	AAH60100 /// Q8CGF7 /// Q8CHT8 /// Q9R0R5
1421033_a_at Tceg1	transcription elongation regulator 1 (CA150)	0.58 AV046403	Q8C490 /// Q8BQ2 /// Q8CD81 /// Q91VW9 /// Q9CSC5 /// Q9ESY5
1415689_s_at Zfp307	zinc finger protein 307	0.59 BC007473	Q8C252 /// Q8BQ2 /// Q8CD81 /// Q91VW9 /// Q9CSC5 /// Q9CSE2
1429207_at Bcl7a	B-cell CLL/lymphoma 7A	0.59 AK014498	Q8C361 /// Q8C8M8 /// Q8VD15 /// Q9CXE2
1429519_at Fggt	fucose-1-phosphate guanylyltransferase	0.59 BB303906	CAC81971 /// Q8C1A2
1449557_at 1600012F09Rik	RIKEN cDNA 1600012F09 gene	0.59 NM_025904	Q8BPG2 /// Q9CS38 /// Q9D033 /// Q9D053 /// Q9D064 /// Q9DAY6
1418380_at Tef1	telomeric repeat binding factor 1	0.59 NM_009352	P70371 /// Q7TSK8
1417030_at 2310028N02Rik	RIKEN cDNA 2310028N02 gene	0.59 NM_025864	Q9CZV9 /// Q9D771
1451146_at Zfp386	zinc finger protein 386 (Krueppel-like)	0.59 BC004747	Q99KB9 /// Q9QZP7
1448104_at Aldh6a1	aldehyde dehydrogenase family 6, subfamily A1	0.59 NM_134042	Q8CIB4 /// Q8K0L1 /// Q9EQ20
1429897_a_at D16Etd472e	DNA segment, Chr 16, ERATO Dcl 472, expressed	0.59 AK009258	Q8VE27 /// Q9D7G4
1448600_s_at Vav3	vav 3 oncogene	0.59 BC027242	Q7TS85 /// Q8BRV2 /// Q8CCF5 /// Q8R076 /// Q9JLS6 /// Q9R0C8
1425934_a_at B4gal4	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4	0.59 AF158746	Q8BR54 /// Q9J104 /// Q9QY12
1425498_at Prip4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	0.59 U48737	AAH59713 /// Q61136 /// Q8BND8 /// Q8C5G1 /// Q99L76
1453221_at Gopc	golgi associated PDZ and coiled-coil motif containing	0.59 AA437924	Q8BH60 /// Q8BSV4 /// Q8R025 /// Q920R1 /// Q9ET11
1427108_at 9530068E07Rik	RIKEN cDNA 9530068E07 gene	0.59 BM233467	Q8K201 /// Q922L7 /// Q9CVN1
1417981_at Insig2	insulin induced gene 2	0.59 AV257512	Q8BWP1 /// Q91WG1
1452989_at 2900009J20Rik	RIKEN cDNA 2900009J20 gene	0.59 BB315961	---
1423572_at Bcl2l2	Bcl2-like 2	0.59 BB485989	BAB23468 /// P70345 /// Q8CFR2 /// Q8CGL4 /// Q9CYW5 /// Q9D1Y5
1445194_at Cnk2-pending	connector enhancer of KSR2	0.59 BB355006	AAH60716 /// Q80TP2 /// Q80YA9
1437030_at Plcd4	phospholipase C, delta 4	0.59 AV257260	---
1420822_s_at Sppp1	sphingosine-1-phosphate phosphatase 1	0.59 NM_030750	Q9J199
1433457_s_at Grs1	G-rich RNA sequence binding factor 1	0.59 AV090328	Q8BR05 /// Q8BRG7 /// Q8C298 /// Q8C5Q4
1438071_at Pns1	postmeiotic segregation increased 1 (S. cerevisiae)	0.59 BM200777	Q8BL19 /// Q8K119
1455954_x_at Gpaal	GPI anchor attachment protein 1	0.59 BB332286	Q9WTK3
1430526_a_at Smarca2	SWI/SNF related, matrix associated, actin dependent	0.59 AK011935	Q35846 /// Q7TND4 /// Q8R1W7 /// Q99KH6 /// Q9CTU8 /// Q9D007
1440818_s_at Sf3b1	regulator of chromatin, subfamily a, member 2	0.59 BB161546	Q8C2Y9 /// Q99NB9
1458433_at Rbtlb1	regulator of chromosome condensation (RCC1) and	0.59 BB000798	AAH67005 /// Q8BTZ6 /// Q8BZV0
1423301_at Copb1	BTB (POZ) domain containing protein 1	0.59 BF147382	AAH30837 /// Q9JIF7
	coatomer protein complex, subunit beta 1		

1428409_at	Mak3p	Mak3p homolog (S. cerevisiae)	0.60 AK013287	AAH57117 /// Q7TML2 /// Q80VE3 /// Q9D0Q8
1434228_at	---	Mus musculus, Similar to pyruvate dehydrogenase phosphatase, clone IMAGE:6492665, mRNA	---	---
1441879_x_at	Mkm1	makorin, ring finger protein, 1	0.60 AV255921	Q8C5B6 /// Q8C5V4 /// Q99LD7 /// Q9DB86 /// Q9QXP6
1421812_at	Tapbp	TAP binding protein	0.60 AF043943	Q8C6N4 /// Q91W5 /// Q9D679 /// Q9R233
1437980_at	9130230N09Rik	RIKEN cDNA 9130230N09 gene	0.60 BB814947	---
1434580_at	Enpp4	ectonucleotide pyrophosphatase/phosphodiesterase 4	0.60 AV280361	Q8BTJ4 /// Q8K1L3
1458261_at	---	Mus musculus transcribed sequence with weak similarity to protein ref:NP_081764.1 (M.musculus)	---	---
1452661_at	Trfr	transferrin receptor	0.60 BB701997	---
1438349_at	LOC381067	Similar to zinc finger protein 52	0.60 AK011596	BAC40674 /// Q62351 /// Q8C872 /// Q8JZS3
1415686_at	Rab14	RAB14, member RAS oncogene family	0.60 BG069331	Q80ZY7
1434062_at	8430421H08Rik	RIKEN cDNA 8430421H08 gene	0.60 AV339290	AAH56648 /// Q91V41
1455342_at	6330414G02Rik	RIKEN cDNA 6330414G02 gene	0.60 AV226672	---
1421530_a_at	Gm8	glutamate receptor, metabotropic 8	0.60 BM232966	---
1426939_at	2310007F12Rik	RIKEN cDNA 2310007F12 gene	0.60 NM_008174	P47743
1436051_at	9630007J19Rik	RIKEN cDNA 9630007J19 gene	0.60 BG070464	Q8C8T8 /// Q8R3M9
1455261_at	Luc7l	Luc7 homolog (S. cerevisiae)-like	0.60 BQ174518	---
1434839_s_at	8030499H02Rik	RIKEN cDNA 8030499H02 gene	0.60 BB400102	Q9CYI4
1428235_at	Sdhb	succinate dehydrogenase complex, subunit D, integral membrane protein	0.60 BG071620	Q8BHJ5 /// Q8C4A2
1433891_at	Gpr48	G protein-coupled receptor 48	0.60 AK013962	Q9CXV1 /// Q9D6J9
1417999_at	Itm2b	integral membrane protein 2B	0.60 B1017632	AAH56637 /// Q80T31 /// Q8BXS9 /// Q8BZR7
1424366_at	Tmem15	transmembrane protein 15	BAB22220 /// BAB22877 /// BAB23828 /// BAC36212 /// BAC36822 /// O89051 /// Q9CWW90 ///	---
1418591_at	DnaJ4	DnaJ (Hsp40) homolog, subfamily A, member 4	0.60 NM_008410	Q9D103 /// Q9JME4
1451688_at	C530043G21Rik	RIKEN cDNA C530043G21 gene	0.60 BC026973	Q8R2Y3
1460359_at	Armcx3	armadillo repeat containing, X-linked 3	0.60 NM_021422	BAC32747 /// BAC36232 /// Q8R1X2 /// Q9JMC3
1434383_at	Pja2	praja 2, RING-H2 motif containing	0.60 BG060641	BAC97964 /// Q8VCS3
1455257_at	Igfb3	integrin beta 3	0.60 AK004598	Q8BHS6 /// Q91VP8 /// Q9DC32
1415741_at	Tparl	TPA regulated locus	0.60 BM114949	Q80U04 /// Q810E3 /// Q91W46 /// Q99KC0
1454723_at	1110033M05Rik	RIKEN cDNA 1110033M05 gene	0.60 AV352983	---
1420441_at	Cenpc	centromere autubantigen C	0.61 NM_011626	P52875
1428970_at	Mak3p	Mak3p homolog (S. cerevisiae)	0.61 AV141095	AAH57380 /// Q8BVS2 /// Q8C770 /// Q9DAC9 /// Q9Z106
1440423_at	D430004I08Rik	RIKEN cDNA D430004I08 gene	0.61 NM_007683	P49452 /// Q9CRZ7
1440926_at	---	Mus musculus transcribed sequences	0.61 AV113878	AAH57117 /// Q7TML2 /// Q80VE3 /// Q9D0Q8
1437168_at	Srp-pending	serine-arginine repressor protein	0.61 AV363211	Q8C3U9 /// Q8C5F2
1448123_s_at	Tgfb1	transforming growth factor, beta induced	0.61 BB555042	---
1451096_at	Ndufs2	NADH dehydrogenase (ubiquinone) Fe-S protein 2	0.61 BB335578	Q8C8K3
1423350_at	Socs5	suppressor of cytokine signaling 5	0.61 NM_009369	P82198
1423599_a_at	Pdcl	prolactin-like	0.61 BC016097	Q91WD5 /// Q99L23
1441139_at	B330003H21	hypothetical protein B330003H21	0.61 AA510713	O54928 /// Q7TSK1
1427475_a_at	Nrap	nebulin-related anchoring protein	0.61 AK004704	BAC26056 /// BAC26133 /// Q923E8
1434052_at	Al593442	expressed sequence Al593442	0.61 BB321858	Q8C8M4
1431873_a_at	Tube1	epsilon-tubulin, 1	0.61 BC002020	O35884 /// Q80V40 /// Q80XB4
1436044_at	Scn7a	sodium channel, voltage-gated, type VI, alpha polypeptide	0.61 AV327193	Q8BPR8 /// Q8CC42
1425662_at	Cdadcl	cytidine and dCMP deaminase domain containing 1	0.61 AK010005	AAH62179 /// Q8BYF9 /// Q9D6T1
			0.61 BB452990	Q62467
			0.61 BC006901	Q8BMD5 /// Q8BYL2 /// Q8BYN1 /// Q8C014 /// Q922P4 /// Q99KL2 /// Q9D7F3

ATP-binding cassette, sub-family G (WHITE), member 2				
1422906_at	Abcg2	RIKEN cDNA 1110057H19 gene	0.61 NM_011920	Q7TMS5 /// Q9R004 /// Q9Z1T0
1448702_at		vesicle-associated membrane protein 4	0.61 BE287896	Q9CR20
1422895_at	Vamp4	expressed sequence AW146242	0.61 NM_016796	O70480 /// Q8BSN6 /// Q9D095
1423812_s_at	AW146242		0.61 BC024822	Q8C0B7 /// Q8R1C3
			AAH58262	/// BAC98072 /// Q8BIH9 /// Q8COE8 /// Q8K011 /// Q920B0 /// Q920B1 ///
1438169_a_at	Frm4b	FERM domain containing 4B	0.62 BB009122	Q9ESP9
1449494_at	Rab3c	RAB3C, member RAS oncogene family	0.62 AY026947	BAC37689 /// Q63482 /// Q9CXS2
1438358_x_at	Pfdn5	prefoldin 5	0.62 AV124256	BAB24185 /// BAC25814 /// Q9DAJ0 /// Q9WU28
1434485_a_at	Ugp2	UDP-glucose pyrophosphorylase 2	0.62 AW146314	AAH61208 /// Q8R0M2 /// Q8R3D2 /// Q91ZJ5
1449893_a_at	Nqo2	NAD(P)H dehydrogenase, quinone 2	0.62 NM_020282	Q9CVF5 /// Q9CVI1 /// Q9J175
1429600_at	1110019K23Rik	RIKEN cDNA 1110019K23 gene	0.62 AK003824	---
1416200_at	9230117N10Rik	RIKEN cDNA 9230117N10 gene	0.62 NM_133775	Q8BVZ5 /// Q99L46
1449227_at	Ch25h	cholesterol 25-hydroxylase	0.62 NM_009890	Q8CHQ2 /// Q9Z0F5
1453312_at	120006M05Rik	RIKEN cDNA 120006M05 gene	0.62 BB264725	Q8BK50 /// Q9DC22
1420821_at	Sgpp1	sphingosine-1-phosphate phosphatase 1	0.62 NM_030750	Q9J199
		solute carrier organic anion transporter family, member 1a5	0.62 NM_130861	Q91YY5 /// Q99K89
1449203_at	Slo1a5	retinol dehydrogenase 10 (all-trans)	0.62 BG069583	---
1460632_at	Rdh10	diazepam binding inhibitor	0.62 AV019984	BAB25730 /// BAB25755 /// BAB32175 /// BAC25658 /// P31786
1455976_x_at	Dbl	hyaluronic acid binding protein 4	0.62 NM_019986	Q9D450 /// Q9JKS5
1418927_a_at	Halp4	Mus musculus transcribed sequences	0.62 BQ175978	P16388 /// Q8CA58
1455785_at	---	Wilms' tumour 1-associated protein	0.62 AV141160	AAH46416 /// BAC36191 /// Q9ER69
1425197_at	Ptpn2	protein tyrosine phosphatase, non-receptor type 2	0.62 BG076152	Q06180 /// Q922E7
1452598_at	2810418N01Rik	RIKEN cDNA 2810418N01 gene	0.62 AK013116	BAC97891 /// Q8K1A2 /// Q9CZ15
1433565_at	2410002M20Rik	RIKEN cDNA 2410002M20 gene	0.62 BM209793	AAH59875 /// Q8BVY2
1451415_at	1810011O10Rik	RIKEN cDNA 1810011O10 gene	0.62 BC016562	Q9D915
1426899_at	4930451A13Rik	RIKEN cDNA 4930451A13 gene	0.62 AV209678	Q8K0F1 /// Q8VE48
		Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230348D21	0.62 BB314596	---
1436599_at	---	product:unknown EST, full insert sequence microtubule-associated protein 4	0.62 BB280360	P27546 /// Q60638 /// Q7TPC6 /// Q7TPD4 /// Q80YQ5 /// Q8CFP5
1437855_at	Mtap4			
		Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630066H14	0.62 BM247146	---
1438295_at	---	product:unknown EST, full insert sequence	0.62 AV021813	AAH58110 /// BAC97954 /// Q8BZC7 /// Q8C173 /// Q8VDM3 /// Q9CSL7
1457139_at	---	Mus musculus transcribed sequences	O70318 /// Q7TPN6 /// Q80UE3 /// Q80UE4 /// Q80UE5 /// Q811B2 /// Q811C0 /// Q8BSR4 ///	
1433490_s_at	Epb4.112	erythrocyte protein band 4.1-like 2	0.62 BE951907	Q8C928 /// Q8CGJ6 /// Q9EPM7 /// Q9EPM8
1459774_at	---	Mus musculus transcribed sequences	0.62 A1662002	---
1429005_at	Mfnas1	malignant fibrous histiocytoma amplified sequence 1	0.62 BB107412	Q8C4N5
		Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:C630020C21		
1455014_at	---	product:unknown EST, full insert sequence		
1419975_at	Scp2	steroid carrier protein 2, liver	0.63 BM213104	---
1434229_a_at	Polb	polymerase (DNA directed), beta	0.63 C76618	P32020
1423489_at	Mimd	monocyte to macrophage differentiation-associated	0.63 BG094331	AAH60998 /// Q8K409
1435556_at	4933407K12Rik	RIKEN cDNA 4933407K12 gene	0.63 BC021914	AAR08388 /// Q9CQY7
			0.63 AV270881	---

1425048_a_at	Hmgob1	high mobility group box 1	0.63 U00431	AAH64790 /// BAC29802 /// BAC39289 /// P07155 /// Q8BNM0 /// Q8BQ02 /// Q8C7C4
1417948_s_at	Ilf2	interleukin enhancer binding factor 2	0.63 NM_026374	Q99KS3 /// Q9CXY6
1458528_at	---	Mus musculus transcribed sequences	0.63 AW491643	---
1443665_at	---	Mus musculus transcribed sequences	0.63 BE994639	---
1450484_a_at	Tyki	thymidylate kinase family LPS-inducible member	0.63 AK004595	AAH57565 /// Q9DC34
1436300_at	C430014H23Rik	RIKEN cDNA C430014H23 gene	0.63 BB435342	---
1423952_a_at	Krt2-7	keratin complex 2, basic, gene 7	0.63 BC010337	Q9DCV7
1459961_at	Mme	membrane metallo endopeptidase	0.63 AV174022	AAH6840 /// Q61391 /// Q8BNU9 /// Q8K251
1453766_a_at	4931407K02Rik	RIKEN cDNA 4931407K02 gene	0.63 AK016516	AAH56955 /// Q9D2D8
1423025_a_at	Schp1	schwannomin interacting protein 1	0.63 NM_013928	AAH60529 /// Q9JLR0
1417365_a_at	Calm1	calmodulin 1	0.63 AU079514	AAH54805 /// BAC23462 /// BAC40168 /// P02593 /// Q9D6G4
1426204_a_at	Opr1	opioid receptor-like	0.63 AF043276	BAC30067 /// BAC37672 /// P35377 /// Q80WU7
1429036_at	Otop3	otopetrin 3	0.63 AK009293	Q810B4 /// Q9D7E9
1420478_at	Nap1l1	nucleosome assembly protein 1-like 1	0.63 BG064031	P28656 /// Q8BSH9 /// Q9CSP8
1433626_at	Plscr4	phospholipid scramblase 4	0.63 BB826296	P58196 /// Q8BH62 /// Q8BV91 /// Q8BW59 /// Q8BZC5
1452763_at	1110027G09Rik	RIKEN cDNA 1110027G09 gene	0.63 BB770774	---
1436072_at	---	---	0.64 BG070468	---
1436561_at	Suv39h2	suppressor of variegation 3-9 homolog 2 (Drosophila)	0.64 BB440055	Q8BNK2 /// Q8K085 /// Q9EQQ0
1439526_at	---	Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130022D06	---	---
1420846_at	Mrs2	product/unknown EST, full insert sequence	0.64 AV375160	---
1451724_at	Ankmy2	mitochondrial ribosomal protein S2	0.64 AV031454	Q8BQ99 /// Q924T2
1420808_at	Nco4	ankyrin repeat and MYND domain containing 2	0.64 BC024959	Q8BK14 /// Q8BYW5 /// Q8R3N4 /// Q921J1
1442138_at	4933402E03Rik	nuclear receptor coactivator 4	0.64 NM_019744	Q8BSH1 /// Q8K2F6 /// Q9CUF2 /// Q9CXF3 /// Q9VW42
1449915_at	Zfp202	RIKEN cDNA 4933402E03 gene	0.64 BE955672	---
1438156_x_at	Opl1a	zinc finger protein 202	0.64 NM_030713	Q8C879 /// Q99PG8 /// Q99PG9
1423200_at	Ncor1	cardiac fatty acid synthase 1, liver	0.64 BB119196	P97742 /// Q7TQD5 /// Q80SW3 /// Q8BP98 /// Q8C7H8
1424550_at	Zfyve27	nuclear receptor co-repressor 1	0.64 U22016	Q60974 /// Q8CHB6 /// Q8VDE8 /// Q9CUV3
1440057_at	Hsd17b7	zinc finger, FYVE domain containing 27	0.64 BB663137	Q8CFP8 /// Q8R1D3
1429476_s_at	Dnaja2	hydroxysteroid (17-beta) dehydrogenase 7	0.64 AV322070	BAC25918 /// BAC34124 /// Q88736 /// Q8C5N9 /// Q921L1
1453174_at	2310076G13Rik	DnaJ (Hsp40) homolog, subfamily A, member 2	0.64 BG063818	BAC36946 /// BAC38809 /// Q9QYJ0
1454939_at	E130113K22Rik	RIKEN cDNA 2310076G13 gene	0.64 AK010199	---
1430226_at	2900036K24Rik	RIKEN cDNA E130113K22 gene	0.64 BB268102	---
1419291_x_at	Gas5	RIKEN cDNA 2900036K24 gene	0.64 AK013623	---
1448537_at	Ttc1	growth arrest specific 5	0.64 NM_013525	Q99KJ3
1455384_x_at	D030056L22	tetratricopeptide repeat domain 1	0.64 NM_133795	Q91Z38 /// Q9CTZ9
1424616_s_at	Frag1	hypothetical protein D030056L22	0.64 BB256746	Q8BLJ5 /// Q8VCE4
1452899_at	Rlan	FGF receptor activating protein 1	0.64 BG063931	---
1460602_at	Dlc1	RNA imprinted and accumulated in nucleus	0.64 BG063931	---
1450897_at	AU014947	deleted in liver cancer 1	0.64 AK017440	Q9R0Z9
1435695_a_at	A030007L17Rik	expressed sequence AU014947	0.64 AA673177	Q9D7X8
1428905_at	Raga	RIKEN cDNA A030007L17 gene	0.64 AI118026	Q80X95 /// Q8C1S2 /// Q8CFU3
1460286_at	---	Ras-related GTP binding A	0.64 NM_007868	BAC40453 /// Q8C2L2 /// Q8C406 /// Q8C848 /// Q9R1T4
1417307_at	Dmd	sepin 6	0.64 AI585679	---
1436740_at	2610005L07Rik	dystrophin, muscular dystrophy	0.65 BB390675	BAC98009 /// Q7TTN66 /// Q8K310
1438368_a_at	Matr3	RIKEN cDNA 2610005L07 gene	0.65 BB193360	---
1441693_at	1100001H14Rik	matrin 3	0.65 AU067804	Q8R2U2
1455781_at	BC027231	RIKEN cDNA 1100001H14 gene	0.65 BB024498	AAH59229 /// Q91VG0 /// Q9D3P5
1456582_x_at	5230400G24Rik	cDNA sequence BC027231	---	---
1456582_x_at	5230400G24Rik	RIKEN cDNA 5230400G24 gene	---	---

1446594_at	---	Mus musculus transcribed sequence with weak similarity to protein p1r-S60335 (H.sapiens) S60335	0.65 BB205215	---
1415908_at	Tspyl	TGF-beta receptor interacting protein 1 - human	0.65 AF042180	O88552
1416669_s_at	Naca	nascent polypeptide-associated complex alpha polypeptide	0.65 NM_013608	Q60817
1437455_a_at	Btg1	B-cell translocation gene 1, anti-proliferative	0.65 AW322026	P31607
1416651_at	Spta6	spermatogenesis associated 6	0.65 AK005819	Q8BW97 /// Q99MU6 /// Q9D9J1 /// Q9DAI3
1429358_at	4921533L14Rik	RIKEN cDNA 4921533L14 gene	0.65 AK019549	Q8BX58 /// Q8BZL9 /// Q8K2K2 /// Q9D2J6
1435047_at	---	Mus musculus transcribed sequences	0.65 A1668801	---
1456795_at	---	Mus musculus 13 days embryo heart cDNA, RIKEN full-length enriched library, clone:D330027G24	---	---
1434609_at	B930007L02Rik	product:unclassified, full insert sequence	0.65 BB449568	---
1426328_a_at	Scn3b	RIKEN cDNA B930007L02 gene	0.65 BQ174157	---
1457034_at	Rap140-pending	sodium channel, voltage-gated, type III, beta	0.65 AY049036	Q8BHK2
1447818_x_at	1810036J22Rik	retinoblastoma-associated protein 140	0.65 BM209908	Q9CUD3
1434712_at	A1452372	RIKEN cDNA 1810036J22 gene	0.65 AV271831	Q9D8T3
1442281_at	---	expressed sequence A1452372	0.65 W34859	Q8BGV8 /// Q8C4Y9
1423157_at	Gnpat1	Mus musculus transcribed sequences	0.65 BG069783	---
1450986_at	Crot	glucosamine-phosphate N-acetyltransferase 1	0.65 AK008566	Q9JK38
1450983_at	Akap8	carnitine O-octanoyltransferase	0.65 BB283187	Q92114 /// Q9DC50
1438407_at	9330132E09Rik	A kinase (PRKA) anchor protein 8	0.65 BG069776	Q8BP29 /// Q9DBR0 /// Q9R0L8
1428830_at	C030026E19Rik	RIKEN cDNA 9330132E09 gene	0.65 AV336691	Q8BZP3
1435389_at	---	RIKEN cDNA C030026E19 gene	0.65 AK021102	---
1434343_at	5730403M16Rik	Mus musculus transcribed sequences	0.65 BM899236	---
1434931_at	Neo1	RIKEN cDNA 5730403M16 gene	0.66 AV173406	Q7TNU5 /// Q8BIA9
1434403_at	Spred2	neogenin	0.66 BB667778	P97798 /// Q7TQ35
1454149_a_at	Ccnl2	sprouty protein with EVH-1 domain 2, related sequence	0.66 AV229054	AAH66013 /// Q8K2N1 /// Q924S7
1423678_at	BC017643	cyclin L2	0.66 AK008585	Q60995 /// Q8BLP2 /// Q8CIU8 /// Q99L73 /// Q9CVZ6 /// Q9D814 /// Q9JJA7 /// Q9QXH5
1433452_at	B630019K06Rik	cDNA sequence BC017643	0.66 BC017643	Q8VD13
1431337_a_at	1810055E12Rik	RIKEN cDNA B630019K06 gene	0.66 BB179847	Q7TNS5 /// Q8C8L2
1428682_at	4631426G04Rik	RIKEN cDNA 1810055E12 gene	0.66 AK004643	Q91WS5 /// Q9D8N2
1438106_at	Pcdhb22	RIKEN cDNA 4631426G04 gene	0.66 AK019473	Q8BYK8
1419737_a_at	Ldh1	protocadherin beta 22	0.66 AV336932	Q8C8Z3 /// Q91XZ8 /// Q925L0
1455048_at	Igsf2	lactate dehydrogenase 1, A chain	0.66 NM_010699	AAH66858 /// BAC41000 /// P06151 /// Q99K20
1416659_at	Eif3s10	immunoglobulin superfamily, member 2	0.66 BB484576	BAC32470 /// BAC35000 /// BAC97961 /// Q7TPV3
1428921_at	2810021B07Rik	eukaryotic translation initiation factor 3, subunit 10 (theta)	0.66 AW701127	P23116
1452209_at	Pkp4	RIKEN cDNA 2810021B07 gene	0.66 AK021189	Q9CZC6 /// Q9D011
1420798_s_at	Pcdha1	plakophilin 4	0.66 AV286396	Q8BK47 /// Q8BVH1 /// Q9CRE3
1437075_at	Fmrd3	protocadherin alpha 1	0.66 NM_054072	---
1459850_x_at	Glib	FERM domain containing 3	0.66 BB099015	Q8BHD4 /// Q8BV94 /// Q8C045 /// Q9D7L5 /// Q9D7M6
1424310_at	Mocs2	glycine receptor, beta subunit	0.66 BB345174	BAC38831 /// P48168
1417275_at	Mal	molybdenum cofactor synthesis 2	0.66 A1447812	Q8C5E5 /// Q8R1M7 /// Q9Z223 /// Q9Z224
1441165_s_at	C1str2	myelin and lymphocyte protein, T-cell differentiation protein	0.66 NM_010762	BAB23430 /// O09198 /// Q9D2R2
		calysinterin 2	0.66 A1448973	AAH63058 /// Q9ER65

1439899_at	Galnt13	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 13	0.66 BE995677	Q8BLE4 /// Q8BYT3 /// Q8CF93
1448628_at	Scg3	secretogranin III	0.66 NM_009130	P47867 /// Q8R1D7
1425580_a_at	Plk3c3	phosphoinositide-3-kinase, class 3	0.66 BC024675	AAH57678 /// Q8R3S8
1434486_x_at	Ugp2	UDP-glucose pyrophosphorylase 2	0.66 AW146314	AAH61208 /// Q8R0M2 /// Q8R3D2 /// Q91ZJ5
1437539_at	C130083N04Rik	RIKEN cDNA C130083N04 gene	0.66 BM236715	Q8BUX6
1427050_at	5730420B22Rik	RIKEN cDNA 5730420B22 gene	0.66 BC027108	Q7TN22 /// Q8BL40 /// Q8R2W8 /// Q9CS82
1450072_at	Ash1	ash1 (absent, small, or homeotic)-like (Drosophila)	0.66 EG694892	Q80VY5 /// Q8BM69 /// Q8BTX0 /// Q8BZY6
1438772_at	Zfp367	zinc finger protein 367	0.67 BB227141	Q8BH90 /// Q8BIA4 /// Q8BI53 /// Q8BI88
1450939_at	Entpd1	ectonucleoside triphosphate diphosphohydrolase 1	0.67 B1151440	BAC27039 /// P55772 /// Q8CDV7 /// Q8CEB1 /// Q921Q6
1453035_at	Lnp	limb and neural patterns	0.67 BM200788	AAH57961 /// AAH60153 /// Q7TQ95
1419031_at	Fads2	fatty acid desaturase 2	0.67 NM_019699	AAH57189 /// Q9Z0R9
1456097_a_at	Itgb3bp	integrin beta 3 binding protein (beta3-endonexin)	0.67 BB830191	Q9CQ82
1460697_s_at	2610209M04Rik	RIKEN cDNA 2610209M04 gene	0.67 BC027564	Q8K194
1433583_at	Zfp365	zinc finger protein 365	0.67 AV327248	AAQ11828 /// CAD56774 /// Q80TQ4 /// Q8BG89 /// Q8BK39 /// Q8BXM9 /// Q8BXT2
1434841_at	7330405111	hypothetical protein 7330405111	0.67 A117751	Q8BQK5
1448763_at	Atiad1	ATPase family, AAA domain containing 1	0.67 NM_026487	Q9D5T0 /// Q9D7A4 /// Q9D9C1
1436214_at	C430010P07Rik	RIKEN cDNA C430010P07 gene	0.67 AV023018	Q8BNM1 /// Q8C4R5
1431055_a_at	Snx10	sorting nexin 10	0.67 AK010399	Q8BY15 /// Q8C1E0 /// Q9CWT3
1424114_s_at	Lamb1-1	laminin B1 subunit 1	0.67 BG970109	P02469 /// Q8K271 /// Q9CRX6
1435051_at	2610034K17Rik	RIKEN cDNA 2610034K17 gene	0.67 AV375936	AAH68151 /// Q8BIZ7 /// Q8BTS1 /// Q8BZS8
1453160_at	1110067M05Rik	RIKEN cDNA 1110067M05 gene	0.67 BB244704	---
1419655_at	Tie3	transducin-like enhancer of split 3, homolog of Drosophila E(spl)	0.67 NM_009389	AAH56465 /// Q08122 /// Q80TC1
1418839_at	Glmn	glomulin, FKBP associated protein	0.67 NM_133248	Q8BZM1
1434097_at	---	Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430088G18	0.67 BM218328	---
1419081_at	Apg10l	product: hypothetical Zinc finger, C2H2 type containing protein, full insert sequence	0.67 NM_025770	Q8BPAS /// Q8R1P4 /// Q9D3J7
1418942_at	Ccdc2	autophagy 10-like (S. cerevisiae)	0.67 NM_026319	Q80Z13 /// Q8BKE9 /// Q8CGJ7 /// Q9CSY1 /// Q9CUS0 /// Q9D9T5
1441063_at	---	coiled-coil domain containing 2	---	---
1427450_x_at	Myo1b	Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230383O11	0.67 BB229155	Q8CJF9
1434558_at	1810073M12Rik	product: unknown EST, full insert sequence	0.67 BI080370	P46735 /// Q7TQD7 /// Q80VD8 /// Q91Z16
1418434_at	Mkrn1	myosin IB	0.67 BG075633	Q80TP4 /// Q8C8E3 /// Q8CEH9 /// Q8CGF6
1420608_at	Rbm18	RIKEN cDNA 1810073M12 gene	0.68 BQ176661	Q8C5B6 /// Q8C5V4 /// Q99LD7 /// Q9DB86 /// Q9QXP6
1457954_at	---	makorin, ring finger protein, 1	0.68 AV116216	Q8CBD4 /// Q9CR83
1457161_at	9530029O12Rik	RNA binding motif protein 18	0.68 BE980601	Q8C986 /// Q8K244
1455970_at	---	Mus musculus transcribed sequences	0.68 BB111383	---
1457118_at	6230417E10Rik	RIKEN cDNA 9530029O12 gene	0.68 BE370618	---
1435171_at	---	Mus musculus transcribed sequences	0.68 AV353605	AAR19362 /// Q8CB26
1431772_a_at	Sh3d1B	RIKEN cDNA 6230417E10 gene	0.68 BB667085	Q9CRK3
1434729_at	mKIAA1166	Mus musculus transcribed sequences	0.68 AK015445	Q80TG5 /// Q8C9C3 /// Q8CD59 /// Q9CQD9 /// Q9Z0R6
1417520_at	Nfe2l3	SH3 domain protein 1B	0.68 BM120178	BAC98112
1423130_a_at	Sfrs5	mKIAA1166 protein	0.68 NM_010903	Q9D246 /// Q9D3M5 /// Q9WTM4
1418823_at	Arf6	nuclear factor, erythroid derived 2, like 3	0.68 AW1212917	Q9D8S5
1418397_at	Zfp275	splicing factor, arginine/serine-rich 5 (SRp40, HRS)	0.68 BI248938	P26438
		ADP-ribosylation factor 6	0.68 BC019962	Q8VE24 /// Q9D319
		Zinc finger protein 275		

1425350_a_at	Myel2	myelin basic protein expression factor 2, repressor	0.68 U13262	AAH60946 /// BAC98146 /// Q60690 /// Q8BS80 /// Q8C854 /// Q8QZZ1 /// Q9JLR3
1428779_at	8430415N23Rik	RIKEN cDNA 8430415N23 gene	0.68 BB526541	---
1418545_at	Wasf1	WASP family 1	0.68 NM_031877	Q8R5H6 /// Q91W51 /// Q9ERQ9
1426723_at	8430408H12Rik	RIKEN cDNA 8430408H12 gene	0.68 BE570732	AAH62967 /// Q80TD4 /// Q80X0 /// Q8BH57 /// Q8BRM0 /// Q92229 /// Q9CRR1 /// Q9CSL0
1456030_at	Klf13	Kruppel-like factor 13	0.68 BE949230	Q9JUZ6
1428347_at	Cyfp2	cytoplasmic FMR1 interacting protein 2	0.68 AK005148	AAH56974 /// Q810V4 /// Q8BSW0 /// Q8CHA9 /// Q8K118 /// Q924D3 /// Q9R181
1455184_at	B230364F10	hypothetical protein B230364F10	0.68 BG071991	---
1426961_at	6820402O20Rik	RIKEN cDNA 6820402O20 gene	0.68 BB308157	AAH60121 /// Q8BLG0 /// Q8BZ14
1434843_at	C130034K06	hypothetical protein C130034K06	0.68 BG070968	AAH62107 /// Q8CA10
1418433_at	Cab39	calcium binding protein 39	0.68 AK005226	Q8K312 /// Q8VDZ8
1449152_at	Cdkn2b	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	0.68 AF059567	AAC14569 /// P55271
1458341_x_at	---	Mus musculus transcribed sequences	0.68 BB397841	---
1460712_s_at	Ap1g1	adaptor protein complex AP-1, gamma 1 subunit	0.68 C86561	P22892 /// Q8BSZ7 /// Q8CBB7 /// Q8CC03
1448525_a_at	Brip3l	BCL2/adenovirus E1B 19kDa-interacting protein 3-like	0.69 AK018668	BAB23456 /// BAB25351 /// BAB28869 /// Q91Z78 /// Q9Z2F7
1429146_at	6620401M08Rik	RIKEN cDNA 6620401M08 gene	0.69 BF011349	---
1436098_at	Bche	butyrylcholinesterase	0.69 BB667452	---
1433791_at	Rab9b	RAB9B, member RAS oncogene family budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae)	0.69 BB084626	Q8BHH2
1448473_at	Bub3	Mus musculus transcribed sequences	0.69 BE986800	AAH25089 /// BAC40409 /// Q8BH42 /// Q9CS16 /// Q9WVA3
1444077_at	---	kinesin family member 13A	0.69 BE983694	---
1455746_at	Klf13a	RIKEN cDNA 5730414N17 gene	0.69 BF166390	Q8CA55 /// Q8CDQ6 /// Q9EQW7
1429899_at	5730414N17Rik	RIKEN cDNA 5730414N17 gene	0.69 BB039237	---
1458940_at	9430076K19Rik	RIKEN cDNA 9430076K19 gene	0.69 BF147707	---
1454607_s_at	Psat1	phosphoserine aminotransferase 1 Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4931440N07 product/hypothetical Type-1 copper (blue) domain/Leucine-rich region containing protein, full insert sequence	0.69 AV216491	BAC33959 /// Q8BTJ1 /// Q99JU9 /// Q99K85
1439590_at	---	polyribonucleotide nucleotidyltransferase 1	0.69 AV273072	AAH57035 /// Q8C0T0
1452677_at	Prp11	RIKEN cDNA 2310042M24 gene	0.69 BB777815	Q810U7 /// Q812B3 /// Q8K1R3 /// Q8R2U3
1452130_at	2310042M24Rik	FERM domain containing 4A	0.69 B1790903	Q8BW13 /// Q9D710
1434285_at	Fmrd4a	Unc-51 like kinase 2 (C. elegans)	0.69 BB701578	---
1417847_at	Ulk2	protein phosphatase 1A, magnesium dependent, alpha isoform	0.69 NM_013881	Q80TV7 /// Q9QY01 /// Q9WTP4
1425537_at	Ppm1a	channel-interacting PDZ domain protein	0.69 AF259672	P49443 /// Q8R4T7 /// Q9EQE2 /// Q9EQE3
1418983_at	Cipp	RIKEN cDNA E130013N09 gene	0.69 AV287690	AAH57124 /// AAH62194 /// Q70471 /// Q80YR8 /// Q8BPB9 /// Q8VE63
1434292_at	E130013N09Rik	cDNA sequence BC002236	0.69 B1731047	---
1415788_at	BC002236	RIKEN cDNA 9030023J02 gene	0.69 BF158817	AAH56652 /// Q8BGR9 /// Q99LT3
1455337_at	9030023J02Rik	arginine vasopressin receptor 1A	0.69 BQ175875	---
1418603_at	Avpr1a	RAB1, member RAS oncogene family	0.69 D49729	Q62463
1436034_at	Rab1	calpastatin	0.69 AW550283	BAC28697 /// BAC98287 /// P11476 /// Q811M4
1451413_at	Cast	heparan sulfate 2-O-sulfotransferase 1	0.69 AD026997	P51125 /// Q8BS37 /// Q8C281 /// Q8CB83 /// Q8CE04 /// Q8CE80 /// Q921U7
1450729_at	Hs2st1	ADP-ribosylation factor 2	0.69 AB346600	AAH59008 /// Q88464 /// Q8R3H7 /// Q9JLK2
1416458_at	Arf2	collectin sub-family member 12	0.69 NM_007477	BAC31426 /// BAC35273 /// BAC36882 /// P16500 /// Q8BSL7 /// Q91VR9
1419693_at	Colec12	cyclin-dependent kinase-like 2 (CDC2-related kinase)	0.69 NM_130449	AAH57936 /// Q8K4Q8 /// Q8VIF6
1449229_a_at	Cdk12	cyclin-dependent kinase-like 2 (CDC2-related kinase)	0.69 NM_016912	Q9QUK0 /// Q9QY11 /// Q9QY12

1418071_s_at	Cdyl	chromodomain protein, Y chromosome-like	0.69 AF081260	AAH62123 /// Q9WTK2	/// Q9CSL9
1437543_at	D3Etd330e	DNA segment, Chr 3, ERATO Doi 330, expressed	0.69 BB488001	Q91WJ8	
1428543_at	Ppat	phosphoribosyl pyrophosphate amidotransferase	0.69 AV305746	Q8CIH9	
1419736_a_at	Eflray	eukaryotic translation initiation factor 1A, Y-linked	0.69 NM_025437	AAH27284 /// BAC41069 /// Q60872 /// Q8BJZ2 /// Q8BMH8 /// Q8BMJ3	
1448527_at	Pcd10	programmed cell death 10	0.69 AV094856	Q8VE70 /// Q9DAR3 /// Q9WV43	
1455102_at	D330037H05Rik	RIKEN cDNA D330037H05 gene	0.70 BB213860	Q8BWM4 /// Q9D6P9	
1438306_at	3110001E11Rik	RIKEN cDNA 3110001E11 gene	0.70 AV340072	Q80ZX1 /// Q8CCR1 /// Q9CXV6	
1435701_at	---	Mus musculus 10 days neonate medulla oblongata cDNA, RIKEN full-length enriched library, clone:B830010I11 product:unclassified, full insert sequence	0.70 BM118858	---	
1448761_a_at	Copg2	coatomer protein complex, subunit gamma 2	0.70 NM_017478	---	
1435446_a_at	Chpt1	choline phosphotransferase 1	0.70 BF180212	AAR16089 /// Q8C025 /// Q8K0H2 /// Q91W91	
1427105_at	2610510J17Rik	RIKEN cDNA 2610510J17 gene	0.70 BM230253	AAH58243 /// Q8R2W7 /// Q9CZW2	
1443119_at	6330570A01Rik	RIKEN cDNA 6330570A01 gene	0.70 AV335221	---	
1423911_at	Ppp2r5a	protein phosphatase 2, regulatory subunit B (B56), alpha isoform	0.70 BC023062	AAH59026 /// Q8R1U7	
1416161_at	Rad21	RAD21 homolog (S. pombe)	0.70 AF332085	BAC97860 /// Q61550 /// Q810A8	
1427160_at	2500001H09Rik	RIKEN cDNA 2500001H09 gene	0.70 AV374246	Q80V88 /// Q8K0S1 /// Q8R2P5 /// Q99KH9	
1431328_at	Ppp1cb	protein phosphatase 1, catalytic subunit, beta isoform	0.70 AK017392	AAH46832 /// BAC40636 /// P37140 /// Q8C285 /// Q9DBY2	
1428460_at	Syn2	synapsin II	0.70 AK013810	AAH66004 /// Q8CE19 /// Q9QWV7	
1425262_at	Cabpg	CC-AAT/enhancer binding protein (C/EBP), gamma	0.70 AB012273	BAA25311 /// BAC34355 /// P53568	
1428317_at	4833415N24Rik	RIKEN cDNA 4833415N24 gene	0.70 A1510221	AAH61464 /// Q80VT2 /// Q80YD9 /// Q8BSM8 /// Q9D617 /// Q9D6K8	
1435603_at	SST3	secreted protein SST3	0.70 BB487754	CAE48492 /// Q810H2 /// Q8BMD9	
1444097_at	BC019776	cDNA sequence BC019776	0.70 BB544962	Q8R1J2 /// Q8VE43	
1443282_at	2410002M20Rik	RIKEN cDNA 2410002M20 gene	0.71 BB556993	AAH59875 /// Q8BYY2	
1456665_at	B130023L16Rik	RIKEN cDNA B130023L16 gene	0.71 BB476944	---	
1459332_at	---	Mus musculus transcribed sequence with moderate similarity to protein p1r-S12207 (M.musculus) S12207	0.71 BM197626	---	
1460163_at	---	hypothetical protein (B2 element) - mouse	0.71 BB039211	---	
1417166_at	Psp2	Mus musculus transcribed sequences	0.71 NM_133948	Q80WQ7 /// Q99JF7 /// Q99JF8 /// Q99LR4 /// Q9CT03	
1428237_at	2700059D21Rik	PC4 and SFRS1 interacting protein 2	0.71 B1689227	---	
1424357_at	BC018222	RIKEN cDNA 2700059D21 gene	0.71 BC026654	Q8VCZ2	
1417962_s_at	Ghr	cDNA sequence BC018222	0.71 NM_010284	P16882 /// Q8BPQ3	
1428203_at	C030002O17Rik	growth hormone receptor	0.71 A1844535	Q8BT41	
1445173_at	mKIAA1377	RIKEN cDNA C030002O17 gene	0.71 BF472675	BAC98151	
1451493_at	Ndfip1	Nedd4 family interacting protein 1	0.71 BC026372	Q8R0W6 /// Q9EQH8	
1454754_a_at	Aamp	angio-associated migratory protein	0.71 BF468097	Q8K2C1	
1433602_at	Gabra5	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 5	0.71 BQ175863	AAH62112 /// Q88964 /// Q8BHJ7	
1423295_at	Tn9s12	transmembrane 9 superfamily member 2	0.71 BB747462	BAC33215 /// BAC40645 /// P58021 /// Q8C6H4 /// Q8C7F9	
1423251_at	Luc712	LUC7-like 2 (S. cerevisiae)	0.71 BG075618	AAH56383 /// AAH56970 /// Q7TNC4	
1435946_at	D5Etd135e	DNA segment, Chr 5, ERATO Doi 135, expressed	0.72 BB401993	AAH62133 /// Q8BZS6	
1446959_at	---	Mus musculus transcribed sequences	0.72 BG068073	---	
1438613_at	Kona4	potassium voltage-gated channel, shaker-related subfamily, member 4	0.72 BB131475	Q8CBF8	
1460003_at	---	Mus musculus transcribed sequences	0.72 AV234963	---	
1426369_at	3732409C05Rik	RIKEN cDNA 3732409C05 gene	0.72 BG094874	Q8BZS2 /// Q922J9 /// Q9CXE8 /// Q9D0Q1 /// Q9DAU2	

1438886_at	Heyl	hairly/enhancer-of-split related with YRPW motif-like	0.72 BB310549	Q9DBX7 /// Q9JJV6 /// Q9QXW8
1429430_at	8430411F12Rik	RIKEN cDNA 8430411F12 gene	0.72 AK018402	AAH64801 /// P59913
1425202_a_at	Ank3	ankyrin 3, epithelial	0.72 BC021657	Q61307 /// Q8CBN3 /// Q8CCD5 /// Q8VC68 /// Q9QXH1
1433669_at	Akap8	A kinase (PRKA) anchor protein 8	0.72 BB037566	Q8BP29 /// Q9DBR0 /// Q9R0L8
1450863_a_at	Dcamk1l	double cortin and calcium/calmodulin-dependent protein kinase-like 1	0.72 BQ174703	AAH64783 /// Q80VB6 /// Q8BQN2 /// Q8CCN4 /// Q8CHG1 /// Q8VDT3 /// Q9JLM6 /// Q9JLM7 /// Q9JLM8
1454720_at	Apba3	amyloid beta (A4) precursor protein-binding, family A, member 3	0.72 AV328620	Q88888 /// Q8BR09
1426216_at	Cog6	component of oligomeric golgi complex 6	0.72 BC025427	Q8BRB0 /// Q8BSNT /// Q8CTY2 /// Q8CHB1 /// Q8R3I3
1429159_at	4631408O11Rik	RIKEN cDNA 4631408O11 gene	0.72 AK018605	---
1424693_at	4933407N01Rik	RIKEN cDNA 4933407N01 gene	0.72 BC018468	Q8BYN6 /// Q8VEH8 /// Q9CWA6
1452395_at	2410018M14Rik	RIKEN cDNA 2410018M14 gene	0.72 AA111022	---
1435436_at	---	Mus musculus transcribed sequences	0.72 B1647951	---
1451971_at	Cul4a	cullin 4A	0.72 BC024113	Q8BJG5 /// Q8R1T2 /// Q91VY0 /// Q91Z44 /// Q9CTG1 /// Q9CWI5
1450479_x_at	Ptgn12	protein tyrosine phosphatase, non-receptor type 12	0.72 X63440	P35831 /// Q80UM4
1418310_a_at	Rlbp1	retinaldehyde binding protein 1	0.72 NM_020599	BAB29216 /// Q9Z275
1423646_at	Zdhnc3	zinc finger, DHHC domain containing 3	0.72 BB815190	AAO27359 /// Q8R173
1454794_at	Spg4	spastic paraplegia 4 homolog (human)	0.72 AV298495	BAC98092 /// Q80VE0 /// Q9CVK0 /// Q9QYY8
1436889_at	Gabra1	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 1	0.72 BQ268470	BAC28585 /// BAC30368 /// P18504
1451679_at	6530401D17Rik	RIKEN cDNA 6530401D17 gene	0.72 BC016270	Q8BK31 /// Q9D365
1448430_a_at	Naca	nascent polypeptide-associated complex alpha polypeptide	0.72 NM_013608	Q60817
1452371_at	2610019N13Rik	RIKEN cDNA 2610019N13 gene	0.72 AW261583	Q8BV04 /// Q8BYD3 /// Q8C0Z3 /// Q8CFF2 /// Q8CGI3 /// Q9CT17
1450723_at	Isl1	ISL1 transcription factor, LIM/homeodomain (islet 1)	0.72 BQ176915	P61372 /// Q8BTH7
1434503_s_at	Lamp2	lysosomal membrane glycoprotein 2	0.73 BB490768	P17047 /// Q8BSG8 /// Q8C876 /// Q9CZU7
1423684_at	Hnrpk	heterogeneous nuclear ribonucleoprotein K	0.73 BC006694	Q07244 /// Q8BGQ8
1460449_at	C030032C09Rik	RIKEN cDNA C030032C09 gene	0.73 BQ174247	Q8BIZ1 /// Q8BJ47 /// Q8BL49 /// Q8BZM2
1450038_s_at	Usp9x	ubiquitin specific protease 9, X chromosome	0.73 AW107303	P70398 /// Q8BR77 /// Q8BS89
1454651_x_at	Mbp	myelin basic protein	0.73 BE994609	AAH51094 /// BAC30679 /// BAC37705 /// P04370
1422457_s_at	Sumo3	SMT3 suppressor of mif two 3 homolog 3 (yeast)	0.73 NM_019929	Q9Z172
1418723_at	Edg7	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor 7	0.73 NM_022983	BAC31159 /// Q9EQ31
1422520_at	Nef3	neurofilament 3, medium	0.73 NM_008691	P08553 /// Q8BQ20
1439341_at	---	Mus musculus transcribed sequence with weak similarity to protein pir:T00340 (H.sapiens) T00340	0.73 BB203252	---
1423078_a_at	Sc4mol	hypothetical protein KIAA057 - human	0.73 AK005441	BAC32201 /// Q9CRA4
1448261_at	Cdh1	sterol-C4-methyl oxidase-like cadherin 1	0.73 NM_009864	P09803
1437132_x_at	Nedd9	neural precursor cell expressed, developmentally down-regulated gene 9	0.73 BB535494	O35177
1436511_at	BC031781	cDNA sequence BC031781	0.73 BM935102	Q8BJX1 /// Q8K1J5
1452804_at	1700010A17Rik	RIKEN cDNA 1700010A17 gene	0.73 BG298252	Q9DAI9
1431296_at	4933439K08Rik	RIKEN cDNA 4933439K08 gene	0.73 AA555873	---
1455907_x_at	---	Mus musculus transcribed sequences	0.73 BB059017	---
1455904_at	Gas5	growth arrest specific 5	0.73 B1650268	Q99KJ3
1426607_at	3110070M22Rik	RIKEN cDNA 3110070M22 gene	0.73 BG068872	Q8VDR5 /// Q9CXM1 /// Q9DAQ7
1417663_a_at	Ndr3	N-myc downstream regulated 3	0.74 BE631549	BAB23475 /// BAC29818 /// Q8CDY0 /// Q8VCV2 /// Q9QYF9
1436302_at	2410193C02Rik	RIKEN cDNA 2410193C02 gene	0.74 BB770006	Q8BV58 /// Q8BYD0 /// Q9CWD6
1422744_at	Phka1	phosphorylase kinase alpha 1	0.74 NM_008832	P18826 /// Q8BSV5 /// Q8CBA7

1423176_at	Tob1	transducer of ErbB-2.1	0.74 BQ266486	---	
1452062_at	Prpsap2	phosphoribosyl pyrophosphate synthetase-associated protein 2	0.74 BB246540	BAC30096 /// BAC36491 /// Q8BK37 /// Q8R574	
1430500_s_at	Mxb2	metaxin 2	0.74 AK005233	BAC40046 /// O88441 /// Q8C454	
1435058_x_at	Sxpp3	synixin binding protein 3	0.74 AI528529	AAH62901 /// Q60770 /// Q8C7H4	
1415844_at	Syf4	synaptotagmin 4	0.74 AV336547	P40749	
1435061_at	Nudt11	nudix (nucleoside diphosphate linked moiety X)-type motif 11	0.74 AI853080	Q8BKF4 /// Q9JUD3	
1445519_at	Kons3	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	0.74 C77819	Q8BQZ8	
1455446_x_at	Acadsb	acyl-Coenzyme A dehydrogenase, short/branched chain	0.74 BF228057	Q7TMY2 /// Q9DBL1	
1453365_at	8430421H08Rik	RIKEN cDNA 8430421H08 gene	0.74 AK018430	---	
1460116_s_at	Spred1	sprouty protein with EVH-1 domain 1, related sequence	0.74 AI450584	AAH57874 /// Q924S8	
1438024_at	6230416A05Rik	RIKEN cDNA 6230416A05 gene	0.74 AW554392	---	
1435021_at	Gabrb3	gamma-aminobutyric acid (GABA-A) receptor, subunit beta 3	0.74 BQ175666	BAC30230 /// P15433 /// Q8C446	
1443992_at	4921518A06Rik	RIKEN cDNA 4921518A06 gene	0.74 BB203972	Q7TNS4 /// Q8BKV4 /// Q8CES9 /// Q9CUC6	
1452872_at	2900054D09Rik	RIKEN cDNA 2900054D09 gene	0.74 BM217754	---	
1453328_at	2700008G24Rik	RIKEN cDNA 2700008G24 gene	0.74 AW495672	---	
1428086_at	Dnm1l	dynamitin 1-like	0.74 BM249101	Q8BNQ5 /// Q8BQ64 /// Q8CGD0 /// Q8K1A1 /// Q8K1M6	
1416253_at	Cdkn2d	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	0.74 BC013898	Q60773 /// Q91YV3	
1428453_at	5730533P17Rik	RIKEN cDNA 5730533P17 gene	0.74 AK017805	Q7TN07 /// Q8CES0	
1451620_at	Pter	phosphotriesterase related	0.75 BB768838	---	
1438413_at	2810413I22Rik	RIKEN cDNA 2810413I22 gene	0.75 AV231698	AAH58593 /// AAH64127 /// Q80TA3 /// Q8BUH8 /// Q9CQN9 /// Q9CRF0 /// Q9CX65	
1426948_at	Tpr	translocated promoter region	0.75 BM214109	Q8BIX0 /// Q8BK71 /// Q8BU18 /// Q8K2T9 /// Q8R4A0 /// Q91ZA5	
1438093_x_at	Dbi	diazepam binding inhibitor	0.75 BB115327	BAB25730 /// BAB25755 /// BAB32175 /// BAC25658 /// P31786	
1453565_at	Ndufab1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1	0.75 AV221509	AAH60951 /// BAC40751 /// Q9CR21	
1452230_at	Dnajc10	DnaJ (Hsp40) homolog, subfamily C, member 10	0.75 AV114239	AAQ14555 /// Q8CH78 /// Q8CIB0 /// Q99LV4 /// Q9CRX9 /// Q9CUG0 /// Q9DC23	
1419362_at	Mpl35	mitochondrial ribosomal protein L35	0.75 BF787384	Q9CQL6	
1453212_at	1110003H10Rik	RIKEN cDNA 1110003H10 gene	0.75 BB705379	---	
1448670_at	Ube2e3	ubiquitin-conjugating enzyme E2E 3, UBC4/5 homolog (yeast)	0.75 AW120830	P52483 /// Q8BXB0	
1419650_at	Zfr	zinc finger RNA binding protein	0.75 NM_011767	AAH58570 /// Q88532 /// Q8BS85 /// Q8CGG5 /// Q91VZ0 /// Q9CT34	
1417702_a_at	Hnmt	histamine N-methyltransferase	0.75 NM_080462	Q91VF2	
1452214_at	9130011J04Rik	RIKEN cDNA 9130011J04 gene	0.75 AK018608	---	
1439817_at	AI451465	expressed sequence AI451465	0.75 AI451465	---	
1440879_at	Abca9	ATP-binding cassette transporter sub-family A member 9	0.75 AW046072	Q8BIS4 /// Q8C114 /// Q8K449	
1452592_at	Mgst2	microsomal glutathione S-transferase 2	0.75 AV066880	Q8R032	
1428124_at	Gtf2e1	general transcription factor II E, polypeptide 1 (alpha subunit)	0.75 AK011543	BAC27436 /// Q8BV40 /// Q9D0D5	
1424872_at	2310001H12Rik	RIKEN cDNA 2310001H12 gene	0.75 BC012405	Q8BJ78	
1425332_at	Zfp106	zinc finger protein 106	0.75 BI452653	Q88465 /// Q88466 /// Q8C235 /// Q8CDZ8 /// Q8R314	
1419170_at	2310044D20Rik	RIKEN cDNA 2310044D20 gene	0.75 BB667295	Q8CC46 /// Q8VDR1 /// Q9D238 /// Q9D3L0 /// Q9D6W5 /// Q9D6Z3	
1425542_a_at	Ppp2r5c	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	0.75 BC003979	AAR26474 /// BAC97852 /// Q60996 /// Q8C8H4 /// Q99KW8 /// Q99N67 /// Q99N68	

1450779_at	Fabp7	fatty acid binding protein 7, brain	0.75 NM_021272 P51880
1434284_at	G630013P12Rik	RIKEN cDNA G630013P12 gene	0.75 BQ031214 Q8BT14 /// Q8K0U7
1433540_x_at	Ppp1cb	protein phosphatase 1, catalytic subunit, beta isoform	0.75 AW823525 AAH46832 /// BAC40636 /// P37140 /// Q8C285 /// Q9DBY2
1426978_at	Klh2	kelch-like 2, Mayven (Drosophila)	0.75 AW682368 Q8CCU0 /// Q8IZP3 /// Q8R3U4
1416412_at	Nsmaf	neutral sphingomyelinase (N-SMase) activation associated factor	0.76 NM_010945 Q35242
1438725_at	Thrap1	thyroid hormone receptor associated protein 1	0.76 BB212816 BAC97978
1438324_at	9330182L06Rik	RIKEN cDNA 9330182L06 gene	0.76 AW550882 Q8BJM9 /// Q8BJN9 /// Q8BJT7 /// Q8BKX9 /// Q8BL89 /// Q8BLT1 /// Q8BM91 /// Q8K107
1437259_at	Slc9a2	solute carrier family 9 (sodium/hydrogen exchanger), member 2	0.76 AV274006 Q9WUJ4
1420748_a_at	Adat1	adenosine deaminase, tRNA-specific 1	0.76 NM_013925 Q8VE23 /// Q9JH2
1417481_at	Ramp1	receptor (calcitonin) activity modifying protein 1	0.76 NM_016894 Q8VIT7 /// Q9CT80 /// Q9WTJ5
1425468_at	Plp	proteolipid protein (myelin)	0.76 BB768495 P60202 /// Q62079
1422510_at	Ctdspl	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	0.76 NM_133710 CAC69078 /// P58465
1441946_at	Itih5	inter-alpha (globulin) inhibitor H5	0.76 AV239969 AAH62196 /// Q80VG0 /// Q8BJD1 /// Q8BK33 /// Q8BMS5
1460292_a_at	Smarca1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	0.76 NM_053123 AAH57115 /// Q8BS67 /// Q8BSS1 /// Q91Y58
1435303_at	4932409F03Rik	RIKEN cDNA 4932409F03 gene	0.76 AV373814 Q8C0S6
1455003_at	---	Mus musculus mRNA similar to hypothetical protein FLJ10477 (cDNA clone MGC:47985 IMAGE:5118383), complete cds	0.76 BQ032496 ---
1452015_at	6330416G13Rik	RIKEN cDNA 6330416G13 gene	0.76 AV326978 Q8BMN2 /// Q8C07 /// Q8CIJ7 /// Q8R239
1429383_at	Csnk1g3	casein kinase 1, gamma 3	0.76 BM195380 Q8BM57 /// Q8C001 /// Q8K079
1435234_at	Ncoa2	nuclear receptor coactivator 2	0.76 BM234716 Q61026 /// Q7TPTU7 /// Q8C961 /// Q8CBM5 /// Q8CE59
1456137_at	Nrxn3	neurexin III	0.76 BB132137 AAH60719 /// BAC98015 /// Q88724 /// Q8C985 /// Q8CBZ2 /// Q8CCT8
1429685_at	C030002O17Rik	RIKEN cDNA C030002O17 gene	0.76 BB313857 ---
1423246_at	Txnrd4	thioredoxin domain containing 4 (endoplasmic reticulum)	0.76 B1100077 Q9D1Q6
1451531_at	BC018472	cDNA sequence BC018472	0.77 BC018472 Q7TSA8 /// Q8K399 /// Q8VEH6
1445438_at	Ddhd1	DDHD domain containing 1	0.77 BB132393 BAC98235 /// Q80YA3
1452168_x_at	Gspt1	G1 to phase transition 1	0.77 AB003502 Q8BPH0 /// Q8CAS6 /// Q8CCV1 /// Q8K2E1 /// Q8R050
1436298_x_at	Paics	phosphoribosylaminimidazole carboxylase, phosphoribosylaminimidazole, succinocarboxamide synthetase	0.77 BB066556 Q9CQ38 /// Q9DCL9
1423856_at	Rpl17	ribosomal protein L17	0.77 BC003896 Q9ES81
1433872_at	2410042D21Rik	RIKEN cDNA 2410042D21 gene	0.77 BB143137 Q8C7R6 /// Q9CWLJ3
1417214_at	Rab27b	RAB27b, member RAS oncogene family	0.77 BB121259 BAB86914 /// BAC87832 /// Q99P58
1446331_at	Plgfr	prostaglandin F receptor	0.77 AV244075 ---
1426260_a_at	Ugt1a1	UDP-glucuronosyltransferase 1 family, member 1	0.77 D87867 ---
1440209_at	2900024D24Rik	RIKEN cDNA 2900024D24 gene	0.77 A1449126 AAH66008 /// Q8C294 /// Q8CBA1
1430535_at	1810043J12Rik	RIKEN cDNA 1810043J12 gene	0.77 BB045401 AAH58221 /// Q9CVK3
1416872_at	Tm4sf6	transmembrane 4 superfamily member 6	0.77 NM_019656 Q70401 /// Q99L96
1429158_at	Foxo28	F-box protein 28	0.77 AV302798 Q7TMH9 /// Q8BIF5 /// Q8BIG4
1433465_a_at	A1467606	expressed sequence A1467606	0.77 BB234337 AAH38694 /// AAH64101 /// Q8C708
1451355_at	CRG-L1	cancer related gene-liver 1	0.77 AF282864 AAH59819 /// Q8BUG3 /// Q8VD53
1429284_at	8430436F23Rik	RIKEN cDNA 8430436F23 gene	0.77 BB248684 ---

1437408_at	Gpr126	G protein-coupled receptor 126	0.77	BB812574	Q811E4	
1428642_at	Slc35d3	solute carrier family 35, member D3	0.77	AK018094	Q8BGF8 /// Q8CXD4	
1433527_at	Irb2	iron responsive element binding protein 2	0.77	BB080732	Q70235 /// Q811J3 /// Q8BWZ6 /// Q8BZL2	
1426819_at	Fosb	FBJ osteosarcoma oncogene B	0.77	BG076079	P13346	
1426578_s_at	Snap25bp	synaptosomal-associated protein 25 binding protein	0.77	BB667523	Q9Z266	
1438816_at	Elys	embryonic large molecule derived from yolk sac	0.78	BM247201	Q8BVJ5 /// Q8R1T9 /// Q8VD55	
1452249_at	Prickle1	prickle like 1 (Drosophila)	0.78	BC022643	Q8CGJ0	
1416923_a_at	Bnip3l	BCL2/adenovirus E1B 19kDa-interacting protein 3-like	0.78	AK018668	BAB23456 /// BAB25351 /// BAB28869 /// Q91Z78 /// Q9Z2F7	
1422094_a_at	Riken cDNA 2810439M05Rik	RIKEN cDNA 2810439M05 gene	0.78	NM_026046	Q8BKL5 /// Q9CYV4 /// Q9D459	
1442379_at	Chdc1	calponin homology (CH) domain containing 1	0.78	A1552548	BAC98074	
1433536_at	Lrp11	low density lipoprotein receptor-related protein 11	0.78	BB435348	AAH59874 /// Q8CB67	
1451744_a_at	Zadn1	zinc binding alcohol dehydrogenase, domain containing 1	0.78	BC021466	Q8BZA2 /// Q8VDQ1 /// Q9D1W8	
1450135_at	Fzd3	fizzled homolog 3 (Drosophila)	0.78	AU043193	Q61086	
1458379_at	9330159F19	hypothetical protein 9330159F19	0.78	BB079733	---	
1434866_x_at	Cpt1a	carnitine palmitoyltransferase 1, liver	0.78	BB021753	P97742 /// Q7TQD5 /// Q80SW3 /// Q8BP98 /// Q8C7H8	
1460360_at	Asrg1l	asparaginase like 1	0.78	AU040643	Q8COM9 /// Q91WC8 /// Q9CVX3	
1417565_at	Abhd5	abhydrolase domain containing 5	0.78	AK007421	Q922Z5 /// Q9CTY3 /// Q9DBL9	
1427084_a_at	Map4k5	mitogen-activated protein kinase kinase kinase 5	0.78	BG067961	AAH57930 /// Q8BPM2 /// Q8BRE4	
1452074_at	2810439K08Rik	RIKEN cDNA 2810439K08 gene	0.78	AV225967	Q8BSY5 /// Q8C8G3 /// Q8CCZ6 /// Q8CE78 /// Q9CYV5	
1423046_s_at	Ncbp2	nuclear cap binding protein subunit 2	0.78	BE285362	Q9CQ49	
1418382_at	AB023957	cDNA sequence AB023957	0.78	BB770932	Q9R0R2	
1434376_at	Cd44	CD44 antigen	0.78	AW146109	P15379 /// Q80X37	
1454074_a_at	1500011J06Rik	RIKEN cDNA 1500011J06 gene	0.78	AK005213	---	
1419918_at	3930401E15Rik	RIKEN cDNA 3930401E15 gene	0.79	AW545765	---	
1460119_at	---	---	0.79	BB245904	---	
1426395_s_at	Elf3s1	eukaryotic translation initiation factor 3, subunit 1 alpha	0.79	BB379268	Q8BUW6 /// Q99JK5	
1423606_at	Postn	periostin, osteoblast specific factor	0.79	BI110565	Q62009	
1449677_s_at	D4Erd89e	DNA segment, Chr 4, ERATO Doi 89, expressed	0.79	C77858	Q9DAV9	
1417372_a_at	Pell1	pellino 1	0.79	BC016515	Q8C669	
1421137_a_at	Pklb	protein kinase inhibitor beta, cAMP dependent, testis specific	0.79	AV047342	AAH61162 /// Q04758 /// Q8BNE5	
1455406_at	---	Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833431M13	0.79	AV251542	---	
1437243_at	A1325464	product:unknown EST, full insert sequence expressed sequence A1325464	0.79	AV349520	Q8BU06 /// Q8CIM3	
1459274_at	Gpr135	G protein-coupled receptor 135	0.79	AV221890	Q7TQP2	
1426015_s_at	Asph	aspartate-beta-hydroxylase	0.79	AF302653	AAH61098 /// Q8BQK0 /// Q8BSY0 /// Q8CBM2 /// Q8CH79 /// Q91WG6 /// Q920F7 /// Q9EQ63 /// Q9EQ64 /// Q9EQ66	
1428785_at	Amotl1	angiomotin-like 1	0.79	BG917015	Q9D4H4	
1423220_at	Elf4e	eukaryotic translation initiation factor 4E	0.79	BB406487	P20415 /// Q8C470	
1422484_at	Cycs	cytochrome c, somatic	0.79	NM_007808	BAB22313 /// BAB22617 /// BAB23959 /// BAB27091 /// P00009	
1448503_at	Mcl1	myeloid cell leukemia sequence 1	0.79	BC003839	P97287 /// Q9CIR4	
1448830_at	Dusp1	dual specificity phosphatase 1	0.79	NM_013642	P28563	
1434765_at	Ep300	E1A binding protein p300	0.79	A1844888	Q8BJ14	
1445531_at	Csmd1	CUB and Sushi multiple domains 1	0.79	BB179947	Q923L3	

1454722_at	2310035O07Rik	RIKEN cDNA 2310035O07 gene	0.79 BG792618	
1444501_at	G6pdx	glucose-6-phosphate dehydrogenase X-linked	0.80 A1853202	
1429468_at	1110018F16Rik	RIKEN cDNA 1110018F16 gene	0.80 AK003775	
1422631_at	Ahr	aryl-hydrocarbon receptor	P30561	/// Q8R4S5 /// Q8R4S6
1426987_at	5430417L22Rik	RIKEN cDNA 5430417L22 gene	0.80 BB028755	
1421195_at	Cckar	cholecystokinin A receptor	0.80 BC020534	
1450954_at	Yme11	YME1-like 1 (S. cerevisiae)	O08786	
1437382_at	Acvr2	activin receptor IIA	O8967	/// Q8C597
			P27038	/// Q8BRV4
1433835_at	Ppp3cb	protein phosphatase 3, catalytic subunit, beta isoform	0.80 BE825122	
1436405_at	6330411N01Rik	RIKEN cDNA 6330411N01 gene	AAH66000	/// P48453
1448471_a_at	Ctla2a	cytotoxic T lymphocyte-associated protein 2 alpha	0.80 BG068753	
1427676_a_at	Grik1	glutamate receptor, ionotropic, kainate 1	0.80 NM_007796	
1453187_at	1810027I20Rik	RIKEN cDNA 1810027I20 gene	0.80 X66118	
1429144_at	2310032D16Rik	RIKEN cDNA 2310032D16 gene	0.80 AV062896	
			Q80TD5	/// Q8BKJ7 /// Q8BKW7 /// Q8C0L9 /// Q8CFW2 /// Q9D759
1418780_at	Cyp39a1	cytochrome P450, family 39, subfamily a, polypeptide 1	0.80 NM_018887	
1423177_a_at	Abi1	abi-interactor 1	BAC27530	/// Q8CFY8 /// Q9JKJ9
1441229_at	D230019N24Rik	RIKEN cDNA D230019N24 gene	0.80 AW912678	
1418968_at	Rb1cc1	RB1-inducible coiled-coil 1	Q60747	/// Q8CBW3 /// Q91ZM5 /// Q92319 /// Q99KH4
1421851_at	Ddx26	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26	0.80 BA468551	
1459205_at		Mus musculus transcribed sequences	AAH66152	/// Q61384 /// Q8BRY9 /// Q8BT47 /// Q8CHH8 /// Q9ESK9 /// Q9JK14
1429106_at	4921509J17Rik	RIKEN cDNA 4921509J17 gene	0.80 BB731480	
1450684_at	Ev1	ets variant gene 1	AAH58637	/// AAH59263 /// Q61204 /// Q8BQZ7 /// Q8C9M9
1423298_at	Add3	adducin 3 (gamma)	0.80 BI076746	
1416060_at	Tbc1d15	TBC1 domain family, member 15	0.80 AK014853	
1416539_at	Ysg2	yolk sac gene 2	0.80 NM_007960	
1451726_at	Mtmr6	myotubularin related protein 6	Q8BJH2	/// Q8BM29 /// Q8JZT6 /// Q9JLE2 /// Q9QYB5
1423591_at	Fgfr1op2	FGFR1 oncogene partner 2	0.80 BM239842	
1423672_at	2510042P03Rik	RIKEN cDNA 2510042P03 gene	0.81 BF577643	
1450840_a_at	Rpl39	ribosomal protein L39	0.81 BF577643	
1447875_x_at		Mus musculus transcribed sequences	0.81 NM_011734	
1443260_at	Meis1	myeloid ecotropic viral integration site 1	BAC26049	/// P70665 /// Q8CBM6 /// Q8CC41 /// Q8CEB7
1453106_a_at	Rnmt	RNA (guanine-7-) methyltransferase	0.81 BC020019	
1424925_at	Sec63	SEC63-like (S. cerevisiae)	0.81 AK004662	
1420021_s_at	D11Etd530e	DNA segment, Chr 11, ERATO Doi 530, expressed	Q8VE11	
1429573_at	4921520P21Rik	RIKEN cDNA 4921520P21 gene	0.81 BC026507	
1428438_s_at	2700023B17Rik	RIKEN cDNA 2700023B17 gene	0.81 AK014934	
1454885_at	2610021A01Rik	RIKEN cDNA 2610021A01 gene	0.81 AV107150	
			P02404	
1427371_at	Abca8a	ATP-binding cassette, sub-family A (ABC1), member 8a	0.81 BB332055	
1425956_a_at	Cdadcl1	cytidine and dCMP deaminase domain containing 1	0.81 BB051155	
1437481_s_at	2810441O16Rik	RIKEN cDNA 2810441O16 gene	0.81 AK015403	
1446735_at	Sh3d1B	SH3 domain protein 1B	0.81 C76103	
1435496_at	5730469M10Rik	RIKEN cDNA 5730469M10 gene	0.81 AU022339	
			0.81 AK014934	
			Q9DSU3	/// Q9D9R7
			Q8K2F8	/// Q9CTG8
			0.81 BM211194	
			AAH60032	/// Q8C0A9 /// Q8K442 /// Q8R0R4
			Q8BMD5	/// Q8BYL2 /// Q8BYN1 /// Q8C014 /// Q922P4 /// Q99KL2 /// Q9D7F3
			Q80VS9	/// Q91YJ1 /// Q9CSC1
			Q80TG5	/// Q8C9C3 /// Q8CD59 /// Q9CQD9 /// Q9Z0R6
			AAH56635	/// Q9CYH2
1440370_at	Abca13	ATP-binding cassette, sub-family A (ABC1), member 13	0.81 BB277120	
1427183_at	Etemp1	epidermal growth factor-containing fibulin-like	Q80T20	/// Q8BHZ2
1429084_at	Vezf1	extracellular matrix protein 1	AAO37642	/// AAP79577 /// Q8BPPB5 /// Q8K0J4 /// Q8R1U8
		vascular endothelial zinc finger 1	Q8K1B7	/// Q9Z162

1417411_at	Nap1l5-pending	nucleosome assembly protein 1-like 5	0.81 NM_021432	Q80U90 /// Q8CFQ0 /// Q9CTE1 /// Q9CYM1 /// Q9JF0
1434424_at	9630055N22Rik	RIKEN cDNA 9630055N22 gene	0.81 BB276950	Q8CAM2 /// Q91XE2
1449310_at	Ptger2	prostaglandin E receptor 2 (subtype EP2)	0.81 BC005440	BAC35664 /// Q62053
1429451_at	2610301B20Rik	RIKEN cDNA 2610301B20 gene	0.82 AK011950	AAH58777 /// Q9D005
1434136_at	6332401019Rik	RIKEN cDNA 6332401019 gene	0.82 BE571820	Q8BN70
1425210_s_at	Zfp84	zinc finger protein 84	0.82 A465811	Q60911 /// Q8BL69 /// Q922D0 /// Q9D654
1424769_s_at	Cald1	caldesmon 1	0.82 B1248947	Q7TMN5 /// Q8VCQ8 /// Q8VD79
1439829_at	Adcy5	adenylate cyclase 5	0.82 BE946363	--
1452762_at	8430436O14Rik	RIKEN cDNA 8430436O14 gene	0.82 AK018466	--
1420971_at	Ubr1	ubiquitin protein ligase E3 component n-recognin 1	0.82 BQ173927	Q70481 /// Q8BN40 /// Q8C5K3
1439268_x_at	Elf3s6	eukaryotic translation initiation factor 3, subunit 6	0.82 BB032885	AAC53346 /// P60229 /// Q8BNE6 /// Q9CT23
1448955_s_at	Cadps	Ca ²⁺ -dependent activator protein for secretion	0.82 NM_012061	AAH57065 /// Q61374 /// Q80TJ1
1419549_at	Arg1	arginase 1, liver	0.82 NM_007482	Q61176 /// Q80VH4
1455914_at	Al987944	expressed sequence Al987944	0.82 AW554430	--
1428856_at	2610207H6Rik	RIKEN cDNA 2610207H6 gene	0.82 BM200015	Q8C3H3 /// Q99JH2 /// Q99LV2
1455590_at	4930482L21Rik	RIKEN cDNA 4930482L21 gene	0.82 AV380561	Q60854 /// Q8BZR2
1437671_x_at	2310046G15Rik	RIKEN cDNA 2310046G15 gene	0.82 BB378796	BAC28708 /// BAC37319 /// Q8BZS4 /// Q8CF39 /// Q9D6X6
1434732_x_at	1110020J08Rik	RIKEN cDNA 1110020J08 gene	0.82 AV044898	Q9D173
1424232_a_at	BC025546	cDNA sequence BC025546	0.82 BC025546	Q8BWQ4 /// Q8R3E7
1429175_at	2810417M05Rik	RIKEN cDNA 2810417M05 gene	0.82 AK014196	Q8CEU4 /// Q9CZ16
1438201_at	--	Mus musculus, Similar to pyruvate dehydrogenase phosphatase, clone IMAGE:6492665, mRNA	0.82 AV290622	--
1460544_at	Mak10	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	0.82 BG083730	AAH56435 /// Q8BYJ5 /// Q8BYJ9 /// Q8K3H2
1422936_at	Mas1	MAS1 oncogene	0.82 NM_008552	P30554 /// Q8BHI8
1439185_x_at	--	Mus musculus transcribed sequences	0.82 BB433489	Q8VCF0
1430219_at	Fts	fused toes	0.82 AK017861	Q64362
1436761_s_at	4921522K17Rik	RIKEN cDNA 4921522K17 gene	0.82 BB461323	AAH66835 /// Q8BLV7 /// Q99LJ4 /// Q9DBR2
1434751_at	Ids	iduronate 2-sulfatase	0.82 BB493523	Q08890 /// Q8CJ15
1460320_at	Becn1	bedlin 1 (coiled-coil, myosin-like BCL2-interacting protein)	0.82 NM_019584	O88597 /// Q99J03
1428156_at	Gng2	guanine nucleotide binding protein (G protein), gamma 2 subunit	0.82 AV021455	P16874
1419286_s_at	Cdv1	carnitine deficiency-associated gene expressed in ventricle 1	0.82 NM_009879	O35594
1426736_at	Gsp11	G1 to phase transition 1	0.83 AB003502	Q8BPH0 /// Q8CAS6 /// Q8CCV1 /// Q8K2E1 /// Q8R050
1451177_at	DnaJb4	DnaJ (Hsp40) homolog, subfamily B, member 4	0.83 BC017161	BAC25720 /// Q8BP73 /// Q9D832
1449407_at	Cdv1	carnitine deficiency-associated gene expressed in ventricle 1	0.83 NM_009879	O35594
1449530_at	Trps1	trichorhinophalangeal syndrome 1 (human)	0.83 NM_032000	Q80V18 /// Q8BZ62 /// Q8K1J0 /// Q925H1
1420367_at	Denr	density-regulated protein	0.83 AK010394	Q9CQJ6
1428791_at	Ube2h	ubiquitin-conjugating enzyme E2H	0.83 BB183512	AAH08517 /// P37286
1452411_at	Lrrc1	leucine rich repeat containing 1	0.83 BG966295	Q80VQ1 /// Q8BKR1 /// Q8BUS9 /// Q8QZU1
1447861_x_at	Mrg1	myeloid ectotropic viral integration site-related gene 1	0.83 AV329543	AAH17375 /// P97367
1449643_s_at	Btf3	basic transcription factor 3	0.83 AA220626	AAH08233 /// AAH64010 /// Q64152 /// Q9D9L3
1437067_at	Phf2	putative homeodomain transcription factor 2	0.83 BM228625	Q77PX6 /// Q8C975 /// Q8C9D2 /// Q8CB19 /// Q8CBQ3
1428603_at	Glc1	glucocorticoid induced transcript 1	0.83 AK009885	Q80YT1 /// Q8CEA5 /// Q8K3I9 /// Q925C1 /// Q9D6W9
1427058_at	Elf4a1	eukaryotic translation initiation factor 4A1	0.83 AK010844	AAH49915 /// BAB27678 /// BAC36796 /// P60843 /// Q64341 /// Q99LR0
1433853_at	Mib1	mindbomb homolog 1 (Drosophila)	0.83 BG063791	AAH18022 /// BAC98141 /// Q80SY4 /// Q8BNR1 /// Q8C6W2 /// Q921Q1
1426717_at	3830408P04Rik	RIKEN cDNA 3830408P04 gene	0.83 BF787442	Q8KOM0 /// Q921M1 /// Q9CSH1 /// Q9DON5 /// Q9JJC8

1443269_at	---	Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130009B15	0.83 BB451348	---	
1447927_at	Alf595338	product:unknown EST, full insert sequence	0.83 BG092512	AAH57969 /// BAC87667 /// Q61594 /// Q77MV8 /// Q8K0G1 /// Q9D3E4	
1433575_at	Sox4	expressed sequence Alf595338	0.84 BG083485	Q06831 /// Q8BPK5 /// Q8BQ53 /// Q8CE55	
1435239_at	Gria1	SRY-box containing gene 4	0.84 BQ175316	AAH60702 /// P23818 /// Q7TNB5	
		glutamate receptor, ionotropic, AMPA1 (alpha 1)			
		Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730031J22			
1459325_at	---	product:unknown EST, full insert sequence	0.84 AV329840	---	
1425149_a_at	Pdcl	phosducin-like	0.84 BC006578	BAC26056 /// BAC26133 /// Q923E8	
1415834_at	Dusp6	dual specificity phosphatase 6	0.84 NM_026268	BAC40372 /// BAC40489 /// Q9DBB1	
		proteasome (prosome, macropain) 26S subunit, ATPase, 6			
1417769_at	Psmo6	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930564M06	0.84 AW208944	AAH57997 /// Q810A6 /// Q8QZS9 /// Q92524 /// Q9CXH9	
		product:inferred: cadherin-11 [Mus musculus], full insert sequence			
1441565_at	---	RIKEN cDNA 2400002F02 gene	0.84 BB016866	---	
1429596_at	2400002F02Rik	RIKEN cDNA 4930469P12 gene	0.84 AK010254	---	
1459793_s_at	4930469P12Rik	Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:6530427L06	0.84 AV301944	---	
		product:unknown EST, full insert sequence			
1438073_at	---	hypothetical protein A930017M01	0.84 AW047633	---	
1437076_at	A930017M01	RIKEN cDNA 4732435N03 gene	0.84 BB279424	Q8C4W1	
1452366_at	4732435N03Rik	zinc finger, CW-type with coiled-coil domain 3	0.84 AV371987	Q8B1Q9 /// Q8BWW9 /// Q8BZU7 /// Q8C195 /// Q8CBT0 /// Q8R0M6	
1420091_s_at	Zcwc3	NHL repeat containing 2	0.84 AI452146	Q8R0R0	
1433929_at	Nhlrc2		0.84 BB785641	Q8OXU0 /// Q8BZW8 /// Q8C1S8 /// Q9CWB4	
1422414_a_at	Calm2	calmodulin 2	0.84 NM_007589	AAH21347 /// AAH51444 /// BAB28116 /// BAB28319 /// BAB28631 /// P02593 /// Q91VQ9	
1455372_at	Cpeb3	cytoplasmic polyadenylation element binding protein 3	0.84 BB770826	Q7TN99 /// Q8CHC2	
1426747_at	Abcf3	ATP-binding cassette, sub-family F (GCN20), member 3	0.84 AI552141	Q8K268 /// Q9JL49	
1456700_x_at	Marcks	myristoylated alanine rich protein kinase C substrate	0.84 BB100920	P26645	
1428973_s_at	0610012D17Rik	RIKEN cDNA 0610012D17 gene	0.84 AK007178	AAH59716 /// Q9CQ66 /// Q9CQJ9	
1420402_at	Atp2b2	ATPase, Ca++ transporting, plasma membrane 2	0.84 NM_009723	Q9R0K7	
1422561_at	Adams5	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecaenase-2)	0.84 BB658835	Q8BGP4 /// Q9R001	
1418066_at	Cfil2	cofilin 2, muscle	0.84 AI323758	P45591	
		Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130058B11			
1439204_at	---	product:unknown EST, full insert sequence	0.85 BB096886	Q62204	
1427331_at	---	Mus musculus transcribed sequences	0.85 BB518668	CAD88592 /// Q60612 /// Q8BGU7 /// Q8CAH1 /// Q8R0M5	
1419245_at	Rab14	RAB14, member RAS oncogene family	0.85 AV339290	AAH56648 /// Q91V41	
1428408_a_at	D12Erd551e	DNA segment, Chr 12, ERATO Doi 551, expressed	0.85 BI102044	AAH59230 /// Q9D5Y7	
		TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor			
1441982_at	Taf7		0.85 BB551747	BAC26429 /// BAC36313 /// Q8BPH4 /// Q8C291 /// Q9R1C0	
1427464_s_at	Hspa6	heat shock 70kD protein 5 (glucose-regulated protein)	0.85 AJ002387	AAH50927 /// BAC36166 /// P20029 /// Q7TMA3 /// Q9DC41	

1437921_x_at	C330029B10Rik	RIKEN cDNA C330029B10 gene	0.85 AW744723	---
1441545_at	9230115F04Rik	RIKEN cDNA 9230115F04 gene	0.85 BM243297	---
1423725_at	Pls3	platin 3 (T-isoform)	0.85 BC005459	Q99K51
1448899_s_at	Rad51ap1	RAD51 associated protein 1	0.85 BC003738	O55219 /// Q8BP36 /// Q8C551 /// Q8C551 /// Q99L94 /// Q9D0J0
1435230_at	Al447928	expressed sequence Al447928	0.85 BB277613	Q80TP9 /// Q8BR16 /// Q8CBV4
1425518_at	Rapgef4	Rap guanine nucleotide exchange factor (GEF) 4	0.85 AK004874	Q8CCU5 /// Q9CS95 /// Q9EQZ6
1448760_at	Zfp68	Zinc finger protein 68	0.85 NM_013844	Q88238 /// Q60910 /// Q8BLK6 /// Q8VEM6 /// Q9Z116
1455875_x_at	Tm9sf2	transmembrane 9 superfamily member 2	0.85 BB131843	BAC33215 /// BAC40645 /// P58021 /// Q8C6H4 /// Q8C7F9
1434888_a_at	Matr3	matrin 3	0.85 BM219545	BAC38009 /// Q7TN66 /// Q8K310
1435129_at	Ptp4a2	protein tyrosine phosphatase 4a2	0.85 AW495875	O70274
1433542_at	Inpp5f	inositol polyphosphate-5-phosphatase F	0.85 BB085335	AAH67200 /// BAC98059 /// Q8C8G7 /// Q8CBW2 /// Q8CDA1
1453314_x_at	2610039C10Rik	RIKEN cDNA 2610039C10 gene	0.85 AK012533	Q9CXR6 /// Q9CZJ6 /// Q9D086
1435001_at	lnrs1abp	influenza virus NS1A binding protein	0.85 BM198417	Q8C6C4
1417815_a_at	Tde1	tumor differentially expressed 1	0.85 NM_012032	Q8C6L8 /// Q9DCF0 /// Q9QZ19
1455963_at	6332401O19Rik	RIKEN cDNA 6332401O19 gene	0.85 AV317707	Q8BN70
1435174_at	Rsb1	rosbin, round spermatid basic protein 1	0.85 AW546080	Q7TNJ3 /// Q80T69 /// Q8BGC6 /// Q8BQ56 /// Q8C2Z3
1435675_at	Tbc1d12	TBC1D12: TBC1 domain family, member 12	0.85 BF228251	Q8K257
1422437_at	Col5a2	collagen, type V, alpha 2	0.85 AV229424	Q61431 /// Q7TMS0 /// Q80VS8 /// Q8BNA3
1430992_s_at	1500009M05Rik	RIKEN cDNA 1500009M05 gene	0.86 BE916591	AAH58279 /// Q9CQB5 /// Q9D0Y0
1418472_at	Aspa	aspartoacylase (aminoacylase) 2	0.86 BC024934	Q8BZC2 /// Q8R3P0
1456856_at	E130120L08Rik	RIKEN cDNA E130120L08 gene	0.86 A1854225	Q8BS59
1424353_at	Lpprc	leucine-rich PPR-motif containing osteoglycin	0.86 BC004681	AAH59862 /// Q8K4V0 /// Q99KF9 /// Q9CRX4
1419663_at	Ogn	osteoglycin	0.86 BB542051	BAC35462 /// Q62000
1439409_x_at	Tyrp1	tyrosinase-related protein 1	0.86 BB006219	P07147
1451510_s_at	Thecd1	thioesterase domain containing 1	0.86 BC025001	Q8R197
1435518_at	Rap1b	RAS related protein 1b	0.86 BM246972	AAH33382 /// AAH52480 /// Q99J16
1428976_at	Tmpo	thymopoietin	0.86 AK017463	BAB27960 /// Q61029 /// Q61033 /// Q9CPQ7
1428579_at	Fmn12	formin-like 2	0.86 AK017338	AAH64731 /// Q7TPA8 /// Q80VH6 /// Q8BI62
1429601_x_at	1110019K23Rik	RIKEN cDNA 1110019K23 gene	0.86 AK003824	---
1455901_at	Chpt1	choline phosphotransferase 1	0.86 A1642069	AAR16089 /// Q8C025 /// Q8K0H2 /// Q91W91
1420866_at	Zfp161	zinc finger protein 161	0.86 NM_009547	BAC29858 /// Q08376
1450418_a_at	2310034L04Rik	RIKEN cDNA 2310034L04 gene	0.87 NM_026417	Q8C407 /// Q99KZ9
1416083_at	Za20d2	zinc finger, A20 domain containing 2	0.87 AA124553	BAC36321 /// Q88878 /// Q9D3C9
1426276_at	Ifih1	interferon induced with helicase C domain 1	0.87 AY075132	Q8BYC9 /// Q8BZ01 /// Q8K5C7 /// Q8R144 /// Q8R5F7 /// Q8VE79 /// Q99KS4 /// Q9D2Z5
1440882_at	Lrp8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	0.87 BB750940	Q924X6
1428268_at	Psd2	pleckstrin and Sec7 domain containing 2	0.87 AK018116	AAH56437 /// AAH62930 /// AAH65053 /// AAH65055 /// AAH66026 /// AAH66036 ///
1456111_at	C130036J11	hypothetical protein C130036J11	0.87 BB072624	Q8BHR9 /// Q9D3B8
1434848_at	Gpr27	G protein-coupled receptor 27	0.87 BB259283	Q8BKV4
1449175_at	Gpr65	G-protein coupled receptor 65	0.87 NM_008152	Q61038
1433751_at	Slc39a10	solute carrier family 39 (zinc transporter), member 10	0.87 BM250411	AAH59214 /// AAH62918 /// Q80TG2 /// Q8BX42 /// Q8C0L2
1421284_at	Pign	phosphatidylinositol glycan, class N	0.87 NM_013784	Q8VCC3 /// Q9R1S2 /// Q9R1S3
1452593_a_at	Tceb1	transcription elongation factor B (SII), polypeptide 1	0.87 A1019214	Q63182
1426407_at	1600010O03Rik	RIKEN cDNA 1600010O03 gene	0.87 B1412951	---
1455181_at	Rasa2	RAS p21 protein activator 2	0.87 BM228516	P58069
1433441_at	Fbx15	F-box and leucine-rich repeat protein 5	0.87 BQ173911	Q8C2S5
1423963_at	Wdr26	WD repeat domain 26	0.87 BC020044	AAH58601 /// Q8C6G8

1424782_at	RIKEN cDNA 2610318G18 gene	0.88 BC024458	Q9CR48 /// Q9D520 /// Q9D835
1460073_at	Mus musculus transcribed sequences	0.88 BE980582	---
1426863_at	RNA binding motif protein, X chromosome	0.88 BM123721	Q8C2U6 /// Q9R0Y0 /// Q9WVW02
1427235_at	ubiquitously transcribed tetra-tripeptide repeat gene, X chromosome	0.88 BG076105	O70546 /// Q7TSG4 /// Q8C4Z1 /// Q8R2W5
1434460_at	Bardet-Biedl syndrome 4 homolog (human)	0.88 BG067572	Q8C1Z7
1454736_at	RIKEN cDNA 4921515A04 gene	0.88 BM119297	Q7TSA5 /// Q8BWN1 /// Q8C0J6 /// Q8C650
1426707_at	tubulin, gamma complex associated protein 3	0.88 BC025647	AAH58566 /// P58854 /// Q8BKJ3
1429033_at	golgi coiled coil 1	0.88 AV339946	AAH66807 /// Q8VC84 /// Q9D4H2
1417191_at	DnaJ (Hsp40) homolog, subfamily B, member 9	0.88 NM_013760	AAH42713 /// Q9QYI6
1441662_at	cytochrome P450, family 4, subfamily X, polypeptide 1	0.88 BB171122	Q8BYS0
1436883_at	RIKEmembrane-bound transcription factor protease, site 2	0.88 BB264953	---
1444602_at	---	0.88 BE136101	---
1448192_s_at	phosphoribosyl pyrophosphate synthetase 1	0.88 AK011304	AAH54772 /// BAA84686 /// BAB27530 /// BAC40697 /// Q9D7G0
1423829_at	RIKEN cDNA 0910001A06 gene	0.88 BC011343	Q921M7
1437156_at	EF hand calcium binding protein 1	0.88 BB392041	AAH67055 /// Q80W91 /// Q8BG18
1441481_at	microfibrillar-associated protein 3-like	0.89 AV262974	Q80TV6 /// Q9D3X9
1427971_at	hyperparathyroidism 2 homolog (human)	0.89 BB622571	Q8JZM7
1450928_at	inhibitor of DNA binding 4	0.89 BB121406	BAC30845 /// P41139
1420514_at	transmembrane 4 superfamily member 10	0.89 NM_138751	Q8C0H5 /// Q9JJG6
1427075_s_at	RIKEN cDNA 5330414D10 gene	0.89 BM117243	Q8BHD8
1428950_s_at	nucleolar protein 8	0.89 AK017551	Q80VB9 /// Q8CDJ7 /// Q9CUR0
1433930_at	heparanase	0.89 BG094050	AAN41636 /// AAQ15188 /// Q8K3K3
1443638_at	Mus musculus transcribed sequences	0.89 BM197773	---
1454642_a_at	COMM domain containing 3	0.89 BB230296	Q8C9P5
1457990_at	RIKEN cDNA C030032C09 gene	0.89 BB080832	Q8BIZ1 /// Q8BJ47 /// Q8BJ49 /// Q8BZM2
1436772_at	glutamate receptor, ionotropic, AMPA4 (alpha 4)	0.89 BB330347	---
1443924_at	protein kinase, lysine deficient 3	0.89 BB084132	AAH60731 /// Q80XP9
1457385_at	translocase of inner mitochondrial membrane 8	0.89 BB796239	---
1459701_x_at	homolog a (yeast)	0.89 AA67488	---
1453070_at	RIKEN cDNA C030033F14 gene	0.90 BB305930	---
1438171_x_at	RIKEN cDNA 0610012D09 gene	0.90 BB056666	AAH68124 /// Q8BJU4 /// Q8R567 /// Q9CTJ3 /// Q9EPL4 /// Q9JJ88
1433788_at	Mus musculus transcribed sequences	0.90 BM942887	---
1422843_at	monooxygenase, DBH-like 1	0.90 NM_021509	AAH57652 /// Q8BUZ7 /// Q8R394 /// Q9CXI3 /// Q8JJJA6
1456812_at	ATP-binding cassette, sub-family D (ALD), member 2	0.90 AW456685	Q61285 /// Q8BQ63 /// Q8C4B6
1420665_at	integrin beta 3 binding protein (beta3-endonexin)	0.90 NM_026348	Q9CQ82
1454764_s_at	solute carrier family 38, member 1	0.90 BF165681	AAH66815 /// Q8BHI3 /// Q8BXE2 /// Q8K2P7 /// Q99PR1
1437791_s_at	RIKEN cDNA 1700016A15 gene	0.90 AV230748	Q8BRL0 /// Q8K0U5 /// Q8R2W0
1441258_at	cDNA sequence AF529169	0.90 BB316516	Q8BQW5 /// Q8K3V7
1418772_at	cDNA sequence BC016423	0.90 NM_134063	BAC87659 /// Q91W76
1457473_at	chromodomain helicase DNA binding protein 1	0.90 AB51787	P40201 /// Q8C9F3 /// Q9CRD9 /// Q9D5K6
1439011_at	RIKEN cDNA 2010109K11 gene	0.90 BB333400	---
1426725_s_at	E26 avian leukemia oncogene 1, 5' domain	0.90 BB151715	AAR00342 /// AAR87824 /// P27577 /// Q8BVW8 /// Q8K3Q9 /// Q921D8
1455177_at	Abelson helper integration site	0.91 BQ175532	AAH65146 /// Q7TNV2 /// Q8K3E4 /// Q8K3E5 /// Q9CVY1
1434045_at	cyclin-dependent kinase inhibitor 1B (P27)	0.91 BB354528	---
1452682_at	RIKEN cDNA 4632404H22 gene	0.91 AK019480	AAH66167 /// Q8BRG5 /// Q8CBB0 /// Q9D2N2

1435350_at	Traf6	Tnf receptor-associated factor 6	0.91 AV377471	AAH60705 /// P70196
1428755_at	3526402H21Rik	RIKEN cDNA 3526402H21 gene	0.91 AK014391	Q9D6D2
1428749_at	6430411K14Rik	RIKEN cDNA 6430411K14 gene	0.91 AK018275	---
1419267_at	Nfyb	nuclear transcription factor-Y beta	0.91 AV250496	P22569 /// Q8C590 /// Q9D056
1438035_at	---	Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430015D03	0.91 BB748934	Q8BSE0 /// Q8CIF1
1442812_at	Anapc5	product:hypothetical protein, full insert sequence anaphase-promoting complex subunit 5	0.91 BB156332	---
1448254_at	Ptn	pleiotrophin	0.91 BC002064	AAH61695 /// BAB27557 /// P20935 /// Q9CSX6
145880_s_at	Becn1	beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)	0.91 C86082	O88597 /// Q99J03
1433856_at	AW555814	expressed sequence AW555814	0.91 AW555814	BAC97950 /// Q7TPL4 /// Q80V47 /// Q8BWK5
1460369_at	LOC233987	similar to zinc finger protein 97	0.92 BC003267	---
1419925_s_at	6430411B10Rik	RIKEN cDNA 6430411B10 gene	0.92 AV259382	AAH57139 /// BAC98261 /// Q8BXZ1 /// Q8BZB8
1428083_at	2310043N10Rik	RIKEN cDNA 2310043N10 gene	0.92 AK018202	---
1460381_at	LOC232855	similar to zinc finger protein 113	0.92 BC023179	Q8R573
1448484_at	Amd1	S-adenosylmethionine decarboxylase 1	0.92 NM_009665	P31154
1448689_at	Rras2	related RAS viral (r-ras) oncogene homolog 2	0.92 NM_025846	P17082 /// Q8C5D1 /// Q9CTF6 /// Q9D0H6
1460252_s_at	Zfp105	zinc finger protein 105	0.92 NM_009544	O88412 /// Q80WR2
1422045_a_at	Ptpn12	protein tyrosine phosphatase, non-receptor type 12	0.92 X63440	P35831 /// Q80UM4
1433857_at	Fath	fat tumor suppressor homolog (Drosophila)	0.92 AV088463	AAP82173 /// Q60833 /// Q80VA2 /// Q80XT9 /// Q9QXA3
1458820_at	---	Mus musculus transcribed sequences	0.92 AV300514	---
1424243_at	Icam1	intercellular adhesion molecule	0.92 AK005797	Q8CAP7 /// Q9CPR1
1460403_at	Psp2	PC4 and SFRS1 interacting protein 2	0.92 BF117241	Q8WQZ7 /// Q99JF7 /// Q99JF8 /// Q99LR4 /// Q9CT03
1456735_x_at	C13009A20Rik	RIKEN cDNA C13009A20 gene	0.92 BB458645	Q8BHA9 /// Q8BZ12 /// Q8BZD5
1448954_at	Nrip3	nuclear receptor interacting protein 3	0.92 NM_020610	Q9JJR9
1428663_at	5133401H06Rik	RIKEN cDNA 5133401H06 gene	0.92 AK017223	---
1435084_at	C730049O14Rik	RIKEN cDNA C730049O14 gene	0.92 BB200607	---
1439441_x_at	Lats2	large tumor suppressor 2	0.93 BB134767	Q7TSJ6 /// Q8CDJ4 /// Q8VHE1 /// Q8VHE2 /// Q9JMI3
1451360_at	1200009B18Rik	RIKEN cDNA 1200009B18 gene	0.93 BC018188	AAH64749 /// Q9CR89 /// Q9CWM6 /// Q9CYA2 /// Q9D4R1 /// Q9D8Z9
1455511_at	Seph1	selenophosphate synthetase 1	0.93 BB354974	AAH65165 /// AAH66037 /// Q8BH69 /// Q8BL02
1423408_a_at	2500003M10Rik	RIKEN cDNA 2500003M10 gene	0.93 BE592070	Q8C5N4 /// Q99KL5 /// Q9CY57 /// Q9D7T3 /// Q9DB03 /// Q9DC54 /// Q9JJ95
1438657_x_at	Ptp4a1	protein tyrosine phosphatase 4a1	0.93 BB043450	Q63739
1420174_s_at	Tax1bp1	Tax1 (human T-cell leukemia virus type I) binding protein 1	0.93 C85320	Q91YT6 /// Q9CVF0 /// Q9DC45
1451217_a_at	1500034J20Rik	RIKEN cDNA 1500034J20 gene	0.93 BC008259	Q9CQU8
1421479_at	Zfp318	zinc finger protein 318	0.93 NM_021346	Q8BMX9 /// Q99PP2 /// Q9JJO1
1425794_at	Polr2	polymerase (DNA directed), alpha 2	0.93 BC006945	AAH64795 /// P33611 /// Q8CIL1 /// Q8VDR3 /// Q922M1 /// Q9CTS2
1426709_a_at	Usp33	ubiquitin specific protease 33	0.93 BG075953	Q80TK2 /// Q80VA4 /// Q8KOI3 /// Q8R5K2 /// Q99K22
1433925_at	---	Mus musculus cDNA clone MGC:76410 IMAGE:6405596, complete cds	0.93 BM212035	AAH58645
1438210_at	9630018L10Rik	RIKEN cDNA 9630018L10 gene	0.93 BB126999	Q80T52 /// Q8BXA3 /// Q8BZC0
1426271_at	Smc5l1	SMC5 structural maintenance of chromosomes 5-like 1 (yeast)	0.93 AV257384	Q80TW7 /// Q8BKX5 /// Q8CG46 /// Q8CHX5 /// Q922K3
1423641_s_at	Cnot7	CCR4-NOT transcription complex, subunit 7	0.93 BC006021	BAC31969 /// Q60809
1428178_s_at	Trappc6b	trafficking protein particle complex 6B	0.93 BG066452	Q8CBK8 /// Q9D289
1429013_at	5330432J06Rik	RIKEN cDNA 5330432J06 gene	0.93 AK021126	Q8BLE6 /// Q8BMO4 /// Q8C0A6 /// Q9D2A4
1433795_at	Tgfb3	transforming growth factor, beta receptor III	0.94 BM122301	O88393
1449079_s_at	Slat10	sialyltransferase 10 (alpha-2,3-sialyltransferase VI)	0.94 NM_018784	Q80UR7 /// Q8BLV1 /// Q8K0W8 /// Q8VIB3 /// Q9CVM3 /// Q9VWV2

1460048_at	---	Mus musculus transcribed sequences	0.94 BB462453	---
1453915_a_at	Slc37a3	solute carrier family 37 (glycerol-3-phosphate transporter), member 3	0.94 AK012071	Q8BVY2 /// Q99JR0
1430996_at	Etnk1	ethanolamine kinase 1	0.94 BG867902	Q8BWW4 /// Q8BXQ0 /// Q8BZY0 /// Q9D4V0
145206_at	C130006E23	hypothetical protein C130006E23	0.94 BQ175276	---
1449056_at	E330009J07Rik	RIKEN cDNA E330009J07 gene	0.94 NM_133929	Q80T18 /// Q8C6M2
1452717_at	Slc25a24	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 24	0.94 BM230959	Q7TPC2 /// Q8BMD8 /// Q8R225
1420618_at	Cpeb4	cytoplasmic polyadenylation element binding protein 4	0.94 NM_026252	Q7TN98 /// Q9D5F3 /// Q9D5G2
1423474_at	Top1	topoisomerase (DNA) I	0.94 BG068053	Q04750 /// Q8BND6
1437500_at	---	Mus musculus transcribed sequence with weak similarity to protein ref NP_081764.1 (M.musculus)	0.94 AV306749	---
1419821_s_at	ldh1	RIKEN cDNA 5730493B19 [Mus musculus]	0.95 A178952	Q88844 /// Q8C338
1448108_at	Tde2	isocitrate dehydrogenase 1 (NADP+), soluble	0.95 AK005203	Q8C5F9 /// Q9QZ18
1436957_at	Gabra3	tumor differentially expressed 2	0.95 AW557545	---
1417340_at	Txn12	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 3	0.95 NM_023140	Q9CQM9
1434461_at	2610041B18Rik	thioredoxin-like 2	0.95 AV025957	AAH57313 /// Q88232 /// Q8CGF2 /// Q8CGG0 /// Q9D082
1418659_at	Clock	circadian locomotor output cycles kaput	0.95 BB203106	BAC97928 /// Q08785 /// Q8BRU1 /// Q8C9W6 /// Q8K1L9
1416488_at	Ccng2	cyclin G2	0.95 U95826	Q08918 /// Q8C9K5
1433478_at	Noc4	neighbor of Cox4	0.95 BQ174254	AAH09103 /// Q70378
1426476_at	Rasa1	RAS p21 protein activator 1	0.95 AA124924	Q91YX7
1449861_at	Nek4	NIMA (never in mitosis gene a)-related expressed kinase 4	0.95 BF181187	AAH57939 /// Q9Z1J2
1431340_a_at	2310002J21Rik	RIKEN cDNA 2310002J21 gene	0.95 AK010048	---
1448745_s_at	Lor	loricrin	0.96 NM_008508	P18165
1437263_at	A730089K16Rik	RIKEN cDNA A730089K16 gene	0.96 BB138441	Q8C904
1429599_a_at	1110019K23Rik	RIKEN cDNA 1110019K23 gene	0.96 AK003824	---
1420809_a_at	1500003O03Rik	RIKEN cDNA 1500003O03 gene	0.96 NM_019769	AAH54733 /// AAH64784 /// BAC32532 /// P61022 /// Q8C6H3
1429534_a_at	Imnt	inner membrane protein, mitochondrial	0.96 BB222675	AAH61010 /// Q7TNE2 /// Q8CAQ8 /// Q9D9F6
1433905_at	Akap7	A kinase (PRKA) anchor protein 7	0.96 BF730930	O55074 /// Q7TN79 /// Q8BVR3
1434776_at	Sema5a	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	0.96 BQ176610	AAH65137 /// Q62217 /// Q8BYL6
1427411_s_at	Dleu2	deleted in lymphocytic leukemia, 2	0.96 BB812902	---
1439904_at	Fstl5	ollistatin-like 5	0.96 BB374771	Q80TG3 /// Q8BFF2 /// Q8C4T3
1416176_at	Hmgb1	high mobility group box 1	0.96 BF166000	AAH64790 /// BAC29902 /// BAC39289 /// P07155 /// Q8BNM0 /// Q8BQ02 /// Q8C7C4
1440325_at	2610209L14Rik	RIKEN cDNA 2610209L14 gene	0.96 AV332226	---
1434553_at	C730036B01Rik	RIKEN cDNA C730036B01 gene	0.96 BB667728	Q8CGF5 /// Q9D4Q8
1436818_a_at	Msi2h	Musashi homolog 2 (Drosophila)	0.97 BB479807	Q920Q6 /// Q920Q7
1433985_at	Abi2	abi-interactor 2	0.97 AV263684	AAH56345
1452960_at	1200016D23Rik	RIKEN cDNA 1200016D23 gene	0.97 BB274851	AAH66800 /// Q8BQC9 /// Q8BRJ1 /// Q8C8F4 /// Q9DBQ7
1428107_at	Sh3bgl	SH3-binding domain glutamic acid-rich protein like solute carrier family 25 (mitochondrial carrier, Graves disease autoantigen), member 16	0.97 AK004519	Q8BHV4 /// Q9JJU8
1434996_at	Slc25a16	APG4 (ATG4) autophagy-related homolog C (S. cerevisiae)	0.97 AV316233	AAH62168 /// Q8C0K5
1434014_at	Apg4c	hypothetical protein C730026J16	0.97 BB291836	AAH58981
1434687_at	C730026J16	hypothetical protein C730026J16	0.97 BE456566	Q8BIL1 /// Q8BW24 /// Q8BW71

1450858_a_at Ube2d3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	0.97 AK009276	P61079 /// Q9D1S1 /// Q9D7F5
1438933_x_at ---	Mus musculus, Similar to RAS, guanyl releasing protein 2, clone IMAGE:4481738, mRNA	0.97 BE688720	O09004 /// Q80WCO /// Q8BSC8 /// Q9QUG9
1441799_at ---	Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030422H21 product:unknown EST, full insert sequence	---	---
1417980_a_at Insig2	Insulin induced gene 2	0.97 A098139	Q8BWP1 /// Q91WG1
1423032_at Rpl39	ribosomal protein L39	0.97 AV107150	P02404
1426448_at Pta1	praja1, RING-H2 motif containing	0.97 BM199789	O55176
1422244_at Pkdrej	polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like	0.97 NM_011105	Q8C0Z9
1416267_at Socc	short coiled-coil protein	0.97 NM_019708	BAB22159 /// Q8C6K2 /// Q9CWN2 /// Q9CY27 /// Q9WU55
1449047_at Hpol-pending	2-hydroxyphytanoyl-CoA lyase	0.97 NM_019975	BAC31032 /// BAC34059 /// Q9QXEO
1427277_at Six1	sine oculis-related homeobox 1 homolog (Drosophila)	0.97 BB137929	Q62231 /// Q8BSP4
1455407_at Zfp236	zinc finger protein 236	0.97 BB282741	Q8BI89 /// Q8BIE3
1434194_at Mtap2	microtubule-associated protein 2	0.97 AV337593	P20357 /// Q80X35 /// Q80ZL4
1415864_at Bpgm	2,3-bisphosphoglycerate mutase	0.97 NM_007563	BAC31541 /// BAC37133 /// P15327
1434889_at A430081P20Rik	RIKEN cDNA A430081P20 gene	0.97 B1905111	Q8BYE3
1421519_a_at Zfp120	zinc finger protein 120	0.97 NM_023266	Q8BZW4 /// Q9EQK2 /// Q9EQK4 /// Q9JIB8
1449972_s_at Zfp97	zinc finger protein 97	0.97 NM_011765	---
1456199_x_at ---	Mus musculus, clone IMAGE:6512643, mRNA	0.97 BB106402	---
1421830_at Ak4	adenylate kinase 4	0.97 NM_009647	Q9WUR9
1423543_at Swap70	SWAP complex protein	0.97 AK019882	AAH65136 /// O88443
1457124_at ---	Mus musculus transcribed sequences	0.98 AV328224	---
1418070_at Cdy1	chromodomain protein, Y chromosome-like	0.98 AF081260	AAH62123 /// Q9WTK2
1426999_at 1700016A15Rik	RIKEN cDNA 1700016A15 gene	0.98 BM198642	Q8BIY8 /// Q8BJ05 /// Q8R3Q8 /// Q8R3R2 /// Q9DAA8
1425826_a_at Sorbs1	sorbin and SH3 domain containing 1	0.98 AF078667	Q62417 /// Q80TF8 /// Q8BZ13 /// Q8K3Y2 /// Q921F8 /// Q9Z0Z8 /// Q9Z0Z9
1430314_at 4933437F05Rik	RIKEN cDNA 4933437F05 gene	0.98 BB217068	Q9D3S5
1454826_at Cltc	clathrin, heavy polypeptide (Hc)	0.98 BM211219	Q8OU89 /// Q8K2I5
1442760_x_at ---	Mus musculus transcribed sequences	0.98 BB206454	---
1423114_at Ube2d3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	0.98 AK009276	P61079 /// Q9D1S1 /// Q9D7F5
1456060_at Maf	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog	0.98 AV284857	---
1436981_a_at Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	0.98 BB706206	---
1421750_a_at Vbp1	von Hippel-Lindau binding protein 1	0.98 NM_011692	Q15765 /// Q9CPZ0
1417549_at Zip68	Zinc finger protein 68	0.99 NM_013844	O88238 /// Q60910 /// Q8BLK6 /// Q8VEM6 /// Q9Z116
1422576_at Sca10	spinocerebellar ataxia 10 homolog (human)	0.99 NM_016843	BAC32981 /// BAC37285 /// P28658 /// Q8BWX1
1434278_at ---	---	0.99 BG976607	---
1445367_at ---	Mus musculus transcribed sequences	0.99 C76202	---
1432195_s_at Ccnl2	cyclin L2	0.99 AK008585	Q60995 /// Q8BLP2 /// Q8CIJ8 /// Q99L73 /// Q9CVZ6 /// Q9D814 /// Q9JJA7 /// Q9QXH5
1416861_at Stam	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	0.99 NM_011484	P70297
1416998_at Rrs1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	0.99 NM_021511	Q9CYH6

1423096_at	Capn7	calpain 7	0.99 BQ257745	Q9R1S8
1456862_at	Six4	sine oculis-related homeobox 4 homolog (Drosophila)	0.99 A1893638	Q61321
1427504_s_at	Sfrs2	splicing factor, arginine/serine-rich 2 (SC-35)	0.99 AF250133	BAC39610 /// BAC40111 /// Q06477 /// Q62093 /// Q8C671 /// Q99MY4 /// Q99MY5
1428471_at	Sorbs1	sorbin and SH3 domain containing 1	0.99 BQ176684	Q62417 /// Q80TF8 /// Q8BZ13 /// Q8K3Y2 /// Q921F8 /// Q920Z8 /// Q9Z0Z9
1423378_at	Adam23	a disintegrin and metalloprotease domain 23	0.99 A1838132	AAS49900 /// AAS49901 /// Q9R1V7
1418529_at	Osgp	O-sialoglycoprotein endopeptidase	0.99 NM_133676	Q8BWU5
1454980_at	AU018056	expressed sequence AU018056	0.99 BB667201	BAC98282 /// Q7TSQ8
1428938_at	Gnaq	guanine nucleotide binding protein, alpha q polypeptide	0.99 W41916	AAH57583 /// P21279 /// Q8C6U1
1418150_at	Mtmr4	myotubularin related protein 4	0.99 BQ032797	AAH58091 /// AAH58364 /// Q91XS1
1424895_at	Gpsm2	G-protein signalling modulator 2 (AGS3-like, C. elegans)	0.99 BC021308	Q8BLX3 /// Q8VDU0
1451133_s_at	8430437G11Rik	RIKEN cDNA 8430437G11 gene	0.99 BC007160	Q91VX9
1450899_at	Nedd1	neural precursor cell expressed, developmentally down-regulated gene 1	1.00 BB829652	AAH66870 /// P33215 /// Q8BN12 /// Q8BN86 /// Q8BQL9 /// Q9CWNK2
1419181_at	Zfp326	zinc finger protein 326	1.00 NM_018759	O88291 /// Q8BSJ5 /// Q8K1X9 /// Q9CYG9
1448502_at	Slc16a7	solute carrier family 16 (monocarboxylic acid transporters), member 7	1.00 NM_011391	BAC36415 /// OT0451
1415894_at	Enpp2	ectonucleotide pyrophosphatase/phosphodiesterase 2	1.00 BC003264	AAH58759 /// Q8CAF0 /// Q9R1E6
1458693_at	---	Mus musculus transcribed sequences	1.00 BB461850	---
1419252_at	Eps15	epidermal growth factor receptor pathway substrate 15	1.00 BG067649	P42567 /// Q80ZL3 /// Q8C431
1433976_at	---	Mus musculus, clone IMAGE:5355681, mRNA	1.00 B1249740	---
1451047_at	Ilm2a	integral membrane protein 2A	1.00 B1966443	Q61500 /// Q8K0H4 /// Q9CRW4
1448933_at	Pcdhb17	protocadherin beta 17	1.00 NM_053142	Q80TB2 /// Q91VD8 /// Q925L4
1424873_at	Rnr2	ring finger protein 2	1.00 BC020122	O35699 /// O35729 /// Q8C1X8 /// Q9CQJ4
1435990_at	5730596K20Rik	RIKEN cDNA 5730596K20 gene	1.00 BB795103	---
1425494_s_at	Bmpr1a	bone morphogenetic protein receptor, type 1A	1.00 BM939768	AAQ64630 /// P36895
1427269_at	2610019N13Rik	RIKEN cDNA 2610019N13 gene	1.00 AW261583	Q8BV04 /// Q8BYD3 /// Q8C0Z3 /// Q8CFF2 /// Q8CGI3 /// Q9CT17
1457568_at	C230004L04	hypothetical protein C230004L04	1.00 BB380198	---
1449128_at	D11Erd707e	DNA segment, Chr 11, ERATO Doi 707, expressed transmembrane 6 superfamily member 1	1.00 NM_025918	AAH58520 /// AAH61076 /// Q9CR29
1424443_at	Tm6sf1	transmembrane 6 superfamily member 1	1.00 AV378394	P56749 /// Q8BUN7
1441145_at	D030065N23Rik	RIKEN cDNA D030065N23 gene	1.01 BB448266	---
1435042_at	9130004C02Rik	RIKEN cDNA 9130004C02 gene	1.01 BG296454	---
1426558_x_at	3100002L24Rik	RIKEN cDNA 3100002L24 gene	1.01 BB283527	Q8BHI0
1442210_at	1700058C01Rik	RIKEN cDNA 1700058C01 gene	1.01 AV273577	Q8BII1
1428103_at	Adam10	a disintegrin and metalloprotease domain 10	1.01 AV327574	AAH66207 /// O35598
1420772_a_at	Gliz	glucocorticoid-induced leucine zipper	1.01 NM_010286	Q8K160 /// Q9EQN0 /// Q9EQN1 /// Q9EQN2 /// Q9Z2S7
1428011_a_at	Erbp2ip	Erbp2 interacting protein	1.01 BC028256	Q80TH2 /// Q8BQ14 /// Q8K171 /// Q99JU3 /// Q9J147
1452659_at	Dek	DEK oncogene (DNA binding)	1.02 AK007546	Q7TNV0 /// Q80VC5 /// Q8BZV6 /// Q9CVL7
1434339_at	2610318I01Rik	RIKEN cDNA 2610318I01 gene	1.02 AW548221	Q8K012
1428652_at	0610010F05Rik	RIKEN cDNA 0610010F05 gene	1.02 BB469274	BAC98264 /// Q8BPK6 /// Q9CWA7
1419750_at	Dnm12	DNA methyltransferase 2	1.02 BB010597	O50555 /// Q8C7F0 /// Q8CE27
1457741_at	Tex2	testis expressed gene 2	1.02 AV377040	---
1448922_at	Dusp19	dual specificity phosphatase 19	1.02 NM_024438	Q8K4T5 /// Q99N12 /// Q9CRR3 /// Q9D6P6
1428693_at	2610044O15Rik	RIKEN cDNA 2610044O15 gene	1.02 AK011776	Q8BG62
1442810_x_at	---	Mus musculus transcribed sequences	1.02 BB452274	Q62205
1435190_at	Chl1	close homolog of L1	1.02 BB378591	P70232 /// Q8BS24 /// Q8C6W0 /// Q8C823

1455029_at	Klf21a	kinesin family member 21A Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630041108	1.02 BB342219	AAH60698 /// AAH62896 /// BAC98236 /// Q8BWZ9 /// Q8BXF1 /// Q8BXG5 /// Q9QXL2
1439732_at	---	product:unknown EST, full insert sequence	---	---
1420675_at	Zfp113	zinc finger protein 113	1.02 BB129764	---
1435181_at	A461788	expressed sequence A461788	1.03 NM_019747	AAH56445 /// Q8C889
1435899_at	9430079B08Rik	RIKEN cDNA 9430079B08 gene	1.03 BG073348	Q8BMU8 /// Q8C107
1418649_at	Egln3	EGL nine homolog 3 (C. elegans)	1.03 BE136439	---
1448557_at	1200015N20Rik	RIKEN cDNA 1200015N20 gene	1.03 BB284358	Q91UZ4
1452328_s_at	Pja2	praja 2, RING-H2 motif containing	1.03 NM_024244	AAH66835 /// Q8BLV7 /// Q99LJ4 /// Q9D8R2
1440651_at	Dusp16	dual specificity phosphatase 16	1.03 BF160731	Q8OU04 /// Q810E3 /// Q91W46 /// Q99KC0
1439806_at	---	Mus musculus adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330007G10	1.03 BM238701	---
1450950_at	Cspg6	product:unknown EST, full insert sequence	1.03 BB184086	---
1450017_at	Ccng1	chondroitin sulfate proteoglycan 6	1.03 AK005647	AAH36330 /// AAH57345 /// AAH62935 /// Q9CW03
1416015_s_at	Abce1	ATP-binding cassette, sub-family E (OABP), member 1	1.04 BG065754	AAH05534 /// P51945
1424156_at	Rbl1	retinoblastoma-like 1 (p107)	1.04 NM_015751	AAH66794 /// AAH66836 /// P61222 /// Q8C2N8
1434191_at	A530016O06Rik	RIKEN cDNA A530016O06 gene	1.04 U27177	AAH60124 /// Q64701 /// Q8BTA6 /// Q8CCD4
1426088_at	---	---	1.04 A790538	Q8BS35 /// Q8C7H5 /// Q8CAA6
1429690_at	1300003B13Rik	RIKEN cDNA 1300003B13 gene	1.04 BC004015	---
1424733_at	P2y14	purinergic receptor P2Y, G-protein coupled, 14	1.04 AK004870	Q8K3B4
1422869_at	Merk	c-met proto-oncogene tyrosine kinase	1.04 AF177211	BAC30456 /// Q9ESG6
1435265_at	---	Mus musculus transcribed sequences	1.04 NM_008587	Q60805 /// Q8C584 /// Q8CE52
1451626_x_at	---	---	1.04 BF466929	---
1418308_at	Hus1	Hus1 homolog (S. pombe)	1.05 U58494	---
1459321_at	---	Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330109G15	1.05 NM_008316	AAH61249 /// O70543 /// Q8BQY8
1428522_at	Thf2	product:unknown EST, full insert sequence	1.05 BB075541	---
1451127_at	AW146242	transcription termination factor, RNA polymerase II	1.05 BB283807	---
1441980_at	C030007I09Rik	expressed sequence AW146242	1.05 BC024822	Q8C0B7 /// Q8R1C3
1421546_a_at	Racgap1	RIKEN cDNA C030007I09 gene	1.05 BB355593	Q8BQT9
1418664_at	Mpdz	Rac GTPase-activating protein 1	1.05 NM_012025	Q9WVM1
1422702_at	Oazin	multiple PDZ domain protein	AAH61504 /// AAL37377	/// Q08783 /// Q80ZY8 /// Q8C0H8 /// Q8VBV5 /// Q8VBX6 ///
1427208_at	Zfp451	ornithine decarboxylase antizyme inhibitor	Q8VBY0 /// Q9Z1K3	Q8VBY0 /// Q9Z1K3
1416187_s_at	Pncr2	zinc finger protein 451	1.05 AK019164	BAC33870 /// BAC40494 /// Q35484 /// Q8C2R8 /// Q8K1E5
1458075_at	---	proline-rich nuclear receptor coactivator 2	1.05 BE626090	AAH62154 /// Q80TA4 /// Q811K1 /// Q8C0P7 /// Q8R0N3 /// Q8R1L1 /// Q8R5E1 /// Q8VCL4
1439012_a_at	Dck	Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B930079L03	1.05 BC024435	/// Q9CUK0
1435590_at	D430047L21Rik	product:unknown EST, full insert sequence	1.05 NM_026383	Q9CR73 /// Q9CXC6
1439753_x_at	Six4	deoxycytidine kinase	1.05 BB350401	---
1415863_at	Eif4g2	RIKEN cDNA D430047L21 gene	1.06 BB030204	BAB23394 /// BAB27131 /// BAC33307 /// BAC40203 /// P43346 /// Q8OUS6
1423824_at	5031439A09Rik	sine oculis-related homeobox 4 homolog (Drosophila)	1.06 AV325177	---
		eukaryotic translation initiation factor 4, gamma 2	1.06 AI898638	Q61321
		RIKEN cDNA 5031439A09 gene	1.06 NM_013507	AAH64810 /// Q62448
			1.06 BC018381	Q8CD50 /// Q8CDZ6 /// Q8CE42 /// Q9D2B7

1416700_at	Arie	ras homolog gene family, member E	1.06 BC009002	BAC28975 /// P61588	
1426405_at	Rnf11	ring finger protein 11	1.06 B1150320	Q9QYK7	
1455164_at	Cdgap	Cdc42 GTPase-activating protein	1.06 AV308092	BAC98119 /// Q9WV94	
1429908_at	6530403A03Rik	RIKEN cDNA 6530403A03 gene	1.06 AK004216	Q8BIU0 /// Q8BJ30 /// Q8BMZ0 /// Q8CFF6 /// Q8VDQ5 /// Q9CSG3 /// Q9CVM5 /// Q9D361	
1435543_at	Laiba	lactalbumin, alpha	1.06 BM124893	P70382 /// Q61315 /// Q8BNP7 /// Q8BRD8 /// Q8C919	
1426880_at	9430077C05Rik	RIKEN cDNA 9430077C05 gene	1.06 BM250266	BAD14929 /// BAD14930 /// Q80VK2 /// Q8BHX8 /// Q8BHY1 /// Q8CHA8 /// Q8ROK6 ///	
1443657_at	Hook3	hook homolog 3 (Drosophila)	1.06 BB825115	Q8CX18	
1434109_at	Sh3bgr12	SH3 domain binding glutamic acid-rich protein like 2	1.06 BB825115	Q8BIUK6	
1422059_at	Camk2d	calcium/calmodulin-dependent protein kinase II, delta	1.06 AV291265	Q8BG73 /// Q8C073 /// Q8C0Z4	
1428248_at	Nfx1	nuclear transcription factor, X-box binding 1	1.07 NM_023813	AAH52894 /// Q70459 /// Q8C3F8 /// Q8C413 /// Q8CBX9 /// Q8CAC5 /// Q8CCM0 /// Q9CZE2	
1459843_s_at	Smad1	MAD homolog 1 (Drosophila)	1.07 AK005038	Q7TPT4 /// Q8C6R0 /// Q8CC59 /// Q8D9E1 /// Q9DBC8 /// Q9JKW7	
1434413_at	Igf1	insulin-like growth factor 1	1.07 BB257769	AAH58693 /// BAC35658 /// P70340 /// Q8CB69	
1455938_x_at	Rad21	insulin-like growth factor 1	1.07 BG092677	AAL34535 /// P05017 /// P05018 /// Q8C4U6 /// Q8CAR0	
1453399_at	Ccnt2	RAD21 homolog (S. pombe)	1.07 AV025454	BAC97860 /// Q61550 /// Q810A8	
1436594_at	Fusip1	cyclin T2	1.07 AK013634	Q7TQK0 /// Q8VCM9 /// Q9D6H3	
1423982_at	Sparg1	RIKEN cDNA C630016O21 gene	1.07 BB281667	Q8BIV1	
1416114_at	Sparg1	FUS interacting protein (serine-arginine rich) 1	1.07 AF060490	Q8CF51 /// Q9ROU0	
1439026_at	Sparg1	SPARC-like 1 (mast9, hev9)	1.07 NM_010097	P70663	
1428875_at	Golp4	RIKEN cDNA 6330504P12 gene	1.07 BB125842	---	
1457632_s_at	Mrg1	golgi phosphoprotein 4	1.07 BE981485	Q8BV17 /// Q8BWP9 /// Q8BXA1	
1416688_at	Snap91	myeloid ecotropic viral integration site-related gene 1	1.07 BB207647	AAH17375 /// P97367	
1428944_at	5730469D23Rik	synaptosomal-associated protein 91	1.07 NM_013669	Q61548 /// Q7T120 /// Q8BQA2 /// Q8CHE0 /// Q8K0D4	
1457392_at	A1450757	RIKEN cDNA 5730469D23 gene	1.07 BB417360	AAH63048 /// Q8C7R4	
1434671_at	B230337E12Rik	expressed sequence A1450757	1.07 BB055966	AAH63761 /// Q8BZX4	
1459991_at	4732465J09Rik	RIKEN cDNA B230337E12 gene	1.08 BM120593	---	
1426218_at	Glccl1	RIKEN cDNA 4732465J09 gene	1.08 BB104162	Q8DY92 /// Q8COU0 /// Q8C170	
1452953_at	1810036I24Rik	glucocorticoid induced transcript 1	1.08 AA152997	Q8DYT1 /// Q8CEA5 /// Q8K319 /// Q925C1 /// Q9D6W9	
1419062_at	Epb4.1l3	erythrocyte protein band 4.1-like 3	1.08 AK017572	Q9D8T4	
1452291_at	Centd1	centaurin, delta 1	1.08 NM_013813	Q8BT38 /// Q9WV92	
1448584_at	1200013F24Rik	RIKEN cDNA 1200013F24 gene	1.08 AV375176	Q80TX2 /// Q8BY88 /// Q8BYL0 /// Q8BZ05 /// Q8C3T2 /// Q8VEL6	
1435993_at	---	Mus musculus transcribed sequences	1.08 NM_025822	Q80XR9 /// Q8BR75 /// Q8CF54 /// Q8CF40 /// Q9CSR8 /// Q9D0Y1	
1434759_at	Lrrtm3	leucine rich repeat transmembrane neuronal 3	1.08 BB027219	---	
1416440_at	Cd164	CD164 antigen	1.08 NM_016898	Q8BGJ7 /// Q8BZ81 /// Q8BZA0	
1452750_at	---	Mus musculus, clone IMAGE:3676181, mRNA	1.08 BB820846	---	
1427042_at	Mal2	mal, T-cell differentiation protein 2	1.08 BB127697	Q8BI08	
1452876_x_at	2610040I015Rik	RIKEN cDNA 2610040I015 gene	1.08 AK011776	Q8BG62	
1452054_at	6130401J04Rik	RIKEN cDNA 6130401J04 gene	1.08 BB796558	Q8BVJ8 /// Q8YDVW4 /// Q9D5H3	
1444425_at	---	Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630017L16	1.08 BE994902	---	
1426924_at	2900024N03Rik	product unknown EST, full insert sequence	1.09 AA709668	---	
1451867_x_at	Arhgap6	RIKEN cDNA 2900024N03 gene	1.09 AF177664	O54834 /// Q8BG83 /// Q8C842 /// Q8C8B2	
1435459_at	Fmo2	Rho GTPase activating protein 6	1.09 BM936480	Q8K2I3 /// Q9QZF7	
1424369_at	Psmf1	flavin containing monooxygenase 2	1.09 BC012260	Q8BHL8 /// Q8C0G9 /// Q91X47	
1451033_a_at	Trpc4	proteasome (prosome, macropain) inhibitor subunit 1	1.09 BB271442	Q8BNT2 /// Q9QUO5	
1428883_at	1110007C24Rik	transient receptor potential cation channel, subfamily C, member 4	1.09 AK003528	AAH56944 /// AAQ64008 /// Q7TQE6 /// Q80SV6 /// Q80YA4 /// Q9CTI0	

1458709_a_at	2810423G08Rik	RIKEN cDNA 2810423G08 gene	1.09 AV274704	---
1418815_at	Cdh2	cadherin 2	1.09 BC022107	AAH22107 /// P15116 /// Q8BSI9
1456359_at	4632422M10Rik	RIKEN cDNA 4632422M10 gene	1.09 AV23215	Q8C908 /// Q8CEC6
1433894_at	Pde3b	phosphodiesterase 3B, cGMP-inhibited	1.09 AV270888	---
1442598_at	Prkrip1	Prkr interacting protein 1 (IL11 inducible)	1.09 AV324577	Q8BL85 /// Q9CWW6 /// Q9CXA5 /// Q9CY32
1418357_at	Foxg1	forkhead box G1	1.09 NM_008241	Q60987 /// Q80VP3
1423549_at	Slc1a4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	1.09 BB277461	O35874 /// Q8BXT5 /// Q9ESU8
1426065_a_at	lfd2	induced in fatty liver dystrophy 2	1.09 BC012955	CAD55728 /// Q8K4K2
1449886_s_at	Scp2	sterol carrier protein 2, liver	1.10 C76618	P32020
1417622_at	Slc12a2	solute carrier family 12, member 2	1.10 BG069505	P55012
1436791_at	Vnt5a	wingless-related MMTV integration site 5A	1.10 BB067079	P22725 /// Q8BM17 /// Q8BMF9 /// Q8VCV6
1433537_at	4833408C14Rik	RIKEN cDNA 4833408C14 gene	1.10 AV112912	---
1425485_at	Mtmr6	myotubularin related protein 6	1.10 BC020019	Q8VE11
1435637_at	2310047C21Rik	RIKEN cDNA 2310047C21 gene	1.10 AW554709	Q99KW9
1451324_s_at	3830421F13Rik	RIKEN cDNA 3830421F13 gene	1.10 BC010204	Q8BVM8 /// Q8K361 /// Q91Z49 /// Q921B0 /// Q9D6A8
1443392_at	Trpv1	transient receptor potential cation channel, subfamily V, member 1; capsaicin receptor; vanilloid receptor subtype 1	1.10 BB346256	---
1434283_at	Dest	developmentally and sexually retarded with transient immune abnormalities	1.10 BB079486	Q8BM75
1434860_at	---	Mus musculus transcribed sequences	1.10 BQ176197	---
1447985_s_at	Ank1b1	ankyrin repeat and IBR domain containing 1	1.11 C80642	BAC98153
1453152_at	Mamdc2	MAM domain containing 2	1.11 AK004794	Q8CG85
1457164_at	Anktn1	ANKTM1	1.11 BB309395	Q8BLA8
1429371_at	2810426N06Rik	RIKEN cDNA 2810426N06 gene	1.11 AK013166	AAH27798 /// Q8BUQ3 /// Q9CRL6 /// Q9CZ01
1434302_at	9430025M21Rik	RIKEN cDNA 9430025M21 gene	1.11 AV307311	---
1449431_at	Trpc6	transient receptor potential cation channel, subfamily C, member 6	1.11 NM_013838	AAH67391 /// AAH68310 /// Q61143
1426840_at	Ythdf3	YTH domain family 3	1.11 BB183208	Q8R5D2
1417770_s_at	Psmc6	proteasome (prosome, macropain) 26S subunit, ATPase, 6	1.11 AW208944	AAH57997 /// Q810A6 /// Q8QZS9 /// Q92524 /// Q9CXH9
1416152_a_at	Sfrs3	splicing factor, arginine/serine-rich 3 (SRp20)	1.11 NM_013663	AAH68111 /// BAC37445 /// P23152 /// Q8C3H6 /// Q9D6W4
1452176_at	Nup153	nucleoporin 153	1.11 BB292874	Q8OUN3 /// Q80WR07 /// Q8BRF6 /// Q8R2M9
1433502_s_at	AW550801	expressed sequence AW550801	1.12 BM213835	BAC98160 /// Q8K2F5
1426358_at	2810468K05Rik	RIKEN cDNA 2810468K05 gene	1.12 BB272466	Q8JX2 /// Q8VE26 /// Q91VG7 /// Q9D3K9
1451624_a_at	1700048E23Rik	RIKEN cDNA 1700048E23 gene	1.12 BC025612	Q9D9M5
1427167_at	Al448196	expressed sequence Al448196	1.12 BE865094	Q8K2R3 /// Q8R103
1439059_at	BC031748	cDNA sequence BC031748	1.12 BB709811	Q8K2D0
1440226_at	9430018I06	hypothetical protein 9430018I06	1.12 BB088782	Q8C9G1
1437111_at	A230108E06	hypothetical protein A230108E06	1.12 BB183628	---
1436202_at	9430072K23Rik	RIKEN cDNA 9430072K23 gene	1.12 AI853644	---
1451074_at	Rnf13	ring finger protein 13	1.12 AF037205	AAH58182 /// O54965 /// Q8CB78
1439088_at	Pdzk8	PDZ domain containing 8	1.12 BB102308	---
1460357_at	Ythdf2	YTH domain family 2	1.13 BB455932	Q8BM70 /// Q8BUJ8 /// Q8K325 /// Q91YT7
1453456_at	2900084O13Rik	RIKEN cDNA 2900084O13 gene	1.13 BM117709	---
1428607_at	Araf	raf-related oncogene	1.13 AK010060	P04627 /// Q8CAD1
1435167_at	Ranbp6	RAN binding protein 6	1.13 AW108431	Q8BNV3

1455434_a_at	Ktn1	kinectin 1	Q61595 /// Q8BG49 /// Q8BHF4 /// Q8BHM8 /// Q8C9Y5 /// Q8CG51 /// Q8CG52 /// Q8CG55 /// Q8CG54 /// Q8CG55 /// Q8CG56 /// Q8CG57 /// Q8CG58 /// Q8CG59 /// Q8CG60 ///
1454666_at	9930027G08Rik	RIKEN cDNA 9930027G08 gene	
1440354_at	Elov17	ELOVL family member 7, elongation of long chain fatty acids (yeast)	
1427683_at	Egr2	early growth response 2	1.13 BF162017 1.13 AV230488
1447522_s_at	5430432P15Rik	RIKEN cDNA 5430432P15 gene	1.13 AV230488 1.13 AV230488
1440354_at	Elov17	ELOVL family member 7, elongation of long chain fatty acids (yeast)	1.13 BB149977 1.13 X06746
1427683_at	Egr2	early growth response 2	1.13 X06746 1.13 A1662480
1447522_s_at	5430432P15Rik	RIKEN cDNA 5430432P15 gene	1.13 A1662480 1.13 A1662480
1460044_at	---	---	1.13 BB389395 1.13 NM_133739
141417222_a_at	2310075C12Rik	Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230062K19 product:unknown EST, full insert sequence	Q8CEX4 /// Q91Z22 BAC97984 /// Q9CTE0 /// Q9JLV5
14343717_at	Cul3	culin 3	1.13 BM198837 1.13 BI076832
1433784_at	9030612M13Rik	RIKEN cDNA 9030612M13 gene	1.13 BI076832 1.13 BB745314
1429108_at	Msl2	male-specific lethal-2 homolog (Drosophila)	1.13 BB745314 1.14 W91587
1427195_at	---	---	1.14 W91587 1.14 BB031756
141419087_s_at	Sf3a1	Mus musculus, clone IMAGE:3983419, mRNA splicing factor 3a, subunit 1	1.14 BB031756 1.14 NM_026106
1416018_at	Dr1	down-regulator of transcription 1	Q91WV0 Q8R1T0 /// Q924D0
1417668_at	Rtn4p1	reticulon 4 interacting protein 1	1.14 NM_130892 1.14 NM_130892
1418736_at	B3gal13	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 3	1.14 BC003835 1.14 NM_019484
1422993_s_at	Thoc4	THO complex 4	O08583 1.14 AV234245
1427131_s_at	1810012N18Rik	RIKEN cDNA 1810012N18 gene	1.14 AV234245 1.15 AV174556
1425020_at	Ubx4	UBX domain containing 4	1.15 AV174556 1.15 BB817800
1438029_at	4930535B03Rik	RIKEN cDNA 4930535B03 gene	1.15 BB817800 1.15 BC021522
1418997_at	4930469P12Rik	RIKEN cDNA 4930469P12 gene	AAH67054 /// BAC97960 /// Q8BU73 /// Q9D4Z4 Q8VDL7 /// Q91V16
1454768_at	Kcnf1	potassium voltage-gated channel, subfamily F, member 1	1.15 AV337635 1.15 BG261945
1451840_at	Kcnip4	Kv channel interacting protein 4	AAH51130 /// Q8CAD0 /// Q8R4I2 /// Q9EQ01
1416487_a_at	Yap	yap-associated protein	AAH39125 /// P46938 /// Q91WL1
1454795_at	Cobl1	Cobl-like 1	1.15 NM_009534 1.15 AV080881
1429063_s_at	Kif16b	kinesin family member 16B	AAH67007 /// Q7TQM8 /// Q8BJK8 /// Q8BWB9 /// Q8BWH3
1436231_at	2900052N01Rik	RIKEN cDNA 2900052N01 gene	1.15 BG066903 1.15 AU067665
1424674_at	Sic39a6	solute carrier family 39 (metal ion transporter), member 6	Q8C7N3 /// Q8CAM6 Q7TTPP /// Q7TQE0 /// Q8C145 /// Q8R518
1453188_at	6230424C14Rik	RIKEN cDNA 6230424C14 gene	1.16 BB825002 1.16 A1553459
1427432_a_at	Sfrs10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	1.16 BM238387 1.16 BB452274
14472809_at	---	Mus musculus transcribed sequences	Q62205 1.16 NM_133736
14147466_at	Rgs5	regulator of G-protein signaling 5	BAC31773 /// BAC35655 /// O08850 /// Q99JV0
1454869_at	Wdr40b	WD repeat domain 40B	1.16 BB274776 1.16 NM_133736
1436432_at	B230343J05Rik	RIKEN cDNA B230343J05 gene	AAH68319 /// Q8C8E2 /// Q8CA30 /// Q8CAL3 /// Q8CBW4 /// Q8CBX8
1436997_x_at	Sh3bgr1	SH3-binding domain glutamic acid-rich protein like	1.16 BM941461 1.16 BB248904
1418046_at	Nap112	nucleosome assembly protein 1-like 2	Q8BHV4 /// Q9JJU8 P51860 /// Q8K3R9
1450934_at	Eif4a2	eukaryotic translation initiation factor 4A2	1.16 NM_008671 1.16 BM240314
1419599_s_at	Ms4a6d	membrane-spanning 4-domains, subfamily A, member 6D	BAC36372 /// P10630 /// Q8BTU6 1.16 NM_026835
1447977_x_at	---	---	1.16 NM_026835 1.17 C77009
1434106_at	Epm2a1p1	EPH2A (laforin) interacting protein 1	1.17 AV340515 Q80TS4 /// Q8VEH5

1429940_at	8430414L16Rik	RIKEN cDNA 8430414L16 gene	1.17 BM935271	Q8JZM7	
1429177_x_at	Sox17	SRY-box containing gene 17	1.17 AK004781	AAH60812 /// Q61473	
1437635_at	Dcbl2	discolidin, CUB and LCC1 domain containing 2	1.17 AW146002	AAH66097 /// Q8BK14 /// Q91ZH3 /// Q91ZV3 /// Q9D9K5	
1438673_at	Sic4a7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	1.17 AV555750	Q8BTY2 /// Q8BWMZ4 /// Q5JLQ9	
1459713_s_at	AU040576	expressed sequence AU040576	1.17 AU040576	AAH62959 /// Q8BHY3 /// Q8BI26 /// Q99JK1	
1452700_s_at	1110008P08Rik	RIKEN cDNA 1110008P08 gene	1.17 AK003597	---	
1433885_at	---	Mus musculus, Similar to IQ motif containing GTPase activating protein 2, clone IMAGE:3596508, mRNA, partial cds	1.17 BM240173	Q7TMU5 /// Q811L1 /// Q8BV47 /// Q8C9I3	
1437403_at	E130306M17Rik	RIKEN cDNA E130306M17 gene	1.17 BB308071	Q8BJC5	
1454084_a_at	Serp8	SUMO/sentrin specific protease family member 8	1.18 AK018606	BAC33554 /// Q9DZ24	
1436325_at	Rora	RAR-related orphan receptor alpha	1.18 BB306272	P51448 /// Q8BRL5 /// Q8C3F5	
1423839_a_at	Btf3	basic transcription factor 3	1.18 BC008233	AAH08233 /// AAH64010 /// Q64152 /// Q9D9L3	
1438435_at	Pfca	phytoceramidase, alkaline	1.18 BB329313	Q8CIG2 /// Q9D099	
1417974_at	Kpna4	karyopherin (importin) alpha 4	1.18 BF018653	O35343	
1452660_s_at	Klhl7	kelch-like 7 (<i>Drosophila</i>)	1.18 AK012326	Q8BUL5 /// Q8K2Z1 /// Q9CZP4	
1456898_at	---	Mus musculus transcribed sequence with weak similarity to protein pir:A36298 (H.sapiens) A36298 proline-rich protein PRB3M (null) - human (fragment)	1.18 A426862	P42669 /// Q00577 /// Q8C6E9	
1426205_at	Ppp1cb	protein phosphatase 1, catalytic subunit, beta isoform	1.18 M27073	AAH46832 /// BAC40636 /// P37140 /// Q8C285 /// Q9DBY2	
1425095_at	BC002059	cDNA sequence BC002059	1.18 BC002059	---	
1433631_at	Eif5	eukaryotic translation initiation factor 5	1.18 BQ176989	AAH56633 /// P59325 /// Q8BWW6	
1416745_x_at	Uap1	UDP-N-acetylglucosamine pyrophosphorylase 1	1.18 NM_133806	Q8BG76 /// Q8BXD6 /// Q8VD59 /// Q91YN5	
1433897_at	Smc4l1	SMC4 structural maintenance of chromosomes 4-like 1 (yeast)	1.19 BQ176744	---	
1428113_at	4930403J22Rik	RIKEN cDNA 4930403J22 gene	1.19 BB278364	Q8BG19 /// Q8CAD2 /// Q8CAC3 /// Q8K0I2 /// Q9CS83 /// Q9D5P3	
1436317_at	9030223K07Rik	RIKEN cDNA 9030223K07 gene	1.19 BM115569	---	
1439006_x_at	AW260253	expressed sequence AW260253	1.19 BB093996	AAH62956 /// Q8BHS0 /// Q8BHV8 /// Q8BHW5 /// Q8BHZ6	
1439903_at	AU021838	expressed sequence AU021838	1.19 BM227771	---	
1439807_at	B230382K22Rik	RIKEN cDNA B230382K22 gene	1.19 BB816169	Q8BQU7	
1455604_at	---	Mus musculus transcribed sequences	1.19 BB795235	---	
1434659_at	5830411G16Rik	RIKEN cDNA 5830411G16 gene	1.20 BB514213	Q8OU56	
1434468_at	4930431L18Rik	RIKEN cDNA 4930431L18 gene	1.20 BM238914	Q80TL3 /// Q9CJUN2	
1434955_at	2900024D24Rik	RIKEN cDNA 2900024D24 gene	1.20 BB134696	AAH66008 /// Q8C294 /// Q8CBA1	
1453481_at	Zdhc2	zinc finger, DHHC domain containing 2	1.20 BB342242	P59267	
1450938_at	Pnn	pinin	1.20 AV135835	O35691 /// Q8CD89 /// Q9CV89	
1436387_at	C330006P03Rik	RIKEN cDNA C330006P03 gene	1.20 BB398124	---	
1456599_at	Nx2	nuclear transport factor 2-like export factor 2	1.20 BB745947	AAH64727 /// AAH68166 /// Q8C070	
1448936_at	Sx12	syntaxin 12	1.20 BC010669	Q9ER00	
1428777_at	Spred1	sprouty protein with EVH-1 domain 1, related sequence	1.20 AK017680	AAH57874 /// Q924S8	
1429771_at	3110073H01Rik	RIKEN cDNA 3110073H01 gene	1.21 AK014252	---	
1452766_at	2900041A09Rik	RIKEN cDNA 2900041A09 gene	1.21 AK013631	Q7TQD2	
1420859_at	Pkia	protein kinase inhibitor, alpha	1.21 AK010212	AAH48244 /// P27776	
1458704_at	---	Mus musculus transcribed sequences	1.21 A452119	---	
1450642_at	3110001I20Rik	RIKEN cDNA 3110001I20 gene	1.21 NM_133725	---	
1443858_at	1110039I09Rik	RIKEN cDNA 1110039I09 gene	1.21 B1653857	Q99PP3 /// Q99PP4 /// Q99PP5 /// Q99PP6	
1436719_at	Sic35f1	solute carrier family 35, member F1	1.21 BB758319	AAH59075 /// Q8BGK5 /// Q8BKD4 /// Q8BX52	

1429131_at	Ube2v2	ubiquitin-conjugating enzyme E2 variant 2	1.21 AV010904	AAH58374 /// Q8BGH6 /// Q8CE99 /// Q8K2V7 /// Q9CYD7 /// Q9D2M8 /// Q9ER18
1433761_at	RIKEN cDNA 9430063L05Rik	RIKEN cDNA 9430063L05 gene	1.21 AV374669	Q80U00 /// Q80YT7 /// Q8BKQ2 /// Q8C9H5 /// Q8K240
1428592_s_at	Usp38	ubiquitin specific protease 38	1.21 BG064874	BAC98274 /// Q8BW70
1450870_at	Rala	v-ral simian leukemia viral oncogene homolog A (ras related)	1.22 BG073338	AAG23136 /// AAH31741 /// P05810 /// Q9CXY0
1419971_s_at	Sic35a5	solute carrier family 35, member A5	1.22 C86506	Q921R7 /// Q9DC72
1416426_at	Rab5a	RAB5A, member RAS oncogene family	1.22 NM_025887	Q8BPE8 /// Q9CQD1
1441598_at	Tneff2	transmembrane protein with EGF-like and two follistatin-like domains 2	1.22 AV246773	Q8CDH1 /// Q9JJE3 /// Q9QYM9
1422769_at	Syncrip	synaptotagmin binding, cytoplasmic RNA interacting protein	1.22 BG920261	Q7TMK9
1428915_at	Sirt5	sirtuin 5 (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	1.22 AK002609	Q8K2C6
1427185_at	Mef2a	myocyte enhancer factor 2A	1.22 AV255689	AAH61128
1434039_at	Appbp2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	1.22 BB553604	Q80U61 /// Q9CUT5 /// Q9DAX9
1416744_at	Uap1	UDP-N-acetylglucosamine pyrophosphorylase 1	1.22 NM_133806	Q8BG76 /// Q8BXD6 /// Q8VD59 /// Q91YN5
1455083_at	A330005H02Rik	RIKEN cDNA A330005H02 gene	1.22 BG068357	---
1429167_at	8430438M01Rik	RIKEN cDNA 8430438M01 gene	1.23 BM221159	---
1438221_at	C130065N10Rik	RIKEN cDNA C130065N10 gene	1.23 A875682	---
1455009_at	Cpd	carboxypeptidase D	1.23 AW550842	O89001
1435504_at	---	Mus musculus transcribed sequences	1.23 BM217861	Q8BW09 /// Q8C196 /// Q921Q4 /// Q9D2S6
1436816_at	---	Mus musculus cDNA clone IMAGE:6839226, partial cds	1.23 BB559624	Q8CDZ5 /// Q8R0G9
1417489_at	Npy2r	neuropeptide Y receptor Y2	1.23 NM_008731	P97295 /// Q8BWW1
1423535_at	Strn3	striatin, calmodulin binding protein 3	1.23 BF148627	Q9ERG2
1455324_at	---	Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930035P11	1.24 BQ176176	---
1415861_at	Tyrl	product:unknown EST, full insert sequence	1.24 BB762957	P07147
1447757_x_at	Inpp5f	tyrosinase-related protein 1	1.24 AV033355	AAH67200 /// BAC98059 /// Q8C8G7 /// Q8CBW2 /// Q8CDA1
1416151_at	Sfrs3	inositol polyphosphate-5-phosphatase F splicing factor, arginine/serine-rich 3 (SRp20)	1.24 NM_013663	AAH68111 /// BAC37445 /// P23152 /// Q8C3H6 /// Q9D6W4
1428437_at	2700023B17Rik	RIKEN cDNA 2700023B17 gene	1.25 B1662680	Q8K2F8 /// Q9CTG8
1443869_at	E430028B21Rik	RIKEN cDNA E430028B21 gene	1.25 BM114886	AAH64450 /// Q8BKH8 /// Q8BTS8 /// Q8BUQ5 /// Q8C3G9 /// Q8CB54
1435990_at	Adams2	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 2	1.25 BG073461	Q8C9W3
1449176_a_at	Dok	deoxyctidine kinase	1.25 NM_007632	BAB23394 /// BAB27131 /// BAC33307 /// BAC40203 /// P43346 /// Q80US6
1429335_at	Snapc1	small nuclear RNA activating complex, polypeptide 1	1.25 AK012317	Q8K0S9
1450664_at	Gabpa	GA repeat binding protein, alpha	1.26 NM_008065	Q00422 /// Q7TT22 /// Q91YY8 /// Q9CT91
1424683_at	1810015C04Rik	RIKEN cDNA 1810015C04 gene	1.26 BC019494	Q7TMV5 /// Q8VE91 /// Q9CUJ4 /// Q9D8Z5
1442077_at	2310076G05Rik	RIKEN cDNA 2310076G05 gene	1.26 BB197581	---
1451077_at	Rpl5	ribosomal protein L5	1.26 BM114165	P47962
1425562_s_at	Trnt1	tRNA nucleotidyl transferase, CCA-adding, 1	1.27 BM225164	Q8K1J6
1435286_at	AW125296	expressed sequence AW125296	1.27 BB304438	---
1433585_at	Tnpo1	transportin 1	1.27 B1696984	Q8BFY9
1455602_x_at	1190030G24	hypothetical protein 1190030G24	1.27 AV023018	Q8BNM1 /// Q8C4R5
1455607_at	Thsd2	thrombospondin, type I, domain 2	1.27 BG072958	Q8BVW2 /// Q9CSB2
1422729_at	Pcdhb10	protocadherin beta 10	1.27 NM_053135	Q91VE5
1416814_at	Tia1	cytotoxic granule-associated RNA binding protein 1	1.28 BG518542	BAC40385 /// P52912 /// Q80ZW7 /// Q8BT02 /// Q8C1I5

1417716_at	GoI2	glutamate oxaloacetate transaminase 2, mitochondrial	1.28 U82470	P05202	
1423195_at	Hiat1	hippocampus abundant gene transcript 1	1.28 BM208582	P70187 /// Q9DBS0	
1435014_at	Rab39b	RAB39B, member RAS oncogene family	1.28 AV162168	Q8BHC1	
1457707_at	---	Mus musculus transcribed sequences	1.29 BB817942	---	
1448176_a_at	Hnrpk	heterogeneous nuclear ribonucleoprotein K	1.29 NM_025279	Q07244 /// Q8BGQ8	
1442226_at	Sema3e	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	1.29 AV348197	AAH57956 /// BAC33823 /// BAC97926 /// P70275 /// Q8CCCK6 /// Q9QX23	
1427915_s_at	Toeb1	transcription elongation factor B (SII), polypeptide 1	1.29 A1019214	Q63182	
1425994_a_at	Asa12	N-acylsphingosine amidohydrolase 2	1.29 AB037111	Q8BNP0 /// Q8BQN7 /// Q8R236 /// Q9JHE3	
1440357_at	---	Mus musculus transcribed sequences	1.29 BM938290	---	
1418843_at	Slc30a4	solute carrier family 30 (zinc transporter), member 4	1.29 NM_011774	Q35149	
1438666_at	Al194318	expressed sequence Al194318	1.29 BB534423	Q8CCS0 /// Q8CDR7	
1435060_at	---	Mus musculus transcribed sequences	1.30 BB667124	AAH61124 /// Q8BGX9 /// Q9CUK4 /// Q9JJK7	
1434294_at	---	Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230361M20	1.30 BB183166	Q8K2D0	
1449664_s_at	Rnf20	ring finger protein 20	1.30 AW540162	Q7TTT11 /// Q8BKA8 /// Q8BKN8 /// Q8BUF7 /// Q8BVU4	
1429691_at	5430405N12Rik	RIKEN cDNA 5430405N12 gene	1.30 AK017277	---	
1435862_at	Son	Son cell proliferation protein	1.30 BG067046	Q80TM4 /// Q811G3 /// Q8BM30 /// Q8BS91 /// Q8C9T5 /// Q9QX47	
1450394_at	Golph3	golgi phosphoprotein 3	1.30 AV174110	Q99KY1 /// Q9CRA5	
1427682_a_at	Egr2	early growth response 2	1.30 X06746	P08152	
1438592_at	---	Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530008K05	1.30 BB418199	---	
1460303_at	Nr3c1	product:unclassified, full insert sequence	1.30 NM_008173	P06537	
1437154_at	4933426L22Rik	nuclear receptor subfamily 3, group C, member 1	1.30 BB667247	Q8BJW2 /// Q9D3Z0	
1450387_s_at	Ak4	RIKEN cDNA 4933426L22 gene	1.30 NM_009647	Q9WJUR9	
1455196_s_at	AA987161	adenylate kinase 4	1.31 AA987127	Q80VNA	
1434585_at	Fbl	expressed sequence AA987161	1.31 BB667130	---	
1455123_at	St18	fibroblast	1.31 BB178719	Q80TY4 /// Q811B4 /// Q8K098	
1448140_at	Ciapi1	suppression of tumorigenicity 18	1.31 NM_134141	AAS09959 /// Q8VC24 /// Q8WTY4	
1426827_at	A730098D12Rik	cytokine induced apoptosis inhibitor 1	1.31 AV025877	Q80V25 /// Q8C4W4 /// Q8R5E6	
1452261_at	Shprh	RIKEN cDNA A730098D12 gene	1.31 BC006883	Q7TFQ3 /// Q7TQ27 /// Q7TQ28 /// Q7TQ29 /// Q8BKE2 /// Q8BUW0 /// Q8BXM1 /// Q922Q3	
1452761_a_at	8430436O14Rik	SNF2 histone linker PHD RING helicase	1.31 AK018466	---	
1418816_at	281040511Rik	RIKEN cDNA 8430436O14 gene	1.31 BG073376	Q99LU0 /// Q9CXR5	
1428586_at	D7Etd743e	RIKEN cDNA 2810405H11 gene	1.31 BB823331	Q8C1X2 /// Q8CBS5 /// Q8CBU5 /// Q8K1A5	
1439295_x_at	9930105H17Rik	DNA segment, Chr 7, ERATO Dof 743, expressed	1.31 BB371300	---	
1459882_at	Asf1a	RIKEN cDNA 9930105H17 gene	1.32 AV312905	Q9CQE6	
1420376_a_at	H3f3b	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	1.32 NM_008211	AAH37730 /// BAB22464 /// BAC40130 /// P06351 /// Q8VDJ2 /// Q9D0H3	
1453059_at	2310046A06Rik	H3 histone, family 3B	1.32 AK009836	Q9D6X9	
1418428_at	Kif5b	kinasin family member 5B	1.33 B1328541	Q61768 /// Q8CFE7 /// Q9CUT6	
1456130_at	---	Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930002I12	1.33 BG068705	---	
1455142_at	A730004F22Rik	product:unclassified, full insert sequence	1.33 BB244749	---	
		RIKEN cDNA A730004F22 gene			

1430667_at	Pcdh10	protocadherin 10	1.33 BB077413	AAH65695 /// Q80TE2 /// Q8CA99 /// Q8CC37 /// Q925I8 /// Q9CU33 /// Q9Z1B1
1416653_at	Sbcbp3	syntaxin binding protein 3	1.33 NM_011504	AAH62901 /// Q60770 /// Q8C7H4
1422569_at	Yy1	YY1 transcription factor	1.34 BI665246	Q00899 /// Q8C6B5
1429062_at	Kif16b	kinesin family member 16B	1.34 BG066903	BAC98211 /// O35056 /// Q8BZZ9
1434272_at	Opeb2	cytoplasmic polyadenylation element binding protein 2	1.34 AV231491	Q812E0
1435050_at	---	Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B930094H20	1.34 BB353607	---
1434108_at	Fbxo11	product:unknown EST, full insert sequence	1.34 BM250184	Q7TPD1
1458841_at	---	F-box only protein 11	1.34 BB499674	---
1439779_at	---	Mus musculus transcribed sequences	1.34 BB356939	---
1438223_at	---	Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630050J22	1.35 BG065705	---
1437995_x_at	---	product:unknown EST, full insert sequence	1.35 AV219419	O55131 /// Q8C2A3
1455173_at	Gsp11	sepin 7	1.35 AW537663	Q8BPH0 /// Q8CAS6 /// Q8CCV1 /// Q8K2E1 /// Q8R050
1445642_at	4930540I23Rik	G1 to phase transition 1	1.35 AV156411	---
1451064_a_at	Psat1	RIKEN cDNA 4930540I23 gene	1.35 BC004827	BAC33959 /// Q8BTJ1 /// Q99JU9 /// Q99K85
1415963_at	Hmrh2	phosphoserine aminotransferase 1	1.35 NM_019868	P70333
1439397_at	---	heterogeneous nuclear ribonucleoprotein H2	1.36 BB164513	---
1452784_at	Itgav	Mus musculus transcribed sequences	1.36 AK003416	P43406 /// Q80Y67
1451301_at	Tmod2	integrin alpha V	1.36 BB633110	AAH61124 /// Q8BGX9 /// Q9CUK4 /// Q9JKK7
1430651_s_at	Zfp191	tropomodulin 2	1.36 AI504586	Q8C2B8 /// Q91VN1
1416613_at	Cyp11b1	zinc finger protein 191	1.36 BI251808	Q64429 /// Q80V82 /// Q8BRY0 /// Q8C685 /// Q9CUA1
1454612_at	Rkhd2	cytochrome P450, family 1, subfamily b, polypeptide 1	1.36 BI656279	---
1448405_a_at	Cr1	ring finger and KH domain containing 2	1.37 BC010712	Q8BP25 /// Q9CQ17 /// Q9CYM0 /// Q9CZL9 /// Q9DCR4
1427418_a_at	Hif1a	CREBBP/EP300 inhibitory protein 1	1.37 X95580	Q61221
1421052_a_at	Sms	hypoxia inducible factor 1, alpha subunit	1.37 NM_009214	AAH58688 /// P97355 /// Q8C7P4 /// Q9CT09
1415688_at	Ube2g1	spermine synthase	1.37 NM_025985	Q99462
1440066_at	---	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)	1.38 BB531653	---
1428804_at	Map3l	Mus musculus transcribed sequences	1.38 AK017269	Q80TV6 /// Q9D3X9
1419754_at	Myo5a	microfibrillar-associated protein 3-like	1.38 NM_010864	Q99104
1448943_at	Nrp	myosin Va	1.39 AK011144	AAH60129 /// P97333 /// Q80X28
1418501_a_at	Oxr1	neuropilin	1.39 AW548944	Q8C715 /// Q99L06 /// Q99MK1 /// Q99MP4
1437734_at	Ppp1r12a	oxidation resistance 1	1.39 AV309184	Q9DBR7
1434075_at	MGC40669	protein phosphatase 1, regulatory (inhibitor) subunit 12A	1.39 AV374294	Q8C784 /// Q8K0V1
1423821_at	8430437G11Rik	hypothetical protein MGC40669	1.39 BC007160	Q91VX9
1435120_at	---	RIKEN cDNA 8430437G11 gene	1.39 AV300631	---
1441928_x_at	Eli	Mus musculus transcribed sequences	1.39 BB139475	AAH24894 /// O08856
1450121_at	---	elongation factor RNA polymerase II	1.39 AV336781	Q62206
1428252_at	1190006E07Rik	Mus musculus sodium channel 27 mRNA fragment.	1.39 AA881383	Q80UZ4 /// Q8BJF9 /// Q9CT65
1423297_at	Add3	RIKEN cDNA 1190006E07 gene	1.40 BM239842	Q8BJH2 /// Q8BM29 /// Q8JZT6 /// Q9JLE2 /// Q9QYB5
1417074_at	Ceacam10	adducin 3 (gamma)	1.40 NM_007675	Q61400 /// Q99LD6 /// Q9D329
1451179_a_at	Qk	CEA-related cell adhesion molecule 10	1.40 AF090403	AAH56346 /// O88972 /// Q61110 /// Q61111 /// Q9CW34 /// Q9QUH4 /// Q9QYS9 /// Q9Z246
1451179_a_at	Qk	quaking	---	---

1439249_at	A230035H12Rik	RIKEN cDNA A230035H12 gene mitogen-activated protein kinase kinase kinase	1.41 BB822150	---
1427083_a_at	Map4k5	5	1.41 BG067961	AAH57930 /// Q8BPM2 /// Q8BRE4
1444615_x_at	Cbfa2t1h	CBFA2T1 identified gene homolog (human)	1.42 AV327778	G61909 /// Q8C066
1435251_at	Snx13	sorting nexin 13	1.42 AV377013	AAH56394 /// AAH67201 /// Q80TT7
1456026_at	8030451K01Rik	RIKEN cDNA 8030451K01 gene	1.42 AV303159	Q8CCH2 /// Q8CDW5
1456596_at	6430550H21Rik	RIKEN cDNA 6430550H21 gene	1.42 BB093996	AAH62956 /// Q8BHS0 /// Q8BHV8 /// Q8BHW5 /// Q8BHZ6
1424752_x_at	Zfp71-rs1	zinc finger protein 71, related sequence 1	1.42 BC016248	G60915 /// Q8BY64 /// Q91W94
1433740_at	2610301K12Rik	RIKEN cDNA 2610301K12 gene	1.43 BG070008	Q8BKU8 /// Q8K0G0 /// Q9D001
1429639_at	2310032D16Rik	RIKEN cDNA 2310032D16 gene	1.43 AK009137	Q80TD5 /// Q8BKJ7 /// Q8BKW7 /// Q8C0L9 /// Q8CFW2 /// Q9D759
1424717_at	Misc12	MIS12 homolog (yeast)	1.43 BC026790	Q9CY25
1437087_at	---	Mus musculus 2 days neonate thymus thymic cells	---	---
1434172_at	Cnr1	cDNA, RIKEN full-length enriched library, clone: C920025L08 product: hypothetical RNI-like structure containing protein, full insert sequence	1.43 AV079268	---
1437137_at	AW260253	cannabinoid receptor 1 (brain)	1.44 BQ177934	---
1429642_at	Anub1	expressed sequence AW260253	1.44 AV280875	AAH62956 /// Q8BHS0 /// Q8BHV8 /// Q8BHW5 /// Q8BHZ6
1418058_at	Elt1	AN1, ubiquitin-like, homolog (Xenopus laevis)	1.44 AK012639	Q80ZS6
1435132_at	Disp1	EGF, latrophilin seven transmembrane domain containing 1	1.45 BC017134	Q923X1
1434179_at	Mil3	dispatched homolog 1 (Drosophila)	1.45 AI056598	AAH59225 /// Q80ZZ8 /// Q8CGS3 /// Q8CIP6 /// Q8CIQ9 /// Q9CT62
1423042_at	Fin14	myeloid/lymphoid or mixed-lineage leukemia 3	1.45 AV297525	BAC98187 /// Q8BRH4 /// Q8BZX5
1438606_a_at	Clic4	fibroblast growth factor inducible 14	1.46 BF123067	---
1449893_a_at	Lrig1	chloride intracellular channel 4 (mitochondrial)	1.46 BB814844	BAC33601 /// Q9QYB1
1421849_at	Stag2	leucine-rich repeats and immunoglobulin-like domains 1	1.46 NM_008377	P70193
1434677_at	Hps5	stromal antigen 2	1.46 NM_021465	AAH66041 /// Q35638 /// Q8BSB5
1456699_s_at	A730098D12Rik	Hermansky-Pudlak syndrome 5 homolog (human)	1.46 BG067097	BAC98075 /// P59438
1433847_at	D330017J20Rik	RIKEN cDNA A730098D12 gene	1.48 AA561825	Q80V25 /// Q8CAW4 /// Q8R5E6
1420429_at	Pcdhb3	RIKEN cDNA D330017J20 gene	1.48 BB098407	Q80T16 /// Q8C7A2 /// Q8C9H6
1431748_a_at	1700051E09Rik	protocadherin beta 3	1.48 NM_053128	Q91XZ7 /// Q925M6
1450937_at	Lin7c	RIKEN cDNA 1700051E09 gene	1.48 AK015806	AAO42677 /// BAC87665 /// Q9D543 /// Q9D9B1
1455995_at	D10Bwg1379e	lin 7 homolog c (C. elegans)	1.48 BQ176612	O88952 /// Q99KF6
1419589_at	C1qr1	DNA segment, Chr 10, Brigham & Women's Genetics	1.49 BB125269	Q80TH0
1417768_at	1200006O19Rik	1379 expressed	1.49 BB039247	BAC37518 /// Q89103 /// Q8C5P4
1456485_at	Npat	complement component 1, q subcomponent, receptor 1	1.49 BC019364	Q8K1N1 /// Q8VECO /// Q9CVC9 /// Q9DC20
1428333_at	6530401D17Rik	RIKEN cDNA 1200006O19 gene	1.50 BM207451	Q8BMA5 /// Q8BWA9 /// Q8BY06
1457424_at	Eya1	nuclear protein in the AT region	1.50 AK013740	Q8BK31 /// Q9D365
1439968_x_at	---	eyes absent 1 homolog (Drosophila)	1.50 BB760085	AAH60260 /// AAH66860 /// P97767 /// Q8C9D0
1426585_s_at	Mapk1	Mus musculus adult male corpora quadrigemina cDNA, product: unknown EST, full insert sequence	1.50 BE949296	---
1420895_at	Tgfb1	RIKEN full-length enriched library, clone: B230215D24	1.51 BM209765	AAH56258 /// BAC29053 /// BAC33251 /// BAC40044 /// P27703 /// Q922X7 /// Q9D319
1440177_at	---	mitogen activated protein kinase 1	1.51 BM248342	Q64729 /// Q9CVP4
1451652_a_at	5033428A16Rik	transforming growth factor, beta receptor I	1.51 BM899529	---
1439618_at	Pde10a	hypothetical protein 9630027E11	1.51 BC018498	---
		RIKEN cDNA 5033428A16 gene	1.51 A1448308	Q8C8M0 /// Q8CA95 /// Q9WV11
		phosphodiesterase 10A		

1418500_at	Nap1l3	nucleosome assembly protein 1-like 3	1.53 NM_138742	O54802
1430187_at	RIKEN cDNA 6330516O17	gene	1.53 AK018216	Q9D388
1455258_at	AW047325	expressed sequence AW047325	1.53 BQ174236	--
1420609_at	Axot	axotrophin	1.53 NM_020575	Q9WW66
1448147_at	Tnfrsf19	tumor necrosis factor receptor superfamily, member 19	1.54 NM_013869	Q80T13 /// Q812G3 /// Q8BUM7 /// Q8BWR1 /// Q9JLL3
1415855_at	Kitl	kit ligand	1.54 BB815530	P20826 /// Q61854 /// Q64384
1416174_at	Rbbp9	retinoblastoma binding protein 9	Q88851 /// Q80YU9	
1427898_at	Rnf6	ring finger protein (C3H2C3 type) 6	1.54 BC011107	Q8K565 /// Q9DBU5
1434601_at	Amigo2-pending	amphoterin induced gene and ORF 2	1.55 B1738010	Q80ZD9
1440201_at	Mapk10	mitogen activated protein kinase 10	1.55 AV315087	Q61831 /// Q80W80 /// Q80W81 /// Q80W82 /// Q8C9D4
1449322_at	Ptp4a1	protein tyrosine phosphatase 4a1	1.56 BB313689	Q63739
1418488_s_at	Ankrd3	ankyrin repeat domain 3	1.56 AF302127	AAH57871 /// Q9CV04 /// Q9ERK0
1418162_at	Tlr4	toll-like receptor 4	1.56 AF185285	AAH57574 /// BAC75668 /// P48432 /// Q8CCY4
1416967_at	Sox2	SRY-box containing gene 2	1.56 U31967	Q811E4
1437409_s_at	Gpr126	G protein-coupled receptor 126	1.57 BB812574	Q8B8M8 /// Q8BV50 /// Q8BXV6 /// Q8BYA5 /// Q8BYB0 /// Q8R1E4
1435768_at	Arid4b	AT rich interactive domain 4B (Rbp1 like)	1.57 AV371758	Q80UU4
1438079_at	MGC60963	hypothetical protein MGC60963	1.57 AV290754	Q8CHQ0 /// Q99JG8 /// Q9D4Y5
1427121_at	Fbxo4	F-box only protein 4	1.58 BF455337	
1417600_at	Slc15a2	solute carrier family 15 (H+/peptide transporter), member 2	1.58 NM_021301	Q80XC0 /// Q8VEK9 /// Q9CXC0 /// Q9JM03
1416444_at	Elovl2	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	1.58 NM_019423	BAC26646 /// BAC32079 /// BAC34236 /// Q9JLL4
1427081_at	A630072M18Rik	RIKEN cDNA A630072M18 gene	1.59 BB246700	--
1452974_at	Nol8	nucleolar protein 8	1.59 AK017551	Q80VB9 /// Q8CDJ7 /// Q9CUR0
1440527_at	--	Mus musculus transcribed sequences	1.59 B1440542	--
1451268_at	Tram1l1	translocation associated membrane protein 1-like 1	1.59 BC027120	Q8C455 /// Q8C8X6 /// Q8QZR0
1423592_at	Rock2	Rho-associated coiled-coil forming kinase 2	1.60 BB761686	P70336 /// Q8CC95
1454714_x_at	Phgdh	3-phosphoglycerate dehydrogenase	1.61 AA561726	Q61753 /// Q8C603
1444437_at	Usp34	ubiquitin specific protease 34	1.61 BB086152	AAH63062 /// BAC97975 /// Q7TMJ6 /// Q8CCHO
1422032_a_at	Za2d03	zinc finger, A20 domain containing 3	1.61 NM_022985	Q9DCH6
1427670_a_at	Tcf12	transcription factor 12	1.61 M97636	Q61286 /// Q8BP24 /// Q8K1X3
1433571_at	A130038L21Rik	RIKEN cDNA A130038L21 gene	1.61 BQ175260	AAH62131 /// Q80ZH8 /// Q8BHJ6 /// Q8CHM0
1435514_at	Lztf11	leucine zipper transcription factor-like 1	1.62 BB700884	Q8BRX8 /// Q8CDG8 /// Q8CDS2 /// Q9JHQ5
1434313_at	6330407D12Rik	RIKEN cDNA 6330407D12 gene	1.62 BB762434	Q8BIS8
1436662_at	--	Mus musculus transcribed sequences	1.62 BB022723	--
1417493_at	Bmi1	B lymphoma Mo-MLV insertion region 1	1.63 M64279	P25916
1454783_at	Il13ra1	interleukin 13 receptor, alpha 1	1.63 B1081033	Q09030 /// Q7TTT7 /// Q8BNM4 /// Q8C1Z3 /// Q8VDP7
1456573_x_at	Nnt	nicotinamide nucleotide transhydrogenase	1.63 BB205930	Q61941 /// Q8BGK0 /// Q8C1W8 /// Q8C3H2 /// Q8C9V5 /// Q922E1 /// Q9CTX5
1433779_at	--	Mus musculus, clone IMAGE:5068832, mRNA, partial cds	1.63 AV311104	AAH64446 /// AAR26704 /// AAR26705 /// Q8BQ39 /// Q8C4Z2 /// Q8K2M1
1425115_at	C030034J04Rik	RIKEN cDNA C030034J04 gene	1.63 BC025874	Q8R399
1446899_at	--	Mus musculus transcribed sequences with weak similarity to protein ref:NP_081764.1 (M.musculus)	1.64 BB165801	--
1420907_at	Cd2ap	CD2-associated protein	1.64 BB398671	Q9JLQ0
1436948_a_at	6430550H21Rik	RIKEN cDNA 6430550H21 gene	1.64 BB520013	AAH62956 /// Q8BHS0 /// Q8BHV8 /// Q8BHW5 /// Q8BHZ6
1448293_at	Ebf1	early B-cell factor 1	1.65 BB125261	Q07802 /// Q8BSM3 /// Q8C955 /// Q8CBL7
1437029_at	Tacr3	tachykinin receptor 3	1.65 AV328460	AAH66845 /// P47937
1426895_at	Zfp191	zinc finger protein 191	1.65 BB579760	Q8C2B8 /// Q91VN1

1454862_at	Phldb2	pleckstrin homology-like domain, family B, member 2	1.66 AV253284	AAH60683 /// Q80Y16 /// Q8BKV3 /// Q8BZE3 /// Q8K1N2
1456943_a_at	---	Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230215D24	---	---
1426371_at	3732409C05Rik	product unknown EST, full insert sequence	1.67 BE949296	---
1428236_at	Acbd5	acyl-Coenzyme A binding domain containing 5	1.67 BG094874	Q8BZS2 /// Q922J9 /// Q9CXE8 /// Q9DQ1 /// Q9DAU2
1428664_at	Vip	vasoactive intestinal polypeptide	1.67 AK005001	AAH61484 /// Q7TSC2 /// Q8BKU6 /// Q8CI99 /// Q9CW41
1436093_at	---	Mus musculus transcribed sequences	1.68 AK018599	Q9D2Z7
1419552_at	Echdc1	enoyl Coenzyme A hydratase domain containing 1	1.68 BE981269	---
1415999_at	Hey1	hair/enhancer-of-split related with YRPW motif 1	1.68 NM_025855	AAH66183 /// Q8C185 /// Q8R5A8 /// Q9CTC5 /// Q9CTK2 /// Q9CTM5 /// Q9D9V3
1424229_at	Dyrk3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	1.68 NM_010423	Q9D0R0 /// Q9QUIM5 /// Q9WV93
1452224_at	Zowcc3	zinc finger, CW-type with coiled-coil domain 3	1.69 BC006704	Q8BM34 /// Q922Y0
1436590_at	Ppp1r3b	protein phosphatase 1, regulatory (inhibitor) subunit 3B	1.69 BC026506	Q8R0R0
1419186_a_at	Siat8d	sialyltransferase 8 (alpha-2, 8-sialyltransferase) D	1.70 BG071940	AAH60261 /// Q8C767
1459722_at	2900036G02Rik	RIKEN cDNA 2900036G02 gene	1.70 NM_009183	AAH60112 /// CAA11685 /// Q64692 /// Q8BY70
1435588_at	Wdfy1	WD40 and FYVE domain containing 1	1.71 A427602	---
1422479_s_at	Rcn2	reticulocalbin 2	1.71 BQ031098	Q8R3I5 /// Q9DAD3
1434298_at	Zfhx1b	zinc finger homeobox 1b	1.71 NM_011992	O70341 /// Q8BP39 /// Q8BP92
1452281_at	Sos2	Son of sevenless homolog 2 (Drosophila)	1.72 BM117243	Q8BHD8
1417183_at	Dnaj2	DnaJ (Hsp40) homolog, subfamily A, member 2	1.73 BQ174116	AAH60699 /// Q80TX6 /// Q8BSG9 /// Q8CD37 /// Q9R0G7
1422504_at	Grib	glycine receptor, beta subunit	1.74 Z11664	Q02384
1428091_at	Khl7	kelch-like 7 (Drosophila)	1.75 C77509	BAC36946 /// BAC38809 /// Q9QYJ0
1426293_at	6330581L23Rik	RIKEN cDNA 6330581L23 gene	1.75 NM_010298	BAC38831 /// P48168
1434099_at	Casp7	caspase 7	1.76 AK012326	Q8BUL5 /// Q8K2Z1 /// Q9CZP4
1459750_s_at	Gpr123	G protein-coupled receptor 123	1.77 BG068796	Q80XZ2 /// Q91VW8
1436223_at	4832412006Rik	RIKEN cDNA 4832412006 gene	1.78 BB752393	Q8BRP2 /// Q8CCT1
1434434_s_at	Tcerg1	transcription elongation regulator 1 (CA150)	1.79 AU015577	---
1416950_at	Tnfrsf8	tumor necrosis factor, alpha-induced protein 8	1.81 BB504737	---
1456851_at	Bmp5	bone morphogenetic protein 5	1.85 AW557777	Q8C490 /// Q8CGF7 /// Q8CHT8 /// Q9R0R5
1438752_at	A230058F20Rik	RIKEN cDNA A230058F20 gene	1.85 NM_134131	Q8BTH4 /// Q921Z5
1435162_at	Ptkg2	protein kinase, cGMP-dependent, type II	1.85 AV032115	P49003 /// Q8CCE0
1424123_at	BC011209	cDNA sequence BC011209	1.90 AV327739	---
1459989_at	---	Mus musculus transcribed sequences	1.90 BB823350	Q61410 /// Q8C4R2 /// Q8CAH8
1453064_at	5730466H23Rik	RIKEN cDNA 5730466H23 gene	1.92 BC011209	Q8BQK2 /// Q91X85
1460718_s_at	Mtch1	mitochondrial carrier homolog 1 (C. elegans)	1.93 AV271189	---
1442542_at	B130023L16Rik	RIKEN cDNA B130023L16 gene	1.95 AK018594	Q8BZM6 /// Q8K332 /// Q9CS19 /// Q9D2Z9
1416390_at	Cnc1	chromosome condensation 1-like	1.95 AF192558	Q8CEY5 /// Q8R0T0 /// Q8R1T8 /// Q8R2T2 /// Q9QZA5 /// Q9QZP4
1416958_at	Nr1d2	nuclear receptor subfamily 1, group D, member 2	1.96 BB363812	---
1450757_at	Cdh11	cadherin 11	2.00 NM_134083	Q8BMG2 /// Q99LJ7
1418142_at	Kcnj8	potassium inwardly-rectifying channel, subfamily J, member 8	2.00 NM_011584	Q60674 /// Q8C598 /// Q8C6J1 /// Q8CCE4 /// Q922C3
1428582_at	2010208K18Rik	RIKEN cDNA 2010208K18 gene	2.02 NM_009866	P55288 /// Q8C7Q6
1428608_at	Itm2a	integral membrane protein 2A	2.03 NM_008428	P97794
1439795_at	Gpr64	G protein-coupled receptor 64	2.06 AK008476	Q9D853
1435338_at	583041120	hypothetical protein 583041120	2.06 B1968443	Q61500 /// Q8K0H4 /// Q9CRW4
			2.10 AV242919	Q8BLU3 /// Q8CJ12
			2.11 BM238926	---

1437967_at	---	Mus musculus transcribed sequences	2.11 AV365582	---
1435098_at	Al317395	expressed sequence Al317395	2.14 BF658992	---
1435233_at	Ncoa2	nuclear receptor coactivator 2	2.20 BM234716	Q61026 /// Q77TPU7 /// Q8C961 /// Q8CBM5 /// Q8CE59
1452286_at	5033405K12Rik	RIKEN cDNA 5033405K12 gene	2.22 BG081701	BAC98175 /// Q8BHV0 /// Q8CI08 /// Q8VCP7
1433623_at	Zfp367	zinc finger protein 367	2.34 BE629588	Q8BH90 /// Q8BI44 /// Q8BI53 /// Q8BI88
1450655_at	2310035O07Rik	RIKEN cDNA 2310035O07 gene	2.38 AA214868	BAC36545 /// BAC40525 /// O08586 /// Q8BJP9 /// Q8BSR7
1447854_s_at	Hist2h2bb	histone 2, H2bb	2.44 AV127319	Q64524
1448573_a_at	Ceacam10	CEA-related cell adhesion molecule 10	2.50 NM_007675	Q61400 /// Q99LD6 /// Q9D329

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CLAIMS

1. A method of identifying a compound capable of reducing or preventing prolonged
5 sensory neuron hyper-excitability comprising the steps of:
 (a) administering the compound to an experimental non-human animal having
prolonged sensory neuron hyper-excitability;
 (b) generating an expression profile of the genes modulated in the Nodose Ganglia
(NG) of the animal of step (a);
10 (c) comparing the expression profile obtained in (b) with the expression profile of
a corresponding panel of genes expressed in the NG of an experimental non-human
animal having no prolonged sensory neuron hyper-excitability;
 wherein a positive correlation of the expression profiles is indicative that the
compound is capable of reducing or preventing prolonged sensory neuron hyper-
15 excitability in NG.
2. The method according to claim 1, wherein the modulated NG genes whose
expression is to be compared comprise at least one gene selected from the group
consisting of those genes listed in Table 1.
- 20 3. The method according to claim 1 or 2, wherein the modulated NG genes whose
expression is to be compared comprise at least one gene selected from the group
consisting the genes listed in Table 2.
- 25 4. The method according to any one of claims 1 to 3, wherein the modulated genes
expressed in the NG are compared at the nucleic acid level.
5. The method according to any one of claims 1 to 4, wherein the modulated NG
genes whose expression is to be compared comprise at least the vanilloid receptor VR1
30 (*Trpv1*), cholecystokinin receptor A (*Cckar*), serotonin receptor 3A (*Htr3a*) and
somatostatin 2 receptor (*Sstr2*).

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6. The method according to any preceding claim, wherein the method comprises comparing the expression of a panel of at least 40 genes selected from the group consisting of those genes listed in Table 1.

5 7. The method according to any preceding claim, wherein the method comprises comparing the expression of a panel of at least 51 genes comprising those genes listed in Table 2.

8. The method according to any preceding claim, wherein the expression profile of
10 the NG genes is assessed at the transcript level or at the protein level.

9. The method according to claim 8 wherein the expression profile of the NG genes is assessed at the mRNA level.

15 10. A method according to any preceding claim, wherein at least 1 probe which hybridises to the NG modulated gene expression product is affixed to a solid support.

11. The method according to claim 10 wherein the probes are in an arrayed form.

20 12. A microarray comprising at least 1 nucleic acid probe immobilised on a solid support capable of hybridizing with the expression product of a gene modulated in NG neurons having prolonged sensory neuron hyper-excitability

13. The microarray according to claim 12 comprising at least 40 nucleic acid probes
25 capable of hybridizing to sequences selected from the group consisting of nucleic acid sequences representing genes from Table 1.

14. The microarray according to claim 12 comprising at least 40 nucleic acid probes
30 capable of hybridizing to sequences selected from the group consisting of nucleic acid sequences representing genes from Table 2.

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15. A method according to claim 1, wherein the experimental non-human animal is a rodent.

16. A method according to claim 15, wherein the rodent is a mouse.

5

17. The method according to claims 15 or 16, wherein the rodent is previously infected with a parasitic helminth selected from Table 3, in particular infected with *Nippostrongylus brasiliensis*.

10 18. A method of treating a subject with a disease condition related to prolonged sensory neuron hyper-excitability, comprising administering to a subject an effective amount of an agent that modulates NG sensory neuron activity.

15 19. The method according to claim 18, wherein the agent administered to the subject is an agent that modulates the expression or activity of one or more genes products selected from the group encoded by those genes listed in Table 1.

20 20. The method according to claim 18 or 19, wherein the agent modulates the expression or activity of one or more gene products selected from the group encoded by those genes listed in Table 2.

21. The method according to claim 18 or 19 wherein the agent modulates the expression or activity of one or more receptors selected from the group consisting of the vanilloid receptor VR1 (*Trpv1*), cholecystokinin receptor A (*Cckar*), serotonin receptor 3A (*Htr3a*) and somatostatin 2 receptor (*Sstr2*).

25

22. The method according to any one of claims 18 to 21, wherein the disease condition associated with prolonged sensory neuron hyper-excitability is a gastrointestinal (GI) tract disorder or stress-related disorder.

30

23. The method according to claim 22, wherein the disease is a bowel disorder, selected from the group consisting of, ulcerative colitis, Crohn's disease, ileitis, proctitis,

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celiacdisease, enteropathy associated with arthropathies, microscopic or collagenous colitis, eosinophilic gastroenteritis or pouchitis resulting after proctocolectomy ,post ileoanal anastomosis, functional dyspepsia, functional vomiting, oesophagitis, gastric ulcer, duodenal ulcer, irritable bowel syndrome or depression.

5

24. The method according to claim 22 or 23, wherein the disease is irritable bowel syndrome.

10 25. A pharmaceutical composition for the treatment of a disease or disorder related to prolonged sensory neuron hyper-excitability comprising a compound identified by the method of claim 1 and at least one pharmaceutically acceptable diluent or excipient.

15 26. Use of a compound identified by the method of claim 1 in the manufacture of a medicament for the treatment of a disease or disorder related to prolonged sensory neuron hyper-excitability.

27. The use of claim 26, wherein disease or disorder related to prolonged sensory neuron hyper-excitability is a GI tract disorder or stress-related disorder.

20 28. The use of claim 26 or 27, wherein the disorder comprises a bowel disorder, selected from the group comprising, ulcerative colitis, Crohn's disease, ileitis, proctitis, celiacdisease, enteropathy associated with arthropathies, microscopic or collagenous colitis, eosinophilic gastroenteritis or pouchitis resulting after proctocolectomy, post ileoanal anastomosis, functional dyspepsia, functional vomiting, oesophagitis, gastric
25 ulcer, duodenal ulcer, irritable bowel syndrome or depression.

29. The use of any one of claims 26 to 28, wherein the disorder is irritable bowel syndrome

30 30. A method of making a pharmaceutical composition for the treatment of a disease or disorder related to prolonged sensory neuron hyper-excitability, comprising combining a compound identified according to the method of claim 1 or having the modulating

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activity as defined in claim 19 or 20 together with a pharmaceutically acceptable diluent or excipient..

31. A method for identifying a compound capable of reducing or preventing

5 prolonged sensory neuron hyper-excitability comprising the steps of:

(a) administering the compound to a test cell population;

(b) generating an expression profile of the prolonged sensory neuron hyper-excitability modulated genes in the cell population of step (a);

10 (c) comparing the expression profile obtained in (b) with the expression profile of the prolonged sensory neuron hyper-excitability modulated genes in a reference cell population;

wherein a positive correlation of the expression profiles is indicative that the compound is capable of reducing or preventing prolonged sensory neuron hyper-excitability in NG.

15

32. A method according to claim 31, wherein the test cell population is derived from the NG of an experimental non-human animal according to claim 17.

33. A method according to claim 31 wherein the reference cell population is derived
20 from NG of an experimental non-human animal not having prolonged sensory neuron hyper-excitability.

34. A method for identifying a compound capable of reducing or preventing prolonged sensory neuron hyper-excitability comprising the steps of:

25 (a) administering the compound to NG having prolonged sensory neuron hyper-excitability; and

(b) determining the effect of said compound on the NG sensory neuron activity of said cells.

30 35. A method according to claim 34, wherein the NG are derived from the NG of an experimental non-human animal according to claim 17.

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36. A method according to claim 34, wherein the activity of the NG is assessed using electrophysiological or fluorometric or other techniques.

37. Use of antisense nucleotides or gene silencing to validate as pharmaceutical
5 targets any one or more of the genes shown in Table 1 in the treatment of a G.I. tract disorders or stress-related disorders.

38. The use according to claim 37 wherein, the gene silencing technique is siRNA.

10 39. The use as claimed in claim 37 or 38 wherein, the disorders are as defined in claim 23.

40. A method for identifying a compound capable of reducing or preventing prolonged sensory neuron hyper-excitability comprising the steps of:

- 15 (a) administering the compound to an experimental non-human animal having prolonged sensory neuron hyper-excitability; and
(b) determining the effect of said compound in a nociceptive assay.

41. A method according to claim 40, wherein said nociceptive assay is a visceral
20 nociceptive assay.

42. A method according to claim 40, wherein said nociceptive assay is a somatic nociceptive assay.

25 43. A method according to any one of claims 40 to 42, wherein the experimental non-human animal having prolonged sensory neuron hyper-excitability is a rodent previously infected with a parasitic helminth selected from Table 3, in particular infected with *Nippostrongylus brasiliensis*.

30 44. A method according to claim 34, wherein the nociceptive assay is the pressor-depressor model.

Fig 1

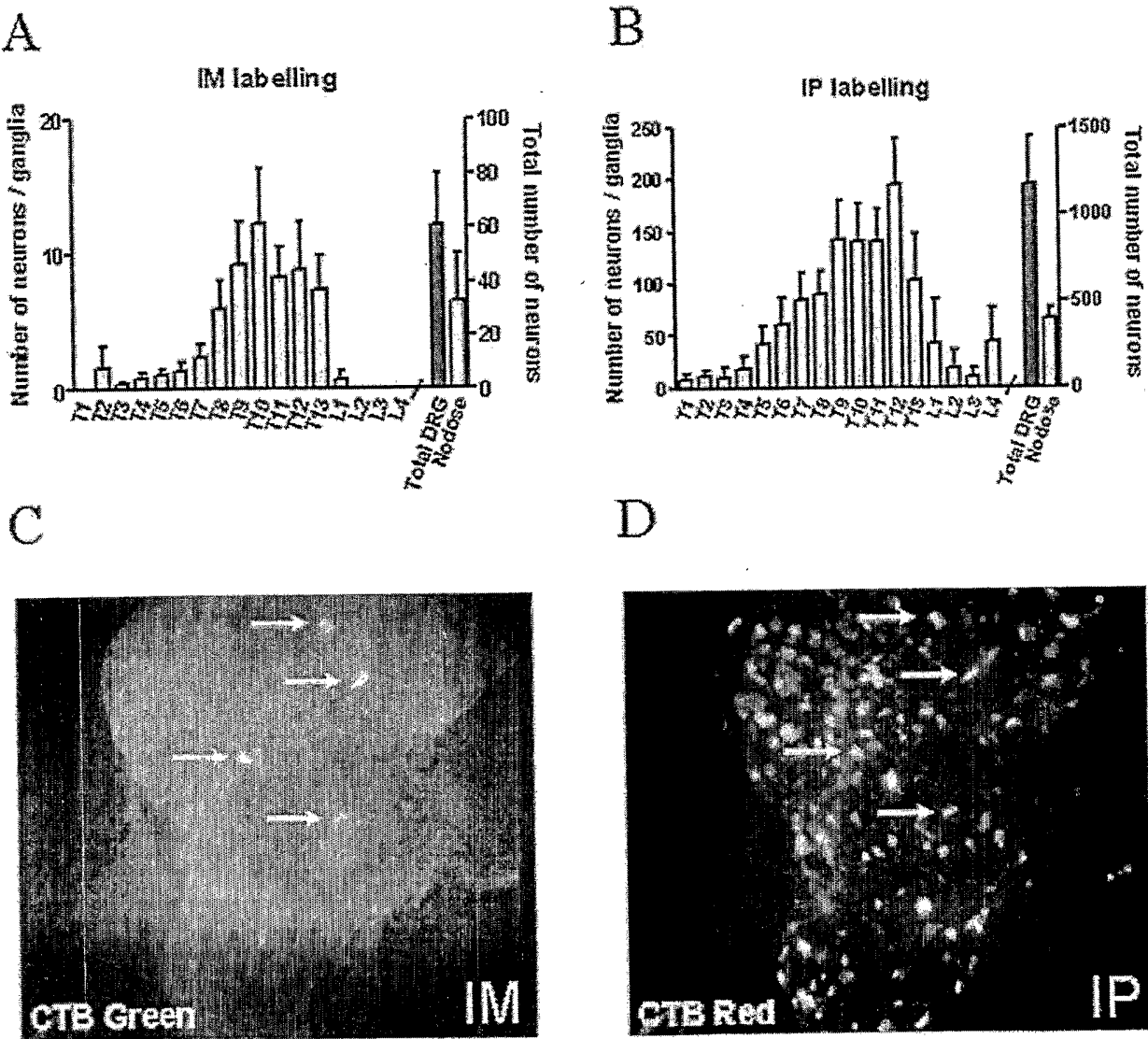
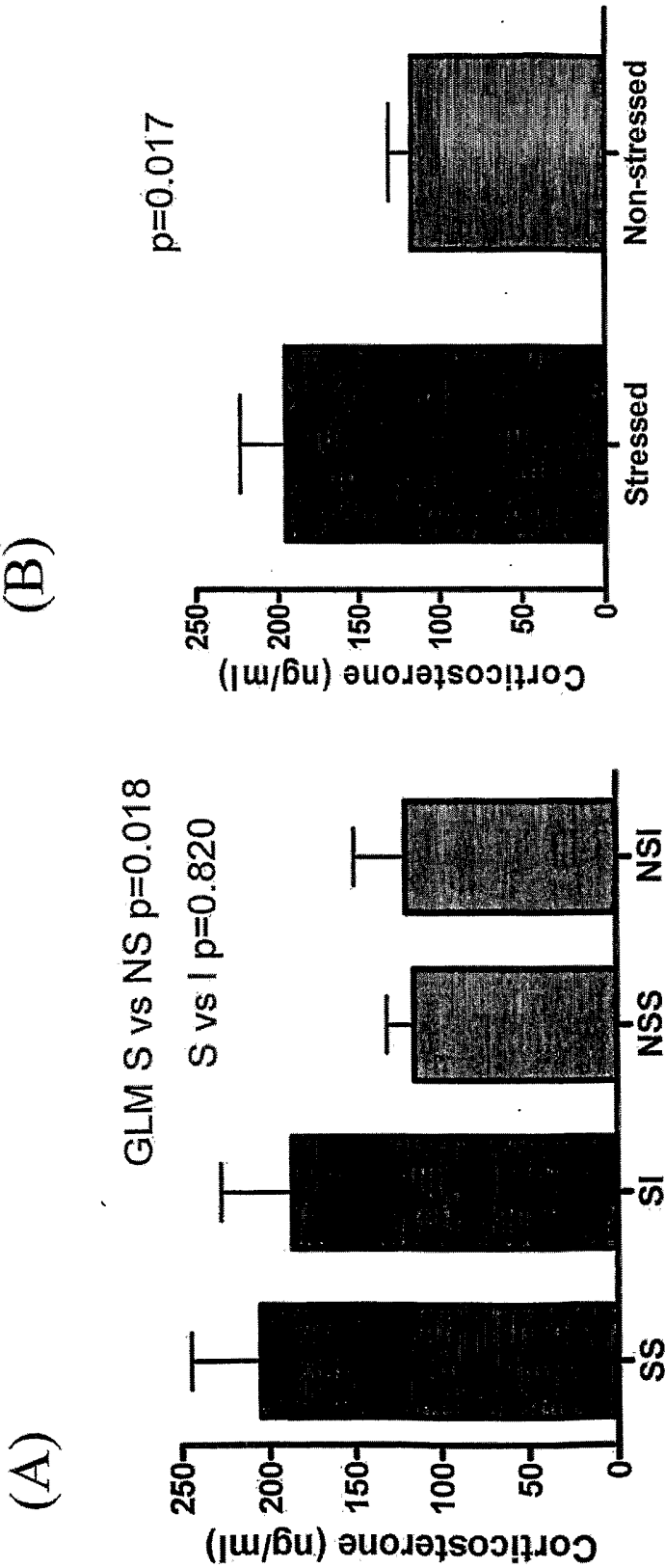


Fig 2

Corticosterone plasma levels after 5 weeks in different environments



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Fig 4

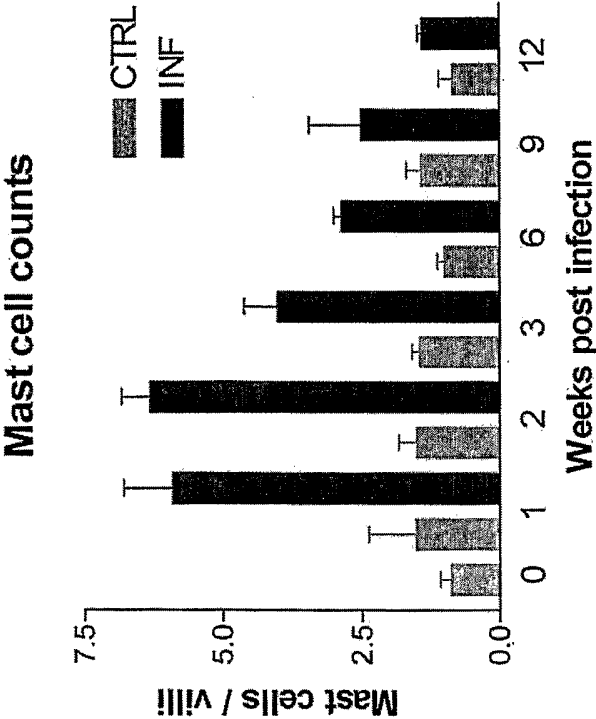


Fig 3B

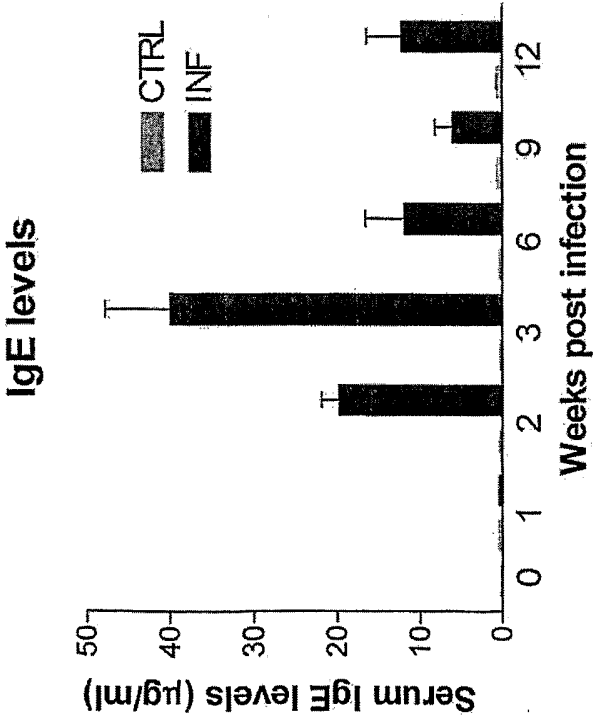


Fig 3A

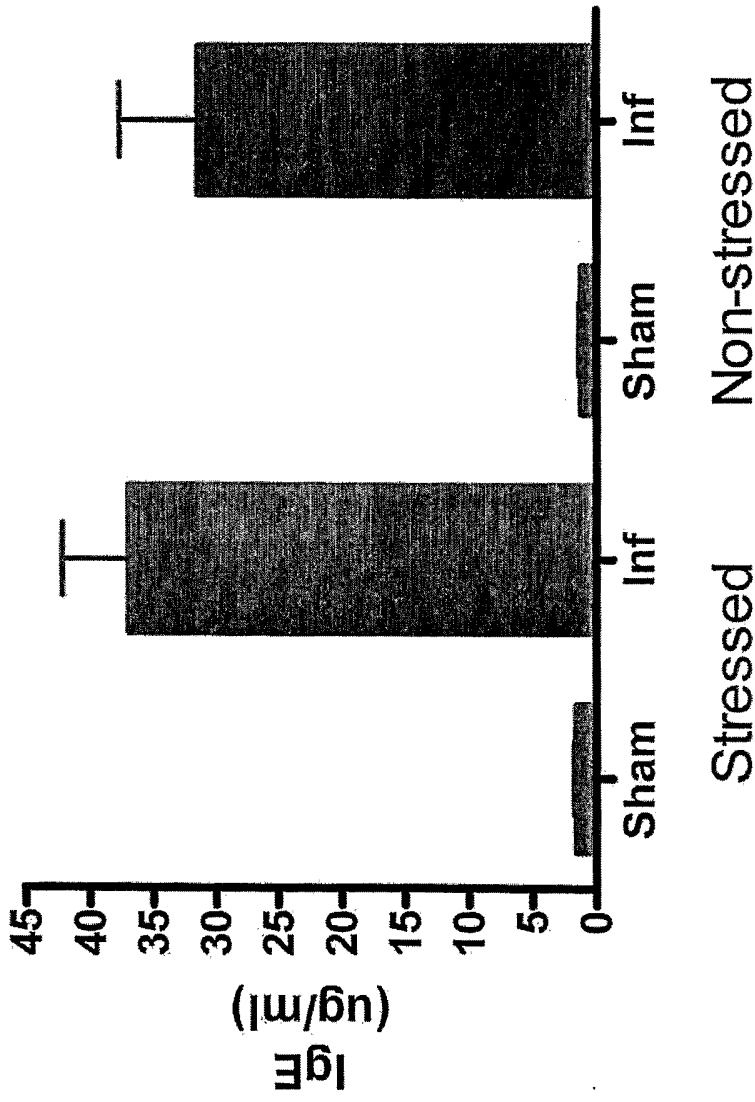


Fig. 5

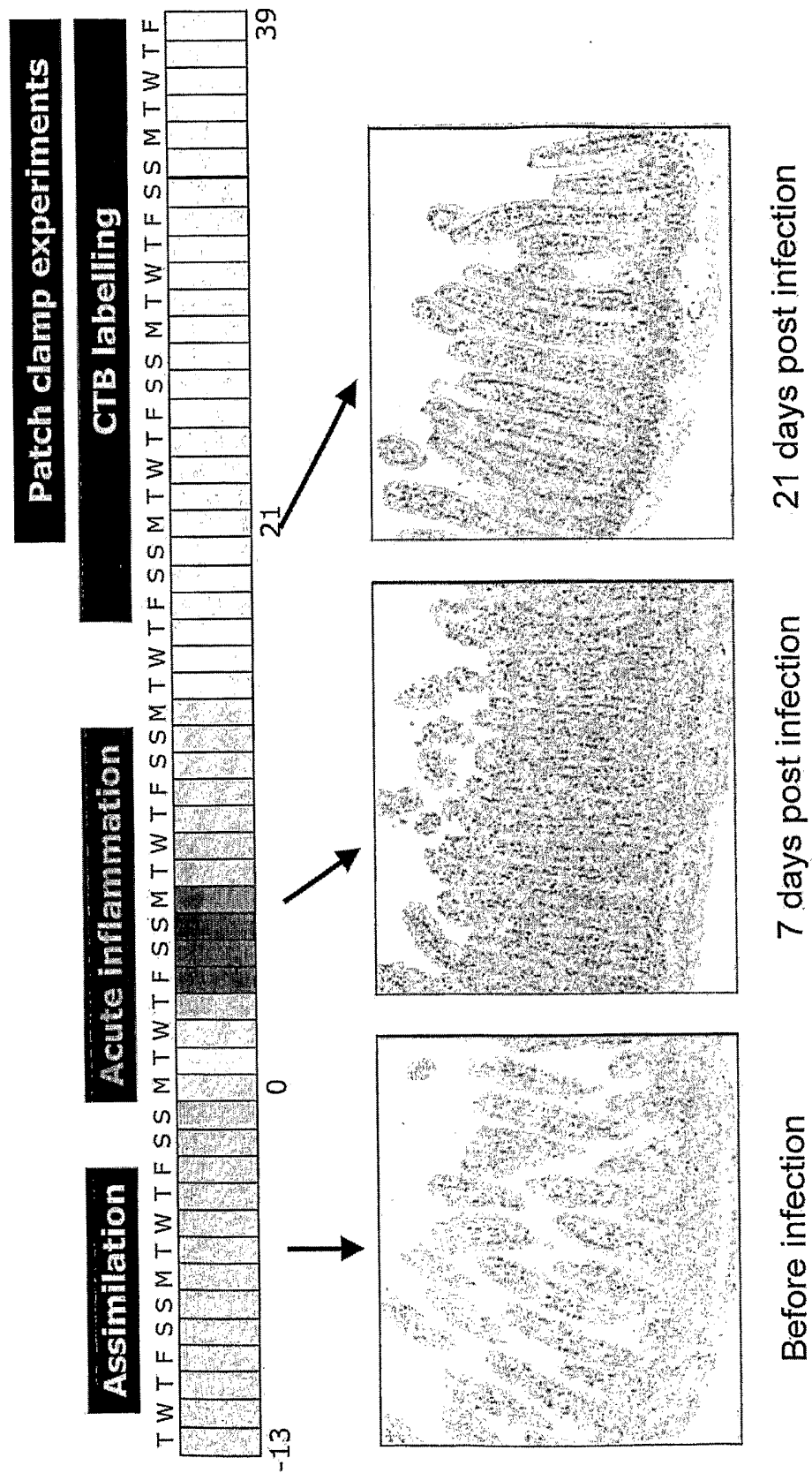
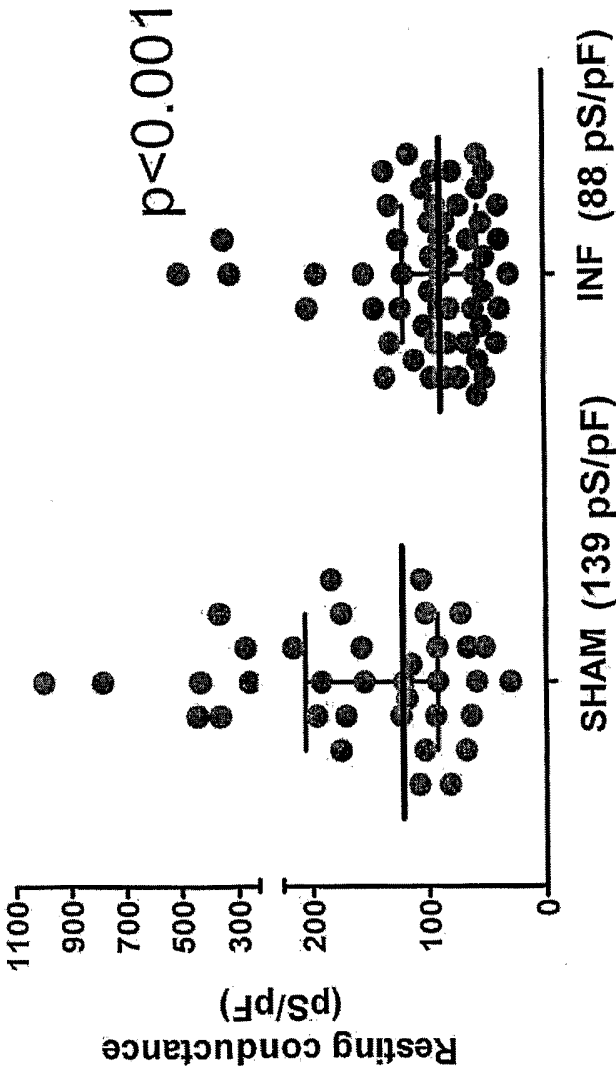


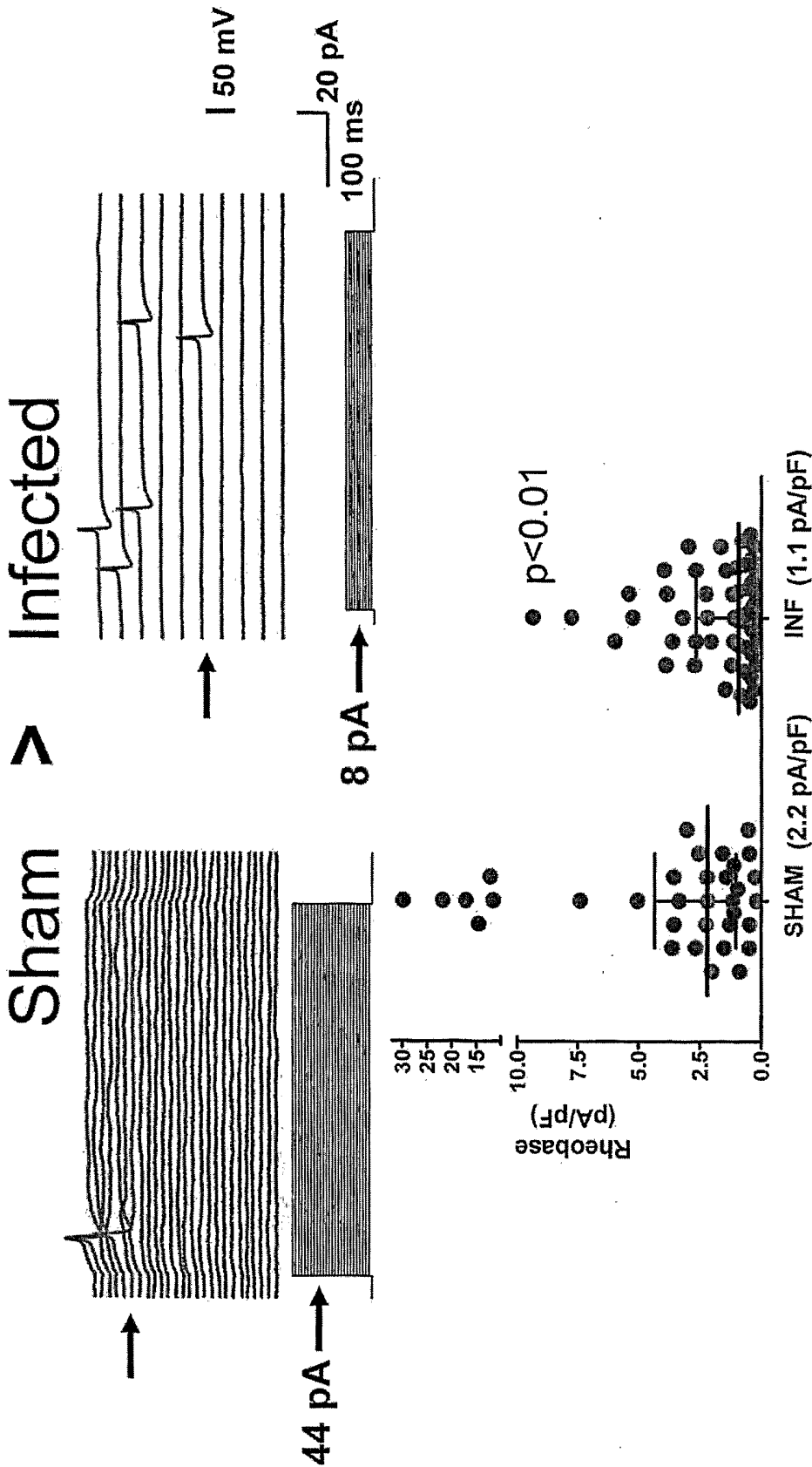
Fig 6
Sham > Infected



Data expressed as median $\pm$ interquartile range (IQR)
Significance determined by Mann-Whitney test, 2 tailed.

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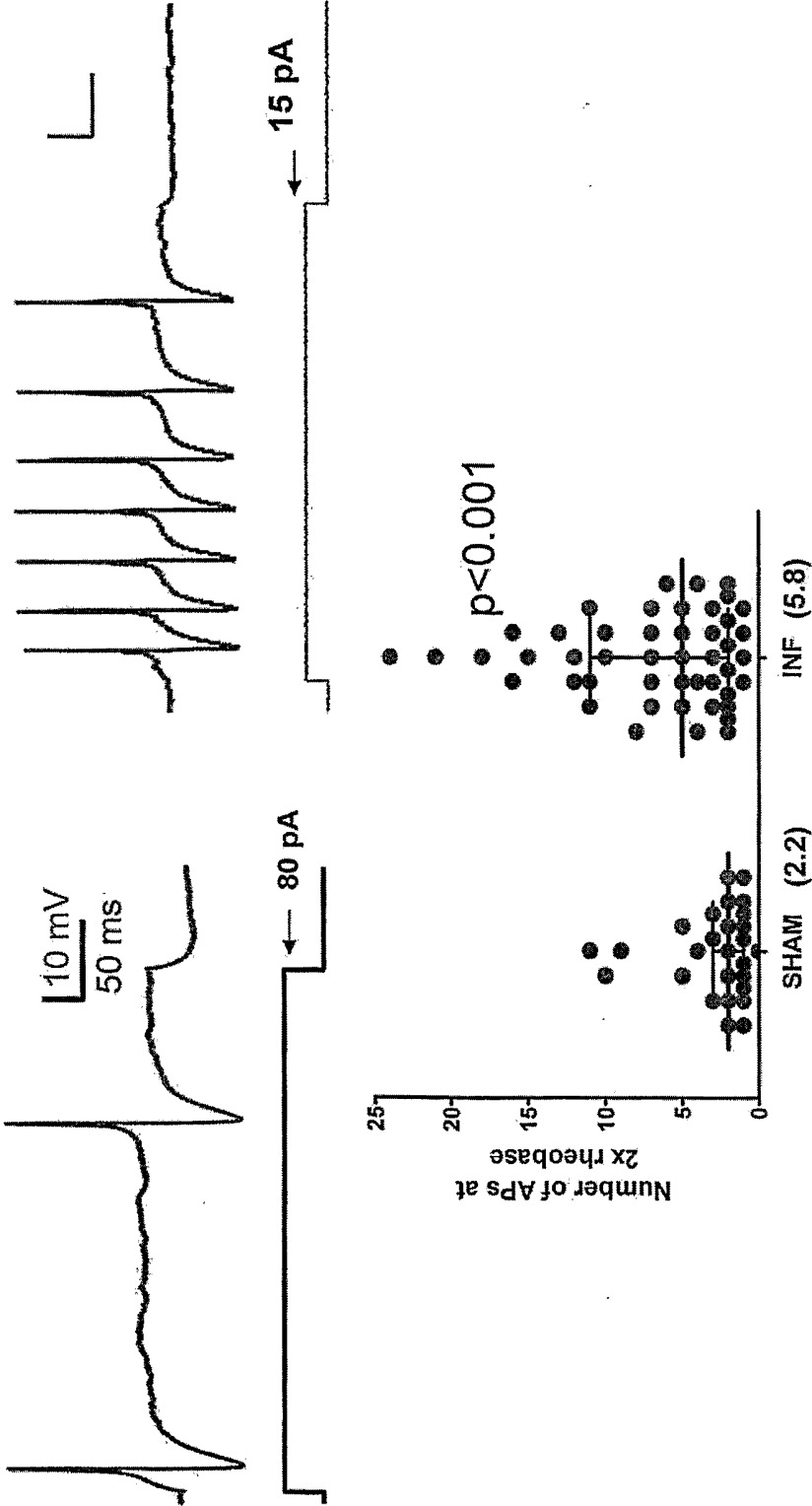
Fig 7



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Fig 8

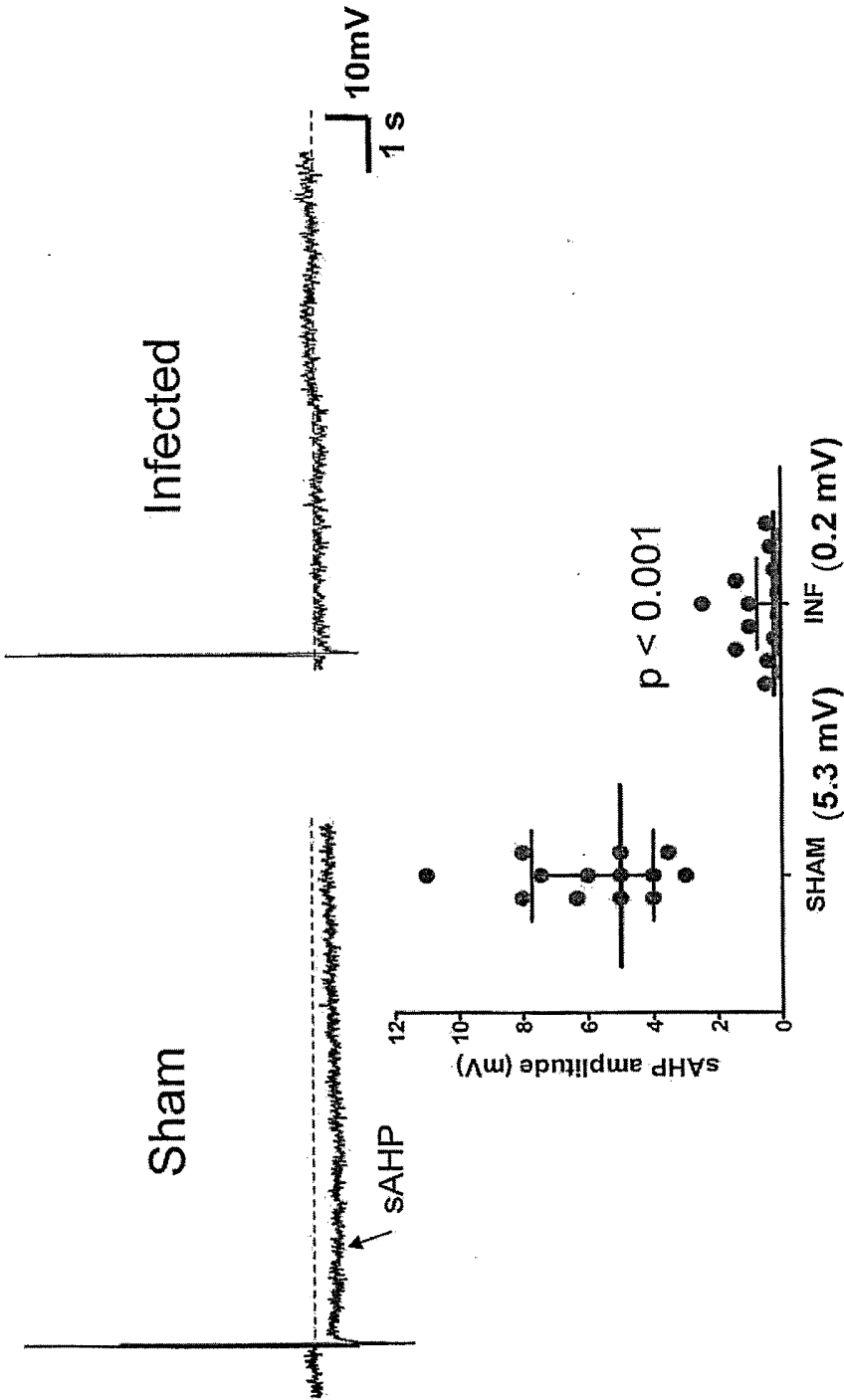
Sham < Infected



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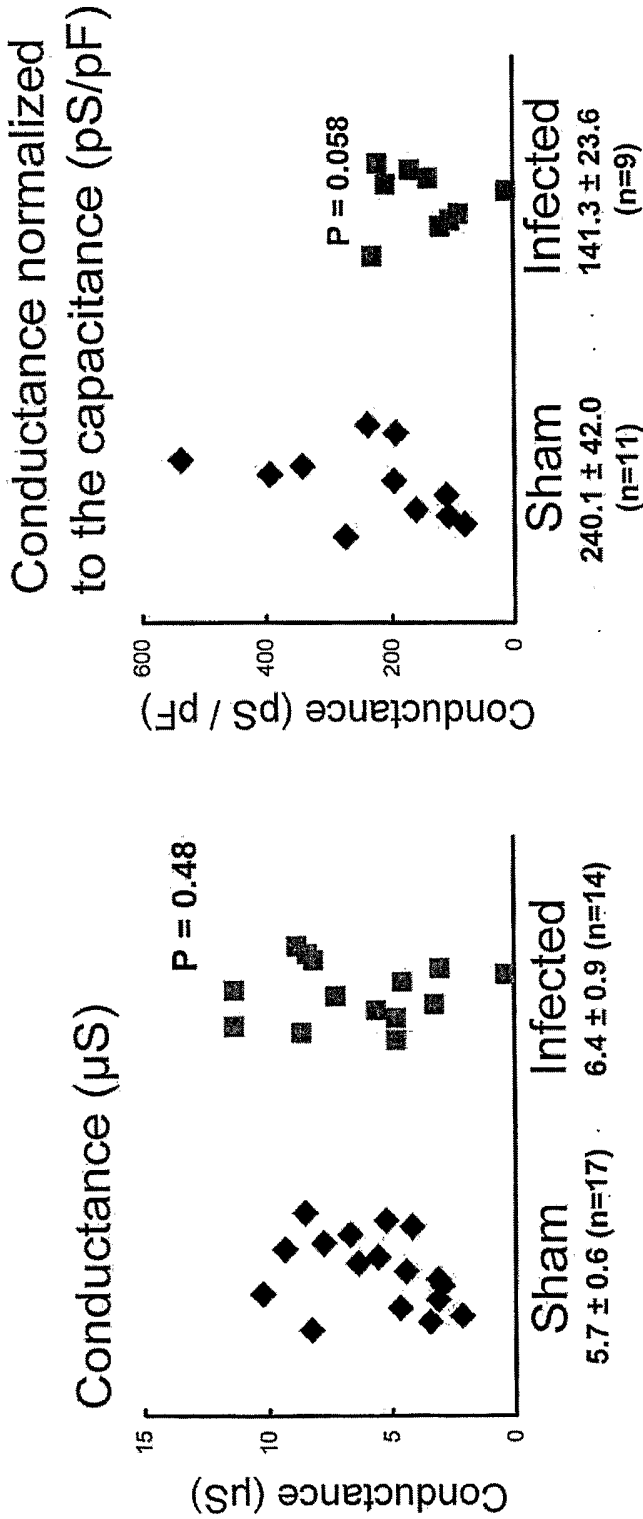
Fig 9

Sham > Infected



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Fig 10



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Fig 11

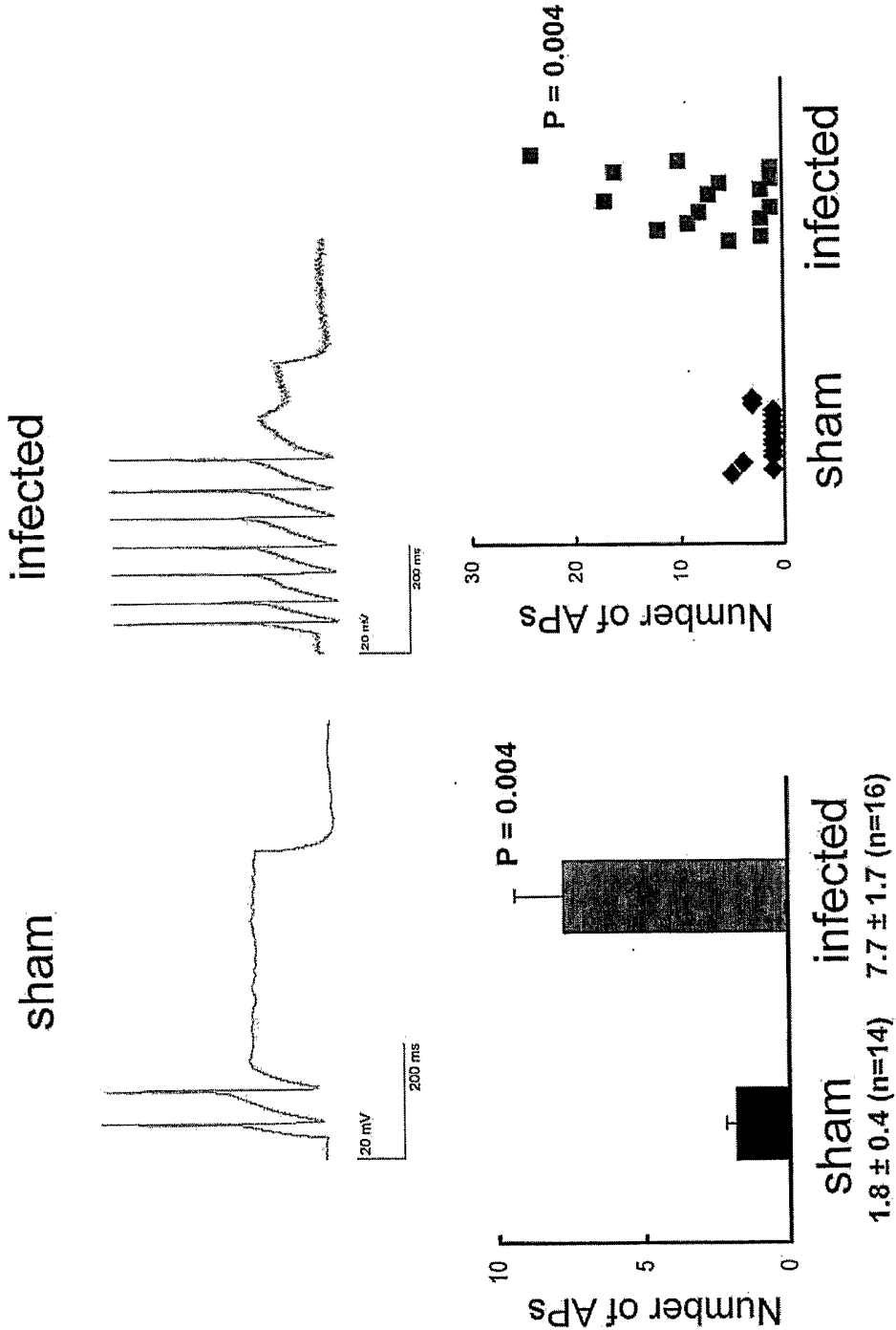
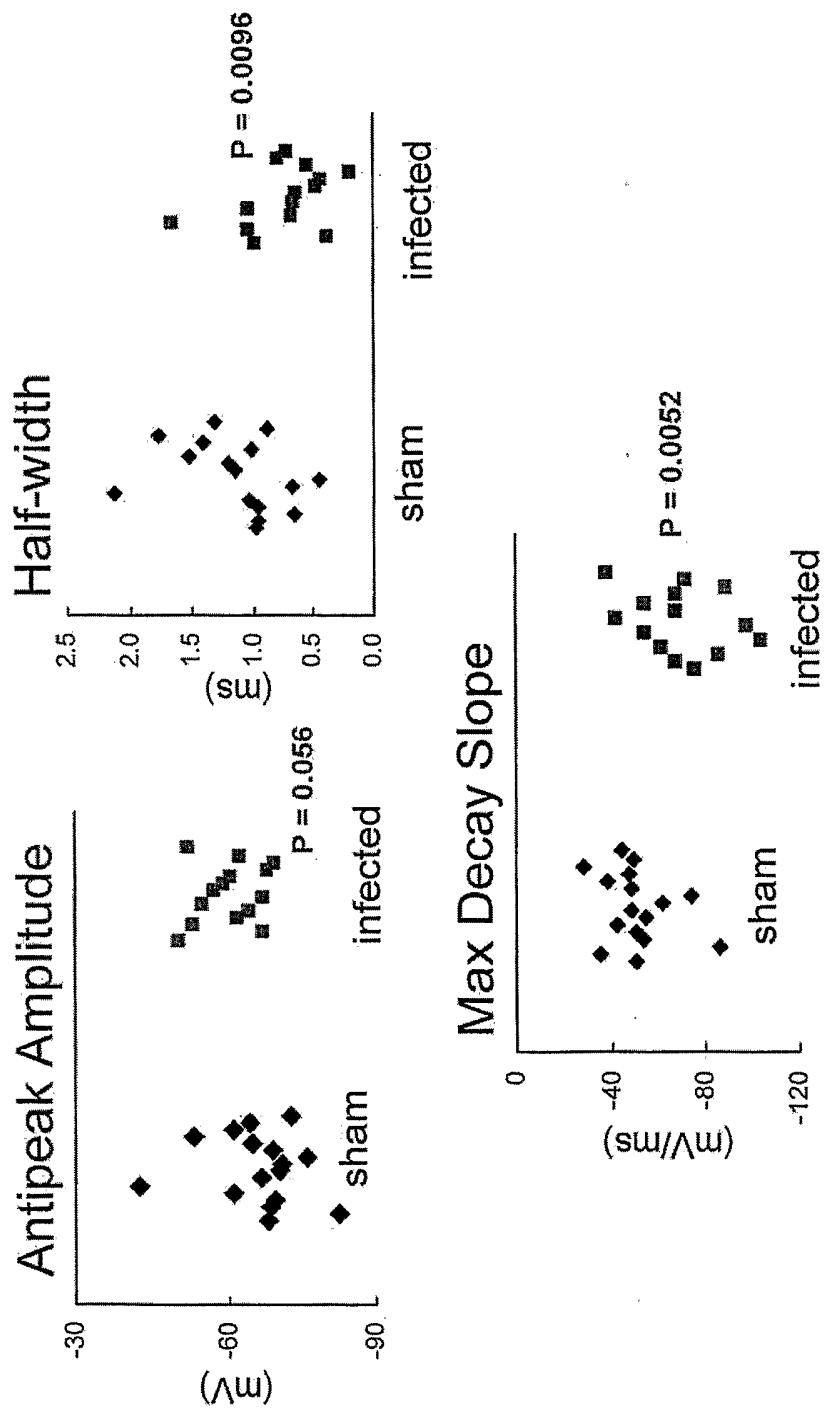


Fig 12



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Fig 13

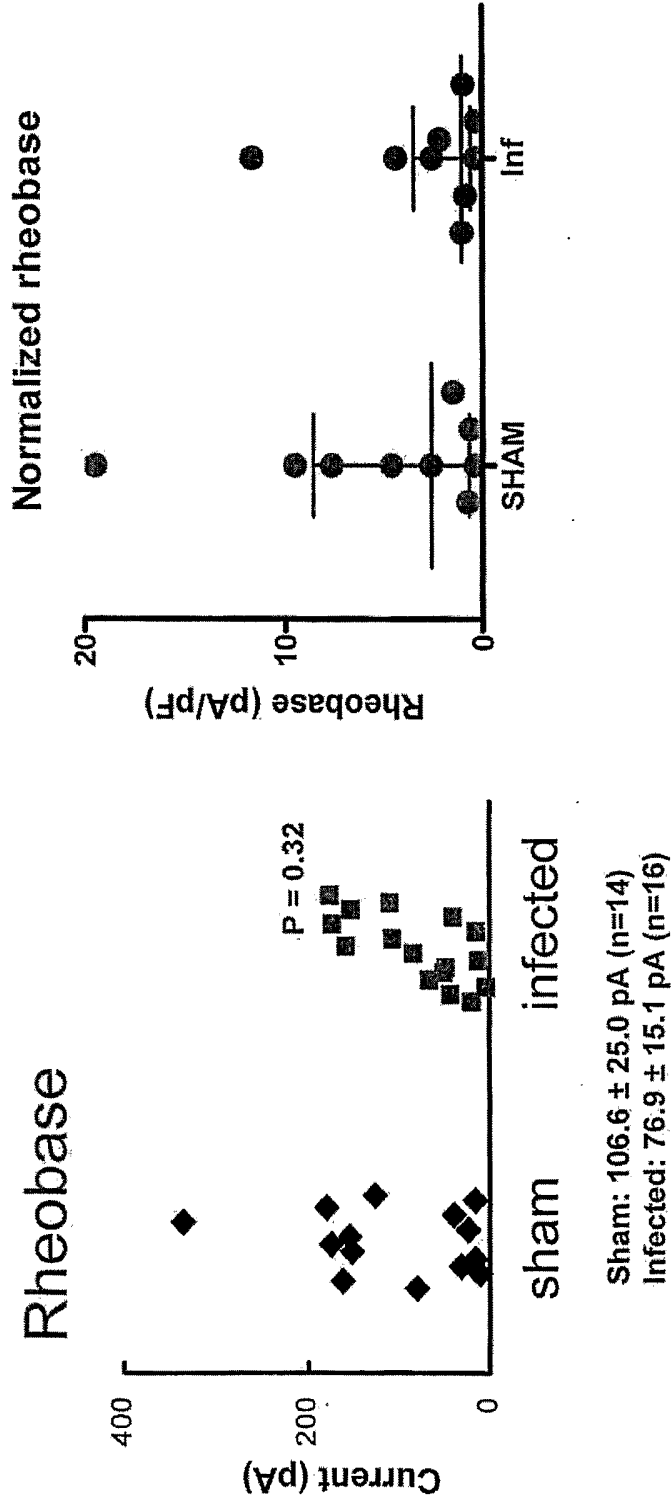


Fig 14

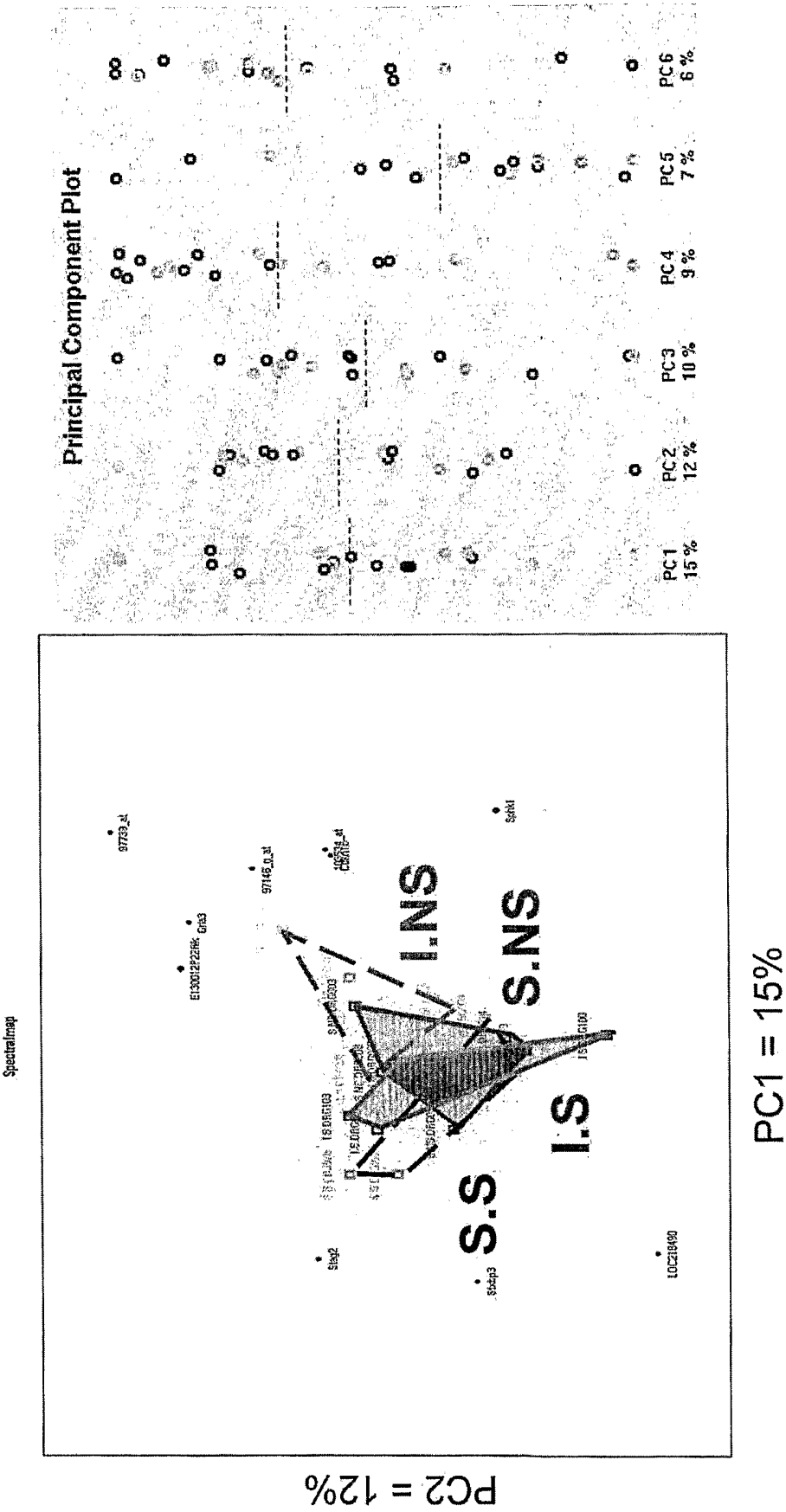
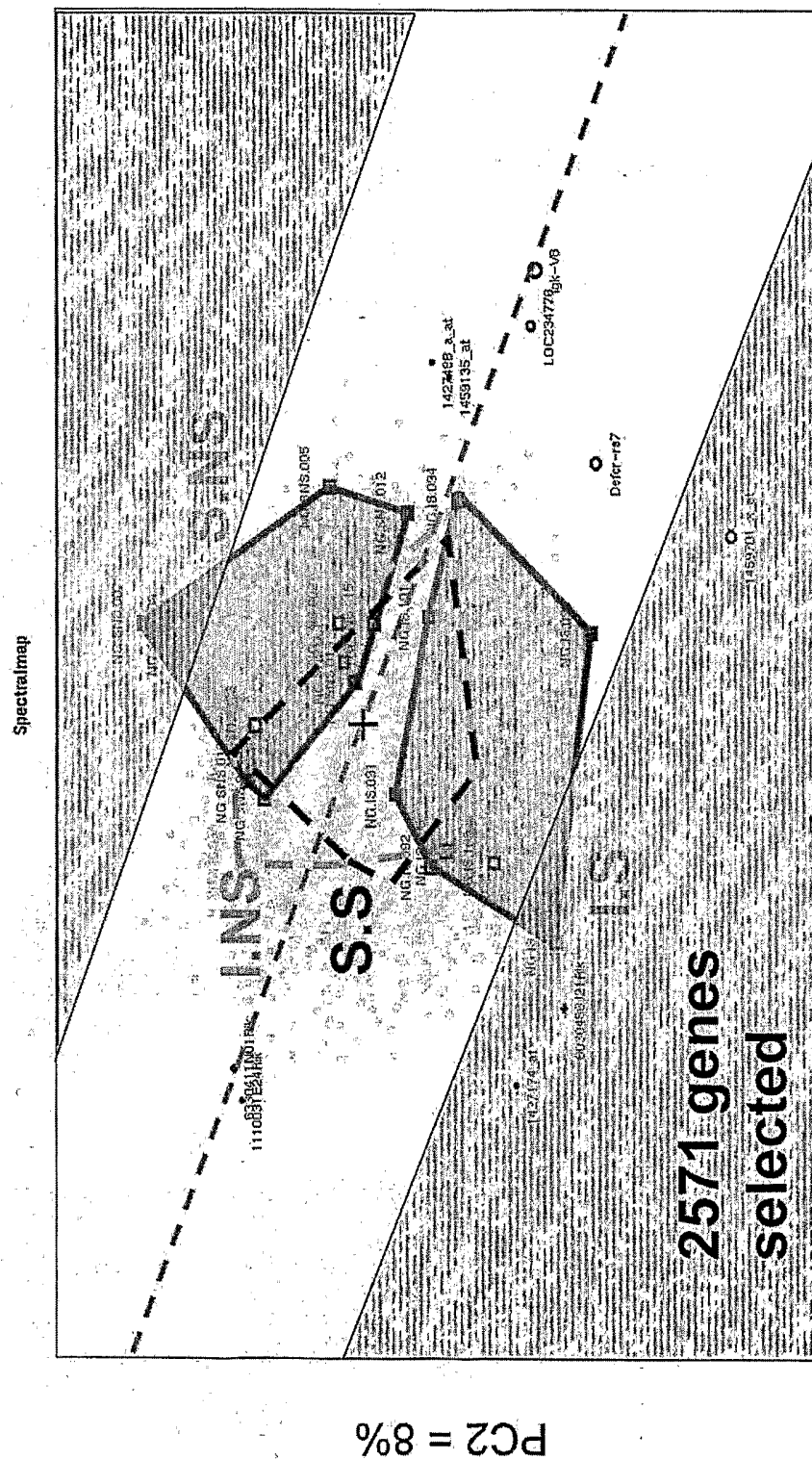


Fig 15



PC1 = 24%

Closure = none, Center = double, Norm. = global, Scale = uvc, RW = mean, CW = constant

2571 genes selected

Fig16

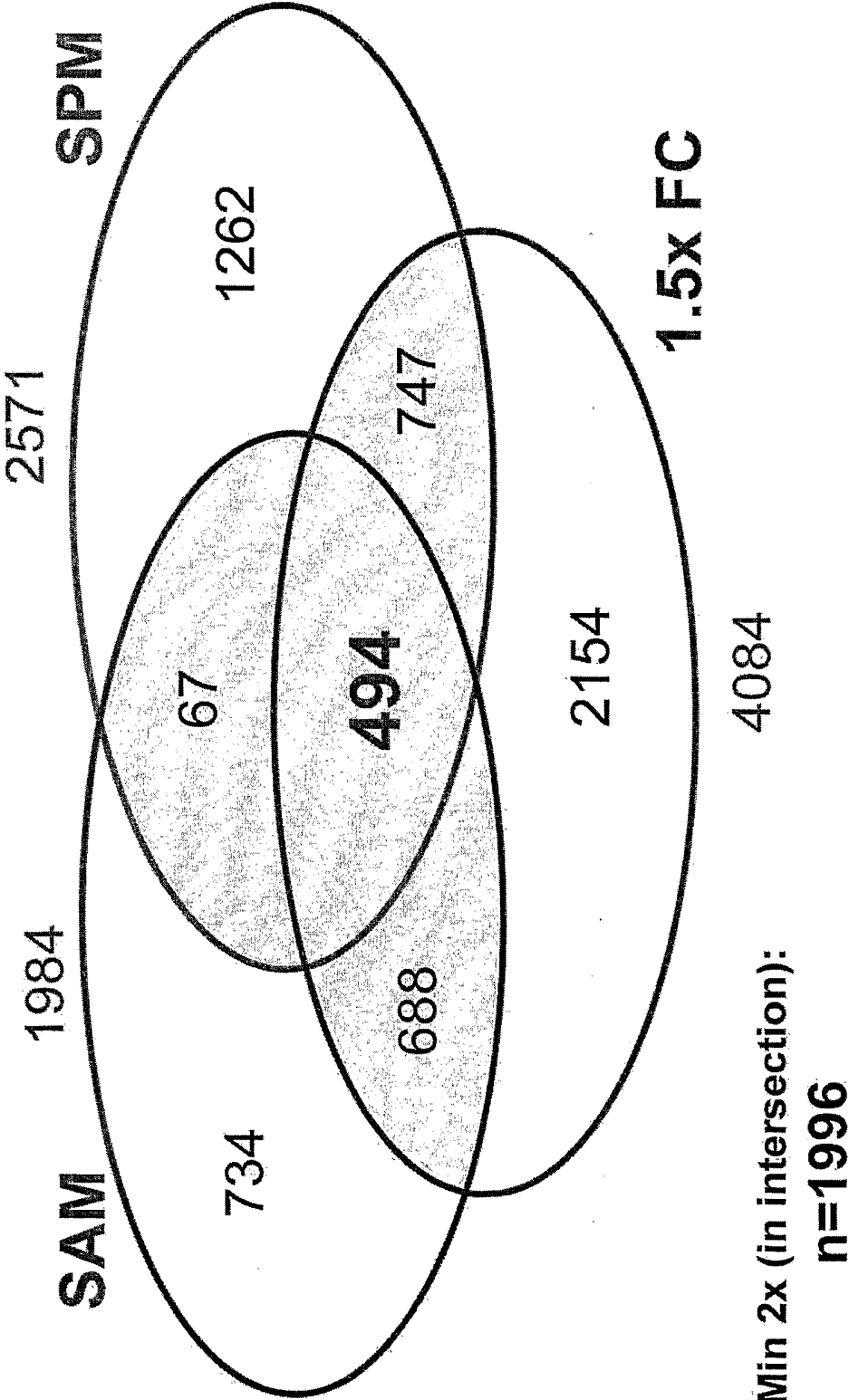
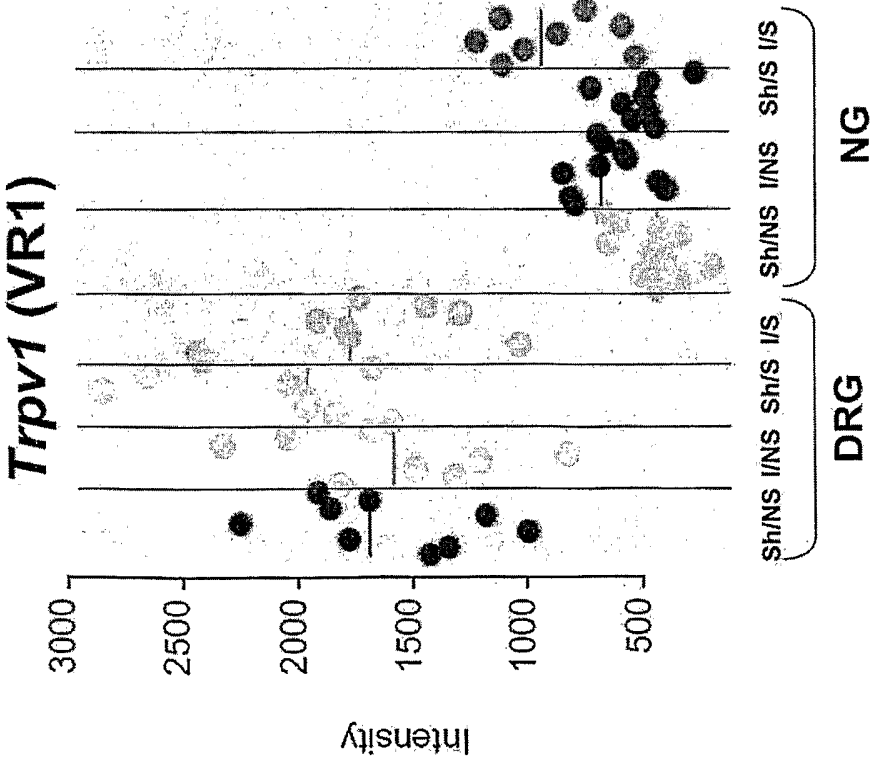


Fig 17

A



B

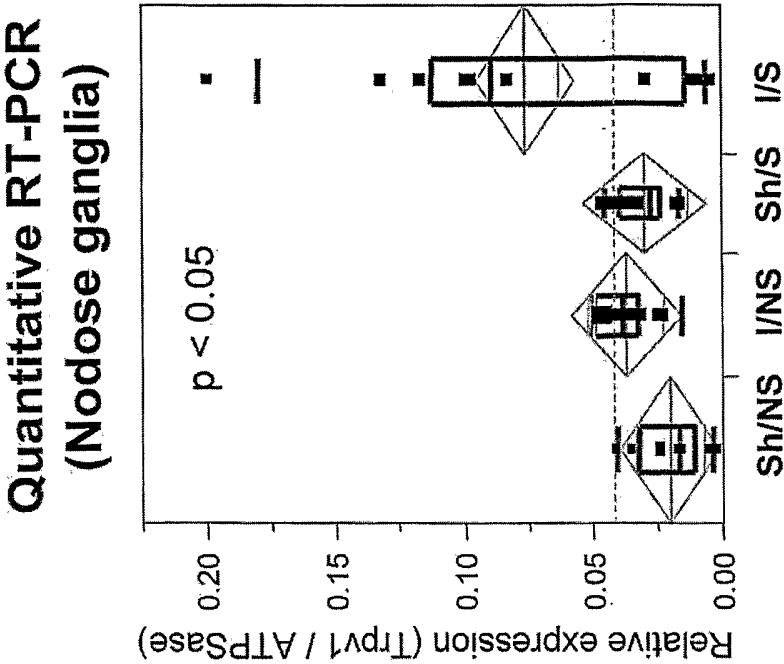


Fig 18

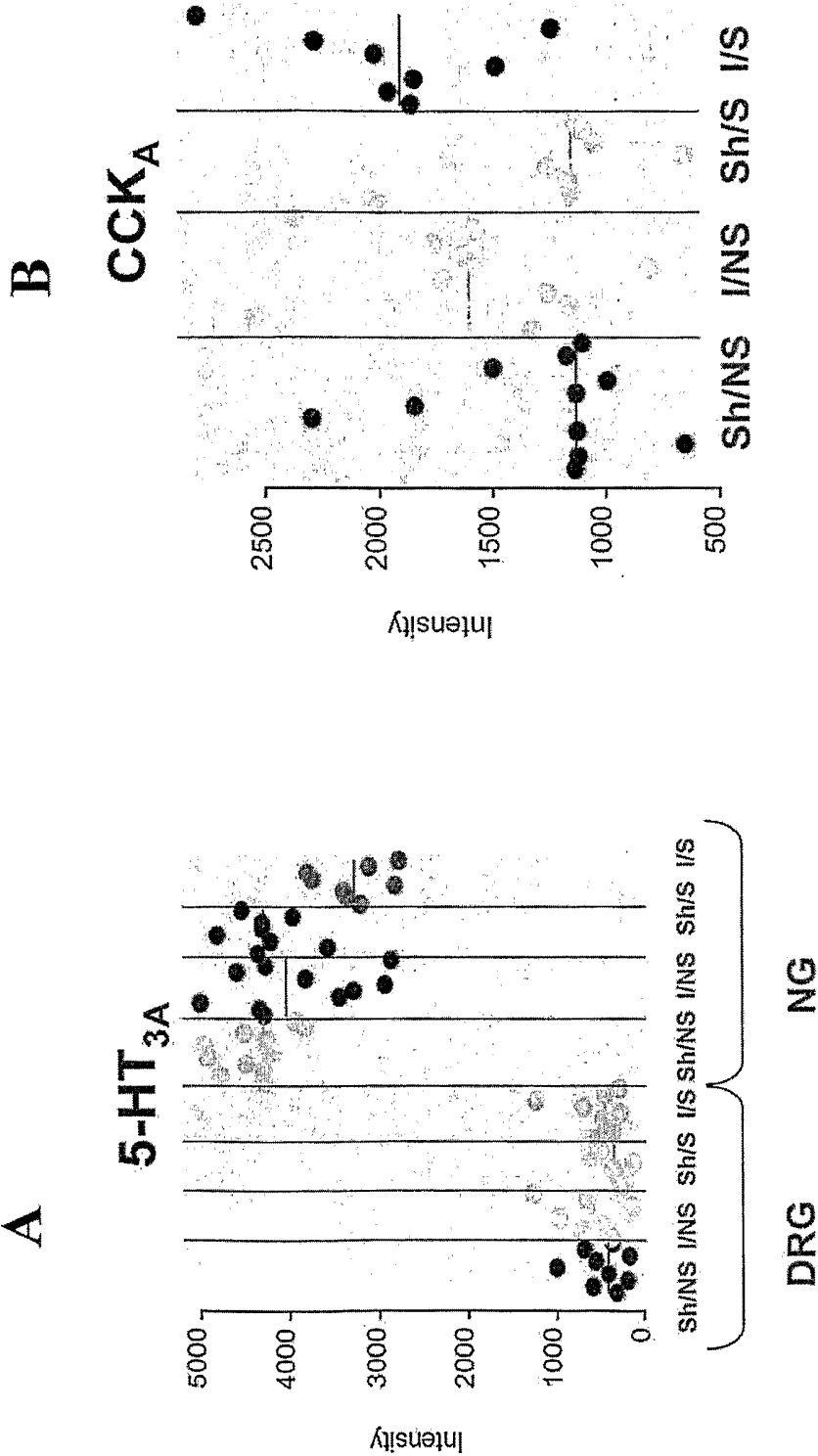


Fig 19

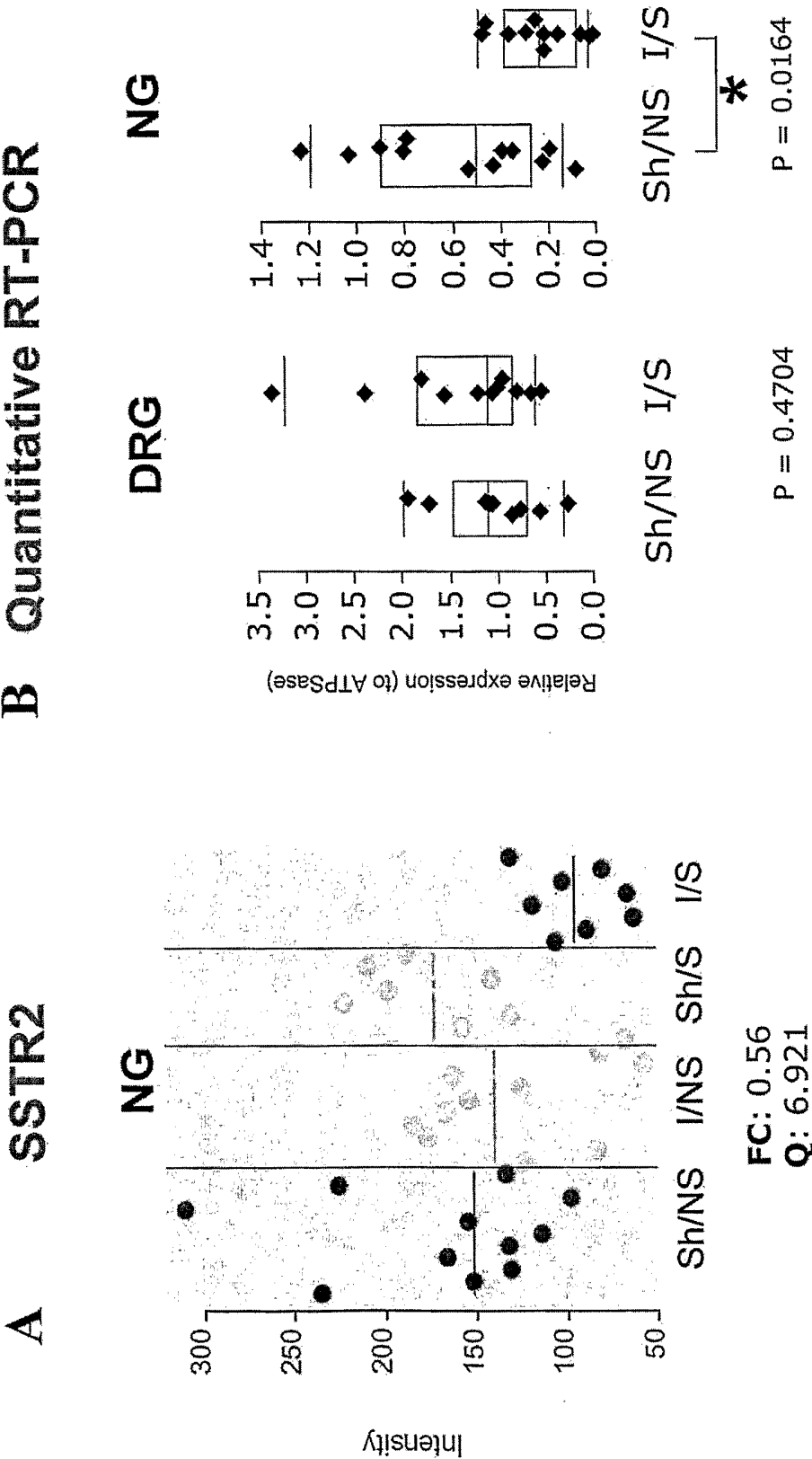


Fig 20

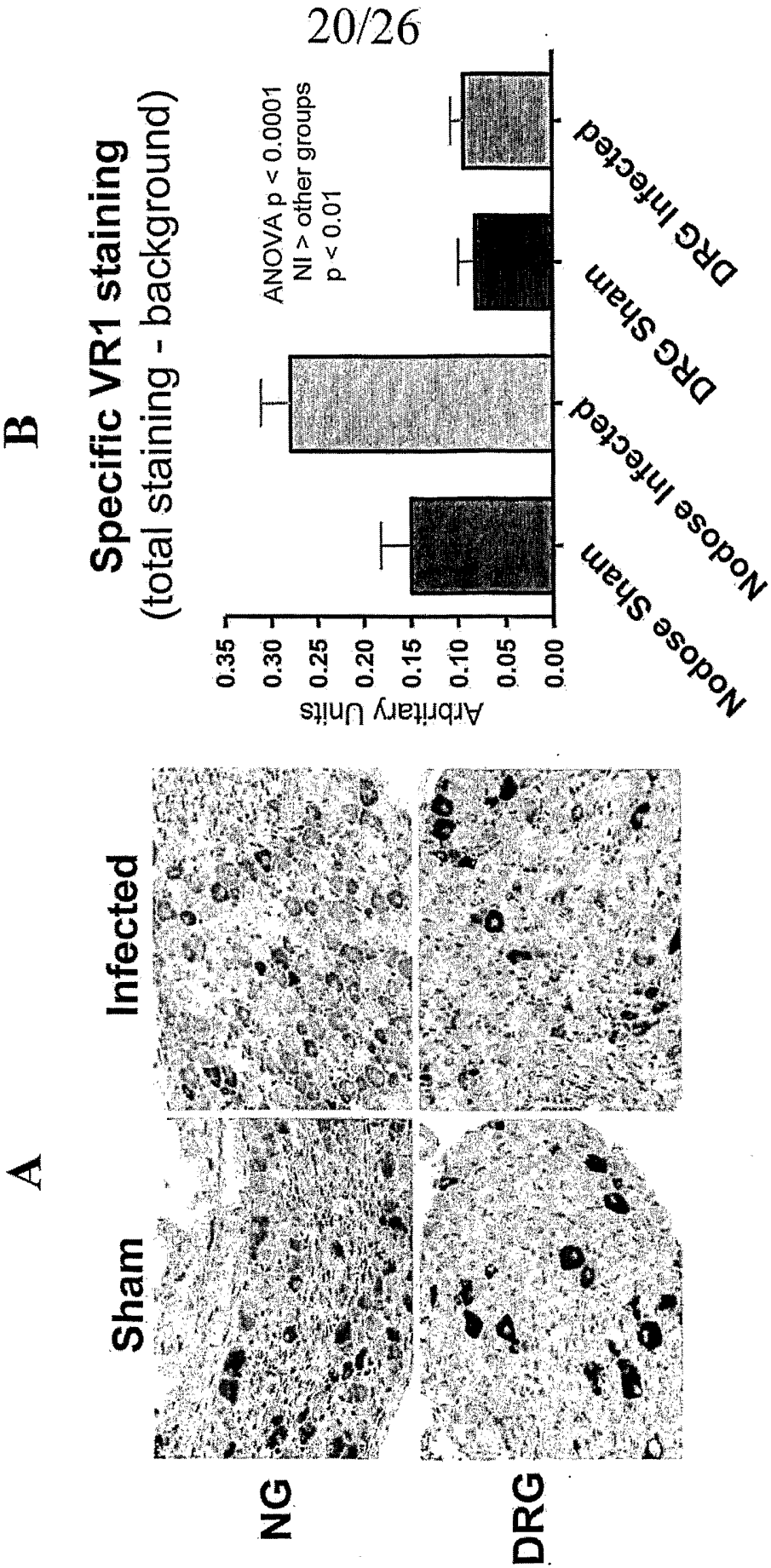


Fig 21

Effect of jejunal distension on pressor responses – Sham vs. Day 21 Post Nb infection

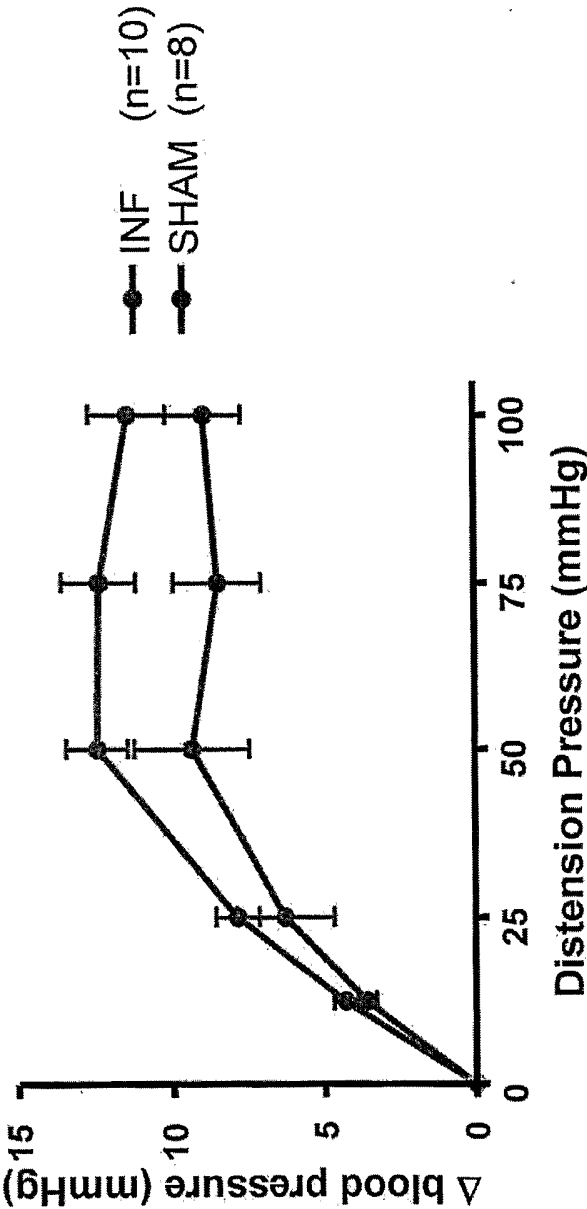


Fig 22

Effect of colonic distension on pressor responses – Sham vs. Day 21 Post Nb infection

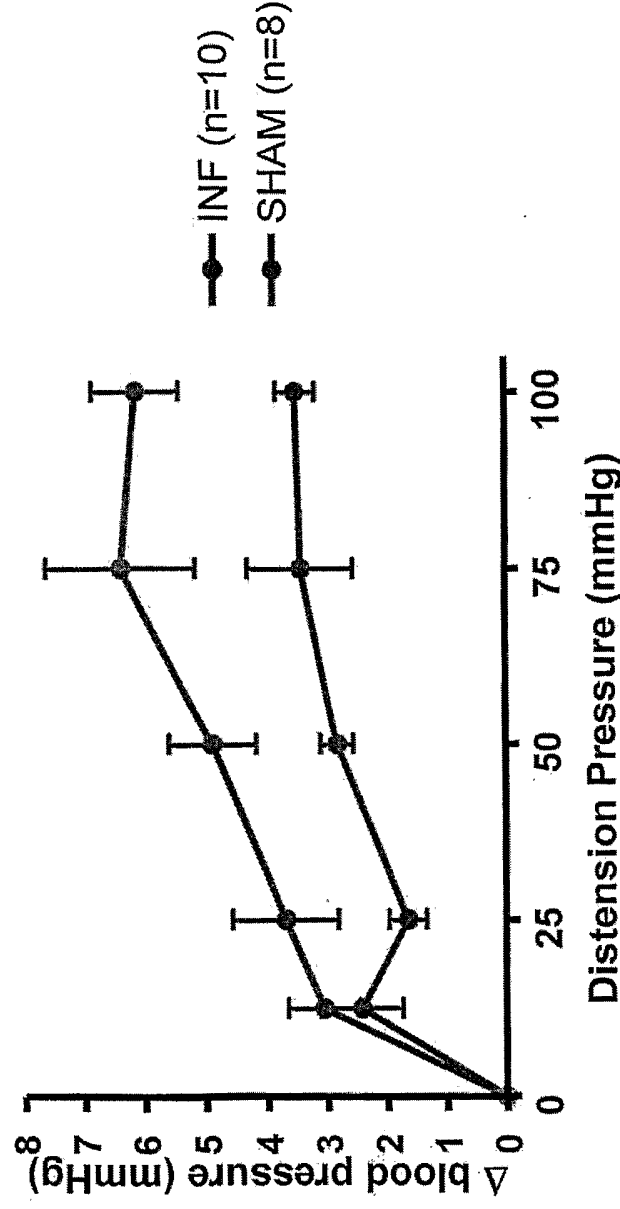
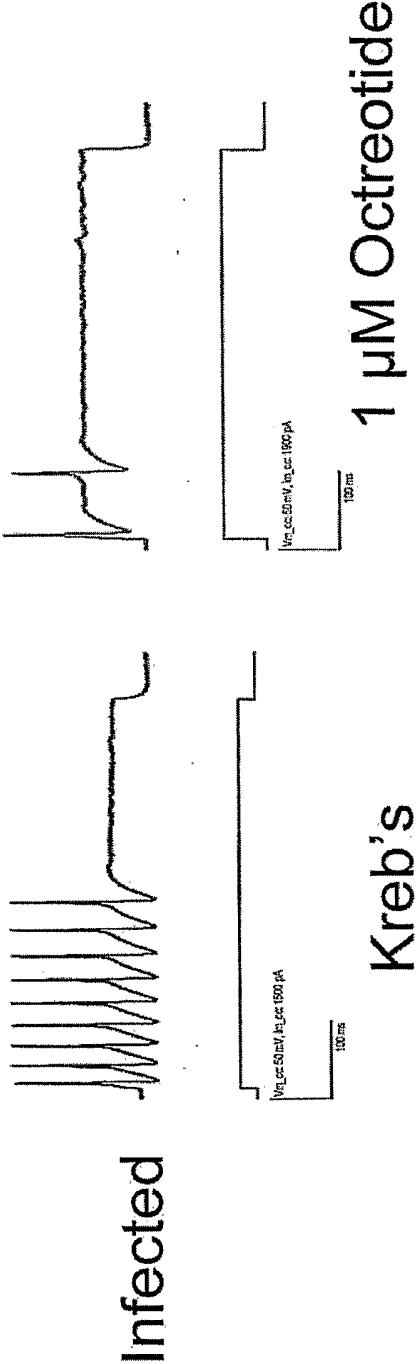
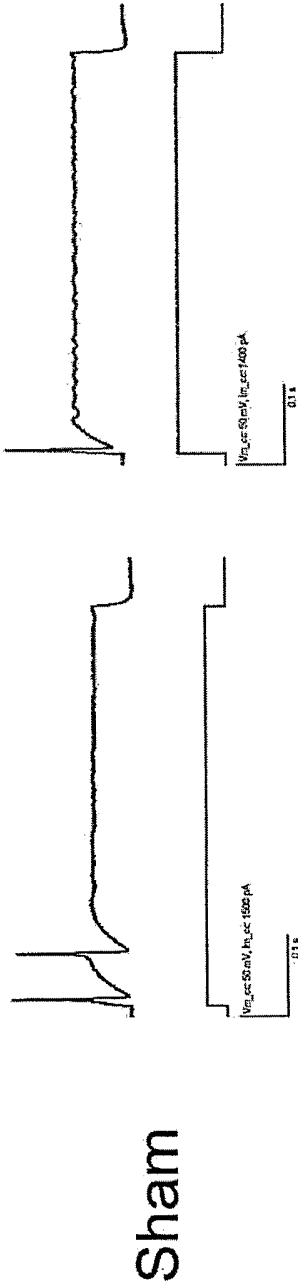


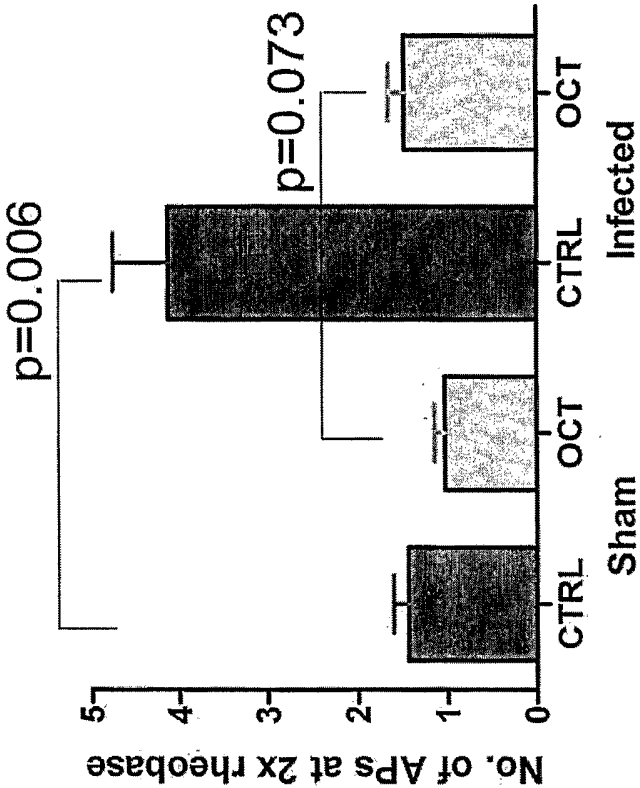
Fig 23

2 x Rheobase



Octreotide reduced multiple discharges

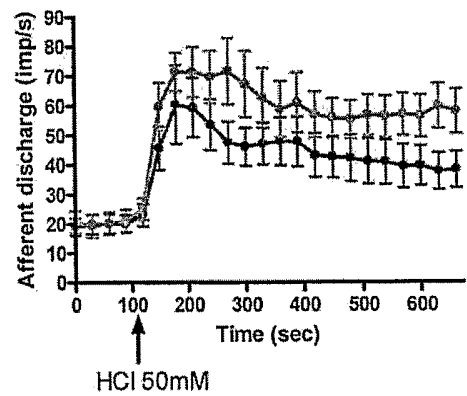
Fig 24



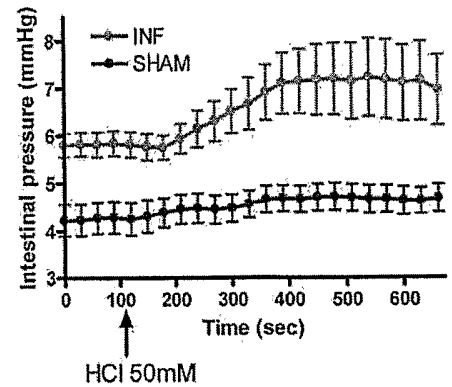
Octreotide reduces number of discharges at 2x rheobase

FIG 25

A: Afferent Nerve Activity



B: Intraluminal Pressure



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FIG 26

