An old protein in unexpected places: alpha- and beta- globin expression in mesencephalic dopaminergic neurons and glial cells.

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CANDIDATE
Milena Pinto

SUPERVISOR
Prof. Stefano Gustincich

Declaration

The work described in this thesis was carried out at the International School for Advanced Studies, Trieste, between October 2005 and August 2009 with the exception of

- Solexa Illumina Sequencing that was performed at Genome Science Laboratory, RIKEN, Wako main Campus, Hirosawa 2-1 Wako, Japan under the supervision of Piero Carninci
- FACS sorting that was performed at Centro Interdipartimentale Medicina Rigenerativa (CIME), University of Udine, Udine, Italy under the supervision professor Carlo Alberto Beltrami.

The work described in this thesis is included in:

Milena Pinto (*), Marta Biagioli (*), Daniela Cesselli, Marta Zaninello, Dejan Lazarevic, Paola Roncaglia, Roberto Simone, Christina Vlachouli, Charles Plessy, Nicolas Bertin, Antonio Beltrami, Kazuto Kobayashi, Vittorio Gallo, Claudio Santoro, Isidro Ferrer, Stefano Rivella, Carlo Alberto Beltrami, Piero Carninci, Elio Raviola and Stefano Gustincich.
Unexpected expression of α- and β- globin in mesencephalic dopaminergic neurons and glial cells.

Abbreviations:

Hb-IR, Hemoglobin-ImmunoReactivity;
mDA, Mesencephalic Dopaminergic neurons;
PD, Parkinson's Disease;
SN, *Substantia Nigra*;
VTA, *Ventral Tegmental Area*;
TH, Tyrosine Hydroxilase;
LCM, Laser Capture Microdissection;
CAGE, Cap Analysis of Gene Expression;
FACS, Fluorescent Activated Cell Sorting;
IHC, immunohistochemistry
eGFP, enhanced Green Fluorescent Protein;
NO, Nitric Oxide.

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ABSTRACT

Dopaminergic neurons (DA) are an anatomically and functionally heterogeneous group of cells involved in a wide range of neuronal network activities and behaviour. Among them, mesencephalic dopaminergic neurons (mDA) are the major source of dopamine in the brain. They present two main groups of projecting cells: the A9 neurons of the *Substantia Nigra* (SN) and the A10 cells of the *Ventral Tegmental Area* (VTA).

A9 neurons form the nigrostriatal pathway and are involved in regulating voluntary movements and postural reflexes. Their selective degeneration leads to Parkinson's disease (PD) and the loss of DA synapses in the striatum is believed to be primary cause for the disruption of the ability to control movements (E. Hirsch *et al.* 1988).

A10 cells constitute the mesocorticolimbic pathway playing a fundamental role in reward and attention. Their abnormal function has been linked to schizophrenia, attention deficit and addiction while they are relatively spared in PD (Meyer-Lindenberg *et al.* 2002).

The description of the repertory of genes of mDA neurons may provide crucial information on their physiology as well as on the mechanisms of cell-type specific dysfunction. Interestingly, in previous gene expression profiling experiments, mDA cells groups presented a limited number of differentially expressed genes with A9-enriched transcripts mainly related to energy metabolism and mitochondrial function (C. Y. Chung *et al.* 2005; James G Greene *et al.* 2005).

A crucial requirement for metabolically active aerobic cells is a steady supply of oxygen. To this purpose, hemoglobin-like molecules occur widely in organisms ranging form bacteria to human (Vandergon 1998). Vertebrate hemoglobin is the oxygen- and carbon dioxide-carrying protein in cells of erythroid lineage and is responsible for oxygen delivery to the respiring tissues of the body. Additional vertebrate heme-containing proteins with structural homology to globin chains include cytoglobin, mostly described in connective tissues (M. Schmidt *et al.* 2004), and neuroglobin, broadly expressed in the brain (Burmester 2000; Burmester 2004).

Surprisingly, hemoglobin chains have been recently detected in non-erythroid cells including macrophages, alveolar cells, eye's lens and mesangial cells of the kidney (Dugas *et al.* 2006; L. Liu *et al.* 1999; Newton *et al.* 2006; Nishi *et al.* 2008).

By a combination of different gene expression platforms with Laser Capture Microdissection (LCM), we have identified the transcripts of hemoglobin alpha, adult chain 1 (Hba-a1) and hemoglobin beta, adult chain 1 (Hbb-b1) in A9 neurons.

Interestingly, Hemoglobin-ImmunoReactivity (Hb-IR) decorated the large majority of A9 cells while stained only less than 5% of A10 neurons. Furthermore, we detected hemoglobin expression in almost all oligodendrocytes as well as in cortical and hippocampal astrocytes and proved that this pattern of expression was conserved in mammals. Importantly, A9 DA neurons from human *post mortem* brain showed hemoglobin expression.

By gene expression analysis of mouse dopaminergic neuroblastoma cell lines stably transfected with alpha- and beta-chains, we observed changes in genes involved in oxygen homeostasis as well as in oxidative phosphorylation, suggesting a link between hemoglobin and mitochondrial activity.

These results open a new scenario for hemoglobin role in brain physiology and in PD pathogenesis.

1. INTRODUCTION

1.1 PARKINSON' S DISEASE

1.1.1 HISTORY AND CLINICAL FEATURES

Parkinson's Disease (PD) was originally described by James Parkinson in 1817 in his monograph "An Essay on the Shaking Palsy". He described the symptoms of the disease as *"Involuntary tremolous motion, with lessened muscular power, in parts not in action and even when supported; with a propensity to bend the trunk forewords and to pass from a walking to a running pace: the senses and the intellect being ininjured"* (Parkinson S.d.).

During the 1950s and 1960s, Arvid Carlsson (Nobel Prize in 2000) demonstrated that PD patients showed a massive loss of Dopamine (DA) in the brain, which can be clinically reverted by treatment with Levodopa.

Nowadays PD is the second most common progressive neurodegenerative disorder (six million patients worldwide) after Alzheimer's Disease (AD). It affects 1-2 % of all individuals above the age of 65 years old, increasing to 4-5% by the age of 85.

PD is now known as a slowly progressive neurodegenerative disorder that gradually worsens in severity and usually affects one side of the body before spreading to the other side. It is characterized by six cardinal features: tremor at rest, rigidity, bradikinesia, hypokinesia and akinesia, flexed posture of neck, trunk and limbs, loss of postural reflexes and freezing phenomenon. The early symptoms of PD are usually alleviated by the treatment with Levodopa and DA agonists. As PD advances from year to year, late symptoms such as flexed posture, loss of postural reflexes and freezing phenomenon as well as bradykinesia don't respond to the same doses of Levodopa treatment any longer. While motor symptoms dominate PD clinical features, many patients show non-motor symptoms. These include fatigue, depression, anxiety, sleep disturbances, constipation, bladder and other autonomic disturbances (sexual and gastrointestinal), sensory complaints, decreased motivation, apathy and a decline in cognition that can progress to dementia (Braak *et al.* 2004).

1.1.2 NEUROPATHOLOGICAL FEATURES OF PD

Analysis of PD patients *post mortem* human brains show three major pathological features: depigmentation of the *substantia nigra* (SN) caused by the loss of dopaminergic neurons projecting in the striatum (principal cause of PD motor symptoms) presence of intraneuronal inclusions known as Lewy bodies within the surviving neurons of the SN as well as other brain regions and iron deposits.

Loss of midbrain dopaminergic neurons and consequent dopamine depletion in striatum

Motor dysfunctions are key features of PD.

Voluntary movements originate at motor cortex level: signals are sent through the encephalic trunk (*mesencephalon, pons and medulla*) to the brain stem and spinal cord. These signalling pathways are controlled by different sub-cortical structures (*thalamus, putamen and subthalamic nuclei*) that modulate movements thanks to a complex network of excitatory and inhibitory signals (**Fig.1 left)**. These nuclei are, in turn, innervated and modulated by ventral midbrain dopaminergic neurons, subdivided into three main groups: A8 (retrorubral field; RRF), A9 (*substantia nigra pars compacta* SNc), and A10 (ventral tegmental area; VTA).

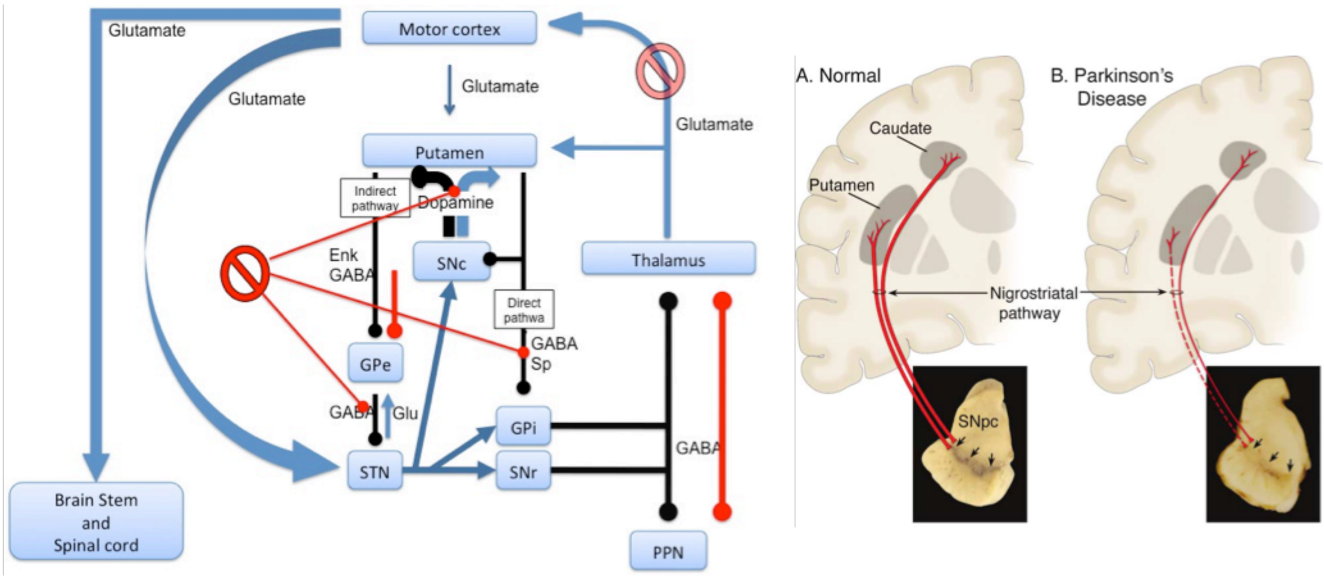


Fig.1: **on the left**: schematic illustration of the basal ganglia-thalamocortical "motor" circuit and its neurotrasmitters. Blue arrows represent excitatory transmission and black arrows inhibitory transmission, red symbols represent the pathway disregulations that happen in PD. (GPe, GPi *globus pallidus* external and internal segment, STN subthalamic nucleus, PPN pedunculopontine nucleus) . **On the right**: a schematic representation of the (A) normal nigrostriatal pathway (in red). SNc neurons project (thick solid red lines) to the basal ganglia and synapse in the striatum. In Parkinson's disease (B), the nigrostriatal pathway degenerates: there is a marked loss of dopaminergic neurons that project to the putamen (dashed line) and a much more modest loss of those that project to the caudate (thin red solid line) (Dauer et al. 2003).

The sensorimotor striatum involved in control of movement (*putamen*) is mainly innervated by dopaminergic cells of the ventral SNc whereas the limbic ventral striatum and the *thalamus* are targeted preferentially by VTA and dorsal SNc neurons.

The characteristic motor symptoms of PD are due to the alteration of this movement control system, in particular, to the selective, slow and progressive loss of dopaminergic neurons in the SNc. Their loss leads to a profound reduction in striatal dopamine that provokes an unbalance between excitatory and inhibitory trasmission in the basal ganglia-thalamocortical “motor” circuit (**Fig.1 left**) (Dauer & Przedborski 2003). The decreased striatal dopamine causes increased inhibitory output from the *globus pallidus* internal segment and *substantia nigra pars reticulata* (GPi/SNr) that, in turn, suppresses movement. On one hand, decreased striatal dopamine stimulation causes the direct reduction of the inhibition of the GPi/SNr; on the other hand, decreased dopamine inhibition causes increased inhibition of the *globus pallidus* external segment (GPe), resulting in blocking the inhibition of the subtalamic nucleus (STN). Increased STN output increases GPi/SNr inhibitory output to the thalamus that can not regulate the activity of the motor cortex any longer (**Fig.1 left**).

The pattern of progressive cell loss is not homogeneous, but rather displays a complex topographical and regional organization: the degeneration starts from the most lateral part of SNc and spreads to the most medialis region. Furthermore, nigrostriatal projections to the putamen are more sensitive than those to caudate and nucleus accumbens regions (**Fig.1 right**), whereas VTA projections to the ventral striatum are selectively spared in PD patients.

While loss of the nigral dopaminergic neurons and terminals are responsible for the movement disorders associated with PD, it has become clear that additional neuronal populations throughout the brain are also affected in the disease (Braak *et al.* 2004).

Lewy Bodies

Typical pathological hallmarks of the desease are Lewy Bodies (LBs), discovered in 1919 by Trétiakoff, and dystrophic neuritis, also called Lewy Neurites (LNs) first described by Friederich Lewy in the dorsal motor nucleus of the vagus nerve and in the *substantia innominata* from patients with PD (1912).

LBs and LNs are present in PD patients’ brains in some of the surviving dopaminergic neurons and in other regions like dorsal motor nucleus of the vagus, locus ceruleus, thalamus, amygdala, olfactory nuclei, pediculopontine nucleus, and cerebral cortex. In late stages of PD, when patients manifest all motor and cognitive clinical symptoms, inclusion bodies decorate the entire neocortex comprising the sensory association area (Braak *et al.* 2004).

LBs are round cytoplasmatic eosinophilic inclusions, 5–25 μm in diameter (**Fig. 2**). The ultrastructure show that they are composed of a dense core of filamentous and granular material, surrounded by radially orientated filaments of 10–20 nm in diameter.

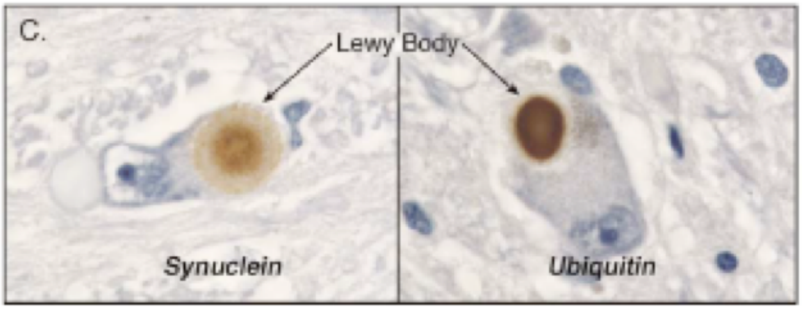


Fig 2: Immunohistochemical staining of Lewy Bodies found in dopaminergic neurons of PD patients in *Substantia Nigra pars compacta.* Unsoluble fibrous component of aggregates are detected with anti-α-synuclein antibody and anti-ubiquitin \cite{Dauer:2003km}.

LBs are composed by the accumulation of cytoplasmic aggregates containing a variety of proteins, like α-synuclein, the major component, but also, parkin and UCHL1 (genes whose mutations have been correlated with PD) and many others like Hsp70, ubiquitin and components of the proteasome (Spillantini & Goeder S.d.).

LNs are abnormal neurites that contain the same proteins and abnormal filaments found in Lewy bodies.

The mechanism causing the abnormal accumulation of proteins in Lewy bodies and Lewy neurites is not yet known and their toxic or protective role in neurodegenerative process is still matter of debate because till now there is no clear correlation between inclusion formation and neuronal cell death. If LBs are considered toxic, cytoplasmic protein aggregates may interfere with intracellular trafficking or sequestrate proteins important for cell survival. On the other hand, LBs are present in surviving cells that seem to be healthier, by morphological and biochemical analysis, than neighbouring cells (Tompkins & W. D. Hill 1997). Moreover, LBs have been also found in people without evident neuronal loss or clinical signs of PD, so they could be a protective structure in which proteins accumulate after the pathological failure of protein degradation.

Iron accumulation

Iron is important for different biological processes. It is coordinated by heme, and it is an essential component of cytochromes as well as a cofactor of many different enzymes involved in the normal function of neuronal tissue. For example, tyrosine hydroxylase, which is required for dopamine synthes, is a non-heme iron enzyme.

Large amounts of iron are sequestered in neuromelanin granules in the dopaminergic neurons of the *substantia nigra* and the noradrenergic neurons of the locus ceruleus. Neuromelanin is synthesized by the oxidation of excess cytosolic catechols that are not accumulated in synaptic vesicles by vesicular monoamine transporter-2 (VMAT2). Interestingly, it binds iron avidly.

Iron accumulation in *Substantia Nigra* and *Globus Pallidus* has been also described as pathological hallmark of PD. Large amounts of iron are sequestered in neuromelanin granules in the dopaminergic neurons of the *substantia nigra* and the noradrenergic neurons of the *locus ceruleus*.

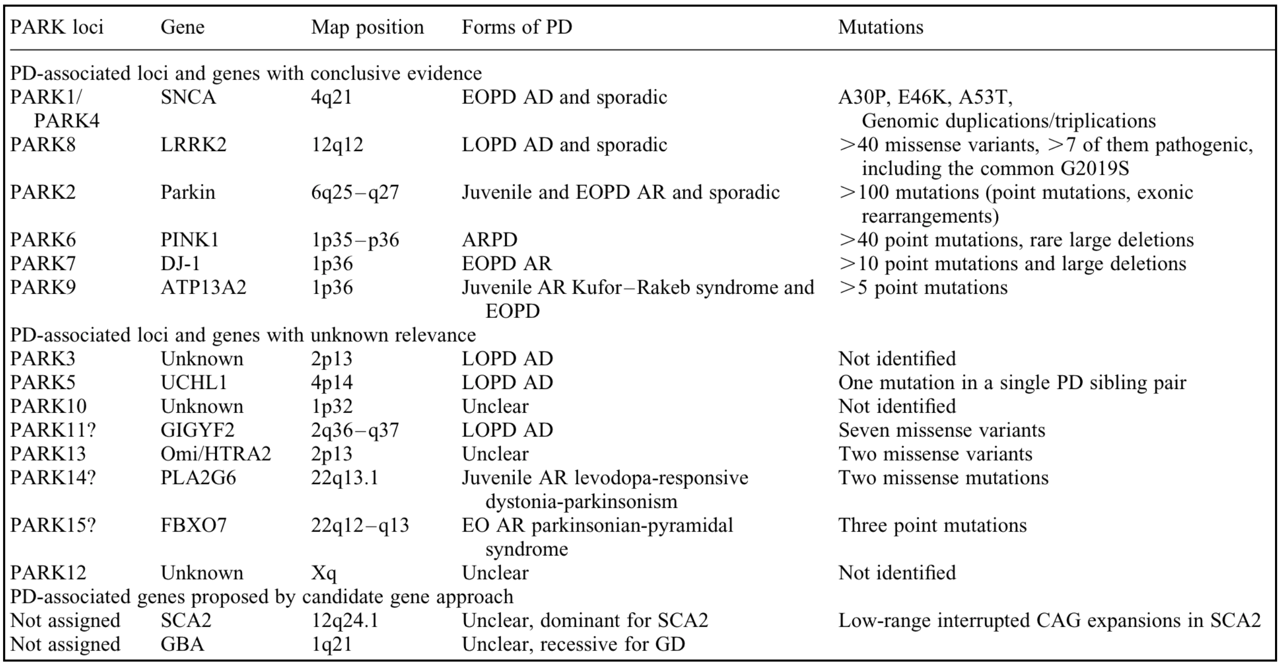
The role of iron in neurodegenerative diseases, particularly PD, has not been clarified yet but different evidences show how its role, in combination with age, could be critical for the dopaminergic cells neurodegeneration. To underline the toxic effect of iron in PD pathology it is important also to mention that iron chelators, when administered prior to the exogenous toxin mimicking PD pathogenesis, appears neuroprotective in mice and non-human primates (Kaur et al. 2003).

1.1.3 ETIOLOGY OF PD

PD is a multifactorial disease caused by both environmental and genetic factors. The cause of sporadic PD is unknown, but the environmental hypothesis was dominant for much of the 20th century for he discovery that an exogenous toxin can mimic the clinical and pathological features of PD: in 1983 Langston *et al.* discovered that people intoxicated with 1-methyl-4-phenyl-1,2,3,4-tetrahydropyrydine (MPTP) developed a syndrome nearly identical to PD (Langston *et al.* 1983). Moreover, human epidemiological studies have correlated residence in rural environment and related exposure to herbicide (i.e. Paraquat) (Tanner *et al.* 1989) and pesticides (i.e. Rotenone) (Betarbet & J. Timothy Greenamyre 2000) with an elevated risk for PD.

Although PD was longly considered a non-genetic disorder of sporadic origin, 5–10% of patients are now known to have monogenic forms of the disease. 13 loci and 9 genes

(**Table 1**) have been associated so far to both autosomal dominant and recessive form of the disease. The discovery of these genes and of their pathological mutations led to a better understanding of the mechanisms underlying the disease.



PARK loci	Gene	Map position	Forms of PD	Mutations
PD-associated loci and genes with conclusive evidence				
PARK1/ PARK4	SNCA	4q21	EOPD AD and sporadic	A30P, E46K, A53T, Genomic duplications/triplications
PARK8	LRRK2	12q12	LOPD AD and sporadic	>40 missense variants, >7 of them pathogenic, including the common G2019S
PARK2	Parkin	6q25–q27	Juvenile and EOPD AR and sporadic	>100 mutations (point mutations, exonic rearrangements)
PARK6	PINK1	1p35–p36	ARPD	>40 point mutations, rare large deletions
PARK7	DJ-1	1p36	EOPD AR	>10 point mutations and large deletions
PARK9	ATP13A2	1p36	Juvenile AR Kufor–Rakeb syndrome and EOPD	>5 point mutations
PD-associated loci and genes with unknown relevance				
PARK3	Unknown	2p13	LOPD AD	Not identified
PARK5	UCHL1	4p14	LOPD AD	One mutation in a single PD sibling pair
PARK10	Unknown	1p32	Unclear	Not identified
PARK11?	GIGYF2	2q36–q37	LOPD AD	Seven missense variants
PARK13	Omi/HTRA2	2p13	Unclear	Two missense variants
PARK14?	PLA2G6	22q13.1	Juvenile AR levodopa-responsive dystonia-parkinsonism	Two missense mutations
PARK15?	FBXO7	22q12–q13	EO AR parkinsonian-pyramidal syndrome	Three point mutations
PARK12	Unknown	Xq	Unclear	Not identified
PD-associated genes proposed by candidate gene approach				
Not assigned	SCA2	12q24.1	Unclear, dominant for SCA2	Low-range interrupted CAG expansions in SCA2
Not assigned	GBA	1q21	Unclear, recessive for GD	

Table 1: Genetic *loci* and genes identified in PD. Modified by Suzanne Lesage and Alexis Brice, Human molecular genetics (Lesage *et al*. 2009).

Whatever the initial insult is, the analysis of human *post mortem* brains of PD patients as well as studies on PD animal models (neurotoxin-treated or genetic-modificated) suggest the involvement of two major, possibly interconnected, pathways in dopaminergic neurodegeneration:

- protein misfolding and aggregation
- mitochondrial dysfunctions: oxidative stress and alterated fusion/fission machinery

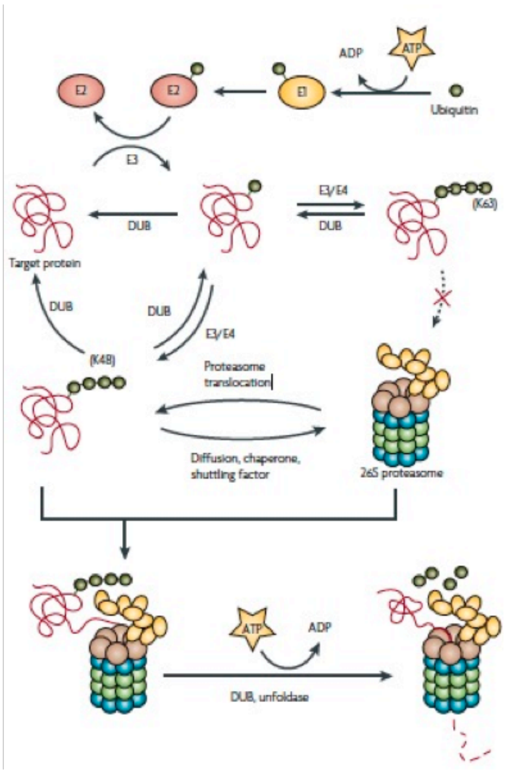
Protein misfolding and aggregation:

Alteration of protein folding, ubiquitin proteasome system (UPS) and autophagy are considered among the main molecular mechanisms in aggregate formation.

The most important proteins involved in the correct folding of polypeptides are chaperons: this highly conserved class of proteins prevents inappropriate interactions within and between non-native polypeptides, enhances the efficiency of *de novo* protein folding and promote the refolding of stress-induced misfolded proteins (Hartl & Hayer-Hartl 2002).

When misfolded proteins cannot be “repaired” by chaperons, they have to be degraded. In the classical mechanism of degradation, proteins are poly-ubiquitinated to be addressed to the proteasome for degradation. Ubiquitination of a substrate requires a cascade of enzymes: ubiquitin-activating enzyme (E1), ubiquitin-conjugating enzymes (E2s) and ubiquitin-protein ligases (E3s) that are responsible for highly specific target recognition in this system through physical interactions with the substrate. Proteasome is a multisubunit protein complex composed by a 20S core complex where proteins are degraded, a 19S regulatory complex that removes the ubiquitin and unfolds the protein for translocation into the 20S chamber and the so called 11S complex (or REG or PA28) that is thought to activate the 20S (**Fig.3, left**).

A relatively new discovered mechanism through which proteins can be degraded is authophagy. Most long-lived proteins, cytoplasmic constituents, including organelles, are sequestered into double-membraned autophagosomes, which subsequently fuse with lysosomes where their contents are degraded thanks to proteolitic enzymes (**Fig.3, right**).



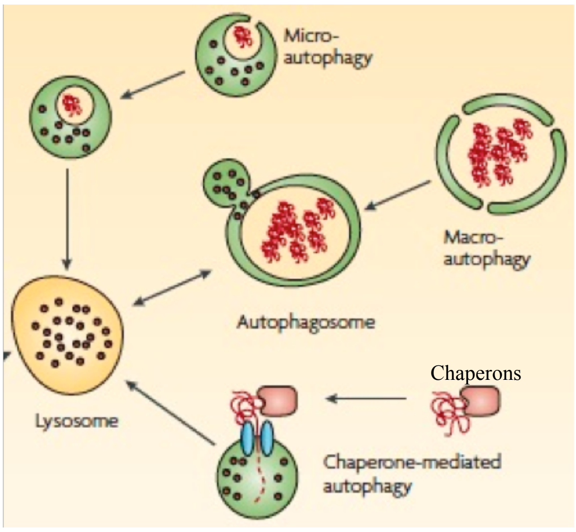


Fig3.left: Scheme of the Ubiquitin-proteasome system (UPS); **right:** scheme of the chaperon-mediated autophagy. (modified from Tai & schuman 2008)

When misfolded proteins are not correctly degraded and one of the previously described mechanisms is misregulated, there is the formation of toxic aggregates.

It is interesting to note that LBs are immunoreactive against chaperone proteins (i.e. Hsp-70), ubiquitin, and components of the 20S of the proteosome system.

Interestingly, accumulation of autophagic vacuoles has been seen in dopaminergic neurons of histopathological sections of PD patients *post mortem* brains (Nedelsky *et al.* 2008).

Several genetic and environmental factors have been associated with protein misfolding and aggregation. One of the mechanism by which mutations lead to conformational changes is destabilization of the normal protein structure. Environmental factors might also catalyse protein misfolding like changes in metal ions, pathological chaperone proteins, pH or oxidative stress, macromolecular crowding and increases in the concentration of the misfolded protein. Many of these alterations are associated with aging, consistent with the late onset of PD.

To explain how protein misfolding and aggregation might be associated with neuronal degeneration, different hypotheses have been described (C. Soto 2003): neurodegeneration could be due to the loss of normal activity of the misfolded protein, to the gain of a toxic activity or to the recruitment by the intracellular aggregate of factors that are essential for cell viability. Moreover, abnormal protein aggregates act as irritants and cause a chronic inflammatory reaction in the brain that leads to neuronal death and synaptic changes (Wyss-Coray & Lennart Mucke 2002).

PD-associated genetic mutations and misfolded protein aggregation

PD-linked mutations have been identified in genes encoding proteins that have been found in LBs and LNs. In particular, some of these proteins are incline to aggregate in some environments or in presence of particular stressors, others have a role in the previously described protein degradation mechanisms. In the last years, the strongest evidence that UPS and autophagy have a role in PD emerged from studies of genes whose mutated forms are associated with familial PD: SNCA, PARKIN, UCHL1, DJ-1 and LRRK2.

SNCA (PARK1 and PARK4) (a-synuclein) is one of the major components of LBs and LNs and mutations in this gene have been associated with early onset autosomal dominant forms of PD. It belongs to the family of natively unfolded proteins because it lacks secondary or tertiary structure, like many chaperones and it accumulates in presynaptic nerve terminals associated with membranes of synaptic vescicles. In addiction, KO mice survive with no evident brain defects (Chandra & Sudhof S.d.).

α-synuclein is a natively unfolded protein and has a great propensity to aggregate both *in vitro* and *in vivo*, especially in the presence of oxidative stress and several herbicide and pesticide. Two PD-linked mutants (Ala30Pro and Ala52Thr) show a great propensity to form protofibrils, an intermediate in the process of aggregate formation.

Pesticides (such as rotenone, dieldrin and paraquat), metal ions (copper, iron) and other factors accelerate a-snuclein fibrillation.

The *in vitro* expression of α-synuclein in dopaminergic neurons also results in inclusion body formation and triggers pronounced (~50%) neuronal loss.

Finally, transgenic mice expressing the wild-type human gene for α-synuclein develop several of the clinicopathological features of PD like accumulation of LBs in neurons of the neocortex, hippocampus and *substantia nigra* and loss of dopaminergic terminals in the basal ganglia (Masliah *et al.* 2000).

PARKIN (PARK2) is an E3 ubiquitin protein ligase that is up-regulated under unfolded protein stress. Mutations in PARKIN were first linked to early onset autosomal recessive forms of PD and are the most frequent cause of autosomal recessive PD.

PARKIN can ubiquitinate specific substrates (such as Cyclin E, α-synuclein, Pael Receptor and Synphilin-1) and target them for proteasomal degradation. Considering that the majority of the patients with PARKIN mutation lacks LBs pathology and that in sporadic PD patients these inclusions are immunoreactive for some of PARKIN substrates, it has been suggested that PARKIN may promote LBs formation (T M Dawson 2006).

Moreover, Drosophila KO for this protein shows a loss of mitochondrial integrity and function and in this model PARKIN seems to promote mitochondrial autophagy (Narendra *et al.* 2009).

UCH-L1 (PARK5) hydrolyzes ubiquitin from polymeric chains and from ubiquitinated proteins producing monomeric units. Mutations in this gene are correlated with late onset autosomal dominant forms of PD. UCH-L1 has been found in the LBs of patients with sporadic PD. This finding provides an additional evidence for the involvement of aberrant ubiquitination and aggregates formation in the PD pathogenesis (Yasuda *et al.* 2009).

DJ-1 (PARK7) is a ubiqutously expressed protein whose function has not yet been completely clarified. Mutations in the DJ-1 gene were recently associated with early onset autosomal recessive forms of PD (Bonifati *et al.* 2003).

A recent study (Shendelman *et al.* 2004) shows how DJ-1 functions as a cytoplasmic redox-sensitive molecular chaperone *in vitro* and *in vivo*. In particular it inhibits the aggregation of α-synuclein in neuronal cell lines at an early step of the aggregation process and its loss leads to increased accumulation of insoluble α-synuclein.

Shendelman *et al.* also hypothesize that DJ-1 may promote the degradation of misfolded proteins, either through the proteasome or through chaperone-mediated autophagy.

LRRK2 (PARK8), also known as "dardarin", is one of last discovered genes involved in late onset autosomal dominant forms of PD.

Transgenic mice that express the mutated form of LRRK2 (R1441G) recapitulate most of the PD motor symptoms like age-dependent and progressive reduced mobility, late visually apparent immobility that are reverted by the somministration of Levodopa (Yanping Li *et al.* 2009).

Its function is not yet fully characterized but it seems to be involved in aggregate formation because its full length form has the capacity to phosphorylate serine 129 of α-synuclein, been such phosphorylated form the major component of LBs. Moreover, the mutated form of Lrrk2, which is the most common genetic determinant of PD, has a significantly greater capacity than wild-type to phosphorylate α-synuclein (Qing *et al.* 2009).

Mitochondrial dysfunction and oxidative stress

A consequence of the mitochondrial dysfunction is oxidative stress and *vice versa*. Ninety-five percent of the molecular oxygen is metabolized within the mitochondria by the electron-transport chain: thus mitochondria are highly exposed and damaged by oxidative stress and this leads to a more intense and perpetuating cycle in which reactive oxygen species (ROS) are generated.

ROS cause functional alterations in proteins, lipids and DNA. Lipid damage leads to loss of membrane integrity and ions permeability, promoting excitotoxicity (Halliwell 1992). Although ROS levels cannot be directly measured, the assessment of their reaction products and of the resulting damage in *post mortem* tissues is as an indirect index of their levels (Foley & Riederer 2000).

Over the last several decades, evidence has accumulated that mitochondrial dysfunction is associated with PD. A mild deficiency in mitochondrial respiratory electron transport chain NADH dehydrogenase activity (Complex I) was first found in the *substantia nigra* of patients with PD (Mann *et al.* 1994; Schapira *et al.* 1989), followed by studies identifying a similar Complex I deficit in platelets (Blandini *et al.* 1998; Haas *et al.* 1995; D. Krige *et al.* 1992), lymphocytes (Barroso *et al.* 1993; Yoshino *et al.* 1992), and, less consistently, in muscle tissue (Penn *et al.* 1995; D. J. Taylor *et al.* 1994) from PD patients. The hypothesis that oxidative stress plays a role in the pathogenesis of PD was also previously proposed by the discovery that MPTP blocks the mitochondrial electron transport chain by inhibiting complex I (Nicklas *et al.* 1987). MPTP is highly lipophilic, and it crosses the blood brain barrier within minutes. Once in the brain, it is oxidized to 1-methyl-4 phenyl-2,3-dihydropyridinium (MPDP$^+$) by monoamine oxidase B (MAO B) in glial cells and serotoninergic neurons and then is spontaneously oxidized to MPP$^+$. Due to its high affinity for the DA transporter (DAT), it is selectively accumulated in dopaminergic neurons, where it causes toxicity and neuronal death through complex I inhibition (**Fig. 4**).

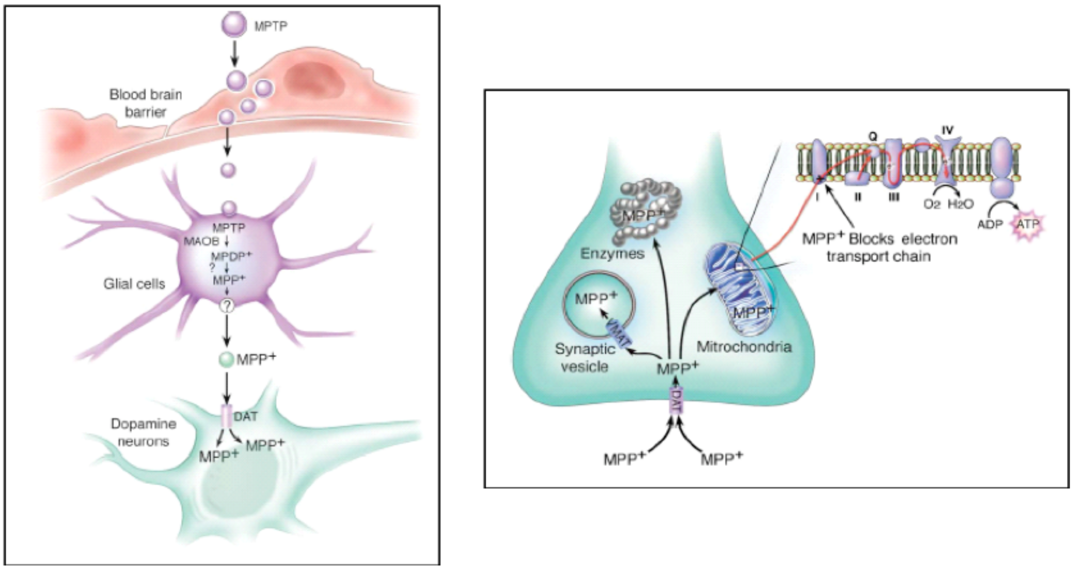


Fig 4: a) Schematic representation of the MPTP metabolism and b) of MPP$^+$ intracellular pathway (Dauer et al. 2003).

Similar toxic effects are produced by the common herbicide 1,1’-dimethyl-4,4’-5 bipyridinium (Paraquat) coupled with the administration of the fungicide manganese ethylenepistithiocarbamate (Maneb). While Paraquat, which is structurally similar to MPTP, blocks the mitochondrial complex I, Maneb inhibits the mitochondrial complex III. Rotenone, that freely crosses cellular membranes and accumulates in subcellular organelles such as mitochondria, impairs oxidative phosphorylation by inhibiting complex I of the electron transport chain and leads to neuropathologic and behavioural changes in rats similar to human PD (Alam & W. J. Schmidt 2002).

Other important and complex processes involved in mitochondrial dysfunction are alteration in mitochondrial fusion and fission. Mitochondrial fission and fusion are important mechanisms that maintain the integrity of mitochondria, their electrical and biochemical connectivity, their turnover, and the segregation, stabilization, and protection of mitochondrial DNA (mtDNA). When altered, they cause morphological and functional mitochondrial abnormalities.

The correlation between oxidative stress and fission/fusion machinery is still matter of debate but it seems that the presence of ROS can alter mitochondria morphology due to a disregulation of genes involved in this process like Mfn1, Fis1 and Drp1 (Liot *et al.* 2009; H. Zhang *et al.* 2009).

These mechanisms are of high interest in neurons because these cells have unique features such as post-mitotic state and long processes with higher energy requirements, therefore a fine regulation of dynamic fission and fusion processes in these cells are particularly important.

In addiction, mitochondrial fission/fusion machinery is intimately and critically involved in the formation of synapses and dendritic spines; preventing mitochondrial fission leads to a loss of mitochondria from dendritic spines and a reduction of synapse formation, whereas increasing fission increases synapse formation (Zheng Li *et al.* 2004). In addition, the absence of the mitochondrial fission protein Drp1 has been shown to prevent mitochondria from distributing to synapses and to lead to synaptic dysfunction (Verstreken *et al.* 2005).

PD-associated genetic mutations and mitochondrial dysfunctions

PD-linked mutations have been identified in genes encoding both mitochondria-targeted proteins and proteins involved in mitochondrial function and/or oxidative stress responses. In the last years, the strongest evidence that mitochondrial dynamics have a role in PD is emerging from studies of genes whose mutated forms are associated with familial PD: PARKIN, PINK1 and DJ-1.

First evidences that **PARKIN** is involved in mitochondrial function came from several studies performed in *Drosophila*: both PARKIN loss-of-function and overexpression of one pathogenic PARKIN mutation, R275W, make *Drosophila* more sensitive to oxygen radical stress; the mutants exhibit also dopaminergic cell loss and severe mitochondrial damage in muscle and germline tissues that included swollen mitochondria and fragmented *cristae* (Jessica C Greene *et al.* 2003; Pesah *et al.* 2004). Similar observations were also obtained from brains of PARKIN-knockout and PARKIN-mutant transgenic mice showing mitochondrial respiratory defects and morphological abnormalities (Palacino *et al.* 2004; Stichel *et al.* 2007). Moreover, mitochondrial defects were also found in leukocytes from PD patients with PARKIN mutations (Mortiboys *et al.* 2008; Müftüoglu *et al.* 2004) and in primary fibroblasts from patients carrying mutations in PARKIN. These phenotypes are linked to the loss of functional PARKIN protein as also demonstrated by experiments using control fibroblasts treated with siRNA against PARKIN or control fibroblasts treated with siRNA against PARKIN.

Since PARKIN is not a mitochondrial protein, it must be translocated into the organelle by other components of a more complex pathway to mediate mitochondrial maintenance.

PINK1 (PARK6) is a mitochondrial-targeted kinase (PTEN-induced putative kinase 1) and mutations in its gene have been associated with a late onset autosomal recessive form of PD.

Similarly to what observed for PARKIN, the characteristic phenotypes (mitochondrial morphological defects, increased susceptibility to oxidative stress, decreased cellular ATP levels, reduced mtDNA content) and their location (tissues appearance) were also observed in transgenic *Drosophila* fruit fly expressing loss-of-function PINK1 mutants as well as in PINK1-deficient lines.

Interestingly, the mitochondrial morphologies and tissues in which they were observed were remarkably similar to those of parkin mutant: disorganized indirect flight muscle fibers, swollen mitochondria with disorganized *cristae* in muscle tissue and dopaminergic neurons, and dopaminergic neuron degeneration (I. E. Clark *et al.* 2006; J. Park *et al.* 2006; Y. Yang *et al.* 2008).

Moreover, in PINK1 knock-out mice dissociated neurons, ATP levels were reduced, as well as mitochondrial membrane potential and respiratory complex I+III+IV activity.

Loss of PINK1 significantly impairs striatal neurons mitochondrial respiration but it seems that no gross changes in the ultrastructure or the total number of mitochondria are present (Gautier *et al.* 2008), even though a recent study by Dagda *et al.* shows how overexpression of wild-type PINK1 in a human neuroblastoma cell line increased mitochondrial interconnectivity and elongation while stable knockdown of PINK1 induced mitochondria fragmentation (Dagda *et al.* 2009)

A significant reduction in dopamine content in the striatum was also observed, even though this phenotype was not correlated to any loss of dopaminergic neurons in SN (Gispert *et al.* 2009).

Strong evidences suggest that PARKIN and PINK1 belong to the same pathway. In particular PARKIN seems to be downstream of PINK1: in flies, in fact, PARKIN overexpression, completely rescued the effect of the loss of PINK1 activity but not *vice versa.*

Compared to PARKIN and PINK1, there is less evidence that **DJ-1** has a direct role in mitochondrial function; in fact DJ-1 loss-of-function doesn't lead to mitochondrial morphological defects. However, although endogenous DJ-1 localization is predominantly cytosolic, in mouse brain it can be found in the mitochondrial matrix and intermembrane space and this partial mitochondrial localization might suggest a role for DJ-1 in mitochondrial function. Moreover, *in vitro* studies have reported physical interactions of DJ-1 with PINK1 (B. Tang *et al.* 2006) and, under oxidative conditions, with PARKIN (Moore *et al.* 2005), but it remains unclear whether these associations occur *in vivo*. An indirect correlation between DJ-1 deficiency and mitochondrial dysfunction has been proposed. DJ-1 deficiency increases sensitivity to cell death induced by oxidative stress, whereas overexpression is protective and these effects seem to be specific to oxidative stress because primary neurons from DJ-1 KO mice are more sensitive to H_2O_2 and rotenone but not to various non-oxidative stresses (Raymond H Kim *et al.* 2005).

Because defective mitochondrial respiration can increase ROS production, a reasonable hypothesis is that DJ-1 functions to detect and/or defend against oxidative stress associated with mitochondrial respiration.

Crosstalk between pathways: protein aggregation, oxidative stress and iron accumulation

Many factors lead to oxidative stress in SNpc. The reduced content of the anti-oxidant glutathione in the SNpc of PD brains lowers the capability to clear H_2O_2. Moreover, the increased free iron level can promote OH^* formation and DA oxidation into toxic dopamine-quinone species (Graham *et al.* 1978). The impairment of the complex I system may be central in PD pathogenesis of DA neurons since its defects and inhibition cause dopaminergic cell death and induce the formation of filamentous inclusions containing α-synuclein. Therefore there is a complex interaction between mitochondrial dysfunction, oxidative stress and the propensity to form aggregates (**Fig. 5**). Complex I inhibitors causes a reduction in the proteasomal activity (Shen & Cookson 2004) and conversely proteasomal inhibition can cause mitochondrial damage (Höglinger *et al.* 2003).

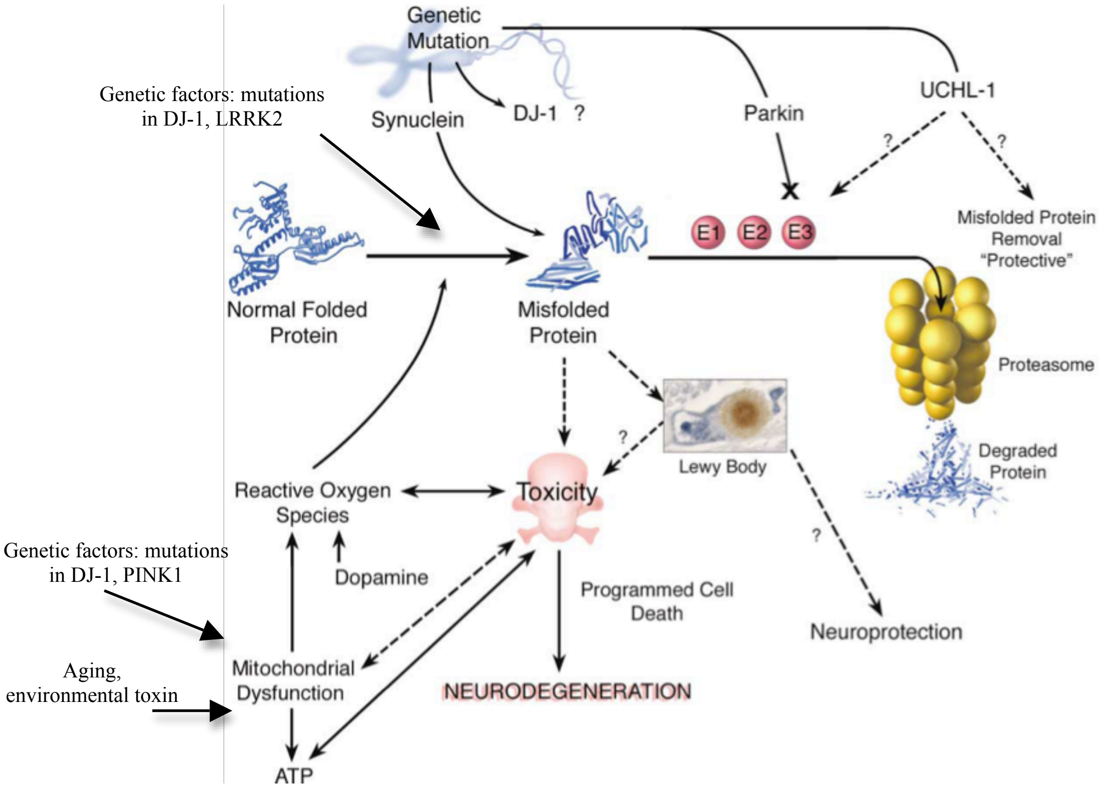


Fig 5: Mechanism of neurodegeneration: linking oxidative stress and mitochondrial damage to UPS impairment and aggregates formation. (modified from Dauer et al. 2003).

Moreover, iron represents an important catalyst in these processes. Even though its role in this pathology has not been clarified yet, we have to take in consideration that iron imbalance contributes to the enhanced generation of ROS; in fact ferrous iron ($Fe2^+$) can be oxidized to ferric iron ($Fe3^+$) catalyzing the conversion of hydrogen peroxide into a hydroxide ion and a hydroxyl free radical.

In neuroblastoma cells, iron produces oxidative stress (Sangchot *et al.* 2002), and contributes to the aggregation of α-synuclein. In the presence of iron and dopamine or hydrogen peroxide, human neuroblastoma cells that over-express α-synuclein produce intracellular aggregates (Ostrerova-Golts *et al.* 2000). This is prevented by the action of the iron chelator desferrioxamine. Such aggregates disturb the cytosolic environment and interact with vesicles and their dopamine transporters and intraneuronal mitochondria, and these disturbances might result in activation of cell-death cascades.

In vitro fibrillization studies also indicate that iron accelerates α-synuclein aggregation (Uversky *et al.* 2001) and that iron-catalysed oxidative reactions mediated by the heme-containing cytochrome c and hydrogen peroxide might be crucially involved in promoting protein aggregation (Hashimoto *et al.* 1999).

1.1.4 CELLULAR DIVERSITY IN *Substantia Nigra* DOPAMINERGIC CELLS

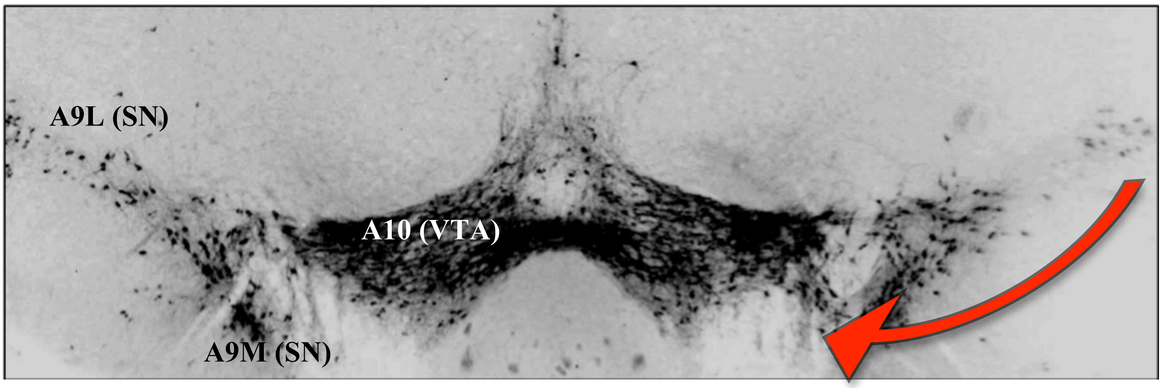


Fig.6: dopaminergic neurons of mouse midbrain. From the left different groups of dopaminergic neurons: A9 lateralis and medialis neurons forming *Substantia Nigra* (SN) and A10 neurons, forming *Ventral Tegmental Area* (VTA). The red arrow on the right indicates the direction of progressive neurodegeneration observed in PD that affects first A9L and then spreads to A9M. Notably, A10 neurons are almost spared even in severe cases of the desease.

One key question is why only specific sets of neurons die in PD.

As mentioned above, neurons in the ventral and lateral SN are much more sensitive to neurodegeneration than neurons in the VTA (**Fig. 6**); this differential vulnerability is a key characteristic of the disease and it is well recapitulated in PD animal models like rodents or primates (Ted Dawson *et al.* 2002).

What makes these particular sets of neurons vulnerable to PD is not known, but uncovering their physiological and molecular peculiarities might be crucial to the understanding of the neurodegeneration mechanisms in PD.

Strikingly, these two populations of DA neurons have many common features. They present long and thin axons, and the axons have little or no myelination (Braak *et al.* 2004). They have an high energy demand, feature which renders these neurons particularly dependent on proper mitochondrial dynamics.

On the contrary, Liang *et al.* (2007) recently found that the cytoplasmic area occupied by mitochondria in the dopaminergic neurons in the *substantia nigra* (susceptible to PD degeneration) is lower than in neighbouring non-dopaminergic neurons or in dopaminergic neurons of the ventral tegmental area (resistant in PD), suggesting the possibility that the vulnerable neurons may be more susceptible to subtle changes in mitochondrial maintenance (C. Liang *et al.* 2007).

These specific characteristics, however, are not sufficient to explain the different susceptibility of SN neurons to neurodegeneration. For this reason, in the last decade, a lot of efforts have been done by independent groups to determine the critical molecular differences between A9 and A10 neurons that could result in vulnerability or provide opportunities for neuroprotection. In particular, the availability of new tools and techniques like laser capture microdissection (that has led to isolate A9 and A10 cells) and high throughput techniques, like microarray analysis, CAGE and nanoCAGE technologies have represented a way to analyze the difference between A9 and A10, obtaining gene expression profiles of the two dopaminergic neurons populations.

Despite an overall high similarity between the two groups of cells, several pathways show interesting differences between them (**Fig.7**).

In comparison to A10 neurons, A9 cells show higher expression of genes related to metabolism and genes encoding mitochondrial proteins as well as genes involved in protein, lipid and vesicle-mediated transport but not ion transport.

Interestingly, the level of metabolic transcripts correlates directly with susceptibility of the two cell populations to complex I toxins (James G Greene *et al.* 2005).

Several genes related to small GTPase-mediated signaling and synaptic vesicle recycling, including RAB and RAS proteins, are elevated in A9 cells.

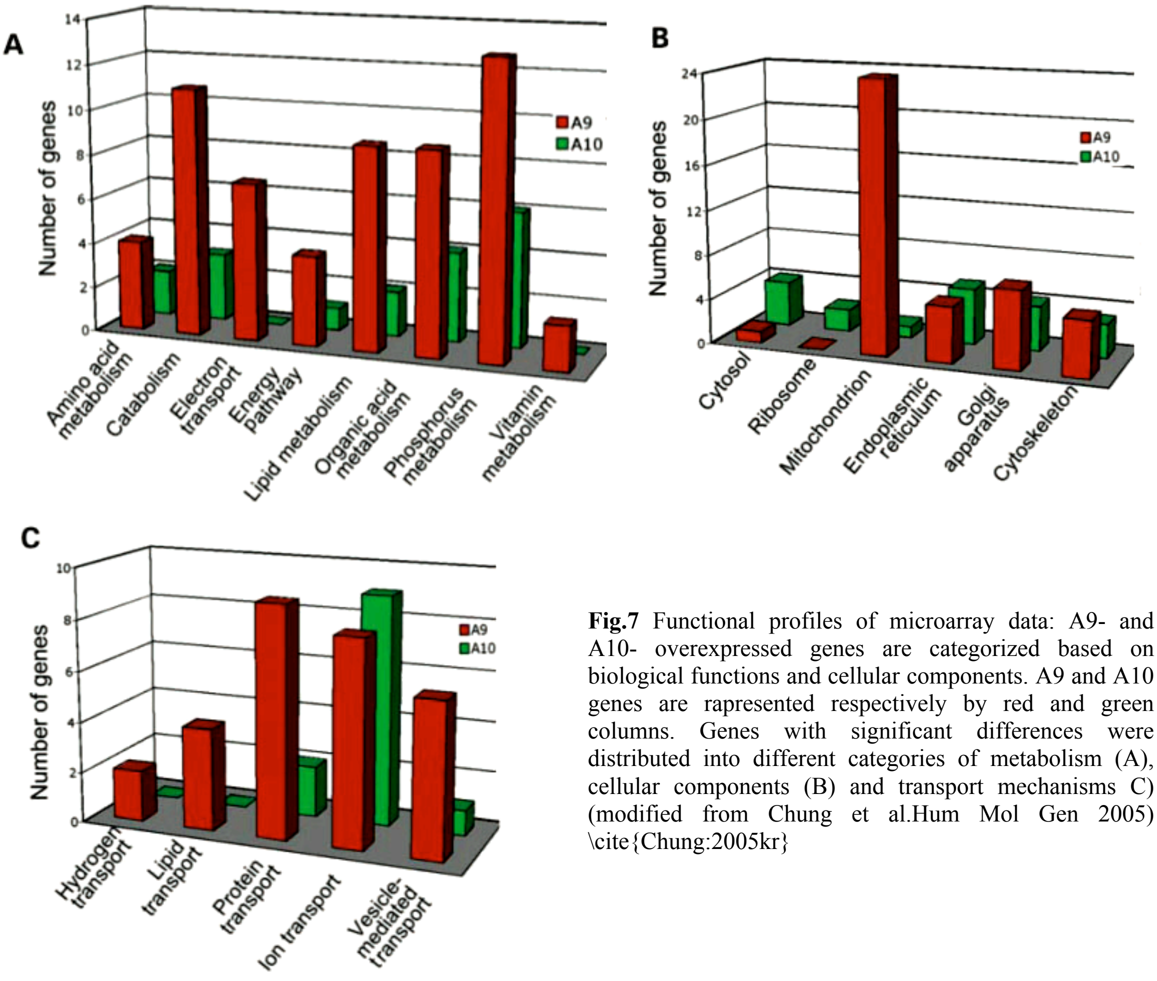


Fig.7 Functional profiles of microarray data: A9- and A10- overexpressed genes are categorized based on biological functions and cellular components. A9 and A10 genes are rapresented respectively by red and green columns. Genes with significant differences were distributed into different categories of metabolism (A), cellular components (B) and transport mechanisms C) (modified from Chung et al.Hum Mol Gen 2005) \cite{Chung:2005kr}

Transcripts related to neuropeptide signaling and neurotrophic factors like BDNF, NGF or VGF were also markedly different between A9 and A10 cells (James G Greene *et al.* 2005; C. Y. Chung *et al.* 2005).

1.1.5 nanoCAGE

These new data have rapidly turned into an array of exciting and somewhat overwhelming challenges that is probably requiring new and/or updated technologies and altered points of view.

Tagging technologies, which include for example SAGE and nanoCAGE are aimed at the description of new transcripts and their transcription start sites (TSSs). Being the strategy of tagging methods related in no way to pre-existing sequence information or prediction, their main advantage is the complete transcriptional scanning of a target genome.

CAGE (Cap-Analysis of Gene Expression) is a powerful tagging technique set up at RIKEN Institute in Japan. It is based on the production of short tag sequences close to the 5'-end of the transcript and the ligation of tags into groups of concatamers, followed by cloning and sequencing of ligation products (Gustincich *et al.* 2006; R. Kodzius 2006; Shiraki *et al.* 2003).

Through statistical calculations assessing the number of tags related to a specific transcripts normalized per million of sequenced tags (tags per million, TPM) the information derived by CAGE data are quantitative.

The advantages of CAGE over other methodologies such as microarrays in identifying new promoters and new TSSs are becoming more evident as the sequencing technologies become more affordable. A major issue of classic CAGE technology was the need for a large amount of starting RNA from the target tissue of cell type; recent advancements in 5'-end tagging and sequence technologies have made possible to develop a new CAGE protocol suitable for starting total RNA quantities as low as 50 nanograms. This new technique, named "nanoCAGE", has been developed in the laboratories of P. Carninci (RIKEN) and S. Gusticich (SISSA). It has a tremendous potential in the analyses of transcriptomes and promotomes of small RNA samples, for example those derived from Laser Capture Microdissection, Fluorescence-Activated Cell Sorters (FACS) and similar technologies.

In this thesis nanoCAGE technique has been used to obtain gene expression profiles of A9 and A10 cells and hemoglobin was found as a differentially expressed protein, as it will be discussed in details later.

1.2 HEMOGLOBIN

In 1962 Felix Hoppe Seyler used for the first time the word “haemoglobin” to describe the blood’s red pigment. Subsequently Stokes described the reversibility of the binding with oxygen and in 1912 Kuster analyzed the heme structure. In 1962 Perutz won the chemistry Nobel Prize with his assay “*X-ray analysis of haemoglobin*” for his studies on globular proteins tridimentional structure

1.2.1 HEMOGLOBIN STRUCTURE

Hemoglobin is an etero-tetrameric protein composed of two couples of identical subunits. Human hemoglobin coding genes are distinguished in two groups: alpha (α) and zeta (ζ) chains belong to the first group, on the chromosome 16, beta (β), epsilon (ε), gamma (γ) and delta (δ) chains belong to the second, on the chromosome 11. During development, different couples of genes are expressed, forming at least five different hemoglobin tetramers: in temporal order, the first is composed by two ζ and two ε chains and it’s called Gower Hb ($\zeta_2\varepsilon_2$), the second is called Portland Hb ($\zeta_2\gamma_2$), the third is the fetal Hb, HbF ($\alpha_2\gamma_2$). During adult life both β and δ chains are expressed, forming adult Hb, HbA ($\alpha_2\beta_2$) and HbA$_2$ ($\alpha_2\delta_2$). In adulthood, HbA accounts for approximately 97% of the protein molecules, HbA$_2$ for about 2% and HbF for only 1%.

HbA is composed by two α chains of 141 aminoacids and two β chains of 146 aminoacids, held together by non-covalent interactions. Each chain is folded around a heme group that coordinates an iron atom, responsible for the binding with oxygen **(Fig.8)**.

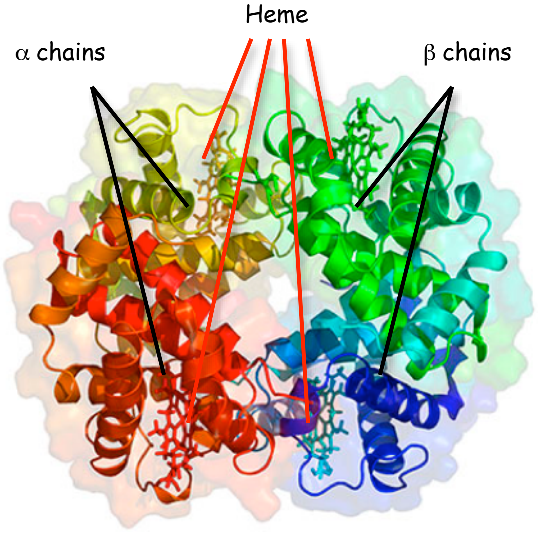


Fig.8: tetrmeric structure of adult hemoglobin

The primary and secondary structures of the two chains do not share a high similarity, but the tertiary one is very conserved. Each polypeptide chain is made up of eight or nine alpha-helical segments and an equal number of non-helical ones placed at the corners between them and at the ends of the chain. The helices are named A-H, starting from the amino acid terminal (**Fig.9**).

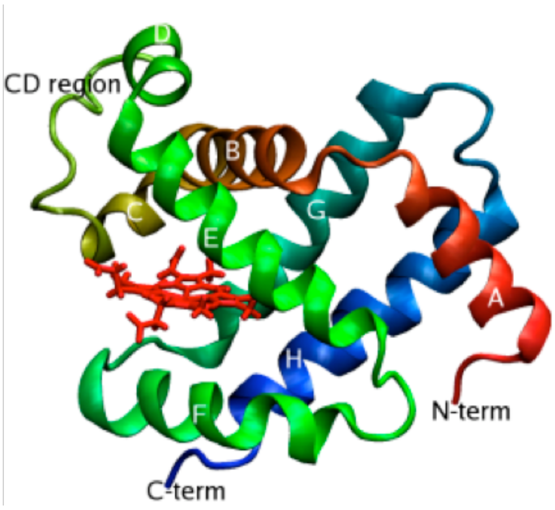


Fig.9 The classical globin fold (human hemoglobin beta unit). The helices are labeled from N-terminal to C-terminal (A,B,..H). Heme group is redStructure of a single chain

The most conserved aminoacids are the *proximal* Histidines (87th residue in alpha chain and 92nd in the beta chain), the *distal* Histidines (58th residue in alpha chain and 63rd in beta chain) involved in the binding with heme, and the residues involved in the interaction between the four chains.

The heme consists of an organic part, porphyrin, and an iron atom. Porphyrin is made up of four pyrrole groups that are linked by methane bridges to form a tetrapyrrole ring. The particular porphyrin found in hemoglobin is protoporphyrin IX, which contains four methyl, two vinyl, and two propionate side chains. The iron atom (Fe^{2+}) in deoxyhemoglobin is pentacoordinated: four of its ligands are nitrogens residues in the centre of the protoporphyrin ring, the fifth is the nitrogen atom of the *proximal* His. In the oxyhemoglobin the iron atom is exacoordinated because it binds also an oxygen atom. The second oxygen atom is linked to the *distal* His through an hydrogen bond. The hydrophobic environment in which the heme group is located prevent the iron atom from oxidation; if hemoglobin comes in contact with air, the iron atom become oxidized (Fe^{3+}), forming the so called methemoglobin in which the oxygen binding site is occupied from H_2O and becomes inactive.

1.2.2 HEMOGLOBIN GENES

In humans

The α-like globin genes (chromosome 16) are in a region of ubiquitously expressed genes near the telomere. The β-like genes (chromosome 11) are in a region that contains multiple DNA sequences that act as strong tissue and developmental stage-specific enhancers of transcription.

Fig.10 shows the human cluster for α- and for β-globin genes: the first is composed by only 3 coding genes (ζ, α1, α2) and at least 4 pseudogenes whereas, in the second one, there are 5 coding genes (ε, Gγ, Aγ, δ, β) and only one pseudogene (Schechter 2008).

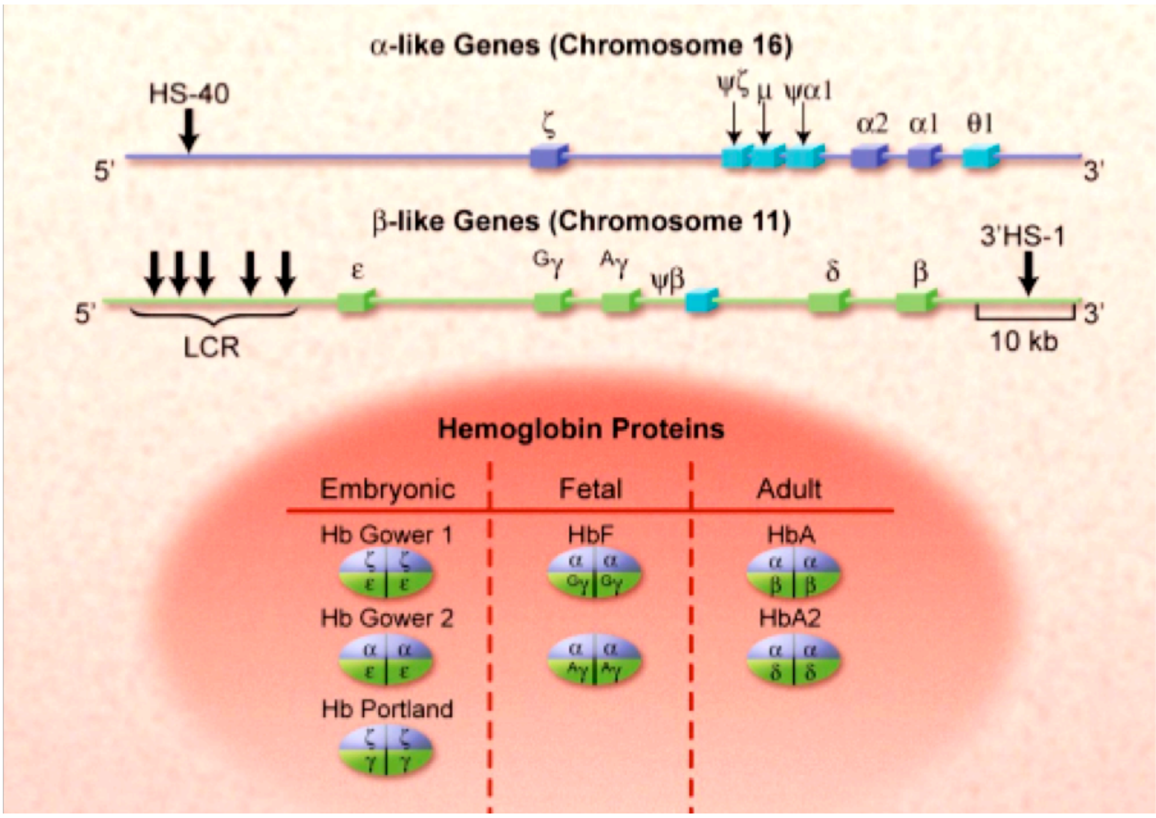


Fig.10: The genomic structure of α- and β-globin clusters: The functional α-like and β-like genes are respectively in dark blue and light green. Pseudogenes are in light blue. The important control elements, HS-40 and the LCR, are also shown at their approximate locations. The various hemoglobin species formed from these genes, with their prime developmental stages, are shown in the lower part of the figure (Schechter 2008).

The expression of the different genes is controlled by multiple *cis*-acting elements like promoters, enhancers, silencer, insulators, MARs/SAR/s and LCR, because of their fine regulation from embryonic to adult life. The β-globin cluster is the most regulated because it has to control the perfect switch between 5 genes during development: in particular its proximity to a group of 5 LCR contribute significantly to regulation of the sequential 5'-to-3' expression of the globin genes during development, as well as their very high level of expression, with matched contributions from the α-locus, in normal erythrocyte. Although this cluster is one of the most historically studied, it always appears to be more and more complex: sequencing of the globin gene clusters has revealed an enormous number of other DNA motifs, that appear to be binding sites for many other proteins that also contribute to enhancing or silencing transcription.

The molecular mechanisms of the β-globin LCR have been only partially elucidated: they are major regulators of globin gene expression, both as a strong general enhancer of transcription and as a specific mediator of developmental control. They are supposed to "open" the chromatin allowing the transcription initiation complex and other *trans*-acting factors to bind at the appropriate gene (R. Kodzius 2006; Shiraki *et al.* 2003; Gustincich *et al.* 2006).

The most studied transcription regulatory protein with a strong erythroid specificity is GATA-1 but many other like FOG-1, TAL-1, EKLF, Gfi-1b and BCL11A, have a role in fine control of individual globin genes or their sequential expression (Mahajan *et al.* 2007).

In mouse

Murine α- and β- clusters have some differences compared to human's: α-cluster is on chromosome 11 and is composed by 3 coding genes (Hba-x, Hba-a1 and Hba-a2) that encode for X embryonic chain and α adult chains and 2 pseudogenes. There are also present 2 other genes (Hbq1 and Hbq2) encoding for adult θ-globins that in homo sapiens are evolved in a pseudogene (Storz *et al.* 2008). β-cluster is on chromosome 7 and is composed by 4 coding genes (Hbb-y, Hbb-bh1, Hbb-b1 and Hbb-b2) that encode for Y, Z embryonic chains and β^{minor} , β^{major} adult chains and 3 pseudogenes.

In mouse embryo three different types of tetramers are expressed: X_2Y_2, α_2Y_2 and α_2Z_2; the switch to adult hemoglobin occurs between 14th and 15th gestation day.

1.2.3 HEMOGLOBIN LIGANDS AND FUNCTIONS

Oxygen

In mammals, the most studied function of hemoglobin is to transport oxygen from the lungs to tissues and the most abundant sites of expression are the red blood cells.

The binding with oxygen for α and β subunits does not happen contemporary: when the first oxygen molecule binds to the iron atom of one chain, it "pulls" the *proximal* His and induces a conformational change that propagates to all the chain structure. This change induces, in turn, conformational rearrangements of the other chains and the consequent increase of their affinity for oxygen. In this way the binding of the other three oxygen molecules is much faster. The *vice versa*, the release of oxygen, follows the same mechanism.

The already described cooperative binding of hemoglobin by its ligand oxygen dramatically increases its physiological oxygen-carrying capacity: in the lungs the partial pressure of oxygen (pO_2) is relatively high (100 torr) and hemoglobin becomes nearly saturated with oxygen (98% of the oxygen-binding sites are occupied); in the tissues pO_2 is much lower (20 torr) and hemoglobin saturation level drops to 32%. The cooperative binding of oxygen by hemoglobin enables it to deliver about 2 times as much oxygen as it would if the sites were independent.

However, the cooperative binding only partially explains the behavioural of hemoglobin in efficiently transporting oxygen: other allosteric effectors like CO_2, pH and 2,3-bisphosphoglycerate (2,3-BPG) regulate hemoglobin structural changes and function.

CO_2 stabilizes deoxyhemoglobin by reacting with the terminal amino groups to form carbamate groups, so the presence of CO_2 in tissues decreases hemoglobin affinity for oxygen, facilitating its release. On the other hand, in lungs, the high concentration of oxygen stabilizes the oxyhemoglobin, inducing the release of CO_2.

Moreover, a portion of CO_2 reacts with H_2O becoming HCO_3^- with the release of a H^+, responsible of the *Bohr effect.* In fact the oxygen affinity of hemoglobin decreases as pH decreases. As hemoglobin moves into a region of low pH, for example from lungs to tissues, its tendency to release oxygen increases due to conformational changes in the four chains.

Another allosteric effector is 2,3-diphosphoglycerate (2,3-DPG). This highly anionic compound is present in red blood cells and gives to hemoglobin the capacity to act as an extremely efficient oxygen transporter. Single molecules of DPG bind to deoxyhemoglobin and stabilize it, reducing the oxygen affinity and increasing the capacity to release oxygen. DPG binding to hemoglobin has other crucial physiological consequences in the passage of oxygen from maternal to fetal red blood cells. Fetal hemoglobin tetramers include two α chains and two γ chains in which there is the substitution of a serine residue for His143 of the β chain of the DPG-binding site. This change reduces the affinity of DPG for fetal hemoglobin, thereby increasing the oxygen-binding affinity of fetal hemoglobin relative to that of maternal (adult) hemoglobin. This difference in oxygen affinity allows oxygen to be effectively transferred from maternal to fetal red blood cells.

Nitric oxide

Nitric oxide is present in all the tissues of the organism and its concentration increases in ischemic conditions. It is a ubiquitously produced cell signalling molecule, acting via soluble guanylyl cyclase production of cyclic GMP and through other mechanisms. It is especially important in mammals in the regulation of vascular tone, cell interactions, and neural function.

Under basal conditions, in blood vessels, NO are produced by endothelial NO synthase enzymes to activate soluble guanylyl cyclase (sGC) to produce cyclic GMP and regulate vascular tone.

In neurons it is synthesised by NO synthase (NOS type1) and acts as a neuromodulator in different processes like memory, neuronal plasticity or nociception. It is also a toxic molecule at high concentration and in presence of ROS: it reacts in particular with anion superoxide ($O_2\bullet^-$) to form peroxinitrite ($ONOO^-$), a highly reactive molecule that oxidise cellular molecules and inhibits Glutamate transporter (Trotti *et al.* 1996).

The presence of nitrosilated molecules in *post mortem* human brains of PD, SLA and Alzheimer patients lead to the hypothesis of a role of NO in neurodegenerative diseases (Beal *et al.* 1997; Good *et al.* 1996).

NO can bind hemoglobin in different ways (**Fig.13**): it can react with iron atom of deoxyhemoglobin to form nitrosyl(heme)hemoglobin (NO-hemoglobin) and it can also bind the cystein in position 93 of the β-chain to form *S*-nitrosylhemoglobin (SNO-hemoglobin). The first reaction had generally been assumed to be irreversible, however, there is now evidence that NO-hemoglobin in the circulating red blood cell may release NO molecules, potentially allowing a mechanism for hemoglobin-based, endocrine-like transport of NO from one tissue to another within the body.

Also SNO-hemoglobin seems to be able to dissociate and to release NO at low oxygen concentration. This could be a mechanism for homeostatic control of blood flow to tissues, because NO promotes vascular dilatation and increases blood flow and oxygen delivery, but this hypothesis is still controversial (Singel & Jonathan S Stamler 2005).

NO reacts also with oxyhemoglobin to produce methemoglobin, with ferric iron ($Fe3^+$) and nitrate ions. Recent work suggests that most of the methemoglobin circulating in red blood cells is derived from this oxidation process which is normally reversed by the erythrocytic methemoglobin reductase system.

More recently, an alternative hypothesis to account for the transport of NO by erythrocytes has been proposed. It has been suggested that nitrite ions within erythrocytes could be reduced to NO by deoxyhemoglobin in regions of relative hypoxia (Dejam *et al.*

2004).

It’s important to considerate that the interactions of NO, produced by endothelial cells under physiological condition, with red cells is limited by several barriers. Whereas, in case of hemolysis, cell-free oxyhemoglobin acts as an efficient scavenger of NO, causing vasoconstriction and perhaps pathological organ conditions.

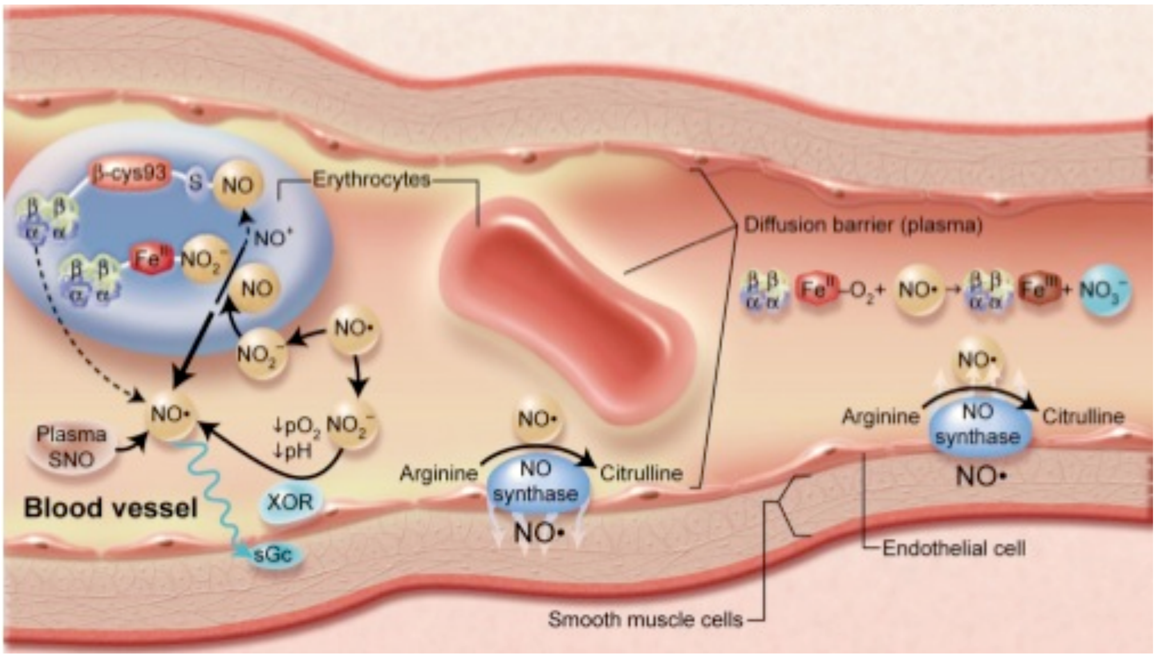


Fig.13: A representation of nitric oxide (NO)/hemoglobin reactions in the arterial microcirculation. (Adapted from Schechter 2008).

1.2.4 GLOBIN FAMILY

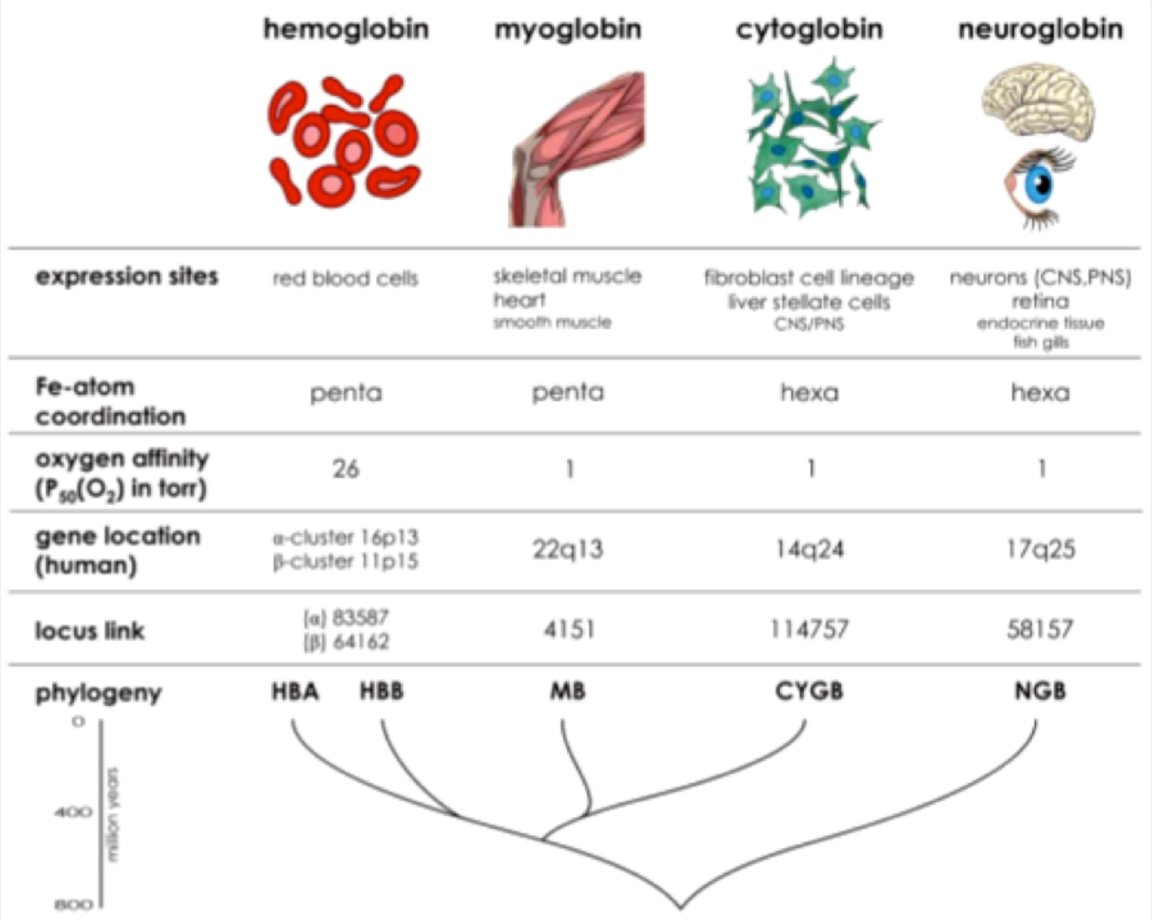
Globin family members are characterized by the coordination of heme group and by the consequent binding with oxygen that is the essential ligand for their function.

Globins have been identified in different organisms like in plants (leghemoglobin) where single-chain globins are involved with electron tranfer, oxygen storage and scavenging, in yeast (flavohemoglobin) or in bacteria where they seem to be primarily NO dioxygenases for detoxifying NO (Hardison 1998).

Beside their role of transport and storage of oxygen, other functions have been identified like enzymatic and detoxifying functions (Minning *et al.* 1999).

Four main components of the family have been discovered and characterized in mammals up to now: hemoglobin, myoglobin, cytoglobin and neuroglobin (**Fig.11**) (Hankeln *et al.* 2005).

All these proteins share a similar tertiary structure even though their primary sequences have less than 50% of homology. However the residues responsible for the binding with heme are conserved.



	hemoglobin	myoglobin	cytoglobin	neuroglobin
expression sites	red blood cells	skeletal muscle heart smooth muscle	fibroblast cell lineage liver stellate cells CNS/PNS	neurons (CNS,PNS) retina endocrine tissue fish gills
Fe-atom coordination	penta	penta	hexa	hexa
oxygen affinity ($P_{50}(O_2)$ in torr)	26	1	1	1
gene location (human)	α-cluster 16p13 β-cluster 11p15	22q13	14q24	17q25
locus link	(α) 83587 (β) 64162	4151	114757	58157

Fig.11: human globins characteristics: tissue distribution, biochemical and philogenetic aspects of the four globins (Hankeln 2005).

Myoglobin

Myoglobin is a monomeric protein strongly resembling one single hemoglobin chain. It coordinates an heme group and its oxygen binding site has an higher affinity for the ligand in comparison to the other globins. It is mainly expressed by the muscular and cardiac tissue and its classical function is to store oxygen and to release it instantaneously under high request of energy by muscular tissue, in particular it facilitates oxygen diffusion to mitochondria. It also helps maintain nitric oxide homeostasis (acting as a NO dioxygenase and nitrite reductase), and scavenge reactive oxygen species (Garry *et al.*

2003). Although it has been studied since 40's, a detailed understanding of its function has still not been achieved; interestingly, knockout mice for myoglobin have almost normal physiology (Gödecke et al. 1999).

Cytoglobin

Cytoglobin (Cygb) is one of the newly discovered oxygen-binding members of the globin family (Burmester 2000). It's monomeric and very similar to myoglobin in the tertiary structure. Mammalian Cygb is longer than most globins and covers 190 amino acids instead of the typical 140 –150 aminoacids. This is due to two 20 amino acid extensions at both the N- and the C- terminal. Its affinity for oxygen is similar to myoglobin's, moreover it can bind CO and NO like hemoglobin but with a weaker affinity.

It is prevalently cytoplasmic and is expressed by almost all the cells, in particular by cells that actively produce components of the extracellular matrix like fibroblasts, chondrocytes and bone cells but also by neurons, where its subcellular localization is both cytoplasmic and nuclear (M. Schmidt *et al.* 2004).

Its function is still unknown and many hypotheses have been made on a possible implication in oxygen sensing or storage and in ROS scavenging. Up to now several studies show only that it is over-expressed under hypoxic conditions (Singh *et al.* 2009), Cygb is correlated with cell respiration and proliferation in fibroblast via NO dioxygenation (Halligan *et al.* 2009) and with collagen synthesis. It also seems to be a tumor suppressor, in fact it has been demonstrated that its down-regulation is a key event in a familial cancer syndrome of the upper aerodigestive tract (Shivapurkar *et al.* 2008).

Neuroglobin

Neuroglobin (Ngb) was first observed in vertebrate brain (Burmester 2004), now it is known how it is widely expressed in vertebral CNS and peripheral nerve system as well as in retina and endocrine tissues (M. Schmidt *et al.* 2005). Like myoglobin and cytoglobin, it is monomeric but unlike cytoglobin, it is exclusively cytoplasmic.

Previous studies demonstrated that expression of Ngb increases in response to oxygen deprivation and that it is neuroprotective against hypoxic/ischemic brain injuries (Xiaoying Wang *et al.* 2008; J. Liu *et al.* 2009; Y. Sun 2001; Y. Sun 2003). Although different hypothesis have been made, (**Fig.12**) its neuroprotective mechanism still remains unclear. It's important to note that Ngb is expressed by metabolically most active oxygen-consuming cell types, including neurons that are particularly sensitive to hypoxic/ischemic insults. The low average concentration of Ngb in the brain (~1 mM), its tendency to autooxidize and its relatively low oxygen affinity under physiological conditions seem to suggest a primary role other than oxygen storage. Hypothetical mechanisms of neuroprotection mediated by Ngb in hypoxic or ischemic injury include oxygen sensing and transport, scavenging of reactive oxygen-containing species (ROS) or reactive nitrogen-containing species (RNS) (Greenberg *et al.* 2008). Ngb can also act as a guanine nucleotide dissociation inhibitor (GDI) regulating the signal transduction (Wakasugi *et al.* 2003).

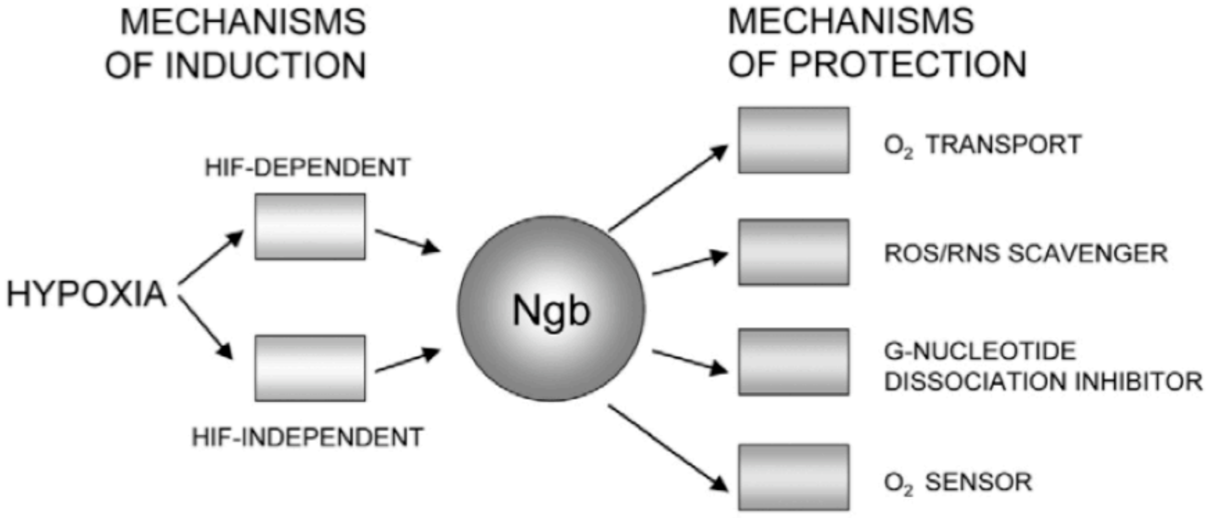


Fig.12: hypothetical mechanisms of protection by Ngb from hypoxic insult (Greenberg 2008).

1.2.5 ATYPICAL EXPRESSION SITES

In the last years it has becoming clear that hemoglobin expression is not restricted to erythrocytes and his precursors. For this reason other potential functions have been postulated.

In 1999 Liu *et al.* described the expression of β^{min} chain of hemoglobin in murine macrophages (L. Liu *et al.* 1999): they showed that both an immortalized macrophagic cell line and primary macrophages expressed β^{min} chain of hemoglobin after treatment with IFN-γ and LPS, inducers of inflammatory response. The role of this induction is still unknown but it suggest alternative functions for globins in mammalian cells and challenge the prevailing view that the expression of alpha- and beta- globin genes is always balanced and coordinated. In fact the functional properties of the single chains compared to those of the tetramer, are very different: alpha- chain monomer is very unstable and doesn't aggregate in tetramers; on the contrary beta- chain can form tetramers (known as HbH, isolated from the blood of alpha-thalassemic or HbH disease patients (Tongsong *et al.* 2009)) with a high affinity for oxygen. β_4 tetramer biochemical properties can be affected by pH and by BPG like hemoglobin. However, its physiological role, if any, is still under investigation.

In 2006 Newton *et al.* demonstrated the expression of both alpha- and beta- chains in alveolar epithelial cells and Clara cells, the primary producers of pulmonary surfactant, implicating then in the physiology and pathology of the lung (Newton *et al.* 2006).

Moreover, in 2008 Nishi *et al.* observed an up-regulation of hemoglobin in the hypoxic kidney, in particular in rat glomerular mesangial cells. With the support of *in vitro* studies, they hypothesized a protective role of this protein against oxidative stress induced by hydrogen peroxide and superoxide anion (Nishi *et al.* 2008).

Other sites of globin subunits mRNAs expression have been reported included the pituitary of neonatal rats after exposure to estrogen and human cardiac ventricular tissue after ischemia-reperfusion (Leffers *et al.* 2006; Arab *et al.* 2007).

In this thesis hemoglobin has been found in midbrain dopaminergic cells as well as in a subpopulation of hyppocampal and cortex astrocytes and in almost all oligodendrocytes.

2. MATERIALS AND METHODS

2.1 ANIMAL PROCEDURES

All the experiments involving the use of animals were performed in accordance with the Italian ethical committee and local authority veterinary service.

2.2 LASER CAPTURE MICRODISSECTION OF DA NEURONS FROM TH-GFP MICE.

8 to 12-weeks old mice were deeply anesthetized with polyurethane (10% solution in distilled water; 2mg/g, i.p), and intensively perfused transcardially with Tris Buffered Saline (TBS) followed by 1x zinc fixative (BD) diluted in RNase free water (Ambion). Brains were removed and post-fixed in 1X zinc fixative for 8 h at +4°C. The region containing the *substantia nigra* was isolated and included in freezing medium Neg-50 (Richard Allan scientific). To obtain a quick freezing the block was put in a box containing frozen isopentane, immersed in liquid nitrogen. The frozen block was brought into cryostat (Microm International, Walldorf, Germany) and left at -21°C for 30 minutes. Coronal sections of midbrain (14 μm) were cut, transferred on Superfrost Plus glass slides (Menzel-Glaser, Menzel GmbH & co KG) and air-dried for 5 minutes. Dopaminergic neurons were visualized at fluorescent LCM microscope (Zeiss), single neurons were microdissected, catapulted, collected in adhesive caps (Zeiss) and immediately processed (**Fig.14**).

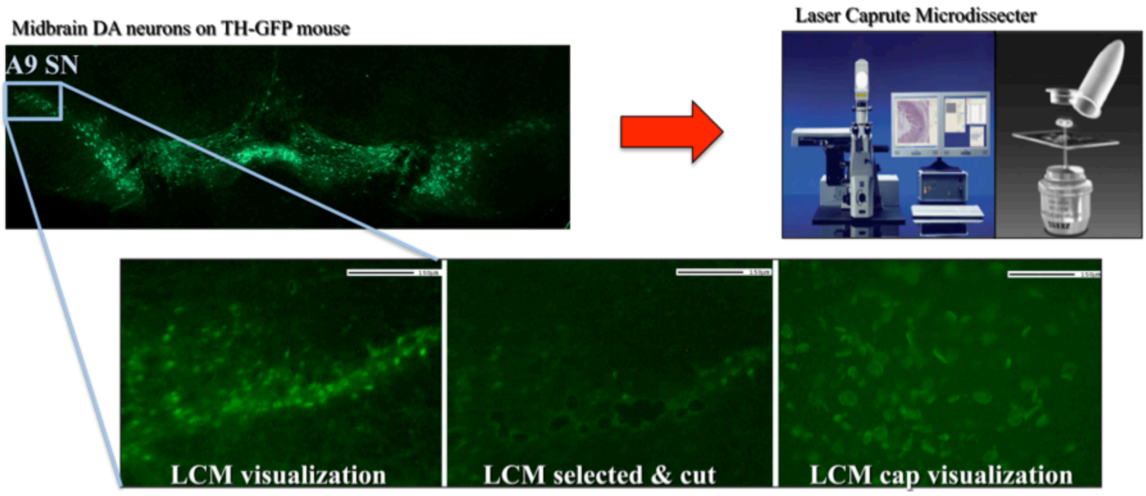


Fig.14: LCM process, in bottom panel DA neurons are shown before and after the cut

2.3 RNA ISOLATION, REVERSE TRANSCRIPTION, qPCR, CLONING AND SEQUENCING

RNA was extracted from cell lines and blood using TRIZOL reagent (Invitrogen) according to manufacturer's instructions.

RNA was extracted from LCM- or FACS- purified cells with Absolutely RNA® Nanoprep Kit (Stratagene). Single strand cDNA was obtained from purified RNA using the iSCRIPT^{TM} cDNA Synhesis Kit (Bio-Rad) according to manufacturer's instructions. Quantitative RT-PCR was performed using SYBER-Green PCR Master Mix and iQ5 Real-Time PCR Detection System (Bio-Rad).

Quantitative RT-PCR was performed with an iCycler IQ (Bio-Rad); β-actin was used as an endogenous control to normalize the expression level of target genes. Primers were chosen using the software Beacon Designer 2.0 (PREMIER Biosoft International). Primer sequences are presented in **Tab.1a-b**. Results were normalized to β-actin and the initial amount of the template of each sample was determined as relative expression versus one of the samples chosen as reference. The relative expression of each sample was calculated by the formula 2exp-ΔΔCt (User Bulletin 2 of the ABI Prism 7700 Sequence Detection System). PCR and qPCR amplicons were cloned in pGEM-TEasy vector (Promega) and sequenced using T7/Sp6 primers by LI-COR Global Edition DNA sequencer.

GENE NAME	FWD PRIMER (5'-->3')	REV PRIMER (5'-->3')
Hba-a1	GCCCTGGAAAGGATGTTTG	GCATCGGCGACCTTCTTG
Hbb-b1	GAGAACTTCAGGCTCCTGG	CACTCCAGCCACCACCTTC
Th	CCGTCTCAGAGCAGGATACC	CGAATACCACAGCCTCCAATG
Alas 2	CTCAGCGCTCTTCTCCTCCTG	CACCACTGTTGCGAATGC
Spna	GCAGAAGAAGTTTGACGAGTTC	CAGCCACTTTGTTGATGTCC
Beta-actin	CACACCCGCCACCAGTTC	CCCATTCCCACCATCACACC
Dmp1	CCCGTCCTGCTTTATTTGTG	CACTACTTCAACTATGGCATCG
Egln3	GGCTGGGCAAATACTATGTC	CCCTCCGTGTAACTTGGC
Fis1	AAGGAATATGAAAAGGCTCTAAAG	AAGGCGATGGTGAGGATG
Hif1a	AGGAAATGAGAGAAATGCTTACAC	GGTTGGTTACTGTTGGTATCATAG
March5	CTATCTATTGGACAGCCGTGAC	CGCCATAGTCTAAGCACATAGTC
Mfn1	TGGTGGAAATACAGGGCTACAG	CTCAGGAAGCAGTTGGTTGTG
Mnf2	TCCAAGTGTCCGCTCCTG	GAACTGCTTCTCCGTCTGC
Mt1	ACTATGCGTGGGCTGGAG	ACGGAGTAAGTGAGGAGAAGG
Ndufa3	CCTCCGCTCTTGGCATTTG	GCACTCTTCTCTGACTCTGTAG
Ndufa6	TCGGTGAAGCCCATTTTC	GCCTTGGTGTTTCTGTTTC
Ndufv2	CGAAAGCCAGTTGGGAAGTAC	AAAGTTTGTCAGGTGTAGTCTCTC

Nos1	AGGAATCCAGGTGGACAGAGAC	GAAGGACTGCCATTCTTGGTAGG
Opa-1	ATTGTCGGAGCAGGAATC	TCACTAAGGATTGGCAGAC
Ret	GGCACCTTCTACCACTTCC	CCTCCAGCACATACTTCTCC
Vegfc	AGTATTGATATTGAGTGGAGAAAG	CAAACAACGTCTTGCTGAG
Vhl	TTGCCAACATCACATTGCCAGTG	GCTCAGTCGCTGTATGTCCTTCC

Tab.1a: List of primers used for qPCR. All the primers have been design with Beacon Designer 2.0

GENE NEME	**Fwd primer (5'-->3')**	**Rev primer (5'-->3')**
Hba-a1	AAGCCCTGGAAAGGATGTTTG	CAGAGGCAAGGAATTTGTCC
Hbb-b1	GGTGAACGCCGATGAAGTTGGTG	GTGAAATCCTTGCCCAGGTGGTG
TH	GTCTGACGATGTGCGCAGTGCCAGAG	TCGCAGCTGGAAGCCAGTCCGTTCC
Alas 2	CACAGCCCTCAGATGATG	GCATAGGTGGTAACATATTGG
Gypa	GATGGCAGGGATTATCGGAAC	AACATTGGAGGACTCTTCATTAGG
GFAP	GGATGTGGCCAAGCCAGACCTCAC	CTTAATGACCTCACCATCCCGCA
CNPase	GCTTTTTGAAATGGCAGACC	CCTTGGGTTCATCTCCAGAA

Tab.1b: List of primers used for simle PCR.

2.4 *In situ* HYBRIDIZATION

After perfusion with 4% paraformaldehyde in PBS, the mouse brain was removed, post-fixed for 1h at room temperature and cryoprotected over night at 4°C in 30% sucrose, then it was frozen and cut with criostat (16μm).

Sense and antisense probes were generated by *in vitro* transcription from the cDNA encoding mouse beta-globin (NM_008220.3) and mouse alpha-globin (NM_008218.2). To avoid cross hybridization between other globin mRNA we decided to include in the probe also part of the 5' and 3' untraslated region, where the homology with the other chains is very low: the beta-globin probe includes the complete CDS, 28bp in the 5'UTR and 97bp in the 3'UTR, the alpha-globin probe includes the complete CDS, 24bp in the 5'UTR and 47bp in the 3'UTR (**Fig.15**)

Probes were labeled with digoxigenin using the DIG RNA Labeling Mix (Roche Applied Science) and digoxigenin incorporation was tested by Northern Blot. Hybridization was performed with probes at a concentration of 4 μg/ml at 60°C for 16h. Sections were then washed and incubated with anti-DIG AP conjugate antibody (Roche Applied Science) for 3 hours at RT. Colorimetric reactions were performed with NBT/BCIP solution (Sigma-Aldrich, St. Louis, MO). To perform also immunohistochemistry, sections were washed and incubated with primary antibody for 2h at RT and then with secondary Ab for 1h RT (see paragraph 2.6). Sections were mounted with Vectashield and analyzed with both transmitted light and fluorescence.

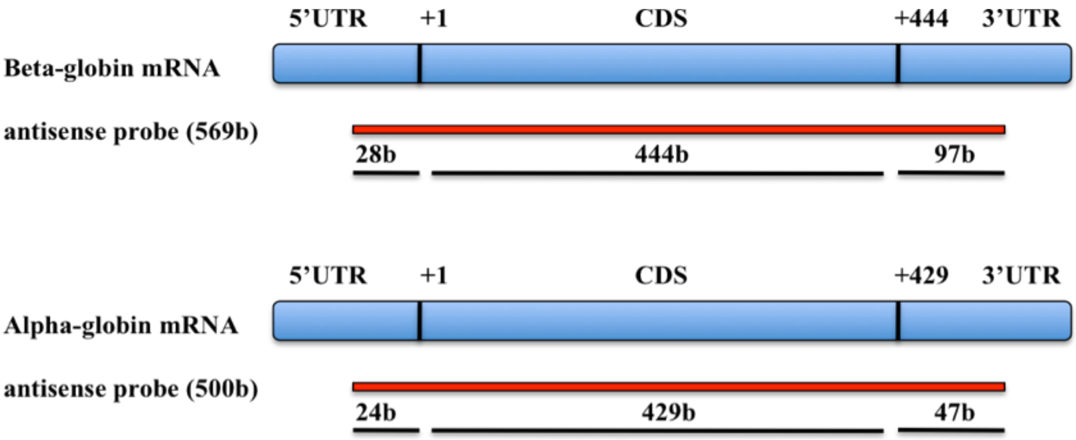


Fig.15: Scheme of the antisense probes designed for *in situ* hybridization.

2.5 SINGLE CELL DISSOCIATION AND FACS SORTING

To isolate dopaminergic neurons, astrocytes and oligodendrocytes, transgenic mice including TH-GFP (Matsushita 2002; Sawamoto 2001), GFAP-GFP (Jackson Laboratories) and CNPase-GFP (Yuan *et al.* 2002) were respectively used. For dopaminergic neurons and cortical or hippocampal astrocytes, P4-P8 pups were used. Oligodendrocytes were collected using P13/P20 animals. Solitary dopaminergic neurons were prepared as previously described (David Sulzer online protocol http://www.sulzerlab.org/Sulzer_VM_culture_4.1.pdf). Briefly, midbrain was isolated from transgenic TH-GFP mice. The pieces were enzymatically dissociated (Papain) under continuous oxygenation (5% CO_2 and 95% O_2 gas mixture) with slow stirring at 33°C (kynurenate 0.5M is added to the solution).

After 40 minutes the reaction was stopped with enzyme inhibitors and the cell suspension was gently triturated with p1000 tip. Undissociated tissue was allowed to settle down and the supernatant was collected; the procedure was repeated twice.

Single cells were then resuspended in panning buffer and incubated on lectin coated panning plates for 15' at RT. Non-adherent cells were transferred to next panning plate (4 pannings, 15' each). Then, non-adherent cells were collected, centrifuged and resuspended in serum free neuronal medium or PBS.

A similar procedure was also followed for the dissociation of cortical and hippocampal astrocytes as well as for oligodendrocytes.

Medium for astrocytes and oligodendrocytes (200 ml)

Component	Amount
1. MEM	180 ml
2. Calf serum fresh, *not* heat-inactivated	20 ml
3. Glucose 45%	1.5 ml
4. Pen-Strep	0.24 ml
5. Insulin (25 mg/ml)	40 µl, dissolve in 20mM HCl
6. Glutamine (200 mM)	0.5 ml

Medium for neurons (200 ml)

1. BSA	0.50 g
2. MEM liquid	94 ml Sigma
3. DME liquid	80 ml Sigma
4. F-12 liquid	20 ml Sigma
5. Glucose 45% liquid	1.5 ml Sigma solution
6. Glutamine 200 mM	0.50 ml Sigma solution
7. DiPorzio Conc.	2.0 ml
8. Calf Serum	2.0 ml Gibco, heat-inactivated
9. Liquid Catalase	0.10 ml Sigma solution
10. Kynurenic acid 0.5M	200 µl (0.5 M kynurenic acid is 946 mg in 10mL. Dissolve in 1N NaOH
11. HCl 5N	50 µl

Before sorting, a cell strainer with 70µm nylon mesh (BD Falcon) was used to obtain a single cell suspension from previous dissociation. 7-Amino-actinomycin D (7-AAD) (Beckman-Coulter) was added to the cell suspension before sorting: it is excluded by viable cells but can penetrate membranes of dying or dead cells and it intercalates into double-stranded nucleic acids. A high-speed cell sorter (MoFlo) was used to sort subpopulation of cells expressing GFP. Sorting parameters used for the three different populations are visualized on **Fig.16**: we first excluded from the analysis cell doublets and debris on the basis of their Pulse Width vs. Forward Scatter (PW/FSC) dot plot. Physical parameters such as FSC and Side Scatter (SSC) were then used to remove a part of dead cells and debris. 7-AAD exclusion was also employed in order to exclude cells with loss in the membrane integrity and, finally, a subpopulation of cells with increased GFP emission was identified and sorted. To confirm the high purity of our preparations, we performed a re-analysis on the FACS sorted samples (on the right of **Fig.16**).

For GFAP-GFP mice two populations of astrocytes with different intensities (DIM, range between 101-102 and Bright 102-104) were sorted and purified. Due to the higher grade of purity of the bright cell population, we used this second parameter sets for further experiments.

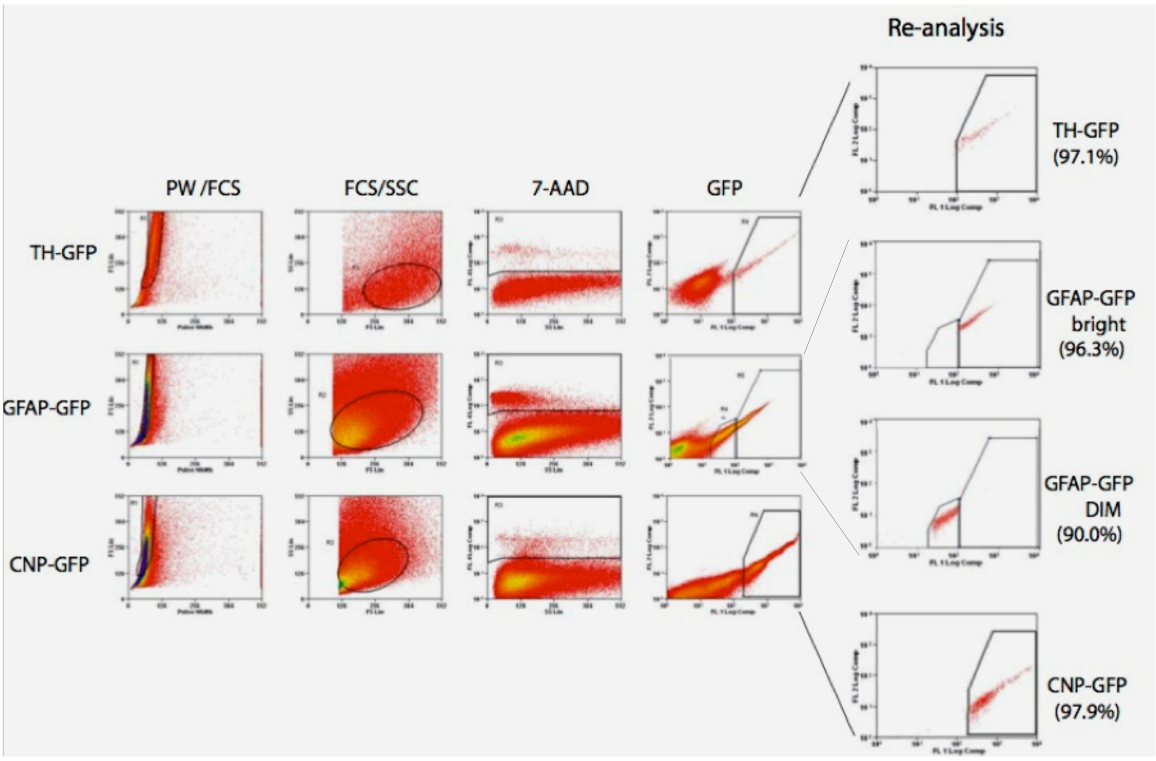


Fig.16: Gating and sorting strategies: different graohs of sorting parameters (see text for detailed description)

2.6 IMMUNOCYTOCHEMISTRY AND IMMUNOHISTOCHEMISTRY

For immunocytochemistry experiments, cells were fixed in 4% paraformaldehyde (Tousimis Research Corporation) directly added to culture medium for 10 minutes, then washed with PBS two times, treated with 0.1M glycine for 4 minutes in PBS and permeabilized with 0.1% Triton X-100 in PBS for another 4 minutes. After washing with PBS and blocking with 0.2% BSA, 1% NGS, 0.1% Triton X-100 in PBS (blocking solution), cells were incubated with the indicated antibodies diluted in blocking solution for 90 minutes at room temperature. After washes in PBS, cells were incubated with labeled secondary antibodies for 60 minutes. For nuclear staining, cells were incubated with 1μg/ml DAPI for 5 minutes. Cells were washed and mounted with Vectashield mounting medium (Vector).

For immunohistochemistry (IHC), 8 to 12-weeks old C57/B6 mice (Jackson Laboratories) were deeply anesthetized and intensively perfused transcardially with PBS followed by 4% paraformaldehyde diluted in PBS. Brains were removed and post-fixed in 4% paraformaldehyde for 1h at room temperature. The region containing the *Substantia Nigra* was isolated and cut with a vibratome (40 µm). Slides were blocked with PBS, 10% NGS, 1% BSA, 1% Fish gelatin (filtered) for 1h at RT, the primary and secondary antibodies were diluted in PBS, 1% BSA, 0.1% Fish gelatin, 0.3% tritonX-100. Incubation with primary antibodies was performed for 16h at RT; incubation with secondary antibodies was performed for 2h at RT. Nuclei were labeled with DAPI. Slides were mounted with mounting medium for fluorescence Vectashield (Vector Lab.) and observed at confocal microscope.

Immunohistochemistry on human *post mortem* brain sections was performed as described (Waldvogel *et al.* 2006).

For detection, Alexa Fluor -488, -594 or -405 (Invitrogen) antibodies were used. For double immunohistochemistry with two antibodies raised in rabbit, Zenon Rabbit IgG Labeling Kits (Molecular Probes, Invitrogen) was used following the manufacturer instructions. Nuclei were visualized with DAPI. All images were collected using a confocal microscope (LEICA TCS SP2).

The following antibodies were used for this study:

ANTIGEN	**COMPANY**	**DILUTION**
Myc	Cell Signalling	1:1000
Flag	Sigma	1:1000
m-hemoglobin	Cappel	1:1000
m-hemoglobin	ICL	1:300
CNPase	Chemicon	1:500
TH	SIGMA	1:1000
Gata-1	Santa Cruz	1:200
Tal1	Santa Cruz	1:200,
GFAP	SIGMA	1:1000
NeuN	Chemicon	1:1000
NG2	Chemicon	1:300
Iba-1	(kind provided by Dr. Imai, Japan)	1:200
h-hemoglobin	Biomeda	1:100
h-hemoglobin	Santa Cruz	1:200

2.7 *post mortem* HUMAN BRAIN SAMPLES

Brain samples were obtained from the Brain Banks of the Institute of Neuropathology, Bellvitge Hospital, and of the University of Barcelona. The Ethics Committee of the University of Barcelona obtained human brains at autopsy with the informed consent of patients or their relatives and the institutional approval. The samples were from 3 caucasian males, age matched (39-56 years old).

The time between death and brain processing was between 3 and 5h. SN and *amygdala* were excised, cryo-protected with 30% sucrose in 4% formaldehyde, frozen in dry ice and stored at −80°C until use.

2.8 CONSTRUCTS

Full-length mouse sequences of adult and embryonic globin chains as well as myoglobin and cytoglobin were obtained from the FANTOM2 RIKEN clone libraries collection (Okazaki 2002). Mouse neuroglobin full-length sequence was obtained from RZPD (Germany). Coding sequences were sub-cloned by PCR into pIRES2-EGFP (Clontech, BD Biosciences) in frame with C-terminal myc tag (**Fig.17**).

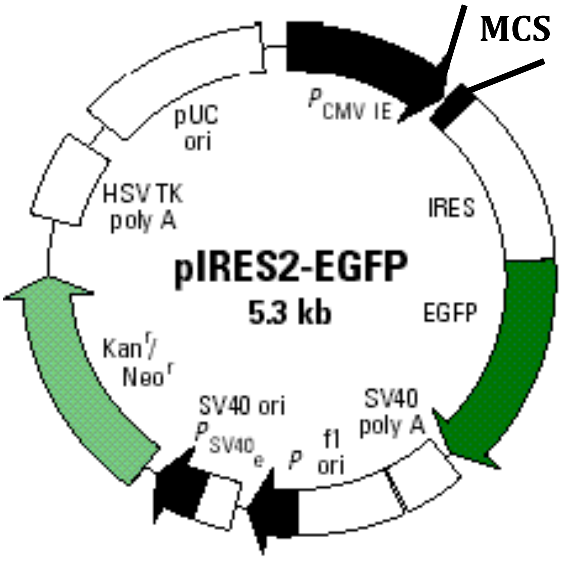


Fig17. Scheme of pIRES-EGFP plasmid

We took advantage of pBudCE 4.1 vector (Invitrogen), designed for the independent expression of two genes from a single plasmid, in order to express alpha- and beta- chains of mouse hemoglobin in MN9D cells. A fragment composed by beta-globin-Myc-tag-IRES-EGFP was cloned into the CMV-MCS (*Sal* I/*Xba* I) whether 2xFlag-alpha-globin was placed into EF-1 alpha-MCS (*Kpn* I/*Xho* I).

A control vector containing only IRES-EGFP in CMV-MCS (*Sal* I/*Xho* I) was also created (**Fig.18**).

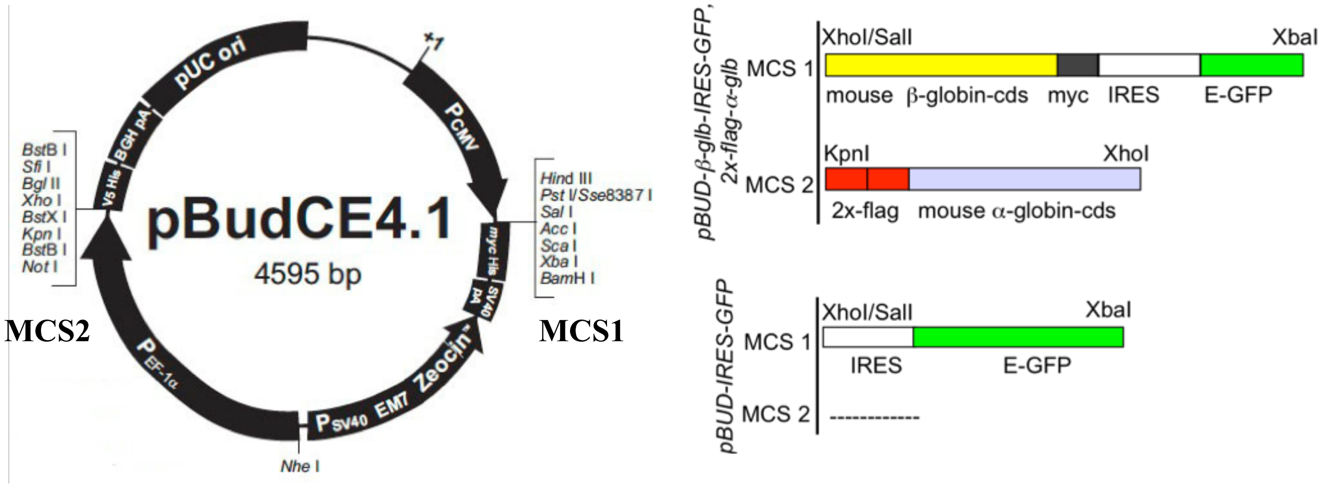


Fig.18 Cloning strategy scheme of respectively *pBUD-IRES-GFP* (Empty vector) and *pBUD-*β*-glb-Myc-IRES-GFP*, *2x-flag-*α*-glb* (alpha and beta vector). β-globin-myc-IRES-GFP or IRES-GFP alone was inserted into CMV-MCS, while 2x.flag-α-globin was inserted into the EF-1a –MCS of pBUDCE 4.1 vector.

2.9 CELL CULTURE AND TRANSFECTION

HEK-293T (human embryonic kidney) cells were grown in DMEM (GIBCO) supplemented with 10% fetal bovine serum (SIGMA-ALDRICH), 100 IU/ml penicillin and 100µm/ml streptomycin (SIGMA) at 37°C in a humidified CO_2 incubator. HEK cells were transfected with standard calcium phosphate method.

The mouse dopaminergic neuroblastoma cell line MN9D was obtained by Dr. Michael J. Zigmond, University of Pittsburgh (U.S.A.) and maintained in culture using D-MEM with 10% fetal bovine serum, 100 µg/ml penicillin and 100 µg/ml streptomycin. MN9D cells were transfected using LipofectamineTM 2000 (Invitrogen) following manufacturer instructions. After 24 hours from transfection, cells were collected and an high-speed cell sorter (MoFlo) was used to sort subpopulation of cells expressing GFP. Sorting parameters are summarized on **Fig.19**.

After sorting, cells were re-plated and 48 hours later, Zeocyn (300µg/ml) was added for selection.

After 3 weeks polyclonal cell populations expressing tagged alpha- and beta-chains of mouse hemoglobin or empty vector were obtained and confirmed by western blot analysis, immunofluorescence and quantitative real-time PCR (see results).

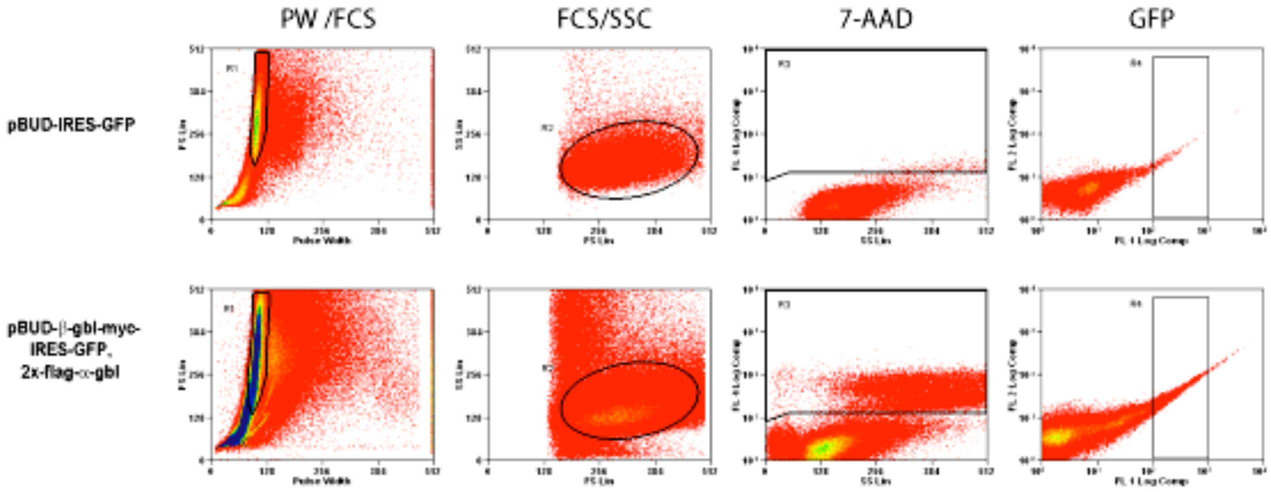


Fig.19 Polyclonal stable cell lines overexpressing *pBUD*-β-*glb-Myc-IRES-GFP, 2x-flag*-α-*glb* or *pBUD-IRES-GFP* were purified using FACS sorter. FACS parameters used were similar to those employed previously (see S6). Briefly, we first excluded from the analysis cell doublets and debris (PW/FSC), then physical parameters (FSC and SSC) as well as 7-AAD exclusion were used in order to exclude dead cells. Finally, a subpopulation of cells with comparable GFP emission intensity (102-103) was identified and sorted for the two cell populations.

2.10 IMMUNOPRECIPITATION EXPERIMENTS

For immunoprecipitation and co-immunoprecipitation, cell were lysed in immunoprecipitation buffer (IP) (300 mM NaCl, 50 mM TRIS pH 7.5, 1% NP40, 10% glycerol), supplemented with complete EDTA-free protease inhibitor cocktail (Roche Diagnostics) for 30 minutes at 4°C. Lysates were cleared at 15,000 g for 20 minutes. Cellular lysates were incubated with the appropriate antibodies [anti-Myc (Cell Signalling), anti-Flag (Sigma), anti-Hb (Cappel)] or corresponding controls [mouse IgG and rabbit IgG (Sigma)]. Immunoprecipitation was performed for 2 h at 4°C. After washing, immunoprecipitated proteins were eluted with 2 X SDS sample buffer, boiled and analysed by western blot. Washes of immunoprecipitated proteins were performed with the same IP buffer.

For western blot analysis, samples were resolved on 10-15% SDS-PAGE as needed and proteins were transferred to nitrocellulose membrane (Schleicher & Schuell).

Membrane was blocked with 5% non-fat milk in Tris Buffer Saline Solution (TBS-T), then incubated with primary antibodies overnight at 4°C or at room temperature for 2 hours. Proteins were detected by horseradish peroxidase-conjugated secondary antibodies (DakoCytomation) and enhanced chemiluminescence reagents (GE Healthcare).

2.11 MICROARRAY ANALYSIS

Total RNA was isolated using TRIzol (Invitrogen) according to manufacturer's instructions, treated with DnaseI (Ambion) and purified with RNeasy Mini kit (Qiagen). RNA quality and quantity was assessed using an Agilent 2100 Bioanalyzer (Agilent Technologies) and NanoDrop 1000 spectrophotometer (Thermo Scientific).

2µg of each total RNA sample was labeled according to standard one-cycle amplification and labeling protocol (Affymetrix).

Labeled cRNA was hybridized on Affymetrix GeneChip Mouse Genome 430A 2.0 Arrays, containing 22,690 probesets corresponding to approximately 14,000 well-characterized mouse genes. Hybridized arrays were stained, washed (GeneChip Fluidics Station 450) and scanned (GeneChip Scanner 3000 7G). Cell intensity values and probe detection calls were computed using the Affymetrix GeneChip Operating Software (GCOS). Four biological replicas were processed for each experimental condition. One replicate from empty vector condition didn't pass the quality control analysis and was discarded from further study. Further data processing was performed in the R computing environment (http://www.r-project.org/) version 2.8.0 with BioConductor packages (http://www.bioconductor.org/).

Robust Multi-Array Average (RMA) normalization was applied (Irizarry *et al.* 2003). Data were then filtered based on Affymetrix detection call and probeset intensity, so that only probesets that had a present call and intensity value >100 in at least one of the arrays were retained. Statistical analysis was performed with limma (Smyth 2004).

P-values were adjusted for multiple testing using Benjamini and Hochberg's method to control the false discovery rate (Hochberg & Benjamini 1990). Genes with adjusted P values below 0.05 were considered differentially expressed. A threshold value of 0.2 Log fold change was applied. Data were analysed through the use of Ingenuity Pathways Analysis (Ingenuity Systems®, www.ingenuity.com).

Microarray data are deposited in the GEO database with Accession Number GSE16192 (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16192).

Heatmap cell values were obtained as ratios between each probe intensity value and the median of all control sample intensities for that probe. Hierarchical clustering analysis (average linkage) was performed on genes and samples as implemented in the MultiExperiment Viewer version 4.0 (Saeed *et al.* 2003).

2.12 STATYSTICAL ANALYSIS

All data were obtained by at least three indipendent experiments and were expressed as mean ± stadard deviation. Student’s t-test was used for comparison. Significance to reference samples were shown as (*) $p<0.05$ or (**) $p<0.01$.

3 RESULTS

3.1 IDENTIFICATION OF ALPHA- AND BETA- GLOBIN TRANSCRIPTS BY EXPRESSION ANALYSIS OF A9 DA NEURONS.

To study the cellular physiology of A9 DA neurons, we determined their gene expression profiles with two independent techniques: cDNA microarrays and nanoCAGE. To this purpose we took advantage of transgenic mice that selectively express green fluorescent protein (GFP) in catecholaminergic cells under the control of tyrosine hydroxylase (TH) gene promoter (TH-GFP mice). In this mouse line we can identify the majority of mDA neurons for their GFP labeling. Furthermore, we can distinguish A9 neurons from A10 for their anatomical localization. LCM and pressure catapulting were used to harvest A9 neurons after fixation with a Zinc-fix-based method that assured the preservation of both tissue morphology and RNA integrity. RNA was then used as template in two different gene expression approaches.

In the cDNA microarray experiment, RNA was processed by μMACS amplification kit (Miltenyi), labeled and used as a target to monitor gene expression on a custom-made cDNA microarray platform (SISSA arrays). All the experiments were performed in three biological replicates. The complete description of the transcripts expressed in A9 neurons is presented elsewhere (Christina Vlachouli PhD Thesis). Interestingly, among the genes expressed in A9 cells, transcripts for the alpha and beta chains of mouse hemoglobin were identified.

For the nanoCAGE transcriptome analysis, 2000 A9 cells were harvested with LCM on TH-GFP mice, full length cDNAs were produced and, after cleavage with a class IIS restriction endonuclease, 5' end tags were purified and sequenced by using the second generation of sequencers (Roberto Simone PhD thesis). Finally, Transcription Start Sites (TSS) were identified by mapping tags to the genome (Valen *et al.* 2009; R. Kodzius 2006). This kind of analysis unveiled TSS on the mouse chromosomes 11 and 7, in the genomic regions corresponding to the 5'-end of Hba-a1 (NM_008218.2) and Hbb-b1 (NM_008220.3) transcripts (**Fig.20**). In **Tab2** a list of nanoCAGE tags in A9 neurons is provided for these two loci.

Therefore, cDNA microarray data and CAGE tags distribution suggested that A9 neurons express transcripts for alpha- and beta- chains of hemoglobin.

Locus	*Tags sequences*	*Chr.*	*Position*	*Tags count*
Hbb-a1	GACACTTCTGATTCTGACAGACTCA	Chr.11	32183671-695	328.802
Hbb-a1	ACTTCTGATTCTGACAGACTCAGGA	Chr.11	32183674-698	662.67
Hbb-a1	AAGACAAAAGCAACATCAAGGCTGC	Chr.11	32183723-747	21.866
Hbb-a1	CACCAAGACCTACTTCCCTCACTTT	Chr.11	32183945-963	41.884
Hbb-a1	CTGCAGCATTGGCCAGAGCATCGGC	Chr.11	32184017-041	36.667

Locus	*Tags sequences*	*Chr.*	*Position*	*Tags count*
Hbb-b1	ATAGTTGTGTTGACTCACAACCCCA	Chr.7	110976400-426	65.08
Hbb-b1	ACATTTGCTTCTGACATAGTTGTGT	Chr.7	110976415-441	393

Tab.2: List of nanoCAGE tags for alpha- and beta- loci in A9 neurons: a list of cage tags sequences is presented for both alpha- and beta-transcripts expressed in A9 neurons. The nucleotide sequences and their position along the chromosomes are indicated as well as the number of tags shown in TPM (tags per million)

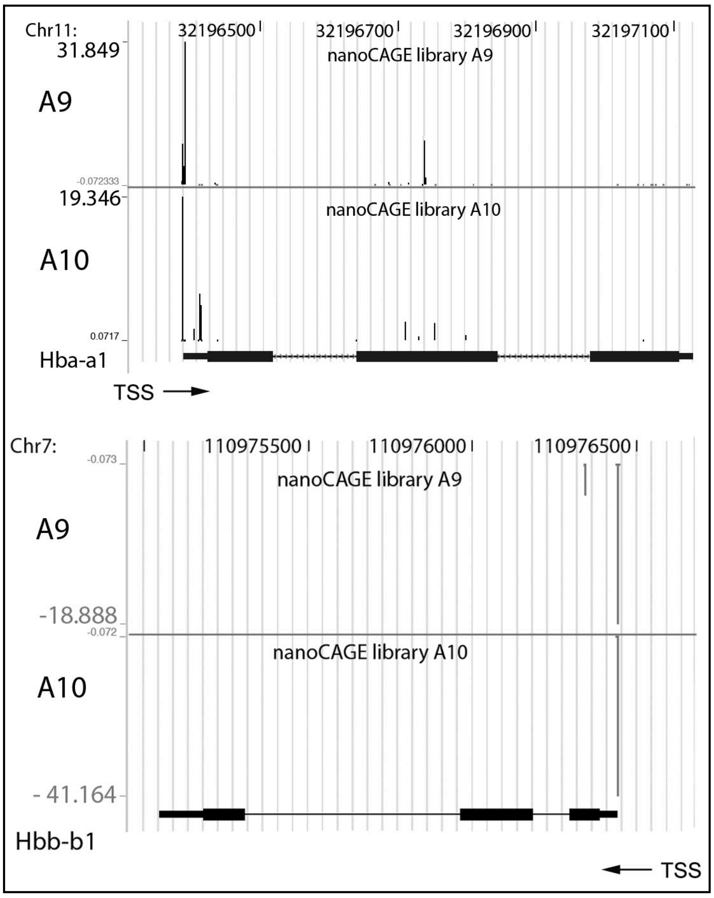


Fig.20 Expression of alpha- and beta-globin transcripts in A9 and A10 neurons. nanoCAGE tracks visualization concerning Hbb-a1 (Chr.11) and Hbb-b1 (Chr.7) gene loci. A Genome Browser view is presented. A9 library is indicated and the tags per million (TPM) for each gene are reported. The structure of Hbb-a1 and Hbb-b1 transcripts is depicted on the bottom. Transcriptional start sites (TSS) are indicated at the 5' un-transcribed region of each transcript, where the maximum amount of CAGE tags accumulates.

To estimate potential blood contamination, we monitored the expression of several erythrocyte-specific transcripts: no expression was detected for Rhesus blood group-associated A glycoprotein (Rhag; NM_011269.2), glycophorin A (Gypa; NM_010369.3), aminolevulinic acid synthase 2 (Alas2; NM_009653.2), spectrin alpha 1 (Spna1; NM_011465.3) and erythrocyte protein band 4.2 (Epb4.2; NM_013513).

3.2 VALIDATION OF THE EXPRESSION OF ALPHA- AND BETA- GLOBIN TRANSCRIPTS IN A9 DA CELLS.

We then validated the expression of alpha- and beta- globin transcripts in A9 DA neurons by two independent approaches.

We studied the precise distribution of alpha- and beta- globin transcripts in the mouse midbrain by *in situ* hybridization. Experimental procedures and antisense RNA probes were first tested on bone marrow as a positive control for globin expression (**Fig.21**).

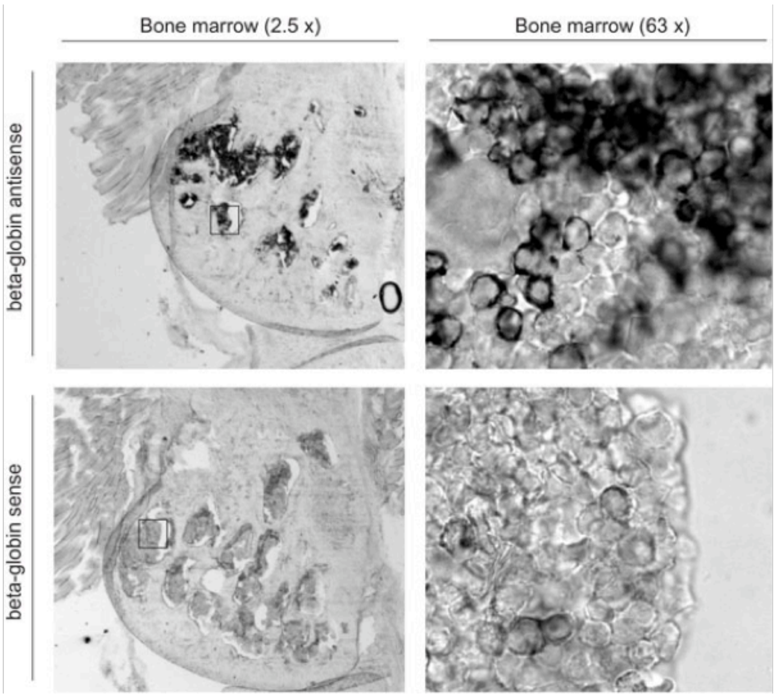


Fig.21 *In situ* hybridization on mouse bone marrow (BM): Slices probed with antisense (top) and sense (bottom) transcripts for beta-globin are presented. In the pictures at lower magnification (2,5x), the morphology of bone marrow tissue is evident; higher magnification (63x, area in the boxes)) single cells strongly labelled for the *in situ* signal are clearly visible (antisense probe), whereas no labelling was visualized using sense probe. Similar results were also obtained using antisense and sense probe for alpha-globin.

Then brains were fixed using conventional methods (with PFA 4%) after extensive perfusion with PBS in order to minimize blood contamination. As shown in the **Fig.22a**, antisense probes gave specific and reproducible signals in A9 neurons that were identified by anti-TH immunoreactivity and anatomical localization. Interestingly, a specific labeling for the antisense probes was also evident in A10 neurons (**Fig.22b**). Higher magnification of the merged images showed co-localization of the antisense signals for each hemoglobin chains in the cytosol of TH-positive A9 and A10 DA cells.

We then took advantage of LCM to collect 500 TH-GFP-positive neurons for each mDA cell group. After RNA extraction and cDNA synthesis, qPCR amplification was carried out to detect the expression of alpha- and beta- globin. As visualized in **Fig.22c**, the qPCR showed that alpha- and beta- globin transcripts were two fold more expressed in A9 than in A10 neurons.

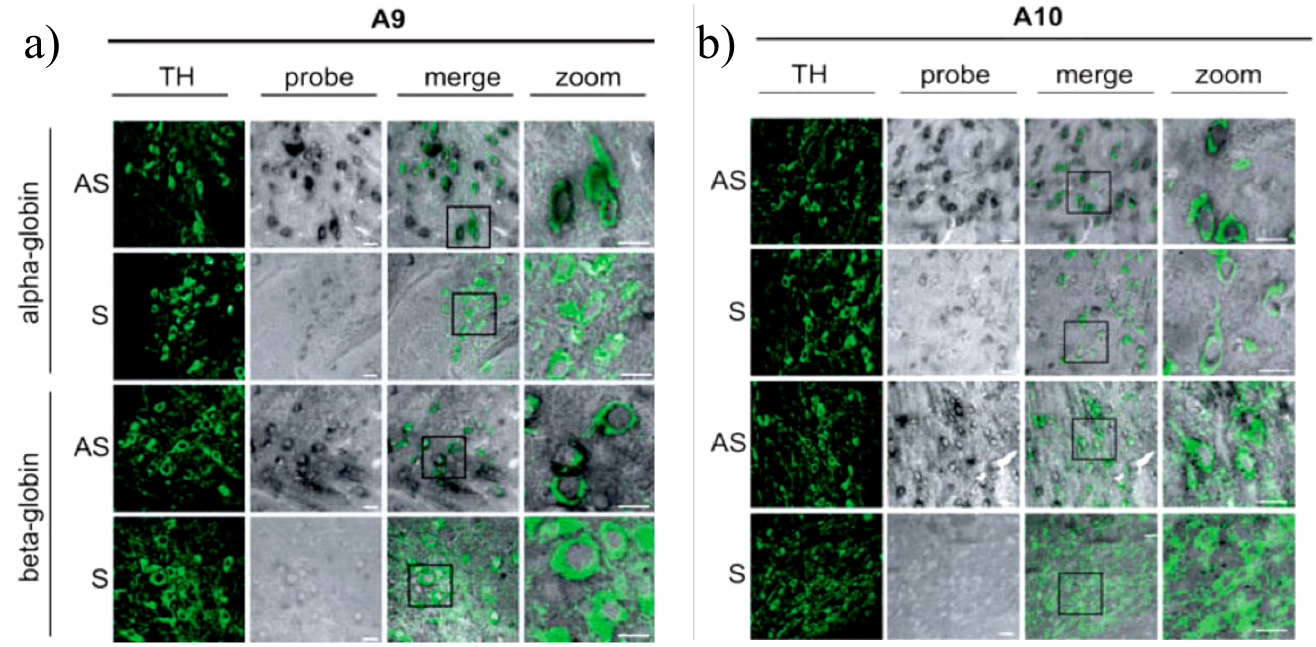


Fig.22a-b: *In situ* hybridization of alpha- and beta- globin transcripts on A9 (a) and in A10 (b) DA neurons: ventral midbrain slices were processed with antisense (AS) and sense (S) probes for the two globins transcripts. DA neurons were visualized by IHC using an anti-TH antibody (green).

The overlay (merge) shows co-localization of the transcripts of alpha- and beta-globin in the cytoplasm of A9 and A10 neurons. Probes obtained from sense transcripts were used as negative controls. The zoom offers magnifications of the overlay images (area in the boxes). Scale bars indicate 20 μm.

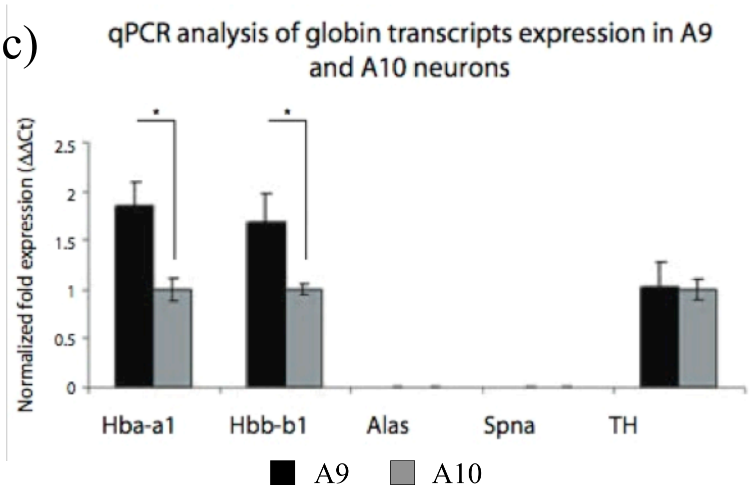
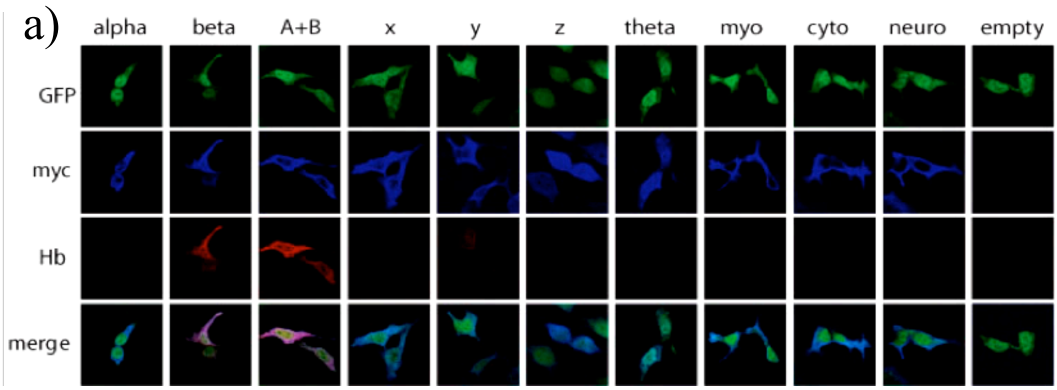


Fig.22c: qPCR starting from 500 LCM-isolated neurons from A9 and A10 regions of the ventral midbrain of TH-GFP mice. TH, alpha-globin and beta-globin transcripts were amplified and the absence of blood contamination was evaluated using primers for Alas and Spna. Alpha and beta-transcripts are more expressed in A9 neurons (~2 fold), four biological replicas, $P < 0.05$.

3.3 HB-IR IS PRESENT IN DA NEURONS OF THE SN

To characterize hemoglobin expression at protein level, we used a commercial antibody produced against highly purified total mouse hemoglobin (Cappel). For the high homology among proteins of the globin family and for the expression of atypical globins in neurons, we first verified the repertory of immunoreactivity of the Cappel antibody in immunofluorescence experiments (**Fig.23a**). We transfected HEK cells with expression vectors carrying myc-tagged globin isoforms (Hba-a1, Hbb-b1, Hba-x, Hbb-y, Hbb-bh1, Hbq1) and atypical globins (Cygb, Ngb, Mg). Cappel antibody reactivity was then monitored in parallel with anti-myc staining. A strong signal was obtained for beta-globin chain. A weaker labeling was also detected when the Hbb-y embryonic chain was expressed. Importantly, no cross-reaction was present with any of the atypical globins normally expressed in neurons.



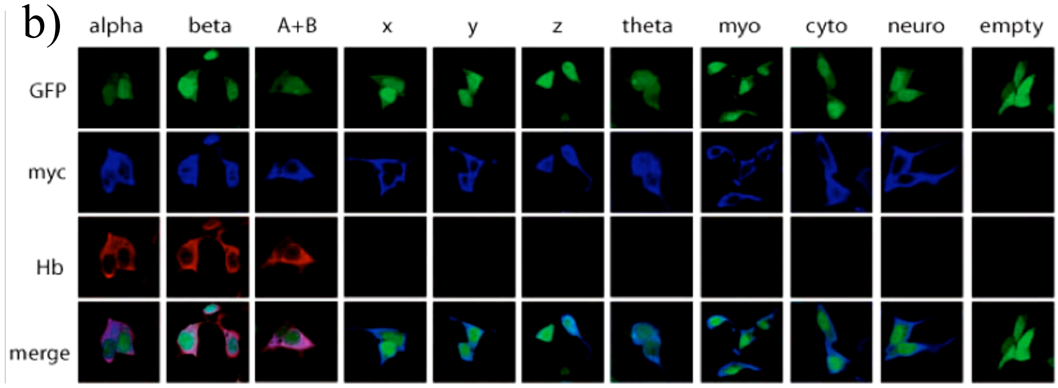


Fig.23a: Hek-293 cells transfected with different constructs expressing typical and atypical globin chains [Hbb-a1 (alpha), Hbb-b1 (beta), co-expression of alpha- and beta-globin (A+B), Hba-x (x), Hbb-y (y), Hba-z (z), Hbq1 (theta), myoglobin (Myo), cytoglobin (cyto) and neuroglobin (neuro)] were subjected to double immunofluorescence using anti-Myc (blue) and anti-hemoglobin (Cappel) (red) antibodies. The transfected constructs also expressed GFP (green). pIRES2-EGFP empty vectors were transfected as control. Cappel anti-mouse hemoglobin antibody specifically recognized beta-chains of mouse hemoglobin. No cross-reaction with the atypical globins was observed (magnification 63X).

Fig.23b: Similar experiment was performed using the second antibody anti-mouse hemoglobin (ICL). The ICL antibody showed different chain recognition abilities since it detected both alpha- and beta-globin. No cross-reaction was observed with the atypical globins.

Therefore, an immunohistochemical analysis of the mouse mesencephalon was carried out. To avoid strong reactivity from blood cells, brains were extensively washed in PBS during perfusion before fixation. IHC on mouse midbrain revealed a complex pattern of protein expression (**Fig.24**). In the SN, 65,8 ± 6,1% of A9 DA neurons was positive for Hb staining. On the contrary, a very limited number of DA neurons in the A10 region was labeled (2,9 ± 0.82%). Interestingly, Hb-immunoreactivity in mDA neurons was localized both in the cytoplasm as well as in the nucleus excepted for the nucleolus. Importantly, the specificity of the antibody was further verified by competition assays using mouse spleen extracts on midbrain sections (**Fig.24**).

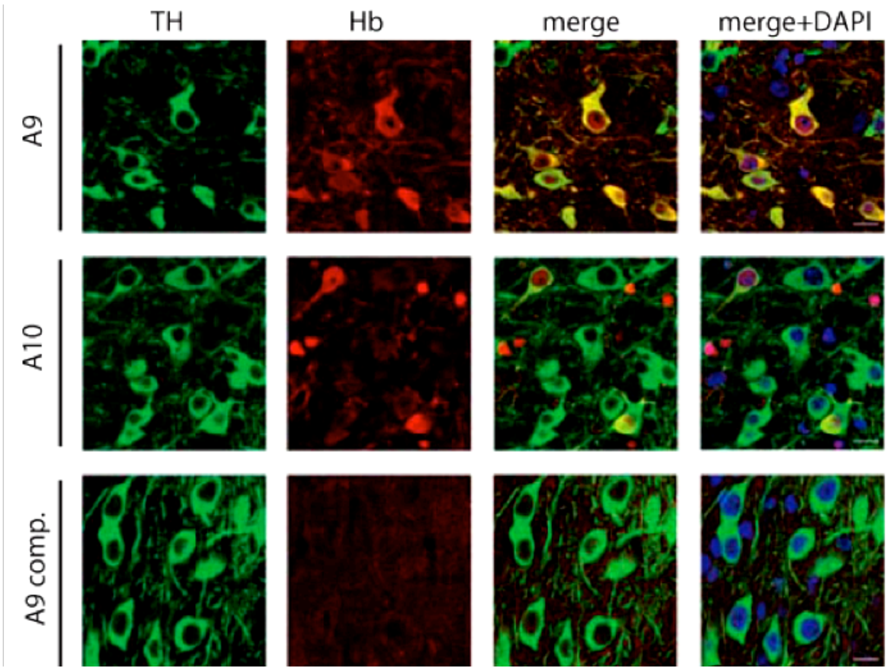


Fig.24: Hb protein is expressed in A9 and A10 DA neurons of mouse brain.

A double IHC using anti-Hb (red), anti-TH (green) and DAPI (blue) is presented: nearly 70% of A9 but only 3% of A10 neurons were double labelled for Hb and TH (merge). Hb staining is present both in the nucleus, except for the nucleolus, and in the cytoplasm. Adsorbtion of the anti-Hb antibody with spleen extract completely prevents Hb staining (A9 comp). Scale bar indicates 20 mm.

To further confirm Hb staining, we then used a second commercial antibody against purified mouse hemoglobin (ICL Labs). First, we proved that its chain specificity pattern is limited to the detection of both alpha- and beta- chains and that no cross-reaction with other typical or atypical globins was observed (**Fig.23b**). Then we confirmed an extensive overlap of Hb staining for DA neurons between Cappel and ICL antibodies (**Fig.25**). Experiments performed on brains without perfusion showed a strong labeling of red blood cells that were clearly different in size, location and number from DA neurons (**Fig.26**).

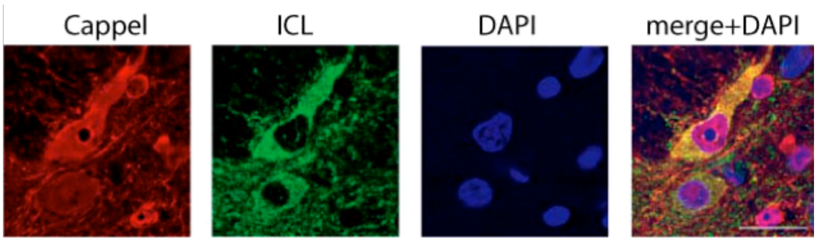


Fig.25: Comparison of the staining obtained using two different anti-mouse hemoglobin antibodies. Double IHC with Cappel (red) and ICL (green) antibodies in the ventral midbrain of adult mouse is presented. An extensive overlap of globin-IR for mDA neurons is confirmed using both antibodies (merge). Scale bars 20 μm

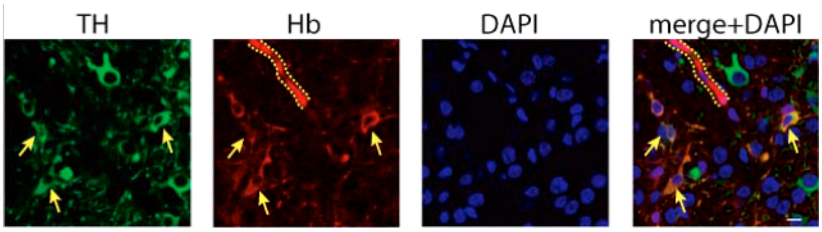


Fig.26: Double IHC on a brain with no perfusion. Anti-Hb antibody (red), anti-TH antibody (green) and DAPI (blue) were used. Dashed lines decorated a blood vessel containing several erythrocytes strongly labelled with anti-Hb antibody. Hb-IR mDA neurons (arrows) are morphologically and topographically different from red blood cells. Scale bars 20 μ

To further analyze if only dopaminergic neurons of *substantia nigra* were positive for Hb staining, we analyzed also other groups of dopaminergic cells in olfactory bulbs and in locus ceruleus and we confirmed that they don't present any imunoreactivity for Cappel antibody (**Fig.27**).

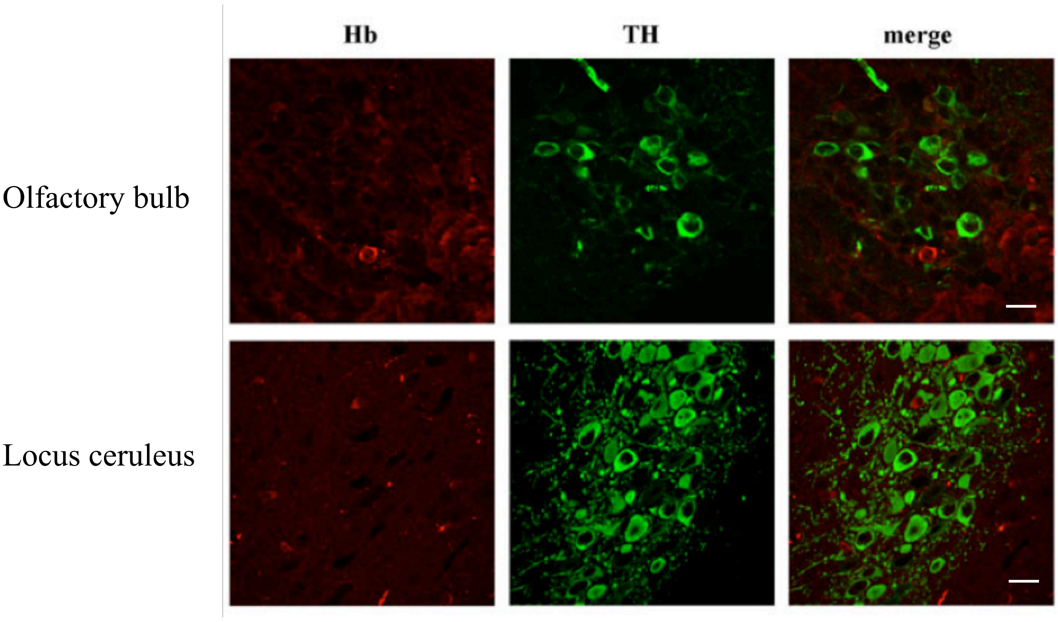


Fig.27: Double IHC on olfactory bulb and locus ceruleus with Ab anti Hb (red) and anti-TH (green) showed that other groups of dopaminergic neurons are negative for Hb staining. Scale bar 20μm.

Since nanoCAGE data showed that both alpha- and beta- chains synthesis involved the same transcriptional starting site used in blood, we investigated whether the major transcription factors implicated in controlling primitive and definitive erythroid lineages may be involved in mDA cells transcription. Notably, the expression of Gata family members and SCL/*Tal-1* transcription factors has been also described in the midbrain and hindbrain (Tsai *et al.* 1994; Pandolfi *et al.* 1995; Herberth *et al.* 2005; Ogilvy *et al.* 2007; Bradley *et al.* 2006; Nardelli 1999).

As shown in **Fig.28**, several (~50%) DA neurons were positive for both Gata-1 and Hb staining.

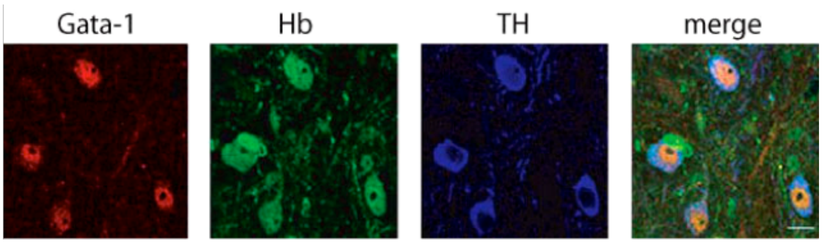


Fig.28: Triple IHC using anti-Gata-1 (red), anti-Hb (green) and anti-TH (blue) antibodies. A subpopulation of DA neurons (nearly 50%) were positive for Hb, Gata-1 and TH. Scale bars 20 µm

3.4 ADDITIONAL HB-IR CELLS ARE PRESENT IN DISTINCT AREAS THROUGHOUT THE BRAIN.

Together with mDA neurons (**Fig.29**; left), two additional TH-negative cell types were labeled by the anti-Hb antibody (Cappel) in brain sections: cell type I were large cells located in the cortex and in the hippocampus, faintly labeled in the cytoplasm and in the nucleus (approx. diameter: 15-18 µm) (**Fig.29**; center); cell type II were small cells widely diffused in all the brain regions analyzed, strongly labeled in the thin cytoplasm as well as in the nucleus (approx. diameter: 7-10 µm) (**Fig.29**; right).

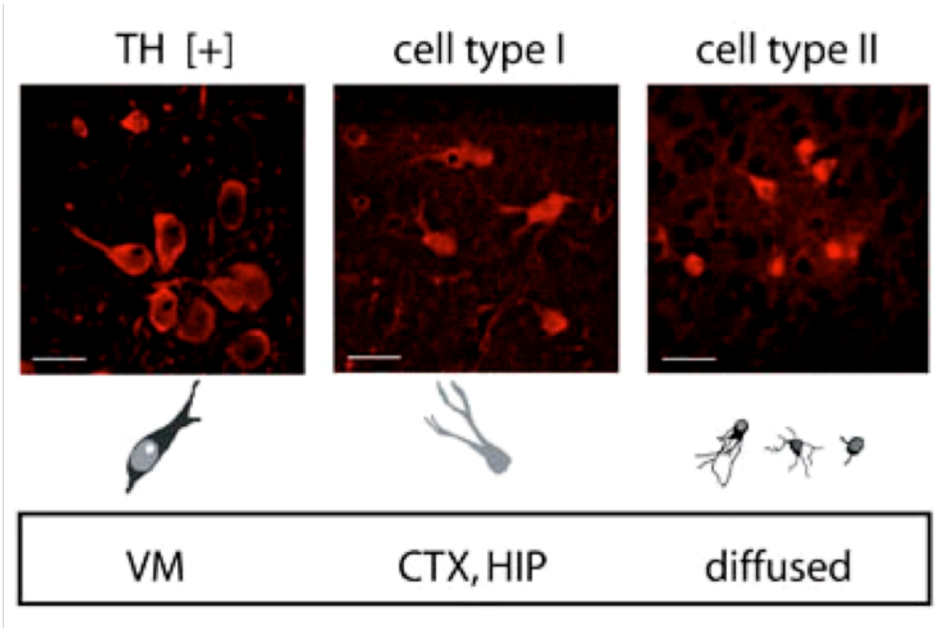


Fig.29: IHC using anti-Hb antibody on mouse brain revealed different Hb–IR cells: large neurons located in the ventral midbrain, positive for TH (TH [+], already described); cell type I) large cells located in the cortex (CTX) and in the hippocampus (HIP); and cell type II) small cells, widely diffused in all the brain regions tested and presenting a strong Hb-IR. On the bottom of the figure a schematic representation of the morphologies of Hb–IR cells is presented. Scale bars 20 mm.

In order to identify these cells, we carried out extensive double-IHC on mouse midbrain slices with anti-Hb antibody together with antibodies specific for different neuronal and glial cell populations: NG2, marker of oligodendrocyte precursors, Iba-1, microglial marker, NeuN, neuronal marker, GFAP, glial marker and CNPase, marker of mature oligodendrocytes.

As described in **Fig.30a-b**, we found a specific and reproducible Hb staining in a subpopulation (73,2 ± 4,8 %) of hippocampal and cortical cells positive for anti-GFAP antibody as well as in a large fraction (>99%) of mature oligodendrocites, characterized by the expression of CNPase. We also confirmed Hb staining in these cells with competition assay using spleen extract. No Hb positive cells were labeled with NG2, NeuN and Iba1 (**Fig.30c**).

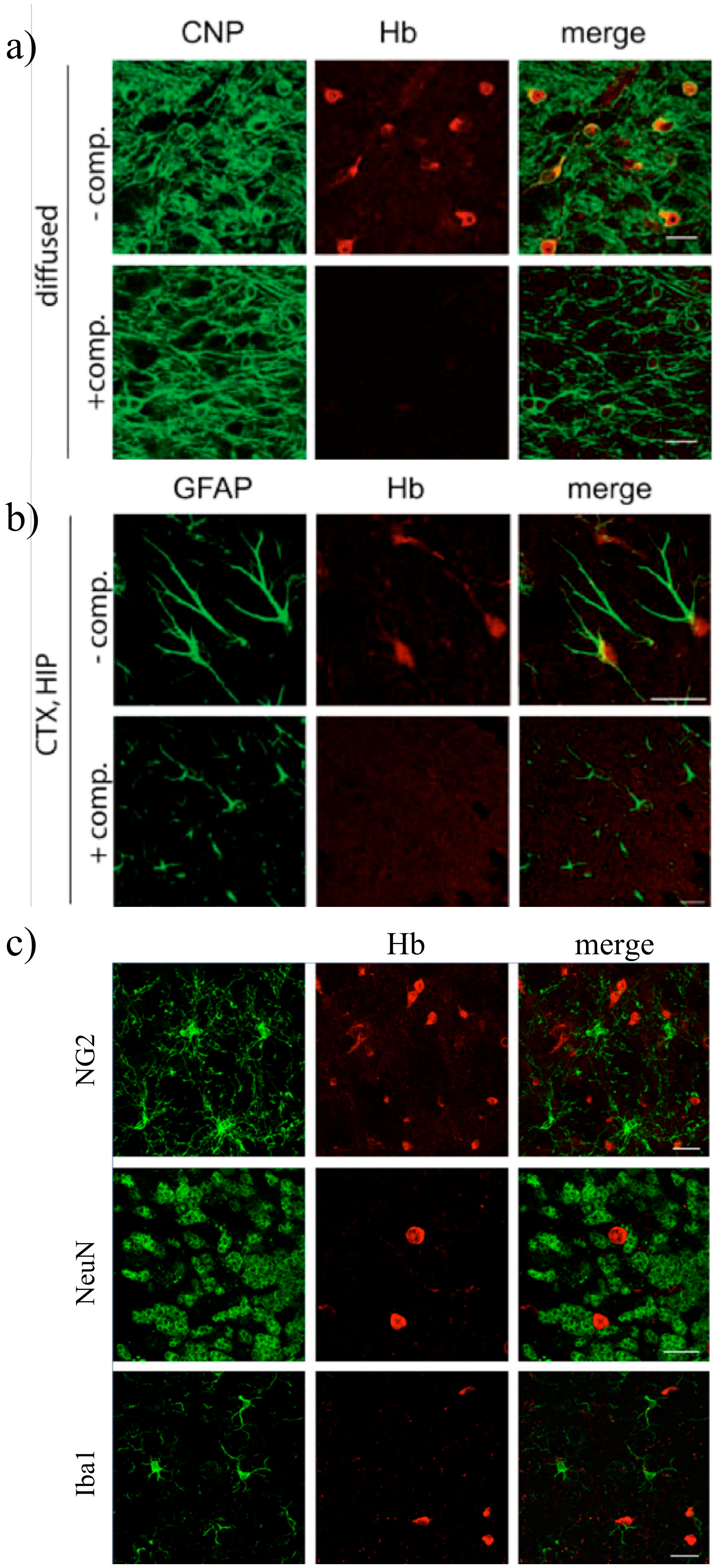


Fig.30 (a-b): Double IHC using anti-Hb antibody (red) together with oligodendrocytes and astrocytes markers (CNP and GFAP, green). In the cortex (CTX) and in the hippocampus (HIP), Hb–IR cell type II colocalizes with the oligodendrocytes marker CNP (a); cell type I colocalizes with GFAP staining (b). In the bottom panels, Hb-IR adsorbtion of the anti-Hb antibody with spleen extract completely prevents Hb staining (+ comp).

(c): double IHC with antibody anti-Hb (red) and different cellular markers (green) shows no colocalization between Hb positive type II cells and cells positive for NG2, NeuN or Iba1.

Scale bars 20 μm.

Astrocytes with a radial glia-like morphology in the subgranular zone of the dentate gyrus of hyppocampus are considered stem cells (Kempermann *et al.* 2004); they extend a long branching process through the granule cell layer and express GFAP and nestin (Satoshi Fukuda *et al.* 2003; Filippov *et al.* 2003; Hüttmann *et al.* 2003).

To analyze if GFAP/Hb positive cells in the dentate gyrus were precursors, we also performed a double IHC with Ab anti-nestin but we found that they were negative for this marker (**Fig.31**).

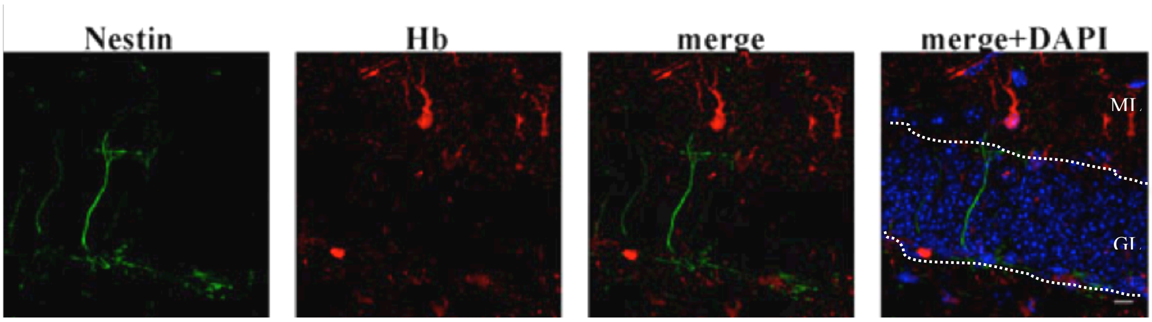


Fig.31: double IHC with antibody anti-Nestin (green) and anti Hb (red) on dentate gyrus of hippocampus shows that Hb+ cellspresent in hyppocampus are negative for nestin. GL: granular layer, ML: molecular layer of hippocampus.

3.5 PRIMARY CULTURES OF HB-IR NEURONAL AND GLIAL CELL POPULATIONS.

We studied globin expression at mRNA and protein level *in vitro* on primary cultures obtained from dissociated mouse ventral midbrain, cortex or hippocampus. Immunofluorescence experiments confirmed the expression pattern observed *in vivo*: Hb-IR was found in a subpopulation of TH-positive DA neurons, in cortical GFAP-positive astrocytes and in the large majority of CNP-positive oligodendrocytes (**Fig.32a**).

Taking advantage of TH-GFP, GFAP-GFP and CNP-GFP transgenic mice lines, we next validated the expression of alpha- and beta- chains transcripts after resorting to Fluorescent-Activated Cell Sorting (FACS) for purifying respectively mDA neurons, astrocytes and oligodendrocytes. After enzymatic digestion and mechanical trituration of dissected regions, the cell suspension was sequentially panned on four *Bandeiraea Simplicifolia* lectin I-coated dishes (Cahoy *et al.* 2008). This step minimized endothelial, microglial and red-blood cells contamination of the preparation. Then, the FACS sorting procedure was applied and GFP-positive cells were collected. FACS-purified cell culture showed an elevated enrichment of the cells of interest (98% for mDA, 96% for astrocytes and 97,8% for oligodendrocytes). RNA was then extracted from 2000 GFP-positive cells for each cell type and, after RT-PCR amplification, the specific amplicons of alpha- and beta- globins were observed in TH-, GFAP- and CNP- enriched cells (**Fig.32b**). Cloning and sequencing confirmed the identity of PCR products.

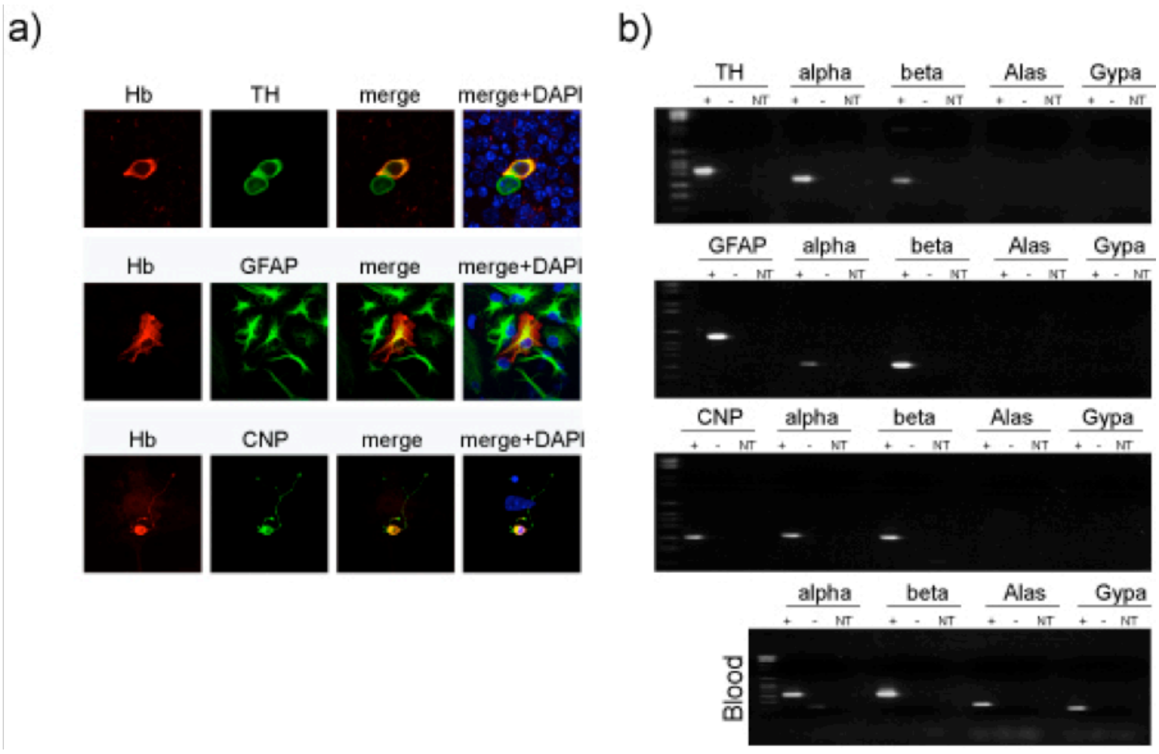


Fig.32: (a) Immunofluorescence on primary cultures of DA neurons, cortical and hippocampal astrocytes and oligodendrocytes. Specific cell population markers and Hb stainigs are shown in green and red respectively (magnification 63X).

b) RT-PCR results obtained from 2000 single FACS-sorted cells. Alpha- and beta-globin transcripts as well as the population-specific marker (TH, GFAP, CNP respectively) were amplified (+). The absence of blood contamination was evaluated using primers for Alas and Gypa. Negative controls, retrotranscriptase free (-) and no-template control samples (NT) are presented. RNA extracted from blood was used as positive control (lower panel).

3.6 HB-IR PATTERN IS CONSERVED IN MAMMALS.

We then addressed whether the characteristic pattern of globin expression described for C57BL/6J line is conserved in different genetic backgrounds. IHC of BALB/cJ, FVB/NJ, CD-1 mouse strains was carried out showing the same morphological and topographical organization of Hb-IR cells.

Furthermore, Hb-IR in mDA neurons, cortical and hippocampal astrocytes as well as in oligodendrocytes was confirmed as early as postnatal day 6. Importantly, other rodents, like *Rattus norvegicus*, showed the same pattern of Hb-IR in the adult brain (**Fig.33a**).

We then analyzed the SN of human *post mortem* brains. The expression pattern was very much resembling what was observed on mouse mDA neurons (**Fig.33b**): only a subset of TH-positive neurons was Hb-IR. Since the state of preservation of human *post mortem* brain samples is very critical, we introduced several additional controls.

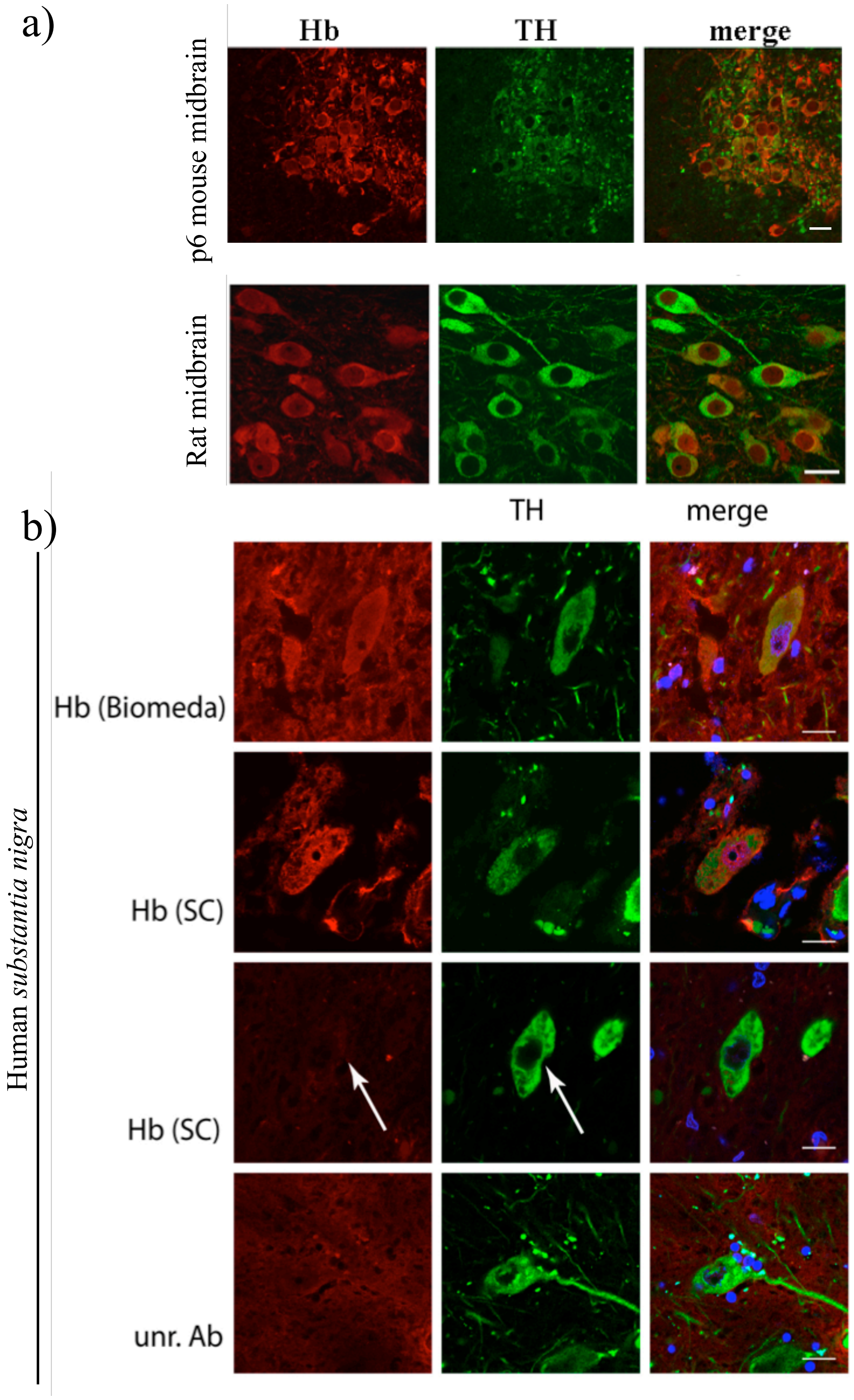


Fig.33: (a) Double IHC on p6 mouse and adult rat midbrain with antibody anti Hb (red) and anti-TH (green) showed the same Hb-IR pattern that in adult mouse brain.
(b) double IHC on human *post mortem* midbrain (SN). For the human brain two different anti-human Hb antibodies are presented. Santa Cruz (SC) as well as Biomeda antibody co-stain several TH-positive neurons in the SN. Several TH-positive Hb-negative neurons were also described (arrow). Unrelated antibodies (unr. Ab), host-matched with those of human hemoglobin, were used as negative controls (one representative picture is shown). Scale bars 20μm.

We stained the sections using both Biomeda and Santa Cruz (SC) antibodies obtaining a similar pattern. We also performed double IHC for TH-positive neurons with unrelated antibodies that were host-matched with anti-Hb (**Fig.33b**). Therefore, we can conclude that Hb-IR in the brain is conserved from mouse to human.

3.7 HB OVEREXPRESSION ON MOUSE NEUROBLASTOMA CELL LINE MN9D CHANGES THE EXPRESSION OF GENES INVOLVED IN OXYGEN HOMEOSTASIS AND MITOCHONDRIAL OXIDATIVE PHOSPHORYLATION

To address the role of Hb in DA neurons, we took advantage of the MN9D dopaminergic neuroblastoma cell lines.

To first monitor hemoglobin expression, RT-PCR was carried out on MN9D RNA demonstrating that transcripts for alpha- and beta- chains of mouse hemoglobin were indeed expressed. RNA from mouse blood was used as positive control. By using a specific antibody against mouse hemoglobin, protein expression was detected by western blot although Hb level was very low. By resorting to immunoprecipitation, a clear band of 17 kDa was specifically enriched from cell lysates (**Fig.34**).

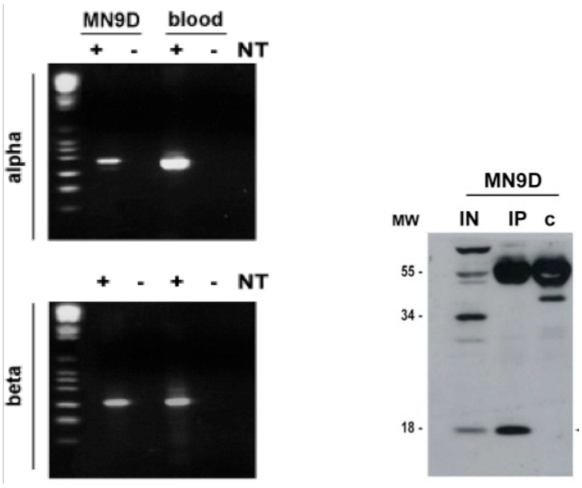


Fig.34: left: RT-PCR of alpha- and beta-chains of hemoglobin from MN9D cells and mouse blood. Alpha- and beta-globin transcripts were clearly amplified in mouse dopaminergic cell line MN9D (left). RNA extracted from blood was used as positive control (right). Amplicons identities were confirmed by sequencing.
Right: Immunoprecipitation of Hb protein from MN9D cell line. A clear band of 17 kDa was enriched from MN9D lysate after resorting to immunoprecipitation (IP) using anti-mouse Hb antibody (Cappel). Rabbit IgG were used as immunoprecipitation control (c). IN indicates input of MN9D lysate.

As Hb is likely to act as heterotetramer of two different subunits, we took advantage of pBUDCE 4.1 vector to over-express tagged alpha- and beta-chains of mouse hemoglobin in MN9D cells (see materials and methods **Fig.18**). By the use of an Internal Ribosomal Entry Site (IRES) driving the expression of eGFP, two stable polyclonal cell lines were obtained by FACS (see materials and methods **Fig.19**) and zeocyn selection: *MN9D-pBUD-β-glb-IRES-GFP, 2x-flag-α-glb* (expressing tagged alpha- and beta- chains of mouse hemoglobin together with eGFP) and *MN9D-pBUD-IRES-GFP* (expressing only eGFP). The expression of alpha- and beta- chains was analysed by qPCR and by co-immunoprecipitation experiments (**Fig.35**).

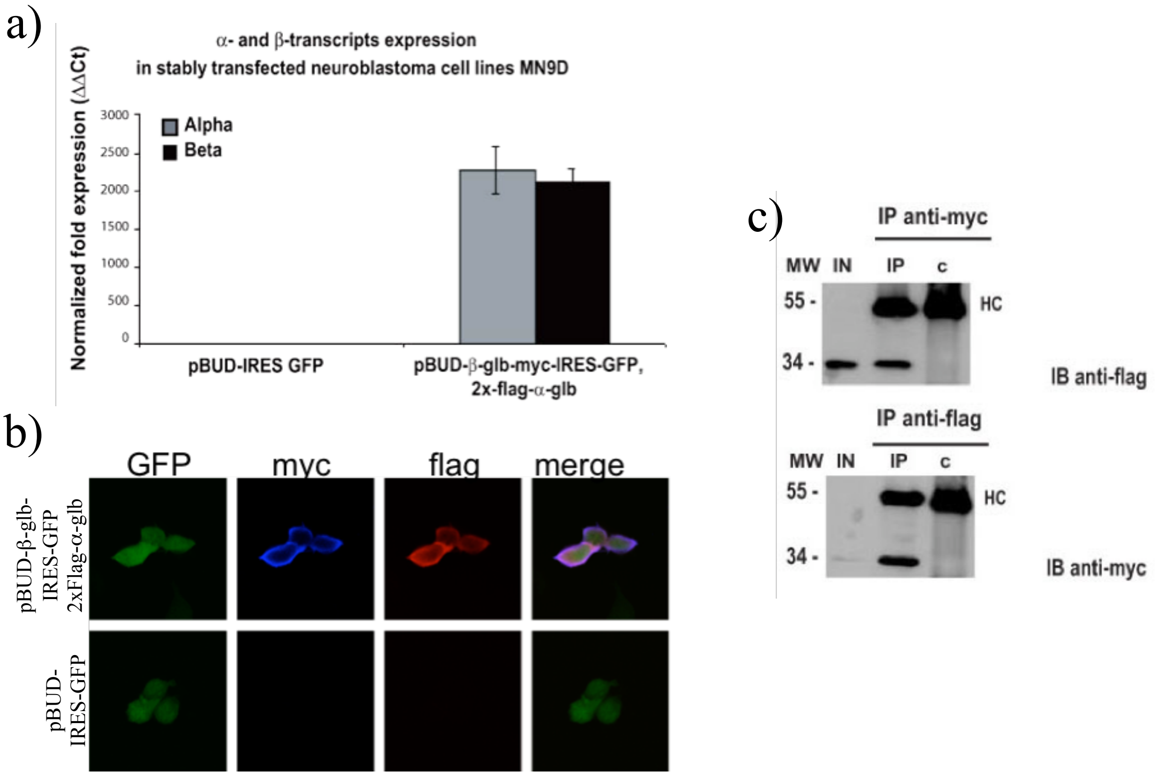


Fig. 35: a) qPCR experiments demonstrated that the levels of expression of the two Hb chains was thousands fold up-regulated in MN9D-*pBUD*-β-*glb-Myc-IRES-GFP, 2x-flag*-α-*glb* in comparison to MN9D-*pBUD-IRES-GFP*. Moreover, qPCR revealed comparable levels of alpha- and beta- chains expression in MN9D-*pBUD*-β-*glb-Myc-IRES-GFP, 2x-flag*-α-*glb* cell line.

b) A double immunofluorescence of MN9D-*pBUD*-β-*glb-Myc-IRES-GFP, 2x-flag*-α-*glb* and MN9D-*pBUD-IRES-GFP* was carried out using anti-Myc (blue) and anti-FLAG (red) antibodies. Beta-globin-myc-tag and 2x-flag-alpha-globin co-localise in the cytoplasm and, partially, in the nucleus of MN9D stable cell lines. The transfected constructs also expressed GFP (green).

c) Immunoprecipitation (IP) of beta-globin (IP anti-myc) from MN9D-*pBUD*-β- *glb-Myc-IRES-GFP, 2x-flag*-α-*glb* co-immunoprecipitated alpha-globin (immunoblot, IB, anti-flag) demonstrating that the transfected chains are able to form hetero-dimers. Reverse co-immunoprecipitation confirm this result (IP anti-Flag, IB anti-myc). Mouse IgG were use has IP control (c).

We then took advantage of the Affymetrix platform to interrogate the GeneChip® Mouse Genome 430A 2.0 Array for gene expression differences between *MN9D-pBUD-β-glb-IRES-GFP, 2x-flag-α-glb* and *MN9D-pBUD-IRES-GFP* (see Materials and methods for details). The experiment was carried out with 3 biological replicas.

A total of 4617 genes was found to be differentially expressed with a fold change higher than 1.2. 2057 genes were up-regulated in alpha- and beta- chains over-expressing clones and 2560 genes were down-regulated. qPCR confirmed microarrays data for all genes tested for validation. A complete list of genes is provided in Supplementary table 4.

By applying Ingenuity software, two major pathways resulted affected: oxygen homeostasis and oxidative phopshorylation (**Fig.36**).

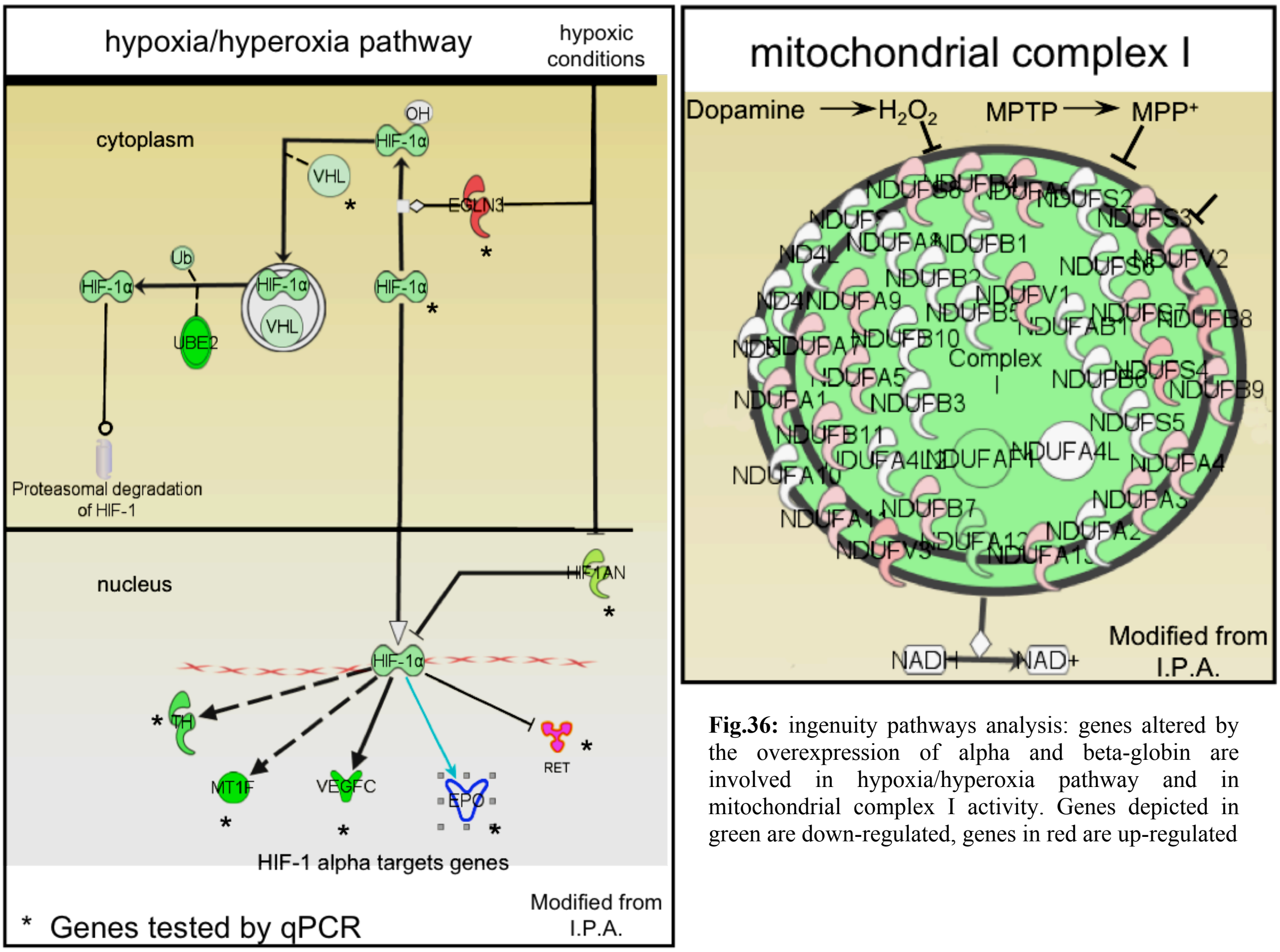


Fig.36: ingenuity pathways analysis: genes altered by the overexpression of alpha and beta-globin are involved in hypoxia/hyperoxia pathway and in mitochondrial complex I activity. Genes depicted in green are down-regulated, genes in red are up-regulated

Other changes involved genes in oxidative stress, iron metabolism as well as in NO synthesis. **Tab.3** provides a list of selected, differentially expressed genes, sorted into distinct functional categories. Arrays expression values (LogFC) and Affymetrix probes ID are indicated. When tested, qPCR data is provided, confirming the expression changes observed in the arrays.

Oxygen homeostasis mainly occurs through the activity of Hif1a, a transcription factor which expression is decreased in globin-over-expressing cells (Sharp & Bernaudin 2004). Its physiological activity is regulated by egl nine homolog 3 (Egln3), an oxygen-regulated prolyl-4-hydroxilase that mediates Hif1a hydroxylation, and by the Von Hippel-Lindau tumor suppressor gene (Vhl), a component of an E3 ubiquitin ligase complex that targets

Hif1a for degradation (Willam *et al.* 2004). The overexpression of alpha- and beta-chains decreased Vhl mRNA while strongly increased Egln3 transcripts (**Fig.37a**).

Interestingly, the expression of TH and Ret, two targets of Hif1a, was also changed (Elvidge *et al.* 2006; Kramer *et al.* 2007).

Genes involved in mitochondrial oxidative phosphorylation were increased in the stable cell line over-expressing Hb chains. 36 out of 78 genes that encode for subunits of mitochondrial complex I-V were up-regulated. This induction occurred mainly in complex I (20 genes out of 46), and to a lesser extent in complex II (1 gene), III (3 genes), IV (6 genes) and V (5 genes). Interestingly, the mitochondrial, proton carrier, Uncoupling Protein 2 (Ucp2), was also strongly up-regulated (**Fig.37b**).

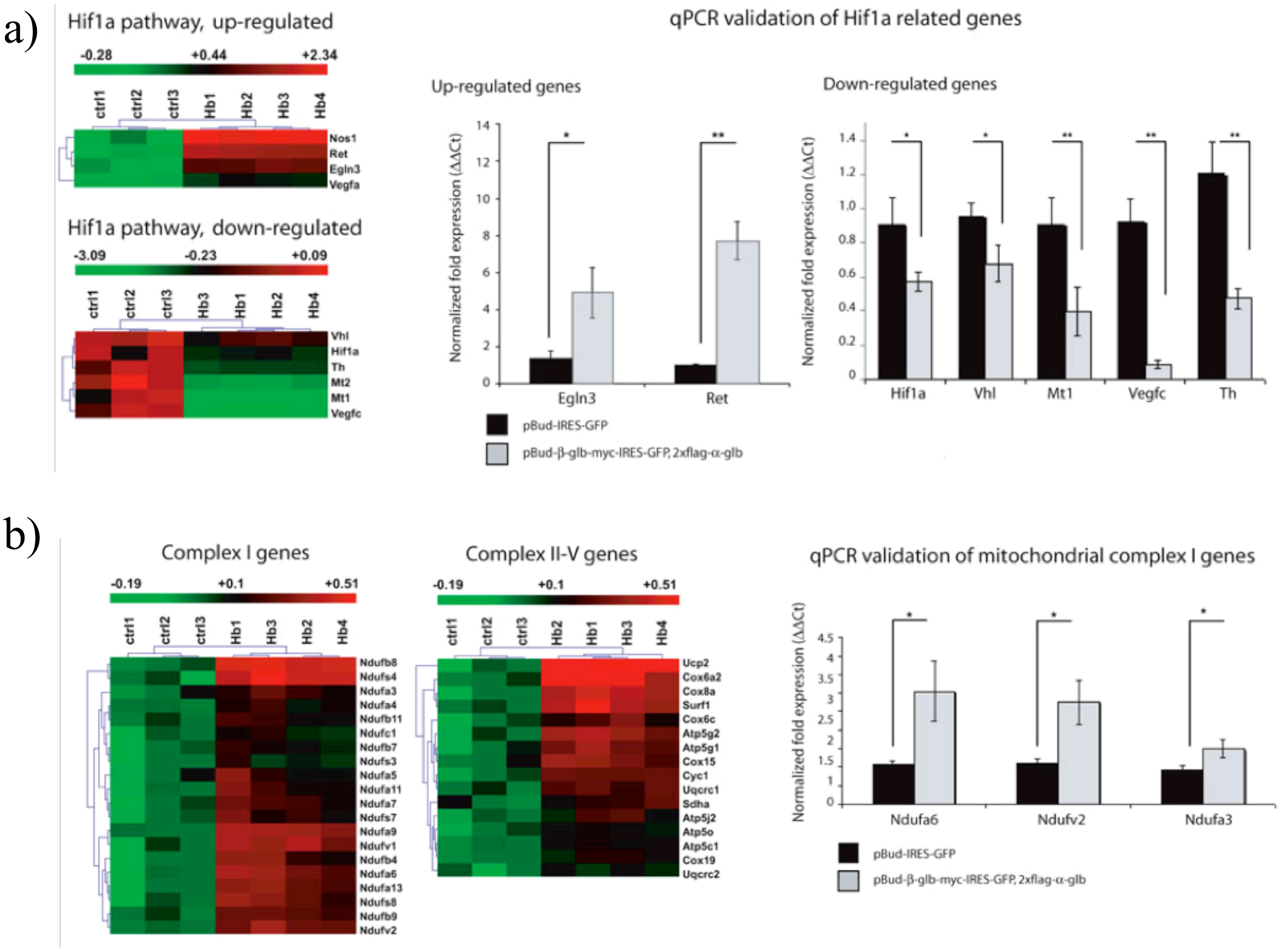


Fig. 37: a) Genes involved in Hif1a pathway are presented. Heatmaps of genes up-regulated (upper, left) and down-regulated (bottom, left) highlighted the levels of fold change; on the right, qPCR experiments of selected genes validate array results.

b) Genes involved in mitochondrial oxidative phosphorylation pathway. Heatmaps of genes belonging to complex I (left), complex II-V (center) are presented. On the right, qPCR experiments validate randomly selected genes of mitochondrial complex I. (* P-value <0,05; ** P-value <0,01)

Mitochondrial fission/fusion machinery is an unexpected pathway affected by the presence of α- and β-globin. Both genes involved in mitochondrial fission, like Drp1, and genes involved in mitochondrial fusion, like Mfn1, Mfn2 and Opa, were down-regulated. Furthermore, expression of Fis1 and March5, involved in fission process didn't change (**Fig.38**).

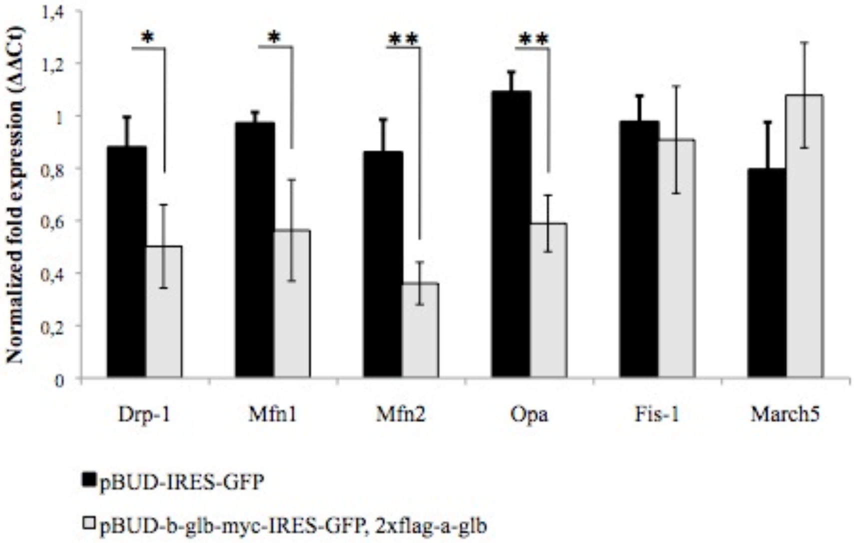


Fig.38: qPCR validation of genes involved in mitochondrial fission/fusion machinery. (* P-value <0,05; ** P-value <0,01)

Other genes involved in iron metabolism like hemocromatosis, hemocromatosis type2 (Hfe, Hfe2), ferritin light chain 1 (Ftl1), ferroportin 1 (Fpn1) and trasferrin receptor 2 (Tfr2) were also tested by qPCR but their expression didn't change significatively.

Finally, genes well known as detoxifying agents from cellular free radicals as superoxide dismutase 2, peroxiredoxin 5, Prdx5, glutathione peroxidase 4, Gpx4, thioredoxin 2, Trn2 and thioredoxin reductase 2, Txnrd2 were also up-regulated (**Tab.3**).

Importantly, nitric oxide synthase 1, neuronal, Nos1 was induced in alpha- and beta-globin over-expressing cells.

Tab.3

Gene symbol	Gene description	Affymetrix probes ID (mouse 430A 2.0)	Array (LogFC)	qPCR(ΔΔCt)
HIF-1 alpha pathway				
Egln3	EGL nine homolog 3 (C. elegans)	1418648_at	+1.05	+1.71
Hif1a	hypoxia inducible factor 1, alpha subunit	1448183_a_at	-0.39	-1.00
Mt2	metallothionein 2	1428942_at	-1.63	-1.36
Nos1	nitric oxide synthase 1, neuronal	1438483_at	+2,31	+3.47
Mt1	metallothionein 1	1422557_s_at	-2.09	
Ret	ret proto-oncogene	1421359_at	+1.63	+2.95
Th	tyrosine hydroxylase	1420546_at	-0.70	-0.79
Vegfa	vascular endothelial growth factor A	1420909_at	+0.39	
Vegfc	vascular endothelial growth factor C	1419417_at	-2.82	-3.64
Vhl	von Hippel-Lindau syndrome	1421071_at	-0.19	-0.58
Oxidative Phosphorilation				
Complex I				
Ndufa3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3	1428464_at	+0.15	+0.58
Ndufa4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	1424085_at	+0.13	
Ndufa5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5	1417285_a_at	+0.16	
Ndufa6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6	1448427_at	+0.35	+1.61
Ndufa7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7	1428360_x_at	+0.22	
Ndufa9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	1416663_at	+0.34	
Ndufa11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11	1429708_at	+0.23	
Ndufa13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	1430713_s_at	+0.32	
Ndufb4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4	1428076_s_at	+0.27	
Ndufb7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 7	1416417_a_at	+0.14	
Ndufb8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	1448198_a_at	+0.45	
Ndufb9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 9	1436803_a_at	+0.21	
Ndufb11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 11	1455911_x_at	+0.14	
Ndufc1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1	1448284_a_at	+0.14	
Ndufs3	NADH dehydrogenase (ubiquinone) Fe-S protein 3	1423737_at	+0.11	
Ndufs4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	1418117_at	+0.46	
Ndufs7	NADH dehydrogenase (ubiquinone) Fe-S protein 7	1451312_at	+0.22	
Ndufs8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	1434579_x_at	+0.31	
Ndufv1	NADH dehydrogenase (ubiquinone) flavoprotein 1	1415966_a_at	+0.38	

Ndufv2	NADH dehydrogenase (ubiquinone) flavoprotein 2	1428179_at	+0.25	+1.46
Complex II				
Sdha	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	1426689_s_at	+0.14	
Complex III				
Cyc1	cytochrome c-1	1416604_at	+0.25	
Uqcrc1	ubiquinol-cytochrome c reductase core protein 1	1428782_a_at	+0.20	
Uqcrc2	ubiquinol-cytochrome c reductase core protein 2	1428631_a_at	+0.10	
Complex IV				
Cox6a2	cytochrome c oxidase, subunit VI a, polypeptide 2	1417607_at	+0.48	
Cox6c	cytochrome c oxidase, subunit VIc	1434491_a_at	+0.24	
Cox8a	cytochrome c oxidase, subunit VIIIa	1416112_at	+0.41	
Cox15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	1452146_a_at	+0.27	
Cox19	COX19 cytochrome c oxidase assembly homolog (S. cerevisiae)	1434923_at	+0.12	
Surf1	surfeit gene 1	1450561_a_at	+0.39	
Complex V				
Atp5o	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	1437164_x_at	+0.16	
Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	1416058_s_at	+0.12	
Atp5j2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	1416269_at	+0.15	
Atp5g2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	1415980_at	+0.33	
Atp5g1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	1416020_a_at	+0.27	
Proton Pump				
Ucp2	uncoupling protein 2 (mitochondrial, proton carrier)	1448188_at	+0.82	
Detoxifying agents				
Sod2	superoxide dismutase 2, mitochondrial	1448610_a_at	+0.30	
Prdx5	peroxiredoxin 5	1416381_a_at	+0.39	
Gpx4	glutathione peroxidase 4	1456193_x_at	+0.50	
Txn2	thioredoxin 2	1452782_a_at	+0.25	
Txnrd2	thioredoxin reductase 2	1449097_at	+0.16	
Iron metabolism				
Fth1	ferritin heavy chain 1	1448771_a_at	+0.39	+0.89
Tfrc	transferrin receptor	1422967_a_at	-0.38	-0.21
Nitric oxide metabolism				
Nos1	nitric oxide synthase 1, neuronal	1438483_at	+2.31	+3.47

4. DISCUSSION

The first descriptions of globins in the nervous tissue date back to the 19th century. More recently, hemoglobin and globin-like molecules have been detected in neurons of various invertebrates (Vandergon 1998). In the bivalve mollusc *Tellina alternate*, neural excitability is sustained as long as oxygen can be delivered by a neural globin (Kraus & Colacino 1986). In Aplysia, a gastropod mollusc, the firing activity of the neural ganglia is proportional to the degree of oxygenation of the neural globin. Natural variation in a neural globin in *Caenorhabditis elegans* strains has been linked to changes in electrophysiological responses as well as in sensory behaviours (McGrath *et al.* 2009).

Recently, neuroglobin has been identified in mammalian brains where it is probably involved in the hypoxia response (Y. Sun 2001; Y. Sun 2003; Burmester 2004).

Here we show that alpha- and beta- chains transcripts as well as Hb-IR are present in a subpopulation of DA neurons, cortical and hippocampal astrocytes as well as in all mature oligodendrocytes.

Significantly, here we also proved the expression of hemoglobin in A9 DA neurons of human *post mortem* brain. The selective expression of Hb in the neuronal site of typical degeneration in PD may suggest its active role in the disease although it is still unclear whether as a neuroprotective or toxic molecule.

The establishment of a series of transgenic mice with cell type-specific globin gene knock out in DA neurons as well as in astrocytes and oligodendrocytes will provide an essential tool to unveil hemoglobin function in the brain, but unfortunatelly it is of note that to our knowledge no *loxP* mouse line for globin genes is currently available

4.1 ALPHA- AND BETA- GLOBIN EXPRESSION IN DA NEURONS OF *substantia nigra*

We observed the expression of globin transcripts in DA cells using four different approaches: cDNA microarrays, nanoCAGE, RT-PCR and *in situ* hybridization. Furthermore, we took advantage of two different methods to isolate a pure population of DA neurons: LCM and FACS.

Interestingly, when analyzing Hb-IR we found that Hb protein expression does not fully overlap with transcript distribution: the large majority of A10 DA cells and a small number of A9 neurons showed mRNA expression but not Hb-IR. There were several supporting evidences of the specificity of the Hb-IR staining including the use of two anti-Hb antibodies raised in different hosts, competition experiments, reproducible patterns in different mouse strains as well as in rat and human. There are thus at least three potential explanations for this discrepancy: the level of Hb expression in those DA cells is lower and below antibody sensitivity; antibody staining in different cells depends on the vagaries of fixation; hemoglobin protein expression may be regulated at post-transcriptional level. Interestingly, our *in situ* hybridization data may suggest the expression of mRNA for globin chains in hippocampal neurons. When we profiled the gene expression of hippocampal GABAergic interneurons from GAD-67-GFP mice and pyramidal cells, we indeed detected alpha- and beta- chains transcripts in both cell types (*data not shown*). However, no Hb-IR was evident with both antibodies. Future experiments will be needed to address this issue. It must be noted that Hb-IR was localized both in the cytoplasm and in the nucleus. This pattern was first described for cytoglobin although its significance is still unknown (Geuens *et al.* 2003).

4.2 ALPHA- AND BETA- GLOBIN EXPRESSION IN HIPPOCAMPAL AND CORTICAL ASTROCYTES AND IN OLYGODENDROCYTES

Globin RNAs and protein expression overlap in hippocampal and cortical astrocytes as well as in almost all mature oligodendrocytes. Globin mRNAs have been previously detected as differentially expressed between acutely purified and cultured oligodendrocytes (Dugas *et al.* 2006) and during regeneration of the sciatic nerve (Setton-Avruj *et al.* 2007). Here we observed globin staining in the oligodendrocytes of all the brain regions including striatum, corpus callosum and medulla oblongata.

In the adult brain, no NG2-positive cells were Hb-IR thus Hb expression seems restricted to mature oligodendrocytes, but we found Hb-positive cells in perinatal pups with a very specific morphology resembling oligodendrocyte precursors (OLP) (Nishiyama *et al.* 2009). These cells have long and thin processes in p0 midbrain and a more “bushy” shape at p6, with a higher number of short processes (**Fig.39**). We performed a double IHC with anti A2B5 antibody, marker for OLP, and we found that Hb positive cells were negative for A2B5 staining. Further studies have to be performed to analyze if these cells are OLP and at what maturation state they start to express Hb.

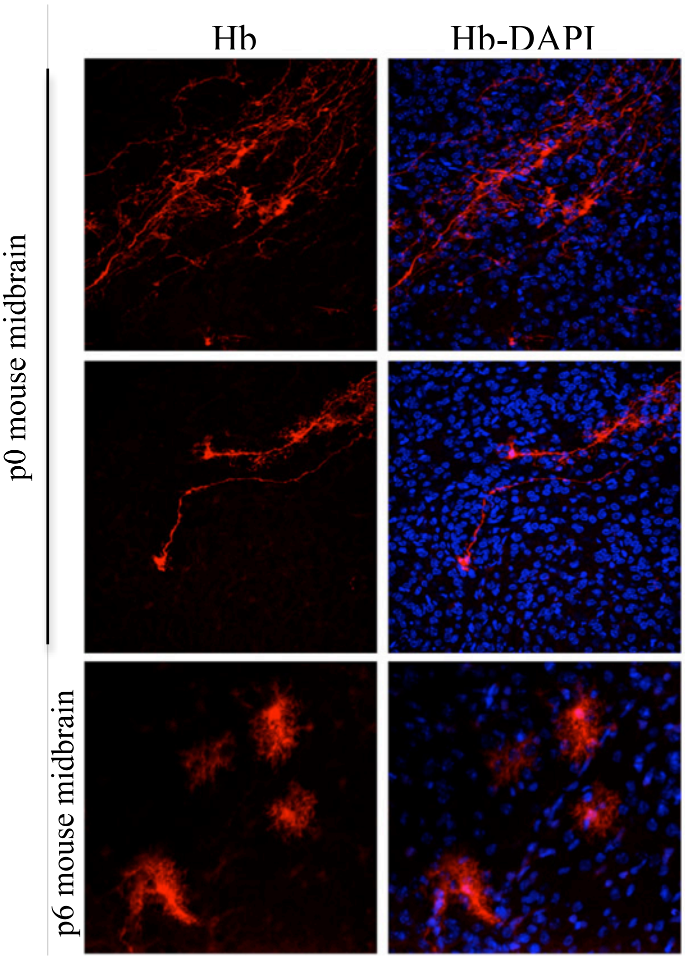


Fig.39 IHC with anti-Hb un p0 and p6 mouse brains. Antibody anti-Hb decorates a population of cells whose morphology resembles that of OLP.

4.3 HYPOTHESIS ON THE ROLE OF ALPHA- AND BETA-GLOBIN IN DA NEURONS

Although Hb function in the brain remains to be investigated *in vivo*, here we have provided some interesting cues using MN9D cells, mouse dopaminergic neuroblastoma which represent a well-accepted *in vitr*o model to study dopaminergic cell physiology and dysfunction (H. K. Choi *et al.* 1991; W. S. Choi *et al.* 1999).

We created two stable cell lines over-expressing or alpha- and beta-globin or the corresponding empty vector and we analyzed the differentially expressed genes between the two cell lines.

We found that several pathways were affected by the presence of alpha- and beta-globin and we decided to focus on three main groups of genes involved in hypoxia/hyperoxia mechanism, mitochondria complex I activity and free radical detoxification. In this choice we took in consideration that mitochondrial oxidative phosphorylation, oxidative stress, iron deposits and NO metabolism are all important components of PD pathogenesis (C. Y. Chung *et al.* 2005; Berg & Hochstrasser 2006).

Hypoxia/hyperoxia pathway

By carrying out a gene expression analysis of MN9D stably transfected with alpha- and beta-chains we found that Hb expression acts on the main elements of oxygen homeostasis. This was not surprising since Hb may act as an oxygen storage and transport molecule. Nerve tissue in vertebrates has a high-energy demand, mainly used for maintaining ion gradients for action potentials and for transport of molecules throughout the nerve fibre. It is well known that hyperoxia and hypoxia could be both detrimental to cellular physiology and, while hyperoxia may be linked to DNA damage and premature aging (Diringer 2008), hypoxia occurs in ischemia and other pathological conditions, such as epilepsy (Sanchez *et al.* 2001) or parkinsonism (Swaminath *et al.* 2006). Moreover, genes involved in familiar cases of Parkinson's disease have been related to hypoxia signalling (Vasseur *et al.* 2009) and brief ischemic–anoxic insult in a mouse pups induces apoptosis in DA neurons of the *substantia nigra* (T F Oo *et al.* 1995; R E Burke *et al.* 1992), suggesting a broader role of this pathway in neurodegenerative diseases.

Brain hemoglobin may then act as storage of oxygen to provide a homeostatic mechanism in anoxic conditions. This is especially important for A9 DA neurons that have an elevated metabolism with a high requirement for energy production.

Extending this model to the other Hb-expressing cells in the brain, the widespread distribution of oligodendrocytes as well as their localization adjacent to neuronal cells may provide a net of oxygen-storage cells. In hypoxia conditions, oxygen may then be released and provide to the neighbouring neurons some highly needed relief for the maintenance of the aerobic metabolism.

Mitochondria complex I activity and biogenesis

It is well known that oxygen tension regulates mitochondrial DNA-encoded Complex I gene expression (Piruat & López-Barneo 2005) and high oxygen concentration induces mitochondrial biogenesis (Gutsaeva *et al.* 2006). It's to be noted that deficits in the subunits and activity of mitochondrial complex I of the electron transport chain have been consistently detected in the SN and blood platelets of PD patients (Mann *et al.* 1992). Furthermore, in PD animal models administration of the toxic metabolite MPP^+ as well as the pesticides rotenone and paraquat cause dopaminergic degeneration in part by mitochondrial complex I inhibition.

Interestingly, the level of transcripts of genes involved in mitochondrial oxidative phosphorylation correlates directly with susceptibility of A9 and A10 dopaminergic neurons to complex I toxins (James G Greene *et al.* 2005). According to one hypothesis, SN dopamine neurons may be normally closer to their maximal metabolic capacity, giving them less capability to respond to a metabolic insult. It is possible that neurons in the VTA may have compensatory mechanisms available that allow them to recover more quickly or maintain energy metabolism despite inhibition of complex I. Higher metabolic rate may cause greater levels of oxidative stress in SN neurons, making them more vulnerable to complex I inhibition.

36 out of 78 genes that encode for subunits of complex I-V were induced in the stable cell lines over-expressing alpha- and beta-chains of Hb. Although the fold change of most of respiratory transcripts did not exceed 2-fold, the observation that the major part (46%) of mitochondrial subunit transcripts share the same trend highlighted the biological significance of these findings. Moreover, It is becoming clear, especially for mitochondrial oxidative phosphorylation genes, that the biological outcome of gene expression changes is not necessarily dependent on the level of differential expression (Preston *et al.* 2008). Interestingly, rotenone application to undifferentiated SK-N-MC neuroblastoma cells *in vitro* induced the expression of a set of complex I subunits as a compensatory response that largely overlap with Hb-dependent gene expression. One challenging hypothesis could be that Hb-mediated oxygen availability may regulate mitochondrial oxidative phosphorylation and cellular metabolism. Further analysis will elucidate if the eventual role of hemoglobin in this pathway is protective or toxic.

Regulation of mitochondria fusion/fission machinery is another important mechanism linked to Parkinson's disease. Genes whose mutations are implicated in monogenic forms of PD are closely related to mitochondrial dynamics.

Overexpression of the mitochondrial fission protein Drp1 or loss-of-function mutations affecting the mitochondrial fusion-promoting factors OPA1 and Mfn2 rescued mitochondrial abnormalities and other defects present in the absence of PINK1 or Parkin (Poole *et al.* 2008; Y. Yang *et al.* 2008)(Deng *et al.* 2008).

Even though the precise regulation and role of fusion/fission in neurodegeneration is still unknown, these results show that genetic manipulations that shift the net mitochondrial dynamics toward fission and inhibiting fusion might be protective.

In our *in vitro* model, overexpression of alpha- and beta-globin lead to a downregulation of all genes analyzed involved in fusion process (Mfn1, Mfn2, Opa1) and 1 out of 3 fission-promoting genes (Drp1). Preliminary results on mitochondrial morphology in globin-overexpressing cells seem not to show any changes in fission/fusion machinery, however it would be very interesting to further investigate possible roles of hemoglobin in this complex mechanism.

Free radical detoxification

High mitochondrial activity is usually linked to oxidative stress. This may be especially detrimental for A9 neurons since they are normally under intense oxidative stress due to the production of hydrogen peroxide via autoxidation and/or MAO-mediated deamination of dopamine and the subsequent reaction of accessible ferrous iron to generate highly toxic hydroxyl radicals (Youdim & Lavie 1994). In this respect, it is interesting that an animal model of nutritional iron deficiency shows a very specific reduction of central dopamine neurotransmission, linking iron metabolism regulation to neurodegeneration (Youdim *et al.* 1989). Hemoglobin may indeed play homeostatic roles both as an antioxidant and as a regulator of iron metabolism. In rat mesangial cells Hb carries out an antioxidant function (Nishi *et al.* 2008). In our gene expression data, this ability may be mediated by components of the well-known detoxifying agents from cellular free radicals like superoxide dismutase 2 (SOD2, up-regulated in alpha- and beta-overexpressing cells with a LogFC +0,30), peroxiredoxin 5 (Prdx5, +0,39), glutathione peroxidase 4 (Gpx4, +0,5), thioredoxin 2 (Txn2, +0,25), thioredoxin reductase 2 (Txnrd2, +0,16).

Finally, Hemoglobin and invertebrate globins have been also shown acting as NO-detoxifying agents carrying a NO reductase activity (Z. Huang *et al.* 2005). Interestingly, nitric oxide synthase 1, neuronal, Nos1 was induced in alpha- and beta-globin overexpressing cells.

4.4 A SPECULATIVE LINK BETWEEN A PROTECTIVE ROLE OF ERYTHROPOIETIN IN PD AND HEMOGLOBIN EXPRESSION IN DA NEURONS

In the last 30-40 years an increasing interest is focusing on the role of erythropoietin (EPO) as a neuroprotectant.

EPO is produced mainly by fetal liver and adult kidney, it binds to its receptor (EPOr) expressed on erythroid precursor cells in bone marrow and stimulates erythropoiesis inhibiting apoptosis of erythroid precursor cells and supporting their proliferation and differentiation into mature red blood cells.

However, EPO and EpoR are also expressed in the nervous system by neurons, glial cells and endothelial cells (Csete *et al.* 2004). Several evidences show that EPO and EPOr have important roles in neurodevelopment, in neuroprotective mechanisms following different types of stress (ischemic, hypoxic, metabolic, neurotoxic and excitotoxic) as well as in modulation of neurotransmission (Sermin Genc *et al.* 2004).

Recent studies suggest that EPO is an effective neuroprotective agent for dopaminergic neurons and may be useful in reversing the behavioral deficits associated with PD (S Genc *et al.* 2001; Xue *et al.* 2007; Signore *et al.* 2006). Some mechanisms, such as direct neuroprotection, anti-inflammatory, anti-apoptotic, anti-oxidant effects, stimulation of neurogenesis, and modulation of neurotransmission have been suggested as putative bases underlying the beneficial effects of EPO (Sermin Genc *et al.* 2004).

Here, we showed that hemoglobin is specifically expressed in DA neurons of SN as well as in astrocytes of hippocampus and cortex and in oligodendrocytes.

Even though there are no evidences of an EPO direct regulation of alpha- and beta-globin mRNA expression, this hormone induces, in erythrocyte lineage, the phosphorylation and activation of GATA-1, one of the main transcription factors involved in hemoglobin transcription (W. Zhao *et al.* 2006).

Moreover, Schelshorn *et al.* show that neuronal hemoglobin is up-regulated by injection or transgenic overexpression of erythropoietin and is accompanied by enhanced brain oxygenation (Schelshorn *et al.* 2008).

Although several experiments will be needed to explore this possibility, it will be very interesting to investigate an hypothetical novel mechanism for the neuroprotective action of erythropoietin through induction of hemoglobin expression.

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Affymetrix probe ID	Gene name	Gene symbol	LogFC	adj.P.Val
1452757_s_at	hemoglobin alpha, adult chain 1	Hba-a1	7.152	1.54E-09
1428361_x_at	hemoglobin alpha, adult chain 1	Hba-a1	5.843	3.12E-11
1417714_x_at	hemoglobin alpha, adult chain 1	Hba-a1	5.163	9.81E-10
1423824_at	G protein-coupled receptor 177	Gpr177	3.728	1.69E-09
1456250_x_at	transforming growth factor, beta induced	Tgfbi	3.42	4.43E-09
1424525_at	gastrin releasing peptide	Grp	3.294	2.99E-07
1419063_at	UDP galactosyltransferase 8A	Ugt8a	3.28	1.45E-08
1416239_at	argininosuccinate synthetase 1	Ass1	3.15	1.54E-09
1437434_a_at	G protein-coupled receptor 177	Gpr177	3.073	4.32E-08
1423691_x_at	keratin 8	Krt8	3.01	2.80E-09
1448123_s_at	transforming growth factor, beta induced	Tgfbi	2.977	2.50E-09
1418910_at	bone morphogenetic protein 7	Bmp7	2.953	4.95E-08
1420797_at	otogelin	Otog	2.922	3.64E-09
1415871_at	transforming growth factor, beta induced	Tgfbi	2.824	4.95E-08
1420647_a_at	keratin 8	Krt8	2.77	4.98E-09
1418476_at	cytokine receptor-like factor 1	Crlf1	2.746	9.55E-09
1448194_a_at	H19 fetal liver mRNA	H19	2.724	1.44E-08
1435989_x_at	keratin 8	Krt8	2.672	1.25E-09
1421180_at	limb expression 1 homolog (chicken)	Lix1	2.655	9.81E-10
1432410_a_at	bone morphogenetic protein 7	Bmp7	2.63	7.28E-09
1451268_at	translocation associated membrane protein 1-like 1	Tram1l1	2.561	7.28E-09
1448392_at	secreted acidic cysteine rich glycoprotein	Sparc	2.557	1.33E-07
1455626_at	homeo box A9	Hoxa9	2.475	6.41E-08
1420360_at	dickkopf homolog 1 (Xenopus laevis)	Dkk1	2.327	1.25E-09
1438483_at	nitric oxide synthase 1, neuronal	Nos1	2.311	2.35E-07
1416589_at	secreted acidic cysteine rich glycoprotein	Sparc	2.302	2.80E-09
1451348_at	DEP domain containing 6	Depdc6	2.3	9.81E-10
1452107_s_at	NA	NA	2.298	3.23E-09
1424797_a_at	paired-like homeodomain transcription factor 2	Pitx2	2.262	2.12E-07
1434745_at	cyclin D2	Ccnd2	2.256	3.01E-07
1423825_at	G protein-coupled receptor 177	Gpr177	2.141	3.00E-08
1437463_x_at	transforming growth factor, beta induced	Tgfbi	2.134	1.47E-06
1416168_at	serine (or cysteine) peptidase inhibitor, clade F, member 1	Serpinf1	2.128	1.45E-08
1448254_at	pleiotrophin	Ptn	2.115	1.15E-07
1422476_at	interferon gamma inducible protein 30	Ifi30	2.036	1.25E-09
1423611_at	alkaline phosphatase, liver/bone/kidney	Alpl	1.998	7.66E-08
1416122_at	cyclin D2	Ccnd2	1.992	1.41E-08
1415832_at	angiotensin II receptor, type 2	Agtr2	1.986	2.66E-07
1423135_at	thymus cell antigen 1, theta	Thy1	1.941	3.44E-08
1425528_at	paired related homeobox 1	Prrx1	1.935	1.65E-08
1452106_at	nephronectin	Npnt	1.929	7.66E-08
1435106_at	LIM and calponin homology domains 1	Limch1	1.908	5.67E-08
1449632_s_at	FK506 binding protein 10	Fkbp10	1.86	5.90E-08
1418507_s_at	suppressor of cytokine signaling 2	Socs2	1.855	1.12E-08
1426243_at	cystathionase (cystathionine gamma-lyase)	Cth	1.848	5.42E-09
1436363_a_at	nuclear factor I/X	Nfix	1.772	1.56E-08
1435479_at	NA	NA	1.77	9.63E-09
1427127_x_at	heat shock protein 1B	Hspa1b	1.756	9.11E-08
1455531_at	major facilitator superfamily domain containing 4	Mfsd4	1.751	1.25E-05
1451204_at	scavenger receptor class A, member 5 (putative)	Scara5	1.726	1.45E-08
1427537_at	epiplakin 1	Eppk1	1.708	1.43E-07
1448201_at	secreted frizzled-related protein 2	Sfrp2	1.69	1.90E-06

1430127_a_at	cyclin D2	Ccnd2	1.69	1.85E-06
1427320_at	coatomer protein complex, subunit gamma 2, antisense 2	Copg2as2	1.672	3.89E-07
1416832_at	solute carrier family 39 (metal ion transporter), member 8	Slc39a8	1.661	2.99E-07
1449109_at	suppressor of cytokine signaling 2	Socs2	1.652	2.38E-07
1452217_at	AHNAK nucleoprotein (desmoyokin)	Ahnak	1.64	8.92E-07
1451297_at	gulonolactone (L-) oxidase	Gulo	1.637	1.54E-06
1421359_at	ret proto-oncogene	Ret	1.635	2.59E-07
1455956_x_at	cyclin D2	Ccnd2	1.631	2.23E-07
1448519_at	TEA domain family member 2	Tead2	1.624	3.07E-07
1426561_a_at	nephronectin	Npnt	1.622	5.75E-07
1435321_at	LIM and calponin homology domains 1	Limch1	1.609	3.41E-08
1431530_a_at	tetraspanin 5	Tspan5	1.609	7.98E-07
1448229_s_at	cyclin D2	Ccnd2	1.589	2.45E-07
1436448_a_at	prostaglandin-endoperoxide synthase 1	Ptgs1	1.583	2.23E-07
1418268_at	5-hydroxytryptamine (serotonin) receptor 3A	Htr3a	1.579	1.15E-07
1427123_s_at	coatomer protein complex, subunit gamma 2, antisense 2	Copg2as2	1.578	3.32E-06
1418497_at	fibroblast growth factor 13	Fgf13	1.575	2.48E-07
1448926_at	homeo box A5	Hoxa5	1.574	1.44E-06
1454903_at	nerve growth factor receptor (TNFR superfamily, member 16)	Ngfr	1.57	1.37E-06
1448700_at	G0/G1 switch gene 2	G0s2	1.566	1.14E-06
1420362_a_at	BCL2-interacting killer	Bik	1.563	4.06E-07
1427100_at	meteorin, glial cell differentiation regulator	Metrn	1.56	1.69E-08
1450297_at	interleukin 6	Il6	1.551	7.22E-08
1423493_a_at	nuclear factor I/X	Nfix	1.544	2.21E-06
1422760_at	peptidyl arginine deiminase, type IV	Padi4	1.539	1.24E-07
1436767_at	LUC7-like 2 (S. cerevisiae)	Luc7l2	1.524	5.30E-05
1427126_at	heat shock protein 1B	Hspa1b	1.523	9.87E-07
1425527_at	paired related homeobox 1	Prrx1	1.517	1.09E-06
1436021_at	major facilitator superfamily domain containing 4	Mfsd4	1.513	9.55E-05
1435162_at	protein kinase, cGMP-dependent, type II	Prkg2	1.512	1.14E-06
1425458_a_at	growth factor receptor bound protein 10	Grb10	1.511	3.25E-07
1423414_at	prostaglandin-endoperoxide synthase 1	Ptgs1	1.508	1.33E-08
1434777_at	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	Mycl1	1.501	2.08E-06
1417741_at	liver glycogen phosphorylase	Pygl	1.471	5.67E-08
1434553_at	transmembrane protein 56	Tmem56	1.467	4.92E-08
1450769_s_at	StAR-related lipid transfer (START) domain containing 5	Stard5	1.467	2.15E-07
1451461_a_at	aldolase C, fructose-bisphosphate	Aldoc	1.46	8.16E-08
1449151_at	PCTAIRE-motif protein kinase 3	Pctk3	1.459	2.35E-07
1422949_at	nitric oxide synthase 1, neuronal	Nos1	1.448	7.82E-07
1452318_a_at	heat shock protein 1B	Hspa1b	1.433	2.43E-06
1424292_at	DEP domain containing 1a	Depdc1a	1.429	3.29E-06
1417065_at	early growth response 1	Egr1	1.428	1.08E-07
1438610_a_at	crystallin, zeta	Cryz	1.424	1.31E-07
1419669_at	proteinase 3	Prtn3	1.409	1.58E-06
1430128_a_at	receptor accessory protein 6	Reep6	1.405	2.73E-07
1436364_x_at	nuclear factor I/X	Nfix	1.391	9.85E-07
1419248_at	regulator of G-protein signaling 2	Rgs2	1.384	3.60E-08
1419247_at	regulator of G-protein signaling 2	Rgs2	1.383	2.79E-07
1426640_s_at	tribbles homolog 2 (Drosophila)	Trib2	1.37	9.11E-08
1419033_at	poly (A) polymerase alpha	Papola	1.346	2.38E-05

1450644_at	zinc finger protein 36, C3H type-like 1	Zfp36l1	1.334	1.89E-05
1453571_at	DEP domain containing 6	Depdc6	1.329	6.01E-07
1436922_at	peptidylprolyl isomerase (cyclophilin) like 5	Ppil5	1.323	6.51E-07
1415951_at	FK506 binding protein 10	Fkbp10	1.317	2.95E-07
1435495_at	adenosine A1 receptor	Adora1	1.313	1.16E-05
1460343_at	neuralized-like homolog (Drosophila)	Neurl	1.275	2.48E-07
1417707_at	NEDD4 binding protein 2-like 1	N4bp2l1	1.273	3.53E-08
1424704_at	runt related transcription factor 2	Runx2	1.271	1.40E-05
1448609_at	thiosulfate sulfurtransferase, mitochondrial	Tst	1.267	6.50E-06
1422088_at	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	Mycl1	1.261	9.85E-08
1432129_a_at	paired related homeobox 1	Prrx1	1.256	1.89E-06
1425526_a_at	paired related homeobox 1	Prrx1	1.254	1.95E-06
1450044_at	frizzled homolog 7 (Drosophila)	Fzd7	1.243	3.53E-08
1436766_at	LUC7-like 2 (S. cerevisiae)	Luc7l2	1.226	4.73E-05
1423266_at	RIKEN cDNA 2810405K02 gene	2810405K02Rik	1.221	4.66E-05
1455899_x_at	suppressor of cytokine signaling 3	Socs3	1.22	2.43E-06
1422072_a_at	glutathione S-transferase, mu 6	Gstm6	1.212	2.66E-07
1424544_at	nuclear receptor binding protein 2	Nrbp2	1.208	4.99E-05
1426641_at	tribbles homolog 2 (Drosophila)	Trib2	1.194	1.24E-05
1425753_a_at	uracil DNA glycosylase	Ung	1.188	1.21E-07
1450177_at	nerve growth factor receptor (TNFR superfamily, member 16)	Ngfr	1.185	4.33E-08
1451191_at	cellular retinoic acid binding protein II	Crabp2	1.174	7.22E-08
1419420_at	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	St6galnac5	1.174	2.43E-05
1418175_at	vitamin D receptor	Vdr	1.173	8.88E-07
1420762_a_at	Y box protein 2	Ybx2	1.165	1.11E-06
1427286_at	DNA segment, Chr 11, Brigham & Women's Genetics 0517 expressed	D11Bwg0517e	1.157	3.33E-06
1422545_at	T-box 2	Tbx2	1.153	6.25E-06
1419148_at	advillin	Avil	1.15	1.72E-06
1438948_x_at	translocator protein	Tspo	1.15	1.93E-07
1417179_at	tetraspanin 5	Tspan5	1.15	1.90E-06
1431170_at	similar to Ephrin A3	LOC100046031	1.143	4.21E-08
1419687_at	MACRO domain containing 1	Macrod1	1.129	4.68E-07
1424130_a_at	polymerase I and transcript release factor	Ptrf	1.127	1.15E-07
1431856_a_at	C1q and tumor necrosis factor related protein 6	C1qtnf6	1.12	1.67E-06
1424900_at	solute carrier family 29 (nucleoside transporters), member 4	Slc29a4	1.115	5.53E-06
1419032_at	poly (A) polymerase alpha	Papola	1.113	1.44E-05
1449956_at	protein kinase C, epsilon	Prkce	1.108	3.56E-07
1448482_at	solute carrier family 39 (metal ion transporter), member 8	Slc39a8	1.108	3.20E-06
1456005_a_at	BCL2-like 11 (apoptosis facilitator)	Bcl2l11	1.105	2.79E-05
1419414_at	guanine nucleotide binding protein (G protein), gamma 13	Gng13	1.101	3.97E-05
1455422_x_at	septin 4	Sept4	1.099	6.98E-06
1416700_at	Rho family GTPase 3	Rnd3	1.098	5.58E-06
1417408_at	coagulation factor III	F3	1.096	1.65E-07
1422839_at	neurogenin 2	Neurog2	1.094	3.82E-06
1449005_at	solute carrier family 16 (monocarboxylic acid transporters), member 3	Slc16a3	1.092	2.10E-06
1433579_at	transmembrane protein 30B	Tmem30b	1.087	1.82E-06
1415874_at	sprouty homolog 1 (Drosophila)	Spry1	1.084	9.85E-08
1421429_a_at	nephronectin	Npnt	1.072	0.000109756

1422922_at	RecQ protein-like 4	Recql4	1.069	8.39E-06
1456251_x_at	translocator protein	Tspo	1.059	7.12E-07
1421045_at	mannose receptor, C type 2	Mrc2	1.058	6.85E-06
1454783_at	interleukin 13 receptor, alpha 1	Il13ra1	1.056	2.60E-05
1418648_at	EGL nine homolog 3 (C. elegans)	Egln3	1.052	3.09E-06
1418176_at	vitamin D receptor	Vdr	1.05	4.40E-06
1428781_at	dermokine	Dmkn	1.047	4.15E-06
1416778_at	serum deprivation response	Sdpr	1.046	1.93E-07
1416695_at	translocator protein	Tspo	1.044	6.57E-08
1424378_at	low density lipoprotein receptor adaptor protein 1	Ldlrap1	1.037	6.29E-06
1424037_at	inositol 1,4,5-trisphosphate 3-kinase A	Itpka	1.034	1.14E-06
1452010_at	cholinergic receptor, nicotinic, alpha polypeptide 3	Chrna3	1.033	1.72E-06
1426560_a_at	nephronectin	Npnt	1.032	1.14E-06
1454838_s_at	expressed sequence AW548124	AW548124	1.031	6.73E-07
1424181_at	septin 6	Sept6	1.027	7.08E-07
1442028_at	beta-1,4-N-acetyl-galactosaminyl transferase 2	B4galnt2	1.022	9.64E-06
1438244_at	nuclear factor I/B	Nfib	1.02	0.000421573
1422121_at	opioid receptor, delta 1	Oprd1	1.02	0.000410012
1417933_at	insulin-like growth factor binding protein 6	Igfbp6	1.015	6.73E-07
1421022_x_at	acylphosphatase 1, erythrocyte (common) type	Acyp1	1.012	1.77E-06
1452878_at	protein kinase C, epsilon	Prkce	1.011	2.30E-06
1421992_a_at	insulin-like growth factor binding protein 4	Igfbp4	1.006	2.59E-06
1419137_at	SH3/ankyrin domain gene 3	Shank3	1.005	3.27E-06
1434437_x_at	ribonucleotide reductase M2	Rrm2	1	8.32E-06
1421863_at	vesicle-associated membrane protein 1	Vamp1	1	1.67E-05
1421991_a_at	insulin-like growth factor binding protein 4	Igfbp4	0.999	4.43E-05
1417821_at	DNA segment, Chr 17, human D6S56E 5	D17H6S56E-5	0.997	1.16E-05
1452398_at	phospholipase C, epsilon 1	Plce1	0.994	1.30E-05
1455931_at	cholinergic receptor, nicotinic, alpha polypeptide 3	Chrna3	0.993	1.65E-07
1423556_at	aldo-keto reductase family 1, member B7	Akr1b7	0.991	8.88E-07
1422087_at	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	Mycl1	0.989	1.44E-05
1450095_a_at	acylphosphatase 1, erythrocyte (common) type	Acyp1	0.988	5.12E-07
1422822_at	StAR-related lipid transfer (START) domain containing 5	Stard5	0.987	4.27E-05
1450731_s_at	tumor necrosis factor receptor superfamily, member 21	Tnfrsf21	0.986	1.57E-06
1422711_a_at	pregnancy upregulated non-ubiquitously expressed CaM kinase	Pnck	0.981	1.18E-05
1448475_at	olfactomedin-like 3	Olfml3	0.981	1.14E-06
1455642_a_at	tetraspanin 17	Tspan17	0.978	3.49E-06
1416647_at	branched chain ketoacid dehydrogenase E1, alpha polypeptide	Bckdha	0.977	1.67E-06
1416286_at	regulator of G-protein signaling 4	Rgs4	0.971	1.80E-06
1420928_at	beta galactoside alpha 2,6 sialyltransferase 1	St6gal1	0.969	1.04E-06
1422821_s_at	StAR-related lipid transfer (START) domain containing 5	Stard5	0.967	2.43E-06
1436026_at	zinc finger protein 703	Zfp703	0.967	4.03E-07
1438245_at	NA	NA	0.966	0.001303566
1416779_at	serum deprivation response	Sdpr	0.961	2.40E-06
1460411_s_at	expressed sequence AW548124	AW548124	0.96	7.35E-06
1436970_a_at	platelet derived growth factor receptor, beta polypeptide	Pdgfrb	0.96	2.83E-06
1455220_at	frequently rearranged in advanced T-cell lymphomas 2	Frat2	0.949	4.05E-06

1451978_at	lysyl oxidase-like 1	Loxl1	0.947	4.87E-06
1449335_at	tissue inhibitor of metalloproteinase 3	Timp3	0.943	0.000174785
1438169_a_at	FERM domain containing 4B	Frmd4b	0.943	4.05E-05
1456212_x_at	suppressor of cytokine signaling 3	Socs3	0.94	6.73E-05
1460324_at	DNA methyltransferase 3A	Dnmt3a	0.938	9.12E-07
1421595_at	RIKEN cDNA 9630031F12 gene	9630031F12Rik	0.937	1.81E-05
1448720_at	leucine rich repeat containing 40	Lrrc40	0.935	5.04E-06
1449202_at	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G	Sema4g	0.925	1.19E-06
1448729_a_at	septin 4	Sept4	0.923	7.15E-06
1448226_at	ribonucleotide reductase M2	Rrm2	0.922	3.49E-06
1450842_a_at	centromere protein A	Cenpa	0.922	2.82E-06
1455214_at	microphthalmia-associated transcription factor	Mitf	0.922	5.93E-06
1417034_at	trafficking protein particle complex 6A	Trappc6a	0.921	9.16E-06
1460419_a_at	protein kinase C, beta	Prkcb	0.912	4.16E-06
1427243_at	RELT-like 1	Rell1	0.911	2.12E-06
1451848_a_at	crystallin, zeta	Cryz	0.909	9.51E-07
1449056_at	RIKEN cDNA E330009J07 gene	E330009J07Rik	0.909	2.10E-06
1423756_s_at	insulin-like growth factor binding protein 4	Igfbp4	0.909	8.35E-07
1427489_at	integrin alpha 8	Itga8	0.905	9.17E-05
1455466_at	G protein-coupled receptor 133	Gpr133	0.904	0.000139767
1454737_at	dual specificity phosphatase 9	Dusp9	0.902	4.69E-07
1418301_at	interferon regulatory factor 6	Irf6	0.9	2.44E-05
1454047_a_at	RIKEN cDNA 2410017P07 gene	2410017P07Rik	0.891	1.69E-05
1419582_at	cytochrome P450, family 2, subfamily c, polypeptide 55	Cyp2c55	0.891	1.74E-05
1418184_at	centromere protein M	Cenpm	0.889	1.24E-06
1436613_at	coronin, actin binding protein 6	Coro6	0.886	7.41E-05
1417890_at	pyridoxal (pyridoxine, vitamin B6) phosphatase	Pdxp	0.881	2.65E-06
1422723_at	stimulated by retinoic acid gene 6	Stra6	0.877	3.16E-05
1416713_at	tubulin polymerization-promoting protein family member 3	Tppp3	0.876	1.09E-05
1428443_a_at	Rap1 GTPase-activating protein	Rap1gap	0.875	1.70E-06
1423757_x_at	insulin-like growth factor binding protein 4	Igfbp4	0.874	2.64E-06
1445689_at	NA	NA	0.873	0.001860808
1449876_at	protein kinase, cGMP-dependent, type I	Prkg1	0.869	1.49E-05
1434116_at	chromobox homolog 2 (Drosophila Pc class)	Cbx2	0.868	3.13E-07
1452773_at	RIKEN cDNA 5730494N06 gene	5730494N06Rik	0.864	1.82E-05
1416992_at	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	Mfng	0.862	7.59E-07
1424488_a_at	pyrophosphatase (inorganic) 2	Ppa2	0.86	3.24E-07
1416531_at	glutathione S-transferase omega 1	Gsto1	0.86	3.56E-07
1450950_at	structural maintenace of chromosomes 3	Smc3	0.86	3.33E-06
1419400_at	microsomal triglyceride transfer protein	Mttp	0.858	3.64E-06
1452359_at	RELT-like 1	Rell1	0.858	4.99E-06
1448598_at	matrix metallopeptidase 17	Mmp17	0.858	2.00E-06
1423122_at	arginine vasopressin-induced 1	Avpi1	0.857	3.20E-06
1423747_a_at	pyruvate dehydrogenase kinase, isoenzyme 1	Pdk1	0.856	4.45E-05
1460684_at	transmembrane 7 superfamily member 2	Tm7sf2	0.856	3.26E-06
1418649_at	EGL nine homolog 3 (C. elegans)	Egln3	0.854	1.39E-06
1431182_at	heat shock protein 8	Hspa8	0.854	7.12E-06
1419553_a_at	RAB geranylgeranyl transferase, b subunit	Rabggtb	0.847	2.23E-07
1417437_at	X-ray repair complementing defective repair in Chinese hamster cells 6	Xrcc6	0.847	1.24E-06
1422866_at	collagen, type XIII, alpha 1	Col13a1	0.843	5.95E-05
1415909_at	stress-induced phosphoprotein 1	Stip1	0.839	3.49E-06

1416120_at	ribonucleotide reductase M2	Rrm2	0.835	1.75E-05
1456014_s_at	tRNA phosphotransferase 1	Trpt1	0.834	2.10E-05
1424194_at	RCSD domain containing 1	Rcsd1	0.832	0.000408289
1426526_s_at	oviductal glycoprotein 1	Ovgp1	0.83	0.000598826
1451532_s_at	six transmembrane epithelial antigen of the prostate 1	Steap1	0.829	1.25E-06
1418569_at	filamin binding LIM protein 1	Fblim1	0.828	6.91E-06
1449383_at	adenylosuccinate synthetase like 1	Adssl1	0.827	1.73E-06
1448326_a_at	cellular retinoic acid binding protein I	Crabp1	0.826	4.16E-06
1427165_at	interleukin 13 receptor, alpha 1	Il13ra1	0.826	6.42E-05
1420348_at	LIM homeobox protein 5	Lhx5	0.825	0.00093407
1427004_at	F-box protein 2	Fbxo2	0.824	8.67E-06
1418711_at	platelet derived growth factor, alpha	Pdgfa	0.823	3.91E-06
1448188_at	uncoupling protein 2 (mitochondrial, proton carrier)	Ucp2	0.821	3.65E-06
1422530_at	peripherin	Prph	0.82	5.07E-06
1416683_at	plexin B2	Plxnb2	0.817	2.39E-06
1448417_at	ninjurin 1	Ninj1	0.817	3.25E-05
1438114_x_at	embryonal Fyn-associated substrate	Efs	0.814	7.64E-05
1424379_at	carbonic anhydrase 11	Car11	0.812	1.21E-05
1420801_at	neuronal PAS domain protein 1	Npas1	0.811	2.37E-06
1419011_at	crystallin, beta A2	Cryba2	0.81	2.95E-06
1433845_x_at	dual specificity phosphatase 9	Dusp9	0.81	1.38E-06
1451264_at	FERM domain containing 6	Frmd6	0.809	3.09E-07
1433521_at	ankyrin repeat domain 13c	Ankrd13c	0.809	9.40E-07
1450726_at	N-acylsphingosine amidohydrolase 2	Asah2	0.809	6.25E-06
1449581_at	EMI domain containing 1	Emid1	0.806	7.67E-06
1421546_a_at	Rac GTPase-activating protein 1	Racgap1	0.805	4.03E-07
1418161_at	junctophilin 3	Jph3	0.805	1.08E-06
1424938_at	six transmembrane epithelial antigen of the prostate 1	Steap1	0.804	2.52E-05
1454735_at	similar to outer dense fiber of sperm tails 2	LOC100047199	0.801	1.90E-06
1452603_at	RIKEN cDNA 5330431N19 gene	5330431N19Rik	0.8	1.83E-06
1427912_at	carbonyl reductase 3	Cbr3	0.799	1.91E-06
1460337_at	SH3-domain kinase binding protein 1	Sh3kbp1	0.797	1.98E-06
1417168_a_at	ubiquitin specific peptidase 2	Usp2	0.797	7.03E-06
1421821_at	low density lipoprotein receptor	Ldlr	0.796	3.29E-07
1417823_at	glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	Gcat	0.793	1.86E-06
1439995_at	Na+/H+ exchanger domain containing 2	Nhedc2	0.792	3.28E-06
1418949_at	growth differentiation factor 15	Gdf15	0.791	3.32E-05
1439381_x_at	MARVEL (membrane-associating) domain containing 1	Marveld1	0.789	1.32E-06
1438928_x_at	ninjurin 1	Ninj1	0.788	7.15E-07
1426960_a_at	fatty acid 2-hydroxylase	Fa2h	0.788	3.29E-06
1448907_at	thimet oligopeptidase 1	Thop1	0.786	1.68E-05
1448285_at	regulator of G-protein signaling 4	Rgs4	0.786	4.12E-05
1417404_at	ELOVL family member 6, elongation of long chain fatty acids (yeast)	Elovl6	0.784	5.59E-07
1426122_a_at	coronin, actin binding protein 6	Coro6	0.782	2.05E-05
1434311_at	CCR4-NOT transcription complex, subunit 6-like	Cnot6l	0.78	0.000755862
1438933_x_at	RAS, guanyl releasing protein 2	Rasgrp2	0.78	0.000253836
1417167_at	exosome component 5	Exosc5	0.779	5.93E-06
1449187_at	platelet derived growth factor, alpha	Pdgfa	0.779	4.51E-06
1416326_at	cysteine-rich protein 1 (intestinal)	Crip1	0.779	4.62E-05
1417801_a_at	protein tyrosine phosphatase, receptor-type, F	Ppfibp2	0.778	3.49E-06

	interacting protein, binding protein 2			
1423063_at	DNA methyltransferase 3A	Dnmt3a	0.778	4.04E-06
1448277_at	polymerase (DNA directed), delta 2, regulatory subunit	Pold2	0.777	1.89E-06
1426981_at	proprotein convertase subtilisin/kexin type 6	Pcsk6	0.776	2.36E-06
1439148_a_at	phosphofructokinase, liver, B-type	Pfkl	0.775	9.87E-07
1453647_at	RIKEN cDNA E130112N10 gene	E130112N10Rik	0.775	2.52E-05
1422256_at	somatostatin receptor 2	Sstr2	0.773	2.43E-06
1428574_a_at	chimerin (chimaerin) 2	Chn2	0.773	1.95E-05
1436584_at	sprouty homolog 2 (Drosophila)	Spry2	0.773	7.15E-05
1427101_at	meteorin, glial cell differentiation regulator	Metrn	0.773	0.000149398
1417226_at	F-box and WD-40 domain protein 4	Fbxw4	0.772	1.98E-06
1420363_at	BCL2-interacting killer	Bik	0.771	0.000132322
1417644_at	sarcospan	Sspn	0.768	1.57E-06
1448812_at	hippocalcin-like 1	Hpcal1	0.767	2.07E-06
1433428_x_at	transglutaminase 2, C polypeptide	Tgm2	0.767	7.25E-06
1417323_at	proline/serine-rich coiled-coil 1	Psrc1	0.767	0.000118465
1416287_at	regulator of G-protein signaling 4	Rgs4	0.766	7.89E-07
1428573_at	chimerin (chimaerin) 2	Chn2	0.765	1.19E-05
1417580_s_at	selenium binding protein 2	Selenbp2	0.765	9.58E-05
1422444_at	integrin alpha 6	Itga6	0.76	5.59E-07
1454159_a_at	insulin-like growth factor binding protein 2	Igfbp2	0.76	6.68E-05
1452240_at	bruno-like 4, RNA binding protein (Drosophila)	Brunol4	0.76	2.43E-06
1460689_at	DNA segment, Chr 15, Wayne State University 75, expressed	D15Wsu75e	0.759	9.55E-07
1418796_at	C-type lectin domain family 11, member a	Clec11a	0.756	2.21E-06
1418471_at	placental growth factor	Pgf	0.756	6.98E-06
1417643_at	radial spoke head 1 homolog (Chlamydomonas)	Rsph1	0.756	2.10E-06
1425457_a_at	growth factor receptor bound protein 10	Grb10	0.754	9.87E-05
1448104_at	aldehyde dehydrogenase family 6, subfamily A1	Aldh6a1	0.754	0.000117543
1424648_at	RAB, member of RAS oncogene family-like 4	Rabl4	0.754	3.29E-06
1456036_x_at	glutathione S-transferase omega 1	Gsto1	0.753	2.70E-06
1417541_at	helicase, lymphoid specific	Hells	0.753	2.74E-05
1421862_a_at	vesicle-associated membrane protein 1	Vamp1	0.752	0.000105822
1422445_at	integrin alpha 6	Itga6	0.748	4.26E-07
1452123_s_at	FERM domain containing 4B	Frmd4b	0.748	0.000399902
1455900_x_at	transglutaminase 2, C polypeptide	Tgm2	0.748	1.32E-05
1423068_at	intraflagellar transport 172 homolog (Chlamydomonas)	Ift172	0.747	1.91E-06
1417311_at	cysteine rich protein 2	Crip2	0.74	2.12E-06
1450670_at	dopamine beta hydroxylase	Dbh	0.74	2.11E-05
1434243_s_at	translocase of outer mitochondrial membrane 70 homolog A (yeast)	Tomm70a	0.739	1.37E-06
1420876_a_at	septin 6	Sept6	0.739	1.00E-05
1427900_at	phosphatidylinositol-4-phosphate 5-kinase-like 1	Pip5kl1	0.738	0.000177245
1432052_at	exosome component 1	Exosc1	0.738	5.99E-06
1451775_s_at	interleukin 13 receptor, alpha 1	Il13ra1	0.738	0.000383864
1449907_at	beta-carotene 15,15'-monooxygenase	Bcmo1	0.737	2.72E-06
1436819_at	septin 6	Sept6	0.737	1.69E-05
1448546_at	Ras association (RalGDS/AF-6) domain family member 3	Rassf3	0.736	3.81E-06
1451119_a_at	fibulin 1	Fbln1	0.733	2.39E-06
1415834_at	dual specificity phosphatase 6	Dusp6	0.733	7.44E-07
1415984_at	acyl-Coenzyme A dehydrogenase, medium	Acadm	0.733	1.89E-06

	chain			
1424376_at	CDC42 effector protein (Rho GTPase binding) 1	Cdc42ep1	0.733	1.21E-05
1418402_at	a disintegrin and metallopeptidase domain 19 (meltrin beta)	Adam19	0.732	1.14E-05
1421014_a_at	citrate lyase beta like	Clybl	0.731	2.30E-06
1451634_at	RIKEN cDNA 2810051F02 gene	2810051F02Rik	0.73	0.002677775
1419089_at	tissue inhibitor of metalloproteinase 3	Timp3	0.727	0.000199729
1452202_at	phosphodiesterase 2A, cGMP-stimulated	Pde2a	0.726	3.10E-06
1448377_at	secretory leukocyte peptidase inhibitor	Slpi	0.725	6.67E-06
1417403_at	ELOVL family member 6, elongation of long chain fatty acids (yeast)	Elovl6	0.724	2.52E-05
1422438_at	epoxide hydrolase 1, microsomal	Ephx1	0.723	2.39E-06
1419449_a_at	guanine nucleotide binding protein (G protein), alpha inhibiting 2	Gnai2	0.723	2.80E-05
1438559_x_at	solute carrier family 44, member 2	Slc44a2	0.72	8.39E-05
1423470_at	polypyrimidine tract binding protein 2	Ptbp2	0.72	0.000201938
1422779_at	sphingomyelin phosphodiesterase 3, neutral	Smpd3	0.719	4.50E-05
1422115_a_at	FMS-like tyrosine kinase 3 ligand	Flt3l	0.717	5.27E-05
1448661_at	phospholipase C, beta 3	Plcb3	0.717	4.97E-06
1435191_at	corneodesmosin	Cdsn	0.717	2.10E-06
1418743_a_at	tescalcin	Tesc	0.716	0.000129293
1422710_a_at	calcium channel, voltage-dependent, T type, alpha 1H subunit	Cacna1h	0.716	0.000118465
1419767_at	peptidyl arginine deiminase, type III	Padi3	0.715	0.000114104
1425326_at	ATP citrate lyase	Acly	0.715	1.08E-05
1417212_at	RIKEN cDNA 9530058B02 gene	9530058B02Rik	0.713	2.62E-05
1436092_at	NA	NA	0.713	2.97E-05
1416978_at	Fc receptor, IgG, alpha chain transporter	Fcgrt	0.712	6.91E-06
1433909_at	synaptotagmin XVII	Syt17	0.71	3.39E-06
1449987_at	anaplastic lymphoma kinase	Alk	0.709	3.78E-05
1438527_at	ribosomal protein L3	Rpl3	0.709	0.000653499
1450048_a_at	isocitrate dehydrogenase 2 (NADP+), mitochondrial	Idh2	0.708	7.58E-06
1418865_at	zinc finger protein 385A	Zfp385a	0.708	6.44E-05
1416352_s_at	glycoprotein, synaptic 2	Gpsn2	0.707	4.11E-06
1454636_at	chromobox homolog 5 (Drosophila HP1a)	Cbx5	0.707	8.58E-06
1451475_at	plexin D1	Plxnd1	0.706	2.39E-06
1430195_at	RIKEN cDNA 2810043O03 gene	2810043O03Rik	0.705	0.030627311
1457094_at	src homology 2 domain-containing transforming protein E	She	0.704	2.01E-05
1424470_a_at	Rap guanine nucleotide exchange factor (GEF) 3	Rapgef3	0.702	1.19E-05
1416442_at	immediate early response 2	Ier2	0.702	2.24E-05
1438982_s_at	FLYWCH family member 2	Flywch2	0.701	1.61E-05
1449491_at	caspase recruitment domain family, member 10	Card10	0.701	2.75E-06
1423305_at	exostoses (multiple)-like 1	Extl1	0.701	1.45E-05
1450269_a_at	phosphofructokinase, liver, B-type	Pfkl	0.701	3.82E-06
1439459_x_at	ATP citrate lyase	Acly	0.7	1.95E-06
1424334_at	tetraspanin 17	Tspan17	0.697	7.74E-06
1420877_at	septin 6	Sept6	0.697	2.82E-06
1435448_at	BCL2-like 11 (apoptosis facilitator)	Bcl2l11	0.697	4.64E-05
1421882_a_at	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	Elavl2	0.696	0.000135365
1448330_at	glutathione S-transferase, mu 1	Gstm1	0.694	1.32E-05
1422589_at	RAB3A, member RAS oncogene family	Rab3a	0.693	1.08E-05

1424220_a_at	porcupine homolog (Drosophila)	Porcn	0.693	0.000191638
1449141_at	filamin binding LIM protein 1	Fblim1	0.689	1.20E-05
1427176_s_at	expressed sequence AI428936	AI428936	0.687	2.94E-06
1429681_a_at	glycoprotein, synaptic 2	Gpsn2	0.686	1.19E-05
1435013_at	HEAT repeat containing 2	Heatr2	0.685	9.96E-06
1424382_at	reticulocalbin 3, EF-hand calcium binding domain	Rcn3	0.68	1.25E-05
1418634_at	Notch gene homolog 1 (Drosophila)	Notch1	0.678	5.16E-05
1434299_x_at	RAB, member of RAS oncogene family-like 4	Rabl4	0.677	8.09E-05
1416246_a_at	coronin, actin binding protein 1A	Coro1a	0.676	1.89E-05
1418010_a_at	SH3-domain GRB2-like B1 (endophilin)	Sh3glb1	0.675	8.68E-06
1419307_at	tumor necrosis factor receptor superfamily, member 13c	Tnfrsf13c	0.675	2.75E-06
1423586_at	AXL receptor tyrosine kinase	Axl	0.671	0.000447274
1439959_at	fibroblast growth factor 11	Fgf11	0.671	0.000113158
1416416_x_at	glutathione S-transferase, mu 1	Gstm1	0.671	1.05E-05
1437406_x_at	insulin-like growth factor binding protein 4	Igfbp4	0.669	4.29E-06
1416701_at	Rho family GTPase 3	Rnd3	0.669	0.000135142
1426955_at	collagen, type XVIII, alpha 1	Col18a1	0.669	1.73E-06
1417500_a_at	transglutaminase 2, C polypeptide	Tgm2	0.668	7.67E-06
1439436_x_at	inner centromere protein	Incenp	0.667	3.85E-05
1418966_a_at	discoidin, CUB and LCCL domain containing 1	Dcbld1	0.667	2.40E-05
1438312_s_at	SCY1-like 1 (S. cerevisiae)	Scyl1	0.666	0.000169912
1448508_at	Traf3 interacting protein 2	Traf3ip2	0.665	7.60E-06
1451666_at	ATP citrate lyase	Acly	0.665	8.55E-07
1437277_x_at	transglutaminase 2, C polypeptide	Tgm2	0.664	2.91E-05
1460409_at	carnitine palmitoyltransferase 1a, liver	Cpt1a	0.663	1.91E-06
1417862_at	RIKEN cDNA A830059I20 gene	A830059I20Rik	0.663	6.28E-06
1431335_a_at	WAP four-disulfide core domain 1	Wfdc1	0.662	4.31E-05
1417353_x_at	small nuclear ribonucleoprotein polypeptide A'	Snrpa1	0.662	4.45E-05
1460367_at	high mobility group box transcription factor 1	Hbp1	0.662	2.43E-06
1422803_at	follistatin-like 3	Fstl3	0.661	1.05E-05
1423233_at	CCAAT/enhancer binding protein (C/EBP), delta	Cebpd	0.661	8.35E-06
1417133_at	peripheral myelin protein 22	Pmp22	0.66	3.36E-06
1429597_at	developmental pluripotency associated 4	Dppa4	0.66	3.49E-06
1422847_a_at	protein kinase C, delta	Prkcd	0.659	6.08E-06
1420996_at	plexin A3	Plxna3	0.659	3.64E-05
1449522_at	unc-5 homolog C (C. elegans)	Unc5c	0.659	1.58E-05
1437012_x_at	Rap guanine nucleotide exchange factor (GEF) 3	Rapgef3	0.658	8.43E-05
1436954_at	WAS/WASL interacting protein family, member 1	Wipf1	0.656	2.62E-05
1426642_at	fibronectin 1	Fn1	0.656	3.78E-06
1438651_a_at	apelin receptor	Aplnr	0.656	0.002277796
1418773_at	fatty acid desaturase 3	Fads3	0.655	9.16E-06
1427164_at	interleukin 13 receptor, alpha 1	Il13ra1	0.655	3.64E-05
1428283_at	cytochrome P450, family 2, subfamily s, polypeptide 1	Cyp2s1	0.654	3.22E-05
1421883_at	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	Elavl2	0.653	5.19E-05
1435026_at	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2	Spock2	0.651	1.14E-06
1426930_at	bruno-like 4, RNA binding protein (Drosophila)	Brunol4	0.65	5.33E-05
1448650_a_at	polymerase (DNA directed), epsilon	Pole	0.65	5.58E-06
1419592_at	unc-5 homolog C (C. elegans)	Unc5c	0.649	4.24E-05
1422059_at	chromobox homolog 2 (Drosophila Pc class)	Cbx2	0.647	0.000950285

1450627_at	progressive ankylosis	Ank	0.646	1.72E-05
1448477_at	carbohydrate sulfotransferase 12	Chst12	0.646	5.55E-06
1448205_at	cyclin B1, related sequence 1	Ccnb1-rs1	0.645	9.33E-05
1417351_a_at	small nuclear ribonucleoprotein polypeptide A'	Snrpa1	0.644	4.26E-06
1433538_at	MARVEL (membrane-associating) domain containing 1	Marveld1	0.643	5.11E-06
1451386_at	biliverdin reductase B (flavin reductase (NADPH))	Blvrb	0.642	6.94E-05
1426040_a_at	outer dense fiber of sperm tails 2	Odf2	0.642	0.000107612
1452650_at	tripartite motif-containing 62	Trim62	0.641	6.47E-05
1426260_a_at	UDP glucuronosyltransferase 1 family, polypeptide A6A	Ugt1a6a	0.641	0.000111479
1436528_at	Kazal-type serine peptidase inhibitor domain 1	Kazald1	0.641	1.75E-05
1418744_s_at	tescalcin	Tesc	0.64	7.35E-06
1435780_at	pleckstrin and Sec7 domain containing	Psd	0.639	6.85E-06
1448181_at	Kruppel-like factor 15	Klf15	0.639	1.09E-05
1451181_at	transmembrane protein 121	Tmem121	0.638	5.96E-05
1416780_at	phosphofructokinase, muscle	Pfkm	0.637	1.57E-06
1450713_at	chondroitin sulfate proteoglycan 5	Cspg5	0.636	0.000394534
1451872_a_at	neuralized-like homolog (Drosophila)	Neurl	0.636	4.94E-05
1433530_at	ribosomal protein L41	Rpl41	0.635	3.56E-05
1451358_a_at	Rac GTPase-activating protein 1	Racgap1	0.635	1.57E-05
1417896_at	tight junction protein 3	Tjp3	0.634	2.81E-05
1438480_a_at	thymocyte nuclear protein 1	Thyn1	0.633	0.000546061
1428465_at	transmembrane protein 147	Tmem147	0.633	4.05E-06
1417352_s_at	small nuclear ribonucleoprotein polypeptide A'	Snrpa1	0.632	8.39E-05
1423844_s_at	cystathionine beta-synthase	Cbs	0.632	1.75E-05
1419076_a_at	breast cancer 2	Brca2	0.632	0.000670307
1419495_at	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	Immp2l	0.631	5.39E-06
1427140_at	plasmacytoma variant translocation 1	Pvt1	0.629	6.12E-05
1425093_at	purinergic receptor P2X, ligand-gated ion channel, 3	P2rx3	0.628	6.18E-05
1418086_at	protein phosphatase 1, regulatory (inhibitor) subunit 14A	Ppp1r14a	0.628	0.000132805
1450992_a_at	Meis homeobox 1	Meis1	0.627	9.66E-06
1424988_at	myosin regulatory light chain interacting protein	Mylip	0.626	3.03E-05
1419072_at	glutathione S-transferase, mu 7	Gstm7	0.626	2.04E-05
1419399_at	microsomal triglyceride transfer protein	Mttp	0.625	8.33E-06
1424519_at	mitochondrial GTPase 1 homolog (S. cerevisiae)	Mtg1	0.624	1.54E-06
1418715_at	pantothenate kinase 1	Pank1	0.624	3.91E-05
1418881_at	N-terminal EF-hand calcium binding protein 2	Necab2	0.624	4.05E-06
1416400_at	pyrroline-5-carboxylate reductase-like	Pycrl	0.621	2.21E-06
1416625_at	serine (or cysteine) peptidase inhibitor, clade G, member 1	Serping1	0.621	9.10E-05
1423698_at	non-SMC condensin II complex, subunit H2	Ncaph2	0.621	1.67E-05
1451377_a_at	achalasia, adrenocortical insufficiency, alacrimia	Aaas	0.62	1.80E-06
1451888_a_at	odd Oz/ten-m homolog 4 (Drosophila)	Odz4	0.62	2.48E-05
1450520_at	calcium channel, voltage-dependent, gamma subunit 3	Cacng3	0.619	4.85E-05
1418840_at	programmed cell death 4	Pdcd4	0.619	1.13E-05
1454632_at	RIKEN cDNA 6330442E10 gene	6330442E10Rik	0.619	4.97E-06
1451542_at	single-stranded DNA binding protein 2	Ssbp2	0.617	0.000175575
1435105_at	ring finger protein 208	Rnf208	0.617	3.29E-06
1416576_at	suppressor of cytokine signaling 3	Socs3	0.617	0.00025743

1449836_x_at	BCL2-interacting killer	Bik	0.617	9.60E-05
1452330_a_at	matrix-remodelling associated 8	Mxra8	0.616	1.13E-05
1448491_at	enoyl coenzyme A hydratase 1, peroxisomal	Ech1	0.613	2.24E-05
1452412_at	homeo box C8	Hoxc8	0.613	0.005609546
1451336_at	lectin, galactose binding, soluble 4	Lgals4	0.613	0.000884362
1427356_at	RIKEN cDNA 2310031A18 gene	2310031A18Rik	0.612	3.66E-06
1433844_a_at	dual specificity phosphatase 9	Dusp9	0.611	4.35E-06
1428289_at	RIKEN cDNA 2310051E17 gene	2310051E17Rik	0.611	1.88E-05
1432329_a_at	megakaryocyte-associated tyrosine kinase	Matk	0.611	0.000193344
1416383_a_at	pyruvate carboxylase	Pcx	0.611	6.98E-06
1448547_at	Ras association (RalGDS/AF-6) domain family member 3	Rassf3	0.61	4.98E-06
1455030_at	protein tyrosine phosphatase, receptor type, J	Ptprj	0.61	5.64E-05
1422308_a_at	lectin, galactose binding, soluble 7	Lgals7	0.61	0.000114815
1418376_at	fibroblast growth factor 15	Fgf15	0.608	4.60E-05
1417092_at	parathyroid hormone receptor 1	Pthr1	0.607	1.74E-05
1455106_a_at	creatine kinase, brain	Ckb	0.607	2.40E-05
1448648_at	RIKEN cDNA 9130005N14 gene	9130005N14Rik	0.607	0.000141864
1438156_x_at	carnitine palmitoyltransferase 1a, liver	Cpt1a	0.606	0.000152105
1417822_at	DNA segment, Chr 17, human D6S56E 5	D17H6S56E-5	0.606	6.85E-06
1422952_at	Ng23 protein	Ng23	0.604	0.000364532
1418665_at	inositol (myo)-1(or 4)-monophosphatase 2	Impa2	0.604	0.001652483
1432108_at	polycomb group ring finger 6	Pcgf6	0.604	4.04E-05
1417229_at	calpain 1	Capn1	0.604	3.80E-06
1438009_at	histone cluster 1, H2ae	Hist1h2ae	0.603	0.000663038
1427674_a_at	seizure related gene 6	Sez6	0.602	2.45E-05
1425764_a_at	branched chain aminotransferase 2, mitochondrial	Bcat2	0.602	1.71E-05
1416716_at	embryonal Fyn-associated substrate	Efs	0.6	3.42E-05
1417753_at	polycystic kidney disease 2	Pkd2	0.6	5.19E-05
1437270_a_at	cardiotrophin-like cytokine factor 1	Clcf1	0.599	0.000403366
1456495_s_at	oxysterol binding protein-like 6	Osbpl6	0.597	0.000103212
1420564_at	insulin receptor-related receptor	Insrr	0.597	3.14E-05
1438932_at	RAS, guanyl releasing protein 2	Rasgrp2	0.595	0.001888555
1423092_at	inner centromere protein	Incenp	0.594	5.00E-06
1450157_a_at	hyaluronan mediated motility receptor (RHAMM)	Hmmr	0.594	2.23E-05
1438769_a_at	thymocyte nuclear protein 1	Thyn1	0.594	2.23E-05
1424471_at	Rap guanine nucleotide exchange factor (GEF) 3	Rapgef3	0.593	7.35E-06
1428113_at	transmembrane and tetratricopeptide repeat containing 4	Tmtc4	0.593	4.11E-05
1425245_a_at	regulator of G-protein signaling 11	Rgs11	0.592	5.64E-05
1423192_at	paraspeckle protein 1	Pspc1	0.591	1.33E-05
1436549_a_at	heterogeneous nuclear ribonucleoprotein A1	Hnrnpa1	0.591	0.00015857
1435336_at	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)	Celsr2	0.591	2.25E-05
1456424_s_at	phospholipid transfer protein	Pltp	0.591	0.003135531
1426972_at	Sec24 related gene family, member D (S. cerevisiae)	Sec24d	0.59	2.40E-05
1450772_at	wingless-related MMTV integration site 11	Wnt11	0.59	2.53E-05
1449893_a_at	leucine-rich repeats and immunoglobulin-like domains 1	Lrig1	0.588	6.14E-05
1416207_at	tafazzin	Taz	0.587	4.65E-05
1416936_at	apoptosis-associated tyrosine kinase	Aatk	0.587	2.59E-06
1418090_at	plasmalemma vesicle associated protein	Plvap	0.586	3.83E-06
1420995_at	plexin A3	Plxna3	0.586	0.000435063

1423774_a_at	protein regulator of cytokinesis 1	Prc1	0.585	3.53E-06
1421881_a_at	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	Elavl2	0.584	4.89E-05
1434784_s_at	transmembrane protein 106C	Tmem106c	0.583	1.25E-05
1448286_at	hydroxysteroid (17-beta) dehydrogenase 10	Hsd17b10	0.581	1.91E-06
1451911_a_at	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	Ace	0.581	2.58E-05
1448647_at	mannosidase 2, alpha 1	Man2a1	0.58	9.00E-05
1451891_a_at	dysferlin	Dysf	0.579	3.72E-05
1426517_at	guanine nucleotide binding protein, alpha z subunit	Gnaz	0.579	0.000107352
1460222_at	SH3-domain binding protein 1	Sh3bp1	0.579	8.82E-06
1451906_at	UBX domain protein 10	Ubxn10	0.579	7.07E-05
1437333_x_at	aldehyde dehydrogenase 18 family, member A1	Aldh18a1	0.578	1.57E-06
1435386_at	Von Willebrand factor homolog	Vwf	0.578	0.000256268
1449324_at	ERO1-like (S. cerevisiae)	Ero1l	0.577	4.04E-06
1422739_at	heparan sulfate 2-O-sulfotransferase 1	Hs2st1	0.577	0.000407108
1454987_a_at	H2-K region expressed gene 6	H2-Ke6	0.577	9.79E-05
1452056_s_at	protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca	0.577	9.64E-06
1435941_at	rhomboid, veinlet-like 3 (Drosophila)	Rhbdl3	0.576	1.08E-05
1452283_at	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	Rassf8	0.576	2.51E-05
1434981_at	RIKEN cDNA E130303B06 gene	E130303B06Rik	0.576	4.06E-05
1426803_at	RNA binding motif protein 26	Rbm26	0.576	0.004181737
1419583_at	chromobox homolog 4 (Drosophila Pc class)	Cbx4	0.576	5.58E-06
1425047_a_at	RIKEN cDNA 4921517L17 gene	4921517L17Rik	0.575	8.79E-06
1460370_at	DNA topoisomerase 1, mitochondrial	Top1mt	0.575	2.05E-05
1436824_x_at	ring finger protein 26	Rnf26	0.575	1.18E-05
1429212_a_at	leucine rich repeat containing 51	Lrrc51	0.574	2.52E-05
1420776_a_at	AU RNA binding protein/enoyl-coenzyme A hydratase	Auh	0.574	7.07E-05
1422549_at	ADP-ribosylation factor-like 2	Arl2	0.574	9.69E-06
1419569_a_at	interferon-stimulated protein	Isg20	0.574	1.82E-05
1422540_at	fibulin 1	Fbln1	0.574	6.72E-06
1449418_s_at	F-box protein 36	Fbxo36	0.573	3.70E-05
1455696_a_at	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	Prpf4b	0.573	0.000149398
1451857_a_at	notum pectinacetylesterase homolog (Drosophila)	Notum	0.573	0.000186997
1456341_a_at	Kruppel-like factor 9	Klf9	0.572	1.56E-05
1460354_a_at	mitochondrial ribosomal protein L13	Mrpl13	0.572	3.49E-06
1419943_s_at	cyclin B1	Ccnb1	0.571	2.38E-05
1422955_at	synaptotagmin XVII	Syt17	0.571	4.41E-05
1438115_a_at	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	Slc9a3r1	0.571	6.03E-06
1434235_at	solute carrier family 20, member 2	Slc20a2	0.57	5.55E-06
1421923_at	SH3-domain binding protein 5 (BTK-associated)	Sh3bp5	0.57	2.18E-06
1452242_at	centrosomal protein 55	Cep55	0.569	0.000177878
1450122_at	protein tyrosine phosphatase, receptor type, G	Ptprg	0.569	0.000153483
1420142_s_at	proliferation-associated 2G4	Pa2g4	0.569	9.76E-06
1427789_s_at	GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus	Gnas	0.567	6.07E-05
1424112_at	insulin-like growth factor 2 receptor	Igf2r	0.566	8.80E-06
1417971_at	nurim (nuclear envelope membrane protein)	Nrm	0.566	3.27E-06
1417297_at	inositol 1,4,5-triphosphate receptor 3	Itpr3	0.565	6.73E-05

1434959_at	desert hedgehog	Dhh	0.565	3.63E-05
1421112_at	NK2 transcription factor related, locus 2 (Drosophila)	Nkx2-2	0.565	0.00015105
1419499_at	glycerol-3-phosphate acyltransferase, mitochondrial	Gpam	0.564	1.86E-05
1416367_at	RIKEN cDNA 1110001J03 gene	1110001J03Rik	0.564	0.000542088
1454168_a_at	ClpB caseinolytic peptidase B homolog (E. coli)	Clpb	0.564	0.000740419
1419529_at	interleukin 23, alpha subunit p19	Il23a	0.564	6.28E-06
1437325_x_at	aldehyde dehydrogenase 18 family, member A1	Aldh18a1	0.563	5.96E-06
1450162_at	D4, zinc and double PHD fingers, family 3	Dpf3	0.562	2.57E-05
1426787_at	Sfi1 homolog, spindle assembly associated (yeast)	Sfi1	0.561	0.004747684
1435216_a_at	outer dense fiber of sperm tails 2	Odf2	0.561	0.000625281
1425108_a_at	cDNA sequence BC004728	BC004728	0.561	3.48E-05
1417272_at	RIKEN cDNA 9130005N14 gene	9130005N14Rik	0.561	3.39E-05
1452050_at	calcium/calmodulin-dependent protein kinase ID	Camk1d	0.56	4.83E-06
1425822_a_at	deltex 1 homolog (Drosophila)	Dtx1	0.56	1.68E-05
1428288_at	RIKEN cDNA 2310051E17 gene	2310051E17Rik	0.559	4.43E-06
1426905_a_at	DnaJ (Hsp40) homolog, subfamily C, member 10	Dnajc10	0.559	0.000963618
1435524_at	NA	NA	0.559	3.06E-05
1448688_at	podocalyxin-like	Podxl	0.559	6.33E-06
1438391_x_at	hydroxysteroid (17-beta) dehydrogenase 10	Hsd17b10	0.558	7.88E-05
1424138_at	rhomboid family 1 (Drosophila)	Rhbdf1	0.558	7.21E-05
1416746_at	H2A histone family, member X	H2afx	0.557	4.41E-06
1449468_at	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	St6galnac5	0.557	4.88E-05
1427680_a_at	nuclear factor I/B	Nfib	0.557	0.000192223
1421755_at	G protein-coupled receptor 132	Gpr132	0.557	0.000284303
1417604_at	calcium/calmodulin-dependent protein kinase I	Camk1	0.556	6.58E-06
1420643_at	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	Lfng	0.556	0.000436267
1415803_at	chemokine (C-X3-C motif) ligand 1	Cx3cl1	0.555	8.21E-05
1424204_at	mitochondrial ribosomal protein L13	Mrpl13	0.554	2.40E-05
1422329_a_at	neurotrophic tyrosine kinase, receptor, type 3	Ntrk3	0.554	5.58E-05
1423804_a_at	isopentenyl-diphosphate delta isomerase	Idi1	0.554	0.000276701
1417019_a_at	cell division cycle 6 homolog (S. cerevisiae)	Cdc6	0.554	6.71E-05
1427161_at	centromere protein F	Cenpf	0.553	0.000174842
1417018_at	epidermal growth factor-containing fibulin-like extracellular matrix protein 2	Efemp2	0.552	1.75E-05
1455740_at	heterogeneous nuclear ribonucleoprotein A1	Hnrnpa1	0.552	0.003935317
1434691_at	splicing factor, arginine/serine-rich 2, interacting protein	Sfrs2ip	0.55	5.97E-06
1417575_at	OTU domain, ubiquitin aldehyde binding 2	Otub2	0.549	2.88E-05
1437658_a_at	small nucleolar RNA, C/D box 22	Snord22	0.549	0.000304398
1433443_a_at	similar to Hmgcs1 protein	LOC100040592	0.548	2.55E-05
1423847_at	non-SMC condensin I complex, subunit D2	Ncapd2	0.548	5.97E-06
1435110_at	unc-5 homolog B (C. elegans)	Unc5b	0.548	1.45E-05
1416007_at	special AT-rich sequence binding protein 1	Satb1	0.547	2.11E-05
1422528_a_at	zinc finger protein 36, C3H type-like 1	Zfp36l1	0.546	0.00050575
1460286_at	septin 6	Sept6	0.546	8.20E-05
1416076_at	cyclin B1, related sequence 1	Ccnb1-rs1	0.546	0.000101753
1451586_at	testis enhanced gene transcript	Tegt	0.546	1.13E-05
1454675_at	thyroid hormone receptor alpha	Thra	0.546	1.04E-05

1451547_at	iodotyrosine deiodinase	Iyd	0.545	9.84E-05
1425815_a_at	hyaluronan mediated motility receptor (RHAMM)	Hmmr	0.545	0.000197004
1451672_at	G protein-coupled receptor kinase 6	Grk6	0.545	1.12E-05
1416842_at	glutathione S-transferase, mu 5	Gstm5	0.544	1.45E-05
1418075_at	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	St6galnac4	0.544	1.37E-05
1437724_x_at	phosphatidylinositol transfer protein, membrane-associated 1	Pitpnm1	0.543	0.000110272
1428835_at	myosin, heavy polypeptide 14	Myh14	0.543	3.63E-05
1451147_x_at	cold shock domain containing C2, RNA binding	Csdc2	0.543	9.58E-05
1419512_at	PRP40 pre-mRNA processing factor 40 homolog B (yeast)	Prpf40b	0.543	0.000162942
1423298_at	adducin 3 (gamma)	Add3	0.542	1.35E-05
1424081_at	polycomb group ring finger 6	Pcgf6	0.541	3.88E-06
1438091_a_at	H2A histone family, member Z	H2afz	0.541	7.35E-06
1419613_at	collagen, type VII, alpha 1	Col7a1	0.541	0.000440407
1421340_at	mitogen-activated protein kinase kinase kinase 5	Map3k5	0.539	4.09E-05
1452388_at	heat shock protein 1A	Hspa1a	0.539	0.001979236
1449484_at	stanniocalcin 2	Stc2	0.538	8.20E-06
1434291_a_at	small EDRK-rich factor 1	Serf1	0.538	0.000488656
1432143_a_at	high mobility group box transcription factor 1	Hbp1	0.537	7.21E-05
1420518_a_at	immunoglobulin superfamily, member 9	Igsf9	0.537	0.000478624
1428197_at	tetraspanin 9	Tspan9	0.536	1.44E-05
1420903_at	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3	St6galnac3	0.535	2.47E-05
1416918_at	discs, large homolog 3 (Drosophila)	Dlg3	0.535	0.000136396
1426866_at	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 14	Chst14	0.535	0.000104003
1434866_x_at	carnitine palmitoyltransferase 1a, liver	Cpt1a	0.534	5.57E-05
1424553_at	hedgehog acyltransferase-like	Hhatl	0.534	1.47E-05
1417780_at	LAG1 homolog, ceramide synthase 4	Lass4	0.533	0.000161923
1448689_at	related RAS viral (r-ras) oncogene homolog 2	Rras2	0.533	0.000101826
1456241_a_at	solute carrier family 38, member 10	Slc38a10	0.533	1.00E-05
1415977_at	myo-inositol 1-phosphate synthase A1	Isyna1	0.533	5.38E-05
1419503_at	stanniocalcin 2	Stc2	0.533	1.20E-05
1452608_at	c-myc binding protein	Mycbp	0.533	4.18E-05
1438116_x_at	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	Slc9a3r1	0.532	3.56E-05
1434783_at	transmembrane protein 106C	Tmem106c	0.532	4.98E-05
1450023_at	GTP binding protein 1	Gtpbp1	0.531	1.80E-05
1426666_a_at	unc-84 homolog A (C. elegans)	Unc84a	0.53	4.04E-06
1418264_at	centromere protein K	Cenpk	0.53	0.000508911
1449290_at	dihydropyrimidinase-like 5	Dpysl5	0.53	2.60E-05
1419686_at	testis specific gene A14	Tsga14	0.529	5.20E-05
1425266_a_at	RAP1, GTP-GDP dissociation stimulator 1	Rap1gds1	0.529	2.42E-05
1428421_a_at	glyoxalase domain containing 4	Glod4	0.528	2.27E-05
1460652_at	estrogen related receptor, alpha	Esrra	0.528	3.76E-05
1455006_at	RIKEN cDNA 2310016M24 gene	2310016M24Rik	0.528	2.57E-05
1435966_x_at	mitochondrial ribosomal protein L13	Mrpl13	0.528	5.24E-05
1451782_a_at	solute carrier family 29 (nucleoside transporters), member 1	Slc29a1	0.528	1.76E-05
1419125_at	protein tyrosine phosphatase, non-receptor type 18	Ptpn18	0.527	4.46E-05
1423597_at	ATPase, aminophospholipid transporter	Atp8a1	0.526	0.000183261

	(APLT), class I, type 8A, member 1			
1423563_at	proline-rich transmembrane protein 1	Prrt1	0.526	0.000138258
1425627_x_at	glutathione S-transferase, mu 1	Gstm1	0.526	4.92E-05
1422704_at	glycerol kinase	Gyk	0.525	0.000478846
1424773_at	RIKEN cDNA 1110012M11 gene	1110012M11Rik	0.525	0.00034078
1424140_at	galactose-4-epimerase, UDP	Gale	0.525	3.15E-05
1448269_a_at	kelch-like 13 (Drosophila)	Klhl13	0.525	0.00016896
1418012_at	SH3-domain GRB2-like B1 (endophilin)	Sh3glb1	0.524	4.99E-05
1439360_x_at	non-SMC condensin II complex, subunit H2	Ncaph2	0.524	9.84E-06
1451718_at	proteolipid protein (myelin) 1	Plp1	0.523	0.00806868
1455677_s_at	chloride channel Ka	Clcnka	0.523	0.000156497
1428789_at	Ral GEF with PH domain and SH3 binding motif 2	Ralgps2	0.522	0.000139389
1437279_x_at	syndecan 1	Sdc1	0.522	5.19E-05
1427541_x_at	hyaluronan mediated motility receptor (RHAMM)	Hmmr	0.522	6.99E-05
1450287_at	neuronal PAS domain protein 3	Npas3	0.521	0.001621306
1427523_at	sine oculis-related homeobox 3 homolog (Drosophila)	Six3	0.521	2.43E-05
1418529_at	O-sialoglycoprotein endopeptidase	Osgep	0.521	8.79E-06
1424242_at	biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen)	Bphl	0.521	2.99E-05
1429041_at	RIKEN cDNA 6820431F20 gene	6820431F20Rik	0.52	9.54E-05
1423078_a_at	sterol-C4-methyl oxidase-like	Sc4mol	0.519	5.19E-05
1418379_s_at	G protein-coupled receptor 124	Gpr124	0.519	0.000249538
1453573_at	histone cluster 2, H3c1	Hist2h3c1	0.519	2.19E-05
1427034_at	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	Ace	0.519	4.59E-05
1431875_a_at	E2F transcription factor 1	E2f1	0.518	4.88E-05
1455008_at	NA	NA	0.518	1.35E-05
1448992_at	internexin neuronal intermediate filament protein, alpha	Ina	0.518	4.43E-05
1427405_s_at	RAB11 family interacting protein 5 (class I)	Rab11fip5	0.518	0.001285943
1423845_at	cold shock domain containing C2, RNA binding	Csdc2	0.517	8.36E-05
1422659_at	calcium/calmodulin-dependent protein kinase II, delta	Camk2d	0.517	0.000112459
1460675_at	immunoglobulin superfamily, member 8	Igsf8	0.517	8.46E-06
1425623_a_at	cystathionine beta-synthase	Cbs	0.517	5.44E-05
1419212_at	icos ligand	Icosl	0.517	0.00025296
1418957_at	src homology three (SH3) and cysteine rich domain	Stac	0.517	3.36E-05
1455061_a_at	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	Acaa2	0.516	0.00024381
1427962_at	coiled-coil domain containing 102A	Ccdc102a	0.516	9.69E-05
1450414_at	platelet derived growth factor, B polypeptide	Pdgfb	0.515	0.000423222
1417282_at	matrix metallopeptidase 23	Mmp23	0.515	0.000116546
1424628_a_at	RIKEN cDNA 1500032D16 gene	1500032D16Rik	0.515	4.61E-05
1415836_at	aldehyde dehydrogenase 18 family, member A1	Aldh18a1	0.514	5.30E-05
1455820_x_at	scavenger receptor class B, member 1	Scarb1	0.514	8.43E-05
1448991_a_at	internexin neuronal intermediate filament protein, alpha	Ina	0.514	2.36E-05
1423522_at	nucleoplasmin 3	Npm3	0.514	3.85E-05
1419658_at	histocompatibility 2, T region locus 23	H2-T23	0.513	0.00868148
1437405_a_at	insulin-like growth factor binding protein 4	Igfbp4	0.512	2.47E-05
1448490_at	aarF domain containing kinase 4	Adck4	0.512	3.02E-05
1437667_a_at	BTB and CNC homology 2	Bach2	0.512	0.000618685

1418403_at	a disintegrin and metallopeptidase domain 19 (meltrin beta)	Adam19	0.512	8.90E-05
1436737_a_at	sorbin and SH3 domain containing 1	Sorbs1	0.512	6.69E-05
1425494_s_at	bone morphogenetic protein receptor, type 1A	Bmpr1a	0.511	0.000145207
1455269_a_at	coronin, actin binding protein 1A	Coro1a	0.511	0.000927755
1437043_a_at	RIKEN cDNA 1110012M11 gene	1110012M11Rik	0.511	7.07E-05
1443949_at	NA	NA	0.511	0.024460833
1454703_x_at	small nucleolar RNA host gene (non-protein coding) 1	Snhg1	0.511	0.000297141
1450995_at	folate receptor 1 (adult)	Folr1	0.51	5.97E-05
1428172_at	PRP39 pre-mRNA processing factor 39 homolog (yeast)	Prpf39	0.51	0.000598337
1428526_at	LSM domain containing 1	Lsmd1	0.509	8.56E-05
1418049_at	latent transforming growth factor beta binding protein 3	Ltbp3	0.508	0.000109073
1438092_x_at	H2A histone family, member Z	H2afz	0.507	1.43E-05
1438478_a_at	protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca	0.506	4.04E-05
1427918_a_at	ras homolog gene family, member Q	Rhoq	0.506	9.10E-05
1422811_at	solute carrier family 27 (fatty acid transporter), member 1	Slc27a1	0.505	5.14E-05
1419647_a_at	immediate early response 3	Ier3	0.505	2.80E-05
1436277_at	ring finger protein 207	Rnf207	0.504	0.002937249
1456193_x_at	glutathione peroxidase 4	Gpx4	0.504	4.04E-06
1450920_at	cyclin B2	Ccnb2	0.504	1.06E-05
1451695_a_at	glutathione peroxidase 4	Gpx4	0.504	0.000121112
1431973_at	septin 6	Sept6	0.504	8.21E-05
1418687_at	activity regulated cytoskeletal-associated protein	Arc	0.504	0.00093774
1433830_at	heterogeneous nuclear ribonucleoprotein A2/B1	Hnrnpa2b1	0.503	0.000273429
1426097_a_at	coiled-coil domain containing 106	Ccdc106	0.503	0.000121425
1450854_at	proliferation-associated 2G4	Pa2g4	0.503	1.01E-05
1452839_at	DPH5 homolog (S. cerevisiae)	Dph5	0.502	2.00E-05
1424785_at	angiopoietin-like 6	Angptl6	0.502	4.69E-05
1423717_at	adenylate kinase 3	Ak3	0.502	1.75E-05
1421910_at	transcription factor 20	Tcf20	0.501	0.000122049
1434943_at	MORN repeat containing 4	Morn4	0.501	5.76E-06
1451516_at	Ras homolog enriched in brain like 1	Rhebl1	0.501	4.93E-05
1460351_at	S100 calcium binding protein A11 (calgizzarin)	S100a11	0.5	9.90E-05
1449215_at	solute carrier family 22 (organic cation transporter), member 21	Slc22a21	0.499	0.001905187
1426931_s_at	DNA segment, Chr 19, Brigham & Women's Genetics 1357 expressed	D19Bwg1357e	0.499	1.17E-05
1452609_at	RIKEN cDNA 1190005I06 gene	1190005I06Rik	0.499	9.17E-05
1416008_at	special AT-rich sequence binding protein 1	Satb1	0.498	3.00E-05
1436759_x_at	similar to calponin 3, acidic	LOC100047856	0.498	0.000220372
1452068_at	N-acylethanolamine acid amidase	Naaa	0.497	0.000173184
1450480_a_at	G protein-coupled receptor kinase 6	Grk6	0.495	7.39E-05
1448559_at	flotillin 1	Flot1	0.495	1.51E-05
1419456_at	dicarbonyl L-xylulose reductase	Dcxr	0.495	9.92E-05
1422851_at	high mobility group AT-hook 2	Hmga2	0.495	4.12E-05
1427141_at	RIKEN cDNA 2700099C18 gene	2700099C18Rik	0.495	0.000217956
1417398_at	related RAS viral (r-ras) oncogene homolog 2	Rras2	0.495	1.99E-05
1418538_at	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	Kdelr3	0.494	1.29E-05
1427175_at	expressed sequence AI428936	AI428936	0.494	0.001296518
1423475_at	cyclin M2	Cnnm2	0.494	0.000152144

1431592_a_at	SH3-domain kinase binding protein 1	Sh3kbp1	0.494	0.001231411
1423775_s_at	protein regulator of cytokinesis 1	Prc1	0.494	6.10E-05
1439040_at	centromere protein E	Cenpe	0.493	0.000320041
1448259_at	follistatin-like 1	Fstl1	0.493	6.43E-06
1421841_at	fibroblast growth factor receptor 3	Fgfr3	0.493	4.58E-05
1452579_at	IscU iron-sulfur cluster scaffold homolog (E. coli)	Iscu	0.493	0.000177245
1427191_at	natriuretic peptide receptor 2	Npr2	0.492	1.56E-05
1454120_a_at	polycomb group ring finger 6	Pcgf6	0.492	9.71E-05
1423963_at	WD repeat domain 26	Wdr26	0.492	8.42E-05
1420508_at	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	Sema3f	0.491	0.000111397
1450781_at	high mobility group AT-hook 2	Hmga2	0.491	7.77E-05
1417228_at	calpain 1	Capn1	0.491	2.96E-05
1421061_at	guanylate cyclase activator 1a (retina)	Guca1a	0.49	0.000476254
1417703_at	poliovirus receptor-related 2	Pvrl2	0.49	2.88E-05
1426801_at	septin 8	Sept8	0.489	7.60E-06
1438316_a_at	coiled-coil domain containing 102A	Ccdc102a	0.489	0.005438837
1449291_a_at	discoidin, CUB and LCCL domain containing 1	Dcbld1	0.489	2.88E-05
1448860_at	rad and gem related GTP binding protein 2	Rem2	0.489	0.000176107
1452961_at	RIKEN cDNA 1200009O22 gene	1200009O22Rik	0.488	0.000121094
1424252_at	heterogeneous nuclear ribonucleoprotein D-like	Hnrpdl	0.488	0.000483577
1416498_at	peptidylprolyl isomerase C	Ppic	0.488	3.19E-05
1450981_at	calponin 2	Cnn2	0.487	1.13E-05
1436750_a_at	3-oxoacid CoA transferase 1	Oxct1	0.486	0.00075322
1416890_at	WD repeat domain 74	Wdr74	0.486	3.79E-05
1434400_at	TGFB-induced factor homeobox 2	Tgif2	0.485	8.06E-06
1418057_at	T-cell lymphoma invasion and metastasis 1	Tiam1	0.484	8.25E-05
1427338_at	ciliary rootlet coiled-coil, rootletin	Crocc	0.483	0.001682355
1460038_at	POU domain, class 3, transcription factor 1	Pou3f1	0.483	0.000243603
1426626_at	general transcription factor IIF, polypeptide 2	Gtf2f2	0.483	0.000225917
1426621_a_at	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	Ppp2r2b	0.482	0.000363778
1460542_s_at	transformed mouse 3T3 cell double minute 4	Mdm4	0.482	0.00011617
1454681_at	RNA binding motif protein 35A	Rbm35a	0.482	0.000716183
1419273_at	expressed sequence C80913	C80913	0.482	0.000137622
1416718_at	brevican	Bcan	0.481	0.00033006
1417299_at	NIMA (never in mitosis gene a)-related expressed kinase 2	Nek2	0.481	2.25E-05
1434889_at	pleckstrin homology domain containing, family A member 7	Plekha7	0.481	2.23E-05
1437620_x_at	aldehyde dehydrogenase 18 family, member A1	Aldh18a1	0.48	0.000110781
1454652_at	zinc finger, RAN-binding domain containing 2	Zranb2	0.48	0.001766235
1436763_a_at	Kruppel-like factor 9	Klf9	0.479	0.000263904
1454801_at	ankyrin repeat domain 28	Ankrd28	0.479	2.74E-05
1449381_a_at	protein kinase C and casein kinase substrate in neurons 1	Pacsin1	0.479	0.000529716
1426830_a_at	S-adenosylhomocysteine hydrolase-like 1	Ahcyl1	0.477	6.29E-06
1448288_at	nuclear factor I/B	Nfib	0.477	0.003107035
1448685_at	RIKEN cDNA 2900010M23 gene	2900010M23Rik	0.477	0.000141542
1428105_at	TPX2, microtubule-associated protein homolog (Xenopus laevis)	Tpx2	0.477	2.35E-05
1418072_at	histone cluster 1, H2bc	Hist1h2bc	0.477	6.34E-05
1417985_at	Notch-regulated ankyrin repeat protein	Nrarp	0.476	0.00041804
1433702_at	endoplasmic reticulum metallopeptidase 1	Ermp1	0.476	7.21E-05

1426401_at	protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca	0.476	2.90E-05
1455796_x_at	olfactomedin 1	Olfm1	0.476	0.002310148
1431012_a_at	peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase	Peci	0.476	1.12E-05
1421312_a_at	kinesin family member C2	Kifc2	0.476	8.49E-05
1460366_at	echinoderm microtubule associated protein like 3	Eml3	0.476	0.001109979
1417607_at	cytochrome c oxidase, subunit VI a, polypeptide 2	Cox6a2	0.476	0.0001131
1423294_at	mesoderm specific transcript	Mest	0.476	8.19E-06
1424556_at	pyrroline-5-carboxylate reductase 1	Pycr1	0.475	5.30E-05
1451490_at	lysophospholipase-like 1	Lyplal1	0.475	2.11E-05
1432269_a_at	SH3-domain kinase binding protein 1	Sh3kbp1	0.475	0.000167619
1420927_at	beta galactoside alpha 2,6 sialyltransferase 1	St6gal1	0.475	0.000224838
1427901_at	mitochondrial ribosomal protein S18C	Mrps18c	0.475	0.000115421
1449118_at	dihydrolipoamide branched chain transacylase E2	Dbt	0.474	0.00018575
1417967_at	MMS19 (MET18 S. cerevisiae)	Mms19	0.474	1.48E-05
1418178_at	internexin neuronal intermediate filament protein, alpha	Ina	0.474	2.85E-05
AFFX-PyruCarbMur/L09192_3_at	pyruvate carboxylase	Pcx	0.474	0.000162686
1435855_x_at	aldehyde dehydrogenase 18 family, member A1	Aldh18a1	0.473	0.000140351
1455570_x_at	calponin 3, acidic	Cnn3	0.473	0.000257554
1422814_at	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	Aspm	0.473	0.000355306
1426450_at	phospholipase C-like 2	Plcl2	0.473	0.000125699
1425396_a_at	lymphocyte protein tyrosine kinase	Lck	0.473	7.60E-06
1417356_at	paternally expressed 3	Peg3	0.472	0.000101572
1435652_a_at	guanine nucleotide binding protein (G protein), alpha inhibiting 2	Gnai2	0.472	0.000382501
1417046_at	tumor suppressor candidate 4	Tusc4	0.471	7.59E-05
1426932_at	DNA segment, Chr 19, Brigham & Women's Genetics 1357 expressed	D19Bwg1357e	0.471	0.000138364
1419030_at	ERO1-like (S. cerevisiae)	Ero1l	0.471	0.000341304
1418229_s_at	NFU1 iron-sulfur cluster scaffold homolog (S. cerevisiae)	Nfu1	0.471	8.40E-05
1419457_at	Rho-guanine nucleotide exchange factor	Rgnef	0.47	3.20E-05
1449074_at	RIKEN cDNA 1700019N12 gene	1700019N12Rik	0.47	0.001141814
1427535_s_at	obscurin-like 1	Obsl1	0.47	2.01E-05
1417109_at	tubulointerstitial nephritis antigen-like 1	Tinagl1	0.47	1.82E-05
1418481_at	protein kinase, membrane associated tyrosine/threonine 1	Pkmyt1	0.47	2.83E-05
1421477_at	complexin 2	Cplx2	0.47	0.000115817
1456135_s_at	paxillin	Pxn	0.469	6.07E-05
1437171_x_at	gelsolin	Gsn	0.469	0.000538387
1415818_at	annexin A6	Anxa6	0.469	7.40E-05
1424171_a_at	hydroxyacyl glutathione hydrolase	Hagh	0.469	0.004305547
1450780_s_at	high mobility group AT-hook 2	Hmga2	0.468	0.000182641
1450975_at	calcium channel, voltage-dependent, gamma subunit 4	Cacng4	0.468	2.88E-05
1455099_at	monoacylglycerol O-acyltransferase 2	Mogat2	0.468	5.95E-05
1425161_a_at	TraB domain containing	Trabd	0.468	0.000378449
1425784_a_at	olfactomedin 1	Olfm1	0.468	0.000271325
1424008_a_at	RNA binding protein with multiple splicing 2	Rbpms2	0.468	0.000287746

1424434_at	cDNA sequence BC024814	BC024814	0.468	5.00E-05
1449815_a_at	single-stranded DNA binding protein 2	Ssbp2	0.468	2.02E-05
1448468_a_at	potassium voltage-gated channel, shaker-related subfamily, beta member 1	Kcnab1	0.466	5.74E-05
1417668_at	reticulon 4 interacting protein 1	Rtn4ip1	0.466	0.000178298
1423129_at	soc-2 (suppressor of clear) homolog (C. elegans)	Shoc2	0.466	0.000276064
1426992_at	xenotropic and polytropic retrovirus receptor 1	Xpr1	0.465	1.03E-05
1416029_at	Kruppel-like factor 10	Klf10	0.465	2.14E-05
1437958_at	xenotropic and polytropic retrovirus receptor 1	Xpr1	0.465	0.007603081
1423418_at	farnesyl diphosphate synthetase	Fdps	0.465	3.51E-05
1434190_at	spermine synthase	Sms	0.465	0.001153942
1417585_at	nucleoporin 210	Nup210	0.464	8.52E-05
1424967_x_at	troponin T2, cardiac	Tnnt2	0.464	0.000543883
1430811_a_at	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	Nuf2	0.464	1.98E-05
1438717_a_at	oxysterol binding protein-like 6	Osbpl6	0.463	0.000655895
1427986_a_at	collagen, type XVI, alpha 1	Col16a1	0.463	0.00026579
1417934_at	DnaJ (Hsp40) homolog, subfamily C, member 4	Dnajc4	0.463	2.48E-05
1456584_x_at	3-phosphoglycerate dehydrogenase	Phgdh	0.463	1.23E-05
1448134_at	cDNA sequence X99384	X99384	0.463	2.17E-05
1437378_x_at	scavenger receptor class B, member 1	Scarb1	0.462	4.57E-05
1419817_s_at	ankyrin repeat and zinc finger domain containing 1	Ankzf1	0.462	0.000590641
1417605_s_at	calcium/calmodulin-dependent protein kinase I	Camk1	0.461	0.000137967
1434930_at	two pore channel 1	Tpcn1	0.461	0.000197386
1450258_a_at	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)	Elavl4	0.46	8.81E-05
1435222_at	forkhead box P1	Foxp1	0.46	0.000317603
1425840_a_at	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	Sema3f	0.46	0.000194931
1426902_at	coenzyme Q6 homolog (yeast)	Coq6	0.46	2.45E-05
1416791_a_at	nuclear RNA export factor 1 homolog (S. cerevisiae)	Nxf1	0.459	9.37E-05
1418117_at	NADH dehydrogenase (ubiquinone) Fe-S protein 4	Ndufs4	0.459	4.09E-05
1419267_at	nuclear transcription factor-Y beta	Nfyb	0.459	2.51E-05
1422443_at	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	Xpnpep1	0.458	1.40E-05
1416362_a_at	FK506 binding protein 4	Fkbp4	0.458	0.00028397
1424835_at	glutathione S-transferase, mu 4	Gstm4	0.458	2.81E-05
1452504_s_at	chitobiase, di-N-acetyl-	Ctbs	0.458	9.31E-05
1433733_a_at	cryptochrome 1 (photolyase-like)	Cry1	0.458	0.000446899
1417169_at	ubiquitin specific peptidase 2	Usp2	0.458	0.000134007
1423809_at	transcription factor 19	Tcf19	0.457	1.01E-05
1450001_a_at	Usher syndrome 1C homolog (human)	Ush1c	0.457	0.000298959
1452621_at	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2	Pcbd2	0.457	1.05E-05
1424113_at	laminin B1 subunit 1	Lamb1-1	0.456	0.003162985
1415944_at	syndecan 1	Sdc1	0.456	7.81E-05
1421026_at	guanine nucleotide binding protein, alpha 12	Gna12	0.456	0.001596265
1417629_at	proline dehydrogenase	Prodh	0.456	0.000153721
1423373_at	ribonuclease P/MRP 30 subunit (human)	Rpp30	0.455	1.43E-05
1416221_at	follistatin-like 1	Fstl1	0.455	1.11E-05
1450706_a_at	ADP-ribosylation factor-like 3	Arl3	0.455	1.57E-05
1418512_at	serine/threonine kinase 3 (Ste20, yeast	Stk3	0.455	0.000205195

	homolog)			
1455685_at	microtubule associated monoxygenase, calponin and LIM domain containing 2	Mical2	0.455	0.000201213
1452233_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	Abcc1	0.454	3.58E-05
1418269_at	lysyl oxidase-like 3	Loxl3	0.454	0.000250177
1417035_at	SAC3 domain containing 1	Sac3d1	0.454	0.000264724
1420256_x_at	NA	NA	0.454	0.000230987
1424230_at	exocyst complex component 6	Exoc6	0.454	0.00022643
1438430_at	high mobility group box transcription factor 1	Hbp1	0.454	4.41E-05
1419062_at	erythrocyte protein band 4.1-like 3	Epb4.1l3	0.453	3.01E-05
1437480_at	RIKEN cDNA 1110001A07 gene	1110001A07Rik	0.453	0.000613732
1417333_at	RAS p21 protein activator 4	Rasa4	0.453	0.000858847
1453596_at	inhibitor of DNA binding 2	Id2	0.453	0.008201045
1456543_at	prokineticin receptor 1	Prokr1	0.453	0.00117945
1450097_s_at	guanine nucleotide binding protein, alpha 12	Gna12	0.452	0.00018566
1450951_at	structural maintenace of chromosomes 3	Smc3	0.452	9.23E-05
1451409_at	RIKEN cDNA 2210021J22 gene	2210021J22Rik	0.452	4.31E-05
1455927_x_at	non-SMC element 1 homolog (S. cerevisiae)	Nsmce1	0.452	3.95E-05
1417701_at	protein phosphatase 1, regulatory (inhibitor) subunit 14c	Ppp1r14c	0.451	0.000116378
1428485_at	carbonic anyhydrase 12	Car12	0.451	4.09E-05
1419703_at	collagen, type V, alpha 3	Col5a3	0.451	5.19E-05
1428140_at	3-oxoacid CoA transferase 1	Oxct1	0.45	2.14E-05
1452894_at	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)	Elavl4	0.45	9.79E-05
1451128_s_at	kinesin family member 22	Kif22	0.45	0.000753345
1423297_at	adducin 3 (gamma)	Add3	0.45	7.75E-05
1423856_at	ribosomal protein L17	Rpl17	0.45	0.000186041
1455045_at	serine racemase	Srr	0.45	0.000133618
1423626_at	dystonin	Dst	0.45	0.001155174
1416934_at	X-linked myotubular myopathy gene 1	Mtm1	0.45	0.000840312
1425483_at	thymocyte selection-associated high mobility group box	Tox	0.449	0.000261318
1421963_a_at	cell division cycle 25 homolog B (S. pombe)	Cdc25b	0.449	0.000192185
1418228_at	NFU1 iron-sulfur cluster scaffold homolog (S. cerevisiae)	Nfu1	0.449	4.67E-05
1427385_s_at	actinin, alpha 1	Actn1	0.449	0.001109979
1460184_at	hydroxyacyl-Coenzyme A dehydrogenase	Hadh	0.449	1.05E-05
1420772_a_at	TSC22 domain family, member 3	Tsc22d3	0.449	3.68E-05
1451148_at	PTEN induced putative kinase 1	Pink1	0.448	7.51E-05
1436851_at	protein kinase N1	Pkn1	0.448	0.000519004
1424882_a_at	5'-nucleotidase domain containing 2	Nt5dc2	0.448	0.000203195
1448187_at	polymerase (DNA directed), delta 1, catalytic subunit	Pold1	0.448	3.96E-05
1415964_at	stearoyl-Coenzyme A desaturase 1	Scd1	0.447	1.30E-05
1450909_at	eukaryotic translation initiation factor 4E	Eif4e	0.447	0.000236048
1424105_a_at	pituitary tumor-transforming 1	Pttg1	0.447	0.000322867
1434767_at	expressed sequence C79407	C79407	0.447	0.002137877
1450493_at	KISS1 receptor	Kiss1r	0.447	0.000176936
1416163_at	COP9 (constitutive photomorphogenic) homolog, subunit 4 (Arabidopsis thaliana)	Cops4	0.447	6.55E-05
1449845_a_at	Eph receptor B4	Ephb4	0.447	7.21E-05
1421336_at	prospero-related homeobox 1	Prox1	0.447	0.026681122
1437843_s_at	nucleoporin like 1	Nupl1	0.447	0.000210525
1452954_at	ubiquitin-conjugating enzyme E2C	Ube2c	0.446	0.000700547
1448198_a_at	NADH dehydrogenase (ubiquinone) 1 beta	Ndufb8	0.446	1.17E-05

	subcomplex 8			
1437863_at	butyrylcholinesterase	Bche	0.446	0.000146997
1418011_a_at	SH3-domain GRB2-like B1 (endophilin)	Sh3glb1	0.446	0.000157673
1435315_s_at	RIKEN cDNA 2900034E22 gene	2900034E22Rik	0.445	0.002867157
1421115_a_at	zinc finger, DHHC domain containing 16	Zdhhc16	0.445	1.33E-05
1419286_s_at	intraflagellar transport 81 homolog (Chlamydomonas)	Ift81	0.445	0.000455432
1416050_a_at	scavenger receptor class B, member 1	Scarb1	0.445	1.25E-05
1433684_at	chromatin modifying protein 6	Chmp6	0.445	2.60E-05
1420824_at	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	Sema4d	0.445	8.06E-06
1426769_s_at	mastermind like 1 (Drosophila)	Maml1	0.444	2.44E-05
1417015_at	Ras association (RalGDS/AF-6) domain family member 3	Rassf3	0.443	0.000142753
1436991_x_at	gelsolin	Gsn	0.443	0.000609887
1438292_x_at	adenosine kinase	Adk	0.443	0.000124235
1449509_at	small EDRK-rich factor 1	Serf1	0.443	9.60E-05
1453208_at	RIKEN cDNA 2700089E24 gene	2700089E24Rik	0.443	0.00051432
1449675_at	cyclin B1	Ccnb1	0.442	0.033886689
1452215_at	RIKEN cDNA 9130401M01 gene	9130401M01Rik	0.442	2.18E-05
1419031_at	fatty acid desaturase 2	Fads2	0.441	8.00E-06
1423119_at	radial spokehead-like 2B	Rshl2b	0.441	8.73E-05
1455877_a_at	nanos homolog 1 (Drosophila)	Nanos1	0.441	8.73E-05
1437917_at	RIKEN cDNA D530037H12 gene	D530037H12Rik	0.441	0.047626461
1420524_a_at	mannan-binding lectin serine peptidase 2	Masp2	0.44	0.005736704
1433445_x_at	similar to Hmgcs1 protein	LOC100040592	0.44	1.95E-05
1417524_at	cornichon homolog 2 (Drosophila)	Cnih2	0.44	7.90E-05
1418478_at	LIM domain only 1	Lmo1	0.44	0.000697398
1419835_s_at	plectin 1	Plec1	0.439	0.00020845
1417411_at	nucleosome assembly protein 1-like 5	Nap1l5	0.439	4.66E-05
1451370_at	hypothetical protein LOC622404	RP23-195K8.6	0.439	0.00059742
1434695_at	denticleless homolog (Drosophila)	Dtl	0.438	8.97E-05
1415945_at	minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	Mcm5	0.438	1.25E-05
1415708_at	taurine upregulated gene 1	Tug1	0.438	4.01E-05
1415727_at	apolipoprotein A-I binding protein	Apoa1bp	0.438	7.45E-05
1426516_a_at	lipin 1	Lpin1	0.438	2.74E-05
1436689_a_at	aldehyde dehydrogenase 9, subfamily A1	Aldh9a1	0.438	2.38E-05
1424363_at	Mycbp associated protein	Mycbpap	0.437	0.000107941
1417360_at	mutL homolog 1 (E. coli)	Mlh1	0.437	1.28E-05
1419266_at	nuclear transcription factor-Y beta	Nfyb	0.437	3.39E-05
1421506_at	olfactory receptor 78	Olfr78	0.437	0.002387802
1431028_a_at	pantothenate kinase 1	Pank1	0.437	0.000606512
1419664_at	serine racemase	Srr	0.436	0.003456347
1428181_at	electron transferring flavoprotein, beta polypeptide	Etfb	0.436	1.43E-05
1424027_at	paxillin	Pxn	0.436	0.000208404
1448154_at	N-myc downstream regulated gene 2	Ndrg2	0.435	9.28E-05
1422747_at	CHK2 checkpoint homolog (S. pombe)	Chek2	0.435	2.82E-05
1420722_at	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3	Elovl3	0.435	0.001497715
1416492_at	cyclin E1	Ccne1	0.435	4.45E-05
1429246_a_at	annexin A6	Anxa6	0.435	9.33E-05
1430848_a_at	RIKEN cDNA 2410017P07 gene	2410017P07Rik	0.435	0.000805853
1417267_s_at	FK506 binding protein 11	Fkbp11	0.435	0.000736426
1426782_at	G protein-coupled receptor 125	Gpr125	0.435	1.51E-05

1433675_at	small nucleolar RNA, C/D box 22	Snord22	0.435	7.51E-05
1452500_at	NA	NA	0.435	0.026456566
1428699_at	spermine synthase	Sms	0.435	0.000116369
1448461_a_at	THO complex 7 homolog (Drosophila)	Thoc7	0.434	5.54E-05
1415812_at	gelsolin	Gsn	0.434	6.76E-05
1428394_at	phytanoyl-CoA dioxygenase domain containing 1	Phyhd1	0.433	4.11E-05
1450982_at	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	Slc9a3r1	0.433	5.75E-05
1456393_at	programmed cell death 4	Pdcd4	0.433	0.000697269
1417750_a_at	solute carrier family 25, member 37	Slc25a37	0.432	4.17E-05
1425524_at	RNA binding motif protein 25	Rbm25	0.432	0.001841956
1415943_at	syndecan 1	Sdc1	0.432	2.13E-05
1440201_at	solute carrier family 8 (sodium/calcium exchanger), member 1	Slc8a1	0.432	0.049208467
1456603_at	RIKEN cDNA 1500005K14 gene	1500005K14Rik	0.432	9.60E-05
1448807_at	histamine receptor H3	Hrh3	0.431	5.59E-05
1419886_at	DNA segment, Chr X, ERATO Doi 223, expressed	DXErtd223e	0.431	0.001484527
1424210_at	ER lipid raft associated 1	Erlin1	0.431	0.000136286
1423463_a_at	DNA segment, Chr 2, ERATO Doi 750, expressed	D2Ertd750e	0.431	0.000349579
1448314_at	cell division cycle 2 homolog A (S. pombe)	Cdc2a	0.431	0.000152181
1455758_at	protein kinase C, gamma	Prkcc	0.431	4.61E-05
1416185_a_at	alcohol dehydrogenase 5 (class III), chi polypeptide	Adh5	0.431	2.85E-05
1425241_a_at	WD repeat and SOCS box-containing 1	Wsb1	0.431	8.24E-05
1436946_s_at	predicted gene, 100041120	100041120	0.431	0.00026579
1455972_x_at	hydroxyacyl-Coenzyme A dehydrogenase	Hadh	0.43	6.85E-05
1428353_at	forkhead box K2	Foxk2	0.43	1.22E-05
1449098_a_at	polymerase (DNA directed), iota	Poli	0.43	0.00025849
1423093_at	inner centromere protein	Incenp	0.43	6.45E-05
1429615_at	zinc finger protein 91	Zfp91	0.43	0.000329317
1450127_a_at	glucagon receptor	Gcgr	0.43	0.000165503
1433446_at	similar to Hmgcs1 protein	LOC100040592	0.43	7.31E-05
1451364_at	polymerase (RNA) III (DNA directed) polypeptide G like	Polr3gl	0.429	6.73E-05
1417596_at	B9 protein domain 1	B9d1	0.429	0.000140351
1438789_s_at	dihydropyrimidinase-like 3	Dpysl3	0.429	0.000547628
AFFX-PyruCarbMur/L09192_MB_at	pyruvate carboxylase	Pcx	0.429	2.81E-05
1452195_s_at	Sfi1 homolog, spindle assembly associated (yeast)	Sfi1	0.429	0.002517253
1438390_s_at	pituitary tumor-transforming 1	Pttg1	0.429	0.000218871
1456315_a_at	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a	Ptpla	0.429	3.36E-05
1451126_at	MAF1 homolog (S. cerevisiae)	Maf1	0.429	7.66E-05
1426502_s_at	glutamic pyruvic transaminase, soluble	Gpt	0.429	1.42E-05
1418530_at	nucleoporin 160	Nup160	0.428	3.39E-05
1448113_at	stathmin 1	Stmn1	0.428	0.000879252
1460278_a_at	DNA segment, Chr 15, Wayne State University 75, expressed	D15Wsu75e	0.428	0.000206855
1421431_at	polymerase I and transcript release factor	Ptrf	0.427	0.007919027
1424351_at	WAP four-disulfide core domain 2	Wfdc2	0.427	2.13E-05
1417301_at	frizzled homolog 6 (Drosophila)	Fzd6	0.427	6.38E-05
1450970_at	glutamate oxaloacetate transaminase 1, soluble	Got1	0.427	0.000222432

1420046_s_at	MAF1 homolog (S. cerevisiae)	Maf1	0.427	1.72E-05
1419229_at	reproductive homeobox 4B	Rhox4b	0.426	4.04E-05
1427579_at	rhomboid, veinlet-like 3 (Drosophila)	Rhbdl3	0.426	0.000330302
1422470_at	BCL2/adenovirus E1B interacting protein 3	Bnip3	0.426	0.000180618
1416439_at	RIKEN cDNA 2410015N17 gene	2410015N17Rik	0.425	8.82E-05
1448441_at	CDC28 protein kinase 1b	Cks1b	0.425	0.000127254
1418030_at	solute carrier organic anion transporter family, member 3a1	Slco3a1	0.425	5.65E-05
1460361_at	RIKEN cDNA 5033414D02 gene	5033414D02Rik	0.425	0.000100874
1417420_at	cyclin D1	Ccnd1	0.425	5.59E-05
1449059_a_at	3-oxoacid CoA transferase 1	Oxct1	0.425	1.87E-05
1452151_at	GRAM domain containing 4	Gramd4	0.425	2.17E-05
1418305_s_at	nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs)	Nola1	0.425	1.94E-05
1423598_at	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	Atp8a1	0.424	0.000733173
1419274_at	expressed sequence C80913	C80913	0.424	6.70E-05
1422653_at	centrosomal protein 70	Cep70	0.424	0.000225917
1439399_a_at	small nucleolar RNA host gene (non-protein coding) 1	Snhg1	0.424	3.79E-05
1417313_at	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)	Lsm7	0.424	5.76E-05
1417457_at	CDC28 protein kinase regulatory subunit 2	Cks2	0.424	5.24E-05
1415735_at	damage specific DNA binding protein 1	Ddb1	0.423	1.39E-05
1415890_at	3'-phosphoadenosine 5'-phosphosulfate synthase 1	Papss1	0.423	4.47E-05
1450350_a_at	Jun dimerization protein 2	Jdp2	0.423	4.87E-05
1432384_a_at	methyltransferase like 6	Mettl6	0.423	3.79E-05
1423642_at	tubulin, beta 2c1	Tubb2c1	0.422	0.000195806
1426430_at	jagged 2	Jag2	0.422	9.54E-05
1455363_at	brain-specific angiogenesis inhibitor 1	Bai1	0.422	0.000309568
1451405_at	propionyl-Coenzyme A carboxylase, alpha polypeptide	Pcca	0.422	6.85E-05
1426929_at	bruno-like 4, RNA binding protein (Drosophila)	Brunol4	0.422	0.000515769
1425492_at	bone morphogenetic protein receptor, type 1A	Bmpr1a	0.422	5.19E-05
1437271_at	cardiotrophin-like cytokine factor 1	Clcf1	0.421	5.19E-05
1454785_at	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	Dusp11	0.421	0.00032516
1428029_a_at	H2A histone family, member V	H2afv	0.421	0.000121073
1448498_at	ribosomal protein S6 kinase, polypeptide 4	Rps6ka4	0.421	9.46E-05
1448143_at	aldehyde dehydrogenase 2, mitochondrial	Aldh2	0.421	0.000364532
1435221_at	forkhead box P1	Foxp1	0.42	0.007603081
1417886_at	integrator complex subunit 5	Ints5	0.42	0.00043454
1419581_at	discs, large homolog 4 (Drosophila)	Dlg4	0.42	9.78E-06
1422771_at	MAD homolog 6 (Drosophila)	Smad6	0.419	0.000743683
1417507_at	cytochrome b-561	Cyb561	0.419	1.94E-05
1416956_at	potassium voltage-gated channel, shaker-related subfamily, beta member 2	Kcnab2	0.418	0.000317665
1448447_at	vacuolar protein sorting 28 (yeast)	Vps28	0.418	3.89E-05
1433683_at	RNA binding motif protein 35b	Rbm35b	0.417	5.59E-05
1420530_at	D4, zinc and double PHD fingers family 1	Dpf1	0.417	7.95E-05
1421052_a_at	spermine synthase	Sms	0.417	0.000218558
1418448_at	Harvey rat sarcoma oncogene, subgroup R	Rras	0.416	5.59E-05
1423220_at	eukaryotic translation initiation factor 4E	Eif4e	0.416	0.000379285
1434445_at	DNA segment, Chr 15, Wayne State University 169, expressed	D15Wsu169e	0.416	0.000197022
1416623_at	thrombospondin 3	Thbs3	0.416	0.004527628

1449325_at	fatty acid desaturase 2	Fads2	0.416	0.000109073
1453527_a_at	neuralized-like homolog (Drosophila)	Neurl	0.415	0.000727519
1426667_a_at	unc-84 homolog A (C. elegans)	Unc84a	0.415	0.001824251
1427373_at	adhesion molecule with Ig like domain 1	Amigo1	0.415	0.000172615
1417466_at	regulator of G-protein signaling 5	Rgs5	0.415	0.001130407
1426606_at	cartilage acidic protein 1	Crtac1	0.415	0.000105546
1450111_a_at	nudix (nucleoside diphosphate linked moiety X)-type motif 8	Nudt8	0.414	0.000100247
1422479_at	acyl-CoA synthetase short-chain family member 2	Acss2	0.414	8.21E-05
1416112_at	cytochrome c oxidase, subunit VIIIa	Cox8a	0.414	3.31E-05
1417555_at	ATPase family, AAA domain containing 1	Atad1	0.413	0.003561874
1433444_at	similar to Hmgcs1 protein	LOC100040592	0.413	5.42E-05
1416954_at	solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10	Slc25a10	0.413	5.80E-05
1434210_s_at	leucine-rich repeats and immunoglobulin-like domains 1	Lrig1	0.413	3.96E-05
1427787_at	trans-acting transcription factor 6	Sp6	0.412	0.000204158
1419045_at	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	Slc25a23	0.412	5.38E-05
1424118_a_at	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	Spc25	0.412	9.87E-05
1450156_a_at	hyaluronan mediated motility receptor (RHAMM)	Hmmr	0.412	0.0010114
1448669_at	dickkopf homolog 3 (Xenopus laevis)	Dkk3	0.412	0.0001172
1451012_a_at	cold shock domain protein A	Csda	0.412	0.000737237
1424763_at	RIKEN cDNA 1700027N10 gene	1700027N10Rik	0.412	0.000483577
1449511_a_at	single stranded DNA binding protein 4	Ssbp4	0.412	0.000284614
1452098_at	CTF18, chromosome transmission fidelity factor 18 homolog (S. cerevisiae)	Chtf18	0.411	2.70E-05
1434119_at	DNA segment, Chr 2, Wayne State University 81, expressed	D2Wsu81e	0.411	5.34E-05
1417878_at	E2F transcription factor 1	E2f1	0.411	9.36E-05
1423065_at	DNA methyltransferase 3A	Dnmt3a	0.411	0.001120373
1451928_a_at	RAD18 homolog (S. cerevisiae)	Rad18	0.411	0.000860634
1422203_at	solute carrier family 18 (vesicular monoamine), member 3	Slc18a3	0.41	1.65E-05
1417576_a_at	OTU domain, ubiquitin aldehyde binding 2	Otub2	0.41	0.000767702
1427989_at	anti-Mullerian hormone type 2 receptor	Amhr2	0.409	0.000430937
1452371_at	splicing factor, arginine/serine-rich 11	Sfrs11	0.409	5.42E-05
1421066_at	Janus kinase 2	Jak2	0.409	0.000205425
1427153_at	branched chain ketoacid dehydrogenase E1, beta polypeptide	Bckdhb	0.409	9.48E-05
1423066_at	DNA methyltransferase 3A	Dnmt3a	0.409	0.001021258
1424511_at	aurora kinase A	Aurka	0.409	4.31E-05
1423650_at	ring finger protein 26	Rnf26	0.408	1.36E-05
1426657_s_at	3-phosphoglycerate dehydrogenase	Phgdh	0.408	0.000158015
1423183_at	leucine-rich repeat LGI family, member 1	Lgi1	0.408	5.61E-05
1454639_x_at	ribosomal protein L41	Rpl41	0.408	0.000242155
1422692_at	SUB1 homolog (S. cerevisiae)	Sub1	0.408	0.000708477
1459983_at	inositol (myo)-1(or 4)-monophosphatase 2	Impa2	0.407	6.09E-05
1427294_a_at	solute carrier family 38, member 10	Slc38a10	0.407	0.000238692
1419173_at	aminoacylase 1	Acy1	0.407	1.89E-05
1424561_at	endothelin converting enzyme 2	Ece2	0.406	0.016262836
1455385_at	SH3-domain GRB2-like B1 (endophilin)	Sh3glb1	0.406	0.000492376
1421276_a_at	dystonin	Dst	0.406	0.0024842
1436038_a_at	phosphatidylinositol glycan anchor biosynthesis, class P	Pigp	0.406	0.000176107

1438974_x_at	phosphatidylinositol transfer protein, membrane-associated 1	Pitpnm1	0.406	0.000504878
1452316_at	integrator complex subunit 12	Ints12	0.406	0.000799781
1438853_x_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	Ddx54	0.405	4.73E-05
1427505_a_at	CASP2 and RIPK1 domain containing adaptor with death domain	Cradd	0.405	0.000308164
1456037_x_at	prolactin regulatory element binding	Preb	0.405	0.013210568
1448938_at	replication protein A3	Rpa3	0.405	0.000414086
1425615_a_at	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	Pck2	0.405	0.000503259
1452683_at	DnaJ (Hsp40) homolog, subfamily C, member 8	Dnajc8	0.405	7.17E-05
1436959_x_at	nasal embryonic LHRH factor	Nelf	0.404	8.60E-05
1422264_s_at	Kruppel-like factor 9	Klf9	0.404	0.012479312
1437841_x_at	cold shock domain containing C2, RNA binding	Csdc2	0.404	0.001139962
1437908_a_at	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	Ergic1	0.404	9.92E-05
1436121_a_at	non-SMC element 1 homolog (S. cerevisiae)	Nsmce1	0.404	4.67E-05
1452342_at	amyloid beta (A4) precursor protein-binding, family B, member 2	Apbb2	0.403	9.57E-05
1439269_x_at	minichromosome maintenance deficient 7 (S. cerevisiae)	Mcm7	0.403	0.000109073
1451180_a_at	5'-nucleotidase, cytosolic III-like	Nt5c3l	0.403	0.000250971
1424095_at	RNA terminal phosphate cyclase domain 1	Rtcd1	0.403	2.86E-05
1423224_at	tectonic family member 2	Tctn2	0.403	0.000339559
1417584_at	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	Slc11a2	0.403	7.55E-05
1419580_at	discs, large homolog 4 (Drosophila)	Dlg4	0.403	0.000146237
1426917_s_at	secernin 3	Scrn3	0.403	0.000211994
1424776_a_at	solute carrier family 25, member 28	Slc25a28	0.403	0.000101175
1449080_at	histone deacetylase 2	Hdac2	0.403	0.000202995
1416188_at	GM2 ganglioside activator protein	Gm2a	0.402	0.000242388
1426724_at	calponin 3, acidic	Cnn3	0.402	9.90E-05
1416757_at	Zwilch, kinetochore associated, homolog (Drosophila)	Zwilch	0.402	0.002163484
1454149_a_at	cyclin L2	Ccnl2	0.402	0.000342792
1416828_at	synaptosomal-associated protein 25	Snap25	0.401	0.000148681
1420565_at	homeo box A1	Hoxa1	0.401	0.000332251
1418902_at	chitinase domain containing 1	Chid1	0.401	4.50E-05
1448806_at	matrix metallopeptidase 24	Mmp24	0.401	0.000182687
1434610_at	plectin 1	Plec1	0.401	0.000722742
1455242_at	forkhead box P1	Foxp1	0.401	0.000225917
1430776_s_at	ankyrin repeat domain 24	Ankrd24	0.401	0.000680973
1448555_at	RNA polymerase II associated protein 3	Rpap3	0.401	2.87E-05
1448363_at	yes-associated protein 1	Yap1	0.4	0.000564269
1448371_at	myosin light chain, phosphorylatable, fast skeletal muscle	Mylpf	0.4	0.000114323
1437208_at	septin 10	Sept10	0.4	0.002250175
1427048_at	smoothened homolog (Drosophila)	Smo	0.4	9.96E-05
1417645_at	sarcospan	Sspn	0.4	0.002408064
1418181_at	protein tyrosine phosphatase 4a3	Ptp4a3	0.4	0.0003536
1436838_x_at	coactosin-like 1 (Dictyostelium)	Cotl1	0.4	0.000137389
1417155_at	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	Mycn	0.399	0.000109797
1452598_at	GINS complex subunit 1 (Psf1 homolog)	Gins1	0.399	9.90E-05
1417094_at	acyl-CoA thioesterase 7	Acot7	0.398	0.000329057
1451305_at	chibby homolog 1 (Drosophila)	Cby1	0.398	8.80E-05
1437621_x_at	3-phosphoglycerate dehydrogenase	Phgdh	0.398	0.000357255

1425271_at	proteasome (prosome, macropain) 26S subunit, ATPase 3, interacting protein	Psmc3ip	0.398	8.74E-05
1426624_a_at	yippee-like 3 (Drosophila)	Ypel3	0.398	5.27E-05
1452026_a_at	phospholipase A2, group XIIA	Pla2g12a	0.398	0.000763374
1429043_at	survival motor neuron domain containing 1	Smndc1	0.397	0.000212622
1425491_at	bone morphogenetic protein receptor, type 1A	Bmpr1a	0.397	0.000198697
1448130_at	farnesyl diphosphate farnesyl transferase 1	Fdft1	0.397	3.02E-05
1420674_at	phospholipase A2, group IIE	Pla2g2e	0.397	9.15E-05
1418128_at	adenylate cyclase 6	Adcy6	0.397	0.000251514
1439443_x_at	transketolase	Tkt	0.397	4.98E-05
1427357_at	cytidine deaminase	Cda	0.396	0.000112704
1425272_at	epithelial membrane protein 2	Emp2	0.396	0.001994339
1422021_at	sprouty homolog 4 (Drosophila)	Spry4	0.396	0.001232903
1420909_at	vascular endothelial growth factor A	Vegfa	0.396	0.00010213
1418751_at	suppression inducing transmembrane adaptor 1	Sit1	0.395	0.000268044
1425012_at	guanine nucleotide binding protein (G protein), gamma 5	Gng5	0.395	0.007535461
1422616_s_at	WD repeat domain 54	Wdr54	0.395	9.96E-05
1449914_at	RIB43A domain with coiled-coils 1	Ribc1	0.394	0.000211415
1450191_a_at	SRY-box containing gene 13	Sox13	0.394	0.000138654
1451122_at	isopentenyl-diphosphate delta isomerase	Idi1	0.394	0.000404186
1452094_at	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	P4ha1	0.394	5.33E-05
1428093_at	TraB domain containing	Trabd	0.394	0.000149179
1423213_at	plexin C1	Plxnc1	0.393	9.89E-05
1449633_s_at	5'-nucleotidase, cytosolic III-like	Nt5c3l	0.393	0.00164285
1434787_at	ADP-ribosylation factor 3	Arf3	0.393	6.57E-05
1451260_at	aldehyde dehydrogenase 1 family, member B1	Aldh1b1	0.392	0.001057269
1425310_a_at	EMI domain containing 2	Emid2	0.392	5.59E-05
1456003_a_at	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	Slc1a4	0.392	0.000218172
1436566_at	Rab40b, member RAS oncogene family	Rab40b	0.392	0.000339736
1449219_at	fatty acid desaturase 3	Fads3	0.392	0.001555755
1456055_x_at	polymerase (DNA directed), delta 1, catalytic subunit	Pold1	0.391	0.000251641
1427882_at	deoxynucleotidyltransferase, terminal, interacting protein 2	Dnttip2	0.391	3.18E-05
1421154_at	hyperpolarization-activated, cyclic nucleotide-gated K+ 2	Hcn2	0.391	0.001330646
1417047_at	prominin 2	Prom2	0.391	9.58E-05
1428328_at	nucleoporin 50	Nup50	0.391	5.24E-05
1454694_a_at	topoisomerase (DNA) II alpha	Top2a	0.391	2.83E-05
1432360_a_at	transmembrane and tetratricopeptide repeat containing 4	Tmtc4	0.39	0.000246029
1418295_s_at	diacylglycerol O-acyltransferase 1	Dgat1	0.39	0.000330056
1425656_a_at	brain-specific angiogenesis inhibitor 1-associated protein 2	Baiap2	0.39	0.002630771
1434931_at	neogenin	Neo1	0.39	7.65E-05
1416674_at	protein tyrosine phosphatase, receptor type, U	Ptpru	0.389	0.000107724
1416553_at	stimulated by retinoic acid 13	Stra13	0.389	3.59E-05
1421065_at	Janus kinase 2	Jak2	0.389	8.10E-05
1450730_at	heparan sulfate 2-O-sulfotransferase 1	Hs2st1	0.389	9.67E-05
1456541_x_at	ATPase family, AAA domain containing 3A	Atad3a	0.388	0.000193714
1450376_at	Max interacting protein 1	Mxi1	0.388	6.73E-05
1416381_a_at	peroxiredoxin 5	Prdx5	0.388	2.42E-05

1450561_a_at	surfeit gene 1	Surf1	0.388	0.000162686
1425318_a_at	transmembrane protein 116	Tmem116	0.388	0.000172909
1426668_at	solute carrier family 30 (zinc transporter), member 9	Slc30a9	0.388	5.44E-05
1423718_at	adenylate kinase 3	Ak3	0.388	0.000181565
1433605_at	inositol polyphosphate-5-phosphatase A	Inpp5a	0.387	4.66E-05
1427021_s_at	eukaryotic translation initiation factor 3, subunit F	Eif3f	0.387	5.44E-05
1456307_s_at	adenylate cyclase 7	Adcy7	0.387	0.000547523
1450383_at	low density lipoprotein receptor	Ldlr	0.387	0.0031306
1428585_at	actinin, alpha 1	Actn1	0.387	0.000160694
1421081_a_at	barrier to autointegration factor 1	Banf1	0.386	0.000171163
1433924_at	NA	NA	0.386	0.000348937
1437651_a_at	dystrobrevin, beta	Dtnb	0.386	0.001205482
1418185_at	RIKEN cDNA 4733401H18 gene	4733401H18Rik	0.386	0.000314126
1456380_x_at	calponin 3, acidic	Cnn3	0.386	4.39E-05
1451015_at	transketolase	Tkt	0.386	0.002457828
1436517_at	H1 histone family, member X	H1fx	0.386	0.001466312
1452011_a_at	UDP-glucuronate decarboxylase 1	Uxs1	0.385	0.000700547
1417986_at	Notch-regulated ankyrin repeat protein	Nrarp	0.385	0.002886104
1424250_a_at	Rho guanine nucleotide exchange factor (GEF) 3	Arhgef3	0.385	0.000736414
1428333_at	RIKEN cDNA 2900062L11 gene	2900062L11Rik	0.385	6.79E-05
1453355_at	WNK lysine deficient protein kinase 2	Wnk2	0.385	0.002876389
1425560_a_at	S100 calcium binding protein A16	S100a16	0.385	0.003286219
1450813_a_at	troponin I, skeletal, slow 1	Tnni1	0.385	0.000153483
1424277_at	UCHL5 interacting protein	Uchl5ip	0.385	0.000244444
1451508_at	La ribonucleoprotein domain family, member 2	Larp2	0.384	7.85E-05
1423673_at	leucine zipper, down-regulated in cancer 1-like	Ldoc1l	0.384	0.000172069
1417276_at	tubby-like protein 2	Tulp2	0.384	0.000172203
1448485_at	gamma-glutamyltransferase 1	Ggt1	0.384	0.005859831
1425029_a_at	membrane bound O-acyltransferase domain containing 2	Mboat2	0.383	0.000187162
1416730_at	RNA terminal phosphate cyclase-like 1	Rcl1	0.383	4.49E-05
1417768_at	patatin-like phospholipase domain containing 8	Pnpla8	0.383	2.95E-05
1439368_a_at	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	Slc9a3r2	0.383	0.000164969
1426731_at	desmin	Des	0.383	0.000213847
1431231_at	histone cluster 1, H3f	Hist1h3f	0.383	0.003339248
1449076_x_at	acireductone dioxygenase 1	Adi1	0.383	5.24E-05
1438761_a_at	predicted gene, EG666231	EG666231	0.383	0.000100247
1451002_at	aconitase 2, mitochondrial	Aco2	0.382	6.73E-05
1417977_at	eukaryotic translation initiation factor 4E member 3	Eif4e3	0.382	6.73E-05
1448771_a_at	ferritin heavy chain 1	Fth1	0.382	0.000514539
1437327_x_at	enolase-phosphatase 1	Enoph1	0.382	0.000136827
1427055_at	thioesterase superfamily member 4	Them4	0.382	0.000291628
1426052_at	mutL homolog 3 (E coli)	Mlh3	0.381	0.000862124
1417234_at	matrix metallopeptidase 11	Mmp11	0.381	8.08E-05
1415966_a_at	NADH dehydrogenase (ubiquinone) flavoprotein 1	Ndufv1	0.381	0.000377138
1418713_at	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 1	Pcbd1	0.381	0.000138487
1422716_a_at	acid phosphatase 1, soluble	Acp1	0.381	0.03042085
1417355_at	paternally expressed 3	Peg3	0.381	5.58E-05
1417147_at	RIKEN cDNA B230317C12 gene	B230317C12Rik	0.381	0.000836785

1425522_at	RNA binding motif protein 25	Rbm25	0.381	0.003424707
1424753_at	nudix (nucleoside diphosphate linked moiety X)-type motif 14	Nudt14	0.38	0.0005733
1417516_at	DNA-damage inducible transcript 3	Ddit3	0.38	0.000367734
1425041_at	LIM homeobox protein 3	Lhx3	0.38	0.000194256
1424991_s_at	thymidylate synthase	Tyms	0.379	0.000139279
1433999_at	STE20-like kinase (yeast)	Slk	0.379	0.000257791
1421083_x_at	barrier to autointegration factor 1	Banf1	0.379	0.00051432
1436952_at	Kruppel-like factor 9	Klf9	0.379	0.000174118
1420491_at	eukaryotic translation initiation factor 2, subunit 1 alpha	Eif2s1	0.379	0.000388448
1450914_at	protein phosphatase 1, regulatory (inhibitor) subunit 14B	Ppp1r14b	0.378	0.003611357
1448222_x_at	cytochrome c oxidase, subunit VIIIa	Cox8a	0.378	2.31E-05
1449939_s_at	delta-like 1 homolog (Drosophila)	Dlk1	0.378	0.000828781
1434239_at	ribosomal RNA processing 12 homolog (S. cerevisiae)	Rrp12	0.378	0.00238231
1417978_at	eukaryotic translation initiation factor 4E member 3	Eif4e3	0.378	0.000116996
1426431_at	jagged 2	Jag2	0.378	0.003445073
1448698_at	cyclin D1	Ccnd1	0.378	0.000236748
1434261_at	signal-induced proliferation-associated 1 like 2	Sipa1l2	0.378	0.000112935
1423477_at	zinc finger protein of the cerebellum 1	Zic1	0.378	0.0296979
1450748_at	sphingomyelin phosphodiesterase 3, neutral	Smpd3	0.377	0.044220457
1448740_at	RAN guanine nucleotide release factor	Rangrf	0.377	0.000164205
1437563_at	PHD finger protein 20-like 1	Phf20l1	0.377	0.004131455
1416069_at	phosphofructokinase, platelet	Pfkp	0.376	0.000178873
1454714_x_at	3-phosphoglycerate dehydrogenase	Phgdh	0.376	0.000158609
1418159_at	transcription factor CP2	Tcfcp2	0.376	0.001082737
1428065_at	solute carrier family 44, member 2	Slc44a2	0.375	0.000407763
1448315_a_at	pyrroline-5-carboxylate reductase family, member 2	Pycr2	0.375	2.51E-05
1418778_at	coiled-coil domain containing 109B	Ccdc109b	0.375	4.31E-05
1451248_at	protein arginine N-methyltransferase 7	Prmt7	0.375	6.13E-05
1455434_a_at	kinectin 1	Ktn1	0.375	5.95E-05
1416030_a_at	minichromosome maintenance deficient 7 (S. cerevisiae)	Mcm7	0.375	0.000259324
1452540_a_at	histone cluster 1, H2bp	Hist1h2bp	0.375	0.000418214
1455291_s_at	zinc and ring finger 2	Znrf2	0.374	0.000376264
1423680_at	fatty acid desaturase 1	Fads1	0.374	0.000335933
1427533_at	ALS2 C-terminal like	Als2cl	0.374	0.001247785
1452324_at	plasmacytoma variant translocation 1	Pvt1	0.374	0.000113608
1428225_s_at	heterogeneous nuclear ribonucleoprotein D-like	Hnrpdl	0.374	0.000526878
1460396_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	Ddx54	0.374	0.000912264
1416245_at	aurora kinase A interacting protein 1	Aurkaip1	0.373	0.000661555
1422774_at	RIKEN cDNA 1700088E04 gene	1700088E04Rik	0.373	0.000122049
1451759_at	mannan-binding lectin serine peptidase 2	Masp2	0.373	0.001979902
1426767_at	WD repeat domain 90	Wdr90	0.373	0.001751663
1438731_at	N-sulfoglucosamine sulfohydrolase (sulfamidase)	Sgsh	0.373	0.000573591
1421082_s_at	barrier to autointegration factor 1	Banf1	0.373	2.60E-05
1419809_s_at	component of oligomeric golgi complex 4	Cog4	0.373	0.000521115
1422186_s_at	cytochrome b5 reductase 3	Cyb5r3	0.373	4.15E-05
1448005_at	SAM and SH3 domain containing 1	Sash1	0.373	3.23E-05
1448241_at	GM2 ganglioside activator protein	Gm2a	0.373	2.99E-05
1422762_at	kinesin family member 17	Kif17	0.373	0.000336659

1438173_x_at	polyamine-modulated factor 1	Pmf1	0.373	0.000132805
1424365_at	RIKEN cDNA 1810037I17 gene	1810037I17Rik	0.373	0.000450048
1415936_at	breast cancer anti-estrogen resistance 3	Bcar3	0.372	0.0019238
1424205_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	Smarca5	0.372	0.00187762
1424555_at	RIKEN cDNA 9430015G10 gene	9430015G10Rik	0.372	0.00091581
1418102_at	hairy and enhancer of split 1 (Drosophila)	Hes1	0.371	0.000198891
1424231_s_at	exocyst complex component 6	Exoc6	0.371	0.000169912
1433674_a_at	small nucleolar RNA, C/D box 22	Snord22	0.371	2.06E-05
1425760_a_at	phosphatidylinositol transfer protein, membrane-associated 1	Pitpnm1	0.371	0.008853965
1437343_x_at	ATPase family, AAA domain containing 3A	Atad3a	0.371	0.000603742
1455812_x_at	vasorin	Vasn	0.37	0.019365703
1425017_at	protocadherin alpha 6	Pcdha6	0.37	0.000142448
1460198_a_at	proteasome (prosome, macropain) subunit, beta type 3	Psmb3	0.37	0.001766218
1435736_x_at	RAB, member of RAS oncogene family-like 4	Rabl4	0.37	0.000133336
1452073_at	RIKEN cDNA 6720460F02 gene	6720460F02Rik	0.37	0.00120096
1425830_a_at	RIKEN cDNA 2810452K22 gene	2810452K22Rik	0.369	6.73E-05
1454833_at	ribosomal protein L35	Rpl35	0.369	0.016508155
1433543_at	anillin, actin binding protein	Anln	0.369	0.000244618
1421926_at	mitogen-activated protein kinase 11	Mapk11	0.368	0.000184888
1448930_at	RIKEN cDNA 3010026O09 gene	3010026O09Rik	0.368	0.00106544
1423407_a_at	fibulin 2	Fbln2	0.368	0.000357629
1438178_x_at	ATPase family, AAA domain containing 3A	Atad3a	0.368	0.000137205
1428069_at	cell division cycle associated 7	Cdca7	0.368	7.39E-05
1438758_at	acireductone dioxygenase 1	Adi1	0.368	0.00010346
1429427_s_at	transcription factor 7-like 2, T-cell specific, HMG-box	Tcf7l2	0.367	0.001809185
1416841_at	RIKEN cDNA 1110059E24 gene	1110059E24Rik	0.367	0.001540388
1448903_at	selenoprotein	15-Sep	0.367	9.88E-05
1423967_at	paralemmin	Palm	0.367	0.001976644
1449555_a_at	fetuin beta	Fetub	0.367	0.000168812
1423478_at	protein kinase C, beta	Prkcb	0.367	0.002887419
1434551_at	heterogeneous nuclear ribonucleoprotein U-like 2	Hnrnpul2	0.367	0.000122794
1435659_a_at	triosephosphate isomerase 1	Tpi1	0.367	0.001223459
1422073_a_at	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)	Celsr2	0.367	0.000287808
1424632_a_at	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae)	Rev3l	0.366	0.001204496
1435630_s_at	acetyl-Coenzyme A acetyltransferase 2	Acat2	0.366	0.00048205
1428122_s_at	RIKEN cDNA 2610528K11 gene	2610528K11Rik	0.366	5.03E-05
1453567_s_at	transmembrane protein 216	Tmem216	0.366	0.000136229
1452585_at	mitochondrial ribosomal protein S28	Mrps28	0.366	0.000160213
1423100_at	FBJ osteosarcoma oncogene	Fos	0.366	0.017606601
1425626_at	glutathione S-transferase, mu 1	Gstm1	0.366	0.003162985
1450692_at	kinesin family member 4	Kif4	0.365	9.86E-05
1417245_at	G protein-coupled receptor 180	Gpr180	0.365	0.000385547
1451357_at	MPN domain containing	Mpnd	0.365	0.000121112
1452067_at	N-acylethanolamine acid amidase	Naaa	0.365	5.58E-05
1424787_a_at	nuclear respiratory factor 1	Nrf1	0.365	0.000660043
1417976_at	adenosine deaminase	Ada	0.364	0.000524394
1434079_s_at	minichromosome maintenance deficient 2 mitotin (S. cerevisiae)	Mcm2	0.364	9.57E-05
1415918_a_at	triosephosphate isomerase 1	Tpi1	0.364	0.000230875

1425424_at	hypothetical protein LOC620031	MGC7817	0.363	0.046881481
1418053_at	synuclein, beta	Sncb	0.363	0.000138364
1425834_a_at	glycerol-3-phosphate acyltransferase, mitochondrial	Gpam	0.363	0.00144999
1452415_at	actinin, alpha 1	Actn1	0.363	0.000604576
1418791_at	SH3-domain GRB2-like 2	Sh3gl2	0.363	0.000167717
1449307_at	dysbindin (dystrobrevin binding protein 1) domain containing 1	Dbndd1	0.363	0.000190246
1438322_x_at	farnesyl diphosphate farnesyl transferase 1	Fdft1	0.363	6.71E-05
1417830_at	structural maintenance of chromosomes 1A	Smc1a	0.363	0.000469897
1417384_at	ectonucleoside triphosphate diphosphohydrolase 5	Entpd5	0.363	0.001157698
1435103_x_at	phenylalanyl-tRNA synthetase, beta subunit	Farsb	0.362	0.000427127
1437100_x_at	proviral integration site 3	Pim3	0.362	0.000600087
1418930_at	chemokine (C-X-C motif) ligand 10	Cxcl10	0.362	0.000743683
1425323_a_at	family with sequence similarity 173, member A	Fam173a	0.362	8.09E-05
1429428_at	transcription factor 7-like 2, T-cell specific, HMG-box	Tcf7l2	0.361	0.00049557
1424051_at	collagen, type IV, alpha 2	Col4a2	0.361	0.000434455
1421446_at	protein kinase C, gamma	Prkcc	0.361	0.000159271
1423136_at	fibroblast growth factor 1	Fgf1	0.361	0.004839939
1424172_at	hydroxyacyl glutathione hydrolase	Hagh	0.361	0.000252996
1436512_at	ADP-ribosylation factor-like 4C	Arl4c	0.361	0.000332783
1427229_at	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	Hmgcr	0.361	0.000822259
1436780_at	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	Ogt	0.36	0.024540614
1438910_a_at	stomatin	Stom	0.36	0.000587492
1427295_at	solute carrier family 38, member 10	Slc38a10	0.36	0.000301576
1451019_at	cathepsin F	Ctsf	0.36	0.000218172
1423985_at	guanine nucleotide binding protein (G protein), gamma 5	Gng5	0.359	7.41E-05
1426275_a_at	UDP-glucuronate decarboxylase 1	Uxs1	0.359	0.000118303
1424211_at	solute carrier family 25, member 33	Slc25a33	0.359	9.79E-05
1417969_at	F-box protein 31	Fbxo31	0.359	0.000126706
1449114_at	serine/threonine kinase 3 (Ste20, yeast homolog)	Stk3	0.359	0.013537462
1422619_at	phosphatidic acid phosphatase 2a	Ppap2a	0.359	0.000263659
1425994_a_at	N-acylsphingosine amidohydrolase 2	Asah2	0.359	0.001667161
1422628_at	RIKEN cDNA 4632417K18 gene	4632417K18Rik	0.359	0.001830163
1423802_at	CaM kinase-like vesicle-associated	Camkv	0.359	0.001224493
1424925_at	SEC63-like (S. cerevisiae)	Sec63	0.359	7.19E-05
1420448_at	reproductive homeobox 2A	Rhox2a	0.359	6.20E-05
1448777_at	minichromosome maintenance deficient 2 mitotin (S. cerevisiae)	Mcm2	0.358	0.000219814
1455752_a_at	transmembrane protein 134	Tmem134	0.358	8.40E-05
1449017_at	nuclear transport factor 2	Nutf2	0.358	6.25E-05
1428529_at	RIKEN cDNA 2810026P18 gene	2810026P18Rik	0.358	8.71E-05
1418929_at	intraflagellar transport 57 homolog (Chlamydomonas)	Ift57	0.358	0.000149799
1417781_at	LAG1 homolog, ceramide synthase 4	Lass4	0.358	0.000778399
1437313_x_at	high mobility group box 2	Hmgb2	0.358	0.005261305
1448995_at	platelet factor 4	Pf4	0.358	0.004001845
1437033_a_at	S-phase kinase-associated protein 2 (p45)	Skp2	0.357	0.000264724
1456015_x_at	NADH dehydrogenase (ubiquinone) flavoprotein 1	Ndufv1	0.357	0.000329307

1448613_at	extracellular matrix protein 1	Ecm1	0.357	9.63E-05
1424295_at	developmental pluripotency-associated 3	Dppa3	0.357	0.000695657
1456606_a_at	phosphatase and actin regulator 1	Phactr1	0.357	0.002477425
1455343_at	pleckstrin homology domain containing, family A member 7	Plekha7	0.357	0.016112166
1438712_at	DENN/MADD domain containing 2D	Dennd2d	0.356	0.003880635
1454605_a_at	phosphatidylinositol 4-kinase type 2 alpha	Pi4k2a	0.356	0.000101729
1438549_a_at	serine racemase	Srr	0.356	0.000193714
1460711_at	DnaJ (Hsp40) homolog, subfamily C, member 21	Dnajc21	0.356	0.000180733
1417999_at	integral membrane protein 2B	Itm2b	0.356	0.000198697
1417075_at	RIKEN cDNA 2010309E21 gene	2010309E21Rik	0.356	0.000155124
1425006_a_at	vaccinia related kinase 1	Vrk1	0.355	5.04E-05
1436934_s_at	aconitase 2, mitochondrial	Aco2	0.355	0.000387499
1449198_a_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	St3gal5	0.355	0.000135829
1455084_x_at	serine hydroxymethyltransferase 2 (mitochondrial)	Shmt2	0.355	7.89E-05
1426658_x_at	3-phosphoglycerate dehydrogenase	Phgdh	0.355	0.001476539
1422461_at	ATPase family, AAA domain containing 3A	Atad3a	0.355	0.000354006
1421140_a_at	forkhead box P1	Foxp1	0.355	0.000225917
1422607_at	ets variant gene 1	Etv1	0.355	0.000653779
1456466_x_at	ataxin 10	Atxn10	0.355	0.000659534
1439022_at	phosphatase and actin regulator 1	Phactr1	0.355	0.00061271
1415993_at	squalene epoxidase	Sqle	0.354	3.43E-05
1416948_at	mitochondrial ribosomal protein L23	Mrpl23	0.354	0.002598871
1427011_a_at	LanC (bacterial lantibiotic synthetase component C)-like 1	Lancl1	0.354	7.98E-05
1450896_at	Rho GTPase activating protein 5	Arhgap5	0.354	0.001484155
1425893_a_at	fragile histidine triad gene	Fhit	0.354	0.000195022
1449020_at	phospholipid scramblase 3	Plscr3	0.354	0.000185249
1451700_a_at	RIKEN cDNA 1110007L15 gene	1110007L15Rik	0.354	0.000547042
1450472_s_at	MAD homolog 3 (Drosophila)	Smad3	0.354	0.002913527
1451989_a_at	microtubule-associated protein, RP/EB family, member 2	Mapre2	0.353	0.024850822
1449088_at	fructose bisphosphatase 2	Fbp2	0.353	8.42E-05
1418288_at	lipin 1	Lpin1	0.353	0.000134641
1417419_at	cyclin D1	Ccnd1	0.353	0.002122934
1416770_at	serine/threonine kinase 25 (yeast)	Stk25	0.353	0.000231027
1426022_a_at	villin-like	Vill	0.353	0.000170386
1425493_at	bone morphogenetic protein receptor, type 1A	Bmpr1a	0.353	0.000920608
1450908_at	eukaryotic translation initiation factor 4E	Eif4e	0.353	0.000820658
1421872_at	RAB24, member RAS oncogene family	Rab24	0.352	0.00060037
1415965_at	stearoyl-Coenzyme A desaturase 1	Scd1	0.352	0.001669753
1426004_a_at	transglutaminase 2, C polypeptide	Tgm2	0.352	0.000435374
1417893_at	sideroflexin 3	Sfxn3	0.352	0.000119571
1416011_x_at	EH-domain containing 1	Ehd1	0.352	0.000691146
1460178_at	lon peptidase 2, peroxisomal	Lonp2	0.351	0.000289319
1452799_at	FGGY carbohydrate kinase domain containing	Fggy	0.351	6.13E-05
1417242_at	eukaryotic translation initiation factor 4A, isoform 3	Eif4a3	0.351	7.15E-05
1433913_at	expressed sequence C80913	C80913	0.351	0.004010783
1448770_a_at	ATPase inhibitory factor 1	Atpif1	0.351	0.000507583
1423101_at	progestin and adipoQ receptor family member IV	Paqr4	0.351	0.000116522
1419384_at	protein interacting with C kinase 1	Pick1	0.351	0.002785069
1436708_x_at	minichromosome maintenance deficient 4	Mcm4	0.351	0.001712667

	homolog (S. cerevisiae)			
1427416_x_at	dual specificity phosphatase 7	Dusp7	0.351	0.000952578
1451473_a_at	crystallin, zeta (quinone reductase)-like 1	Cryzl1	0.351	0.000124235
1427658_at	chitobiase, di-N-acetyl-	Ctbs	0.35	0.000561554
1425111_at	sortilin-related VPS10 domain containing receptor 3	Sorcs3	0.35	0.004227424
1416001_a_at	coactosin-like 1 (Dictyostelium)	Cotl1	0.35	0.000935574
1449345_at	coiled-coil domain containing 34	Ccdc34	0.35	0.009540481
1439042_at	adenylate cyclase activating polypeptide 1 receptor 1	Adcyap1r1	0.35	0.002794821
1424711_at	transmembrane protein 2	Tmem2	0.35	0.002590423
1418237_s_at	collagen, type XVIII, alpha 1	Col18a1	0.349	0.000753345
1417963_at	phospholipid transfer protein	Pltp	0.349	0.00174726
1423318_at	RAD18 homolog (S. cerevisiae)	Rad18	0.349	4.12E-05
1448465_at	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. elegans)	Nipsnap1	0.349	0.000170386
1425801_x_at	coactosin-like 1 (Dictyostelium)	Cotl1	0.349	9.37E-05
1426904_s_at	DnaJ (Hsp40) homolog, subfamily C, member 10	Dnajc10	0.348	0.001694435
1448191_at	polo-like kinase 1 (Drosophila)	Plk1	0.348	0.000202177
1456312_x_at	gelsolin	Gsn	0.348	0.005392949
1448923_at	protein kinase, interferon inducible double stranded RNA dependent activator	Prkra	0.348	0.000206084
1417587_at	timeless homolog (Drosophila)	Timeless	0.348	0.000336044
1460241_a_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	St3gal5	0.347	5.67E-05
1422807_at	ADP-ribosylation factor 5	Arf5	0.347	0.000618685
1448427_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	Ndufa6	0.346	0.000700501
1423813_at	kinesin family member 22	Kif22	0.346	0.001384596
1421891_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	St3gal2	0.346	0.000484644
1452336_at	zinc finger protein 395	Zfp395	0.346	0.005521375
1422478_a_at	acyl-CoA synthetase short-chain family member 2	Acss2	0.346	0.004411468
AFFX-MURINE_b1_at	NA	NA	0.345	9.90E-05
1426997_at	thyroid hormone receptor alpha	Thra	0.345	0.000257554
1452155_a_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	Ddx17	0.345	0.000162537
1430421_a_at	transmembrane protein 205	Tmem205	0.344	0.001404877
1417458_s_at	CDC28 protein kinase regulatory subunit 2	Cks2	0.344	0.000932922
1449380_at	protein kinase C and casein kinase substrate in neurons 1	Pacsin1	0.344	9.79E-05
1436623_at	ectonucleoside triphosphate diphosphohydrolase 7	Entpd7	0.344	0.001119097
1428689_at	trypsin domain containing 1	Tysnd1	0.344	4.24E-05
1423165_a_at	metastasis-associated gene family, member 2	Mta2	0.343	6.68E-05
1424114_s_at	laminin B1 subunit 1	Lamb1-1	0.343	0.000357292
1456032_x_at	H2A histone family, member Z	H2afz	0.343	0.000208527
1451981_at	gene trap ROSA b-geo 22	Gtrgeo22	0.343	0.000124791
1419077_at	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)	Mpp3	0.343	3.69E-05
1418257_at	solute carrier family 12, member 7	Slc12a7	0.343	0.000263904
1425281_a_at	TSC22 domain family, member 3	Tsc22d3	0.343	0.000573198
1455804_x_at	3-oxoacid CoA transferase 1	Oxct1	0.343	0.001769631
1451458_at	transmembrane protein 2	Tmem2	0.342	0.000604576
1424550_at	zinc finger, FYVE domain containing 27	Zfyve27	0.342	0.000541688

1448896_at	phosphatidylinositol glycan anchor biosynthesis, class F	Pigf	0.342	0.001245119
1416214_at	minichromosome maintenance deficient 4 homolog (S. cerevisiae)	Mcm4	0.342	0.001304956
1456471_x_at	3-phosphoglycerate dehydrogenase	Phgdh	0.342	8.89E-05
1448557_at	RIKEN cDNA 1200015N20 gene	1200015N20Rik	0.342	0.021338177
1428868_a_at	ornithine decarboxylase antizyme 1	Oaz1	0.342	6.85E-05
1420529_at	D4, zinc and double PHD fingers family 1	Dpf1	0.342	0.003750815
1435950_at	hairless	Hr	0.342	0.000687157
1435444_at	activating transcription factor 6	Atf6	0.341	8.55E-05
1448622_at	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	Lsm4	0.341	0.000281243
1450707_at	double C2, gamma	Doc2g	0.341	0.003782543
1419377_at	mediator of RNA polymerase II transcription, subunit 9 homolog (yeast)	Med9	0.341	0.000102491
1455491_at	heterogeneous nuclear ribonucleoprotein H3	Hnrnph3	0.341	0.000407246
1422185_a_at	cytochrome b5 reductase 3	Cyb5r3	0.34	4.99E-05
1416663_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	Ndufa9	0.34	4.80E-05
1456225_x_at	tribbles homolog 3 (Drosophila)	Trib3	0.34	6.94E-05
1426545_at	trinucleotide repeat containing 6b	Tnrc6b	0.34	0.001413553
1415849_s_at	stathmin 1	Stmn1	0.34	8.52E-05
1418259_a_at	ectonucleoside triphosphate diphosphohydrolase 2	Entpd2	0.339	0.000543844
1438759_x_at	acireductone dioxygenase 1	Adi1	0.339	0.000103134
1426565_at	insulin-like growth factor I receptor	Igf1r	0.339	0.002238521
1424206_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	Smarca5	0.339	8.82E-05
1416915_at	mutS homolog 6 (E. coli)	Msh6	0.339	0.000252528
1426993_at	xenotropic and polytropic retrovirus receptor 1	Xpr1	0.339	0.005840749
1433478_at	presenilin associated, rhomboid-like	Parl	0.339	7.07E-05
1449046_a_at	Josephin domain containing 2	Josd2	0.339	0.000944769
1419963_at	DEP domain containing 6	Depdc6	0.339	0.000910923
1418586_at	adenylate cyclase 9	Adcy9	0.339	0.001296509
1455288_at	RIKEN cDNA 1110036O03 gene	1110036O03Rik	0.339	0.001387937
1415999_at	hairy/enhancer-of-split related with YRPW motif 1	Hey1	0.339	0.000392546
1415681_at	mitochondrial ribosomal protein L43	Mrpl43	0.338	0.001757064
1418969_at	S-phase kinase-associated protein 2 (p45)	Skp2	0.338	0.000501103
1449969_at	tropomodulin 4	Tmod4	0.338	0.009542819
1427364_a_at	ornithine decarboxylase, structural 1	Odc1	0.338	0.000132805
1419351_a_at	lethal, Chr 7, Rinchik 6	l7Rn6	0.337	0.010325306
1415967_at	NADH dehydrogenase (ubiquinone) flavoprotein 1	Ndufv1	0.337	9.37E-05
1422518_at	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	Cask	0.337	9.13E-05
1420349_at	prostaglandin F receptor	Ptgfr	0.337	0.000727275
1418446_at	solute carrier family 16 (monocarboxylic acid transporters), member 2	Slc16a2	0.337	0.000134388
1436342_a_at	UBX domain protein 1	Ubxn1	0.337	0.003903808
1436810_x_at	RIKEN cDNA 2900010M23 gene	2900010M23Rik	0.337	0.016496816
1424437_s_at	ATP-binding cassette, sub-family G (WHITE), member 4	Abcg4	0.336	8.59E-05
1417066_at	chaperone, ABC1 activity of bc1 complex like (S. pombe)	Cabc1	0.336	0.000344929
1418463_at	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 beta)	Pik3r2	0.336	0.000180406

1426913_at	lanosterol synthase	Lss	0.335	0.000198697
1422693_a_at	SUB1 homolog (S. cerevisiae)	Sub1	0.335	0.000165924
1455715_at	predicted gene, 100038868	100038868	0.335	0.018008014
1426719_at	amyloid beta (A4) precursor protein-binding, family B, member 2	Apbb2	0.335	0.00020278
1456748_a_at	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. elegans)	Nipsnap1	0.335	0.000112904
1428405_at	host cell factor C1 regulator 1 (XPO1-dependent)	Hcfc1r1	0.335	0.006796024
1455158_at	integrin alpha 3	Itga3	0.335	0.0005733
1428114_at	solute carrier family 14 (urea transporter), member 1	Slc14a1	0.335	0.011964446
1427782_a_at	corticotropin releasing hormone receptor 1	Crhr1	0.335	0.004253098
1426535_at	KTEL (Lys-Tyr-Glu-Leu) containing 1	Ktelc1	0.334	0.000162686
1426983_at	formin binding protein 1	Fnbp1	0.334	0.001275545
1435800_a_at	cold shock domain protein A	Csda	0.334	0.000244444
1425845_a_at	soc-2 (suppressor of clear) homolog (C. elegans)	Shoc2	0.334	0.001669061
1417705_at	OTU domain, ubiquitin aldehyde binding 1	Otub1	0.334	0.001135816
1426481_at	kelch-like 22 (Drosophila)	Klhl22	0.334	8.88E-05
1419737_a_at	lactate dehydrogenase A	Ldha	0.333	0.000128269
1452999_at	survival motor neuron domain containing 1	Smndc1	0.333	0.000914013
1449476_at	renal tumor antigen	Rage	0.333	0.000347465
1426352_s_at	Tia1 cytotoxic granule-associated RNA binding protein-like 1	Tial1	0.333	0.003093809
1449349_at	nudix (nucleoside diphosphate linked moiety X)-type motif 1	Nudt1	0.333	8.74E-05
1423549_at	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	Slc1a4	0.332	0.000834205
1416955_at	solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10	Slc25a10	0.332	0.00247682
1450696_at	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2)	Psmb9	0.332	0.000514362
1452458_s_at	peptidylprolyl isomerase (cyclophilin) like 5	Ppil5	0.331	0.003314342
1419708_at	wingless-related MMTV integration site 6	Wnt6	0.331	5.38E-05
1417382_at	ectonucleoside triphosphate diphosphohydrolase 5	Entpd5	0.33	0.003845618
1438675_at	splicing factor, arginine/serine-rich 8	Sfrs8	0.33	0.004148504
1429207_at	RIKEN cDNA 5730408K05 gene	5730408K05Rik	0.329	0.001531494
1453840_at	poly A binding protein, cytoplasmic 1	Pabpc1	0.329	0.025566594
1445459_at	somatostatin receptor 5	Sstr5	0.329	0.005888372
1415980_at	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	Atp5g2	0.329	0.000313075
1421945_a_at	brix domain containing 1	Bxdc1	0.329	0.000525909
1460358_s_at	nudix (nucleoside diphosphate linked moiety X)-type motif 22	Nudt22	0.329	0.000386543
1416578_at	ring-box 1	Rbx1	0.328	8.40E-05
1420554_a_at	RAS-related C3 botulinum substrate 3	Rac3	0.328	0.000235824
1417077_at	B-cell receptor-associated protein 29	Bcap29	0.328	0.000266898
1424917_a_at	WD repeat domain, phosphoinositide interacting 1	Wipi1	0.328	0.001738082
1426065_a_at	tribbles homolog 3 (Drosophila)	Trib3	0.328	0.000107103
1416293_at	nuclear factor I/B	Nfib	0.327	0.000970372
1438354_x_at	calponin 3, acidic	Cnn3	0.327	0.001324888
1431815_a_at	MMS19 (MET18 S. cerevisiae)	Mms19	0.327	0.000349023
1435631_x_at	SH3-domain GRB2-like B1 (endophilin)	Sh3glb1	0.327	0.000260499
1454837_at	ceroid-lipofuscinosis, neuronal 6	Cln6	0.327	0.000214409

1450409_a_at	RIKEN cDNA 4930570C03 gene	4930570C03Rik	0.327	0.002173915
1448660_at	Rho GDP dissociation inhibitor (GDI) gamma	Arhgdig	0.327	0.000494766
1427475_a_at	PDZ and LIM domain 5	Pdlim5	0.327	0.00110467
1429582_at	BTB (POZ) domain containing 14A	Btbd14a	0.326	0.001296518
1453804_a_at	origin recognition complex, subunit 4-like (S. cerevisiae)	Orc4l	0.326	9.92E-05
1421378_s_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	Abcc1	0.326	0.00686535
1418546_a_at	Stam binding protein like 1	Stambpl1	0.325	0.00020845
1419513_a_at	ect2 oncogene	Ect2	0.325	0.00187762
1417010_at	zinc finger protein 238	Zfp238	0.325	0.0031957
1424412_at	opioid growth factor receptor-like 1	Ogfrl1	0.325	0.002439032
1435857_s_at	amyloid beta (A4) precursor-like protein 1	Aplp1	0.325	0.000115421
1427197_at	ataxia telangiectasia and Rad3 related	Atr	0.325	0.003001866
1423666_s_at	ribosomal protein L5	Rpl5	0.325	0.001010594
1416066_at	CD9 antigen	Cd9	0.324	0.000311277
1419066_at	immediate early response 5-like	Ier5l	0.324	0.005477218
1450923_at	transforming growth factor, beta 2	Tgfb2	0.324	0.001376345
1430713_s_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	Ndufa13	0.324	0.000816515
1416876_at	parvin, gamma	Parvg	0.324	0.009180044
1433654_at	meningioma expressed antigen 5 (hyaluronidase)	Mgea5	0.324	0.000621024
1417586_at	timeless homolog (Drosophila)	Timeless	0.324	0.001493614
1433906_at	retinaldehyde binding protein 1-like 1	Rlbp1l1	0.324	5.50E-05
1423699_at	non-SMC condensin II complex, subunit H2	Ncaph2	0.323	0.000818602
1435628_x_at	cDNA sequence BC005512	BC005512	0.323	0.01651269
1417845_at	claudin 6	Cldn6	0.323	0.024664509
1425252_a_at	mitotic arrest deficient 1-like 1	Mad1l1	0.323	0.000949968
1423592_at	Rho-associated coiled-coil containing protein kinase 2	Rock2	0.323	0.002315022
1419174_at	RIKEN cDNA 2410004B18 gene	2410004B18Rik	0.322	8.82E-05
1450262_at	cardiotrophin-like cytokine factor 1	Clcf1	0.322	0.000115421
1435525_at	potassium channel tetramerisation domain containing 17	Kctd17	0.322	0.001388496
1415744_at	H2-K region expressed gene 2	H2-Ke2	0.322	0.000426328
1417048_at	prominin 2	Prom2	0.322	0.001850605
1451427_a_at	EGF-like domain 7	Egfl7	0.321	0.000140336
1417359_at	microfibrillar-associated protein 2	Mfap2	0.321	0.000431718
1452754_at	cysteine-rich with EGF-like domains 2	Creld2	0.321	0.000357255
1419097_a_at	stomatin	Stom	0.321	6.11E-05
1449374_at	pipecolic acid oxidase	Pipox	0.321	0.000472804
1425329_a_at	cytochrome b5 reductase 3	Cyb5r3	0.321	0.007021426
1422820_at	lipase, hormone sensitive	Lipe	0.321	0.000236703
1427881_at	deoxynucleotidyltransferase, terminal, interacting protein 2	Dnttip2	0.321	0.000376245
1426609_at	DIS3 mitotic control homolog (S. cerevisiae)	Dis3	0.321	0.000516896
1417372_a_at	pellino 1	Peli1	0.321	8.59E-05
1451363_a_at	DENN/MADD domain containing 2D	Dennd2d	0.32	9.48E-05
1434278_at	X-linked myotubular myopathy gene 1	Mtm1	0.32	0.000494043
1434821_at	bromodomain containing 1	Brd1	0.32	0.000467142
1455526_at	DIRAS family, GTP-binding RAS-like 1	Diras1	0.32	0.001971003
1438320_s_at	minichromosome maintenance deficient 7 (S. cerevisiae)	Mcm7	0.32	5.70E-05
1452927_x_at	triosephosphate isomerase 1	Tpi1	0.32	0.000561454
1449062_at	ketohexokinase	Khk	0.32	0.002499379
1436836_x_at	similar to calponin 3, acidic	LOC100047856	0.32	0.000214628

1426700_a_at	ubiquitin specific peptidase 52	Usp52	0.32	0.044710938
1417374_at	tubulin, alpha 4A	Tuba4a	0.32	0.000592463
1428327_at	trafficking protein, kinesin binding 1	Trak1	0.319	0.00119114
1416532_at	transformation/transcription domain-associated protein	Trrap	0.319	0.006155358
1436182_at	NA	NA	0.319	0.000406659
1426825_at	formin-like 3	Fmnl3	0.319	0.000140351
1426844_a_at	programmed cell death 2-like	Pdcd2l	0.319	0.000742093
1448899_s_at	RAD51 associated protein 1	Rad51ap1	0.319	0.000651524
1417435_at	like-glycosyltransferase	Large	0.319	0.003463679
1421929_at	Eph receptor A4	Epha4	0.318	0.001385283
1449139_at	RIKEN cDNA 2310008M10 gene	2310008M10Rik	0.318	0.000257888
1421965_s_at	Notch gene homolog 3 (Drosophila)	Notch3	0.318	0.010254739
1448472_at	valyl-tRNA synthetase	Vars	0.318	0.000596194
1448877_at	distal-less homeobox 2	Dlx2	0.318	0.007292999
1438938_x_at	prohibitin 2	Phb2	0.318	0.001055168
1427568_a_at	intraflagellar transport 80 homolog (Chlamydomonas)	Ift80	0.318	0.001046647
1456128_at	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	Atp5g2	0.318	0.000867825
1416961_at	budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae)	Bub1b	0.318	0.000105136
1452414_s_at	coiled-coil domain containing 86	Ccdc86	0.317	0.003511752
1419688_at	glypican 6	Gpc6	0.317	0.000290693
1460244_at	ureidopropionase, beta	Upb1	0.317	0.000963431
1453924_a_at	prostaglandin F receptor	Ptgfr	0.317	0.001838032
1455126_x_at	RIKEN cDNA 2310028O11 gene	2310028O11Rik	0.317	0.000579116
1422635_at	acetylcholinesterase	Ache	0.317	0.007097896
1455239_at	RIKEN cDNA 6330512M04 gene	6330512M04Rik	0.317	0.00101805
1426574_a_at	adducin 3 (gamma)	Add3	0.317	0.005564251
1424862_s_at	mindbomb homolog 2 (Drosophila)	Mib2	0.316	0.000463266
1456177_x_at	zinc finger protein 706	Zfp706	0.316	0.000345087
1431226_a_at	fibronectin type III domain containing 4	Fndc4	0.316	0.001205482
1421430_at	RAD51-like 1 (S. cerevisiae)	Rad51l1	0.316	0.001416781
1421731_a_at	flap structure specific endonuclease 1	Fen1	0.316	0.000242854
1427079_at	microtubule-associated protein, RP/EB family, member 3	Mapre3	0.315	0.001617124
1435035_at	RNA (guanine-9-) methyltransferase domain containing 2	Rg9mtd2	0.315	0.006555411
1450061_at	ectodermal-neural cortex 1	Enc1	0.315	0.000145971
1416480_a_at	HIG1 domain family, member 1A	Higd1a	0.315	0.001449338
1419237_at	ubiquitin specific peptidase 29	Usp29	0.315	0.018731373
1451825_a_at	coatomer protein complex, subunit zeta 1	Copz1	0.315	0.00012016
1453740_a_at	cyclin L2	Ccnl2	0.315	0.007656767
1416319_at	adenosine kinase	Adk	0.314	0.002517253
1419352_at	lethal, Chr 7, Rinchik 6	l7Rn6	0.314	0.000169853
1448917_at	mediator complex subunit 30	Med30	0.314	9.89E-05
1417638_at	left right determination factor 1	Lefty1	0.314	0.001684295
1422414_a_at	calmodulin 2	Calm2	0.314	0.002721375
1450522_a_at	H1 histone family, member 0	H1f0	0.314	0.000184941
1418927_a_at	hyaluronic acid binding protein 4	Habp4	0.314	0.000881029
1448158_at	syndecan 1	Sdc1	0.314	0.002588794
1448590_at	collagen, type VI, alpha 1	Col6a1	0.314	0.013537506
1437801_at	mortality factor 4 like 1	Morf4l1	0.314	0.017419985
1426339_at	adenylate kinase 5	Ak5	0.313	0.000930269
1426690_a_at	sterol regulatory element binding transcription factor 1	Srebf1	0.313	9.84E-05

1422430_at	fidgetin-like 1	Fignl1	0.313	0.005283227
1451471_at	glutamyl-tRNA synthetase 2 (mitochondrial)(putative)	Ears2	0.313	0.000386543
1416433_at	replication protein A2	Rpa2	0.313	0.00020504
1417152_at	BTB (POZ) domain containing 14A	Btbd14a	0.313	0.016096995
1424612_at	NIPA-like domain containing 2	Npal2	0.312	0.000851781
1452020_a_at	SIVA1, apoptosis-inducing factor	Siva1	0.312	0.000446899
1424006_at	alanyl-tRNA synthetase domain containing 1	Aarsd1	0.312	0.000318435
1424059_at	suppressor of variegation 4-20 homolog 2 (Drosophila)	Suv420h2	0.312	0.001527564
1438166_x_at	NADH dehydrogenase (ubiquinone) Fe-S protein 4	Ndufs4	0.312	0.001559464
1435442_at	WD repeats and SOF domain containing 1	Wdsof1	0.311	0.000186186
1430526_a_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	Smarca2	0.311	0.00221373
1451320_at	Rho GTPase activating protein 8	Arhgap8	0.311	0.000493233
1419216_at	5-azacytidine induced gene 1	Azi1	0.311	0.008885476
1427940_s_at	c-myc binding protein	Mycbp	0.311	0.00598666
1415881_at	growth hormone inducible transmembrane protein	Ghitm	0.311	0.000298407
1424970_at	purine-rich element binding protein G	Purg	0.31	0.031781242
1416943_at	ubiquitin-conjugating enzyme E2E 1, UBC4/5 homolog (yeast)	Ube2e1	0.31	0.000276064
1422620_s_at	phosphatidic acid phosphatase 2a	Ppap2a	0.31	0.000284696
1419472_s_at	nuclear distribution gene C homolog (Aspergillus)	Nudc	0.31	0.001064562
1455505_at	GATA zinc finger domain containing 2A	Gatad2a	0.31	0.000491325
1450288_at	cadherin 6	Cdh6	0.309	0.000764126
1424087_at	proteasome (prosome, macropain) assembly chaperone 3	Psmg3	0.309	0.000691903
1416161_at	RAD21 homolog (S. pombe)	Rad21	0.309	0.000369687
1436344_at	RIKEN cDNA 5830404H04 gene	5830404H04Rik	0.309	0.000225917
1436032_at	NA	NA	0.309	0.028664128
1434884_at	Metadherin	Mtdh	0.309	0.000771106
1423827_s_at	nucleolar complex associated 4 homolog (S. cerevisiae)	Noc4l	0.309	0.000168284
1432287_a_at	syntrophin, gamma 1	Sntg1	0.309	0.019828639
1427844_a_at	CCAAT/enhancer binding protein (C/EBP), beta	Cebpb	0.309	0.018223625
1449770_x_at	transmembrane protein 191C	Tmem191c	0.308	0.003852478
1451574_at	B-cell CLL/lymphoma 9	Bcl9	0.308	0.00694639
1451069_at	proviral integration site 3	Pim3	0.308	0.001092169
1448408_at	Hermansky-Pudlak syndrome 1 homolog (human)	Hps1	0.308	0.001448395
1423453_at	nucleolar protein 12	Nol12	0.307	0.005677601
1426612_at	timeless interacting protein	Tipin	0.307	0.00015868
1417636_at	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	Slc6a9	0.307	0.000398525
1448675_at	ankyrin repeat and zinc finger domain containing 1	Ankzf1	0.307	0.003199666
1416270_at	polymerase (RNA) II (DNA directed) polypeptide G	Polr2g	0.307	0.000368334
1424088_at	melanocyte proliferating gene 1	Myg1	0.307	0.003175828
1424157_at	EH-domain containing 2	Ehd2	0.307	0.003392526
1451808_at	potassium inwardly-rectifying channel, subfamily J, member 4	Kcnj4	0.307	0.000435317
1437711_x_at	ornithine decarboxylase, structural 1	Odc1	0.306	0.00164193

1448175_at	EH-domain containing 1	Ehd1	0.306	0.009363355
1426831_at	S-adenosylhomocysteine hydrolase-like 1	Ahcyl1	0.306	0.002993842
1448819_at	eukaryotic translation initiation factor 2, subunit 2 (beta)	Eif2s2	0.306	0.000435063
1434579_x_at	NADH dehydrogenase (ubiquinone) Fe-S protein 8	Ndufs8	0.306	0.002668285
1426602_at	v-raf murine sarcoma 3611 viral oncogene homolog	Araf	0.306	0.001352554
1454070_a_at	DDHD domain containing 1	Ddhd1	0.306	0.000822387
1416162_at	RAD21 homolog (S. pombe)	Rad21	0.306	0.009807551
1449085_at	PHD finger protein 10	Phf10	0.306	0.000174842
1423709_s_at	phenylalanyl-tRNA synthetase, beta subunit	Farsb	0.306	0.000122233
1456700_x_at	myristoylated alanine rich protein kinase C substrate	Marcks	0.306	0.002604951
1424022_at	oxidative stress induced growth inhibitor 1	Osgin1	0.306	0.002142242
1423918_at	rhomboid domain containing 1	Rhbdd1	0.305	0.000258366
1451313_a_at	RIKEN cDNA 1110067D22 gene	1110067D22Rik	0.305	0.000554434
1455441_at	mitogen-activated protein kinase kinase kinase 7	Map3k7	0.305	0.000419653
1432195_s_at	cyclin L2	Ccnl2	0.305	0.002039126
1449248_at	chloride channel 2	Clcn2	0.305	0.008164486
1450471_at	MAD homolog 3 (Drosophila)	Smad3	0.304	0.001423667
1460350_at	oxysterol binding protein	Osbp	0.304	0.00013838
1416837_at	BCL2-associated X protein	Bax	0.304	0.000521376
1424318_at	RIKEN cDNA 1110067D22 gene	1110067D22Rik	0.304	0.000147795
1448610_a_at	superoxide dismutase 2, mitochondrial	Sod2	0.304	0.000458291
1449984_at	chemokine (C-X-C motif) ligand 2	Cxcl2	0.304	0.049598138
1428454_at	breast carcinoma amplified sequence 3	Bcas3	0.304	0.001076345
1418325_at	selenophosphate synthetase 2	Sephs2	0.304	0.000422092
1422147_a_at	phospholipase A2, group VI	Pla2g6	0.304	0.001609366
1452917_at	replication factor C (activator 1) 5	Rfc5	0.304	0.000165924
1451271_a_at	acetyl-Coenzyme A acetyltransferase 1	Acat1	0.304	0.000260723
1432187_at	nucleoporin 43	Nup43	0.303	0.000448268
1417938_at	RAD51 associated protein 1	Rad51ap1	0.303	0.002002715
1451486_at	solute carrier family 46, member 3	Slc46a3	0.303	0.006008713
1452718_at	ubiquitin protein ligase E3 component n-recognin 5	Ubr5	0.303	0.000172718
1422232_at	paired-like homeobox 2b	Phox2b	0.303	0.007750979
1418866_at	cytochrome P450, family 24, subfamily a, polypeptide 1	Cyp24a1	0.303	0.003795421
1417727_at	splicing factor, arginine/serine rich 9	Sfrs9	0.303	0.00191922
1418445_at	solute carrier family 16 (monocarboxylic acid transporters), member 2	Slc16a2	0.303	0.00079364
1434703_at	exostoses (multiple)-like 3	Extl3	0.303	0.000823046
1424390_at	nucleoporin like 1	Nupl1	0.302	0.00037167
1417119_at	zinc finger like protein 1	Zfpl1	0.302	0.00090941
1450410_a_at	RIKEN cDNA 4930570C03 gene	4930570C03Rik	0.302	0.0002252
1419994_s_at	DNA segment, Chr 10, ERATO Doi 641, expressed	D10Ertd641e	0.302	0.00035567
1422159_at	protein phosphatase, EF hand calcium-binding domain 2	Ppef2	0.302	0.002138111
1419415_a_at	retinoic acid receptor, gamma	Rarg	0.302	0.000314278
1416033_at	transmembrane protein 109	Tmem109	0.301	0.001492575
1416031_s_at	minichromosome maintenance deficient 7 (S. cerevisiae)	Mcm7	0.301	0.0001798
1421142_s_at	forkhead box P1	Foxp1	0.301	0.003148115
1434679_at	neurocan	Ncan	0.301	0.008239229
1416311_s_at	tubulin, alpha 3A	Tuba3a	0.301	0.001819402

1419290_at	methyltransferase like 6	Mettl6	0.3	0.000571731
1437519_x_at	hydroxyacyl glutathione hydrolase	Hagh	0.3	0.000576634
1418164_at	syntaxin 2	Stx2	0.3	7.51E-05
1427027_a_at	general transcription factor III A	Gtf3a	0.3	0.003580105
1454613_at	RIKEN cDNA 9430041P20 gene	9430041P20Rik	0.3	6.88E-05
1418644_a_at	serine/threonine kinase 11	Stk11	0.3	0.00074165
1428351_at	protein phosphatase 1M	Ppm1m	0.299	0.000129747
1429453_a_at	mitochondrial ribosomal protein L55	Mrpl55	0.299	0.000533641
1460685_at	translocase of inner mitochondrial membrane 17b	Timm17b	0.299	0.000198898
1448678_at	RIKEN cDNA 3110048E14 gene	3110048E14Rik	0.298	0.00022936
1452188_at	mastermind like 1 (Drosophila)	Maml1	0.298	0.000146288
1426590_at	G elongation factor, mitochondrial 2	Gfm2	0.298	0.000781823
1437773_x_at	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	Kdelr3	0.298	0.00306203
1450720_at	acid phosphatase 1, soluble	Acp1	0.298	0.000182825
1415810_at	ubiquitin-like, containing PHD and RING finger domains, 1	Uhrf1	0.298	0.000317665
1417445_at	NDC80 homolog, kinetochore complex component (S. cerevisiae)	Ndc80	0.298	0.002081252
1455283_x_at	NADH dehydrogenase (ubiquinone) Fe-S protein 8	Ndufs8	0.298	0.002940737
1418183_a_at	cytohesin 1	Cyth1	0.298	0.000205498
1426674_at	eukaryotic translation initiation factor 3, subunit B	Eif3b	0.298	0.000344547
1418321_at	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase)	Dci	0.298	0.001579371
1423939_a_at	Yip1 interacting factor homolog A (S. cerevisiae)	Yif1a	0.297	0.000245511
1417052_at	proteasome (prosome, macropain) subunit, beta type 3	Psmb3	0.297	0.000295561
1426536_at	NMDA receptor-regulated gene 2	Narg2	0.297	0.017636092
1450684_at	ets variant gene 1	Etv1	0.297	0.003775725
1425921_a_at	RIKEN cDNA 1810055G02 gene	1810055G02Rik	0.297	0.000614864
1417373_a_at	tubulin, alpha 4A	Tuba4a	0.297	0.000289596
1450725_s_at	carbonic anhydrase 14	Car14	0.297	0.018008377
1423264_at	block of proliferation 1	Bop1	0.297	0.000202861
1435352_at	phosphatidylinositol glycan anchor biosynthesis, class K	Pigk	0.297	0.000979362
1419761_a_at	GA repeat binding protein, beta 1	Gabpb1	0.297	0.003283002
1426423_at	serine hydroxymethyltransferase 2 (mitochondrial)	Shmt2	0.297	0.004781654
1417321_at	zinc finger, CCHC domain containing 7	Zcchc7	0.296	0.008144575
1426270_at	structural maintenance of chromosomes 5	Smc5	0.296	0.006919906
1418996_a_at	LYR motif containing 5	Lyrm5	0.296	0.00132268
1454640_at	coiled-coil-helix-coiled-coil-helix domain containing 7	Chchd7	0.296	0.007605101
1451366_at	COP9 (constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana)	Cops6	0.296	0.000254803
1420593_a_at	TEA domain family member 3	Tead3	0.296	0.000434455
1423940_at	Yip1 interacting factor homolog A (S. cerevisiae)	Yif1a	0.295	0.000629172
1438656_x_at	translocase of inner mitochondrial membrane 17b	Timm17b	0.295	0.00041728
1418763_at	nitrilase family, member 2	Nit2	0.295	0.000156268
1429412_at	enhancer of yellow 2 homolog (Drosophila)	Eny2	0.295	0.003448649
1416999_at	sphingomyelin phosphodiesterase 2, neutral	Smpd2	0.295	0.004919858
1417151_a_at	neurotensin receptor 2	Ntsr2	0.295	0.01107526

1432436_a_at	adenylate kinase 3	Ak3	0.294	0.003114891
1416993_at	component of oligomeric golgi complex 4	Cog4	0.294	0.00026818
1439369_x_at	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	Slc9a3r2	0.294	0.000621027
1427049_s_at	smoothened homolog (Drosophila)	Smo	0.294	0.000531643
1452584_at	RIKEN cDNA 1500032L24 gene	1500032L24Rik	0.294	0.000658591
1419458_at	Rho-guanine nucleotide exchange factor	Rgnef	0.294	0.001968714
1424227_at	polymerase (RNA) III (DNA directed) polypeptide H	Polr3h	0.294	0.001132799
1428104_at	TPX2, microtubule-associated protein homolog (Xenopus laevis)	Tpx2	0.294	0.001173831
1416128_at	tubulin, alpha 1C	Tuba1c	0.293	0.011932461
1448878_at	Max dimerization protein 3	Mxd3	0.293	0.000521769
1426943_at	integrator complex subunit 1	Ints1	0.293	0.005870275
1427269_at	splicing factor, arginine/serine-rich 11	Sfrs11	0.293	0.001609366
1423754_at	interferon induced transmembrane protein 3	Ifitm3	0.293	0.000703324
1417383_at	ectonucleoside triphosphate diphosphohydrolase 5	Entpd5	0.293	0.006685163
1433616_a_at	RIKEN cDNA 2310028O11 gene	2310028O11Rik	0.293	0.000401493
1450993_at	PAS domain containing serine/threonine kinase	Pask	0.293	0.000707536
1437398_a_at	aldehyde dehydrogenase 9, subfamily A1	Aldh9a1	0.293	0.000717429
1421925_at	mitogen-activated protein kinase 11	Mapk11	0.293	0.003385189
1434204_x_at	serine hydroxymethyltransferase 2 (mitochondrial)	Shmt2	0.293	0.000257956
1425048_a_at	high mobility group box 1	Hmgb1	0.293	0.00042084
1431145_a_at	CUE domain containing 2	Cuedc2	0.293	0.004498331
1448365_at	exosome component 7	Exosc7	0.293	0.000214079
1425792_a_at	RAR-related orphan receptor gamma	Rorc	0.293	0.000847833
1426409_at	leucine zipper, putative tumor suppressor 2	Lzts2	0.292	0.000912264
1433773_at	ribonucleotide reductase M2 B (TP53 inducible)	Rrm2b	0.292	0.000319365
1451531_at	COBW domain containing 1	Cbwd1	0.292	0.000700936
1431375_s_at	parvin, alpha	Parva	0.292	0.000230664
1428297_at	mitogen-activated protein kinase kinase kinase kinase 2	Map4k2	0.292	0.001091174
1427156_s_at	activating signal cointegrator 1 complex subunit 2	Ascc2	0.292	0.000173615
1451669_at	protein phosphatase 1B, magnesium dependent, beta isoform	Ppm1b	0.292	0.000709478
1449566_at	NK2 transcription factor related, locus 5 (Drosophila)	Nkx2-5	0.292	0.000166477
1425194_a_at	RIKEN cDNA 6330577E15 gene	6330577E15Rik	0.292	0.000802539
1424212_at	RIKEN cDNA 9430023L20 gene	9430023L20Rik	0.292	0.004097596
1434627_at	nuclear respiratory factor 1	Nrf1	0.291	0.00108338
1455895_x_at	RIKEN cDNA 1110012M11 gene	1110012M11Rik	0.291	0.005451631
1421141_a_at	forkhead box P1	Foxp1	0.291	0.003221237
1451104_a_at	U1 small nuclear ribonucleoprotein polypeptide A	Snrp70	0.29	0.005052589
1422020_at	sprouty homolog 4 (Drosophila)	Spry4	0.29	0.020281675
1424419_at	leucine rich repeat containing 14	Lrrc14	0.29	0.000158066
1418242_at	Fas-associated factor 1	Faf1	0.29	0.000220428
1425678_a_at	SNF related kinase	Snrk	0.29	0.000491325
1448384_at	protein O-fucosyltransferase 2	Pofut2	0.29	0.00098379
1416505_at	nuclear receptor subfamily 4, group A, member 1	Nr4a1	0.29	0.000417249
1449328_at	lymphocyte antigen 75	Ly75	0.29	0.003635584
1420800_a_at	potassium voltage-gated channel, subfamily Q,	Kcnq2	0.29	0.002847391

	member 2			
1417562_at	eukaryotic translation initiation factor 4E binding protein 1	Eif4ebp1	0.29	0.000498481
1452012_a_at	exosome component 1	Exosc1	0.29	0.001552296
1449000_at	DNA segment, Chr 10, Johns Hopkins University 81 expressed	D10Jhu81e	0.29	0.00084978
1417486_at	src homology 2 domain-containing transforming protein D	Shd	0.289	0.000244364
1452216_at	malonyl CoA:ACP acyltransferase (mitochondrial)	Mcat	0.289	0.000444778
1425531_at	zinc finger, HIT domain containing 1	Znhit1	0.289	0.002250236
1460247_a_at	S-phase kinase-associated protein 2 (p45)	Skp2	0.289	0.001440472
1434148_at	transcription factor 4	Tcf4	0.289	0.002004996
1449705_x_at	minichromosome maintenance deficient 3 (S. cerevisiae)	Mcm3	0.289	0.000508565
1448232_x_at	tubulin, alpha 1C	Tuba1c	0.289	0.008880523
1448179_at	upregulated during skeletal muscle growth 5	Usmg5	0.289	0.001285285
1439200_x_at	erythroid differentiation regulator 1	Erdr1	0.289	0.014875909
1437767_s_at	retinoblastoma-like 2	Rbl2	0.289	0.009970929
1425350_a_at	myelin basic protein expression factor 2, repressor	Myef2	0.289	0.001200998
1451643_a_at	RAB4B, member RAS oncogene family	Rab4b	0.288	0.001048238
1418540_a_at	protein tyrosine phosphatase, receptor type, E	Ptpre	0.288	0.01254104
1448800_at	reticulon 4 interacting protein 1	Rtn4ip1	0.288	0.000218736
1428085_at	RIKEN cDNA 1110057K04 gene	1110057K04Rik	0.288	0.000276064
1416877_a_at	mitochondrial ribosomal protein L51	Mrpl51	0.288	0.004587836
1422731_at	LIM domains containing 1	Limd1	0.288	0.000261024
1450022_at	GTP binding protein 1	Gtpbp1	0.288	0.002716808
1460414_at	obscurin-like 1	Obsl1	0.288	0.001685561
1416359_at	sorting nexin 18	Snx18	0.288	0.001927761
1417730_at	exostoses (multiple) 1	Ext1	0.288	0.000817683
1438640_x_at	phosphoglycerate kinase 1	Pgk1	0.288	0.003582356
1456624_at	WD repeat domain, phosphoinositide interacting 1	Wipi1	0.287	0.005394265
1421018_at	RIKEN cDNA 1110018J18 gene	1110018J18Rik	0.287	0.001296518
1452334_at	centromere protein F	Cenpf	0.287	0.002302442
1448530_at	guanosine monophosphate reductase	Gmpr	0.287	0.001327539
1451428_x_at	EGF-like domain 7	Egfl7	0.287	0.002192403
1448592_at	cartilage associated protein	Crtap	0.286	0.001421647
1438961_s_at	bleomycin hydrolase	Blmh	0.286	0.000368334
1460300_a_at	leukocyte tyrosine kinase	Ltk	0.286	0.007980629
1449121_at	FUS interacting protein (serine-arginine rich) 1	Fusip1	0.286	0.005679134
1424783_a_at	UDP glucuronosyltransferase 1 family, polypeptide A9	Ugt1a9	0.286	0.031960421
1452016_at	arachidonate 5-lipoxygenase activating protein	Alox5ap	0.286	0.002124003
1424581_at	SH3 and cysteine rich domain 2	Stac2	0.286	0.000435317
1433893_s_at	sperm associated antigen 5	Spag5	0.286	0.001200557
1433709_at	calcium activated nucleotidase 1	Cant1	0.285	0.000300111
1423702_at	H1 histone family, member 0	H1f0	0.285	9.84E-05
1460455_at	ubiquitin protein ligase E3 component n-recognin 3	Ubr3	0.285	0.006337006
1426884_at	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	Rmnd5a	0.285	0.0002131
1428068_at	sorting and assembly machinery component 50 homolog (S. cerevisiae)	Samm50	0.285	0.000243056
1416535_at	microspherule protein 1	Mcrs1	0.285	0.00058231
1427064_a_at	scribbled homolog (Drosophila)	Scrib	0.285	0.003672127
1452273_at	expressed sequence AA409316	AA409316	0.284	0.002386989

1416010_a_at	EH-domain containing 1	Ehd1	0.284	0.000306323
1426529_a_at	transgelin 2	Tagln2	0.284	0.000276362
1426105_a_at	UBX domain protein 11	Ubxn11	0.284	0.000668404
1455290_at	zinc and ring finger 2	Znrf2	0.284	0.001538239
1452882_at	progesterone receptor membrane component 2	Pgrmc2	0.284	0.000435063
1460464_at	RIKEN cDNA 2700089E24 gene	2700089E24Rik	0.283	0.001851077
1418513_at	serine/threonine kinase 3 (Ste20, yeast homolog)	Stk3	0.283	0.006854405
1426010_a_at	erythrocyte protein band 4.1-like 3	Epb4.1l3	0.283	0.002102365
1438152_at	NA	NA	0.283	0.007339097
1425731_at	ankyrin repeat domain 24	Ankrd24	0.283	0.000420523
1419305_a_at	F-box protein 36	Fbxo36	0.282	0.000352291
1416618_at	protoporphyrinogen oxidase	Ppox	0.282	0.020024031
1417514_at	synovial sarcoma, X breakpoint 2 interacting protein	Ssx2ip	0.282	0.002995361
1448618_at	major vault protein	Mvp	0.282	0.014001732
1415913_at	ribosomal protein S13	Rps13	0.282	0.016371704
1449536_at	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1	Kcnn1	0.282	0.004283679
1438842_at	mitochondrial carrier homolog 2 (C. elegans)	Mtch2	0.282	0.047131994
1416134_at	amyloid beta (A4) precursor-like protein 1	Aplp1	0.282	0.000803223
1436724_a_at	ligatin	Lgtn	0.282	0.001976479
1417312_at	dickkopf homolog 3 (Xenopus laevis)	Dkk3	0.281	0.000961819
1415968_a_at	kidney androgen regulated protein	Kap	0.281	0.02262829
1434353_at	Scm-like with four mbt domains 2	Sfmbt2	0.281	0.00158551
1452385_at	ubiquitin specific peptidase 53	Usp53	0.281	0.028683474
1417594_at	G kinase anchoring protein 1	Gkap1	0.281	0.000199248
1426836_s_at	methionyl aminopeptidase 1	Metap1	0.281	0.001633167
1451176_at	RIKEN cDNA D430028G21 gene	D430028G21Rik	0.281	0.003136057
1416896_at	ribosomal protein S6 kinase polypeptide 1	Rps6ka1	0.281	0.000149332
1436884_x_at	Ewing sarcoma breakpoint region 1	Ewsr1	0.281	0.002607885
1451965_at	V(kappa) gene product	LOC672450	0.281	0.000294703
1426024_a_at	drebrin 1	Dbn1	0.281	0.000895674
1425242_at	RIKEN cDNA 1810006K21 gene	1810006K21Rik	0.28	0.000300895
1417371_at	pellino 1	Peli1	0.28	0.000540903
1449095_at	vacuolar protein sorting 54 (yeast)	Vps54	0.28	0.001129086
1428096_at	importin 11	Ipo11	0.28	0.000214054
1439380_x_at	maternally expressed 3	Meg3	0.28	0.029898605
1429382_at	translocase of outer mitochondrial membrane 40 homolog-like (yeast)	Tomm40l	0.28	0.000404475
1418380_at	telomeric repeat binding factor 1	Terf1	0.28	0.002632278
1426909_at	uridine-cytidine kinase 2	Uck2	0.28	0.000212622
1427359_at	jumonji C domain-containing histone demethylase 1 homolog D (S. cerevisiae)	Jhdm1d	0.28	0.007547596
1426959_at	3-hydroxybutyrate dehydrogenase, type 1	Bdh1	0.28	0.000772912
1416605_at	nucleolar protein family A, member 2	Nola2	0.28	0.005736704
1416347_at	multiple endocrine neoplasia 1	Men1	0.28	0.000762428
1418455_at	coatomer protein complex, subunit zeta 2	Copz2	0.28	0.000289596
1451504_at	coiled-coil-helix-coiled-coil-helix domain containing 3	Chchd3	0.28	0.000888541
1416938_at	coiled-coil-helix-coiled-coil-helix domain containing 1	Chchd1	0.28	0.001965895
1420578_at	opticin	Optc	0.279	0.01398526
1417818_at	WW domain containing transcription regulator 1	Wwtr1	0.279	0.002791762

1454045_a_at	phosphatidylglycerophosphate synthase 1	Pgs1	0.279	0.001996998
1436244_a_at	transducin-like enhancer of split 2, homolog of Drosophila E(spl)	Tle2	0.279	0.001926125
1428510_at	latrophilin 1	Lphn1	0.279	0.002839574
1415877_at	dihydropyrimidinase-like 3	Dpysl3	0.279	0.001950699
1451234_at	cDNA sequence BC021381	BC021381	0.278	0.001884399
1424880_at	tribbles homolog 1 (Drosophila)	Trib1	0.278	0.000637287
1452230_at	DnaJ (Hsp40) homolog, subfamily C, member 10	Dnajc10	0.278	0.00422277
1427099_at	MYC-associated zinc finger protein (purine-binding transcription factor)	Maz	0.278	0.000894979
1418356_at	mercaptopyruvate sulfurtransferase	Mpst	0.278	0.003162023
1448901_at	carboxypeptidase X 1 (M14 family)	Cpxm1	0.278	0.001769631
1420885_a_at	seizure related gene 6	Sez6	0.278	0.000727526
1435889_at	MAP/microtubule affinity-regulating kinase 2	Mark2	0.278	0.003909284
1452307_at	Cdk5 and Abl enzyme substrate 2	Cables2	0.278	0.000364532
1417460_at	interferon induced transmembrane protein 2	Ifitm2	0.278	0.000545802
1449040_a_at	selenophosphate synthetase 2	Sephs2	0.278	0.031179799
1448948_at	recombination activating gene 1 activating protein 1	Rag1ap1	0.277	0.000615607
1455985_x_at	serine hydroxymethyltransferase 2 (mitochondrial)	Shmt2	0.277	0.002525729
1423708_a_at	phenylalanyl-tRNA synthetase, beta subunit	Farsb	0.277	0.000384336
1451353_at	transmembrane 6 superfamily member 1	Tm6sf1	0.277	0.00039974
1423471_at	polypyrimidine tract binding protein 2	Ptbp2	0.277	0.043007678
1448584_at	arginine/serine-rich coiled-coil 1	Rsrc1	0.277	0.000394095
1435360_at	zinc finger protein 651	Zfp651	0.277	0.003928449
1416376_at	transmembrane protein 97	Tmem97	0.277	0.000636473
1424060_at	nei like 3 (E. coli)	Neil3	0.277	0.001016835
1450131_a_at	B-box and SPRY domain containing	Bspry	0.277	0.000318002
1437614_x_at	zinc finger, DHHC domain containing 14	Zdhhc14	0.277	0.002019616
1454197_a_at	coiled-coil domain containing 86	Ccdc86	0.277	0.003369946
1416486_at	small inducible cytokine subfamily E, member 1	Scye1	0.276	0.00052832
1452464_a_at	methionine aminopeptidase-like 1	Metapl1	0.276	0.003580105
1426367_at	calcium binding protein 39-like	Cab39l	0.276	0.00235973
1451352_s_at	metastasis associated 3	Mta3	0.276	0.002091206
1419573_a_at	lectin, galactose binding, soluble 1	Lgals1	0.276	0.000147475
1427552_a_at	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	Gstz1	0.276	0.000449972
1454908_x_at	small EDRK-rich factor 1	Serf1	0.276	0.000716453
1417061_at	solute carrier family 40 (iron-regulated transporter), member 1	Slc40a1	0.276	0.012712881
1452692_a_at	NADH dehydrogenase (ubiquinone) flavoprotein 2	Ndufv2	0.276	0.000389518
1426845_at	programmed cell death 2-like	Pdcd2l	0.276	0.000117095
1423012_at	synaptotagmin VII	Syt7	0.276	0.025212849
1438161_s_at	replication factor C (activator 1) 4	Rfc4	0.275	0.00357884
1427762_x_at	histone cluster 1, H2bp	Hist1h2bp	0.275	0.009480526
1436243_at	FERM domain containing 5	Frmd5	0.275	0.021957223
1448388_a_at	RIKEN cDNA 1110002B05 gene	1110002B05Rik	0.275	0.000308451
1436236_x_at	coactosin-like 1 (Dictyostelium)	Cotl1	0.275	0.001251838
1460254_at	RIKEN cDNA 1810049H13 gene	1810049H13Rik	0.275	0.00509868
1433887_at	DnaJ (Hsp40) homolog, subfamily C, member 3	Dnajc3	0.275	0.01107526
1426802_at	septin 8	Sept8	0.275	0.002455335
1450721_at	acid phosphatase 1, soluble	Acp1	0.275	0.000143758

1418119_at	RNA binding motif protein 8a	Rbm8a	0.275	0.000138487
1453851_a_at	growth arrest and DNA-damage-inducible 45 gamma	Gadd45g	0.275	0.026550922
1446244_at	zyg-II homolog B (C. elegans)	Zyg11b	0.275	0.014352121
1452346_at	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	B3gnt1	0.275	0.002964142
1417302_at	REST corepressor 2	Rcor2	0.275	0.000277457
1424685_at	exosome component 4	Exosc4	0.274	0.001281946
1415765_at	heterogeneous nuclear ribonucleoprotein U-like 2	Hnrnpul2	0.274	0.001796851
1416703_at	mitogen-activated protein kinase 14	Mapk14	0.274	0.000267013
1438673_at	solute carrier family 4, sodium bicarbonate cotransporter, member 7	Slc4a7	0.274	0.001553385
1448743_at	synovial sarcoma, X breakpoint 2 interacting protein	Ssx2ip	0.274	0.000719191
1452864_at	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)-like	Med12l	0.274	0.046596148
1438606_a_at	chloride intracellular channel 4 (mitochondrial)	Clic4	0.274	0.000328944
1452146_a_at	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	Cox15	0.274	0.001858413
1423311_s_at	trophoblast glycoprotein	Tpbg	0.273	0.000997639
1419238_at	ATP-binding cassette, sub-family A (ABC1), member 7	Abca7	0.273	0.014529077
1457272_at	NA	NA	0.273	0.004781654
1416583_at	BCL2-associated agonist of cell death	Bad	0.273	0.003579566
1422900_at	meningioma expressed antigen 5 (hyaluronidase)	Mgea5	0.273	0.002270211
1415974_at	mitogen-activated protein kinase kinase 2	Map2k2	0.273	0.011503393
1416014_at	ATP-binding cassette, sub-family E (OABP), member 1	Abce1	0.273	0.000991556
1450838_x_at	ribosomal protein L37	Rpl37	0.273	0.004582736
1460718_s_at	mitochondrial carrier homolog 1 (C. elegans)	Mtch1	0.272	0.009055581
1415673_at	phosphoserine phosphatase	Psph	0.272	0.000660456
1421729_a_at	fer (fms/fps related) protein kinase, testis specific 2	Fert2	0.272	0.000349994
1449708_s_at	checkpoint kinase 1 homolog (S. pombe)	Chek1	0.272	0.005539015
1416773_at	WEE 1 homolog (S. pombe)	Wee1	0.272	0.002415362
1457285_at	zinc finger protein 187	Zfp187	0.272	0.007467252
1451422_at	myosin XVIIIa	Myo18a	0.271	0.000707536
1428076_s_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4	Ndufb4	0.271	0.004160736
1424149_at	non-SMC element 2 homolog (MMS21, S. cerevisiae)	Nsmce2	0.271	0.001846147
1448308_at	adaptor-related protein complex 3, mu 1 subunit	Ap3m1	0.271	0.001696961
1456057_x_at	transmembrane protein 109	Tmem109	0.271	0.007792937
1448953_at	Bloom syndrome homolog (human)	Blm	0.271	0.000389742
1418862_at	enoyl Coenzyme A hydratase domain containing 3	Echdc3	0.27	0.001636315
1420823_at	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	Sema4d	0.27	0.012548005
1416020_a_at	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	Atp5g1	0.27	0.001139115
1423376_a_at	docking protein 4	Dok4	0.27	0.001735632
1421887_a_at	amyloid beta (A4) precursor-like protein 2	Aplp2	0.269	0.003794909
1438550_x_at	serine racemase	Srr	0.269	0.002535803
1418483_a_at	glycoprotein galactosyltransferase alpha 1, 3	Ggta1	0.269	0.007556251

1430536_a_at	enhancer of rudimentary homolog (Drosophila)	Erh	0.269	0.000326991
1434149_at	transcription factor 4	Tcf4	0.269	0.006826291
1443762_s_at	SET binding factor 2	Sbf2	0.269	0.001372675
1432188_s_at	nucleoporin 43	Nup43	0.269	0.001387937
1417091_at	conserved helix-loop-helix ubiquitous kinase	Chuk	0.268	0.004777286
1455092_at	hypothetical protein LOC100043601	LOC100043601	0.268	0.01916816
1448959_at	NADH dehydrogenase (ubiquinone) Fe-S protein 4	Ndufs4	0.268	0.001313634
1456028_x_at	myristoylated alanine rich protein kinase C substrate	Marcks	0.268	0.008358434
1452087_at	epithelial stromal interaction 1 (breast)	Epsti1	0.268	0.005703119
1417189_at	proteasome (prosome, macropain) 28 subunit, beta	Psme2	0.268	0.002065579
1430291_at	dedicator of cytokinesis 5	Dock5	0.268	0.002396927
1455073_at	cytidine and dCMP deaminase domain containing 1	Cdadc1	0.268	0.007525701
1455800_x_at	sorting and assembly machinery component 50 homolog (S. cerevisiae)	Samm50	0.268	0.000284107
1417340_at	glutaredoxin 3	Glrx3	0.268	0.014179761
1439060_s_at	WD repeat domain, phosphoinositide interacting 1	Wipi1	0.267	0.00448256
1421873_s_at	RAB24, member RAS oncogene family	Rab24	0.267	0.00330012
1416415_a_at	H2A histone family, member Z	H2afz	0.267	0.000189155
1427964_at	CKLF-like MARVEL transmembrane domain containing 8	Cmtm8	0.267	0.00171381
1417591_at	prostaglandin E synthase 2	Ptges2	0.267	0.00121021
1437733_at	eukaryotic translation initiation factor 4E binding protein 2	Eif4ebp2	0.267	0.000560717
1453683_a_at	centrosomal protein 55	Cep55	0.267	0.023552075
1452742_at	trafficking protein, kinesin binding 1	Trak1	0.267	0.006707156
1416668_at	tetratricopeptide repeat domain 35	Ttc35	0.267	0.001001022
1423907_a_at	NADH dehydrogenase (ubiquinone) Fe-S protein 8	Ndufs8	0.267	0.012005182
1451283_at	RIKEN cDNA 1810073G14 gene	1810073G14Rik	0.266	0.000147922
1438095_x_at	nucleolar complex associated 4 homolog (S. cerevisiae)	Noc4l	0.266	0.001263959
1422598_at	calsequestrin 1	Casq1	0.266	0.036960878
1456244_x_at	glutaredoxin 3	Glrx3	0.266	0.021354202
1422009_at	ATPase, Na+/K+ transporting, beta 2 polypeptide	Atp1b2	0.266	0.001042411
1423823_at	MRT4, mRNA turnover 4, homolog (S. cerevisiae)	Mrto4	0.265	0.00163814
1451307_at	mitochondrial ribosomal protein L14	Mrpl14	0.265	0.000180654
1452604_at	StAR-related lipid transfer (START) domain containing 13	Stard13	0.265	0.005455268
1419199_at	chromobox homolog 8 (Drosophila Pc class)	Cbx8	0.265	0.013487618
1424291_at	nucleoporin 93	Nup93	0.265	0.000174842
1426217_at	transmembrane protein 216	Tmem216	0.265	0.001858413
1425668_a_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	St3gal4	0.265	0.001948421
1450519_a_at	protein kinase, cAMP dependent, catalytic, alpha	Prkaca	0.265	0.00049082
1415973_at	myristoylated alanine rich protein kinase C substrate	Marcks	0.264	0.002875932
1417126_a_at	ribosomal protein L22 like 1	Rpl22l1	0.264	0.010470671
1434420_x_at	translocase of outer mitochondrial membrane 22 homolog (yeast)	Tomm22	0.264	0.002348575
1451768_a_at	solute carrier family 20, member 2	Slc20a2	0.264	0.000635389

1455237_at	ubiquitin specific peptidase 36	Usp36	0.264	0.000209504
1423219_a_at	mitochondrial ribosomal protein L49	Mrpl49	0.264	0.002272423
1425195_a_at	acetyl-Coenzyme A acetyltransferase 3	Acat3	0.264	0.006634603
1448016_at	spindle assembly 6 homolog (C. elegans)	Sass6	0.264	0.001712667
1460631_at	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	Ogt	0.264	0.005392341
1417079_s_at	lectin, galactose-binding, soluble 2	Lgals2	0.264	0.000645429
1423924_s_at	tetraspanin 14	Tspan14	0.264	0.000448044
1449407_at	intraflagellar transport 81 homolog (Chlamydomonas)	Ift81	0.264	0.000429163
1428843_at	membrane-associated ring finger (C3HC4) 5	5-Mar	0.264	0.000400173
1451293_at	RRP9, small subunit (SSU) processome component, homolog (yeast)	Rrp9	0.263	0.001282586
1418286_a_at	ephrin B1	Efnb1	0.263	0.000971019
1424692_at	RIKEN cDNA 2810055F11 gene	2810055F11Rik	0.263	0.004527628
1426994_at	PH domain and leucine rich repeat protein phosphatase	Phlpp	0.263	0.000459478
1416763_at	cell division cycle 123 homolog (S. cerevisiae)	Cdc123	0.263	0.00057432
1448345_at	translocase of outer mitochondrial membrane 34	Tomm34	0.263	0.000306796
1448822_at	proteasome (prosome, macropain) subunit, beta type 6	Psmb6	0.263	0.002172644
1450144_at	phospholipase A2 receptor 1	Pla2r1	0.263	0.004140506
1416675_s_at	phospholipase C, delta 1	Plcd1	0.263	0.003616247
1427955_a_at	differentially expressed in B16F10 1	Deb1	0.263	0.005710074
1451333_a_at	proacrosin binding protein	Acrbp	0.262	0.029826336
1449620_s_at	adenylate cyclase 9	Adcy9	0.262	0.000770174
1426562_a_at	olfactomedin 1	Olfm1	0.262	0.049700878
1425732_a_at	Max interacting protein 1	Mxi1	0.262	0.014339587
1425576_at	S-adenosylhomocysteine hydrolase-like 1	Ahcyl1	0.262	0.011370963
1449413_at	Mpv17 transgene, kidney disease mutant-like	Mpv17l	0.262	0.000430937
1448523_at	nephronophthisis 1 (juvenile) homolog (human)	Nphp1	0.262	0.000462126
1420028_s_at	minichromosome maintenance deficient 3 (S. cerevisiae)	Mcm3	0.262	0.000379838
1452154_at	isoleucine-tRNA synthetase	Iars	0.262	0.000307099
1425364_a_at	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	Slc3a2	0.262	0.000298162
1417414_at	septin 3	Sept3	0.261	0.002415362
1422715_s_at	acid phosphatase 1, soluble	Acp1	0.261	0.001649115
1439407_x_at	transgelin 2	Tagln2	0.261	0.000743683
1450466_at	cyclin-dependent kinase 5, regulatory subunit 2 (p39)	Cdk5r2	0.261	0.003859392
1429485_a_at	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	Utp11l	0.261	0.00155109
1418746_at	paroxysmal nonkinesiogenic dyskinesia	Pnkd	0.261	0.000447274
1452264_at	tensin like C1 domain-containing phosphatase	Tenc1	0.261	0.008518051
1417258_at	chaperonin containing Tcp1, subunit 5 (epsilon)	Cct5	0.261	0.000189641
1419485_at	forkhead box C1	Foxc1	0.261	0.009794216
1451143_at	RIKEN cDNA 1110006G06 gene	1110006G06Rik	0.261	0.001434218
1424132_at	Harvey rat sarcoma virus oncogene 1	Hras1	0.261	0.002019616
1419811_at	adenylate cyclase 9	Adcy9	0.261	0.000915528
1418260_at	hormonally upregulated Neu-associated kinase	Hunk	0.26	0.00118555
1451555_at	neurolysin (metallopeptidase M3 family)	Nln	0.26	0.000521323
1436791_at	wingless-related MMTV integration site 5A	Wnt5a	0.26	0.00134857
1452048_at	mitochondrial ribosomal protein L12	Mrpl12	0.26	0.007786448

1424224_at	ankyrin repeat and SOCS box-containing 8	Asb8	0.26	0.000387499
1453076_at	basic leucine zipper transcription factor, ATF-like 3	Batf3	0.26	0.000387398
1423948_at	BCL2-associated athanogene 2	Bag2	0.26	0.00100032
1426090_a_at	fer (fms/fps related) protein kinase, testis specific 2	Fert2	0.26	0.000628256
1422034_a_at	paralemmin	Palm	0.259	0.012733937
1425073_at	pleckstrin homology domain containing, family G (with RhoGef domain) member 6	Plekhg6	0.259	0.018933778
1428073_a_at	nucleoporin 88	Nup88	0.259	0.000466337
1426312_at	brain and reproductive organ-expressed protein	Bre	0.259	0.000860634
1427447_a_at	TRIO and F-actin binding protein	Triobp	0.259	0.000530789
1434214_at	RIKEN cDNA 0910001L09 gene	0910001L09Rik	0.259	0.001856397
1417782_at	LAG1 homolog, ceramide synthase 4	Lass4	0.259	0.007384754
1416641_at	ligase I, DNA, ATP-dependent	Lig1	0.259	0.001559873
1451982_at	mitogen-activated protein kinase kinase 4	Map2k4	0.258	0.002138689
1455605_at	RUN and FYVE domain containing 3	Rufy3	0.258	0.015035953
1424097_at	ELOVL family member 7, elongation of long chain fatty acids (yeast)	Elovl7	0.258	0.000189129
1418332_a_at	ATP/GTP binding protein 1	Agtpbp1	0.258	0.003059102
1422678_at	diacylglycerol O-acyltransferase 2	Dgat2	0.258	0.002327032
1460348_at	MAD2 mitotic arrest deficient-like 2 (yeast)	Mad2l2	0.258	0.011947759
1424826_s_at	metastasis suppressor 1	Mtss1	0.258	0.001099924
1423239_at	inosine 5'-phosphate dehydrogenase 1	Impdh1	0.258	0.000558489
1450704_at	Indian hedgehog	Ihh	0.257	0.043264096
1453016_at	heat shock protein family B (small), member 11	Hspb11	0.257	0.002685777
1439463_x_at	RIKEN cDNA 2810416G20 gene	2810416G20Rik	0.257	0.018305627
1428143_a_at	patatin-like phospholipase domain containing 2	Pnpla2	0.257	0.005003464
1425826_a_at	sorbin and SH3 domain containing 1	Sorbs1	0.257	0.00222515
1420807_a_at	delta-like 2 homolog (Drosophila)	Dlk2	0.257	0.001329132
1450959_at	RIKEN cDNA D930014E17 gene	D930014E17Rik	0.256	0.003709698
1427441_a_at	succinate-Coenzyme A ligase, GDP-forming, beta subunit	Suclg2	0.256	0.004858062
1450082_s_at	ets variant gene 5	Etv5	0.256	0.001407248
1453253_a_at	RNA pseudouridylate synthase domain containing 1	Rpusd1	0.256	0.001883077
1435977_at	hepatoma-derived growth factor, related protein 3	Hdgfrp3	0.256	0.000620379
1424535_at	tectonic family member 3	Tctn3	0.256	0.002590294
1439185_x_at	RIKEN cDNA D430028G21 gene	D430028G21Rik	0.256	0.000764126
1450628_at	solute carrier family 2, (facilitated glucose transporter), member 8	Slc2a8	0.256	0.001301399
1451668_at	RIKEN cDNA C530043G21 gene	C530043G21Rik	0.255	0.000471044
1460170_at	exostoses (multiple) 2	Ext2	0.255	0.000494366
1455868_a_at	tubulin, gamma complex associated protein 2	Tubgcp2	0.255	0.000336818
1416032_at	transmembrane protein 109	Tmem109	0.255	0.001071619
1416299_at	Shc SH2-domain binding protein 1	Shcbp1	0.255	0.007547596
1418074_at	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	St6galnac4	0.255	0.008898932
1422252_a_at	cell division cycle 25 homolog C (S. pombe)	Cdc25c	0.255	0.001007675
1451382_at	ChaC, cation transport regulator-like 1 (E. coli)	Chac1	0.255	0.000342936
1426693_x_at	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	Cox15	0.255	0.002092933
1448227_at	growth factor receptor bound protein 7	Grb7	0.255	0.0008935
1448253_at	glutamate dehydrogenase 1	Glud1	0.255	0.00028382
1455955_s_at	sorting nexin 17	Snx17	0.254	0.010621005

1426837_at	methionyl aminopeptidase 1	Metap1	0.254	0.001176838
1418425_at	Sp7 transcription factor 7	Sp7	0.254	0.0200443
1452296_at	slit homolog 3 (Drosophila)	Slit3	0.254	0.003408066
1415823_at	stearoyl-Coenzyme A desaturase 2	Scd2	0.254	0.003396158
1427791_a_at	a disintegrin and metallopeptidase domain 1a	Adam1a	0.254	0.001769631
1418329_at	pyroglutamyl-peptidase I	Pgpep1	0.254	0.002221912
1423908_at	NADH dehydrogenase (ubiquinone) Fe-S protein 8	Ndufs8	0.254	0.00596773
1434035_at	DnaJ (Hsp40) homolog, subfamily B, member 6	Dnajb6	0.253	0.000451757
1449003_a_at	vesicle transport through interaction with t-SNAREs 1B homolog	Vti1b	0.253	0.000386461
1426323_x_at	SIVA1, apoptosis-inducing factor	Siva1	0.253	0.003399528
1419118_at	V-set and transmembrane domain containing 2B	Vstm2b	0.253	0.001125886
1424225_at	ankyrin repeat and SOCS box-containing 8	Asb8	0.253	0.001694435
1452782_a_at	thioredoxin 2	Txn2	0.253	0.00526166
1423431_a_at	MYB binding protein (P160) 1a	Mybbp1a	0.253	0.00057432
1428954_at	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	Slc9a3r2	0.253	0.005994244
1428125_at	predicted gene, ENSMUSG00000074747	ENSMUSG00000074747	0.253	0.000243267
1416242_at	kelch-like 13 (Drosophila)	Klhl13	0.253	0.045844383
1429104_at	LIM domain containing 2	Limd2	0.253	0.000493056
1424508_at	tetratricopeptide repeat domain 5	Ttc5	0.253	0.001099924
1427090_at	zinc finger, BED domain containing 4	Zbed4	0.252	0.000345087
1423701_at	Coenzyme A synthase	Coasy	0.252	0.008245503
1437997_x_at	mitochondrial ribosomal protein L48	Mrpl48	0.252	0.002863253
1453013_at	zinc finger protein 740	Zfp740	0.252	0.003579566
1438563_s_at	mitochondrial ribosomal protein S24	Mrps24	0.252	0.029103385
1452343_at	DNA segment, Chr 18, ERATO Doi 653, expressed	D18Ertd653e	0.252	0.007151408
1452919_a_at	jagged 2	Jag2	0.252	0.00509868
1423826_at	nucleolar complex associated 4 homolog (S. cerevisiae)	Noc4l	0.252	0.0108431
1452271_at	xenotropic and polytropic retrovirus receptor 1	Xpr1	0.252	0.003138388
1437982_x_at	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	Cox15	0.252	0.005296875
1427233_at	teashirt zinc finger family member 1	Tshz1	0.252	0.003393277
1424615_at	FGF receptor activating protein 1	Frag1	0.252	0.003194285
1423814_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	Ddx41	0.251	0.001684436
1452241_at	topoisomerase (DNA) II binding protein 1	Topbp1	0.251	0.000673917
1417665_a_at	cleavage and polyadenylation specific factor 1	Cpsf1	0.251	0.001194528
1422407_s_at	Harvey rat sarcoma virus oncogene 1	Hras1	0.251	0.004670725
1435881_at	mitogen-activated protein kinase kinase kinase 12	Map3k12	0.251	0.000980564
1423750_a_at	splicing factor 1	Sf1	0.251	0.001512534
1433750_at	solute carrier family 31, member 1	Slc31a1	0.251	0.000894979
1424263_at	RIKEN cDNA 2810003C17 gene	2810003C17Rik	0.251	0.001917918
1418655_at	beta-1,4-N-acetyl-galactosaminyl transferase 1	B4galnt1	0.251	0.011684089
1452078_a_at	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	Slc11a2	0.251	0.003932231
1450932_s_at	dedicator of cytokinesis 9	Dock9	0.251	0.000657625
1454454_at	NA	NA	0.251	0.016663237
1460676_at	Josephin domain containing 1	Josd1	0.251	0.00074548
1423067_at	CDK5 regulatory subunit associated protein 3	Cdk5rap3	0.251	0.001127345
1416002_x_at	coactosin-like 1 (Dictyostelium)	Cotl1	0.25	0.000561056
1436232_a_at	GA repeat binding protein, beta 1	Gabpb1	0.25	0.000729228

1427893_a_at	phosphomevalonate kinase	Pmvk	0.25	0.000610564
1449406_at	cysteine and histidine rich 1	Cyhr1	0.25	0.006477565
1424048_a_at	cytochrome b5 reductase 1	Cyb5r1	0.25	0.000355306
1452662_a_at	eukaryotic translation initiation factor 2, subunit 1 alpha	Eif2s1	0.25	0.000853953
1417533_a_at	integrin beta 5	Itgb5	0.25	0.00138035
1416016_at	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2)	Psmb9	0.25	0.001042338
1423254_x_at	ribosomal protein S27-like	Rps27l	0.25	0.004373636
1416892_s_at	RIKEN cDNA 3110001A13 gene	3110001A13Rik	0.25	0.004362271
1427599_at	bol, boule-like (Drosophila)	Boll	0.249	0.024843212
1449980_a_at	gamma-aminobutyric acid (GABA-A) receptor, subunit delta	Gabrd	0.249	0.006155358
1416536_at	melanoma associated antigen (mutated) 1	Mum1	0.249	0.001483424
1460424_at	transmembrane protein 160	Tmem160	0.249	0.00179184
1424312_at	adiponectin receptor 1	Adipor1	0.249	0.002448531
1451904_a_at	a disintegrin and metallopeptidase domain 33	Adam33	0.249	0.000602276
1451362_at	RAB7, member RAS oncogene family-like 1	Rab7l1	0.248	0.038280524
1423550_at	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	Slc1a4	0.248	0.003747655
1425806_a_at	mediator complex subunit 21	Med21	0.248	0.003744361
1433661_at	NLR family member X1	Nlrx1	0.248	0.001620933
1449423_at	microtubule associated serine/threonine kinase 1	Mast1	0.248	0.006477744
1418490_at	serine dehydratase-like	Sdsl	0.248	0.002803826
1452173_at	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	Hadha	0.248	0.001246553
1415953_s_at	MAP/microtubule affinity-regulating kinase 2	Mark2	0.248	0.004063713
1415804_at	chemokine (C-X3-C motif) ligand 1	Cx3cl1	0.248	0.007614111
1436000_a_at	S-phase kinase-associated protein 2 (p45)	Skp2	0.248	0.00063461
1460722_at	sterol O-acyltransferase 2	Soat2	0.247	0.00247682
1427482_a_at	carbonic anhydrase 8	Car8	0.247	0.001714059
1450058_at	aspartate-beta-hydroxylase	Asph	0.247	0.002159495
1429061_at	RIKEN cDNA 1810063B05 gene	1810063B05Rik	0.247	0.008915703
1423134_at	Rab interacting lysosomal protein-like 2	Rilpl2	0.247	0.004611633
1428406_s_at	host cell factor C1 regulator 1 (XPO1-dependent)	Hcfc1r1	0.247	0.002479499
1424421_at	lens epithelial protein	Lenep	0.246	0.001015718
1416604_at	cytochrome c-1	Cyc1	0.246	0.000381897
1419869_s_at	high density lipoprotein (HDL) binding protein	Hdlbp	0.246	0.004429857
1418607_at	zinc finger with KRAB and SCAN domains 14	Zkscan14	0.246	0.000652887
1417037_at	origin recognition complex, subunit 6-like (S. cerevisiae)	Orc6l	0.246	0.001008314
1438653_x_at	ataxin 10	Atxn10	0.246	0.000569974
1451139_at	solute carrier family 39 (zinc transporter), member 4	Slc39a4	0.246	0.002648495
1435143_at	ELK3, member of ETS oncogene family	Elk3	0.246	0.000836138
1428179_at	NADH dehydrogenase (ubiquinone) flavoprotein 2	Ndufv2	0.246	0.002095566
1419522_at	zinc finger, MYND domain containing 19	Zmynd19	0.246	0.002430523
1423195_at	hippocampus abundant gene transcript 1	Hiat1	0.246	0.001492641
1434011_a_at	integrator complex subunit 5	Ints5	0.246	0.001273816
1417058_a_at	keratinocyte associated protein 2	Krtcap2	0.245	0.046359501
1420712_a_at	hepsin	Hpn	0.245	0.005239341
1450423_s_at	brix domain containing 1	Bxdc1	0.245	0.001063614
1451959_a_at	vascular endothelial growth factor A	Vegfa	0.245	0.019437313

1426916_at	secernin 3	Scrn3	0.245	0.011818884
1424858_at	L-2-hydroxyglutarate dehydrogenase	L2hgdh	0.245	0.001516965
1417237_at	phospholipase D2	Pld2	0.245	0.017391924
1430769_s_at	RIKEN cDNA 2900009I07 gene	2900009I07Rik	0.245	0.000602085
1417354_at	endoplasmic reticulum chaperone SIL1 homolog (S. cerevisiae)	Sil1	0.245	0.001163485
1455071_at	zinc finger and BTB domain containing 7B	Zbtb7b	0.245	0.004734649
1423429_at	reproductive homeobox 5	Rhox5	0.244	0.000244433
1416006_at	midkine	Mdk	0.244	0.00623732
1452767_at	ribosome binding protein 1	Rrbp1	0.244	0.00855075
1437253_at	RIKEN cDNA A630054L15 gene	A630054L15Rik	0.244	0.000814276
1426389_at	calcium/calmodulin-dependent protein kinase ID	Camk1d	0.244	0.006319665
1419438_at	single-minded homolog 2 (Drosophila)	Sim2	0.244	0.000942656
1427180_at	solute carrier family 27 (fatty acid transporter), member 3	Slc27a3	0.244	0.001569482
1419978_s_at	DNA segment, Chr 10, ERATO Doi 610, expressed	D10Ertd610e	0.244	0.02516294
1426898_at	mitogen-activated protein kinase kinase kinase 7 interacting protein 1	Map3k7ip1	0.244	0.005434698
1448817_at	OTU domain, ubiquitin aldehyde binding 1	Otub1	0.244	0.00144999
1452653_at	solute carrier family 25 (mitochondrial carrier, glutamate), member 22	Slc25a22	0.243	0.00076628
1448387_at	ring-box 1	Rbx1	0.243	0.000300569
1426652_at	minichromosome maintenance deficient 3 (S. cerevisiae)	Mcm3	0.243	0.001250905
1424364_a_at	RIKEN cDNA 1110020P15 gene	1110020P15Rik	0.243	0.001463684
1448539_a_at	aspartoacylase (aminoacylase) 3	Acy3	0.243	0.003305051
1433829_a_at	heterogeneous nuclear ribonucleoprotein A2/B1	Hnrnpa2b1	0.243	0.004761648
1449859_at	golgi transport 1 homolog B (S. cerevisiae)	Golt1b	0.242	0.004969018
1434491_a_at	cytochrome c oxidase, subunit VIc	Cox6c	0.242	0.010716836
1418285_at	ephrin B1	Efnb1	0.242	0.00091581
1417599_at	CD276 antigen	Cd276	0.242	0.000887136
1425099_a_at	aryl hydrocarbon receptor nuclear translocator-like	Arntl	0.242	0.000435063
1434658_at	RIKEN cDNA 3110056O03 gene	3110056O03Rik	0.242	0.002648495
1415995_at	caspase 6	Casp6	0.242	0.002677775
1449679_s_at	syntaxin 5A	Stx5a	0.242	0.001110465
1416651_at	zinc finger, HIT domain containing 2	Znhit2	0.242	0.015488377
1448509_at	RIKEN cDNA 3110001A13 gene	3110001A13Rik	0.242	0.014727826
1416723_at	transcription factor 4	Tcf4	0.242	0.00400926
1424395_at	asparaginase like 1	Asrgl1	0.242	0.000994273
1460732_a_at	periplakin	Ppl	0.242	0.04757676
1451329_at	nudix (nucleoside diphosphate linked moiety X)-type motif 22	Nudt22	0.242	0.001494667
1426835_at	methionyl aminopeptidase 1	Metap1	0.241	0.000311797
1456133_x_at	integrin beta 5	Itgb5	0.241	0.001784305
1428823_at	HD domain containing 2	Hddc2	0.241	0.016446928
1428072_a_at	dolichyl pyrophosphate phosphatase 1	Dolpp1	0.241	0.002092838
1426180_a_at	submaxillary gland androgen regulated protein 2	Smr2	0.241	0.037322655
1428128_at	predicted gene, ENSMUSG00000074747	ENSMUSG00000074747	0.241	0.000862124
1424396_a_at	asparaginase like 1	Asrgl1	0.241	0.000479263
1423834_s_at	golgi associated, gamma adaptin ear containing, ARF binding protein 1	Gga1	0.241	0.001697253
1441013_at	expressed sequence C81521	C81521	0.24	0.015892771

1449157_at	nuclear receptor subfamily 2, group C, member 1	Nr2c1	0.24	0.004388746
1437394_at	centaurin, gamma 2	Centg2	0.24	0.012302668
1423696_a_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	Psmd6	0.24	0.008635012
1428955_x_at	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	Slc9a3r2	0.24	0.001494294
1423120_at	insulin degrading enzyme	Ide	0.24	0.00031994
1424183_at	acetyl-Coenzyme A acetyltransferase 1	Acat1	0.24	0.000300087
1449047_at	2-hydroxyacyl-CoA lyase 1	Hacl1	0.24	0.00594294
1415796_at	DAZ associated protein 2	Dazap2	0.24	0.000757816
1448662_at	frizzled homolog 6 (Drosophila)	Fzd6	0.239	0.010919821
1452812_at	latrophilin 1	Lphn1	0.239	0.004595928
1423360_at	YME1-like 1 (S. cerevisiae)	Yme1l1	0.239	0.01729158
1423251_at	LUC7-like 2 (S. cerevisiae)	Luc7l2	0.239	0.004388202
1416113_at	FK506 binding protein 8	Fkbp8	0.239	0.001054078
1416900_s_at	LAG1 homolog, ceramide synthase 1	Lass1	0.239	0.002464232
1455730_at	discs, large (Drosophila) homolog-associated protein 5	Dlgap5	0.239	0.001228597
1452885_at	splicing factor, arginine/serine-rich 2, interacting protein	Sfrs2ip	0.239	0.005493973
1418277_at	retinitis pigmentosa 9 (human)	rp9	0.238	0.005995184
1429103_at	translocase of outer mitochondrial membrane 22 homolog (yeast)	Tomm22	0.238	0.001764496
1416606_s_at	nucleolar protein family A, member 2	Nola2	0.238	0.007781196
1455676_x_at	Tia1 cytotoxic granule-associated RNA binding protein-like 1	Tial1	0.238	0.008992601
1449362_a_at	misshapen-like kinase 1 (zebrafish)	Mink1	0.238	0.004429857
1460701_a_at	mitochondrial ribosomal protein L52	Mrpl52	0.238	0.01064922
1428048_at	cDNA sequence BC027582	BC027582	0.238	0.032687174
1451064_a_at	phosphoserine aminotransferase 1	Psat1	0.237	0.000620837
1426735_at	isoleucine-tRNA synthetase 2, mitochondrial	Iars2	0.237	0.000737746
1455901_at	choline phosphotransferase 1	Chpt1	0.237	0.046059194
1438056_x_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	Abcc5	0.237	0.004908966
1437848_x_at	ADP-dependent glucokinase	Adpgk	0.237	0.021635921
1428995_at	predicted gene, ENSMUSG00000071724	ENSMUSG00000071724	0.237	0.016970909
1454904_at	X-linked myotubular myopathy gene 1	Mtm1	0.237	0.002588354
1450799_at	adenylate cyclase activating polypeptide 1 receptor 1	Adcyap1r1	0.237	0.01604711
1427606_at	ubiquitin specific peptidase 27, X chromosome	Usp27x	0.237	0.001606496
1448796_s_at	transforming growth factor beta regulated gene 4	Tbrg4	0.237	0.006039506
1424274_at	USO1 homolog, vesicle docking protein (yeast)	Uso1	0.237	0.003085897
1415882_at	growth hormone inducible transmembrane protein	Ghitm	0.237	0.003493598
1424282_at	PET112-like (yeast)	Pet112l	0.237	0.006198846
1427951_s_at	coiled-coil domain containing 28A	Ccdc28a	0.237	0.011280809
1421019_at	RIKEN cDNA 1700021F05 gene	1700021F05Rik	0.237	0.001664068
1419209_at	chemokine (C-X-C motif) ligand 1	Cxcl1	0.237	0.008525997
1452665_at	tetratricopeptide repeat domain 27	Ttc27	0.237	0.002110523
1428707_at	parathymosin	Ptms	0.237	0.000709478
1416678_at	COP9 (constitutive photomorphogenic) homolog, subunit 3 (Arabidopsis thaliana)	Cops3	0.236	0.0005275
1428063_at	ankyrin repeat domain 46	Ankrd46	0.236	0.000610564
1423456_at	basic leucine zipper and W2 domains 2	Bzw2	0.236	0.00999168
1451927_a_at	mitogen-activated protein kinase 14	Mapk14	0.236	0.025771753

1428388_at	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	Tnks2	0.236	0.007264796
1428389_s_at	WD repeat domain 43	Wdr43	0.236	0.000754502
1418042_a_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	Abcc5	0.236	0.001347518
1450905_at	plexin C1	Plxnc1	0.236	0.01031953
1426744_at	sterol regulatory element binding factor 2	Srebf2	0.236	0.001281007
1426094_at	rhomboid, veinlet-like 1 (Drosophila)	Rhbdl1	0.236	0.001971739
1452456_at	nuclear receptor interacting protein 2	Nrip2	0.236	0.013317923
1416510_at	mitochondrial ribosomal protein L4	Mrpl4	0.236	0.001941442
1434976_x_at	eukaryotic translation initiation factor 4E binding protein 1	Eif4ebp1	0.235	0.004657195
1422997_s_at	acyl-CoA thioesterase 2	Acot2	0.235	0.022838719
1449043_at	N-acetyl galactosaminidase, alpha	Naga	0.235	0.000972295
1438477_a_at	methylmalonyl CoA epimerase	Mcee	0.235	0.012800439
1429655_at	NudC domain containing 1	Nudcd1	0.235	0.005888372
1416814_at	cytotoxic granule-associated RNA binding protein 1	Tia1	0.235	0.010330977
1426817_at	antigen identified by monoclonal antibody Ki 67	Mki67	0.235	0.007046179
1428302_at	mitochondrial ribosomal protein L48	Mrpl48	0.235	0.001400374
1433775_at	expressed sequence C77080	C77080	0.234	0.003138091
1422244_at	polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like	Pkdrej	0.234	0.009753615
1460228_at	upstream transcription factor 2	Usf2	0.234	0.001595043
1423472_at	septin 2	Sept2	0.234	0.003338946
1423055_at	neuron specific gene family member 1	Nsg1	0.234	0.005111462
1451383_a_at	conserved helix-loop-helix ubiquitous kinase	Chuk	0.234	0.005903671
1419180_at	B-cell CLL/lymphoma 9-like	Bcl9l	0.234	0.007990184
1428075_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4	Ndufb4	0.234	0.004897794
1452637_a_at	bolA-like 1 (E. coli)	Bola1	0.234	0.002172415
1424818_at	asparagine-linked glycosylation 12 homolog (yeast, alpha-1,6-mannosyltransferase)	Alg12	0.234	0.003291132
1423655_a_at	RIKEN cDNA 1500010J02 gene	1500010J02Rik	0.234	0.007715908
1438082_at	protein phosphatase 2, regulatory subunit B (B56), alpha isoform	Ppp2r5a	0.234	0.039432664
1427820_at	NA	NA	0.234	0.009499527
1433953_at	zinc finger protein 277	Zfp277	0.234	0.001115648
1417848_at	zinc finger protein 704	Zfp704	0.234	0.022973344
1417722_at	6-phosphogluconolactonase	Pgls	0.233	0.006680246
1451209_at	LAG1 homolog, ceramide synthase 5	Lass5	0.233	0.002479499
1425072_at	S-phase kinase-associated protein 2 (p45)	Skp2	0.233	0.003707359
1452097_a_at	dual specificity phosphatase 7	Dusp7	0.233	0.003610173
1449841_at	kinesin family member 3A	Kif3a	0.233	0.002346188
1434427_a_at	ring finger protein 157	Rnf157	0.233	0.042744264
1450630_at	queuine tRNA-ribosyltransferase 1	Qtrt1	0.233	0.007776837
1418853_at	apolipoprotein N	Apon	0.233	0.009753615
1438058_s_at	prostate tumor over expressed gene 1	Ptov1	0.233	0.004213918
1452838_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	Ddx10	0.233	0.003904394
1456390_at	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	Ppp2ca	0.233	0.003928072
1428635_at	catechol-O-methyltransferase domain containing 1	Comtd1	0.233	0.018733312
1437008_x_at	transmembrane protein 109	Tmem109	0.233	0.022718239
1456377_x_at	LIM domain containing 2	Limd2	0.232	0.045395485
1448060_at	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D	Sema6d	0.232	0.020982318

1437684_at	FtsJ methyltransferase domain containing 1	Ftsjd1	0.232	0.024376326
1434036_at	metastasis suppressor 1	Mtss1	0.232	0.001338268
1437618_x_at	G protein-coupled receptor 85	Gpr85	0.232	0.009063143
1425230_at	N-acetylglutamate synthase	Nags	0.232	0.002664018
1451024_at	sphingosine-1-phosphate receptor 4	S1pr4	0.232	0.003825519
1451144_at	brix domain containing 2	Bxdc2	0.232	0.000705293
1435429_x_at	ribosomal protein S27-like	Rps27l	0.232	0.003369663
1428107_at	SH3-binding domain glutamic acid-rich protein like	Sh3bgrl	0.232	0.018379677
1416919_a_at	nephronophthisis 1 (juvenile) homolog (human)	Nphp1	0.232	0.013550726
1448489_at	platelet-activating factor acetylhydrolase 2	Pafah2	0.232	0.006427358
1420929_at	catenin (cadherin associated protein), alpha-like 1	Ctnnal1	0.231	0.009355828
1452844_at	POU domain, class 6, transcription factor 1	Pou6f1	0.231	0.00157961
1421683_at	t-complex-associated testis expressed 3	Tcte3	0.231	0.00235973
1420930_s_at	catenin (cadherin associated protein), alpha-like 1	Ctnnal1	0.231	0.011416604
1423705_at	enolase-phosphatase 1	Enoph1	0.231	0.002108236
1451809_s_at	RWD domain containing 3	Rwdd3	0.231	0.021057956
1455229_x_at	phosphatidylglycerophosphate synthase 1	Pgs1	0.231	0.001294435
1452925_a_at	membrane-associated ring finger (C3HC4) 5	5-Mar	0.231	0.021507049
1448209_a_at	solute carrier family 22 (organic cation transporter), member 17	Slc22a17	0.231	0.000736717
1422719_s_at	nucleoporin 50	Nup50	0.23	0.004140506
1423960_at	lysophosphatidylcholine acyltransferase 3	Lpcat3	0.23	0.000390159
1419195_at	WAP four-disulfide core domain 15B	Wfdc15b	0.23	0.005483424
1426271_at	structural maintenance of chromosomes 5	Smc5	0.23	0.001695743
1417726_at	Sjogren's syndrome/scleroderma autoantigen 1 homolog (human)	Sssca1	0.229	0.003705421
1448574_at	non-metastatic cells 6, protein expressed in (nucleoside-diphosphate kinase)	Nme6	0.229	0.001791009
1427920_at	PHD finger protein 19	Phf19	0.229	0.00468574
1427560_at	sine oculis-related homeobox 5 homolog (Drosophila)	Six5	0.229	0.034326445
1416726_s_at	ubiquitin-conjugating enzyme E2S	Ube2s	0.229	0.011147013
1451075_s_at	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	Ctdsp2	0.229	0.000847958
1427232_at	teashirt zinc finger family member 1	Tshz1	0.229	0.002991607
1424311_at	RIKEN cDNA 0710008K08 gene	0710008K08Rik	0.229	0.001755679
1449477_s_at	solute carrier family 2 (facilitated glucose transporter), member 10	Slc2a10	0.229	0.032578703
1416197_at	U1 small nuclear ribonucleoprotein C	Snrpc	0.229	0.002044421
1426865_a_at	neural cell adhesion molecule 1	Ncam1	0.228	0.039389897
1416582_a_at	BCL2-associated agonist of cell death	Bad	0.228	0.002611553
1417170_at	leucine zipper transcription factor-like 1	Lztfl1	0.228	0.01212063
1426840_at	YTH domain family 3	Ythdf3	0.228	0.023476359
1448257_at	solute carrier family 29 (nucleoside transporters), member 2	Slc29a2	0.228	0.004253855
1422321_a_at	splicing factor 1	Sf1	0.228	0.003424088
1428706_at	proline-rich polypeptide 6	Prr6	0.228	0.000725747
1427246_at	membrane associated guanylate kinase, WW and PDZ domain containing 1	Magi1	0.228	0.010850472
1449068_at	zinc finger protein 148	Zfp148	0.228	0.011414783
1421339_at	exostoses (multiple)-like 3	Extl3	0.228	0.029103385
1451211_a_at	ligatin	Lgtn	0.227	0.001891805
1417138_s_at	polymerase (RNA) II (DNA directed) polypeptide E	Polr2e	0.227	0.001007616

1428193_at	ubiquitin specific peptidase 9, X chromosome	Usp9x	0.227	0.027735233
1449799_s_at	plakophilin 2	Pkp2	0.227	0.006860006
1415822_at	stearoyl-Coenzyme A desaturase 2	Scd2	0.227	0.0004905
1425557_x_at	TSC22 domain family, member 3	Tsc22d3	0.227	0.000625015
1424323_at	nucleolar complex associated 2 homolog (S. cerevisiae)	Noc2l	0.227	0.022668014
1423334_at	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	Ergic1	0.227	0.002489949
1426855_at	DNA segment, Chr 10, ERATO Doi 610, expressed	D10Ertd610e	0.227	0.031108648
1416577_a_at	ring-box 1	Rbx1	0.226	0.011611312
1415779_s_at	actin, gamma, cytoplasmic 1	Actg1	0.226	0.000764126
1433940_at	sperm associated antigen 7	Spag7	0.226	0.01593167
1449146_at	Notch gene homolog 4 (Drosophila)	Notch4	0.226	0.032634743
1444028_s_at	dedicator of cytokinesis 9	Dock9	0.226	0.005644507
1429708_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11	Ndufa11	0.226	0.007434023
1434017_at	zinc and ring finger 2	Znrf2	0.226	0.001649115
1449474_a_at	nasal embryonic LHRH factor	Nelf	0.226	0.002785213
1422576_at	ataxin 10	Atxn10	0.226	0.002276251
1450084_s_at	influenza virus NS1A binding protein	Ivns1abp	0.226	0.004225726
1451734_a_at	drebrin 1	Dbn1	0.226	0.01350789
1427202_at	RIKEN cDNA 4833442J19 gene	4833442J19Rik	0.226	0.006416873
1434213_x_at	NADH dehydrogenase (ubiquinone) Fe-S protein 8	Ndufs8	0.225	0.006025093
1424388_at	clusterin associated protein 1	Cluap1	0.225	0.001580216
1451288_s_at	RIKEN cDNA 1810043G02 gene	1810043G02Rik	0.225	0.001339109
1428329_a_at	intraflagellar transport 80 homolog (Chlamydomonas)	Ift80	0.225	0.002080569
1449441_a_at	WW domain binding protein 1	Wbp1	0.225	0.002907323
1428090_at	pentatricopeptide repeat domain 3	Ptcd3	0.225	0.001147881
1416273_at	tumor necrosis factor, alpha-induced protein 2	Tnfaip2	0.225	0.002795143
1437308_s_at	coagulation factor II (thrombin) receptor	F2r	0.225	0.027309164
1450244_a_at	mitogen-activated protein kinase kinase kinase kinase 2	Map4k2	0.224	0.008189087
1424284_at	protein-O-mannosyltransferase 1	Pomt1	0.224	0.004855451
1450925_a_at	ribosomal protein S27-like	Rps27l	0.224	0.006715504
1418412_at	tumor protein D52-like 1	Tpd52l1	0.224	0.003003393
1425993_a_at	heat shock 105kDa/110kDa protein 1	Hsph1	0.224	0.000669945
1436384_at	ribosomal protein S10	Rps10	0.224	0.007770434
1423656_x_at	RIKEN cDNA 1500010J02 gene	1500010J02Rik	0.224	0.001712667
1418792_at	SH3-domain GRB2-like 2	Sh3gl2	0.224	0.0030614
1448218_s_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	Ywhaz	0.224	0.00507546
1426751_s_at	nucleoporin 107	Nup107	0.223	0.000893126
1449171_at	Ttk protein kinase	Ttk	0.223	0.020988299
1438793_x_at	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	Ergic1	0.223	0.012011461
1455462_at	adenylate cyclase 2	Adcy2	0.223	0.002725905
1432136_s_at	zinc finger, DHHC domain containing 4	Zdhhc4	0.223	0.001296509
1418108_at	rhotekin 2	Rtkn2	0.223	0.00806868
1420053_at	proteasome (prosome, macropain) subunit, beta type 1	Psmb1	0.223	0.035764455
1422626_at	matrix metallopeptidase 16	Mmp16	0.223	0.00816078
1418736_at	UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 1	B3galnt1	0.223	0.001565341
1426277_at	RIKEN cDNA C730025P13 gene	C730025P13Rik	0.223	0.00148343

1416573_at	protein O-fucosyltransferase 2	Pofut2	0.223	0.009644718
1449353_at	zinc finger matrin type 3	Zmat3	0.223	0.004938684
1416910_at	DnaJ (Hsp40) homolog, subfamily C, member 15	Dnajc15	0.223	0.001015098
1416679_at	ATP-binding cassette, sub-family D (ALD), member 3	Abcd3	0.223	0.002023554
1434180_at	fermitin family homolog 2 (Drosophila)	Fermt2	0.223	0.001170576
1419046_at	brain protein 16	Brp16	0.223	0.003849715
1416571_at	Tnf receptor associated factor 4	Traf4	0.222	0.000884362
1424443_at	transmembrane 6 superfamily member 1	Tm6sf1	0.222	0.002761668
1455177_at	Abelson helper integration site 1	Ahi1	0.222	0.002857676
1451369_at	COMM domain containing 5	Commd5	0.222	0.004823644
1416698_a_at	CDC28 protein kinase 1b	Cks1b	0.222	0.00244745
1449635_at	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	Prpf19	0.222	0.002164924
1436955_at	tumor suppressing subtransferable candidate 1	Tssc1	0.222	0.008720638
1448656_at	calcium channel, voltage-dependent, beta 3 subunit	Cacnb3	0.222	0.010986118
1417050_at	C1q and tumor necrosis factor related protein 4	C1qtnf4	0.222	0.044941731
1451218_at	ER degradation enhancer, mannosidase alpha-like 1	Edem1	0.222	0.002207514
1460583_at	golgi transport 1 homolog B (S. cerevisiae)	Golt1b	0.222	0.005903401
1424609_a_at	predicted gene, 100039204	100039204	0.222	0.016907304
1417193_at	superoxide dismutase 2, mitochondrial	Sod2	0.222	0.004448363
1453686_x_at	nephronophthisis 1 (juvenile) homolog (human)	Nphp1	0.222	0.003359912
1434199_at	transmembrane protein 151B	Tmem151b	0.221	0.007904001
1449283_a_at	mitogen-activated protein kinase 12	Mapk12	0.221	0.011640526
1418901_at	CCAAT/enhancer binding protein (C/EBP), beta	Cebpb	0.221	0.001883077
1423653_at	ATPase, Na+/K+ transporting, alpha 1 polypeptide	Atp1a1	0.221	0.000631097
1438976_x_at	methionine adenosyltransferase II, alpha	Mat2a	0.221	0.030003751
1419153_at	RIKEN cDNA 2810417H13 gene	2810417H13Rik	0.221	0.002630215
1418377_a_at	SIVA1, apoptosis-inducing factor	Siva1	0.221	0.006122572
1435364_at	cysteine and histidine rich 1	Cyhr1	0.221	0.001093942
1428360_x_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	Ndufa7	0.221	0.002231899
1435152_at	leukocyte receptor cluster (LRC) member 8	Leng8	0.221	0.005655735
1421476_a_at	calcium activated nucleotidase 1	Cant1	0.221	0.008624271
1417123_at	vav 3 oncogene	Vav3	0.22	0.005124391
1451274_at	oxoglutarate dehydrogenase (lipoamide)	Ogdh	0.22	0.004271316
1435067_at	RIKEN cDNA B230208H17 gene	B230208H17Rik	0.22	0.005600967
1452421_at	homeo box A3	Hoxa3	0.22	0.00324569
1448627_s_at	PDZ binding kinase	Pbk	0.22	0.001422726
1455938_x_at	RAD21 homolog (S. pombe)	Rad21	0.22	0.013115066
1418986_a_at	ubiquitously expressed transcript	Uxt	0.22	0.038994704
1434005_at	RNA binding motif, single stranded interacting protein 1	Rbms1	0.22	0.00492538
1451265_at	coiled-coil domain containing 115	Ccdc115	0.22	0.003766808
1460657_at	wingless related MMTV integration site 10a	Wnt10a	0.22	0.015816518
1439081_at	meningioma expressed antigen 5 (hyaluronidase)	Mgea5	0.219	0.024972589
1451765_a_at	ectonucleoside triphosphate diphosphohydrolase 5	Entpd5	0.219	0.009078917
1452620_at	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	Pck2	0.219	0.014132328
1417864_at	phosphoglycerate kinase 1	Pgk1	0.219	0.000729556
1424407_s_at	chromobox homolog 6	Cbx6	0.219	0.003822992

1436971_x_at	bromodomain containing 2	Brd2	0.219	0.002784112
1421260_a_at	spermidine synthase	Srm	0.219	0.005122979
1460296_a_at	fibroblast growth factor 22	Fgf22	0.219	0.002250236
1433720_s_at	coiled-coil-helix-coiled-coil-helix domain containing 10	Chchd10	0.219	0.001208609
1451198_at	GATA zinc finger domain containing 2A	Gatad2a	0.219	0.024631956
1422462_at	ubiquitin-conjugating enzyme E2T (putative)	Ube2t	0.218	0.001385175
1436349_at	RIKEN cDNA 2700094K13 gene	2700094K13Rik	0.218	0.002885993
1417919_at	protein phosphatase 1, regulatory (inhibitor) subunit 7	Ppp1r7	0.218	0.003582655
1448884_at	general transcription factor II E, polypeptide 2 (beta subunit)	Gtf2e2	0.218	0.000801788
1425480_at	CCR4-NOT transcription complex, subunit 6-like	Cnot6l	0.218	0.007655036
1426820_at	RIKEN cDNA 2610507B11 gene	2610507B11Rik	0.218	0.001981999
1426597_s_at	expressed sequence C79267	C79267	0.218	0.004920966
1455439_a_at	lectin, galactose binding, soluble 1	Lgals1	0.218	0.001412226
1417153_at	BTB (POZ) domain containing 14A	Btbd14a	0.218	0.004693942
1437175_at	PDLIM1 interacting kinase 1 like	Pdik1l	0.218	0.004166505
1420942_s_at	regulator of G-protein signaling 5	Rgs5	0.218	0.039827064
1451354_at	FAD-dependent oxidoreductase domain containing 1	Foxred1	0.217	0.008622514
1416537_at	cysteine-rich with EGF-like domains 1	Creld1	0.217	0.000744976
1434529_x_at	checkpoint with forkhead and ring finger domains	Chfr	0.217	0.041776743
1419285_s_at	cysteine and histidine rich 1	Cyhr1	0.217	0.00185661
1451745_a_at	zinc finger, HIT domain containing 1	Znhit1	0.217	0.006680573
1426459_s_at	expressed sequence AW549877	AW549877	0.216	0.040890118
1452041_at	kelch-like 26 (Drosophila)	Klhl26	0.216	0.010411354
1459994_x_at	transferrin receptor 2	Trfr2	0.216	0.0311243
1437716_x_at	kinesin family member 22	Kif22	0.216	0.000999061
1426694_at	RIKEN cDNA 9030624J02 gene	9030624J02Rik	0.216	0.005268064
1449261_at	pre B-cell leukemia transcription factor 2	Pbx2	0.216	0.001365028
1424422_s_at	lens epithelial protein	Lenep	0.216	0.003819995
1451312_at	NADH dehydrogenase (ubiquinone) Fe-S protein 7	Ndufs7	0.216	0.012124178
1426834_s_at	RIKEN cDNA D930015E06 gene	D930015E06Rik	0.216	0.000915528
1427763_a_at	calcium/calmodulin-dependent protein kinase II, delta	Camk2d	0.216	0.031574195
1434557_at	huntingtin interacting protein 1	Hip1	0.216	0.007021282
1423936_at	potassium channel tetramerisation domain containing 5	Kctd5	0.216	0.003086018
1425674_a_at	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast)	Ssu72	0.216	0.018316259
1418372_at	adenylosuccinate lyase	Adsl	0.215	0.007556409
1417176_at	casein kinase 1, epsilon	Csnk1e	0.215	0.009670918
1424098_at	ELOVL family member 7, elongation of long chain fatty acids (yeast)	Elovl7	0.215	0.007129084
1419657_a_at	solute carrier family 25, member 36	Slc25a36	0.215	0.043174434
1423064_at	DNA methyltransferase 3A	Dnmt3a	0.215	0.002317165
1436341_at	homeobox containing 1	Hmbox1	0.215	0.004308906
1426722_at	solute carrier family 38, member 2	Slc38a2	0.215	0.000509134
1424767_at	cadherin 22	Cdh22	0.215	0.018523125
1424029_at	TSPY-like 4	Tspyl4	0.215	0.001139206
1451077_at	ribosomal protein L5	Rpl5	0.215	0.004671006
1427509_at	BAI1-associated protein 3	Baiap3	0.215	0.019441141
1454607_s_at	phosphoserine aminotransferase 1	Psat1	0.215	0.004220565
1451210_at	phosphatidic acid phosphatase type 2c	Ppap2c	0.214	0.000661765

1425211_at	glutamyl-tRNA(Gln) amidotransferase, subunit C homolog (bacterial)	Gatc	0.214	0.002352758
1422268_a_at	ribosomal protein S6 kinase, polypeptide 2	Rps6kb2	0.214	0.021130052
1431812_a_at	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	Slc6a9	0.214	0.001854522
1451604_a_at	activin A receptor, type II-like 1	Acvrl1	0.214	0.004501451
1435824_at	YY1 transcription factor	Yy1	0.214	0.001882133
1448918_at	solute carrier organic anion transporter family, member 3a1	Slco3a1	0.214	0.004027428
1448321_at	SPARC related modular calcium binding 1	Smoc1	0.214	0.001415742
1426525_at	AT rich interactive domain 2 (ARID, RFX-like)	Arid2	0.214	0.002540823
1454753_at	arginyl aminopeptidase (aminopeptidase B)-like 1	Rnpepl1	0.214	0.009970929
1452174_at	sterol regulatory element binding factor 2	Srebf2	0.214	0.001916536
1438690_at	thymidylate synthase	Tyms	0.214	0.0253469
1421402_at	metastasis associated 3	Mta3	0.214	0.007786448
1423990_at	RAB28, member RAS oncogene family	Rab28	0.214	0.001466312
1436167_at	Src homology 2 domain containing F	Shf	0.213	0.022205947
1450509_at	carbohydrate sulfotransferase 11	Chst11	0.213	0.037961125
1425979_a_at	Fas (TNFRSF6) binding factor 1	Fbf1	0.213	0.006965794
1424670_s_at	zinc finger, FYVE domain containing 21	Zfyve21	0.213	0.004239688
1423440_at	RIKEN cDNA 1110001A07 gene	1110001A07Rik	0.213	0.013732492
1436567_a_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	Ndufa7	0.213	0.005702788
1419029_at	ERO1-like (S. cerevisiae)	Ero1l	0.213	0.019904874
1417725_a_at	Sjogren's syndrome/scleroderma autoantigen 1 homolog (human)	Sssca1	0.213	0.022199696
1423697_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	Psmd6	0.213	0.001439522
1420375_at	kinesin family member 3A	Kif3a	0.213	0.009263735
1418838_at	ATP-binding cassette, sub-family D (ALD), member 1	Abcd1	0.213	0.000864169
1437611_x_at	kinesin family member 2C	Kif2c	0.213	0.01039623
1423566_a_at	heat shock 105kDa/110kDa protein 1	Hsph1	0.213	0.002951498
1439439_x_at	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	Eef1d	0.213	0.00785205
1434555_at	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	Anp32a	0.213	0.001649289
1425018_at	malignant T cell amplified sequence 1	Mcts1	0.212	0.000887136
1450927_at	leucine-zipper-like transcriptional regulator, 1	Lztr1	0.212	0.004185196
1417734_at	A kinase (PRKA) anchor protein 8-like	Akap8l	0.212	0.021578368
1415972_at	myristoylated alanine rich protein kinase C substrate	Marcks	0.212	0.002499379
1431435_at	NA	NA	0.212	0.019104848
1436803_a_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	Ndufb9	0.212	0.00133869
1426483_at	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)	Prkrir	0.212	0.001094927
1419839_x_at	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	Prpf19	0.212	0.003644229
1422976_x_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	Ndufa7	0.212	0.004903034
1420104_at	NA	NA	0.212	0.014341637
1449200_at	nucleoporin 155	Nup155	0.212	0.007643802
1418080_at	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2	B4galt2	0.212	0.038001601
1424828_a_at	fumarate hydratase 1	Fh1	0.211	0.003282342

1439422_a_at	C1q domain containing 2	C1qdc2	0.211	0.008507148
1444508_s_at	arrestin domain containing 1	Arrdc1	0.211	0.005142977
1424367_a_at	homer homolog 2 (Drosophila)	Homer2	0.211	0.001170019
1448211_at	ATPase, H+ transporting, lysosomal V0 subunit E2	Atp6v0e2	0.211	0.001394413
1450677_at	checkpoint kinase 1 homolog (S. pombe)	Chek1	0.211	0.042598554
1422797_at	mitogen-activated protein binding protein interacting protein	Mapbpip	0.211	0.007618985
1452287_at	NA	NA	0.211	0.002874593
1428853_at	patched homolog 1	Ptch1	0.211	0.003705752
1424653_at	tetraspanin 15	Tspan15	0.211	0.002019442
1453928_a_at	Sjogren syndrome antigen B	Ssb	0.211	0.013370732
1451491_at	BCDIN3 domain containing	Bcdin3d	0.211	0.003150308
1433883_at	RIKEN cDNA 2610528G24 gene	2610528G24Rik	0.211	0.003710034
1438941_x_at	adenosine monophosphate deaminase 2 (isoform L)	Ampd2	0.211	0.008866233
1450406_a_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	St3gal3	0.211	0.010375029
1456279_a_at	B-cell receptor-associated protein 31	Bcap31	0.211	0.001878999
1449935_a_at	DnaJ (Hsp40) homolog, subfamily A, member 3	Dnaja3	0.21	0.000654627
1428684_at	RIKEN cDNA 1500001M20 gene	1500001M20Rik	0.21	0.00384695
1427720_a_at	ribosomal RNA processing 1 homolog (S. cerevisiae)	Rrp1	0.21	0.004287507
1452269_at	spectrin beta 3	Spnb3	0.21	0.001432259
1428674_at	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	Prpf38b	0.21	0.001024333
1448615_at	copper chaperone for superoxide dismutase	Ccs	0.21	0.000893056
1452120_at	N-acetyltransferase 11	Nat11	0.21	0.005270497
1426977_at	ubiquitin specific peptidase 47	Usp47	0.21	0.000737746
1438159_x_at	NADH dehydrogenase (ubiquinone) flavoprotein 2	Ndufv2	0.21	0.000705293
1416973_at	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	Nhp2l1	0.21	0.002435559
1449373_at	DnaJ (Hsp40) homolog, subfamily C, member 3	Dnajc3	0.21	0.005435874
1456059_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	Psmd11	0.21	0.001934647
1421960_at	adenylate cyclase 3	Adcy3	0.21	0.001663269
1418167_at	transcription factor AP4	Tcfap4	0.21	0.016126996
1415707_at	anaphase promoting complex subunit 2	Anapc2	0.21	0.000853859
1416960_at	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	B3gat3	0.21	0.013934578
1433519_at	nuclear casein kinase and cyclin-dependent kinase substrate 1	Nucks1	0.209	0.045108112
1449011_at	solute carrier family 12, member 7	Slc12a7	0.209	0.029420344
AFFX-MUR_b2_at	NA	NA	0.209	0.02599971
1424942_a_at	myelocytomatosis oncogene	Myc	0.209	0.015422175
1426936_at	hypothetical protein LOC215866	LOC215866	0.209	0.014900321
1460042_at	solute carrier family 23 (nucleobase transporters), member 3	Slc23a3	0.209	0.036978961
1427669_a_at	citron	Cit	0.209	0.004227424
1418348_a_at	activating signal cointegrator 1 complex subunit 2	Ascc2	0.209	0.022208564
1416972_at	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	Nhp2l1	0.209	0.002199715
1452197_at	structural maintenance of chromosomes 4	Smc4	0.209	0.003120732
1423636_at	WD repeat domain 31	Wdr31	0.209	0.011632972

1460210_at	polycystic kidney disease 1 homolog	Pkd1	0.209	0.017816567
1451049_at	B-cell receptor-associated protein 31	Bcap31	0.209	0.000658274
1418669_at	perlecan (heparan sulfate proteoglycan 2)	Hspg2	0.209	0.004820976
1449855_s_at	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	Uchl3	0.209	0.006157901
1456456_x_at	melanoma antigen	Mela	0.208	0.003393277
1451694_at	tubulin tyrosine ligase-like family, member 3	Ttll3	0.208	0.0108431
1435431_at	proteasome (prosome, macropain) assembly chaperone 4	Psmg4	0.208	0.006023746
1419452_at	ubiquitin carboxyl-terminal esterase L5	Uchl5	0.208	0.00125881
1423130_a_at	splicing factor, arginine/serine-rich 5 (SRp40, HRS)	Sfrs5	0.208	0.002961973
1454046_x_at	phosphatidylglycerophosphate synthase 1	Pgs1	0.208	0.004527628
1415970_at	cytochrome c oxidase, subunit VIc	Cox6c	0.208	0.001187947
1428708_x_at	parathymosin	Ptms	0.208	0.001451894
1455928_x_at	leucine-zipper-like transcriptional regulator, 1	Lztr1	0.208	0.005231052
1433574_at	cell division cycle 37 homolog (S. cerevisiae)-like 1	Cdc37l1	0.208	0.015503816
1460346_at	arylsulfatase A	Arsa	0.208	0.001280019
1460445_at	splicing factor, arginine/serine-rich 2, interacting protein	Sfrs2ip	0.208	0.016835095
1423416_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	Smarcc1	0.207	0.000713863
1416015_s_at	ATP-binding cassette, sub-family E (OABP), member 1	Abce1	0.207	0.003728936
1422103_a_at	signal transducer and activator of transcription 5B	Stat5b	0.207	0.007122969
1427966_at	cDNA sequence BC087945	BC087945	0.207	0.001034921
1434325_x_at	protein kinase, cAMP dependent regulatory, type I beta	Prkar1b	0.207	0.001834479
1426492_at	tyrosyl-DNA phosphodiesterase 1	Tdp1	0.207	0.001082737
1428577_at	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	Ppfia4	0.207	0.016129579
1419885_at	DNA segment, Chr X, ERATO Doi 223, expressed	DXErtd223e	0.207	0.021813055
1451185_at	splicing factor 3b, subunit 5	Sf3b5	0.207	0.021728788
1451986_s_at	leucine-rich repeat kinase 1	Lrrk1	0.207	0.00447133
1428265_at	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	Ppp2r1b	0.207	0.015208779
1448811_at	mitochondrial ribosomal protein L2	Mrpl2	0.207	0.007129084
1427557_at	asparagine-linked glycosylation 12 homolog (yeast, alpha-1,6-mannosyltransferase)	Alg12	0.207	0.008843924
1416199_at	kinesin family member C3	Kifc3	0.207	0.002977897
1419514_at	paired-like homeodomain transcription factor 1	Pitx1	0.207	0.018658894
1449341_a_at	stomatin	Stom	0.206	0.037685922
1415787_at	alpha glucosidase 2 alpha neutral subunit	Ganab	0.206	0.00348685
1451985_at	leucine-rich repeat kinase 1	Lrrk1	0.206	0.004595484
1423982_at	FUS interacting protein (serine-arginine rich) 1	Fusip1	0.206	0.033496678
1456134_x_at	Yip1 interacting factor homolog A (S. cerevisiae)	Yif1a	0.206	0.003106999
1421129_a_at	ATPase, Ca++ transporting, ubiquitous	Atp2a3	0.206	0.006777733
1460360_at	asparaginase like 1	Asrgl1	0.206	0.0024932
1419275_at	DAZ associated protein 1	Dazap1	0.206	0.001447664
1429568_x_at	ubiquitin-conjugating enzyme E2F (putative)	Ube2f	0.206	0.001407929
1423157_at	glucosamine-phosphate N-acetyltransferase 1	Gnpnat1	0.206	0.003871126
AFFX-	NA	NA	0.206	0.027099318

18SRNAMur/X00686_3_at				
1455936_a_at	RNA binding protein gene with multiple splicing	Rbpms	0.206	0.001997787
1450818_a_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	Ndufa7	0.206	0.004130053
1450865_s_at	mitochondrial ribosomal protein S24	Mrps24	0.206	0.016544867
1420813_at	histone deacetylase 7	Hdac7	0.206	0.001627049
1436997_x_at	SH3-binding domain glutamic acid-rich protein like	Sh3bgrl	0.206	0.048064121
1454677_at	tissue inhibitor of metalloproteinase 2	Timp2	0.206	0.002373791
1436292_a_at	ornithine decarboxylase antizyme 1	Oaz1	0.205	0.000784551
1424315_at	RIKEN cDNA 1110004E09 gene	1110004E09Rik	0.205	0.005713326
1451984_at	heterogeneous nuclear ribonucleoprotein U-like 1	Hnrnpul1	0.205	0.002166049
1448267_at	syntaxin 5A	Stx5a	0.205	0.006257416
1454704_at	scavenger receptor class B, member 2	Scarb2	0.205	0.003939115
1438646_x_at	RIKEN cDNA 2510039O18 gene	2510039O18Rik	0.205	0.017174206
1418462_at	exosome component 9	Exosc9	0.205	0.004413029
1419471_a_at	nuclear distribution gene C homolog (Aspergillus)	Nudc	0.205	0.00492538
1424191_a_at	transmembrane protein 41a	Tmem41a	0.205	0.00084816
1417779_at	RIKEN cDNA 2310079N02 gene	2310079N02Rik	0.205	0.00655087
1420629_a_at	DnaJ (Hsp40) homolog, subfamily A, member 3	Dnaja3	0.205	0.013734887
1432177_a_at	menage a trois 1	Mnat1	0.204	0.000841222
1455675_a_at	Tia1 cytotoxic granule-associated RNA binding protein-like 1	Tial1	0.204	0.008063315
1424463_at	RIKEN cDNA 2210010L05 gene	2210010L05Rik	0.204	0.002709757
1435056_x_at	protein O-fucosyltransferase 2	Pofut2	0.204	0.019397357
1428477_at	elaC homolog 2 (E. coli)	Elac2	0.204	0.003209507
1426554_a_at	phosphoglycerate mutase 1	Pgam1	0.204	0.007258138
1427938_at	c-myc binding protein	Mycbp	0.204	0.005703119
1419525_at	carbonic anhydrase 5a, mitochondrial	Car5a	0.204	0.030772085
1424460_s_at	lysophosphatidylcholine acyltransferase 1	Lpcat1	0.204	0.005232631
1451187_at	RIKEN cDNA 0610037P05 gene	0610037P05Rik	0.204	0.002613572
1443414_at	EST C78513	C78513	0.203	0.008863572
1424607_a_at	predicted gene, 100039204	100039204	0.203	0.031748821
1451093_at	polymerase (RNA) II (DNA directed) polypeptide E	Polr2e	0.203	0.041918879
1452314_at	kinesin family member 11	Kif11	0.203	0.020524872
1449152_at	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	Cdkn2b	0.203	0.008067044
1427939_s_at	c-myc binding protein	Mycbp	0.203	0.020612709
1437642_at	HIV-1 Rev binding protein-like	Hrbl	0.203	0.001763039
1439435_x_at	phosphoglycerate kinase 1	Pgk1	0.203	0.004969018
1417358_s_at	sorbin and SH3 domain containing 1	Sorbs1	0.203	0.007316605
1427275_at	structural maintenance of chromosomes 4	Smc4	0.203	0.003346129
1437345_a_at	Bernardinelli-Seip congenital lipodystrophy 2 homolog (human)	Bscl2	0.203	0.002138689
1426705_s_at	isoleucine-tRNA synthetase	Iars	0.203	0.000621324
1425964_x_at	heat shock protein 1	Hspb1	0.203	0.008813479
1455152_at	expressed sequence AI462493	AI462493	0.203	0.004436077
1422944_a_at	diaphanous homolog 3 (Drosophila)	Diap3	0.203	0.004683061
1437622_x_at	mitochondrial ribosomal protein L28	Mrpl28	0.203	0.001598071
1416724_x_at	transcription factor 4	Tcf4	0.203	0.02451006
1450172_at	Pbx/knotted 1 homeobox	Pknox1	0.202	0.014552447
1448956_at	START domain containing 10	Stard10	0.202	0.03043181

1448141_at	ribosomal RNA processing 7 homolog A (S. cerevisiae)	Rrp7a	0.202	0.015430873
1431241_at	coiled-coil-helix-coiled-coil-helix domain containing 3	Chchd3	0.202	0.048153203
1437852_x_at	cleavage and polyadenylation specificity factor 3	Cpsf3	0.202	0.009721799
1416368_at	glutathione S-transferase, alpha 4	Gsta4	0.202	0.02982753
1427450_x_at	myosin IB	Myo1b	0.202	0.001261597
1450542_s_at	melanoma antigen, family A, 3	Magea3	0.202	0.014132328
1432273_a_at	Duffy blood group, chemokine receptor	Darc	0.202	0.035558589
1422943_a_at	heat shock protein 1	Hspb1	0.202	0.002806493
1415915_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	Ddx1	0.202	0.001634159
1425977_a_at	STE20-like kinase (yeast)	Slk	0.202	0.02045208
1417470_at	apolipoprotein B editing complex 3	Apobec3	0.202	0.001223691
1455618_x_at	tetraspanin 33	Tspan33	0.201	0.001489269
1419486_at	forkhead box C1	Foxc1	0.201	0.01940606
1438655_a_at	ribosomal protein L34	Rpl34	0.201	0.001027552
1418120_at	RNA binding motif protein 8a	Rbm8a	0.201	0.007547596
1434103_at	solute carrier family 35, member E1	Slc35e1	0.201	0.002484867
1428782_a_at	ubiquinol-cytochrome c reductase core protein 1	Uqcrc1	0.201	0.002550927
1418123_at	unc-119 homolog (C. elegans)	Unc119	0.2	0.020325288
1448706_at	Traf and Tnf receptor associated protein	Ttrap	0.2	0.001502476
1424532_at	YLP motif containing 1	Ylpm1	0.2	0.00448256
1455713_x_at	prohibitin 2	Phb2	0.2	0.004903034
1421218_at	butyrylcholinesterase	Bche	0.2	0.013874254
1416690_at	GTP binding protein 2	Gtpbp2	0.2	0.012799396
1451165_at	limb region 1 like	Lmbr1l	0.2	0.007665555
1417842_at	calcium modulating ligand	Caml	-0.2	0.006537745
1451042_a_at	myc induced nuclear antigen	Mina	-0.2	0.001090211
1422513_at	cyclin F	Ccnf	-0.2	0.002720007
1423733_a_at	Flt3 interacting zinc finger protein 1	Fiz1	-0.201	0.00247682
1426623_a_at	Rho GTPase activating protein 17	Arhgap17	-0.201	0.013728049
1423284_at	MANSC domain containing 1	Mansc1	-0.201	0.044163088
1460541_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	Slc7a6	-0.201	0.00403768
1423111_at	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	Atp5a1	-0.201	0.001270448
1451317_at	YTH domain family 2	Ythdf2	-0.201	0.009117494
1456604_a_at	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	Pcmt1	-0.201	0.010162575
1426601_at	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	Slc37a1	-0.201	0.00247682
1451642_at	kinesin family member 1B	Kif1b	-0.201	0.025478689
1417515_at	U7 snRNP-specific Sm-like protein LSM10	Lsm10	-0.201	0.003913405
1422732_at	polymerase (DNA-directed), delta interacting protein 2	Poldip2	-0.201	0.008961446
1423384_s_at	testis expressed gene 261	Tex261	-0.201	0.002974332
1438438_at	Rab interacting lysosomal protein-like 1	Rilpl1	-0.201	0.031130555
1455946_x_at	thymosin, beta 10	Tmsb10	-0.201	0.002042148
1453169_a_at	general transcription factor II H, polypeptide 1	Gtf2h1	-0.201	0.003520784
1453256_at	polymerase (RNA) III (DNA directed) polypeptide C	Polr3c	-0.201	0.019608578
1450555_at	testis expressed gene 13	Tex13	-0.201	0.001713885
1437566_at	guanine nucleotide binding protein-like 2 (nucleolar)	Gnl2	-0.201	0.034493568
1415704_a_at	carnitine deficiency-associated gene expressed in ventricle 3	Cdv3	-0.201	0.001277864

1455611_at	protein inhibitor of activated STAT 1	Pias1	-0.202	0.00496471
1450756_s_at	cullin 3	Cul3	-0.202	0.003994756
1416447_at	transmembrane protein 30A	Tmem30a	-0.202	0.006186576
1421120_at	myosin VI	Myo6	-0.202	0.002626311
1416866_at	blocked early in transport 1 homolog (S. cerevisiae)	Bet1	-0.202	0.005263996
1426822_at	ras homolog gene family, member T2	Rhot2	-0.202	0.009061982
1436885_a_at	RIKEN cDNA 1700030K09 gene	1700030K09Rik	-0.202	0.023041628
1451895_a_at	24-dehydrocholesterol reductase	Dhcr24	-0.202	0.007952792
1428848_a_at	microtubule-actin crosslinking factor 1	Macf1	-0.202	0.009589669
1416648_at	dynein cytoplasmic 1 heavy chain 1	Dync1h1	-0.202	0.01556256
1438817_at	DNA replication helicase 2 homolog (yeast)	Dna2	-0.202	0.036485627
1450693_at	regulator of G-protein signaling 17	Rgs17	-0.202	0.00789111
1420839_at	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 3	Plekha3	-0.202	0.011612079
1415906_at	thymosin, beta 4, X chromosome	Tmsb4x	-0.202	0.004704765
1425354_a_at	angiogenic factor with G patch and FHA domains 1	Aggf1	-0.202	0.000726292
1433496_at	glycosyltransferase 25 domain containing 1	Glt25d1	-0.202	0.027323202
1415698_at	golgi membrane protein 1	Golm1	-0.202	0.006204274
1427185_at	myocyte enhancer factor 2A	Mef2a	-0.202	0.002576892
1449972_s_at	zinc finger protein 97	Zfp97	-0.203	0.00304416
1423693_at	elastase 1, pancreatic	Ela1	-0.203	0.001149235
1456486_at	zinc finger protein 574	Zfp574	-0.203	0.018788357
1419984_s_at	zinc finger protein 644	Zfp644	-0.203	0.009933574
1422045_a_at	protein tyrosine phosphatase, non-receptor type 12	Ptpn12	-0.203	0.013789344
1423876_at	expressed sequence AI450540	AI450540	-0.203	0.019987297
1459021_at	NA	NA	-0.203	0.018782802
1455678_at	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	Sema4b	-0.203	0.016002017
1423133_at	CWC15 homolog (S. cerevisiae)	Cwc15	-0.203	0.005427293
1453064_at	Ewing's tumor-associated antigen 1	Etaa1	-0.203	0.024260043
1426021_a_at	cell division cycle 7 (S. cerevisiae)	Cdc7	-0.203	0.009953005
1421433_at	zinc finger homeodomain 4	Zfhx4	-0.203	0.004802152
1460211_a_at	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	Kdelr1	-0.204	0.002943024
1424810_at	taspase, threonine aspartase 1	Tasp1	-0.204	0.007017543
1421495_a_at	RIKEN cDNA 1700052N19 gene	1700052N19Rik	-0.204	0.013665609
1417501_at	F-box protein 6	Fbxo6	-0.204	0.002003012
1451214_at	kelch repeat and BTB (POZ) domain containing 2	Kbtbd2	-0.204	0.001893452
1416035_at	hypoxia inducible factor 1, alpha subunit	Hif1a	-0.204	0.005879366
1417773_at	N-acetylneuraminic acid synthase (sialic acid synthase)	Nans	-0.204	0.003754481
1452413_at	RIKEN cDNA C230081A13 gene	C230081A13Rik	-0.204	0.047213039
1449045_at	AFG3(ATPase family gene 3)-like 1 (yeast)	Afg3l1	-0.204	0.011278337
1452335_at	major facilitator superfamily domain containing 8	Mfsd8	-0.204	0.004837079
1460303_at	nuclear receptor subfamily 3, group C, member 1	Nr3c1	-0.204	0.001891805
1423703_at	peter pan homolog (Drosophila)	Ppan	-0.204	0.027454356
1421360_at	inositol polyphosphate-4-phosphatase, type I	Inpp4a	-0.204	0.043097508
1417632_at	ATPase, H+ transporting, lysosomal V0 subunit A1	Atp6v0a1	-0.204	0.003520784
1430289_a_at	WD repeat domain 77	Wdr77	-0.204	0.01008769

1425508_s_at	ADP-ribosylation factor related protein 1	Arfrp1	-0.204	0.002654251
1429800_at	RIKEN cDNA 9130221H12 gene	9130221H12Rik	-0.205	0.009514849
1425803_a_at	methyl-CpG binding domain protein 2	Mbd2	-0.205	0.04939565
1448163_at	glucosamine-6-phosphate deaminase 1	Gnpda1	-0.205	0.002500922
1418719_at	RIKEN cDNA 2410004L22 gene	2410004L22Rik	-0.205	0.00398598
1416083_at	zinc finger, AN1-type domain 5	Zfand5	-0.205	0.024610229
1448431_at	ankyrin repeat and SOCS box-containing 6	Asb6	-0.205	0.004972821
1460239_at	tetraspanin 13	Tspan13	-0.205	0.004098189
1418774_a_at	ATPase, Cu++ transporting, alpha polypeptide	Atp7a	-0.205	0.023629117
1426055_a_at	phosphatidylinositol glycan anchor biosynthesis, class Q	Pigq	-0.205	0.005748407
1416354_at	RNA binding motif protein, X chromosome	Rbmx	-0.205	0.001049174
1437591_a_at	WD repeat domain 1	Wdr1	-0.205	0.003381186
1425833_a_at	hippocalcin	Hpca	-0.205	0.009716437
1427078_at	sorting nexin 19	Snx19	-0.205	0.004615753
1431645_a_at	guanosine diphosphate (GDP) dissociation inhibitor 2	Gdi2	-0.206	0.012123171
1426310_at	zinc finger, DHHC domain containing 5	Zdhhc5	-0.206	0.002590423
1451350_a_at	leptin receptor overlapping transcript	Leprot	-0.206	0.004768826
1451233_at	Tnf receptor-associated factor 2	Traf2	-0.206	0.007883775
1435638_at	RIKEN cDNA 9130221H12 gene	9130221H12Rik	-0.206	0.002660377
1431304_a_at	transmembrane protein 183A	Tmem183a	-0.206	0.015585675
1420639_at	junction-mediating and regulatory protein	Jmy	-0.206	0.00483278
1427916_at	suppression of tumorigenicity 7-like	St7l	-0.206	0.003066503
1417947_at	proliferating cell nuclear antigen	Pcna	-0.206	0.001522476
1451449_at	RIKEN cDNA 4933407N01 gene	4933407N01Rik	-0.206	0.001155396
1415791_at	ring finger protein 34	Rnf34	-0.206	0.004220743
1437465_a_at	prolyl 4-hydroxylase, beta polypeptide	P4hb	-0.206	0.000748139
1422477_at	Cdk5 and Abl enzyme substrate 1	Cables1	-0.206	0.024540614
1416548_at	solute carrier family 35, member B4	Slc35b4	-0.207	0.025897822
1449934_at	purine rich element binding protein A	Pura	-0.207	0.011362738
1451525_at	Rho GTPase activating protein 12	Arhgap12	-0.207	0.008116242
1417959_at	PDZ and LIM domain 7	Pdlim7	-0.207	0.015540137
1421031_a_at	RIKEN cDNA 2310016C08 gene	2310016C08Rik	-0.207	0.020930463
1450845_a_at	basic leucine zipper and W2 domains 1	Bzw1	-0.207	0.008570373
1422858_at	thyroid hormone receptor interactor 4	Trip4	-0.207	0.013748217
1451485_at	RIKEN cDNA 3300001P08 gene	3300001P08Rik	-0.207	0.038541603
1427186_a_at	myocyte enhancer factor 2A	Mef2a	-0.208	0.003106999
1417141_at	interferon gamma induced GTPase	Igtp	-0.208	0.004835595
1433520_at	SREBF chaperone	Scap	-0.208	0.003482029
1459880_at	alanine-glyoxylate aminotransferase 2-like 2	Agxt2l2	-0.208	0.036879089
1418098_at	adenylate cyclase 4	Adcy4	-0.208	0.007935483
1417082_at	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	Anp32b	-0.208	0.001727326
1416474_at	neighbor of Punc E11	Nope	-0.208	0.020554058
1426467_s_at	RIKEN cDNA 0610037L13 gene	0610037L13Rik	-0.208	0.015873235
1433869_at	ZXD family zinc finger C	Zxdc	-0.208	0.020060108
1427030_at	coiled-coil domain containing 52	Ccdc52	-0.208	0.00717212
1428873_a_at	RIKEN cDNA 4121402D02 gene	4121402D02Rik	-0.208	0.004605537
1448626_at	CDK5 regulatory subunit associated protein 1	Cdk5rap1	-0.208	0.001135816
1416267_at	short coiled-coil protein	Scoc	-0.208	0.02012067
1438943_x_at	ribophorin I	Rpn1	-0.208	0.002636353
1424021_at	ADP-ribosylation factor-like 6 interacting protein 6	Arl6ip6	-0.208	0.017816567
1436801_x_at	CDC42 effector protein (Rho GTPase binding) 4	Cdc42ep4	-0.208	0.027550296
1448702_at	immediate early response 3 interacting protein	Ier3ip1	-0.208	0.033192444

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1452139_at	solute carrier family 35, member C1	Slc35c1	-0.208	0.012255949
1460403_at	PC4 and SFRS1 interacting protein 1	Psip1	-0.208	0.002108255
1433502_s_at	TSR1, 20S rRNA accumulation, homolog (yeast)	Tsr1	-0.209	0.002032092
1433612_at	adaptor-related protein complex 2, sigma 1 subunit	Ap2s1	-0.209	0.0214389
1451638_s_at	armadillo repeat containing 1	Armc1	-0.209	0.001649115
1451146_at	zinc finger protein 386 (Kruppel-like)	Zfp386	-0.209	0.019465448
1448369_at	polymerase (DNA directed), alpha 2	Pola2	-0.209	0.002677775
1454985_at	autophagy/beclin 1 regulator 1	Ambra1	-0.209	0.009557638
1450629_at	LIM domain and actin binding 1	Lima1	-0.209	0.02037503
1460279_a_at	general transcription factor II I	Gtf2i	-0.209	0.026252506
1437364_at	coenzyme Q3 homolog, methyltransferase (yeast)	Coq3	-0.209	0.00747071
1429108_at	male-specific lethal 2-like 1 (Drosophila)	Msl2l1	-0.209	0.016549377
1419548_at	karyopherin (importin) alpha 1	Kpna1	-0.209	0.011403345
1418145_at	tuftelin interacting protein 11	Tfip11	-0.209	0.00752396
1423822_a_at	transmembrane protein 168	Tmem168	-0.21	0.005069632
1417922_at	kelch repeat and BTB (POZ) domain containing 4	Kbtbd4	-0.21	0.017894621
1420497_a_at	CCAAT/enhancer binding protein zeta	Cebpz	-0.21	0.026919952
1456565_s_at	poly(rC) binding protein 2	Pcbp2	-0.21	0.03493725
1437807_x_at	catenin (cadherin associated protein), alpha 1	Ctnna1	-0.21	0.004263665
1419816_s_at	ERBB receptor feedback inhibitor 1	Errfi1	-0.21	0.00386033
1431676_x_at	general transcription factor II I	Gtf2i	-0.21	0.031169034
1422577_at	citrate synthase	Cs	-0.21	0.00598666
1448242_at	Sec61 alpha 1 subunit (S. cerevisiae)	Sec61a1	-0.21	0.004946695
1452364_at	suppressor of zeste 12 homolog (Drosophila)	Suz12	-0.21	0.014987839
1423787_at	nucleoporin 133	Nup133	-0.21	0.001808665
1448354_at	glucose-6-phosphate dehydrogenase X-linked	G6pdx	-0.21	0.004030794
1425525_a_at	purinergic receptor P2X, ligand-gated ion channel 4	P2rx4	-0.21	0.001447664
1428137_at	ADP-ribosylation factor-like 8B	Arl8b	-0.21	0.006550388
1450321_at	zinc finger protein 354C	Zfp354c	-0.211	0.039336874
1424425_a_at	methylthioadenosine phosphorylase	Mtap	-0.211	0.024222068
1416372_at	phosphatidylserine synthase 1	Ptdss1	-0.211	0.001609773
1452363_a_at	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	Atp2a2	-0.211	0.010861851
1419026_at	Fas death domain-associated protein	Daxx	-0.211	0.002128416
1434608_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	Ddx52	-0.211	0.017390973
1434744_at	yrdC domain containing (E.coli)	Yrdc	-0.211	0.019608578
1416257_at	calpain 2	Capn2	-0.211	0.003154541
1437380_x_at	phosphogluconate dehydrogenase	Pgd	-0.211	0.006322004
1451164_a_at	mitochondrial ribosomal protein S18B	Mrps18b	-0.211	0.002499379
1449840_at	syntrophin, basic 2	Sntb2	-0.211	0.041905982
1426146_a_at	choline phosphotransferase 1	Chpt1	-0.212	0.005260966
1424402_at	RUN and FYVE domain containing 3	Rufy3	-0.212	0.001762991
1436547_at	diacylglycerol kinase, epsilon	Dgke	-0.212	0.009071777
1417198_at	WW, C2 and coiled-coil domain containing 2	Wwc2	-0.212	0.039966532
1428587_at	transmembrane protein 41B	Tmem41b	-0.212	0.007499741
1422119_at	RAB5B, member RAS oncogene family	Rab5b	-0.212	0.029712202
1449659_s_at	M-phase phosphoprotein 9	Mphosph9	-0.212	0.031539303
1417207_at	dishevelled 2, dsh homolog (Drosophila)	Dvl2	-0.212	0.001723917
1426924_at	ring finger and CCCH-type zinc finger domains 2	Rc3h2	-0.212	0.042965024
1452648_at	transforming growth factor beta regulated gene	Tbrg1	-0.212	0.004835065

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1419630_a_at	tripartite motif-containing 11	Trim11	-0.212	0.0092364
1449078_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	St3gal6	-0.212	0.007585861
1427572_at	NA	NA	-0.212	0.04951582
1422946_a_at	DNA methyltransferase (cytosine-5) 1	Dnmt1	-0.212	0.000866238
1426759_at	mitogen-activated protein kinase kinase kinase kinase 3	Map4k3	-0.212	0.000539531
1448026_at	chromodomain helicase DNA binding protein 7	Chd7	-0.212	0.018177471
1452581_at	regulation of nuclear pre-mRNA domain containing 1B	Rprd1b	-0.213	0.026423378
1421487_a_at	non-catalytic region of tyrosine kinase adaptor protein 1	Nck1	-0.213	0.003491822
1451728_at	WD repeat domain 13	Wdr13	-0.213	0.001048261
1418622_at	RAB2A, member RAS oncogene family	Rab2a	-0.213	0.00247168
1427462_at	E2F transcription factor 3	E2f3	-0.213	0.006552076
1421149_a_at	atrophin 1	Atn1	-0.213	0.031067657
1417027_at	tripartite motif-containing 2	Trim2	-0.213	0.002598517
1428080_at	phosphoglycerate mutase family member 5	Pgam5	-0.213	0.002475281
1417489_at	neuropeptide Y receptor Y2	Npy2r	-0.213	0.009970929
1418284_at	vacuolar protein sorting 72 (yeast)	Vps72	-0.213	0.010761068
1434823_x_at	myeloma overexpressed 2	Myeov2	-0.213	0.005798561
1427112_at	tubulin tyrosine ligase	Ttl	-0.213	0.015356548
1419812_s_at	coiled-coil domain containing 56	Ccdc56	-0.213	0.001120319
1436902_x_at	thymosin, beta 10	Tmsb10	-0.213	0.044833318
1432444_a_at	E2F-associated phosphoprotein	Eapp	-0.213	0.030384694
1448787_at	modulator of apoptosis 1	Moap1	-0.214	0.003272399
1428492_at	GLI pathogenesis-related 2	Glipr2	-0.214	0.003526658
1420990_at	chromodomain helicase DNA binding protein 1	Chd1	-0.214	0.007231914
1421016_at	immunoglobulin mu binding protein 2	Ighmbp2	-0.214	0.049115447
1425684_at	RIKEN cDNA 2310005E10 gene	2310005E10Rik	-0.214	0.002649486
1428316_a_at	FUN14 domain containing 2	Fundc2	-0.214	0.003344425
1418643_at	tetraspanin 13	Tspan13	-0.214	0.004343442
1426393_a_at	stromal cell derived factor 4	Sdf4	-0.214	0.00115553
1424324_at	establishment of cohesion 1 homolog 1 (S. cerevisiae)	Esco1	-0.214	0.021503813
1416036_at	FK506 binding protein 1a	Fkbp1a	-0.214	0.001625986
1423194_at	Rho GTPase activating protein 5	Arhgap5	-0.214	0.009014725
1424717_at	MIS12 homolog (yeast)	Mis12	-0.214	0.00438684
1425497_a_at	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	Prpf4b	-0.214	0.0106849
1454116_a_at	MTERF domain containing 1	Mterfd1	-0.214	0.012954569
1426874_at	enhancer of mRNA decapping 4	Edc4	-0.215	0.010177425
1426324_at	histocompatibility 2, K1, K region	H2-K1	-0.215	0.002781737
1425058_at	zinc finger protein 472	Zfp472	-0.215	0.020981101
1417493_at	Bmi1 polycomb ring finger oncogene	Bmi1	-0.215	0.001235125
1456340_at	methyltransferase like 11A	Mettl11a	-0.215	0.003862131
1423877_at	chromatin assembly factor 1, subunit B (p60)	Chaf1b	-0.215	0.006046639
1417987_at	biotinidase	Btd	-0.215	0.02025266
1427014_at	DENN/MADD domain containing 4B	Dennd4b	-0.215	0.00063696
1448059_at	mirror-image polydactyly gene 1 homolog (human)	Mipol1	-0.215	0.015886803
1418570_at	nicastrin	Ncstn	-0.215	0.001006974
1417774_at	N-acetylneuraminic acid synthase (sialic acid synthase)	Nans	-0.215	0.003619412
1434814_x_at	glucose phosphate isomerase 1	Gpi1	-0.215	0.001032961
1455727_at	zinc finger (CCCH type), RNA binding motif	Zrsr2	-0.215	0.000991556

	and serine/arginine rich 2			
1424161_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	Ddx27	-0.215	0.048325494
1448352_at	leucine zipper protein 1	Luzp1	-0.215	0.03622779
1423479_at	nucleolar protein 11	Nol11	-0.216	0.003449652
1433504_at	brain glycogen phosphorylase	Pygb	-0.216	0.00256146
1426726_at	protein phosphatase 1, regulatory subunit 10	Ppp1r10	-0.216	0.008015061
1448718_at	RIKEN cDNA 2400001E08 gene	2400001E08Rik	-0.216	0.004723254
1424347_at	protein phosphatase 6, catalytic subunit	Ppp6c	-0.216	0.00395457
1415828_a_at	stress-associated endoplasmic reticulum protein 1	Serp1	-0.216	0.010389279
1437589_x_at	Lck interacting transmembrane adaptor 1	Lime1	-0.216	0.037654257
1434893_at	ATPase, Na+/K+ transporting, alpha 2 polypeptide	Atp1a2	-0.216	0.032003138
1416665_at	demethyl-Q 7	Coq7	-0.216	0.001391942
1418464_at	matrilin 4	Matn4	-0.216	0.011572368
1451346_at	methylthioadenosine phosphorylase	Mtap	-0.216	0.002256932
1454107_a_at	kinesin family member 2A	Kif2a	-0.216	0.018976898
1428098_a_at	transmembrane 7 superfamily member 3	Tm7sf3	-0.216	0.003659116
1420386_at	SEH1-like (S. cerevisiae	Seh1l	-0.217	0.019016289
1421101_a_at	LIM domain binding 2	Ldb2	-0.217	0.002919945
1428935_at	calnexin	Canx	-0.217	0.017419985
1449066_a_at	Rho guanine nucleotide exchange factor (GEF7)	Arhgef7	-0.217	0.000691555
1449465_at	reelin	Reln	-0.217	0.015567415
1448042_s_at	ring finger protein 2	Rnf2	-0.217	0.033862654
1428337_at	RIKEN cDNA 1810034K20 gene	1810034K20Rik	-0.217	0.003303079
1448463_at	RIKEN cDNA 4933434E20 gene	4933434E20Rik	-0.217	0.00222515
1452527_a_at	purinergic receptor P2X, ligand-gated ion channel 4	P2rx4	-0.217	0.00134076
1417699_at	general transcription factor IIF, polypeptide 1	Gtf2f1	-0.217	0.001154629
1427162_a_at	ELK4, member of ETS oncogene family	Elk4	-0.217	0.004906264
1425488_at	SLU7 splicing factor homolog (S. cerevisiae)	Slu7	-0.217	0.007568708
1420966_at	solute carrier family 25 (mitochondrial carrier ornithine transporter), member 15	Slc25a15	-0.217	0.016502374
1460562_at	elongation factor Tu GTP binding domain containing 1	Eftud1	-0.217	0.005211156
1448050_s_at	mitogen-activated protein kinase kinase kinase kinase 4	Map4k4	-0.217	0.013242457
1417032_at	ubiquitin-conjugating enzyme E2G 2	Ube2g2	-0.217	0.002241422
1449183_at	catechol-O-methyltransferase 1	Comt1	-0.217	0.008506708
1427449_a_at	ADP-ribosylhydrolase like 2	Adprhl2	-0.217	0.020069424
1417342_at	protein phosphatase 1, regulatory (inhibitor) subunit 2	Ppp1r2	-0.218	0.043123715
1415826_at	ATPase, H+ transporting, lysosomal V1 subunit H	Atp6v1h	-0.218	0.001512905
1416403_at	ATP-binding cassette, sub-family B (MDR/TAP), member 10	Abcb10	-0.218	0.004140506
1448207_at	LIM and SH3 protein 1	Lasp1	-0.218	0.024514194
1419036_at	casein kinase 2, alpha 1 polypeptide	Csnk2a1	-0.218	0.002993565
1449319_at	R-spondin homolog (Xenopus laevis)	Rspo1	-0.218	0.003114891
1420391_at	par-3 (partitioning defective 3) homolog (C. elegans)	Pard3	-0.218	0.029778846
1417964_at	adaptor-related protein complex 3, delta 1 subunit	Ap3d1	-0.218	0.002195584
1416688_at	synaptosomal-associated protein 91	Snap91	-0.218	0.001193577
1423652_at	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	Isca1	-0.218	0.003419029
1431232_a_at	MAX gene associated	Mga	-0.218	0.043744324

1452445_at	solute carrier family 41, member 2	Slc41a2	-0.218	0.006973993
1455105_at	protein tyrosine phosphatase, non-receptor type 12	Ptpn12	-0.218	0.004136973
1423369_at	fragile X mental retardation syndrome 1 homolog	Fmr1	-0.218	0.003369555
1452611_at	zinc finger protein 294	Zfp294	-0.218	0.027573372
1435970_at	nemo like kinase	Nlk	-0.218	0.002781119
1451094_at	gamma-glutamyltransferase 7	Ggt7	-0.218	0.002479499
1452836_at	lipin 2	Lpin2	-0.218	0.00148608
1429109_at	male-specific lethal 2-like 1 (Drosophila)	Msl2l1	-0.218	0.005736704
1426078_a_at	G protein-coupled receptor 108	Gpr108	-0.218	0.003092094
1452720_a_at	FIP1 like 1 (S. cerevisiae)	Fip1l1	-0.219	0.012590254
1434128_a_at	zinc finger protein 574	Zfp574	-0.219	0.002173238
1440255_at	MBD2-interacting zinc finger	Mizf	-0.219	0.001474611
1431768_a_at	protein arginine N-methyltransferase 3	Prmt3	-0.219	0.046192953
1419587_s_at	retinitis pigmentosa 2 homolog (human)	Rp2h	-0.219	0.010758273
1450949_at	katanin p60 (ATPase-containing) subunit A1	Katna1	-0.219	0.001099522
1432848_a_at	FERM domain containing 8	Frmd8	-0.219	0.00250707
1427620_at	p53-associated parkin-like cytoplasmic protein	Parc	-0.219	0.009148418
1448855_at	Ras association (RalGDS/AF-6) domain family member 1	Rassf1	-0.219	0.001210849
1416275_at	solute carrier family 26, member 6	Slc26a6	-0.219	0.001801116
1431827_a_at	tousled-like kinase 2 (Arabidopsis)	Tlk2	-0.219	0.004656
1451480_at	E2F transcription factor 4	E2f4	-0.219	0.006468651
1416092_a_at	microtubule-associated protein 4	Mtap4	-0.219	0.006204456
1421812_at	TAP binding protein	Tapbp	-0.219	0.010606444
1415814_at	ATPase, H+ transporting, lysosomal V1 subunit B2	Atp6v1b2	-0.219	0.000750846
1454305_at	chromobox homolog 3 (Drosophila HP1 gamma)	Cbx3	-0.219	0.005846219
1451237_s_at	RNA binding motif protein 7	Rbm7	-0.219	0.002776025
1449273_at	cytoplasmic FMR1 interacting protein 2	Cyfip2	-0.219	0.010752244
1454789_x_at	PRP6 pre-mRNA splicing factor 6 homolog (yeast)	Prpf6	-0.219	0.032260084
1423054_at	WD repeat domain 1	Wdr1	-0.22	0.009043297
1460317_s_at	guanine nucleotide binding protein, alpha 13	Gna13	-0.22	0.003200003
1426215_at	dopa decarboxylase	Ddc	-0.22	0.005351445
1424766_at	excision repair cross-complementing rodent repair deficiency complementation group 6 -like	Ercc6l	-0.22	0.013939992
1452673_at	RAN binding protein 3	Ranbp3	-0.22	0.000565074
1437738_at	ATPase, Ca++-sequestering	Atp2c1	-0.22	0.01690555
1421606_a_at	sulfotransferase family 4A, member 1	Sult4a1	-0.22	0.014684335
1451195_a_at	thioredoxin domain containing 1	Txndc1	-0.22	0.002042148
1419269_at	deoxyuridine triphosphatase	Dut	-0.22	0.007019144
1421349_x_at	cell cycle exit and neuronal differentiation 1	Cend1	-0.22	0.013544116
1431804_a_at	trans-acting transcription factor 3	Sp3	-0.22	0.001792648
1421450_a_at	mitogen-activated protein kinase kinase kinase 4	Map3k4	-0.22	0.002790803
1418728_at	steroidogenic acute regulatory protein	Star	-0.22	0.021502872
1420937_at	cleavage and polyadenylation specific factor 2	Cpsf2	-0.22	0.012062753
1454905_at	inhibitor of Bruton agammaglobulinemia tyrosine kinase	Ibtk	-0.22	0.015103319
1422680_at	Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	Ctr9	-0.22	0.002043129
1455236_x_at	small EDRK-rich factor 2	Serf2	-0.22	0.000525909
1416212_at	mago-nashi homolog, proliferation-associated (Drosophila)	Magoh	-0.22	0.002584343

1423040_at	basic leucine zipper and W2 domains 1	Bzw1	-0.22	0.010224802
1419460_at	ribonuclease P 14 subunit (human)	Rpp14	-0.221	0.001242077
1448744_at	galactosamine (N-acetyl)-6-sulfate sulfatase	Galns	-0.221	0.003538804
1451381_at	RIKEN cDNA 1810020D17 gene	1810020D17Rik	-0.221	0.001636817
1425713_a_at	ring finger protein 146	Rnf146	-0.221	0.014159185
1439460_a_at	ADP-ribosylation factor GTPase activating protein 2	Arfgap2	-0.221	0.007380497
1425991_a_at	KN motif and ankyrin repeat domains 2	Kank2	-0.221	0.002415362
1416105_at	nicotinamide nucleotide transhydrogenase	Nnt	-0.221	0.000592152
1427335_at	RIKEN cDNA 6720456H20 gene	6720456H20Rik	-0.221	0.000854279
1420579_s_at	cystic fibrosis transmembrane conductance regulator homolog	Cftr	-0.221	0.02469169
1424350_s_at	lysophosphatidylglycerol acyltransferase 1	Lpgat1	-0.221	0.020585114
1422039_at	tumor necrosis factor receptor superfamily, member 22	Tnfrsf22	-0.221	0.018972988
1420535_a_at	negative regulator of ubiquitin-like proteins 1	Nub1	-0.221	0.002884073
1424478_at	Bardet-Biedl syndrome 2 (human)	Bbs2	-0.221	0.01892632
1418347_at	coiled-coil domain containing 22	Ccdc22	-0.222	0.002699772
1452444_at	N-ethylmaleimide sensitive fusion protein attachment protein beta	Napb	-0.222	0.049569048
1452347_at	myocyte enhancer factor 2A	Mef2a	-0.222	0.000660475
1448757_at	promyelocytic leukemia	Pml	-0.222	0.007651878
1451564_at	poly (ADP-ribose) polymerase family, member 14	Parp14	-0.222	0.023940768
1433546_at	glucosamine (N-acetyl)-6-sulfatase	Gns	-0.222	0.000717953
1417098_s_at	mitochondrial trans-2-enoyl-CoA reductase	Mecr	-0.222	0.001796618
1450826_a_at	serum amyloid A 3	Saa3	-0.222	0.011953578
1426360_at	zinc finger CCCH type containing 11A	Zc3h11a	-0.222	0.014199604
1431760_a_at	serologically defined colon cancer antigen 3	Sdccag3	-0.222	0.013856583
1452920_a_at	peptidylprolyl isomerase (cyclophilin)-like 2	Ppil2	-0.222	0.005924679
1427139_at	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 10	Adamts10	-0.222	0.004162174
1449084_s_at	SH3 domain protein D19	Sh3d19	-0.223	0.010351081
1418984_at	InaD-like (Drosophila)	Inadl	-0.223	0.005438485
1426975_at	amplified in osteosarcoma	Os9	-0.223	0.007007297
1451412_a_at	intraflagellar transport 20 homolog (Chlamydomonas)	Ift20	-0.223	0.004162174
1418341_at	RAB4A, member RAS oncogene family	Rab4a	-0.223	0.009997556
1424507_at	Ras and Rab interactor 1	Rin1	-0.223	0.028588195
1451735_at	ADP-ribosylation factor related protein 1	Arfrp1	-0.223	0.001547945
1438458_a_at	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	Sfpq	-0.223	0.029433366
1420919_at	serum/glucocorticoid regulated kinase 3	Sgk3	-0.223	0.027781937
1422517_a_at	zinc ribbon domain containing, 1	Znrd1	-0.223	0.002535803
1418906_at	nucleotide binding protein 1	Nubp1	-0.223	0.003346581
1418333_at	metal response element binding transcription factor 1	Mtf1	-0.224	0.00130285
1426415_a_at	tripartite motif-containing 25	Trim25	-0.224	0.01574181
1416152_a_at	splicing factor, arginine/serine-rich 3 (SRp20)	Sfrs3	-0.224	0.007550966
1422063_a_at	peroxisome biogenesis factor 5	Pex5	-0.224	0.003480271
1451266_at	mitochondrial ribosomal protein L50	Mrpl50	-0.224	0.019844169
1419765_at	cullin 2	Cul2	-0.224	0.004309179
1424428_at	NO80 complex subunit E	Ino80e	-0.224	0.003491822
1419883_s_at	ATPase, H+ transporting, lysosomal V1 subunit B2	Atp6v1b2	-0.224	0.019983698
1452045_at	zinc finger protein 281	Zfp281	-0.224	0.001574644

1427798_x_at	NA	NA	-0.224	0.010999134
1448317_at	transmembrane protein 128	Tmem128	-0.224	0.000533979
1434705_at	C-terminal binding protein 2	Ctbp2	-0.225	0.009848549
1460334_at	drebrin-like	Dbnl	-0.225	0.007993727
1419450_at	ORM1-like 3 (S. cerevisiae)	Ormdl3	-0.225	0.004398426
1431792_a_at	serine/threonine kinase 11 interacting protein	Stk11ip	-0.225	0.02493337
1415683_at	N-myristoyltransferase 1	Nmt1	-0.225	0.001421647
1450052_at	kinesin family member 2A	Kif2a	-0.225	0.003227303
1425249_a_at	TYRO3 protein tyrosine kinase 3	Tyro3	-0.225	0.038093913
1425614_x_at	histocompatibility 2, K1, K region	H2-K1	-0.225	0.007271792
1427998_at	LSM12 homolog (S. cerevisiae)	Lsm12	-0.225	0.003771111
1428710_at	Ras-like without CAAX 1	Rit1	-0.225	0.006658809
1428264_at	WD repeat domain 57 (U5 snRNP specific)	Wdr57	-0.225	0.000882695
1449981_a_at	N-acetyltransferase 2 (arylamine N-acetyltransferase)	Nat2	-0.225	0.003421422
1438644_x_at	COMM domain containing 9	Commd9	-0.226	0.003447876
1438556_a_at	tropomodulin 3	Tmod3	-0.226	0.006868574
1424630_a_at	breast cancer 1	Brca1	-0.226	0.025958666
1427332_at	mediator of RNA polymerase II transcription, subunit 19 homolog (yeast)	Med19	-0.226	0.009978076
1433640_at	far upstream element (FUSE) binding protein 1	Fubp1	-0.226	0.020496301
1426133_a_at	MIT, microtubule interacting and transport, domain containing 1	Mitd1	-0.226	0.003865351
1424420_at	cell cycle progression 1	Ccpg1	-0.226	0.027735233
1438170_x_at	adhesion regulating molecule 1	Adrm1	-0.226	0.024165899
1422555_s_at	guanine nucleotide binding protein, alpha 13	Gna13	-0.226	0.000509874
1438459_x_at	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	Sfpq	-0.226	0.008476414
1427110_at	ribonucleoprotein, PTB-binding 1	Raver1	-0.226	0.004409526
1431939_a_at	myc induced nuclear antigen	Mina	-0.226	0.002332534
1424202_at	SEH1-like (S. cerevisiae	Seh1l	-0.226	0.008751832
1450396_at	stromal antigen 2	Stag2	-0.226	0.009608439
1429288_x_at	syntaxin 18	Stx18	-0.226	0.00526164
1424438_a_at	leptin receptor overlapping transcript	Leprot	-0.226	0.001530951
1418732_s_at	RIKEN cDNA 1500041N16 gene	1500041N16Rik	-0.226	0.002387978
1426074_at	NA	NA	-0.226	0.03074717
1448674_at	ring finger protein 25	Rnf25	-0.226	0.004595928
1452607_at	RIKEN cDNA 2610030H06 gene	2610030H06Rik	-0.227	0.004536706
1427730_a_at	zinc finger protein 148	Zfp148	-0.227	0.029717026
1451034_at	zinc finger protein 36, C3H type-like 2	Zfp36l2	-0.227	0.035740721
1454629_at	RIKEN cDNA A930037G23 gene	A930037G23Rik	-0.227	0.004425474
1423671_at	delta/notch-like EGF-related receptor	Dner	-0.227	0.001943761
1451290_at	microtubule-associated protein 1 light chain 3 alpha	Map1lc3a	-0.227	0.009564039
1452803_at	GLI pathogenesis-related 2	Glipr2	-0.227	0.015647183
1432013_a_at	RIKEN cDNA 2610016C23 gene	2610016C23Rik	-0.227	0.003635915
1438537_at	NA	NA	-0.227	0.003422861
1452708_a_at	Luc7 homolog (S. cerevisiae)-like	Luc7l	-0.227	0.00900504
1421774_at	ventral anterior homeobox containing gene 1	Vax1	-0.227	0.003088662
1423644_at	aconitase 1	Aco1	-0.227	0.00445583
1425031_at	fukutin	Fktn	-0.227	0.003640188
1423984_a_at	Meis homeobox 3	Meis3	-0.227	0.003369663
1455880_s_at	beclin 1, autophagy related	Becn1	-0.227	0.002003012
1451980_at	CAS1 domain containing 1	Casd1	-0.228	0.041676587
1418265_s_at	interferon regulatory factor 2	Irf2	-0.228	0.01043684
1420478_at	nucleosome assembly protein 1-like 1	Nap1l1	-0.228	0.001363224

1427125_s_at	leucine rich repeat containing 41	Lrrc41	-0.228	0.000743658
1422753_a_at	polymerase (RNA) III (DNA directed) polypeptide K	Polr3k	-0.228	0.003476154
1456293_s_at	cyclin H	Ccnh	-0.228	0.001619534
1459902_at	RIKEN cDNA 2700007P21 gene	2700007P21Rik	-0.228	0.005452599
1452288_at	myotubularin related protein 10	Mtmr10	-0.228	0.001497062
1416739_a_at	BRCA1 associated protein	Brap	-0.228	0.026033095
1418427_at	kinesin family member 5B	Kif5b	-0.228	0.009501984
1417843_s_at	EPS8-like 2	Eps8l2	-0.228	0.011067849
1431753_x_at	ubiquitin related modifier 1 homolog (S. cerevisiae)	Urm1	-0.228	0.001208251
1424189_at	phosphatidylinositol glycan anchor biosynthesis, class C	Pigc	-0.228	0.000816951
1432115_a_at	phosphatidylinositol glycan anchor biosynthesis, class N	Pign	-0.228	0.024518235
1453960_a_at	capping protein (actin filament) muscle Z-line, beta	Capzb	-0.228	0.021816552
1418515_at	metal response element binding transcription factor 2	Mtf2	-0.228	0.02411654
1425652_s_at	RNA binding protein gene with multiple splicing	Rbpms	-0.228	0.007544053
1423994_at	kinesin family member 1B	Kif1b	-0.228	0.004432623
1427539_a_at	ZW10 interactor	Zwint	-0.228	0.004514814
1418370_at	troponin C, cardiac/slow skeletal	Tnnc1	-0.229	0.018278837
1418411_at	F-box and leucine-rich repeat protein 8	Fbxl8	-0.229	0.012302668
1429172_a_at	on-SMC condensin I complex, subunit G	Ncapg	-0.229	0.009456734
1415741_at	transmembrane protein 165	Tmem165	-0.229	0.00071563
1422491_a_at	BCL2/adenovirus E1B interacting protein 2	Bnip2	-0.229	0.001636414
1417211_a_at	RIKEN cDNA 1110032A03 gene	1110032A03Rik	-0.229	0.026624698
1418459_at	coiled-coil domain containing 91	Ccdc91	-0.229	0.001500962
AFFX-TransRecMur/X57349_3_at	transferrin receptor	Tfrc	-0.229	0.013856583
1418033_s_at	zinc finger with KRAB and SCAN domains 6	Zkscan6	-0.229	0.002873012
1427314_at	transmembrane emp24 protein transport domain containing 7	Tmed7	-0.229	0.002250175
1456746_a_at	Cd99 antigen-like 2	Cd99l2	-0.229	0.006122572
1456438_x_at	ribophorin I	Rpn1	-0.229	0.00087595
1448031_at	guanine nucleotide binding protein, alpha O	Gnao1	-0.229	0.005895488
1423402_at	cAMP responsive element binding protein 1	Creb1	-0.229	0.021629572
1428050_a_at	transmembrane BAX inhibitor motif containing 4	Tmbim4	-0.229	0.00149924
1427328_a_at	CLIP associating protein 2	Clasp2	-0.229	0.003602351
1424500_at	UTP6, small subunit (SSU) processome component, homolog (yeast)	Utp6	-0.229	0.001434218
1419380_at	zinc finger protein 423	Zfp423	-0.229	0.006372041
1417721_s_at	lysosomal-associated protein transmembrane 5	Laptm5	-0.229	0.019505392
1417479_at	protein phosphatase 2, regulatory subunit B'', gamma	Ppp2r3c	-0.229	0.008012707
1452545_a_at	integrin beta 1 (fibronectin receptor beta)	Itgb1	-0.229	0.027640386
1427023_at	phytanoyl-CoA hydroxylase interacting protein-like	Phyhipl	-0.23	0.002660377
1452986_at	homogentisate 1, 2-dioxygenase	Hgd	-0.23	0.001415742
1454814_s_at	expressed sequence AU021838	AU021838	-0.23	0.00247682
1439017_x_at	adiponectin receptor 1	Adipor1	-0.23	0.000479603
1417097_at	mitochondrial trans-2-enoyl-CoA reductase	Mecr	-0.23	0.002492389
1421043_s_at	rho/rac guanine nucleotide exchange factor (GEF) 2	Arhgef2	-0.23	0.00063235

1423622_a_at	cyclin L1	Ccnl1	-0.23	0.011932215
1423406_at	synaptic vesicle glycoprotein 2 a	Sv2a	-0.23	0.00437983
1423501_at	Max protein	Max	-0.23	0.039907624
1453307_a_at	anaphase-promoting complex subunit 5	Anapc5	-0.23	0.009557681
1417086_at	platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit	Pafah1b1	-0.23	0.002761237
1421813_a_at	prosaposin	Psap	-0.23	0.001652483
1450953_at	cytosolic iron-sulfur protein assembly 1 homolog (S. cerevisiae)	Ciao1	-0.23	0.000370888
1451345_at	methylthioadenosine phosphorylase	Mtap	-0.23	0.010979024
1422563_at	complement component (3b/4b) receptor 1-like	Cr1l	-0.23	0.000732172
1449442_at	peroxisomal biogenesis factor 11a	Pex11a	-0.23	0.02004798
1426020_at	thymopoietin	Tmpo	-0.23	0.005702154
1423356_at	synaptosomal-associated protein 29	Snap29	-0.23	0.000781214
1415926_at	nucleoporin 62	Nup62	-0.23	0.000691737
1460199_a_at	platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit	Pafah1b1	-0.231	0.002439571
1450496_a_at	RIKEN cDNA 2810433K01 gene	2810433K01Rik	-0.231	0.008311519
1451559_a_at	dehydrogenase/reductase (SDR family) member 4	Dhrs4	-0.231	0.000658972
1448621_a_at	sphingomyelin phosphodiesterase 1, acid lysosomal	Smpd1	-0.231	0.00171381
1456740_x_at	component of oligomeric golgi complex 1	Cog1	-0.231	0.049351288
1448672_a_at	ADP-ribosylation factor GTPase activating protein 2	Arfgap2	-0.231	0.001885451
1418168_at	zinc finger, CCHC domain containing 14	Zcchc14	-0.231	0.00428635
1456000_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	Ddx18	-0.231	0.048750965
1431058_at	HIV TAT specific factor 1	Htatsf1	-0.231	0.026741257
1422146_at	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B	Sema5b	-0.231	0.016753245
1454174_a_at	RIKEN cDNA C330007P06 gene	C330007P06Rik	-0.231	0.021631017
1422935_x_at	chromobox homolog 1 (Drosophila HP1 beta)	Cbx1	-0.231	0.003025171
1422568_at	nuclear distribution gene E-like homolog 1 (A. nidulans)	Ndel1	-0.231	0.002386989
1424028_at	RIKEN cDNA 5830457O10 gene	5830457O10Rik	-0.231	0.000774542
1422763_at	GIPC PDZ domain containing family, member 1	Gipc1	-0.231	0.008062684
1427430_at	expressed sequence AI848100	AI848100	-0.232	0.004277965
1422966_a_at	transferrin receptor	Tfrc	-0.232	0.03603295
1422954_at	zinc finger protein 60	Zfp60	-0.232	0.018327693
1421543_at	F-box protein 4	Fbxo4	-0.232	0.002417634
1422118_at	syncoilin	Sync	-0.232	0.012011081
1460308_a_at	immature colon carcinoma transcript 1	Ict1	-0.232	0.0027338
1428188_at	RIKEN cDNA 2610019A05 gene	2610019A05Rik	-0.232	0.003520077
1420977_at	mannosidase, alpha, class 1A, member 2	Man1a2	-0.232	0.000691903
1450890_a_at	abl-interactor 1	Abi1	-0.232	0.001792492
1422293_a_at	potassium channel tetramerisation domain containing 1	Kctd1	-0.232	0.046674402
1421896_at	ELK1, member of ETS oncogene family	Elk1	-0.232	0.002362307
1422512_a_at	opioid growth factor receptor	Ogfr	-0.232	0.004042498
1450777_at	5'-3' exoribonuclease 2	Xrn2	-0.232	0.004088823
1447947_at	zinc finger, FYVE domain containing 16	Zfyve16	-0.232	0.009154684
1417421_at	S100 calcium binding protein A1	S100a1	-0.232	0.001558048
1419389_at	phosphodiesterase 10A	Pde10a	-0.233	0.008472942
1424385_at	RIKEN cDNA 5830417I10 gene	5830417I10Rik	-0.233	0.004937539
1428745_a_at	RIKEN cDNA 2310003L22 gene	2310003L22Rik	-0.233	0.001034921

1425510_at	MAP/microtubule affinity-regulating kinase 1	Mark1	-0.233	0.002231617
1456310_a_at	RIKEN cDNA 2610002J02 gene	2610002J02Rik	-0.233	0.00195326
1423358_at	endothelin converting enzyme 2	Ece2	-0.233	0.00044427
1423599_a_at	phosducin-like	Pdcl	-0.233	0.010290399
1418657_at	INO80 complex subunit B	Ino80b	-0.233	0.019707456
1427958_at	abhydrolase domain containing 10	Abhd10	-0.233	0.002839574
1423480_at	nucleolar protein 11	Nol11	-0.233	0.000490092
1429003_at	SNW domain containing 1	Snw1	-0.233	0.003114891
1455326_at	C-type lectin domain family 16, member A	Clec16a	-0.233	0.002463175
1451351_at	tetratricopeptide repeat domain 13	Ttc13	-0.233	0.000734297
1425599_a_at	GATA zinc finger domain containing 1	Gatad1	-0.233	0.003794048
1449395_at	RIKEN cDNA 4921520G13 gene	4921520G13Rik	-0.233	0.046967259
1417106_at	tumor protein D52-like 2	Tpd52l2	-0.233	0.00121052
1424849_at	WD repeat domain 62	Wdr62	-0.233	0.008108975
1428033_at	predicted gene, EG245174	EG245174	-0.233	0.001270328
1454606_at	RIKEN cDNA 4933426M11 gene	4933426M11Rik	-0.233	0.008129466
1453946_a_at	serologically defined colon cancer antigen 8	Sdccag8	-0.233	0.006260644
1448957_at	recombination signal binding protein for immunoglobulin kappa J region	Rbpj	-0.233	0.003029852
1451770_s_at	DEAH (Asp-Glu-Ala-His) box polypeptide 9	Dhx9	-0.233	0.001943431
1427151_at	glutamine and serine rich 1	Qser1	-0.233	0.044692768
1456411_at	RCC1 domain containing 1	Rccd1	-0.233	0.002888144
1434403_at	sprouty-related, EVH1 domain containing 2	Spred2	-0.233	0.001496632
1422854_at	src homology 2 domain-containing transforming protein C1	Shc1	-0.234	0.000982044
1420021_s_at	suppressor of zeste 12 homolog (Drosophila)	Suz12	-0.234	0.004663707
1452523_a_at	coiled-coil domain containing 130	Ccdc130	-0.234	0.045239166
1424079_x_at	ubiquitin related modifier 1 homolog (S. cerevisiae)	Urm1	-0.234	0.000429127
AFFX-TransRecMur/X57349_5_at	transferrin receptor	Tfrc	-0.234	0.037379439
1431003_a_at	RIKEN cDNA 2610002J02 gene	2610002J02Rik	-0.234	0.002960699
1416738_at	BRCA1 associated protein	Brap	-0.234	0.00595115
1417154_at	solute carrier family 25 (mitochondrial carrier, brain), member 14	Slc25a14	-0.234	0.003092414
1454928_at	scaffold attachment factor B	Safb	-0.234	0.000948401
1418592_at	DnaJ (Hsp40) homolog, subfamily A, member 4	Dnaja4	-0.234	0.001766235
1416189_a_at	Sec61 alpha 1 subunit (S. cerevisiae)	Sec61a1	-0.234	0.000687668
1448500_a_at	Lck interacting transmembrane adaptor 1	Lime1	-0.234	0.029118461
1418704_at	S100 calcium binding protein A13	S100a13	-0.234	0.003456006
1419158_a_at	histidyl-tRNA synthetase 2, mitochondrial (putative)	Hars2	-0.234	0.00121052
1450955_s_at	sortilin 1	Sort1	-0.234	0.018094596
1460650_at	ATPase, H+ transporting, lysosomal V0 subunit A1	Atp6v0a1	-0.234	0.010132593
1418733_at	twist gene homolog 1 (Drosophila)	Twist1	-0.234	0.035469284
1452059_at	solute carrier family 35, member F5	Slc35f5	-0.234	0.001744496
1428100_at	splicing factor, arginine/serine-rich 1 (ASF/SF2)	Sfrs1	-0.234	0.001580341
1424283_at	jumping translocation breakpoint	Jtb	-0.234	0.000363349
1428619_at	RIKEN cDNA 2310005N03 gene	2310005N03Rik	-0.235	0.033146238
1422591_at	transcription elongation factor B (SIII), polypeptide 3	Tceb3	-0.235	0.004109718
1424663_at	cDNA sequence BC017647	BC017647	-0.235	0.004625504
1426269_at	vesicle-associated membrane protein 7	Vamp7	-0.235	0.014526556

1424481_s_at	armadillo repeat containing, X-linked 5	Armcx5	-0.235	0.007614649
1424472_at	nucleolar protein family 6 (RNA-associated)	Nol6	-0.235	0.000489231
1421832_at	twisted gastrulation homolog 1 (Drosophila)	Twsg1	-0.235	0.013458909
1416493_at	dolichyl-di-phosphooligosaccharide-protein glycotransferase	Ddost	-0.235	0.000407246
1451459_at	AT hook containing transcription factor 1	Ahctf1	-0.235	0.009463805
1460649_at	interleukin-1 receptor-associated kinase 1	Irak1	-0.235	0.007770761
1452150_at	expressed sequence AU040320	AU040320	-0.235	0.000711041
1448287_at	RNA polymerase 1-3	Rpo1-3	-0.235	0.002174421
1419652_s_at	Na+/K+ transporting ATPase interacting 1	Nkain1	-0.236	0.002531139
1420558_at	selectin, platelet	Selp	-0.236	0.023381794
1455644_at	vacuolar protein sorting 53 (yeast)	Vps53	-0.236	0.000715943
1448843_at	signal sequence receptor, alpha	Ssr1	-0.236	0.00493311
1455202_at	gene model 50, (NCBI)	Gm50	-0.236	0.020060108
1425495_at	zinc finger protein 62	Zfp62	-0.236	0.029974419
1419833_s_at	centaurin, delta 3	Centd3	-0.236	0.011611312
1425944_a_at	RAD51-like 3 (S. cerevisiae)	Rad51l3	-0.236	0.009265346
1422286_a_at	TGFB-induced factor homeobox 1	Tgif1	-0.236	0.002091771
1448149_at	catenin (cadherin associated protein), alpha 1	Ctnna1	-0.236	0.000309879
1432027_a_at	TBC1 domain family, member 14	Tbc1d14	-0.236	0.023860772
1429921_at	RIKEN cDNA 9530068E07 gene	9530068E07Rik	-0.236	0.038994704
1448624_at	CD2 antigen (cytoplasmic tail) binding protein 2	Cd2bp2	-0.236	0.003284821
1435353_a_at	Sfi1 homolog, spindle assembly associated (yeast)	Sfi1	-0.236	0.004089412
1416137_at	annexin A7	Anxa7	-0.236	0.00111002
1418543_s_at	coiled-coil domain containing 43	Ccdc43	-0.237	0.002093583
1417786_a_at	regulator of G-protein signaling 19	Rgs19	-0.237	0.026663201
1419805_s_at	similar to Ggps1 protein	LOC100045315	-0.237	0.002102365
1434914_at	RAB6B, member RAS oncogene family	Rab6b	-0.237	0.001628685
1423860_at	prostaglandin D2 synthase (brain)	Ptgds	-0.237	0.03225476
1426379_at	eukaryotic translation initiation factor 4B	Eif4b	-0.237	0.008798469
1449333_at	splicing factor 3a, subunit 1	Sf3a1	-0.237	0.003520784
1450103_a_at	cytohesin 2	Cyth2	-0.237	0.012587025
1448607_at	nicotinamide phosphoribosyltransferase	Nampt	-0.237	0.00307758
1422994_at	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III	Pip5k3	-0.237	0.01715605
1429962_at	CCAAT/enhancer binding protein zeta	Cebpz	-0.237	0.001042691
1423299_at	thioredoxin-like 1	Txnl1	-0.237	0.000853874
1460295_s_at	interleukin 6 signal transducer	Il6st	-0.237	0.014862358
1434334_at	protein kinase D2	Prkd2	-0.237	0.002277796
1438602_s_at	mannan-binding lectin serine peptidase 1	Masp1	-0.238	0.006931803
1421030_at	zinc finger protein 64	Zfp64	-0.238	0.001137303
1460388_at	acyl-CoA thioesterase 6	Acot6	-0.238	0.038377129
1453865_a_at	OTU domain containing 5	Otud5	-0.238	0.003114891
1425603_at	transmembrane protein 176A	Tmem176a	-0.238	0.00247682
1416563_at	cytidine 5'-triphosphate synthase	Ctps	-0.238	0.000932922
1453920_a_at	motile sperm domain containing 2	Mospd2	-0.238	0.008203914
1451631_at	regulation of nuclear pre-mRNA domain containing 1A	Rprd1a	-0.238	0.019549833
1427412_s_at	Rap guanine nucleotide exchange factor (GEF) 6	Rapgef6	-0.238	0.01194403
1433786_x_at	small EDRK-rich factor 2	Serf2	-0.238	0.00036253
1448353_x_at	ribophorin I	Rpn1	-0.238	0.005009093
1426879_at	RIKEN cDNA 1190005F20 gene	1190005F20Rik	-0.238	0.003357879
1425969_a_at	huntingtin	Htt	-0.239	0.006879491

1422243_at	fibroblast growth factor 7	Fgf7	-0.239	0.009540481
1430610_at	mitochondrial ribosomal protein L38	Mrpl38	-0.239	0.026851802
1431292_a_at	twinfilin, actin-binding protein, homolog 2 (Drosophila)	Twf2	-0.239	0.019146627
1456043_at	ubiquitin specific peptidase 22	Usp22	-0.239	0.008050375
1422560_at	regulatory solute carrier protein, family 1, member 1	Rsc1a1	-0.239	0.000736717
1421961_a_at	DnaJ (Hsp40) homolog, subfamily B, member 5	Dnajb5	-0.239	0.007117897
1416568_a_at	apoptotic chromatin condensation inducer 1	Acin1	-0.239	0.020281675
1437503_a_at	shisa homolog 5 (Xenopus laevis)	Shisa5	-0.239	0.007547596
1451726_at	myotubularin related protein 6	Mtmr6	-0.239	0.006007877
1438264_a_at	tripeptidyl peptidase II	Tpp2	-0.239	0.006109518
1425844_a_at	RNA guanylyltransferase and 5'-phosphatase	Rngtt	-0.239	0.006618985
1448958_at	interferon alpha responsive gene	Ifrg15	-0.24	0.00300322
1416768_at	RIKEN cDNA 1110003E01 gene	1110003E01Rik	-0.24	0.002860133
1420899_at	RAB18, member RAS oncogene family	Rab18	-0.24	0.039314998
1448129_at	actin related protein 2/3 complex, subunit 5	Arpc5	-0.24	0.000479263
1439069_a_at	RIKEN cDNA 4933439C20 gene	4933439C20Rik	-0.24	0.004050601
1451325_at	forty-two-three domain containing 1	Fyttd1	-0.24	0.005675557
1424506_at	zinc finger protein 768	Zfp768	-0.24	0.013696364
1426342_at	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	Stt3b	-0.24	0.000491325
1418222_at	RIKEN cDNA 2610024G14 gene	2610024G14Rik	-0.24	0.000664359
1418233_a_at	trafficking protein particle complex 5	Trappc5	-0.241	0.004895546
1434037_s_at	K(lysine) acetyltransferase 2B	Kat2b	-0.241	0.001344732
1421094_at	zinc finger and BTB domain containing 33	Zbtb33	-0.241	0.024204633
1448335_s_at	cyclin I	Ccni	-0.241	0.005291294
1435803_a_at	eukaryotic translation initiation factor 4E member 2	Eif4e2	-0.241	0.003491154
1456869_at	zinc finger protein 787	Zfp787	-0.241	0.01976756
1452813_a_at	transmembrane protein 188	Tmem188	-0.241	0.002381497
1435578_s_at	disabled homolog 1 (Drosophila)	Dab1	-0.241	0.002003012
1428230_at	protein kinase D3	Prkd3	-0.241	0.015864581
1451303_at	cDNA sequence BC002230	BC002230	-0.241	0.007792937
1450701_a_at	general transcription factor II H, polypeptide 2	Gtf2h2	-0.241	0.002795247
1426949_s_at	translocated promoter region	Tpr	-0.242	0.001666724
1426846_at	centromere protein T	Cenpt	-0.242	0.005273775
1423105_a_at	YEATS domain containing 4	Yeats4	-0.242	0.000927755
1435350_at	Tnf receptor-associated factor 6	Traf6	-0.242	0.001042411
1434922_at	PHD finger protein 12	Phf12	-0.242	0.004330672
1420114_s_at	RIKEN cDNA 2410022L05 gene	2410022L05Rik	-0.242	0.018379677
1424349_a_at	lysophosphatidylglycerol acyltransferase 1	Lpgat1	-0.242	0.005545051
1424241_at	solute carrier family 30 (zinc transporter), member 6	Slc30a6	-0.242	0.000367912
1432159_a_at	testis expressed gene 13	Tex13	-0.242	0.002243863
1448438_at	Der1-like domain family, member 2	Derl2	-0.242	0.017508646
1452529_a_at	cAMP responsive element binding protein 1	Creb1	-0.242	0.013303556
1431777_a_at	high mobility group nucleosomal binding domain 3	Hmgn3	-0.242	0.001440472
1417022_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3	Slc7a3	-0.242	0.001366534
1436917_s_at	DNA segment, Chr 2, Brigham & Women's Genetics 1335 expressed	D2Bwg1335e	-0.242	0.011922859
1438397_a_at	RNA binding motif protein 39	Rbm39	-0.243	0.001303566
1420879_a_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta	Ywhab	-0.243	0.0005478

	polypeptide			
1450965_at	testis expressed gene 261	Tex261	-0.243	0.000288832
1427283_at	myeloid/lymphoid or mixed-lineage leukemia 1	Mll1	-0.243	0.028568852
1426112_a_at	CD72 antigen	Cd72	-0.243	0.010046722
1419260_a_at	small nuclear ribonucleoprotein B	Snrpb	-0.243	0.001474506
1423174_a_at	par-6 (partitioning defective 6) homolog beta (C. elegans)	Pard6b	-0.243	0.0145904
1448684_at	protein phosphatase 1, regulatory (inhibitor) subunit 2	Ppp1r2	-0.243	0.000800295
1425358_at	RIO kinase 1 (yeast)	Riok1	-0.243	0.000590721
1416735_at	N-acylsphingosine amidohydrolase 1	Asah1	-0.243	0.001386216
1423600_a_at	Treacher Collins Franceschetti syndrome 1, homolog	Tcof1	-0.243	0.027077488
1430999_a_at	short coiled-coil protein	Scoc	-0.243	0.002501503
1426023_a_at	rabaptin, RAB GTPase binding effector protein 1	Rabep1	-0.243	0.008518811
1417163_at	dual specificity phosphatase 10	Dusp10	-0.244	0.010459065
1425148_a_at	sorting nexin 6	Snx6	-0.244	0.003734576
1449181_at	ferrochelatase	Fech	-0.244	0.003140353
1448565_at	protein phosphatase 1, regulatory (inhibitor) subunit 11	Ppp1r11	-0.244	0.000493682
1434859_at	uridine monophosphate synthetase	Umps	-0.244	0.00631142
1438422_at	leucine rich repeat containing 20	Lrrc20	-0.244	0.009382712
1426486_at	UBX domain protein 4	Ubxn4	-0.244	0.00147905
1416385_a_at	mannose-6-phosphate receptor, cation dependent	M6pr	-0.244	0.001407248
1450458_at	nuclear receptor coactivator 2	Ncoa2	-0.244	0.00718318
1421144_at	retinitis pigmentosa GTPase regulator interacting protein 1	Rpgrip1	-0.244	0.005699765
1416108_a_at	transmembrane emp24 domain containing 3	Tmed3	-0.244	0.002213495
1416107_at	neuron specific gene family member 2	Nsg2	-0.244	0.000972152
1448904_at	DNA segment, Chr 6, Wayne State University 176, expressed	D6Wsu176e	-0.244	0.002690587
1450778_a_at	RNA U, small nuclear RNA export adaptor	Rnuxa	-0.244	0.003147738
1426706_s_at	xylulokinase homolog (H. influenzae)	Xylb	-0.245	0.009670883
1417024_at	histidyl-tRNA synthetase	Hars	-0.245	0.000356043
1422497_at	solute carrier family 30 (zinc transporter), member 5	Slc30a5	-0.245	0.000257791
1425253_a_at	mucosal vascular addressin cell adhesion molecule 1	Madcam1	-0.245	0.007548262
1417767_at	cytochrome b5 type B	Cyb5b	-0.245	0.001742896
1419366_at	zinc finger, matrin type 5	Zmat5	-0.245	0.00235973
1450966_at	carnitine O-octanoyltransferase	Crot	-0.245	0.00393424
1425572_a_at	development and differentiation enhancing	Ddef1	-0.245	0.00116377
1452149_at	ubiquitin protein ligase E3B	Ube3b	-0.245	0.001866483
1432155_at	Wiskott-Aldrich syndrome-like (human)	Wasl	-0.245	0.000745268
1419252_at	epidermal growth factor receptor pathway substrate 15	Eps15	-0.245	0.005593069
1418591_at	DnaJ (Hsp40) homolog, subfamily A, member 4	Dnaja4	-0.245	0.016032647
1425368_a_at	numb gene homolog (Drosophila)	Numb	-0.245	0.016320684
1420607_at	RNA binding motif protein 18	Rbm18	-0.245	0.017419985
1421075_s_at	cytochrome P450, family 7, subfamily b, polypeptide 1	Cyp7b1	-0.245	0.021349765
1452374_at	zinc finger protein 322a	Zfp322a	-0.245	0.010127945
1425487_at	SLU7 splicing factor homolog (S. cerevisiae)	Slu7	-0.245	0.029900719
1421257_at	phosphatidylinositol glycan anchor biosynthesis, class B	Pigb	-0.245	0.00560827

1425611_a_at	cut-like homeobox 1	Cux1	-0.246	0.016250572
1422469_at	TANK-binding kinase 1	Tbk1	-0.246	0.001033803
1424454_at	transmembrane protein 87A	Tmem87a	-0.246	0.003066503
1426810_at	jumonji domain containing 1A	Jmjd1a	-0.246	0.000576632
1449503_at	karyopherin (importin) alpha 1	Kpna1	-0.246	0.025933507
1418876_at	forkhead box D1	Foxd1	-0.246	0.003761123
1451523_a_at	MIF4G domain containing	Mif4gd	-0.246	0.011904859
1453733_a_at	RIKEN cDNA 4933434E20 gene	4933434E20Rik	-0.246	0.002540823
1418819_at	ADP-ribosylation factor-like 8B	Arl8b	-0.246	0.00694468
1451658_a_at	polymerase (RNA) III (DNA directed) polypeptide C	Polr3c	-0.246	0.023800817
1416620_at	Swi/SNF related matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	Smarcal1	-0.246	0.001127642
1434196_at	DnaJ (Hsp40) homolog, subfamily A, member 4	Dnaja4	-0.246	0.001244554
1452179_at	PHD finger protein 17	Phf17	-0.247	0.001388496
1418078_at	proteaseome (prosome, macropain) 28 subunit, 3	Psme3	-0.247	0.006433749
1436187_at	RIKEN cDNA 1110054M08 gene	1110054M08Rik	-0.247	0.01729158
1426893_at	RIKEN cDNA C230093N12 gene	C230093N12Rik	-0.247	0.046003416
1427971_at	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	Cdc73	-0.247	0.004871711
1456601_x_at	FXYD domain-containing ion transport regulator 2	Fxyd2	-0.247	0.010290647
1420986_s_at	kinesin family member 3B	Kif3b	-0.247	0.003538155
1436462_at	RIKEN cDNA 3100002L24 gene	3100002L24Rik	-0.247	0.008630726
1420620_a_at	ring finger protein 13	Rnf13	-0.247	0.018250433
1424280_at	motile sperm domain containing 1	Mospd1	-0.247	0.009942048
1433627_at	Sec23 interacting protein	Sec23ip	-0.247	0.000773237
1448037_at	NA	NA	-0.247	0.00157961
1434059_at	RIKEN cDNA B230312A22 gene	B230312A22Rik	-0.248	0.005646369
1416085_s_at	zinc finger, AN1-type domain 5	Zfand5	-0.248	0.001996998
1451223_a_at	basic transcription factor 3-like 4	Btf3l4	-0.248	0.01199005
1431270_a_at	asteroid homolog 1 (Drosophila)	Aste1	-0.248	0.003871126
1416437_a_at	mitogen-activated protein kinase 8 interacting protein 3	Mapk8ip3	-0.248	0.003964183
1450035_a_at	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	Prpf40a	-0.248	0.030860268
1431644_a_at	islet cell autoantigen 1	Ica1	-0.248	0.004995269
1422546_at	interleukin enhancer binding factor 3	Ilf3	-0.248	0.016810558
1417406_at	SERTA domain containing 1	Sertad1	-0.248	0.007824694
1448244_at	lysophospholipase 1	Lypla1	-0.248	0.005575374
1433946_at	zinc finger protein interacting with K protein 1	Zik1	-0.248	0.011168577
1424057_at	ganglioside-induced differentiation-associated-protein 2	Gdap2	-0.248	0.005434779
1425646_at	cDNA sequence BC016495	BC016495	-0.248	0.007776401
1422770_at	RAD51-like 3 (S. cerevisiae)	Rad51l3	-0.248	0.01013178
1420507_a_at	SFRS12-interacting protein 1	Sfrs12ip1	-0.248	0.001343644
1426095_a_at	tumor necrosis factor receptor superfamily, member 22	Tnfrsf22	-0.248	0.009244933
1438403_s_at	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	Malat1	-0.249	0.02507586
1460450_at	AMME chromosomal region gene 1-like	Ammecr1l	-0.249	0.001349114
1434038_at	DnaJ (Hsp40) homolog, subfamily C, member 13	Dnajc13	-0.249	0.000649694
1451310_a_at	cathepsin L	Ctsl	-0.249	0.000262003
1448761_a_at	coatomer protein complex, subunit gamma 2	Copg2	-0.249	0.002025128

1433628_at	coenzyme Q10 homolog A (yeast)	Coq10a	-0.249	0.001517059
1437455_a_at	similar to myocardial vascular inhibition factor	LOC100047353	-0.249	0.002396927
1433541_a_at	ubiquitin associated protein 2-like	Ubap2l	-0.249	0.000517704
1418651_at	spermatogenesis associated 6	Spata6	-0.249	0.033200834
1450849_at	heterogeneous nuclear ribonucleoprotein U	Hnrnpu	-0.249	0.00171104
1450672_a_at	three prime repair exonuclease 1	Trex1	-0.249	0.012961792
1453993_a_at	BCL2/adenovirus E1B interacting protein 2	Bnip2	-0.25	0.004867305
1416138_at	annexin A7	Anxa7	-0.25	0.000481984
1419339_at	neuraminidase 3	Neu3	-0.25	0.003648172
1424058_at	proline-rich coiled-coil 1	Prrc1	-0.25	0.004434875
1433609_s_at	surfeit gene 2	Surf2	-0.25	0.006262322
1427691_a_at	interferon (alpha and beta) receptor 2	Ifnar2	-0.25	0.000723602
1452600_at	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor	Taf6l	-0.251	0.002362999
1450537_at	midline 2	Mid2	-0.251	0.008740002
1416476_a_at	ubiquitin-conjugating enzyme E2D 2	Ube2d2	-0.251	0.000667877
1423322_at	lin-7 homolog C (C. elegans)	Lin7c	-0.251	0.006644776
1452002_at	ADNP homeobox 2	Adnp2	-0.251	0.000349075
1423601_s_at	Treacher Collins Franceschetti syndrome 1, homolog	Tcof1	-0.251	0.008961446
1431602_a_at	UDP-glucose ceramide glucosyltransferase-like 2	Ugcgl2	-0.251	0.011675033
1419454_x_at	protein inhibitor of activated STAT 2	Pias2	-0.251	0.032011329
1427526_at	FGFR1 oncogene partner 2	Fgfr1op2	-0.251	0.038483212
1423552_at	leptin receptor overlapping transcript-like 1	Leprotl1	-0.251	0.005035528
1426696_at	low density lipoprotein receptor-related protein associated protein 1	Lrpap1	-0.251	0.005703119
1436609_a_at	low density lipoprotein receptor-related protein associated protein 1	Lrpap1	-0.251	0.003776583
1416786_at	activin A receptor, type 1	Acvr1	-0.251	0.024165899
1449120_a_at	pericentriolar material 1	Pcm1	-0.251	0.022208162
1422015_a_at	ATP-binding cassette, sub-family B (MDR/TAP), member 8	Abcb8	-0.251	0.001338179
1451026_at	FtsJ homolog 3 (E. coli)	Ftsj3	-0.251	0.001060266
1417446_at	solute carrier family 12, member 4	Slc12a4	-0.251	0.002489949
1437741_at	RAB21, member RAS oncogene family	Rab21	-0.251	0.000691903
1424520_at	RIKEN cDNA 2010305A19 gene	2010305A19Rik	-0.251	0.000444824
1422005_at	eukaryotic translation initiation factor 2-alpha kinase 2	Eif2ak2	-0.252	0.005859831
1438504_x_at	transmembrane 7 superfamily member 3	Tm7sf3	-0.252	0.031617166
1460387_a_at	sialic acid acetylesterase	Siae	-0.252	0.003482186
1420318_at	NA	NA	-0.252	0.00224246
1452015_at	RIKEN cDNA 6330416G13 gene	6330416G13Rik	-0.252	0.00251123
1442145_at	ATPase type 13A3	Atp13a3	-0.252	0.040688121
1429528_at	RAE1 RNA export 1 homolog (S. pombe)	Rae1	-0.252	0.002822763
1425297_at	zinc finger protein 825	Zfp825	-0.252	0.016901203
1453063_at	clathrin, light polypeptide (Lcb)	Cltb	-0.252	0.001729417
1423690_s_at	G-protein signalling modulator 1 (AGS3-like, C. elegans)	Gpsm1	-0.252	0.004842024
1460353_at	transmembrane protein 48	Tmem48	-0.252	0.005600571
1428920_at	high mobility group 20A	Hmg20a	-0.252	0.008108975
1451140_s_at	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	Prkag2	-0.253	0.000746054
1428372_at	suppression of tumorigenicity 5	St5	-0.253	0.024683939
1425200_at	chloride channel CLIC-like 1	Clcc1	-0.253	0.01090245
1417288_at	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member	Plekha2	-0.253	0.00666622

	2			
1420890_at	holocytochrome c synthetase	Hccs	-0.253	0.000402316
1427944_at	caprin family member 2	Caprin2	-0.253	0.002115783
1418667_at	RIKEN cDNA 2410002O22 gene	2410002O22Rik	-0.253	0.005661206
1451414_at	DNA segment, Chr 13, Wayne State University 177, expressed	D13Wsu177e	-0.253	0.008376218
1427448_at	rabaptin, RAB GTPase binding effector protein 1	Rabep1	-0.253	0.001285328
1431166_at	chromodomain helicase DNA binding protein 1	Chd1	-0.253	0.00125881
1437185_s_at	thymosin, beta 10	Tmsb10	-0.253	0.007989055
1417100_at	CD320 antigen	Cd320	-0.253	0.001486849
1423212_at	polyhomeotic-like 1 (Drosophila)	Phc1	-0.253	0.000959554
1452776_a_at	negative regulator of ubiquitin-like proteins 1	Nub1	-0.253	0.000766838
1426114_at	heterogeneous nuclear ribonucleoprotein A/B	Hnrnpab	-0.253	0.005803411
1424538_at	ubiquitin-like 4	Ubl4	-0.253	0.001032635
1423131_at	RIKEN cDNA 5730427N09 gene	5730427N09Rik	-0.253	0.003667963
1438888_at	germ cell-less homolog 1 (Drosophila)	Gmcl1	-0.253	0.011296736
1426671_a_at	RNA binding motif protein 39	Rbm39	-0.253	0.002139823
1419749_at	tRNA aspartic acid methyltransferase 1	Trdmt1	-0.253	0.0097583
1416004_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	Ywhah	-0.254	0.000420968
1426047_a_at	protein tyrosine phosphatase, receptor type, R	Ptprr	-0.254	0.007214834
1421797_a_at	sorting nexin 12	Snx12	-0.254	0.002230569
1451752_at	forkhead box K1	Foxk1	-0.254	0.000449494
1448264_a_at	eukaryotic translation initiation factor 3, subunit I	Eif3i	-0.254	0.002439032
1426125_a_at	caspase 9	Casp9	-0.254	0.01128724
1455777_x_at	hydroxysteroid (17-beta) dehydrogenase 4	Hsd17b4	-0.254	0.001496632
1453100_at	NA	NA	-0.254	0.005891687
1426406_at	SET domain containing (lysine methyltransferase) 8	Setd8	-0.254	0.001375269
1421395_at	zinc finger protein interacting with K protein 1	Zik1	-0.254	0.006209414
1448726_at	small nuclear RNA activating complex, polypeptide 2	Snapc2	-0.254	0.007155574
1415680_at	anaphase promoting complex subunit 1	Anapc1	-0.254	0.000376933
1417248_at	ralA binding protein 1	Ralbp1	-0.254	0.017348361
1438721_a_at	interferon regulatory factor 3	Irf3	-0.254	0.039402818
1452467_at	methylmalonic aciduria (cobalamin deficiency) type B homolog (human)	Mmab	-0.254	0.001387518
1437985_a_at	RIKEN cDNA 2310061I04 gene	2310061I04Rik	-0.254	0.014331176
1456620_at	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	Gnptab	-0.254	0.007656911
1417666_at	deoxynucleotidyltransferase, terminal, interacting protein 1	Dnttip1	-0.254	0.000781555
1417927_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19a	Ddx19a	-0.254	0.001916536
1418062_at	eukaryotic translation elongation factor 1 alpha 2	Eef1a2	-0.254	0.000535136
1450053_at	kinesin family member 2A	Kif2a	-0.254	0.001038197
1452443_s_at	helicase with zinc finger domain	Helz	-0.255	0.000756823
1449237_at	arachidonate lipoxygenase 3	Aloxe3	-0.255	0.00561356
1452192_at	nuclear assembly factor 1 homolog (S. cerevisiae)	Naf1	-0.255	0.000853859
1424643_at	Treacher Collins Franceschetti syndrome 1, homolog	Tcof1	-0.255	0.004969018
1417101_at	heat shock protein 2	Hspa2	-0.255	0.002502698
1427831_s_at	zinc finger protein 260	Zfp260	-0.255	0.008116985
1439405_x_at	cyclin N-terminal domain containing 1	Cntd1	-0.255	0.009894887

1426826_at	RNA binding motif protein 16	Rbm16	-0.255	0.000312095
1419668_at	sarcoglycan, beta (dystrophin-associated glycoprotein)	Sgcb	-0.255	0.000344846
1428169_at	autophagy-related 16-like 1 (yeast)	Atg16l1	-0.255	0.001573498
1451349_at	EF-hand calcium binding domain 7	Efcab7	-0.255	0.012585972
1416558_at	maternal embryonic leucine zipper kinase	Melk	-0.255	0.0005275
1448396_at	transmembrane protein 131	Tmem131	-0.256	0.001354688
1426316_at	RIKEN cDNA 6330416G13 gene	6330416G13Rik	-0.256	0.015374487
1424819_a_at	resistance to inhibitors of cholinesterase 8 homolog (C. elegans)	Ric8	-0.256	0.000604576
1434735_at	hepatic leukemia factor	Hlf	-0.256	0.019030006
1448347_a_at	cell cycle associated protein 1	Caprin1	-0.256	0.000474718
1426387_x_at	RIKEN cDNA 4933439C20 gene	4933439C20Rik	-0.256	0.002141556
1452122_at	expressed sequence AI314180	AI314180	-0.256	0.000489828
1448976_at	tuftelin interacting protein 11	Tfip11	-0.256	0.000506059
1421874_a_at	mitochondrial ribosomal protein S23	Mrps23	-0.256	0.002113507
1419971_s_at	solute carrier family 35, member A5	Slc35a5	-0.256	0.008306696
1426484_at	UBX domain protein 4	Ubxn4	-0.256	0.009499527
1426958_at	ribosomal protein S9	Rps9	-0.256	0.029585412
1450011_at	hydroxysteroid (17-beta) dehydrogenase 12	Hsd17b12	-0.256	0.000439052
1452187_at	RNA binding motif protein 5	Rbm5	-0.257	0.005428861
1436525_at	adaptor-related protein complex 3, sigma 2 subunit	Ap3s2	-0.257	0.00439251
1422314_at	chloride channel 6	Clcn6	-0.257	0.005186965
1450747_at	kelch-like ECH-associated protein 1	Keap1	-0.257	0.006952328
1435738_x_at	small EDRK-rich factor 2	Serf2	-0.257	0.000313514
1451654_x_at	zinc finger protein 825	Zfp825	-0.257	0.01350553
1419055_a_at	protein tyrosine phosphatase, non-receptor type 21	Ptpn21	-0.257	0.009848549
1452353_at	G protein-coupled receptor 155	Gpr155	-0.257	0.00448988
1450166_at	iduronate 2-sulfatase	Ids	-0.257	0.0193105
1460698_a_at	SEC11 homolog C (S. cerevisiae)	Sec11c	-0.257	0.001927145
1449048_s_at	RAB4A, member RAS oncogene family	Rab4a	-0.257	0.002761668
1427248_at	Wolf-Hirschhorn syndrome candidate 2 (human)	Whsc2	-0.257	0.002097161
1423732_at	translocating chain-associating membrane protein 1	Tram1	-0.258	0.000798067
1450886_at	germ cell-specific gene 2	Gsg2	-0.258	0.00386033
1418169_at	zinc finger, CCHC domain containing 14	Zcchc14	-0.258	0.005128138
1422910_s_at	structural maintenance of chromosomes 6	Smc6	-0.258	0.041661381
1423325_at	pinin	Pnn	-0.258	0.015438254
1425766_x_at	NA	NA	-0.258	0.024310659
1451308_at	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4	Elovl4	-0.258	0.0004905
1417548_at	squamous cell carcinoma antigen recognized by T-cells 3	Sart3	-0.258	0.032626019
1438629_x_at	granulin	Grn	-0.259	0.003154609
1415792_at	RanBP-type and C3HC4-type zinc finger containing 1	Rbck1	-0.259	0.006079779
1450072_at	ash1 (absent, small, or homeotic)-like (Drosophila)	Ash1l	-0.259	0.001099154
1460646_at	casein kinase 2, alpha prime polypeptide	Csnk2a2	-0.259	0.004242614
1455860_at	phosphatidylinositol glycan anchor biosynthesis, class H	Pigh	-0.259	0.001931609
1424667_a_at	cut-like homeobox 1	Cux1	-0.259	0.01729158
1417341_a_at	protein phosphatase 1, regulatory (inhibitor) subunit 2	Ppp1r2	-0.259	0.0067314
1433482_a_at	far upstream element (FUSE) binding protein 1	Fubp1	-0.259	0.001770706

1416911_a_at	akirin 1	Akirin1	-0.259	0.012253278
1420796_at	aryl-hydrocarbon receptor repressor	Ahrr	-0.259	0.008976299
1423532_at	ring finger protein 44	Rnf44	-0.259	0.001717861
1420485_at	nucleolar protein 7	Nol7	-0.259	0.003888715
1431707_a_at	cytohesin 3	Cyth3	-0.259	0.032400771
1426805_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	Smarca4	-0.259	0.043951787
1434155_a_at	RIKEN cDNA 2310061I04 gene	2310061I04Rik	-0.26	0.001643647
1421273_at	suppressor of cytokine signaling 4	Socs4	-0.26	0.019190135
1447976_at	expressed sequence AI596198	AI596198	-0.26	0.019827717
1420048_at	expressed sequence C78859	C78859	-0.26	0.001984771
1431059_x_at	HIV TAT specific factor 1	Htatsf1	-0.26	0.002362999
1422456_at	N-ethylmaleimide sensitive fusion protein	Nsf	-0.26	0.001504517
1452674_a_at	eukaryotic translation initiation factor 3, subunit K	Eif3k	-0.26	0.002939146
1426655_a_at	RIKEN cDNA 4930504E06 gene	4930504E06Rik	-0.26	0.004681995
1451624_a_at	phosphatase, orphan 2	Phospho2	-0.26	0.00164193
1454899_at	LIM domain containing preferred translocation partner in lipoma	Lpp	-0.26	0.015284679
1424049_at	leucine rich repeat containing 42	Lrrc42	-0.26	0.001249591
1428838_a_at	deoxycytidine kinase	Dck	-0.26	0.026401054
1435057_x_at	polymerase (RNA) I polypeptide E	Polr1e	-0.26	0.002629044
1424429_s_at	NO80 complex subunit E	Ino80e	-0.261	0.000196478
1421908_a_at	transcription factor 12	Tcf12	-0.261	0.006973993
1423789_at	cDNA sequence BC005624	BC005624	-0.261	0.000518186
1448668_a_at	interleukin-1 receptor-associated kinase 1	Irak1	-0.261	0.001125886
1454018_at	tousled-like kinase 2 (Arabidopsis)	Tlk2	-0.261	0.00081146
1437142_a_at	phosphatidylinositol glycan anchor biosynthesis, class O	Pigo	-0.261	0.02493337
1422945_a_at	kinesin family member 5C	Kif5c	-0.261	0.00471022
1419295_at	cAMP responsive element binding protein 3-like 1	Creb3l1	-0.261	0.002593284
1430022_at	SUMO1 activating enzyme subunit 1	Sae1	-0.261	0.003349018
1452232_at	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransferase 7	Galnt7	-0.261	0.003928142
1427253_s_at	suppressor of zeste 12 homolog (Drosophila)	Suz12	-0.261	0.002811086
1425932_a_at	CUG triplet repeat, RNA binding protein 1	Cugbp1	-0.262	0.008077119
1424665_at	G patch domain containing 8	Gpatch8	-0.262	0.002787888
1427086_at	slit homolog 3 (Drosophila)	Slit3	-0.262	0.004395381
1453972_x_at	mediator complex subunit 1	Med1	-0.262	0.00176265
1422764_at	microtubule-associated protein, RP/EB family, member 1	Mapre1	-0.262	0.002604951
1420946_at	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	Atrx	-0.262	0.017065264
1415748_a_at	dynactin 5	Dctn5	-0.262	0.000205065
1418375_at	methyl-CpG binding domain protein 6	Mbd6	-0.263	0.001928484
1415845_at	synaptotagmin IV	Syt4	-0.263	0.000574684
1428505_at	coiled-coil domain containing 90B	Ccdc90b	-0.263	0.000174842
1451896_a_at	calcium homeostasis endoplasmic reticulum protein	Cherp	-0.263	0.000421573
1425966_x_at	ubiquitin C	Ubc	-0.263	0.000959949
1448654_at	mitochondrial carrier homolog 2 (C. elegans)	Mtch2	-0.263	0.000961819
1418905_at	nucleotide binding protein 1	Nubp1	-0.263	0.001372675
1435202_at	zinc finger protein 574	Zfp574	-0.263	0.004612419
1429173_at	deoxyribonuclease 1-like 1	Dnase1l1	-0.263	0.001189674

1426356_at	RIKEN cDNA 6330578E17 gene	6330578E17Rik	-0.263	0.005173709
1455940_x_at	WD repeat domain 6	Wdr6	-0.263	0.000602904
1451099_at	membrane bound C2 domain containing protein	Mbc2	-0.263	0.010213424
1420371_at	syntrophin, basic 2	Sntb2	-0.264	0.009764804
1416344_at	lysosomal-associated membrane protein 2	Lamp2	-0.264	0.000763374
1453324_at	RIKEN cDNA 6330509M23 gene	6330509M23Rik	-0.264	0.000840868
1460707_at	protein tyrosine phosphatase 4a2	Ptp4a2	-0.264	0.000450048
1434118_at	mitochondrial ubiquitin ligase activator of NFKB 1	Mul1	-0.264	0.000645502
1417188_s_at	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast)	Ube2k	-0.264	0.002951029
1416883_at	cleft lip and palate associated transmembrane protein 1	Clptm1	-0.264	0.000201823
1417217_at	melanoma antigen, family L, 2	Magel2	-0.264	0.000431982
1452116_s_at	activating transcription factor 2	Atf2	-0.264	0.000276064
1423902_s_at	Rho guanine nucleotide exchange factor (GEF) 12	Arhgef12	-0.264	0.001379993
1449622_s_at	ATPase, H+ transporting, lysosomal accessory protein 1	Atp6ap1	-0.264	0.000221861
1418013_at	camello-like 1	Cml1	-0.264	0.006617924
1422609_at	cAMP-regulated phosphoprotein 19	Arpp19	-0.264	0.015805545
1422766_at	staufen (RNA binding protein) homolog 1 (Drosophila)	Stau1	-0.264	0.000318002
1424216_a_at	poly (A) polymerase alpha	Papola	-0.264	0.007614111
1449234_at	carbonic anhydrase 15	Car15	-0.264	0.001275545
1425835_a_at	bobby sox homolog (Drosophila)	Bbx	-0.264	0.000964171
1451311_a_at	adiponectin receptor 1	Adipor1	-0.264	0.00019521
1449628_s_at	START domain containing 7	Stard7	-0.264	0.001885451
1460194_at	phytanoyl-CoA hydroxylase	Phyh	-0.264	0.001394413
1448167_at	interferon gamma receptor 1	Ifngr1	-0.264	0.004227424
1424066_at	dihydrouridine synthase 3-like (S. cerevisiae)	Dus3l	-0.265	0.011856325
1427460_at	TAF4A RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf4a	-0.265	0.003436405
1423518_at	c-src tyrosine kinase	Csk	-0.265	0.004329997
1420443_at	protocadherin beta 19	Pcdhb19	-0.265	0.023155046
1434900_at	MKL (megakaryoblastic leukemia)/myocardin-like 1	Mkl1	-0.265	0.01090245
1427991_s_at	ubiquitin specific petidase 45	Usp45	-0.265	0.007017543
1422681_at	Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	Ctr9	-0.265	0.003369663
1436703_x_at	small nuclear RNA activating complex, polypeptide 2	Snapc2	-0.265	0.000483577
1457676_at	toll-interleukin 1 receptor (TIR) domain-containing adaptor protein	Tirap	-0.265	0.001695049
1425461_at	F-box and WD-40 domain protein 11	Fbxw11	-0.265	0.015080272
1416109_at	fucosidase, alpha-L- 1, tissue	Fuca1	-0.265	0.002412755
1416358_at	major facilitator superfamily domain containing 10	Mfsd10	-0.265	0.002671062
1455534_s_at	oxysterol binding protein-like 11	Osbpl11	-0.265	0.002450458
1450994_at	Rho-associated coiled-coil containing protein kinase 1	Rock1	-0.265	0.00463715
1426100_a_at	thymidine kinase 2, mitochondrial	Tk2	-0.265	0.004806701
1419690_at	RIKEN cDNA 2610002M06 gene	2610002M06Rik	-0.265	0.00121021
1428092_at	cell division cycle 5-like (S. pombe)	Cdc5l	-0.266	0.004285078
1424164_at	mitochondrial ribosomal protein L50	Mrpl50	-0.266	0.00249236
1451494_at	WW domain containing adaptor with coiled-coil	Wac	-0.266	0.002233365
1450021_at	ubiquilin 2	Ubqln2	-0.266	0.000680597

1451730_at	zinc finger protein 62	Zfp62	-0.266	0.010902612
1455058_at	myotubularin related protein 9	Mtmr9	-0.266	0.002613894
1452411_at	leucine rich repeat containing 1	Lrrc1	-0.266	0.001894351
1450650_at	myosin X	Myo10	-0.266	0.002034979
1460230_at	synapsin II	Syn2	-0.266	0.000291628
1422126_a_at	nudix (nucleoside diphosphate linked moiety X)-type motif 13	Nudt13	-0.266	0.003303296
1416912_at	akirin 1	Akirin1	-0.266	0.000264238
1419069_at	RAB guanine nucleotide exchange factor (GEF) 1	Rabgef1	-0.266	0.002903599
1449278_at	eukaryotic translation initiation factor 2 alpha kinase 3	Eif2ak3	-0.266	0.000238964
1452544_x_at	histocompatibility 2, D region locus 1	H2-D1	-0.266	0.001278549
1460352_s_at	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 4, p150	Pik3r4	-0.267	0.001882133
1460712_s_at	adaptor protein complex AP-1, gamma 1 subunit	Ap1g1	-0.267	0.00238231
1452070_at	death effector domain-containing DNA binding protein 2	Dedd2	-0.267	0.000515769
1419651_at	Na+/K+ transporting ATPase interacting 1	Nkain1	-0.267	0.009213118
1426978_at	kelch-like 2, Mayven (Drosophila)	Klhl2	-0.267	0.000872795
1453426_a_at	WD repeat and FYVE domain containing 1	Wdfy1	-0.267	0.000242116
1423986_a_at	shisa homolog 5 (Xenopus laevis)	Shisa5	-0.267	0.000205913
1418249_at	calcitonin gene-related peptide-receptor component protein	Crcp	-0.267	0.000389078
1416470_a_at	ribophorin I	Rpn1	-0.268	0.00022276
1453997_a_at	nestin	Nes	-0.268	0.048262854
1417689_a_at	PDZK1 interacting protein 1	Pdzk1ip1	-0.268	0.004629097
1423843_at	leucine rich repeat containing 61	Lrrc61	-0.268	0.001499859
1460203_at	inositol 1,4,5-triphosphate receptor 1	Itpr1	-0.268	0.003445073
1434986_a_at	Sec61 alpha 1 subunit (S. cerevisiae)	Sec61a1	-0.268	0.000430993
1416429_a_at	catalase	Cat	-0.268	0.021455232
1449379_at	kinase insert domain protein receptor	Kdr	-0.268	0.017258209
1455131_at	optic atrophy 3 (human)	Opa3	-0.268	0.000742093
1452768_at	testis expressed gene 261	Tex261	-0.268	0.000547628
1420651_at	arginyltransferase 1	Ate1	-0.268	0.009735046
1430701_a_at	RIKEN cDNA 5730528L13 gene	5730528L13Rik	-0.268	0.00164285
1424145_at	proline-rich polypeptide 3	Prr3	-0.268	0.000545179
1426891_at	RNA polymerase II associated protein 1	Rpap1	-0.268	0.005493398
1434033_at	transducin-like enhancer of split 1, homolog of Drosophila E(spl)	Tle1	-0.268	0.00049914
1427992_a_at	RAB12, member RAS oncogene family	Rab12	-0.269	0.000465672
1456080_a_at	serine incorporator 3	Serinc3	-0.269	0.004162174
1418151_at	myotubularin related protein 4	Mtmr4	-0.269	0.0008935
1425621_at	tripartite motif-containing 35	Trim35	-0.269	0.005368911
1424690_at	RIKEN cDNA 5930434B04 gene	5930434B04Rik	-0.269	0.022615634
1452582_at	galactose mutarotase	Galm	-0.269	0.006307891
1421875_a_at	mitochondrial ribosomal protein S23	Mrps23	-0.269	0.001482643
1425280_at	leukocyte receptor cluster (LRC) member 1	Leng1	-0.269	0.005798561
1427954_at	cDNA sequence BC048403	BC048403	-0.269	0.004777286
1417513_at	ecotropic viral integration site 5	Evi5	-0.269	0.001129077
1420088_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	Nfkbia	-0.269	0.005010317
1452395_at	mediator of RNA polymerase II transcription, subunit 19 homolog (yeast)	Med19	-0.269	0.001490916
1431030_a_at	ring finger protein 14	Rnf14	-0.269	0.011735577
1451674_at	solute carrier family 12, member 5	Slc12a5	-0.27	0.002257377

1434785_at	calcium channel, voltage-dependent, gamma subunit 5	Cacng5	-0.27	0.001683543
1434575_at	erythrocyte protein band 4.1-like 1	Epb4.1l1	-0.27	0.003705735
1453025_at	MACRO domain containing 2	Macrod2	-0.27	0.009336485
1420534_at	guanylate cyclase 1, soluble, alpha 3	Gucy1a3	-0.27	0.001274085
1450587_at	histocompatibility 2, M region locus 10.1	H2-M10.1	-0.27	0.011779497
1418345_at	tumor necrosis factor (ligand) superfamily, member 13	Tnfsf13	-0.27	0.002207514
1424416_at	NFKB inhibitor interacting Ras-like protein 2	Nkiras2	-0.27	0.000611975
1428195_at	S-adenosylhomocysteine hydrolase-like 2	Ahcyl2	-0.27	0.02056521
1451800_at	GRIP and coiled-coil domain containing 2	Gcc2	-0.27	0.013269558
1421954_at	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	Crkl	-0.27	0.007494673
1448632_at	proteasome (prosome, macropain) subunit, beta type 10	Psmb10	-0.271	0.001254182
1426534_a_at	ADP-ribosylation factor GTPase activating protein 3	Arfgap3	-0.271	0.000210506
1455805_x_at	coiled-coil domain containing 22	Ccdc22	-0.271	0.006591016
1425593_at	transportin 2 (importin 3, karyopherin beta 2b)	Tnpo2	-0.271	0.001199261
1449600_at	predicted gene, 100042198	100042198	-0.271	0.018937488
1425278_at	ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)	Ube4a	-0.271	0.0253469
1420959_at	aspartate-beta-hydroxylase	Asph	-0.271	0.003103145
1417378_at	cell adhesion molecule 1	Cadm1	-0.271	0.001547945
1451175_at	signal peptidase complex subunit 3 homolog (S. cerevisiae)	Spcs3	-0.272	0.002065579
1416977_at	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	Stam2	-0.272	0.042955624
1426524_at	glucosamine-6-phosphate deaminase 2	Gnpda2	-0.272	0.003586671
1450080_at	CAAX box 1 homolog C (human)	Cxx1c	-0.272	0.000581607
1449800_x_at	PHD finger protein 7	Phf7	-0.272	0.006950875
1424406_at	BCL2-like 13 (apoptosis facilitator)	Bcl2l13	-0.272	0.000654275
1449317_at	CASP8 and FADD-like apoptosis regulator	Cflar	-0.272	0.005851264
1429623_at	zinc finger protein 644	Zfp644	-0.272	0.000451158
1448695_at	protein kinase C, iota	Prkci	-0.272	0.017177196
1448837_at	villin 1	Vil1	-0.272	0.000614864
1428742_at	F-box protein 45	Fbxo45	-0.272	0.004042498
1420148_at	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	Slc6a6	-0.272	0.013242457
1423448_at	RAB11B, member RAS oncogene family	Rab11b	-0.272	0.000827456
1416772_at	carnitine palmitoyltransferase 2	Cpt2	-0.273	0.000173715
1416927_at	transformation related protein 53 inducible nuclear protein 1	Trp53inp1	-0.273	0.012302668
1420895_at	transforming growth factor, beta receptor I	Tgfbr1	-0.273	0.001456383
1453238_s_at	RIKEN cDNA 1200016E24 gene	1200016E24Rik	-0.273	0.00384046
1421927_at	transducin (beta)-like 2	Tbl2	-0.273	0.037892315
1438669_at	WD repeat domain 40A	Wdr40a	-0.273	0.000430937
1460164_at	spindlin 1	Spin1	-0.273	0.010537475
1417465_at	farnesyltransferase, CAAX box, alpha	Fnta	-0.273	0.000226544
1417535_at	F-box protein 25	Fbxo25	-0.273	0.000587492
1450090_at	zinc finger protein 101	Zfp101	-0.273	0.00856881
1426403_at	ARP1 actin-related protein 1 homolog B, centractin beta (yeast)	Actr1b	-0.273	0.001473665
1448751_at	adaptor-related protein complex 3, mu 2 subunit	Ap3m2	-0.273	0.000322471
1435998_at	cyclin B1 interacting protein 1	Ccnb1ip1	-0.274	0.03043181
1416667_at	phenylalkylamine Ca2+ antagonist (emopamil) binding protein	Ebp	-0.274	0.000219059

1452889_at	RIKEN cDNA 2310007H09 gene	2310007H09Rik	-0.274	0.000721733
1449197_at	WD repeat domain 20a	Wdr20a	-0.274	0.002172557
1422650_a_at	RIO kinase 3 (yeast)	Riok3	-0.274	0.001891805
1434053_x_at	ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e	Atp5k	-0.274	0.004627301
1421951_at	LIM homeobox protein 1	Lhx1	-0.274	0.001617645
1427932_s_at	RIKEN cDNA 1200016E24 gene	1200016E24Rik	-0.274	0.001757064
1432488_a_at	splicing factor 3a, subunit 3	Sf3a3	-0.274	0.005155232
1416670_at	SET domain, bifurcated 1	Setdb1	-0.274	0.021532701
1454635_at	F-box and leucine-rich repeat protein 3	Fbxl3	-0.274	0.000734425
1426227_s_at	vacuolar protein sorting 37C (yeast)	Vps37c	-0.274	0.000354159
1420650_at	zinc finger homeobox 3	Zfhx3	-0.274	0.016187053
1447924_at	nuclear casein kinase and cyclin-dependent kinase substrate 1	Nucks1	-0.274	0.005043183
1423623_at	RIKEN cDNA 2810021B07 gene	2810021B07Rik	-0.275	0.000324666
1426635_at	acyl-Coenzyme A binding domain containing 3	Acbd3	-0.275	0.019958434
1426610_a_at	transcription termination factor, RNA polymerase I	Ttf1	-0.275	0.002980991
1423401_at	ets variant gene 6 (TEL oncogene)	Etv6	-0.275	0.005102443
1432435_s_at	RIKEN cDNA C030004A17Rik	C030004A17Rik	-0.275	0.001555755
1449857_at	RIKEN cDNA 1200011I18 gene	1200011I18Rik	-0.275	0.017919182
1450066_at	ubiquitin protein ligase E3 component n-recognin 1	Ubr1	-0.275	0.000492865
1421994_a_at	HCLS1 binding protein 3	Hs1bp3	-0.275	0.009556249
1429619_a_at	RIKEN cDNA 8430406I07 gene	8430406I07Rik	-0.275	0.007086272
1427088_at	cyclin T2	Ccnt2	-0.276	0.003935888
1415901_at	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	Plod3	-0.276	0.00031994
1460290_at	lipin 2	Lpin2	-0.276	0.000525909
1449142_a_at	Yip1 domain family, member 5	Yipf5	-0.276	0.000469897
1423735_a_at	WD repeat domain 36	Wdr36	-0.276	0.000164205
1455065_x_at	predicted gene, EG667410	EG667410	-0.276	0.000344095
1417941_at	N-acetylneuraminic acid phosphatase	Nanp	-0.276	0.000131998
1423840_at	coiled-coil domain containing 56	Ccdc56	-0.276	0.012653511
1423755_at	zinc finger, CCHC domain containing 8	Zcchc8	-0.276	0.000174644
1452619_a_at	ATP/GTP binding protein-like 3	Agbl3	-0.277	0.004441797
1417344_at	RIKEN cDNA 2900064A13 gene	2900064A13Rik	-0.277	0.000186637
1416084_at	zinc finger, AN1-type domain 5	Zfand5	-0.277	0.000715943
1422016_a_at	centromere protein H	Cenph	-0.277	0.002039126
1425544_at	pleckstrin homology domain containing, family A member 5	Plekha5	-0.277	0.017155781
1420533_at	guanylate cyclase 1, soluble, alpha 3	Gucy1a3	-0.277	0.004842203
1417589_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3	Galnt3	-0.277	0.015403393
1417300_at	sphingomyelin phosphodiesterase, acid-like 3B	Smpdl3b	-0.277	0.000417073
1448670_at	ubiquitin-conjugating enzyme E2E 3, UBC4/5 homolog (yeast)	Ube2e3	-0.277	0.000135195
1420645_at	polycomb group ring finger 2	Pcgf2	-0.277	0.0024932
1417028_a_at	tripartite motif-containing 2	Trim2	-0.277	0.000755862
1437537_at	caspase 9	Casp9	-0.277	0.000429369
1430117_a_at	zinc finger protein 64	Zfp64	-0.278	0.004605537
1419611_at	RIKEN cDNA 4632415L05 gene	4632415L05Rik	-0.278	0.000381445
1415788_at	ubiquitin-like domain containing CTD phosphatase 1	Ublcp1	-0.278	0.001158676
1440221_at	expressed sequence AA408650	AA408650	-0.278	0.002250043
1455976_x_at	diazepam binding inhibitor	Dbi	-0.278	0.001131216

1423762_at	aarF domain containing kinase 1	Adck1	-0.278	0.00059127
1437026_at	cDNA sequence BC057893	BC057893	-0.279	0.001316839
1425288_at	sterile alpha motif domain containing 11	Samd11	-0.279	0.003501952
1423672_at	tetratricopeptide repeat domain 30B	Ttc30b	-0.279	0.001763528
1449107_at	nudix (nucleoside diphosphate linked moiety X)-type motif 4	Nudt4	-0.279	0.006641202
1416565_at	cytochrome c oxidase, subunit VIb polypeptide 1	Cox6b1	-0.279	0.000216847
1423246_at	thioredoxin domain containing 4 (endoplasmic reticulum)	Txndc4	-0.279	0.000385547
1450750_a_at	nuclear receptor subfamily 4, group A, member 2	Nr4a2	-0.279	0.002470114
1451939_a_at	sushi-repeat-containing protein	Srpx	-0.279	0.011038838
1418685_at	toll-interleukin 1 receptor (TIR) domain-containing adaptor protein	Tirap	-0.279	0.001614545
1428737_s_at	GRAM domain containing 3	Gramd3	-0.279	0.020861254
1453367_a_at	abhydrolase domain containing 12	Abhd12	-0.279	0.003536195
1460355_at	BUD13 homolog (yeast)	Bud13	-0.28	0.003355549
1451105_at	vasohibin 2	Vash2	-0.28	0.000176946
1437143_a_at	thioredoxin domain containing 1	Txndc1	-0.28	0.000289319
1450743_s_at	synaptotagmin binding, cytoplasmic RNA interacting protein	Syncrip	-0.28	0.003874821
1418899_at	ubiquitin-fold modifier 1	Ufm1	-0.28	0.001331257
1422733_at	four jointed box 1 (Drosophila)	Fjx1	-0.28	0.006477744
1428272_at	eukaryotic translation initiation factor 1B	Eif1b	-0.28	0.001693701
1451596_a_at	sphingosine kinase 1	Sphk1	-0.28	0.004960657
1451321_a_at	RNA binding motif protein 43	Rbm43	-0.28	0.000395557
1438321_x_at	RIKEN cDNA 4930504E06 gene	4930504E06Rik	-0.28	0.00031109
1422772_at	core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1	C1galt1	-0.28	0.006142383
1418308_at	Hus1 homolog (S. pombe)	Hus1	-0.28	0.000761681
1449372_at	DnaJ (Hsp40) homolog, subfamily C, member 3	Dnajc3	-0.28	0.007097896
1451988_s_at	chromatin modifying protein 4B	Chmp4b	-0.28	0.000344929
1456745_x_at	ERGIC and golgi 3	Ergic3	-0.281	0.000763374
1440936_at	serine active site containing 1	Serac1	-0.281	0.012833087
1431734_a_at	DnaJ (Hsp40) homolog, subfamily B, member 4	Dnajb4	-0.281	0.001019402
1423160_at	sprouty protein with EVH-1 domain 1, related sequence	Spred1	-0.281	0.001417255
1423764_s_at	mitochondrial ribosomal protein L37	Mrpl37	-0.281	0.001352554
1420917_at	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	Prpf40a	-0.281	0.029005452
1427319_at	RIKEN cDNA A230046K03 gene	A230046K03Rik	-0.281	0.000473331
1423490_at	F-box protein 3	Fbxo3	-0.281	0.001818078
1416412_at	neutral sphingomyelinase (N-SMase) activation associated factor	Nsmaf	-0.281	0.007873116
1452088_at	zinc finger, BED domain containing 3	Zbed3	-0.281	0.020544484
1417522_at	F-box protein 32	Fbxo32	-0.281	0.000240078
1452190_at	prolylcarboxypeptidase (angiotensinase C)	Prcp	-0.282	0.001694903
1426394_at	eukaryotic translation initiation factor 3, subunit J	Eif3j	-0.282	0.002314195
1450397_at	microtubule-associated protein 1B	Mtap1b	-0.282	0.009350985
1419505_a_at	geranylgeranyl diphosphate synthase 1	Ggps1	-0.282	0.003827991
1460399_at	coiled-coil domain containing 117	Ccdc117	-0.282	0.001139696
1423578_at	collagen, type XI, alpha 2	Col11a2	-0.282	0.020389772
1437553_at	BRCA1/BRCA2-containing complex, subunit 3	Brcc3	-0.282	0.000658972

1418936_at	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)	Maff	-0.282	0.000663038
1451340_at	AT rich interactive domain 5A (MRF1-like)	Arid5a	-0.282	0.000383311
1448642_at	poly(rC) binding protein 1	Pcbp1	-0.282	0.001188513
1422006_at	eukaryotic translation initiation factor 2-alpha kinase 2	Eif2ak2	-0.282	0.000799055
1433705_at	zinc finger protein 213	Zfp213	-0.282	0.000556288
1421252_a_at	myocyte enhancer factor 2A	Mef2a	-0.283	0.000637287
1417865_at	tumor necrosis factor, alpha-induced protein 1 (endothelial)	Tnfaip1	-0.283	0.000195755
1420745_a_at	cyclin D-type binding-protein 1	Ccndbp1	-0.283	0.000310134
1426293_at	zinc finger protein 790	Zfp790	-0.283	0.016428337
1425816_at	zinc finger protein 287	Zfp287	-0.283	0.002393928
1426453_at	pitrilysin metallepetidase 1	Pitrm1	-0.283	0.000150172
1421046_a_at	poly A binding protein, cytoplasmic 4	Pabpc4	-0.283	0.000317015
1452822_at	integrator complex subunit 7	Ints7	-0.283	0.00013278
1426410_at	pyruvate dehydrogenase kinase, isoenzyme 3	Pdk3	-0.283	0.001757064
1450067_a_at	RIKEN cDNA 1810034K20 gene	1810034K20Rik	-0.284	0.001566294
1455252_at	tuberous sclerosis 1	Tsc1	-0.284	0.000601055
1433736_at	host cell factor C1	Hcfc1	-0.284	0.000393733
1431507_a_at	synaptojanin 2 binding protein	Synj2bp	-0.284	0.001507177
1416937_at	gamma-aminobutyric acid receptor associated protein	Gabarap	-0.284	0.000381561
1448863_a_at	tumor necrosis factor, alpha-induced protein 1 (endothelial)	Tnfaip1	-0.284	0.000218172
1428503_a_at	NFKB inhibitor interacting Ras-like protein 1	Nkiras1	-0.284	0.001415507
1419365_at	peroxisomal biogenesis factor 11a	Pex11a	-0.284	0.004587836
1450915_at	adaptor-related protein complex 3, beta 1 subunit	Ap3b1	-0.284	0.005501349
1434087_at	5,10-methylenetetrahydrofolate reductase	Mthfr	-0.284	0.00167786
1426786_s_at	DEAH (Asp-Glu-Ala-His) box polypeptide 38	Dhx38	-0.284	0.000407108
1451457_at	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae)	Sc5d	-0.284	0.000299939
1419646_a_at	myelin basic protein	Mbp	-0.285	0.008025702
1439450_x_at	RIKEN cDNA A230046K03 gene	A230046K03Rik	-0.285	0.000307099
1426842_at	YTH domain family 3	Ythdf3	-0.285	0.009894887
1415745_a_at	Down syndrome critical region gene 3	Dscr3	-0.285	0.003520784
1423931_s_at	anaphase promoting complex subunit 4	Anapc4	-0.285	0.000505764
1424656_s_at	ubiquitin specific peptidase 19	Usp19	-0.285	0.000435347
1452222_at	utrophin	Utrn	-0.285	0.001270328
1416165_at	RAB31, member RAS oncogene family	Rab31	-0.285	0.000808449
1415743_at	histone deacetylase 5	Hdac5	-0.285	0.000569782
1439214_a_at	apoptosis inhibitor 5	Api5	-0.286	0.021183823
1450064_at	formin 2	Fmn2	-0.286	0.002939212
1434025_at	NA	NA	-0.286	0.001058519
1418888_a_at	selenoprotein X 1	Sepx1	-0.286	0.000259333
1426656_at	RIKEN cDNA 4930504E06 gene	4930504E06Rik	-0.286	0.001189502
1416935_at	transient receptor potential cation channel, subfamily V, member 2	Trpv2	-0.286	0.000351295
1449773_s_at	growth arrest and DNA-damage-inducible 45 beta	Gadd45b	-0.286	0.007265361
1418343_at	GTF2I repeat domain containing 2	Gtf2ird2	-0.286	0.000844064
1450785_at	thyroid hormone receptor interactor 4	Trip4	-0.286	0.007200113
1427747_a_at	lipocalin 2	Lcn2	-0.286	0.010995728
1417566_at	abhydrolase domain containing 5	Abhd5	-0.287	0.001721321
1419058_at	polymerase (RNA) I polypeptide E	Polr1e	-0.287	0.002454361
1429787_x_at	ZW10 interactor	Zwint	-0.287	0.000131696

1426681_at	unkempt homolog (Drosophila)	Unk	-0.287	0.000346003
1426709_a_at	ubiquitin specific peptidase 33	Usp33	-0.287	0.000771285
1452383_at	ribosomal protein S6 kinase polypeptide 3	Rps6ka3	-0.287	0.007759122
1460720_at	transient receptor potential cation channel, subfamily C, member 4 associated protein	Trpc4ap	-0.287	0.001194025
1437945_x_at	nucleosome assembly protein 1-like 1	Nap1l1	-0.287	0.000110272
1430778_a_at	nucleotide binding protein 1	Nubp1	-0.287	0.006423719
1426425_at	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	Sugt1	-0.287	0.000827084
1419814_s_at	S100 calcium binding protein A1	S100a1	-0.287	0.000318435
1423838_s_at	RIKEN cDNA 2400003C14 gene	2400003C14Rik	-0.287	0.000186072
1417178_at	GIPC PDZ domain containing family, member 2	Gipc2	-0.288	0.000201867
1416534_at	D4, zinc and double PHD fingers family 2	Dpf2	-0.288	0.000830322
1423099_a_at	methyltransferase-like 3	Mettl3	-0.288	0.000386461
1452387_a_at	angiomotin-like 2	Amotl2	-0.288	0.00063118
1426716_at	tudor domain containing 7	Tdrd7	-0.288	0.000203195
1423882_at	ring finger and WD repeat domain 3	Rfwd3	-0.288	0.001361319
1452474_a_at	ADP-ribosyltransferase 3	Art3	-0.288	0.012389866
1460205_at	dephospho-CoA kinase domain containing	Dcakd	-0.288	0.001016259
1423106_at	ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)	Ube2b	-0.289	0.000350992
1452503_a_at	bromodomain and WD repeat domain containing 1	Brwd1	-0.289	0.014422113
1426669_at	RIKEN cDNA C530044N13 gene	C530044N13Rik	-0.289	0.002024781
1450622_at	breast cancer anti-estrogen resistance 1	Bcar1	-0.289	0.005142977
1417455_at	transforming growth factor, beta 3	Tgfb3	-0.289	0.000652459
1424296_at	glutamate-cysteine ligase, catalytic subunit	Gclc	-0.289	0.000724834
1426259_at	pantothenate kinase 3	Pank3	-0.289	0.000479521
1437102_at	YTH domain family 1	Ythdf1	-0.289	0.004181737
1436986_at	syntrophin, basic 2	Sntb2	-0.289	0.006909494
1416958_at	nuclear receptor subfamily 1, group D, member 2	Nr1d2	-0.289	0.000953294
1433737_at	U2AF homology motif (UHM) kinase 1	Uhmk1	-0.289	0.000296949
1415930_a_at	microtubule-associated protein 1 light chain 3 beta	Map1lc3b	-0.289	0.000627504
1448313_at	tripeptidyl peptidase I	Tpp1	-0.289	0.000204685
1423240_at	Rous sarcoma oncogene	Src	-0.289	0.000594374
1428248_at	nuclear transcription factor, X-box binding 1	Nfx1	-0.289	0.000497346
1430092_at	serine active site containing 1	Serac1	-0.289	0.004804243
1415821_at	neuroplastin	Nptn	-0.289	0.000198639
1426889_at	zinc finger protein 821	Zfp821	-0.289	0.001917918
1433442_at	kelch-like 9 (Drosophila)	Klhl9	-0.289	0.000761681
1449137_at	pyruvate dehydrogenase E1 alpha 1	Pdha1	-0.29	0.001950699
1415740_at	protease (prosome, macropain) 26S subunit, ATPase 5	Psmc5	-0.29	0.000171785
1416823_a_at	oxysterol binding protein-like 1A	Osbpl1a	-0.29	0.002185955
1427313_at	prostaglandin I receptor (IP)	Ptgir	-0.29	0.000115421
1427188_at	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila)	Arih1	-0.29	0.00542001
1449390_at	G patch domain containing 4	Gpatch4	-0.29	0.020958688
1437239_x_at	polyhomeotic-like 2 (Drosophila)	Phc2	-0.29	0.001222615
1435695_a_at	RIKEN cDNA A030007L17 gene	A030007L17Rik	-0.29	0.007380497
1452289_a_at	ring finger protein 135	Rnf135	-0.29	9.11E-05
1452052_s_at	eukaryotic translation initiation factor 3, subunit J	Eif3j	-0.29	0.000111028
1426207_at	inhibitor of kappaB kinase beta	Ikbkb	-0.29	0.001081556

1418843_at	solute carrier family 30 (zinc transporter), member 4	Slc30a4	-0.29	0.000254397
1435129_at	NA	NA	-0.29	0.008476414
1432295_a_at	RIKEN cDNA 2310035K24 gene	2310035K24Rik	-0.291	0.000257791
1440192_at	tetratricopeptide repeat domain 39B	Ttc39b	-0.291	0.012263523
1452331_s_at	glutamine and serine rich 1	Qser1	-0.291	0.009615491
1421407_at	coagulation factor II (thrombin) receptor-like 2	F2rl2	-0.291	0.020048361
1425514_at	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	Pik3r1	-0.291	0.003270164
1426076_at	cell division cycle 27 homolog (S. cerevisiae)	Cdc27	-0.291	0.009266318
1424222_s_at	RAD23b homolog (S. cerevisiae)	Rad23b	-0.291	0.00049557
1451010_at	nucleolar protein 11	Nol11	-0.291	0.001981999
1427193_at	bromodomain containing 8	Brd8	-0.291	0.049332309
1451569_at	nuclear receptor subfamily 2, group C, member 2	Nr2c2	-0.291	0.000543844
1452210_at	DNA replication helicase 2 homolog (yeast)	Dna2	-0.291	0.005898051
1451622_at	LMBR1 domain containing 1	Lmbrd1	-0.291	0.000519415
1418322_at	cAMP responsive element modulator	Crem	-0.292	0.004400212
1426895_at	zinc finger protein 191	Zfp191	-0.292	0.001091174
1422327_s_at	glucose-6-phosphate dehydrogenase 2	G6pd2	-0.292	0.000831744
1438093_x_at	diazepam binding inhibitor	Dbi	-0.292	0.000685582
1423457_at	solute carrier family 35, member A5	Slc35a5	-0.292	0.000573591
1455517_at	RNA binding motif protein 4	Rbm4	-0.292	0.000715943
1423706_a_at	phosphogluconate dehydrogenase	Pgd	-0.292	0.000382501
1421042_at	rho/rac guanine nucleotide exchange factor (GEF) 2	Arhgef2	-0.292	0.006008404
1424513_at	ATPase, H+ transporting, lysosomal V0 subunit A2	Atp6v0a2	-0.292	0.007063617
1417124_at	destrin	Dstn	-0.292	0.000197004
1459884_at	cytochrome c oxidase, subunit VIIc	Cox7c	-0.292	0.031177749
1430575_a_at	tripeptidyl peptidase II	Tpp2	-0.293	0.007232284
1425085_at	RIKEN cDNA 6330416L07 gene	6330416L07Rik	-0.293	0.010346238
1448537_at	tetratricopeptide repeat domain 1	Ttc1	-0.294	0.00075967
1420679_a_at	androgen-induced 1	Aig1	-0.294	0.000379421
1428249_at	pygopus 2	Pygo2	-0.294	0.0001702
1451444_s_at	HEAT repeat containing 6	Heatr6	-0.294	0.000484009
1449553_at	Na+/K+ transporting ATPase interacting 1	Nkain1	-0.294	0.000384336
1418097_a_at	cytokine receptor-like factor 2	Crlf2	-0.294	0.001636269
1434357_a_at	karyopherin (importin) beta 1	Kpnb1	-0.294	0.001862894
1452350_at	bromodomain containing 8	Brd8	-0.295	0.017399518
1452418_at	RIKEN cDNA 1200016E24 gene	1200016E24Rik	-0.295	0.001990901
1454712_at	mitochondrial carrier triple repeat 1	Mcart1	-0.295	0.000204991
1417343_at	FXYD domain-containing ion transport regulator 6	Fxyd6	-0.295	0.001249591
1450351_a_at	CAP-GLY domain containing linker protein 1	Clip1	-0.295	0.001129086
1418024_at	NMDA receptor-regulated gene 1	Narg1	-0.295	0.00032995
1433511_at	RIKEN cDNA 6330549H03 gene	6330549H03Rik	-0.295	0.002627992
1419867_a_at	ankyrin repeat and KH domain containing 1	Ankhd1	-0.295	0.001682355
1426429_at	THAP domain containing 7	Thap7	-0.295	0.001666724
1420548_a_at	RIKEN cDNA 2310008H09 gene	2310008H09Rik	-0.295	0.001903542
1435863_at	COMM domain containing 6	Commd6	-0.295	0.000927755
1428543_at	phosphoribosyl pyrophosphate amidotransferase	Ppat	-0.295	0.004609756
1434757_at	core-binding factor, runt domain, alpha subunit 2, translocated to, 2 (human)	Cbfa2t2	-0.295	0.000110365
1418851_at	tripartite motif-containing 39	Trim39	-0.295	0.000456349
1450436_s_at	DnaJ (Hsp40) homolog, subfamily B, member	Dnajb5	-0.295	0.003683356

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1454007_a_at	zinc finger protein 142	Zfp142	-0.295	0.005321202
1418896_a_at	ribophorin II	Rpn2	-0.296	0.000304398
1428468_at	RIKEN cDNA 3110043O21 gene	3110043O21Rik	-0.296	0.001340357
1437009_a_at	ring finger protein 115	Rnf115	-0.296	0.000680958
1450710_at	jumonji, AT rich interactive domain 2	Jarid2	-0.296	0.001751768
1415746_at	capicua homolog (Drosophila)	Cic	-0.296	0.000978687
1424913_at	RIKEN cDNA 2310044G17 gene	2310044G17Rik	-0.296	0.010649154
1427353_at	CLIP associating protein 1	Clasp1	-0.296	0.014647925
1422206_at	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	B3galt1	-0.296	0.002243616
1425831_at	zinc finger protein 101	Zfp101	-0.296	0.000439052
1427677_a_at	SRY-box containing gene 6	Sox6	-0.296	0.004116732
1438215_at	splicing factor, arginine/serine-rich 3 (SRp20)	Sfrs3	-0.296	0.017812409
1433477_at	active BCR-related gene	Abr	-0.296	0.007219883
1420744_at	cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal)	Chrnb2	-0.296	0.012150561
1454229_a_at	exonuclease domain containing 1	Exod1	-0.297	0.001878306
1436487_x_at	F-box and WD-40 domain protein 2	Fbxw2	-0.297	0.004766768
1437844_x_at	component of oligomeric golgi complex 1	Cog1	-0.297	0.002262753
1427278_at	CAP-GLY domain containing linker protein family, member 4	Clip4	-0.297	0.004185703
1451227_a_at	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	Slc10a3	-0.297	0.000440407
1434348_at	fasciculation and elongation protein zeta 2 (zygin II)	Fez2	-0.297	0.000383532
1417241_at	archaelysin family metallopeptidase 2	Amz2	-0.297	0.000400173
1424299_at	OMA1 homolog, zinc metallopeptidase (S. cerevisiae)	Oma1	-0.297	0.000339677
1451337_at	proteasome (prosome, macropain) inhibitor subunit 1	Psmf1	-0.297	0.000276064
1426117_a_at	solute carrier family 19 (thiamine transporter), member 2	Slc19a2	-0.298	0.019053653
1434471_at	cDNA sequence BC003331	BC003331	-0.298	0.004620133
1417045_at	BH3 interacting domain death agonist	Bid	-0.298	9.61E-05
1449192_at	activating transcription factor 7 interacting protein	Atf7ip	-0.298	0.000251046
1423695_at	ER degradation enhancer, mannosidase alpha-like 2	Edem2	-0.298	0.000388448
1448480_at	nuclear import 7 homolog (S. cerevisiae)	Nip7	-0.298	0.000910923
1437159_at	NA	NA	-0.298	0.000653779
1427679_at	large tumor suppressor	Lats1	-0.298	0.014545515
1438510_a_at	histidyl-tRNA synthetase	Hars	-0.298	0.000284842
1420684_at	acyl-Coenzyme A oxidase 3, pristanoyl	Acox3	-0.298	0.003303902
1433514_at	ethanolamine kinase 1	Etnk1	-0.299	0.000543883
1416190_a_at	Sec61 alpha 1 subunit (S. cerevisiae)	Sec61a1	-0.299	0.002121635
1416656_at	chloride intracellular channel 1	Clic1	-0.299	0.000251387
1450964_a_at	oxysterol binding protein-like 9	Osbpl9	-0.299	0.001961749
1419371_s_at	golgi SNAP receptor complex member 2	Gosr2	-0.299	7.08E-05
1453412_a_at	SEC14-like 1 (S. cerevisiae)	Sec14l1	-0.3	0.000476531
1460384_a_at	AT rich interactive domain 4B (RBP1-like)	Arid4b	-0.3	0.001633167
1422572_at	ras homolog gene family, member G	Rhog	-0.3	0.000522418
1450656_at	guanine nucleotide binding protein, alpha 13	Gna13	-0.3	0.000474112
1452376_at	zinc finger protein 444	Zfp444	-0.3	0.006252908
1423204_at	transmembrane 9 superfamily protein member 4	Tm9sf4	-0.3	0.000321995
1421906_at	mediator complex subunit 1	Med1	-0.3	0.011164066
1420835_at	solute carrier family 25, member 30	Slc25a30	-0.3	0.000520076

1425340_a_at	protein tyrosine phosphatase, receptor type, A	Ptpra	-0.3	0.000799253
1437683_x_at	small EDRK-rich factor 2	Serf2	-0.3	0.00055338
1448159_at	RAB7, member RAS oncogene family	Rab7	-0.3	0.00124862
1416191_at	Sec61 alpha 1 subunit (S. cerevisiae)	Sec61a1	-0.3	0.001182551
1418781_at	NAT9	Nat9	-0.3	0.001721974
1424916_x_at	zinc finger protein 764	Zfp764	-0.3	0.000858847
1420997_a_at	glucose phosphate isomerase 1	Gpi1	-0.3	0.000927755
1448538_a_at	DNA segment, Chr 4, Wayne State University 53, expressed	D4Wsu53e	-0.3	0.013696364
1427228_at	palladin, cytoskeletal associated protein	Palld	-0.3	0.000473058
1420509_at	serum response factor binding protein 1	Srfbp1	-0.3	0.00055652
1426745_at	ribonuclease, RNase K	Rnasek	-0.3	0.001018583
1418636_at	ets variant gene 3	Etv3	-0.3	0.016096995
1426618_a_at	protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase	Pomgnt1	-0.301	0.00016034
1421759_a_at	forkhead box K1	Foxk1	-0.301	0.010515289
1417090_at	reticulocalbin 1	Rcn1	-0.301	0.000116582
1460688_s_at	unc-119 homolog B (C. elegans)	Unc119b	-0.301	0.00011845
1421866_at	nuclear receptor subfamily 3, group C, member 1	Nr3c1	-0.301	0.013499518
1428820_at	microtubule-associated protein, RP/EB family, member 1	Mapre1	-0.301	0.006792957
1448247_at	B-cell CLL/lymphoma 7B	Bcl7b	-0.301	0.000984998
1420472_at	myotrophin	Mtpn	-0.301	0.017025641
1452382_at	dynamin 3, opposite strand	Dnm3os	-0.301	0.00576556
1449440_at	lipin 3	Lpin3	-0.301	0.012005182
1429170_a_at	metal response element binding transcription factor 1	Mtf1	-0.301	0.000924564
1419667_at	sarcoglycan, beta (dystrophin-associated glycoprotein)	Sgcb	-0.301	0.00676859
1438070_at	PHD finger protein 3	Phf3	-0.301	0.002341302
1427984_at	SUMO/sentrin specific peptidase 6	Senp6	-0.301	0.006452524
1423874_at	WD repeat domain 33	Wdr33	-0.302	0.016172439
1424726_at	transmembrane protein 150	Tmem150	-0.302	0.000411749
1420022_s_at	NA	NA	-0.302	0.037423457
1425755_at	mature T-cell proliferation 1	Mtcp1	-0.302	0.003069136
1452837_at	lipin 2	Lpin2	-0.302	0.000640433
1426446_at	RIKEN cDNA 6430548M08 gene	6430548M08Rik	-0.302	0.000472045
1426523_a_at	glucosamine-6-phosphate deaminase 2	Gnpda2	-0.302	0.004334426
1421334_x_at	myoneurin	Mynn	-0.302	0.00423209
1455475_at	RIKEN cDNA 3110057O12 gene	3110057O12Rik	-0.302	0.003853625
1450253_a_at	mitogen-activated protein kinase kinase kinase 4	Map3k4	-0.302	0.000651305
1415802_at	solute carrier family 16 (monocarboxylic acid transporters), member 1	Slc16a1	-0.303	0.000245104
1435039_a_at	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	Pip5k1a	-0.303	0.000498525
1425659_at	target of myb1-like 2 (chicken)	Tom1l2	-0.303	0.010162575
1416067_at	interferon-related developmental regulator 1	Ifrd1	-0.303	0.000121146
1429227_x_at	nucleosome assembly protein 1-like 1	Nap1l1	-0.303	9.00E-05
1425490_a_at	WD repeat domain 13	Wdr13	-0.303	0.003269118
1449128_at	coiled-coil domain containing 43	Ccdc43	-0.304	0.002975281
1427155_at	RELT-like 2	Rell2	-0.304	0.004650485
1417369_at	hydroxysteroid (17-beta) dehydrogenase 4	Hsd17b4	-0.304	0.000114511
1451747_a_at	autophagy-related 12 (yeast)	Atg12	-0.304	0.000217293
1420004_s_at	NOL1/NOP2/Sun domain family, member 5	Nsun5	-0.304	0.002250175
1427342_at	FAST kinase domains 1	Fastkd1	-0.304	0.00021056

1425393_a_at	mitogen-activated protein kinase kinase 7	Map2k7	-0.304	0.007251644
1424571_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	Ddx46	-0.304	0.001246553
1422810_at	zinc finger protein 191	Zfp191	-0.304	0.000137496
1448597_at	cleavage stimulation factor, 3' pre-RNA, subunit 1	Cstf1	-0.304	0.000251085
1416611_at	secretory carrier membrane protein 2	Scamp2	-0.304	0.000199386
1419612_at	RIKEN cDNA 4632415L05 gene	4632415L05Rik	-0.304	0.017630735
1456262_at	RNA binding motif protein 5	Rbm5	-0.304	0.004431943
1417510_at	vacuolar protein sorting 4a (yeast)	Vps4a	-0.304	0.000174101
1434975_x_at	RIKEN cDNA 4933439C20 gene	4933439C20Rik	-0.304	0.000800295
1415738_at	thioredoxin domain containing 12 (endoplasmic reticulum)	Txndc12	-0.304	0.000121288
1418505_at	nudix (nucleoside diphosphate linked moiety X)-type motif 4	Nudt4	-0.305	0.000723345
1451111_at	nucleoporin 133	Nup133	-0.305	0.00428284
1448722_s_at	phosphopantothenoylcysteine synthetase	Ppcs	-0.305	0.007494673
1449217_at	caspase 8 associated protein 2	Casp8ap2	-0.305	0.009111327
1416530_a_at	purine-nucleoside phosphorylase 1	Pnp1	-0.305	0.002016742
1427216_at	interferon zeta	Ifnz	-0.305	0.001754419
1419954_s_at	zinc finger, AN1-type domain 3	Zfand3	-0.305	0.000678926
1448535_at	elongation protein 4 homolog (S. cerevisiae)	Elp4	-0.305	0.001667557
1448310_at	intestinal cell kinase	Ick	-0.305	0.000418995
1426494_at	RNA (guanine-9-) methyltransferase domain containing 3	Rg9mtd3	-0.305	0.000186589
1450987_a_at	RIKEN cDNA 2310004I24 gene	2310004I24Rik	-0.305	0.000201302
1428997_at	PHD finger protein 23	Phf23	-0.306	0.000491325
1449884_at	EF-hand calcium binding domain 2	Efcab2	-0.306	0.005667121
1452667_at	RAB2B, member RAS oncogene family	Rab2b	-0.306	0.001499859
1423383_a_at	oxysterol binding protein-like 9	Osbpl9	-0.306	0.00125038
1451125_at	poly(A) binding protein interacting protein 2B	Paip2b	-0.306	0.000160857
1418712_at	CDC42 effector protein (Rho GTPase binding) 5	Cdc42ep5	-0.306	0.007419481
1421139_a_at	zinc finger protein 386 (Kruppel-like)	Zfp386	-0.306	0.002192403
1417033_at	ubiquitin-conjugating enzyme E2G 2	Ube2g2	-0.306	0.002310148
1421967_at	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	B4galt5	-0.306	0.003425376
1419470_at	guanine nucleotide binding protein (G protein), beta 4	Gnb4	-0.306	0.001979902
1417870_x_at	cathepsin Z	Ctsz	-0.306	0.000539749
1425248_a_at	TYRO3 protein tyrosine kinase 3	Tyro3	-0.306	0.004663707
1416233_at	eukaryotic translation initiation factor 3, subunit I	Eif3i	-0.306	0.00030412
1429555_at	claudin domain containing 1	Cldnd1	-0.306	0.005260066
1424201_a_at	SEH1-like (S. cerevisiae	Seh1l	-0.306	0.021390998
1460381_at	cDNA sequence BC023179	BC023179	-0.306	0.004840079
1425532_a_at	bridging integrator 1	Bin1	-0.307	0.000844073
1455191_x_at	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	Pip5k1a	-0.307	0.001633942
1460320_at	beclin 1, autophagy related	Becn1	-0.307	0.000199919
1422044_at	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	Ndst1	-0.307	0.015705847
1451252_at	interferon regulatory factor 2 binding protein 1	Irf2bp1	-0.307	0.000157826
1420124_s_at	T-cell leukemia translocation altered gene	Tcta	-0.307	0.001179389
1448271_a_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	Ddx21	-0.307	0.003479755
1448943_at	neuropilin 1	Nrp1	-0.307	0.006639223
1420640_at	junction-mediating and regulatory protein	Jmy	-0.307	0.00053499
1425642_at	centrosomal protein 290	Cep290	-0.307	0.000613456

1420953_at	adducin 1 (alpha)	Add1	-0.307	0.000436267
1455975_x_at	ring finger protein 114	Rnf114	-0.307	8.48E-05
1426234_s_at	cDNA sequence BC002199	BC002199	-0.307	7.29E-05
1428097_at	RIKEN cDNA 2510009E07 gene	2510009E07Rik	-0.308	0.045568273
1460665_a_at	CCR4-NOT transcription complex, subunit 7	Cnot7	-0.308	0.003883427
1447631_at	MYST histone acetyltransferase 2	Myst2	-0.308	0.001019402
1451495_at	WW domain containing adaptor with coiled-coil	Wac	-0.308	0.004605537
1416751_a_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	Ddx20	-0.308	9.85E-05
1427189_at	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila)	Arih1	-0.308	0.001570342
1439408_a_at	mediator complex subunit 1	Med1	-0.308	0.003150246
1460725_at	xeroderma pigmentosum, complementation group A	Xpa	-0.308	0.000639236
1451017_at	ERGIC and golgi 3	Ergic3	-0.308	0.000884362
1450634_at	ATPase, H+ transporting, lysosomal V1 subunit A	Atp6v1a	-0.308	0.001216283
1429533_at	inner membrane protein, mitochondrial	Immt	-0.308	0.003583037
1423206_s_at	RIKEN cDNA 2310003F16 gene	2310003F16Rik	-0.308	0.000461109
1429761_at	reticulon 1	Rtn1	-0.308	0.00307758
1417980_a_at	insulin induced gene 2	Insig2	-0.308	0.000545425
1415770_at	WD repeat domain 6	Wdr6	-0.308	0.000153721
1433745_at	triple functional domain (PTPRF interacting)	Trio	-0.308	0.001027552
1427062_at	retinoblastoma binding protein 8	Rbbp8	-0.308	0.001509159
1427258_at	tripartite motif-containing 24	Trim24	-0.309	0.00091581
1426699_at	expressed sequence AU040320	AU040320	-0.309	0.001822853
1420025_s_at	AP2 associated kinase 1	Aak1	-0.309	0.00526166
1427063_at	RIKEN cDNA 5330417C22 gene	5330417C22Rik	-0.309	0.001110754
1438377_x_at	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	Slc13a3	-0.309	0.001059399
1450762_s_at	zinc finger protein 191	Zfp191	-0.309	0.009542819
1452393_at	AT-hook transcription factor	Akna	-0.309	0.002126598
1434768_at	tripeptidyl peptidase I	Tpp1	-0.309	0.000307952
1449915_at	zinc finger protein 202	Zfp202	-0.309	0.007816319
1421904_at	trimethylguanosine synthase homolog (S. cerevisiae)	Tgs1	-0.309	0.000764126
1442006_at	NA	NA	-0.309	0.000153197
1449115_at	metal response element binding transcription factor 2	Mtf2	-0.309	0.000599868
1450860_at	leucine aminopeptidase 3	Lap3	-0.309	0.000666048
1425206_a_at	ubiquitin protein ligase E3A	Ube3a	-0.31	0.011787074
1426434_at	transmembrane protein 43	Tmem43	-0.31	0.000598826
1449519_at	growth arrest and DNA-damage-inducible 45 alpha	Gadd45a	-0.31	0.001675667
1451805_at	pleckstrin homology domain interacting protein	Phip	-0.31	0.006561673
1425592_at	transportin 2 (importin 3, karyopherin beta 2b)	Tnpo2	-0.31	0.003480271
1435517_x_at	v-ral simian leukemia viral oncogene homolog B (ras related)	Ralb	-0.31	0.001015961
1421216_a_at	iduronate 2-sulfatase	Ids	-0.31	0.013179543
1432270_a_at	chromatin modifying protein 5	Chmp5	-0.31	0.000732918
1416602_a_at	RAD52 homolog (S. cerevisiae)	Rad52	-0.31	0.000928545
1418576_at	Yip1 domain family, member 5	Yipf5	-0.31	9.63E-05
1451544_at	TAP binding protein-like	Tapbpl	-0.311	0.000653779
1422691_at	serine palmitoyltransferase, long chain base subunit 1	Sptlc1	-0.311	0.001112352
1425565_at	RE1-silencing transcription factor	Rest	-0.311	0.000931599
1448339_at	transmembrane protein 30A	Tmem30a	-0.311	0.001270448
1452286_at	SLAIN motif family, member 2	Slain2	-0.311	0.000373555

1427622_at	maternal embryonic message 1	Mem1	-0.311	0.000525255
1421553_at	epilepsy, progressive myoclonic epilepsy, type 2 gene alpha	Epm2a	-0.311	0.000817798
1424244_at	RWD domain containing 4A	Rwdd4a	-0.311	0.001418521
1430124_x_at	aldo-keto reductase family 1, member A4 (aldehyde reductase)	Akr1a4	-0.311	6.29E-05
1424539_at	ubiquitin-like 4	Ubl4	-0.311	0.000265239
1451997_at	zinc finger protein 426	Zfp426	-0.311	0.003332917
1425410_at	Tp53rk binding protein	Tprkb	-0.311	0.007719137
1456567_x_at	granulin	Grn	-0.312	0.000134159
1426777_a_at	Wiskott-Aldrich syndrome-like (human)	Wasl	-0.312	0.011304507
1448836_s_at	GPN-loop GTPase 2	Gpn2	-0.312	0.001021956
1423605_a_at	transformed mouse 3T3 cell double minute 2	Mdm2	-0.312	0.000316837
1450742_at	bystin-like	Bysl	-0.312	0.000114923
1417412_at	factor 8-associated gene A	F8a	-0.312	0.000136558
1421582_a_at	cAMP responsive element binding protein 1	Creb1	-0.313	0.019330118
1422883_at	ubiquitin specific peptidase 8	Usp8	-0.313	0.00074165
1428904_at	AMME chromosomal region gene 1-like	Ammecr1l	-0.313	0.000118465
1421720_a_at	deltex 2 homolog (Drosophila)	Dtx2	-0.313	0.001330646
1460192_at	oxysterol binding protein-like 1A	Osbpl1a	-0.313	0.000651686
1418495_at	zinc finger CCCH type containing 8	Zc3h8	-0.313	0.007724196
1448429_at	glycogenin	Gyg	-0.313	0.000245756
1451556_a_at	RIKEN cDNA 2700078E11 gene	2700078E11Rik	-0.313	0.000128132
1417512_at	ecotropic viral integration site 5	Evi5	-0.314	0.001881724
1450804_at	kinesin family member 5C	Kif5c	-0.314	0.004401595
1424542_at	S100 calcium binding protein A4	S100a4	-0.314	0.001010911
1427959_at	abhydrolase domain containing 10	Abhd10	-0.314	0.000320103
1426796_at	karyopherin (importin) alpha 6	Kpna6	-0.314	0.000357255
1423044_at	proline synthetase co-transcribed	Prosc	-0.314	0.000151935
1436149_at	cytochrome c oxidase, subunit Vb	Cox5b	-0.314	0.001257763
1428135_a_at	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	Eef1d	-0.315	0.003304522
1460191_at	YKT6 homolog (S. Cerevisiae)	Ykt6	-0.315	0.003659116
1450872_s_at	lysosomal acid lipase A	Lipa	-0.315	0.000252335
1418482_at	cytochrome b-561 domain containing 2	Cyb561d2	-0.315	0.000419084
1423089_at	tropomodulin 3	Tmod3	-0.315	0.011341856
1456405_at	death inducer-obliterator 1	Dido1	-0.315	0.000482105
1460733_at	unc-119 homolog B (C. elegans)	Unc119b	-0.315	0.000430937
1449615_s_at	high density lipoprotein (HDL) binding protein	Hdlbp	-0.315	0.035292686
1452636_x_at	GTP binding protein 5	Gtpbp5	-0.315	0.000418984
1452497_a_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	Nfatc3	-0.315	0.000830373
1425366_a_at	Hus1 homolog (S. pombe)	Hus1	-0.315	0.007451031
1423309_at	trans-golgi network protein	Tgoln1	-0.315	0.000203124
1448892_at	dedicator of cytokinesis 7	Dock7	-0.315	0.000536288
1420951_a_at	Son DNA binding protein	Son	-0.315	0.001251851
1439263_at	deafness, autosomal dominant 5 homolog (human)	Dfna5h	-0.315	0.008043663
1448947_at	RIKEN cDNA 2810004N23 gene	2810004N23Rik	-0.315	0.000992609
1460168_at	stem-loop binding protein	Slbp	-0.316	7.64E-05
1452422_a_at	U2 small nuclear ribonucleoprotein B	Snrpb2	-0.316	0.000774945
1452115_a_at	polo-like kinase 4 (Drosophila)	Plk4	-0.316	0.0101589
1451503_at	nucleolar protein 3 (apoptosis repressor with CARD domain)	Nol3	-0.316	0.006790197
1437256_at	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	Dcun1d5	-0.316	0.003640489
1417376_a_at	cell adhesion molecule 1	Cadm1	-0.316	0.00212689

1450028_a_at	LanC (bacterial lantibiotic synthetase component C)-like 2	Lancl2	-0.316	6.98E-05
1450030_at	dynactin 4	Dctn4	-0.316	0.008124855
1437103_at	insulin-like growth factor 2 mRNA binding protein 2	Igf2bp2	-0.316	0.002065785
1425616_a_at	coiled-coil domain containing 23	Ccdc23	-0.316	0.000229369
1421348_a_at	cell cycle exit and neuronal differentiation 1	Cend1	-0.316	0.004693422
1427707_a_at	Scl/Tal1 interrupting locus	Stil	-0.316	0.001186759
1432004_a_at	dynamin 2	Dnm2	-0.316	0.044609122
1418780_at	cytochrome P450, family 39, subfamily a, polypeptide 1	Cyp39a1	-0.317	0.024901241
1450247_a_at	secretory carrier membrane protein 5	Scamp5	-0.317	0.000549486
1448120_at	growth differentiation factor 9	Gdf9	-0.317	0.003586148
1416881_at	myeloid cell leukemia sequence 1	Mcl1	-0.317	0.000892118
1424039_at	transmembrane protein 66	Tmem66	-0.317	0.000197288
1430032_at	RNA binding motif protein 4B	Rbm4b	-0.317	0.007292999
1422537_a_at	inhibitor of DNA binding 2	Id2	-0.317	0.022181647
1415717_at	ring finger protein 220	Rnf220	-0.317	0.000381445
1437050_s_at	angel homolog 2 (Drosophila)	Angel2	-0.317	0.000600492
1451269_at	PDZ domain containing 11	Pdzd11	-0.317	7.21E-05
1434109_at	SH3 domain binding glutamic acid-rich protein like 2	Sh3bgrl2	-0.317	0.000503289
1431675_a_at	general transcription factor II I	Gtf2i	-0.317	0.026661789
1434702_at	RIKEN cDNA 2600009E05 gene	2600009E05Rik	-0.317	0.000352469
1451793_at	kelch-like 24 (Drosophila)	Klhl24	-0.318	0.011480308
1448256_at	golgi SNAP receptor complex member 1	Gosr1	-0.318	0.002558659
1437882_s_at	RIKEN cDNA 6330416L07 gene	6330416L07Rik	-0.318	0.009622547
1421972_s_at	host cell factor C1	Hcfc1	-0.318	0.001213112
1426703_at	cyclin G associated kinase	Gak	-0.318	0.000898496
1418662_at	RIKEN cDNA 2210012G02 gene	2210012G02Rik	-0.318	0.00179184
1432144_a_at	ring finger and CHY zinc finger domain containing 1	Rchy1	-0.318	0.000746584
AFFX-TransRecMur/X57349_M_at	transferrin receptor	Tfrc	-0.318	0.018275283
1431722_a_at	arylformamidase	Afmid	-0.318	0.010567243
1417677_at	opsin 3	Opn3	-0.318	0.001162196
1430487_at	AU RNA binding protein/enoyl-coenzyme A hydratase	Auh	-0.318	0.01173367
1420827_a_at	cyclin G1	Ccng1	-0.319	0.000304167
1448343_a_at	neighbor of Brca1 gene 1	Nbr1	-0.319	5.85E-05
1436944_x_at	RIKEN cDNA 4933439C20 gene	4933439C20Rik	-0.319	0.000421669
1420933_a_at	eyes absent 3 homolog (Drosophila)	Eya3	-0.319	0.002550927
1448737_at	tetraspanin 7	Tspan7	-0.319	0.000125381
1455905_at	RIKEN cDNA 2610507B11 gene	2610507B11Rik	-0.319	0.02037956
1419190_at	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	Vti1a	-0.319	0.001528092
1448832_a_at	complexin 1	Cplx1	-0.319	0.000117095
1460490_at	mitochondrial ribosomal protein L15	Mrpl15	-0.319	0.000720759
1427990_at	ubiquitin specific petidase 45	Usp45	-0.319	0.003057962
1425411_at	ADP-ribosylation factor-like 4A	Arl4a	-0.319	0.038590028
1427425_at	RIKEN cDNA 9130208E07 gene	9130208E07Rik	-0.32	0.007936815
1425405_a_at	adenosine deaminase, RNA-specific	Adar	-0.32	0.00104611
1421785_at	UEV and lactate/malate dehyrogenase domains	Uevld	-0.32	0.010678352
1418244_at	N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae)	Nat5	-0.32	0.000479263

1434054_at	sirtuin 7 (silent mating type information regulation 2, homolog) 7 (S. cerevisiae)	Sirt7	-0.32	0.005767981
1438415_s_at	coactivator-associated arginine methyltransferase 1	Carm1	-0.32	0.007544129
1452438_s_at	TAF4A RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf4a	-0.32	0.000534333
1460356_at	endothelial cell-specific adhesion molecule	Esam	-0.32	0.00101805
1435133_at	UDP-glucose ceramide glucosyltransferase	Ugcg	-0.32	0.000136558
1451081_a_at	transcription factor 25 (basic helix-loop-helix)	Tcf25	-0.32	0.000357743
1436900_x_at	leptin receptor overlapping transcript	Leprot	-0.32	0.000980194
1430708_a_at	ubiquitin specific petidase 45	Usp45	-0.32	0.002046765
1434167_at	solute carrier family 35, member E4	Slc35e4	-0.32	0.011904837
1418965_at	nitric oxide synthase interacting protein	Nosip	-0.32	0.00033761
1424947_at	dynein cytoplasmic 1 light intermediate chain 1	Dync1li1	-0.32	0.020060108
1438097_at	RAB20, member RAS oncogene family	Rab20	-0.321	0.006867652
1417279_at	inositol 1,4,5-triphosphate receptor 1	Itpr1	-0.321	0.002816308
1454914_at	RIKEN cDNA 2610101N10 gene	2610101N10Rik	-0.321	0.000619476
1425348_a_at	signal recognition particle receptor, B subunit	Srprb	-0.321	0.001383107
1424276_at	sorting nexin 16	Snx16	-0.321	0.001251838
1434625_at	RIKEN cDNA 4930432O21 gene	4930432O21Rik	-0.321	0.002489949
1422508_at	ATPase, H+ transporting, lysosomal V1 subunit A	Atp6v1a	-0.322	0.001352554
1428241_at	RIKEN cDNA 2310035K24 gene	2310035K24Rik	-0.322	0.000720357
1448454_at	splicing factor, arginine/serine-rich 6	Sfrs6	-0.322	0.00032839
1417527_at	adaptor-related protein complex 3, mu 2 subunit	Ap3m2	-0.322	0.001333158
1423584_at	polymerase (RNA) II (DNA directed) polypeptide B	Polr2b	-0.322	0.001559542
1423363_at	sortilin 1	Sort1	-0.322	0.003513701
1418371_at	dynein light chain LC8-type 2	Dynll2	-0.322	0.000833728
1435335_a_at	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	Gnptab	-0.322	0.000182157
1426963_at	phosphofurin acidic cluster sorting protein 2	Pacs2	-0.322	0.0001213
1452612_at	zinc finger protein 294	Zfp294	-0.322	0.000589622
1426753_at	PHD finger protein 17	Phf17	-0.322	0.017697331
1430271_x_at	Josephin domain containing 3	Josd3	-0.322	0.00027013
1450104_at	a disintegrin and metallopeptidase domain 10	Adam10	-0.322	0.002154162
1417981_at	insulin induced gene 2	Insig2	-0.322	0.000216236
1420475_at	myotrophin	Mtpn	-0.322	0.00154427
1425739_at	phospholipase D1	Pld1	-0.323	0.001716741
1452254_at	myotubularin related protein 9	Mtmr9	-0.323	0.000611962
1449318_at	tubulin, gamma 2	Tubg2	-0.323	0.000768383
1433723_s_at	small EDRK-rich factor 2	Serf2	-0.323	0.001941384
1419250_a_at	PFTAIRE protein kinase 1	Pftk1	-0.323	0.004623308
1453005_at	PRP31 pre-mRNA processing factor 31 homolog (yeast)	Prpf31	-0.323	0.000187826
1417377_at	cell adhesion molecule 1	Cadm1	-0.323	8.62E-05
1421850_at	microtubule-associated protein 1B	Mtap1b	-0.323	0.010910797
1425550_a_at	protein kinase, cAMP dependent regulatory, type I, alpha	Prkar1a	-0.323	0.00017463
1422795_at	cullin 3	Cul3	-0.324	0.023192285
1421050_at	vacuolar protein sorting 25 (yeast)	Vps25	-0.324	0.001792492
1450733_at	bicaudal D homolog 2 (Drosophila)	Bicd2	-0.324	0.000853874
1436670_x_at	RIKEN cDNA 1700019G17 gene	1700019G17Rik	-0.324	0.000156202
1423930_at	anaphase promoting complex subunit 4	Anapc4	-0.324	0.000182995
1448916_at	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian)	Mafg	-0.324	0.000263551

1424658_at	TAO kinase 1	Taok1	-0.324	0.018839757
1439075_at	polymerase (RNA) III (DNA directed) polypeptide F	Polr3f	-0.324	0.000111397
1452629_at	scaffold attachment factor B2	Safb2	-0.324	0.005881251
1424391_at	nardilysin, N-arginine dibasic convertase, NRD convertase 1	Nrd1	-0.324	0.00021596
1420889_at	holocytochrome c synthetase	Hccs	-0.325	0.002774255
1435137_s_at	RIKEN cDNA 1200016E24 gene	1200016E24Rik	-0.325	0.000170923
1416461_at	cell cycle associated protein 1	Caprin1	-0.325	0.000341304
1450408_at	chloride channel 7	Clcn7	-0.325	0.001097198
1420476_a_at	nucleosome assembly protein 1-like 1	Nap1l1	-0.325	0.000456116
1430125_s_at	PQ loop repeat containing 1	Pqlc1	-0.325	0.000123714
1451368_at	asparagine-linked glycosylation 1 homolog (yeast, beta-1,4-mannosyltransferase)	Alg1	-0.325	0.000108698
1422791_at	platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit	Pafah1b2	-0.325	0.005462642
1424126_at	aminolevulinic acid synthase 1	Alas1	-0.325	0.003196141
1451296_x_at	poly A binding protein, cytoplasmic 4	Pabpc4	-0.326	0.000361479
1433805_at	Janus kinase 1	Jak1	-0.326	0.000138654
1426584_a_at	sorbitol dehydrogenase	Sord	-0.326	0.000313075
1415789_a_at	similar to ubiquitin-like domain containing CTD phosphatase 1	LOC100045709	-0.326	0.004972821
1450957_a_at	sequestosome 1	Sqstm1	-0.326	8.49E-05
1417874_at	TMEM9 domain family, member B	Tmem9b	-0.326	0.00050575
1430989_a_at	RIKEN cDNA 1700020I14 gene	1700020I14Rik	-0.326	0.011210252
1423649_at	transmembrane protein 68	Tmem68	-0.326	0.000533883
1421320_a_at	queuine tRNA-ribosyltransferase domain containing 1	Qtrtd1	-0.327	0.012868925
1418189_s_at	receptor (calcitonin) activity modifying protein 2	Ramp2	-0.327	0.001224493
1448667_x_at	transducer of ERBB2, 2	Tob2	-0.327	0.000863054
1418964_at	phosphatidylinositol glycan anchor biosynthesis, class M	Pigm	-0.327	0.000463266
1449094_at	gap junction protein, gamma 1	Gjc1	-0.327	7.21E-05
1433901_at	cell cycle associated protein 1	Caprin1	-0.327	0.000138435
1416928_at	RNA binding motif protein 12	Rbm12	-0.327	0.000167717
1422995_at	BCL2 modifying factor	Bmf	-0.327	0.002761668
1434541_x_at	KH domain containing, RNA binding, signal transduction associated 1	Khdrbs1	-0.327	0.000336283
1434546_at	Smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)	Smg5	-0.327	0.001622216
1418160_at	makorin, ring finger protein, 3	Mkrn3	-0.327	0.001361177
1426979_at	MLX interacting protein	Mlxip	-0.327	0.0002541
1421847_at	WD repeat and SOCS box-containing 2	Wsb2	-0.327	8.09E-05
1425641_at	AF4/FMR2 family, member 1	Aff1	-0.327	0.013243638
1419988_at	mitogen-activated protein kinase kinase kinase 7	Map3k7	-0.327	0.000248066
1419635_at	RIKEN cDNA 4833420G17 gene	4833420G17Rik	-0.327	0.001588006
1422018_at	human immunodeficiency virus type I enhancer binding protein 2	Hivep2	-0.327	0.000763374
1434585_at	tubby like protein 4	Tulp4	-0.327	0.000344418
1417112_at	ADP-ribosylation factor-like 2 binding protein	Arl2bp	-0.327	7.41E-05
1416653_at	syntaxin binding protein 3A	Stxbp3a	-0.328	5.33E-05
1435681_s_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	Ddx49	-0.328	0.01496718
1425948_a_at	solute carrier family 25, member 30	Slc25a30	-0.328	0.003027071
1451183_at	myosin XIX	Myo19	-0.328	8.11E-05
1422769_at	synaptotagmin binding, cytoplasmic RNA interacting protein	Syncrip	-0.329	0.00096708
1426559_at	sno, strawberry notch homolog 1 (Drosophila)	Sbno1	-0.329	0.000635454

1416294_at	secretory carrier membrane protein 3	Scamp3	-0.329	0.000144344
1419249_at	PFTAIRE protein kinase 1	Pftk1	-0.329	0.000473331
1415723_at	eukaryotic translation initiation factor 5	Eif5	-0.329	6.89E-05
1415843_at	G protein beta subunit-like	Gbl	-0.329	0.000576634
1451773_s_at	polymerase (RNA) III (DNA directed) polypeptide F	Polr3f	-0.329	0.00269288
1419382_a_at	dehydrogenase/reductase (SDR family) member 4	Dhrs4	-0.329	0.000636901
1417456_at	glyceronephosphate O-acyltransferase	Gnpat	-0.329	0.000985554
1454236_a_at	RIKEN cDNA C030004A17Rik	C030004A17Rik	-0.329	0.000375765
1415880_a_at	lysosomal-associated membrane protein 1	Lamp1	-0.33	6.11E-05
1418587_at	Tnf receptor-associated factor 3	Traf3	-0.33	0.000185345
1418955_at	zinc finger protein 93	Zfp93	-0.33	0.000522418
1420528_at	G patch domain containing 2	Gpatch2	-0.33	0.000474202
1434071_a_at	pelota homolog (Drosophila)	Pelo	-0.33	0.001280019
1417191_at	DnaJ (Hsp40) homolog, subfamily B, member 9	Dnajb9	-0.33	0.000743379
1419235_s_at	helicase (DNA) B	Helb	-0.33	0.000772155
1455504_a_at	makorin, ring finger protein, 1	Mkrn1	-0.33	0.00151013
1452057_at	ARP1 actin-related protein 1 homolog B, centractin beta (yeast)	Actr1b	-0.33	0.000149179
1421157_at	frizzled homolog 3 (Drosophila)	Fzd3	-0.33	0.00063696
1450168_at	ankyrin repeat domain 12	Ankrd12	-0.33	0.001609565
1419236_at	helicase (DNA) B	Helb	-0.33	0.000717887
1460486_at	RAB GTPase activating protein 1	Rabgap1	-0.331	0.002606601
1421208_at	inhibitor of kappaB kinase gamma	Ikbkg	-0.331	0.005677601
1451322_at	carboxymethylenebutenolidase-like (Pseudomonas)	Cmbl	-0.331	0.000338036
1426734_at	cDNA sequence BC022623	BC022623	-0.331	0.000254712
1421275_s_at	suppressor of cytokine signaling 4	Socs4	-0.331	0.001649039
1430123_a_at	aldo-keto reductase family 1, member A4 (aldehyde reductase)	Akr1a4	-0.331	8.33E-05
1456577_x_at	pitrilysin metallepetidase 1	Pitrm1	-0.331	0.006020125
1449878_a_at	solute carrier family 12, member 6	Slc12a6	-0.331	0.000772155
1417783_at	amyotrophic lateral sclerosis 2 (juvenile) homolog (human)	Als2	-0.331	0.000171466
1453712_a_at	mitogen-activated protein kinase kinase 5	Map2k5	-0.331	0.008938647
1415868_at	chaperonin containing Tcp1, subunit 4 (delta)	Cct4	-0.331	0.000132427
1425076_at	DnaJ (Hsp40) homolog, subfamily C, member 18	Dnajc18	-0.331	9.00E-05
1417329_at	solute carrier family 23 (nucleobase transporters), member 2	Slc23a2	-0.332	0.00011845
1423615_at	ring finger protein 115	Rnf115	-0.332	0.000597995
1456097_a_at	integrin beta 3 binding protein (beta3-endonexin)	Itgb3bp	-0.332	0.001657828
1439295_x_at	predicted gene, EG434179	EG434179	-0.332	0.000435373
1435333_at	RIKEN cDNA 1110007M04 gene	1110007M04Rik	-0.332	0.000294703
1427317_at	antigenic determinant of rec-A protein	Kin	-0.332	0.000138364
1426303_at	xylosylprotein beta1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)	B4galt7	-0.332	0.001480989
1437062_s_at	RIKEN cDNA 1200015N20 gene	1200015N20Rik	-0.332	0.006642723
1454947_a_at	ubiquitin-like domain containing CTD phosphatase 1	Ublcp1	-0.332	0.001191045
1416430_at	catalase	Cat	-0.332	0.0003979
1417746_at	complexin 1	Cplx1	-0.332	0.00039485
1452253_at	cysteine rich transmembrane BMP regulator 1 (chordin like)	Crim1	-0.332	0.005877401
1421060_at	myeloid/lymphoid or mixed-lineage leukemia	Mllt1	-0.332	0.00587836

	(trithorax homolog, Drosophila); translocated to, 1			
1456379_x_at	delta/notch-like EGF-related receptor	Dner	-0.332	0.027873837
1426938_at	neuro-oncological ventral antigen 1	Nova1	-0.332	0.001410046
1456054_a_at	pumilio 1 (Drosophila)	Pum1	-0.333	0.000622243
1452778_x_at	nucleosome assembly protein 1-like 1	Nap1l1	-0.333	7.67E-05
1425384_a_at	ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)	Ube4a	-0.333	0.00067713
1423332_at	syndecan binding protein	Sdcbp	-0.333	0.000400173
1450745_at	core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1	C1galt1	-0.334	0.008448737
1448952_at	RIKEN cDNA A030009H04 gene	A030009H04Rik	-0.334	0.000269846
1422038_a_at	tumor necrosis factor receptor superfamily, member 22	Tnfrsf22	-0.334	0.003419435
1416458_at	ADP-ribosylation factor 2	Arf2	-0.334	5.80E-05
1452635_x_at	Josephin domain containing 3	Josd3	-0.334	0.000154805
1424384_a_at	zinc and ring finger 1	Znrf1	-0.334	0.000327988
1421053_at	kinesin family member 1A	Kif1a	-0.334	0.004679125
1436589_x_at	protein kinase D2	Prkd2	-0.334	0.000864129
1437719_x_at	RIKEN cDNA A230046K03 gene	A230046K03Rik	-0.334	0.000662756
1448999_at	trafficking protein particle complex 5	Trappc5	-0.335	0.001742896
1450853_at	transducin-like enhancer of split 4, homolog of Drosophila E(spl)	Tle4	-0.335	0.003147763
1421846_at	WD repeat and SOCS box-containing 2	Wsb2	-0.335	0.000364532
1451073_at	signal peptide peptidase 3	Sppl3	-0.335	0.000149398
1420954_a_at	adducin 1 (alpha)	Add1	-0.335	0.008244985
1427085_at	RIKEN cDNA 2810432D09 gene	2810432D09Rik	-0.335	0.000430937
1426225_at	retinol binding protein 4, plasma	Rbp4	-0.335	0.000186041
1416831_at	neuraminidase 1	Neu1	-0.335	0.000380704
1452148_at	low density lipoprotein receptor-related protein associated protein 1	Lrpap1	-0.335	0.000166694
1451746_a_at	autophagy-related 12 (yeast)	Atg12	-0.335	0.003745128
1420487_at	nucleolar protein 7	Nol7	-0.335	0.014260559
1424732_s_at	transmembrane protein 192	Tmem192	-0.336	0.000172535
1422432_at	diazepam binding inhibitor	Dbi	-0.336	0.003458082
1426086_a_at	fragile X mental retardation syndrome 1 homolog	Fmr1	-0.336	0.001861012
1426468_at	RIKEN cDNA 0610037L13 gene	0610037L13Rik	-0.336	0.000635945
1428115_a_at	RAB2B, member RAS oncogene family	Rab2b	-0.336	0.002174914
1450659_at	regulator of G protein signaling 7	Rgs7	-0.336	0.001386504
1424830_at	cyclin K	Ccnk	-0.336	0.004368096
1440831_at	BTB and CNC homology 1	Bach1	-0.336	0.000884362
1427270_a_at	BSD domain containing 1	Bsdc1	-0.337	0.000225437
1416098_at	synaptogyrin 3	Syngr3	-0.337	0.000283681
1423081_a_at	translocase of outer mitochondrial membrane 20 homolog (yeast)	Tomm20	-0.337	0.000977444
1422556_at	guanine nucleotide binding protein, alpha 13	Gna13	-0.337	0.001427872
1424892_at	zinc finger with KRAB and SCAN domains 5	Zkscan5	-0.337	0.000117095
1424281_at	ubiquitin-associated protein 2	Ubap2	-0.337	7.47E-05
1417692_at	developmentally regulated GTP binding protein 2	Drg2	-0.337	0.000441301
1460252_s_at	zinc finger protein 105	Zfp105	-0.337	0.000313075
1450478_a_at	protein tyrosine phosphatase, non-receptor type 12	Ptpn12	-0.337	0.002064472
1417180_at	proprotein convertase subtilisin/kexin type 7	Pcsk7	-0.337	0.000247834
1418170_a_at	zinc finger, CCHC domain containing 14	Zcchc14	-0.338	0.00050575

1451619_at	golgi phosphoprotein 3-like	Golph3l	-0.338	0.002637205
1424034_at	RAR-related orphan receptor alpha	Rora	-0.338	0.000160694
1417224_a_at	CD2 antigen (cytoplasmic tail) binding protein 2	Cd2bp2	-0.338	0.000507351
1439032_at	centrosomal protein 27	Cep27	-0.338	0.000232818
1420479_a_at	nucleosome assembly protein 1-like 1	Nap1l1	-0.338	0.001570064
1420123_at	T-cell leukemia translocation altered gene	Tcta	-0.338	0.000117095
1460179_at	DnaJ (Hsp40) homolog, subfamily A, member 1	Dnaja1	-0.339	0.000247207
1423543_at	SWA-70 protein	Swap70	-0.339	0.001451144
1435235_at	thioredoxin-like 1	Txnl1	-0.339	0.003346129
1415947_at	cellular repressor of E1A-stimulated genes 1	Creg1	-0.339	0.000231566
1452049_at	ribosomal protein L7-like 1	Rpl7l1	-0.339	0.000154593
1428132_at	CDC42 small effector 1	Cdc42se1	-0.339	0.00214826
1417380_at	IQ motif containing GTPase activating protein 1	Iqgap1	-0.339	3.76E-05
1416343_a_at	lysosomal-associated membrane protein 2	Lamp2	-0.339	0.005266447
1455482_at	adaptor protein complex AP-2, alpha 2 subunit	Ap2a2	-0.339	0.000451158
1421298_a_at	homeodomain interacting protein kinase 1	Hipk1	-0.34	0.030218188
1415903_at	solute carrier family 38, member 1	Slc38a1	-0.34	0.0001803
1417869_s_at	cathepsin Z	Ctsz	-0.34	0.001588347
1450264_a_at	choline kinase alpha	Chka	-0.34	0.000131694
1427299_at	ribosomal protein S6 kinase polypeptide 3	Rps6ka3	-0.34	0.000197237
1420862_at	dynactin 4	Dctn4	-0.34	0.000477181
1437993_x_at	quinoid dihydropteridine reductase	Qdpr	-0.341	0.000180377
1427091_at	zinc finger, NFX1-type containing 1	Znfx1	-0.341	0.000504878
1417401_at	retinoic acid induced 14	Rai14	-0.341	0.004702118
1450204_a_at	myoneurin	Mynn	-0.341	0.000125666
1421469_a_at	signal transducer and activator of transcription 5A	Stat5a	-0.341	0.000132864
1448922_at	dual specificity phosphatase 19	Dusp19	-0.341	0.001517059
1420113_s_at	RIKEN cDNA 2410022L05 gene	2410022L05Rik	-0.341	0.000171801
1448810_at	glucosamine	Gne	-0.341	0.000192548
1423374_at	nuclear receptor coactivator 6	Ncoa6	-0.341	0.0001707
1450505_a_at	RIKEN cDNA 1810015C04 gene	1810015C04Rik	-0.341	0.000866238
1426336_at	calcium channel, voltage-dependent, gamma subunit 7	Cacng7	-0.341	0.009472004
1421681_at	neuregulin 4	Nrg4	-0.341	0.004705568
1451021_a_at	Kruppel-like factor 5	Klf5	-0.341	0.002588552
1452618_at	CDK5 regulatory subunit associated protein 2	Cdk5rap2	-0.341	0.000196265
1420844_at	ubiquilin 2	Ubqln2	-0.341	0.003036867
1422768_at	synaptotagmin binding, cytoplasmic RNA interacting protein	Syncrip	-0.341	0.000531643
1451467_s_at	GTP binding protein 5	Gtpbp5	-0.341	0.00015192
1435651_a_at	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1	Smarcad1	-0.342	0.000844745
1433991_x_at	diazepam binding inhibitor	Dbi	-0.342	0.000848492
1448644_at	penta-EF hand domain containing 1	Pef1	-0.342	0.000109797
1428094_at	lysosomal-associated membrane protein 2	Lamp2	-0.342	0.001926125
1420774_a_at	RIKEN cDNA 4930583H14 gene	4930583H14Rik	-0.342	0.001705632
1427937_at	RIKEN cDNA 2610030H06 gene	2610030H06Rik	-0.342	0.010418372
1420675_at	zinc finger protein 113	Zfp113	-0.342	0.002196012
1448780_at	solute carrier family 12, member 2	Slc12a2	-0.343	0.003052695
1449682_s_at	tubulin, beta 2a, pseudogene 2	Tubb2a-ps2	-0.343	0.000948465
1448963_at	nuclear transcription factor-Y gamma	Nfyc	-0.343	0.001055133
1419683_at	transformation related protein 53 regulating	Trp53rk	-0.343	0.000205195

	kinase			
1451682_at	zinc finger protein 142	Zfp142	-0.343	0.000709794
1425506_at	myosin, light polypeptide kinase	Mylk	-0.344	0.008897203
1423275_at	RIKEN cDNA E130113E03 gene	E130113E03Rik	-0.344	0.000235824
1421333_a_at	myoneurin	Mynn	-0.344	0.005954455
1450739_at	transducin (beta)-like 1X-linked receptor 1	Tbl1xr1	-0.344	0.000884362
1449414_at	zinc finger protein 53	Zfp53	-0.344	0.000805499
1450081_x_at	glucose phosphate isomerase 1	Gpi1	-0.344	0.001197483
1452461_a_at	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	Gnptab	-0.345	0.006038449
1449936_at	RIKEN cDNA 8430419L09 gene	8430419L09Rik	-0.345	0.000156363
1450105_at	a disintegrin and metallopeptidase domain 10	Adam10	-0.345	0.001628905
1420413_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 11	Slc7a11	-0.345	0.005987611
1426692_at	coiled-coil domain containing 97	Ccdc97	-0.345	0.008173935
1450918_s_at	Rous sarcoma oncogene	Src	-0.345	0.000747063
1417324_at	microtubule associated serine/threonine kinase 2	Mast2	-0.345	0.003576628
1451553_at	ADP-ribosyltransferase 5	Art5	-0.345	0.003382744
1426333_a_at	inhibitor of kappaB kinase beta	Ikbkb	-0.345	0.000514584
1448853_at	synaptojanin 2 binding protein	Synj2bp	-0.345	0.000449763
1428878_a_at	phosphatidylinositol transfer protein, cytoplasmic 1	Pitpnc1	-0.345	0.004037571
1454628_at	RIKEN cDNA A930037G23 gene	A930037G23Rik	-0.345	0.000505764
1452668_x_at	RAB2B, member RAS oncogene family	Rab2b	-0.345	0.000521872
1425186_at	LMBR1 domain containing 1	Lmbrd1	-0.345	0.000320563
1423658_at	signal peptide peptidase 3	Sppl3	-0.345	0.000344095
1424159_at	RIKEN cDNA 1300010M03 gene	1300010M03Rik	-0.345	0.003883009
1422322_at	choroideremia-like	Chml	-0.345	0.001144621
1448402_at	talin 1	Tln1	-0.345	0.002861801
1424403_a_at	RUN and FYVE domain containing 3	Rufy3	-0.346	9.07E-05
1452137_at	acyl-Coenzyme A binding domain containing 3	Acbd3	-0.346	0.013934917
1426194_x_at	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae)	Rev3l	-0.346	0.008085538
1439388_s_at	breast cancer anti-estrogen resistance 1	Bcar1	-0.346	0.000110826
1426242_at	polymerase (RNA) II (DNA directed) polypeptide A	Polr2a	-0.346	0.001421504
1417564_at	mediator complex subunit 7	Med7	-0.346	6.32E-05
1423346_at	degenerative spermatocyte homolog 1 (Drosophila)	Degs1	-0.346	0.000144408
1424040_at	microtubule-associated protein 7 domain containing 1	Mtap7d1	-0.346	0.000337038
1425617_at	DEAH (Asp-Glu-Ala-His) box polypeptide 9	Dhx9	-0.347	0.004334318
1419027_s_at	glycolipid transfer protein	Gltp	-0.347	0.001343644
1426279_at	RIKEN cDNA 5830415L20 gene	5830415L20Rik	-0.347	0.001125886
1449424_at	pleckstrin 2	Plek2	-0.347	0.003428196
1427687_at	protocadherin alpha 10	Pcdha10	-0.348	0.010042628
1423445_at	Rho-associated coiled-coil containing protein kinase 1	Rock1	-0.348	0.00021756
1418025_at	basic helix-loop-helix domain containing, class B2	Bhlhb2	-0.348	0.00033681
1436242_a_at	chemokine-like factor	Cklf	-0.348	0.002105333
1423821_at	transmembrane protein 168	Tmem168	-0.348	0.000331683
1434175_s_at	RIKEN cDNA 2210010N04 gene	2210010N04Rik	-0.348	0.001345351
1448671_at	ubiquitin-conjugating enzyme E2E 3, UBC4/5 homolog (yeast)	Ube2e3	-0.348	0.013797746
1451193_x_at	tetratricopeptide repeat domain 4	Ttc4	-0.348	0.002606601
1425541_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	Ddx27	-0.348	0.003795947

1433803_at	Janus kinase 1	Jak1	-0.348	6.13E-05
1450140_a_at	cyclin-dependent kinase inhibitor 2A	Cdkn2a	-0.349	0.010553613
1421911_at	signal transducer and activator of transcription 2	Stat2	-0.349	0.000217023
1423161_s_at	sprouty protein with EVH-1 domain 1, related sequence	Spred1	-0.349	0.000131195
1451036_at	spastic paraplegia 21 homolog (human)	Spg21	-0.349	0.000496025
1424053_a_at	transcription factor 25 (basic helix-loop-helix)	Tcf25	-0.349	0.00139814
1434856_at	ankyrin repeat domain 44	Ankrd44	-0.349	0.000723602
1460204_at	cytoplasmic tyrosine kinase, Dscr28C related (Drosophila)	Tec	-0.349	0.003060197
1425331_at	zinc finger protein 106	Zfp106	-0.349	0.00176265
1417164_at	dual specificity phosphatase 10	Dusp10	-0.35	0.000440407
1451640_a_at	arginine/serine-rich coiled-coil 2	Rsrc2	-0.35	0.001463157
1425795_a_at	mitogen-activated protein kinase kinase kinase 7	Map3k7	-0.35	0.001015231
1448886_at	GATA binding protein 3	Gata3	-0.35	0.000260456
1448844_at	cytochrome b5 type B	Cyb5b	-0.35	0.003928142
1419446_at	TBC1 domain family, member 1	Tbc1d1	-0.35	0.007656767
1424684_at	RAB5C, member RAS oncogene family	Rab5c	-0.35	9.39E-05
1418048_at	RIKEN cDNA 1110059G10 gene	1110059G10Rik	-0.351	0.000127754
1452340_at	zinc finger protein 518B	Zfp518b	-0.351	0.00212216
1420878_a_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	Ywhab	-0.351	0.001649115
1418100_at	RIKEN cDNA A030009H04 gene	A030009H04Rik	-0.351	0.000125564
1432130_a_at	tetratricopeptide repeat domain 14	Ttc14	-0.351	0.020988299
1451527_at	procollagen C-endopeptidase enhancer 2	Pcolce2	-0.351	0.005372607
1424929_a_at	tripartite motif-containing 26	Trim26	-0.351	8.36E-05
1421901_at	eukaryotic translation initiation factor 2 alpha kinase 1	Eif2ak1	-0.351	5.92E-05
1427895_at	RIKEN cDNA 2310004N24 gene	2310004N24Rik	-0.351	0.000723345
1423355_at	synaptosomal-associated protein 29	Snap29	-0.351	0.007764356
1430718_s_at	DnaJ (Hsp40) homolog, subfamily C, member 24	Dnajc24	-0.351	0.002774255
1423423_at	protein disulfide isomerase associated 3	Pdia3	-0.352	0.000110781
1416974_at	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	Stam2	-0.352	0.00098063
1418707_at	BCL2-associated athanogene 4	Bag4	-0.352	0.004693942
1423304_a_at	ring finger 111	Rnf111	-0.353	0.000444917
1424163_at	required for meiotic nuclear division 5 homolog B (S. cerevisiae)	Rmnd5b	-0.353	4.14E-05
1419123_a_at	platelet-derived growth factor, C polypeptide	Pdgfc	-0.353	0.011735577
1428155_at	COMM domain containing 9	Commd9	-0.353	7.94E-05
1419586_at	retinitis pigmentosa 2 homolog (human)	Rp2h	-0.353	0.00779603
1425601_a_at	rhotekin	Rtkn	-0.353	0.00081482
1421279_at	laminin, gamma 2	Lamc2	-0.353	0.00209706
1452356_at	IQ motif containing C	Iqcc	-0.353	0.000407714
1424319_at	oral cancer overexpressed 1	Oraov1	-0.353	0.00019044
1451158_at	thyroid hormone receptor interactor 12	Trip12	-0.353	0.001306482
1449262_s_at	lin-7 homolog C (C. elegans)	Lin7c	-0.353	0.009379077
1423488_at	monocyte to macrophage differentiation-associated	Mmd	-0.353	0.000230447
1424418_at	solute carrier family 25, member 38	Slc25a38	-0.353	0.00026825
1451200_at	kinesin family member 1B	Kif1b	-0.354	5.75E-05
1423499_at	synuclein, alpha interacting protein (synphilin)	Sncaip	-0.354	0.006008404
1436272_at	RAB3 GTPase activating protein subunit 2	Rab3gap2	-0.354	0.00013629

1423724_at	ZW10 interactor	Zwint	-0.354	8.73E-05
1430798_x_at	mitochondrial ribosomal protein L15	Mrpl15	-0.354	7.41E-05
1416600_a_at	regulator of calcineurin 1	Rcan1	-0.354	0.000189129
1416424_at	mannose-6-phosphate receptor binding protein 1	M6prbp1	-0.354	0.000554434
1430838_x_at	methyl-CpG binding domain protein 1	Mbd1	-0.355	0.000106917
1426573_at	malic enzyme 2, NAD(+)-dependent, mitochondrial	Me2	-0.355	0.002960699
1451389_at	DnaJ (Hsp40) homolog, subfamily C, member 24	Dnajc24	-0.355	0.026372634
1418516_at	metal response element binding transcription factor 2	Mtf2	-0.355	0.000117171
1448360_s_at	angel homolog 2 (Drosophila)	Angel2	-0.355	8.21E-05
1450076_at	RIKEN cDNA 4933411K20 gene	4933411K20Rik	-0.355	0.002166049
1421844_at	interleukin 1 receptor accessory protein	Il1rap	-0.355	0.006723569
1427463_at	CAS1 domain containing 1	Casd1	-0.355	0.00447439
1415731_at	angel homolog 2 (Drosophila)	Angel2	-0.355	5.19E-05
1423489_at	monocyte to macrophage differentiation-associated	Mmd	-0.355	0.000414893
1452274_at	zinc finger, AN1-type domain 3	Zfand3	-0.355	0.000410198
1427198_at	cDNA sequence BC022960	BC022960	-0.355	0.011252776
1423995_at	kinesin family member 1B	Kif1b	-0.356	0.000128946
1415992_at	phosphatidylinositol glycan anchor biosynthesis, class O	Pigo	-0.356	0.000153756
1448008_at	ankyrin repeat and KH domain containing 1	Ankhd1	-0.356	0.000894521
1417866_at	tumor necrosis factor, alpha-induced protein 1 (endothelial)	Tnfaip1	-0.356	0.000111028
1425007_at	zinc finger protein 566	Zfp566	-0.356	8.23E-05
1450425_a_at	RIKEN cDNA 2700062C07 gene	2700062C07Rik	-0.356	0.000542442
1424176_a_at	annexin A4	Anxa4	-0.356	0.00025296
1452372_at	BSD domain containing 1	Bsdc1	-0.356	0.000799549
1436027_at	oxysterol binding protein-like 11	Osbpl11	-0.356	0.000173184
1423127_at	inositol (myo)-1(or 4)-monophosphatase 1	Impa1	-0.356	0.001082873
1424247_at	ELKS/RAB6-interacting/CAST family member 1	Erc1	-0.356	0.000129482
1422467_at	palmitoyl-protein thioesterase 1	Ppt1	-0.357	8.40E-05
1417538_at	solute carrier family 35 (CMP-sialic acid transporter), member 1	Slc35a1	-0.357	6.98E-05
1419034_at	casein kinase 2, alpha 1 polypeptide	Csnk2a1	-0.357	0.001208251
1415790_at	ubiquitin-like domain containing CTD phosphatase 1	Ublcp1	-0.357	0.001170069
1426582_at	activating transcription factor 2	Atf2	-0.357	9.89E-05
1449304_at	RIKEN cDNA 2310061J03 gene	2310061J03Rik	-0.357	0.001020564
1426615_s_at	N-myc downstream regulated gene 4	Ndrg4	-0.357	0.000517704
1435176_a_at	inhibitor of DNA binding 2	Id2	-0.357	0.000213992
1455184_at	MOB1, Mps One Binder kinase activator-like 1A (yeast)	Mobkl1a	-0.358	0.001020239
1419638_at	ephrin B2	Efnb2	-0.358	0.000119322
1434827_at	THO complex 6 homolog (Drosophila)	Thoc6	-0.358	8.38E-05
1450116_at	DNA segment, Chr 3, ERATO Doi 300, expressed	D3Ertd300e	-0.358	0.000669074
1460545_at	thyroid hormone receptor associated protein 3	Thrap3	-0.359	8.59E-05
1427121_at	F-box protein 4	Fbxo4	-0.359	0.000228705
1451301_at	tropomodulin 2	Tmod2	-0.359	0.00010168
1437000_at	diacylglycerol kinase, theta	Dgkq	-0.359	0.002243863
1426714_at	solute carrier family 46, member 1	Slc46a1	-0.359	0.000110839
1437881_at	RIKEN cDNA 6330416L07 gene	6330416L07Rik	-0.36	0.017816567
1454690_at	inhibitor of kappaB kinase gamma	Ikbkg	-0.36	0.000360956

1418290_a_at	enhancer of zeste homolog 1 (Drosophila)	Ezh1	-0.36	0.006948598
1450846_at	basic leucine zipper and W2 domains 1	Bzw1	-0.36	0.004096893
1417792_at	zinc finger, matrin-like	Zfml	-0.36	0.001135816
1424686_at	HEAT repeat containing 6	Heatr6	-0.36	0.001054045
1417129_a_at	Meis homeobox 2	Meis2	-0.36	0.000573591
1448302_at	potassium channel tetramerisation domain containing 20	Kctd20	-0.36	0.000774555
1438183_x_at	sorbitol dehydrogenase	Sord	-0.36	0.000222249
1437742_at	RAB21, member RAS oncogene family	Rab21	-0.36	0.0006219
1449515_at	zinc finger protein 292	Zfp292	-0.36	0.001667884
1427097_at	WW domain containing E3 ubiquitin protein ligase 1	Wwp1	-0.361	7.66E-05
1420612_s_at	protein tyrosine phosphatase 4a2	Ptp4a2	-0.361	0.000743683
1448971_at	RIKEN cDNA 2410022L05 gene	2410022L05Rik	-0.361	0.001528092
1426567_a_at	PQ loop repeat containing 1	Pqlc1	-0.361	0.000180847
1422092_at	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	Pfkfb2	-0.361	0.002762524
1448435_at	mediator complex subunit 15	Med15	-0.361	7.03E-05
1421127_at	transmembrane protein 42	Tmem42	-0.361	0.000266294
1456039_at	sorting nexin 14	Snx14	-0.361	3.98E-05
1431691_a_at	RAB31, member RAS oncogene family	Rab31	-0.361	0.001040831
1424683_at	RIKEN cDNA 1810015C04 gene	1810015C04Rik	-0.361	0.007547596
1434514_at	RNA binding motif protein 15	Rbm15	-0.361	0.000264096
1416477_at	ubiquitin-conjugating enzyme E2D 2	Ube2d2	-0.361	7.29E-05
1450969_at	propionyl Coenzyme A carboxylase, beta polypeptide	Pccb	-0.362	9.33E-05
1417731_at	polyglutamine binding protein 1	Pqbp1	-0.362	0.004132501
1426613_a_at	U2 small nuclear ribonucleoprotein B	Snrpb2	-0.362	0.000317059
1416806_at	ferredoxin reductase	Fdxr	-0.362	0.001199864
1452397_at	RIKEN cDNA 2810474O19 gene	2810474O19Rik	-0.362	0.003843088
1421253_at	nebulin-related anchoring protein	Nrap	-0.362	0.000137226
1424569_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	Ddx46	-0.362	0.002694062
1426009_a_at	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	Pip5k1a	-0.362	0.000632473
1425337_at	solute carrier family 12, member 5	Slc12a5	-0.363	0.002835521
1449504_at	karyopherin (importin) alpha 1	Kpna1	-0.363	0.002673026
1423126_at	ATPase, Na+/K+ transporting, beta 3 polypeptide	Atp1b3	-0.363	5.72E-05
1416897_at	poly (ADP-ribose) polymerase family, member 9	Parp9	-0.363	0.000355306
1425937_a_at	hexamethylene bis-acetamide inducible 1	Hexim1	-0.363	0.001664696
1421771_a_at	IAP promoted placental gene	Ipp	-0.363	7.18E-05
1422773_at	myelin transcription factor 1	Myt1	-0.363	0.000343723
1451189_at	zinc finger, SWIM domain containing 1	Zswim1	-0.363	6.04E-05
1424559_at	RNA polymerase II associated protein 2	Rpap2	-0.363	0.001546338
1417736_at	structural maintenance of chromosomes 6	Smc6	-0.364	0.000914954
1436872_at	transforming, acidic coiled-coil containing protein 3	Tacc3	-0.364	0.016371704
1416462_at	cell cycle associated protein 1	Caprin1	-0.364	0.000159317
1425581_s_at	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransferase 7	Galnt7	-0.364	0.000117967
1431280_at	expressed sequence AI597468	AI597468	-0.364	0.001803483
1456066_a_at	RNA polymerase 1-4	Rpo1-4	-0.364	0.000727526
1415795_at	spindlin 1	Spin1	-0.364	0.001939709
1427967_at	CDK5 regulatory subunit associated protein 2	Cdk5rap2	-0.364	0.028967679
1418152_at	nucleosome binding protein 1	Nsbp1	-0.364	0.000551824

1451847_s_at	AT rich interactive domain 4B (RBP1-like)	Arid4b	-0.364	0.00121052
1424487_x_at	thioredoxin reductase 1	Txnrd1	-0.364	0.00259226
1417502_at	tetraspanin 7	Tspan7	-0.365	0.002489949
1434503_s_at	lysosomal-associated membrane protein 2	Lamp2	-0.365	0.001838512
1424518_at	apolipoprotein L 9a	Apol9a	-0.365	0.00386321
1435170_at	TSR2, 20S rRNA accumulation, homolog (S. cerevisiae)	Tsr2	-0.365	0.000110272
1421143_at	diaphanous homolog 1 (Drosophila)	Diap1	-0.365	0.00214703
1417747_at	complexin 1	Cplx1	-0.365	0.000203124
1418589_a_at	myeloid leukemia factor 1	Mlf1	-0.365	0.00383712
1452225_at	NA	NA	-0.365	0.000159317
1455809_x_at	resistance to inhibitors of cholinesterase 8 homolog (C. elegans)	Ric8	-0.365	0.000744217
1449275_at	RIKEN cDNA 2310038H17 gene	2310038H17Rik	-0.365	6.20E-05
1448119_at	2,3-bisphosphoglycerate mutase	Bpgm	-0.365	7.21E-05
1435860_at	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	Slc5a6	-0.366	0.00033006
1433595_at	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	Slc35d1	-0.366	0.00384695
1450073_at	kinesin family member 3B	Kif3b	-0.366	0.000899065
1418967_a_at	Suppression of tumorigenicity 7	St7	-0.366	8.89E-05
1421219_at	tubulin tyrosine ligase-like family, member 3	Ttll3	-0.366	0.009891752
1419469_at	guanine nucleotide binding protein (G protein), beta 4	Gnb4	-0.366	0.000116258
1433552_a_at	polymerase (RNA) II (DNA directed) polypeptide B	Polr2b	-0.366	7.26E-05
1426900_at	jumonji domain containing 1C	Jmjd1c	-0.366	0.000626858
1448216_at	synaptogyrin 3	Syngr3	-0.366	0.001056607
1418640_at	sirtuin 1 (silent mating type information regulation 2, homolog) 1 (S. cerevisiae)	Sirt1	-0.366	0.000403436
1418637_at	ets variant gene 3	Etv3	-0.367	0.000402315
1450379_at	moesin	Msn	-0.367	0.001347559
1451998_at	taspase, threonine aspartase 1	Tasp1	-0.367	0.000323517
1426377_at	zinc finger protein 281	Zfp281	-0.367	0.000319993
1431744_a_at	stromal membrane-associated protein 1	Smap1	-0.367	0.009032544
1426184_a_at	programmed cell death 6 interacting protein	Pdcd6ip	-0.367	0.002844089
1427279_at	CAP-GLY domain containing linker protein family, member 4	Clip4	-0.367	0.001779984
1433691_at	protein phosphatase 1, regulatory (inhibitor) subunit 3C	Ppp1r3c	-0.367	0.001341004
1460214_at	Purkinje cell protein 4	Pcp4	-0.367	0.000763374
1417956_at	cell death-inducing DNA fragmentation factor, alpha subunit-like effector A	Cidea	-0.367	0.002173238
1454711_at	triple functional domain (PTPRF interacting)	Trio	-0.367	5.38E-05
1450691_at	CASK-interacting protein 2	Caskin2	-0.367	0.000101902
1437688_x_at	ATPase, H+ transporting, lysosomal accessory protein 2	Atp6ap2	-0.368	0.000866344
1451292_at	Zinc finger protein 212	Zfp212	-0.368	9.16E-05
1425687_at	CASP8 and FADD-like apoptosis regulator	Cflar	-0.368	0.000414086
1453470_a_at	guanine nucleotide binding protein, alpha 13	Gna13	-0.368	0.000771446
1427646_a_at	rho/rac guanine nucleotide exchange factor (GEF) 2	Arhgef2	-0.368	0.001419933
1419429_at	ciliary neurotrophic factor receptor	Cntfr	-0.368	0.000290693
1431055_a_at	sorting nexin 10	Snx10	-0.368	0.00011759
1415768_a_at	ubiquitin-conjugating enzyme E2R 2	Ube2r2	-0.369	6.80E-05
1418514_at	metal response element binding transcription factor 2	Mtf2	-0.369	0.00386033

1417316_at	thioesterase superfamily member 2	Them2	-0.369	0.003086111
1419448_at	TBC1 domain family, member 1	Tbc1d1	-0.369	0.00216715
1419035_s_at	casein kinase 2, alpha 1 polypeptide	Csnk2a1	-0.369	0.000249538
1426218_at	glucocorticoid induced transcript 1	Glcci1	-0.369	0.000176946
1450010_at	hydroxysteroid (17-beta) dehydrogenase 12	Hsd17b12	-0.37	4.77E-05
1430972_x_at	aquarius	Aqr	-0.37	0.003538804
1449357_at	RIKEN cDNA 2310030G06 gene	2310030G06Rik	-0.37	0.001445653
1449300_at	CTTNBP2 N-terminal like	Cttnbp2nl	-0.37	0.000831744
1417139_at	DSN1, MIND kinetochore complex component, homolog (S. cerevisiae)	Dsn1	-0.37	0.000289319
1448528_at	programmed cell death 10	Pdcd10	-0.37	0.003278076
1428299_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	Dyrk1a	-0.37	0.0013392
1420863_at	dynactin 4	Dctn4	-0.37	0.000250354
1460017_at	predicted gene, EG434179	EG434179	-0.37	0.000179769
1451436_at	sno, strawberry notch homolog 1 (Drosophila)	Sbno1	-0.37	0.000545676
1448657_a_at	DnaJ (Hsp40) homolog, subfamily B, member 2	Dnajb2	-0.371	0.000100247
1436241_s_at	histone cell cycle regulation defective homolog A (S. cerevisiae)	Hira	-0.371	0.000525292
1448333_at	ADP-ribosylarginine hydrolase	Adprh	-0.371	0.001214765
1452207_at	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	Cited2	-0.371	0.000106888
1424724_a_at	DNA segment, Chr 16, ERATO Doi 472, expressed	D16Ertd472e	-0.371	0.000235824
1452180_at	PHD finger protein 17	Phf17	-0.371	0.000674702
1425573_a_at	development and differentiation enhancing	Ddef1	-0.371	0.000333439
1453299_a_at	purine-nucleoside phosphorylase 2	Pnp2	-0.371	7.21E-05
1435011_x_at	aldo-keto reductase family 1, member A4 (aldehyde reductase)	Akr1a4	-0.372	7.31E-05
1452093_at	transmembrane protein 185B	Tmem185b	-0.372	0.00011845
1417675_a_at	midasin homolog (yeast)	Mdn1	-0.372	0.000496868
1432160_at	G protein-coupled receptor kinase-interactor 2	Git2	-0.372	0.003377006
1425513_at	mitogen-activated protein kinase kinase 7	Map2k7	-0.372	0.000105947
1451680_at	sulfiredoxin 1 homolog (S. cerevisiae)	Srxn1	-0.372	0.000394095
1416924_at	brain protein I3	Bri3	-0.372	0.000519415
1416370_at	zinc finger and SCAN domain containing 21	Zscan21	-0.372	0.000115421
1431890_a_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3	Mllt3	-0.373	3.93E-05
1424996_at	CASP8 and FADD-like apoptosis regulator	Cflar	-0.373	0.002122764
1420947_at	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	Atrx	-0.373	0.006559225
1419179_at	thioredoxin-like 4A	Txnl4a	-0.373	0.006825852
1424638_at	cyclin-dependent kinase inhibitor 1A (P21)	Cdkn1a	-0.373	0.000251126
1448824_at	ubiquitin-conjugating enzyme E2, J1	Ube2j1	-0.373	0.000342234
1418701_at	catechol-O-methyltransferase 1	Comt1	-0.374	0.001869766
1450089_a_at	signal recognition particle receptor, B subunit	Srprb	-0.374	0.000823046
1431295_a_at	syntaxin 18	Stx18	-0.374	0.004612692
1426607_at	predicted gene, EG633640	EG633640	-0.374	3.58E-05
1452221_a_at	CXXC finger 1 (PHD domain)	Cxxc1	-0.374	6.18E-05
1450322_s_at	schlafen 3	Slfn3	-0.375	0.002076893
1416484_at	tetratricopeptide repeat domain 3	Ttc3	-0.375	9.44E-05
1438045_at	early endosome antigen 1	Eea1	-0.375	6.73E-05
1451247_at	major facilitator superfamily domain containing 1	Mfsd1	-0.375	2.93E-05
1448920_at	zinc finger with KRAB and SCAN domains 6	Zkscan6	-0.375	0.000597584

1424142_at	inhibitor of kappa light polypeptide enhancer in B-cells, kinase complex-associated protein	Ikbkap	-0.375	0.003106999
1423391_at	G protein-coupled receptor kinase-interactor 2	Git2	-0.375	0.000593371
1438865_at	histocompatibility 13	H13	-0.375	0.003124873
1424360_at	cDNA sequence BC019943	BC019943	-0.376	0.000267673
1436714_at	LIM domain containing preferred translocation partner in lipoma	Lpp	-0.376	0.001111262
1415981_at	HERPUD family member 2	Herpud2	-0.376	2.55E-05
1423452_at	serine/threonine kinase 17b (apoptosis-inducing)	Stk17b	-0.376	0.001559464
1415985_at	splicing factor 3b, subunit 3	Sf3b3	-0.376	8.18E-05
1417982_at	insulin induced gene 2	Insig2	-0.376	0.001495937
1426254_at	TM2 domain containing 1	Tm2d1	-0.376	0.000119891
1423444_at	Rho-associated coiled-coil containing protein kinase 1	Rock1	-0.376	0.000243056
1427578_a_at	eukaryotic translation initiation factor 6	Eif6	-0.376	3.93E-05
1435394_s_at	ras homolog gene family, member C	Rhoc	-0.376	0.000360005
1422967_a_at	transferrin receptor	Tfrc	-0.376	0.016387403
1418635_at	ets variant gene 3	Etv3	-0.376	0.000138654
1418432_at	calcium binding protein 39	Cab39	-0.376	0.00030412
1437747_at	ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)	Ube4a	-0.376	0.00162161
1448361_at	tetratricopeptide repeat domain 3	Ttc3	-0.377	0.000281243
1448251_at	RIKEN cDNA 9030425E11 gene	9030425E11Rik	-0.377	0.001143082
1449889_a_at	OCIA domain containing 1	Ociad1	-0.377	3.10E-05
1433515_s_at	ethanolamine kinase 1	Etnk1	-0.377	0.000362751
1426715_s_at	solute carrier family 46, member 1	Slc46a1	-0.377	0.000540584
1424749_at	WD repeat and FYVE domain containing 1	Wdfy1	-0.377	7.58E-05
1424055_at	nuclear receptor coactivator 5	Ncoa5	-0.377	8.67E-05
1423507_a_at	sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae)	Sirt2	-0.378	9.83E-05
1425702_a_at	ectonucleotide pyrophosphatase/phosphodiesterase 5	Enpp5	-0.378	0.000554847
1452079_s_at	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	Dcun1d1	-0.378	0.000555844
1452030_a_at	heterogeneous nuclear ribonucleoprotein R	Hnrnpr	-0.378	0.000867484
1428279_a_at	ataxin 7-like 1	Atxn7l1	-0.378	0.001474611
1420634_a_at	MAD homolog 2 (Drosophila)	Smad2	-0.378	7.00E-05
1423104_at	insulin receptor substrate 1	Irs1	-0.378	0.003156858
1419568_at	mitogen-activated protein kinase 1	Mapk1	-0.379	0.010699397
1423832_at	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	Prkag2	-0.379	0.000386145
1423686_a_at	proline rich 13	Prr13	-0.379	2.66E-05
1424068_at	T-cell leukemia translocation altered gene	Tcta	-0.379	0.000184888
1427997_at	RIKEN cDNA 1110007M04 gene	1110007M04Rik	-0.379	0.00031477
1433780_at	ubinuclein 1	Ubn1	-0.379	0.000545802
1426875_s_at	sulfiredoxin 1 homolog (S. cerevisiae)	Srxn1	-0.379	8.17E-05
1427528_a_at	Eph receptor A7	Epha7	-0.38	0.003439857
1416976_at	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	Stam2	-0.38	0.000220262
1425868_at	histone cluster 2, H2bb	Hist2h2bb	-0.38	0.001148678
1451969_s_at	poly (ADP-ribose) polymerase family, member 3	Parp3	-0.38	0.000526236
1428309_s_at	p53 and DNA damage regulated 1	Pdrg1	-0.381	9.11E-05
1435802_at	zinc finger and BTB domain containing 45	Zbtb45	-0.381	0.000299939
1415892_at	sphingosine phosphate lyase 1	Sgpl1	-0.381	0.000106599
1451052_at	peptide deformylase (mitochondrial)	Pdf	-0.381	0.000680998
1441342_at	dipeptidylpeptidase 4	Dpp4	-0.381	0.002001531

1424982_a_at	RIKEN cDNA 2700078E11 gene	2700078E11Rik	-0.381	0.000224112
1424169_at	Tax1 (human T-cell leukemia virus type I) binding protein 3	Tax1bp3	-0.381	7.21E-05
1448451_at	adenylate kinase 2	Ak2	-0.381	0.000260682
1423570_at	ATP-binding cassette, sub-family G (WHITE), member 1	Abcg1	-0.382	5.24E-05
1426240_at	chromatin modifying protein 4B	Chmp4b	-0.382	2.17E-05
1416856_at	RIKEN cDNA 3230401D17 gene	3230401D17Rik	-0.382	3.90E-05
1427103_at	pleckstrin homology domain containing, family O member 2	Plekho2	-0.382	4.26E-05
1427569_a_at	utrophin	Utrn	-0.382	0.000516021
1454014_a_at	McKusick-Kaufman syndrome protein	Mkks	-0.382	0.00632847
1451022_at	low density lipoprotein receptor-related protein 6	Lrp6	-0.382	0.002310148
1448440_x_at	DNA segment, Chr 17, Wayne State University 104, expressed	D17Wsu104e	-0.382	0.000259182
1417252_at	5',3'-nucleotidase, cytosolic	Nt5c	-0.383	0.000116369
1436848_x_at	inositol (myo)-1(or 4)-monophosphatase 1	Impa1	-0.383	0.000514584
1425351_at	sulfiredoxin 1 homolog (S. cerevisiae)	Srxn1	-0.383	0.000254918
1421116_a_at	reticulon 4	Rtn4	-0.383	9.18E-05
1422450_at	catenin (cadherin associated protein), delta 1	Ctnnd1	-0.383	0.003348881
1422051_a_at	gamma-aminobutyric acid (GABA-B) receptor, 1	Gabbr1	-0.383	0.017391924
1449063_at	SEC22 vesicle trafficking protein homolog B (S. cerevisiae)	Sec22b	-0.383	0.000171785
1418716_at	mitochondrial ribosomal protein S25	Mrps25	-0.383	0.000181774
1416154_at	signal recognition particle 54a	Srp54a	-0.383	0.014326969
1425821_at	chloride channel 7	Clcn7	-0.383	0.001803483
1456739_x_at	armadillo repeat containing, X-linked 2	Armcx2	-0.383	0.014807179
1425054_a_at	RIKEN cDNA 2510006D16 gene	2510006D16Rik	-0.384	0.000380204
1448289_at	collapsin response mediator protein 1	Crmp1	-0.384	2.82E-05
1419754_at	myosin Va	Myo5a	-0.384	0.000535387
1416048_at	polyhomeotic-like 2 (Drosophila)	Phc2	-0.384	0.001615944
1420956_at	adenomatosis polyposis coli	Apc	-0.384	0.000251641
1423548_s_at	ERGIC and golgi 3	Ergic3	-0.384	0.000513087
1438957_x_at	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	Cds2	-0.384	7.80E-05
1423372_at	polymerase (DNA-directed), epsilon 4 (p12 subunit)	Pole4	-0.384	0.000394534
1437111_at	zinc finger CCCH type containing 12C	Zc3h12c	-0.385	0.002096585
1448616_at	dishevelled 2, dsh homolog (Drosophila)	Dvl2	-0.385	0.003710843
1417570_at	anaphase promoting complex subunit 1	Anapc1	-0.385	0.001536933
1456492_at	RIKEN cDNA 9130404D08 gene	9130404D08Rik	-0.385	0.002051793
1430519_a_at	CCR4-NOT transcription complex, subunit 7	Cnot7	-0.385	0.003162985
1425624_at	EPM2A (laforin) interacting protein 1	Epm2aip1	-0.385	0.003576628
1434886_at	optic atrophy 3 (human)	Opa3	-0.385	0.000141108
1425347_a_at	zinc finger protein 318	Zfp318	-0.386	0.00526166
1423842_a_at	ring finger protein 41	Rnf41	-0.386	0.000169067
1437915_at	target of myb1-like 2 (chicken)	Tom1l2	-0.386	0.008332418
1421953_at	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	Crkl	-0.387	0.00289387
1418470_at	Yamaguchi sarcoma viral (v-yes) oncogene homolog 1	Yes1	-0.387	0.000531223
1420095_s_at	zinc finger and SCAN domain containing 21	Zscan21	-0.387	5.05E-05
1427195_at	NA	NA	-0.387	4.36E-05
1434796_at	vesicle-associated membrane protein 4	Vamp4	-0.387	0.000574764
1427673_a_at	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	Sema3e	-0.387	0.000438592

1436180_at	DnaJ (Hsp40) homolog, subfamily C, member 5	Dnajc5	-0.387	2.07E-05
1421267_a_at	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	Cited2	-0.388	0.001316839
1426193_at	otospiralin	Otos	-0.388	0.034891591
1448200_at	transcobalamin 2	Tcn2	-0.388	5.75E-05
1417723_at	ubiquitin-conjugating enzyme E2, J1	Ube2j1	-0.388	0.000311797
1415982_at	HERPUD family member 2	Herpud2	-0.388	0.001232956
1425173_s_at	golgi phosphoprotein 3-like	Golph3l	-0.388	0.000635389
1424570_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	Ddx46	-0.388	0.000195043
1419390_at	phosphodiesterase 10A	Pde10a	-0.388	0.001265562
1424333_at	RNA (guanine-9-) methyltransferase domain containing 1	Rg9mtd1	-0.388	0.000371432
1419234_at	helicase (DNA) B	Helb	-0.389	0.001055685
1426592_a_at	F-box protein 22	Fbxo22	-0.389	7.43E-05
1421321_a_at	neuroepithelial cell transforming gene 1	Net1	-0.389	9.41E-05
1452870_at	apoptotic peptidase activating factor 1	Apaf1	-0.389	0.000120181
1451795_at	target of myb1-like 2 (chicken)	Tom1l2	-0.39	0.006380007
1418795_at	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	Cds2	-0.39	0.000475009
1451445_at	uridine monophosphate synthetase	Umps	-0.39	3.25E-05
1425679_a_at	mitogen-activated protein kinase 8 interacting protein 1	Mapk8ip1	-0.39	0.000212169
1421111_at	RING1 and YY1 binding protein	Rybp	-0.39	0.005943372
1452236_at	ATP-binding cassette, sub-family F (GCN20), member 1	Abcf1	-0.39	0.003106557
1435592_at	eukaryotic translation initiation factor 5B	Eif5b	-0.39	9.36E-05
1427559_a_at	activating transcription factor 2	Atf2	-0.39	0.010359173
1425014_at	nuclear receptor subfamily 2, group C, member 2	Nr2c2	-0.39	0.000106599
1438680_at	autism susceptibility candidate 2	Auts2	-0.391	7.78E-05
1460341_at	pleckstrin homology domain containing, family B (evectins) member 2	Plekhb2	-0.391	6.70E-05
1448183_a_at	hypoxia inducible factor 1, alpha subunit	Hif1a	-0.392	0.006632207
1435097_at	methylmalonic aciduria (cobalamin deficiency) type B homolog (human)	Mmab	-0.392	0.000383181
1417289_at	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 2	Plekha2	-0.392	0.000438612
1426049_a_at	telomeric repeat binding factor 2, interacting protein	Terf2ip	-0.392	9.89E-05
1453725_a_at	mitchondrial ribosomal protein S7	Mrps7	-0.392	0.000187224
1424741_s_at	cAMP responsive element binding protein 3	Creb3	-0.393	4.85E-05
1459546_s_at	ectonucleotide pyrophosphatase/phosphodiesterase 1	Enpp1	-0.393	0.000201868
1449030_at	synapsin II	Syn2	-0.393	0.001774352
1450270_at	protocadherin beta 11	Pcdhb11	-0.393	0.009824294
1423047_at	toll interacting protein	Tollip	-0.393	3.22E-05
1416601_a_at	regulator of calcineurin 1	Rcan1	-0.393	0.000371875
1421900_at	eukaryotic translation initiation factor 2 alpha kinase 1	Eif2ak1	-0.393	0.00026579
1449443_at	2,4-dienoyl CoA reductase 1, mitochondrial	Decr1	-0.393	0.000328944
1450402_at	mediator complex subunit 1	Med1	-0.393	0.002746738
1417742_a_at	DNA methyltransferase 1-associated protein 1	Dmap1	-0.394	0.000321995
1451465_at	ubiquitin-like 7 (bone marrow stromal cell-derived)	Ubl7	-0.394	0.001140401
1429244_at	RIKEN cDNA 2610524H06 gene	2610524H06Rik	-0.394	3.53E-05
1427152_at	glutamine and serine rich 1	Qser1	-0.394	0.000331683

1421679_a_at	cyclin-dependent kinase inhibitor 1A (P21)	Cdkn1a	-0.394	0.000114022
1455282_x_at	aminolevulinic acid synthase 1	Alas1	-0.394	0.00016428
1423152_at	vesicle-associated membrane protein, associated protein B and C	Vapb	-0.394	0.008635012
1416018_at	down-regulator of transcription 1	Dr1	-0.394	5.62E-05
1418590_at	karyopherin (importin) alpha 6	Kpna6	-0.394	0.01043684
1450378_at	TAP binding protein	Tapbp	-0.394	0.000250912
1425660_at	BTB (POZ) domain containing 3	Btbd3	-0.394	0.012975483
1423820_at	elongation factor 1 homolog (ELF1, S. cerevisiae)	Elof1	-0.394	9.12E-05
1431933_a_at	DCP1 decapping enzyme homolog A (S. cerevisiae)	Dcp1a	-0.395	0.00250868
1418254_at	APAF1 interacting protein	Apip	-0.395	8.43E-05
1450049_a_at	histone cell cycle regulation defective homolog A (S. cerevisiae)	Hira	-0.395	0.004339865
1424710_a_at	golgi reassembly stacking protein 2	Gorasp2	-0.395	4.66E-05
1421235_s_at	RecQ protein-like 5	Recql5	-0.395	0.000164148
1451641_at	debranching enzyme homolog 1 (S. cerevisiae)	Dbr1	-0.395	0.000144408
1422506_a_at	cystatin B	Cstb	-0.395	0.000166185
1424196_at	Yip1 domain family, member 1	Yipf1	-0.395	0.000802714
1455281_at	WD repeat domain 33	Wdr33	-0.395	0.026251156
1439456_x_at	ATPase, H+ transporting, lysosomal accessory protein 2	Atp6ap2	-0.396	0.000533112
1451035_a_at	aldo-keto reductase family 1, member A4 (aldehyde reductase)	Akr1a4	-0.396	0.000327463
1419706_a_at	A kinase (PRKA) anchor protein (gravin) 12	Akap12	-0.396	0.000260682
1423919_at	cDNA sequence BC023882	BC023882	-0.396	0.000106843
1426546_at	testis-specific kinase 2	Tesk2	-0.396	0.00028397
1420971_at	ubiquitin protein ligase E3 component n-recognin 1	Ubr1	-0.396	0.000220372
1418985_at	CTTNBP2 N-terminal like	Cttnbp2nl	-0.396	5.59E-05
1448275_at	transmembrane protein 19	Tmem19	-0.397	3.18E-05
1427347_s_at	tubulin, beta 2a	Tubb2a	-0.397	3.93E-05
1418006_at	zinc finger CCCH-type containing 18	Zc3h18	-0.397	0.001478185
1450108_at	kinesin family member 1A	Kif1a	-0.397	0.000159271
1451217_a_at	IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae)	Immp1l	-0.397	0.000184273
1427469_at	helicase with zinc finger domain	Helz	-0.397	0.002551917
1455204_at	phosphatidylinositol transfer protein, cytoplasmic 1	Pitpnc1	-0.397	0.00011845
1448781_at	Ngfi-A binding protein 1	Nab1	-0.397	0.000788061
1437924_at	Son DNA binding protein	Son	-0.397	0.000705001
1456464_x_at	synaptotagmin XI	Syt11	-0.397	3.64E-05
1423117_at	pumilio 1 (Drosophila)	Pum1	-0.397	0.000172203
1449813_at	zinc finger protein 30	Zfp30	-0.398	0.000403366
1418312_at	zinc finger protein (C2H2 type) 276	Zfp276	-0.398	0.000563886
1421268_at	UDP-glucose ceramide glucosyltransferase	Ugcg	-0.398	0.000744217
1451505_at	coiled-coil-helix-coiled-coil-helix domain containing 5	Chchd5	-0.398	4.93E-05
1416637_at	solute carrier family 4 (anion exchanger), member 2	Slc4a2	-0.399	0.000993397
1420502_at	spermidine/spermine N1-acetyl transferase 1	Sat1	-0.399	9.86E-05
1434150_a_at	methyltransferase like 7A1	Mettl7a1	-0.399	0.002982059
1451818_at	mindbomb homolog 1 (Drosophila)	Mib1	-0.399	0.001386216
1416799_at	transient receptor potential cation channel, subfamily M, member 7	Trpm7	-0.399	6.45E-05
1451327_a_at	transmembrane emp24 domain containing 1	Tmed1	-0.399	4.98E-05
1425473_at	mediator complex subunit 17	Med17	-0.399	1.43E-05

1454633_at	ethanolamine kinase 1	Etnk1	-0.399	0.001100418
1418336_at	AFG3(ATPase family gene 3)-like 1 (yeast)	Afg3l1	-0.399	0.00059127
1450047_at	heparan sulfate 6-O-sulfotransferase 2	Hs6st2	-0.4	7.09E-05
1428141_at	golgi associated, gamma adaptin ear containing, ARF binding protein 2	Gga2	-0.4	2.59E-05
1416308_at	UDP-glucose dehydrogenase	Ugdh	-0.4	0.000927988
1430656_a_at	asparagine synthetase domain containing 1	Asnsd1	-0.4	0.000104003
1431326_a_at	tropomodulin 2	Tmod2	-0.4	0.001891025
1423003_at	SET domain containing (lysine methyltransferase) 7	Setd7	-0.4	0.000860634
1417062_at	armadillo repeat containing 10	Armc10	-0.4	0.000129368
1426179_a_at	twisted gastrulation homolog 1 (Drosophila)	Twsg1	-0.4	0.015391852
1424047_at	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)	Dera	-0.4	2.74E-05
1421005_at	centrosomal protein 110	Cep110	-0.401	0.001528127
1452446_a_at	transmembrane and ubiquitin-like domain containing 2	Tmub2	-0.401	2.47E-05
1417305_at	SPEG complex locus	Speg	-0.401	0.00039974
1416261_at	transmembrane protein 19	Tmem19	-0.401	3.80E-05
1418629_a_at	KH domain containing, RNA binding, signal transduction associated 1	Khdrbs1	-0.401	0.00010556
1435504_at	CAP-GLY domain containing linker protein family, member 4	Clip4	-0.401	0.000339559
1437113_s_at	phospholipase D1	Pld1	-0.401	0.000274706
1417626_at	phosphodiesterase 4D interacting protein (myomegalin)	Pde4dip	-0.402	6.01E-05
1421147_at	telomeric repeat binding factor 2	Terf2	-0.403	0.000104763
1450333_a_at	GATA binding protein 2	Gata2	-0.403	5.91E-05
1416126_at	RNA polymerase 1-2	Rpo1-2	-0.403	3.78E-05
1421459_a_at	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	Lrp8	-0.403	0.010867303
1453113_at	WD repeat, SAM and U-box domain containing 1	Wdsub1	-0.403	0.00031994
1425919_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	Ndufa12	-0.404	0.025448437
1416920_at	RNA binding motif protein 4	Rbm4	-0.404	4.12E-05
1418129_at	24-dehydrocholesterol reductase	Dhcr24	-0.404	0.024875799
1452112_a_at	RNA binding motif protein 4B	Rbm4b	-0.404	0.000494889
1416373_at	nitrogen fixation gene 1 (S. cerevisiae)	Nfs1	-0.404	4.25E-05
1424839_a_at	NOL1/NOP2/Sun domain family, member 4	Nsun4	-0.404	7.05E-05
1418227_at	origin recognition complex, subunit 2-like (S. cerevisiae)	Orc2l	-0.405	0.001963225
1460215_at	RNA polymerase 1-4	Rpo1-4	-0.405	0.002561642
1418710_at	CD59a antigen	Cd59a	-0.405	0.000140137
1430837_a_at	methyl-CpG binding domain protein 1	Mbd1	-0.405	0.002502698
1449664_s_at	ring finger protein 20	Rnf20	-0.405	0.000734425
1460740_at	clathrin, light polypeptide (Lcb)	Cltb	-0.405	0.000481499
1451192_a_at	tetratricopeptide repeat domain 4	Ttc4	-0.405	0.00049824
1460325_at	pumilio 1 (Drosophila)	Pum1	-0.405	5.42E-05
1422853_at	src homology 2 domain-containing transforming protein C1	Shc1	-0.406	0.002525729
1425721_at	pleckstrin homology domain interacting protein	Phip	-0.406	0.00162148
1423388_at	adaptor protein complex AP-1, gamma 1 subunit	Ap1g1	-0.406	0.000456117
1421240_at	endoplasmic reticulum (ER) to nucleus signalling 1	Ern1	-0.406	0.001649115
1415776_at	aldehyde dehydrogenase family 3, subfamily A2	Aldh3a2	-0.406	1.98E-05

1433497_at	aquarius	Aqr	-0.406	3.96E-05
1423046_s_at	nuclear cap binding protein subunit 2	Ncbp2	-0.406	5.66E-05
1423831_at	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	Prkag2	-0.407	0.000190268
1450847_at	nuclear cap binding protein subunit 2	Ncbp2	-0.407	0.003680357
1426417_at	Yip1 domain family, member 4	Yipf4	-0.407	5.85E-05
1423689_a_at	G-protein signalling modulator 1 (AGS3-like, C. elegans)	Gpsm1	-0.407	0.000806843
1420976_at	mannosidase, alpha, class 1A, member 2	Man1a2	-0.407	0.000417073
1415911_at	imprinted and ancient	Impact	-0.408	0.000153502
1449494_at	RAB3C, member RAS oncogene family	Rab3c	-0.408	1.52E-05
1450899_at	neural precursor cell expressed, developmentally down-regulated gene 1	Nedd1	-0.408	0.000991556
1448933_at	protocadherin beta 17	Pcdhb17	-0.408	0.000137496
1422754_at	tropomodulin 1	Tmod1	-0.408	0.003644229
1418508_a_at	growth factor receptor bound protein 2	Grb2	-0.409	1.22E-05
1433668_at	proline-rich nuclear receptor coactivator 1	Pnrc1	-0.409	0.00031994
1417363_at	zinc finger protein 61	Zfp61	-0.409	0.000375731
1438988_x_at	hematological and neurological expressed sequence 1	Hn1	-0.409	3.45E-05
1437399_at	claudin domain containing 1	Cldnd1	-0.409	0.004604553
1428308_at	p53 and DNA damage regulated 1	Pdrg1	-0.409	2.60E-05
1426628_at	transmembrane protein 184C	Tmem184c	-0.409	2.62E-05
1419524_at	tryptophan hydroxylase 1	Tph1	-0.409	0.005432929
1423770_at	transmembrane channel-like gene family 6	Tmc6	-0.41	0.000181565
1453853_a_at	Rho guanine nucleotide exchange factor (GEF) 12	Arhgef12	-0.41	0.001067292
1419311_at	tripartite motif-containing 10	Trim10	-0.41	0.001128623
1434659_at	RIKEN cDNA 5830411G16 gene	5830411G16Rik	-0.41	0.000875528
1426226_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	Dyrk1a	-0.41	0.004400212
1437112_at	phospholipase D1	Pld1	-0.411	0.000663038
1448439_at	DNA segment, Chr 17, Wayne State University 104, expressed	D17Wsu104e	-0.411	4.46E-05
1453750_x_at	phosphatidylinositol transfer protein, cytoplasmic 1	Pitpnc1	-0.411	0.000609887
1425158_at	T-box 20	Tbx20	-0.411	0.011222078
1418330_at	CCCTC-binding factor	Ctcf	-0.411	3.66E-05
1449910_at	RIKEN cDNA 2210418O10 gene	2210418O10Rik	-0.411	0.000189129
1453030_at	male-specific lethal 2-like 1 (Drosophila)	Msl2l1	-0.412	0.000335933
1420532_at	membrane associated guanylate kinase, WW and PDZ domain containing 2	Magi2	-0.412	0.000357292
1450178_at	bromodomain, testis-specific	Brdt	-0.412	0.000991556
1450708_at	secretogranin II	Scg2	-0.412	9.11E-05
1415949_at	carboxypeptidase E	Cpe	-0.412	0.00014104
1417434_at	glycerol phosphate dehydrogenase 2, mitochondrial	Gpd2	-0.413	2.60E-05
1450216_at	protocadherin beta 16	Pcdhb16	-0.413	0.005260066
1426395_s_at	eukaryotic translation initiation factor 3, subunit J	Eif3j	-0.413	9.37E-05
1417349_at	pallidin	Pldn	-0.413	3.93E-05
1423141_at	lysosomal acid lipase A	Lipa	-0.414	0.003450473
1450017_at	cyclin G1	Ccng1	-0.414	4.73E-05
1417049_at	Rh blood group, D antigen	Rhd	-0.414	0.00010221
1423169_at	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf7	-0.414	0.000132805
1420816_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma	Ywhag	-0.414	0.012938387

	polypeptide			
1426593_a_at	F-box protein 22	Fbxo22	-0.414	0.001067087
1449460_at	ankyrin repeat and SOCS box-containing 13	Asb13	-0.414	0.000182648
1438069_a_at	RNA binding motif protein 5	Rbm5	-0.415	0.000991556
1424317_at	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19	Slc25a19	-0.415	0.00026825
1426495_at	RIKEN cDNA 2410042D21 gene	2410042D21Rik	-0.415	0.00013772
1433935_at	expressed sequence AU020206	AU020206	-0.415	0.000180618
1460460_a_at	golgi reassembly stacking protein 2	Gorasp2	-0.415	0.000217293
1437396_at	cAMP responsive element binding protein 3-like 2	Creb3l2	-0.415	0.000254251
1421223_a_at	annexin A4	Anxa4	-0.415	0.000437483
1449730_s_at	frizzled homolog 3 (Drosophila)	Fzd3	-0.416	0.000409591
1415807_s_at	splicing factor, arginine/serine-rich 2 (SC-35)	Sfrs2	-0.416	0.000510187
1423545_a_at	zinc finger protein 207	Zfp207	-0.416	0.000749146
1424640_at	ADP-ribosylation factor-like 8A	Arl8a	-0.416	5.08E-05
1431737_at	predicted gene, EG629820	EG629820	-0.416	0.004855752
1424552_at	caspase 8	Casp8	-0.416	0.000860634
1419575_s_at	zinc finger protein 292	Zfp292	-0.417	4.89E-05
1422959_s_at	ring finger protein 114	Rnf114	-0.417	0.000381445
1416745_x_at	UDP-N-acetylglucosamine pyrophosphorylase 1	Uap1	-0.417	4.80E-05
1425378_at	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	Herc1	-0.417	0.001310757
1451671_at	golgi reassembly stacking protein 1	Gorasp1	-0.417	2.76E-05
1427174_at	predicted gene, OTTMUSG00000016321	OTTMUSG00000016321	-0.417	0.00049914
1433448_at	solute carrier family 25, member 44	Slc25a44	-0.417	0.00014104
1450381_a_at	B-cell leukemia/lymphoma 6	Bcl6	-0.418	0.000767702
1419735_at	casein kappa	Csn3	-0.418	0.001061465
1425356_at	zinc finger protein 142	Zfp142	-0.418	8.66E-05
1417013_at	heat shock protein 8	Hspb8	-0.418	1.22E-05
1448404_at	secretory carrier membrane protein 2	Scamp2	-0.419	3.83E-05
1452599_s_at	expressed sequence AI413582	AI413582	-0.419	0.000278343
1449268_at	glutamine fructose-6-phosphate transaminase 1	Gfpt1	-0.419	0.001875649
1415865_s_at	2,3-bisphosphoglycerate mutase	Bpgm	-0.419	1.85E-05
1420384_at	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	Col4a3bp	-0.419	0.002050863
1424748_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 11	Galnt11	-0.42	0.000167395
1426083_a_at	B-cell translocation gene 1, anti-proliferative	Btg1	-0.42	2.12E-05
1452907_at	galactosylceramidase	Galc	-0.42	3.29E-05
1437728_at	alkB, alkylation repair homolog 5 (E. coli)	Alkbh5	-0.42	0.000195235
1420387_at	Mpv17 transgene, kidney disease mutant	Mpv17	-0.42	0.000208666
1451318_a_at	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog	Lyn	-0.42	0.000237816
1452931_at	RIKEN cDNA 2810408M09 gene	2810408M09Rik	-0.42	1.39E-05
1426338_a_at	netrin G1	Ntng1	-0.421	0.00022936
1423371_at	polymerase (DNA-directed), epsilon 4 (p12 subunit)	Pole4	-0.421	0.002103529
1423761_at	RIKEN cDNA 5630401D24 gene	5630401D24Rik	-0.421	0.000119571
1425664_at	kelch-like 20 (Drosophila)	Klhl20	-0.421	0.005302476
1423150_at	secretogranin V	Scg5	-0.422	6.22E-05
1424851_at	coiled-coil-helix-coiled-coil-helix domain containing 5	Chchd5	-0.422	0.000388456

1430671_a_at	RIKEN cDNA 0610010K06 gene	0610010K06Rik	-0.422	0.002276251
1425498_at	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	Prpf4b	-0.422	0.000355373
1425097_a_at	zinc finger protein 106	Zfp106	-0.422	0.002420834
1426210_x_at	poly (ADP-ribose) polymerase family, member 3	Parp3	-0.422	0.009117494
1424431_at	chondroitin sulfate N-acetylgalactosaminyltransferase 2	Csgalnact2	-0.422	0.001426282
1449459_s_at	ankyrin repeat and SOCS box-containing 13	Asb13	-0.422	5.75E-05
1423862_at	pleckstrin homology domain containing, family F (with FYVE domain) member 2	Plekhf2	-0.423	0.000230567
1451977_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	Dyrk1a	-0.423	0.00041043
1429222_at	hydrolethalus syndrome 1	Hyls1	-0.423	0.000384371
1422131_at	DCP1 decapping enzyme homolog A (S. cerevisiae)	Dcp1a	-0.423	0.002249651
1422022_at	zinc finger protein 319	Zfp319	-0.423	0.006159615
1421640_a_at	TRAF family member-associated Nf-kappa B activator	Tank	-0.423	8.10E-05
1448778_at	splicing factor, arginine/serine-rich 4 (SRp75)	Sfrs4	-0.423	2.34E-05
1425125_at	oncoprotein induced transcript 3	Oit3	-0.423	0.000225437
1427993_at	RUN and FYVE domain-containing 2	Rufy2	-0.423	0.00039994
1452185_at	importin 8	Ipo8	-0.424	0.001554984
1450878_at	sorcin	Sri	-0.424	9.46E-05
1426998_at	zinc finger, AN1-type domain 3	Zfand3	-0.424	0.001330646
1426746_at	RIKEN cDNA 1810026J23 gene	1810026J23Rik	-0.424	1.79E-05
1451897_a_at	neighbor of Brca1 gene 1	Nbr1	-0.424	0.000386543
1419353_at	dolichol-phosphate (beta-D) mannosyltransferase 1	Dpm1	-0.424	7.55E-05
1426458_at	sarcolemma associated protein	Slmap	-0.425	0.00212689
1418188_a_at	receptor (calcitonin) activity modifying protein 2	Ramp2	-0.425	0.004820048
1422452_at	BCL2-associated athanogene 3	Bag3	-0.425	0.000192548
1415986_at	chloride channel 4-2	Clcn4-2	-0.425	0.000110171
1452595_at	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 4	Adamts4	-0.425	4.42E-05
1422617_at	predicted gene, ENSMUSG00000073257	ENSMUSG00000073257	-0.426	0.000172395
1427718_a_at	transformed mouse 3T3 cell double minute 2	Mdm2	-0.426	0.00062987
1428045_a_at	E74-like factor 2	Elf2	-0.426	0.008067044
1435053_s_at	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1	Plekhh1	-0.426	0.00227937
1448551_a_at	tripartite motif-containing 2	Trim2	-0.427	0.000122672
1417631_at	MAP kinase-interacting serine/threonine kinase 1	Mknk1	-0.427	0.000423384
1428078_at	ring finger protein, transmembrane 1	Rnft1	-0.428	0.000496605
1431382_a_at	CAP-GLY domain containing linker protein family, member 4	Clip4	-0.428	0.003580105
1437055_x_at	major facilitator superfamily domain containing 1	Mfsd1	-0.428	0.000118152
1454708_at	actin-binding LIM protein 1	Ablim1	-0.428	0.000176039
1417833_at	zinc finger CCCH type containing 10	Zc3h10	-0.428	5.38E-05
1423613_at	sperm specific antigen 2	Ssfa2	-0.428	4.05E-05
1419372_at	golgi SNAP receptor complex member 2	Gosr2	-0.428	0.000479089
1454643_at	ubiquitin associated protein 2-like	Ubap2l	-0.429	1.03E-05
1452218_at	coiled-coil domain containing 117	Ccdc117	-0.429	0.000168961
1426644_at	TBC1 domain family, member 20	Tbc1d20	-0.429	5.22E-05
1423875_at	expressed sequence AI450540	AI450540	-0.429	0.000158066

1422842_at	5'-3' exoribonuclease 2	Xrn2	-0.429	0.000164669
1450016_at	cyclin G1	Ccng1	-0.429	0.001440472
1448312_at	proprotein convertase subtilisin/kexin type 2	Pcsk2	-0.429	7.36E-05
1456228_x_at	myelin basic protein	Mbp	-0.429	0.000822259
1427874_at	ring finger protein 114	Rnf114	-0.43	7.94E-05
1417174_at	transmembrane protein 218	Tmem218	-0.43	4.67E-05
1416386_a_at	mannose-6-phosphate receptor, cation dependent	M6pr	-0.43	0.000168767
1416538_at	sialic acid acetylesterase	Siae	-0.43	0.001003678
1448944_at	neuropilin 1	Nrp1	-0.43	0.000509351
1456086_x_at	polyglutamine binding protein 1	Pqbp1	-0.43	8.22E-05
1424645_at	trinucleotide repeat containing 6C	Tnrc6c	-0.431	8.79E-05
1421768_a_at	homer homolog 1 (Drosophila)	Homer1	-0.431	0.000207685
1421230_a_at	Musashi homolog 2 (Drosophila)	Msi2	-0.431	0.039071934
1448838_at	topoisomerase I binding, arginine/serine-rich	Topors	-0.431	0.000203092
1427917_s_at	single-stranded DNA binding protein 3	Ssbp3	-0.431	0.000124507
1420857_at	LanC (bacterial lantibiotic synthetase component C)-like 2	Lancl2	-0.431	0.000114537
1426750_at	filamin, beta	Flnb	-0.431	4.69E-05
1418650_at	spermatogenesis associated 6	Spata6	-0.431	0.002443067
1452175_at	RIKEN cDNA 1810026J23 gene	1810026J23Rik	-0.432	0.000140351
1422629_s_at	shroom family member 3	Shroom3	-0.432	9.89E-05
1452517_at	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1	Plekhh1	-0.432	0.000145207
1456316_a_at	acyl-Coenzyme A binding domain containing 3	Acbd3	-0.432	0.000123818
1421600_a_at	tripartite motif-containing 26	Trim26	-0.432	0.000281814
1439008_at	zinc finger protein 319	Zfp319	-0.433	6.27E-05
1420809_a_at	RIKEN cDNA 1500003O03 gene	1500003O03Rik	-0.433	0.000435063
1416929_at	RNA binding motif protein 12	Rbm12	-0.433	0.000381561
1451058_at	malignant T cell amplified sequence 2	Mcts2	-0.433	7.21E-05
1452439_s_at	splicing factor, arginine/serine-rich 2 (SC-35)	Sfrs2	-0.433	0.002295833
1450259_a_at	signal transducer and activator of transcription 5A	Stat5a	-0.433	0.00173769
1427935_at	LYR motif containing 2	Lyrm2	-0.433	6.80E-05
1425204_s_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19b	Ddx19b	-0.433	7.45E-05
1419160_at	golgi autoantigen, golgin subfamily a, 3	Golga3	-0.433	0.003273465
1426711_at	transmembrane and coiled-coil domains 3	Tmco3	-0.433	0.000498285
1423664_at	quinoid dihydropteridine reductase	Qdpr	-0.433	2.42E-05
1425686_at	CASP8 and FADD-like apoptosis regulator	Cflar	-0.433	0.000376063
1419979_s_at	cAMP responsive element binding protein 3	Creb3	-0.434	0.001189727
1454184_a_at	inhibitor of kappaB kinase beta	Ikbkb	-0.434	0.000538073
1454979_at	diaphanous homolog 1 (Drosophila)	Diap1	-0.434	0.000109073
1456615_a_at	bromodomain PHD finger transcription factor	Bptf	-0.434	0.000161174
1424983_a_at	RIKEN cDNA 2700078E11 gene	2700078E11Rik	-0.434	0.000229161
1419038_a_at	casein kinase 2, alpha 1 polypeptide	Csnk2a1	-0.435	0.000537094
1439241_x_at	steroid 5 alpha-reductase 3	Srd5a3	-0.435	0.000840728
1460287_at	tissue inhibitor of metalloproteinase 2	Timp2	-0.435	0.000118303
1450071_at	ash1 (absent, small, or homeotic)-like (Drosophila)	Ash1l	-0.436	6.85E-05
1417438_at	retinol dehydrogenase 14 (all-trans and 9-cis)	Rdh14	-0.436	0.001316328
1416419_s_at	gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1	Gabarapl1	-0.436	2.23E-05
1424666_at	G patch domain containing 8	Gpatch8	-0.436	4.81E-05
1435731_x_at	peroxiredoxin 4	Prdx4	-0.437	0.000614788
1433575_at	SRY-box containing gene 4	Sox4	-0.437	6.13E-05
1421968_a_at	non imprinted in Prader-Willi/Angelman syndrome 2 homolog (human)	Nipa2	-0.437	0.00024277

1441182_at	bromodomain and WD repeat domain containing 3	Brwd3	-0.437	0.000653781
1424831_at	copine II	Cpne2	-0.437	1.85E-05
1421392_a_at	baculoviral IAP repeat-containing 3	Birc3	-0.437	0.000491669
1430292_a_at	RIKEN cDNA 1810030N24 gene	1810030N24Rik	-0.437	0.00023022
1422011_s_at	X-linked lymphocyte-regulated complex	Xlr	-0.437	0.00035084
1450083_at	CCR4-NOT transcription complex, subunit 4	Cnot4	-0.437	0.000145971
1455871_s_at	predicted gene, OTTMUSG00000012893	OTTMUSG00000012893	-0.438	2.62E-05
1427071_at	F-box protein 42	Fbxo42	-0.438	9.24E-05
1421885_at	Son of sevenless homolog 1 (Drosophila)	Sos1	-0.438	0.001477741
1420826_at	leucine zipper-EF-hand containing transmembrane protein 1	Letm1	-0.438	0.00109171
1416459_at	ADP-ribosylation factor 2	Arf2	-0.438	0.000119258
1423679_at	RIKEN cDNA 2810432L12 gene	2810432L12Rik	-0.438	1.04E-05
1416824_at	RIKEN cDNA B230118H07 gene	B230118H07Rik	-0.438	0.00028149
1427274_at	ring finger protein 214	Rnf214	-0.438	0.000114739
1417270_at	WD repeat domain 12	Wdr12	-0.439	0.000165924
1433942_at	myosin VI	Myo6	-0.439	9.15E-05
1436339_at	RIKEN cDNA 1810058I24 gene	1810058I24Rik	-0.439	0.000266292
1448356_at	ubiquitin-conjugating enzyme E2D 2	Ube2d2	-0.439	1.59E-05
1424740_at	cAMP responsive element binding protein 3	Creb3	-0.439	2.67E-05
1427461_at	NA	NA	-0.439	3.51E-05
1425338_at	phospholipase C, beta 4	Plcb4	-0.439	0.000547523
1434271_at	glucosidase beta 2	Gba2	-0.439	0.002327032
1436669_at	RIKEN cDNA 1700019G17 gene	1700019G17Rik	-0.44	4.47E-05
1436923_at	RAB2B, member RAS oncogene family	Rab2b	-0.44	0.001173607
1434481_at	RIKEN cDNA 4121402D02 gene	4121402D02Rik	-0.44	0.000658094
1460362_at	RIKEN cDNA 2410001C21 gene	2410001C21Rik	-0.44	6.12E-05
1417473_a_at	phosphopantothenoylcysteine synthetase	Ppcs	-0.441	0.0001987
1437419_at	BMP2 inducible kinase	Bmp2k	-0.441	2.74E-05
1430993_at	ubiquitin associated protein 2-like	Ubap2l	-0.441	8.79E-06
1427699_a_at	protein tyrosine phosphatase, non-receptor type 11	Ptpn11	-0.441	0.000113587
1423812_s_at	expressed sequence AW146242	AW146242	-0.441	0.000364493
1431203_at	serologically defined colon cancer antigen 8	Sdccag8	-0.441	0.000122794
1416671_a_at	mucolipin 1	Mcoln1	-0.442	8.62E-05
1449149_at	Tnf receptor-associated factor 3	Traf3	-0.442	0.001144621
1415976_a_at	calcium regulated heat stable protein 1	Carhsp1	-0.442	0.000204431
1431938_a_at	phosphomannomutase 2	Pmm2	-0.442	8.79E-06
1437586_at	CCR4-NOT transcription complex, subunit 4	Cnot4	-0.442	0.000339559
1421008_at	radical S-adenosyl methionine domain containing 2	Rsad2	-0.442	0.007897054
1424261_at	zinc finger protein 672	Zfp672	-0.443	0.000276064
1448965_at	INO80 homolog (S. cerevisiae)	Ino80	-0.443	0.00072178
1421166_at	attractin	Atrn	-0.443	0.000134007
1448646_at	WD repeat domain 12	Wdr12	-0.443	4.72E-05
1421021_at	AE binding protein 2	Aebp2	-0.443	0.000298407
1427271_at	zinc finger and BTB domain containing 44	Zbtb44	-0.443	0.000119571
1417834_at	synaptojanin 2 binding protein	Synj2bp	-0.443	8.25E-05
1452007_at	vesicle-associated membrane protein 7	Vamp7	-0.444	0.000867274
1420422_at	protocadherin beta 21	Pcdhb21	-0.444	9.71E-05
1417225_at	ADP-ribosylation factor-like 6 interacting protein 5	Arl6ip5	-0.444	2.58E-05
1436890_at	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	Uap1l1	-0.444	8.09E-05
1416303_at	LPS-induced TN factor	Litaf	-0.444	3.38E-05

1425227_a_at	ATPase, H+ transporting, lysosomal V0 subunit A1	Atp6v0a1	-0.444	0.001856305
1434736_at	hepatic leukemia factor	Hlf	-0.445	0.00033761
1432272_a_at	excision repair cross-complementing rodent repair deficiency, complementation group 4	Ercc4	-0.445	0.001447664
1435066_at	phosphatidylinositol transfer protein, cytoplasmic 1	Pitpnc1	-0.445	7.57E-05
1420979_at	p21 (CDKN1A)-activated kinase 1	Pak1	-0.445	2.79E-05
1416173_at	pescadillo homolog 1, containing BRCT domain (zebrafish)	Pes1	-0.445	4.40E-05
1450027_at	syndecan 3	Sdc3	-0.445	1.39E-05
1450698_at	dual specificity phosphatase 2	Dusp2	-0.446	0.00050575
1428649_at	cullin associated and neddylation disassociated 1	Cand1	-0.446	0.000158066
1422618_x_at	predicted gene, ENSMUSG00000073257	ENSMUSG00000073257	-0.446	9.72E-05
1449389_at	T-cell acute lymphocytic leukemia 1	Tal1	-0.446	0.000129353
1431712_a_at	RIKEN cDNA 2310022A10 gene	2310022A10Rik	-0.447	1.46E-05
1456473_x_at	ADP-ribosylation factor 2	Arf2	-0.447	0.000363004
1420613_at	protein tyrosine phosphatase 4a2	Ptp4a2	-0.448	0.000699303
1418977_at	SAP30 binding protein	Sap30bp	-0.448	4.99E-05
1417480_at	f-box protein 9	Fbxo9	-0.448	0.00020845
1434496_at	polo-like kinase 3 (Drosophila)	Plk3	-0.448	0.000145207
1417630_at	MAP kinase-interacting serine/threonine kinase 1	Mknk1	-0.449	2.68E-05
1432432_a_at	RAB3C, member RAS oncogene family	Rab3c	-0.449	0.000242177
1452209_at	plakophilin 4	Pkp4	-0.449	7.70E-05
1455994_x_at	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	Elovl1	-0.449	4.62E-05
1452441_at	PHD finger protein 3	Phf3	-0.45	5.24E-05
1451762_a_at	kinesin family member 1B	Kif1b	-0.45	0.002856021
1455625_at	NA	NA	-0.45	6.99E-05
1448596_at	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	Slc6a8	-0.45	3.75E-05
1417014_at	heat shock protein 8	Hspb8	-0.45	4.71E-05
1421205_at	ataxia telangiectasia mutated homolog (human)	Atm	-0.45	0.001399242
1428189_at	RIKEN cDNA 5730494M16 gene	5730494M16Rik	-0.45	0.001935105
1422249_s_at	zinc finger protein, autosomal	Zfa	-0.45	0.016563235
1422751_at	transducin-like enhancer of split 1, homolog of Drosophila E(spl)	Tle1	-0.451	0.000423424
1448385_at	solute carrier family 15, member 4	Slc15a4	-0.451	1.47E-05
1421269_at	UDP-glucose ceramide glucosyltransferase	Ugcg	-0.451	0.000135829
1423989_at	RIKEN cDNA 2210010N04 gene	2210010N04Rik	-0.451	0.000244028
1421175_at	myelin transcription factor 1-like	Myt1l	-0.452	0.000243261
1416672_s_at	mucolipin 1	Mcoln1	-0.452	9.23E-05
1429707_at	phospholipase A2, activating protein	Plaa	-0.452	3.20E-05
1451524_at	F-box and WD-40 domain protein 2	Fbxw2	-0.452	5.18E-05
1449110_at	ras homolog gene family, member B	Rhob	-0.453	8.62E-05
1418172_at	heme binding protein 1	Hebp1	-0.453	7.05E-05
1426098_a_at	calpastatin	Cast	-0.453	1.91E-05
1425426_a_at	myocyte enhancer factor 2A	Mef2a	-0.453	0.009851439
1450967_at	protein tyrosine phosphatase-like A domain containing 2	Ptplad2	-0.453	0.000235235
1425650_at	transducin-like enhancer of split 4, homolog of Drosophila E(spl)	Tle4	-0.453	0.003045336
1431423_a_at	mediator of RNA polymerase II transcription, subunit 8 homolog (yeast)	Med8	-0.454	1.25E-05

1424624_at	RIKEN cDNA 2900011O08 gene	2900011O08Rik	-0.454	1.43E-05
1416448_at	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	Itpa	-0.454	3.69E-05
1425906_a_at	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	Sema3e	-0.454	0.002138223
1424778_at	receptor accessory protein 3	Reep3	-0.454	5.62E-05
1425860_x_at	chemokine-like factor	Cklf	-0.454	0.000166694
1416296_at	interleukin 2 receptor, gamma chain	Il2rg	-0.455	0.00104238
1425608_at	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Dusp3	-0.455	1.80E-05
1449870_a_at	ATPase, H+ transporting, lysosomal V0 subunit A2	Atp6v0a2	-0.455	0.000275598
1426821_at	component of oligomeric golgi complex 8	Cog8	-0.455	0.000235824
1423913_at	HECT domain containing 3	Hectd3	-0.455	5.18E-05
1421504_at	trans-acting transcription factor 4	Sp4	-0.455	5.30E-05
1449931_at	cytoplasmic polyadenylation element binding protein 4	Cpeb4	-0.455	0.00642239
1454670_at	arginine glutamic acid dipeptide (RE) repeats	Rere	-0.455	0.000148496
1438140_a_at	zinc finger protein 64	Zfp64	-0.456	0.000378675
1425077_at	DnaJ (Hsp40) homolog, subfamily C, member 18	Dnajc18	-0.456	0.015288373
1418731_at	ring finger protein 12	Rnf12	-0.456	0.001620279
1416857_at	stromal cell derived factor 2	Sdf2	-0.456	1.40E-05
1435240_at	bromodomain adjacent to zinc finger domain, 2B	Baz2b	-0.456	0.001664893
1452131_at	U2 small nuclear ribonucleoprotein B	Snrpb2	-0.456	0.00057432
1428816_a_at	GATA binding protein 2	Gata2	-0.457	0.000556056
1448481_at	neuraminidase 1	Neu1	-0.457	0.000195755
1423922_s_at	integrator complex subunit 3	Ints3	-0.457	4.74E-05
1415763_a_at	RIKEN cDNA 2510006D16 gene	2510006D16Rik	-0.457	7.28E-05
1449229_a_at	cyclin-dependent kinase-like 2 (CDC2-related kinase)	Cdkl2	-0.458	8.25E-05
1419682_a_at	transformation related protein 53 regulating kinase	Trp53rk	-0.458	0.000197237
1417103_at	D-dopachrome tautomerase	Ddt	-0.458	2.02E-05
1449126_at	zinc finger protein 90	Zfp90	-0.458	2.72E-05
1421346_a_at	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	Slc6a6	-0.458	1.48E-05
1424650_at	protein disulfide isomerase associated 5	Pdia5	-0.458	3.25E-05
1421377_at	Tnf receptor-associated factor 6	Traf6	-0.458	0.001555755
1438155_x_at	phosphatidylinositol glycan anchor biosynthesis, class O	Pigo	-0.458	1.58E-05
1424706_at	zinc finger protein 51	Zfp51	-0.458	0.000163834
1416627_at	serine protease inhibitor, Kunitz type 1	Spint1	-0.458	4.31E-05
1420987_at	kinesin family member 3B	Kif3b	-0.458	0.000538073
1433631_at	eukaryotic translation initiation factor 5	Eif5	-0.459	0.000203124
1418401_a_at	dual specificity phosphatase 16	Dusp16	-0.459	3.04E-05
1423229_at	inositol polyphosphate-5-phosphatase E	Inpp5e	-0.459	1.60E-05
1435347_at	staufen (RNA binding protein) homolog 1 (Drosophila)	Stau1	-0.459	2.13E-05
1431032_at	amylo-1,6-glucosidase, 4-alpha-glucanotransferase	Agl	-0.459	0.001392054
1415988_at	high density lipoprotein (HDL) binding protein	Hdlbp	-0.46	0.00185661
1455017_a_at	zinc finger, MYM-type 3	Zmym3	-0.46	4.43E-05
1425098_at	zinc finger protein 106	Zfp106	-0.46	0.004527696
1416475_at	ubiquitin-conjugating enzyme E2D 2	Ube2d2	-0.46	0.001393153
1423433_at	TROVE domain family, member 2	Trove2	-0.46	1.86E-05
1456530_x_at	elongation of very long chain fatty acids	Elovl1	-0.461	2.47E-05

	(FEN1/Elo2, SUR4/Elo3, yeast)-like 1			
1452379_at	autism susceptibility candidate 2	Auts2	-0.461	0.000365333
1416216_at	RalBP1 associated Eps domain containing protein	Reps1	-0.461	4.66E-05
1448666_s_at	transducer of ERBB2, 2	Tob2	-0.461	0.000203195
1448605_at	ras homolog gene family, member C	Rhoc	-0.461	5.26E-05
1418917_at	heme binding protein 2	Hebp2	-0.461	0.000162075
1452360_a_at	jumonji, AT rich interactive domain 1A (Rbp2 like)	Jarid1a	-0.461	0.013343564
1433799_at	retinol dehydrogenase 13 (all-trans and 9-cis)	Rdh13	-0.461	2.19E-05
1430586_at	RIKEN cDNA 2700007P21 gene	2700007P21Rik	-0.461	0.00255966
1450439_at	host cell factor C1	Hcfc1	-0.462	0.000364532
1416192_at	N-ethylmaleimide sensitive fusion protein attachment protein alpha	Napa	-0.462	5.26E-05
1427037_at	eukaryotic translation initiation factor 4, gamma 1	Eif4g1	-0.462	0.008910691
1451338_at	nischarin	Nisch	-0.462	8.58E-05
1425045_at	hypothetical protein LOC433466	LOC433466	-0.462	1.71E-05
1416579_a_at	tumor-associated calcium signal transducer 1	Tacstd1	-0.462	0.000181355
1452744_at	RIKEN cDNA 2210016F16 gene	2210016F16Rik	-0.462	6.66E-05
1450056_at	adenomatosis polyposis coli	Apc	-0.462	0.000160257
1434343_at	RIKEN cDNA 5730403M16 gene	5730403M16Rik	-0.462	5.75E-05
1426017_a_at	RIKEN cDNA 0610011L14 gene	0610011L14Rik	-0.463	2.55E-05
1417953_at	DNA segment, Chr 6, Wayne State University 176, expressed	D6Wsu176e	-0.463	1.43E-05
1451219_at	ORM1-like 1 (S. cerevisiae)	Ormdl1	-0.463	3.63E-05
1449295_at	SAP30 binding protein	Sap30bp	-0.463	0.000147337
1423033_at	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)	Stt3a	-0.464	0.001225876
1448664_a_at	SPEG complex locus	Speg	-0.464	0.000260499
1419574_at	zinc finger protein 292	Zfp292	-0.465	2.20E-05
1431773_at	chromobox homolog 1 (Drosophila HP1 beta)	Cbx1	-0.465	1.46E-05
1417539_at	solute carrier family 35 (CMP-sialic acid transporter), member 1	Slc35a1	-0.465	3.72E-05
1451518_at	zinc finger protein 709	Zfp709	-0.465	0.00055652
1423713_at	ATP-binding cassette, sub-family B (MDR/TAP), member 8	Abcb8	-0.465	0.002785069
1424486_a_at	thioredoxin reductase 1	Txnrd1	-0.465	0.002413177
1422806_x_at	inhibitor of growth family, member 3	Ing3	-0.465	5.14E-05
1438118_x_at	vimentin	Vim	-0.465	0.000149288
1428879_at	phosphatidylinositol transfer protein, cytoplasmic 1	Pitpnc1	-0.466	0.00052837
1452646_at	transformation related protein 53 inducible nuclear protein 2	Trp53inp2	-0.466	1.43E-05
1451008_at	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	St8sia3	-0.466	0.001296518
1418313_at	zinc finger protein (C2H2 type) 276	Zfp276	-0.466	0.000155743
1425448_x_at	ATPase, H+ transporting, lysosomal V0 subunit B	Atp6v0b	-0.466	4.16E-05
1425010_at	zinc finger protein 119	Zfp119	-0.466	0.000145207
1424560_at	proline-serine-threonine phosphatase-interacting protein 1	Pstpip1	-0.467	0.000731113
1441986_at	zinc finger, CCHC domain containing 6	Zcchc6	-0.467	0.000114537
1419280_at	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	Pip4k2a	-0.468	0.001854662
1420631_a_at	bladder cancer associated protein homolog (human)	Blcap	-0.469	2.31E-05
1420506_a_at	syntaxin binding protein 1	Stxbp1	-0.469	0.001891805

1448199_at	ankyrin repeat domain 10	Ankrd10	-0.469	5.24E-05
1418032_at	integrin alpha FG-GAP repeat containing 2	Itfg2	-0.469	1.73E-05
1426471_at	zinc finger protein 52	Zfp52	-0.469	0.008108975
1429786_a_at	ZW10 interactor	Zwint	-0.47	0.000128317
1423886_at	laminin, gamma 1	Lamc1	-0.47	0.00747071
1426315_a_at	RIKEN cDNA 6330416G13 gene	6330416G13Rik	-0.47	0.000215871
1437389_x_at	KH domain containing, RNA binding, signal transduction associated 1	Khdrbs1	-0.47	0.000134007
1426018_a_at	SRY-box containing gene 6	Sox6	-0.47	0.000560717
1426343_at	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	Stt3b	-0.47	0.000111033
1423726_at	vesicle amine transport protein 1 homolog (T californica)	Vat1	-0.47	6.73E-05
1423662_at	ATPase, H+ transporting, lysosomal accessory protein 2	Atp6ap2	-0.47	1.89E-05
1455488_at	RIKEN cDNA 6230416J20 gene	6230416J20Rik	-0.47	0.000207579
1426480_at	Shwachman-Bodian-Diamond syndrome homolog (human)	Sbds	-0.471	6.70E-05
1434333_a_at	protein kinase D2	Prkd2	-0.471	3.00E-05
1450797_a_at	chromobox homolog 1 (Drosophila HP1 beta)	Cbx1	-0.471	0.000438612
1419536_a_at	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	Rela	-0.471	3.98E-05
1426951_at	cysteine rich transmembrane BMP regulator 1 (chordin like)	Crim1	-0.472	0.000366518
1418898_at	lin-7 homolog C (C. elegans)	Lin7c	-0.472	0.005595061
1450457_at	Casitas B-lineage lymphoma	Cbl	-0.472	0.001166377
1448148_at	granulin	Grn	-0.473	0.000134007
1417828_at	aquaporin 8	Aqp8	-0.473	0.002785213
1420719_at	testis expressed gene 15	Tex15	-0.473	0.005254465
1421201_a_at	trophinin	Tro	-0.474	6.78E-05
1415948_at	cellular repressor of E1A-stimulated genes 1	Creg1	-0.474	1.82E-05
1419401_at	ankyrin repeat and SOCS box-containing 13	Asb13	-0.474	6.30E-05
1416800_at	transient receptor potential cation channel, subfamily M, member 7	Trpm7	-0.474	2.18E-05
1419616_at	bone morphogenic protein receptor, type II (serine/threonine kinase)	Bmpr2	-0.474	0.000414753
1431611_a_at	cell adhesion molecule 1	Cadm1	-0.474	6.73E-05
1438677_at	plakophilin 4	Pkp4	-0.474	4.93E-05
1420547_at	galactosylceramidase	Galc	-0.474	0.004815594
1451690_a_at	poliovirus receptor-related 4	Pvrl4	-0.474	0.000105822
1424952_at	OCIA domain containing 1	Ociad1	-0.475	0.000273317
1433439_at	RNA binding motif protein 12	Rbm12	-0.475	2.34E-05
1420906_at	CD2-associated protein	Cd2ap	-0.475	0.000100247
1439122_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	Ddx6	-0.475	0.001071619
1415975_at	calcium regulated heat stable protein 1	Carhsp1	-0.476	7.68E-06
1417172_at	ubiquitin-conjugating enzyme E2L 6	Ube2l6	-0.476	0.00489956
1429859_a_at	ADP-ribosylation factor-like 2 binding protein	Arl2bp	-0.476	0.000312677
1426986_at	RIKEN cDNA 2810485I05 gene	2810485I05Rik	-0.476	0.003792118
1423861_at	pleckstrin homology domain containing, family F (with FYVE domain) member 2	Plekhf2	-0.477	9.59E-06
1449371_at	histidyl-tRNA synthetase 2, mitochondrial (putative)	Hars2	-0.478	5.70E-05
1415749_a_at	Ras-related GTP binding C	Rragc	-0.478	9.78E-06
1449718_s_at	RIKEN cDNA 4930453N24 gene	4930453N24Rik	-0.478	0.001366095
1455179_at	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	Mpp7	-0.478	0.000367886
1451098_at	chromatin modifying protein 1A	Chmp1a	-0.478	5.85E-05
1428760_at	small nuclear RNA activating complex,	Snapc3	-0.478	1.60E-05

	polypeptide 3			
1416994_at	tetratricopeptide repeat domain 1	Ttc1	-0.479	0.000262238
1433531_at	acyl-CoA synthetase long-chain family member 4	Acsl4	-0.479	8.13E-05
1424779_at	receptor accessory protein 3	Reep3	-0.479	5.91E-05
1449512_a_at	zinc finger protein X-linked	Zfx	-0.479	0.003153614
1421756_a_at	G protein-coupled receptor 19	Gpr19	-0.479	8.79E-06
1421177_at	THAP domain containing, apoptosis associated protein 2	Thap2	-0.479	0.00039311
1450341_at	protocadherin beta 8	Pcdhb8	-0.479	0.000849949
1418131_at	SAM domain and HD domain, 1	Samhd1	-0.479	2.09E-05
1425676_a_at	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	Elovl1	-0.479	1.25E-05
1416065_a_at	ankyrin repeat domain 10	Ankrd10	-0.479	5.65E-05
1416830_at	RIKEN cDNA 0610031J06 gene	0610031J06Rik	-0.48	1.29E-05
1424935_at	ganglioside-induced differentiation-associated protein 1-like 1	Gdap1l1	-0.48	6.55E-05
1423073_at	cytidine monophosphate (UMP-CMP) kinase 1	Cmpk1	-0.48	6.67E-06
1424889_at	nucleoporin like 2	Nupl2	-0.48	4.05E-05
1416482_at	tetratricopeptide repeat domain 3	Ttc3	-0.48	2.72E-05
1450971_at	growth arrest and DNA-damage-inducible 45 beta	Gadd45b	-0.48	0.000320109
1453468_at	centrosomal protein 290	Cep290	-0.481	0.00049914
1421328_at	microtubule-associated protein 2	Mtap2	-0.481	0.003943226
1425203_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19b	Ddx19b	-0.481	0.000364532
1424992_at	Tp53rk binding protein	Tprkb	-0.481	2.57E-05
1425025_at	transmembrane protein 106A	Tmem106a	-0.481	0.000348533
1429400_at	chloride channel 5	Clcn5	-0.481	4.71E-05
1430147_a_at	Josephin domain containing 3	Josd3	-0.481	0.000146997
1427701_a_at	sine oculis-related homeobox 4 homolog (Drosophila)	Six4	-0.481	0.003003393
1419211_s_at	RIKEN cDNA 4933424B01 gene	4933424B01Rik	-0.482	2.81E-05
1417128_at	pleckstrin homology domain containing, family O member 1	Plekho1	-0.482	0.000180631
1455965_at	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 4	Adamts4	-0.482	0.000162686
1421940_at	stromal antigen 1	Stag1	-0.482	5.65E-05
1455350_at	transmembrane protein 62	Tmem62	-0.482	3.07E-05
1423045_at	nuclear cap binding protein subunit 2	Ncbp2	-0.483	0.000121425
1426498_at	jumonji, AT rich interactive domain 1C (Rbp2 like)	Jarid1c	-0.483	0.001891025
1425287_at	zinc finger protein 189	Zfp189	-0.483	0.00129664
1436482_a_at	syndecan 3	Sdc3	-0.484	6.07E-05
1427310_at	bromodomain PHD finger transcription factor	Bptf	-0.484	1.21E-05
1419251_at	epidermal growth factor receptor pathway substrate 15	Eps15	-0.484	0.000568556
1452647_a_at	DPH2 homolog (S. cerevisiae)	Dph2	-0.484	8.71E-06
1416933_at	P450 (cytochrome) oxidoreductase	Por	-0.484	5.69E-05
1422865_at	runt related transcription factor 1	Runx1	-0.484	0.001696276
1417856_at	avian reticuloendotheliosis viral (v-rel) oncogene related B	Relb	-0.484	9.89E-05
1450074_at	kinesin family member 3B	Kif3b	-0.485	0.000304845
1416868_at	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	Cdkn2c	-0.485	0.000112343
1438034_at	RIKEN cDNA 2410005O16 gene	2410005O16Rik	-0.486	0.005961168
1416697_at	dipeptidylpeptidase 4	Dpp4	-0.486	3.02E-05
1417793_at	interferon inducible GTPase 2	Iigp2	-0.487	0.001415742

1426084_a_at	torsin A interacting protein 1	Tor1aip1	-0.487	9.07E-05
1429739_a_at	POZ (BTB) and AT hook containing zinc finger 1	Patz1	-0.487	1.18E-05
1416975_at	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	Stam2	-0.487	0.001137159
1425555_at	Cdc2-related kinase, arginine/serine-rich	Crkrs	-0.487	8.69E-05
1431033_x_at	amylo-1,6-glucosidase, 4-alpha-glucanotransferase	Agl	-0.487	0.000468395
1431072_a_at	coiled-coil domain containing 50	Ccdc50	-0.487	0.0007289
1427267_at	trinucleotide repeat containing 18	Tnrc18	-0.487	0.00919485
1451379_at	RAB22A, member RAS oncogene family	Rab22a	-0.487	1.80E-05
1428133_at	Smad nuclear interacting protein 1	Snip1	-0.488	2.19E-05
1418384_at	apolipoprotein O-like	Apool	-0.488	6.33E-05
1421193_a_at	pre B-cell leukemia transcription factor 3	Pbx3	-0.489	1.65E-05
1431431_a_at	nitrogen fixation gene 1 (S. cerevisiae)	Nfs1	-0.489	0.000134007
1426219_at	sterol carrier protein 2, liver	Scp2	-0.489	2.62E-05
1424817_at	sperm flagellar 1	Spef1	-0.489	0.000328985
1426725_s_at	E26 avian leukemia oncogene 1, 5' domain	Ets1	-0.489	0.007155574
1426521_at	RIKEN cDNA D230025D16 gene	D230025D16Rik	-0.489	7.85E-05
1454664_a_at	eukaryotic translation initiation factor 5	Eif5	-0.49	5.25E-06
1451127_at	expressed sequence AW146242	AW146242	-0.491	0.000884362
1448513_a_at	Niemann Pick type C2	Npc2	-0.491	0.000281243
1418941_at	protocadherin beta 22	Pcdhb22	-0.491	0.000392367
1451142_at	exocyst complex component 1	Exoc1	-0.491	2.62E-05
1423307_s_at	trans-golgi network protein	Tgoln1	-0.491	0.000638944
1423711_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1	Ndufaf1	-0.491	2.36E-05
1436188_a_at	N-myc downstream regulated gene 4	Ndrg4	-0.491	2.47E-05
1431293_a_at	claudin domain containing 1	Cldnd1	-0.491	0.000203881
1424548_at	zinc finger, CCCH-type with G patch domain	Zgpat	-0.491	0.000289182
1451020_at	glycogen synthase kinase 3 beta	Gsk3b	-0.491	6.15E-05
1418501_a_at	oxidation resistance 1	Oxr1	-0.492	0.000175147
1424129_at	major facilitator superfamily domain containing 1	Mfsd1	-0.492	4.61E-05
1427128_at	protein tyrosine phosphatase, non-receptor type 23	Ptpn23	-0.492	0.00024968
1426781_at	tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)	Tyw1	-0.493	7.18E-05
1456488_at	WD repeat domain 33	Wdr33	-0.493	0.000298457
1418908_at	peptidylglycine alpha-amidating monooxygenase	Pam	-0.494	0.000124204
1428662_a_at	HOP homeobox	Hopx	-0.494	7.68E-06
1421534_at	hypothetical LOC14210	LOC14210	-0.494	0.000288192
1417974_at	karyopherin (importin) alpha 4	Kpna4	-0.495	7.07E-06
1422737_at	nuclear receptor coactivator 3	Ncoa3	-0.495	7.18E-05
1427388_at	leucine rich repeat containing 2	Lrrc2	-0.496	0.001789889
1423345_at	degenerative spermatocyte homolog 1 (Drosophila)	Degs1	-0.496	1.28E-05
1425567_a_at	annexin A5	Anxa5	-0.496	6.98E-06
1450530_at	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	B3galt1	-0.497	0.001099154
1423617_at	peptide deformylase (mitochondrial)	Pdf	-0.497	9.87E-05
1427124_at	RIKEN cDNA 4932416H05 gene	4932416H05Rik	-0.498	3.27E-05
1439116_at	NA	NA	-0.498	0.001757064
1420985_at	ash1 (absent, small, or homeotic)-like (Drosophila)	Ash1l	-0.498	0.000193714
1434216_a_at	nudix (nucleoside diphosphate linked moiety X)-type motif 19	Nudt19	-0.498	4.06E-05

1424617_at	interferon-induced protein 35	Ifi35	-0.499	2.15E-05
1452450_at	ATPase, class I, type 8B, member 2	Atp8b2	-0.499	0.000338036
1423154_at	cDNA sequence BC005537	BC005537	-0.499	0.000459478
1432646_a_at	RIKEN cDNA 2900097C17 gene	2900097C17Rik	-0.499	0.005703518
1423155_at	sorcin	Sri	-0.499	7.75E-05
1425115_at	retinoblastoma binding protein 6	Rbbp6	-0.499	7.94E-05
1433645_at	solute carrier family 44, member 1	Slc44a1	-0.5	1.10E-05
1451972_at	similar to glucocorticoid induced transcript 1	LOC100046012	-0.5	9.60E-05
1424457_at	amyloid beta (A4) precursor protein-binding, family B, member 3	Apbb3	-0.5	1.90E-05
1420522_at	coiled-coil domain containing 50	Ccdc50	-0.5	0.002371058
1420383_a_at	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	Col4a3bp	-0.501	0.000773237
1438165_x_at	vesicle amine transport protein 1 homolog (T californica)	Vat1	-0.501	0.000122951
1457695_at	AP1 gamma subunit binding protein 1	Ap1gbp1	-0.501	0.00046182
1425181_at	SH3-domain GRB2-like (endophilin) interacting protein 1	Sgip1	-0.501	2.35E-05
1418597_at	topoisomerase (DNA) III alpha	Top3a	-0.502	2.87E-05
1455076_a_at	RIKEN cDNA 4933424B01 gene	4933424B01Rik	-0.502	0.000131942
1449445_x_at	microfibrillar-associated protein 1A	Mfap1a	-0.502	4.34E-06
1424232_a_at	FtsJ methyltransferase domain containing 1	Ftsjd1	-0.503	0.000113608
1425304_s_at	proline rich membrane anchor 1	Prima1	-0.504	9.92E-05
1456056_a_at	DNA segment, Chr 6, Wayne State University 116, expressed	D6Wsu116e	-0.504	3.44E-05
1448690_at	potassium channel, subfamily K, member 1	Kcnk1	-0.504	0.000231566
1427273_at	ring finger protein 214	Rnf214	-0.505	2.60E-05
1433690_at	RIKEN cDNA 2210016L21 gene	2210016L21Rik	-0.505	3.86E-05
1419132_at	toll-like receptor 2	Tlr2	-0.505	0.000380204
1426485_at	UBX domain protein 4	Ubxn4	-0.505	0.000435317
1453554_a_at	WD repeat domain 33	Wdr33	-0.506	0.000138654
1419760_a_at	RWD domain containing 2B	Rwdd2b	-0.506	5.78E-05
1423865_at	solute carrier family 44, member 1	Slc44a1	-0.507	0.002316584
1425399_at	feline leukemia virus subgroup C cellular receptor 1	Flvcr1	-0.507	4.98E-05
1418491_a_at	pseudouridine synthase 3	Pus3	-0.507	4.04E-05
1419502_at	GH3 domain containing	Ghdc	-0.507	2.39E-05
1419459_a_at	magnesium transporter 1	Magt1	-0.507	4.93E-05
1452378_at	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	Malat1	-0.507	0.002639357
1424091_at	expressed sequence AI449175	AI449175	-0.508	0.000636901
1449167_at	erythrocyte protein band 4.1-like 4a	Epb4.1l4a	-0.508	0.000132322
1460335_at	LysM, putative peptidoglycan-binding, domain containing 3	Lysmd3	-0.508	3.49E-06
1449292_at	RB1-inducible coiled-coil 1	Rb1cc1	-0.508	0.000378242
1424453_at	phosphate cytidylyltransferase 1, choline, alpha isoform	Pcyt1a	-0.508	9.36E-05
1427490_at	ATP-binding cassette, sub-family B (MDR/TAP), member 7	Abcb7	-0.508	0.001151814
1435369_at	U box domain containing 5	Ubox5	-0.508	1.44E-05
1420894_at	transforming growth factor, beta receptor I	Tgfbr1	-0.508	0.002698047
1448306_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	Nfkbia	-0.508	0.000124809
1452940_x_at	phosphatidylinositol transfer protein, cytoplasmic 1	Pitpnc1	-0.509	3.43E-05
1450941_at	syndecan binding protein	Sdcbp	-0.509	0.000378449
1428905_at	Ras-related GTP binding A	Rraga	-0.509	2.45E-05
1450403_at	signal transducer and activator of transcription	Stat2	-0.509	4.66E-05

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1427293_a_at	autism susceptibility candidate 2	Auts2	-0.509	8.07E-05
1450428_at	LIM homeobox protein 1	Lhx1	-0.51	0.003029852
1434840_at	HIV-1 Rev binding protein	Hrb	-0.51	3.47E-05
1424495_a_at	chemokine-like factor	Cklf	-0.51	5.67E-05
1448250_at	RIKEN cDNA 9030425E11 gene	9030425E11Rik	-0.51	2.72E-05
1416046_a_at	fucosidase, alpha-L- 2, plasma	Fuca2	-0.51	3.50E-05
1420056_s_at	jumonji domain containing 6	Jmjd6	-0.51	1.01E-05
1416661_at	eukaryotic translation initiation factor 3, subunit A	Eif3a	-0.511	0.00224775
1424446_at	armadillo repeat containing 7	Armc7	-0.511	3.58E-05
1450641_at	vimentin	Vim	-0.511	4.19E-05
1452583_s_at	galactose mutarotase	Galm	-0.511	0.000778399
1424971_at	coiled-coil domain containing 99	Ccdc99	-0.511	6.45E-06
1449847_a_at	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	Col4a3bp	-0.512	3.33E-05
1454663_at	eukaryotic translation initiation factor 5	Eif5	-0.512	9.89E-05
1417921_at	RIKEN cDNA 2610029G23 gene	2610029G23Rik	-0.513	3.98E-05
1422805_a_at	inhibitor of growth family, member 3	Ing3	-0.513	1.25E-05
1438686_at	eukaryotic translation initiation factor 4, gamma 1	Eif4g1	-0.513	0.023207623
1420654_a_at	glucan (1,4-alpha-), branching enzyme 1	Gbe1	-0.513	0.000140756
1450223_at	apoptotic peptidase activating factor 1	Apaf1	-0.513	0.000235745
1452490_a_at	adaptor protein complex AP-2, alpha 2 subunit	Ap2a2	-0.513	0.000116546
1456088_at	X-linked inhibitor of apoptosis	Xiap	-0.514	0.000847475
1436645_a_at	CCR4-NOT transcription complex, subunit 4	Cnot4	-0.514	0.000188862
1423162_s_at	sprouty protein with EVH-1 domain 1, related sequence	Spred1	-0.514	0.000242177
1434256_s_at	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	Cds2	-0.514	6.98E-06
1452140_at	TBC1 domain family, member 20	Tbc1d20	-0.514	7.46E-05
1438221_at	DNA segment, Chr 1, ERATO Doi 53, expressed	D1Ertd53e	-0.515	0.000992609
1448497_at	excision repair cross-complementing rodent repair deficiency, complementation group 3	Ercc3	-0.515	0.000120848
1421935_at	ribosomal protein S20	Rps20	-0.515	0.000521295
1416844_at	protein arginine N-methyltransferase 2	Prmt2	-0.515	5.12E-05
1420583_a_at	RAR-related orphan receptor alpha	Rora	-0.515	2.29E-05
1427209_at	bromodomain adjacent to zinc finger domain, 2A	Baz2a	-0.516	0.01929764
1428277_at	OTU domain containing 6B	Otud6b	-0.516	6.95E-06
1436042_at	talin 1	Tln1	-0.516	2.65E-05
1450051_at	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	Atrx	-0.517	0.004126084
1435362_at	forkhead box J3	Foxj3	-0.517	1.19E-05
1448883_at	legumain	Lgmn	-0.517	2.58E-05
1442745_x_at	RNA binding motif protein 39	Rbm39	-0.518	0.000681374
1451374_x_at	chemokine-like factor	Cklf	-0.518	0.000118465
1431921_a_at	stromal antigen 1	Stag1	-0.518	0.000132322
1421062_s_at	clathrin, light polypeptide (Lca)	Clta	-0.518	7.25E-06
1416727_a_at	cytochrome b-5	Cyb5	-0.519	4.14E-05
1417542_at	ribosomal protein S6 kinase, polypeptide 2	Rps6ka2	-0.519	8.32E-06
1420908_at	CD2-associated protein	Cd2ap	-0.519	9.13E-05
1435454_a_at	cDNA sequence BC006779	BC006779	-0.52	0.000132805
1434846_at	DENN/MADD domain containing 4C	Dennd4c	-0.52	2.58E-05
1439154_at	nucleoporin 98	Nup98	-0.52	1.79E-05
1451902_at	zinc finger protein 758	Zfp758	-0.52	0.000980564

1417379_at	IQ motif containing GTPase activating protein 1	Iqgap1	-0.52	3.25E-05
1452657_at	adaptor-related protein complex 1, sigma 2 subunit	Ap1s2	-0.521	3.29E-05
1450868_at	heparan-alpha-glucosaminide N-acetyltransferase	Hgsnat	-0.521	1.69E-05
1427285_s_at	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	Malat1	-0.521	0.002338945
1417861_at	cyclin C	Ccnc	-0.521	0.000209504
1422036_at	striatin, calmodulin binding protein	Strn	-0.521	0.000144957
1416271_at	PERP, TP53 apoptosis effector	Perp	-0.521	3.70E-05
1449731_s_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	Nfkbia	-0.522	1.24E-05
1448161_a_at	chloride channel 4-2	Clcn4-2	-0.523	2.19E-05
1419213_at	N-acetyltransferase 6	Nat6	-0.523	0.000169058
1426451_at	spastic paraplegia 11	Spg11	-0.524	1.40E-05
1452003_at	RNA binding motif protein 14	Rbm14	-0.524	0.000164923
1423196_at	neural precursor cell expressed, developmentally down-regulated gene 1	Nedd1	-0.524	0.000526486
1431107_at	serine/threonine kinase 35	Stk35	-0.524	8.36E-05
1433565_at	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	Prpf38a	-0.524	8.16E-06
1425305_at	zinc finger protein 295	Zfp295	-0.525	8.29E-06
1420810_at	RIKEN cDNA 1500003O03 gene	1500003O03Rik	-0.526	1.72E-05
1420973_at	AT rich interactive domain 5B (MRF1-like)	Arid5b	-0.526	0.001735341
1423308_at	trans-golgi network protein	Tgoln1	-0.526	0.000135365
1418431_at	kinesin family member 5B	Kif5b	-0.526	0.000636989
1427471_at	F-box and leucine-rich repeat protein 3	Fbxl3	-0.526	0.000493233
1417663_a_at	N-myc downstream regulated gene 3	Ndrg3	-0.527	2.90E-05
1432207_a_at	target of EGR1, member 1 (nuclear)	Toe1	-0.527	1.19E-05
1424083_at	ROD1 regulator of differentiation 1 (S. pombe)	Rod1	-0.527	0.000183385
1425240_at	cDNA sequence BC011426	BC011426	-0.528	0.000608683
1428761_a_at	small nuclear RNA activating complex, polypeptide 3	Snapc3	-0.528	9.27E-05
1448121_at	WW domain binding protein 2	Wbp2	-0.528	0.000114434
1448967_at	nipsnap homolog 3A (C. elegans)	Nipsnap3a	-0.529	7.41E-06
1437165_a_at	procollagen C-endopeptidase enhancer protein	Pcolce	-0.529	0.0002027
1449444_a_at	microfibrillar-associated protein 1A	Mfap1a	-0.529	1.49E-05
1438824_at	solute carrier family 20, member 1	Slc20a1	-0.529	0.000991556
1452419_at	HEAT repeat containing 1	Heatr1	-0.53	0.00383712
1435250_at	integrator complex subunit 8	Ints8	-0.53	3.79E-05
1431606_a_at	angel homolog 2 (Drosophila)	Angel2	-0.531	9.36E-05
1438427_at	RIKEN cDNA 4932442K08 gene	4932442K08Rik	-0.531	9.78E-06
1450401_at	trimethylguanosine synthase homolog (S. cerevisiae)	Tgs1	-0.531	2.09E-05
1450863_a_at	doublecortin-like kinase 1	Dclk1	-0.532	0.000469652
1450760_a_at	inhibitor of growth family, member 3	Ing3	-0.532	5.59E-05
1426195_a_at	cystatin C	Cst3	-0.532	2.88E-05
1426404_a_at	ring finger protein 11	Rnf11	-0.532	4.98E-05
1427544_a_at	poly (A) polymerase alpha	Papola	-0.532	5.38E-05
1419455_at	interleukin 10 receptor, beta	Il10rb	-0.532	7.32E-05
1422718_at	adaptor-related protein complex 3, sigma 2 subunit	Ap3s2	-0.533	8.35E-06
1451425_a_at	makorin, ring finger protein, 1	Mkrn1	-0.533	0.000168767
1451439_at	cDNA sequence BC027231	BC027231	-0.533	6.31E-06
1452084_at	zinc finger, CCHC domain containing 17	Zcchc17	-0.533	7.60E-06
1419717_at	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	Sema3e	-0.534	0.000570516

1456292_a_at	vimentin	Vim	-0.534	1.82E-05
1450420_at	stromal antigen 1	Stag1	-0.535	6.16E-05
1430275_a_at	aquarius	Aqr	-0.535	5.30E-05
1436746_at	WNK lysine deficient protein kinase 1	Wnk1	-0.535	0.000481886
1416959_at	nuclear receptor subfamily 1, group D, member 2	Nr1d2	-0.535	0.000135955
1435526_at	torsin A interacting protein 2	Tor1aip2	-0.535	1.65E-05
1416541_at	ClpB caseinolytic peptidase B homolog (E. coli)	Clpb	-0.536	9.05E-05
1448747_at	F-box protein 32	Fbxo32	-0.536	0.000487016
1451653_a_at	RIKEN cDNA 4930430E16 gene	4930430E16Rik	-0.537	8.59E-05
1424303_at	DEP domain containing 7	Depdc7	-0.537	5.55E-06
1418872_at	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	Abcb1b	-0.537	2.14E-05
1424974_at	zinc finger protein 418	Zfp418	-0.538	0.001042532
1449119_at	ariadne homolog 2 (Drosophila)	Arih2	-0.538	0.000365573
1422633_at	RIKEN cDNA 1700020D05 gene	1700020D05Rik	-0.538	0.000966386
1419256_at	spectrin beta 2	Spnb2	-0.539	0.001480989
1451816_at	zinc finger protein 451	Zfp451	-0.539	0.001021892
1421493_a_at	regulator of G-protein signaling 20	Rgs20	-0.539	0.000163871
1452550_a_at	fragile X mental retardation syndrome 1 homolog	Fmr1	-0.539	0.000797138
1451991_at	Eph receptor A7	Epha7	-0.539	0.004738255
1449028_at	ras homolog gene family, member U	Rhou	-0.54	1.75E-05
1419552_at	enoyl Coenzyme A hydratase domain containing 1	Echdc1	-0.541	0.000350297
1421070_at	DNA segment, Chr 3, ERATO Doi 300, expressed	D3Ertd300e	-0.541	0.000189129
1428552_at	RIKEN cDNA 2610001J05 gene	2610001J05Rik	-0.541	2.07E-05
1450417_a_at	ribosomal protein S20	Rps20	-0.541	0.003092094
1424598_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	Ddx6	-0.541	0.001088199
1431024_a_at	AT rich interactive domain 4B (RBP1-like)	Arid4b	-0.541	7.31E-05
1451080_at	ubiquitin specific peptdiase 1	Usp1	-0.542	2.44E-05
1437835_a_at	RIKEN cDNA 0610011L14 gene	0610011L14Rik	-0.542	0.000474202
1425940_a_at	single-stranded DNA binding protein 3	Ssbp3	-0.542	2.92E-05
1427408_a_at	thyroid hormone receptor associated protein 3	Thrap3	-0.543	3.96E-05
1424574_at	transmembrane emp24 protein transport domain containing 5	Tmed5	-0.543	0.000108669
1418659_at	circadian locomoter output cycles kaput	Clock	-0.543	4.03E-05
1451281_at	zinc finger and SCAN domain containing 12	Zscan12	-0.543	4.11E-05
1460363_at	trinucleotide repeat containing 6C	Tnrc6c	-0.544	2.55E-05
1449732_at	zinc finger and SCAN domain containing 21	Zscan21	-0.545	5.00E-05
1417883_at	glutathione S-transferase, theta 2	Gstt2	-0.545	1.44E-05
1416304_at	LPS-induced TN factor	Litaf	-0.545	7.60E-06
1449983_a_at	NAD(P)H dehydrogenase, quinone 2	Nqo2	-0.545	0.000282295
1448180_a_at	hematological and neurological expressed sequence 1	Hn1	-0.546	3.91E-06
1425521_at	polyadenylate binding protein-interacting protein 1	Paip1	-0.547	0.00016428
1450107_a_at	renin binding protein	Renbp	-0.547	3.75E-06
1428442_at	cDNA sequence BC029722	BC029722	-0.547	5.28E-05
1420856_a_at	LanC (bacterial lantibiotic synthetase component C)-like 2	Lancl2	-0.547	0.000988642
1427024_at	SLAIN motif family, member 2	Slain2	-0.547	5.19E-05
1424217_at	poly (A) polymerase alpha	Papola	-0.548	0.003003393
1449002_at	pleckstrin homology-like domain, family A, member 3	Phlda3	-0.548	1.11E-05
1418628_at	KH domain containing, RNA binding, signal	Khdrbs1	-0.548	6.07E-05

	transduction associated 1			
1423483_s_at	TATA box binding protein (Tbp)-associated factor, RNA polymerase I, C	Taf1c	-0.548	1.78E-05
1417330_at	solute carrier family 23 (nucleobase transporters), member 2	Slc23a2	-0.548	0.005056267
1426456_a_at	protein inhibitor of activated STAT 2	Pias2	-0.549	5.34E-05
1421869_at	tripartite motif-containing 44	Trim44	-0.549	0.001793858
1427534_at	RIKEN cDNA 4930535I16 gene	4930535I16Rik	-0.549	3.66E-05
1417240_at	zyxin	Zyx	-0.55	7.13E-06
1420340_at	centrosome and spindle pole associated protein 1	Cspp1	-0.55	0.000104749
1450675_at	stromal membrane-associated GTPase-activating protein 2	Smap2	-0.55	2.63E-06
1452639_at	ectonucleotide pyrophosphatase/phosphodiesterase 4	Enpp4	-0.55	3.79E-05
1417409_at	Jun oncogene	Jun	-0.551	4.66E-05
1419287_at	transmembrane protein 208	Tmem208	-0.551	4.03E-06
1418520_at	trans-golgi network protein	Tgoln1	-0.552	0.000638047
1417350_at	pallidin	Pldn	-0.552	0.000529716
1423663_at	folliculin	Flcn	-0.552	3.83E-05
1424597_at	open reading frame 19	ORF19	-0.552	1.05E-05
1437544_at	far upstream element (FUSE) binding protein 1	Fubp1	-0.553	0.000419653
1417664_a_at	N-myc downstream regulated gene 3	Ndrg3	-0.553	1.69E-05
1424293_s_at	transmembrane protein 55A	Tmem55a	-0.553	1.46E-05
1426886_at	ceroid-lipofuscinosis, neuronal 5	Cln5	-0.553	8.44E-06
1418850_at	enhancer of polycomb homolog 1 (Drosophila)	Epc1	-0.553	1.44E-05
1425848_a_at	dual specificity phosphatase 26 (putative)	Dusp26	-0.554	6.95E-06
1419585_at	retinitis pigmentosa 2 homolog (human)	Rp2h	-0.554	0.000635389
1416174_at	retinoblastoma binding protein 9	Rbbp9	-0.554	5.19E-05
1418366_at	histone cluster 2, H2aa1	Hist2h2aa1	-0.554	3.29E-05
1448433_a_at	procollagen C-endopeptidase enhancer protein	Pcolce	-0.554	0.000149179
1428855_at	histocompatibility 13	H13	-0.554	7.95E-05
1432211_a_at	f-box protein 9	Fbxo9	-0.554	0.00010993
1417029_a_at	tripartite motif-containing 2	Trim2	-0.555	0.000621324
1432332_a_at	nudix (nucleoside diphosphate linked moiety X)-type motif 19	Nudt19	-0.555	6.67E-06
1448014_s_at	ubiquitin specific peptidase 24	Usp24	-0.556	4.73E-05
1431320_a_at	myosin Va	Myo5a	-0.557	1.30E-05
1436058_at	radical S-adenosyl methionine domain containing 2	Rsad2	-0.557	0.001254182
1427077_a_at	adaptor-related protein complex 2, beta 1 subunit	Ap2b1	-0.557	1.71E-05
1432181_s_at	SCO cytochrome oxidase deficient homolog 2 (yeast)	Sco2	-0.557	4.10E-05
1425598_a_at	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog	Lyn	-0.558	3.47E-05
1450683_at	transgelin 3	Tagln3	-0.558	8.82E-06
1423184_at	intersectin 2	Itsn2	-0.558	0.00134076
1420603_s_at	retinoic acid early transcript 1, alpha	Raet1a	-0.559	2.62E-05
1448068_at	sterol O-acyltransferase 1	Soat1	-0.559	0.004359392
1434499_a_at	lactate dehydrogenase B	Ldhb	-0.559	0.000651497
1424564_at	RIKEN cDNA 2410001C21 gene	2410001C21Rik	-0.56	2.99E-05
1452416_at	interleukin 6 receptor, alpha	Il6ra	-0.56	0.000742637
1421107_at	serine/threonine kinase 4	Stk4	-0.561	9.40E-05
1424504_at	RAB22A, member RAS oncogene family	Rab22a	-0.562	0.000456217
1449542_at	pre B-cell leukemia transcription factor 1	Pbx1	-0.563	1.90E-05
1457833_at	expressed sequence AI450241	AI450241	-0.564	0.000340297

1416142_at	ribosomal protein S6	Rps6	-0.564	6.29E-06
1434282_at	inhibitor of Bruton agammaglobulinemia tyrosine kinase	Ibtk	-0.564	0.00017914
1416059_at	SEC23B (S. cerevisiae)	Sec23b	-0.564	2.59E-06
1428229_at	protein kinase D3	Prkd3	-0.564	7.19E-05
1454891_at	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	Cds2	-0.564	0.001254182
1416901_at	Niemann Pick type C2	Npc2	-0.564	4.01E-06
1418794_at	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	Cds2	-0.564	0.000180298
1459911_at	cerebellar degeneration-related protein 2-like	Cdr2l	-0.564	5.58E-06
1416744_at	UDP-N-acetylglucosamine pyrophosphorylase 1	Uap1	-0.564	0.000214079
1449686_s_at	sterol carrier protein 2, liver	Scp2	-0.565	0.000123714
1435042_at	RIKEN cDNA 9130004C02 gene	9130004C02Rik	-0.566	0.001174164
1425769_x_at	chemokine-like factor	Cklf	-0.566	8.07E-05
1454109_a_at	jumonji domain containing 6	Jmjd6	-0.566	0.000174344
1422661_at	lectin, galactose binding, soluble 8	Lgals8	-0.566	1.33E-05
1451201_s_at	ribonuclease/angiogenin inhibitor 1	Rnh1	-0.566	1.18E-05
1418536_at	histocompatibility 2, Q region locus 7	H2-Q7	-0.567	0.00031477
1450099_a_at	glucosidase, beta, acid	Gba	-0.567	6.06E-06
1428357_at	RIKEN cDNA 2610019F03 gene	2610019F03Rik	-0.567	1.62E-05
1426016_a_at	trophinin	Tro	-0.568	9.84E-05
1455857_a_at	RAB2B, member RAS oncogene family	Rab2b	-0.568	0.000774555
1450997_at	serine/threonine kinase 17b (apoptosis-inducing)	Stk17b	-0.568	0.000200291
1455176_a_at	synaptotagmin XI	Syt11	-0.568	1.98E-06
1429897_a_at	DNA segment, Chr 16, ERATO Doi 472, expressed	D16Ertd472e	-0.569	1.08E-05
1451273_x_at	FtsJ methyltransferase domain containing 1	Ftsjd1	-0.569	1.19E-05
1452373_at	RIKEN cDNA 1700081L11 gene	1700081L11Rik	-0.57	1.16E-05
1419370_a_at	microfibrillar-associated protein 1A	Mfap1a	-0.571	2.04E-05
1428025_s_at	phosphatidylinositol transfer protein, cytoplasmic 1	Pitpnc1	-0.571	1.38E-05
1452377_at	myeloid/lymphoid or mixed-lineage leukemia 1	Mll1	-0.571	0.000230011
1424289_at	oxidative stress induced growth inhibitor family member 2	Osgin2	-0.571	1.36E-05
1457588_at	expressed sequence C76213	C76213	-0.571	8.12E-05
1450231_a_at	X-linked inhibitor of apoptosis	Xiap	-0.572	0.003707359
1437044_a_at	glucosidase, beta, acid	Gba	-0.572	2.73E-06
1425682_a_at	Tp53rk binding protein	Tprkb	-0.572	3.02E-05
1418714_at	dual specificity phosphatase 8	Dusp8	-0.573	2.27E-05
1425059_at	protein arginine N-methyltransferase 6	Prmt6	-0.573	2.99E-06
1438011_at	phosphate cytidylyltransferase 1, choline, alpha isoform	Pcyt1a	-0.574	1.44E-05
1423170_at	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf7	-0.574	0.000761681
1451347_at	NO80 complex subunit E	Ino80e	-0.575	5.93E-05
1422101_at	tumor necrosis factor receptor superfamily, member 23	Tnfrsf23	-0.575	0.000120181
1417277_at	cytochrome P450, family 4, subfamily f, polypeptide 16	Cyp4f16	-0.576	0.000100247
1427334_s_at	RIKEN cDNA 2810474O19 gene	2810474O19Rik	-0.576	2.70E-05
1416942_at	endoplasmic reticulum aminopeptidase 1	Erap1	-0.576	0.000128132
1449258_at	DNA segment, Chr 11, Wayne State University 99, expressed	D11Wsu99e	-0.577	0.000128576
1415886_at	SH2 domain containing 3C	Sh2d3c	-0.577	2.19E-05
1426856_at	hydroxysteroid dehydrogenase like 2	Hsdl2	-0.577	7.21E-05

1433588_at	DNA segment, Chr 6, Wayne State University 116, expressed	D6Wsu116e	-0.577	5.91E-06
1416666_at	serine (or cysteine) peptidase inhibitor, clade E, member 2	Serpine2	-0.577	7.29E-05
1416258_at	thymidine kinase 1	Tk1	-0.577	7.13E-06
1451776_s_at	HOP homeobox	Hopx	-0.577	1.10E-05
1456302_at	peroxisomal biogenesis factor 6	Pex6	-0.577	0.000208666
1419074_at	ChaC, cation transport regulator homolog 2 (E. coli)	Chac2	-0.578	2.38E-05
1422877_at	protocadherin beta 12	Pcdhb12	-0.578	7.00E-05
1434300_at	RIKEN cDNA 2610101N10 gene	2610101N10Rik	-0.579	0.000222719
1438033_at	thyrotroph embryonic factor	Tef	-0.579	0.00655087
1423557_at	interferon gamma receptor 2	Ifngr2	-0.58	2.64E-05
1450400_at	trimethylguanosine synthase homolog (S. cerevisiae)	Tgs1	-0.58	2.20E-05
1427217_at	zinc finger protein 455	Zfp455	-0.581	0.001114821
1426765_at	COMM domain containing 7	Commd7	-0.581	2.44E-06
1425114_at	retinoblastoma binding protein 6	Rbbp6	-0.581	0.000201247
1450007_at	RIKEN cDNA 1500003O03 gene	1500003O03Rik	-0.581	0.000357255
1418978_at	SAP30 binding protein	Sap30bp	-0.581	2.59E-06
1416262_at	transmembrane protein 19	Tmem19	-0.581	4.05E-06
1454604_s_at	tetraspanin 12	Tspan12	-0.581	9.12E-05
1426614_at	protein kinase C binding protein 1	Prkcbp1	-0.582	2.01E-06
1418873_at	sideroflexin 4	Sfxn4	-0.582	0.000357743
1423249_at	natural killer tumor recognition sequence	Nktr	-0.582	0.000653779
1437234_x_at	protein arginine N-methyltransferase 2	Prmt2	-0.582	4.97E-06
1421322_a_at	interferon regulatory factor 9	Irf9	-0.582	1.12E-05
1424369_at	proteasome (prosome, macropain) inhibitor subunit 1	Psmf1	-0.582	5.47E-06
1417888_at	tripartite motif-containing 13	Trim13	-0.582	0.00012924
1436176_at	RIKEN cDNA 1500004A13 gene	1500004A13Rik	-0.583	0.000276064
1433659_at	tubulin, gamma complex associated protein 4	Tubgcp4	-0.583	6.72E-05
1438661_a_at	ADP-ribosylation factor 2	Arf2	-0.583	0.000236446
1431074_a_at	phosphatidylinositol transfer protein, cytoplasmic 1	Pitpnc1	-0.583	0.001127363
1417968_a_at	methyl-CpG binding domain protein 1	Mbd1	-0.584	3.68E-06
1448694_at	Jun oncogene	Jun	-0.584	2.10E-05
1419155_a_at	SRY-box containing gene 4	Sox4	-0.584	3.09E-06
1449027_at	ras homolog gene family, member U	Rhou	-0.584	5.25E-06
1457964_at	RIKEN cDNA 1810044D09 gene	1810044D09Rik	-0.585	7.15E-05
1416418_at	gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1	Gabarapl1	-0.586	1.35E-05
1418502_a_at	oxidation resistance 1	Oxr1	-0.587	0.000290595
1429830_a_at	CD59a antigen	Cd59a	-0.587	5.00E-06
1417488_at	fos-like antigen 1	Fosl1	-0.588	3.48E-06
1455700_at	MTERF domain containing 3	Mterfd3	-0.588	1.74E-05
1427950_at	zinc finger protein 294	Zfp294	-0.588	0.000229288
1416463_at	cell cycle associated protein 1	Caprin1	-0.588	4.45E-06
1423674_at	ubiquitin specific peptdiase 1	Usp1	-0.589	8.14E-05
1427098_at	WW domain containing E3 ubiquitin protein ligase 1	Wwp1	-0.589	5.34E-06
1423890_x_at	ATPase, Na+/K+ transporting, beta 1 polypeptide	Atp1b1	-0.589	4.77E-05
1455930_at	NA	NA	-0.589	0.000363276
1420367_at	density-regulated protein	Denr	-0.589	1.19E-05
1419442_at	matrilin 2	Matn2	-0.59	0.000347659
1422054_a_at	SKI-like	Skil	-0.59	0.000826909

1448850_a_at	DnaJ (Hsp40) homolog, subfamily C, member 5	Dnajc5	-0.592	1.05E-05
1426527_at	target of EGR1, member 1 (nuclear)	Toe1	-0.592	5.95E-05
1422468_at	palmitoyl-protein thioesterase 1	Ppt1	-0.592	2.03E-05
1452058_a_at	ring finger protein 11	Rnf11	-0.593	7.25E-06
1423185_a_at	ubiquitin-associated protein 1	Ubap1	-0.593	1.45E-05
1450068_at	bromodomain adjacent to zinc finger domain, 1B	Baz1b	-0.593	0.00550171
1449527_at	protocadherin beta 7	Pcdhb7	-0.593	0.005382428
1450557_at	sodium channel, voltage-gated, type IV, alpha	Scn4a	-0.593	2.20E-05
1418915_at	methylmalonic aciduria cblC type, with homocystinuria	Mmachc	-0.594	8.35E-06
1425285_a_at	RAB27A, member RAS oncogene family	Rab27a	-0.594	4.04E-05
1420915_at	signal transducer and activator of transcription 1	Stat1	-0.594	0.00015914
1425339_at	phospholipase C, beta 4	Plcb4	-0.594	4.83E-05
1417487_at	fos-like antigen 1	Fosl1	-0.594	5.57E-05
1452133_at	ubiquinol-cytochrome c reductase hinge protein	Uqcrh	-0.594	2.75E-06
1425810_a_at	cysteine and glycine-rich protein 1	Csrp1	-0.596	1.58E-05
1451299_at	protein kinase, X-linked	Prkx	-0.596	4.43E-05
1429110_a_at	NOL1/NOP2/Sun domain family, member 4	Nsun4	-0.597	5.34E-06
1419087_s_at	splicing factor 3a, subunit 1	Sf3a1	-0.597	3.13E-06
1456870_at	RIKEN cDNA A430107D22 gene	A430107D22Rik	-0.597	8.98E-05
1452361_at	ring finger protein 20	Rnf20	-0.597	0.000123996
1434618_at	CREB/ATF bZIP transcription factor	Crebzf	-0.598	2.32E-05
1437120_at	sorting nexin family member 30	Snx30	-0.598	0.000305806
1421209_s_at	inhibitor of kappaB kinase gamma	Ikbkg	-0.599	3.25E-05
1418296_at	FXYD domain-containing ion transport regulator 5	Fxyd5	-0.6	7.08E-05
1453077_a_at	small nuclear RNA activating complex, polypeptide 3	Snapc3	-0.6	8.45E-05
1434751_at	iduronate 2-sulfatase	Ids	-0.602	0.0003447
1432430_a_at	RIKEN cDNA 1700081L11 gene	1700081L11Rik	-0.602	7.21E-05
1415893_at	sphingosine phosphate lyase 1	Sgpl1	-0.603	0.000167472
1431591_s_at	predicted gene, 677168	677168	-0.603	5.18E-05
1416852_a_at	neurochondrin	Ncdn	-0.604	8.25E-05
1422250_at	mitogen-activated protein kinase kinase kinase 2	Map3k2	-0.604	0.004140506
1418073_at	acyl-CoA thioesterase 9	Acot9	-0.604	2.03E-05
1450434_s_at	phosphate cytidylyltransferase 1, choline, alpha isoform	Pcyt1a	-0.605	1.35E-05
1451685_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	Mllt6	-0.605	0.002254922
1418045_at	inositol polyphosphate-1-phosphatase	Inpp1	-0.605	5.97E-06
1425087_at	RIKEN cDNA 2310003F16 gene	2310003F16Rik	-0.607	0.00148608
1426066_a_at	dystrobrevin alpha	Dtna	-0.607	0.002058155
1424090_at	syndecan binding protein (syntenin) 2	Sdcbp2	-0.607	0.000473353
1452191_at	prolylcarboxypeptidase (angiotensinase C)	Prcp	-0.608	1.61E-05
1437645_at	activating transcription factor 7	Atf7	-0.608	0.005142434
1421237_at	thymopoietin	Tmpo	-0.608	0.000450415
1435634_at	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	Pcmtd1	-0.609	0.000560717
1422627_a_at	McKusick-Kaufman syndrome protein	Mkks	-0.609	1.15E-05
1422562_at	Ras-related associated with diabetes	Rrad	-0.61	3.03E-05
1420961_a_at	influenza virus NS1A binding protein	Ivns1abp	-0.61	5.33E-05
1436179_a_at	DnaJ (Hsp40) homolog, subfamily C, member	Dnajc5	-0.61	3.24E-05

	5			
1455346_at	mannan-binding lectin serine peptidase 1	Masp1	-0.61	0.000603742
1418367_x_at	histone cluster 2, H2aa1	Hist2h2aa1	-0.611	1.67E-05
1425811_a_at	cysteine and glycine-rich protein 1	Csrp1	-0.611	1.01E-05
1425180_at	SH3-domain GRB2-like (endophilin) interacting protein 1	Sgip1	-0.611	1.06E-05
1448128_at	cathepsin A	Ctsa	-0.611	4.68E-06
1424084_at	ROD1 regulator of differentiation 1 (S. pombe)	Rod1	-0.611	5.13E-05
1449257_at	DNA segment, Chr 11, Wayne State University 99, expressed	D11Wsu99e	-0.612	1.19E-05
1448830_at	dual specificity phosphatase 1	Dusp1	-0.612	1.19E-05
1460304_a_at	upstream binding transcription factor, RNA polymerase I	Ubtf	-0.613	0.000412001
1449024_a_at	hexosaminidase A	Hexa	-0.615	2.75E-06
1448746_at	nibrin	Nbn	-0.615	3.33E-05
1424239_at	RIKEN cDNA 2310066E14 gene	2310066E14Rik	-0.615	1.11E-05
1451152_a_at	ATPase, Na+/K+ transporting, beta 1 polypeptide	Atp1b1	-0.615	0.000210009
1456120_at	RIKEN cDNA 3110001I20 gene	3110001I20Rik	-0.615	0.00033852
1418496_at	forkhead box A1	Foxa1	-0.615	5.26E-05
1456112_at	translocated promoter region	Tpr	-0.616	7.00E-05
1416167_at	peroxiredoxin 4	Prdx4	-0.616	7.39E-05
1448013_at	ubiquitin specific peptidase 24	Usp24	-0.616	8.77E-06
1451908_a_at	SEC14-like 1 (S. cerevisiae)	Sec14l1	-0.616	0.000131673
1427017_at	special AT-rich sequence binding protein 2	Satb2	-0.617	1.45E-05
1450100_a_at	transcription elongation regulator 1 (CA150)	Tcerg1	-0.617	3.80E-05
1424286_at	protein kinase, X-linked	Prkx	-0.617	2.10E-06
1427476_a_at	tripartite motif-containing 32	Trim32	-0.618	4.12E-05
1416853_at	neurochondrin	Ncdn	-0.618	3.82E-06
1449968_s_at	acyl-CoA thioesterase 10	Acot10	-0.619	3.64E-05
1429137_at	RIKEN cDNA 2810422O20 gene	2810422O20Rik	-0.619	0.000238524
1423675_at	ubiquitin specific peptdiase 1	Usp1	-0.62	9.76E-06
1422741_a_at	bobby sox homolog (Drosophila)	Bbx	-0.62	0.000132427
1442744_at	RNA binding motif protein 39	Rbm39	-0.622	4.05E-05
1460257_a_at	5, 10-methenyltetrahydrofolate synthetase	Mthfs	-0.622	0.000624046
1423546_at	zinc finger protein 207	Zfp207	-0.623	0.00849964
1429654_at	developmental pluripotency associated 2	Dppa2	-0.624	4.91E-05
1426405_at	ring finger protein 11	Rnf11	-0.625	0.002637205
1416635_at	sphingomyelin phosphodiesterase, acid-like 3A	Smpdl3a	-0.625	0.000395557
1419156_at	SRY-box containing gene 4	Sox4	-0.627	3.24E-06
1419239_at	zinc finger protein 54	Zfp54	-0.627	0.000225437
1438167_x_at	folliculin	Flcn	-0.627	4.45E-06
1417543_at	ribosomal protein S6 kinase, polypeptide 2	Rps6ka2	-0.628	1.19E-05
1421566_at	plasmacytoma expressed transcript 2	Pet2	-0.628	7.60E-06
1460592_at	erythrocyte protein band 4.1-like 1	Epb4.1l1	-0.629	1.83E-06
1435226_at	ring finger protein 19B	Rnf19b	-0.629	1.28E-05
1450459_at	RIKEN cDNA 2010106G01 gene	2010106G01Rik	-0.63	4.31E-05
1449042_at	CCCTC-binding factor	Ctcf	-0.63	0.000169067
1422785_at	RAS p21 protein activator 2	Rasa2	-0.63	1.18E-05
1426928_at	coiled-coil domain containing 93	Ccdc93	-0.631	4.98E-05
1423086_at	Niemann Pick type C1	Npc1	-0.631	6.98E-06
1434540_a_at	clathrin, light polypeptide (Lca)	Clta	-0.632	1.44E-05
1417623_at	solute carrier family 12, member 2	Slc12a2	-0.633	0.000243261
1417461_at	CAP, adenylate cyclase-associated protein 1 (yeast)	Cap1	-0.633	1.53E-06
1427934_at	LYR motif containing 2	Lyrm2	-0.633	1.13E-05
1421840_at	ATP-binding cassette, sub-family A (ABC1),	Abca1	-0.633	1.04E-05

	member 1			
1424290_at	oxidative stress induced growth inhibitor family member 2	Osgin2	-0.634	1.04E-06
1430240_a_at	calmegin	Clgn	-0.635	3.44E-06
1446914_at	expressed sequence C80425	C80425	-0.636	0.000123472
1451100_a_at	carnitine deficiency-associated gene expressed in ventricle 3	Cdv3	-0.636	0.00081124
1455388_at	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	Pcmtd1	-0.637	5.97E-06
1449514_at	G protein-coupled receptor kinase 5	Grk5	-0.637	8.35E-06
1448239_at	heme oxygenase (decycling) 1	Hmox1	-0.637	0.000135365
1422455_s_at	N-ethylmaleimide sensitive fusion protein	Nsf	-0.637	6.50E-05
1420850_at	Crn, crooked neck-like 1 (Drosophila)	Crnkl1	-0.637	1.23E-05
1438220_at	forkhead box J3	Foxj3	-0.637	3.67E-06
1424370_s_at	proteasome (prosome, macropain) inhibitor subunit 1	Psmf1	-0.637	1.97E-06
1417060_at	protein phosphatase 1, regulatory (inhibitor) subunit 11	Ppp1r11	-0.638	3.09E-06
1426063_a_at	GTP binding protein (gene overexpressed in skeletal muscle)	Gem	-0.638	1.00E-05
1448541_at	kinesin light chain 1	Klc1	-0.639	0.000217293
1422662_at	lectin, galactose binding, soluble 8	Lgals8	-0.639	1.13E-05
1424573_at	transmembrane emp24 protein transport domain containing 5	Tmed5	-0.64	4.73E-05
1434369_a_at	crystallin, alpha B	Cryab	-0.64	5.85E-05
1419157_at	SRY-box containing gene 4	Sox4	-0.641	8.76E-06
1435639_at	RIKEN cDNA 2610528A11 gene	2610528A11Rik	-0.641	5.52E-05
1421117_at	dystonin	Dst	-0.641	0.000175422
1436909_at	solute carrier family 25, member 44	Slc25a44	-0.641	7.49E-06
1420893_a_at	transforming growth factor, beta receptor I	Tgfbr1	-0.644	0.000880255
1425205_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19b	Ddx19b	-0.645	4.67E-05
1423465_at	ferric-chelate reductase 1	Frrs1	-0.645	5.93E-06
1448966_a_at	nuclear factor of activated T-cells 5	Nfat5	-0.646	6.75E-06
1448124_at	glucuronidase, beta	Gusb	-0.646	3.09E-06
1416408_at	acyl-Coenzyme A oxidase 1, palmitoyl	Acox1	-0.646	2.26E-06
1437110_at	RIKEN cDNA 2810474O19 gene	2810474O19Rik	-0.647	1.20E-05
1418911_s_at	acyl-CoA synthetase long-chain family member 4	Acsl4	-0.649	2.95E-05
1425698_a_at	CREB/ATF bZIP transcription factor	Crebzf	-0.649	2.07E-05
1422919_at	HRAS-like suppressor	Hrasls	-0.649	2.99E-05
1424687_at	HEAT repeat containing 6	Heatr6	-0.65	0.000235824
1418887_a_at	DNA segment, Chr 11, Wayne State University 99, expressed	D11Wsu99e	-0.65	2.49E-05
1415864_at	2,3-bisphosphoglycerate mutase	Bpgm	-0.651	1.20E-05
1416106_at	KTI12 homolog, chromatin associated (S. cerevisiae)	Kti12	-0.651	9.95E-06
1416047_at	fucosidase, alpha-L- 2, plasma	Fuca2	-0.651	7.86E-05
1416166_a_at	peroxiredoxin 4	Prdx4	-0.651	0.000261195
1427573_at	cysteine-rich hydrophobic domain 1	Chic1	-0.652	1.16E-05
1418354_at	component of oligomeric golgi complex 1	Cog1	-0.652	7.25E-06
1425141_at	lactamase, beta 2	Lactb2	-0.652	5.97E-06
1449875_s_at	histocompatibility 2, T region locus 10	H2-T10	-0.653	6.82E-06
1450119_at	dystonin	Dst	-0.653	2.43E-05
1421358_at	histocompatibility 2, M region locus 3	H2-M3	-0.654	2.42E-05
1417755_at	topoisomerase I binding, arginine/serine-rich	Topors	-0.654	0.000160087
1436343_at	chromodomain helicase DNA binding protein 4	Chd4	-0.654	0.000496517
1437082_at	A kinase (PRKA) anchor protein (yotiao) 9	Akap9	-0.654	0.001313302

1418617_x_at	calmegin	Clgn	-0.655	1.90E-05
1448707_at	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Taf13	-0.656	6.00E-05
1436620_at	coiled-coil domain containing 45	Ccdc45	-0.658	3.10E-06
1448328_at	SH3-domain binding protein 2	Sh3bp2	-0.659	1.98E-06
1430889_a_at	thiopurine methyltransferase	Tpmt	-0.659	0.000629908
1452470_at	centrosomal protein 350	Cep350	-0.659	0.000450415
1422507_at	cystatin B	Cstb	-0.66	8.06E-06
1419057_at	solute carrier family 5 (sodium/glucose cotransporter), member 1	Slc5a1	-0.66	2.81E-05
1426253_at	RIKEN cDNA 4933428G09 gene	4933428G09Rik	-0.66	6.48E-05
1425193_at	RIKEN cDNA 2010106G01 gene	2010106G01Rik	-0.661	1.13E-05
1421939_a_at	stromal antigen 1	Stag1	-0.661	6.45E-05
1417038_at	septin 9	Sept9	-0.662	4.61E-06
1428046_a_at	zinc finger protein X-linked	Zfx	-0.662	0.001301399
1450988_at	leucine rich repeat containing G protein coupled receptor 5	Lgr5	-0.662	3.54E-06
1449823_at	dachshund 2 (Drosophila)	Dach2	-0.664	0.00062259
1421132_at	poliovirus receptor-related 3	Pvrl3	-0.666	5.70E-05
1421957_a_at	phosphate cytidylyltransferase 1, choline, alpha isoform	Pcyt1a	-0.666	7.68E-06
1417754_at	topoisomerase I binding, arginine/serine-rich	Topors	-0.667	0.00027099
1449053_s_at	component of oligomeric golgi complex 1	Cog1	-0.669	8.94E-07
1450893_a_at	ubiquitin-associated protein 1	Ubap1	-0.671	1.13E-05
1423048_a_at	toll interacting protein	Tollip	-0.671	0.000312595
1449370_at	SRY-box containing gene 4	Sox4	-0.671	1.98E-05
1422748_at	zinc finger E-box binding homeobox 2	Zeb2	-0.672	2.60E-05
1422136_at	U2AF homology motif (UHM) kinase 1	Uhmk1	-0.673	0.000413576
1448562_at	uridine phosphorylase 1	Upp1	-0.673	1.83E-06
1423921_at	integrator complex subunit 3	Ints3	-0.673	6.39E-05
1450763_x_at	wingless-related MMTV integration site 3	Wnt3	-0.674	0.000514584
1454106_a_at	CXXC finger 1 (PHD domain)	Cxxc1	-0.676	0.000222432
1452521_a_at	plasminogen activator, urokinase receptor	Plaur	-0.676	1.42E-05
1424775_at	2'-5' oligoadenylate synthetase 1G	Oas1g	-0.676	1.06E-05
1428047_s_at	zinc finger protein X-linked	Zfx	-0.678	0.000574655
1433589_at	DNA segment, Chr 6, Wayne State University 116, expressed	D6Wsu116e	-0.679	8.06E-06
1452448_at	aquarius	Aqr	-0.68	0.0001702
1426464_at	nuclear receptor subfamily 1, group D, member 1	Nr1d1	-0.681	4.95E-06
1421011_at	hydroxysteroid (17-beta) dehydrogenase 11	Hsd17b11	-0.681	7.88E-05
1425043_s_at	RIKEN cDNA 0610037D15 gene	0610037D15Rik	-0.682	0.000230988
1416455_a_at	crystallin, alpha B	Cryab	-0.683	3.84E-05
1425403_at	dynamin 3	Dnm3	-0.684	6.06E-06
1451921_a_at	nuclear factor of activated T-cells 5	Nfat5	-0.685	0.000108942
1448862_at	intercellular adhesion molecule 2	Icam2	-0.685	3.34E-06
1434642_at	hydroxysteroid (17-beta) dehydrogenase 11	Hsd17b11	-0.685	8.56E-06
1452290_at	transmembrane protein 106B	Tmem106b	-0.687	2.45E-05
1450161_at	inhibitor of kappaB kinase gamma	Ikbkg	-0.688	0.000116855
1423573_at	steroid 5 alpha-reductase 3	Srd5a3	-0.688	2.25E-05
1424076_at	glycerophosphodiester phosphodiesterase domain containing 1	Gdpd1	-0.689	1.10E-05
1416013_at	phospholipase D family, member 3	Pld3	-0.692	1.47E-05
1448450_at	adenylate kinase 2	Ak2	-0.692	5.94E-06
1448348_at	cell cycle associated protein 1	Caprin1	-0.692	0.000362879
1449264_at	synaptotagmin XI	Syt11	-0.692	4.80E-05
1423331_a_at	poliovirus receptor-related 3	Pvrl3	-0.693	2.11E-05

1426857_a_at	hydroxysteroid dehydrogenase like 2	Hsdl2	-0.693	8.82E-06
1431464_a_at	phosphomannomutase 2	Pmm2	-0.693	2.20E-05
1425140_at	lactamase, beta 2	Lactb2	-0.694	3.18E-05
1449271_a_at	heme binding protein 2	Hebp2	-0.695	1.83E-06
1420898_at	synaptosomal-associated protein 23	Snap23	-0.696	2.55E-05
1416769_s_at	ATPase, H+ transporting, lysosomal V0 subunit B	Atp6v0b	-0.697	1.16E-06
1449999_a_at	calcium channel, voltage-dependent, alpha2/delta subunit 1	Cacna2d1	-0.698	4.09E-05
1431422_a_at	dual specificity phosphatase 14	Dusp14	-0.7	1.12E-06
1420546_at	tyrosine hydroxylase	Th	-0.7	6.87E-06
1454807_a_at	sorting nexin 12	Snx12	-0.702	4.02E-06
1417158_at	ZXD family zinc finger C	Zxdc	-0.702	2.56E-05
1425556_at	Cdc2-related kinase, arginine/serine-rich	Crkrs	-0.703	9.99E-05
1423914_at	RIKEN cDNA C630004H02 gene	C630004H02Rik	-0.703	1.40E-05
1419932_s_at	G protein-coupled receptor 137B	Gpr137b	-0.704	1.13E-05
1433532_a_at	myelin basic protein	Mbp	-0.705	1.04E-05
1423071_x_at	RIKEN cDNA 6720475J19 gene	6720475J19Rik	-0.706	4.12E-05
1421383_at	coiled-coil domain containing 82	Ccdc82	-0.708	0.000479263
1416702_at	serine (or cysteine) peptidase inhibitor, clade I, member 1	Serpini1	-0.709	0.000159271
1436677_at	RIKEN cDNA 1810032O08 gene	1810032O08Rik	-0.709	0.000357292
1433859_at	INO80 complex subunit C	Ino80c	-0.71	2.43E-06
1450229_at	mediator complex subunit 14	Med14	-0.711	9.19E-05
1416259_at	peroxisomal biogenesis factor 12	Pex12	-0.711	2.81E-06
1429139_at	OTU domain containing 7B	Otud7b	-0.711	2.43E-06
1427923_at	zinc metallopeptidase, STE24 homolog (S. cerevisiae)	Zmpste24	-0.714	2.60E-06
1416019_at	down-regulator of transcription 1	Dr1	-0.716	4.24E-05
1450033_a_at	signal transducer and activator of transcription 1	Stat1	-0.717	1.09E-05
1421330_at	protein tyrosine phosphatase, non-receptor type 4	Ptpn4	-0.718	2.57E-05
1448233_at	prion protein	Prnp	-0.719	1.45E-06
1453427_at	casein kinase 2, alpha 1 polypeptide	Csnk2a1	-0.719	0.001803483
1425861_x_at	calcium channel, voltage-dependent, alpha2/delta subunit 1	Cacna2d1	-0.719	0.003036867
1421399_at	insulinoma-associated 1	Insm1	-0.719	2.17E-05
1420849_at	Crn, crooked neck-like 1 (Drosophila)	Crnkl1	-0.72	1.21E-06
1456691_s_at	steroid 5 alpha-reductase 3	Srd5a3	-0.72	2.40E-05
1452643_at	grainyhead-like 2 (Drosophila)	Grhl2	-0.721	2.23E-05
1420938_at	heparan sulfate 6-O-sulfotransferase 2	Hs6st2	-0.721	0.000222783
1428303_at	RIKEN cDNA 1500005I02 gene	1500005I02Rik	-0.722	0.0001987
1422646_at	MAX gene associated	Mga	-0.722	0.000218736
1428182_at	phosphoribosyl pyrophosphate synthetase-associated protein 1	Prpsap1	-0.722	8.55E-07
1452669_at	RIKEN cDNA 2810012G03 gene	2810012G03Rik	-0.722	1.67E-06
1451448_a_at	RIKEN cDNA 1110005A03 gene	1110005A03Rik	-0.725	8.35E-06
1452428_a_at	beta-2 microglobulin	B2m	-0.726	5.62E-06
1422729_at	protocadherin beta 10	Pcdhb10	-0.726	9.09E-05
1422951_at	protocadherin beta 4	Pcdhb4	-0.726	2.38E-05
1449391_at	zinc finger protein 37	Zfp37	-0.727	6.45E-06
1460426_at	phosphodiesterase 4D interacting protein (myomegalin)	Pde4dip	-0.727	7.47E-05
1437013_x_at	ATPase, H+ transporting, lysosomal V0 subunit B	Atp6v0b	-0.728	3.75E-06
1455156_at	striatin, calmodulin binding protein	Strn	-0.728	0.000197004

1430971_a_at	aquarius	Aqr	-0.73	0.000603742
1420896_at	synaptosomal-associated protein 23	Snap23	-0.73	4.84E-06
1449702_at	zinc finger, AN1-type domain 2A	Zfand2a	-0.731	1.69E-06
1417551_at	ceroid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	Cln3	-0.731	1.11E-06
1438476_a_at	chromodomain helicase DNA binding protein 4	Chd4	-0.732	0.001115085
1460428_at	ankyrin repeat domain 13a	Ankrd13a	-0.732	8.03E-07
1415941_s_at	zinc finger, AN1-type domain 2A	Zfand2a	-0.733	2.17E-06
1423450_a_at	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	Hs3st1	-0.733	6.06E-06
1423091_a_at	glycoprotein m6b	Gpm6b	-0.733	3.66E-06
1417462_at	CAP, adenylate cyclase-associated protein 1 (yeast)	Cap1	-0.735	1.11E-05
1416028_a_at	hematological and neurological expressed sequence 1	Hn1	-0.735	2.15E-05
1460729_at	Rho-associated coiled-coil containing protein kinase 1	Rock1	-0.735	0.000107724
1450034_at	signal transducer and activator of transcription 1	Stat1	-0.736	1.16E-06
1424316_at	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19	Slc25a19	-0.736	1.70E-06
1421644_at	schlafen 3	Slfn3	-0.737	8.12E-05
1436385_at	glucosidase, alpha; neutral C	Ganc	-0.739	1.54E-05
1420843_at	protein tyrosine phosphatase, receptor type, F	Ptprf	-0.741	3.66E-06
1448471_a_at	cytotoxic T lymphocyte-associated protein 2 alpha	Ctla2a	-0.741	1.01E-05
1419207_at	zinc finger protein 37	Zfp37	-0.746	6.80E-05
1421519_a_at	zinc finger protein 120	Zfp120	-0.746	2.99E-06
1449289_a_at	PHD finger protein 20-like 1	Phf20l1	-0.747	1.54E-06
1425060_s_at	CAP-GLY domain containing linker protein 1	Clip1	-0.747	0.000649694
1423895_a_at	CUG triplet repeat, RNA binding protein 2	Cugbp2	-0.748	8.59E-05
1426362_at	transmembrane protein 144	Tmem144	-0.749	4.04E-06
1431164_at	Ras-related GTP binding D	Rragd	-0.75	2.74E-05
1422864_at	runt related transcription factor 1	Runx1	-0.751	7.52E-05
1416340_a_at	mannosidase 2, alpha B1	Man2b1	-0.754	9.15E-06
1417490_at	cathepsin B	Ctsb	-0.754	1.21E-06
1450716_at	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1	Adamts1	-0.754	0.000107826
1424769_s_at	caldesmon 1	Cald1	-0.755	1.37E-05
1419276_at	ectonucleotide pyrophosphatase/phosphodiesterase 1	Enpp1	-0.756	6.24E-05
1420923_at	ubiquitin specific peptidase 9, X chromosome	Usp9x	-0.76	0.000428053
1451413_at	calpastatin	Cast	-0.762	1.48E-06
1418892_at	ras homolog gene family, member J	Rhoj	-0.765	0.000781823
1449111_a_at	growth factor receptor bound protein 2	Grb2	-0.767	3.64E-06
1428856_at	histocompatibility 13	H13	-0.767	0.000122233
1436212_at	transmembrane protein 71	Tmem71	-0.768	0.000156497
1454144_a_at	cyclin C	Ccnc	-0.768	0.000140651
1454006_a_at	UBX domain protein 8	Ubxn8	-0.768	2.72E-06
1434500_at	tweety homolog 2 (Drosophila)	Ttyh2	-0.769	2.29E-06
1421386_at	ankyrin repeat domain 6	Ankrd6	-0.772	4.99E-06
1453223_s_at	developmental pluripotency associated 2	Dppa2	-0.772	1.51E-05
1455873_a_at	vacuolar protein sorting 18 (yeast)	Vps18	-0.772	7.60E-06
1418825_at	immunity-related GTPase family M member 1	Irgm1	-0.773	2.53E-06
1448785_at	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	Runx1t1	-0.773	0.000104003
1422090_a_at	6-phosphofructo-2-kinase/fructose-2,6-	Pfkfb2	-0.774	5.68E-05

	biphosphatase 2			
1428312_at	leucine rich repeat containing 57	Lrrc57	-0.775	1.41E-05
1454822_x_at	adenomatosis polyposis coli down-regulated 1	Apcdd1	-0.776	5.82E-05
1424077_at	glycerophosphodiester phosphodiesterase domain containing 1	Gdpd1	-0.776	4.98E-06
1450787_at	chloride channel 5	Clcn5	-0.778	0.000324228
1427978_at	RIKEN cDNA 4732418C07 gene	4732418C07Rik	-0.781	8.72E-06
1423630_at	cytoglobin	Cygb	-0.782	1.27E-05
1437874_s_at	hexosaminidase B	Hexb	-0.785	7.33E-06
1449583_at	protocadherin beta 20	Pcdhb20	-0.787	6.98E-06
1420842_at	protein tyrosine phosphatase, receptor type, F	Ptprf	-0.788	1.59E-06
1433804_at	Janus kinase 1	Jak1	-0.789	9.49E-05
1421009_at	radical S-adenosyl methionine domain containing 2	Rsad2	-0.789	0.000117095
1424338_at	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	Slc6a13	-0.791	4.12E-06
1421905_at	trimethylguanosine synthase homolog (S. cerevisiae)	Tgs1	-0.792	0.00015868
1418630_at	KH domain containing, RNA binding, signal transduction associated 1	Khdrbs1	-0.792	0.000262314
1449130_at	CD1d1 antigen	Cd1d1	-0.792	5.94E-06
1416811_s_at	cytotoxic T lymphocyte-associated protein 2 alpha	Ctla2a	-0.793	7.13E-06
1436905_x_at	lysosomal-associated protein transmembrane 5	Laptm5	-0.794	9.64E-06
1455631_at	histocompatibility 13	H13	-0.794	1.76E-06
1455978_a_at	matrilin 2	Matn2	-0.794	1.47E-05
1416409_at	acyl-Coenzyme A oxidase 1, palmitoyl	Acox1	-0.797	7.84E-07
1432478_a_at	ring finger protein 19B	Rnf19b	-0.797	2.30E-06
1423694_at	potassium channel tetramerisation domain containing 10	Kctd10	-0.798	1.73E-06
1415978_at	tubulin, beta 3	Tubb3	-0.798	1.08E-05
1416130_at	prion protein	Prnp	-0.801	5.12E-06
1430172_a_at	cytochrome P450, family 4, subfamily f, polypeptide 16	Cyp4f16	-0.807	3.37E-06
1460415_a_at	CD40 antigen	Cd40	-0.807	4.56E-06
1416077_at	adrenomedullin	Adm	-0.807	2.43E-06
1415806_at	plasminogen activator, tissue	Plat	-0.808	1.20E-05
1424770_at	caldesmon 1	Cald1	-0.808	7.27E-06
1448318_at	adipose differentiation related protein	Adfp	-0.808	4.03E-07
1427304_at	vacuolar protein sorting 18 (yeast)	Vps18	-0.81	4.06E-06
1420989_at	RIKEN cDNA 4933411K20 gene	4933411K20Rik	-0.81	0.00063461
1427982_s_at	synaptic nuclear envelope 2	Syne2	-0.811	6.73E-05
1455431_at	solute carrier family 5 (sodium/glucose cotransporter), member 1	Slc5a1	-0.812	0.000427635
1430332_a_at	glucuronidase, beta	Gusb	-0.814	3.24E-06
1427483_at	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 24	Slc25a24	-0.814	8.67E-07
1425383_a_at	pre B-cell leukemia transcription factor 1	Pbx1	-0.815	4.47E-05
1418453_a_at	ATPase, Na+/K+ transporting, beta 1 polypeptide	Atp1b1	-0.815	6.91E-06
1420897_at	synaptosomal-associated protein 23	Snap23	-0.815	2.43E-06
1417540_at	E74-like factor 1	Elf1	-0.815	1.14E-06
1426740_s_at	armadillo repeat containing 5	Armc5	-0.816	1.50E-05
1421385_a_at	myosin VIIa	Myo7a	-0.816	2.45E-06
1421178_at	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme C (putative)	Mgat4c	-0.817	2.82E-05

1424674_at	solute carrier family 39 (metal ion transporter), member 6	Slc39a6	-0.817	8.55E-07
1450500_at	U2AF homology motif (UHM) kinase 1	Uhmk1	-0.818	0.000424587
1426246_at	protein S (alpha)	Pros1	-0.819	6.29E-06
1415940_at	zinc finger, AN1-type domain 2A	Zfand2a	-0.819	2.59E-06
1422069_at	melanocortin 1 receptor	Mc1r	-0.82	3.01E-05
1448443_at	serine (or cysteine) peptidase inhibitor, clade I, member 1	Serpini1	-0.821	1.50E-06
1452163_at	E26 avian leukemia oncogene 1, 5' domain	Ets1	-0.822	2.21E-06
1455798_at	galactokinase 2	Galk2	-0.822	1.14E-06
1425719_a_at	N-myc (and STAT) interactor	Nmi	-0.822	1.26E-05
1455271_at	predicted gene, OTTMUSG00000014994	OTTMUSG00000014994	-0.823	2.75E-06
1416693_at	forkhead box C2	Foxc2	-0.826	1.50E-06
1430045_at	translin-associated factor X	Tsnax	-0.829	2.21E-06
1455581_x_at	sterile alpha motif domain containing 9-like	Samd9l	-0.83	2.15E-05
1424325_at	establishment of cohesion 1 homolog 1 (S. cerevisiae)	Esco1	-0.831	4.66E-05
1425284_a_at	RAB27A, member RAS oncogene family	Rab27a	-0.831	2.69E-05
1420559_a_at	short stature homeobox 2	Shox2	-0.831	9.60E-05
1460498_a_at	DnaJ (Hsp40) homolog, subfamily C, member 5	Dnajc5	-0.832	0.000201213
1452042_a_at	transmembrane protein 144	Tmem144	-0.834	6.80E-07
1427277_at	sine oculis-related homeobox 1 homolog (Drosophila)	Six1	-0.834	1.90E-05
1434620_s_at	RIKEN cDNA 2610024E20 gene	2610024E20Rik	-0.834	1.56E-05
1425197_at	protein tyrosine phosphatase, non-receptor type 2	Ptpn2	-0.835	2.21E-06
1449070_x_at	adenomatosis polyposis coli down-regulated 1	Apcdd1	-0.836	2.45E-05
1446148_x_at	RNA binding motif protein 39	Rbm39	-0.836	3.64E-05
1449037_at	cAMP responsive element modulator	Crem	-0.84	1.21E-05
1431429_a_at	ADP-ribosylation factor-like 4A	Arl4a	-0.842	5.65E-06
1449473_s_at	CD40 antigen	Cd40	-0.846	2.54E-06
1418535_at	ral guanine nucleotide dissociation stimulator,-like 1	Rgl1	-0.846	3.71E-06
1434714_at	ERO1-like beta (S. cerevisiae)	Ero1lb	-0.848	2.43E-06
1449131_s_at	CD1d1 antigen	Cd1d1	-0.85	1.63E-06
1449948_at	ERO1-like beta (S. cerevisiae)	Ero1lb	-0.85	2.28E-05
1426806_at	oligonucleotide/oligosaccharide-binding fold containing 2A	Obfc2a	-0.851	1.40E-06
1421090_at	erythrocyte protein band 4.1-like 1	Epb4.1l1	-0.851	4.02E-05
1421978_at	glutamic acid decarboxylase 2	Gad2	-0.852	2.40E-05
1416406_at	phosphoprotein enriched in astrocytes 15A	Pea15a	-0.852	8.61E-07
1451832_at	chemokine-like factor	Cklf	-0.852	0.000133336
1435635_at	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	Pcmtd1	-0.855	2.43E-05
1425162_at	RAR-related orphan receptor beta	Rorb	-0.86	1.52E-06
1427979_at	RIKEN cDNA 4732418C07 gene	4732418C07Rik	-0.862	1.43E-05
1416041_at	serum/glucocorticoid regulated kinase 1	Sgk1	-0.863	5.14E-07
1449311_at	BTB and CNC homology 1	Bach1	-0.865	0.00015868
1455151_at	A kinase (PRKA) anchor protein (yotiao) 9	Akap9	-0.867	0.000233427
1417975_at	karyopherin (importin) alpha 4	Kpna4	-0.867	4.15E-05
1448851_a_at	DnaJ (Hsp40) homolog, subfamily C, member 5	Dnajc5	-0.868	0.000190268
1416023_at	fatty acid binding protein 3, muscle and heart	Fabp3	-0.87	1.76E-06
1448732_at	cathepsin B	Ctsb	-0.873	1.57E-06
1452312_at	RIKEN cDNA 2810002D19 gene	2810002D19Rik	-0.874	4.16E-06
1419191_at	homeodomain interacting protein kinase 3	Hipk3	-0.875	5.70E-05

1433508_at	Kruppel-like factor 6	Klf6	-0.876	3.29E-07
1416407_at	phosphoprotein enriched in astrocytes 15A	Pea15a	-0.876	7.84E-07
1452203_at	oligonucleotide/oligosaccharide-binding fold containing 2A	Obfc2a	-0.876	3.07E-05
1457810_at	zinc finger and BTB domain containing 37	Zbtb37	-0.886	3.79E-05
1427742_a_at	Kruppel-like factor 6	Klf6	-0.886	8.61E-06
1439036_a_at	ATPase, Na+/K+ transporting, beta 1 polypeptide	Atp1b1	-0.887	2.57E-06
1459921_at	neurexophilin 1	Nxph1	-0.888	0.000218736
1417005_at	kinesin light chain 1	Klc1	-0.889	2.66E-07
1427511_at	NA	NA	-0.892	0.000396716
1423072_at	RIKEN cDNA 6720475J19 gene	6720475J19Rik	-0.894	5.09E-05
1427640_a_at	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	Runx1t1	-0.894	1.08E-05
1446147_at	RNA binding motif protein 39	Rbm39	-0.896	2.11E-05
1423574_s_at	steroid 5 alpha-reductase 3	Srd5a3	-0.896	4.11E-06
1421839_at	ATP-binding cassette, sub-family A (ABC1), member 1	Abca1	-0.897	4.73E-05
1417399_at	growth arrest specific 6	Gas6	-0.9	7.89E-07
1427256_at	versican	Vcan	-0.904	5.66E-05
1450227_at	ankyrin repeat domain 6	Ankrd6	-0.905	1.36E-06
1421727_at	eyes absent 1 homolog (Drosophila)	Eya1	-0.905	5.49E-06
1424287_at	protein kinase, X-linked	Prkx	-0.906	1.40E-05
1420841_at	protein tyrosine phosphatase, receptor type, F	Ptprf	-0.908	8.44E-06
1420664_s_at	protein C receptor, endothelial	Procr	-0.909	2.36E-07
1424380_at	vacuolar protein sorting 37B (yeast)	Vps37b	-0.91	3.89E-06
1427943_at	acylphosphatase 2, muscle type	Acyp2	-0.911	2.08E-06
1418469_at	nuclear receptor interacting protein 1	Nrip1	-0.912	3.96E-05
1451620_at	C1q-like 3	C1ql3	-0.916	1.82E-05
1418046_at	nucleosome assembly protein 1-like 2	Nap1l2	-0.918	6.46E-06
1424524_at	RIKEN cDNA 1200002N14 gene	1200002N14Rik	-0.919	8.56E-06
1427488_a_at	baculoviral IAP repeat-containing 6	Birc6	-0.924	0.003621652
1451484_a_at	synapsin I	Syn1	-0.924	1.65E-07
1424271_at	doublecortin-like kinase 1	Dclk1	-0.926	7.10E-07
1421694_a_at	versican	Vcan	-0.926	1.14E-05
1418571_at	tumor necrosis factor receptor superfamily, member 12a	Tnfrsf12a	-0.929	2.73E-06
1460180_at	hexosaminidase B	Hexb	-0.929	5.06E-07
1418357_at	forkhead box G1	Foxg1	-0.932	1.87E-07
1416968_a_at	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	Hsd3b7	-0.933	5.27E-06
1459929_at	zinc finger protein 568	Zfp568	-0.934	5.28E-05
1417491_at	cathepsin B	Ctsb	-0.934	1.54E-06
1449874_at	lymphocyte antigen 96	Ly96	-0.938	0.000146237
1452631_at	RUN and FYVE domain-containing 2	Rufy2	-0.95	0.000152144
1417696_at	sterol O-acyltransferase 1	Soat1	-0.953	4.69E-05
1451289_at	doublecortin-like kinase 1	Dclk1	-0.959	2.10E-05
1424099_at	RIKEN cDNA 2310016C16 gene	2310016C16Rik	-0.961	4.36E-06
1420957_at	adenomatosis polyposis coli	Apc	-0.962	0.001570064
1421179_at	tweety homolog 2 (Drosophila)	Ttyh2	-0.964	3.48E-05
1426605_at	BRCA1/BRCA2-containing complex, subunit 3	Brcc3	-0.965	5.18E-06
1417695_a_at	sterol O-acyltransferase 1	Soat1	-0.967	1.83E-06
1420859_at	protein kinase inhibitor, alpha	Pkia	-0.968	2.18E-05
1436747_at	RIKEN cDNA 1110014K08 gene	1110014K08Rik	-0.975	1.66E-07
1421251_at	zinc finger protein 40	Zfp40	-0.975	0.000161626
1451828_a_at	acyl-CoA synthetase long-chain family member 4	Acsl4	-0.975	5.34E-06

1418572_x_at	tumor necrosis factor receptor superfamily, member 12a	Tnfrsf12a	-0.981	4.78E-06
1424768_at	caldesmon 1	Cald1	-0.982	2.59E-06
1449305_at	coagulation factor X	F10	-0.982	7.77E-06
1436839_at	RIKEN cDNA 2010109K11 gene	2010109K11Rik	-0.984	7.29E-06
1452352_at	cytotoxic T lymphocyte-associated protein 2 beta	Ctla2b	-0.991	1.53E-05
1448577_x_at	synaptogyrin 2	Syngr2	-0.991	7.12E-07
1448845_at	ribonuclease P 25 subunit (human)	Rpp25	-0.992	3.75E-06
1416503_at	latexin	Lxn	-0.996	3.96E-06
1424270_at	doublecortin-like kinase 1	Dclk1	-0.998	2.58E-05
1427046_at	grainyhead-like 2 (Drosophila)	Grhl2	-1.001	7.49E-07
1427985_at	spindlin family, member 4	Spin4	-1.002	3.79E-05
1449089_at	nuclear receptor interacting protein 1	Nrip1	-1.002	1.12E-05
1418163_at	toll-like receptor 4	Tlr4	-1.004	1.39E-06
1452238_at	HIV-1 Rev binding protein	Hrb	-1.007	8.55E-07
1417081_a_at	synaptogyrin 2	Syngr2	-1.026	1.02E-06
1448316_at	CKLF-like MARVEL transmembrane domain containing 3	Cmtm3	-1.027	4.80E-07
1424339_at	2'-5' oligoadenylate synthetase-like 1	Oasl1	-1.029	1.50E-05
1417073_a_at	quaking	Qk	-1.032	2.43E-05
1425942_a_at	glycoprotein m6b	Gpm6b	-1.034	3.64E-06
1450069_a_at	CUG triplet repeat, RNA binding protein 2	Cugbp2	-1.035	2.30E-05
1460521_a_at	oligonucleotide/oligosaccharide-binding fold containing 2A	Obfc2a	-1.037	5.91E-06
1449168_a_at	A kinase (PRKA) anchor protein 2	Akap2	-1.039	1.09E-05
1416302_at	early B-cell factor 1	Ebf1	-1.04	9.88E-05
1418580_at	receptor transporter protein 4	Rtp4	-1.042	3.78E-06
1421549_at	protocadherin beta 15	Pcdhb15	-1.043	4.20E-07
1416801_at	transient receptor potential cation channel, subfamily M, member 7	Trpm7	-1.045	1.21E-05
1422644_at	SH3-binding domain glutamic acid-rich protein	Sh3bgr	-1.05	1.16E-06
1417697_at	sterol O-acyltransferase 1	Soat1	-1.052	3.56E-07
1449124_at	ral guanine nucleotide dissociation stimulator,-like 1	Rgl1	-1.053	3.24E-07
1424940_s_at	cDNA sequence BC022687	BC022687	-1.055	1.11E-07
1418191_at	ubiquitin specific peptidase 18	Usp18	-1.062	2.12E-06
1426452_a_at	RAB30, member RAS oncogene family	Rab30	-1.069	7.12E-06
1421936_at	dual adaptor for phosphotyrosine and 3-phosphoinositides 1	Dapp1	-1.075	2.44E-05
1422218_at	purinergic receptor P2X, ligand-gated ion channel, 7	P2rx7	-1.077	6.85E-06
1422836_at	muscleblind-like 3 (Drosophila)	Mbnl3	-1.081	2.79E-05
1421001_a_at	carbonic anhydrase 6	Car6	-1.081	2.43E-06
1433765_at	ubiquitin-conjugating enzyme E2O	Ube2o	-1.091	5.72E-07
1433708_at	signal recognition particle 68	Srp68	-1.093	3.44E-08
1421818_at	B-cell leukemia/lymphoma 6	Bcl6	-1.094	1.44E-05
1434865_a_at	exocyst complex component 7	Exoc7	-1.108	1.19E-06
1418280_at	Kruppel-like factor 6	Klf6	-1.115	8.55E-07
1451407_at	immunoglobulin superfamily, member 5	Igsf5	-1.121	1.35E-05
1437458_x_at	clusterin	Clu	-1.121	1.48E-07
1437689_x_at	clusterin	Clu	-1.124	8.87E-08
1417441_at	DnaJ (Hsp40) homolog, subfamily C, member 12	Dnajc12	-1.124	5.17E-06
1424675_at	solute carrier family 39 (metal ion transporter), member 6	Slc39a6	-1.126	1.96E-06
1419497_at	cyclin-dependent kinase inhibitor 1B	Cdkn1b	-1.135	0.001071959

1425597_a_at	quaking	Qk	-1.144	1.50E-06
1423280_at	stathmin-like 2	Stmn2	-1.146	7.22E-08
1448894_at	aldo-keto reductase family 1, member B8	Akr1b8	-1.155	4.92E-08
1454849_x_at	clusterin	Clu	-1.155	5.22E-08
1434272_at	cytoplasmic polyadenylation element binding protein 2	Cpeb2	-1.169	6.45E-06
1451878_a_at	junction-mediating and regulatory protein	Jmy	-1.173	6.20E-05
1425775_at	zinc finger protein 820	Zfp820	-1.176	3.27E-06
1427311_at	bromodomain PHD finger transcription factor	Bptf	-1.179	0.000543844
1426923_at	HIV-1 Rev binding protein	Hrb	-1.186	1.64E-07
1427795_s_at	NA	NA	-1.187	3.89E-07
1451533_at	cDNA sequence BC022687	BC022687	-1.192	3.21E-07
1423281_at	stathmin-like 2	Stmn2	-1.197	9.40E-07
1450392_at	ATP-binding cassette, sub-family A (ABC1), member 1	Abca1	-1.204	5.64E-05
1453943_a_at	acid phosphatase, prostate	Acpp	-1.208	4.62E-05
1418626_a_at	clusterin	Clu	-1.225	6.24E-08
1423608_at	integral membrane protein 2A	Itm2a	-1.227	2.26E-06
1418673_at	snail homolog 2 (Drosophila)	Snai2	-1.229	5.94E-06
1423164_at	G protein-coupled receptor 137B, pseudogene	Gpr137b-ps	-1.239	4.88E-08
1420858_at	protein kinase inhibitor, alpha	Pkia	-1.245	5.55E-06
1449164_at	CD68 antigen	Cd68	-1.25	7.99E-06
1420911_a_at	milk fat globule-EGF factor 8 protein	Mfge8	-1.253	2.00E-08
1427044_a_at	amphiphysin	Amph	-1.279	2.48E-07
1424278_a_at	baculoviral IAP repeat-containing 5	Birc5	-1.28	4.61E-08
1449286_at	netrin G1	Ntng1	-1.291	0.000216761
1416808_at	nidogen 1	Nid1	-1.296	1.11E-07
1448293_at	early B-cell factor 1	Ebf1	-1.297	3.20E-05
1428034_a_at	tumor necrosis factor receptor superfamily, member 9	Tnfrsf9	-1.299	7.42E-07
1429527_a_at	phospholipid scramblase 1	Plscr1	-1.304	1.93E-07
1426892_at	utrophin	Utrn	-1.32	0.000116233
1418162_at	toll-like receptor 4	Tlr4	-1.329	3.14E-05
1449579_at	Sh3 domain YSC-like 1	Sh3yl1	-1.349	1.18E-06
1426922_s_at	HIV-1 Rev binding protein	Hrb	-1.351	7.22E-08
1453181_x_at	phospholipid scramblase 1	Plscr1	-1.362	3.81E-07
1424976_at	ras homolog gene family, member V	Rhov	-1.366	8.16E-08
1419223_a_at	dystrobrevin alpha	Dtna	-1.369	5.33E-05
1418105_at	stathmin-like 4	Stmn4	-1.391	2.43E-08
1418219_at	interleukin 15	Il15	-1.395	1.54E-06
1449122_at	UBX domain protein 2B	Ubxn2b	-1.399	2.53E-06
1448469_at	nidogen 1	Nid1	-1.4	4.67E-06
1452237_at	HIV-1 Rev binding protein	Hrb	-1.401	3.60E-08
1417492_at	cathepsin B	Ctsb	-1.404	5.37E-08
1450881_s_at	G protein-coupled receptor 137B, pseudogene	Gpr137b-ps	-1.407	1.45E-08
1425681_a_at	prion protein dublet	Prnd	-1.425	8.88E-07
1451154_a_at	CUG triplet repeat, RNA binding protein 2	Cugbp2	-1.438	5.66E-06
1433756_at	S100P binding protein	S100pbp	-1.439	3.00E-08
1429775_a_at	G protein-coupled receptor 137B, pseudogene	Gpr137b-ps	-1.48	2.45E-07
1439256_x_at	G protein-coupled receptor 137B, pseudogene	Gpr137b-ps	-1.482	8.16E-08
1419595_a_at	gamma-glutamyl hydrolase	Ggh	-1.507	6.56E-07
1439255_s_at	similar to Gpr137b protein	LOC100044979	-1.51	7.22E-08
1425705_a_at	ERO1-like beta (S. cerevisiae)	Ero1lb	-1.517	1.57E-06
1448303_at	glycoprotein (transmembrane) nmb	Gpnmb	-1.529	7.44E-07
1420429_at	protocadherin beta 3	Pcdhb3	-1.535	2.93E-06
1429768_at	dystrobrevin alpha	Dtna	-1.542	1.44E-06

1422906_at	ATP-binding cassette, sub-family G (WHITE), member 2	Abcg2	-1.546	1.21E-05
1415855_at	kit ligand	Kitl	-1.549	2.57E-05
1450882_s_at	G protein-coupled receptor 137B, pseudogene	Gpr137b-ps	-1.571	1.16E-07
1428942_at	metallothionein 2	Mt2	-1.633	3.68E-08
1449670_x_at	G protein-coupled receptor 137B	Gpr137b	-1.634	4.32E-08
1426622_a_at	glutaminyl-peptide cyclotransferase (glutaminyl cyclase)	Qpct	-1.638	7.22E-08
1436172_at	sterile alpha motif domain containing 9-like	Samd9l	-1.648	1.79E-05
1453196_a_at	2'-5' oligoadenylate synthetase-like 2	Oasl2	-1.654	3.68E-08
1419759_at	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	Abcb1a	-1.664	7.28E-09
1416295_a_at	interleukin 2 receptor, gamma chain	Il2rg	-1.751	4.68E-07
1418248_at	galactosidase, alpha	Gla	-1.829	1.11E-07
1421424_a_at	alanyl (membrane) aminopeptidase	Anpep	-1.831	4.31E-08
1449006_at	galactosidase, alpha	Gla	-1.845	4.03E-05
1428780_at	threonine aldolase 1	Tha1	-1.88	5.09E-08
1451451_at	grancalcin	Gca	-1.887	8.70E-07
1424698_s_at	grancalcin	Gca	-1.936	1.93E-07
1419758_at	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	Abcb1a	-1.965	7.43E-07
1422007_at	aquaporin 3	Aqp3	-1.975	3.44E-08
1427550_at	paternally expressed 10	Peg10	-2.016	1.71E-07
1426808_at	lectin, galactose binding, soluble 3	Lgals3	-2.035	5.67E-08
1417672_at	solute carrier family 4, sodium bicarbonate cotransporter-like, member 10	Slc4a10	-2.074	3.70E-07
1422557_s_at	metallothionein 1	Mt1	-2.09	7.50E-08
1419417_at	vascular endothelial growth factor C	Vegfc	-2.823	4.88E-08
1450460_at	aquaporin 3	Aqp3	-2.864	2.89E-08
1456069_at	dystrobrevin alpha	Dtna	-3.135	7.28E-09
1422008_a_at	aquaporin 3	Aqp3	-3.853	2.36E-10

Unexpected expression of α- and β-globin in mesencephalic dopaminergic neurons and glial cells

Marta Biagioli[a,b,1], Milena Pinto[a,1], Daniela Cesselli[c], Marta Zaninello[a], Dejan Lazarevic[a,b,d], Paola Roncaglia[a], Roberto Simone[a,b], Christina Vlachouli[a], Charles Plessy[e], Nicolas Bertin[e], Antonio Beltrami[c], Kazuto Kobayashi[f], Vittorio Gallo[g], Claudio Santoro[h], Isidro Ferrer[i], Stefano Rivella[j], Carlo Alberto Beltrami[c], Piero Carninci[e], Elio Raviola[k], and Stefano Gustincich[a,b,2]

[a]Sector of Neurobiology, International School for Advanced Studies, [b]The Giovanni Armenise–Harvard Foundation Laboratory, and [d]Consorzio per il Centro di Biomedicina Molecolare, AREA Science Park, Basovizza, 34012 Trieste, Italy; [c]Centro Interdipartimentale Medicina Rigenerativa, University of Udine, 33100 Udine, Italy; [e]RIKEN Omics Science Center, Yokohama Institute 1-7-22 Suehiro-cho Tsurumi-ku Yokohama, Kanagawa 230-0045, Japan; [f]Department of Molecular Genetics, Fukushima Medical University School of Medicine, 1 Hikarigaoka, Fukushima 960-1295, Japan; [g]Center for Neuroscience Research, Children's National Medical Center, 111 Michigan Avenue NW, Washington, DC 20010; [h]Department of Medical Sciences, University of Eastern Piedmont, 28100 Novara, Italy; [i]Institute of Neuropathology, Institut d'Investigació Biomèdica de Bellvitge–University Hospital Bellvitge, University of Barcelona, 08907 Llobregat, Spain; [j]Department of Pediatric Hematology–Oncology, Weill Medical College of Cornell University, 515 East 71st Street, New York, NY 10021; and [k]Department of Neurobiology, Harvard Medical School, 220 Longwood Avenue, Boston, MA 02115

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The mesencephalic dopaminergic (mDA) cell system is composed of two major groups of projecting cells in the *substantia nigra* (SN) (A9 neurons) and the ventral tegmental area (VTA) (A10 cells). A9 neurons form the nigrostriatal pathway and are involved in regulating voluntary movements and postural reflexes. Their selective degeneration leads to Parkinson's disease. Here, we report that gene expression analysis of A9 dopaminergic neurons (DA) identifies transcripts for α- and β-chains of hemoglobin (Hb). Globin immunoreactivity decorates the majority of A9 DA, a subpopulation of cortical and hippocampal astrocytes and mature oligodendrocytes. This pattern of expression was confirmed in different mouse strains and in rat and human. We show that Hb is expressed in the SN of human postmortem brain. By microarray analysis of dopaminergic cell lines overexpressing α- and β-globin chains, changes in genes involved in O_2 homeostasis and oxidative phopshorylation were observed, linking Hb expression to mitochondrial function. Our data suggest that the most famed oxygen-carrying globin is not exclusively restricted to the blood, but it may play a role in the normal physiology of the brain and neurodegenerative diseases.

astrocytes | hemoglobin | oligodendrocytes | oxidative phosphorylation | Parkinson

Dopaminergic neurons (DA) are an anatomically and functionally heterogeneous group of cells involved in a wide range of neuronal network activities and behavior. Among them, mesencephalic DA (mDA) are the major source of dopamine in the brain. They present two main groups of projecting cells: the A9 neurons of the substantia nigra (SN) and the A10 cells of the ventral tegmental area (VTA).

A9 neurons form the nigrostriatal pathway and are involved in regulating voluntary movements and postural reflexes. Their selective degeneration leads to Parkinson's disease (PD), and the loss of DA synapses in the striatum is believed to be primary cause for the disruption of the ability to control movements (1). A10 cells constitute the mesocorticolimbic pathway, playing a fundamental role in reward and attention. Their abnormal function has been linked to schizophrenia, attention deficit, and addiction, whereas they are relatively spared in PD (2).

The description of the repertory of genes of mDA neurons may provide crucial information on their physiology and on the mechanisms of cell-type specific dysfunction. Interestingly, in previous gene expression profiling experiments, mDA cell groups presented a limited number of differentially expressed genes with A9-enriched transcripts mainly related to energy metabolism and mitochondrial function (3–5).

A crucial requirement for metabolically active aerobic cells is a steady supply of oxygen. To this purpose, hemoglobin (Hb)-like molecules occur widely in organisms ranging from bacteria to human (6). Vertebrate Hb is the oxygen- and carbon dioxide-carrying protein in cells of erythroid lineage and is responsible for oxygen delivery to the respiring tissues of the body. Additional vertebrate heme-containing proteins with structural homology to globin chains include cytoglobin, mostly described in connective tissues (7), and neuroglobin, broadly expressed in the brain (8).

Surprisingly, Hb chains have been recently detected in nonerythroid cells including macrophages, alveolar cells, eye's lens, and mesangial cells of the kidney (9–12).

By a combination of different gene expression platforms with laser capture microdissection (LCM), we have identified the transcripts of Hb α, adult chain 1 (Hba-a1), and Hb β, adult chain 1 (Hbb-b1) in A9 neurons. Interestingly, Hb immunoreactivity (Hb-IR) decorated the large majority of A9 cells, whereas it stained only <5% of A10 neurons. Furthermore, we detected Hb expression in almost all oligodendrocytes and cortical and hippocampal astrocytes and proved that this pattern of expression was conserved in mammals. Importantly, A9 DA neurons from human postmortem brain showed Hb expression.

By gene expression analysis of mouse dopaminergic cell lines stably transfected with α- and β-chains, we observed changes in genes involved in O_2 homeostasis and oxidative phosphorylation, suggesting a link between Hb and mitochondrial activity.

These results open a scenario for a role for Hb in brain physiology and PD pathogenesis.

Results

Identification of α- and β-Globin Transcripts by Expression Analysis of A9 DA Neurons. To study the cellular physiology of A9 DA neurons, we determined their gene expression profiles with two

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Author contributions: M.B., M.P., E.R., and S.G. designed research; M.B., M.P., D.C., M.Z., D.L., R.S., C.V., and C.P. performed research; A.B., K.K., V.G., C.S., I.F., S.R., C.A.B., and P.C. contributed new reagents/analytic tools; M.B., M.P., D.C., D.L., P.R., R.S., C.V., C.P., N.B., S.R., C.A.B., P.C., and S.G. analyzed data; and M.B. and S.G. wrote the paper.

The authors declare no conflict of interest.

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Data deposition: The data reported in this paper have been deposited in the Gene Expression Omnibus (GEO) database, www.ncbi.nlm.nih.gov/geo (accession no. GSE16192).

[1]M.B. and M.P. contributed equally to this work.

[2]To whom correspondence should be addressed. E-mail: gustinci@sissa.it.

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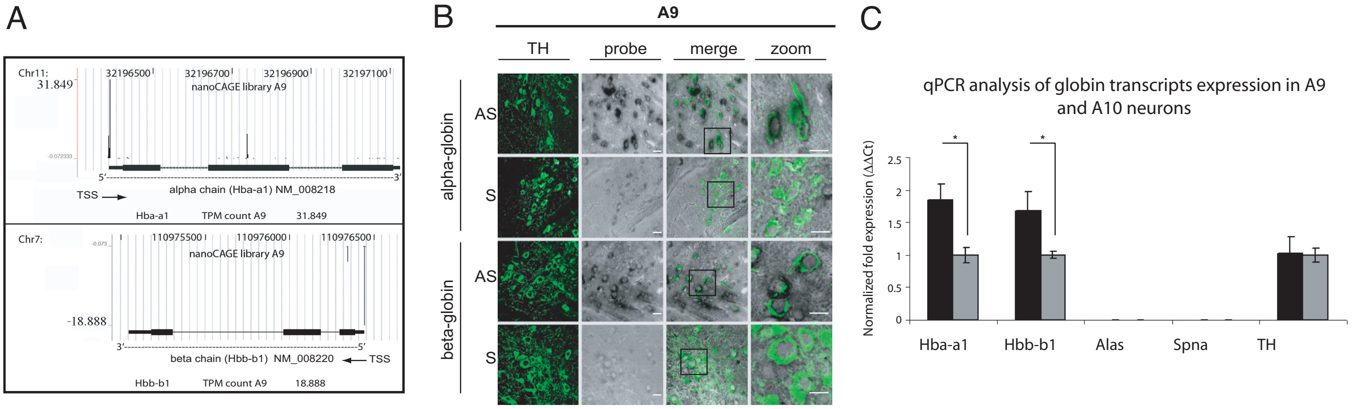

Fig. 1. Expression of α- and β-globin transcripts in A9 and A10 neurons. (*A*) NanoCAGE tracks visualization concerning Hbb-a1 (Chr.11) and Hbb-b1 (Chr.7) gene loci. A Genome Browser view is presented. A9 library is indicated, and the tags per million (TPM) for each gene are reported. The structure of Hbb-a1 and Hbb-b1 transcripts is depicted at the bottom. Transcriptional start sites (TSS) are indicated at the 5′ untranscribed region of each transcript. (*B*) In situ hybridization of α- and β-globin transcripts on A9 DA neurons: ventral midbrain slices were processed with antisense (AS) and sense (S) probes for the two globins transcripts. DA neurons were visualized by immunohistochemistry using an anti-TH antibody (green). The overlay (merge) shows colocalization of the transcripts of α- and β-globin in the cytoplasm of A9 neurons. Probes synthesis from sense transcripts were used as negative controls. The zoom offers magnifications of the area in the boxes of the overlay images. (Scale bars: 20 μm.) (*C*) qPCR starting from 500 LCM-isolated neurons from A9 (black column) and A10 (grey column) regions of the ventral midbrain of TH-GFP mice. TH, α-globin, and β-globin transcripts were amplified and the absence of blood contamination was evaluated by using primers for Alas and Spna. α- and β-transcripts are more expressed in A9 neurons (≈2-fold), four biological replicas, $P < 0.05$.

independent techniques: cDNA microarrays and a nanoscale version of the cap analysis of gene expression (nanoCAGE). To this purpose we took advantage of transgenic mice that selectively express green fluorescent protein (GFP) in catecholaminergic cells under the control of tyrosine hydroxylase (TH) gene promoter (TH-GFP mice) (13). In this mouse line we can identify the majority of mDA neurons for their GFP labeling. Furthermore, we can distinguish A9 neurons from A10 for their anatomical localization. Thus, LCM and pressure catapulting were used to harvest A9 neurons after fixation with a zinc fix-based method that assured the preservation of both tissue morphology and RNA integrity. RNA was then used as template in two different gene expression approaches.

In the cDNA microarray experiment, RNA was processed with a μMACS amplification kit (Miltenyi), labeled, and used as a target to monitor gene expression on a custom-made cDNA microarray platform. All of the experiments were performed in three biological replicates. The complete description of the transcripts expressed in A9 neurons will be presented elsewhere. Interestingly, among the genes expressed in A9 cells, transcripts for the α- and β-chains of mouse Hb were identified.

For the nanoCAGE transcriptome analysis, 2000 A9 cells were harvested, full-length cDNAs were produced and, after cleavage with a class IIS restriction endonuclease, 5′ end tags were purified and sequenced by using the second generation of sequencers. Finally, transcription start sites (TSS) were identified by mapping tags to the genome (15). This kind of analysis unveiled TSS on the mouse chromosomes 11 and 7 in the genomic regions corresponding to the 5′ end of Hba-a1 (NM_008218.2) and Hbb-b1 (NM_008220.3) transcripts (Fig. 1*A*). In Table S1 a list of nanoCAGE tags in A9 neurons is provided for these two loci.

Therefore, cDNA microarray data and CAGE tags distribution suggested that A9 neurons express transcripts for α- and β-chains of Hb.

To estimate potential blood contamination, we monitored the expression of several erythrocyte-specific transcripts: no expression was detected for Rhag, Gypa, Alas2, Spna1, and Epb4.2.

Validation of the Expression of α- and β-Globin Transcripts in A9 DA Cells. We then validated the expression of α- and β-globin transcripts in A9 DA neurons by two independent approaches.

We studied the precise distribution of α- and β-globin transcripts in the mouse midbrain by in situ hybridization. Experimental procedures and antisense RNA probes were first tested on bone marrow as a positive control for globin expression (Fig. S1). Brains were fixed by using conventional methods after extensive perfusion with PBS to minimize blood contamination. As shown in Fig. 1*B*, antisense probes gave specific and reproducible signals in A9 neurons that were identified by anti-TH immunoreactivity and anatomical localization. Interestingly, a specific labeling for the antisense probe was also evident in A10 neurons (Fig. S2). Higher magnification of the merged images showed colocalization of the antisense signals for each Hb chains in the cytosol of TH-positive A9 and A10 DA cells.

We then took advantage of LCM to collect 500 TH-GFP-positive neurons for each mDA cell group. After RNA extraction and cDNA synthesis, quantitative PCR (qPCR) amplification was carried out to detect the expression of α- and β-globin. As visualized in Fig. 1*C*, the qPCR showed that α- and β-globin transcripts were 2-fold more expressed in A9 than in A10 neurons.

Hb-IR Is Present in DA Neurons of the SN. To characterize Hb expression at protein level, we took advantage of a commercial antibody produced against highly purified total mouse Hb (Cappel). For the high homology among proteins of the globin family and the well-described expression of atypical globins in neurons (7, 8), we first verified the repertory of immunoreactivity of the Cappel antibody in immunofluorescence experiments (Fig. S3*a*). We transfected HEK cells with expression vectors carrying myc-tagged globin isoforms (Hba-a1, Hbb-b1, Hba-x, Hbb-y, Hbb-bh1, and Hbq1) and atypical globins (Cygb, Ngb, and Mg). Cappel antibody reactivity was then monitored in parallel with anti-myc staining. A strong signal was obtained for β-globin chain. A weaker labeling was also detected when the Hbb-y embryonic chain was expressed. Importantly, no cross-reaction was present with any of the atypical globins normally expressed in neurons.

Therefore, an immunohistochemical analysis of the mouse mesencephalon was carried out. To avoid strong reactivity from blood cells, brains were extensively washed in PBS during perfusion before fixation. Immunohistochemistry on mouse midbrain revealed a complex pattern of protein expression

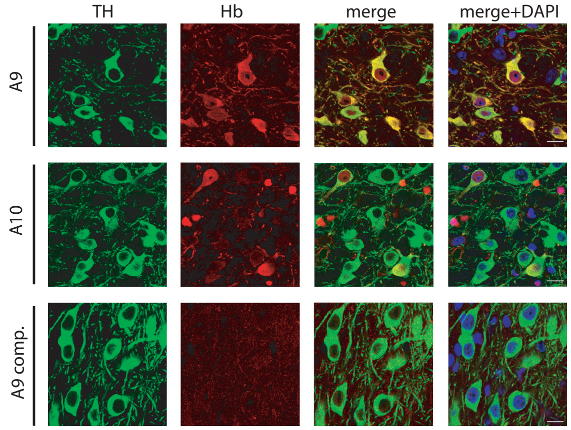

Fig. 2. Hb protein is expressed in A9 and A10 DA neurons of mouse brain. A double immunohistochemistry analysis using anti-Hb (red), anti-TH (green), and DAPI (blue) is presented: nearly 70% of A9 but only 3% of A10 neurons were double labeled for Hb and TH (merge). Hb staining is present in the nucleus, except for the nucleolus, and in the cytoplasm. Adsorption of the anti-Hb antibody with spleen extract completely prevents Hb staining (A9 comp). (Scale bar: 20 μm.)

(Fig. 2). In the SN, 65.8 ± 6.1% of A9 DA neurons were presenting Hb-IR. On the contrary, a very limited number of DA neurons in the A10 region were stained (2.9 ± 0.82%). Interestingly, Hb-IR in mDA neurons was localized in both the cytoplasm and the nucleus. Importantly, the specificity of the antibody was further verified by competition assays using mouse spleen extracts on midbrain sections (Fig. 2). Experiments performed on brains without perfusion showed a strong labeling of red blood cells that were clearly different in size, location, and number from DA neurons (Fig. S4*a*). To further confirm Hb-IR, we then used a second commercial antibody against purified mouse Hb (ICL Labs). First, we proved that its chain specificity pattern is limited to the detection of both β- and α-chains and that no cross-reaction with other typical or atypical globins was observed (Fig. S3*b*). Then we confirmed an extensive overlap of Hb-IR for DA neurons between Cappel and ICL antibodies (Fig. S4*b*).

Because nanoCAGE data shows that both α- and β-chains synthesis involve the same TSS used in blood, we investigated whether the major transcription factors implicated in controlling primitive and definitive erythroid lineages may be involved in mDA cells transcription. Notably, the expression of Gata family members has been also described in the midbrain and hindbrain (16, 17). Interestingly, as shown in Fig. S4*c*, several DA neurons (≈50%) were decorated for both Gata-1 and Hb staining.

Additional Hb-IR Cells Are Present in Distinct Areas Throughout the Brain. Together with mDA neurons (Fig. 3*A Left*), two additional TH-negative cell types were labeled by the Cappel antibody in brain sections.

Cell type I are large cells located in the cortex and the hippocampus, faintly labeled in the cytoplasm and the nucleus (approximate diameter: 15–18 μm) (Fig. 3*A Center*).

Cell type II are small cells widely diffused in all of the brain regions analyzed, strongly labeled in the thin cytoplasm and the nucleus (approximate diameter: 7–10 μm) (Fig. 3*A Right*).

To identify these cells, we carried out extensive double immunohistochemistry on mouse midbrain slices with the Cappel antibody and antibodies specific for different neuronal and glial cell populations (NG2, Iba-1, NeuN, GFAP, and CNP). As shown in Fig. 3*B*, we found a specific and reproducible Hb-IR in a subpopulation (73.2 ± 4.8%) of hippocampal and cortical astrocytes labeled with anti-GFAP antibody and in a large fraction (>99%) of mature oligodendrocites, characterized by the expression of CNP.

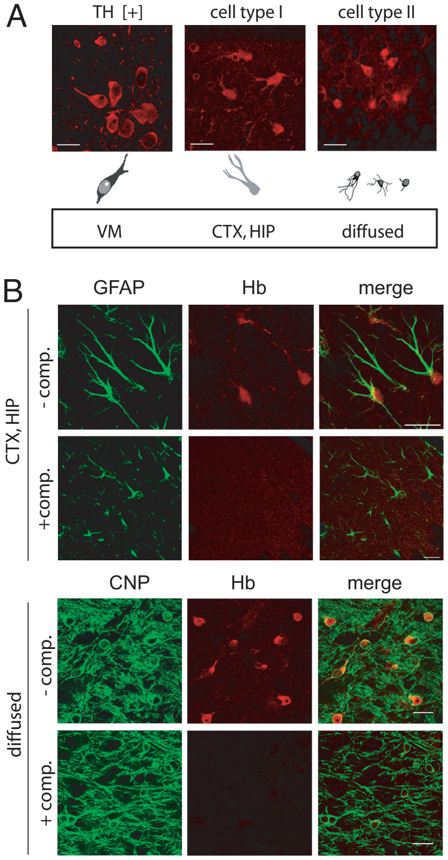

Fig. 3. Hb protein is expressed in different regions of the mouse brain. (*A*) (*Upper*) Immunohistochemistry using anti-Hb antibody on mouse brain revealed different Hb-IR cells: large neurons located in the ventral midbrain, positive for TH (TH$^+$); cell type I large cells located in the cortex (CTX) and hippocampus (HIP); and cell type II small cells, widely diffused in all of the brain regions tested and presenting a strong Hb-IR. (Scale bars: 20 μm.) (*Lower*) A schematic representation of the morphologies of Hb-IR cells is presented. (*B*) Double immunohistochemistry using anti-Hb antibody (red) together with astrocytes and oligodendrocytes markers (GFAP and CNP, green). (*Upper*) In the cortex (CTX) and in the hippocampus (HIP), Hb–IR cell type I colocalizes with GFAP staining. (*Lower*) Hb-IR cell type II colocalizes with the oligodendrocytes marker CNP. Adsorption of the anti-Hb antibody with spleen extract completely prevents Hb staining (+ comp). (Scale bars: 20 μm.)

Primary Cultures of Hb-IR Neuronal and Glial Cell Populations. We studied globin expression at the mRNA and protein levels in vitro on primary cultures obtained from dissociated mouse ventral midbrain, cortex, or hippocampus. Immunofluorescence experiments confirmed the expression pattern observed in vivo: Hb-IR was found in a subpopulation of TH-positive DA neurons, cortical GFAP-positive astrocytes, and the large majority of CNP-positive oligodendrocytes (Fig. 4*A*).

Taking advantage of TH-GFP, GFAP-GFP (Jackson Laboratory), and CNP-GFP transgenic mice lines (18), we next validated the expression of α- and β-chains transcripts after resorting to FACS for purifying, respectively, mDA neurons, astrocytes, and oligodendrocytes. After enzymatic digestion and mechanical trituration of dissected regions, the cell suspension was sequentially panned on four *Bandeiraea Simplicifolia* lectin I-coated dishes (19). This step minimized endothelial, microglial, and red blood cell contamination of the preparation. Then, the FACS procedure was applied and

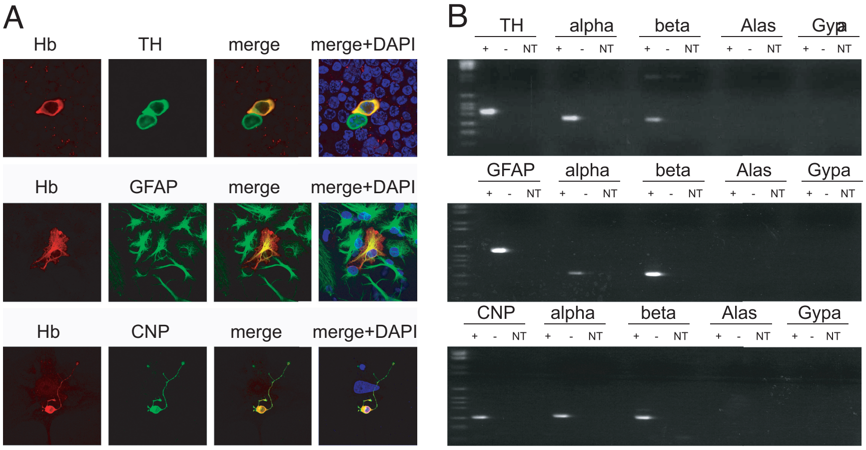

Fig. 4. Primary cultures of DA neurons, astrocytes, and oligodendrocytes: immunofluorescence and RT-PCR. (*A*) Immunofluorescence on primary cultures of DA neurons, cortical and hippocampal astrocytes, and oligodendrocytes. (Magnification: 63×.) Specific cell population markers (green) and Hb staining (red) are shown. (*B*) RT-PCR results obtained from 2,000 single FACS-sorted cells. α- and β-globin transcripts and the population-specific markers (TH, GFAP, and CNP, respectively) were amplified (+). The absence of blood contamination was evaluated by using primers for Alas and Gypa. Negative controls, retrotranscriptase free (−), and no-template control samples (NT) are presented. RNA extracted from blood was used as positive control (Fig. S9).

GFP-positive cells were collected. FACS-purified cell culture showed an elevated enrichment of the cells of interest (98% for mDA, 96% for astrocytes, and 97.8% for oligodendrocytes). RNA was then extracted from 2,000 GFP-positive cells for each cell type and, after RT-PCR amplification, the specific amplicons of α- and β-globins were observed in TH-, GFAP-, and CNP-enriched cells (Fig. 4*B*). The identity of PCR products was confirmed by cloning and sequencing.

Hb-IR Pattern Is Conserved in Mammals. We then addressed whether the characteristic pattern of globin expression described for C57BL/6J line is conserved in different genetic backgrounds. Immunohistochemistry of BALB/cJ, FVB/NJ, and CD-1 mouse strains was carried out by showing the same morphological and topographical organization of Hb-IR cells. Furthermore, Hb-IR in mDA neurons, cortical and hippocampal astrocytes, and oligodendrocytes was confirmed as early as postnatal day 6. Importantly, other rodents, like *Rattus norvegicus*, presented the same pattern of Hb-IR, as shown in Fig. S5*a* for the adult mesencephalon.

We then analyzed the SN of human postmortem brains by two different antibodies: a subset of TH-positive neurons was Hb-immunoreactive, proving that Hb expression in the brain is conserved from mouse to human (Fig. S5*b*).

Hb Overexpression on Mouse DA Cell Line MN9D Changes the Expression of Genes Involved in O_2 Homeostasis and Mitochondrial Oxidative Phosphorylation. We took advantage of the MN9D dopaminergic cell line to address the function of Hb in DA neurons. RT-PCR demonstrated that transcripts for α- and β-chains of mouse Hb were indeed expressed. RNA from mouse blood was used as positive control. By using a specific antibody against mouse Hb, protein expression was detected by Western blot analysis although Hb level was very low. By resorting to immunoprecipitation, a clear band of 17 kDa was specifically enriched from cell lysates (Fig. S6).

As Hb is likely to act as heterotetramer of two different subunits, we took advantage of pBUDCE 4.1 vector to overexpress both mouse globin chains in a series of stably transfected MN9D cell lines (Fig. S7). The expression of α- and β-chains was verified by qPCR and immunocytochemistry, and the presence of α/β heterodimers was confirmed by coimmunoprecipitation experiments (Fig. S7).

We then took advantage of the Affymetrix platform to interrogate the GeneChip Mouse Genome 430A 2.0 Array for gene expression differences between control and globin chain stable cell lines (see *Materials and Methods* for details). The experiment was carried out with three biological replicas.

A total of 4,617 genes was found to be differentially expressed with a fold change >1.2. A total of 2,057 were up-regulated in α- and β-chains over-expressing clones, and 2,560 were down-regulated. qPCR confirmed microarrays data for all 14 genes tested for validation. A complete list of genes is provided in Table S2.

By applying Ingenuity software, two major pathways were affected: O_2 homeostasis and oxidative phopshorylation (Fig. 5). Other changes were observed in genes involved in oxidative stress, iron metabolism, and nitric oxide (NO) synthesis (Table S3).

O_2 homeostasis mainly occurs through the activity of Hif1a, a transcription factor whose expression is decreased in globin-overexpressing cells (Fig. 5) (20). Its physiological activity is regulated by Egln3, a mediator of Hif1a hydroxylation, and Vhl that targets Hif1a for degradation. The overexpression of α- and β-chains decreased Vhl mRNA whereas it strongly increased Egln3 transcripts. Interestingly, the expression of TH and Ret, two targets of Hif1a, was also changed (Fig. 5).

Importantly, genes involved in mitochondrial oxidative phosphorylation were increased upon overexpression of Hb chains. A total of 36 of 78 genes that encode for subunits of mitochondrial complex I–V were up-regulated. This induction occurred mainly in complex I (20 genes of 46) and to a lesser extent in complex II (1 gene), III (3 genes), IV (6 genes), and V (5 genes). Interestingly, the mitochondrial, proton carrier, uncoupling protein 2, was also strongly up-regulated.

Discussion

The first descriptions of globins in the nervous tissue date back to the 19th century. More recently, globin-like molecules have been detected in neurons of various invertebrates (6). In the bivalve mollusc *Tellina alternate*, neural excitability is sustained as long as oxygen can be delivered by a neural globin (21). In *Aplysia*, a gastropod mollusc, the firing activity of the neural ganglia is proportional to the degree of oxygenation of the neural globin. Natural variation in a neural globin in *Caenorhabditis elegans* strains has been linked to changes in electrophysiological responses and sensory behaviors (22).

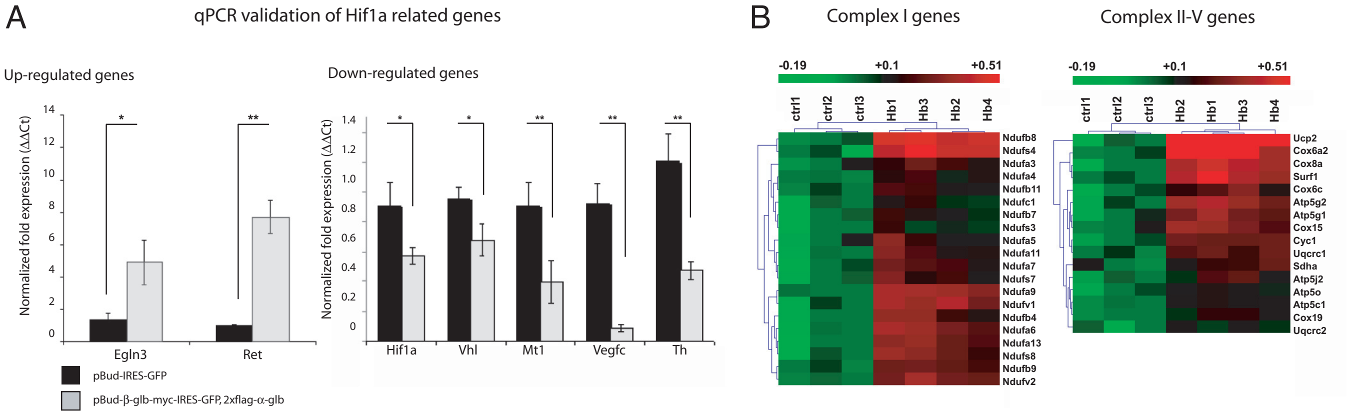

Fig. 5. Array analysis of Hb overexpressing mouse dopaminergic cell line reveals changes in the expression of genes involved in O_2 homeostasis and mitochondrial oxidative phosphorylation. (*A*) Genes involved in Hif1a pathway are presented. qPCR experiments of selected genes, up-regulated (*Left*) and down-regulated (*Right*), validate array data. (*B*) Genes involved in mitochondrial oxidative phosphorylation pathway. Heat maps of genes components of complex I (*Left*) and complexes II–V (*Right*) are presented.

Recently, neuroglobin has been identified in mammalian brains where it is probably involved in the hypoxia response (8, 23).

Here, we show that α- and β-chains transcripts of Hb and Hb-IR are present in a subpopulation of DA neurons, cortical and hippocampal astrocytes, and all mature oligodendrocytes.

We observed the expression of Hb transcripts in DA cells by using four different approaches: cDNA microarrays, nanoCAGE, RT-PCR, and in situ hybridization. Furthermore, we took advantage of two different methods (LCM and FACS) to isolate a pure population of DA neurons.

Interestingly, when analyzing Hb-IR we found that Hb protein expression does not fully overlap with transcript distribution: the large majority of A10 DA cells and a small number of A9 neurons showed mRNA expression but not Hb-IR. There are thus at least two potential explanations for this discrepancy: the level of Hb expression in those DA cells is lower and below antibody sensitivity and/or Hb protein expression may be regulated at posttranscriptional level. Interestingly, our in situ hybridization data may suggest the expression of mRNA for Hb chains in hippocampal neurons as recently proposed (24, 25).

Globin RNAs and protein expression overlap in hippocampal and cortical astrocytes and almost all mature oligodendrocytes. Globin mRNAs have been detected as differentially expressed between acutely purified and cultured oligodendrocytes (11) and during regeneration of the sciatic nerve (26). Here, we observed globin staining in the oligodendrocytes of all of the brain regions including striatum, corpus callosum, and medulla oblongata. We also found Hb-immunoreactive cells in perinatal pups. In the adult, no NG2-positive cells were Hb-immunoreactive, thus Hb expression seems restricted to mature oligodendrocytes.

Although Hb function in the brain remains to be investigated in vivo, here we have provided some interesting cues by using MN9D cells, a mouse dopaminergic cell line that represents a well-accepted in vitro model to study dopaminergic cell physiology and dysfunction (27, 28).

By carrying out a gene expression analysis of MN9D stably transfected with α- and β-chains we found that Hb expression acts on the main elements of O_2 homeostasis. This observation was not surprising because Hb may function as an oxygen storage and transport molecule. It is well known that both hyperoxia and hypoxia can be detrimental to cellular physiology in the nervous system (29). Brain Hb may then act as storage of oxygen to provide a homeostatic mechanism in anoxic conditions, which is especially important for A9 DA neurons that have an elevated metabolism with a high requirement for energy production.

Extending this model to other Hb-expressing cells in the brain, the widespread distribution of oligodendrocytes and their localization adjacent to neuronal cells may provide a net of oxygen-storage cells. In hypoxia conditions, oxygen may then be released and provide to the neighboring neurons some highly needed relief for the maintenance of the aerobic metabolism.

Interestingly, 46% of genes that encode for subunits of mitochondrial complex I–V were induced in the stable cell lines overexpressing Hb chains. It is well known that oxygen tension regulates mtDNA-encoded complex I gene expression (30) and high oxygen concentration induces mitochondrial biogenesis (31). Complex I plays a central role in PD because deficits in its subunits and activity have been consistently detected in the SN of PD patients (32). Furthermore, in PD animal models administration of the toxic metabolite MPP^+ and the pesticides rotenone and paraquat cause dopaminergic degeneration in part by mitochondrial complex I inhibition. Therefore, these gene expression data may suggest Hb as a central player in the control of mitochondrial function in normal and pathological conditions.

High mitochondrial activity is usually linked to oxidative stress, which may be especially detrimental for A9 neurons because they are normally under intense oxidative stress caused by the production of hydrogen peroxide via autoxidation and/or monoamine oxidase (MAO)-mediated deamination of dopamine and the subsequent reaction of accessible ferrous iron to generate highly toxic hydroxyl radicals (33).

Hemoglobin may indeed play homeostatic roles as both an antioxidant and a regulator of iron metabolism. In rat mesangial cells Hb carries out an antioxidant function (12). According to our gene expression data, this ability may be mediated by well-known detoxifying agents from cellular free radicals (Table S3).

Mitochondrial oxidative phosphorylation, oxidative stress, and iron deposits are all important components of PD pathogenesis (34, 35). Significantly, here we proved the expression of Hb in A9 DA neurons of human postmortem brain. Interestingly, a functional polymorphism in the gene for the Hb-binding protein haptoglobin has been shown influencing susceptibility for idiopathic PD (14).

The establishment of a series of transgenic mice with cell type-specific globin gene knockout in DA neurons, astrocytes, and oligodendrocytes will provide an essential tool for unveiling Hb function in the brain. It is of note that to our knowledge no *loxP* mouse line for globin genes is currently available: the unexpected expression of this old protein in the brain will soon change this surprising shortfall.

Materials and Methods

Animal Procedures. All of the experiments involving the use of animals were performed in accordance with guidelines of the international and Italian ethical committees and under the supervision of local veterinary services.

LCM of mDA Neurons from TH-GFP Mice. Eight- to 12-week-old mice were deeply anesthetized and extensively perfused transcardially with TBS followed by 1× zinc fixative (BD) diluted in RNase free water (Ambion). Brains were removed and postfixed in 1× zinc fixative for 8 h at + 4 °C. The region containing the SN was isolated, included in freezing medium Neg-50 (Richard Allan Scientific), and frozen on dry ice for 10 min. The frozen block was brought into cryostat (Microm International) and left at −21 °C for 30 min. Coronal sections of midbrain (14 μm) were cut with a clean blade and transferred on Superfrost Plus glass slides (Menzel-Glaser Menzel). Glass slides were air-dried for 5 min; selections of single DA were marked with a LCM microscope, microdissected, collected in adhesive caps (Zeiss), and immediately processed.

Dissociation and FACS. To isolate DA, astrocytes, and oligodendrocytes, transgenic mice including TH-GFP (13), GFAP-GFP (Jackson Laboratories), and CNP-GFP mice (18) were used, respectively. For DA and cortical or hippocampal astrocytes P4-P8 pups were used. Oligodendrocytes were collected by using P13/P20 animals. Solitary DA were prepared as described (see *SI Text*). A similar procedure was followed for the dissociation of cortical and hippocampal astrocytes and oligodendrocytes.

A cell strainer with 70-μm nylon mesh was used to obtain a single-cell suspension (BD Falcon) before sorting. 7-Amino-actinomycin D (7-AAD) (Beckman–Coulter) was added to the cell suspension to exclude dead cells. Subpopulation of cells expressing GFP emission was isolated with a high-speed cell sorter (MoFlo). Sorting parameters for the three different populations are visualized in Fig. S8.

See *SI Text* for detailed description of experimental procedures.

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Supporting Information

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SI Text

RNA Isolation, Reverse Transcription, qPCR, Cloning, and Sequencing. RNA was extracted from cell lines and blood by using TRIzol reagent (Invitrogen) and following vendor instructions.

RNA was extracted from LCM- or FACS-purified cells with an Absolutely RNA Nanoprep Kit (Stratagene). Single-strand cDNA was obtained from purified RNA by using the iSCRIPT cDNA Synhesis Kit (Bio-Rad) according to the manufacturer's instructions. Quantitative RT-PCR was performed by using SYBER-Green PCR Master Mix and an iQ5 Real-Time PCR Detection System (Bio-Rad).

Quantitative RT-PCR was performed with an iCycler IQ (Bio-Rad); β-actin was used as an endogenous control to normalize the expression level of target genes. Primers were chosen by using the software Beacon Designer 2.0 (Biosoft International). Primer sequences are available on request. Results were normalized to β-actin, and the initial amount of the template of each sample was determined as relative expression versus one of the samples chosen as reference. The relative expression of each sample was calculated by the formula $2\exp^{-\Delta\Delta Ct}$ (User Bulletin 2 of the ABI Prism 7700 Sequence Detection System).

PCR and qPCR amplicons were cloned in pGEM-TEasy vector (Promega) and sequenced with T7/Sp6 primers with a LI-COR Global Edition DNA sequencer.

In Situ Hybridization. After perfusion with 4% paraformaldehyde in PBS, the mouse brain was removed, postfixed, and cryoprotected overnight at 4 °C in 30% sucrose. In situ hybridization was performed on criostat slices (16 μm).

Sense and antisense probes were generated by in vitro transcription from the cDNA encoding mouse β-globin (NM_008220.3, gene nucleotides +27 to +596; 569 bp: complete CDS, 28 bp in the 5′ UTR, 97 bp in the 3′ UTR), and mouse α-globin (NM_008218.2, gene nucleotides +12 to +521; 509 bp: complete CDS, 24 bp in the 5′ UTR, 47 bp in the 3′ UTR). Probes were labeled with digoxigenin (DIG) by using DIG RNA Labeling Mix (Roche Applied Science), and the digoxigenin incorporation was tested by Northern blot analysis. Hybridization was performed with probes at a concentration of 4 μg/mL at 60 °C for 16 h. Anti-DIG AP conjugate (Roche Applied Science) was used as the detection antibody, and colorimetric reactions were performed with NBT/BCIP solution (Sigma–Aldrich). Sections were then washed, incubated with primary antibody for 3 h at room temperature and with secondary antibody for 1 h at room temperature. Sections were mounted with Vectashield and observed at fluorescence microscope.

Dissociation and FACS. To isolate DA neurons, astrocytes, and oligodendrocytes, transgenic mice including TH-GFP (1), GFAP-GFP (Jackson Laboratories), and CNP-GFP mice (2) were used, respectively. For DA neurons and cortical or hippocampal astrocytes, P4-P8 pups were used. Oligodendrocytes were collected by using P13/P20 animals. Solitary DA neurons were prepared as described by David Sulzer online protocol (http://www.sulzerlab.org/Sulzer_VM_culture_4.1.pdf). Briefly, midbrain was isolated from transgenic TH-GFP mice. The pieces were enzymatically dissociated (Papain) under continuous oxygenation (5% CO_2 and 95% O_2 gas mixture) with slow stirring at 33 °C (0.5 M kynurenate is added to the solution). After 40 min the reaction was stopped with enzyme inhibitors and the cell suspension was gently triturated with p1000 tip. Undissociated tissue was allowed to settle down, the supernatant was collected, and the procedure was repeated twice. Single cells were then resuspended in panning buffer and incubated on lectin-coated panning plates for 15 min at room temperature. Nonadherent cells were transferred to the next panning plate (four pannings, 15 min each). Then, nonadherent cells were collected, centrifuged, and resuspended in serum-free neuronal medium or PBS.

A similar procedure was also followed for the dissociation of cortical and hippocampal astrocytes and oligodendrocytes.

A cell strainer with 70-μm nylon mesh was used to obtain a single-cell suspension (BD Falcon) before sorting. 7-AAD (Beckman–Coulter) was added to the cell suspension to exclude dead cells. A high-speed cell sorter (MoFlo) was used to sort subpopulation of cells expressing GFP. Sorting parameters used for the three different populations are visualized in Fig. S8.

Immunocytofluorescence and Immunohistofluorescence. For immunofluorescence experiments cells were fixed in 4% paraformaldehyde (Tousimis Research) directly added to culture medium for 10 min, then washed with PBS two times, treated with 0.1 M glycine for 4 min in PBS, and permeabilized with 0.1% Triton X-100 in PBS for another 4 min. After washing with PBS and blocking with 0.2% BSA, 1% NGS, and 0.1% Triton X-100 in PBS (blocking solution), cells were incubated with the indicated antibodies diluted in blocking solution for 90 min at room temperature. After washes in PBS, cells were incubated with labeled secondary antibodies for 60 min. For nuclear staining, cells were incubated with 1 μg/mL DAPI for 5 min. Cells were washed and mounted with Vectashield mounting medium (Vector).

For immunohistochemistry, 8- to 12-week-old C57/B6 mice (Jackson Laboratories) were deeply anesthetized and intensively perfused transcardially with PBS followed by 4% paraformaldehyde diluted in PBS. Brains were removed and postfixed in 4% paraformaldehyde for 1 h at room temperature. The region containing the SN was isolated and cut with a vibratome (40 μm). Slides were blocked with PBS, 10% NGS, 1% BSA, and 1% fish gelatin (filtered) for 1 h at room temperature, and the primary and secondary antibodies were diluted in PBS, 1% BSA, 0.1% fish gelatin, and 0.3% Triton X-100. Incubation with primary antibodies was performed for 16 h at room temperature; incubation with secondary antibodies was performed for 2 h at room temperature. Nuclei were labeled with DAPI. Slides were mounted with mounting medium for fluorescence Vectashield (Vector Lab) and observed with a confocal microscope.

Immunohistofluorescence on human postmortem brain sections was performed as described (3).

For detection, Alexa Fluor-488, -594, or -405 (Invitrogen) antibodies were used. For double immunohistofluorescence with two antibodies raised in rabbit, Zenon Rabbit IgG Labeling Kits (Molecular Probes/Invitrogen) was used following the manufacturer's instructions. Nuclei were visualized with DAPI. All images were collected with a confocal microscope (Leica TCS SP2).

The following antibodies were used for this study: anti-Myc (1:1,000; Cell Signaling), anti-Flag (1:1,000; Sigma), anti-mouse Hb (1:1,000; Cappel), chicken anti-mouse Hb (1:300; ICL), anti-CNP (1:500; Chemicon), anti-TH (1:1,000; Sigma), anti-Gata-1 (1:200; SC), anti-Tal1 (1:200; SC), anti-GFAP (1:1,000; Sigma), anti-NeuN (1:1,000; Chemicon), anti-NG2 (1:300; Chemicon), anti Iba-1 (1:200; kind gift of Dr. Yoshinori Imai), goat anti-human Hb (1:100; Biomeda), and mouse anti-human Hb (1:200; Santa Cruz).

Postmortem Human Brain Samples. Brain samples were obtained from the brain banks of the Institute of Neuropathology, Bellvitge Hospital, and the University of Barcelona. Human brains were obtained at autopsy with the informed consent of patients or their relatives and the institutional approval of the Ethics Committee of the University of Barcelona. The samples were from three Caucasian males, age-matched (39–56 years old). The time between death and brain processing was between 3 and 5 h. SN and *amygdala* were excised, cryoprotected with 30% sucrose in 4% formaldehyde, frozen in dry ice, and stored at −80 °C until use.

Constructs. Full-length mouse sequences of adult and embryonic globin chains and myoglobin and cytoglobin were obtained from the FANTOM2 RIKEN clone libraries collection (4). Mouse neuroglobin full-length sequence was obtained from the German Science Centre for Genome Research, Berlin. Coding sequences were subcloned by PCR into pIRES2-EGFP (Clontech/BD Biosciences) in frame with C-terminal myc tag.

We took advantage of pBudCE 4.1 vector (Invitrogen), designed for the independent expression of two genes from a single plasmid, to express α- and β-chains of mouse Hb in MN9D cells. A fragment composed by β-globin-Myc-tag-IRES-EGFP was cloned into the CMV-MCS (SalI/XbaI) and 2×Flag-α-globin was placed into EF-1 α-MCS (KpnI/XhoI).

A control vector containing only IRES-EGFP in CMV-MCS (SalI/XhoI) was also created.

Cell Culture and Transfection. HEK-293T cells were grown in DMEM (GIBCO) supplemented with 10% fetal bovine serum (Sigma–Aldrich), 100 units/mL penicillin, and 100 μm/mL streptomycin (Sigma) at 37 °C in a humidified CO_2 incubator. HEK cells were transfected with standard calcium phosphate method.

The mouse dopaminergic neuroblastoma cell line MN9D was obtained by Michael J. Zigmond and maintained in culture using DMEM with 10% FBS, 100 μg/mL penicillin, and 100 μg/mL streptomycin. MN9D cells were transfected by using Lipofectamine 2000 (Invitrogen) following the manufacturer's instructions. Twenty four hours after transfection, cells were collected, and an high-speed cell sorter (MoFlo) was used to sort subpopulation of cells expressing GFP. Sorting parameters are summarized in Fig. S6. After sorting, cells were replated, and 48 h later, Zeocyn (300 μg/mL) was added for selection. After 3 weeks polyclonal cell populations expressing tagged α- and β-chains of mouse Hb or empty vector were obtained and confirmed by Western blot analysis, immunofluorescence, and quantitative real-time PCR (Fig. S7).

Immunoprecipitation Experiments. For immunoprecipitation and coimmunoprecipitation, cells were lysed in immunoprecipitation buffer [300 mM NaCl, 50 mM Tris (pH 7.5), 1% Nonidet P-40, 10% glycerol], supplemented with complete EDTA-free protease inhibitor mixture (Roche Diagnostics) for 30 min at 4 °C. Lysates were cleared at $15{,}000 \times g$ for 20 min. Cellular lysates were incubated with the appropriate antibodies [anti-Myc (Cell Signaling), anti-Flag (Sigma), anti-Hb (Cappel)], or corresponding controls [mouse IgG and rabbit IgG (Sigma)]. Immunoprecipitation was performed for 2 h at 4 °C. After washing, immunoprecipitated proteins were eluted with $2 \times$ SDS sample buffer, boiled, and analyzed by Western blot. Washes of immunoprecipitated proteins were performed with the same immunoprecipitation buffer.

For Western blot analysis, samples were resolved on 10–15% SDS/PAGE as needed and proteins were transferred to nitrocellulose membrane (Schleicher & Schuell). Membrane was blocked with 5% nonfat milk in TBS solution (TBS + 0.1% Tween20), then incubated with primary antibodies overnight at 4 °C or at room temperature for 2 h. Proteins were detected by horseradish peroxidase-conjugated secondary antibodies (DakoCytomation) and enhanced chemiluminescence reagents (GE Healthcare).

Microarray Analysis. Total RNA was isolated by using TRIzol (Invitrogen) according to the manufacturer's instructions, treated with DnaseI (Ambion), and purified with a RNeasy Mini kit (Qiagen). RNA quality and quantity was assessed with an Agilent 2100 Bioanalyzer (Agilent Technologies) and NanoDrop 1000 spectrophotometer (Thermo Scientific). Two micrograms of each total RNA sample was labeled according to standard one-cycle amplification and labeling protocol (Affymetrix).

Labeled cRNA was hybridized on Affymetrix GeneChip Mouse Genome 430A 2.0 Arrays, containing 22,690 probesets corresponding to ≈14,000 well-characterized mouse genes. Hybridized arrays were stained, washed (GeneChip Fluidics Station 450), and scanned (GeneChip Scanner 3000 7G). Cell intensity values and probe detection calls were computed with Affymetrix GeneChip Operating Software. Four biological replicas were processed for each experimental condition. One replicate from empty vector condition did not pass the quality-control analysis and was discarded from further study. Further data processing was performed in the R computing environment (www.r-project.org), version 2.8.0 with BioConductor packages (www.bioconductor.org).

Robust multiarray average normalization was applied (5). Data were then filtered based on Affymetrix detection call and probeset intensity, so that only probesets that had a present call and intensity value >100 in at least one of the arrays were retained. Statistical analysis was performed with limma (6). P values were adjusted for multiple testing by using Benjamini and Hochberg's method to control the false discovery rate (7). Genes with adjusted $P < 0.05$ were considered differentially expressed. A threshold value of 0.2 Log fold change was applied. Data were analyzed through the use of Ingenuity Pathways Analysis (Ingenuity Systems, www.ingenuity.com).

Microarray data have been deposited in the GEO database with accession no. GSE16192. Heat map cell values were obtained as ratios between each probe intensity value and the median of all control sample intensities for that probe. Hierarchical clustering analysis (average linkage) was performed on genes and samples as implemented in MultiExperiment Viewer, version 4.0 (8).

Statistical Analysis. All data were obtained by at least three independent experiments and are expressed as mean ± SD. Student's t test was used for comparison. Significance to reference samples are shown as $*$, $P < 0.05$ or $**$, $P < 0.01$.

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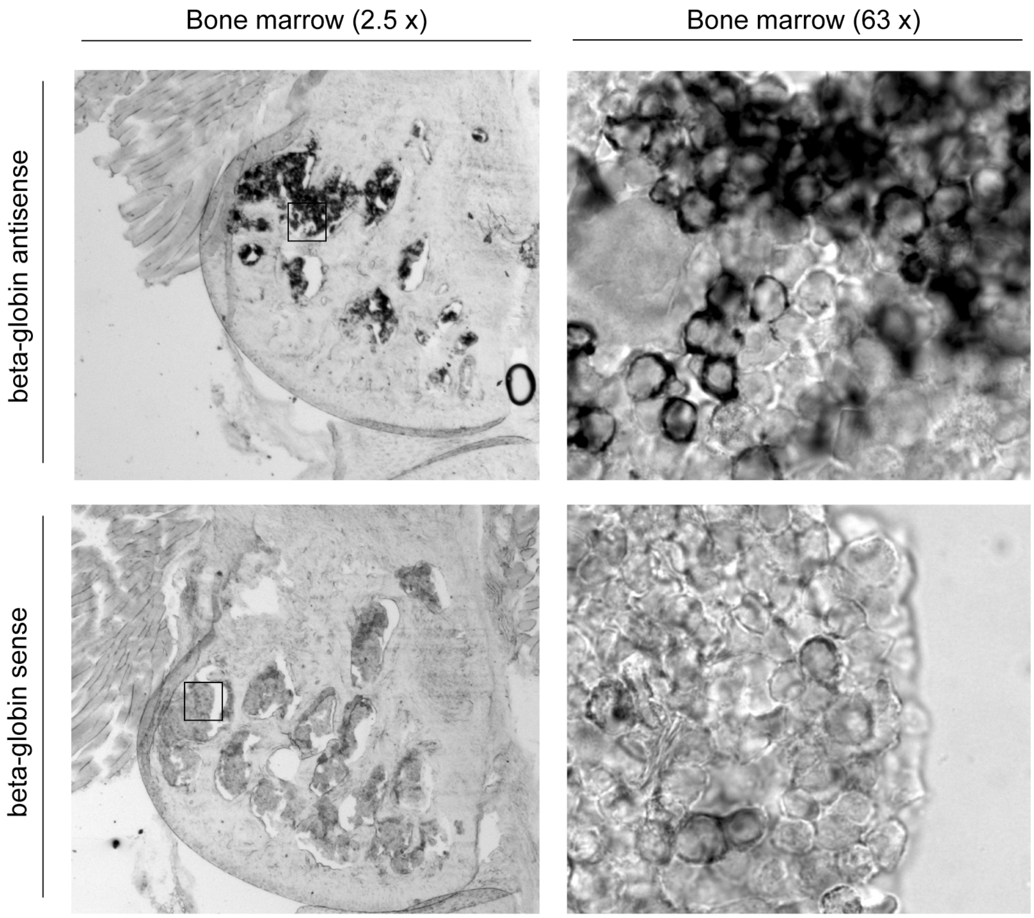

Fig. S1. In situ hybridization on mouse bone marrow (BM). Slices probed with antisense (*Upper*) and sense (*Lower*) transcripts for α- and β-globin are presented. In the pictures at lower magnification (×2.5), the morphology of bone marrow tissue is evident; at higher magnification (×63, square boxes) single cells strongly labeled for the in situ signal are clearly visible (antisense probe), whereas no labeling was visualized with a sense probe. One representative picture for antisense and sense probes of β-globin is shown. Similar results were obtained using antisense and sense probes for α-globin.

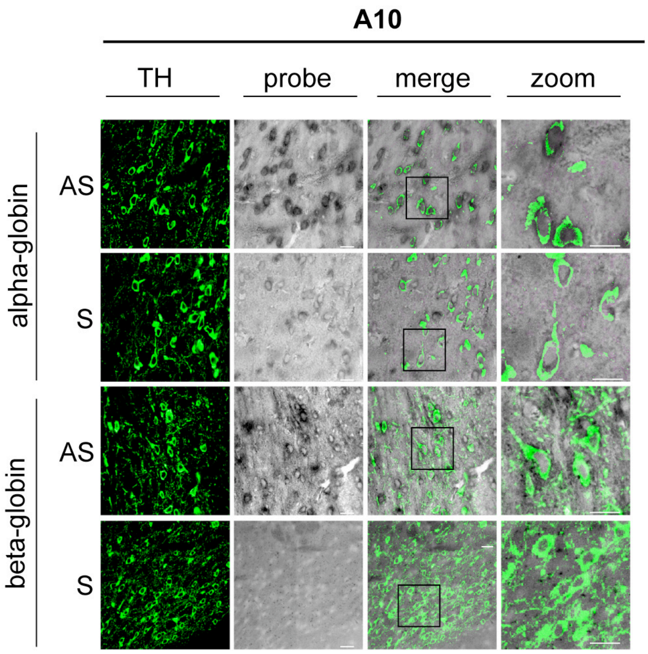

Fig. S2. In situ hybridization of α- and β-globin transcripts on A10 DA neurons: ventral midbrain slices were processed with antisense (AS) and sense (S) probes for the two globins transcripts. DA neurons were visualized by immunohistochemistry using an anti-TH antibody (green). The overlay (merge) shows colocalization of the transcripts of α- and β-globin in the cytoplasm of A10 neurons. Probes obtained from sense transcripts were used as negative controls. The zoom offers magnifications of the area in the boxes of the overlay images. (Scale bars: 20 μm.)

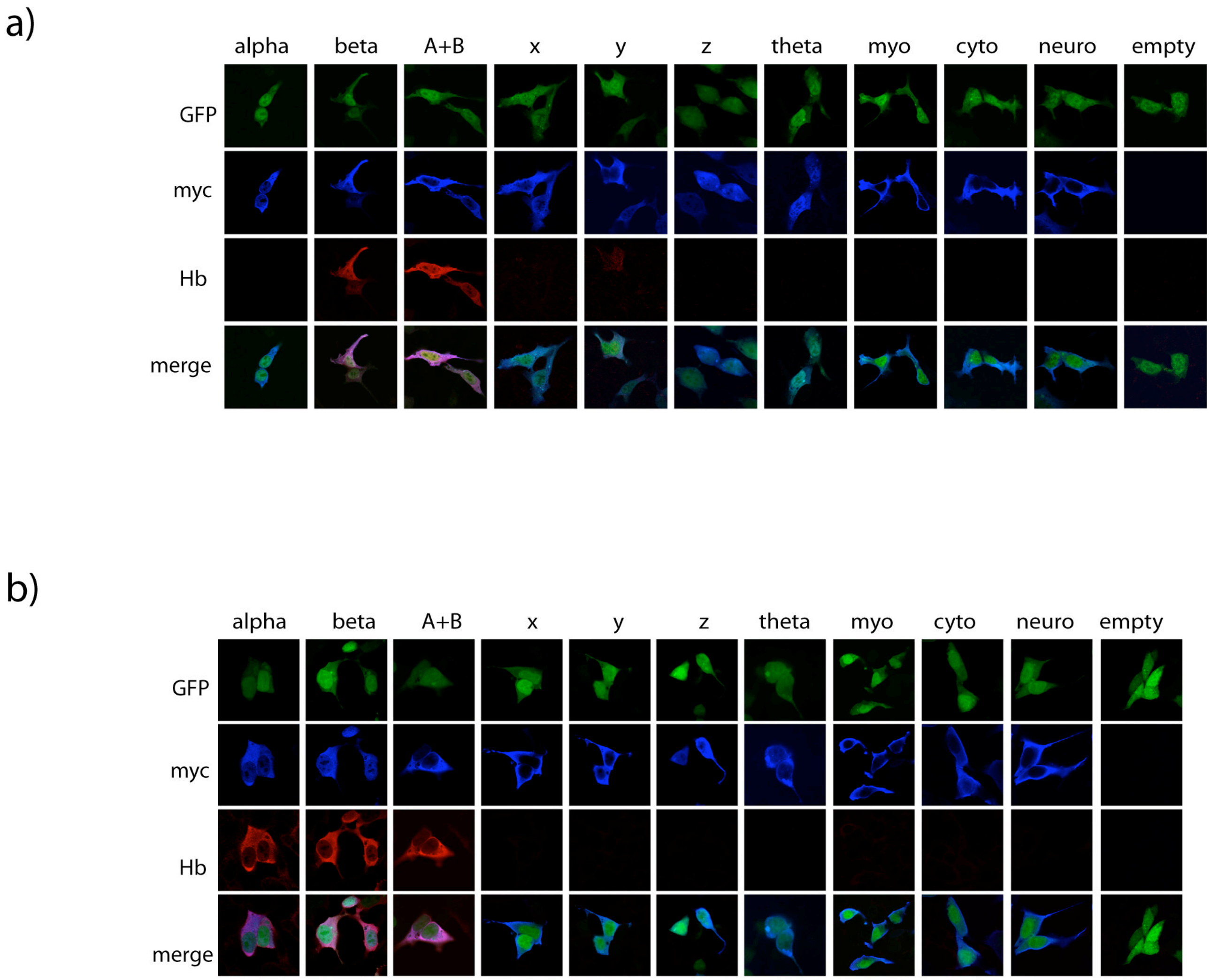

Fig. S3. Antibodies specificity test. (*a*) Hek-293 cells transfected with different constructs expressing typical and atypical globin chains [Hbb-a1 (alpha), Hbb-b1 (beta), Hba-x (x), Hbb-y (y), Hba-z (z), Hbq1 (theta), myoglobin (Myo), cytoglobin (cyto), and neuroglobin (neuro) were subjected to double immunofluorescence using anti-Myc (blue) and anti-Hb (Cappel) (red) antibodies. The transfected constructs also expressed GFP (green). pIRES2-EGFP empty vectors were transfected as control. Cappel anti-mouse Hb antibody specifically recognized β-chains of mouse Hb. No cross-reaction with the atypical globins was observed. (*b*) Similar experiment was performed using the second antibody anti-mouse Hb (ICL). The ICL antibody showed different chain recognition abilities because it detected both α- and β-globin. No cross-reaction was observed with the atypical globins. (Magnification: 63×.)

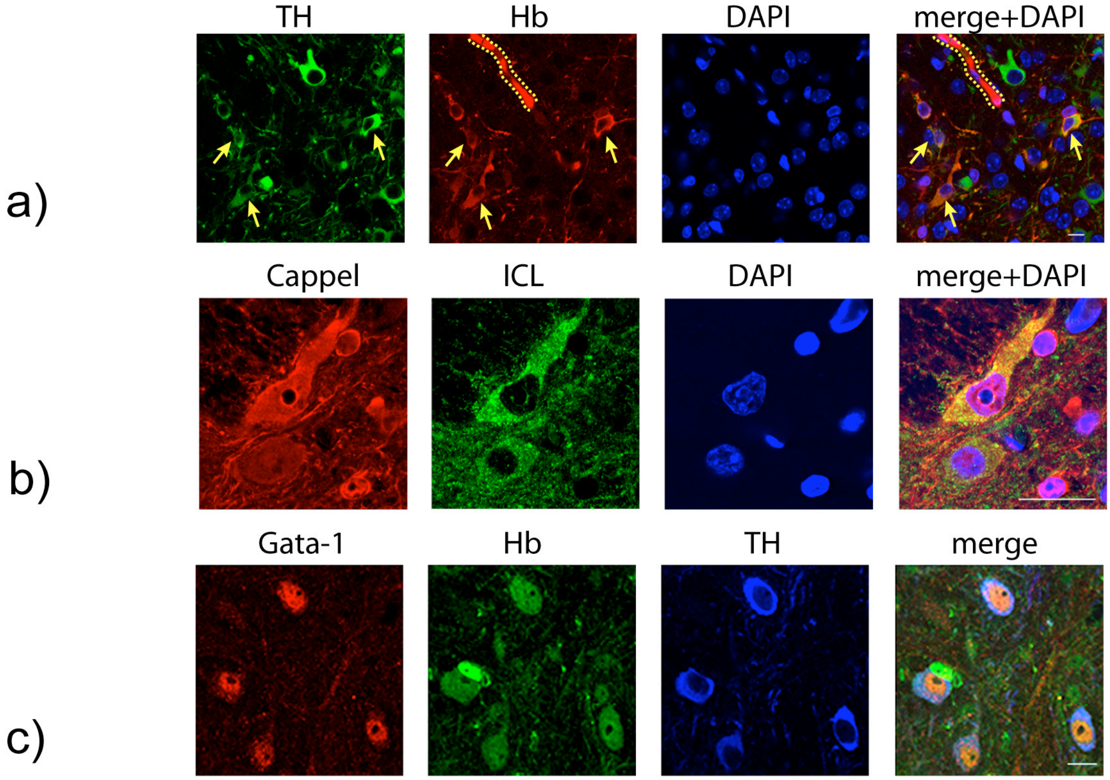

Fig. S4. Additional features for Hb-IR DA. (*a*) Double immunohistochemistry on a brain with no perfusion. Anti-Hb antibody (red), anti-TH antibody (green), and DAPI (blue) were used. Dashed lines decorated a blood vessel containing several erythrocytes strongly labeled with anti-Hb antibody. Hb-IR mDA neurons (arrows) are morphologically and topographically different from red blood cells. (*b*) Comparison of the staining obtained by using two different anti-mouse Hb antibodies. Double immunohistochemistry with Cappel (red) and ICL (green) antibodies in the ventral midbrain of adult mouse is presented. An extensive overlap of globin-IR for mDA neurons is confirmed using both antibodies (merge). (*c*) Triple immunohistochemistry using anti-Gata-1 (red), anti-Hb (green), and anti-TH (blue) antibodies. A subpopulation of DA (nearly 50%) was positive for Hb, Gata-1, and TH. (Scale bars: 20 μm.)

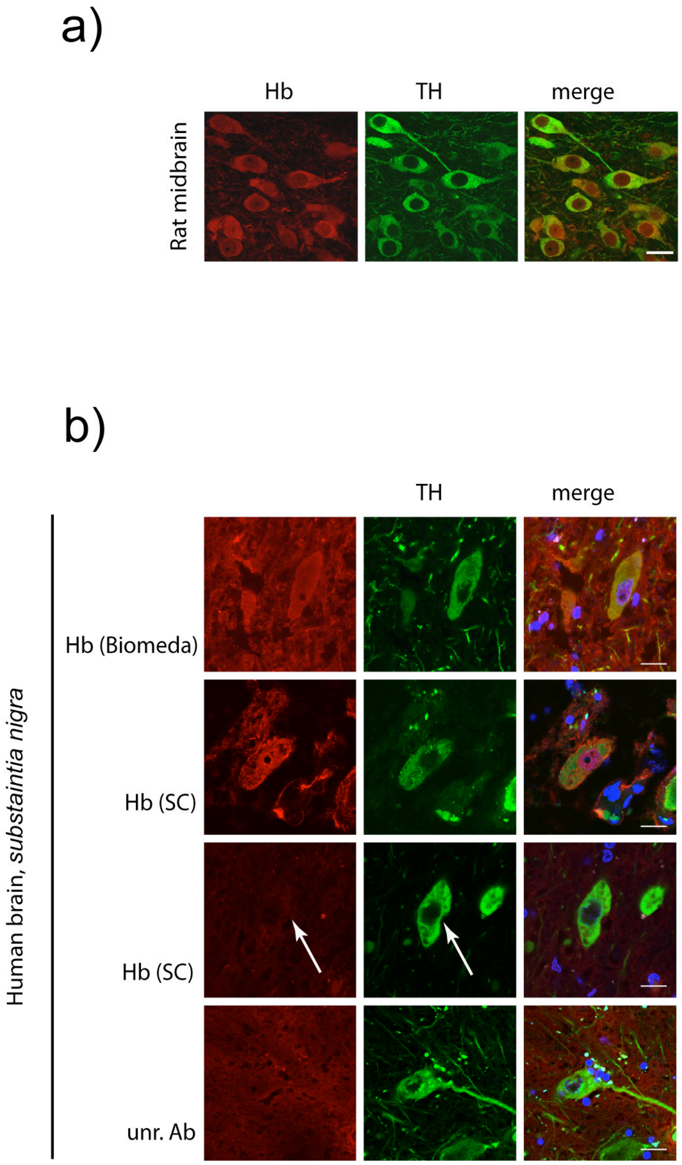

Fig. S5. Hb protein is expressed in DA of rat midbrain and adult postmortem human brain. (*a*) Double immunohystochemistry on rat midbrain. Anti-Hb antibody (red) and anti-TH antibody (green) were used. An extensive overlap of globin-IR for mDA neurons was confirmed (merge). (*b*) Double immunohistochemistry using two different anti-human Hb antibodies is presented. Santa Cruz (SC) and Biomeda antibody costain several TH-positive neurons in the SN. Several TH-positive Hb-negative neurons were also described (arrow). Unrelated antibodies (unr. Ab), host-matched with those of human hemoglobin, were used as negative controls (one representative picture is shown). (Scale bars: 20 μm.)

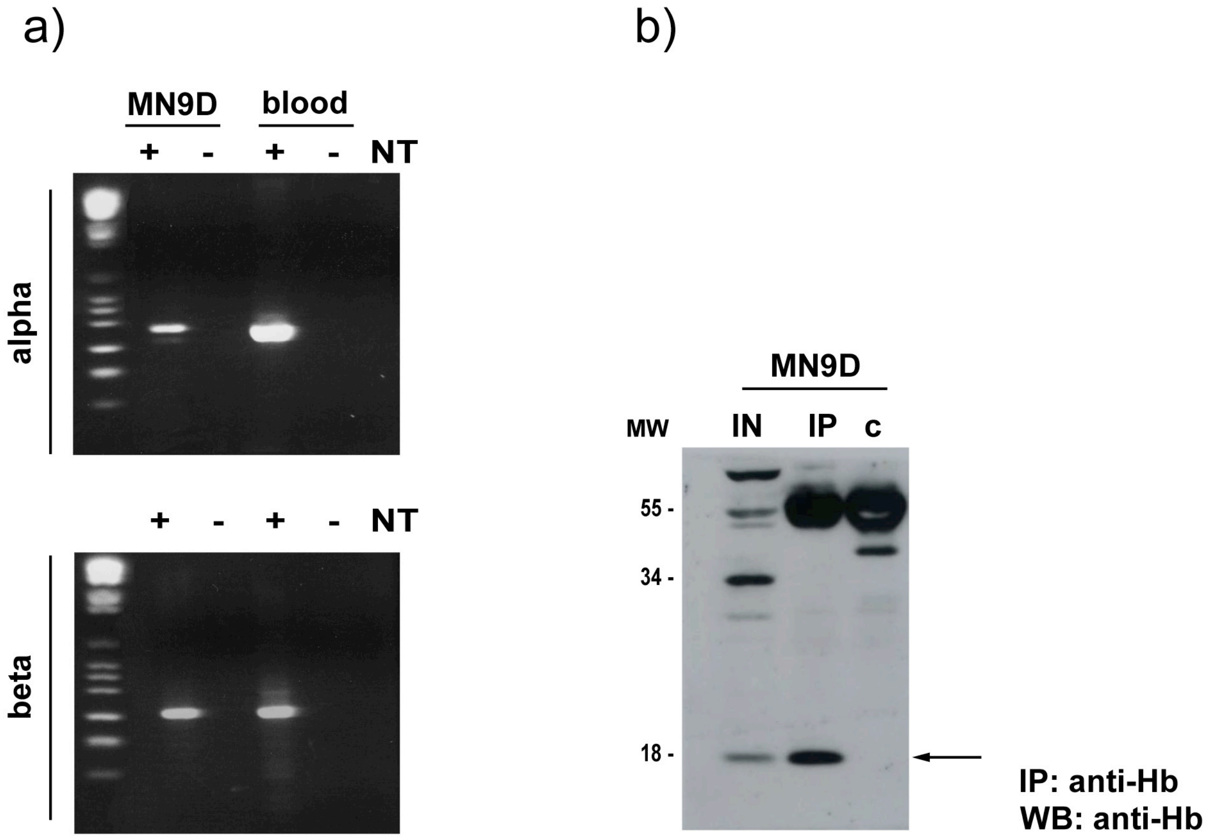

Fig. S6. α- and β-chains of mouse Hb are expressed on MN9D cells. (*a*) RT-PCR of α- and β-chains of hemoglobin from MN9D cells and mouse blood RNA. α- and β-globin transcripts were clearly amplified in mouse dopaminergic cell line MN9D (*Left*). RNA extracted from blood was used as positive control (*Right*). Amplicon identities were confirmed by sequencing. (*b*) Immunoprecipitation of Hb protein from MN9D cell line. A clear band of 17 kDa was enriched from MN9D lysate after resorting to immunoprecipitation (IP) using anti-mouse Hb antibody (Cappel). Rabbit IgG were used as immunoprecipitation control (c). IN indicates input of MN9D lysate. Immunoblot (IB) was probed using the same antibody used for IP.

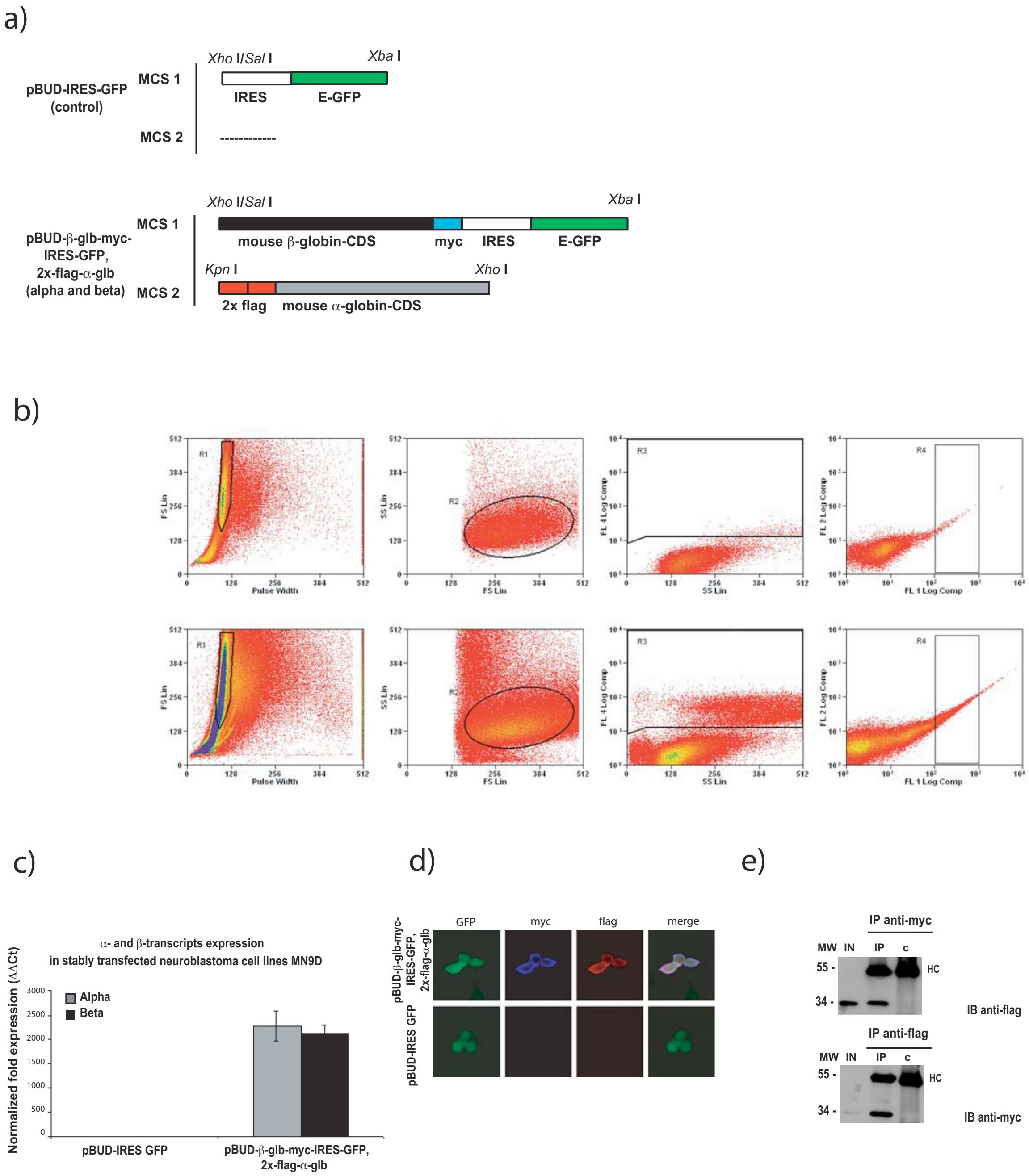

Fig. S7. Polyclonal stable cell lines overexpressing *pBUD-β-glb-Myc-IRES-GFP*, *2x-flag-α-glb*, and *pBUD-IRES-GFP*: cloning strategy and stable cell lines characterization. (*a*) Cloning strategy scheme of, respectively, *pBUD-IRES-GFP* (empty vector) and *pBUD-β-glb-Myc-IRES-GFP*, *2x-flag-α-glb* (α and β vector). β-globin-myc-IRES-GFP or IRES-GFP alone was inserted into CMV-MCS, and 2×flag-α-globin was inserted into the EF-1a–MCS of pBUDCE 4.1 vector. (*b*) Polyclonal stable cell lines overexpressing *pBUD-β-glb-Myc-IRES-GFP*, *2x-flag-α-glb*, or *pBUD-IRES-GFP* were purified by using FACS. FACS parameters used were similar to those used previously (see Fig. S8). Briefly, we first excluded from the analysis cell doublets and debris (PW/FSC), then physical parameters (FSC and SSC) and 7-AAD exclusion were used to exclude dead cells. Finally, a subpopulation of cells with comparable GFP emission intensity (10^2-to 10^3) was identified and sorted for the two cell populations. (*c*) qPCR experiments demonstrated that the levels of expression of the two Hb chains was thousand-fold up-regulated in MN9D-*pBUD-β-glb-Myc-IRES-GFP*, *2x-flag-α-glb* compared with MN9D-*pBUD-IRES-GFP*. Moreover, qPCR revealed comparable levels of α- and β-chains expression in MN9D-*pBUD-β-glb-Myc-IRES-GFP*, *2x-flag-α-glb* cell line. (*d*) A double immunofluorescence of MN9D-*pBUD-β-glb-Myc-IRES-GFP*, *2x-flag-α-glb* and MN9D-*pBUD-IRES-GFP* was carried out using anti-Myc (blue) and anti-FLAG (red) antibodies. β-Globin-myc-tag and 2x-flag-α-globin colocalise in the cytoplasm and, partially, in the nucleus of MN9D stable cell lines. The transfected constructs also expressed GFP (green). (*e*) Immunoprecipitation (IP) of β-globin (IP anti-myc) from MN9D-*pBUD-β-glb-Myc-IRES-GFP*, *2x-flag-α-glb* coimmunoprecipitated α-globin (immunoblot, IB, anti-flag) demonstrating that the transfected chains are able to form heterodimers. Reverse coimmunoprecipitation confirm this result (IP anti-Flag, IB anti-myc). Mouse IgG was use as IP control (c).

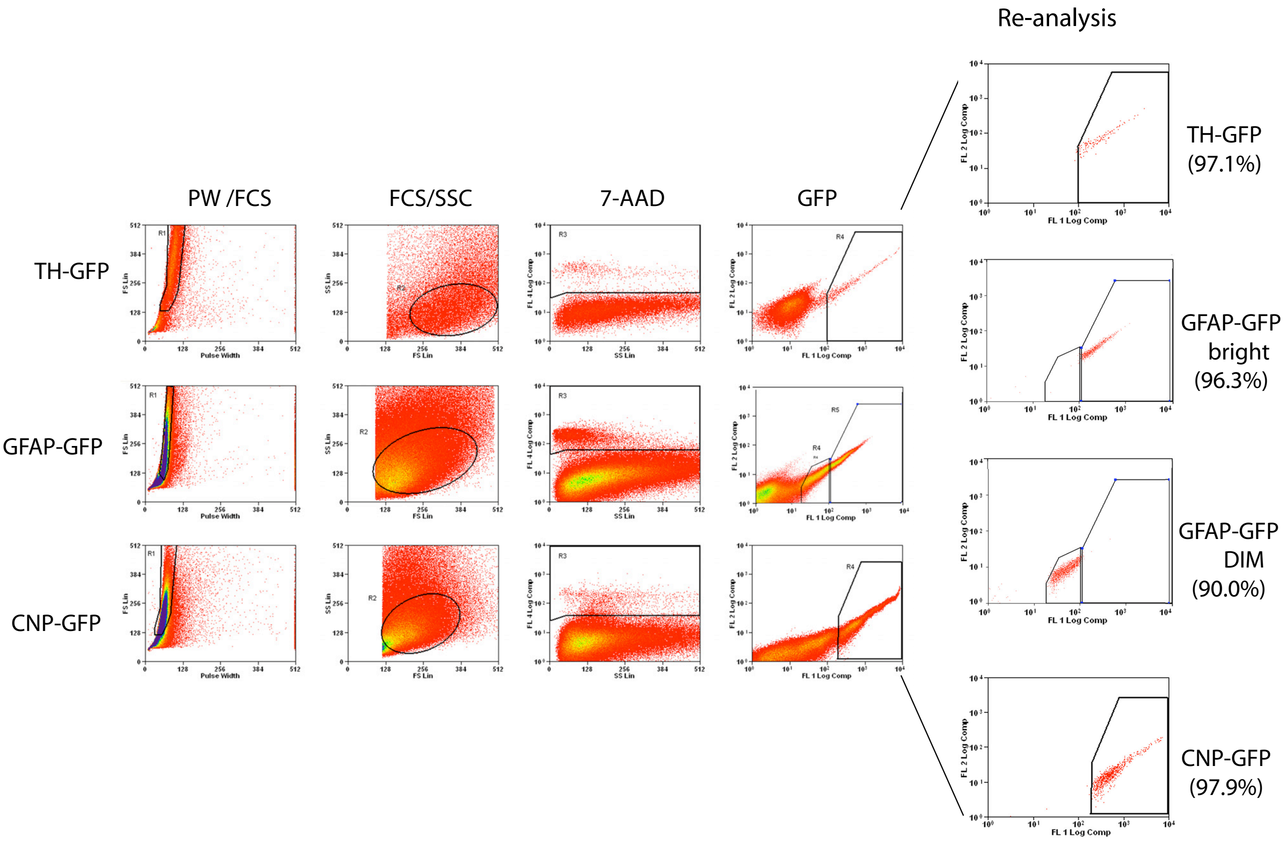

Fig. S8. Gating and sorting strategies. We first excluded from the analysis cell doublets and debris on the basis of their pulse width vs. forward scatter (PW/FSC) dot plot. Physical parameters such as FSC and side scatter (SSC) were then used to remove a part of dead cells and debris. 7-AAD exclusion was also used to exclude cells with loss in the membrane integrity and, finally, a subpopulation of cells with increased GFP emission was identified and sorted. On the right, the results of reanalysis on the FACS-sorted samples confirmed the high purity of our preparations. For GFAP-GFP mice two populations of astrocytes with different intensities (dim, range between 10^1 and 10^2, and bright, range between 10^2 and 10^4) were sorted and purified. Because of the higher grade of purity of the bright cell population, we used these second parameter sets for further experiments.

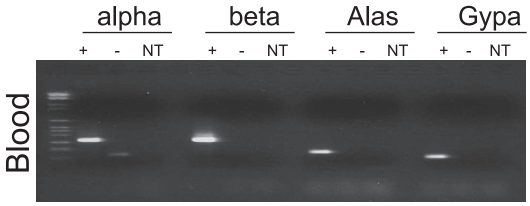

Fig. S9. RT-PCR results obtained using RNA from total mouse blood. α- and β-globin transcripts and blood markers Alas and Gypa were amplified (+). Negative controls, retrotranscriptase free (−), and no-template control samples (NT) are presented.

Other Supporting Information Files

Table S1 (PDF)
Table S2 (PDF)
Table S3 (PDF)