IDENTIFYING PHYSICAL ACTIVITY-ASSOCIATED NEUROPROTECTIVE GENE TRANSCRIPTS

By

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To the many people who have shaped my brain, my life, and my future.

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LIST OF ABBREVIATIONS

ΔCt	Change in Threshold Cycle
18F	Fluorine 18
6-OHDA	6-Hydroxydopamine
AKT/PKB	Protein Kinase B
ALS	Amyotrophic Lateral Sclerosis
AMPK	AMP Activated Protein Kinase
ARC	Activity-Regulated Cytoskeleton-Associated Protein
BDNF	Brain Derive Neurotrophic Factor
BMI	Body Mass Index
DTBZ	Dihydrotetrabenazine
C57BL/6	C 57 Black 6
CaMKIIδ	Calmodulin-Dependent Kinase II δ
CAPN6	Calpain 6
CDC	Centers for Disease Control
cDNA	complementary DNA
CRBN	Cereblon
CREB	cAMP Response Element-Binding
CRL	Crown of Rump Length
CRP	C-Reactive Protein
DAT	Dopamine Transporter
DPF3	D4, Zinc and Double PHD Fingers, Family 3

EAAC	Excitatory Amino Acid Carrier
ELISA	Enzyme Linked Immunosorbent Assay
ERK1/2	Extracellular Regulated MAP Kinase 1 and 2
FDR	False Discovery Rate
FGF2	Fibroblast Growth Factor 2
FOXO3	Forkhead Box O3
GABA(a)β3	Gamma-Aminobutyric Acid
GAD67	Glutamic Acid Decarboxylase 67
GDNF	Glial Derived Neurotrophic Factor
GO	Gene Ontology
GSEA	Gene Set Enrichment Analysis
GSK3	Glutathione Synthase Kinase 3
GST π	Glutathione Transferase pi
HG	Human Genome Microarrays
HUVEC	Human Umbilical Vein Endothelial Cells
IgG	Immunoglobulin G
IQR	Interquartile Range
KEGG	Kyoto Encyclopedia of Genes and Genomes
LDOPA	L-3,4-Dihydrophenylalanine
LRRC27	Leucine Rich Repeat Containing 27
LRRC40	Leucine Rich Repeat Containing 40
MAS5	Microarray Analysis Suite 5
mMAP	Monkey Movement Assessment Panel

MPTP	1-Methyl-4-Phenyl-1,2,3,6-Tetrahydropyridine
MSigDB	Molecular Signatures Database
mTORC1	Mammalian Target of Rapamycin Complex 1
NCBI	National Center for Biotechnology Information
NEUROG3	Neurogenin 3
ng	Nanogram
NGF	Nerve Growth Factor
NOM	Nominal
NTRK3	Neurotrophic Factor Receptor 3
ORC4L	Origin Recognition Complex, Subunit 4-Like
PD	Parkinson's disease
PDK4	Pyruvate Dehydrogenase Kinase, Isozyme 4
PKC	Protein Kinase C
qPCR	quantitative Polymerase Chain Reaction
QTL	Quantitative Trait Locus
R1c	Replicate 1 caudate nucleus
R1p	Replicate 1 putamen
R2c	Replicate 2 caudate nucleus
R2p	Replicate 2 putamen
RhG	Rhesus Genome Microarrays
RIN	RNA Integrity Number
RMA	Robust Multichip Average
SD	Standard Deviation

Ser473	Serine 473
SNpc	Substantia Nigra pars compacta
SPECT	Single-Photon Emission Computed Tomography
SPSS	Statistical Package for the Social Sciences
SRCAP	SnF2-Releatd CREBBP Activator Protein
STX3	Syntaxin 3
tAKT	total AKT
TBL1XR1	Transducin (beta)-Like 1 X-Linked Receptor 1
TBS	Tris-Buffered Saline
TBZ	Tetrabenazine
TH	Tyrosine Hydroxylase
TSC2	Tuberous Sclerosis Protein 2
VEGFA	Vascular Endothelial Growth Factor A
VMAT	Vesicular Monoamine Transporter

CHAPTER I

Introduction

“To get back to my youth I would do anything in the world except take exercise, get up early, or be respectable,” Oscar Wilde, *The Picture of Dorian Gray*.

Both physical activity and exercise greatly benefit overall health. They determine energy balance and weight control, improve bone health, and something as little as 30 minutes of brisk walking, 15 minutes of running, or 45 minutes of playing volleyball is associated with a decreased risk of coronary heart disease, hypertension, diabetes, cancer, and even death (U.S. Department of Health and Human Services, 2007). They elevate mood (Dunn et al., 2005; Lawlor and Hopker, 2001), improve sleep (Driver and Taylor, 2000) and cognition (Colcombe and Kramer, 2003), and are associated with a decreased risk for Alzheimer’s disease (Yaffe et al., 2001; Larson et al., 2006), Parkinson’s disease (Thacker et al., 2008), and a decreased infarct from ischemic stroke (Hu et al., 2000; Lee and Paffenbarger, 1998).

High amounts of physical activity are generally better associated with decreased risks for neurological disorders. In a multivariate analysis controlling for age, BMI, hypertension history, and other covariates physical activity reduced the risk of total and ischemic stroke in a dose responsive manner in a study of 72,488 female nurses over 8 years (Hu et al., 2000). This effect is also seen in men. An 11 year study with over

11,000 men found a decreased risk of stroke at mild energy expenditures (1999 kcal/week) and a further risk decrement at moderate energy expenditures (2000-2999 kcal/week) (Lee and Paffenbarger, 1998).

Additionally, mild physical activity, as little as walking, is associated with decreases in the risk of cognitive decline. In a six year study of 5,925 women (Yaffe et al., 2001) the risk of cognitive decline decreased with the number of blocks walked, and particularly, the greatest risk reduction of dementia associated with voluntary physical activity was in the lower performance levels in a six year smaller study of 1,740 men and women with the limiting factor of a large number of physically active people at baseline (Larson et al., 2006). In a larger study of 143,325 men and women, the lowest risk of Parkinson’s disease was in the highest baseline categories of moderate to vigorous activity (bicycling, aerobics, and tennis) (Thacker et al., 2008). This evidence suggests that physical activity is neuroprotective in a dose response manner in men and women across multiple neurological diseases.

To achieve many of the health benefits from physical activity the Center for Disease Control (CDC) recommends 30 minutes per day, 5 days per week of moderate intensity activity (brisk walking, biking, vacuuming, and gardening) or 20 minutes per day, 3 days per week of vigorous intensity activity (running, aerobics, and heavy yard work). A reported questionnaire conducted by the CDC in the United States in 2007 showed that only 48.8% of people got the recommended amount of physical activity, 37.7% of people got insufficient physical activity, and 13% of people were inactive (U.S. Department of Health and Human Services, 2007), but people commonly over-report their physical activity levels (Troiano et al., 2008).

Automated systems using Actigraph accelerometers, however, provide more accurate physical activity levels (Troiano et al., 2008). In fact lower levels of objective physical activity using waist mounted uniaxial accelerometers correspond to higher levels of self-reported physical activity (Troiano et al., 2008). Even with objective measurements, physical activity declines across age groups with 42% of children and 8% of adolescents getting the recommended 60 minutes of physical activity and 5% of adults obtaining the recommended 30 minutes of physical activity (Troiano et al., 2008). Statistics subjectively or objectively tell the same story – a majority of people do not get the recommended amount of physical activity. Even with the knowledge that exercise greatly improves overall health, as society becomes more digital and is given enhanced, convenient, stimulating, and often sedentary opportunities and activities, many people do not exercise, but this dissertation will show *how* simply increasing overall activity level can provide the same and even better benefits for brain health.

EXPERIENCE INDUCED BRAIN REMODELING

The studies previously mentioned are association studies, and have helped define the relationship between physical activity and a number of illnesses, but they have not precisely defined causation. To understand if and how physical activity decreases the risk of neurodegenerative disorders, such as Parkinson's disease, many have turned to designed studies in animals to elucidate the molecular mechanism by which physical activity influences the central nervous system to combat neurodegenerative and other diseases (Poulton and Muir, 2005; Howells et al., 2005; Caudle et al., 2007; Mabandla et al., 2004; Petzinger et al., 2007; Mandel et al., 2003; O'Dell et al., 2007).

These studies began in the 1970s when researchers saw plasticity in the brains of animals in response to changes in the environment. Cortical maps dynamically remodel in detail in response to behaviorally important experiences throughout life (Buonomano and Merzenich, 1998). The cortex reorganizes its effective local connections following peripheral or central alterations of input and in response to behavior, which partially accounts for certain forms of perceptual and motor learning (Buonomano and Merzenich, 1998). This occurs after lesions in the somatosensory cortex in monkeys (Merzenich et al., 1983; Merzenich et al., 1984; Merzenich and Jenkins, 1993; Buonomano and Merzenich, 1998), in the barrel cortex in rodents (Diamond et al., 1993), in the visual cortex in cats (Kaas, 1995; Wiesel, 1999) and in the auditory cortex in owls, rats, and humans (Plascencia et al., 2003; Untergasser et al., 2003; Hurlstone et al., 2003). Furthermore, cortical representation changes with training. Examples include increases in cortical representation of (a) the left hand in string players (Elbert et al., 1995), (b) nipple bearing skin in rat mothers nursing their young (Xerri et al., 1994), and (c) the fingers after training in monkeys (Jenkins et al., 1990; Recanzone et al., 1993). Cortical maps reorganize in response to experience.

Animals in various environments can, even as adults, remodel features of their cortex, including the number and distribution of synapses (Greenough, 1975). Adult rats in enriched environments for 80 days have higher cortical weight than their counterparts in standard housing; changing the environment increases both dendritic size and complexity (Bennett et al., 1964). Enriched environments in adult animals can increase dendrite length and branching, spine density and numbers, synaptogenesis, neurogenesis, and angiogenesis, and furthermore wheel running seems to increase this most (Greenough and Volkmar, 1973; Diamond and Connor, 1982; Turner and Greenough, 1985; Rampon et al., 2000; Brown et al., 2003; Lazarov et al., 2005). Furthermore, physical activity accompanied with calorie restriction also increases the density of dendritic spines in the entorhinal cortex and hippocampus (Stranahan et al., 2007; Stranahan et al., 2009). These studies suggest that an individual's experience can help the brain gain new neural resources to cope with neurodegeneration (Llorens-Martin et al., 2009).

NEUROTROPHIC FACTORS

What causes these changes in the brain? In search of a soluble factor Neeper et al looked at the expression of brain derived neurotrophic factor (BDNF) and nerve growth factor (NGF) in all regions of the brain (Neeper et al., 1996) after voluntary wheel running in rodents. BDNF and NGF promote the survival and function of forebrain cholinergic and mesencephalic dopaminergic neurons, which are vulnerable to aging and degenerative conditions. Neeper et al found that neurotrophic factors were indeed significantly increased across brain regions in animals that ran on wheels versus animals without running wheels with the greatest increases in the hippocampus and caudal cortex (Neeper et al., 1996). Another group looked at the expression of fibroblast growth factor 2 (FGF2) in the hippocampus and found that it was also increased with physical activity (Gomez-Pinilla et al., 1997). These studies led to a belief that neurotrophic factors were partly responsible for the changes observed in the brain after physical activity and in enriched environmental settings.

Even more precisely the molecular mechanism is thought to involve the methylation of DNA. Stimulation of the dentate gyrus in the hippocampus with electroconvulsive therapy, which induces neuronal activity by direct electrical current, decreases the methylation level of specific regulatory regions of both BDNF and FGF, which result in increases of mRNA and protein (Yu et al., 2011). Even early life stress also has been shown to change the methylation pattern of BDNF (Roth and Sweatt, 2011). This places more attention to how epigenetics affects plasticity.

Other studies using microarrays looked more globally for gene expression changes associated with voluntary wheel running in the hippocampus (Tong et al., 2001a; Molteni et al., 2002), which has given a better picture of the molecular mechanisms of physical activity. Four groups of genes increased with wheel running: neurotrophic factors (NGF, BDNF, and basic fibroblast growth factor, FGF-2), synaptic trafficking proteins (syntaxin, synapsin I, and synaptotagmin), neutrotransmitter systems (ionotropic glutamate receptor subunits NR2A and NR2B, excitatory amino-acid carrier 1 (EAAC1), γ-aminobutyric-acid receptor β3 (GABA_A β3), and glutaminic acid decarboxylase (GAD65)), and signal transduction pathways (CaMKIIδ, ERK1/2, and protein kinase C (PKC)) (Molteni et al., 2002). CAMKIIδ was more highly expressed during acute physical activity (3 days) and ERK1/2 was more highly expressed during chronic physical activity (28 days) (Molteni et al., 2002).

It is now understand that physical activity modulates the BDNF system through intracellular signaling systems such as AKT and the extracellular signal-regulated kinases 1 and 2 (ERK1/2) with endpoint effects on the phosphorylation and function of CREB (Vaynman et al., 2004) (**Figure 1**). AKT also phosphorylates forkhead box O3 (FOXO3), a transcription factor, causing its retention in the cytoplasm. When in the nucleus, FOXO3 likely triggers apoptosis by inducing the expression of genes critical for cell death (Brunet et al., 1999). Keeping FOXO3 in the cytoplasm, therefore, promotes cell survival. This provides an even more detailed mechanism of how physical activity alters and changes neurons that results in plasticity.

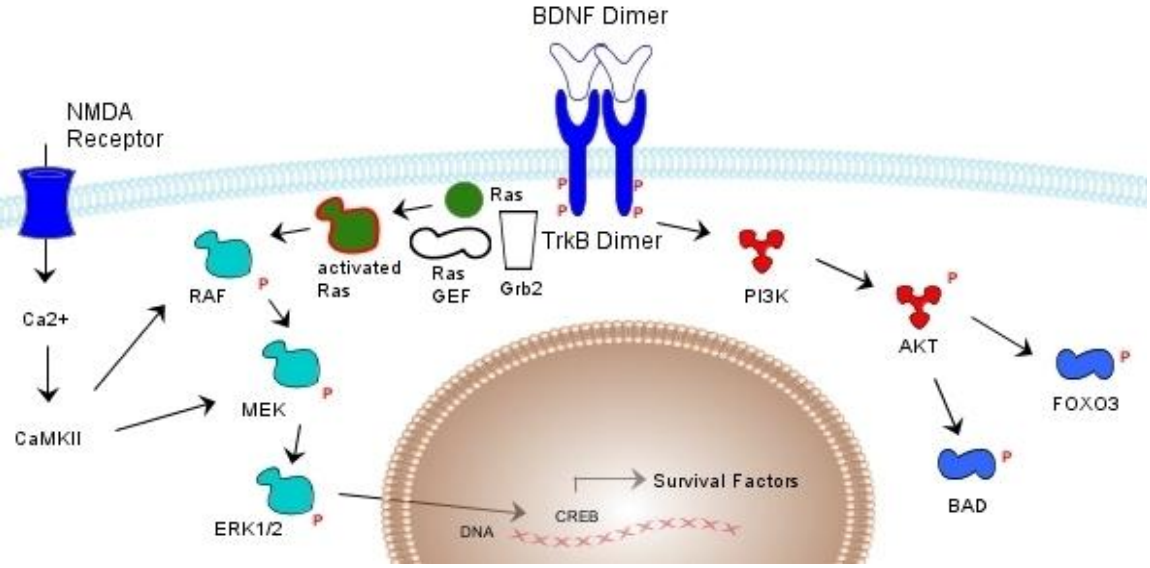

Figure 1. BDNF Signaling Pathways. BDNF activates the AKT and ERK1/2 pathways. PI3K indirectly causes the phosphorylation of AKT, which phosphorylates and inhibits death proteins (FOXO3 and BAD). ERK1/2 is phosphorylated by a kinase cascade (RAF to MEK to ERK1/2) that is activated by RAS, which is activated by RAS-GEF binding to Grb2 bound to phosphorylated TrkB dimers. These pathways also can modulated by other kinases. CaMKII, which is increased with wheel running in rodents, can phosphorylate components of the ERK1/2 pathway (Chen and Russo-Neustadt, 2005; Brunet et al., 1999; Tong et al., 2001a; Molteni et al., 2002).

ANGIOGENESIS AND VASCULAR VOLUME

Plasticity extends to changes in the brain vasculature, which also changes in response to physical activity, exercise, and enriched environments. With exercise the motor cortex, visual cortex, frontal cortex, striatum, and cerebellum increase their capacity to supply blood (Black et al., 1990; Ding et al., 2004; Ding et al., 2006; Swain et al., 2003). In enriched environments capillaries in the visual cortex become larger, and more elaborately branched (Whishaw et al., 1984; Mohammed et al., 1990; Galani et al., 1998). Both exercise and enrichment environment settings must be sustained, however, because increases in vascular volume in the motor cortex of exercised cynomolgus monkeys reverse following a sedentary period (Cameron et al., 2010).

Peripheral factors, such as insulin-like growth factor 1 (IGF-1) and c-reactive protein (CRP), may be responsible for vascular changes in the brain. IGF-1, which has effects similar to other growth factors, increases neuronal survival, angiogenesis, and is increased with physical activity (Llorens-Martin et al., 2009). Other factors, like CRP, have more detrimental effects. Increased levels of CRP can increase tissue damage after stroke (Stewart et al., 2010). CRP of the pentraxin family is involved in host defense related functions, recognizes foreign pathogens and damaged cells, and initiates their elimination by interacting with humoral and cell effector systems in the blood (Stenvinkel, 2006). It is increased in the blood plasma in response to tissue injury, infection, and other inflammatory stimuli and is associated with increased risk for type II diabetes (Lakka et al., 2005), hypertension, cardiovascular disease, and ischemic stroke (Stewart et al., 2010). Exercise can lower CRP levels (Lakka et al., 2005; Gill et al., 2004), and in healthy individuals the concentration of CRP in serum is low (Yeh, 2004).

While some factors positively associated with exercise enrich brain vasculature, others that are negatively associated with exercise are harmful.

BEHAVIORAL AND BIOCHEMICAL SPARING IN PARKINSON'S DISEASE MODELS

Physical activity can also result in neuroplasticity in animal models of Parkinson's disease, but specific and detailed gene expression analyses to determine the mechanisms of neuroprotection are still being researched. Parkinson's disease is characterized by tremor at rest, muscle rigidity, postural instability, and a slowing of physical movement (bradykinesia) that can progress to a complete loss of movement (akinesia) (Betarbet et al., 2002). As disabling motor symptoms are managed with medications (such as L-3, 4-dihydroxyphenylalanine, L-DOPA), other symptoms become more apparent. These include depression, high level cognitive dysfunction, and subtle language problems (Brown et al., 2006; Dagher, 2001). It is thought that symptoms emerge from the progressive loss of dopaminergic neurons in the substantia nigra pars compacta (SNpc). At the onset of motor symptoms dopaminergic neuron loss is already 60-80%. These neurons normally project to the striatum (caudate nucleus and putamen) forming the nigrostriatal dopaminergic pathway (Betarbet et al., 2002). Insufficient action of dopamine (DA) on the striatum is believed to lead to decreased stimulation of the motor cortex and Parkinson's disease symptoms (Brown et al., 2006).

Neuroprotective strategies, such as physical activity, aim to slow dopaminergic neuron loss and lead to improved functioning of the remaining neurons (Mohammed et al., 1990) that will result in improved motor function. In Parkinson's disease patients exercise induces lasting improvements in motor scores, cognitive function, mood, and performance in daily activities (Palmer et al., 1986; Huang et al., 2003; Escudero et al., 2003; Reuter et al., 1999; Reuter et al., 1999; Plaschke et al., 2003). Furthermore, voluntary wheel running, forced limb use, and treadmill running in rodent Parkinson's disease models, unilateral 6-hydroxydopamine (6-OHDA) lesions in rats and bilateral 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine (MPTP) lesions in mice, improve behavioral functioning and provide biochemical sparing in the striatum.

Using a forced limb use paradigm, Tillerson et al demonstrated that early forced use after a unilateral 6-OHDA injection into the medial forebrain bundle improves limb asymmetry and provides biochemical sparing in the striatum. They unilaterally injected 6-OHDA and desipramine (a norepinephrine reuptake inhibitor) into the medial forebrain bundle to selectively kill dopaminergic neurons in the SNpc, cast the unimpaired limb on days 1-7, 3-9, or 7-13 after lesioning, and forced use of the impaired limb. They prevented limb use asymmetry only by casting on days 1-7 and they significantly improved DA and dopamine metabolite (DOPAC and HVA) levels with early forced use (days 1-7 and 3-9 of casting) (Tillerson et al., 2001).

Tillerson switched to a forced treadmill running paradigm, as unilateral forced use is an exercise modality not commonly practiced in humans. They believed that treadmill running, like forced use, would attenuate DA loss and behavior. Rats were given either 6-OHDA and mice were given MPTP and forced to run until day 12 or 30 for behavioral tests and sacrificed for biochemical analysis. Moderate forced treadmill running reversed 6-OHDA movement impairments in rats after one day with 450 m/day of treadmill running, reversed MPTP movement impairments in mice after three days with 50 m/day, and attenuated striatal DA loss and DA terminal marker loss (DAT, VMAT, tyrosine hydroxylase (TH)) in both models (Tillerson et al., 2003). Treadmill running, like forced use, attenuated both movement impairments and dopamine loss.

Numerous other studies demonstrate that voluntary and forced exercise can ameliorate the behavioral and biochemical consequences of 6-OHDA and MPTP lesions (Poulton and Muir, 2005; Howells et al., 2005; Caudle et al., 2007; Mabandla et al., 2004; Petzinger et al., 2007; Mandel et al., 2003) though the time, amount, method of exercise, and type of lesion do affect the behavioral and biochemical outcome. Early physical activity intervention, (Tillerson et al., 2001), before and after the lesion (Mabandla et al., 2004; Poulton and Muir, 2005; O'Dell et al., 2007), and in nonstressful situations (Howells et al., 2005) have proven to be the most beneficial – while limb disuse has been shown to exacerbate both behavioral and biochemical recovery (Caudle et al., 2007).

In all of the studies the number of SNpc cells did not change with exercise and physical activity (Poulton and Muir, 2005; Howells et al., 2005; Caudle et al., 2007; Mabandla et al., 2004; Petzinger et al., 2007; Mandel et al., 2003); rather, we believe behavioral and biochemical sparing comes from neuroplasticity and the sparing of SNpc terminals projecting to the striatum (Petzinger et al., 2007). It has been hypothesized that forced use ameliorates the behavioral and biochemical effects of 6-OHDA and MPTP through a cascade of events that involves glial derived neurotrophic factor, GDNF (Zigmond et al., 2009), a potent survival factor for DA neurons (Cohen et al., 2003). There is a significant increase of striatal GDNF 24 and 72 hours after using a non-impaired limb (Lin et al., 2008). Furthermore, ERK1/2 activation by GDNF in the striatum remains elevated up to 1 month after limb use (Lin et al., 2008; Lindgren et al., 2008).

Dopamine neurons from the SNpc project to the caudate nucleus and putamen of the striatum where they modulate glutamatergic input from the cortex. When SNpc dopaminergic neurons are lost, glutamatergic input to the striatum is no longer properly modulated resulting in overexcitation and the destruction of spine heads of the medium spiny neurons. Physical activity, which induces neuroplasticity and globally increases neurotrophic factors (BDNF, NGF, insulin growth factor-like 1 (IGF-1), FGF-2) (Neeper et al., 1996; Tong et al., 2001a; Molteni et al., 2002; Carro et al., 2001), could ameliorate the behavioral and biochemical effects of this loss, by increasing survival of these spine heads through BDNF, GDNF, and other neurotrophic factors, or by directly causing the protection of dopaminergic projections reaching the striatum. The ultimate goal is to elucidate the mechanism of how physical activity and exercise enhance neuroplasticity in the motor cortex and striatum to protect the brain against neurodegenerative diseases.

HYPOTHESIS AND SPECIFIC AIMS

Mild, moderate, and vigorous physical activity are associated with decreased risks of Alzheimer’s disease, Parkinson’s disease, and a decreased infarct from stroke. Physical activity increases neurogenesis in the hippocampus and upregulates neurotrophic factors throughout the brain, but it largely has been understudied in motor brain regions related to Parkinson’s disease. To understand the mechanisms of physical activity, exercise, and neuroprotection in motor regions of the brain we used three cohorts of monkeys: (1)

spontaneously physically active rhesus monkeys, (2) exercised rhesus monkeys, and (3) spontaneously physically active and exercised rhesus monkeys before and after receiving a MPTP lesion. We hypothesized that aerobic exercise would be protective against a MPTP lesion in Rhesus monkeys and be associated with a distinct gene expression signature in Parkinson’s disease related brain areas, which would allow us to elucidate the mechanisms of physical activity dependent neuroplasticity and neuroprotection.

Specific Aim 1: We believed that spontaneous physical activity and BMI would be associated with distinct gene expression signatures in the brain and sought to establish the gene expression signatures associated with each in the motor cortex and caudate. Using DNA microarrays we investigated gene expression correlates of spontaneous physical activity and body mass index in the motor cortex and caudate nucleus of 14 Rhesus monkeys. Microarray data were verified by qPCR. In addition, we examined the activation of the AKT and ERK1/2 signaling pathways using Western Blots. The activity-associated and BMI-associated gene expression signatures did not overlap – suggesting that different mechanisms are associated with each. These gene expression signatures are discussed in detail in Chapters II and III.

Using the same Rhesus monkey cohort, we cross correlated the level of spontaneous physical activity, blood c-reactive protein (CRP) levels, and the expression of BDNF, and ARC, an immediate early gene, in the brain with CRP. CRP induces vascular changes in the brain and we saw an inverse correlation of CRP with physical activity level and ARC/BDNF expression in the brain, while ARC/BDNF expression are positively correlated with the level of spontaneous activity. These correlations are discussed in Chapter IV.

Specific Aim 2: We believed that in response to exercise different brain areas would share a common mechanism and investigated the gene expression signature associated with exercise in the motor cortex, putamen, and hippocampus. Using DNA microarrays we investigated differentially gene expression associated with exercise in the motor cortex, putamen, and hippocampus of 12 Rhesus monkeys. Rhesus monkeys were pair matched based on initial physical activity levels and placed into two groups: sedentary and 60% maximal heart capacity runners. Runners ran for 5 days a week, 1 hour a day on a human sized treadmill for 3 months while sedentary animals sat on the treadmill. Shared gene expression across the brain regions was minimal suggesting different mechanisms of action in the motor cortex, putamen, and hippocampus. We did, however, find components of the electron transport chain increased in expression across brain regions. These gene expression signatures and proposed mechanisms are discussed in detail in Chapter V.

Specific Aim 3: We believed that exercise would provide behavioral and biochemical sparing in a monkey model of Parkinson's disease using MPTP, and sought to explore the mechanism of exercise and physical activity dependent neuroprotection. Physical activity, not exercise *per se*, protected against the MPTP lesion in a nonhuman primate model. We first demonstrated biochemical sparing and restored functional imaging parameters with physical activity level in nine monkeys treated with MPTP. We next established a gene expression signature associated with physical activity neuroprotection using DNA microarrays in the caudate and putamen. This gene expression signature and proposed mechanism of neuroplasticity and neuroprotection are discussed in detail in Chapter VI.

CHAPTER II

Physical Activity-Associated Gene Expression Signature in Nonhuman Primate Motor Cortex and Caudate Nucleus

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Physical activity plays a critical role in energy balance and weight loss. Looking in our cohort of adult rhesus monkeys (*M. mulatta)* with a wide range of physical activity levels, we previously established that physical activity influences both weight gain and weight loss. The most active monkeys gained the least amount of weight as a part of a weight gain study (Sullivan et al., 2006), and as part of a weight loss study, the animals who did not lose weight compensated for their reduced food intake with a decrease in their activity level (Sullivan and Cameron, 2010). These studies suggest that physical activity levels must be increased to lose significant weight in adulthood.

In addition to its role in the regulation of body weight, physical activity also is associated with a decreased lifetime risk of neurological disorders, such as Parkinson's disease, Alzheimer's disease, and amyotrophic lateral sclerosis (ALS) (Yaffe et al., 2001; Thacker and Ascherio, 2008; Lee and Paffenbarger, 1998; Tsermentseli et al., 2011). In the brain, physical activity most dramatically affects the hippocampus (Neeper et al.,

1996) with increases in neurogenesis (Brown et al., 2003) and growth factors, nerve growth factor (NGF) and brain derived neurotrophic factor (BDNF) (Neeper et al., 1996). In contrast, little attention has been paid to other brain regions that undoubtedly play a role in the interaction between physical activity and neurological disease. The motor cortex is one such area. Motor neurons in this region are devastated in ALS (Tsermentseli et al., 2011). Moreover, the motor cortex is affected with synuclein and tau pathology at the end stages of Parkinson's and Alzheimer's disease (Braak et al., 2006), and physical activity is known to slow the progress of both disorders.

Based on these studies, we hypothesized that spontaneous physical activity is associated with a unique gene expression signature in the motor cortex that may be important in body weight regulation as well as protection against neurodegenerative disease. To test this hypothesis, we performed whole genome expression profiling of the motor cortex of 14 female rhesus monkeys with a wide range of stable physical activity levels using both Affymetrix Rhesus Macaque Genome (RhG) and Human Genome (HG) microarrays (**Figure 2**). Physical activity levels ranged from 46,376 counts per day to 897,948 counts per day with a skew of 1.93, indicating that our activity measurements were skewed right with more animals having low activity values. The rhesus and human genomes share 93% sequence identity (Gibbs et al., 2007) and we have successfully used human microarrays to query rhesus monkey gene expression changes in the past (Sabatini et al., 2007). Whereas the Affymetrix RhG microarrays provided us with the most specific hybridization information for rhesus monkeys, the Affymetrix HG microarrays contained more extensive and higher quality annotations.

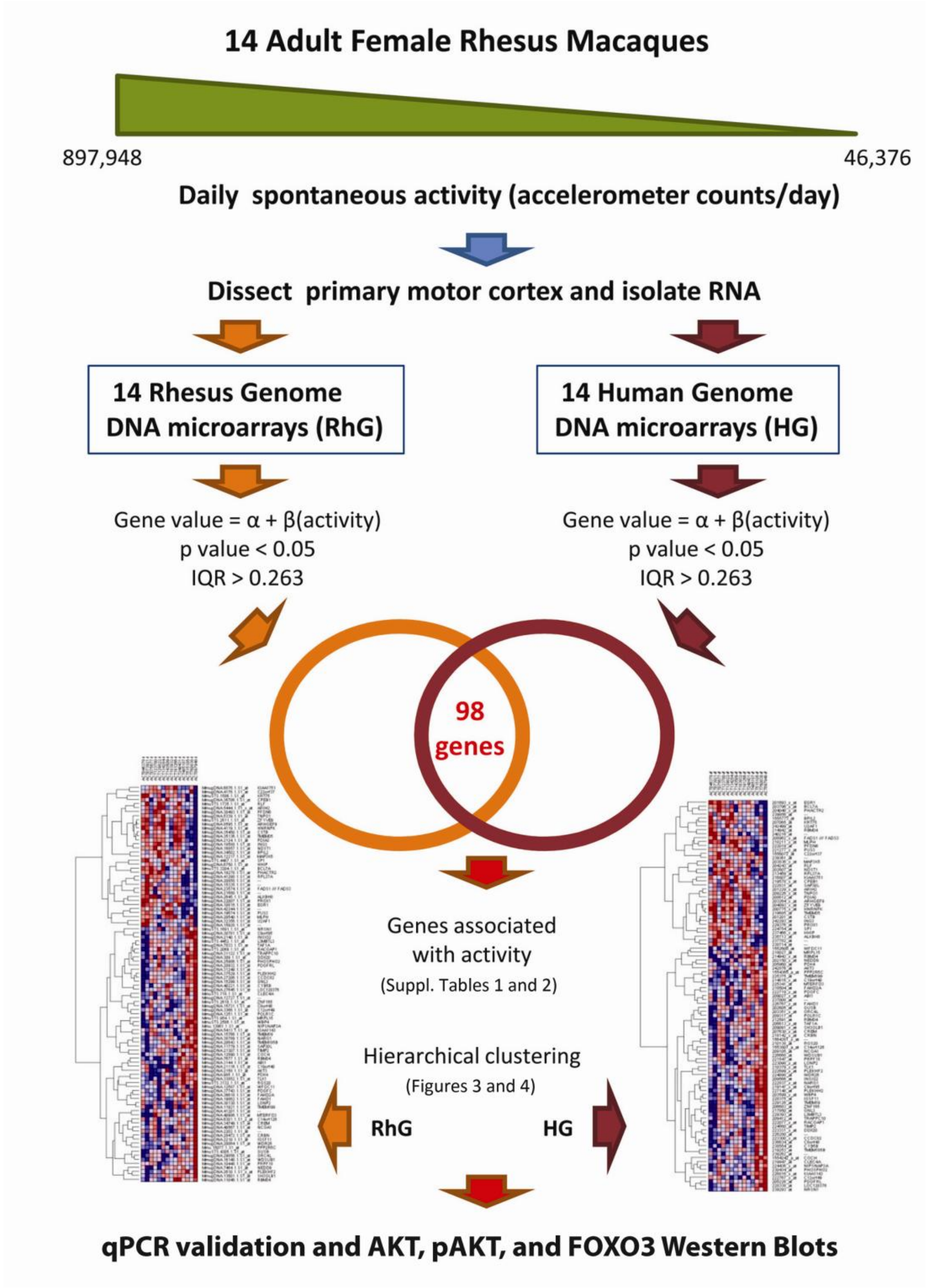


Figure 2. Spontaneous Activity Gene Expression Analysis Experimental Design. Motor cortex and caudate nucleus tissue were harvested respectively from 14 female macaques with vastly different spontaneous activity levels. Their transcriptome was profiled using both Affymetrix Rhesus Macaque Genome microarrays (RhG) and Affymetrix Human Genome U133 2.0 Plus microarrays (HG). We used a linear model to define gene expression associated with physical activity (gene value = α + β (activity)) for both microarrays separately. RhG and HG probes were cross matched based on sequence similarity and a transcript was considered associated with activity if both microarray models (a) were significant with $p < 0.05$, and (b) had an interquartile range (IQR) > 0.263 corresponding to a 20% gene expression change. Significant gene expression changes are reported in Supplementary Tables 1 and 2, and clustered in Figures 3 and 4.

Microarray data were log2 transformed, RMA-normalized (Arion et al., 2007a; Arion et al., 2007b), and linearly modeled with physical activity level. We focused on convergent findings between the RhG and HG microarrays, which enabled us to identify a strong and distinct physical activity associated gene expression signature of ninety-eight significantly altered transcripts (**Supplementary Table 1),** and twenty-eight significantly altered transcripts in the caudate nucleus (**Supplementary Table 2)**. Ninety-six of the ninety-eight significantly altered transcripts changed in the same direction on both microarrays, suggesting a high degree of concordance between the two data sets and a low false discovery rate. Furthermore, our Pearson Hierarchal Clustering (Subramanian et al., 2005) revealed a progression of gene expression levels from monkeys with low activity to monkeys with high activity (**Figures 3 and 4**).

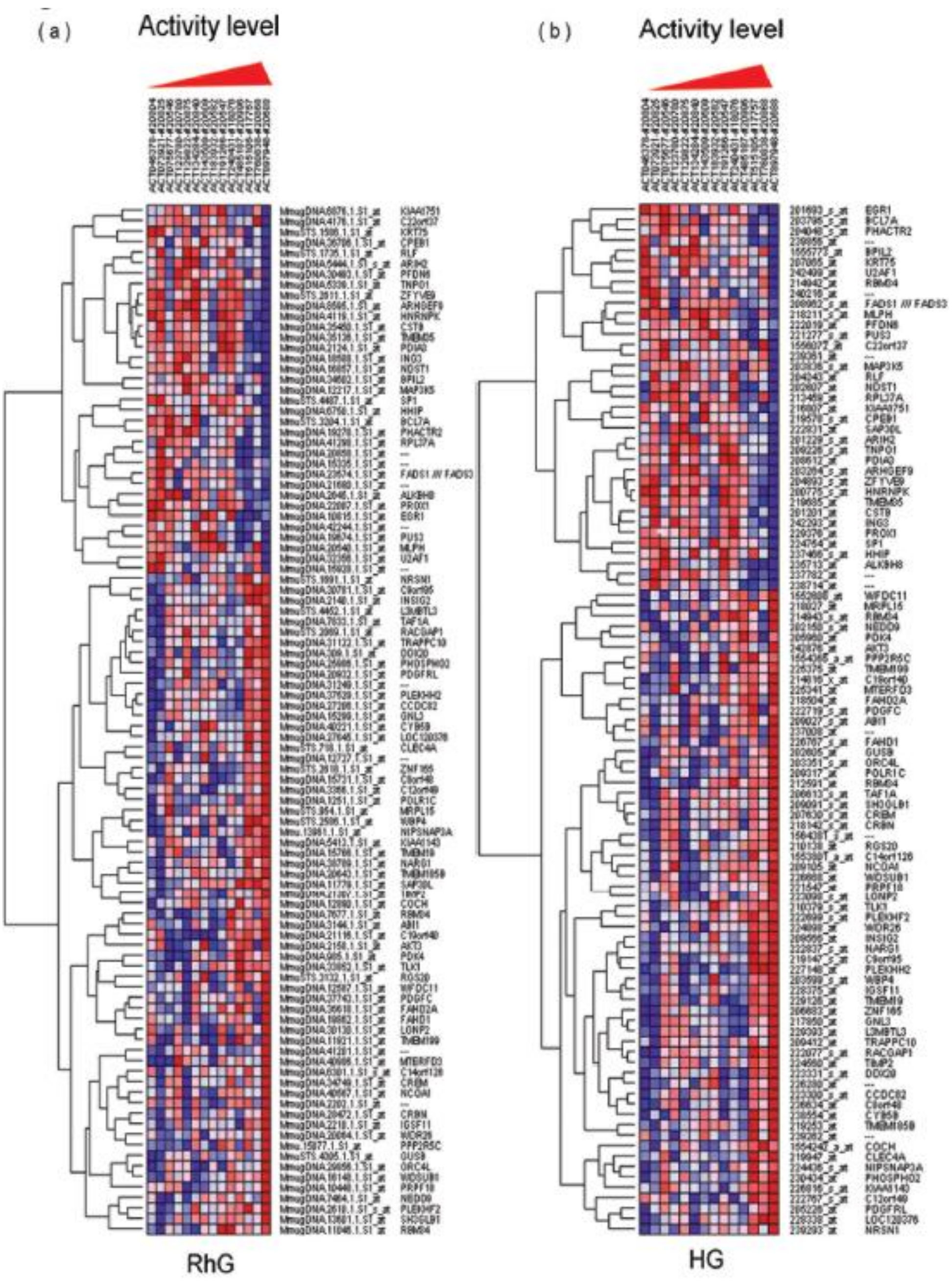


Figure 3. Hierarchal Clustering of Physical Activity Associated Gene Expression in the Motor Cortex. One-way hierarchical clustering was performed on log2-transformed expression levels of 98 differentially expressed genes using GenePattern. Monkeys are arranged by activity level in vertical columns. Monkey identities correspond to level of activity (eg. Monkey ACT046378 had an average daily activity count of 46,378). Genes, denoted by Affymetrix Rhesus and Human Probes and NCBI gene symbols, were clustered horizontally. Each colored square represents a normalized gene expression value with color intensity proportional to magnitude of change (blue indicates lower expression and red indicated increased mRNA levels). (A) Clustering of Rhesus Genome Microarray Data. (B) Clustering of Human Genome Microarray Data. Note the progression of gene expression levels from monkeys with low activity to monkeys with high activity.

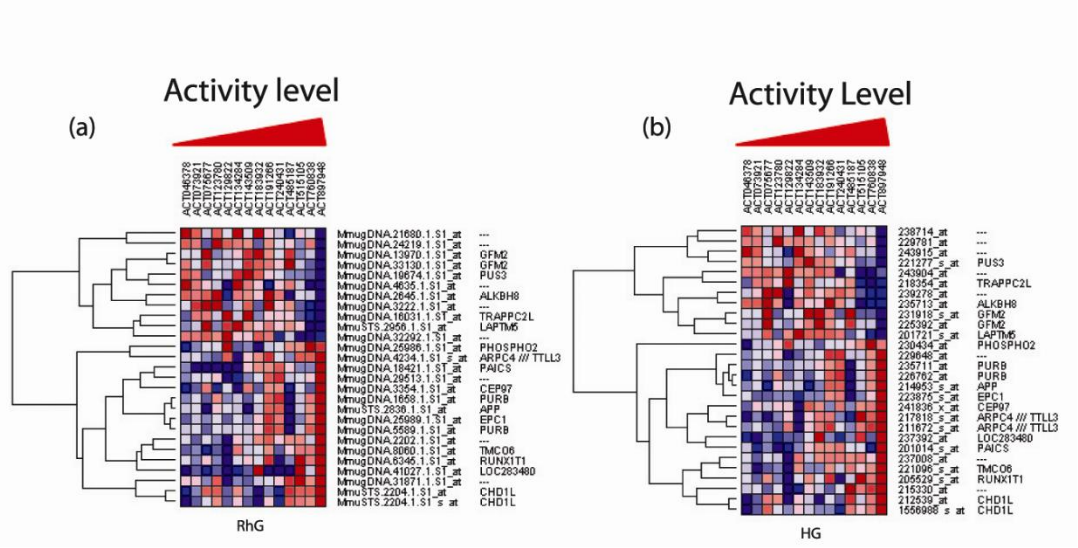
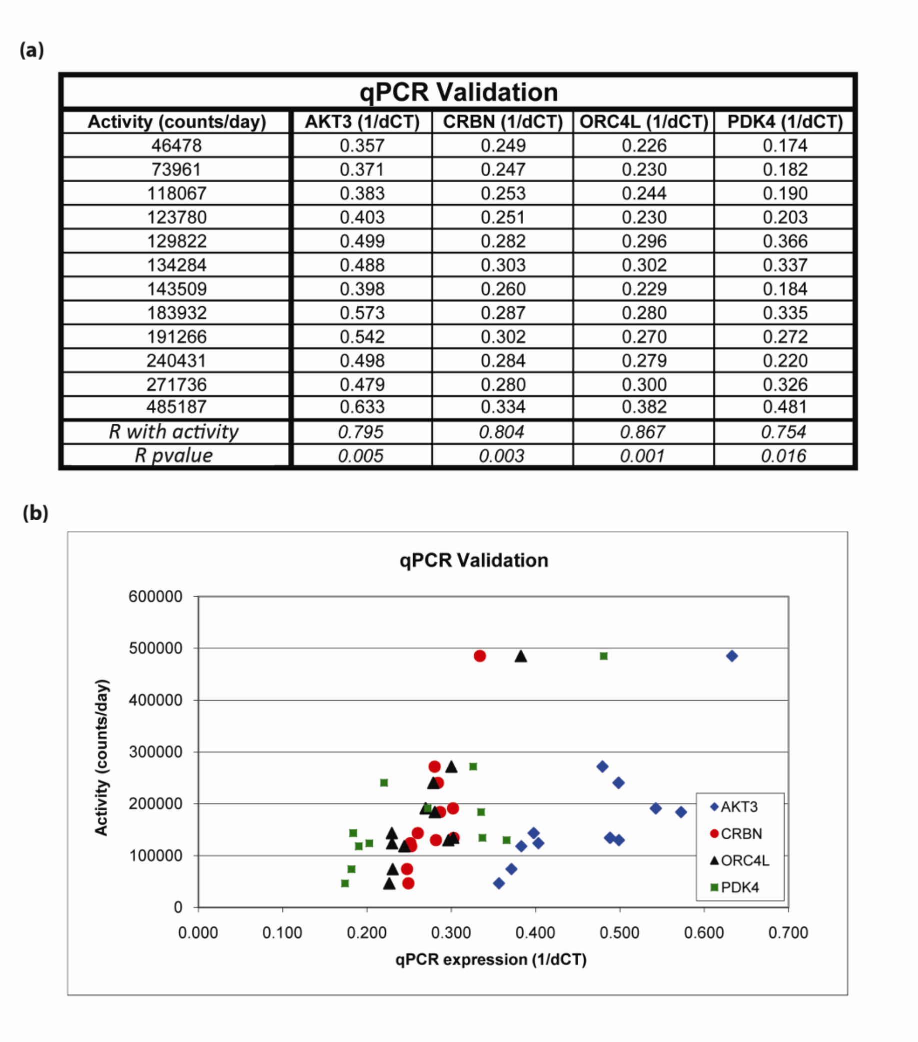


Figure 4. Hierarchal Clustering of Physical Activity Associated Gene Expression in the Caudate Nucleus. One-way hierarchical clustering was performed on log2-transformed expression levels of 28 differentially expressed genes using GenePattern. Monkeys are arranged by activity level in vertical columns. Monkey identities correspond to level of activity (eg. Monkey ACT046378 had an average daily activity count of 46,378). Genes, denoted by Affymetrix Rhesus and Human Probes and NCBI gene symbols, were clustered horizontally. Each colored square represents a normalized gene expression value with color intensity proportional to magnitude of change (blue indicates lower expression and red indicated increased mRNA levels). (a) Clustering of Rhesus Genome Microarray Data. (b) Clustering of Human Genome Microarray Data. Note the progression of gene expression levels from monkeys with low activity to monkeys with high activity.

Several genes with altered transcript levels were part of signaling cascades and nutrient sensing pathways. Namely, AKT3, which showed more than a 2-fold change in expression over the quartile in our dataset, is at the apex of both growth factor signaling and nutrient sensing (Bhaskar and Hay, 2007; Sarbassov et al., 2005). AKT pathway activation is associated with physical activity in the hippocampus (Brunet et al., 1999; Chen and Russo-Neustadt, 2005). When activated, it phosphorylates downstream effectors, such as glycogen synthase kinase (GSK3) (which when inhibited phosphorylation promotes glycogen synthesis) (Wilson et al., 2007), tuberous sclerosis protein 2 (TSC2) (which activates mammalian target of rapamycin complex 1, mTORC1, and is involved in ribosome biogenesis and protein synthesis) (Bhaskar and Hay, 2007), and forkhead box O3 (FOXO3) (which when phosphorylated is no longer recruited to the nucleus where it would bind as a transcription factor to activate transcription of apoptotic related genes (Brunet et al., 1999).



(a)

qPCR Validation				
Activity (counts/day)	AKT3 (1/dCT)	CRBN (1/dCT)	ORC4L (1/dCT)	PDK4 (1/dCT)
46478	0.357	0.249	0.226	0.174
73961	0.371	0.247	0.230	0.182
118067	0.383	0.253	0.244	0.190
123780	0.403	0.251	0.230	0.203
129822	0.499	0.282	0.296	0.366
134284	0.488	0.303	0.302	0.337
143509	0.398	0.260	0.229	0.184
183932	0.573	0.287	0.280	0.335
191266	0.542	0.302	0.270	0.272
240431	0.498	0.284	0.279	0.220
271736	0.479	0.280	0.300	0.326
485187	0.633	0.334	0.382	0.481
R with activity	*0.795*	*0.804*	*0.867*	*0.754*
R pvalue	*0.005*	*0.003*	*0.001*	*0.016*

(b)

Figure 5. Validation of activity associated microarray-reported changes by qPCR. (a) Monkey activity levels were measured in counts/day, while AKT3, CRBN, ORC4L, and PDK4 relative expression levels are reported in threshold cycle difference relative to myelin basic protein (ΔCT). AKT3, CRBN, ORC4L, and PDK4 expressions were significantly positively correlated (R) with activity. (b) Scatter plot showing qPCR expression (1/dCT) versus activity levels (counts/day) for AKT3 (blue diamond), CRBN (red circle), ORC4L (black triangle), and PDK4 (green square).

To validate the correlation of AKT3 gene expression level with physical activity we performed qPCR on 12 of the monkeys studied by microarrays. In addition, we also assessed the expression-activity correlation (R) for two other nutrient genes, cereblon (CRBN) and pyruvate dehydrogenase 4 (PDK4), and origin recognition complex subunit 4-like (ORC4L) (**Figure 5**). CRBN and PDK4 converge on AMP activated protein kinase (AMPK), the master energy sensor. During exercise AMPK activity is known to increase and promote catabolic processes and inhibit anabolic processes thereby increasing cellular energy. CRBN decreases phosphorylation of the α1 subunit of AMPK to inhibit its activity (Lee et al., 2011), while PDK4 is induced by AMPK activity (Kwon et al., 2010). The qPCR validation revealed that AKT3, CRBN, PDK4, and ORC4L showed a positive correlation (R) with increasing physical activity.

Furthermore, we examined AKT protein expression, its phosphorylation state at serine 473, which is required for its full activation (Bhaskar and Hay, 2007), and the protein expression of its downstream effector, FOXO3. While total AKT (tAKT) levels were not changed, we found a significant and positive correlation of active pAKT ($R = 0.624$, $p = 0.017$ for pAKT/tAKT, and $R = 0.542$, $p = 0.045$ for pAKT/actin) with physical activity level (**Figure 6a)**. We also found a significant and positive correlation of FOXO3 protein level with spontaneous activity levels ($R = 0.649$, $p = 0.012$) (**Figure 6b**). Given the striking changes in mRNA levels of AKT3, it seems likely that the immunoblotting data were also assessing changes in this protein. However, we used pan-AKT antibodies that could not distinguish between the different AKT isoforms *per se*. Nonetheless, our data suggest AKT phosphorylation might be a critical molecular effector of physical activity in the motor cortex.

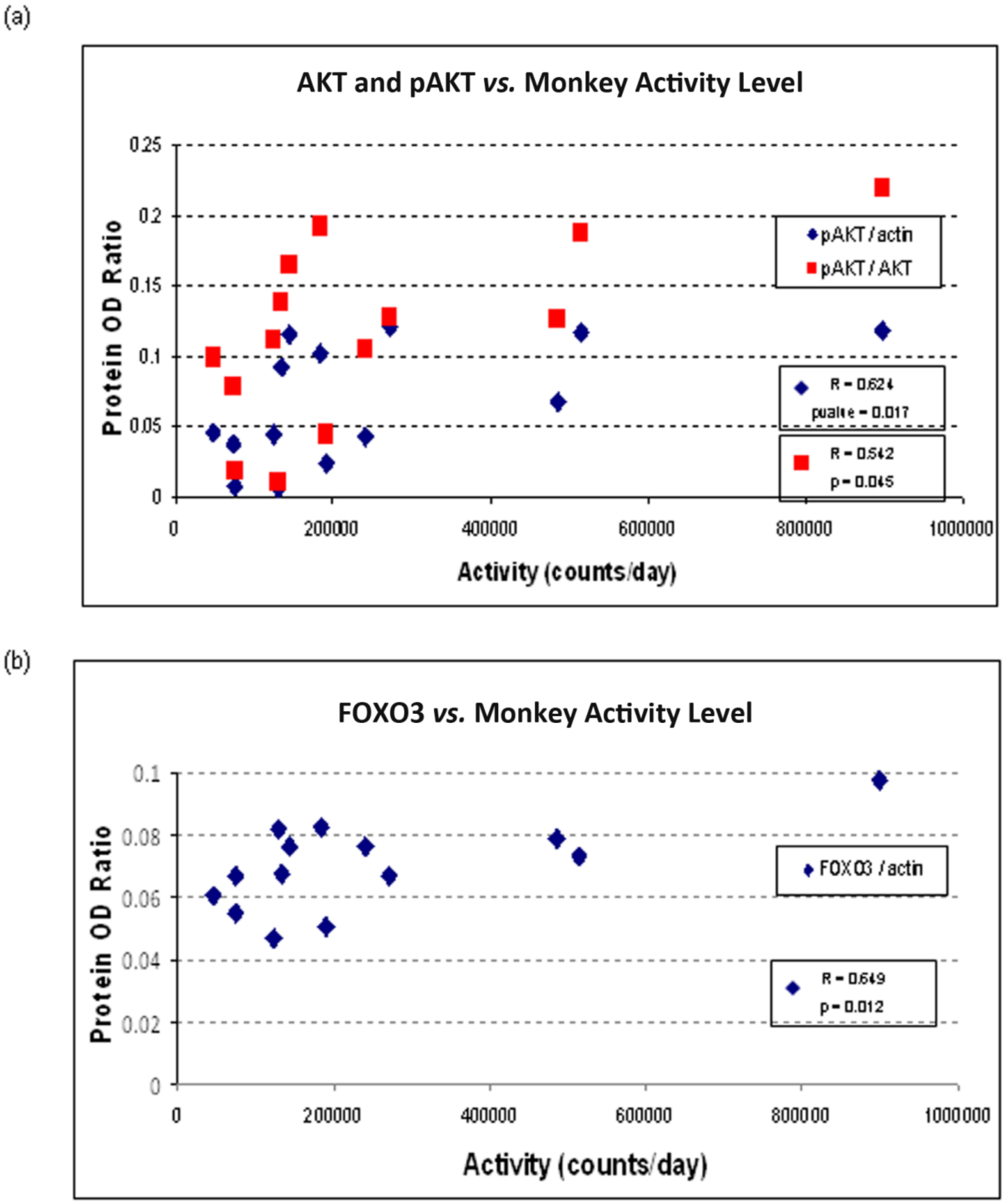


Figure 6. PhosphoAKT and FOXO3 Protein Levels are positively correlated with activity levels. (a) Scatter plot showing activity level (counts/day) versus protein ratios for pAKT/actin (blue diamond) and for pAKT/tAKT (red square) with an insert of the original Western blot data for four monkeys. We observed a significant correlation between activity levels and pAKT expression (p = 0.017 vs. ACT and p = 0.045 vs. tAKT). (b) Scatter plot denotes activity level (counts/day) versus protein ratios for FOXO3/actin (blue diamond) with an insert of the original Western blot data for four monkeys. The analysis revealed a significant correlation between activity level in the monkeys and FOXO3 expression of (p = 0.012). Note that physical activity level is correlated with both pAKT and FOXO3 protein levels.

We ran gene set enrichment analysis (GSEA) (Subramanian et al., 2005) on the human microarray data (HG) for both the motor cortex and the caudate nucleus using the curated C2 pathway gene sets from the Molecular Signatures Database (MSigDB) (Liberzon et al., 2011). We did not find any significantly altered pathways in the motor cortex, but we did find two altered pathways in the caudate nucleus (**Table 1).** These pathways included mTORC1 mediated signaling and the generation of second messenger molecule pathways – both of which are involved in nutrient sensing.

TABLE 1. Caudate Nucleus Gene Set Enrichment Analysis (GSEA) for Physical Activity.

REACTOME Pathway	NOM p-val	FDR q-val	Negatively Enriched Genes
mTORC1 Mediated Signaling	0.004	0.189	EIF4E, RHEB, EEF2K, EIF4EBP1, EIF4B, RPS6KB1
Generation of Second Messenger Molecules	0.000	0.151	HLA-DQB1, HLA-DQA, PAK1, WAS, CD4, ITK, PLCG1, LCK, HLA-DMA, CD3G, HLA-DMB, HLA-DRA, VASP, GRAP2, HLA-DOB, HLA-DRB1, LCP2

Table 1. Caudate Nucleus Gene Set Enrichment Analysis (GSEA) for Physical Activity. Two gene sets from the curated gene lists C2 module of GSEA (Liberzon et al., 2011) were found significantly altered in the caudate nucleus by GSEA. Gene sets are identified by their pathway name, nominal p-value (NOM p-val), and false discovery rate q-value (FDR q-val). Gene sets are enriched with increasing physical activity levels.

In summary, our study reveals that (1) spontaneous physical activity in Rhesus monkeys is associated with a strong and reproducible gene expression signature in the motor cortex, (2) the observed gene expression signature is related to activation of transcriptional machinery, and (3) spontaneous activity is associated with activation of the AKT-FOXO3 signaling pathway and several nutrient sensing transcripts. Given previous findings in the hippocampus, it is noteworthy that we did not observe changes in growth factor or growth factor receptors in the motor cortex, suggesting that spontaneous activity levels and planned exercise might have distinct gene expression profiles across the different brain regions. Whereas planned exercise might be growth factor dependent (and activate the AKT pathway), it is conceivable that growth factor systems still could be activated by non-transcriptional cellular machinery or that spontaneous activity induces AKT/FOXO3 through a different, non-growth factor dependent pathway, but this deserves further investigation. However, our studies did not examine the causality of these changes, but the strong correlational relationship suggests that this is an important avenue for further investigations.

Studies in knockout mice suggest that the three isoforms of AKT play vastly differing roles: mice without AKT1 have decreased body weight, whereas mice without AKT2 have increased fasting plasma glucose levels and diabetes symptoms while mice without AKT3 have decreased brain weight (Dummler et al., 2006; Choi and Sung, 2000). These data also suggest that that AKT3 might be critical for neuronal health, and raise the possibility that activation of the AKT3 signaling pathway may play a crucial role in activity-induced weight loss and the delayed onset of neurological disorders associated with physical activity. Indeed, we have previously found that both physical activity and the neurotrophic factor GDNF increase the phosphorylation state of AKT in the rodent striatum (Smith AD, Castro, SL, Lindgren, N, and Zigmond MJ, unpublished observations). Thus, future studies are warranted to address whether varying levels of spontaneous motor activity are associated with differences in vulnerability to disease models and whether protection against such models can be attenuated by inhibition of AKT signaling.

METHODS

Subjects

The Animal Care and Use Committee of the Oregon National Primate Research Center reviewed and approved all experiments. Fourteen adult female ovariectomized Rhesus monkeys (*Macaca mulatta*) with various levels of spontaneous activity were used in this study with care methods previously published (Sullivan et al., 2006; Sullivan and Cameron, 2010; Mitchell et al., 2010). Their activity levels were measured in counts/day with an accelerometer throughout the study and ranged from 46,378 to 897,948 activity counts per day. These monkeys also participated in a previous weight loss study (Sullivan et al., 2006). Monkeys were deeply anesthetized with ketamine/pentobarbital, quickly decapitated, and the entire brain was removed from the skull. The brain was then hemisected by a midline sagittal cut. The right hemisphere was cut into 5-mm thick coronal blocks, flash-frozen in isopentane over dry ice, and stored at -80 °C until use (Volk et al., 2000).

Sample preparation, hybridization, and DNA microarray processing

Motor cortex was dissected from frozen coronal blocks using anatomical landmarks, homogenized and total RNA isolated using TRIzol® reagent (Invitrogen, Carlsbad, CA) with RNA quality assessed via analysis on an Agilent 2100 Bioanalyzer. Only samples with an RIN > 7.0 were considered for further analysis. The samples were prepared with 2 μg of total RNA using the Enzo BioArray™ Single-Round RNA Amplification and Biotin Labeling System. Fifteen micrograms of the purified and fragmented aRNA were hybridized to 14 GeneChip® Rhesus Macaque Genome (RhG)

Arrays and 14 GeneChip® Human Genome (HG) U133 Plus 2.0 Arrays. Image segmentation analysis and generation of DAT files was performed using Microarray Suite 5.0 (MAS5). Segmented images were normalized and log2 transformed using robust multi-array analysis (RMA) separately for Rhesus and Human arrays (Sabatini et al., 2007). RMA normalized log2 expression levels were utilized for all of our subsequent analyses.

Microarray data analysis

Microarrays were assessed for activity gene expression changes for each probe/gene (**Figure 2**). We tested for skew of the data using the following equation $(n / ((n-1)(n-2))) * \sum ((x_i - \bar{x}) / s)^3$**.** Data from RhG and HG arrays were fit using the model: log transformed gene expression value = $\alpha + \beta$(activity). RhG and HG probe sets were matched on the basis of sequence identity using the Affymetrix HG-U133 Plus 2.0 to Rhesus Best Match Spreadsheet. Gene expression was considered correlated with spontaneous activity if (a) $p < .05$ for testing H_0: $\beta = 0$, using data for RhG and HG microarrays; and if (b) the interquartile range, IQR > 0.263 (measuring the difference between the third and first quartiles was less than 0.263) on the RhG and HG microarrays, which represented a 20% change in gene expression values. One-way hierarchical clustering of the replicating data was performed using GenePattern software (Subramanian 2005) using log2 transformed RMA normalized expression levels utilizing row (gene) centering and Pearson correlation.

Quantitative real-time PCR Validation

We used High Capacity cDNA Archive Kit® (Applied Biosystems, Foster City, CA) to synthesize cDNA from 500 ng of the same total RNA used for microarray analysis. Priming was performed with random hexamers. For each sample, amplified product differences were measured with three independent replicates using SYBR Green chemistry-based detection (Arion et al., 2007a). Myelin basic protein was used as the endogenous reference gene. Primer sequences for myelin basic protein (MBP) were 5' GGG TCT TCC TGG AGA TTT GG 3' and 5' GTG GTT TGG AAA CGA GGT TG 3', for AKT3 were 5' GCA AGG ATT GTA CAC GCT GA 3' and 5' GCA GCA TCT CTT CTC CCA AA 3', for cereblon (CRBN) were 5' CAA GCA TGA ACG GCA GTC TA 3' and 5' CTT CAT GTC CCA TCA ATG ACA 3', for origin recognition complex subunit 4-like (ORC4L) were 5' CAT GCT TTG AAA GAA CTC ATG CT 3' and 5' TGA TCT GCA GCA GTC CAT TT 3', and for pyruvate dehydrogenase kinase 4 (PDK4) were 5' ATT GTC AGC TGC CTG GTC TT 3' and 5' GCC GTT ACT TTG GCA ATT CT 3'. The efficiency for each primer set was assessed prior to qPCR measurements, and a primer set was considered valid if its efficiency was > 90%. The qPCR reactions were carried out on an ABI Prism 7300 thermal cycler (Applied Biosystems Inc.), quantified using ABI Prism 7300 SDS software (with the auto baseline and auto threshold detection options selected) and statistically analyzed using Pearson correlations.

Western Blots

Infrared imaging of immunoblots was used for assessing phosphorylation and total protein state of AKT (Li-Cor Biosciences, Lincoln, NE), and the total protein state of FOXO3. Samples were sonicated in a Triton-based lysis buffer (Cell Signaling, Danvers, MA) and subjected to standard SDS-page immunoblotting procedures. Blots were then blocked in 5% bovine serum albumin in Tris-buffered saline (TBS) with 0.1% Tween for 1 hr prior to incubation overnight at 4^oC in primary antibody made in the same blocking solution. We used mouse anti-total AKT (Cell Signaling), rabbit anti-phospho AKT (Ser473, Cell Signaling), mouse anti-FOXO3 (gift of Anne Brunet's laboratory), and mouse anti-β-actin (Sigma-Aldrich) to control for differences in protein loading. After overnight incubation with primary antibody, blots were washed in TBS-tween and incubated with goat secondary antibodies raised against the appropriate IgG fluorescing in the infrared range (700 and 800 nm, Li-Cor Biosciences). After three washes in TBS-tween, immunostained protein bands on the blots were visualized on an Odyssey Infrared Imager and quantified with Odyssey software (Li-Cor Biosciences).

CHAPTER III

A Distinct BMI Gene Expression Signature in the Motor Cortex and Caudate Nucleus

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Submitted for publication (Mitchell et al., 2011c)

INTRODUCTION

Since 1980 the number of people worldwide considered obese has doubled with over 1.5 billion people now considered overweight (body mass index, BMI, 25 or higher) and 500 million people considered obese (BMI 30 or higher) (WHO, 2006). The negative effects of obesity on health are far reaching. As weight increases to levels defined as overweight and obese, the risks for the following conditions also increases: coronary heart disease, type 2 diabetes, cancers, hypertension, dyslipidemia, stroke, liver and gallbladder disease, sleep apnea, osteoarthritis, and gynecological problems (NIH, 1998; Baba et al., 2002; Yatsuya et al., 2010; Falkstedt et al., 2007). According to the American Medical Association the best ways to decrease the risk of obesity are to eat a diet low in fat and to increase physical activity levels (Kushner, 2003; Gaab et al., 2005)**.** Indeed, modern sedentary life is associated with increased risks for obesity, as well as cardiovascular disease, type II diabetes (Marwick et al., 2009), and depression (Lawlor and Hopker, 2001; Vance et al., 2005).

These co-morbidities strongly suggest that obesity may be associated with alterations in the molecular content of the brain. Decreased brain volume has been seen in the frontal lobe, the temporal lobe, the anterior cingulate, the hippocampus, and the basal ganglia with high BMI (Ho et al., 2010). Using correlations of BMI with brain volumes the same group showed that overweight and obese individual's brains age prematurely (Raji et al., 2010). Other studies also link higher BMI with smaller regional brain volumes (Gustafson et al., 2004; Pannacciulli et al., 2007; Raji et al., 2010; Taki et al., 2008).

Given that high BMI is associated with brain alterations and that physical activity can decrease obesity, we hypothesized that BMI was associated with a unique gene expression signature in motor regions of the brain. Using BMI as a continuous variable we investigated transcriptome changes in motor brains regions (motor cortex and caudate nucleus) of 14 Rhesus monkeys with DNA microarrays. We found a distinct BMI associated gene expression signature in both the motor cortex and the caudate nucleus, and decreased protein phosphorylation of a survival kinase, pERK1/2, in the motor cortex. Our studies indicate that obesity is associated with molecular changes in motor regions of the brain that these changes include alterations in metabolic and apoptotic related genes and that increases in BMI are associated with decreases in the phosphorylation of a survival kinase.

METHODS

Subjects

Fourteen adult female ovariectomized rhesus monkeys (*Macaca mulatta*) were allowed to eat a high fat diet freely for three years (Sullivan et al., 2006; Sullivan and Cameron, 2010) with care methods previously published (Sullivan et al., 2006; Sullivan and Cameron, 2010; Mitchell et al., 2010). Their activity and percent body fat were measured throughout the diet and were found to be extremely stable. As part of a different study they were then placed on a two month calorie reduction diet. Food composition was the same, but their calorie intake was reduced by 30% the first month and 60% the second month from their normal intake. Their BMI was measured in kilograms / crown of rump length squared (kg/CRL^2) at the end of the study. Monkeys were deeply anesthetized with ketamine/pentobarbital, quickly decapitated, and the entire brain was removed from the skull. The brain was then hemisected by a midline sagittal cut. The right hemisphere was cut into 5-mm thick coronal blocks, flash-frozen in isopentane over dry ice, and stored at -80 °C until use (Volk et al., 2000).

Sample preparation and hybridization

Motor cortex and caudate nucleus brain tissue was homogenized and total RNA isolated using TRIzol® reagent (Invitrogen, Carlsbad, CA) with RNA quality assessed via analysis on an Agilent 2100 Bioanalyzer. Only samples with an RIN > 7.0 were considered for further analysis. The samples were prepared using the Enzo BioArray™ Single-Round RNA Amplification and Biotin Labeling System. The samples were primed with a standard T7-oligo(dT) primer and cDNA synthesis was performed using 2 μg of total RNA according to the Affymetrix® manufacturer's protocol. Amplified antisense RNA (aRNA) was produced using in vitro transcription directed by T7 polymerase. Fifteen micrograms of the purified and fragmented aRNA were hybridized to GeneChip® Rhesus Macaque Genome (RhG) Arrays and GeneChip® Human Genome (HG) U133 Plus 2.0 Arrays. Image segmentation analysis and generation of DAT files was performed using Microarray Suite 5.0 (MAS5).

Microarray data analysis

Fourteen RhG arrays for the motor cortex and 14 RhG arrays for the caudate nucleus were scanned and analyzed. Scaling factors ranged from 1.58-3.11 with backgrounds from 29.8-85 and percent present calls from 45-52%. Fourteen HG arrays for the motor cortex and 14 HG arrays for the caudate nucleus were scanned and analyzed. Scaling factors ranged from 6.26-15.28, noise was between 1.2-1.8, and percent present calls were from 31.3% to 35.0%. Segmented images were normalized and log2 transformed using robust multi-array analysis (RMA) separately for Rhesus and Human arrays (Wu and Irizarry, 2004) with RMA normalized expression levels utilized for all of our subsequent analyses.

We analyzed the microarrays for transcripts associated with BMI. We fit data from HG and RhG arrays using the model: log transformed gene expression value = $\alpha + \beta(\text{BMI})$ (Zabawski and Cockerell, 1998). RhG and HG probe sets were matched on the basis of sequence similarity using the Affymetrix HG-U133 Plus 2.0 to Rhesus Best Match Spreadsheet. Genes were considered correlated BMI if (a) $p < 0.05$, where H_0: $\beta =$

0 for RhG arrays; (b) $p < 0.05$, where H_0: $\beta = 0$ for HG arrays; (c) if the interquartile range, IQR > 0.263 on the RhG arrays, measuring the difference between the third and first quartiles was less than 0.263 (representing a 20% change in gene expression values); and (d) if the interquartile range, IQR > 0.263 on the HG arrays, measuring the difference between the third and first quartiles was less than 0.263 (representing a 20% change in gene expression values). The strength of our model was tested for false discovery using a binomial probability test for the direction of change, where the H_0: $p = 0.50$. We tested our model using a binomial probability test with a null hypothesis that $p = 0.50$, which was rejected. Hierarchical clustering of the replicating data was performed using GenePattern software (Subramanian et al., 2005). Clustering was performed on log2 transformed GC-RMA normalized expression levels using row (gene) centering and Pearson correlation.

Gene Ontology (GO) and Gene Set Enrichment Analysis (GSEA)

We assessed our data for the enrichment of functional gene pathways using Gene Ontology (GO) terms (Ashburner et al., 2000) and Gene Set Enrichment Analysis (GSEA) (Subramanian et al., 2007). First, we analyzed the GO terms for all of our transcripts significantly associated with BMI in the motor cortex and caudate nucleus. Second, we performed GSEA (Subramanian et al., 2007) using all of the gene sets in the Molecular Signatures Database (MSigDBv.3.0) for the human (HG) arrays. We report enriched gene sets with a nominal pvalue < 0.01 and a false discovery rate (FDR) < 0.25.

Western Blots

Infrared imaging of immunoblots was used for assessing phosphorylation and total protein state of ERK1/2 and AKT (Li-Cor Biosciences, Lincoln, NE). Samples were sonicated in a Triton-based lysis buffer (Cell Signaling, Danvers, MA) and subjected to standard SDS-page immunoblotting procedures. Blots were then blocked in 5% bovine serum albumin in Tris-buffered saline (TBS) for 1 hr prior to incubation overnight at 4^{o}C in primary antibody made in the same blocking solution with 0.1% Tween. Antibodies used were: rabbit anti-phospho-ERK1/2 (Cell Signaling, Cat. no. 9101), mouse anti-total ERK1/2 (Millipore, Cat. no. 05-1152), rabbit anti-phospho-AKT (Cell Signaling, Cat. no. 9271), mouse anti-total AKT (Cell Signaling, Cat. no. 2920) . Mouse α-tubulin (Sigma-Aldrich, Cat. no. T5168) was used concurrently to control for differences in protein loading. After overnight incubation with primary antibody, blots were washed in TBS-tween and incubated with goat secondary antibodies raised against the appropriate IgG fluorescing in the infrared range (700 and 800 nm, Li-Cor Biosciences). After further washing, immunostained protein bands on the blots were visualized on an Odyssey Infrared Imager and quantified with Odyssey software (Li-Cor Biosciences).

RESULTS

Microarray Data Analysis Reveals a BMI-associated Gene Expression Pattern

We hypothesized that BMI is associated with a unique gene expression signature in the motor cortex and caudate nucleus that may be of importance given observed decreases in brain volume associated with obesity. To test this hypothesis, we performed whole genome expression profiling of the motor cortex of 14 female rhesus monkeys with a wide range of BMIs using both Affymetrix Rhesus Macaque Genome (RhG) and Human Genome (HG) microarrays (**Figure 7**). The rhesus and human genomes share 93% sequence identity (Gibbs et al., 2007) and human microarrays successfully have been used to query rhesus monkey gene expression changes in the past (Sabatini et al., 2007). Whereas the Affymetrix RhG microarrays provided us with the most specific hybridization information for rhesus monkeys, the Affymetrix HG microarrays contained more extensive and higher quality annotations.

Microarray data were log2 transformed, RMA-normalized (Arion et al., 2007a; Arion et al., 2007b) and linearly modeled with BMI. We focused on convergent findings between the RhG and HG microarrays, which enabled us to identify a strong and distinct BMI-associated gene expression signature in the motor cortex and caudate nucleus. Two types of data-mining approaches were employed. First, we identified the transcripts that were associated with BMI, followed by a molecular pathway analysis that revealed the most affected BMI-associated groups of interdependent genes.

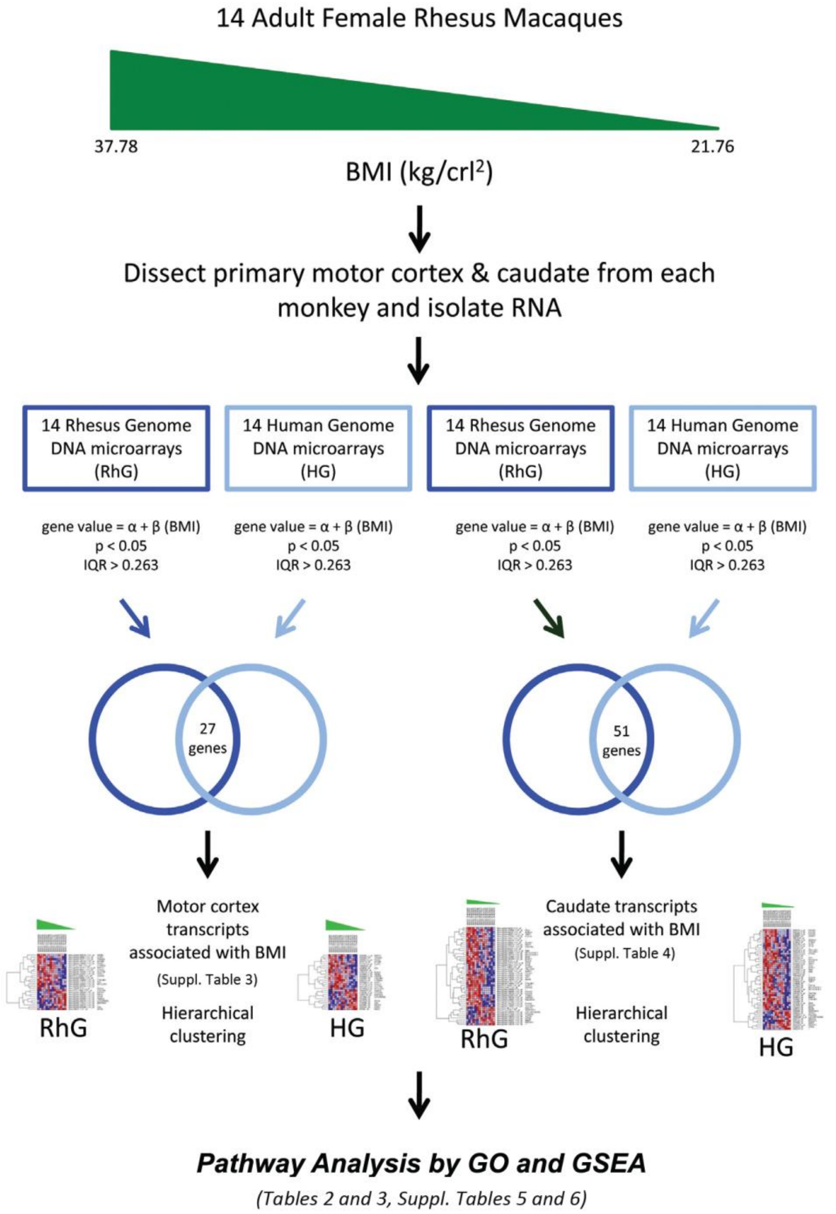

Figure 7. BMI Gene Expression Analysis Experimental Design. Motor cortex and caudate nucleus tissue was harvested from 14 female rhesus macaques with wide ranges of BMI. The motor cortex and caudate nucleus transcriptomes were profiled separately using both Affymetrix Rhesus Macaque Genome microarrays (RhG) and Affymetrix Human Genome U133 2.0 Plus microarrays (HG). We used a linear model to define gene expression associated with BMI (gene value = $\alpha + \beta$ (BMI)) for both microarrays separately. Probes were cross matched based on sequence similarity and significance was defined if both microarray models (i) were significant with $p < 0.05$, and (ii) had an interquartile range (IQR) > 0.263 corresponding to a 20% gene expression change. Significant genes are contained in Supplementary Tables 5 and 6, and clustered in Figure 2. Pathway analysis was performed using both Gene Ontology (GO) contained in Supplementary Tables 3 and 4, and Gene Set Enrichment Analysis (GSEA) contained in Tables 2 and 3. Note that the human and monkey data are highly concordant between the RhG and HG arrays for both the motor cortex and caudate nucleus.

We identified 27 transcripts that were associated with BMI in the motor cortex (17 positively correlated and 10 negatively correlated) and 51 transcripts that were associated with BMI in the caudate nucleus (41 positively correlated and 10 negatively correlated) (**Supplementary Table 3 and 4**). All altered transcripts in the motor cortex and in the caudate nucleus were changed in the same direction on both human and monkey microarrays, suggesting a high degree of concordance between the two data sets, and a very low false discovery rate in our experiment. Furthermore, our Pearson Hierarchal Clustering (Subramanian et al., 2005) revealed a progression of gene expression levels from monkeys with high BMI to monkeys with to low BMI (**Figure 8**).

Next, we performed a pathway analysis using Gene Ontology (GO) terms (**Supplementary Table 5 and 6**) (Ashburner et al., 2000) and GSEA assessment (Subramanian et al., 2007) (**Table 2 and 3**) to decipher which biological processes were involved with the BMI associated gene expression signature. The GO analysis revealed that in the motor cortex (**Supplementary Table 5**) there was an enrichment of apoptosis-related genes, and changes in gene expression in gene involved in metabolism. Similarly, in the caudate nucleus (**Supplementary Table 6**) we also found increased expression of apoptotic related genes, as well as increased expression of signal transduction genes, and changes in genes related to metabolism and transport.

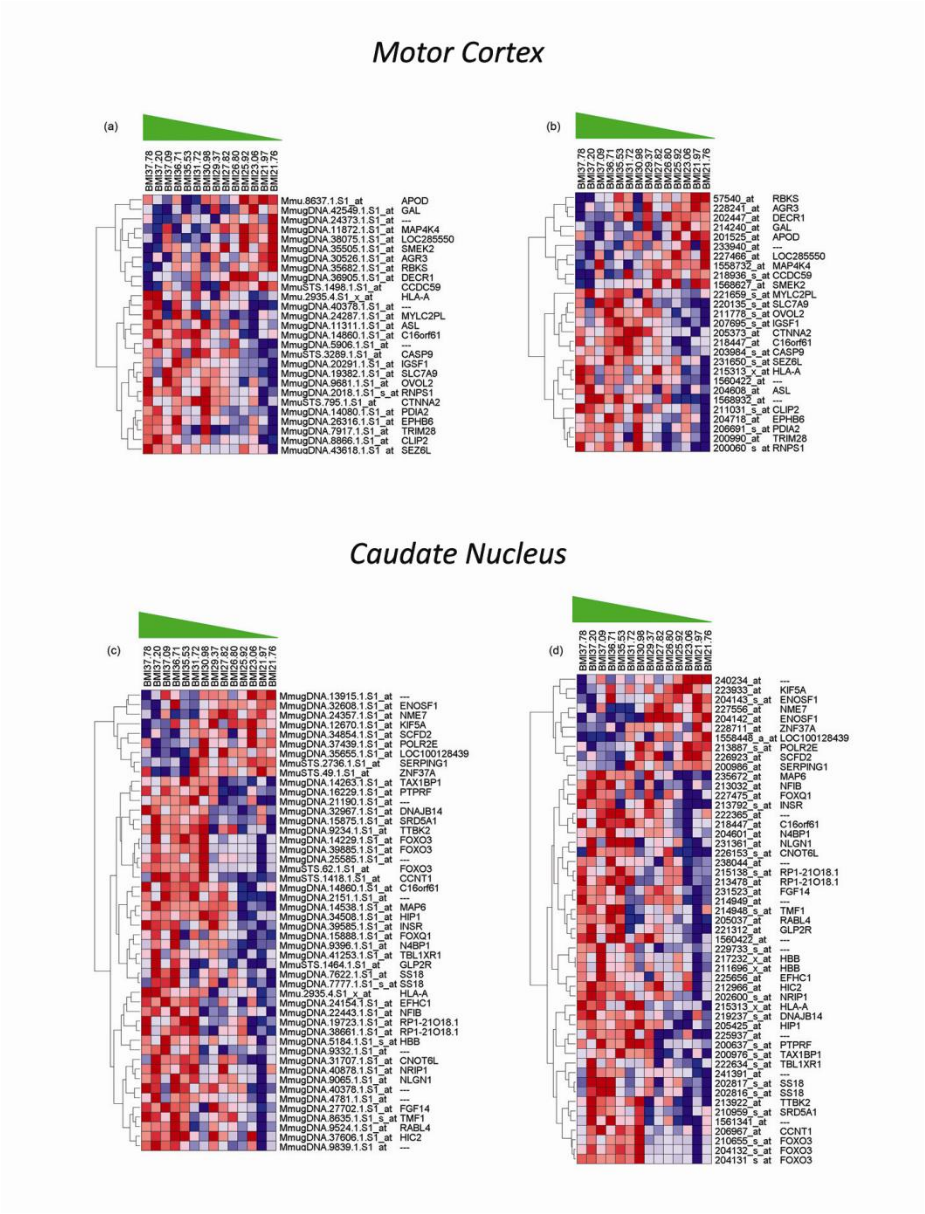

Figure 8. **Hierarchal Clustering of BMI Associated Gene Expression in the Motor Cortex and Caudate Nucleus.** Hierarchical clustering was performed on log2-transformed expression level of genes associated with BMI. Vertical column labels indicate BMI in decreasing order. Genes, denoted by Affymetrix Human Probes and NCBI gene symbols, were clustered horizontally. Each colored square represents a normalized gene expression value with color intensity proportional to magnitude of change (blue indicates a decrease in expression and red an increase). (a) Motor Cortex Gene Expression Signature for Rhesus Genome Microarrays. (b) Motor Cortex Gene Expression Signature for Human Genome Microarrays. (c) Caudate Nucleus Gene Expression Signature for Rhesus Genome Microarrays. (d) Caudate Nucleus Gene Expression Signature for Human Genome Microarrays. Note that in both structures there is a progression of gene expression values from monkeys with low BMI to monkeys with high BMI, and the data are concordant across the human and monkey array platforms.

Table 2. Motor Cortex Gene Set Enrichment Analysis (GSEA) for BMI

Name	Size	NOM p-val	FDR q-val	Correlation with BMI	Enriched Genes
Kuninger IGF1 vs. PDGFB targets up	41	0.000	0.104	+	TPM2, CKM, MYBPH, MYOG, RYR1, USP2, MYL1, TNNT2, TNNI1, ENAH, PYGM, C1QTNF3, PPFIA4, NCAM1, NPNT, SGCA, PKIA, ATP2A1, SMTN
One Carbon Compound Metabolic Process	26	0.000	0.128	+	NSUN2, DMAP1, PRMT5, NSD1, CARM1, DNMT3A, DNMT3B, EHMT1, PRM17, FOS, PRMT2
Module 440	18	0.000	0.173	+	CKM, OAT, ASL, GLUD1, BBOX1, CKB, ODC1, ACY1
ABE VEGFA targets 30 min	19	0.000	0.179	+	HDC, DBC1, C2, EGR2, EGR3, CYR61, NR4A1, TRIB1
Schuring STAT5A targets up	7	0.000	0.184	+	LIF, TRAF4, PIM1
Module 199	57	0.000	0.197	+	EPHB6, TEK, IL4R, KIT, KDR, PTK7, EPHB1, TIE1, IL2RB, MERTK, EPHA4, CCL2, MYLK, AXL, CDK5R1, ERBB2, EPHA7, MAP2K7, PDK4, FGFR3, IL13RA1, IL10RA, ROR2, EFNB3, PDGFRA
Reactome AKT Phosphorylates Targets in the cytosol	14	0.000	0.197	+	AKT2, CASP9, AKT1, TSC2
S Adenosylmethionine Dependent Methyltransferase Activity	22	0.000	0.198	+	METTL1, NSUN2, NSD1, DNMT3A, DNMT3B, EHMT1, PEMT, PRMT7
Methyltransferase Activity	34	0.000	0.216	+	ATIC, METTL1, NSUN2, PRMT5, NSD1, CARM1, DNMT3A, DNMT3B, EHMT1, PBMT, PRMT7, SUV39H1, GART

Table 2. Motor Cortex Gene Set Enrichment Analysis (GSEA) for BMI. Gene Set Enrichment Analysis (GSEA) was performed on the motor cortex data set. The gene set name, size, nominal p-value (NOM p-val), false discovery rate q-value (FDR q-val), correlation with BMI, and core enriched genes are included. Nine gene sets were positively correlated with BMI, had a NOM p-val < 0.001, and a FDR < 0.25. Module 199 and 440 are from the C4 computational gene sets cancer model where they used 1,975 published microarrays to span 22 tumor types. Module 199 is most strongly associated with leukemia and Module 440 is most strongly with associated liver cancer (Segal et al., 2004) .

We also assessed our data for the enrichment of functional gene pathways using Gene Set Enrichment Analysis (GSEA) (Subramanian et al., 2007) using the gene sets in the Molecular Signatures Database (MSigDBv.3.0) for the human (HG) arrays. We found 9 gene sets significantly associated with BMI in the motor cortex (**Table 2)**, and 3 gene sets in the caudate nucleus (**Table 3**). Prominently, in the motor cortex the BMI-associated changes included VEGFA targets (genes upregulated in HUVEC endothelium cells at 30 minutes after VEGFA stimulation (Abe and Sato, 2001)) and AKT phosphorylation targets in the cytosol, while in the caudate nucleus significant gene sets included HDAC targets (genes whose transcription is altered by histone deacetylase inhibitors (Marks, 2007)).

Table 3. Caudate Nucleus Gene Set Enrichment Analysis (GSEA) for BMI

Name	Size	NOM p-val	FDR q-val	Correlation with BMI	Enriched Genes
Cell Maturation	15	0.000	0.137	-	TP53, GADD45B, FAS, GSN, CASP3, GLRX, BAD, CCNE1, TXN, MCM3
Developmental Maturation	17	0.000	0.202	-	KCNIP2, MYH11, ACTA1, KRT19, EREG, IL21, PICK1, MYOZ1
MARKS HDAC targets up	18	0.000	0.238	-	MYH11, ACTA1, KRT19, EREG, IL21, PICK1, MYOZ1

Table 3. Caudate Nucleus Gene Set Enrichment Analysis (GSEA) for BMI. Gene Set Enrichment Analysis (GSEA) was performed on the caudate nucleus data set. Three gene sets were positively correlated with BMI, had a nominal p-value (NOM p-val) < 0.001, and a false discovery rate (FDR) < 0.25.

The observed gene expression changes are putatively a result of altered ERK1/2 signaling

One particular BMI-dependent gene expression attracted further attention. Our data identified inversely correlated mRNA levels of forkhead box O3 (FOXO3) with

BMI. FOXO3 is activated via the growth factor pathway, and involved in apoptosis and neuronal survival (Brunet et al., 1999). Furthermore, as a number of pro-apoptotic genes were positively correlated with BMI, and as both AKT and ERK1/2 are effector signaling pathways of neurotrophic factors (Park and Cho, 2006; Brunet et al., 1999; Lindgren et al., 2008), we next investigated the association of the AKT and ERK protein phosphorylation state with BMI (**Figure 9**) through Western analysis. While AKT levels and its phosphorylation state was unchanged, we identified a strong negative correlation of both ERK1/2 and pERK1/2 levels with BMI (pERK1/2 / tubulin r = -0.663 with p 0.010 and pERK1/2 / ERK1/2 of -0.595 with p = 0.025) (**Figure 9**). As pERK1/2 phosphorylates CREB, a transcription factor in the nucleus to reduce apoptosis (Park and Cho, 2006) and activate transcription of neuronal survival genes (Brunet et al., 1999), the decreased phosphorylation of ERK1/2 with increasing BMIs suggests that this might be a critical signaling pathway mediating some of the detrimental effect of BMI on the gene expression in the brain.

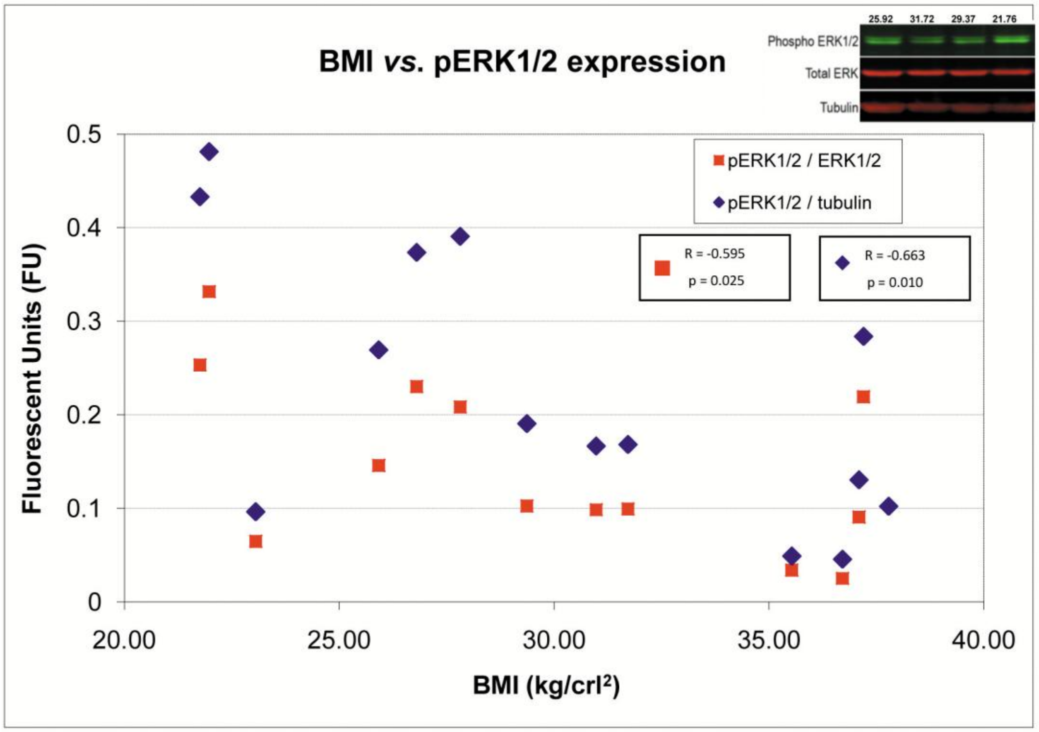

Figure 9. PhosphoERK1/2 levels are negatively correlated with BMI. Figure 9 is a scatterplot showing BMI (kg/CRL^2) versus protein ratios for pERK1/2 / tubulin (blue diamond) and for pERK1/2 / ERK1/2 (red square). There is a significant negative correlation between BMI and pERK1/2 / tubulin protein ratio (r= -0.663; p = 0.010) and a significant negative correlation of BMI and protein ratio for phospho ERK1/2 / total ERK1/2 (r=-0.595; p = 0.025). Inset provides examples of ERK1/2 protein levels in four monkeys with various BMI, with BMI levels denoted above the images.

DISCUSSION

In summary, we discovered a distinct gene expression signature associated with BMI in the motor cortex and caudate nucleus. Our linear model allowed us to model BMI and gene expression continuously, and to find a gene expression signature with 100% concordance in directionality between significant probes on RhG and HG microarrays. We saw increases in apoptotic related genes and changes in metabolic related genes across both brain regions, suggesting that motor regions of the brain are affected at the transcriptional level by obesity. Decreased ERK1/2 phosphorylation was associated with increasing BMI. Activation of this prototypical survival kinase provides a potential explanation for the enrichment of pro-apoptotic genes in animals with high BMI and putatively explains how obesity raises the risk for reduced brain volume (Gustafson et al., 2004; Raji et al., 2010; Pannacciulli et al., 2007; Taki et al., 2008).

Although we did not find evidence of BMI-dependent changes to the AKT signaling pathway, we cannot rule out the possibility of cross talk between the AKT and ERK1/2 pathways (Tang et al., 2010; Shelton et al., 2004; Dai et al., 2009; Levinthal and DeFranco, 2004) in the nonhuman primate brain. Furthermore, our previous data suggest that physical activity is positively correlated with pAKT protein levels in nonhuman primates (Mitchell et al., 2011b), potentially leading to a double-risk to the brain: the sedentary lifestyle might decrease pAKT signaling and increased BMI can repress the activation of the neuronal survival kinase ERK1/2. These two events, in concert might significantly increase brain susceptibility to various insults. Although it is tempting to hypothesize that both of these events are the result of a change in a growth factor signaling pathway, we found relatively meager evidence to support this theory at the level of the transcriptome. However, it is known that growth factor signaling is profoundly regulated at the post-transcriptional level (Lindgren et al., 2008; Chen and Russo-Neustadt, 2007) and this should be a topic of further follow-up experiments.

The positive correlation between the expression of apoptosis-related genes and BMI is also noteworthy. Increased pro-apoptotic gene expression can lead to increased vulnerability of neurons to various environmental insults, and the decreased brain volume observed in persons with high BMI (Gustafson et al., 2004; Pannacciulli et al., 2007; Taki et al., 2008; Raji et al., 2010) might be closed linked to the gene expression changes we uncovered.

Since our monkeys were placed on a calorie restriction diet immediately prior to transcriptome analyses some of the deleterious effects associated with high BMI may have been masked. A number of previous studies have demonstrated many beneficial effects of calorie restriction on health, the rate of aging, and longevity (Kemnitz, 2011). These findings suggest important roles for the plasma membrane redox system in protecting brain cells against age-related increases in oxidative and metabolic stress, and these findings might be directly related to the BMI-correlated increases in pro-apoptotic gene expression (Hyun et al., 2006). Furthermore, our results are also in concordance with previous transcriptome profiling studies performed on monkeys that underwent dietary restriction (Prolla and Mattson, 2001). The neuroprotective effect of dietary restriction reported increased production of neurotrophic factors and protein chaperones, resulting in protection against oxyradical production, stabilization of cellular calcium homeostasis, and inhibition of apoptosis.

Finally, based on our studies and previous literature we conclude that active lifestyles with low BMI create a brain homeostasis more conducive to brain resiliency and neuronal survival. Brain health is clearly linked to body health, and, we now show the converse, that maintaining a health BMI is also essential for maintaining a healthy brain transcriptome.

CHAPTER IV

Molecular correlates of spontaneous activity in nonhuman primates

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INTRODUCTION

A growing body of evidence suggests that mild (Yaffe et al., 2001), moderate, and vigorous physical activity (Thacker et al., 2008) are neuroprotective, decreasing the risk of many brain disorders including ischemic stroke (Hu et al., 2000; Lee and Paffenbarger, 1998), Alzheimer's disease (Yaffe et al., 2001; Larson et al., 2006), and Parkinson's disease (PD) (Thacker et al., 2008). Numerous studies also associate the modern sedentary lifestyle with increased risks for obesity, cardiovascular diseases, type 2 diabetes (Marwick et al., 2009), and depression (Lawlor and Hopker, 2001; Vance et al., 2005).

At the molecular level, exercise is correlated with increased levels of neurotrophic factors (nerve growth factor (NGF), brain derived neurotrophic factor (BDNF), and fibroblast growth factor-2 (FGF-2)), synaptic trafficking genes (syntaxin, synapsin I, and synaptotagmin), and activation of signal transduction pathways (CaMKIIδ, ERK1/2, and PKC) (Neeper et al., 1996; Molteni et al., 2002; Tong et al., 2001b). In a previous study we found that both BDNF and activity regulated cytoskeletal associated protein (ARC) are elevated in mice exposed to enriched environments (Lazarov et al., 2005), suggesting that activation of the ARC-BDNF pathway might be a critical mediator of neuroprotective events. ARC is an immediate early gene induced by neuronal excitation with a role in activity dependent synaptic modification (Steward and Worley, 2002), and active behavior in the hippocampus, neocortex, and striatum (Vazdarjanova et al., 2006).

In contrast, high c-reactive protein (CRP) is associated with increased risks for type II diabetes (Lakka et al., 2005), hypertension, cardiovascular disease, and ischemic stroke (Stewart et al., 2010). It is involved in host defense related functions, recognizes foreign pathogens and damaged cells, and initiates their elimination by interacting with humoral and cell effector systems in the blood (Stenvinkel, 2006). In healthy individuals the concentration of CRP in serum is low (Yeh, 2004). As a result of ischemic infraction CRP binds to phosphocholine expressed on the surface of dead or dying cells in order to activate complement during the acute phase response (Volanakis and Kaplan, 1971) (Stenvinkel, 2006), and is increased in the bloodstream in response to tissue injury, infection, and other inflammatory stimuli (Futterman and Lemberg, 2002). Furthermore, high CRP enhances ischemic tissue damage in rats (Gill et al., 2004), indicating that it may be an active contributor to pathophysiological events.

Recently, it has been shown that exercise can also lower CRP in the blood plasma (Maglott et al., 2011). This finding, combined with well-established activity-dependent elevation of ARC/BDNF expression the brain, leads us to the hypothesis that there is a relationship between spontaneous physical activity, CRP plasma levels, and ARC/BDNF expression in the brain. To test this hypothesis, we measured and correlated CRP serum levels and brain expression of ARC and BDNF in 11 Rhesus monkeys with various levels of spontaneous activity.

METHODS

Experimental animals

All experiments were reviewed and approved by the Animal Care and Use Committee of the Oregon National Primate Research Center. Eleven adult female ovarectomized rhesus monkeys (*Macaca mulatta*) were housed in individual cages (32 x 24 x 27 or 32 x 34 x 27 in.) in a temperature-controlled room (24 ± 2 C), with lights on between 0700 and 1900 h. Two and a half years prior to the initiation of this study, these monkeys were ovariectomized and placed on a diet higher in fat than standard monkey chow (35% of calories from fat) to approximate the conditions experienced by many post-menopausal women in the Western world (Williams et al., 2003). This diet was formulated at the Oregon National Primate Research Center (ONPRC) (Sullivan et al., 2006; Sullivan and Cameron, 2010), following a modification of the recipe developed by Clarkson and colleagues to study diet-induced atherosclerosis (Shadoan et al., 2003; Williams et al., 2003). Monkeys were subsequently placed on a diet of Purina high protein monkey chow (no. 5045; Ralston Purina, St. Louis MO), supplemented with fresh fruits and vegetables for two months. During the first month available calories were reduced to 30% as compared to baseline on the higher fat diet, and in the second month calorie intake was reduced to 60% as compared to baseline.

In vivo Experimental Measures

Throughout the study, food intake was measured at every meal, body weight was measured weekly, and activity was measured continuously using omnidirectional Actical accelerometers (Respironics, Phoenix, AZ), attached to a loose-fitting metal collar, via previously published methods (Sullivan et al., 2006; Sullivan and Cameron, 2010). Percent body fat was determined using dual energy X-ray absorptiometry scans (Sullivan et al., 2006; Sullivan and Cameron, 2010).

Collection of Brain Tissue

Monkeys were deeply anesthetized with ketamine/pentobarbitol, quickly decapitated, and the entire brain was removed from the skull. The brain was then hemi-sected by a midline saggital cut. The right hemisphere was cut into ~5 mm-thick coronal blocks, flash-frozen in isopentane over dry ice, and stored at -80°C until use (Volk et al., 2000).

RNA sample preparation

The motor cortex was identified using anatomical landmarks, and a 2mm x 2mm tissue cube of transcortical gray matter was dissected from the frozen block using surgical tools under RNAse-free conditions. The motor cortex brain material was homogenized and total RNA isolated using TRIzol® reagent (Invitrogen, Carlsbad, CA) with RNA quality assessed via analysis on an Agilent 2100 Bioanalyzer. Only samples with an RIN > 7.0 were considered for further analysis.

Quantitative real-time PCR

cDNA synthesis was performed using two independent reverse transcription reactions for each sample with High Capacity cDNA Archive Kit® (Applied Biosystems). For each 100 μl reaction, we used 700 ng of the same total RNA used for microarray analysis. Priming was performed with random hexamers. For each sample, amplified product differences were measured with 4 independent replicates using SYBR Green chemistry-based detection (Mimmack et al., 2004). β-actin was used as the endogenous reference gene since it has been established as a stable reference gene in the literature (Chen et al., 2001; Arion et al., 2007a; Arion et al., 2007b). Primer sequences for β-actin were 5’ GAT GTG GAT CAG CAA GCA 3’ and 5’ AGA AAG GCT GTA ACG CAA CTA 3’; for BDNF were 5’ GAC TGG ACG ACC ACA CTC AAG 3’ AND 5’ CAA CCT GCT CCA GGC TAA TC 3’; and for ARC 5’ CGC CTG GAG AAG AAT CAG AG 3’ AND 5’ CTC AGC CGG ATT TGA GGA C 3’. The efficiency for each primer set was assessed prior to qPCR measurements, and a primer set was considered valid if its efficiency was > 90%. The qPCR reactions were carried out on an ABI Prism 7300 thermal cycler (Applied Biosystems Inc.), quantified using ABI Prism 7300 SDS software (with the auto baseline and auto threshold detection options selected) and statistically analyzed using Pearson correlations.

CRP measurements

C-reactive protein (CRP) was analyzed using serum drawn immediately prior to termination of the study, after animals had been on a low fat diet for two months following a three-year period on a 35% fat diet. Serum was stored frozen, warmed to make aliquots and then refrozen before use. A quantitative ELISA kit specific for monkey CRP (Alpha Diagnostic international, 96 well) was used to measure serum levels of CRP according to the manufacturers instructions. Serum aliquots were diluted with the Elisa kit diluent between 1:200 and 1:800 in order to cover the range of CRP levels in these animals, and run on a single ELISA plate in triplicate. Results shown were based on a 1:400 dilution, as this range best centered the observed levels within the standard curve, but other dilutions did not alter the conclusions drawn. Optical density of the colored reactant was quantified using an Emax Precision Microplate Reader (Molecular Devices) set to 450nm, measured twice and averaged. A standard curve was generated using known sample concentrations, run on the same ELISA plate in duplicate. Sigma Plot (Systat) was then used to calculate the unknown concentrations of CRP using the standard curve.

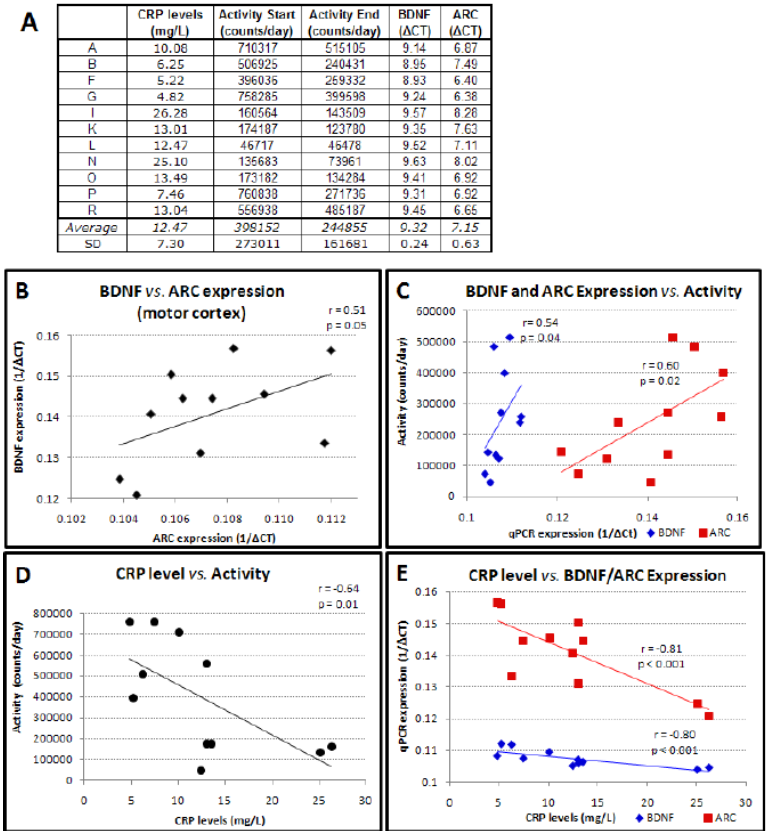
Statistical procedures

BDNF, ARC, CRP and spontaneous activity measurements were correlated using Pearson product-moment correlation coefficient in Microsoft Excel 2007. The significance of the Pearson product-moment correlation coefficient was calculated using $t = r / [(\sqrt{(1 - r^2)} / (N - 2)]$. P-values were obtained from the t-statistic (Lowry, 2010). As higher values mean lower absolute transcript expression, to denote meaningful correlations, in **Figures 10 b-e** qPCR expression data are plotted as a $1/\Delta Ct$.

RESULTS

Spontaneous activity levels activity levels, measured continuously with accelerometers, showed individual variation of more than an order of magnitude, and encompassed a range of 46,717 – 760,838 counts/day (mean = 398,152 counts/day, SD = 273,011 counts/day) at the beginning of the calorie restriction diet and 46,478 - 515,105 counts/day (mean = 244,855 counts/day, SD = 161,681 counts/day) at the end of the calorie restriction diet. Activity measurements at the beginning and end of the calorie restriction diet were highly correlated (r=0.85, p=0.000379), suggesting that diet was not a crucial factor in defining the relative level of spontaneous activity, and that relative activity level was a stable intrinsic characteristic of monkeys over the investigated time window. The monkeys displayed serum concentrations of CRP in the range of 4.82 – 26.28 mg/L (mean concentration = 12.47, SD = 7.30) (**Table 1 in Figure 10a**), while brain expression measurement of BDNF and ARC suggested that both genes were abundantly expressed in the motor cortex, albeit with less individual variability than the CRP levels and spontaneous activity levels.

As we obtained measurements for continuous variables (spontaneous activity, serum CRP, cortical ARC and cortical BDNF), to test our hypotheses we cross-correlated the overall data using Pearson product-moment correlation coefficient. As expected from our previously reported findings (Lazarov et al., 2005), the expression of ARC and BDNF were correlated in the motor cortex (r=0.51, p=0.05) (**Figure 10b**). Furthermore, ARC and BDNF activity were also significantly correlated with spontaneous activity (r=0.60, p=0.02 and r=0.54, p=0.04, respectively) (**Figure 10c**). In contrast, CRP plasma levels were inversely and significantly correlated with spontaneous activity (r=-0.64, p=0.01) (**Figure 10d**). Finally, the CRP levels were also strongly and inversely correlated with the motor cortical expression of ARC and BDNF (r=-0.81, p<0.001 and r=-0.80, p<0.001, respectively) (**Figure 10e**), raising the possibility of a causal co-regulation between these measurements.



A

	CRP levels (mg/L)	Activity Start (counts/day)	Activity End (counts/day)	BDNF (ΔCT)	ARC (ΔCT)
A	10.08	710317	515105	9.14	6.87
B	6.25	506925	240431	8.95	7.49
F	5.22	396036	259332	8.93	6.40
G	4.82	758285	399598	9.24	6.38
I	26.28	160564	143509	9.57	8.28
K	13.01	174187	123780	9.35	7.63
L	12.47	46717	46478	9.52	7.11
N	25.10	135683	73961	9.63	8.02
O	13.49	173182	134284	9.41	6.92
P	7.46	760838	271736	9.31	6.92
R	13.04	556938	485187	9.45	6.65
Average	*12.47*	*398152*	*244855*	*9.32*	*7.15*
SD	7.30	273011	161681	0.24	0.63

Figure 10. Correlation of spontaneous activity, serum CRP levels, and BDNF and ARC expression in motor cortex of 11 Rhesus monkeys. (a) Monkey activity levels were measured in counts/day, CRP in milligrams per liter (mg/L), BDNF and ARC in threshold cycle difference relative to β-actin (ΔCT). **(b)** Scatter plot of ARC expression (X axis) and BDNF expression (Y axis) for the motor cortex of the 11 monkeys included in the study. Solid line represents trend line. Note the correlation between the expression of these two genes. **(c)** X axis denotes gene expression level measured by qPCR for ARC (blue diamonds) and BDNF (red squares) for the 11 monkeys, while Y-axis represent end of experiment spontaneous activity counts. Solid lines denote trend lines. Note that both ARC and BDNF expression are significantly correlated with spontaneous activity in the studied monkeys. **(d)** Scatter plot of serum CRP levels (X axis) vs. spontaneous activity (Y axis). Each symbol represents a single experimental animal. Note the inverse correlation between spontaneous activity and serum CRP levels. **(e)** Correlation of serum CRP level and ARC and BDNF expression in the motor cortex. The figure layout is similar to that of 1c. Note the high inverse correlation between the ARC-CRP and BDNF-CRP measurements.

DISCUSSION

This study gave rise to three major findings. First, spontaneous activity in the primate is stable over time and although a monkey's activity level decreases with calorie restriction (Sullivan and Cameron, 2010) their activity level relative to that of other monkeys remains stable. Second, spontaneous activity is positively correlated with ARC and BDNF expression in the motor cortex of nonhuman primates, and negatively correlated with serum CRP levels. Third, serum CRP levels are strongly and negatively correlated with ARC and BDNF expression in the motor cortex of nonhuman primates.

Previous studies in mice, rats, and monkeys show the same general localization of BDNF and ARC to layers II, III, IV, and VI in the cortex (Link et al., 1995; Grinevich et al., 2009; Hofer et al., 1990; Phillips et al., 1990; Zhang et al., 2007), and both are predominantly expressed in the principal (projection) neurons in the cortex. Thus, we believe that the CRP-correlated cortical expression changes occur in the same population of the projection neurons. Nevertheless, this hypothesis will have to be confirmed in follow up co-localization studies in a different experimental cohort, as our fresh-frozen material is less then ideally suited for such experiments.

Activity, CRP, BDNF and ARC co-regulation raises an important and interesting question: how are peripheral changes in CRP levels in the blood related to the gene expression changes in the motor cortex? Based on previous literature findings, we believe that this relationship could be causal and related to dynamic changes in brain vascularization: 1) CRP can significantly influence gene expression in the vascular endothelium after 24 hours (Wang et al., 2005), 2) increased levels of CRP can increase infarct in rats and enhance ischemic tissue damage (Gill et al., 2004), 3) CRP is also increased in the blood plasma in response to tissue injury, infection, and other inflammatory stimuli (Yeh, 2004), 4) CRP causes blood–brain barrier disruption involving the formation of ROS by the NAD(P)H-oxidase (Kuhlmann et al., 2009), 5) brain endothelial cells express higher levels of CRP receptors and have increased vulnerability of brain endothelial cells to CRP following stroke (Kuhlmann et al., 2009), 6) MPTP administration increases CRP levels in nonhuman primates (De Pablos et al., 2009) and 7) high CRP is associated with increased risk for type II diabetes (Lakka et al., 2005), hypertension, cardiovascular disease, and ischemic stroke (Stewart et al., 2010). Furthermore, exercise results in the reduction of weight and is associated with improvements in CRP (Church et al., 2010).

However, we must also acknowledge the possibility that the correlation between peripheral CRP levels and BDNF/ARC is a result of a more complex, coordinated set of pathophysiological events. This cascade might also involve an insulin-like growth factor (IGF) dependent mechanism: peripheral administration of IGF has also been shown to induce BDNF mRNA expression in the hippocampus and cortex (Carro et al., 2000). Furthermore, exercise increases IGF1 levels in the brain, and IGF1 blocking antibodies administered before a neural injury results in decreased neuroprotection (Carro et al., 2001). Thus, one could hypothesize that the activity-induced increase in IGF1 levels leads to upregulation of BDNF/ARC in the hippocampus and cortex.

Finally, our findings and the literature data raise a critical question: do increased peripheral CRP levels increase the chance of an individual to develop neurodegenerative brain diseases? If so, lowering CRP levels in the periphery might be neuroprotective, and this could be assessed in various *in vitro* and *in vivo* model systems. Further studies of the activity-CRP-ARC-BDNF relationships and the health of the brain are warranted by our findings, and could lead to important new strategies for early detection of, as well as novel treatments for neurodegenerative disorders.

CHAPTER V

Electron Transport Chain Alterations are associated with Exercise in the Hippocampus, Motor Cortex, and Putamen

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INTRODUCTION

Mild (Yaffe et al., 2001), moderate, and vigorous physical activity (Thacker et al., 2008) are associated with a decreased risk of neurodegenerative brain disorders such as Alzheimer’s disease (Yaffe et al., 2001; Aaron et al., 2006), Parkinson’s disease (Thacker and Ascherio, 2008), and the size of the infarct from stroke. Many clinicians routinely recommend physical activity for those suffering from the effects of these diseases. In Parkinson’s disease patients physical activity has been shown to improve gait, tremor, grip strength, balance, and motor coordination (Hirsch et al., 2003; Palmer et al., 1986) while physical activity alone has been shown to improve sleep (Driver and Taylor, 2000), cognition (Colcombe and Kramer, 2003; Weuve et al., 2004), and decrease depression (Dunn et al., 2005; Lawlor and Hopker, 2001; Reuter et al., 1999). It has been hypothesized that exercise is neuroprotective against Parkinson’s disease and other neurodegenerative diseases.

Many people have explored the mechanism of exercise in the brain. Animal studies show that exercise and environmental enrichment increase the production of neurotrophic factors (nerve growth factor, NGF, brain derived growth factor, BDNF, and basic fibroblast growth factor, FGF-2), immediate early genes, synaptic trafficking genes (syntaxin, synapsin I, and synaptotagmin), and signaling transduction molecules (AKT, CaMKIIδ, ERK1/2, and protein kinase C, PKC) throughout the brain with the most dramatic effects in the hippocampus (Neeper et al., 1996; Molteni et al., 2002; Gomez-Pinilla et al., 2002). Physical activity and enriched environments also enhance learning and memory, increase neuronal survival, increase resistance to brain insults, trigger synaptogenesis, promote brain angiogenesis, and promote neurogenesis in the hippocampus (Brown et al., 2003).

Little has been done to evaluate exercise alone in brain regions other than the hippocampus, which is a unique brain region, one of only two sites that undergo adult neurogenesis (Neeper et al., 1996; Molteni et al., 2002; Brown et al., 2003; Tong et al., 2001a), and some studies suggest regional differences in the brain in response to exercise. The hippocampus does show a high frequency of neural activity during exercise, like the motor cortex and striatum (Vissing et al., 1996), but the hippocampus does not show an increase in bioenergetic capacity (McCloskey et al., 2001). This suggests that additional responses to, or mechanisms of, exercise may be seen in regions outside of the hippocampus.

Other models have confirmed the principal that physical activity can provide protection against brain lesions. Animal neurodegeneration models for Alzheimer’s disease and Parkinson’s disease show that physical activity and exercise can decrease the size of the lesion as evidenced in the caudate nucleus and putamen (Tillerson et al., 2001; Tillerson et al., 2003; Howells et al., 2005; Caudle et al., 2007; Mabandla et al., 2004;

Petzinger et al., 2007; Lazarov et al., 2005; Mitchell et al., 2011a). Indeed in our monkey MPTP model of Parkinson's disease we found that overall physical activity level, not exercise alone, protected the brain against neurodegeneration of dopaminergic projections to the caudate and putamen (Mitchell et al., 2011a).

The mechanism of neuroprotection has been explored in greater detail using disease models. Zigmond et al hypothesized that forced use ameliorates the behavioral and biochemical effects of Parkinson's disease using the 6-OHDA model through cascade of events that involves glial derived neurotrophic factor (GDNF) (Zigmond et al., 2009), a potent survival factor for DA neurons (Cohen et al., 2003). There is a significant increase of striatal GDNF 24 and 72 hours after using the non-impaired limb in the unilateral 6-OHDA model of Parkinson's disease (Lin et al., 2008). Furthermore, ERK1/2 activation by GDNF in the striatum remains elevated up to 1 month after limb use (Lin et al., 2008; Lindgren et al., 2008). We have also found that physical activity gene expression in the motor cortex is associated with phosphorylated AKT – a signaling kinase important in cellular survival – and in the caudate nucleus with the mTORC1 nutrient sensing and generation of second messengers pathways (Mitchell et al., 2011b), which indicates that there are some common responses and mechanisms of physical activity across different brain regions.

Thus, we hypothesized that the motor cortex and putamen would share an exercise-associated gene expression signature with the hippocampus, but also would contain unique gene expression changes. We used sedentary and exercising Rhesus monkeys (*Macaca mulatta*) to explore the mechanism of exercise by DNA microarray in the motor cortex, putamen, and hippocampus. We found exercise associated gene expression included solute carrier family (SLC) members, members of the electron transport chain, and translation initiation genes, suggesting that the mechanism of aerobic exercise in the brain differs from that of spontaneous activity.

METHODS

Subjects

Twelve female Rhesus monkeys (*Macaca mulatta)* (15-20 years of age, 5-8 kg) were matched based on initial activity levels and placed into two groups: sedentary and animals that ran 5 days/week on a treadmill at 80% of their maximal heart capacity, intensities that can be tolerated by people with Parkinson's disease (Schenkman et al., 2008).

Sample preparation and hybridization

Hippocampus tissue, motor cortex tissue, and putamen tissue, respectively, were homogenized and total RNA was isolated using TRIzol® reagent (Invitrogen, Carlsbad, CA). RNA quality was assessed on an Agilent 2100 Bioanalyzer. A RNA integrity number (RIN) > 7 was considered acceptable for further analysis. Samples were amplified using the Enzo™ BioArray Single Round RNA Amplification and Biotin Labeling System. They were primed with a standard T7-oligo(dT) primer and cDNA synthesis was performed using 3 µg of total RNA. Amplified antisense RNA (aRNA) was produced using *in vitro* transcription directed by a T7 polymerase. Six µg of each purified and fragmented aRNA was hybridized to GeneChip® HT Human Genome (HG) U133 Plus PM Arrays Plates. Image segmentation analysis and generation of DAT files was performed using Microarray Suite 5.0 (MAS5).

Microarray data analysis

One 24 Affymetrix Human Gene Titan array plate containing hippocampal and motor cortex samples, and one 16 Affymetrix Human Gene Titan array plate containing putamen samples were scanned and analyzed. Segmented images were normalized and log2 transformed using robust multi-array analysis (RMA) separately for hippocampus, motor cortex, and putamen with RMA normalized expression levels utilized for all subsequent analyses. All microarray data will be available at http://mirnicslab.vanderbilt.edu.

Probes with a p-value < 0.05 for both paired and groupwise t-tests, and an average log ratio (ALR) > 0.263 (representing a 20% change) were considered associated with exercise. Gene lists for hippocampus, motor cortex, and putamen exercise-associated were created. Exercise-associated probes from each region were tested for concordance in directionality of gene expression change between the other 2 regions.

We performed gene set enrichments analysis (GSEA) on the motor cortex, putamen, and hippocampus using Broad Institute GenePattern Software (Subramanian et al., 2005) on all gene sets in the Molecular Signatures Database (MSigDB 3.0) (Liberzon et al., 2011). We performed 1000 permutations with a minimum enriched gene set size of five.

RESULTS

We hypothesized that the motor cortex, putamen, and hippocampus would be associated with unique gene expression changes, but also share common gene expression changes relating to neuronal survival. We used two groups of monkeys: 6 sedentary monkeys who sat on treadmills and 6 exercising monkeys who ran on treadmills at 80% of their maximum heart capacity. We isolated RNA from the motor cortex, putamen, and hippocampus, and profiled the transcriptome using Human Genome DNA microarrays (HG) (**Figure 11**).

We identified 434 transcripts that were associated with exercise in the motor cortex (336 increasing with exercise and 98 decreasing with exercise), 265 transcripts that were associated with exercise in the putamen (127 increasing with exercise and 138 decreasing with exercise), and 5508 transcripts that were associated with exercise in the putamen (1673 increasing with exercise and 3835 decreasing with exercise) (**Supplementary Tables 7, 8, and 9**).

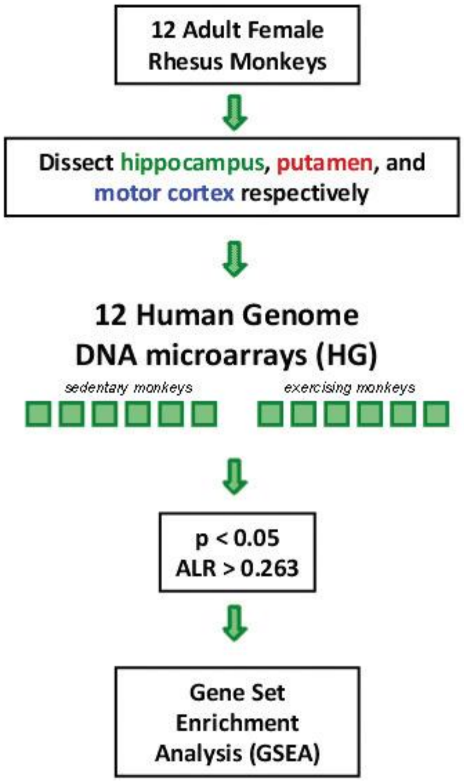

Figure 11. Exercise Gene Expression Analysis Experimental Design. Twelve female rhesus monkeys were placed into either a sedentary group or a group of 80% maximum heart capacity runners to look for transcripts by Human Genome (HG) DNA microarray in the brain associated with exercise. We looked at 3 regions of the brain: motor cortex (blue), putamen (red), and the hippocampus (green). We defined transcripts significantly associated by a groupwise and paired t-test with a p-value<0.05, and an average log ratio (ALR) > 0.263, representing a 20% change. Additionally, we looked for functional pathways associated with each brain region by gene set enrichment analysis (GSEA) (Liberzon et al., 2011).

Our data suggests that the motor cortex and the hippocampus respond differently to exercise. There was no overlap between all three brain regions. Furthermore, we saw only 3 of 55 overlapping gene transcripts between the motor cortex and hippocampus changing in the same direction (**Figure 12**). Between the motor cortex and putamen we saw 4 of 5 overlapping gene transcripts changing in the same direction, and 89 of 91 overlapping gene transcripts changing in the same direction between the hippocampus and putamen.

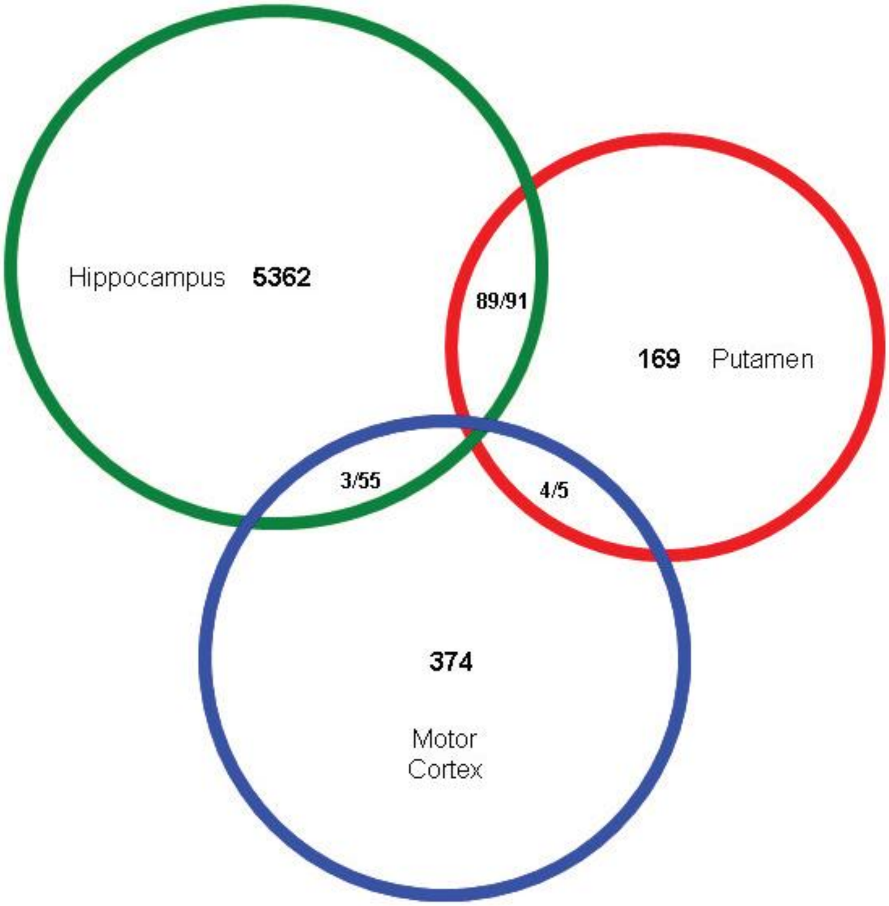

Figure 12. Exercise Related Gene Expression Motor Cortex, Putamen, and Hippocampus Venn Diagram. We used a Venn diagram to compare gene expression associated with exercise in three regions of the brain: motor cortex (blue), putamen (red), and hippocampus (green). There are 434 transcripts in total associated with exercise in the motor cortex, 265 in total associated with exercise in the putamen, and 5508 transcripts in total associated with exercise in the hippocampus. Ninety one transcripts overlap between the hippocampus and putamen, 89 of which are changing in the same direction. Five transcripts overlap between the motor cortex and putamen, 4 of which are changing in the same direction. Fifty five transcripts overlap between the hippocampus and motor cortex, 3 of which are changing in the same direction. This indicates that exercise associated gene expression is different between the hippocampus and motor cortex, and that the putamen shares exercise associated gene expression with the motor cortex and hippocampus.

In all three brain regions we found members of the solute carrier (SLC) family and genes involved in the mitochondria electron transport carrier, and by GSEA in the motor cortex using the Molecular Signatures Database (MSigDB) we found exercise enriched genes in the NADH Dehydrogenase, mitochondrial respiratory chain complex, and respiratory chain complex I gene sets (**Table 4, Figure 13**).

Table 4. Exercise Motor Cortex Gene Set Enrichment Analysis (GSEA)			
Gene Set Name	**Enriched Genes**	**NOM p-val**	**FDR q-val**
NADH Dehydrogenase Complex	NDUFA13, NDUFB6, NDUFS3, NDUFS8, NDUFS7, NDUFV1, NDUFS1	0.000	0.145
Mitochondrial Respiratory Chain Complex I	NDUFA13, NDUFB6, NDUFS3, NDUFS8, NDUFS7, NDUFV1, NDUFS1	0.000	0.073
Respiratory Chain Complex I	NDUFA13, NDUFB6, NDUFS3, NDUFS8, NDUFS7, NDUFV1, NDUFS1	0.000	0.048

Table 4. Motor Cortex Gene Set Enrichment Analysis (GSEA) for Exercise. Three gene sets using all of the gene sets from the Molecule Signatures Database (MSigDB) (Liberzon et al., 2011) were found significantly altered in the motor cortex by GSEA. Gene sets are identified by their pathway name, size, nominal p-value (NOM p-val), and false discovery rate q-value (FDR q-val). Nominal p-values of 0.000 indicate that the value was below 1 / (number of permutations, or 1000). Complex I of the electron transport chain is enriched with exercise in the motor cortex.

In the motor cortex we saw increased in SLC25A27 and SLC25A37 and decreased SLC23A1 and SLC39A13 (**Figure 13**). SLC25A27 is mitochondrial uncoupling protein 4. It reduces the mitochondrial membrane potential and separates oxidative phosphorylation from ATP synthesis with energy dissipated as heat. SLC25A37 is a mitochondria inner membrane protein that imports iron for synthesis into mitochondria heme and iron-sulfur clusters. SLC23A1 is a vitamin C transporter. SLC39A13 is a zinc transporter (Maglott et al., 2011). These mRNA transcript changes suggest that there is an increased capacity to handle oxygen consumption with exercise.

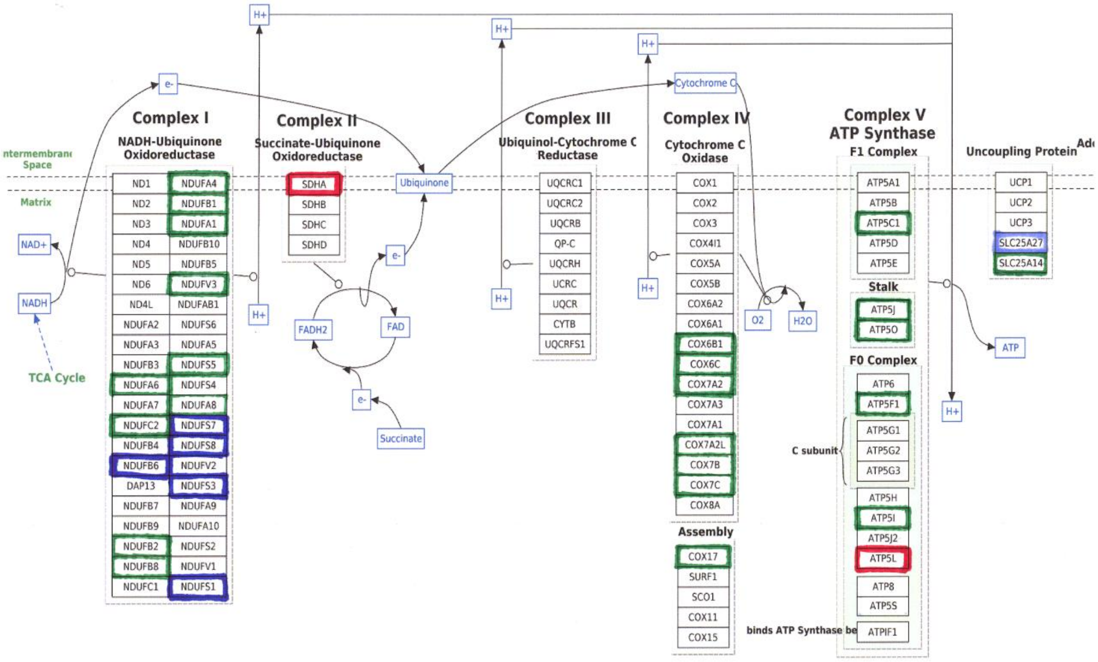

Figure 13. **The Electron Transport Chain.** We found solute carrier family (SLC) members and electron transport chain family members associated with exercise in the motor cortex (light blue), putamen (red), hippocampus (green), and in the motor cortex by GSEA (dark blue). This figure was edited from Wikipathways (Pico et al., 2008).

In the putamen we saw increased SLC25A18, SLC15A2, and SLC37A4 and decreased SLC38A1 and SLC4A4 (**Figure 13**). SLC25A18 is a mitochondrial carrier protein. SLC15A2 is an H+/peptide transporter. SLC37A4 is a glucose 6 phosphate translocase. SLC38A1 is an amino acid transporter that transports glutamine, an intermediate in detoxification of ammonia and production of urea. SLC4A4 is an electrogenic sodium bicarbonate co-transporter (Maglott et al., 2011). These mRNA transcript changes suggest that there are changes in transport of many solutes with exercise in the brain.

In the hippocampus we saw numerous genes involved in the mitochondrial respiratory chain (**Figure 13**). These were involved with Complex 1 (NDUFA6, NDUFB2, NDUFB1, NDUFA1, NDUFA5, and NDUFA8), Complex II (SDHD), Complex III (UQCRC2, UQCRB, and UQCRH), Complex IV (COX5A, COX5B, COX6B1, BOX6C, COX7A2, COXA2L, COX7B, COX7C, and COX17), Complex V (ATP5C1, ATP5J, ATP50, ATP5F1, ATP5I, ATP5J2, AND ATPIF1), and the uncoupling protein (SLC25A27 and SLC25A14) (Maglott et al., 2011). This suggests again that there is an increased capacity to handle oxygen consumption with exercise.

DISCUSSION

We believe that exercise contributes to physical activity level, but that physical activity level itself is neuroprotective. We have looked at spontaneous activity gene expression signatures in the motor cortex, caudate nucleus (Mitchell et al., 2011b)**,** and the putamen (Mitchell et al., 2011a). We found that activity is associated with increases in the phosphorylation state of AKT, a neuronal survival signaling cascade (Mitchell et al., 2011b). This is distinct from weight and BMI gene expression signatures in the brain (Mitchell et al., 2011c) where increases in BMI are associated with decreases in the phosphorylation of ERK1/2, another neuronal survival signaling cascade, and increases in apoptotic factors. Finally, in the caudate nucleus and putamen we find chromatin remodeling and anti-apoptotic factors associated with physical activity-associated neuroprotection (Mitchell et al., 2011a). The physical activity associated gene expression signatures in all 3 regions that we have studied (the motor cortex, caudate, and putamen) promote neuronal survival.

In exploring the exercise associated gene expression signature in the motor cortex, putamen, and hippocampus we found that the putamen shared the most similar gene expression between the regions. After GSEA we found an enrichment of genes in the motor cortex associated with complex I of the electron transport chain (**Table 4**).

These results confirm other results of changes in the electron transport chain in the brain with exercise. In general exercise increases the metabolic rate, the rate of mitochondrial respiration, the rate of oxidative phosphorylation, and oxygen flux (Meydani et al., 1993; Ji et al., 1998). In a recent study the number of mitochondria was found increased, as assessed via mtDNA, with exercise in the brain (Steiner et al., 2011). In the hippocampus of mice uncoupling protein 2 and oxygen consumption were found increased with voluntary exercise (Dietrich et al., 2008). In addition defects in complex I, III, and IV proteins are associated with exercise intolerance (DiMauro, 1999). Some of the best evidence comes from a study using mice running on treadmills. Exercise prevented the decrease in antioxidant enzyme activities (Mn, Cu, and ZN superoxide dismutase and catalase), prevented the decrease in complex III and IV in the brain (Navarro et al., 2004).

These results have implications for aging and disease. Generally there are higher levels of superoxides and progressive oxidative damage with aging (Maklashina et al., 2003), longer lifespans correlate with low reactive oxygen species production by the mitochondria (Perez-Campo et al., 1998), and decreased complex I and IV activity is associated with aging (Bowling et al., 1993; Navarro et al., 2002). Complex I defects may have a role in the etiology of Parkinson’s disease. Though the exact etiology of Parkinson’s disease is unknown, there an increase in peroxides produced by the complex I and decreased proteasome activity may lead to Parkinson’s disease (Chou et al., 2010). In Parkinson’s disease patient cell lines there is increased proton leakage in complex I

(Esteves et al., 2010), and complex I is inhibited by toxins used to create Parkinson's disease lesions in animal models (Betarbet et al., 2002).

Although we did not find neuroprotection by exercise (only by activity level) in our MPTP model of Parkinson's disease in rhesus monkeys (Mitchell et al., 2011a), our data supports the idea that exercise is also important in upregulating transcripts that combat Parkinson's disease in the putamen. This supports the idea that exercise contributes the physical activity in a way that is neuroprotective. This leads us to the belief that exercise is important in promoting brain resiliency to protect the brain against Parkinson's disease and other neurodegenerative diseases.

CHAPTER VI

Physical Activity Protects the Striatum Against MPTP Damage in Nonhuman Primates

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Submitted for publication (Mitchell et al., 2011a)

INTRODUCTION

Studies in rodents have shown that several forms of exercise (wheel-running, treadmill running, and forced use by casting the opposite forelimb) can lead to plastic changes in the brain including angiogenesis, neurogenesis, synaptogenesis, and increased tissue concentrations of trophic factors (Neeper et al., 1996; Cotman and Berchtold, 2002; Kleim et al., 2003; Klintsova et al., 2004). Moreover, in rodents exercise can prevent or significantly mitigate the destruction of nigrostriatal dopamine (DA) neurons and the development of PD symptoms that occurs after exposure to the DA neurotoxins 6-hydroxydopamine (6-OHDA) or 1,2,3,6-methyl-phenyl-tetrahydropyridine (MPTP) (Tillerson et al., 2001; Fisher et al., 2004; Faherty et al., 2005). Interestingly, however, housing animals in an enriched environment with other animals and toys can also decrease damage after DA neurotoxin exposure (Faherty et al., 2005; Urakawa et al., 2007). Since an enriched environment is well known to be associated with increase motor activity, these findings suggest that increasing activity, rather than aerobic exercise *per se*, may lead to neuroprotection of DA neurons.

Increased overall physical activity that does not involve aerobic exercise has been associated with numerous health benefits in humans. An increased level of activity has been correlated with overall better health in older adults, including less risk of arteriosclerosis, hypertension, and hyperglycemia (Kuller et al., 2006; Aoyagi and Shephard, 2009). Physical activity is also positively correlated with a reduced level of metabolic risk factors (Riechman et al., 2002; (Healy et al., 2008; Sisson et al., 2010), a reduced fatty liver index, associated with increased insulin sensitivity and decreased coronary heart disease risk (Gastaldelli et al., 2009), and higher plasma levels of adenopectin (Jurimae et al., 2010), which protects against metabolic diseases in middle- and older-aged adults (Dekker et al., 2008; Fretts et al., 2009). In addition, higher levels of physical activity are associated with a lower risk of osteoporosis (Aoyagi and Shephard, 2009) and gall bladder disease (Kriska et al., 2007).

Given the numerous health benefits provided by increased levels of physical activity in humans, we sought to determine whether objectively measured activity is associated with neuroprotection of DA neurons in a primate model of PD, the MPTP-treated rhesus monkey. A broad range of physical activity levels was studied by taking advantage of stable individual differences in monkeys' daily levels of physical activity (Sullivan et al., 2006; Hunnell et al., 2007; Papailiou et al., 2008), as well as by having some monkeys undertake planned exercise regimens five days a week, which we have previously shown increases an individual monkey's daily activity by two- to four-fold (Sullivan and Cameron, 2010). Furthermore, as neuroprotection by activity and planned exercise is known to be associated with strong transcriptome profile changes (Lazarov et al., 2005), we analyzed the mRNA expression of the caudate and putamen and correlated it with activity and the functional PET measurements of DA system sparing.

METHODS

Animals

Nine female rhesus macaques (Macaca mulatta), aged 14-20 years (mean±SE: 16.44±0.74 years) were housed in social living pens (4m x 4m x 4.7m) that had multiple perches, toys, and a thick layer of sawdust bedding. This housing facility has 20 pens in a wing, such that monkeys in each pen could see and hear other monkeys in a number of other pens. Six monkeys were of Chinese origin (sedentary: n=2; running: n=4) and three were of Indian origin (sedentary: n=1; running: n=2). All monkeys were housed with at least one other monkey. Monkeys were fed Purina Monkey Chow (#5038; Ralston Purina Co., St. Louis, MO) once daily and given fruit, vegetables, nuts and seeds to encourage foraging, as well as *ad libitum* access to drinking water. All monkeys were observed daily for health and menstrual status. All procedures were performed in accordance with the NIH Guide for the Care and Use of Laboratory Animals and were approved by the University of Pittsburgh Institutional Animal Care and Use Committee.

Experimental Design

Monkeys were studied in groups of three: one sedentary monkey, one monkey running at 60% of maximal aerobic capacity, and one running at 80% of maximal aerobic capacity. Prior to MPTP administration, monkeys were studied for a 3-month period, during which the runners ran and sedentary animals sat on a treadmill 5 days/week. All monkeys then received a right intracarotid injection of MPTP-HCl (0.8 mg; Sigma Chemical Co., St. Louis MO), at a concentration of 0.2 mg/mL, delivered at 1mL/min) using previously published techniques (Ovadia et al., 1995; Gash et al., 1996; Grondin et al., 2002). After surgery animals were allowed to recover in quarantine for 4 days to allow for excretion of MPTP.

Activity Monitoring

Activity was measured in each animal using an omnidirectional Actical accelerometer (Respironics, Phoenix, AZ) mounted on a loose-fitting collar (Primate Products, Immokalee, FL), and using previously published methods (Sullivan et al., 2006; Sullivan and Cameron, 2010; Papailiou et al., 2008). Activity counts per minute were recorded. Each group of three animals studied together was chosen so that they were 'activity-matched' prior to the initiation of exercise training. Baseline activity was measured for 7 days prior to the experimental period, and activity during the experimental period was measured for 8-12 weeks prior to MPTP administration. Activity is presented as mean daily activity.

Exercise Training

Monkeys were trained to run a on a human size treadmill (Model 910e, Precor, Inc., Bothell, WA) using procedures developed and previously published by this laboratory (Williams et al., 2007; Williams et al., 2001b; Williams et al., 2001a; Cameron et al., 2010; Rhyu et al., 2010). Briefly, runners were adapted to the treadmill by first sitting on it, then learning to walk at a slow pace, and then increasing the speed and duration of running until they were running 1 hour/day, 5 days/week, at a target speed. Target speed was determined from a maximal exercise test performed after animals had learned to walk on the treadmill, and was set at a speed equivalent to either 60% or 80% of maximal aerobic power. A second maximal exercise test was performed at week 6 of the study and running speed adjusted, so that animals continued to train at 60% or 80% of maximal aerobic power as they became more fit. Monkeys ran for 3 months prior to receiving MPTP and 7 weeks post-MPTP. Sedentary monkeys sat on a treadmill and watched the runners each day.

Monkey Motor Assessment Panel (mMAP) testing

The mMAP is a reward-based test panel that reliably detects subtle improvements or declines in fine motor function by measuring performance time in milliseconds for a monkey to use its hands to retrieve a small food treat from a receptacle chamber attached to a testing cage (Gash et al., 1999; Zhang et al., 2000; Grondin et al., 2000; Grondin et al., 2003). Beginning 4 weeks prior to MPTP exposure, monkeys were placed in a testing cage in a behavioral testing room and adapted to the test apparatus for 10-15 minute periods for 5-6 days. When the animals were routinely retrieving food from the food receptacle with each hand, active testing began. Each monkey was then tested 5 days/week for four weeks pre-MPTP to obtain baseline data. Each testing session consisted of 12 trials, 6 on each side, alternating between the right and left hand. Three tests of increasing difficulty were evaluated: the platform test (Level I), the straight rod test (Level II), and the straight rod placed at a distance test (Level III). Both fine motor performance (i.e., the time the hand was in the receptacle picking up the food reward) and coarse motor performance (i.e., the time for the upper limb to move from the armhole portal to the food receptacle portal and then back from the receptacle portal into the cage, or total time) were recorded. Fine motor performance and total time to complete the task were used for analysis.

PET Imaging

At 6 weeks post-MPTP, all monkeys received positron emission tomography (PET) scans using [^{11}C]dihydrotetrabenazine (DTBZ), which binds to vesicular monoamine transporter (VMAT2) receptors, as a ligand. This radioligand was selected for its high specificity for VMAT2 receptors, and because it is not sensitive to pharmaceutical treatments for PD such as L-DOPA; thus findings in the monkey could be more easily translated to clinical studies. Monkeys were transported to the University of Pittsburgh PET imaging facility, anaesthetized with 10mg/kg IM ketamine hydrochloride (Ketaject, Phoenix Pharmaceuticals Inc., St. Louis, MO), and placed under isofluorane anaesthesia (0.5 - 2.0% minimum alveolar concentration) for the duration of the 90-

minute PET scan. Each animal's body temperature was maintained at a constant 37°C using a recirculating hot water blanket (Gaymar Industries, Inc., Orchard Park, NY) controlled by a rectal temperature probe. A catheter was placed in a saphenous vein for the injection of the radiotracer and administration of isotonic saline for hydration. Vital signs were monitored continuously throughout the experiment. PET imaging was performed on a microPET P4 scanner (Siemens Molecular Imaging, Knoxville TN), according to previously published procedures (Lopresti et al., 2008). The outcome measure was binding potential, which is a unitless measure of radiotracer specific binding that is directly proportional to the ratio of $B_{max,}$ of the free receptor pool, to K_D, the ligand dissociation constant. Binding potential values (B_{max}/K_D) were computed on a voxel-by-voxel basis to generate maps [^{11}C]DTBZ-specific binding, and B_{max}/K_D values were used for analysis.

Tissue Collection

At 7 weeks post-MPTP, subjects were sedated with 10 mg/kg IM ketamine HCl and deeply anesthetized with sodium pentobarbital (30 mg/kg, i.v.; Nembutal, Abbott Laboratories, North Chicago, IL). The carotid arteries were severed, and animals were exsanguinated. The brains were rapidly removed from the skull, immediately placed in ice-cold RNAse-free saline, and then quickly transferred into a custom-made macaque brain mold (Bioanalytical Systems Inc., West Lafayette, IN). The brain was sectioned rostral to caudal every 4 mm using the guides in the mold for placement of blades. Fresh sections were laid flat on glass slides, brain regions of interest were harvested (i.e., punches of caudate and putamen), and the punches and remaining tissue were snap frozen on dry ice and stored at –80ºC.

Biochemical analysis

Tyrosine hydroxylase protein levels in the caudate and putamen were measured by Western Blot analysis, using minor modifications of previous techniques (Leak et al., 2008). Modifications include sonicating monkey tissue in 0.1% sodium dodecyl sulfate (BioRad, Philadelphia PA) in 1x lysis buffer (Cell Signaling Technologies, Danvers, MA) with a protease inhibitor cocktail (Sigma-Aldrich, St. Louis, MO) in 20 volumes of liquid per mg wet tissue weight. After immunoblotting, membranes were visualized on an Odyssey Imager with infrared secondary antibodies (Li-Cor, Lincoln, NE), which were used to bind mouse anti-TH (Millipore, Billerica, MA) and anti-β-actin primary antibodies (mouse monoclonal; Sigma Aldrich). TH is expressed over actin, to control for minor differences in protein loading.

Transcriptome profiling

Expression profiling was performed on four (two for caudate nucleus and two for putamen) independently harvested and analyzed samples from each monkey. Tissue samples were dissected from each animal from frozen coronal blocks using anatomical landmarks, homogenized, and total RNA was isolated using TRIzol® reagent (Invitrogen, Carlsbad, CA) with RNA quality assessed via analysis on an Agilent 2100

Bioanalyzer. Only samples with an RIN > 7.0 were considered for further analysis. The samples were prepared with 2 μg of total RNA using the Enzo BioArray™ Single-Round RNA Amplification and Biotin Labeling System. Purified and fragmented aRNA samples were hybridized to 2 Affymetrix HU133 GeneTitan 24-array plates. Image segmentation analysis and generation of DAT files was performed using Microarray Suite 5.0 (MAS5). Segmented images were normalized and log2 transformed using robust multi-array analysis (RMA) (Sabatini et al., 2007). We obtained RMA normalized data from two pieces of caudate for each animal. The averaged RMA normalized log2 expression levels for each animal were utilized for all of our subsequent analyses.

Statistical Analysis

Linear regression models were used to determine whether mean daily activity counts during exercise training predicted 1) [^{11}C]DTBZ binding to VMAT2 receptors in the caudate and putamen, as well as in the striatum (caudate + putamen), and 2) the TH/β-actin ratio in each of these regions. For each of these measures, the sides of the brain ipsilateral (i.e. the right side) and contralateral (i.e. the left side) the side of the MPTP injection, were examined separately. Activity data during the experimental period was not available for one monkey, and preliminary analysis revealed that a second monkey's mean daily pre-MPTP activity was 2.6 standard deviations greater than the group mean, and significantly higher than any other monkey we have ever recorded activity for, so both were excluded from analyses. The rhesus monkeys used in this study were of both Indian origin (n=3) and Chinese origin (n=6). To determine whether differences in origin influenced each outcome, independent-samples t-tests were employed. Independent-samples t-tests were also used to analyze the mMAP data, with the total duration to complete the task for each hand as the outcome (left vs. right, as MPTP administration to the right side of the brain would be expected to affect left-side motor function). An alpha level of 0.05 was considered statistically significant, and SPSS software (PASW Version 18, Chicago, IL) was used for all analyses.

To examine correlations with the gene expression profile, first, we performed a data reduction step by correlating the replicate harvests R1c and R1c for the caudate nucleus, and R1p and R2p for the putamen across the 8 monkeys used in analyses (**Figure 18**). Only probe sets with a correlation $r > 0.70$ were considered for further data analysis. Next, we correlated RMA normalized log2 gene expression values from each replicate separately with activity, percent loss [^{11}C]DTBZ binding potential (PET) from the affected hemisphere versus the nonaffected hemisphere, and percent loss tyrosine hydroxylase (TH) levels from the affected hemisphere versus the nonaffected hemisphere. In this step, a gene was significantly changed if it showed a correlation in both replicates greater that 0.60 or less than -0.60 ($r>0.6$ or $r<-0.6$). This analysis was separately performed for activity, percent loss [^{11}C]DTBZ binding potential, and percent loss of tyrosine hydroxylase levels. In the final step we queried the data for overlap between the activity, percent loss of [^{11}C]DTBZ binding compared to the nonaffected hemisphere, and percent loss of TH compared to the unlesioned side, identifying the gene expressions changes that best explained DA terminal sparing by the three functional measurements.

Additionally, we profiled the putamen of the nonlesioned hemisphere for three monkeys (one from each group) using DNA microarrays, and compared it to the lesioned hemisphere for each monkey. We used a paired t-test to find differentially expressed genes associated with the lesion with a $p<0.05$ and an average log ratio (ALR) greater than 0.3785, representing a 30% change in expression. Hierarchical clustering was performed using GenePattern software (Subramanian et al., 2005) using log2 transformed RMA normalized expression levels.

RESULTS

Mean daily activity counts significantly predicted the amount of $[^{11}C]$DTBZ binding to VMAT2 receptors in the striatum ipsilateral to MPTP injection, such that monkeys that were more active prior to MPTP exhibited greater binding potentials (striatum: $r^2=0.636$, $p=0.032$; **Figures 14, 15a**). Greater activity also predicted $[^{11}C]$DTBZ binding in the ipsilateral putamen ($r^2=0.698$, $p=0.019$), with a trend toward predicting $[^{11}C]$DTBZ binding in the ipsilateral caudate ($r^2=0.511$, $p=0.07$). Mean daily activity also predicted the percent loss of $[^{11}C]$DTBZ binding in the putamen with reference to the side contralateral to the MPTP injection ($r^2=0.713$, $p=0.017$).

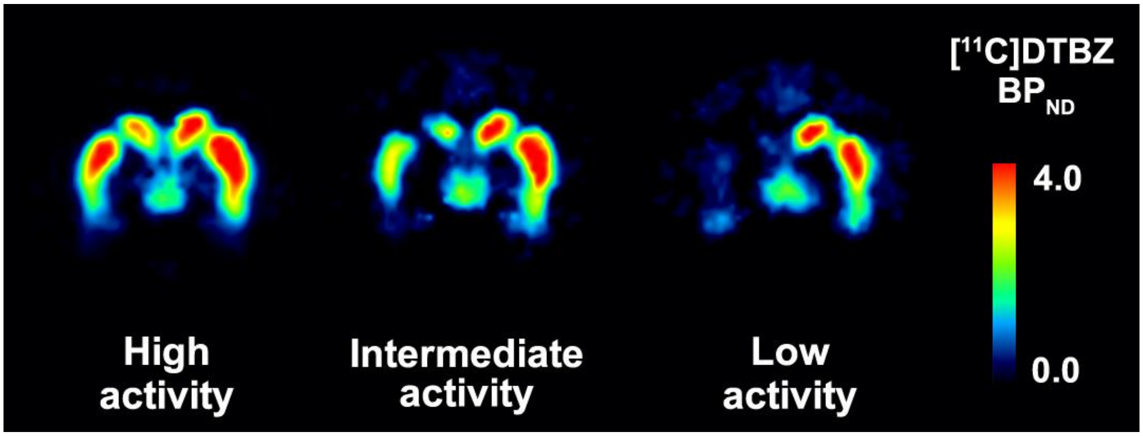

Figure 14. Parametric PET image of [^{11}C] DTBZ binding in a monkey with high (left), intermediate (middle), and low daily activity (right). Distribution Volume Ratio (DVR) is shown rather than binding potential for anatomical reference. Given the same unilateral intracarotid dose of MPTP there was less damage to the ipsilateral striatum in more active animals.

Mean daily activity also significantly predicted TH in the ipsilateral striatum, putamen and caudate (striatum: r^2=0.760, p=0.011; putamen: r^2=0.833, p=0.004; caudate: r^2=0.625, p=0.034; Figure 15b). Further, mean daily activity predicted the percent loss of TH in the striatum and putamen with reference to the side contralateral to the MPTP injection (striatum: r^2=0.572, p=0.05; putamen: r^2=0.682, p=0.022).

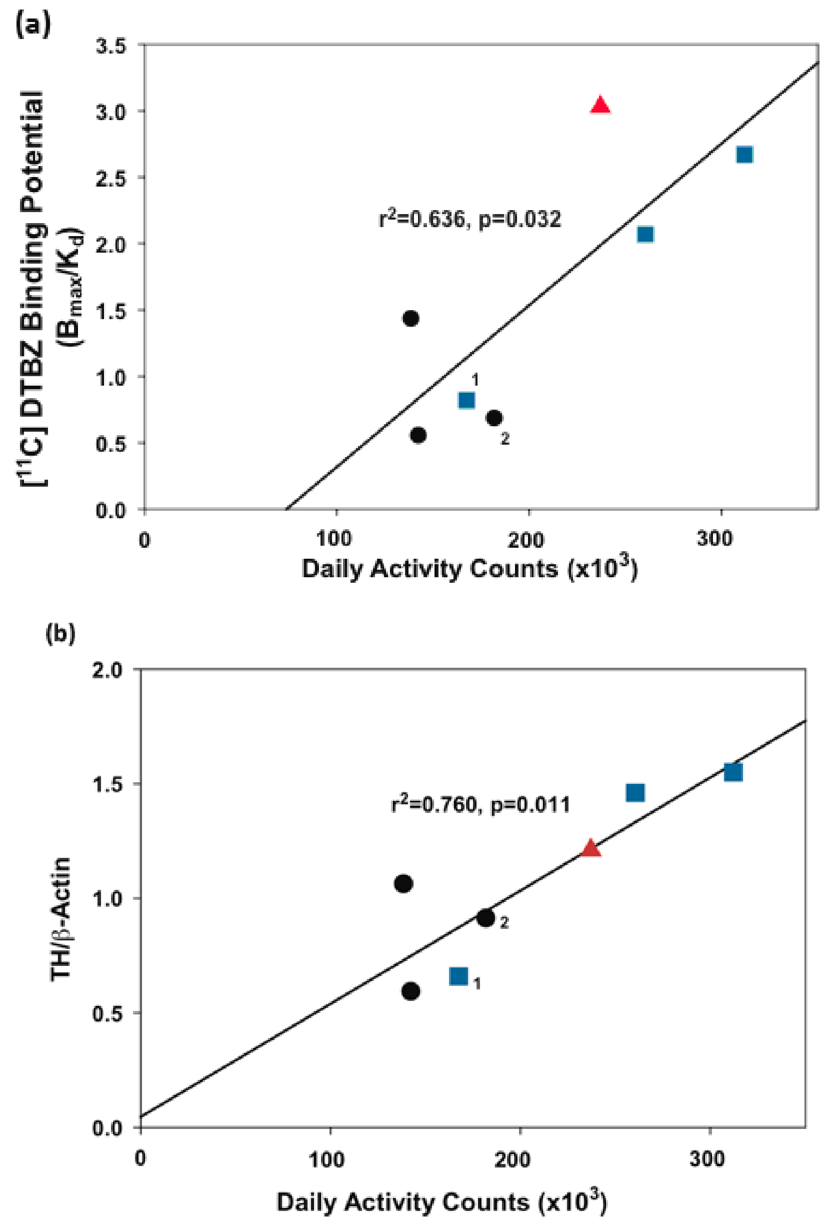

Figure 15. Regression analysis of PET scan data showing (a) average daily level of physical activity vs. [^{11}C] DTBZ binding potential in the striatum and (b) average daily level of physical activity vs. tyrosine hydroxylase/β-actin levels in the striatum. Black circles represent sedentary monkeys, blue squares represent monkeys that ran at 60% maximal heart rate 5 days/week and the red triangle represents a monkey that ran at 80% maximal heart rate 5 days/week. The numbers 1 and 2 indicate monkeys whose 24-hour actigrams are depicted in Figure 17.

Interestingly, we found the rhesus monkeys of Indian origin showed a significantly higher percent loss of TH compared rhesus monkeys of Chinese origin ($t_{(7)}$=2.67; p=0.03; 71.74$\pm$1.73% vs. 38.04$\pm$8.58%; **Figure 16a**). As shown in **Figure**

16b, the sedentary Indian monkey did not use her left hand (the hand affected by MPTP) at anytime after MPTP administration to complete any stage of testing, while she relied on her right hand for both the platform and straight rod near tasks and, as would be expected, performed slightly better with her right hand as testing progressed. In contrast, the 60% runner used both hands similarly for the platform task ($t_{(10)}$=0.68, p=0.51) and while she used both hands for the straight rod near task, she was significantly faster with her right hand (control) than her left hand (MPTP) throughout testing on this task ($t_{(10)}$=-2.27, p=0.03). Most strikingly, the 80% runner used both hands equally well on both the platform and straight rod near task, and was the only monkey to perform the straight rod far task where again she used both hands equally well (p>0.10 for all tasks). Thus it appears that the 60% runner was able to use the hand affected by MPTP moderately well in tests of fine motor skills, while the 80% runner showed no loss of fine motor function. Physiological parameters that we measured did not differ significantly between Chinese and Indian rhesus monkeys, including weight (Chinese: 6.43±0.47, Indian: 7.05±0.37, p=0.33) and mean daily activity (Chinese: 226,140±30,188, Indian: 155,100±12,379, p=0.22).

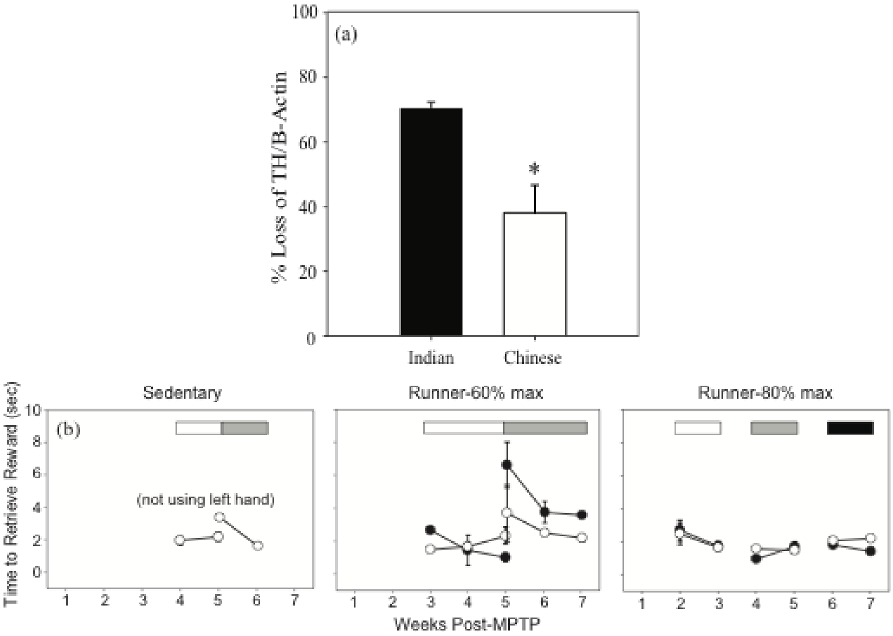

Figure 16. **Monkey Origin and mMAP testing**. (a) Percent loss of tyrosine hydroxylase/β-actin levels in the ipsilateral putamen, with reference to the contralateral putamen, seven weeks after a unilateral intracarotid injection of MPTP. Asterisk indicates a significant difference, $p<0.05$, between monkeys of Indian origin (n=3) compared to monkeys of Chinese origin (n=6). (b) Time to retrieve a lifesaver on a platform (open bars), on a straight-rod place close (grey bars) or on a straight-rod placed at a distance (black bar), with the left hand (closed circles) and right hand (open circles) for the three Indian origin monkeys. Asterisks represent a significant difference in time to retrieve the lifesaver with the right vs. left hand.

Examination of patterns of activity of individual monkeys revealed that there were two patterns of activity that were evident in these monkeys. Monkeys that were exercising an hour a day showed an increased level of activity during the hour of exercise (see **Figure 17**, left panel). In contrast, some monkeys have relatively high levels of mean daily activity and these monkeys tended to show consistent patterns of higher activity throughout the 12-hour light period (see **Figure 17**, right panel). Thus, it was possible for two monkeys with very similar daily mean activity levels (Monkeys 1 and 2; **Figures 15A** and **15B**) to have very different patterns of daily activity (**Figure 17**, left panel vs. right panel).

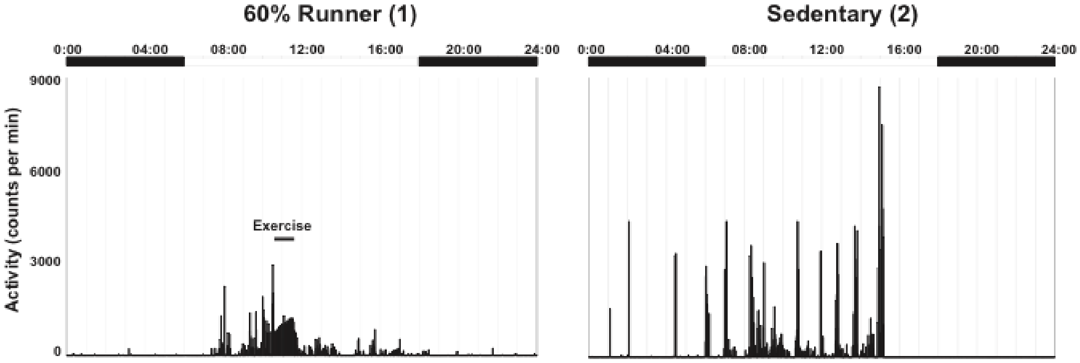

Figure 17. Twenty-four hour actigrams of activity across a 24-hour day for two monkeys identified in Fig. 14a and 14b, which had similar mean daily levels of activity and neuroprotection as indicated by both [^{11}C] DTBZ binding and TH levels. Monkey 1 was a runner who was extremely inactive most of the day, except when exercising. Monkey 2 was a sedentary monkey who showed naturally occurring bouts of substantial activity over the course of a normal day. Black bars at the top of the actigrams indicate periods of lights off; light bars indicate periods of lights on.

A comparable gene expression profile (r>0.70) was seen in 5359 transcripts between the two caudate samples (R1c and R2c), and in 2831 transcripts between the two putamen samples (R1p and R2p) (**Figure 18).** These transcripts were correlated subsequently with monkey activity values, independently for both structures. Seventy-nine transcripts were correlated (r>0.60) with activity in both R1c and R2c caudate samples (34 positively correlated and 45 negative correlated) (**Supplementary Table 10**) and two-hundred fifty seven transcripts were correlated (r>0.60) with activity in both R1p and R2p putamen samples (166 positively correlated and 91 negatively correlated) (**Supplementary Table 11).** When subjected to a two-way hierarchical clustering, both the caudate and putamen samples showed a nice progression of gene expression levels from monkeys with low activity to monkeys to high activity (**Figures 19 and 20**). Interestingly, the activity associated gene expression profiles of the caudate and putamen were quite distinct, with only two genes (vomeronasal 1 receptor 4 and transducin (beta)-like 1 X-linked receptor) overlapping across the two structures.

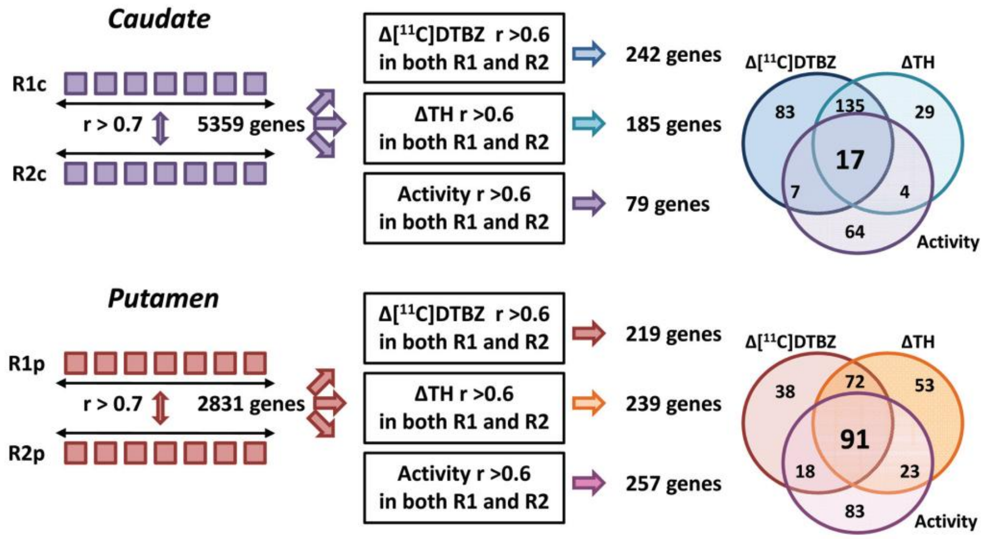

Figure 18. Identifying neuroprotection-associated transcripts in the caudate nucleus and putamen. Gene expression was assessed by two independent, adjacent dissections of caudate nucleus (R1c and R2c) and putamen (R1p and R2p) on the Affymetrix GeneTitan 24-array plate platform. In the caudate 5359 transcripts showed a dataset correlation of r>0.7 between R1c and R2c, while in the putamen 2831 transcripts showed a dataset correlation of r>0.7 between R1p and R2p. These data were subjected to subsequent analysis, where we identified transcripts that were correlated (r>0.6 or r<-0.6) with percent loss of [^{11}C]DTBZ binding, tyrosine hydroxylase levels, and with mean total activity counts (counts/day) in both caudate (R1c and R2c) and both putamen (R1p and R2p) samples. There were 17 overlapping transcripts associated with all 3 measurements in the caudate, and 91 overlapping transcripts associated with all 3 measurements in the putamen.

In both brain regions we identified several genes that target chromatin (DPF3, MDB3L1, SRCAP, TBLR1) (Lange et al., 2008; Zeng et al., 2010; Wong et al., 2007; Jiang et al., 2004; Slupianek et al., 2010; Zhang et al., 2006; Yoon et al., 2005), a few genes previously associated with neuronal survival and apoptosis (CAPN6, NEUROG3, and NTRK3) (Rho et al., 2008; Huang and Wang, 2001; Lee et al., 2003; Nikoletopoulou et al., 2010), two genes with critical functions at the synapse (STX3 and UHRF1BP1L) (Martin-Martin et al., 1999; Binda et al., 2008; Beckman et al., 1998; Haase et al., 2001; Lee et al., 2004; Sung et al., 2003; Dipace et al., 2007; Otto et al., 2010), and two members of the leucine rich repeat family (LRRC27 and LRRC40) (Matsushima et al., 2009; Smith et al., 2005; Lee et al., 2010). All of these genes, in concert, could be considered as potential mediators of activity associated neuroprotection, and deserve a more detailed follow-up in future studies.

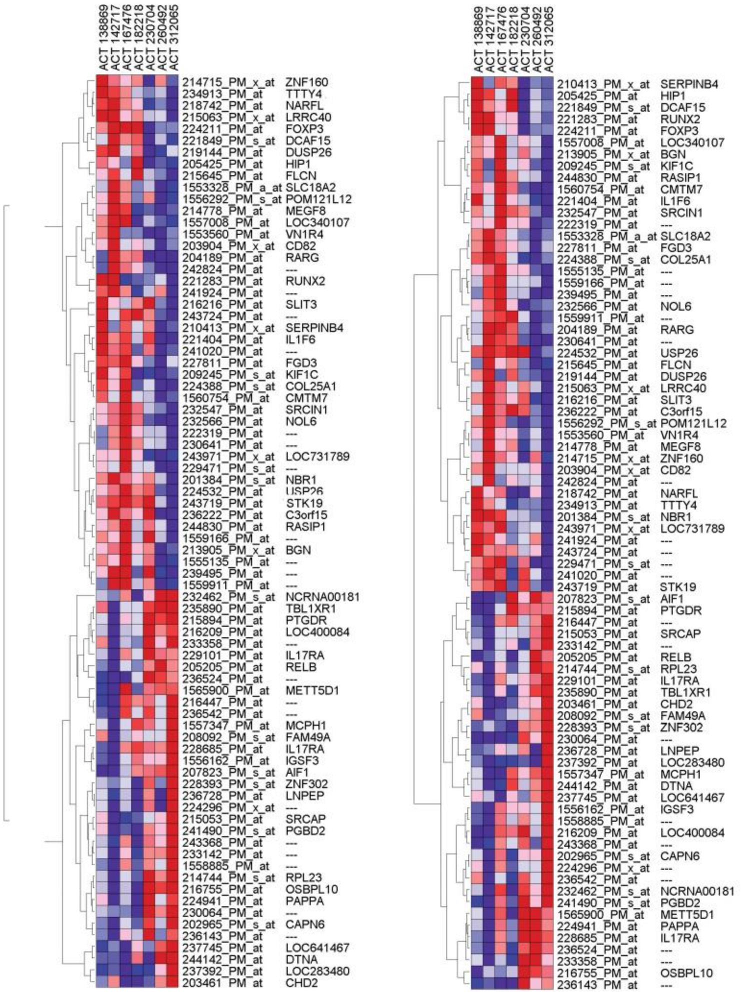

Figure 19. Hierarchal clustering of transcripts associated with mean total activity in the caudate nucleus. One-way hierarchical clustering was performed on the log2-transformed expression levels of caudate (R1c and R2c) replicate transcripts associated with mean total activity. Genes, denoted by their Affymetrix Human Probe Set ID and NCBI gene symbol, were clustered horizontally. Monkeys are identified by their mean total activity. Each colored square represents a normalized gene expression value with color intensity proportional to the level of expression (blue indicates lower expression and red indicates increased mRNA levels). Note the progression of gene expression levels from monkeys with low mean total activity to monkeys with high mean total activity in both caudate replicates.

In the next step we hypothesized that expression of the most critical neuroprotection genes would be correlated with all three of our functional measurements:

activity levels, *in vivo* [^{11}C]DTBZ binding, and TH levels. To test this hypothesis we performed a correlational analysis between all three measurements (**Figure 18**) and gene expression in the caudate and putamen samples. In the caudate we identified 79 activity, 242 [^{11}C]DTBZ binding, and 185 TH correlated transcripts that were present in both R1c and R2c samples.

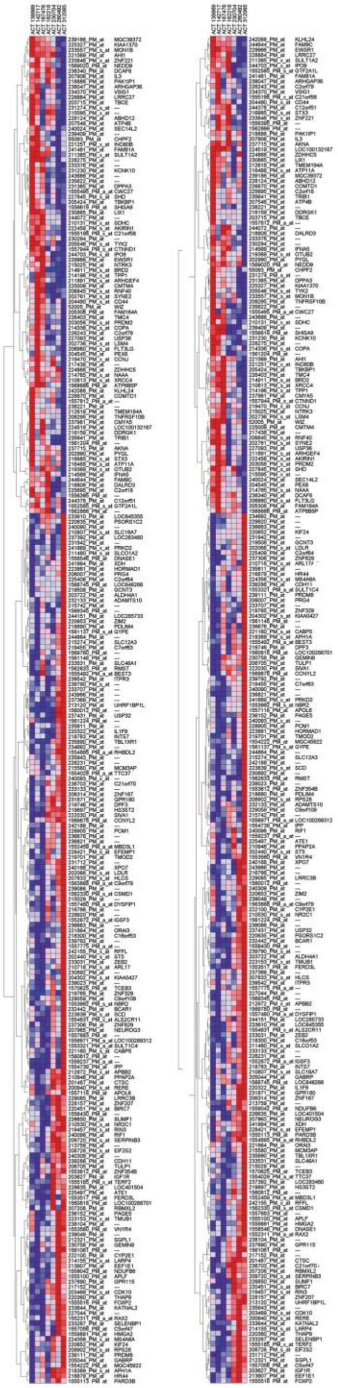

Figure 20. Hierarchal clustering of transcripts associated with mean total activity in the putamen. One-way hierarchical clustering was performed on the log2-transformed expression levels of putamen (R1p and R2p) replicate transcripts associated with mean total activity. Genes, denoted by their Affymetrix Human Probe Set ID and NCBI gene symbol, were clustered horizontally. Monkeys are identified by their mean total activity. Each colored square represents a normalized gene expression value with color intensity proportional to the level of expression (blue indicates lower expression and red indicates increased mRNA levels). Note the progression of gene expression levels from monkeys with low mean total activity to monkeys with high mean total activity in both putamen replicates.

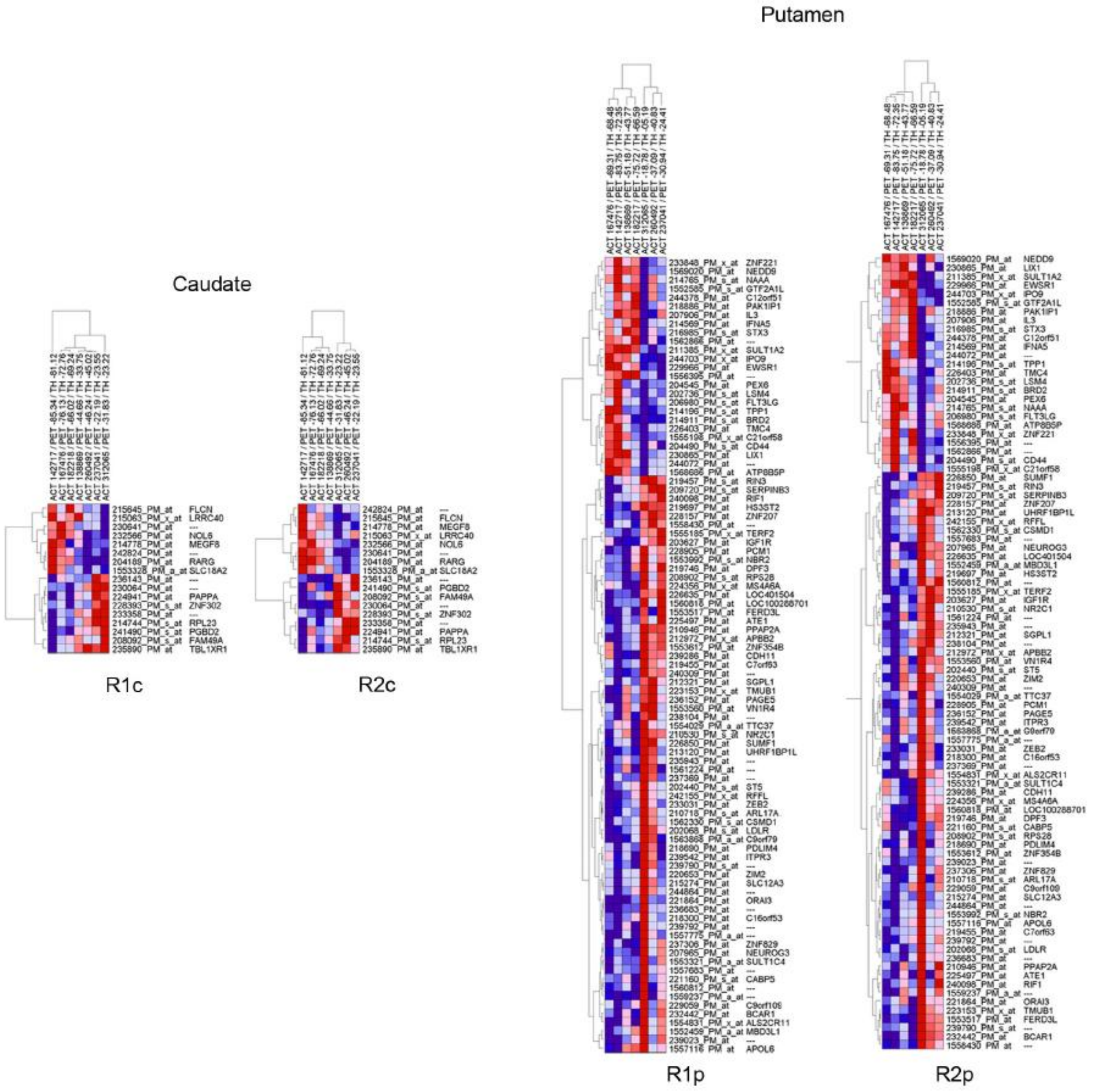

Figure 21. Hierarchal clustering of transcripts associated with mean total activity, percent loss [^{11}C]DTBZ binding, and percent loss TH in the caudate nucleus and putamen. Two-way hierarchical clustering was performed on log2-transformed expression levels on the caudate (R1c and R2c) and putamen (R1p and R2p) replicate samples. Genes, denoted by their Affymetrix Human Probe Set ID and NCBI gene symbol, were clustered horizontally, and monkey samples were clustered vertically. Monkey identifiers denote mean total activity, percent loss [^{11}C]DTBZ binding, and percent TH loss. Each colored square represents a normalized gene expression value with color intensity proportional to the level of expression (blue indicates lower expression and red indicated higher mRNA levels). Note the progression of gene expression levels correlate with mean total activity, percent loss [^{11}C]DTBZ binding, and percent loss TH in both the caudate and putamen replicates.

Of these 17 genes we identified as correlated with all three functional readouts (activity, [^{11}C]DTBZ binding, and TH levels), with 9 showing positive and 8 showing negative correlation (**Supplementary Table 12**). In the putamen, we identified 257 activity, 219 [^{11}C]DTBZ binding, and 239 TH correlated transcripts that were present in both R1p and R2p samples. Of these we identified 91 transcripts as correlated with all three functional readouts (activity levels, [^{11}C]DTBZ binding, and TH levels) with 66 showing a positive correlation and 25 transcripts showing a negative correlation (**Supplementary Table 13**). When these common expression changes were subjected to a two-way hierarchical clustering, both the caudate and putamen samples showed a nice progression of expression levels with all three functional measurements (**Figure 21**). The putamen-correlated expression changes were more numerous than those in the caudate, and this is probably a result of a differential connectivity and distinct effects of MPTP on these two structures. Transcripts associated with all three measurements included LRRC40 and TBL1XR1 in the caudate, and DPF3, MBD3L1, NEUROG3, STX3, UHRF1BP1L, and VN1R4 in the putamen. It is highly unlikely, however, that any single gene alone was responsible for the observed neuroprotection; rather, this pattern is indicative of a collaborative transcript network responsible for the sparing of the DA terminals.

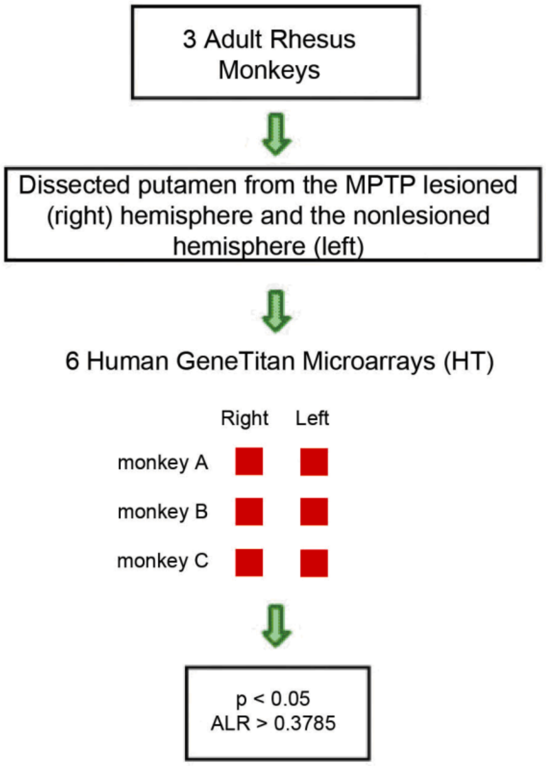

Figure 22. Identifying Differentially Expressed Between the Lesioned and Nonlesioned Putamen. We dissected both the right and left putamen from one monkey from each group (sedentary, 60% runners, and 80% runners) and analyzed gene expression via DNA microarray. Significant differentially expressed transcripts had a $p < 0.05$ and an ALR > 0.3785 (a 30% change).

In addition, we also looked at genes associated with the lesioned hemisphere by assessing significantly differentially expressed transcripts between the lesioned right putamen and the nonlesioned left putamen (**Figure 22)**. We found 384 differentially express transcripts (199 decreasing with the lesion and 185 increasing with the lesion) between the lesioned and nonlesioned hemispheres. We found a gene involved in repair decreased, ataxia telangiectasia and Rad3 related (ATR), a gene involved in apoptosis increased (CASP9), increases in some neurotrophic factor signaling genes (FGF2 and eukaryotic translation initiation factor 4E (EIF4E)), and specifically an increase in syntaxin 3 (**Figure 23** and **Supplementary Table 14**). This supports the idea that some compensatory mechanisms (axon sprouting) promote survival of neurons after a lesion

(Greenough and Volkmar, 1973). These mechanisms include an increase in dopamine release and a decrease in dopamine uptake (Connor and Diamond, 1982; Zigmond et al., 1992; Abercrombie et al., 1990; Snyder et al., 1990). They also confirm the MPTP lesion (decreased in ATR and an increase in CASP9).

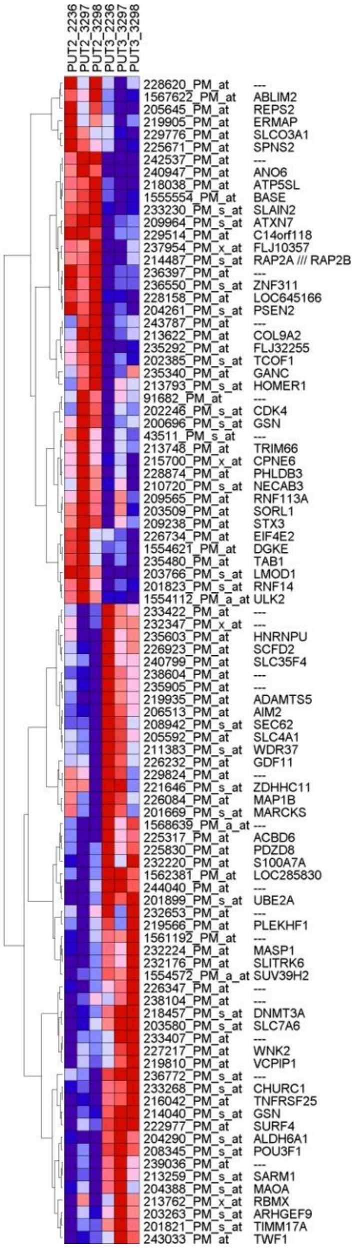

Figure 23. Putamen Transcripts Differentially Expressed Between the Lesioned and Nonlesioned Hemispheres. We found 384 differentially express transcripts (199 decreasing with the lesion and 185 increasing with the lesion) between the lesioned and nonlesioned hemispheres.

DISCUSSION

By several different measures of function (i.e., [^{11}C]DTBZ binding as measured by PET scan, TH levels measured by Western blot), monkeys with higher daily levels of physical activity showed greater protection of nigrostriatal dopaminergic neurons when exposed to the dopaminergic neurotoxin, MPTP. This greater level of neuroprotection translated to greater functional protection after MPTP exposure in monkeys with higher activity levels. Although monkeys with higher levels of physical activity were those that were participating in a planned exercise program of 1 hour of running/day, 5 days/week, both naturally-occurring daily activity and planned exercise contributed to mean daily activity level (as shown in **Figure 17**), such that the monkeys that had the greatest mean daily activity levels were not those that exercised at the greatest intensity. These findings offer strong support for the concept that increased daily activity, at any intensity, is neuroprotective in primates. This is encouraging in that it suggests that maintaining an active lifestyle may protect the brain against neurodegenerative diseases (e.g., Parkinson's disease), yet be accessible to many people regardless of their baseline fitness.

Functional imaging methods, such as PET scans, have been widely applied to non-invasively assess the degree of striatal DA terminal loss in PD patients by determining the specific binding of one of several DAT or VMAT-2 radioligands, including [^{11}C]methylphenidate, [^{11}C]beta-CFT, [^{123}I]beta-CIT, and [^{11}C]DTBZ (Leenders et al., 1986; Brooks et al., 1990; Morrish et al., 1998; Innis et al., 1991; Frost et al., 1993; Guttman et al., 1997; Rinne et al., 1999a; Rinne et al., 1999b). PET assessment of DA terminal degeneration has been shown to correlate with disease stage as well as the severity of bradykinesia and rigidity (Seibyl et al., 1995; Brucke et al., 1997). VMAT-2 is a membrane bound protein found in monoaminergic neurons that translocates monoamines that are either newly synthesized or taken back up via DAT (or other monoaminergic transporters) from the cytosol into synaptic storage vesicles (Schuldiner, 1994). While VMAT-2 transporters are not selective for any one monoamine, more than 95% of VMAT-2 sites in the striatum are associated with the dopaminergic nigrostriatal projection (Vander Borght et al., 1995; Wilson and Kish, 1996). PET and SPECT radioligands developed for imaging VMAT-2 non-invasively are all structural analogs of the potent and selective inhibitor of VMAT-2, tetrabenazine (TBZ) (Efange, 2000). In this study we used a-[^{11}C]dihydrotetrabenazine (DTBZ), a metabolite of TBZ, as a PET imaging agent for VMAT-2. In vitro investigations of [^{3}H]DTBZ demonstrated specific binding to VMAT-2 and low non-specific binding. In postmortem human brain tissue, [^{3}H]DTBZ demonstrated binding to a single high-affinity site (Kd = 7 nM), and the distribution of binding sites was consistent with the distribution of TH immunoreactivity (Thibaut et al., 1995). Likewise, we have found in monkeys that striatal binding of [^{11}C]DTBZ correlates strongly with TH quantified by Western blot (Lopresti et al., 2008). VMAT-2 immunochemistry has shown significant reductions (70-88%) in the caudate and putamen of PD subjects (Miller et al., 1999). Similar reductions in the striatal binding of [^{11}C]DTBZ have been demonstrated in vivo using PET in PD patients (Bohnen et al., 1999; Bohnen et al., 2006; Frey et al., 1996) and in primate models of PD (Doudet et al., 2006). Thus, our finding in this study that monkeys with higher levels of physical activity showed increased [^{11}C]DTBZ binding in the striatum after MPTP lesions is a strong indication that there was less damage to striatal DA neurons in these monkeys.

Experimentally induced striatal DA depletion in animals has proven to be a useful approach for studying many motor aspects of parkinsonism (Blum et al., 2001; Oiwa et al., 2003). In most models, one of two selective toxins is used: 6-OHDA, which acts through oxidative stress by increasing hydrogen peroxide and quinone breakdown products or 1,2,3,6-methyl-phenyl-tetrahydropyridine (MPTP), which causes oxidative stress by inhibition of Complex I of the mitochondrial electron transport chain (Chassain et al., 2001; Jenner, 2003; Barcia et al., 2004). The capacity of MPTP to induce stable parkinsonism in nonhuman primates (Davis et al., 1979; Burns et al., 1983) provides the opportunity to create a primate model of PD. Moreover, the introduction by Bankiewicz and colleagues of an intra-carotid approach to the administration of MPTP in nonhuman primates (Bankiewicz et al., 1986) and its continued development by investigators of the University of Kentucky Udall Center (Ovadia et al., 1995; Gash et al., 1996; Gash et al., 2005; Grondin et al., 2002; Ai et al., 2003; Ding et al., 2008) provides a model with a highly reproducible, unilateral lesion with a quantifiable phenotype. Administration of a moderate dose of MPTP (0.8 mg) leads to a loss of TH+ cells in the substantia nigra and TH+ fiber density in the striatum (Ding et al., 2008). Using these same procedures, here we found that more active monkeys had significantly less loss of TH in the striatum, strongly supporting the conclusion that there was less damage to DA neurons in more active animals. These results support findings in the rodent that exercise or housing in an enriched environment can protect DA terminals from the effects of 6-OHDA or MPTP, as shown by measures of DA content, TH in the striatum, and counts of TH+ cells in the substantia nigra (Tillerson et al., 2002; Tillerson et al., 2001; Tillerson et al., 2003; Bezard et al., 2003; Cohen et al., 2003; Faherty et al., 2005; Anstrom et al., 2007).

Interestingly, we found that genetic origin of the rhesus monkeys in our study (Indian origin vs. Chinese origin) also influenced the degree of response to MPTP, with monkeys of Indian origin having a greater loss of DA terminals after MPTP exposure. Strain differences in nigrostriatal DA neuron response to MPTP have been previously reported in C57BL/6 mice (i.e., MPTP-sensitive) vs. Swiss-Webster (SW) MPTP-resistant mice (Hamre et al., 1999; Smeyne et al., 2007). In these two mice strains differential expression of glutathione-S-transferase (GST) π appears to play a key role in the level of MPTP sensitivity. GST π is expressed in nigrostriatal dopaminergic neurons, and is a detoxifying enzyme that inhibits JNK-activated signaling, blocking the phosphorylation of cJUN and apoptosis of the cell (Wang et al., 2001). C57BL/6 MPTP-sensitive mice show a decrease in GST π levels in nigrostriatal DA neurons after MPTP exposure, whereas SW MPTP-resilient mice show stable levels of GST π post-MPTP (Smeyne et al., 2007). In people, polymorphisms in GST π have been loosely correlated with increased risk of idiopathic PD after exposure to pesticides (Menegon et al., 1998; Kelada et al., 2003). Whether Indian origin rhesus monkeys have lower levels of GST π in nigrostriatal DA neurons is unknown at this time, but this or a similar genetic difference between Indian and Chinese origin rhesus monkeys could account for differences in MPTP toxicity. There are substantial genetic differences in rhesus monkeys of Indian vs. Chinese origin in mitochondrial DNA (Kanthaswamy and Smith, 2004; Satkoski et al., 2008), and in the nuclear genomes as demonstrated by differences in microsatellites (Smith et al., 2006), Major Histocompatability Complex (MHC) loci (Penedo et al., 2005), and SNPs (Ferguson et al., 2007; Hernandez et al., 2007). We did not find a significant difference in mean daily activity between Chinese and Indian monkeys, however, this may be because sample size was low. So it is possible that Indian rhesus monkeys may have lower activity than Chinese rhesus, and if so, that this may contribute to differences in sensitivity to MPTP.

In both humans (Hornykiewicz, 1962; Fearnley and Lees, 1991) and animals (Zigmond and Stricker, 1972) motor impairment does not occur until there is approximately a 70-80% loss of striatal dopamine, we only expected to find motor impairment in the monkeys of Indian origin in this study. And, we did find that the sedentary Indian origin animal essentially would not use her left hand for mMAP testing (as shown in **Figure 17**). However, we found that both exercising monkeys of Indian origin showed much less motor impairment compared to the sedentary animal, with the monkey running at 80% capacity showing no detectable slowness of movement of the left hand compared to the right hand. These findings strongly support a wealth of data in rats (Mabandla et al., 2004; Howells et al., 2005; Poulton and Muir, 2005; Jadavji et al., 2006; Steiner et al., 2006; O'Dell et al., 2007) and mice (Tillerson et al., 2003; Fisher et al., 2004; Petzinger et al., 2007) showing that giving animals access to exercise equipment (i.e., running wheels, treadmills), or housing them in an enriched environment that encourages an increase in physical activity (Bezard et al., 2003; Faherty et al., 2005; Petzinger et al., 2007) leads to a clear reduction in the behavioral consequences of 6-OHDA and MPTP. This also supports evidence that has been mounting over the past decade suggesting benefits of exercise in people in early and mid-stages of PD (Schenkman et al., 2008; Ellis et al., 2005) on general motor function. Our findings would in fact suggest that participation in planned exercise is not necessary but that just being more active in daily activities may slow the progression of PD.

The gene expression profiling studies also led us to several interesting conclusions. After MPTP exposure in a non-human primate model (1) there is a strong association between non-human primate activity and functional measurements of dopamine system sparing ([^{11}C]DTBZ binding and TH levels), and gene expression in the caudate and putamen; (2) caudate and putamen gene expression patterns are distinct, which may be explained by distinct functional connectivity between these two brain regions or differential effect of MPTP on striatal structures., and (3) the neuroprotection-associated gene expression pattern in the caudate and putamen included multiple genes previously associated with chromatin remodeling and anti-apoptotic processes.

We found a number of increased chromatin-remodeling gene transcripts associated with planned physical activity after MPTP exposure. These genes have a unique, but putatively converging function. D4, zinc and double PHD fingers, family 3 (DPF3) is a histone acetylation and methylation reader of the BAF chromatin remodeling complex (Lange et al., 2008). It initiates gene transcription during development by binding histones H3 and H4 in an acetylation sensitive manner (Zeng et al., 2010). In contrast, methyl-CpH binding domain protein 3-like 1 (MBD3L) is a transcriptional repressor that interacts with methyl-CpG-binding protein 2 (MeCP2/MBD2) (Jiang et al., 2004), a protein that plays a critical role in both CNS development and response to cell death (Russell et al., 2007). Snf2-related CREBBP activator protein (SRCAP) is also a chromatin remodeling protein (Wong et al., 2007), and has been shown to enhance the ability of CREB binding protein to activate transcription (Slupianek et al., 2010). Finally, transduction (beta)-like 1 X-linked receptor 1 (TBL1XR1) is a multifunctional co-repressor of transcription (Zhang et al., 2006) that binds preferentially to hypoacetylated histones H2B and H4, and has a critical role in targeting the co-repressor complexes to chromatin in vivo (Yoon et al., 2005). Additional chromatin remodeling genes that were also correlated with activity included chromodomain helicase DNA binding domain 2 (CHD2), microcephalin (MCPH1), and runt-related transcription factor 2 (RUNX2) (Nagarajan et al., 2009; Marfella et al., 2006; Yang et al., 2008; Westendorf et al., 2002). These combined findings suggest that neuroprotection by activity after MPTP exposure is, at least in part, achieved though epigenomic mechanisms that deserve further investigation.

We propose that a second, anti-apoptotic molecular mechanism also might play an important activity-dependent role in sparing the DA terminals after MPTP exposure. Calpain 6 (CAPN6), an atypical protease lacking the active site (Huang and Wang, 2001) has been shown to inhibit apoptosis and facilitate neurogenesis (Rho et al., 2008), potentially counteracting MPTP effect in the stratum. Neurotrophic factor receptor 3 (NTRK3/TrkC) is the high affinity catalytic receptor for the neurotrophin NT-3 mediating neuronal differentiation and survival. TrkC activation instructs developing neurons to die both in vitro and in vivo (Nikoletopoulou et al., 2010), and this is consistent with the repressed TrkC expression level we observed in the monkeys with higher activity. Similarly, the Huntington interacting protein 1 (HIP1) was negatively correlated with our measurements, and this gene is known to induce cell death through the caspases 3, 8, 9 system (Hackam et al., 2000; Wanker, 2002; Choi et al., 2006). Additional anti-apoptotic genes that were also correlated with mean total activity included v-rel reticulotheliosis viral oncogene homolog B (RELB) (El Gazzar et al., 2007) and dual specificity phosphatase 26 (DUSP26) (Shang et al., 2010).

In particular our attention was focused on STX3, as we also found it associated with activity-associated neuroprotection in the putamen and associated with the lesioned hemisphere, albeit a different probe. Syntaxin 3 was decreased with activity, [^{11}C]DTBZ binding, and TH levels, and increased in the lesioned hemisphere. Syntaxins function in vesicle mediated exocytosis of neurotransmitters (Sudhof and Rothman, 2009), and bind synaptotagmin in a calcium dependent way (Sudhof et al., 1993; Lin and Scheller, 1997). There is a coordinated change in the expression of several syntaxin isoforms after long term potentiation (LTP) and learning in the hippocampus. Expression of syntaxin 3A (STX3A) increases 6 hours after LTP while syntaxin 3A (STX3B) decreases 30 minutes after LTP (Rodger et al., 1998). Healthy neurons may prefer STX3A over STX3B, but the role of STX3 in causing damaging and preventing neuroprotection is difficult to determine from current research and the literature, and requires further investigation.

In summary, our findings do suggest that participating in a planned exercise program increases the probability of having high levels of mean daily activity, as indicated by our finding that monkeys in our study with the highest mean daily activity levels were those who ran on treadmills five days a week. However, as can be seen in **Figures 15a** and **15b**, mean daily activity level was not solely dependent on the level of planned exercise that was undertaken. One of the sedentary monkeys with a relatively high level of baseline activity had slightly higher mean daily activity levels than one of the monkeys which ran at 60% maximal capacity 5 days a week. Likewise, one monkey running at 80% maximal capacity had lower mean daily activity levels than two other monkeys that ran at 60% maximal capacity. Mean daily activity strong predicted the level of neuroprotection after neurotoxin exposure, whether daily activity came from planned exercise, high levels of naturally-occurring activity or a combination of both. This finding is particularly encouraging for the aging population, or those in the early stages of diseases that target motor function, in that it suggests that a variety of forms of activity are neuroprotective, not just aerobic exercise that many may have difficulty undertaking. Finally, the identification of the molecular underpinnings of activity-associated expression profile in the striatal structures gives us a glance into the neuroprotective mechanisms at work, and might enable development of targeted therapeutic interventions in follow-up studies.

CHAPTER VII

Gene expression profiling of the brain: Pondering facts and fiction

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It has been over a decade since the publication of the first high-throughput gene expression profiling studies of the brain (Mirnics et al., 2000; Hakak et al., 2001; Lockhart and Barlow, 2001; Pasinetti and Ho, 2001; Mimmack et al., 2002). During the last decade the opinion and attitude of the scientific community has changed toward these technologies multiple times. The first phase, lasting about 3-4 years, was characterized by enthusiasm, excitement, and often unjustified optimism. Many viewed DNA microarray technology as a "magic bullet" that would fundamentally change our understanding of various brain disorders, and during this golden era of microarrays funding agencies were generous in supporting data-driven exploratory efforts. As a result, several important studies were generated, along with a large number of mediocre studies that resulted in long lists of gene dumpouts without meaningful interpretation of the findings. The backlash was predictable, and over a relatively short time period the dominant scientific opinion transformed itself to one of skepticism toward anything that was DNA microarray-generated. In the meanwhile, proteomics became “hot”, followed by other novel “omics” technologies, and microarray expression studies fell in disgrace: microarray manuscripts started to be considered “descriptive studies”, and as such they routinely started to receive editorial rejections by the top journals in the field of neuroscience. The attitude of many journals and editors was best summarized by the boilerplate rejection letter of the Journal of Neuroscience from 2005, stating that *“We tend to be circumspect when we receive an expression array paper.”* (Journal-of-Neuroscience, 2005) - not caring about the quality of the presented science, but condemning the technology. Many microarray enthusiasts jumped on a bandwagon of new, hotter and better-funded “omic” technologies – while the real puritans of microarray technology went to work: they teamed up with expert teams of biostatisticians and bioinformaticians and started to generate standards of performing, reporting (Brazma et al., 2001), analyzing (Tusher et al., 2001; Irizarry et al., 2003; Subramanian et al., 2005) and sharing (Barrett et al., 2005) the experiments. To the classical “most changed gene” analyses novel pathway assessments were added (Mirnics et al., 2000; Mirnics et al., 2001; Dennis et al., 2003; Curtis et al., 2005; Subramanian et al., 2005; Langfelder and Horvath, 2008), and the best microarray experiments started to include both data verification and functional follow-up assays. The gene expression profiling field grew up, entered its current phase of “accepted method” and took its place as a powerful, yet not omnipotent, scientific tool in the exploratory research portfolio.

Being part of this evolution process was both fascinating and frustrating. Over the years we received many criticisms from our peers, editors and reviewers. Some were fully justified and pointed out our own ignorance, while others were clearly malicious and had no foundation in reality. However, a number of observations and statements made in this process constituted great starting points for interesting discussions. The latter ones are the topic of this manuscript, in a hope that public pondering of some of these issues will help achieve better experimental design, higher quality data, enhanced recognition of a good microarray experiment, and improved interpretation of findings.

“Without a testable hypothesis, there is no good science.”

We strongly disagree with this notion. *“I believe in ignorance-based methods because humans have a lot of ignorance and we should play to our strong suit …you take raw ignorance and turn it into processed ignorance, and processed ignorance, well-defined ignorance, well-asked questions that we don't know the answer to, that's the root of experiment.”* - Dr. Eric Lander, founding director of the Broad Institute, eloquently pointed out the prevailing philosophy of data-driven researchers (Lander, 2002). It should be noted that initial and unproven hypotheses *per se* carry little value, and are limited by our current perception of how a biological system might work (Mirnics and Pevsner, 2004; Horvath et al., 2010). Data-driven, hypothesis-free approaches allow simultaneous testing of thousands of unformulated hypotheses: comparing the whole genome transcription machinery allows us to find the truly unknown, the unexpected, and the counterintuitive. It allows us to generate novel hypotheses, which can, and should be followed up in detail, in a hypothesis-driven fashion. Thus, in our experiments the precise initial hypothesis becomes secondary to a stellar experimental design that maximizes the chance of finding meaningful and fundamentally novel data (Mirnics et al., 2006). What to analyze (e.g. which cell types or brain regions), which subjects to include (e.g. co-morbidity, endophenotypes, technical exclusion), how to analyze the dataset are critical, and often very challenging considerations, and the poorly performed expression profiling studies almost invariably fail at this.

"Sample size should be increased…"

In theory, this is true. I have never met a biostatistician who did not advocate an increased sample size. Yet, the reality is that in expression profiling studies sample size will always be limited, especially in postmortem brain studies. We simply cannot even approach the sample size of genome-wide association studies (GWAS) studies (Sullivan, 2010), where thousands of samples are required to perform a meaningful study – we can be considered fortunate if we have several dozens of high-quality postmortem samples to work with (Mirnics et al., 2006). So, due to the limited sample size, should we abandon this line of research? Absolutely not! There is a huge difference between the gene expression profiling and genome wide association studies, which is strongly in favor of transcriptome assessment: invariably the disease associated gene expression signature is much stronger than the genetic association signal! For example, genetics studies of schizophrenia (and also bipolar disorder, ADHD, major depression, and a host of other disorders) could only identify miniscule genetic signals for any putative susceptibility genes (Harrison and Weinberger, 2005), yet, gene expression studies, despite the small sample sizes, have successfully identified expression changes that are characteristic of >50% of the diseased cohort (Mirnics et al., 2000; Hakak et al., 2001; Middleton et al., 2002; Arion et al., 2007a; Garbett et al., 2008). The explanation for this is functional convergence and the fundamental nature of the brain transcriptome itself – gene expression networks are interdependent (Mirnics, 2008; Horvath and Mirnics, 2009; Winden et al., 2009), and the various genetic and environmental insults converge at critical molecular pathways, resulting in common alteration of transcript levels of different origin (Mirnics et al., 2006). As a result, one might argue that while genetic predispositions speak of the *origin*s of the disturbance seen in psychiatric disorders, gene expression changes give us clues about the *mechanisms* by which the pathophysiology progresses and the disease symptoms arise.

"Transcript changes do not matter if the protein levels are not altered."

This is an interesting reasoning, and at the first glance it makes a lot of sense – or does it? Let us follow this line of reasoning for a second. If the transcript alteration does not matter in the absence of an obvious protein change, than the protein level is also unimportant if the protein is not activated or transported to its place of action. Obviously, this trafficking also becomes irrelevant unless it affects the electrical conductivity and the responsiveness of the neuron. Similarly, any change in excitability of the single cell also becomes meaningless unless the activity of a whole neural network is altered and neural network activity fluctuations mean virtually nothing if the behavior of an individual is not altered… This logic could be applied in such a manner to make any important discovery seem meaningless. We believe that such a line of reasoning is deeply flawed, and put serious limits on future discoveries.

Furthermore, the argument that the transcript changes are trivial in the absence of changing protein levels also demonstrates disrespect for the most fundamental principles of brain anatomy. The majority of neurons *project out* from the brain regions where the cell bodies reside, and they traffic proteins from the somata to thousands of synaptic terminals in remote brain regions. So, a proteomic profile of any brain region at any given moment is a sum of proteins that are produced by the cell somata which reside in the harvested area (intrinsic proteins) *and* proteins that are contained within the synaptic terminals that project into the area from other brain regions (extrinsic proteins). Importantly, many proteins (such as synaptic release machinery) have both an intrinsic and an extrinsic source, and bulk tissue proteomics cannot differentiate between them. In contrast, the mRNA expression profile is primarily made up by the somatodendritic transcripts of cells that reside in the harvested brain region (intrinsic transcripts), with a minimal contribution from extrinsic mRNA species. Thus, transcriptomics and proteomics measure different anatomical substrates, and this is very important for the interpretation of both "omics" findings: a change in mRNA, without a corresponding protein change might mean that the intrinsic cell population is affected at both the mRNA and protein level, but the substantial extrinsic source of the same protein (which is unchanged), makes impossible to detect the intrinsic protein change (Pongrac et al., 2002).

“The magnitude of gene expression change is too small to be physiologically relevant”

This is clearly an assumption, yet it is surprising how little discussion it has attracted over the years. The “bigger is better” mentality, while characteristic of our society, is not clearly applicable to biological systems. Homeostatic systems are differently tuned, with various degrees of tolerances. For example, changing the blood pH by 20% is lethal, yet dynamic blood glucose concentration doubling after meals or significant hormonal oscillations are part of normal physiology. The same principle applies to gene expression changes – many knockout animals do not show any readily discernable phenotypes (McMahon et al., 1996; Schluter et al., 1999) and copy-number variations (CNVs) normally occur at a high rate in the disease-free human population (Vogler et al., 2010). Yet, modest decreases in mRNA expression of the 67-kilodalton isoform of glutamic acid decarboxylase (GAD67) appear to be a critical, functional component of schizophrenia pathophysiology (Hashimoto et al., 2008). Thus, it appears that the individual function of the gene, its place in the transcriptome network, other genes performing a similar function, associated regulatory and compensatory mechanisms, simultaneously occurring gene expression changes in the same molecular pathway and many other factors decide the functional consequence of a gene expression change. While the magnitude of the gene expression change is also certainly one part of this equation, by itself it is a poor predictor of functional consequences.

“The most significant expression changes are the most important”

This is clearly another assumption. While statistical assessment is essential, probability values in a transcriptome profiling experiments represent a continuum, and there is no way to predict if a gene expression change associated with a p=0.0001 is more functionally relevant than an expression alteration reporting a p=0.01.

Furthermore, if statistical assessments are not selected carefully, the results can be quite misleading. In the following example, the prefrontal cortex of a genetically altered mouse was compared to the prefrontal cortex of its wild-type littermates using whole-genome expression profiling. The analysis of 5 transgenic and 5 control mice, after RMA normalization, revealed the following $\log_2$ expression values for *Gene X*: 6.0, 6.8, 7.0, 6.2, 6.5 for WT, and 7.2, 10.0, 15.0, 8.0, 7.8 for TG samples. Performing a standard, two-tailed groupwise, equal-variance Student t-test in Microsoft Excel will report a significance of p=0.0637. If not careful, such a result will not be even noticed, and discarded as “non-significant”. In contrast, *Gene Y* in the same experiment might report the following values across the studies samples: 2.2, 2.2, 2.2, 2.3, 2.3 for WT, and 2.4, 2.4, 2.3, 2.3, 2.3 for the TG samples. A similar t-test analysis for *Gene Y* in Microsoft Excel will yield a “significant” p=0.0203, yet *Gene Y* is certainly less promising for follow up than *Gene X*. How did this happen? The variance for Gene X was big and for Gene Y was small (possibly a normalization artifact), and the t-test alone was quite inappropriate to analyze the transcriptome changes.

Involving a knowledgeable biostatistician in your experimental design and discussing the data mining strategies *before* performing the experiment is always a good idea. Determining “true expression changes” and subsequently identifying the “most promising expression changes” requires pulling resources from both biological and statistical knowledge, requiring (an often painful) cross-field education for both the molecular biologist and biostatistician.

“The authors did not apply a Bonferroni correction…”

… because they did not want to throw out the baby with the bath water. False discovery assessment is very important in all transcriptome profiling experiments, but in most cases Bonferroni correction is ill-suited for this purpose. First, in a typical transcriptome profiling experiment the number of genes tested is greater than the number of samples by 3 orders of magnitude. Second, human brain samples show a molecular diversity similar to the genetic and symptom diversity of the disease, postulating that not all the affected brains will have an identical gene expression signature, and this weakens statistical significance measures. Third, in complex brain disorders typical gene expression differences are relatively modest, often in the range of 20-50%, and precise expression measurement can be challenging. As a result, gene expression changes almost never reach significance that that can withstand a whole-genome Bonferroni p-value correction. Should we have applied a Bonferroni correction to the schizophrenia microarray datasets over the last ten years, we would have not obtained any novel leads – and the immune (Arion et al., 2007a), mitochondrial (Middleton et al., 2002), synaptic (Mirnics et al., 2000), oligodendroglial (Hakak et al., 2001) and GABAergic (Hashimoto et al., 2008) changes could have not been identified and consequently replicated.

So, how can we ensure that the gene expression changes we uncovered are “real”, and not a result of experimental noise or cohort bias? There are multiple alternatives to extremely stringent statistical corrections that still ensure that true biological findings, and not experimental artifacts, are uncovered. First, one can use less stringent statistical corrections for multiple comparisons, such as the Benjamini-Hochberg procedure (Sibille et al., 2004). This method is very effective, especially if the gene expression dataset is *a priori* trimmed for non-expressed genes and genes with very low variance: proper “trimming” procedures can reduce the number of performed comparisons by up to 75%, thus reducing the stringency of statistical correction that is required for false discovery assessment. Second, assessment of false discovery by various kinds of permutation analyses has gained great popularity over the years (Gao, 2006; Sohn et al., 2009). At core of all these assessments is mixing the experimental and control samples randomly into two balanced groups, and performing the same analyses repeatedly – for both pathways and individual genes. If the disease effect is bigger than the random noise, the random assignment of microarrays into variously permutated groups will report less differentially expressed genes than the “pure” comparison of control and experimental samples (Unger et al., 2005). In the past such analyses have been challenging for laboratories without strong bioinformatics support, however, recently developed public domain software packages make these assessments (both at the individual gene and pathway level) straightforward (Gentleman et al., 2004; Kuehn et al., 2008). Third, a very elegant, biology-based assessment of false discovery includes defining the differentially expressed transcripts in the initial cohort, and then testing this pattern in a second, independent replication cohort (Lazarov et al., 2005). Although false discovery assessments should always be incorporated in the experimental design, the exact choice of the false discovery analysis method should depend on availability of samples, cohort size, experimental design and many other factors.

“The authors should have employed the analysis strategy by Doe et al, published in Nature”

There is no such a thing as a “universally good” microarray study design. Each experimental design and analysis strategy should be tailored to your own experiment. Applying an experimental design or analysis strategy only because it was published in a high-impact journal is a common mistake made most often by trainees who try to emulate successful studies. Rather, considerations should include sample size, type and diversity, employed technology, number of replicates, and many other factors. Establishing clear and carefully crafted experimental parameters *before* the start of the study goes a long way toward obtaining meaningful experimental data – “patching up” microarray experiments with changing inclusion-exclusion criteria and adding additional samples at a later time usually results in noisy (and often uninterpretable) experimental outcomes.

“In this transcriptome profiling study, genes X and Y and pathway Z were not changed”

This is true, but is potentially misleading: not *finding* gene expression changed and not *being* changed are fundamentally different statements. DNA microarrays studies notoriously carry a high percentage of type II errors – a true biological difference is often not detected in these experiments. The explanation to this is a technical limitation, and has three major sources. First, universal hybridization conditions are never ideal for all of the hundreds of thousands of probes on a single microarray. Second, some DNA microarray probes perform less then ideally, and cross-hybridize to other genes than their own target, and the specificity of the signal is lost. Third, genes that are expressed in only a small subpopulation of cells in the tissue, or are expressed at very low levels, are at the cusp of detection limit even on the highest quality microarrays. Thus, failing to find a gene expression change in a microarray experiment is not a definitive proof that a gene expression is absent between the compared samples (Hollingshead et al., 2005), and negative data must be interpreted with great care.

“Finding hundreds of diverse gene expression changes is uninterpretable”

Not so. Unfortunately, the human brain appears to like simple solutions, and we scientists are not immune to this. A list of several hundred gene expression changes between two conditions is overwhelming, and we would prefer to explain the main pathophysiological process by very few changes in mRNA level. More is less: a big panel of changed genes somehow became less informative than the alteration of only one mRNA. However, the vast majority of complex brain disorders cannot be explained by individual gene dysfunction and the transcriptome profiling results merely reflect this complexity of the pathophysiological process. Unfortunately, many microarray studies fall short of proper interpretation of data by simply discussing the role of several, usually, "most changed" genes. The ability to decipher and interpret the data, and subsequently build a falsifiable model related to the studied pathophysiological process is the trait that sets apart a great expression profiling manuscript from a mediocre one.

So, how can we avoid writing a mediocre manuscript? First, we must reduce the emphasis on single gene changes, and shift our attention to analysis of co-regulated transcript networks (Korade and Mirnics, 2011; Voineagu et al., 2011). This can be achieved by using a number of freely available tools such as weighted gene co-expression network analysis (WGCNA) (Langfelder and Horvath, 2008), WholePathwayScope (Yi et al., 2006), Database for Annotation, Visualization and Integrated Discovery (DAVID) (Dennis et al., 2003), Kyoto Encyclopedia of Genes and Genomes (KEGG) (Aoki and Kanehisa, 2005; Arakawa et al., 2005), Gene Set Enrichment Analysis (GSEA) (Kuehn et al., 2008). Second, we must start more actively comparing our datasets to those generated by other investigators, especially the ones that are deposited in the main microarray data repositories (Barrett et al., 2005; Parkinson et al., 2005). Third, beyond data verification, we should attempt to follow-up our findings with additional experiments, obtaining supporting readouts about the consequences of the observed gene expression changes (Horvath and Mirnics, 2009; Huffaker et al., 2009).

"Transcriptome profiling studies are descriptive"

Actually, gene expression profiling studies are not any more descriptive than anatomical, brain imaging, genetic association or any other "omic" studies. None of these studies can prove causality beyond doubt, yet they all offer critical information about the disease state. On the other hand, transgenic animal models, tissue culture experiments and certain electrophysiology studies test causal relationships, yet they all have serious limitations of a different kind: they will never be able to fully recapitulate complex brain disorders in their model systems: they study biological processes in isolation, and not the disease itself. Furthermore, "mechanistic" studies invariably obtain their leads from "descriptive" scientific discoveries. Is a genetic study reporting a higher proportion of CNVs in schizophrenia (Stefansson et al., 2008) or autism (Sebat et al., 2007) descriptive or causal? Neither of these two findings gave direct insight into the mechanism by which the CNVs might produce a disease, so, they must be considered "descriptive". Yet, they discovered a critical process by which these two devastating diseases might arise, and they suggest causality, so they must be considered "mechanistic" at the same time. Thus, separating studies into "descriptive" and "mechanistic" is highly artificial – the information value of the study is critical, and not the classification of the technology that was employed in the studies.

In summary, nowadays we are fully aware of the interpretational challenges associated with high-throughput expression profiling. We hope that we were able to convince you that a carefully designed, executed, and thoughtfully interpreted expression profiling experiment is a valuable source of scientific data, that our field has high standards, and that we are able to generate valuable leads for brain researchers. We expect that the "circumspect" attitude (Journal-of-Neuroscience, 2005) toward our experiments will fade into the sunset, and we deeply believe that transcriptome profiling studies will continue to be essential for deciphering the pathophysiological mechanisms leading to complex brain disorders.

CHAPTER VII

Discussion

In our model spontaneous activity, not exercise *per se*, predicted the size of the MPTP lesion in Rhesus monkeys. Neuroplasticity and neuroprotective mechanisms associated with spontaneous activity in the brain have been explored via gene expression analyses in depth (**Figure 24**). Exercise does increase the likelihood of having a high activity level, but daily activity can be gained in other ways, as one of the monkeys, who was sedentary, did have a high activity level. This suggests that spontaneous activity gene expression is of more importance to neuronal sparing and plasticity than exercise differentially expressed transcripts, which makes sense given that enriched environments also influence changes in the brain. Furthermore, spontaneous activity gene expression in the motor cortex is inversely correlated with a peripheral protein, c-reactive protein (CRP), a marker of inflammation that has been associated with neuronal death (Stenvinkel, 2006; Futterman and Lemberg, 2002). Increasing physical activity as measured with accelerometers, or pedometers, should be of higher interest than exercise.

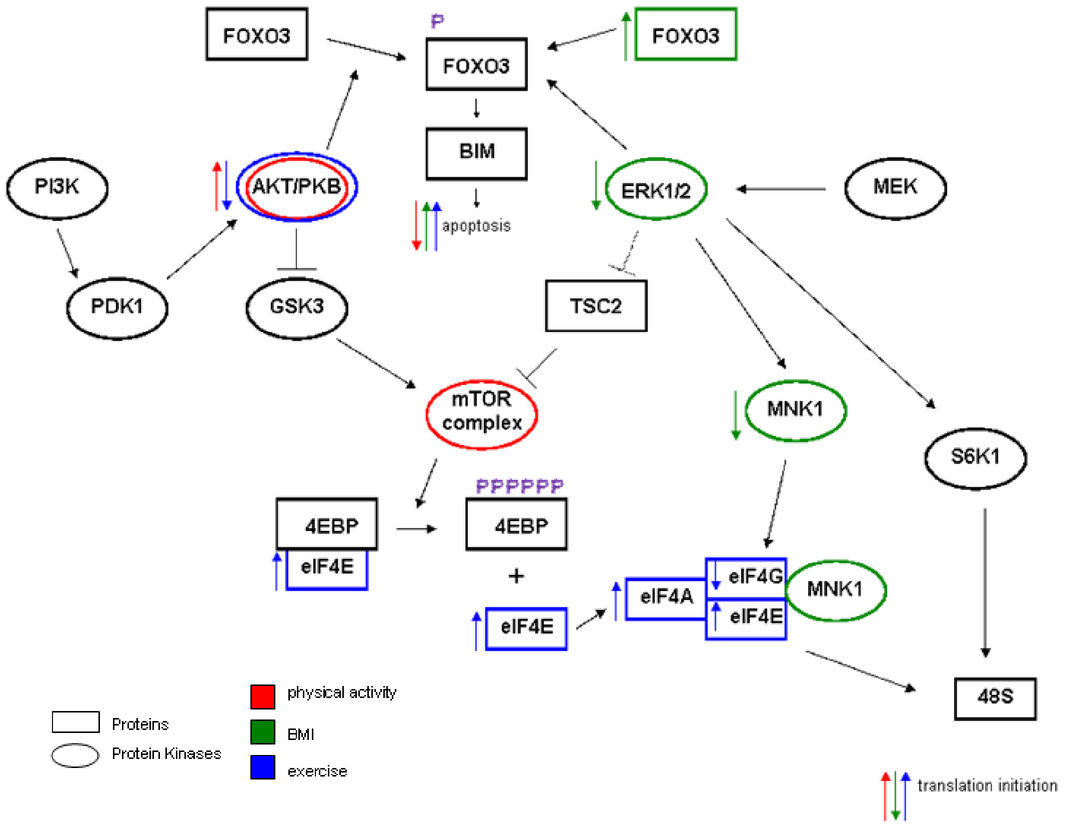

Figure 24. Activity, BMI, and exercise signaling pathways converge.
Proteins highlighted in red are associated with activity, those in green are associated with BMI, and those in blue are associated with exercise. At the transcriptome level activity is associated with increases in AKT in the motor cortex and the mTORC1 signaling pathway by GSEA in the caudate nucleus, BMI is associated with decreases in MNK1 in the motor cortex and increases of FOXO3 in the caudate nucleus, and exercise is associated with increases in eIF4E and eIF4A and decreases in eIF4G. At the protein level activity is associated with phosphorylation of AKT, and BMI is associated with decreased phosphorylation of ERK1/2. In sum, translation initiation is promoted by physical activity and exercise, while apoptosis is promoted by exercise and BMI.

SPONTANEOUSLY ACTIVE RHESUS MONKEY STUDIES

These studies began by looking for gene expression associated with activity and BMI in spontaneously activity Rhesus monkeys. Spontaneous activity and BMI were independent measurements though multiple measurements were taken. The monkeys were fed a high fat diet 3 years prior to the end of the study at which time they received one month of a 30% calorie reduction followed by one month of a 60% calorie reduction. Measurements were taken of CRP (mg/L), body mass index (kg/CRL^2) at the beginning and the end of the calorie reduction, change in BMI over the calorie reduction, weight (kg) at the beginning and the end of the calorie reduction, weight loss after 1 month of a 30% calorie reduction, weight loss after 1 month of a 60% calorie reduction, total weight lost (kg), and activity at the beginning of the diet (counts/day), activity at the end of the diet (counts/day), and change in activity (**Table 5).**

Table 5 . Spontaneously Active Rhesus Monkeys

BMI @ start (kg/CRL2)	BMI @ end (kg/CRL2)	Δ BMI	wt @ start (kg)	wt @ end (kg)	Δ wt @ 30%	Δ wt @ 60%	Δ wt	Activity @start (cts/day)	Activity @end (cts/day)	Δ activity
29.25	29.37	0.12	6.72	6.75	0.03	-2.00	1.64	710317	515105	195212
26.27	25.92	-0.35	7.30	7.20	-0.10	-0.68	2.04	506925	240431	266494
44.96	37.20	-7.76	11.60	9.60	-2.00	5.57	14.48	200427	191266	9161
37.16	35.53	-1.63	9.83	9.40	-0.43	0.25	4.33	188606	183932	4675
29.59	31.72	2.13	8.02	8.60	0.58	-7.89	1.29	95848	75677	20172
37.21	36.71	-0.50	8.67	8.55	-0.12	-1.84	3.25	160564	143509	17054
22.49	26.80	4.31	5.66	6.75	1.09	-12.19	-4.45	1007746	897948	109798
26.69	27.82	1.13	6.72	7.00	0.28	-7.40	3.61	174187	123780	50407
20.99	23.06	2.07	4.82	5.30	0.48	-7.88	-1.19	46717	46478	239
21.11	21.76	0.65	5.72	5.90	0.18	-3.98	1.05	135683	73961	61722
43.78	37.09	-6.68	10.74	9.10	-1.64	4.42	13.02	173182	134284	38898
26.20	21.97	-4.23	6.68	5.60	-1.08	4.00	14.67	760838	271736	489102
33.44	30.98	-2.46	8.20	7.60	-0.60	2.65	5.15	191991	129822	62169
45.72	37.78	-7.94	10.65	8.80	-1.85	4.42	15.89	556938	485187	71751

Table 5. Measurements for Spontaneously Active Rhesus Monkeys. BMI measurements (kilograms per crown of rump length squared) are in green. Weight loss (kg) measurements are in blue. Activity measurements (counts per day) are in red. Measurements taken at the beginning of the calorie reduction diet are indicated by @start, those taken at the end of the diet are indicated by @end, those taken at 30% calorie reduction are indicated by @30%, and those taken at 60% calorie reduction are indicated by @60%.

CRP was not measured in all of the monkeys, but using the monkeys with CRP measurements we also found that CRP was inversely correlated with activity. CRP, which is located in blood plasma, is associated with increased neuronal death from injury (Stenvinkel, 2006; Futterman and Lemberg, 2002), and worse health outcomes such as hypertension and heart attack. Even more interesting CRP was correlated with both BDNF and ARC mRNA levels in the motor cortex, suggesting that CRP could be a peripheral marker of brain health. From the literature it is known that BDNF can cause the activation of ARC, an immediate early gene, in neurons (Zheng et al., 2009), and there was a positive correlation of BDNF and ARC, supporting the idea that high activity levels provide brain resiliency.

To select independent measurements for microarray analyses all of the measurements were correlated with each other (**Table 6**). Since BMI and weight measurements intercorrelated, activity and BMI were used for subsequent microarrays analyses. The continuous gene expression data were modeled a few ways with Pearson correlations and linear models. Linear models proved superior, because genes interacting between activity and BMI could be found. The following formulas were used: gene expression = $\alpha + \beta$(activity), gene expression = $\alpha + \beta$(BMI), and gene expression = $\alpha + \beta_1$(activity) + β_2(BMI) + β_3(activity x BMI). We tested the hypothesis that the slope (β) was not equal to 0 for activity, BMI, and activity x BMI. If the slope (β) of the probeset was significantly different from 0 with a $p < 0.05$, then the probeset (gene) was considered significantly associated with either activity, BMI, or interacting between activity and BMI.

Individually, different gene transcripts, and thus mechanisms, associated with activity and BMI were found. Physical activity was associated with nutrient sensing and neuronal survival genes in both the motor cortex and the caudate nucleus. BMI was associated with apoptosis, insulin signaling, and metabolism in the motor cortex and caudate nucleus. Two kinases downstream of neurotrophic factors involved in neuronal survival were associated individually with each: pAKT was increased with activity levels, whereas pERK1/2 was increased at low BMIs.

Table 6. Spontaneously Active Rhesus Monkeys Correlation Matrix

	BMI @ start	**BMI @ end**	**Δ BMI**	**wt @ start**	**wt @ end**	**Δ wt @ 30%**	**Δ wt @ 60%**	**Δ wt**	**Activity @start**	**Activity @end**	**Δ activity**
BMI @ start											
BMI @ end	**0.933**										
Δ BMI	**-0.834**	**-0.580**									
wt @ start	**0.974**	**0.906**	**-0.817**								
wt @ end	**0.877**	**0.946**	**-0.534**	**0.923**							
Δ wt @ 30%	**0.734**	0.475	**-0.934**	**0.732**	0.449						
Δ wt @ 60%	**0.738**	0.466	**-0.958**	**0.726**	0.429	**0.876**					
Δ wt	**-0.826**	**-0.569**	**0.999**	**-0.813**	**-0.527**	**-0.938**	**-0.956**				
Activity @start	-0.192	-0.238	0.069	-0.232	-0.289	-0.066	-0.007	0.077			
Activity @end	-0.063	-0.008	0.131	-0.124	-0.086	-0.213	-0.137	0.143	**0.901**		
Δ activity	-0.316	-0.513	-0.072	-0.301	-0.492	0.222	0.222	-0.078	**0.661**	0.270	

Table 6. Spontaneously Active Rhesus Monkey Correlation Matrix. Significant correlations ($p<0.05$) are in bold green, blue, or red. All BMI measurements significantly intercorrelated (green bold font), as did weight loss measurements (blue bold font), and activity measurements (red bold font), but BMI also correlated with weight loss measurements. BMI and activity were independent measures.

A host of genes interacting between activity and BMI were found in the interaction model (gene expression = $\alpha + \beta_1(\text{activity}) + \beta_2(\text{BMI}) + \beta_3(\text{activity x BMI})$), suggesting shared mechanisms for activity and BMI, which were difficult to interpret. These results do suggest that activity and BMI interact in complicated ways in the motor cortex and caudate nucleus. To ease the analyses genes associated with either activity or BMI in the simpler models (gene expression = $\alpha + \beta$ (activity) or gene expression = $\alpha + \beta$ (BMI)) were found and interactions in signaling cascades were investigated.

One potential site of crosstalk between AKT, ERK1/2, and even AMPK was FOXO3, as it can be modified by all three kinases. Protein modifications of FOXO3 determine its nuclear/cytoplasmic localization. AKT phosphorylation of FOXO3 results in its retention in the cytoplasm while AKT inhibition leads to its nuclear translocation and activation of its target genes, which induce apoptosis (Brunet et al., 1999; Matsuzaki et al., 2005; Plas and Thompson, 2003; Aoki et al., 2004; Huang and Porter, 2005). AMPK phosphorylation of FOXO3 has been shown to activate FOXO3 transcriptional activity without affecting its subcellular location (Greer et al., 2007).

ERK directly phosphorylates FOXO3, and the phosphorylated FOXO3 can be degraded via an MDM2-mediated ubiquitin-proteasome pathway (Yang et al., 2008). The simultaneous blockade of ERK1/2 and MDM2 signaling upregulates levels of the BH3-only proteins Puma and Bim, in part through the transcriptional up-regulation of FOXO3, which promotes apoptosis (Zhang et al., 2010). Direct evidence of this was seen in our BMI dataset. Low pERK1/2 levels were associated with high BMI's in the motor cortex, along with increases in caspase 9 mRNA, and increases in FOXO3 mRNA with increased BMI. The exact mechanism by which FOXO3 remains in the cytoplasm is not fully understood though AKT, ERK1/2, and AMPK do regulate its location, and this results in changes in neuronal survival and apoptosis.

Exhaustive lists of growth factors associated with activity or BMI were not found, though increases in the insulin receptor (which signals through similar cascades as growth factors) were seen with increased BMI. It is conceivable that growth factor systems still could be activated by non-transcriptional cellular machinery or that spontaneous activity and BMI induce AKT/FOXO3 and ERK1/2 respectively through different, non-growth factor dependent pathway, and this deserves further investigation. However, our studies did not examine the causality of these changes, but the strong correlational relationship suggests that this is an important avenue for further investigations.

In addition, there was upregulation of MAP kinase interacting kinase 1 (MNK1) at low BMIs. MNK1 has been found to be recruited to the eukaryotic initiation factor 4F (eIF4F) complex through association with eIF4G (Pyronnet et al., 1999) (**Figure 24**). This complex has been implicated in preventing the large ribosomal subunit from binding the small subunit before it is ready to start elongation and it helps to position mRNA near the exit site of the 40S ribosome subunit and promote the assembly of the pre-initiation complex. Protein synthesis regulation by the eIF4F complex plays an important role in controlling cell growth and proliferation (Sonenberg and Dever, 2003). It consists of three subunits: eIF4A, eIF4E, and eIF4G. eIF4E binds the 5’ cap of mRNAs and recruits them to the complex. It interacts with eIF4G, which recruits the eIF4A RNA helicase to the complex, unwinds the secondary structure in the mRNA, and facilitates translation initiation by the 40S ribosomal complex. eIF4E activity is partially regulated by phosphorylation through ERK1/2 (Flynn et al., 1997), but also is activated by mammalian target of rapamycin complex 1 (mTORC1) (Bhaskar and Hay, 2007), which is downstream of AKT. Translation initiation can be regulated by AKT, ERK, and MNK1

(**Figure 24**), and could be important in mediating neuroprotection, plasticity, and neuronal survival in motor areas of the brain.

There was significant overlap between both the Rhesus Macaque Genome (RhG) and the Human Genome (HG) microarrays for both activity and BMI – suggesting that both arrays can be used to query rhesus macaque gene expression and providing a strong dataset for analyses. While the RhG arrays are more specific, the HG arrays provide higher quality genome annotations and are more useful in deciphering function from differentially expressed gene transcripts. There were no overlapping transcripts associated with activity and BMI again suggesting that activity and BMI have different mechanisms. While activity provides brain resiliency via AKT, low BMIs provide brain resiliency via ERK1/2, and both activity and BMI provide resiliency by influencing AMPK activity. These resiliencies are mediated molecularly through energy signaling cascades.

EXERCISED RHESUS MONKEYS

Next, gene expression in three brain regions of exercised Rhesus monkeys were analyzed: the motor cortex, the hippocampus, and the putamen. In addition the datasets were analyzed using gene set enrichment analysis (GSEA) for enrichment using all of the gene sets in the Molecular Signatures Database (MSigDB) and gene sets made from the significant gene transcripts from the spontaneous activity, BMI, and MPTP datasets. Differentially expressed gene transcripts varied in number, strength, type, and associated pathways across all three brain regions. The hippocampus contained the highest number of differentially expressed transcripts (5508), which were strong in their magnitude of change (on average an ALR of + or - 0.650, which represents about a 50% change in expression), but not significantly associated with a pathway as assessed by GSEA. The motor cortex, conversely, contained 435 differentially expressed transcripts with exercise, which were intermediate in magnitude (on average an ALR of + or - 0.463, which represents about a 35% change in expression), but significantly associated by GSEA with three pathways associated with complex I of the electron transport chain. These pathways included three genes set: the NADH dehydrogenase complex gene set, the mitochondrial respiratory chain complex I gene set, and the respiratory chain complex I gene set. The putamen contained the smallest number of differentially expressed transcripts (265), which were small in the magnitude of change (on average an ALR of + or – 0.367, which represents about a 30% change in expression).

Overall increases in complex I of the electron transport chain were found in all three brain regions. In the hippocampus a number of transcripts involved in translation initiation, a pathway increased by spontaneous physical activity, were increased (**Figure 24)**. These genes operate downstream of AKT and the mTOR. Additionally, in the motor cortex and putamen there were decreases in AKT3, something that was increased in the motor cortex of spontaneously active rhesus monkeys. Some genes in the motor cortex known to be protective including APOE, AChE, and IGF-1 (Carro et al., 2001) also were increased. CASP9 was also increased in the motor cortex suggesting that apoptotic processes may also be increased with exercise. This is not surprising, considering that exercise results in mitochondrial stress (Mattson et al., 2000; Mattson et al., 2008).

Although, exercise did not significantly predict the size of the MPTP lesion, but alterations in pathways associated with Parkinson's disease also associated with exercise. This suggests that exercise, since it decreases the production of genes involved in Parkinson's disease, likely contributes to total activity levels, and helps to decrease the onset of Parkinson's disease, though it was not significantly associated with the MPTP lesion.

After doing a probe by probe comparison there were no gene transcripts overlapping between all three regions. There was overlap (a) between the putamen and motor cortex of 91 transcripts, 89 which were changing in the same direction, (b) between the putamen and hippocampus of 5 transcripts, 4 of which were changing in the same direction, and (c) between the motor cortex and hippocampus of 55, with only 3 changing in the same direction. This suggests again that different processes are occurring in the motor cortex and the hippocampus – the hippocampus being specifically involved in neurogenesis while the motor cortex seemed to also have hints of apoptosis. Together with transcripts associated with physical activity and BMI we have diagramed exercise related transcripts indicated in blue on an activity, BMI, and exercise pathway diagram (**Figure 24**). In sum apoptosis is promoted by increases in BMI and exercise and prevented by increases in physical activity levels, while translation initiation is promoted by physical activity levels and exercise, and prevented by high BMI.

MPTP TREATED RHESUS MONKEYS

Participating in a planned exercise program increases the probability of having high levels of mean daily activity, as indicated by the finding that monkeys with the highest mean daily activity levels were those who ran on treadmills five days a week. In fact the pvalue for a t-test comparing the activity levels of all monkeys who ran versus those who did not is 0.06, nearing significance (**Table 7)**. Furthermore, there was not a significant difference between the monkey strains based on their activity levels (the pvalue between Indian rhesus monkeys animals and Chinese rhesus monkeys was 0.22 for activity level). Activity levels were significantly correlated with PET and TH in both the caudate nucleus and putamen, indicating that spontaneous activity also predicted the size of the MPTP lesion.

Table 7. MPTP Treated Rhesus Monkeys

Origin	Condition	Activity (cts/day)	PET % DIFF CAU	PET % DIFF PUT	PET % DIFF STR	TH % DIFF CAU	TH % DIFF PUT	TH % DIFF STR
Indian	60% runner	167476	-76.13	-69.31	-70.46	-72.76	-68.48	-70.32
Chinese	60% runner	312065	-31.83	-18.78	-24.62	-23.22	-5.19	-13.65
Chinese	60% runner	260492	-46.24	-37.09	-39.89	-45.02	-40.83	-42.90
Chinese	80% runner	237041	-22.19	-30.94	-27.96	-23.55	-24.41	-24.07
Indian	Sedentary	142717	-85.34	-83.75	-84.59	-81.12	-72.35	-76.48
Chinese	Sedentary	138870	-44.66	-51.18	-48.99	-33.75	-43.77	-39.56
Chinese	Sedentary	182218	-66.02	-75.72	-72.29	-69.24	-66.59	-67.80
ttest for Origin (pvalue)		0.222	0.028	0.100	0.066	0.047	0.103	0.069
ttest for Exercise (pvalue)		0.062	0.268	0.095	0.125	0.318	0.194	0.234
Correlation (R) with Activity		1	0.683	0.844	0.800	0.642	0.826	0.756

Table 7. MPTP Treated Rhesus Monkeys. Monkey origins, exercise group during the study, activity measures (counts/day), and percent loss of PET or TH compared to the nonlesioned hemisphere for the caudate nucleus and putamen. We performed t-tests for the origin of the monkeys and exercise group on all measures and correlated each measure with activity levels.

However, as can be see in **Figures 15a** and **15b**, mean daily activity levels were not solely dependent on the level of planned exercise that was undertaken. One of the sedentary monkeys with a relatively high level of baseline activity had slightly higher mean daily activity levels than one of the monkeys which ran at 60% maximal capacity 5 days a week. Likewise, one monkey running at 80% maximal capacity had lower mean daily activity levels than two other monkeys that ran at 60% maximal capacity. Mean daily activity strongly predicted the level of neuroprotection after neurotoxin exposure, whether daily activity came from planned exercise, high levels of naturally-occurring activity or a combination of both. This finding is particularly encouraging for the aging population, or those in the early stages of diseases that target motor function, in that it suggests that a variety of forms of activity are neuroprotective, not just aerobic exercise that many may have difficulty undertaking.

Studies also show that neuronal plasticity can be achieved by a specific diet, calorie restriction, and physical and cognitive activities (i.e. the individual’s experience) (which also increase levels of GDNF and BDNF and activate signal transduction pathways that involve ERK1/2 and PI3K) (Mattson et al., 2003; Duan et al., 2001; Lee et al., 2000; Lee et al., 2002; Bramham and Messaoudi, 2005), and the brain gains resilience to neurodegeneration by means of creating new neuronal resources (Llorens-Martin et al., 2009). Though we see that physical activity and exercise provide behavioral and biochemical sparing, other activities could also provide neuroprotection.

These results warrant future investigations into exactly how genetics and the environment interact. Monkeys of Indian origin in the study have a more severe MPTP lesion than the monkeys of Chinese origin (**Table 7**) with pvalues reaching < 0.05 for % loss for PET and TH caudate nucleus measures. In mice glutathione-S-transferase (GST) pi plays a key role in the level of MPTP sensitivity. C57BL/6 MPTP-sensitive mice show a decrease in GST π levels in nigrostriatal DA neurons after MPTP exposure, whereas

SW MPTP-resilient mice show stable levels of GST π post-MPTP (Smeyne et al., 2007). GST π is expressed in nigrostriatal dopaminergic neurons, and is a detoxifying enzyme that inhibits JNK-activated signaling, blocking the phosphorylation of cJUN and apoptosis of the cell (Wang et al., 2001). In people, polymorphisms in GST π have been loosely correlated with increased risk of idiopathic PD after exposure to pesticides (Menegon et al., 1998; Kelada et al., 2003).

Indian monkeys were used in the other two studies investigating spontaneous activity and exercise. Whether Indian origin rhesus monkeys have lower levels of GST π in nigrostriatal DA neurons is unknown at this time, but this or a similar genetic difference between Indian and Chinese origin rhesus monkeys could account for differences in MPTP toxicity. There are substantial genetic differences in rhesus monkeys of Indian vs. Chinese origin in mitochondrial DNA (Kanthaswamy and Smith, 2004), (Satkoski et al., 2008), and in the nuclear genomes as demonstrated by differences in microsatellites (Smith et al., 2006), Major Histocompatability Complex (MHC) loci (Penedo et al., 2005), and SNPs (Ferguson et al., 2007; Hernandez et al., 2007). However, there was not a significant difference in mean daily activity between Chinese and Indian monkeys (**Table 7**).

To elucidate the mechanism of physical activity associated neuroprotection gene expression in the caudate nucleus and putamen was assessed. There was a strong gene expression association between non-human primate activity and functional measurements of dopamine system sparing ([^{11}C]DTBZ binding and TH levels) in the caudate and putamen of the MPTP treated Rhesus monkeys. These gene expression signatures were different in each region which may reflect the different functional connectivity of each region and included several transcripts previously associated with chromatin remodeling and anti-apoptotic processes. These combined findings suggest that neuroprotection by activity after MPTP exposure is, at least in part, achieved though epigenetic mechanisms that deserve further investigation.

In addition, genes associated with the lesioned hemisphere were found by assessing significantly differentially expressed transcripts between the lesioned right putamen and the nonlesioned left putamen (**Figure 22)**. These included decreases in a gene involved in repair, ataxia telangiectasia and Rad3 related (ATR), increases in a gene involved in apoptosis increased (CASP9), increases in some neurotrophic factor signaling genes (FGF2 and eukaryotic translation initiation factor 4E (EIF4E)), and specifically an increase in syntaxin 3 (**Figure 23** and **Supplementary Table 12**). This supports the idea that some compensatory mechanisms promote survival of neurons after MPTP exposure. These mechanisms include an increase in dopamine release and a decrease in dopamine uptake (Zigmond et al., 1989; Zigmond et al., 1992; Abercrombie et al., 1990; Snyder et al., 1990). They also confirm the MPTP lesion (decreased in ATR and an increase in CASP9).

In particular attention was focused on STX3, as it was associated with activity-associated neuroprotection in the putamen, albeit with a different probeset. Syntaxin 3 was decreased with activity, [^{11}C]DTBZ binding, and TH levels, and increased in the lesioned hemisphere. Syntaxins function in vesicle mediated exocytosis of neurotransmitters (Sudhof and Rothman, 2009), and bind synaptotagmin in a calcium dependent way (Sudhof et al., 1993; Lin and Scheller, 1997). Healthy neurons may prefer STX1 over STX3, but the role of STX3 in causing damaging and preventing neuroprotection is difficult to determine from current research and the literature.

In summary, physical activity levels were associated with increased protection in the MPTP model of Parkinson's disease in rhesus monkeys. The gene expression associations converge from two separate dissections of caudate nucleus and two separate dissections of putamen from each monkey. This is analogous to performing the same microarray on each brain regions twice for each animal giving us a good measure of true discovery from the experiments. In both the caudate nucleus and the putamen the activity-associated gene transcripts include those involved in chromatin remodeling and anti-apoptosis. In the putamen STX3 decreased with activity, $[^{11}C]$DTBZ binding, and TH levels, and increased with the lesion. This specifically warrants further investigation into how physical activity is associated with chromatin remodeling, how STX3 operates at the synapse, and further suggests that other experiences which are associated with chromatin remodeling also could be associated with neuroprotection.

CONCLUSIONS

We have proven that physical activity, as measured by accelerometers and pedometers, is associated with reduced CRP, protection from a MPTP lesion, and should be of more interest than exercise. Spontaneous activity is associated with activation of the AKT signaling pathway, low BMI is associated with the ERK1/2 signaling pathway, and exercise is associated with the electron transport chain and translation initiation pathway – all of which converges and interact in the cell and when in proper balance promote neuroplasticity and brain resiliency (**Figure 24).** Furthermore, physical activity is associated with a peripheral marker, CRP, is protective in the MPTP model of Parkinson's disease, and results in changes to chromatin remodeling and anti-apoptotic gene transcripts in the caudate nucleus and putamen.

We tested the hypothesis that exercise is neuroprotective in two ways. First, we looked at the mechanisms of exercise alone in rhesus monkeys in the motor cortex, putamen, and hippocampus. We found that components of complex I of the electron transport chain are increased, and these are associated with Parkinson's disease (Chou et al., 2010; Betarbet et al., 2002). Upon directly testing the hypothesis using the MPTP model of Parkinson's disease in exercised Rhesus monkeys, we did not find that exercise decreased the size of the lesion. Instead, we have found that physical activity levels strongly predicted the size of the MPTP lesion.

Further studies are warranted to explore how both genetics and experience interact to protect against neurodegenerative diseases. One way to explore the genetic component of physical activity is by looking for quantitative trait loci (QTL) in mice bred to be highly active or highly inactive. Mouse lines natural have different physical activity levels (Knab et al., 2009). C576J/BL mice have higher activity levels than C3H mice and this has been explained by examining quantitative trait loci (QTL), which have implicated the dopamine system in genetic predispositions to exercise (Bronikowski et al., 2004). Other studies in ADHD patients have linked dopamine markers with activity levels as well (Arnsten, 2006; Li et al., 2006). There is a dopamine model of the genetics of physical activity levels, which suggests that dopamine both affects and is affected by activity levels, but other studies are needed to investigate the other QTL associated with physical activity.

Another way to study if physical activity levels alone protect against neurodegenerative lesions is, in a very well controlled study, to manipulate physical activity levels in mice, who naturally have the same activity levels. A group of mice matched with the same levels of activity could be divided into three groups: (a) one group whose activity levels would be increased, (b) a second group whose activity levels would not be manipulated, and (c) a third group whose activity levels would be reduced. All three groups after three months of their condition would be exposed to MPTP, and seven weeks after the extent of the lesion could be assessed by measuring TH and DAT levels. Studies similar to this have been done and do suggest that physical activity levels protect against Parkinson disease like lesions (Caudle et al., 2007; Mabandla et al., 2004; O'Dell et al., 2007), but they haven't been well controlled specifically for activity levels.

In sum, we provide evidence that an individual's experiences, specifically physical activity levels, are associated with a change in neural resources that change the ability to cope with a MPTP lesion, mimicking Parkinson's disease. The mechanism of these changes includes chromatin remodeling, anti-apoptotic processes, and neuronal survival signaling cascades (Mitchell et al., 2010; Mitchell et al., 2011b; Mitchell et al., 2011c). One's experiences, may that be their physical activity levels, BMI, exercise, or even as suggested by other research the foods they eat and calorie intake (Stranahan et al., 2009), can change his or her neuronal resiliency. Taken together these things help shape the brain's resources to take on highly complex interactions and deal with the onslaught of neurodegeneration.

Supplementary Table 1. Spontaneous Activity Associated Gene Expression Changes in the Motor Cortex. Genes are identified with their HG and RhG probes names, the human gene symbol, the human gene title, percent identity between RhG and HG probes (% ID), both HG and RhG interquartile ranges, and both HG and RhG Entrez Gene ID numbers. Genes decreasing in expression with physical activity level are indicated with (-), genes increasing in expression with physical activity level are indicated with (+), genes changing in different directions on both arrays are indicated with (≠). Note the high degree of concordance between the two datasets: of the ninety-eight probes reporting activity-dependent expression ninety-six reported expression change in the same direction.

SUPPLEMENTARY TABLE 1. Spontaneous Activity-Associated Gene Expression Changes in the Motor Cortex.

HG Probe	RH Probe	% ID	*HG pval*	*RH pval*	Direction	HG IQR	RH IQR	HG Gene Title	HG Gene Symbol	HG Entrez Gene ID	RH Entrez Gene ID
237782_at	MmugDNA.20858.1.S1_at	97.2	***0.005***	***0.034***	-	**0.313**	**0.405**	---	---	---	---
238714_at	MmugDNA.21680.1.S1_at	89.51	***0.009***	***0.043***	-	**0.494**	**0.467**	---	---	---	---
239856_at	MmugDNA.42244.1.S1_at	89.91	***0.010***	***0.004***	-	**0.391**	**0.419**	---	---	---	---
240216_at	MmugDNA.15928.1.S1_at	98.06	***0.039***	***0.042***	-	**0.433**	**0.325**	---	---	---	---
239361_at	MmugDNA.15335.1.S1_at	93.3	***0.007***	***0.029***	-	**0.284**	**0.267**	---	---	---	---
235713_at	MmugDNA.2645.1.S1_at	93.15	***0.016***	***0.028***	-	**0.580**	**1.352**	alkB, alkylation repair homolog 8 (E. coli)	ALKBH8	91801	706917
203264_s_at	MmugDNA.8595.1.S1_at	95.47	***0.025***	***0.039***	-	**0.601**	**1.248**	Cdc42 guanine nucleotide exchange factor (GEF) 9	ARHGEF9	23229	707387
201229_s_at	MmugDNA.5444.1.S1_s_at	91.67	***0.031***	***0.014***	-	**0.643**	**0.568**	ariadne homolog 2 (Drosophila)	ARIH2	10425	719993
203796_s_at	MmuSTS.3204.1.S1_at	93.71	***0.027***	***0.015***	-	**0.368**	**0.357**	B-cell CLL/lymphoma 7A	BCL7A	605	705028
1555773_at	MmugDNA.34502.1.S1_at	89.04	***0.002***	***0.007***	-	**0.484**	**0.462**	bactericidal/permeability-increasing protein-like 2	BPIL2	254240	717287
1556072_at	MmugDNA.4176.1.S1_at	63.51	***0.039***	***0.012***	-	**0.270**	**0.307**	chromosome 22 open reading frame 37	C22orf37	200298	---
219578_s_at	MmugDNA.36706.1.S1_at	97.39	***0.039***	***0.033***	-	**0.429**	**0.268**	cytoplasmic polyadenylation element binding protein 1	CPEB1	64506	694357

201201_at	MmugDNA.35450.1.S1_at	64.01	***0.038***	***0.021***	-	**0.391**	**0.434**	cystatin B (stefin B)	CSTB	1476	713504
201693_s_at	MmugDNA.10815.1.S1_at	98.1	***0.027***	***0.031***	-	**0.456**	**0.389**	early growth response 1	EGR1	1958	716786
208962_s_at	MmugDNA.23574.1.S1_at	93.75	***0.033***	***0.034***	-	**0.752**	**0.772**	fatty acid desaturase 1 /// fatty acid desaturase 3	FADS1 /// FADS3	3992 /// 3995	---
237466_s_at	MmugDNA.6750.1.S1_at	93.39	***0.007***	***0.014***	-	**0.713**	**0.590**	hedgehog interacting protein	HHIP	64399	701205
200775_s_at	MmugDNA.4119.1.S1_at	99.39	***0.021***	***0.033***	-	**0.904**	**1.185**	heterogeneous nuclear ribonucleoprotein K	HNRNPK	3190	709112
242293_at	MmugDNA.18588.1.S1_at	83.63	***0.016***	***0.027***	-	**0.419**	**0.367**	inhibitor of growth family, member 3	ING3	54556	694005
216807_at	MmugDNA.6876.1.S1_at	93.12	***0.018***	***0.038***	-	**0.349**	**0.392**	KIAA1751	KIAA1751	85452	709689
207065_at	MmuSTS.1586.1.S1_at	94.93	***0.009***	***0.046***	-	**0.305**	**0.264**	keratin 75	KRT75	9119	699682
203836_s_at	MmugDNA.12217.1.S1_at	97.1	***0.027***	***0.007***	-	**0.303**	**0.275**	mitogen-activated protein kinase kinase kinase 5	MAP3K5	4217	711382
218211_s_at	MmugDNA.20540.1.S1_at	92.73	***0.001***	***0.029***	-	**0.543**	**1.237**	melanophilin	MLPH	79083	694820
202607_at	MmugDNA.16857.1.S1_at	95.25	***0.024***	***0.014***	-	**0.289**	**0.492**	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	NDST1	3340	712425
208612_at	MmugDNA.2124.1.S1_at	97.67	***0.026***	***0.015***	-	**0.466**	**0.498**	protein disulfide isomerase family A, member 3	PDIA3	2923	711029
222019_at	MmugDNA.30493.1.S1_at	91.41	***0.020***	***0.032***	-	**0.265**	**0.303**	prefoldin subunit 6	PFDN6	10471	718253
204048_s_at	MmugDNA.19278.1.S1_at	92.17	***0.014***	***0.006***	-	**0.466**	**0.631**	phosphatase and actin regulator 2	PHACTR2	9749	700363
229376_at	MmugDNA.22007.1.S1_at	99.3	***0.012***	***0.038***	-	**0.653**	**0.686**	prospero homeobox 1	PROX1	5629	709465
221277_s_at	MmugDNA.19674.1.S1_at	96.85	***0.005***	***0.002***	-	**0.340**	**0.364**	pseudouridylate synthase 3	PUS3	83480	713746
204243_at	MmuSTS.1735.1.S1_at	96.22	***0.045***	***0.014***	-	**0.398**	**0.635**	rearranged L-myc fusion	RLF	6018	693503

213459_at	MmugDNA.41298.1.S1_at	93.14	***0.028***	***0.009***	-	**0.459**	**0.383**	ribosomal protein L37a	RPL37A	6168	696415 /// 707154
224754_at	MmuSTS.4487.1.S1_at	90.96	***0.018***	***0.006***	-	**0.486**	**0.449**	Sp1 transcription factor	SP1	6667	702710
219685_at	MmugDNA.35136.1.S1_at	96.1	***0.014***	***0.041***	-	**0.697**	**0.955**	transmembrane protein 35	TMEM35	59353	702205
209226_s_at	MmugDNA.5339.1.S1_at	31.15	***0.004***	***0.020***	-	**0.298**	**0.551**	transportin 1	TNPO1	3842	707195
242499_at	MmugDNA.32356.1.S1_at	86.12	***0.029***	***0.049***	-	**0.354**	**0.286**	U2 small nuclear RNA auxiliary factor 1	U2AF1	7307	---
204893_s_at	MmuSTS.2611.1.S1_at	91.21	***0.021***	***0.033***	-	**0.583**	**0.793**	zinc finger, FYVE domain containing 9	ZFYVE9	9372	713155
214942_at	MmugDNA.7677.1.S1_at	93.68	***0.011***	***0.010***	≠	**0.274**	**0.355**	RNA binding motif protein 34	RBM34	23029	711962
222831_at	MmugDNA.11779.1.S1_at	0	***0.033***	***0.043***	≠	**0.345**	**0.302**	SAP30-like	SAP30L	79685	714400
1564381_s_at	MmugDNA.41201.1.S1_at	92.28	***0.015***	***0.047***	+	**0.278**	**0.338**	---	---	---	---
239262_at	MmugDNA.12727.1.S1_at	94	***0.017***	***0.013***	+	**0.291**	**0.385**	---	---	---	---
226280_at	MmugDNA.31249.1.S1_at	82.68	***0.018***	***0.026***	+	**0.427**	**0.275**	---	---	---	---
237008_at	MmugDNA.2202.1.S1_at	97.71	***0.043***	***0.039***	+	**0.817**	**0.956**	---	---	---	---
209027_s_at	MmugDNA.3144.1.S1_at	96.83	***0.023***	***0.022***	+	**0.300**	**0.329**	abl-interactor 1	ABI1	10006	707698
242876_at	MmugDNA.2158.1.S1_at	91.92	***0.018***	***0.043***	+	**0.328**	**1.206**	V-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	AKT3	10000	---
222767_s_at	MmugDNA.3366.1.S1_at	95.32	***0.035***	***0.004***	+	**0.401**	**0.300**	chromosome 12 open reading frame 49	C12orf49	79794	713916
1553801_a_at	MmugDNA.6301.1.S1_s_at	97.73	***0.019***	***0.034***	+	**0.310**	**0.328**	chromosome 14 open reading frame 126	C14orf126	112487	717267
214816_x_at	MmugDNA.21116.1.S1_at	78.62	***0.002***	***0.007***	+	**0.315**	**0.469**	chromosome 19 open reading frame 40	C19orf40	91442	---

236634_at	MmugDNA.15731.1.S1_at	95.2	***0.010***	***0.025***	+	**0.452**	**0.382**	chromosome 8 open reading frame 48	C8orf48	157773	700746
219147_s_at	MmugDNA.30781.1.S1_at	95.84	***0.022***	***0.018***	+	**0.346**	**0.468**	chromosome 9 open reading frame 95	C9orf95	54981	703868
223300_s_at	MmugDNA.27206.1.S1_at	93.14	***0.047***	***0.015***	+	**0.469**	**0.324**	coiled-coil domain containing 82	CCDC82	79780	700198
219947_at	MmuSTS.718.1.S1_at	96.24	***0.036***	***0.019***	+	**0.298**	**0.417**	C-type lectin domain family 4, member A	CLEC4A	50856	716122
1554242_a_at	MmugDNA.12890.1.S1_at	91.11	***0.049***	***0.015***	+	**0.489**	**0.516**	coagulation factor C homolog, cochlin (Limulus polyphemus)	COCH	1690	717114
218142_s_at	MmugDNA.28472.1.S1_at	86.33	***0.028***	***0.021***	+	**0.361**	**0.271**	cereblon	CRBN	51185	704436
207630_s_at	MmugDNA.34749.1.S1_at	96.5	***0.035***	***0.029***	+	**0.357**	**0.276**	cAMP responsive element modulator	CREM	1390	698636
238554_at	MmugDNA.40221.1.S1_at	94.77	***0.015***	***0.045***	+	**0.388**	**0.383**	cytochrome b5 type B (outer mitochondrial membrane)	CYB5B	80777	705093
223331_s_at	MmugDNA.309.1.S1_at	96.13	***0.022***	***0.037***	+	**0.340**	**0.340**	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	DDX20	11218	704731
226767_s_at	MmugDNA.19862.1.S1_at	93.73	***0.011***	***0.030***	+	**0.325**	**0.273**	fumarylacetoacetate hydrolase domain containing 1	FAHD1	81889	722505
218504_at	MmugDNA.36618.1.S1_at	96.15	***0.005***	***0.024***	+	**0.414**	**0.474**	fumarylacetoacetate hydrolase domain containing 2A	FAHD2A	51011	706967
217850_at	MmugDNA.15299.1.S1_at	88.46	***0.044***	***0.040***	+	**0.395**	**0.369**	guanine nucleotide binding protein-like 3 (nucleolar)	GNL3	26354	695877
202605_at	MmuSTS.4305.1.S1_at	77.02	***0.037***	***0.003***	+	**0.402**	**0.352**	glucuronidase, beta	GUSB	2990	677692

228375_at	MmugDNA.2210.1.S1_at	90.45	***0.017***	***0.016***	+	**0.301**	**0.287**	immunoglobulin superfamily, member 11	IGSF11	152404	713784
209566_at	MmugDNA.2140.1.S1_at	94.47	***0.018***	***0.044***	+	**0.347**	**0.305**	insulin induced gene 2	INSIG2	51141	693654
226816_s_at	MmugDNA.5413.1.S1_at	90.88	***0.043***	***0.039***	+	**0.634**	**0.586**	KIAA1143	KIAA1143	57456	---
229393_at	MmuSTS.4452.1.S1_at	98.15	***0.031***	***0.022***	+	**0.278**	**0.307**	l(3)mbt-like 3 (Drosophila)	L3MBTL3	84456	710947
228338_at	MmugDNA.27645.1.S1_at	94.04	***0.024***	***0.009***	+	**0.291**	**0.369**	hypothetical protein LOC120376	LOC120376	120376	710801
223098_s_at	MmugDNA.30130.1.S1_at	87.54	***0.035***	***0.028***	+	**0.291**	**0.421**	lon peptidase 2, peroxisomal	LONP2	83752	---
218027_at	MmuSTS.954.1.S1_at	82.4	***0.005***	***0.030***	+	**0.319**	**0.277**	mitochondrial ribosomal protein L15	MRPL15	29088	694274
225341_at	MmugDNA.40986.1.S1_at	97.16	***0.015***	***0.030***	+	**0.372**	**0.321**	MTERF domain containing 3	MTERFD3	80298	703525 /// 703925
222837_s_at	MmugDNA.38789.1.S1_at	74.25	***0.012***	***0.041***	+	**0.426**	**0.343**	NMDA receptor regulated 1	NARG1	80155	697123
209105_at	MmugDNA.40567.1.S1_at	63.5	***0.027***	***0.025***	+	**0.270**	**0.534**	nuclear receptor coactivator 1	NCOA1	8648	693342
202150_s_at	MmugDNA.7464.1.S1_at	97.28	***0.004***	***0.003***	+	**0.290**	**0.291**	neural precursor cell expressed, developmentally down-regulated 9	NEDD9	4739	699359
224436_s_at	Mmu.13961.1.S1_at	82.88	***0.008***	***0.021***	+	**0.342**	**0.476**	nipsnap homolog 3A (C. elegans)	NIPSNAP3A	25934	716188
239293_at	MmuSTS.1691.1.S1_at	92.94	***0.000***	***0.010***	+	**0.330**	**0.271**	neurensin 1	NRSN1	140767	707362
203351_s_at	MmugDNA.29856.1.S1_at	98.72	***0.007***	***0.011***	+	**0.333**	**0.265**	origin recognition complex, subunit 4-like (yeast)	ORC4L	5000	721876
222719_s_at	MmugDNA.37743.1.S1_at	94.83	***0.009***	***0.006***	+	**0.409**	**0.489**	platelet derived growth factor C	PDGFC	56034	700236
205226_at	MmugDNA.20932.1.S1_at	96.3	***0.031***	***0.048***	+	**0.322**	**0.588**	platelet-derived growth factor receptor-like	PDGFRL	5157	703117

205960_at	MmugDNA.985.1.S1_at	87.27	***0.014***	***0.004***	+	**0.393**	**0.475**	pyruvate dehydrogenase kinase, isozyme 4	PDK4	5166	698726
230434_at	MmugDNA.25986.1.S1_at	98.74	***0.024***	***0.019***	+	**0.676**	**0.695**	phosphatase, orphan 2	PHOSPHO2	493911	---
222699_s_at	MmugDNA.2610.1.S1_s_at	94.49	***0.006***	***0.005***	+	**0.384**	**0.381**	pleckstrin homology domain containing, family F (with FYVE domain) member 2	PLEKHF2	79666	701884
227148_at	MmugDNA.37529.1.S1_at	95.49	***0.008***	***0.024***	+	**0.353**	**0.498**	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2	PLEKHH2	130271	713488
209317_at	MmugDNA.1251.1.S1_at	95.74	***0.024***	***0.027***	+	**0.321**	**0.451**	polymerase (RNA) I polypeptide C, 30kDa	POLR1C	9533	700727
1554365_a_at	Mmu.15077.1.S1_at	0	***0.025***	***0.013***	+	**0.270**	**0.273**	protein phosphatase 2, regulatory subunit B', gamma isoform	PPP2R5C	5527	718894
221547_at	MmugDNA.10448.1.S1_at	90.57	***0.016***	***0.042***	+	**0.318**	**0.295**	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)	PRPF18	8559	696401
222077_s_at	MmuSTS.2069.1.S1_at	61.9	***0.034***	***0.038***	+	**0.437**	**0.350**	Rac GTPase activating protein 1	RACGAP1	29127	711887
212591_at	MmugDNA.11046.1.S1_at	95.45	***0.007***	***0.042***	+	**0.577**	**0.479**	RNA binding motif protein 34	RBM34	23029	711962
214943_s_at	MmugDNA.7677.1.S1_at	93.6	***0.049***	***0.010***	+	**0.418**	**0.355**	RNA binding motif protein 34	RBM34	23029	711962
210138_at	MmuSTS.3132.1.S1_at	92.49	***0.020***	***0.027***	+	**0.397**	**0.320**	regulator of G-protein signaling 20	RGS20	8601	693454
209091_s_at	MmugDNA.13601.1.S1_at	0	***0.025***	***0.028***	+	**0.299**	**0.399**	SH3-domain GRB2-like endophilin B1	SH3GLB1	51100	712393

206613_s_at	MmugDNA.7833.1.S1_at	96.64	***0.021***	***0.012***	+	**0.274**	**0.334**	TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kDa	TAF1A	9015	704624
224560_at	MmugDNA.21307.1.S1_at	82.74	***0.019***	***0.016***	+	**0.295**	**0.299**	TIMP metallopeptidase inhibitor 2	TIMP2	7077	---
210379_s_at	MmugDNA.33852.1.S1_at	91.57	***0.050***	***0.020***	+	**0.287**	**0.300**	tousled-like kinase 1	TLK1	9874	701221
219253_at	MmugDNA.20643.1.S1_at	59.09	***0.024***	***0.025***	+	**0.299**	**0.363**	transmembrane protein 185B (pseudogene)	TMEM185B	79134	695744
229126_at	MmugDNA.15766.1.S1_at	92.94	***0.037***	***0.028***	+	**0.427**	**0.401**	transmembrane protein 19	TMEM19	55266	---
225375_at	MmugDNA.11921.1.S1_at	67.81	***0.040***	***0.020***	+	**0.414**	**0.346**	transmembrane protein 199	TMEM199	147007	708298
209412_at	MmugDNA.31122.1.S1_at	96.2	***0.045***	***0.047***	+	**0.359**	**0.370**	trafficking protein particle complex 10	TRAPPC10	7109	---
203599_s_at	MmuSTS.2586.1.S1_at	94.83	***0.046***	***0.037***	+	**0.293**	**0.264**	WW domain binding protein 4 (formin binding protein 21)	WBP4	11193	698220
224898_at	MmugDNA.20064.1.S1_at	96.15	***0.013***	***0.001***	+	**0.489**	**0.505**	WD repeat domain 26	WDR26	80232	704911
226668_at	MmugDNA.16148.1.S1_at	89.23	***0.016***	***0.004***	+	**0.451**	**0.268**	WD repeat, sterile alpha motif and U-box domain containing 1	WDSUB1	151525	699456
1552608_at	MmugDNA.12587.1.S1_at	77.4	***0.005***	***0.040***	+	**0.287**	**0.273**	WAP four-disulfide core domain 11	WFDC11	259239	709928
206683_at	MmuSTS.2618.1.S1_at	98.59	***0.017***	***0.013***	+	**0.573**	**0.392**	zinc finger protein 165	ZNF165	7718	706080

Supplementary Table 2. Spontaneous Activity Associated Gene Expression Changes in the Caudate Nucleus. Genes are identified with their HG and RhG probes names, the human gene symbol, the human gene title, percent identity between RhG and HG probes (% ID), both HG and RhG interquartile ranges, and both HG and RhG Entrez Gene ID numbers. Genes decreasing in expression with physical activity level are indicated with (-), genes increasing in expression with physical activity level are indicated with (+), genes changing in different directions on both arrays are indicated with (≠). Note the high degree of concordance between the two datasets: of the twenty-eight probes reporting activity-dependent expression twenty-eight reported expression change in the same direction.

SUPPLEMENTARY TABLE 2. Spontaneous Activity-Associated Gene Expression Changes in the Caudate Nucleus.

HG Probe	RH Probe	% ID	HG pval	RH pval	Direction	HG IQR	RH IQR	HG Gene Title	HG Gene Symbol	HG Entrez Gene ID	RH Entrez Gene ID
229781_at	MmugDNA.24219.1.S1_at	92.67	0.001	0.024	-	**0.484**	**1.175**	---	---	---	---
243904_at	MmugDNA.32292.1.S1_at	92.51	0.006	0.003	-	**1.156**	**1.816**	---	---	---	---
243915_at	MmugDNA.4635.1.S1_at	91.04	0.017	0.031	-	**0.610**	**1.053**	---	---	---	---
238714_at	MmugDNA.21680.1.S1_at	89.51	0.019	0.018	-	**0.312**	**0.607**	---	---	---	---
239278_at	MmugDNA.3222.1.S1_at	94.99	0.033	0.011	-	**0.280**	**0.401**	---	---	---	---
235713_at	MmugDNA.2645.1.S1_at	93.15	0.014	0.013	-	**0.381**	**0.645**	alkB, alkylation repair homolog 8 (E. coli)	ALKBH8	91801	706917
231918_s_at	MmugDNA.13970.1.S1_at	91.69	0.030	0.016	-	**0.717**	**0.471**	G elongation factor, mitochondrial 2	GFM2	84340	704247
225392_at	MmugDNA.33130.1.S1_at	94.39	0.033	0.003	-	**0.289**	**0.355**	G elongation factor, mitochondrial 2	GFM2	84340	704247
201721_s_at	MmuSTS.2956.1.S1_at	86.83	0.020	0.013	-	**0.316**	**0.270**	lysosomal multispanning membrane protein 5	LAPTM5	7805	---
221277_s_at	MmugDNA.19674.1.S1_at	96.85	0.004	0.008	-	**0.312**	**0.495**	pseudouridylate synthase 3	PUS3	83480	713746
218354_at	MmugDNA.16031.1.S1_at	96.89	0.020	0.022	-	**0.365**	**0.416**	trafficking protein particle complex 2-like	TRAPPC2L	51693	697970
215330_at	MmugDNA.31871.1.S1_at	86.75	0.003	0.022	+	**0.322**	**0.688**	---	---	---	---
237008_at	MmugDNA.2202.1.S1_at	97.71	0.021	0.016	+	**0.441**	**0.422**	---	---	---	---
229648_at	MmugDNA.29513.1.S1_at	87.61	0.033	0.019	+	**0.608**	**0.634**	---	---	---	---

214953_s_at	MmuSTS.2836.1.S1_at	97.77	0.019	0.023	+	**0.986**	**0.915**	amyloid beta (A4) precursor protein	APP	351	708212
217818_s_at	MmugDNA.4234.1.S1_s_at	0	0.002	0.026	+	**0.477**	**1.132**	actin related protein 2/3 complex, subunit 4, 20kDa /// tubulin tyrosine ligase-like family, member 3	ARPC4 /// TTLL3	10093 /// 26140	703147
211672_s_at	MmugDNA.4234.1.S1_s_at	97.38	0.013	0.026	+	**0.730**	**1.132**	actin related protein 2/3 complex, subunit 4, 20kDa /// tubulin tyrosine ligase-like family, member 3	ARPC4 /// TTLL3	10093 /// 26140	703147
241836_x_at	MmugDNA.3354.1.S1_at	85.14	0.019	0.047	+	**0.275**	**0.581**	centrosomal protein 97kDa	CEP97	79598	---
212539_at	MmuSTS.2204.1.S1_at	0	0.018	0.030	+	**0.327**	**0.373**	chromodomain helicase DNA binding protein 1-like	CHD1L	9557	700179
1556988_s_at	MmuSTS.2204.1.S1_s_at	78.32	0.006	0.001	+	**0.265**	**0.322**	chromodomain helicase DNA binding protein 1-like	CHD1L	9557	700179
223875_s_at	MmugDNA.25989.1.S1_at	94.24	0.003	0.022	+	**0.375**	**0.608**	enhancer of polycomb homolog 1 (Drosophila)	EPC1	80314	721332
237392_at	MmugDNA.41027.1.S1_at	94.5	0.010	0.007	+	**0.528**	**0.630**	hypothetical protein LOC283480	LOC283480	283480	---
201014_s_at	MmugDNA.18421.1.S1_at	99.17	0.019	0.020	+	**0.711**	**0.644**	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	PAICS	10606	694743

230434_at	MmugDNA.25986.1.S1_at	98.74	0.039	0.018	+	**0.332**	**0.341**	phosphatase, orphan 2	PHOSPHO2	493911	---
235711_at	MmugDNA.5589.1.S1_at	96.43	0.008	0.037	+	**0.628**	**0.965**	purine-rich element binding protein B	PURB	5814	705519
226762_at	MmugDNA.1658.1.S1_at	97.88	0.027	0.039	+	**1.354**	**1.151**	purine-rich element binding protein B	PURB	5814	705519
205529_s_at	MmugDNA.6345.1.S1_at	98.81	0.026	0.033	+	**0.806**	**0.660**	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	RUNX1T1	862	696934
221096_s_at	MmugDNA.8060.1.S1_at	73.61	0.001	0.000	+	**0.293**	**0.331**	transmembrane and coiled-coil domains 6	TMCO6	55374	697611

Supplementary Table 3. BMI Associated Gene Expression Changes in the Motor Cortex. All genes in the table were significant on both RhG and HG microarrays with a $p < 0.05$. Genes are identified with their HG and RhG probes names, the human gene symbol, the human gene title, percent identity between RhG and HG probes (% ID), both HG and RhG p values (pval), both HG and RhG interquartile ranges (IQR), and both HG and RhG Entrez Gene ID numbers. Genes with negatively correlated expression with BMI are blue and indicated with (-), and genes with positively correlated expression with BMI are red and indicated with (+). There is 100% concordance between the human and monkey microarray datasets.

SUPPLEMENTARY TABLE 3. BMI Associated Gene Expression Changes in the Motor Cortex.

HG Probe	**RH Probe**	**% ID**	***HG pval***	***RH pval***	**Direction**	**HG IQR**	**RH IQR**	**HG Gene Title**	**HG Gene Symbol**	**HG Entrez Gene ID**	**RH Entrez Gene ID**
233940_at	MmugDNA.24373.1.S1_at	95.28	*0.042*	*0.045*	-	**0.277**	**0.310**	---	---	---	---
228241_at	MmugDNA.30526.1.S1_at	96.72	*0.045*	*0.023*	-	**0.590**	**0.541**	anterior gradient homolog 3 (Xenopus laevis)	AGR3	155465	714517
201525_at	Mmu.8637.1.S1_at	63.93	*0.044*	*0.044*	-	**0.489**	**0.793**	apolipoprotein D	APOD	347	709223
218936_s_at	MmuSTS.1498.1.S1_at	90.26	*0.024*	*0.028*	-	**0.657**	**0.782**	coiled-coil domain containing 59	CCDC59	29080	698443
202447_at	MmugDNA.36905.1.S1_at	94.82	*0.013*	*0.020*	-	**0.375**	**0.346**	2,4-dienoyl CoA reductase 1, mitochondrial	DECR1	1666	696035
214240_at	MmugDNA.42549.1.S1_at	94.88	*0.041*	*0.049*	-	**0.876**	**1.052**	galanin prepropeptide	GAL	51083	721572
227466_at	MmugDNA.38075.1.S1_at	89.9	*0.014*	*0.046*	-	**0.364**	**0.612**	hypothetical protein LOC285550	LOC285550	285550	714235
1558732_at	MmugDNA.11872.1.S1_at	87.5	*0.027*	*0.010*	-	**0.602**	**1.941**	mitogen-activated protein kinase kinase kinase kinase 4	MAP4K4	9448	---
57540_at	MmugDNA.35682.1.S1_at	87.14	*0.026*	*0.023*	-	**0.291**	**0.344**	ribokinase	RBKS	64080	702464
1568627_at	MmugDNA.35505.1.S1_at	96.06	*0.022*	*0.042*	-	**0.493**	**0.477**	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	SMEK2	57223	---
1568932_at	MmugDNA.5906.1.S1_at	93.15	*0.001*	*0.010*	+	**0.509**	**0.561**	---	---	---	---
1560422_at	MmugDNA.40378.1.S1_at	92.31	*0.015*	*0.021*	+	**0.719**	**1.079**	---	---	---	---
204608_at	MmugDNA.11311.1.S1_at	85.13	*0.032*	*0.033*	+	**0.391**	**0.448**	argininosuccinate lyase	ASL	435	697109

218447_at	MmugDNA.14860.1.S1_at	83.64	*0.018*	*0.034*	+	**0.530**	**0.368**	chromosome 16 open reading frame 61	C16orf61	56942	---
203984_s_at	MmuSTS.3289.1.S1_at	90.61	*0.021*	*0.032*	+	**0.274**	**0.434**	caspase 9, apoptosis-related cysteine peptidase	CASP9	842	694544
211031_s_at	MmugDNA.8866.1.S1_at	93.41	*0.041*	*0.010*	+	**0.278**	**0.431**	CAP-GLY domain containing linker protein 2	CLIP2	7461	---
205373_at	MmuSTS.795.1.S1_at	98.39	*0.039*	*0.048*	+	**0.264**	**0.273**	catenin (cadherin-associated protein), alpha 2	CTNNA2	1496	712135
204718_at	MmugDNA.26316.1.S1_at	96.85	*0.033*	*0.008*	+	**0.422**	**0.410**	EPH receptor B6	EPHB6	2051	704886
215313_x_at	Mmu.2935.4.S1_x_at	60.42	*0.020*	*0.008*	+	**0.338**	**0.484**	major histocompatibility complex, class I, A	HLA-A	3105	---
207695_s_at	MmugDNA.20291.1.S1_at	96.59	*0.008*	*0.005*	+	**0.268**	**0.399**	immunoglobulin superfamily, member 1	IGSF1	3547	704264
221659_s_at	MmugDNA.24287.1.S1_at	56.5	*0.030*	*0.047*	+	**0.437**	**0.604**	myosin light chain 2, precursor lymphocyte-specific	MYLC2PL	93408	---
211778_s_at	MmugDNA.9681.1.S1_at	96.72	*0.026*	*0.008*	+	**0.413**	**0.422**	ovo-like 2 (Drosophila)	OVOL2	58495	699284
206691_s_at	MmugDNA.14080.1.S1_at	87.6	*0.044*	*0.011*	+	**0.301**	**0.337**	protein disulfide isomerase family A, member 2	PDIA2	64714	694964
200060_s_at	MmugDNA.2018.1.S1_s_at	89.7	*0.005*	*0.004*	+	**0.403**	**0.459**	RNA binding protein S1, serine-rich domain	RNPS1	10921	695816
231650_s_at	MmugDNA.43618.1.S1_at	95.1	*0.019*	*0.022*	+	**0.515**	**0.540**	Seizure related 6 homolog (mouse)-like	SEZ6L	23544	---

220135_s_at	MmugDNA.19382.1.S1_at	77.32	*0.007*	*0.003*	+	**0.458**	**0.456**	solute carrier family 7 (cationic amino acid transporter, y+ system), member 9	SLC7A9	11136	703081
200990_at	MmugDNA.7917.1.S1_at	98.79	*0.033*	*0.041*	+	**0.354**	**0.461**	tripartite motif-containing 28	TRIM28	10155	711982

Supplementary Table 4. BMI Associated Gene Expression Changes in the Caudate Nucleus. All genes in the table were significant on both RhG and HG microarrays with a $p < 0.05$. Genes are identified with their HG and RhG probes names, the human gene symbol, the human gene title, percent identity between RhG and HG probes (% ID), both HG and RhG p values (pval), both HG and RhG interquartile ranges (IQR), and both HG and RhG Entrez Gene ID numbers. Genes with negatively correlated expression with BMI are blue and indicated with (-), and genes with positively correlated expression with BMI are red and indicated with (+). There is 100% concordance between the human and monkey microarray datasets.

SUPPLEMENTARY TABLE 4. BMI Associated Gene Expression Changes in the Caudate Nucleus.

HG Probe	**RH Probe**	**% ID**	***HG pval***	***RH pval***	**Direction**	**HG IQR**	**RH IQR**	**HG Gene Title**	**HG Gene Symbol**	**HG Entrez Gene ID**	**RH Entrez Gene ID**
240234_at	MmugDNA.13915.1.S1_at	84.53	*0.005*	*0.033*	-	**0.269**	**0.845**	---	---	---	---
204142_at	MmugDNA.32608.1.S1_at	92.45	*0.003*	*0.042*	-	**0.381**	**0.547**	enolase superfamily member 1	ENOSF1	55556	697333
204143_s_at	MmugDNA.32608.1.S1_at	89.42	*0.013*	*0.042*	-	**0.415**	**0.547**	enolase superfamily member 1	ENOSF1	55556	697333
223933_at	MmugDNA.12670.1.S1_at	95.24	*0.043*	*0.045*	-	**0.669**	**1.226**	kinesin family member 5A	KIF5A	3798	---
1558448_a_at	MmugDNA.35655.1.S1_at	84.26	*0.001*	*0.034*	-	**0.397**	**0.571**	hypothetical protein LOC100128439	LOC100128439	100128439	---
227556_at	MmugDNA.24357.1.S1_at	97.56	*0.023*	*0.015*	-	**0.941**	**1.085**	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)	NME7	29922	---
213887_s_at	MmugDNA.37439.1.S1_at	95.43	*0.008*	*0.036*	-	**0.423**	**0.393**	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa	POLR2E	5434	721178
226923_at	MmugDNA.34854.1.S1_at	95.9	*0.038*	*0.036*	-	**0.305**	**0.297**	sec1 family domain containing 2	SCFD2	152579	698111
200986_at	MmuSTS.2736.1.S1_at	89.43	*0.035*	*0.006*	-	**0.536**	**0.689**	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	SERPING1	710	703928
228711_at	MmuSTS.49.1.S1_at	94.83	*0.040*	*0.027*	-	**0.325**	**0.418**	zinc finger protein 37A	ZNF37A	7587	701714
222365_at	MmugDNA.2151.1.S1_at	86.82	*0.025*	*0.002*	+	**0.275**	**0.654**	---	---	---	---

1561341_at	MmugDNA.25585.1.S1_at	92.8	*0.021*	*0.008*	+	**0.335**	**0.430**	---	---	---	---
1560422_at	MmugDNA.40378.1.S1_at	92.31	*0.006*	*0.009*	+	**0.818**	**2.226**	---	---	---	---
241391_at	MmugDNA.9839.1.S1_at	79.9	*0.018*	*0.009*	+	**0.287**	**0.737**	---	---	---	---
214949_at	MmugDNA.8635.1.S1_s_at	0	*0.042*	*0.014*	+	**0.330**	**0.437**	---	---	---	706318
238044_at	MmugDNA.4781.1.S1_at	96.22	*0.019*	*0.016*	+	**0.302**	**0.267**	---	---	---	---
229733_s_at	MmugDNA.9332.1.S1_at	93.95	*0.029*	*0.034*	+	**0.602**	**0.919**	---	---	---	---
225937_at	MmugDNA.21190.1.S1_at	96	*0.032*	*0.042*	+	**0.913**	**1.064**	---	---	---	---
218447_at	MmugDNA.14860.1.S1_at	83.64	*0.018*	*0.020*	+	**0.513**	**0.330**	chromosome 16 open reading frame 61	C16orf61	56942	---
206967_at	MmuSTS.1418.1.S1_at	97.44	*0.026*	*0.002*	+	**0.513**	**1.152**	cyclin T1	CCNT1	904	707754
226153_s_at	MmugDNA.31707.1.S1_at	88.08	*0.027*	*0.028*	+	**0.382**	**0.418**	CCR4-NOT transcription complex, subunit 6-like	CNOT6L	246175	697981
219237_s_at	MmugDNA.32967.1.S1_at	96.42	*0.015*	*0.010*	+	**0.364**	**0.558**	DnaJ (Hsp40) homolog, subfamily B, member 14	DNAJB14	79982	711298
225656_at	MmugDNA.24154.1.S1_at	96.76	*0.040*	*0.015*	+	**0.279**	**0.531**	EF-hand domain (C-terminal) containing 1	EFHC1	114327	708517
231523_at	MmugDNA.27702.1.S1_at	95.02	*0.009*	*0.026*	+	**0.462**	**0.423**	fibroblast growth factor 14	FGF14	2259	701077
204131_s_at	MmuSTS.62.1.S1_at	96.66	*0.005*	*0.003*	+	**0.348**	**0.387**	forkhead box O3	FOXO3	2309	700731
210655_s_at	MmugDNA.14229.1.S1_at	77.34	*0.035*	*0.018*	+	**0.370**	**0.408**	forkhead box O3	FOXO3	2309	700731
204132_s_at	MmugDNA.39885.1.S1_at	95.73	*0.008*	*0.028*	+	**0.531**	**0.556**	forkhead box O3	FOXO3	2309	700731
227475_at	MmugDNA.15888.1.S1_at	94.88	*0.045*	*0.034*	+	**0.362**	**0.286**	forkhead box Q1	FOXQ1	94234	722908
221312_at	MmuSTS.1464.1.S1_at	90.19	*0.001*	*0.020*	+	**0.305**	**0.354**	glucagon-like peptide 2 receptor	GLP2R	9340	717783
217232_x_at	MmugDNA.5184.1.S1_s_at	97.37	*0.037*	*0.023*	+	**0.709**	**0.823**	hemoglobin, beta	HBB	3043	---
211696_x_at	MmugDNA.5184.1.S1_s_at	97.37	*0.040*	*0.023*	+	**0.717**	**0.823**	hemoglobin, beta	HBB	3043	---
212966_at	MmugDNA.37606.1.S1_at	95.4	*0.047*	*0.029*	+	**0.333**	**0.613**	hypermethylated in cancer 2	HIC2	23119	698399

205425_at	MmugDNA.34508.1.S1_at	94.41	*0.011*	*0.022*	+	**0.344**	**0.553**	huntingtin interacting protein 1	HIP1	3092	---
215313_x_at	Mmu.2935.4.S1_x_at	60.42	*0.017*	*0.007*	+	**0.343**	**0.444**	major histocompatibility complex, class I, A	HLA-A	3105	---
213792_s_at	MmugDNA.39585.1.S1_at	88.01	*0.011*	*0.003*	+	**0.633**	**0.700**	insulin receptor	INSR	3643	---
235672_at	MmugDNA.14538.1.S1_at	96.34	*0.004*	*0.002*	+	**0.299**	**0.353**	microtubule-associated protein 6	MAP6	4135	696223
204601_at	MmugDNA.9396.1.S1_at	94.36	*0.014*	*0.014*	+	**0.320**	**0.429**	NEDD4 binding protein 1	N4BP1	9683	717876
213032_at	MmugDNA.22443.1.S1_at	96.71	*0.013*	*0.019*	+	**0.363**	**0.300**	nuclear factor I/B	NFIB	4781	714098
231361_at	MmugDNA.9065.1.S1_at	97.21	*0.033*	*0.020*	+	**0.320**	**0.265**	Neuroligin 1	NLGN1	22871	---
202600_s_at	MmugDNA.40878.1.S1_at	94.22	*0.002*	*0.034*	+	**0.585**	**0.506**	nuclear receptor interacting protein 1	NRIP1	8204	693428
200637_s_at	MmugDNA.16229.1.S1_at	97.87	*0.043*	*0.021*	+	**0.294**	**0.378**	protein tyrosine phosphatase, receptor type, F	PTPRF	5792	701160
205037_at	MmugDNA.9524.1.S1_at	95.47	*0.002*	*0.007*	+	**0.509**	**0.544**	RAB, member of RAS oncogene family-like 4	RABL4	11020	697032
215138_s_at	MmugDNA.19723.1.S1_at	98.69	*0.018*	*0.011*	+	**0.370**	**0.320**	kazrin	RP1-21O18.1	23254	---
213478_at	MmugDNA.38661.1.S1_at	90.81	*0.008*	*0.030*	+	**0.842**	**0.765**	kazrin	RP1-21O18.1	23254	---
210959_s_at	MmugDNA.15875.1.S1_at	93.69	*0.036*	*0.029*	+	**0.300**	**0.608**	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	SRD5A1	6715	695103
202817_s_at	MmugDNA.7777.1.S1_s_at	96.84	*0.038*	*0.029*	+	**0.716**	**0.907**	synovial sarcoma translocation, chromosome 18	SS18	6760	709897
202816_s_at	MmugDNA.7622.1.S1_at	98.14	*0.010*	*0.033*	+	**0.632**	**0.716**	synovial sarcoma translocation, chromosome 18	SS18	6760	709897

200976_s_at	MmugDNA.14263.1.S1_at	85.92	*0.049*	*0.031*	+	**0.476**	**0.436**	Tax1 (human T-cell leukemia virus type I) binding protein 1	TAX1BP1	8887	698103
222634_s_at	MmugDNA.41253.1.S1_at	98.44	*0.038*	*0.025*	+	**0.263**	**0.494**	151eparin151ing (beta)-like 1 X-linked receptor 1	TBL1XR1	79718	712740
214948_s_at	MmugDNA.8635.1.S1_s_at	93.77	*0.039*	*0.014*	+	**0.421**	**0.437**	TATA element modulatory factor 1	TMF1	7110	706318
213922_at	MmugDNA.9234.1.S1_at	95.07	*0.011*	*0.031*	+	**0.748**	**0.662**	tau tubulin kinase 2	TTBK2	146057	712249

Supplementary Table 5. Gene Ontology Classification of BMI-associated Expression Changes in the Motor Cortex. GO Biological Process terms were used to determine the function of BMI associated genes in the motor cortex. Genes highlighted in blue denote decreased expression, while genes in red denote increased expression with increased BMI. Note that the most altered BMI-dependent GO terms were associated with apoptosis.

SUPPLEMENTARY TABLE 5. Gene Ontology Classification of BMI-associated Expression Changes in the Motor Cortex

Analysis	GO TERM	# OF GENES	GENE NAMES
GO Biological Process	metabolism	6	ASL, APOD, DECR1, RBK5, RNPS1, SLC6A9
	protein amino acid phosphorylation	2	EPHB6, MAP4K4
	apoptosis	2	CASP9, PDIA2

Supplementary Table 6. Gene Ontology Classification of BMI-associated Expression Changes in the Caudate Nucleus. GO Biological Process terms were used to determine the function of BMI associated genes in the caudate nucleus. Genes highlighted in blue denote decreased expression, while genes in red denote increased expression with increased BMI. Note that the most altered BMI-dependent GO terms were associated with transcription and apoptosis.

SUPPLEMENTARY TABLE 6. Gene Ontology Classification of BMI-associated Expression Changes in the Caudate Nucleus

Analysis	GO TERM	# OF GENES	GENE NAMES
GO Biological Process	transcription	13	CCNT1, CNOT6L, FOXO3B, FOXQ1, HIC2, HIP1, NFIB, NRIP1, POL2E, SS18, SMF, TBLIXR1, ZNF37A
	apoptosis	4	HIP1, PTFRF, TAX1BP1, TTBK2
	metabolism	3	SRD5A1, NME7, ENOSF1
	signal transduction	3	FGF14, GLP2R, INSR
	transport	3	HBB, KIF5A, SCFD2

Supplementary Table 7. Exercise Associated Gene Expression in the Motor Cortex. All transcripts in the table are significant with p<0.05 for both paired and groupwise t-tests. All transcripts are identified by their Probe Set ID, Gene title, Entrez Gene ID, and Gene symbol. Transcript data is listed for the motor cortex (M), putamen (P), and hippocampus (H). For each transcript we calculated their average log ratio (ALR, the average expression change of the exercising monkeys minus the sedentary monkeys), the direction of the change, the p-value for the groupwise and paired t-tests, and if the transcript met the significance cutoff in each brain region. There are 434 transcripts differentially expressed by exercise in the motor cortex.

Supplementary Table 7. Exercise Associated Gene Expression in the Motor Cortex.

Probe Set ID	Gene Title	Entrez Gene ID	Gene Symbol	M ALR	M DIR	M TTEST (GROUP)	M TTEST (PAIR)
235201_PM_at	---	---	---	-0.488	-	0.000	0.007
1561212_PM_at	---	---	---	-0.361	-	0.001	0.009
234674_PM_at	---	---	---	-0.266	-	0.003	0.007
237421_PM_at	---	---	---	-0.383	-	0.006	0.029
1566032_PM_at	---	---	---	-0.269	-	0.009	0.033
234502_PM_at	---	---	---	-0.298	-	0.009	0.018
237583_PM_at	---	---	---	-0.418	-	0.009	0.009
229580_PM_at	---	---	---	-0.378	-	0.013	0.008
233646_PM_at	---	---	---	-0.311	-	0.016	0.034
238191_PM_at	---	---	---	-0.329	-	0.020	0.033
241814_PM_at	---	---	---	-0.269	-	0.020	0.026
1559063_PM_at	---	---	---	-0.287	-	0.022	0.047
238521_PM_at	---	---	---	-0.290	-	0.022	0.032
229531_PM_at	---	---	---	-0.301	-	0.025	0.038
230714_PM_s_at	---	---	---	-0.278	-	0.029	0.015
230913_PM_at	---	---	---	-0.295	-	0.032	0.009
229108_PM_at	---	---	---	-0.399	-	0.037	0.038
241636_PM_x_at	---	---	---	-0.316	-	0.043	0.012
209000_PM_s_at	septin 8	23176	8-Sep	-0.421	-	0.035	0.012
226925_PM_at	acid phosphatase-like 2	92370	ACPL2	-0.394	-	0.035	0.027
204332_PM_s_at	aspartylglucosaminidase	175	AGA	-0.340	-	0.016	0.007
1566989_PM_at	AT rich interactive domain 1B (SWI1-like)	57492	ARID1B	-0.434	-	0.022	0.025

209824_PM_s_at	aryl hydrocarbon receptor nuclear translocator-like	406	ARNTL	-0.348	-	0.021	0.048
234584_PM_s_at	arginyltransferase 1	11101	ATE1	-0.265	-	0.023	0.018
228190_PM_at	ATG4 autophagy related 4 homolog C (S. cerevisiae) /// Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	84938 /// 9646	ATG4C /// CTR9	-0.431	-	0.014	0.023
242230_PM_at	ataxin 1	6310	ATXN1	-0.316	-	0.015	0.021
227373_PM_at	ataxin 1-like	342371	ATXN1L	-0.313	-	0.046	0.024
209964_PM_s_at	ataxin 7	6314	ATXN7	-0.274	-	0.036	0.024
210157_PM_at	chromosome 19 open reading frame 2	8725	C19orf2	-0.428	-	0.003	0.003
218721_PM_s_at	chromosome 1 open reading frame 27	54953	C1orf27	-0.285	-	0.004	0.010
228195_PM_at	chromosome 2 open reading frame 88	84281	C2orf88	-0.279	-	0.001	0.004
200757_PM_s_at	calumenin	813	CALU	-0.292	-	0.021	0.043
236320_PM_at	coiled-coil domain containing 17	149483	CCDC17	-0.284	-	0.045	0.045
213110_PM_s_at	collagen, type IV, alpha 5	1287	COL4A5	-0.643	-	0.025	0.028
52255_PM_s_at	collagen, type V, alpha 3	50509	COL5A3	-0.289	-	0.002	0.009
216204_PM_at	Catechol-O-methyltransferase	1312	COMT	-0.275	-	0.020	0.027
204172_PM_at	coproporphyrinogen oxidase	1371	CPOX	-0.315	-	0.007	0.001
219139_PM_s_at	ciliary rootlet coiled-coil, rootletin-like 2	114819	CROCCL2	-0.283	-	0.002	0.003
213319_PM_s_at	Cold shock domain protein A	8531	CSDA	-0.326	-	0.011	0.009
216680_PM_s_at	EPH receptor B4	2050	EPHB4	-0.567	-	0.022	0.049
227551_PM_at	family with sequence similarity 108, member B1	51104	FAM108B1	-0.283	-	0.012	0.037
224030_PM_s_at	family with sequence similarity 115, member A	9747	FAM115A	-0.297	-	0.039	0.014
235043_PM_at	family with sequence similarity 122A	116224	FAM122A	-0.310	-	0.023	0.047
218510_PM_x_at	family with sequence similarity 134, member B	54463	FAM134B	-0.305	-	0.013	0.013
231001_PM_at	fin bud initiation factor homolog (zebrafish)	387758	FIBIN	-0.419	-	0.013	0.026
230946_PM_at	Formin 2	56776	FMN2	-0.274	-	0.003	0.002
1558199_PM_at	fibronectin 1	2335	FN1	-0.263	-	0.012	0.007
206377_PM_at	forkhead box F2	2295	FOXF2	-0.283	-	0.024	0.012
204145_PM_at	FSHD region gene 1	2483	FRG1	-0.386	-	0.027	0.023
209702_PM_at	fat mass and obesity associated	79068	FTO	-0.326	-	0.038	0.047
201723_PM_s_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	2589	GALNT1	-0.338	-	0.004	0.005

227525_PM_at	glucocorticoid induced transcript 1	113263	GLCCI1	-0.283	-	0.017	0.040
219269_PM_at	homeobox containing 1	79618	HMBOX1	-2.305	-	0.013	0.042
241650_PM_x_at	hemicentin 2	256158	HMCN2	-0.284	-	0.040	0.012
212115_PM_at	hematological and neurological expressed 1-like	90861	HN1L	-0.303	-	0.030	0.030
216517_PM_at	immunoglobulin kappa constant	100291464	IGKC	-0.278	-	0.000	0.001
204302_PM_s_at	KIAA0427	9811	KIAA0427	-0.294	-	0.016	0.041
205631_PM_at	KIAA0586	9786	KIAA0586	-0.358	-	0.027	0.045
223161_PM_at	KIAA1147	57189	KIAA1147	-0.267	-	0.004	0.024
220911_PM_s_at	KIAA1305	57523	KIAA1305	-0.294	-	0.036	0.049
229349_PM_at	lin-28 homolog B (C. elegans)	389421	LIN28B	-0.265	-	0.012	0.012
225793_PM_at	Lix1 homolog (mouse)-like	128077	LIX1L	-0.284	-	0.038	0.036
229179_PM_at	similar to hCG2045012	100288901	LOC100288901	-0.265	-	0.006	0.015
1566449_PM_at	Leucine rich repeat containing 40	55631	LRRC40	-0.288	-	0.011	0.024
218364_PM_at	leucine rich repeat (in FLII) interacting protein 2	9209	LRRFIP2	-0.367	-	0.029	0.018
227839_PM_at	methyl-CpG binding domain protein 5	55777	MBD5	-0.352	-	0.018	0.043
219673_PM_at	minichromosome maintenance complex component 9	254394	MCM9	-0.307	-	0.011	0.012
212872_PM_s_at	mediator complex subunit 20	9477	MED20	-0.304	-	0.043	0.050
242765_PM_at	myelin-associated oligodendrocyte basic protein	4336	MOBP	-0.590	-	0.018	0.040
206001_PM_at	neuropeptide Y	4852	NPY	-0.310	-	0.027	0.043
203814_PM_s_at	NAD(P)H dehydrogenase, quinone 2	4835	NQO2	-0.266	-	0.007	0.034
204622_PM_x_at	nuclear receptor subfamily 4, group A, member 2	4929	NR4A2	-0.445	-	0.014	0.041
216248_PM_s_at	nuclear receptor subfamily 4, group A, member 2	4929	NR4A2	-0.435	-	0.017	0.006
221684_PM_s_at	nyctalopin	60506	NYX	-0.367	-	0.015	0.016
210415_PM_s_at	outer dense fiber of sperm tails 2	4957	ODF2	0.471	-	0.044	0.006
230246_PM_at	placenta-specific 9	219348	PLAC9	-0.468	-	0.007	0.023
77508_PM_r_at	rabaptin, RAB GTPase binding effector protein 2	79874	RABEP2	-0.292	-	0.027	0.017
241433_PM_at	REST corepressor 3	55758	RCOR3	-0.277	-	0.003	0.004
217776_PM_at	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	51109	RDH11	-0.325	-	0.011	0.029
205923_PM_at	reelin	5649	RELN	-0.441	-	0.013	0.026
213459_PM_at	ribosomal protein L37a	6168	RPL37A	-0.287	-	0.016	0.028

204923_PM_at	SAM and SH3 domain containing 3	54440	SASH3	-0.286	-	0.034	0.020
227369_PM_at	SERPINE1 mRNA binding protein 1	26135	SERBP1	-0.297	-	0.049	0.036
223732_PM_at	solute carrier family 23 (nucleobase transporters), member 1	9963	SLC23A1	-0.284	-	0.024	0.013
207827_PM_x_at	synuclein, alpha (non A4 component of amyloid precursor)	6622	SNCA	-0.342	-	0.042	0.040
1563906_PM_at	sine oculis binding protein homolog (Drosophila)	55084	SOBP	-0.376	-	0.009	0.017
203373_PM_at	suppressor of cytokine signaling 2	8835	SOCS2	-0.402	-	0.004	0.012
227426_PM_at	son of sevenless homolog 1 (Drosophila)	6654	SOS1	-0.363	-	0.007	0.048
226822_PM_at	storkhead box 2	56977	STOX2	-0.295	-	0.008	0.016
243766_PM_s_at	TEA domain family member 2	8463	TEAD2	-0.278	-	0.005	0.023
205016_PM_at	transforming growth factor, alpha	7039	TGFA	-0.395	-	0.047	0.036
227804_PM_at	TLC domain containing 1	116238	TLCD1	-0.377	-	0.015	0.011
239265_PM_at	transmembrane protein 20	159371	TMEM20	-0.279	-	0.035	0.012
203049_PM_s_at	tetratricopeptide repeat domain 37	9652	TTC37	-0.426	-	0.006	0.014
228956_PM_at	UDP glycosyltransferase 8	7368	UGT8	-0.525	-	0.030	0.049
221513_PM_s_at	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)	10813 /// 9724	UTP14A /// UTP14C	0.306	-	0.025	0.008
239757_PM_at	Zinc finger, AN1-type domain 6	54469	ZFAND6	-0.295	-	0.012	0.031
204937_PM_s_at	zinc finger protein 274	10782	ZNF274	-0.309	-	0.017	0.019
233511_PM_at	---	---	---	0.337	+	0.001	0.002
236961_PM_at	---	---	---	0.407	+	0.003	0.014
1560327_PM_at	---	---	---	0.339	+	0.005	0.019
238774_PM_at	---	---	---	0.308	+	0.005	0.038
243881_PM_at	---	---	---	0.319	+	0.012	0.013
239684_PM_at	---	---	---	0.414	+	0.018	0.050
237441_PM_at	---	---	---	0.294	+	0.027	0.022
1556904_PM_at	---	---	---	0.480	+	0.028	0.012
1563469_PM_at	---	---	---	0.390	+	0.043	0.046
226454_PM_at	membrane-associated ring finger (C3HC4) 9	92979	9-Mar	0.264	+	0.037	0.009
204343_PM_at	ATP-binding cassette, sub-family A (ABC1), member 3	21	ABCA3	0.326	+	0.004	0.017
225529_PM_at	ArfGAP with coiled-coil, ankyrin repeat and PH domains 3	116983	ACAP3	0.514	+	0.025	0.039
205377_PM_s_at	acetylcholinesterase (Yt blood group)	43	ACHE	0.327	+	0.025	0.032
205378_PM_s_at	acetylcholinesterase (Yt blood group)	43	ACHE	0.471	+	0.047	0.046

222707_PM_s_at	ARP8 actin-related protein 8 homolog (yeast)	93973	ACTR8	0.461	+	0.010	0.011
202740_PM_at	aminoacylase 1	95	ACY1	0.365	+	0.025	0.003
232133_PM_at	ADAM metallopeptidase with thrombospondin type 1 motif, 10	81794	ADAMTS10	0.368	+	0.011	0.030
90265_PM_at	ArfGAP with dual PH domains 1	11033	ADAP1	0.375	+	0.037	0.020
201401_PM_s_at	adrenergic, beta, receptor kinase 1	156	ADRBK1	1.211	+	0.029	0.042
206152_PM_at	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2	116986	AGAP2	0.366	+	0.036	0.042
218480_PM_at	ATP/GTP binding protein-like 5	60509	AGBL5	0.336	+	0.008	0.011
231857_PM_s_at	ATP/GTP binding protein-like 5	60509	AGBL5	0.371	+	0.020	0.010
219723_PM_x_at	1-acylglycerol-3-phosphate O-acyltransferase 3	56894	AGPAT3	0.379	+	0.009	0.036
224282_PM_s_at	1-acylglycerol-3-phosphate O-acyltransferase 3	56894	AGPAT3	0.840	+	0.027	0.043
202139_PM_at	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)	8574	AKR7A2	1.170	+	0.016	0.014
206469_PM_x_at	aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase)	22977	AKR7A3	0.327	+	0.030	0.022
218555_PM_at	anaphase promoting complex subunit 2	29882	ANAPC2	0.644	+	0.034	0.030
213001_PM_at	angiopoietin-like 2	23452	ANGPTL2	0.310	+	0.048	0.007
219081_PM_at	ankyrin repeat and KH domain containing 1	54882	ANKHD1	0.329	+	0.016	0.009
231423_PM_s_at	ankyrin repeat domain 16	54522	ANKRD16	0.353	+	0.019	0.038
201043_PM_s_at	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	8125	ANP32A	1.097	+	0.027	0.014
225754_PM_at	adaptor-related protein complex 1, gamma 1 subunit	164	AP1G1	0.292	+	0.003	0.006
201613_PM_s_at	adaptor-related protein complex 1, gamma 2 subunit	8906	AP1G2	0.513	+	0.003	0.021
212161_PM_at	adaptor-related protein complex 2, alpha 2 subunit	161	AP2A2	0.315	+	0.022	0.001
203382_PM_s_at	apolipoprotein E	348	APOE	0.570	+	0.023	0.040
203219_PM_s_at	adenine phosphoribosyltransferase	353	APRT	1.034	+	0.021	0.027
202547_PM_s_at	Rho guanine nucleotide exchange factor (GEF) 7	8874	ARHGEF7	0.536	+	0.010	0.025
225184_PM_at	AT rich interactive domain 1B (SWI1-like)	57492	ARID1B	0.858	+	0.001	0.007
1552722_PM_at	cyclic AMP-regulated phosphoprotein, 21 kD	10777	ARPP-21	0.519	+	0.014	0.034
1570523_PM_s_at	ATG10 autophagy related 10 homolog (S. cerevisiae)	83734	ATG10	0.373	+	0.001	0.007
228984_PM_at	ATP-grasp domain containing 1	57571	ATPGD1	-0.349	+	0.037	0.038
203452_PM_at	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	26229	B3GAT3	0.444	+	0.011	0.029

210534_PM_s_at	B9 protein domain 1	27077	B9D1	1.079	+	0.012	0.023
1555735_PM_a_at	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	8314	BAP1	0.733	+	0.044	0.033
225674_PM_at	B-cell receptor-associated protein 29	55973	BCAP29	0.372	+	0.011	0.023
200837_PM_at	B-cell receptor-associated protein 31	10134	BCAP31	0.610	+	0.046	0.012
202030_PM_at	branched chain ketoacid dehydrogenase kinase	10295	BCKDK	0.294	+	0.031	0.006
238692_PM_at	BTB (POZ) domain containing 11	121551	BTBD11	0.426	+	0.018	0.008
218220_PM_at	chromosome 12 open reading frame 10	60314	C12orf10	0.393	+	0.033	0.042
225313_PM_at	chromosome 20 open reading frame 177	63939	C20orf177	-0.412	+	0.026	0.041
50314_PM_i_at	chromosome 20 open reading frame 27	54976	C20orf27	0.410	+	0.025	0.026
218081_PM_at	chromosome 20 open reading frame 27	54976	C20orf27	0.401	+	0.037	0.032
223360_PM_at	chromosome 21 open reading frame 56	84221	C21orf56	1.073	+	0.009	0.007
235935_PM_at	chromosome 6 open reading frame 154	221424	C6orf154	0.953	+	0.018	0.024
227000_PM_at	chromosome 7 open reading frame 41	222166	C7orf41	0.412	+	0.014	0.017
211802_PM_x_at	calcium channel, voltage-dependent, T type, alpha 1G subunit	8913	CACNA1G	0.470	+	0.025	0.016
224291_PM_at	calcium channel, voltage-dependent, gamma subunit 6	59285	CACNG6	0.528	+	0.000	0.001
201615_PM_x_at	caldesmon 1	800	CALD1	0.358	+	0.003	0.012
1555608_PM_at	caprin family member 2	65981	CAPRIN2	0.273	+	0.003	0.002
210775_PM_x_at	caspase 9, apoptosis-related cysteine peptidase	842	CASP9	0.377	+	0.006	0.001
1559409_PM_a_at	coiled-coil and C2 domain containing 2A	57545	CC2D2A	0.325	+	0.008	0.015
206037_PM_at	cysteine conjugate-beta lyase, cytoplasmic	883	CCBL1	0.289	+	0.010	0.004
223316_PM_at	coiled-coil domain containing 3	83643	CCDC3	0.338	+	0.004	0.001
226539_PM_s_at	coiled-coil domain containing 42B	387885	CCDC42B	0.278	+	0.019	0.029
204610_PM_s_at	coiled-coil domain containing 85B	11007	CCDC85B	0.624	+	0.032	0.044
217849_PM_s_at	CDC42 binding protein kinase beta (DMPK-like)	9578	CDC42BPB	0.710	+	0.009	0.012
203198_PM_at	cyclin-dependent kinase 9	1025	CDK9	0.426	+	0.026	0.013
208052_PM_x_at	carcinoembryonic antigen-related cell adhesion molecule 3	1084	CEACAM3	0.268	+	0.013	0.009
1554489_PM_a_at	centrosomal protein 70kDa	80321	CEP70	0.365	+	0.007	0.008
224932_PM_at	coiled-coil-helix-coiled-coil-helix domain containing 10	400916	CHCHD10	0.315	+	0.025	0.037
222755_PM_s_at	chromodomain helicase DNA binding protein 7	55636	CHD7	0.655	+	0.004	0.031

1553442_PM_a_at	contactin associated protein-like 4	85445	CNTNAP4	0.747	+	0.008	0.009
203653_PM_s_at	coilin	8161	COIL	0.504	+	0.031	0.023
209132_PM_s_at	COMM domain containing 4	54939	COMMD4	0.268	+	0.026	0.010
218057_PM_x_at	COX4 neighbor	10328	COX4NB	0.269	+	0.028	0.002
225815_PM_at	complexin 2	10814	CPLX2	0.326	+	0.030	0.007
202224_PM_at	v-crk sarcoma virus CT10 oncogene homolog (avian)	1398	CRK	0.303	+	0.020	0.001
206777_PM_s_at	160eparin160ing, beta B2 /// 160eparin160ing, beta B2 pseudogene 1	1415 /// 1416	CRYBB2 /// CRYBB2P1	0.483	+	0.007	0.008
214355_PM_x_at	CTAGE family, member 4	100128553 /// 100142659 /// 119437 /// 220429 /// 340307 /// 4253 /// 441294 /// 643854 /// 647288	CTAGE4	0.292	+	0.029	0.030
201905_PM_s_at	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	10217	CTDSPL	0.461	+	0.037	0.022
227886_PM_at	cathepsin D	1509	CTSD	0.460	+	0.005	0.032
209158_PM_s_at	cytohesin 2	9266	CYTH2	0.386	+	0.035	0.031
1569648_PM_at	dapper, antagonist of beta-catenin, homolog 2 (Xenopus laevis)	168002	DACT2	0.506	+	0.001	0.006
238340_PM_at	DDB1 and CUL4 associated factor 8	50717	DCAF8	0.444	+	0.023	0.014
218892_PM_at	dachsous 1 (Drosophila)	8642	DCHS1	0.283	+	0.007	0.014
231151_PM_at	discs, large (Drosophila) homolog-associated protein 3	58512	DLGAP3	0.446	+	0.008	0.008
230936_PM_at	DnaJ (Hsp40) related, subfamily B, member 13	374407	DNAJB13	0.872	+	0.014	0.033
224612_PM_s_at	DnaJ (Hsp40) homolog, subfamily C, member 5	80331	DNAJC5	0.968	+	0.041	0.046
207648_PM_at	dystrophin related protein 2	1821	DRP2	0.295	+	0.029	0.048
1553983_PM_at	deoxythymidylate kinase (thymidylate kinase)	1841	DTYMK	0.282	+	0.004	0.007
238594_PM_x_at	dual specificity phosphatase 8	1850	DUSP8	0.296	+	0.025	0.038
211079_PM_s_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	1859	DYRK1A	0.268	+	0.007	0.029
1555306_PM_a_at	endothelin converting enzyme 2	9718	ECE2	0.335	+	0.007	0.012

202496_PM_at	enhancer of mRNA decapping 4	23644	EDC4	0.420	+	0.038	0.044
209356_PM_x_at	EGF-containing fibulin-like extracellular matrix protein 2	30008	EFEMP2	0.633	+	0.015	0.029
205249_PM_at	early growth response 2	1959	EGR2	0.268	+	0.004	0.003
1555996_PM_s_at	eukaryotic translation initiation factor 4A, isoform 2	1974	EIF4A2	0.428	+	0.014	0.013
210376_PM_x_at	ELK1, member of ETS oncogene family	2002	ELK1	0.299	+	0.024	0.034
203464_PM_s_at	epsin 2	22905	EPN2	0.298	+	0.010	0.013
202176_PM_at	excision repair cross-complementing rodent repair deficiency, complementation group 3 (xeroderma pigmentosum group B complementing)	2071	ERCC3	0.350	+	0.015	0.049
226411_PM_at	ecotropic viral integration site 5-like	115704	EVI5L	0.389	+	0.036	0.048
210012_PM_s_at	Ewing sarcoma breakpoint region 1	2130	EWSR1	1.002	+	0.009	0.016
218695_PM_at	exosome component 4	54512	EXOSC4	0.388	+	0.011	0.014
225874_PM_at	family with sequence similarity 100, member A	124402	FAM100A	0.604	+	0.012	0.031
229655_PM_at	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	25817	FAM19A5	0.284	+	0.039	0.030
232048_PM_at	family with sequence similarity 76, member B	143684	FAM76B	0.309	+	0.003	0.007
32209_PM_at	family with sequence similarity 89, member B	23625	FAM89B	0.404	+	0.018	0.025
214114_PM_x_at	Fas-activated serine/threonine kinase	10922	FASTK	0.878	+	0.015	0.031
210975_PM_x_at	Fas-activated serine/threonine kinase	10922	FASTK	0.656	+	0.020	0.019
202676_PM_x_at	Fas-activated serine/threonine kinase	10922	FASTK	0.916	+	0.039	0.050
219189_PM_at	F-box and leucine-rich repeat protein 6	26233	FBXL6	0.532	+	0.032	0.005
219305_PM_x_at	F-box protein 2	26232	FBXO2	0.584	+	0.037	0.017
223050_PM_s_at	F-box and WD repeat domain containing 5	54461	FBXW5	0.295	+	0.006	0.008
205866_PM_at	ficolin (collagen/fibrinogen domain containing) 3 (Hakata antigen)	8547	FCN3	0.307	+	0.015	0.029
226705_PM_at	fibroblast growth factor receptor 1	2260	FGFR1	0.512	+	0.024	0.040
208234_PM_x_at	fibroblast growth factor receptor 2	2263	FGFR2	0.667	+	0.023	0.049
244498_PM_x_at	similar to ubiquitin-conjugating enzyme E2Q 2 /// chondroitin sulfate proteoglycan 4 pseudogene /// chondroitin sulfate proteoglycan 4 pseudogene	388165 /// 440297 /// 440300	FLJ43276 /// LOC440297 /// LOC440300	0.338	+	0.030	0.001
201350_PM_at	flotillin 2	2319	FLOT2	0.376	+	0.007	0.016

229272_PM_at	formin binding protein 4	23360	FNBP4	0.640	+	0.024	0.026
218843_PM_at	fibronectin type III domain containing 4	64838	FNDC4	0.377	+	0.004	0.003
221187_PM_s_at	fuzzy homolog (Drosophila)	80199	FUZ	0.530	+	0.032	0.048
203172_PM_at	fragile X mental retardation, autosomal homolog 2	9513	FXR2	0.419	+	0.029	0.047
233437_PM_at	gamma-aminobutyric acid (GABA) A receptor, alpha 4	2557	GABRA4	0.337	+	0.017	0.007
207352_PM_s_at	gamma-aminobutyric acid (GABA) A receptor, beta 2	2561	GABRB2	0.801	+	0.040	0.039
207704_PM_s_at	growth arrest-specific 7	8522	GAS7	0.318	+	0.043	0.043
216860_PM_s_at	growth differentiation factor 11	10220	GDF11	0.287	+	0.005	0.007
35436_PM_at	golgi autoantigen, golgin subfamily a, 2	2801	GOLGA2	0.379	+	0.025	0.029
218193_PM_s_at	golgi transport 1 homolog B (S. cerevisiae)	51026	GOLT1B	0.337	+	0.010	0.036
227215_PM_at	golgi associated PDZ and coiled-coil motif containing	57120	GOPC	0.348	+	0.041	0.031
210009_PM_s_at	golgi SNAP receptor complex member 2	9570	GOSR2	0.404	+	0.005	0.017
206266_PM_at	glycosylphosphatidylinositol specific phospholipase D1	2822	GPLD1	0.266	+	0.026	0.036
225058_PM_at	G protein-coupled receptor 108	56927	GPR108	0.320	+	0.009	0.022
221306_PM_at	G protein-coupled receptor 27	2850	GPR27	0.310	+	0.047	0.050
200736_PM_s_at	glutathione peroxidase 1	2876	GPX1	0.634	+	0.014	0.024
208465_PM_at	glutamate receptor, metabotropic 2	2912	GRM2	0.718	+	0.019	0.015
215333_PM_x_at	glutathione S-transferase mu 1 /// glutathione S-transferase mu 2 (muscle)	2944 /// 2946	GSTM1 /// GSTM2	0.296	+	0.000	0.007
210892_PM_s_at	general transcription factor Iii	2969	GTF2I	0.330	+	0.011	0.020
225245_PM_x_at	H2A histone family, member J	55766	H2AFJ	0.310	+	0.011	0.029
201035_PM_s_at	hydroxyacyl-Coenzyme A dehydrogenase	3033	HADH	0.315	+	0.012	0.034
229181_PM_s_at	HAUS augmin-like complex, subunit 2	55142	HAUS2	0.353	+	0.035	0.027
215193_PM_x_at	major histocompatibility complex, class II, DR beta 1	100133661	HLA-DRB1	1.059	+	0.006	0.029
209675_PM_s_at	heterogeneous nuclear ribonucleoprotein U-like 1	11100	HNRNPUL1	0.516	+	0.025	0.041
221663_PM_x_at	histamine receptor H3	11255	HRH3	0.376	+	0.034	0.017
1552842_PM_at	162eparin sulfate 6-O-sulfotransferase 3	266722	HS6ST3	0.263	+	0.017	0.040
1569905_PM_at	hydroxysteroid (11-beta) dehydrogenase 1-like	374875	HSD11B1L	0.661	+	0.017	0.027
213540_PM_at	hydroxysteroid (17-beta) dehydrogenase 8	7923	HSD17B8	0.418	+	0.023	0.012
211616_PM_s_at	5-hydroxytryptamine (serotonin) receptor 2A	3356	HTR2A	1.013	+	0.015	0.032
201609_PM_x_at	isoprenylcysteine carboxyl methyltransferase	23463	ICMT	0.823	+	0.022	0.031
212203_PM_x_at	interferon induced transmembrane protein 3 (1-8U)	10410	IFITM3	0.362	+	0.019	0.034

226324_PM_s_at	intraflagellar transport 172 homolog (Chlamydomonas)	26160	IFT172	0.265	+	0.005	0.000
209542_PM_x_at	insulin-like growth factor 1 (somatomedin C)	3479	IGF1	0.273	+	0.016	0.011
222963_PM_s_at	interleukin 1 receptor accessory protein-like 1	11141	IL1RAPL1	0.637	+	0.036	0.047
218234_PM_at	inhibitor of growth family, member 4	51147	ING4	0.372	+	0.021	0.040
213651_PM_at	inositol polyphosphate-5-phosphatase J	27124	INPP5J	0.304	+	0.014	0.017
215130_PM_s_at	IQ motif containing K	124152	IQCK	0.285	+	0.006	0.022
223428_PM_s_at	ISY1 splicing factor homolog (S. cerevisiae)	57461	ISY1	0.289	+	0.035	0.021
201189_PM_s_at	inositol 1,4,5-triphosphate receptor, type 3	3710	ITPR3	0.379	+	0.005	0.003
235467_PM_s_at	potassium voltage-gated channel, Shaw-related subfamily, member 4	3749	KCNC4	0.372	+	0.012	0.001
223726_PM_at	potassium voltage-gated channel, subfamily H (eag-related), member 3	23416	KCNH3	0.532	+	0.020	0.009
207141_PM_s_at	potassium inwardly-rectifying channel, subfamily J, member 3	3760	KCNJ3	0.874	+	0.038	0.042
212492_PM_s_at	lysine (K)-specific demethylase 4B	23030	KDM4B	1.233	+	0.033	0.028
203363_PM_s_at	KIAA0652	9776	KIAA0652	0.711	+	0.012	0.028
231842_PM_at	KIAA1462	57608	KIAA1462	0.298	+	0.023	0.037
224746_PM_at	KIAA1522	57648	KIAA1522	0.414	+	0.003	0.018
225140_PM_at	Kruppel-like factor 3 (basic)	51274	KLF3	0.275	+	0.013	0.028
208960_PM_s_at	Kruppel-like factor 6	1316	KLF6	0.362	+	0.034	0.011
209008_PM_x_at	keratin 8	3856	KRT8	0.302	+	0.012	0.002
219061_PM_s_at	L antigen family, member 3	8270	LAGE3	0.264	+	0.033	0.032
224980_PM_at	LEM domain containing 2	221496	LEMD2	0.264	+	0.049	0.008
228762_PM_at	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	3955	LFNG	0.455	+	0.045	0.020
200805_PM_at	lectin, mannose-binding 2	10960	LMAN2	0.516	+	0.029	0.048
219135_PM_s_at	lipase maturation factor 1	64788	LMF1	0.433	+	0.029	0.023
212682_PM_s_at	lipase maturation factor 2	91289	LMF2	0.296	+	0.045	0.020
229636_PM_at	Hypothetical protein LOC100131226	100131226	LOC100131226	0.293	+	0.037	0.046
216967_PM_at	hypothetical protein LOC100288551	100288551	LOC100288551	0.303	+	0.017	0.035

232211_PM_at	similar to protein phosphatase 1, regulatory (inhibitor) subunit 3F /// protein phosphatase 1, regulatory (inhibitor) subunit 3F	100293149 /// 89801	LOC100293149 /// PPP1R3F	0.353	+	0.021	0.046
229528_PM_at	hypothetical protein LOC283378	283378	LOC283378	0.424	+	0.016	0.007
1556042_PM_s_at	hypothetical LOC338799	338799	LOC338799	0.354	+	0.015	0.024
229826_PM_at	similar to CG32736-PA	440957	LOC440957	0.394	+	0.010	0.010
203570_PM_at	lysyl oxidase-like 1	4016	LOXL1	0.310	+	0.028	0.039
1553940_PM_a_at	leucine rich repeat containing 28	123355	LRRC28	0.417	+	0.027	0.017
219922_PM_s_at	latent transforming growth factor beta binding protein 3	4054	LTBP3	0.651	+	0.027	0.010
213176_PM_s_at	latent transforming growth factor beta binding protein 4	8425	LTBP4	0.269	+	0.029	0.016
223234_PM_at	MAD2 mitotic arrest deficient-like 2 (yeast)	10459	MAD2L2	0.654	+	0.028	0.029
203668_PM_at	mannosidase, alpha, class 2C, member 1	4123	MAN2C1	0.371	+	0.028	0.038
215384_PM_s_at	microtubule-associated protein 1A	4130	MAP1A	0.357	+	0.030	0.002
226190_PM_at	mitogen-activated protein kinase kinase kinase 13	9175	MAP3K13	0.406	+	0.039	0.025
41160_PM_at	methyl-CpG binding domain protein 3	53615	MBD3	0.290	+	0.001	0.010
218664_PM_at	mitochondrial trans-2-enoyl-CoA reductase	51102	MECR	0.418	+	0.022	0.046
43544_PM_at	mediator complex subunit 16	10025	MED16	0.693	+	0.041	0.037
221650_PM_s_at	mediator complex subunit 18	54797	MED18	0.313	+	0.039	0.009
211913_PM_s_at	c-mer proto-oncogene tyrosine kinase	10461	MERTK	0.397	+	0.027	0.015
214588_PM_s_at	microfibrillar-associated protein 3	4238	MFAP3	0.358	+	0.021	0.013
214972_PM_at	Meningioma expressed antigen 5 (hyaluronidase)	10724	MGEA5	0.616	+	0.026	0.034
228261_PM_at	mindbomb homolog 2 (Drosophila)	142678	MIB2	0.672	+	0.041	0.045
219332_PM_at	MICAL-like 2	79778	MICALL2	0.328	+	0.003	0.016
232167_PM_at	macrophage migration inhibitory factor (glycosylation-inhibiting factor) /// solute carrier family 2 (facilitated glucose transporter), member 11	4282 /// 66035	MIF /// SLC2A11	0.277	+	0.045	0.001
214625_PM_s_at	misshapen-like kinase 1 (zebrafish)	50488	MINK1	0.496	+	0.026	0.012
220587_PM_s_at	MTOR associated protein, LST8 homolog (S. cerevisiae)	64223	MLST8	0.497	+	0.013	0.032
224207_PM_x_at	matrix metallopeptidase 28	79148	MMP28	0.276	+	0.012	0.006

1557455_PM_s_at	motile sperm domain containing 1	56180	MOSPD1	0.693	+	0.038	0.040
206538_PM_at	muscle RAS oncogene homolog	22808	MRAS	0.407	+	0.037	0.004
219162_PM_s_at	mitochondrial ribosomal protein L11	65003	MRPL11	0.347	+	0.002	0.002
213897_PM_s_at	mitochondrial ribosomal protein L23	6150	MRPL23	0.403	+	0.002	0.012
243579_PM_at	musashi homolog 2 (Drosophila)	124540	MSI2	0.773	+	0.045	0.039
238583_PM_at	methionine sulfoxide reductase B3	253827	MSRB3	0.439	+	0.027	0.036
216222_PM_s_at	myosin X	4651	MYO10	0.287	+	0.029	0.014
210480_PM_s_at	myosin VI	4646	MYO6	0.855	+	0.011	0.025
213607_PM_x_at	NAD kinase	65220	NADK	0.672	+	0.025	0.027
222598_PM_s_at	neuron navigator 2	89797	NAV2	0.324	+	0.013	0.040
40640_PM_at	non-SMC 165eparin165in II complex, subunit H2	29781	NCAPH2	0.340	+	0.013	0.020
242121_PM_at	non-protein coding RNA 182	100302692	NCRNA00182	0.399	+	0.038	0.045
204325_PM_s_at	neurofibromin 1	4763	NF1	0.345	+	0.004	0.007
211094_PM_s_at	neurofibromin 1	4763	NF1	0.320	+	0.012	0.043
213298_PM_at	nuclear factor I/C (CCAAT-binding transcription factor)	4782	NFIC	0.530	+	0.020	0.012
209973_PM_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1	4795	NFKBIL1	0.301	+	0.028	0.017
209261_PM_s_at	nuclear receptor subfamily 2, group F, member 6	2063	NR2F6	0.360	+	0.020	0.006
218359_PM_at	neurensin 2	80023	NRSN2	0.427	+	0.016	0.037
206291_PM_at	neurotensin	4922	NTS	0.279	+	0.035	0.014
222025_PM_s_at	5-oxoprolinase (ATP-hydrolysing)	26873	OPLAH	0.440	+	0.025	0.027
1558426_PM_x_at	ORAI calcium release-activated calcium modulator 2	80228	ORAI2	0.382	+	0.023	0.049
221237_PM_s_at	oxysterol binding protein 2	23762	OSBP2	0.583	+	0.037	0.015
204088_PM_at	purinergic receptor P2X, ligand-gated ion channel, 4	5025	P2RX4	0.314	+	0.030	0.006
1555823_PM_at	phosphofurin acidic cluster sorting protein 2	23241	PACS2	0.608	+	0.014	0.015
227053_PM_at	protein kinase C and casein kinase substrate in neurons 1	29993	PACSIN1	0.316	+	0.021	0.020
1552944_PM_a_at	pannexin 2	56666	PANX2	0.470	+	0.004	0.013
239067_PM_s_at	pannexin 2	56666	PANX2	0.337	+	0.009	0.036
204629_PM_at	parvin, beta	29780	PARVB	0.330	+	0.006	0.010

211392_PM_s_at	POZ (BTB) and AT hook containing zinc finger 1	23598	PATZ1	0.389	+	0.037	0.018
209361_PM_s_at	poly(rC) binding protein 4	57060	PCBP4	0.286	+	0.014	0.024
208823_PM_s_at	PCTAIRE protein kinase 1	5127	PCTK1	0.359	+	0.029	0.040
219165_PM_at	PDZ and LIM domain 2 (mystique)	64236	PDLIM2	0.403	+	0.007	0.020
211564_PM_s_at	PDZ and LIM domain 4	8572	PDLIM4	0.385	+	0.034	0.025
203242_PM_s_at	PDZ and LIM domain 5	10611	PDLIM5	0.402	+	0.035	0.005
223543_PM_at	PDZ domain containing 4	57595	PDZD4	0.334	+	0.032	0.037
320_PM_at	peroxisomal biogenesis factor 6	5190	PEX6	0.408	+	0.012	0.005
55616_PM_at	post-GPI attachment to proteins 3	93210	PGAP3	0.326	+	0.006	0.003
218387_PM_s_at	6-phosphogluconolactonase	25796	PGLS	0.337	+	0.035	0.025
218388_PM_at	6-phosphogluconolactonase	25796	PGLS	0.610	+	0.037	0.034
235149_PM_at	phosphoglucomutase 2-like 1	283209	PGM2L1	0.458	+	0.022	0.034
222622_PM_at	phosphoglycolate phosphatase	283871	PGP	0.269	+	0.006	0.007
200658_PM_s_at	prohibitin	5245	PHB	0.609	+	0.012	0.026
205450_PM_at	phosphorylase kinase, alpha 1 (muscle)	5255	PHKA1	0.415	+	0.019	0.037
210647_PM_x_at	phospholipase A2, group VI (cytosolic, calcium-independent)	8398	PLA2G6	0.264	+	0.005	0.013
202240_PM_at	polo-like kinase 1 (Drosophila)	5347	PLK1	0.269	+	0.000	0.004
212235_PM_at	plexin D1	23129	PLXND1	0.265	+	0.034	0.036
210139_PM_s_at	peripheral myelin protein 22	5376	PMP22	-0.295	+	0.037	0.031
211697_PM_x_at	partner of NOB1 homolog (S. cerevisiae)	56902	PNO1	0.335	+	0.010	0.029
1557700_PM_at	Polymerase (DNA directed), eta	5429	POLH	0.323	+	0.005	0.005
1557701_PM_s_at	polymerase (DNA directed), eta	5429	POLH	0.370	+	0.028	0.036
218997_PM_at	polymerase (RNA) I polypeptide E, 53kDa	64425	POLR1E	0.307	+	0.030	0.009
213368_PM_x_at	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3	8541	PPFIA3	0.495	+	0.033	0.032
228795_PM_at	protein kinase C, beta	5579	PRKCB	0.543	+	0.038	0.029
216088_PM_s_at	proteasome (prosome, macropain) subunit, alpha type, 7	5688	PSMA7	0.517	+	0.023	0.012
232702_PM_at	RAB GTPase activating protein 1-like	9910	RABGAP1L	0.266	+	0.006	0.033
206103_PM_at	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)	5881	RAC3	0.456	+	0.001	0.005
204916_PM_at	receptor (G protein-coupled) activity modifying protein 1	10267	RAMP1	0.316	+	0.019	0.024

203749_PM_s_at	retinoic acid receptor, alpha	5914	RARA	0.264	+	0.012	0.049
223802_PM_s_at	retinoblastoma binding protein 6	5930	RBBP6	0.268	+	0.047	0.009
217622_PM_at	rhomboid domain containing 3	25807	RHBDD3	0.268	+	0.026	0.009
207383_PM_s_at	rhomboid, veinlet-like 1 (Drosophila)	9028	RHBDL1	0.436	+	0.013	0.043
1570253_PM_a_at	Ras homolog enriched in brain like 1	121268	RHEBL1	0.567	+	0.014	0.036
220483_PM_s_at	ring finger protein 19A	25897	RNF19A	0.553	+	0.035	0.050
210706_PM_s_at	ring finger protein 24	11237	RNF24	0.360	+	0.037	0.049
212191_PM_x_at	ribosomal protein L13	6137	RPL13	0.383	+	0.026	0.025
200022_PM_at	ribosomal protein L18	6141	RPL18	0.387	+	0.035	0.035
204632_PM_at	ribosomal protein S6 kinase, 90kDa, polypeptide 4	8986	RPS6KA4	0.392	+	0.025	0.025
203777_PM_s_at	ribosomal protein S6 kinase, 70kDa, polypeptide 2	6199	RPS6KB2	0.338	+	0.011	0.022
212647_PM_at	related RAS viral (r-ras) oncogene homolog	6237	RRAS	0.323	+	0.029	0.009
216831_PM_s_at	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	862	RUNX1T1	0.348	+	0.002	0.001
202426_PM_s_at	retinoid X receptor, alpha	6256	RXRA	0.320	+	0.008	0.013
201844_PM_s_at	RING1 and YY1 binding protein	23429	RYBP	0.309	+	0.006	0.001
230290_PM_at	signal peptide, CUB domain, EGF-like 3	222663	SCUBE3	0.323	+	0.004	0.011
221220_PM_s_at	SCY1-like 2 (S. cerevisiae)	55681	SCYL2	0.544	+	0.029	0.028
202062_PM_s_at	sel-1 suppressor of lin-12-like (C. elegans)	6400	SEL1L	0.505	+	0.025	0.007
202283_PM_at	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	5176	SERPINF1	0.357	+	0.007	0.016
1569106_PM_s_at	SET domain containing 5	55209	SETD5	0.495	+	0.033	0.020
213742_PM_at	splicing factor, arginine/serine-rich 11	9295	SFRS11	0.337	+	0.018	0.034
205367_PM_at	SH2B adaptor protein 2	10603	SH2B2	0.332	+	0.011	0.004
231787_PM_at	solute carrier family 25, member 27	9481	SLC25A27	0.751	+	0.001	0.021
222529_PM_at	solute carrier family 25, member 37	51312	SLC25A37	0.484	+	0.020	0.026
1552295_PM_a_at	solute carrier family 39 (zinc transporter), member 13	91252	SLC39A13	0.356	+	0.035	0.015
216230_PM_x_at	sphingomyelin phosphodiesterase 1, acid lysosomal	6609	SMPD1	0.423	+	0.036	0.042
209877_PM_at	synuclein, gamma (breast cancer-specific protein 1)	6623	SNCG	0.629	+	0.044	0.005

223865_PM_at	SRY (sex determining region Y)-box 6	55553	SOX6	0.267	+	0.049	0.023
222532_PM_at	signal recognition particle receptor, B subunit	58477	SRPRB	0.680	+	0.022	0.015
232322_PM_x_at	StAR-related lipid transfer (START) domain containing 10	10809	STARD10	0.314	+	0.027	0.018
230691_PM_at	syntaxin 1B	112755	STX1B	0.983	+	0.048	0.042
226037_PM_s_at	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	51616	TAF9B	0.353	+	0.032	0.003
1552541_PM_at	T-cell activation RhoGTPase activating protein	117289	TAGAP	0.354	+	0.012	0.027
204877_PM_s_at	TAO kinase 2	9344	TAOK2	0.589	+	0.006	0.005
1554701_PM_a_at	TBC1 domain family, member 16	125058	TBC1D16	0.311	+	0.014	0.015
229192_PM_s_at	tubulin folding cofactor D	6904	TBCD	0.297	+	0.047	0.029
201149_PM_s_at	TIMP metallopeptidase inhibitor 3	7078	TIMP3	1.024	+	0.018	0.046
1552293_PM_at	transmembrane protein 196	256130	TMEM196	0.297	+	0.026	0.025
224981_PM_at	transmembrane protein 219	124446	TMEM219	0.305	+	0.032	0.008
238831_PM_at	transmembrane protein 33	55161	TMEM33	0.356	+	0.027	0.007
1554077_PM_a_at	transmembrane protein 53	79639	TMEM53	0.483	+	0.034	0.033
227570_PM_at	transmembrane protein 86A	144110	TMEM86A	0.265	+	0.008	0.031
219423_PM_x_at	tumor necrosis factor receptor superfamily, member 25	8718	TNFRSF25	0.295	+	0.001	0.000
211841_PM_s_at	tumor necrosis factor receptor superfamily, member 25	8718	TNFRSF25	0.409	+	0.011	0.004
211282_PM_x_at	tumor necrosis factor receptor superfamily, member 25	8718	TNFRSF25	0.788	+	0.035	0.023
239288_PM_at	TRAF2 and NCK interacting kinase	23043	TNIK	0.303	+	0.038	0.047
210585_PM_s_at	transportin 2	30000	TNPO2	0.510	+	0.038	0.042
243834_PM_at	trinucleotide repeat containing 6A	27327	TNRC6A	0.323	+	0.045	0.027
228834_PM_at	transducer of ERBB2, 1	10140	TOB1	0.793	+	0.030	0.031
1554379_PM_a_at	tumor protein p73	7161	TP73	0.277	+	0.010	0.006
210372_PM_s_at	tumor protein D52-like 1	7164	TPD52L1	0.541	+	0.009	0.022
225870_PM_s_at	trafficking protein particle complex 5	126003	TRAPPC5	0.302	+	0.012	0.007
213884_PM_s_at	tripartite motif-containing 3	10612	TRIM3	0.775	+	0.046	0.031
222651_PM_s_at	trichorhinophalangeal syndrome I	7227	TRPS1	0.353	+	0.001	0.001
224852_PM_at	tetratricopeptide repeat domain 17	55761	TTC17	0.340	+	0.006	0.008
201009_PM_s_at	thioredoxin interacting protein	10628	TXNIP	0.380	+	0.022	0.039

211177_PM_s_at	thioredoxin reductase 2	10587	TXNRD2	0.443	+	0.020	0.034
238587_PM_at	ubiquitin associated and SH3 domain containing, B	84959	UBASH3B	0.310	+	0.010	0.016
215544_PM_s_at	U-box domain containing 5	22888	UBOX5	0.305	+	0.024	0.039
224221_PM_s_at	vav 3 guanine nucleotide exchange factor	10451	VAV3	0.285	+	0.002	0.000
224608_PM_s_at	vacuolar protein sorting 25 homolog (S. cerevisiae)	84313	VPS25	0.377	+	0.014	0.004
223293_PM_at	WD repeat domain 24	84219	WDR24	0.301	+	0.037	0.043
224898_PM_at	WD repeat domain 26	80232	WDR26	0.325	+	0.023	0.029
1552811_PM_at	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 1	117166	WFIKKN1	0.511	+	0.041	0.028
203827_PM_at	WD repeat domain, phosphoinositide interacting 1	55062	WIPI1	0.282	+	0.008	0.015
1554821_PM_a_at	zinc finger, BED-type containing 1	9189	ZBED1	0.395	+	0.003	0.013
231908_PM_at	zinc finger, DHHC-type containing 18	84243	ZDHHC18	0.288	+	0.008	0.008
224858_PM_at	zinc finger, DHHC-type containing 5	25921	ZDHHC5	0.423	+	0.014	0.028
222407_PM_s_at	zinc finger protein 106 homolog (mouse)	64397	ZFP106	0.775	+	0.010	0.039
223388_PM_s_at	zinc finger, FYVE domain containing 1	53349	ZFYVE1	0.311	+	0.016	0.041
210291_PM_s_at	zinc finger protein 174	7727	ZNF174	0.337	+	0.049	0.016
219314_PM_s_at	zinc finger protein 219	51222	ZNF219	0.373	+	0.004	0.005
217185_PM_s_at	zinc finger protein 259 /// zinc finger protein 259, pseudogene	442240 /// 8882	ZNF259 /// ZNF259P	0.410	+	0.023	0.013
242684_PM_at	zinc finger protein 425	155054	ZNF425	0.310	+	0.014	0.023
242697_PM_at	zinc finger protein 540	163255	ZNF540	0.267	+	0.033	0.032
213367_PM_at	zinc finger family member 783	155060	ZNF783	0.466	+	0.012	0.028
235448_PM_at	ZXD family zinc finger C	79364	ZXDC	0.306	+	0.001	0.002
215706_PM_x_at	zyxin	7791	ZYX	0.476	+	0.013	0.013
200808_PM_s_at	zyxin	7791	ZYX	0.323	+	0.038	0.050

Supplementary Table 8. Exercise Associated Gene Expression in the Putamen. All transcripts in the table are significant with p<0.05 for both paired and groupwise t-tests. All transcripts are identified by their Probe Set ID, Gene title, Entrez Gene ID, and Gene symbol. Transcript data is listed for the motor cortex (M), putamen (P), and hippocampus (H). For each transcript we calculated their average log ratio (ALR,the average expression change of the exercising monkeys minus the average expression change of the sedentary monkeys), the direction of the change, the p-value for the groupwise and paired t-tests, and if the transcript met the significance cutoff in each brain region. There are 265 transcripts differentially expressed by exercise in the putamen.

Supplementary Table 8. Exercise Associated Gene Expression in the Putamen.

Probe Set ID	Gene Title	Entrez Gene ID	Gene Symbol	P ALR	P DIR	P TTEST (GROUP)	P TTEST (PAIR)
243067_PM_at	---	---	---	-0.284	-	0.003	0.012
1558444_PM_at	---	---	---	-0.303	-	0.003	0.020
233081_PM_at	---	---	---	-0.264	-	0.004	0.020
230868_PM_at	---	---	---	-0.299	-	0.004	0.007
244170_PM_at	---	---	---	-0.359	-	0.005	0.017
216172_PM_at	---	---	---	-0.286	-	0.005	0.024
1563295_PM_at	---	---	---	-0.288	-	0.006	0.013
235150_PM_at	---	---	---	-0.374	-	0.007	0.028
244270_PM_at	---	---	---	-0.279	-	0.008	0.021
231101_PM_at	---	---	---	-0.308	-	0.010	0.040
244711_PM_at	---	---	---	-0.304	-	0.014	0.031
236117_PM_at	---	---	---	-0.311	-	0.017	0.003
236388_PM_at	---	---	---	-0.343	-	0.025	0.022
1562106_PM_at	---	---	---	-0.423	-	0.043	0.032
234862_PM_at	---	---	---	-0.274	-	0.048	0.017
1554878_PM_a_at	ATP-binding cassette, sub-family D (ALD), member 3	5825	ABCD3	-0.299	-	0.038	0.037
217007_PM_s_at	ADAM metallopeptidase domain 15	8751	ADAM15	-0.288	-	0.010	0.039
219393_PM_s_at	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	10000	AKT3	-0.263	-	0.009	0.045
236034_PM_at	angiopoietin 2	285	ANGPT2	-0.265	-	0.001	0.010
201686_PM_x_at	apoptosis inhibitor 5	8539	API5	-0.466	-	0.001	0.007
214959_PM_s_at	apoptosis inhibitor 5	8539	API5	-0.538	-	0.001	0.005

1566989_PM_at	AT rich interactive domain 1B (SWI1-like)	57492	ARID1B	-0.623	-	0.015	0.027
1566990_PM_x_at	AT rich interactive domain 1B (SWI1-like)	57492	ARID1B	-0.352	-	0.030	0.009
225709_PM_at	ADP-ribosylation-like factor 6 interacting protein 6	151188	ARL6IP6	-0.263	-	0.030	0.015
211076_PM_x_at	Atrophin 1	1822	ATN1	-0.378	-	0.006	0.016
219558_PM_at	ATPase type 13A3	79572	ATP13A3	-0.445	-	0.030	0.023
209186_PM_at	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	488	ATP2A2	-0.289	-	0.017	0.014
1557759_PM_at	ATP5S-like	55101	ATP5SL	-0.306	-	0.012	0.033
221484_PM_at	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5	9334	B4GALT5	-0.361	-	0.007	0.026
225472_PM_at	HLA-B associated transcript 4	7918	BAT4	-0.263	-	0.000	0.000
213016_PM_at	bobby sox homolog (Drosophila)	56987	BBX	-0.288	-	0.020	0.043
1553021_PM_s_at	bicaudal D homolog 2 (Drosophila)	23299	BICD2	-0.356	-	0.021	0.030
1555544_PM_a_at	cell adhesion molecule 2	253559	CADM2	-0.326	-	0.000	0.003
200935_PM_at	calreticulin	811	CALR	-0.394	-	0.018	0.047
231729_PM_s_at	calcyphosine	828	CAPS	-0.330	-	0.014	0.048
213055_PM_at	CD47 molecule	961	CD47	-0.517	-	0.010	0.030
204739_PM_at	centromere protein C 1	1060	CENPC1	-0.292	-	0.009	0.014
1557786_PM_s_at	cysteine-rich hydrophobic domain 1	53344	CHIC1	-0.334	-	0.023	0.046
207486_PM_x_at	chimerin (chimaerin) 2	1124	CHN2	-0.264	-	0.015	0.010
206736_PM_x_at	cholinergic receptor, nicotinic, alpha 4	1137	CHRNA4	-0.273	-	0.006	0.010
210866_PM_s_at	CCR4-NOT transcription complex, subunit 4	4850	CNOT4	-0.417	-	0.015	0.032
218975_PM_at	collagen, type V, alpha 3	50509	COL5A3	-0.622	-	0.033	0.000
222686_PM_s_at	calcineurin-like phosphoesterase domain containing 1	55313	CPPED1	-0.376	-	0.038	0.050
206994_PM_at	cystatin S	1472	CST4	-0.341	-	0.004	0.035
220611_PM_at	disabled homolog 1 (Drosophila)	1600	DAB1	-0.612	-	0.001	0.004
222678_PM_s_at	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	54165	DCUN1D1	-0.419	-	0.003	0.007
225442_PM_at	discoidin domain receptor tyrosine kinase 2	4921	DDR2	-0.708	-	0.010	0.002
202516_PM_s_at	discs, large homolog 1 (Drosophila)	1739	DLG1	-0.344	-	0.004	0.007

235341_PM_at	DnaJ (Hsp40) homolog, subfamily C, member 3	5611	DNAJC3	-0.276	-	0.033	0.046
1560916_PM_a_at	dpy-19-like 1 (C. elegans)	23333	DPY19L1	-0.414	-	0.008	0.015
221835_PM_at	deltex homolog 3 (Drosophila)	196403	DTX3	-0.393	-	0.017	0.035
214793_PM_at	dual specificity phosphatase 7	1849	DUSP7	-0.287	-	0.035	0.013
204954_PM_s_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	9149	DYRK1B	-0.302	-	0.003	0.004
226911_PM_at	EGF-like, fibronectin type III and laminin G domains	133584	EGFLAM	-0.270	-	0.003	0.014
219436_PM_s_at	endomucin	51705	EMCN	-0.269	-	0.014	0.030
226432_PM_at	ethanolamine kinase 1	55500	ETNK1	-0.356	-	0.014	0.027
205521_PM_at	endo/exonuclease (5’-3’), endonuclease G-like	9941	EXOG	-0.273	-	0.009	0.028
208092_PM_s_at	family with sequence similarity 49, member A	81553	FAM49A	-0.393	-	0.033	0.032
201787_PM_at	fibulin 1	2192	FBLN1	-0.484	-	0.021	0.029
1564383_PM_s_at	FLJ35934 protein	400579	FLJ35934	-0.484	-	0.003	0.000
215977_PM_x_at	glycerol kinase	2710	GK	-0.420	-	0.017	0.039
216316_PM_x_at	glycerol kinase /// glycerol kinase 3 pseudogene	2710 /// 2713	GK /// GK3P	-0.357	-	0.006	0.022
215966_PM_x_at	glycerol kinase 3 pseudogene	2713	GK3P	-0.738	-	0.007	0.030
205184_PM_at	guanine nucleotide binding protein (G protein), gamma 4	2786	GNG4	-0.298	-	0.010	0.042
203631_PM_s_at	G protein-coupled receptor, family C, group 5, member B	51704	GPRC5B	-0.284	-	0.039	0.044
220142_PM_at	hyaluronan and proteoglycan link protein 2	60484	HAPLN2	-0.287	-	0.018	0.049
231043_PM_at	primary ciliary dyskinesia protein 1	200373	hCG_17324	-0.793	-	0.001	0.004
225116_PM_at	homeodomain interacting protein kinase 2	28996	HIPK2	-1.031	-	0.003	0.025
224016_PM_at	homeodomain interacting protein kinase 2	28996	HIPK2	-0.316	-	0.049	0.033
207764_PM_s_at	homeodomain interacting protein kinase 3	10114	HIPK3	-0.335	-	0.004	0.024
205967_PM_at	histone cluster 1, H4c	8364	HIST1H4C	-0.361	-	0.018	0.010
1563532_PM_at	hemicentin 2	256158	HMCN2	-0.300	-	0.016	0.018
209098_PM_s_at	jagged 1 (Alagille syndrome)	182	JAG1	-0.470	-	0.031	0.044
203849_PM_s_at	kinesin family member 1A	547	KIF1A	-0.336	-	0.035	0.037
225140_PM_at	Kruppel-like factor 3 (basic)	51274	KLF3	-0.289	-	0.015	0.013
223888_PM_s_at	leucyl-tRNA synthetase	51520	LARS	-0.280	-	0.028	0.049
235036_PM_at	Lix1 homolog (mouse)-like	128077	LIX1L	-0.273	-	0.027	0.040
239598_PM_s_at	lysophosphatidylcholine acyltransferase 2	54947	LPCAT2	-0.399	-	0.000	0.004

212272_PM_at	lipin 1	23175	LPIN1	-0.354	-	0.005	0.034
207702_PM_s_at	membrane associated guanylate kinase, WW and PDZ domain containing 2	9863	MAGI2	-0.314	-	0.016	0.011
203841_PM_x_at	microtubule-associated protein, RP/EB family, member 3	22924	MAPRE3	-0.316	-	0.005	0.026
205018_PM_s_at	muscleblind-like 2 (Drosophila)	10150	MBNL2	-0.292	-	0.029	0.017
222590_PM_s_at	nemo-like kinase	51701	NLK	-0.319	-	0.014	0.017
1552932_PM_at	NLR family, pyrin domain containing 6	171389	NLRP6	-0.272	-	0.003	0.012
203964_PM_at	N-myc (and STAT) interactor	9111	NMI	-0.321	-	0.012	0.007
226061_PM_s_at	Nudix (nucleoside diphosphate linked moiety X)-type motif 3	11165	NUDT3	-0.266	-	0.047	0.042
201282_PM_at	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	4967	OGDH	-0.267	-	0.036	0.045
200815_PM_s_at	platelet-activating factor acetylhydrolase, isoform Ib, subunit 1 (45kDa)	5048	PAFAH1B1	-0.307	-	0.023	0.020
1559052_PM_s_at	p21 protein (Cdc42/Rac)-activated kinase 2	5062	PAK2	-0.489	-	0.002	0.000
208875_PM_s_at	p21 protein (Cdc42/Rac)-activated kinase 2	5062	PAK2	-0.287	-	0.005	0.009
211502_PM_s_at	PFTAIRE protein kinase 1	5218	PFTK1	-0.473	-	0.008	0.001
205702_PM_at	putative homeodomain transcription factor 1	10745	PHTF1	-0.343	-	0.004	0.019
1568949_PM_at	phosphatidylinositol transfer protein, cytoplasmic 1	26207	PITPNC1	-0.331	-	0.001	0.011
235958_PM_at	phospholipase A2, group IVF	255189	PLA2G4F	-0.297	-	0.006	0.018
206174_PM_s_at	protein phosphatase 6, catalytic subunit	5537	PPP6C	-0.284	-	0.010	0.016
214545_PM_s_at	proline synthetase co-transcribed homolog (bacterial)	11212	PROSC	-0.511	-	0.021	0.045
209385_PM_s_at	proline synthetase co-transcribed homolog (bacterial)	11212	PROSC	-0.422	-	0.038	0.019
209599_PM_s_at	prune homolog (Drosophila)	58497	PRUNE	-0.325	-	0.043	0.042
211711_PM_s_at	phosphatase and tensin homolog	5728	PTEN	-0.273	-	0.005	0.014
208466_PM_at	RAB3D, member RAS oncogene family	9545	RAB3D	-0.389	-	0.008	0.013
201156_PM_s_at	RAB5C, member RAS oncogene family	5878	RAB5C	-0.354	-	0.001	0.013
212332_PM_at	retinoblastoma-like 2 (p130)	5934	RBL2	-0.288	-	0.017	0.028
203169_PM_at	RGP1 retrograde golgi transport homolog (S. cerevisiae)	9827	RGP1	-0.440	-	0.016	0.004
213430_PM_at	RUN and FYVE domain containing 3	22902	RUFY3	-0.266	-	0.017	0.005
1555819_PM_s_at	sterile alpha motif domain containing 14	201191	SAMD14	-0.270	-	0.011	0.050
233242_PM_at	SCAN domain containing 2 pseudogene	54581	SCAND2	-0.271	-	0.017	0.044

201093_PM_x_at	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	6389	SDHA	0.300	-	0.008	0.047
37462_PM_i_at	splicing factor 3a, subunit 2, 66kDa	8175	SF3A2	-0.268	-	0.018	0.028
214096_PM_s_at	serine hydroxymethyltransferase 2 (mitochondrial)	6472	SHMT2	-0.267	-	0.009	0.033
239435_PM_x_at	shroom family member 1	134549	SHROOM1	-0.310	-	0.008	0.037
218237_PM_s_at	solute carrier family 38, member 1	81539	SLC38A1	-0.279	-	0.007	0.004
210739_PM_x_at	solute carrier family 4, sodium bicarbonate cotransporter, member 4	8671	SLC4A4	-0.404	-	0.003	0.007
211494_PM_s_at	solute carrier family 4, sodium bicarbonate cotransporter, member 4	8671	SLC4A4	-0.608	-	0.024	0.023
34868_PM_at	Smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)	23381	SMG5	-0.328	-	0.003	0.007
212777_PM_at	son of sevenless homolog 1 (Drosophila)	6654	SOS1	-0.299	-	0.008	0.007
212466_PM_at	174epari-related, EVH1 domain containing 2	200734	SPRED2	-0.368	-	0.008	0.030
217903_PM_at	striatin, calmodulin binding protein 4	29888	STRN4	-0.275	-	0.030	0.008
1555052_PM_a_at	synaptotagmin IX	143425	SYT9	-0.496	-	0.009	0.013
244615_PM_x_at	threonyl-tRNA synthetase-like 2	123283	TARSL2	-0.274	-	0.011	0.035
1555189_PM_a_at	tyrosine aminotransferase	6898	TAT	-0.272	-	0.009	0.018
218466_PM_at	TBC1 domain family, member 17	79735	TBC1D17	-0.307	-	0.005	0.024
203167_PM_at	TIMP metallopeptidase inhibitor 2	7077	TIMP2	-0.567	-	0.026	0.038
201001_PM_s_at	TMEM189-UBE2V1 readthrough transcript /// ubiquitin-conjugating enzyme E2 variant 1	387522 /// 7335	TMEM189-UBE2V1 /// UBE2V1	-0.380	-	0.007	0.006
222736_PM_s_at	transmembrane protein 38B	55151	TMEM38B	-0.283	-	0.036	0.046
226083_PM_at	transmembrane protein 70	54968	TMEM70	-0.271	-	0.007	0.001
216695_PM_s_at	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	8658	TNKS	-0.359	-	0.018	0.027
206817_PM_x_at	trinucleotide repeat containing 4	11189	TNRC4	-0.375	-	0.005	0.013
214332_PM_s_at	Ts translation elongation factor, mitochondrial	10102	TSFM	-0.326	-	0.015	0.045
223283_PM_s_at	teashirt zinc finger homeobox 1	10194	TSHZ1	-0.404	-	0.001	0.007
1564386_PM_at	thioredoxin domain containing 8 (spermatozoa)	255220	TXNDC8	-0.343	-	0.039	0.025

218382_PM_s_at	U2 small nuclear RNA auxiliary factor 2	11338	U2AF2	-0.316	-	0.004	0.040
205137_PM_x_at	Usher syndrome 1C (autosomal recessive, severe)	10083	USH1C	-0.383	-	0.001	0.006
220769_PM_s_at	WD repeat domain 78	79819	WDR78	-0.312	-	0.002	0.011
1564053_PM_a_at	YTH domain family, member 3	253943	YTHDF3	-0.322	-	0.008	0.025
1554239_PM_s_at	zinc binding alcohol dehydrogenase domain containing 2	284273	ZADH2	-0.270	-	0.009	0.025
208446_PM_s_at	zinc finger, FYVE domain containing 9	9372	ZFYVE9	-0.310	-	0.009	0.003
1554159_PM_a_at	zinc finger, MYND domain containing 11	10771	ZMYND11	-0.263	-	0.024	0.023
1554958_PM_at	zinc finger protein 641	121274	ZNF641	-0.503	-	0.019	0.027
239080_PM_at	---	---	---	0.264	+	0.000	0.000
235875_PM_at	---	---	---	0.379	+	0.000	0.002
226345_PM_at	---	---	---	0.265	+	0.003	0.006
243992_PM_at	---	---	---	0.350	+	0.006	0.044
244184_PM_at	---	---	---	0.358	+	0.008	0.001
208306_PM_x_at	---	730415	---	0.608	+	0.010	0.015
244633_PM_at	---	---	---	0.317	+	0.013	0.032
228528_PM_at	---	---	---	0.376	+	0.016	0.001
231513_PM_at	---	---	---	0.976	+	0.018	0.004
214353_PM_at	---	---	---	0.306	+	0.018	0.050
1561155_PM_at	---	---	---	0.336	+	0.022	0.018
233005_PM_at	---	---	---	0.333	+	0.028	0.015
243006_PM_at	---	---	---	0.308	+	0.029	0.026
232834_PM_at	---	---	---	0.354	+	0.032	0.030
240655_PM_at	---	---	---	0.446	+	0.032	0.027
243666_PM_at	---	---	---	0.267	+	0.034	0.001
239277_PM_at	---	---	---	0.307	+	0.036	0.018
235657_PM_at	---	---	---	0.392	+	0.044	0.011
228297_PM_at	---	---	---	0.795	+	0.044	0.041
242932_PM_at	---	---	---	0.304	+	0.047	0.028
226394_PM_at	membrane-associated ring finger (C3HC4) 5	54708	5-Mar	0.327	+	0.008	0.007

202144_PM_s_at	adenylosuccinate lyase	158	ADSL	0.455	+	0.044	0.049
210250_PM_x_at	adenylosuccinate lyase	158	ADSL	0.357	+	0.049	0.049
238135_PM_at	Angiotensin II receptor-associated protein	57085	AGTRAP	0.378	+	0.008	0.017
229526_PM_at	aquaporin 11	282679	AQP11	0.397	+	0.012	0.033
225552_PM_x_at	aurora kinase A interacting protein 1	54998	AURKAIP1	0.273	+	0.045	0.046
229720_PM_at	BCL2-associated athanogene	573	BAG1	0.275	+	0.002	0.007
202201_PM_at	biliverdin reductase B (flavin reductase (NADPH))	645	BLVRB	0.263	+	0.044	0.050
1555773_PM_at	bactericidal/permeability-increasing protein-like 2	254240	BPIL2	0.392	+	0.004	0.017
231960_PM_at	bromodomain and WD repeat domain containing 1	54014	BRWD1	0.287	+	0.007	0.041
1555923_PM_a_at	chromosome 10 open reading frame 114	399726	C10orf114	0.267	+	0.035	0.032
230259_PM_at	chromosome 10 open reading frame 125	282969	C10orf125	0.314	+	0.044	0.049
221599_PM_at	chromosome 11 open reading frame 67	28971	C11orf67	0.309	+	0.003	0.019
228721_PM_at	chromosome 3 open reading frame 41	26172	C3orf41	0.305	+	0.038	0.003
219124_PM_at	chromosome 8 open reading frame 41	80185	C8orf41	0.322	+	0.003	0.011
209682_PM_at	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	868	CBLB	0.306	+	0.034	0.043
205899_PM_at	cyclin A1	8900	CCNA1	0.276	+	0.019	0.011
228081_PM_at	cyclin G2	901	CCNG2	0.301	+	0.016	0.031
203493_PM_s_at	centrosomal protein 57kDa	9702	CEP57	0.278	+	0.008	0.046
211862_PM_x_at	CASP8 and FADD-like apoptosis regulator	8837	CFLAR	0.390	+	0.002	0.018
226702_PM_at	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	129607	CMPK2	0.380	+	0.005	0.002
1554377_PM_a_at	contactin associated protein-like 4	85445	CNTNAP4	0.347	+	0.015	0.017
1554241_PM_at	coagulation factor C homolog, cochlin (Limulus polyphemus)	1690	COCH	0.393	+	0.005	0.020
208146_PM_s_at	carboxypeptidase, vitellogenic-like	54504	CPVL	0.265	+	0.024	0.002
240228_PM_at	CUB and Sushi multiple domains 3	114788	CSMD3	0.439	+	0.006	0.002
1554796_PM_at	dipeptidyl-peptidase 6	1804	DPP6	0.350	+	0.000	0.001
211625_PM_s_at	dopamine receptor D3	1814	DRD3	0.314	+	0.036	0.001
206032_PM_at	desmocollin 3	1825	DSC3	0.286	+	0.025	0.028
236649_PM_at	DTW domain containing 1	56986	DTWD1	0.273	+	0.027	0.039
201303_PM_at	eukaryotic translation initiation factor 4A, isoform 3	9775	EIF4A3	0.289	+	0.002	0.004
204824_PM_at	endonuclease G	2021	ENDOG	0.274	+	0.001	0.016

231472_PM_at	F-box protein 15	201456	FBXO15	0.770	+	0.046	0.036
1570183_PM_at	F-box protein 34	55030	FBXO34	0.503	+	0.009	0.008
227298_PM_at	hypothetical gene supported by AK095117	401264	FLJ37798	0.312	+	0.030	0.047
233919_PM_s_at	hyaluronan binding protein 4	22927	HABP4	0.272	+	0.023	0.028
212964_PM_at	hypermethylated in cancer 2	23119	HIC2	0.309	+	0.044	0.019
215193_PM_x_at	major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 3 /// major histocompatibility complex, class II, DR beta 4 /// major histocompatibility complex, class II, DR beta 5 /// similar to HLA class II histocompatibility antigen, DR-W53 beta chain /// similar to HLA class II histocompatibility antigen, DRB1-7 beta chain	100133661 /// 100294036 /// 3123 /// 3125 /// 3126 /// 3127	HLA-DRB1 /// HLA-DRB3 /// HLA-DRB4 /// HLA-DRB5	0.912	+	0.011	0.041
209312_PM_x_at	major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 4	3123 /// 3126	HLA-DRB1 /// HLA-DRB4	1.037	+	0.005	0.023
204670_PM_x_at	major histocompatibility complex, class II, DR beta 1 /// major histocompatibility complex, class II, DR beta 4	3123 /// 3126	HLA-DRB1 /// HLA-DRB4	0.418	+	0.041	0.041
217362_PM_x_at	major histocompatibility complex, class II, DR beta 6 (pseudogene)	3128	HLA-DRB6	0.381	+	0.002	0.002
203960_PM_s_at	heat shock protein family B (small), member 11	51668	HSPB11	0.530	+	0.009	0.028
215691_PM_x_at	heat shock protein family B (small), member 11	51668	HSPB11	0.303	+	0.019	0.038
231183_PM_s_at	Jagged 1 (Alagille syndrome)	182	JAG1	1.363	+	0.024	0.039
215527_PM_at	KH domain containing, RNA binding, signal transduction associated 2	202559	KHDRBS2	0.322	+	0.031	0.048
214961_PM_at	KIAA0774	23281	KIAA0774	0.334	+	0.019	0.048
233916_PM_at	KIAA1486	57624	KIAA1486	0.276	+	0.050	0.046
221841_PM_s_at	Kruppel-like factor 4 (gut)	9314	KLF4	0.278	+	0.026	0.041
202057_PM_at	karyopherin alpha 1 (importin alpha 5)	3836	KPNA1	0.294	+	0.007	0.004
206309_PM_at	leukocyte cell derived chemotaxin 1	11061	LECT1	0.304	+	0.005	0.010
229930_PM_at	similar to hCG1811002	100134361	LOC100134361	0.603	+	0.010	0.026

238473_PM_at	hypothetical LOC100216545	100216545	LOC100216545	0.314	+	0.028	0.025
1559310_PM_at	hypothetical protein LOC100292408	100292408	LOC100292408	0.475	+	0.018	0.046
238207_PM_at	similar to CG32736-PA	440957	LOC440957	0.333	+	0.009	0.004
1569872_PM_a_at	Hypothetical protein LOC650392	650392	LOC650392	0.297	+	0.011	0.021
238534_PM_at	Leucine rich repeat (in FLII) interacting protein 1	9208	LRRFIP1	0.377	+	0.025	0.013
209580_PM_s_at	methyl-CpG binding domain protein 4	8930	MBD4	0.277	+	0.026	0.048
215663_PM_at	muscleblind-like (Drosophila)	4154	MBNL1	0.279	+	0.007	0.006
209087_PM_x_at	melanoma cell adhesion molecule	4162	MCAM	0.389	+	0.006	0.004
207447_PM_s_at	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme C (putative)	25834	MGAT4C	0.346	+	0.029	0.040
224385_PM_s_at	Mov10l1, Moloney leukemia virus 10-like 1, homolog (mouse)	54456	MOV10L1	0.612	+	0.009	0.013
215731_PM_s_at	M-phase phosphoprotein 9	10198	MPHOSPH9	0.291	+	0.003	0.000
222555_PM_s_at	mitochondrial ribosomal protein L44	65080	MRPL44	0.272	+	0.010	0.033
224873_PM_s_at	mitochondrial ribosomal protein S25	64432	MRPS25	0.273	+	0.041	0.012
225240_PM_s_at	musashi homolog 2 (Drosophila)	124540	MSI2	0.309	+	0.010	0.022
1554126_PM_at	methionine sulfoxide reductase B3	253827	MSRB3	-0.338	+	0.008	0.023
222794_PM_x_at	mitochondrial poly(A) polymerase	55149	MTPAP	0.278	+	0.008	0.009
227992_PM_s_at	non-protein coding RNA 85	147650	NCRNA00085	0.287	+	0.046	0.042
214657_PM_s_at	nuclear paraspeckle assembly transcript 1 (non-protein coding)	283131	NEAT1	0.285	+	0.044	0.045
201467_PM_s_at	NAD(P)H dehydrogenase, quinone 1	1728	NQO1	0.318	+	0.037	0.007
212775_PM_at	obscurin-like 1	23363	OBSL1	0.378	+	0.029	0.036
219245_PM_s_at	2-oxoglutarate and iron-dependent oxygenase domain containing 2	79676	OGFOD2	0.297	+	0.027	0.031
218736_PM_s_at	palmdelphin	54873	PALMD	0.512	+	0.002	0.006
230109_PM_at	phosphodiesterase 7B	27115	PDE7B	0.276	+	0.002	0.030
225830_PM_at	PDZ domain containing 8	118987	PDZD8	0.427	+	0.029	0.023
238131_PM_at	polyhomeotic homolog 2 (Drosophila)	1912	PHC2	0.371	+	0.023	0.016
229385_PM_s_at	placenta-specific 2 (non-protein coding)	257000	PLAC2	0.278	+	0.045	0.037

208928_PM_at	P450 (cytochrome) oxidoreductase	5447	POR	0.285	+	0.017	0.026
228217_PM_s_at	proteasome (prosome, macropain) assembly chaperone 4	389362	PSMG4	0.594	+	0.001	0.011
223471_PM_at	RAB3A interacting protein (rabin3)	117177	RAB3IP	0.442	+	0.011	0.013
218526_PM_s_at	RAN guanine nucleotide release factor	29098	RANGRF	0.304	+	0.015	0.011
203696_PM_s_at	replication factor C (activator 1) 2, 40kDa	5982	RFC2	0.342	+	0.010	0.028
213566_PM_at	ribonuclease, Rnase A family, k6	6039	RNASE6	0.465	+	0.008	0.030
226548_PM_at	SH3-binding domain kinase 1	388228	SBK1	0.282	+	0.043	0.032
232983_PM_s_at	secretion regulating guanine nucleotide exchange factor	26297	SERGEF	0.268	+	0.003	0.016
211429_PM_s_at	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	5265	SERPINA1	0.375	+	0.048	0.021
230660_PM_at	SERTA domain containing 4	56256	SERTAD4	0.343	+	0.001	0.002
200685_PM_at	splicing factor, arginine/serine-rich 11	9295	SFRS11	0.265	+	0.006	0.019
204270_PM_at	v-ski sarcoma viral oncogene homolog (avian)	6497	SKI	0.392	+	0.006	0.016
205317_PM_s_at	solute carrier family 15 (H+/peptide transporter), member 2	6565	SLC15A2	0.442	+	0.032	0.033
223605_PM_at	solute carrier family 25 (mitochondrial carrier), member 18	83733	SLC25A18	0.402	+	0.000	0.005
217289_PM_s_at	solute carrier family 37 (glucose-6-phosphate transporter), member 4	2542	SLC37A4	0.410	+	0.002	0.000
226264_PM_at	sushi domain containing 1	64420	SUSD1	0.271	+	0.029	0.004
214348_PM_at	tachykinin receptor 2	6865	TACR2	0.272	+	0.007	0.011
213209_PM_at	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	10629	TAF6L	0.402	+	0.006	0.004
230236_PM_at	testis development related protein 1	732253	TDRG1	0.396	+	0.010	0.031
228906_PM_at	tet oncogene 1	80312	TET1	0.356	+	0.017	0.038
1554379_PM_a_at	tumor protein p73	7161	TP73	0.283	+	0.007	0.018
213748_PM_at	tripartite motif-containing 66	9866	TRIM66	0.308	+	0.023	0.011
211701_PM_s_at	trophinin	7216	TRO	0.277	+	0.032	0.001
213679_PM_at	tetratricopeptide repeat domain 30A	92104	TTC30A	0.662	+	0.012	0.020
244293_PM_at	ubiquinol-cytochrome c reductase binding protein	7381	UQCRB	0.297	+	0.022	0.028
224608_PM_s_at	vacuolar protein sorting 25 homolog (S. cerevisiae)	84313	VPS25	0.277	+	0.001	0.005
236635_PM_at	zinc finger protein 667	63934	ZNF667	0.418	+	0.002	0.009
1553172_PM_at	zinc finger protein 777	27153	ZNF777	0.378	+	0.003	0.012

244180_PM_at	zinc finger protein 793	390927	ZNF793	0.320	+	0.019	0.027
226764_PM_at	zinc finger protein 827	152485	ZNF827	0.407	+	0.001	0.003
222814_PM_s_at	zinc finger, HIT type 2	741	ZNHIT2	0.437	+	0.020	0.031

Supplementary Table 9. Exercise Associated Gene Expression in the Hippocampus. All transcripts in the table are significant with p<0.05 for both paired and groupwise t-tests. All transcripts are identified by their Probe Set ID, Gene title, Entrez Gene ID, and Gene symbol. Transcript data is listed for the motor cortex (M), putamen (P), and hippocampus (H). For each transcript we calculated their average log ratio (ALR, the average expression change of the exercising monkeys minus the sedentary monkeys), the direction of the change, the p-value for the groupwise and paired t-tests, and if the transcript met the significance cutoff in each brain region. There are 5508 transcripts differentially expressed by exercise in the hippocampus

Supplementary Table 9. Exercise Associated Gene Expression in the Hippocampus

Probe Set ID	Gene Title	Entrez Gene ID	Gene Symbol	H ALR	H DIR	H TTEST (GROUP)	H TTEST (PAIR)
229803_PM_s_at	---	84289	---	-0.975	-	1.60E-04	9.63E-04
217211_PM_at	---	55031	---	-0.311	-	4.37E-04	8.71E-03
1566524_PM_a_at	---	6303	---	-0.299	-	4.85E-04	1.79E-03
1560926_PM_at	---	140885	---	-0.283	-	1.04E-03	6.44E-03
239155_PM_at	---	---	---	-0.410	-	1.14E-03	1.44E-02
240482_PM_at	---	5930	---	-0.276	-	1.24E-03	1.47E-03
1553498_PM_at	---	10658	---	-0.270	-	2.24E-03	1.91E-03
242846_PM_at	---	9295	---	-0.324	-	2.68E-03	1.06E-02
238495_PM_at	---	2067	---	-0.594	-	3.29E-03	4.34E-03
1556432_PM_at	---	120	---	-0.327	-	4.24E-03	1.22E-02
242403_PM_at	---	---	---	-0.378	-	4.31E-03	3.92E-03
244306_PM_at	---	---	---	-0.506	-	4.37E-03	3.14E-02
1562473_PM_at	---	9656	---	-1.081	-	4.65E-03	2.30E-03
240216_PM_at	---	---	---	-1.146	-	4.83E-03	9.17E-03
237413_PM_at	---	8897	---	-0.621	-	4.83E-03	2.45E-02
239082_PM_at	---	---	---	-0.323	-	5.11E-03	4.03E-02
241216_PM_at	---	---	---	-0.316	-	5.61E-03	2.98E-02
229244_PM_at	---	4297	---	-0.765	-	5.64E-03	1.92E-02
235381_PM_at	---	65258	---	-0.481	-	5.78E-03	1.07E-02
241929_PM_at	---	---	---	-0.279	-	6.09E-03	6.10E-03
243101_PM_x_at	---	---	---	-0.279	-	6.38E-03	5.77E-03
237964_PM_at	---	---	---	-0.273	-	6.89E-03	3.12E-02

233626_PM_at	---	100129250	---	-0.328	-	7.34E-03	8.03E-03
229297_PM_at	---	10466	---	-1.624	-	7.35E-03	2.77E-02
242850_PM_at	---	---	---	-0.346	-	7.91E-03	1.19E-02
244678_PM_at	---	---	---	-0.286	-	8.37E-03	4.16E-02
236412_PM_at	---	3092	---	-0.266	-	8.92E-03	2.07E-03
215345_PM_x_at	---	79776	---	-0.269	-	8.97E-03	9.17E-04
214807_PM_at	---	51188	---	-0.398	-	9.23E-03	3.24E-02
239742_PM_at	---	100294358	---	-1.862	-	9.63E-03	1.32E-02
239758_PM_at	---	8239	---	-0.269	-	9.73E-03	2.05E-02
229434_PM_at	---	10672	---	-1.830	-	1.04E-02	2.24E-02
1562409_PM_s_at	---	7799	---	-0.288	-	1.20E-02	1.93E-02
211973_PM_at	---	7803	---	-1.404	-	1.21E-02	2.07E-02
244170_PM_at	---	---	---	-2.294	-	1.24E-02	3.48E-02
244358_PM_at	---	---	---	-0.470	-	1.28E-02	4.98E-02
233800_PM_at	---	647589	---	-0.834	-	1.29E-02	3.73E-02
232333_PM_at	---	7707	---	-0.448	-	1.36E-02	3.95E-03
243249_PM_at	---	---	---	-0.274	-	1.45E-02	4.81E-02
234151_PM_at	---	---	---	-0.632	-	1.56E-02	1.54E-02
231259_PM_s_at	---	---	---	-0.514	-	1.57E-02	4.09E-02
215287_PM_at	---	29967	---	-1.132	-	1.65E-02	1.67E-02
1561639_PM_at	---	2274	---	-0.400	-	1.72E-02	4.73E-02
244194_PM_at	---	---	---	-0.341	-	1.76E-02	2.10E-02
242768_PM_at	---	---	---	-0.273	-	1.77E-02	6.64E-03
232058_PM_at	---	---	---	-0.283	-	1.97E-02	4.79E-02
239095_PM_at	---	---	---	-0.843	-	2.00E-02	1.28E-02
227121_PM_at	---	8629	---	-1.068	-	2.81E-02	3.55E-02
243665_PM_s_at	---	91862	---	-0.779	-	3.00E-02	1.81E-02
236636_PM_at	---	---	---	-0.371	-	3.12E-02	4.66E-02
215528_PM_at	---	79862	---	-0.294	-	3.24E-02	1.40E-02
212608_PM_s_at	---	27238	---	-1.408	-	3.36E-02	4.14E-02
243394_PM_at	---	---	---	-0.291	-	3.41E-02	4.23E-02

1558019_PM_at	---	5692	---	-0.279	-	3.69E-02	3.71E-02
229606_PM_at	---	90025	---	-1.012	-	3.88E-02	4.16E-02
217637_PM_at	---	222068	---	-1.202	-	4.06E-02	4.65E-02
213048_PM_s_at	---	2892	---	-2.641	-	4.29E-02	4.86E-02
228218_PM_at	---	54495	---	-0.578	-	4.78E-02	2.08E-02
240157_PM_at	---	730631	---	-0.285	-	4.78E-02	7.96E-03
213655_PM_at	---	5934	---	-1.591	-	4.85E-02	4.26E-02
1555526_PM_a_at	septin 6	4154	3-Mar	-1.129	-	1.68E-03	2.22E-02
200778_PM_s_at	septin 2	8573	3-Mar	-0.676	-	1.12E-02	4.12E-02
1553422_PM_s_at	ataxin 2-binding protein 1	55197	A2BP1	-0.606	-	1.08E-03	9.17E-03
221217_PM_s_at	ataxin 2-binding protein 1	8851	A2BP1	-1.398	-	9.97E-03	1.03E-02
211186_PM_s_at	AP2 associated kinase 1	9462	AAK1	-0.501	-	7.22E-03	1.76E-02
202170_PM_s_at	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	26025 /// 5098 /// 56097 /// 56098 /// 56099 /// 56100 /// 56101 /// 56102 /// 56103 /// 56104 /// 56105 /// 56106 /// 56107 /// 56108 /// 56109 /// 56110 /// 56111 /// 56112 /// 56113 /// 56114 /// 8641 /// 9708	AASDHPPT	-2.342	-	6.49E-03	2.63E-02
210100_PM_s_at	ATP-binding cassette, sub-family A (ABC1), member 2	84899	ABCA2	-2.617	-	7.09E-03	1.90E-02
1554878_PM_a_at	ATP-binding cassette, sub-family D (ALD), member 3	3895	ABCD3	-1.408	-	2.38E-04	3.90E-03
228123_PM_s_at	abhydrolase domain containing 12	5814	ABHD12	-1.934	-	2.91E-02	4.95E-02
87100_PM_at	abhydrolase domain containing 2	54455	ABHD2	-0.281	-	8.07E-03	6.89E-03
221679_PM_s_at	abhydrolase domain containing 6	5453	ABHD6	-1.504	-	2.17E-02	4.65E-02

211793_PM_s_at	abl-interactor 2	284161	ABI2	-0.948	-	3.35E-03	5.27E-03
209856_PM_x_at	abl-interactor 2	84991	ABI2	-0.659	-	1.30E-02	2.24E-02
214671_PM_s_at	active BCR-related gene	55255	ABR	-0.327	-	2.07E-02	1.23E-02
226442_PM_at	ankyrin repeat and BTB (POZ) domain containing 1	6431	ABTB1	-0.361	-	5.80E-03	8.01E-03
1552472_PM_a_at	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2	10044	ACAP2	-0.610	-	2.71E-02	2.98E-02
225529_PM_at	ArfGAP with coiled-coil, ankyrin repeat and PH domains 3	157773	ACAP3	-0.618	-	2.36E-02	3.10E-02
202323_PM_s_at	acyl-Coenzyme A binding domain containing 3	54812	ACBD3	-0.632	-	1.41E-03	1.88E-02
210337_PM_s_at	ATP citrate lyase	54536	ACLY	-1.503	-	3.60E-02	4.04E-02
215728_PM_s_at	acyl-CoA thioesterase 7	55006	ACOT7	-1.824	-	3.60E-02	3.90E-02
200801_PM_x_at	actin, beta	51754	ACTB	-0.407	-	1.94E-02	4.34E-02
208637_PM_x_at	actinin, alpha 1	9927	ACTN1	-1.603	-	2.57E-02	4.30E-02
200720_PM_s_at	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast)	782	ACTR1A	-1.435	-	6.96E-04	1.89E-03
1558015_PM_s_at	ARP2 actin-related protein 2 homolog (yeast)	7388	ACTR2	-3.485	-	2.47E-04	6.08E-03
200727_PM_s_at	ARP2 actin-related protein 2 homolog (yeast)	5788	ACTR2	-2.827	-	5.05E-04	8.79E-03
1554390_PM_s_at	ARP2 actin-related protein 2 homolog (yeast)	9948	ACTR2	-2.711	-	1.04E-03	1.62E-02
208223_PM_s_at	activin A receptor, type IB	4839	ACVR1B	-1.261	-	4.40E-03	8.66E-03
220028_PM_at	activin A receptor, type IIB	11334	ACVR2B	-0.536	-	2.53E-03	5.24E-03
207880_PM_at	ADAM metallopeptidase domain 11	4750	ADAM11	-0.617	-	1.68E-02	2.91E-02
217007_PM_s_at	ADAM metallopeptidase domain 15	51527	ADAM15	-0.419	-	2.39E-02	2.61E-02
206046_PM_at	ADAM metallopeptidase domain 23	51747	ADAM23	-0.812	-	1.06E-02	1.49E-02
1554393_PM_a_at	arginine decarboxylase	9528	ADC	-1.186	-	1.09E-02	2.21E-02
214726_PM_x_at	184eparin184 1 (alpha)	59342	ADD1	-0.636	-	8.02E-04	8.96E-03
205882_PM_x_at	184eparin184 3 (gamma)	81552	ADD3	-1.759	-	2.58E-03	1.31E-02
201752_PM_s_at	184eparin184 3 (gamma)	7171	ADD3	-1.561	-	4.29E-03	1.61E-02
201753_PM_s_at	184eparin184 3 (gamma)	5151	ADD3	-1.028	-	1.42E-02	3.51E-02
216220_PM_s_at	adenosine A1 receptor	51028	ADORA1	-0.326	-	3.11E-02	1.76E-02
201401_PM_s_at	adrenergic, beta, receptor kinase 1	9104	ADRBK1	-1.429	-	1.39E-02	3.24E-02

228998_PM_at	adenylosuccinate lyase /// trinucleotide repeat containing 6B	25925	ADSL /// TNRC6B	-0.358	-	1.30E-02	4.92E-02
217729_PM_s_at	amino-terminal enhancer of split	7046	AES	-0.870	-	1.55E-02	2.48E-02
1555436_PM_a_at	AF4/FMR2 family, member 4	5211	AFF4	-0.359	-	1.24E-02	4.16E-02
217939_PM_s_at	aftiphilin	79813	AFTPH	-1.519	-	1.97E-02	4.69E-02
215080_PM_s_at	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2	79870	AGAP2	-0.517	-	3.46E-02	2.94E-02
231299_PM_at	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	10150	AGAP3	-3.028	-	3.17E-03	1.11E-02
231857_PM_s_at	ATP/GTP binding protein-like 5	84945	AGBL5	-0.489	-	3.78E-03	1.75E-03
213926_PM_s_at	ArfGAP with FG repeats 1	3858	AGFG1	-0.328	-	9.38E-03	9.77E-03
32836_PM_at	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)	758	AGPAT1	-1.424	-	2.68E-02	4.09E-02
224282_PM_s_at	1-acylglycerol-3-phosphate O-acyltransferase 3	84306	AGPAT3	-0.771	-	7.52E-03	5.97E-03
205401_PM_at	alkylglycerone phosphate synthase	6584	AGPS	-0.509	-	2.03E-02	4.87E-02
200850_PM_s_at	adenosylhomocysteinase-like 1	91	AHCYL1	-2.708	-	2.38E-02	4.40E-02
205002_PM_at	AT hook, DNA binding motif, containing 1	4331	AHDC1	-1.296	-	6.21E-03	1.62E-02
215789_PM_s_at	adherens junctions associated protein 1	10776	AJAP1	-0.687	-	2.24E-03	1.83E-03
222862_PM_s_at	adenylate kinase 5	2901	AK5	-1.010	-	1.57E-02	2.36E-02
210625_PM_s_at	A kinase (PRKA) anchor protein 1	7555	AKAP1	-1.255	-	2.05E-02	3.87E-02
218064_PM_s_at	A kinase (PRKA) anchor protein 8-like	353116	AKAP8L	-2.245	-	3.84E-03	1.46E-02
222458_PM_s_at	akirin 1	25976	AKIRIN1	-2.077	-	5.47E-03	1.83E-02
223143_PM_s_at	akirin 2	79817	AKIRIN2	-1.153	-	3.96E-03	1.93E-02
222880_PM_at	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	339479	AKT3	-0.741	-	7.02E-03	1.62E-02
219393_PM_s_at	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	5903	AKT3	-0.386	-	8.83E-03	4.99E-02
210544_PM_s_at	aldehyde dehydrogenase 3 family, member A2	79993	ALDH3A2	-0.318	-	2.83E-02	2.48E-02
204290_PM_s_at	aldehyde dehydrogenase 6 family, member A1	9779	ALDH6A1	-1.242	-	1.19E-03	2.24E-03
201196_PM_s_at	adenosylmethionine decarboxylase 1	5058	AMD1	-0.589	-	9.01E-03	3.49E-02
231973_PM_s_at	anaphase promoting complex subunit 1	3988	ANAPC1	-0.583	-	5.47E-03	1.96E-02
208721_PM_s_at	anaphase promoting complex subunit 5	996	ANAPC5	-1.968	-	1.28E-02	2.50E-02

202921_PM_s_at	ankyrin 2, neuronal	23648	ANK2	-2.013	-	1.96E-02	3.53E-02
207950_PM_s_at	ankyrin 3, node of Ranvier (ankyrin G)	6038	ANK3	-0.775	-	4.36E-04	5.41E-03
209442_PM_x_at	ankyrin 3, node of Ranvier (ankyrin G)	55284	ANK3	-0.855	-	1.67E-02	1.17E-02
223094_PM_s_at	ankylosis, progressive homolog (mouse)	26504	ANKH	-2.268	-	2.38E-03	9.63E-03
233292_PM_s_at	ankyrin repeat and KH domain containing 1 /// ANKHD1-EIF4EBP3 readthrough transcript	7381	ANKHD1 /// ANKHD1-EIF4EBP3	-1.610	-	1.04E-02	2.86E-02
224687_PM_at	ankyrin repeat and IBR domain containing 1	57614	ANKIB1	-1.418	-	5.19E-03	6.19E-03
238642_PM_at	ankyrin repeat domain 13 family, member D	---	ANKRD13D	-0.451	-	2.12E-02	1.22E-02
225852_PM_at	ankyrin repeat domain 17	80124	ANKRD17	-1.912	-	2.43E-03	1.58E-03
211717_PM_at	ankyrin repeat domain 40	114769	ANKRD40	-0.910	-	7.65E-03	2.32E-02
201051_PM_at	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	1859	ANP32A	-0.453	-	1.59E-02	3.07E-02
206200_PM_s_at	annexin A11	8202	ANXA11	-0.609	-	4.93E-02	4.95E-02
200982_PM_s_at	annexin A6	1831	ANXA6	-0.695	-	3.74E-02	4.93E-02
223025_PM_s_at	adaptor-related protein complex 1, mu 1 subunit	79956	AP1M1	-0.849	-	2.19E-02	3.41E-02
205196_PM_s_at	adaptor-related protein complex 1, sigma 1 subunit	1385	AP1S1	-2.263	-	3.35E-02	4.58E-02
209635_PM_at	adaptor-related protein complex 1, sigma 1 subunit	10910	AP1S1	-0.556	-	4.05E-02	1.75E-02
234068_PM_s_at	adaptor-related protein complex 2, alpha 1 subunit	---	AP2A1	-1.758	-	2.52E-03	7.15E-03
223237_PM_x_at	adaptor-related protein complex 2, alpha 1 subunit	79745	AP2A1	-0.525	-	1.42E-02	1.00E-02
208710_PM_s_at	adaptor-related protein complex 3, delta 1 subunit	64759	AP3D1	-1.743	-	2.67E-03	4.51E-03
202652_PM_at	amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65)	10955	APBB1	-0.457	-	3.25E-02	3.85E-02
216933_PM_x_at	adenomatous polyposis coli	65008	APC	-0.365	-	3.24E-02	1.07E-02
201686_PM_x_at	apoptosis inhibitor 5	6598	API5	-2.015	-	1.21E-03	1.42E-02
214959_PM_s_at	apoptosis inhibitor 5	51019	API5	-1.880	-	1.78E-03	2.05E-02
214960_PM_at	apoptosis inhibitor 5	64784	API5	-0.269	-	1.57E-02	6.99E-03
209462_PM_at	amyloid beta (A4) precursor-like protein 1	79101	APLP1	-0.446	-	2.19E-02	1.76E-02
214875_PM_x_at	amyloid beta (A4) precursor-like protein 2	56984	APLP2	-1.545	-	8.69E-03	1.52E-02
208702_PM_x_at	amyloid beta (A4) precursor-like protein 2	55737	APLP2	-1.394	-	8.95E-03	1.41E-02
211404_PM_s_at	amyloid beta (A4) precursor-like protein 2	338692	APLP2	-1.730	-	2.02E-02	3.78E-02
203381_PM_s_at	apolipoprotein E	80031	APOE	-0.676	-	1.38E-02	3.50E-02

210906_PM_x_at	aquaporin 4	148418	AQP4	-0.931	-	1.03E-03	4.54E-03
210068_PM_s_at	aquaporin 4	84240	AQP4	-1.454	-	1.21E-03	6.24E-03
210066_PM_s_at	aquaporin 4	10431	AQP4	-0.882	-	1.40E-02	3.74E-02
211622_PM_s_at	ADP-ribosylation factor 3	196403	ARF3	-1.461	-	3.09E-02	4.57E-02
234001_PM_s_at	ADP-ribosylation factor GTPase activating protein 1	---	ARFGAP1	-0.306	-	1.60E-02	1.13E-02
216689_PM_x_at	Rho GTPase activating protein 1	26995	ARHGAP1	-0.918	-	3.57E-03	5.34E-03
1555020_PM_a_at	Rho GTPase activating protein 20	6386	ARHGAP20	-0.282	-	4.92E-03	6.94E-03
241701_PM_at	Rho GTPase activating protein 21	---	ARHGAP21	-0.748	-	4.75E-02	9.25E-03
1552627_PM_a_at	Rho GTPase activating protein 5	129285	ARHGAP5	-0.641	-	4.82E-02	3.68E-02
201167_PM_x_at	Rho GDP dissociation inhibitor (GDI) alpha	23154	ARHGDIA	-1.697	-	9.11E-03	2.00E-02
206888_PM_s_at	Rho GDP dissociation inhibitor (GDI) gamma	8487	ARHGDIG	-1.356	-	4.12E-02	4.48E-02
1554783_PM_s_at	Rho/Rac guanine nucleotide exchange factor (GEF) 2	5908 /// 643752	ARHGEF2	-0.677	-	2.30E-03	5.48E-03
211891_PM_s_at	Rho guanine nucleotide exchange factor (GEF) 4	57582	ARHGEF4	-2.337	-	1.05E-02	2.52E-02
202547_PM_s_at	Rho guanine nucleotide exchange factor (GEF) 7	51501	ARHGEF7	-0.611	-	1.64E-03	2.97E-03
212152_PM_x_at	AT rich interactive domain 1A (SWI-like)	7072	ARID1A	-0.507	-	2.49E-02	1.10E-02
223111_PM_x_at	AT rich interactive domain 4B (RBP1-like)	54942	ARID4B	-0.881	-	2.55E-04	1.65E-03
218150_PM_at	ADP-ribosylation factor-like 5A	4087	ARL5A	-0.550	-	1.14E-02	6.81E-03
223328_PM_at	armadillo repeat containing 10	79003	ARMC10	-0.280	-	1.28E-02	1.89E-02
217858_PM_s_at	armadillo repeat containing, X-linked 3	55773	ARMCX3	-0.460	-	2.61E-03	2.75E-02
1555902_PM_at	armadillo repeat containing, X-linked 5	9184	ARMCX5	-0.558	-	3.07E-02	4.88E-03
211672_PM_s_at	actin related protein 2/3 complex, subunit 4, 20kDa /// tubulin tyrosine ligase-like family, member 3	196403	ARPC4 /// TTLL3	-2.525	-	1.89E-02	1.89E-02
218554_PM_s_at	ash1 (absent, small, or homeotic)-like (Drosophila)	25851	ASH1L	-0.337	-	3.22E-02	1.71E-02
1553997_PM_a_at	aspartate beta-hydroxylase domain containing 1	23263	ASPHD1	-1.504	-	2.58E-02	4.22E-02
218857_PM_s_at	asparaginase like 1	91775	ASRGL1	-1.005	-	2.79E-02	4.29E-02
244519_PM_at	additional sex combs like 1 (Drosophila)	---	ASXL1	-0.265	-	1.38E-03	6.10E-03
205446_PM_s_at	activating transcription factor 2	8821	ATF2	-0.925	-	2.24E-03	2.56E-02
216208_PM_s_at	activating transcription factor 6 beta	51108	ATF6B	-0.829	-	8.77E-03	1.99E-02

1554487_PM_a_at	activating transcription factor 6 beta	3939	ATF6B	-0.819	-	3.40E-02	2.76E-02
212280_PM_x_at	ATG4 autophagy related 4 homolog B (S. cerevisiae)	66008	ATG4B	-0.572	-	1.36E-02	3.15E-02
211076_PM_x_at	Atrophin 1	11276	ATN1	-0.516	-	5.22E-03	1.40E-02
219558_PM_at	ATPase type 13A3	9646	ATP13A3	-1.120	-	1.98E-03	1.37E-02
201242_PM_s_at	ATPase, Na+/K+ transporting, beta 1 polypeptide	80864 /// 9374	ATP1B1	-1.031	-	1.23E-02	2.35E-02
209186_PM_at	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	29761	ATP2A2	-1.053	-	7.98E-03	1.57E-02
209281_PM_s_at	ATPase, Ca++ transporting, plasma membrane 1	54469	ATP2B1	-2.071	-	1.11E-02	2.87E-02
211586_PM_s_at	ATPase, Ca++ transporting, plasma membrane 2	127544	ATP2B2	-1.585	-	1.62E-03	4.55E-03
201444_PM_s_at	ATPase, H+ transporting, lysosomal accessory protein 2	782	ATP6AP2	-1.363	-	2.62E-02	4.30E-02
205095_PM_s_at	ATPase, H+ transporting, lysosomal V0 subunit a1	11060	ATP6V0A1	-1.710	-	4.36E-03	7.19E-03
201971_PM_s_at	ATPase, H+ transporting, lysosomal 70kDa, V1 subunit A	50488	ATP6V1A	-2.812	-	2.69E-03	1.69E-02
210192_PM_at	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	317649	ATP8A1	-1.630	-	3.65E-03	1.93E-02
203231_PM_s_at	ataxin 1	137872	ATXN1	-1.668	-	7.39E-04	1.78E-03
202685_PM_s_at	AXL receptor tyrosine kinase	51131	AXL	-0.340	-	2.75E-02	2.75E-02
221484_PM_at	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5	4693	B4GALT5	-1.093	-	5.42E-03	9.21E-03
206232_PM_s_at	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	7336	B4GALT6	-1.449	-	6.88E-03	4.00E-02
224335_PM_s_at	beta-site APP-cleaving enzyme 1	133619	BACE1	-1.392	-	2.30E-02	3.71E-02
205293_PM_x_at	BAI1-associated protein 2	3631	BAIAP2	-2.345	-	1.86E-03	2.31E-03
208132_PM_x_at	HLA-B associated transcript 2	23321	BAT2	-1.001	-	2.90E-02	3.90E-02
211948_PM_x_at	BAT2 domain containing 1	7184	BAT2D1	-1.785	-	1.06E-02	4.64E-03
211944_PM_at	BAT2 domain containing 1	4677	BAT2D1	-1.091	-	1.35E-02	2.70E-03
214055_PM_x_at	BAT2 domain containing 1	29799	BAT2D1	-1.219	-	3.65E-02	2.74E-02
222643_PM_s_at	Bardet-Biedl syndrome 1 /// dipeptidyl-peptidase 3	112479	BBS1 /// DPP3	-0.682	-	3.60E-03	2.33E-02
223135_PM_s_at	bobby sox homolog (Drosophila)	29928	BBX	-1.382	-	7.89E-03	2.19E-02
232008_PM_s_at	bobby sox homolog (Drosophila)	285550	BBX	-1.279	-	1.44E-02	1.79E-02
223134_PM_at	bobby sox homolog (Drosophila)	79568	BBX	-1.531	-	1.99E-02	2.83E-02
213015_PM_at	bobby sox homolog (Drosophila)	2922	BBX	-0.848	-	2.52E-02	4.23E-02
91920_PM_at	brevican	11276	BCAN	-0.488	-	9.25E-03	3.19E-02

234979_PM_at	BCDIN3 domain containing	549	BCDIN3D	-0.393	-	6.22E-03	4.08E-03
224310_PM_s_at	B-cell CLL/lymphoma 11B (zinc finger protein)	56893	BCL11B	-0.892	-	1.64E-02	1.07E-02
222895_PM_s_at	B-cell CLL/lymphoma 11B (zinc finger protein)	54765	BCL11B	-0.697	-	3.40E-02	3.80E-02
206665_PM_s_at	BCL2-like 1	7965	BCL2L1	-0.426	-	7.95E-03	2.48E-02
215037_PM_s_at	BCL2-like 1	56180	BCL2L1	-0.965	-	2.88E-02	3.27E-02
223664_PM_x_at	BCL2-like 13 (apoptosis facilitator)	2744	BCL2L13	-1.005	-	3.84E-03	9.65E-03
215990_PM_s_at	B-cell CLL/lymphoma 6	79726	BCL6	-0.806	-	8.05E-03	2.10E-02
201101_PM_s_at	BCL2-associated transcription factor 1	25970	BCLAF1	-2.642	-	2.23E-02	3.54E-02
201169_PM_s_at	basic helix-loop-helix family, member e40	801	BHLHE40	-1.041	-	2.48E-03	1.87E-02
231243_PM_s_at	basic helix-loop-helix family, member e41	57414	BHLHE41	-1.612	-	1.83E-03	1.15E-02
223185_PM_s_at	basic helix-loop-helix family, member e41	79570	BHLHE41	-0.286	-	4.68E-02	2.73E-02
1553021_PM_s_at	bicaudal D homolog 2 (Drosophila)	51008	BICD2	-0.398	-	5.71E-05	3.48E-04
209203_PM_s_at	bicaudal D homolog 2 (Drosophila)	54477	BICD2	-1.013	-	1.09E-02	2.06E-02
202931_PM_x_at	bridging integrator 1	5992	BIN1	-0.761	-	2.20E-02	4.42E-02
210202_PM_s_at	bridging integrator 1	57542	BIN1	-2.238	-	2.32E-02	4.77E-02
1555675_PM_at	BH3-like motif containing, cell death inducer	1488	BLID	-0.321	-	6.89E-03	1.54E-02
207595_PM_s_at	bone morphogenetic protein 1	5930	BMP1	-0.331	-	6.51E-03	3.62E-02
210523_PM_at	bone morphogenetic protein receptor, type IB	8654	BMPR1B	-0.384	-	9.29E-03	6.09E-03
209920_PM_at	bone morphogenetic protein receptor, type II (serine/threonine kinase)	282991	BMPR2	-0.555	-	1.93E-02	4.96E-02
207186_PM_s_at	bromodomain PHD finger transcription factor	9736	BPTF	-1.289	-	7.55E-03	1.08E-02
208685_PM_x_at	bromodomain containing 2	8942	BRD2	-1.544	-	9.62E-04	1.92E-03
214911_PM_s_at	bromodomain containing 2	64748	BRD2	-0.755	-	2.82E-02	2.01E-02
202102_PM_s_at	bromodomain containing 4	5621	BRD4	-1.694	-	1.08E-03	1.01E-03
226054_PM_at	bromodomain containing 4	1601	BRD4	-1.935	-	1.43E-02	1.61E-02
222737_PM_s_at	bromodomain containing 7	2495	BRD7	-1.288	-	2.11E-02	3.12E-02
215010_PM_s_at	BR serine/threonine kinase 2	56034	BRSK2	-0.622	-	4.58E-03	2.14E-02
223653_PM_x_at	189epar-like 4, RNA binding protein (Drosophila)	58515	BRUNOL4	-2.696	-	5.54E-03	8.31E-03
231744_PM_at	189epar-like 5, RNA binding protein (Drosophila)	128077	BRUNOL5	-0.793	-	2.00E-03	1.23E-02
200920_PM_s_at	B-cell translocation gene 1, anti-proliferative	7267	BTG1	-2.718	-	1.97E-02	4.66E-02
201457_PM_x_at	budding uninhibited by benzimidazoles 3 homolog (yeast)	5162	BUB3	-1.374	-	1.33E-02	4.11E-02

200776_PM_s_at	basic leucine zipper and W2 domains 1 /// basic leucine zipper and W2 domains 1 like 1	94134	BZW1 /// BZW1L1	-0.383	-	2.52E-03	9.46E-03
219844_PM_at	chromosome 10 open reading frame 118	10497	C10orf118	-0.402	-	2.67E-03	8.58E-03
227257_PM_s_at	chromosome 10 open reading frame 46	50509	C10orf46	-0.581	-	1.31E-03	3.94E-04
1553566_PM_at	chromosome 12 open reading frame 53	54498	C12orf53	-0.894	-	2.36E-02	3.77E-02
1556299_PM_s_at	chromosome 12 open reading frame 76	8087	C12orf76	-0.345	-	7.54E-04	4.87E-03
203289_PM_s_at	chromosome 16 open reading frame 35	1479	C16orf35	-0.734	-	1.63E-02	3.28E-02
230296_PM_at	Chromosome 16 open reading frame 52	283174	C16orf52	-1.797	-	3.64E-03	2.85E-03
213986_PM_s_at	chromosome 19 open reading frame 6	23398	C19orf6	-1.249	-	4.87E-03	6.06E-03
224727_PM_at	chromosome 19 open reading frame 63	85457	C19orf63	-0.788	-	4.53E-02	3.33E-02
212002_PM_at	chromosome 1 open reading frame 144	6319	C1orf144	-0.544	-	1.15E-02	4.41E-02
243753_PM_at	chromosome 1 open reading frame 173	10783	C1orf173	-0.476	-	3.26E-02	2.89E-02
223127_PM_s_at	chromosome 1 open reading frame 21	54851	C1orf21	-0.988	-	2.48E-02	2.18E-02
233750_PM_s_at	chromosome 1 open reading frame 25	6616	C1orf25	-0.496	-	3.17E-03	8.57E-03
223938_PM_at	chromosome 1 open reading frame 49	84233	C1orf49	-0.269	-	2.90E-03	1.09E-02
223708_PM_at	C1q and tumor necrosis factor related protein 4	84259	C1QTNF4	-1.855	-	1.10E-02	3.28E-02
1557470_PM_at	C1q and tumor necrosis factor related protein 9 /// spermatogenesis associated 13	6392	C1QTNF9 /// SPATA13	-0.275	-	1.26E-02	3.84E-02
224693_PM_at	chromosome 20 open reading frame 108	200916	C20orf108	-0.503	-	8.22E-03	1.69E-02
50314_PM_i_at	chromosome 20 open reading frame 27	152485	C20orf27	-0.470	-	1.77E-02	5.51E-03
218123_PM_at	chromosome 21 open reading frame 59	9949	C21orf59	-0.447	-	1.72E-02	4.87E-02
204757_PM_s_at	C2CD2-like	5279	C2CD2L	-0.408	-	3.46E-02	2.63E-02
1560035_PM_at	chromosome 2 open reading frame 85	2958	C2orf85	-2.919	-	1.82E-02	2.44E-02
241666_PM_at	chromosome 3 open reading frame 23	55554	C3orf23	-0.896	-	2.83E-04	4.67E-03
1553158_PM_at	chromosome 3 open reading frame 34	23281	C3orf34	-0.505	-	4.73E-03	1.72E-02
242753_PM_x_at	chromosome 4 open reading frame 16	347744	C4orf16	-0.428	-	5.61E-03	1.87E-02
233558_PM_s_at	chromosome 4 open reading frame 41	50509	C4orf41	-0.755	-	2.00E-02	4.39E-02
1552660_PM_a_at	chromosome 5 open reading frame 22	55610	C5orf22	-1.506	-	7.64E-03	3.16E-02
48030_PM_i_at	chromosome 5 open reading frame 4	---	C5orf4	-0.794	-	2.59E-02	2.99E-02
1554229_PM_at	chromosome 5 open reading frame 41	6155	C5orf41	-0.383	-	2.89E-02	1.15E-02

217924_PM_at	chromosome 6 open reading frame 106	92906	C6orf106	-0.700	-	2.29E-03	9.82E-03
205457_PM_at	chromosome 6 open reading frame 106	7454	C6orf106	-0.590	-	8.32E-03	1.90E-02
213875_PM_x_at	chromosome 6 open reading frame 62	23243	C6orf62	-2.601	-	1.30E-02	3.24E-02
227000_PM_at	chromosome 7 open reading frame 41	285282	C7orf41	-0.755	-	8.99E-04	7.45E-03
221629_PM_x_at	chromosome 8 open reading frame 30A	55715	C8orf30A	-0.295	-	6.18E-03	3.85E-03
228701_PM_at	chromosome 8 open reading frame 46	55846	C8orf46	-3.348	-	9.25E-03	2.72E-02
228695_PM_at	chromosome 8 open reading frame 46	91057	C8orf46	-2.114	-	2.05E-02	4.80E-02
220712_PM_at	chromosome 8 open reading frame 60	4129	C8orf60	-0.275	-	1.23E-02	3.34E-02
235209_PM_at	chromosome 8 open reading frame 84	9125	C8orf84	-0.851	-	2.41E-02	3.39E-03
224458_PM_at	chromosome 9 open reading frame 125	54602	C9orf125	-0.639	-	4.74E-04	9.24E-04
241781_PM_at	chromosome 9 open reading frame 41	---	C9orf41	-0.290	-	6.07E-04	3.30E-03
223006_PM_s_at	chromosome 9 open reading frame 5	51312	C9orf5	-1.795	-	1.92E-02	1.66E-02
225377_PM_at	chromosome 9 open reading frame 86	64776	C9orf86	-0.577	-	4.53E-02	3.11E-02
224311_PM_s_at	calcium binding protein 39	359948	CAB39	-0.778	-	2.44E-04	5.99E-03
221003_PM_s_at	calcium binding protein 39-like	9308	CAB39L	-0.347	-	4.02E-03	1.76E-02
222542_PM_x_at	chaperone, ABC1 activity of bc1 complex homolog (S. pombe)	1386	CABC1	-0.329	-	9.36E-03	3.31E-02
208320_PM_at	calcium binding protein 1	10369	CABP1	-0.563	-	5.00E-03	3.30E-02
208321_PM_s_at	calcium binding protein 1	9135	CABP1	-1.888	-	1.94E-02	2.73E-02
210181_PM_s_at	calcium binding protein 1	121536	CABP1	-2.517	-	2.06E-02	3.80E-02
207050_PM_at	calcium channel, voltage-dependent, alpha 2/delta subunit 1	54780	CACNA2D1	-0.429	-	7.14E-03	8.82E-03
206996_PM_x_at	calcium channel, voltage-dependent, beta 1 subunit	10962	CACNB1	-0.482	-	5.13E-03	1.00E-02
210967_PM_x_at	calcium channel, voltage-dependent, beta 1 subunit	128229	CACNB1	-0.540	-	6.15E-03	1.44E-02
1555098_PM_a_at	calcium channel, voltage-dependent, beta 2 subunit	3983	CACNB2	-0.308	-	4.10E-02	4.56E-02
207693_PM_at	calcium channel, voltage-dependent, beta 4 subunit	26009	CACNB4	-2.121	-	5.55E-03	8.83E-03
214495_PM_at	calcium channel, voltage-dependent, gamma subunit 2	29074	CACNG2	-2.535	-	1.08E-03	4.48E-03
231737_PM_at	calcium channel, voltage-dependent, gamma subunit 4	---	CACNG4	-0.558	-	9.76E-03	7.46E-03
62987_PM_r_at	calcium channel, voltage-dependent, gamma subunit 4	---	CACNG4	-0.385	-	1.80E-02	4.62E-02
209030_PM_s_at	cell adhesion molecule 1	55129	CADM1	-0.536	-	1.68E-02	1.01E-02
1555544_PM_a_at	cell adhesion molecule 2	9698	CADM2	-0.906	-	2.12E-03	1.66E-02

213948_PM_x_at	cell adhesion molecule 3	286148	CADM3	-0.982	-	2.61E-02	2.57E-02
215258_PM_at	cell adhesion molecule 4	64081	CADM4	-0.752	-	2.32E-02	2.42E-02
233950_PM_at	Ca++-dependent secretion activator	439911	CADPS	-1.236	-	1.62E-02	2.90E-02
234220_PM_at	Ca++-dependent secretion activator	---	CADPS	-0.358	-	3.45E-02	4.89E-02
209563_PM_x_at	calmodulin 1 (phosphorylase kinase, delta)	51390	CALM1	-0.435	-	9.39E-04	9.78E-03
200622_PM_x_at	calmodulin 3 (phosphorylase kinase, delta)	4287	CALM3	-1.375	-	9.22E-03	2.17E-02
200623_PM_s_at	calmodulin 3 (phosphorylase kinase, delta)	10520	CALM3	-0.297	-	2.87E-02	2.79E-02
214845_PM_s_at	calumenin	54951	CALU	-1.775	-	4.60E-03	1.45E-02
200756_PM_x_at	calumenin	8525	CALU	-1.478	-	5.42E-03	9.62E-03
219896_PM_at	calcyon neuron-specific vesicular protein	22856	CALY	-4.585	-	1.65E-03	5.40E-03
204392_PM_at	calcium/calmodulin-dependent protein kinase I	1514	CAMK1	-1.802	-	4.04E-02	4.48E-02
220246_PM_at	calcium/calmodulin-dependent protein kinase ID	10426	CAMK1D	-0.327	-	6.06E-03	1.67E-02
235626_PM_at	calcium/calmodulin-dependent protein kinase ID	392	CAMK1D	-0.928	-	2.00E-02	2.69E-03
207613_PM_s_at	calcium/calmodulin-dependent protein kinase II alpha	158471	CAMK2A	-3.856	-	3.92E-04	1.65E-03
34846_PM_at	calcium/calmodulin-dependent protein kinase II beta	728819	CAMK2B	-1.536	-	2.00E-03	2.10E-03
1552893_PM_at	calcium/calmodulin-dependent protein kinase II inhibitor 2	1388	CAMK2N2	-1.165	-	1.65E-03	7.15E-03
210349_PM_at	calcium/calmodulin-dependent protein kinase IV	1184	CAMK4	-0.885	-	1.72E-04	4.48E-03
212763_PM_at	calmodulin regulated spectrin-associated protein 1-like 1	27292	CAMSAP1L1	-0.800	-	1.69E-02	4.16E-02
208853_PM_s_at	calnexin	58486	CANX	-0.769	-	4.28E-02	2.97E-02
212551_PM_at	CAP, adenylate cyclase-associated protein, 2 (yeast)	79053	CAP2	-2.698	-	2.13E-02	4.99E-02
226289_PM_at	cell cycle associated protein 1	65055	CAPRIN1	-0.993	-	1.10E-02	2.25E-02
200722_PM_s_at	cell cycle associated protein 1	9555	CAPRIN1	-2.298	-	1.87E-02	3.91E-02
201950_PM_x_at	capping protein (actin filament) muscle Z-line, beta	5911 /// 5912	CAPZB	-1.118	-	1.17E-02	2.16E-02
201949_PM_x_at	capping protein (actin filament) muscle Z-line, beta	1936	CAPZB	-0.289	-	4.61E-02	3.84E-02
207620_PM_s_at	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	23142	CASK	-1.999	-	1.75E-03	6.05E-04
238698_PM_at	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	55573	CASK	-0.269	-	7.26E-03	2.55E-03
238699_PM_s_at	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	23528	CASK	-0.785	-	1.49E-02	1.84E-02
211208_PM_s_at	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	10243	CASK	-0.569	-	3.24E-02	4.79E-02
203065_PM_s_at	caveolin 1, caveolae protein, 22kDa	54602	CAV1	-0.351	-	1.78E-02	4.47E-02

209145_PM_s_at	core-binding factor, runt domain, alpha subunit 2; translocated to, 2	51022	CBFA2T2	-0.365	-	1.65E-03	1.18E-02
1554637_PM_a_at	core-binding factor, runt domain, alpha subunit 2; translocated to, 2	151579 /// 9689	CBFA2T2	-0.383	-	1.21E-02	4.32E-02
206724_PM_at	chromobox homolog 4 (Pc class homolog, Drosophila)	51592	CBX4	-0.575	-	4.63E-03	8.20E-03
226085_PM_at	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	9520	CBX5	-0.318	-	3.05E-02	2.82E-02
242487_PM_at	coiled-coil and C2 domain containing 1B	---	CC2D1B	-0.349	-	3.37E-03	3.34E-03
1559409_PM_a_at	coiled-coil and C2 domain containing 2A	11269 /// 55308	CC2D2A	-0.299	-	2.70E-02	2.85E-02
224736_PM_at	cell division cycle and apoptosis regulator 1	4194	CCAR1	-1.073	-	6.31E-03	7.53E-03
1553732_PM_s_at	coiled-coil domain containing 123	54331	CCDC123	-0.300	-	3.04E-03	1.41E-02
225454_PM_at	coiled-coil domain containing 124	144233	CCDC124	-0.658	-	3.34E-02	4.84E-02
1554217_PM_a_at	coiled-coil domain containing 132	4735	CCDC132	-0.611	-	8.18E-03	3.79E-02
228693_PM_at	coiled-coil domain containing 50	---	CCDC50	-0.441	-	3.24E-04	1.32E-03
221078_PM_s_at	coiled-coil domain containing 88A	5422	CCDC88A	-0.574	-	4.33E-03	2.42E-02
227299_PM_at	Cyclin I	56834	CCNI	-1.886	-	1.57E-02	2.66E-02
224651_PM_at	cyclin Y	399959	CCNY	-1.028	-	4.31E-03	7.68E-03
208653_PM_s_at	CD164 molecule, sialomucin	84162	CD164	-0.429	-	2.68E-03	1.91E-02
202257_PM_s_at	CD2 (cytoplasmic tail) binding protein 2	51386	CD2BP2	-0.612	-	6.19E-04	9.94E-03
205049_PM_s_at	CD79a molecule, immunoglobulin-associated alpha	644	CD79A	-0.270	-	2.67E-02	2.61E-02
217881_PM_s_at	cell division cycle 27 homolog (S. cerevisiae)	64983	CDC27	-0.914	-	1.54E-02	4.49E-02
203377_PM_s_at	cell division cycle 40 homolog (S. cerevisiae)	51542	CDC40	-0.556	-	1.07E-02	2.40E-02
1552613_PM_s_at	CDC42 small effector 2	129285	CDC42SE2	-0.846	-	3.23E-03	1.19E-02
1552612_PM_at	CDC42 small effector 2	150290	CDC42SE2	-1.626	-	8.76E-03	4.70E-02
207172_PM_s_at	cadherin 11, type 2, OB-cadherin (osteoblast)	58517	CDH11	-0.646	-	1.87E-02	1.00E-02
203441_PM_s_at	cadherin 2, type 1, N-cadherin (neuronal)	29989 /// 29991	CDH2	-1.345	-	1.51E-02	2.57E-02
210518_PM_at	cadherin 8, type 2	132864	CDH8	-0.885	-	2.94E-02	4.85E-02
210622_PM_x_at	cyclin-dependent kinase 10	23678	CDK10	-0.954	-	7.36E-03	3.61E-02
204996_PM_s_at	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	324	CDK5R1	-1.523	-	1.95E-03	4.26E-03
207143_PM_at	cyclin-dependent kinase 6	689	CDK6	-0.688	-	4.54E-02	1.48E-02

210240_PM_s_at	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	7559	CDKN2D	-0.438	-	4.19E-02	4.99E-02
205709_PM_s_at	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1	6326	CDS1	-0.353	-	4.98E-04	6.77E-03
228746_PM_s_at	CDV3 homolog (mouse)	120534	CDV3	-1.614	-	3.17E-02	2.85E-02
204373_PM_s_at	centrosomal protein 350kDa	5782	CEP350	-0.717	-	3.74E-03	2.29E-02
203491_PM_s_at	centrosomal protein 57kDa	282890	CEP57	-0.533	-	3.56E-03	1.82E-02
207971_PM_s_at	centrosomal protein 68kDa	23254	CEP68	-0.329	-	1.42E-02	4.60E-02
206861_PM_s_at	CGG triplet repeat binding protein 1	4149	CGGBP1	-0.610	-	3.36E-02	2.98E-02
201183_PM_s_at	chromodomain helicase DNA binding protein 4	6509	CHD4	-0.835	-	2.04E-02	2.38E-02
229586_PM_at	chromodomain helicase DNA binding protein 9	---	CHD9	-0.378	-	1.10E-02	4.24E-05
225119_PM_at	chromatin modifying protein 4B	51106	CHMP4B	-1.643	-	2.06E-02	2.19E-02
207993_PM_s_at	calcium binding protein P22	9470	CHP	-3.182	-	1.99E-03	7.81E-03
231783_PM_at	cholinergic receptor, muscarinic 1	---	CHRM1	-0.342	-	1.50E-02	3.98E-03
1564339_PM_a_at	cholinergic receptor, muscarinic 3	7077	CHRM3	-0.688	-	5.35E-03	1.81E-02
1559633_PM_a_at	cholinergic receptor, muscarinic 3	322	CHRM3	-1.142	-	2.13E-02	1.81E-02
230142_PM_s_at	cold inducible RNA binding protein	645460	CIRBP	-2.470	-	1.78E-02	2.96E-02
201735_PM_s_at	chloride channel 3	23213	CLCN3	-1.071	-	5.24E-04	3.13E-03
201732_PM_s_at	chloride channel 3	2036	CLCN3	-1.857	-	6.35E-04	1.57E-03
221881_PM_s_at	chloride intracellular channel 4	545	CLIC4	-1.165	-	1.11E-03	4.34E-03
201768_PM_s_at	clathrin interactor 1	23301	CLINT1	-1.053	-	1.18E-02	4.24E-02
235243_PM_at	CAP-GLY domain containing linker protein 3	---	CLIP3	-2.352	-	1.08E-03	4.21E-03
219944_PM_at	CAP-GLY domain containing linker protein family, member 4	10300	CLIP4	-0.662	-	2.04E-02	1.70E-02
204980_PM_at	clock homolog (mouse)	51430	CLOCK	-0.363	-	1.45E-02	1.43E-02
201640_PM_x_at	cleft lip and palate associated transmembrane protein 1	3516	CLPTM1	-0.281	-	7.04E-03	3.24E-02
211136_PM_s_at	cleft lip and palate associated transmembrane protein 1	51495	CLPTM1	-3.019	-	1.42E-02	2.60E-02
230070_PM_at	cornichon homolog 2 (Drosophila)	83482	CNIH2	-0.300	-	3.74E-02	2.83E-02
1554607_PM_at	connector enhancer of kinase suppressor of Ras 2	8655	CNKSR2	-1.772	-	6.62E-03	2.26E-02
203239_PM_s_at	CCR4-NOT transcription complex, subunit 3	91833	CNOT3	-0.687	-	1.91E-02	4.43E-02
211141_PM_s_at	CCR4-NOT transcription complex, subunit 3	80318	CNOT3	-0.374	-	3.71E-02	4.23E-02
210866_PM_s_at	CCR4-NOT transcription complex, subunit 4	4810	CNOT4	-1.204	-	1.20E-02	1.84E-02

218250_PM_s_at	CCR4-NOT transcription complex, subunit 7	84343	CNOT7	-2.112	-	8.49E-03	2.89E-02
202162_PM_s_at	CCR4-NOT transcription complex, subunit 8	134	CNOT8	-1.075	-	1.29E-02	3.98E-02
207940_PM_x_at	cannabinoid receptor 1 (brain)	6191	CNR1	-0.672	-	6.18E-04	4.42E-03
211203_PM_s_at	contactin 1	57545	CNTN1	-1.828	-	6.78E-03	2.53E-02
215145_PM_s_at	contactin associated protein-like 2	26589	CNTNAP2	-1.656	-	4.59E-02	2.58E-02
203653_PM_s_at	coilin	22866	COIL	-0.880	-	1.23E-03	3.26E-03
218975_PM_at	collagen, type V, alpha 3	84902	COL5A3	-0.880	-	1.42E-04	1.67E-03
52255_PM_s_at	collagen, type V, alpha 3	---	COL5A3	-0.332	-	5.55E-03	2.62E-03
208817_PM_at	catechol-O-methyltransferase	54187	COMT	-0.934	-	3.91E-02	4.53E-02
214336_PM_s_at	coatomer protein complex, subunit alpha	11180	COPA	-1.770	-	2.29E-03	8.99E-03
201942_PM_s_at	carboxypeptidase D	5689	CPD	-0.936	-	4.17E-04	7.27E-03
235479_PM_at	cytoplasmic polyadenylation element binding protein 2	9727	CPEB2	-0.510	-	1.76E-02	4.35E-02
224829_PM_at	cytoplasmic polyadenylation element binding protein 4	388789	CPEB4	-1.993	-	5.70E-04	5.90E-04
224828_PM_at	cytoplasmic polyadenylation element binding protein 4	4163	CPEB4	-2.171	-	1.92E-02	1.51E-02
1554321_PM_a_at	copine I /// NFS1 nitrogen fixation 1 homolog (S. cerevisiae)	6136	CPNE1 /// NFS1	-0.437	-	2.00E-02	4.78E-02
204263_PM_s_at	carnitine palmitoyltransferase 2	9685	CPT2	-0.457	-	3.62E-02	4.20E-02
204312_PM_x_at	cAMP responsive element binding protein 1	23429	CREB1	-1.519	-	4.56E-03	1.46E-02
214513_PM_s_at	cAMP responsive element binding protein 1	51056	CREB1	-0.647	-	9.43E-03	3.51E-02
202978_PM_s_at	CREB/ATF bZIP transcription factor	64895	CREBZF	-0.492	-	1.09E-02	4.10E-02
202226_PM_s_at	v-crk sarcoma virus CT10 oncogene homolog (avian)	1627	CRK	-1.185	-	1.31E-02	2.56E-02
206184_PM_at	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	23176	CRKL	-0.430	-	1.47E-03	1.02E-02
202517_PM_at	195eparin195in response mediator protein 1	64840	CRMP1	-0.814	-	3.33E-02	3.42E-02
222975_PM_s_at	cold shock domain containing E1, RNA-binding	55742	CSDE1	-1.019	-	8.36E-03	2.67E-02
219939_PM_s_at	cold shock domain containing E1, RNA-binding	5156	CSDE1	-0.360	-	8.88E-03	4.57E-02
1553405_PM_a_at	CUB and Sushi multiple domains 1	9444	CSMD1	-0.319	-	3.82E-02	4.91E-02
206562_PM_s_at	casein kinase 1, alpha 1	1628	CSNK1A1	-2.264	-	1.44E-02	3.20E-02
207945_PM_s_at	casein kinase 1, delta	6642	CSNK1D	-0.652	-	2.67E-02	4.12E-02
202332_PM_at	casein kinase 1, epsilon	114883	CSNK1E	-1.037	-	9.50E-04	5.17E-03
231920_PM_s_at	casein kinase 1, gamma 1	22834	CSNK1G1	-0.779	-	2.34E-03	4.27E-03
202574_PM_s_at	casein kinase 1, gamma 2	54542	CSNK1G2	-0.675	-	1.25E-02	2.02E-02

212075_PM_s_at	casein kinase 2, alpha 1 polypeptide	10945	CSNK2A1	-1.881	-	6.24E-03	1.71E-02
212073_PM_at	casein kinase 2, alpha 1 polypeptide /// casein kinase 2, alpha 1 polypeptide pseudogene	6734	CSNK2A1 /// CSNK2A1P	-0.530	-	3.60E-02	3.63E-02
205344_PM_at	chondroitin sulfate proteoglycan 5 (neuroglycan C)	9854	CSPG5	-2.000	-	1.02E-02	2.02E-02
225042_PM_s_at	cysteine-serine-rich nuclear protein 2	23383	CSRNP2	-0.547	-	9.97E-03	2.33E-02
206994_PM_at	cystatin S	2137	CST4	-0.294	-	2.89E-03	2.98E-03
217844_PM_at	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1	64778	CTDSP1	-0.263	-	3.31E-02	3.94E-02
201905_PM_s_at	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	10521	CTDSPL	-0.679	-	3.08E-02	3.77E-02
1558214_PM_s_at	catenin (cadherin-associated protein), alpha 1, 102kDa	8883	CTNNA1	-0.656	-	2.47E-04	1.56E-03
1554411_PM_at	catenin (cadherin-associated protein), beta 1, 88kDa	7534	CTNNB1	-2.351	-	8.43E-03	2.28E-02
213274_PM_s_at	cathepsin B	10492	CTSB	-1.725	-	1.80E-02	4.47E-02
214074_PM_s_at	cortactin	9236	CTTN	-0.854	-	6.47E-05	3.32E-04
228126_PM_x_at	cortexin 1	---	CTXN1	-1.682	-	1.72E-02	3.27E-02
1555467_PM_a_at	CUG triplet repeat, RNA binding protein 1	10456	CUGBP1	-0.927	-	2.75E-03	1.20E-02
204113_PM_at	CUG triplet repeat, RNA binding protein 1	23471	CUGBP1	-0.872	-	1.67E-02	4.20E-02
1554569_PM_a_at	CUG triplet repeat, RNA binding protein 2	7323	CUGBP2	-0.979	-	4.61E-04	2.73E-03
202157_PM_s_at	CUG triplet repeat, RNA binding protein 2	1388	CUGBP2	-0.585	-	7.57E-03	7.21E-03
210257_PM_x_at	cullin 4B	10335	CUL4B	-0.626	-	1.03E-02	4.94E-02
242781_PM_at	chromosome X open reading frame 39	---	Cxorf39	-0.339	-	1.20E-03	1.10E-02
222996_PM_s_at	CXXC finger 5	29105	CXXC5	-1.050	-	6.51E-03	1.48E-02
233955_PM_x_at	CXXC finger 5	53335	CXXC5	-0.971	-	8.58E-03	1.47E-02
1554574_PM_a_at	cytochrome b5 reductase 3	6711	CYB5R3	-1.158	-	2.09E-02	2.23E-02
216607_PM_s_at	cytochrome P450, family 51, subfamily A, polypeptide 1	25897	CYP51A1	-0.878	-	2.71E-03	1.87E-02
202879_PM_s_at	cytohesin 1	81894	CYTH1	-0.524	-	1.61E-03	8.17E-04
216060_PM_s_at	196eparin196in associated activator of morphogenesis 1	57665	DAAM1	-0.843	-	2.49E-03	3.42E-03
220611_PM_at	disabled homolog 1 (Drosophila)	7257	DAB1	-1.857	-	1.22E-04	8.06E-05

225828_PM_at	diacylglycerol lipase, beta	---	DAGLB	-0.416	-	8.86E-03	2.04E-02
225833_PM_at	diacylglycerol lipase, beta	---	DAGLB	-0.541	-	1.78E-02	3.35E-02
211214_PM_s_at	death-associated protein kinase 1	79664	DAPK1	-0.447	-	1.35E-02	2.61E-02
203890_PM_s_at	death-associated protein kinase 3	5048	DAPK3	-0.931	-	2.55E-03	5.54E-03
217025_PM_s_at	drebrin 1	11091	DBN1	-1.363	-	1.32E-02	2.77E-02
209782_PM_s_at	D site of albumin promoter (albumin D-box) binding protein	84811	DBP	-0.934	-	1.90E-02	2.05E-02
224730_PM_at	DDB1 and CUL4 associated factor 7	140901	DCAF7	-0.610	-	1.78E-03	1.18E-02
218508_PM_at	DCP1 decapping enzyme homolog A (S. cerevisiae)	130074	DCP1A	-0.296	-	1.07E-03	4.23E-03
209231_PM_s_at	dynactin 5 (p25)	55140	DCTN5	-0.500	-	8.33E-03	2.64E-02
1553565_PM_s_at	dimethylarginine dimethylaminohydrolase 1	64393	DDAH1	-1.376	-	6.56E-04	8.23E-03
213998_PM_s_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	23066	DDX17	-2.228	-	1.29E-02	3.19E-02
202576_PM_s_at	DEAD (Asp-Glu-Ala-As) box polypeptide 19A /// DEAD (Asp-Glu-Ala-As) box polypeptide 19B	10777	DDX19A /// DDX19B	-0.381	-	3.00E-02	4.63E-02
212514_PM_x_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	5711	DDX3X	-1.120	-	9.63E-04	9.73E-03
201211_PM_s_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	3801	DDX3X	-1.608	-	3.91E-03	2.84E-02
1559954_PM_s_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	8813	DDX42	-2.339	-	9.29E-03	2.46E-02
53991_PM_at	DENN/MADD domain containing 2A	---	DENND2A	-0.274	-	2.55E-02	4.29E-03
234915_PM_s_at	density-regulated protein	10274	DENR	-0.314	-	7.99E-03	3.78E-03
219402_PM_s_at	Der1-like domain family, member 1	1994	DERL1	-0.705	-	1.56E-03	1.63E-02
207556_PM_s_at	diacylglycerol kinase, zeta 104kDa	55818	DGKZ	-1.106	-	3.22E-02	4.11E-02
223138_PM_s_at	DEAH (Asp-Glu-Ala-His) box polypeptide 36	55273	DHX36	-0.417	-	1.59E-02	1.93E-02
213229_PM_at	dicer 1, ribonuclease type III	57798	DICER1	-0.464	-	1.48E-03	1.94E-02
232854_PM_at	DIRAS family, GTP-binding RAS-like 1	51101	DIRAS1	-0.369	-	2.40E-02	1.89E-02
210762_PM_s_at	deleted in liver cancer 1	1387	DLC1	-0.443	-	7.83E-03	2.86E-02
206253_PM_at	discs, large homolog 2 (Drosophila)	8648	DLG2	-1.477	-	6.65E-03	6.57E-03
207732_PM_s_at	discs, large homolog 3 (Drosophila)	11011	DLG3	-0.816	-	2.14E-04	2.62E-04
212729_PM_at	discs, large homolog 3 (Drosophila)	4242	DLG3	-0.665	-	1.23E-02	8.41E-03
210750_PM_s_at	discs, large (Drosophila) homolog-associated protein 1	148423	DLGAP1	-0.431	-	3.21E-02	2.88E-02
231151_PM_at	discs, large (Drosophila) homolog-associated protein 3	56886	DLGAP3	-0.740	-	2.76E-03	1.65E-03

1560300_PM_a_at	DMRT-like family C1 /// DMRT-like family C1B	7726	DMRTC1 /// DMRTC1B	-0.264	-	3.42E-02	2.04E-02
1554429_PM_a_at	dystrophia myotonica, WD repeat containing	6647	DMWD	-1.436	-	3.20E-02	4.81E-02
200664_PM_s_at	DnaJ (Hsp40) homolog, subfamily B, member 1	9877	DNAJB1	-1.218	-	6.23E-03	2.16E-02
222850_PM_s_at	DnaJ (Hsp40) homolog, subfamily B, member 14	8707	DNAJB14	-1.066	-	5.27E-03	1.78E-02
1555360_PM_a_at	DnaJ (Hsp40) homolog, subfamily C, member 11	23646	DNAJC11	-0.421	-	2.16E-02	6.91E-03
1554451_PM_s_at	DnaJ (Hsp40) homolog, subfamily C, member 14	2752	DNAJC14	-1.498	-	1.11E-02	4.15E-02
227166_PM_at	DnaJ (Hsp40) homolog, subfamily C, member 18	4848	DNAJC18	-0.789	-	1.09E-02	2.41E-02
205744_PM_at	double C2-like domains, alpha	56242	DOC2A	-1.206	-	4.19E-02	4.95E-02
215041_PM_s_at	dedicator of cytokinesis 9	64757	DOCK9	-0.454	-	1.62E-02	1.35E-02
207747_PM_s_at	docking protein 4	253959	DOK4	-0.428	-	2.46E-02	4.52E-02
231599_PM_x_at	D4, zinc and double PHD fingers family 1	128854	DPF1	-1.434	-	2.77E-02	4.20E-02
219590_PM_x_at	DPH5 homolog (S. cerevisiae)	23219	DPH5	-0.302	-	4.45E-02	4.05E-02
1560916_PM_a_at	dpy-19-like 1 (C. elegans)	6672	DPY19L1	-0.408	-	5.13E-03	1.52E-02
205492_PM_s_at	dihydropyrimidinase-like 4	51375	DPYSL4	-0.615	-	2.50E-02	4.32E-02
203267_PM_s_at	developmentally regulated GTP binding protein 2	79971	DRG2	-1.670	-	2.35E-02	3.12E-02
211515_PM_s_at	dual serine/threonine and tyrosine protein kinase	163404	DSTYK	-0.881	-	3.33E-02	4.57E-02
208430_PM_s_at	dystrobrevin, alpha	8295	DTNA	-2.087	-	5.04E-03	3.19E-03
211493_PM_x_at	dystrobrevin, alpha	84332	DTNA	-1.474	-	1.56E-02	2.18E-02
210736_PM_x_at	dystrobrevin, alpha	349565	DTNA	-1.924	-	1.78E-02	2.66E-02
49051_PM_g_at	deltex homolog 3 (Drosophila)	100128644	DTX3	-1.507	-	6.52E-03	1.23E-02
221835_PM_at	deltex homolog 3 (Drosophila)	54453	DTX3	-0.804	-	1.41E-02	8.01E-03
49049_PM_at	deltex homolog 3 (Drosophila)	---	DTX3	-1.171	-	2.19E-02	4.11E-02
227098_PM_at	dual specificity phosphatase 18	8539	DUSP18	-0.369	-	3.42E-03	2.68E-02
1553701_PM_a_at	dual specificity phosphatase 18	1033	DUSP18	-0.283	-	2.99E-02	5.44E-04
201538_PM_s_at	dual specificity phosphatase 3	3135	DUSP3	-0.980	-	1.35E-03	6.07E-03
201537_PM_s_at	dual specificity phosphatase 3	7422	DUSP3	-0.277	-	6.55E-03	1.22E-02

203590_PM_at	dynein, cytoplasmic 1, light intermediate chain 2	117584	DYNC1LI2	-0.890	-	2.16E-02	1.70E-02
217270_PM_s_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1B	55540	DYRK1B	-0.483	-	4.10E-02	4.82E-02
202968_PM_s_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	85021	DYRK2	-0.547	-	1.28E-02	2.99E-02
38707_PM_r_at	E2F transcription factor 4, p107/p130-binding	---	E2F4	-0.646	-	8.68E-03	2.02E-02
223243_PM_s_at	ER degradation enhancer, mannosidase alpha-like 3	55336	EDEM3	-1.341	-	7.87E-04	9.14E-04
207379_PM_at	EGF-like repeats and discoidin I-like domains 3	23157 /// 84656	EDIL3	-2.460	-	4.91E-03	3.11E-02
1558643_PM_s_at	EGF-like repeats and discoidin I-like domains 3	7398	EDIL3	-1.296	-	6.77E-03	4.22E-02
204540_PM_at	eukaryotic translation elongation factor 1 alpha 2	3685	EEF1A2	-3.645	-	2.52E-08	1.02E-05
210883_PM_x_at	ephrin-B3	158 /// 23112	EFNB3	-0.564	-	3.13E-02	8.83E-03
201983_PM_s_at	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	23007	EGFR	-0.410	-	8.41E-03	4.55E-02
221497_PM_x_at	egl nine homolog 1 (C. elegans)	1842	EGLN1	-1.128	-	3.70E-03	1.57E-02
223083_PM_s_at	egl nine homolog 2 (C. elegans)	54969	EGLN2	-0.495	-	1.11E-02	2.42E-02
212650_PM_at	EH domain binding protein 1	7443	EHBP1	-0.788	-	5.73E-03	1.41E-02
209037_PM_s_at	EH-domain containing 1	4649	EHD1	-0.307	-	5.53E-03	3.53E-02
201019_PM_s_at	eukaryotic translation initiation factor 1A pseudogene 1 /// eukaryotic translation initiation factor 1A, X-linked	10383	EIF1AP1 /// EIF1AX	-0.760	-	7.06E-03	1.70E-03
201017_PM_at	eukaryotic translation initiation factor 1A, X-linked	509	EIF1AX	-0.597	-	2.57E-02	3.47E-02
225827_PM_at	eukaryotic translation initiation factor 2C, 2	414899	EIF2C2	-0.925	-	2.98E-02	3.21E-02
200596_PM_s_at	eukaryotic translation initiation factor 3, subunit A	8487	EIF3A	-0.479	-	8.58E-03	4.22E-03
240513_PM_at	Eukaryotic translation initiation factor 3, subunit M	55745	EIF3M	-0.274	-	7.55E-03	2.60E-02
211937_PM_at	eukaryotic translation initiation factor 4B	8717	EIF4B	-0.676	-	1.12E-03	5.05E-03
238461_PM_at	eukaryotic translation initiation factor 4E family member 3	202451	EIF4E3	-0.478	-	1.34E-03	1.74E-02
208624_PM_s_at	eukaryotic translation initiation factor 4 gamma, 1	23139	EIF4G1	-0.652	-	1.50E-02	1.17E-02
1554310_PM_a_at	eukaryotic translation initiation factor 4 gamma, 3	9045	EIF4G3	-0.622	-	1.55E-02	1.54E-02
208705_PM_s_at	eukaryotic translation initiation factor 5	51637	EIF5	-0.961	-	6.81E-03	2.06E-03
208427_PM_s_at	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	9380	ELAVL2	-1.628	-	8.29E-03	3.80E-02

1555602_PM_a_at	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	262	ELAVL3	-0.508	-	1.48E-02	3.91E-02
210376_PM_x_at	ELK1, member of ETS oncogene family	10869	ELK1	-0.609	-	2.75E-03	1.25E-02
217039_PM_x_at	ELK1, member of ETS oncogene family /// similar to ETS domain protein Elk-1	23456	ELK1 /// LOC652030	-0.352	-	4.75E-02	1.18E-02
220029_PM_at	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	3720	ELOVL2	-0.570	-	7.82E-03	3.42E-02
221094_PM_s_at	elongation protein 3 homolog (S. cerevisiae)	2028	ELP3	-0.447	-	2.15E-02	2.85E-02
204399_PM_s_at	echinoderm microtubule associated protein like 2	10920	EML2	-0.508	-	9.84E-04	5.88E-04
1570393_PM_at	echinoderm microtubule associated protein like 5	10658	EML5	-0.272	-	4.39E-03	2.81E-02
201340_PM_s_at	ectodermal-neural cortex (with BTB-like domain)	7422	ENC1	-2.149	-	9.63E-04	7.23E-04
212336_PM_at	erythrocyte membrane protein band 4.1-like 1	1666	EPB41L1	-0.792	-	6.83E-03	5.99E-03
206114_PM_at	EPH receptor A4	546	EPHA4	-1.897	-	3.75E-04	3.93E-03
228948_PM_at	EPH receptor A4	9175	EPHA4	-0.991	-	8.20E-03	1.24E-02
229374_PM_at	EPH receptor A4	730094	EPHA4	-0.821	-	2.56E-02	3.62E-02
215664_PM_s_at	EPH receptor A5	63920	EPHA5	-0.702	-	2.45E-02	3.05E-02
200842_PM_s_at	glutamyl-prolyl-tRNA synthetase	83450	EPRS	-1.262	-	8.28E-03	1.16E-02
200841_PM_s_at	glutamyl-prolyl-tRNA synthetase	7916	EPRS	-1.159	-	1.53E-02	1.09E-02
224576_PM_at	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	90441	ERGIC1	-0.397	-	1.32E-02	1.31E-02
202444_PM_s_at	ER lipid raft associated 1	93974	ERLIN1	-0.524	-	5.98E-03	3.51E-02
222646_PM_s_at	ERO1-like (S. cerevisiae)	152559	ERO1L	-0.632	-	4.56E-02	1.19E-02
218859_PM_s_at	ESF1, nucleolar pre-rRNA processing protein, homolog (S. cerevisiae)	343450	ESF1	-0.781	-	2.96E-02	2.18E-02
1555830_PM_s_at	extended synaptotagmin-like protein 2	5500	ESYT2	-0.326	-	1.40E-02	2.04E-02
226432_PM_at	ethanolamine kinase 1	6731	ETNK1	-1.923	-	1.81E-02	3.53E-02
216375_PM_s_at	ets variant 5	79694	ETV5	-1.337	-	2.74E-04	6.31E-03
210012_PM_s_at	Ewing sarcoma breakpoint region 1	55684	EWSR1	-0.744	-	1.65E-02	4.17E-02
1555808_PM_a_at	exonuclease 3’-5’ domain containing 2	5339	EXD2	-0.462	-	1.34E-02	2.04E-02
240528_PM_s_at	exocyst complex component 4	4728	EXOC4	-1.828	-	1.43E-04	4.20E-04
211051_PM_s_at	exostoses (multiple)-like 3	84557	EXTL3	-0.296	-	8.51E-04	2.84E-03

208621_PM_s_at	ezrin	5322	EZR	-1.321	-	2.68E-04	1.18E-03
234963_PM_s_at	fatty acid 2-hydroxylase	1024	FA2H	-1.157	-	1.97E-02	3.41E-02
216080_PM_s_at	fatty acid desaturase 3	56926	FADS3	-1.703	-	3.56E-02	3.72E-02
222511_PM_x_at	Fas (TNFRSF6) associated factor 1	57215	FAF1	-0.325	-	5.04E-03	3.64E-02
212106_PM_at	Fas associated factor family member 2	55233	FAF2	-0.743	-	1.13E-02	4.41E-03
224785_PM_at	family with sequence similarity 100, member B	150684	FAM100B	-0.784	-	2.19E-02	3.84E-02
227869_PM_at	family with sequence similarity 104, member B /// hypothetical LOC100293328	23184	FAM104B /// LOC100293328	-0.518	-	6.83E-04	1.07E-02
209074_PM_s_at	family with sequence similarity 107, member A	56945	FAM107A	-1.023	-	1.46E-02	2.02E-02
223059_PM_s_at	family with sequence similarity 107, member B	54914	FAM107B	-0.479	-	3.04E-02	3.20E-02
221267_PM_s_at	family with sequence similarity 108, member A1	8864	FAM108A1	-3.945	-	5.03E-03	1.74E-02
220285_PM_at	family with sequence similarity 108, member B1	2487	FAM108B1	-1.148	-	3.11E-03	2.13E-02
210529_PM_s_at	family with sequence similarity 115, member A	4215	FAM115A	-2.785	-	9.15E-04	5.82E-03
229739_PM_s_at	family with sequence similarity 116, member B	84859	FAM116B	-0.969	-	5.03E-03	1.88E-02
228678_PM_at	family with sequence similarity 116, member B	10220	FAM116B	-0.384	-	7.95E-03	1.90E-03
200767_PM_s_at	family with sequence similarity 120A	649	FAM120A	-0.651	-	1.09E-03	8.29E-03
1555945_PM_s_at	family with sequence similarity 120A	10856	FAM120A	-0.948	-	7.67E-03	1.99E-02
232806_PM_s_at	family with sequence similarity 131, member A	---	FAM131A	-0.746	-	7.69E-03	2.77E-02
229946_PM_at	family with sequence similarity 168, member B	57380	FAM168B	-0.308	-	1.12E-02	1.77E-02
242762_PM_s_at	family with sequence similarity 171, member B	63934	FAM171B	-1.424	-	6.13E-04	6.64E-03
1554132_PM_a_at	family with sequence similarity 190, member B	7158	FAM190B	-0.411	-	1.13E-02	5.34E-04
208092_PM_s_at	family with sequence similarity 49, member A	135138	FAM49A	-0.740	-	8.90E-03	2.32E-02
243011_PM_at	family with sequence similarity 55, member C	440957	FAM55C	-0.735	-	7.07E-03	3.81E-02
228459_PM_at	family with sequence similarity 84, member A	54542	FAM84A	-0.895	-	1.42E-02	2.39E-02
1556131_PM_s_at	Fas (TNFRSF6) binding factor 1	56681	FBF1	-0.354	-	1.99E-02	2.26E-02
201787_PM_at	fibulin 1	6935	FBLN1	-0.693	-	1.66E-02	1.83E-02
220080_PM_at	F-box and leucine-rich repeat protein 8	51439	FBXL8	-0.265	-	1.07E-03	1.30E-02

220233_PM_at	F-box protein 17 /// seryl-tRNA synthetase 2, mitochondrial	2799	FBXO17 /// SARS2	-0.616	-	4.47E-02	4.32E-02
219305_PM_x_at	F-box protein 2	6659	FBXO2	-0.567	-	1.44E-02	9.72E-03
212229_PM_s_at	F-box protein 21	55186	FBXO21	-1.458	-	4.84E-03	7.07E-03
219608_PM_s_at	F-box protein 38	7320	FBXO38	-0.407	-	1.26E-03	3.68E-03
225100_PM_at	F-box protein 45	51277	FBXO45	-0.352	-	4.91E-04	2.53E-03
1566509_PM_s_at	F-box protein 9	348	FBXO9	-1.200	-	1.95E-02	3.82E-02
209456_PM_s_at	F-box and WD repeat domain containing 11	55364	FBXW11	-1.653	-	3.99E-05	3.63E-04
214212_PM_x_at	fermitin family homolog 2 (Drosophila)	8801	FERMT2	-1.277	-	2.06E-03	4.52E-04
202305_PM_s_at	fasciculation and elongation protein zeta 2 (zygin II)	26354	FEZ2	-0.655	-	2.33E-03	5.36E-03
204819_PM_at	FYVE, RhoGEF and PH domain containing 1	8880	FGD1	-0.326	-	3.86E-02	4.32E-02
207501_PM_s_at	fibroblast growth factor 12	7385	FGF12	-0.637	-	1.97E-02	4.03E-02
207937_PM_x_at	fibroblast growth factor receptor 1	93081	FGFR1	-0.877	-	7.01E-03	1.52E-02
210973_PM_s_at	fibroblast growth factor receptor 1	285313	FGFR1	-1.719	-	9.94E-03	1.65E-02
211401_PM_s_at	fibroblast growth factor receptor 2	6546	FGFR2	-0.620	-	2.72E-02	4.15E-02
204380_PM_s_at	fibroblast growth factor receptor 3	1942	FGFR3	-0.485	-	6.01E-03	1.95E-02
201539_PM_s_at	four and a half LIM domains 1	5799	FHL1	-2.777	-	2.71E-02	4.82E-02
210298_PM_x_at	four and a half LIM domains 1	9946	FHL1	-2.917	-	2.79E-02	4.94E-02
40850_PM_at	FK506 binding protein 8, 38kDa	---	FKBP8	-1.414	-	3.64E-02	4.89E-02
236329_PM_at	hypothetical protein FLJ33996	23011	FLJ33996	-1.886	-	4.83E-03	2.06E-03
208748_PM_s_at	flotillin 1	2287	FLOT1	-1.202	-	3.20E-02	1.36E-02
211299_PM_s_at	flotillin 2	163081	FLOT2	-0.586	-	1.43E-03	1.26E-02
234106_PM_s_at	FLYWCH-type zinc finger 1	---	FLYWCH1	-0.324	-	1.54E-02	3.22E-02
229272_PM_at	formin binding protein 4	91404	FNBP4	-0.525	-	8.08E-03	1.30E-02
228250_PM_at	folliculin interacting protein 1	55802	FNIP1	-0.396	-	3.04E-03	2.56E-02
223997_PM_at	folliculin interacting protein 1	26503	FNIP1	-0.364	-	5.19E-03	7.26E-03
204764_PM_at	farnesyltransferase, CAAX box, beta	9267	FNTB	-1.093	-	2.24E-02	3.98E-02
204131_PM_s_at	forkhead box O3	8451	FOXO3	-0.591	-	4.95E-02	3.85E-02
230146_PM_s_at	frequenin homolog (Drosophila)	283209	FREQ	-0.490	-	1.25E-02	1.27E-02
1554260_PM_a_at	FRY-like	6156	FRYL	-0.650	-	1.29E-02	4.30E-02

201564_PM_s_at	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	10093 /// 26140	FSCN1	-0.429	-	7.24E-03	4.59E-03
210933_PM_s_at	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	9101	FSCN1	-0.312	-	4.17E-02	2.33E-02
203091_PM_at	far upstream element (FUSE) binding protein 1	4774	FUBP1	-0.655	-	2.14E-02	3.51E-02
1565717_PM_s_at	fusion (involved in t(12;16) in malignant liposarcoma) /// nuclear receptor subfamily 1, group H, member 3	5932	FUS /// NR1H3	-2.732	-	1.25E-02	2.28E-02
213594_PM_x_at	FUS interacting protein (serine/arginine-rich) 1	23197	FUSIP1	-1.548	-	4.50E-04	7.89E-03
210178_PM_x_at	FUS interacting protein (serine/arginine-rich) 1	26057	FUSIP1	-1.446	-	1.85E-03	1.83E-02
201635_PM_s_at	fragile X mental retardation, autosomal homolog 1	3688	FXR1	-2.198	-	2.34E-02	4.50E-02
220131_PM_at	FXYD domain containing ion transport regulator 7	55719	FXYD7	-2.472	-	2.88E-02	4.72E-02
211865_PM_s_at	fizzy/cell division cycle 20 related 1 (Drosophila)	9147	FZR1	-0.486	-	7.71E-03	4.38E-02
223254_PM_s_at	G2/M-phase specific E3 ubiquitin ligase	53822	G2E3	-0.372	-	4.05E-02	3.89E-02
201514_PM_s_at	GTPase activating protein (SH3 domain) binding protein 1	2992	G3BP1	-0.284	-	1.88E-02	2.06E-02
206383_PM_s_at	GTPase activating protein (SH3 domain) binding protein 2	10057	G3BP2	-2.274	-	1.73E-03	1.45E-02
208840_PM_s_at	GTPase activating protein (SH3 domain) binding protein 2	29880	G3BP2	-0.985	-	1.57E-02	4.86E-02
207112_PM_s_at	GRB2-associated binding protein 1	9657	GAB1	-0.350	-	5.43E-03	1.05E-02
225998_PM_at	GRB2-associated binding protein 1	8992	GAB1	-0.725	-	8.32E-03	1.41E-02
211679_PM_x_at	gamma-aminobutyric acid (GABA) B receptor, 2	55337	GABBR2	-1.002	-	1.19E-02	1.29E-02
209991_PM_x_at	gamma-aminobutyric acid (GABA) B receptor, 2	80298	GABBR2	-3.259	-	1.36E-02	2.33E-02
217077_PM_s_at	gamma-aminobutyric acid (GABA) B receptor, 2	84937	GABBR2	-3.318	-	1.61E-02	2.85E-02
206678_PM_at	gamma-aminobutyric acid (GABA) A receptor, alpha 1	3305	GABRA1	-2.163	-	3.76E-03	2.25E-02
207210_PM_at	gamma-aminobutyric acid (GABA) A receptor, alpha 3	10137	GABRA3	-1.739	-	1.19E-02	2.29E-02
217280_PM_x_at	gamma-aminobutyric acid (GABA) A receptor, alpha 5	7227	GABRA5	-2.937	-	9.26E-03	2.53E-02
215531_PM_s_at	gamma-aminobutyric acid (GABA) A receptor, alpha 5	10842	GABRA5	-2.920	-	9.54E-03	3.07E-02
229724_PM_at	gamma-aminobutyric acid (GABA) A receptor, beta 3	6657	GABRB3	-1.653	-	1.43E-03	2.76E-03
205850_PM_s_at	gamma-aminobutyric acid (GABA) A receptor, beta 3	6166	GABRB3	-1.389	-	3.75E-03	1.58E-02
208457_PM_at	gamma-aminobutyric acid (GABA) A receptor, delta	2971	GABRD	-1.253	-	1.30E-02	2.88E-02
206670_PM_s_at	glutamate decarboxylase 1 (brain, 67kDa)	23049	GAD1	-2.694	-	3.23E-03	1.13E-02
211810_PM_s_at	galactosylceramidase	83746	GALC	-0.624	-	8.97E-03	5.62E-03
235256_PM_s_at	galactose mutarotase (aldose 1-epimerase)	9659	GALM	-0.280	-	3.53E-03	1.99E-02

217787_PM_s_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2)	84061	GALNT2	-0.471	-	8.32E-04	1.60E-03
1566271_PM_x_at	GTPase activating Rap/RanGAP domain-like 1	11072	GARNL1	-0.269	-	6.75E-03	4.67E-03
208258_PM_s_at	growth arrest-specific 2 like 1	10228	GAS2L1	-0.783	-	6.67E-03	2.55E-02
210872_PM_x_at	growth arrest-specific 7	166968	GAS7	-0.678	-	1.25E-02	3.02E-03
202191_PM_s_at	growth arrest-specific 7	22947 /// 653543 /// 653544 /// 653545 /// 728410	GAS7	-0.403	-	2.03E-02	4.53E-02
208503_PM_s_at	GATA zinc finger domain containing 1	10440	GATAD1	-1.163	-	1.13E-03	3.32E-03
223921_PM_s_at	glucosidase, beta (bile acid) 2	59277	GBA2	-1.346	-	2.77E-02	4.62E-02
221279_PM_at	ganglioside-induced differentiation-associated protein 1	6728	GDAP1	-1.954	-	2.71E-03	1.46E-02
1555606_PM_a_at	glycerophosphodiester phosphodiesterase domain containing 1	5707	GDPD1	-0.645	-	3.54E-03	1.44E-02
217099_PM_s_at	gem (nuclear organelle) associated protein 4	57409	GEMIN4	-0.348	-	2.64E-02	2.93E-02
231917_PM_at	G elongation factor, mitochondrial 2	284214 /// 9229	GFM2	-0.316	-	3.24E-04	1.29E-03
205722_PM_s_at	GDNF family receptor alpha 2	9522	GFRA2	-0.406	-	2.89E-02	2.74E-02
214190_PM_x_at	golgi associated, gamma adaptin ear containing, ARF binding protein 2	284403	GGA2	-0.869	-	5.82E-03	1.00E-02
208915_PM_s_at	golgi associated, gamma adaptin ear containing, ARF binding protein 2	582	GGA2	-1.578	-	1.22E-02	2.10E-02
211815_PM_s_at	golgi associated, gamma adaptin ear containing, ARF binding protein 3	776	GGA3	-1.093	-	1.42E-02	1.01E-02
226471_PM_at	gamma-glutamyltransferase 7	2186	GGT7	-1.639	-	3.74E-03	1.31E-02
215977_PM_x_at	glycerol kinase	51218	GK	-0.442	-	3.25E-04	1.83E-03
229312_PM_s_at	G kinase anchoring protein 1	112487	GKAP1	-0.806	-	6.07E-03	1.69E-03
214730_PM_s_at	golgi apparatus protein 1	80351	GLG1	-0.730	-	4.34E-02	1.52E-02
203158_PM_s_at	glutaminase	221955	GLS	-1.205	-	2.63E-03	1.80E-02
223079_PM_s_at	glutaminase	9419	GLS	-0.283	-	2.76E-02	1.99E-02
217202_PM_s_at	glutamate-ammonia ligase (glutamine synthetase)	5570	GLUL	-2.428	-	1.59E-02	3.48E-02
200648_PM_s_at	glutamate-ammonia ligase (glutamine synthetase)	509	GLUL	-1.986	-	1.93E-02	3.68E-02
221628_PM_s_at	glyoxylate reductase 1 homolog (Arabidopsis)	10787	GLYR1	-0.953	-	7.21E-03	1.25E-02

204762_PM_s_at	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	10775	GNAO1	-0.427	-	2.81E-02	3.11E-03
200745_PM_s_at	guanine nucleotide binding protein (G protein), beta polypeptide 1	2257	GNB1	-1.665	-	6.19E-03	2.14E-02
1555766_PM_a_at	guanine nucleotide binding protein (G protein), gamma 2	1315	GNG2	-1.613	-	6.30E-03	1.54E-02
224965_PM_at	guanine nucleotide binding protein (G protein), gamma 2	441212	GNG2	-0.815	-	8.02E-03	3.94E-02
203676_PM_at	glucosamine (N-acetyl)-6-sulfatase	4668	GNS	-1.113	-	2.25E-03	1.17E-02
35436_PM_at	golgi autoantigen, golgin subfamily a, 2	---	GOLGA2	-0.546	-	5.21E-03	1.04E-02
204384_PM_at	golgi autoantigen, golgin subfamily a, 2	3836	GOLGA2	-0.583	-	1.32E-02	3.14E-03
227214_PM_at	golgi associated PDZ and coiled-coil motif containing	55269	GOPC	-0.752	-	1.03E-02	1.79E-02
227215_PM_at	golgi associated PDZ and coiled-coil motif containing	51542	GOPC	-0.490	-	1.19E-02	7.90E-03
225420_PM_at	glycerol-3-phosphate acyltransferase, mitochondrial	54768	GPAM	-0.795	-	1.15E-02	1.82E-02
211613_PM_s_at	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	51271	GPD2	-0.589	-	4.86E-03	2.19E-02
234941_PM_s_at	gephyrin	9583	GPHN	-1.045	-	3.03E-02	4.78E-02
209167_PM_at	glycoprotein M6B	64067	GPM6B	-0.398	-	2.64E-02	2.14E-03
225058_PM_at	G protein-coupled receptor 108	57631	GPR108	-0.268	-	2.95E-02	1.04E-03
43934_PM_at	G protein-coupled receptor 137	---	GPR137	-1.159	-	4.27E-03	1.02E-02
219430_PM_at	G protein-coupled receptor 137	1345	GPR137	-0.668	-	1.74E-02	3.11E-02
242592_PM_at	G protein-coupled receptor 137C	---	GPR137C	-0.276	-	3.30E-03	1.70E-02
228950_PM_s_at	G protein-coupled receptor 177	6638	GPR177	-1.006	-	1.64E-02	4.97E-02
221306_PM_at	G protein-coupled receptor 27	10603	GPR27	-0.406	-	1.20E-02	1.35E-02
207055_PM_at	G protein-coupled receptor 37 like 1	7301	GPR37L1	-1.289	-	8.47E-03	1.55E-02
203631_PM_s_at	G protein-coupled receptor, family C, group 5, member B	23074	GPRC5B	-2.836	-	3.74E-03	1.41E-02
209410_PM_s_at	growth factor receptor-bound protein 10	9448	GRB10	-1.025	-	1.44E-03	5.68E-03
215075_PM_s_at	growth factor receptor-bound protein 2	60487	GRB2	-0.625	-	7.98E-04	4.39E-03
220794_PM_at	gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)	9649	GREM2	-0.349	-	8.09E-04	6.83E-03
208032_PM_s_at	glutamate receptor, ionotrophic, AMPA 3	57863	GRIA3	-1.937	-	2.37E-03	1.63E-02
206730_PM_at	glutamate receptor, ionotrophic, AMPA 3	90410	GRIA3	-2.472	-	2.95E-03	1.38E-02
217565_PM_at	glutamate receptor, ionotrophic, AMPA 3	65056	GRIA3	-1.747	-	3.65E-03	7.72E-03
214966_PM_at	glutamate receptor, ionotropic, 205eparin 5	51650	GRIK5	-1.204	-	4.36E-03	6.26E-03
217509_PM_x_at	glutamate receptor, ionotropic, 205eparin 5	9991	GRIK5	-0.300	-	4.00E-02	3.57E-02

210781_PM_x_at	glutamate receptor, ionotropic, N-methyl D-aspartate 1	100302736 /// 353376	GRIN1	-1.986	-	1.10E-03	4.14E-03
211125_PM_x_at	glutamate receptor, ionotropic, N-methyl D-aspartate 1	57223	GRIN1	-1.258	-	5.09E-03	6.72E-03
210782_PM_x_at	glutamate receptor, ionotropic, N-methyl D-aspartate 1	65062	GRIN1	-0.918	-	5.91E-03	6.46E-03
205915_PM_x_at	glutamate receptor, ionotropic, N-methyl D-aspartate 1	23039	GRIN1	-1.401	-	7.92E-03	1.99E-02
210412_PM_at	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	85315	GRIN2B	-1.809	-	2.99E-02	1.62E-02
207235_PM_s_at	glutamate receptor, metabotropic 5	100101267 /// 9883	GRM5	-0.465	-	3.56E-03	7.76E-03
217008_PM_s_at	glutamate receptor, metabotropic 7	55437	GRM7	-0.893	-	1.21E-02	3.56E-02
201520_PM_s_at	G-rich RNA sequence binding factor 1	2263	GRSF1	-0.657	-	9.90E-03	3.44E-02
214040_PM_s_at	gelsolin (amyloidosis, Finnish type)	8233	GSN	-1.099	-	8.76E-03	2.23E-02
238585_PM_at	glycosyltransferase-like domain containing 1	---	GTDC1	-0.894	-	1.87E-02	3.68E-02
202355_PM_s_at	general transcription factor IIF, polypeptide 1, 74kDa	81539	GTF2F1	-0.619	-	1.92E-02	3.78E-03
202453_PM_s_at	general transcription factor IIH, polypeptide 1, 62kDa	27247	GTF2H1	-1.177	-	1.50E-02	4.02E-02
210892_PM_s_at	general transcription factor Iii	6326	GTF2I	-0.397	-	2.77E-02	4.65E-02
210620_PM_s_at	general transcription factor IIIC, polypeptide 2, beta 110kDa	143384	GTF3C2	-0.619	-	4.05E-03	2.88E-02
206927_PM_s_at	guanylate cyclase 1, soluble, alpha 2	11235	GUCY1A2	-0.312	-	5.66E-03	2.35E-02
208629_PM_s_at	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	23002	HADHA	-0.929	-	7.33E-03	1.59E-02
240975_PM_x_at	hexaribonucleotide binding protein 3	92482	hCG_1776007	-0.688	-	1.34E-03	1.23E-02
229406_PM_at	hexaribonucleotide binding protein 3	9640	hCG_1776007	-1.442	-	3.43E-03	5.38E-03
1556959_PM_at	hCG2007354	3066	hCG_2007354	-0.347	-	6.68E-03	3.65E-02
1557100_PM_s_at	HECT domain containing 1	2908	HECTD1	-0.481	-	1.17E-03	3.53E-03
241955_PM_at	HECT domain containing 1	---	HECTD1	-0.465	-	4.78E-03	1.88E-02
240703_PM_s_at	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	254251	HERC1	-0.302	-	2.19E-03	1.11E-02
233509_PM_at	hect domain and RLD 4	8548	HERC4	-0.326	-	1.99E-02	2.93E-02
210428_PM_s_at	hepatocyte growth factor-regulated tyrosine kinase substrate	3267	HGS	-0.354	-	1.62E-02	3.95E-02

1556037_PM_s_at	hedgehog interacting protein	8878	HHIP	-0.927	-	1.74E-02	4.60E-02
224078_PM_at	hippocampus abundant transcript-like 2	3038	HIATL2	-0.630	-	6.34E-03	4.65E-02
213763_PM_at	homeodomain interacting protein kinase 2	30849	HIPK2	-1.034	-	8.15E-04	2.12E-04
225116_PM_at	homeodomain interacting protein kinase 2	387923	HIPK2	-0.548	-	7.05E-03	4.22E-02
204806_PM_x_at	major histocompatibility complex, class I, F	7799	HLA-F	-0.799	-	2.56E-02	2.93E-02
221875_PM_x_at	major histocompatibility complex, class I, F	5781	HLA-F	-0.863	-	3.63E-02	4.23E-02
211530_PM_x_at	major histocompatibility complex, class I, G	5170	HLA-G	-0.986	-	8.56E-03	2.25E-02
205822_PM_s_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	7101	HMGCS1	-3.141	-	2.17E-02	3.39E-02
212596_PM_s_at	HMG box domain containing 4	10200	HMGXB4	-0.511	-	1.89E-02	1.69E-02
208765_PM_s_at	heterogeneous nuclear ribonucleoprotein R	23412	HNRNPR	-1.055	-	1.16E-02	3.35E-02
236244_PM_at	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	23476	HNRNPU	-0.406	-	1.68E-02	4.47E-02
209675_PM_s_at	heterogeneous nuclear ribonucleoprotein U-like 1	23786	HNRNPUL1	-0.609	-	1.22E-02	2.97E-03
206997_PM_s_at	207eparin sulfate 6-O-sulfotransferase 1	11183	HS6ST1	-0.337	-	5.81E-03	8.06E-03
1569905_PM_at	hydroxysteroid (11-beta) dehydrogenase 1-like	4216	HSD11B1L	-0.576	-	1.38E-04	3.05E-04
213756_PM_s_at	heat shock transcription factor 1	157567	HSF1	-0.630	-	1.31E-02	4.21E-02
211969_PM_at	heat shock protein 90kDa alpha (cytosolic), class A member 1	4076	HSP90AA1	-0.811	-	3.91E-03	8.75E-03
200064_PM_at	heat shock protein 90kDa alpha (cytosolic), class B member 1	8910	HSP90AB1	-0.280	-	4.27E-02	4.90E-02
200598_PM_s_at	heat shock protein 90kDa beta (Grp94), member 1	8777	HSP90B1	-2.314	-	1.23E-02	3.25E-02
216449_PM_x_at	heat shock protein 90kDa beta (Grp94), member 1	23731	HSP90B1	-1.077	-	1.33E-02	1.77E-02
211016_PM_x_at	heat shock 70kDa protein 4	60509	HSPA4	-0.581	-	3.12E-03	2.46E-02
211015_PM_s_at	heat shock 70kDa protein 4	7391	HSPA4	-0.349	-	9.26E-03	9.50E-03
208814_PM_at	Heat shock 70kDa protein 4	28985	HSPA4	-0.560	-	2.28E-02	9.83E-03
208744_PM_x_at	heat shock 105kDa/110kDa protein 1	54948	HSPH1	-2.723	-	1.08E-02	3.32E-02
202601_PM_s_at	HIV-1 Tat specific factor 1	23590	HTATSF1	-0.499	-	2.65E-03	8.77E-03
207949_PM_s_at	islet cell autoantigen 1, 69kDa	90634	ICA1	-0.274	-	3.31E-02	1.20E-02
206906_PM_at	intercellular adhesion molecule 5, telencephalin	3597	ICAM5	-0.646	-	1.88E-02	1.69E-03
202439_PM_s_at	iduronate 2-sulfatase	152006	IDS	-1.128	-	1.00E-03	9.53E-03
206342_PM_x_at	iduronate 2-sulfatase	2063	IDS	-0.710	-	1.59E-03	8.21E-03
217432_PM_s_at	iduronate 2-sulfatase	84817	IDS	-1.100	-	2.18E-03	5.08E-03
202438_PM_x_at	iduronate 2-sulfatase	29098	IDS	-0.303	-	3.18E-02	3.88E-02

202081_PM_at	immediate early response 2	27352	IER2	-0.269	-	3.62E-03	1.40E-02
243358_PM_at	insulin-like growth factor 1 receptor	---	IGF1R	-0.340	-	5.13E-03	1.70E-03
203424_PM_s_at	insulin-like growth factor binding protein 5	8618	IGFBP5	-0.271	-	8.15E-03	1.53E-02
225025_PM_at	immunoglobulin superfamily, member 8	11278	IGSF8	-0.567	-	6.48E-03	2.25E-02
211027_PM_s_at	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	64682	IKBKB	-0.341	-	1.80E-02	2.23E-02
220086_PM_at	IKAROS family zinc finger 5 (Pegasus)	3488	IKZF5	-0.536	-	1.60E-04	7.03E-03
211612_PM_s_at	interleukin 13 receptor, alpha 1	92579	IL13RA1	-0.597	-	1.17E-03	9.28E-03
210904_PM_s_at	interleukin 13 receptor, alpha 1	80318	IL13RA1	-0.345	-	4.72E-03	1.67E-02
222698_PM_s_at	Impact homolog (mouse)	26156	IMPACT	-0.322	-	4.38E-03	2.17E-02
222093_PM_s_at	INO80 complex subunit B	125061 /// 3423	INO80B	-0.925	-	7.50E-03	2.15E-03
204553_PM_x_at	inositol polyphosphate-4-phosphatase, type I, 107kDa	10613	INPP4A	-0.540	-	1.40E-02	9.97E-03
208363_PM_s_at	inositol polyphosphate-4-phosphatase, type I, 107kDa	8828	INPP4A	-0.700	-	1.96E-02	3.68E-02
1554757_PM_a_at	inositol polyphosphate-5-phosphatase, 40kDa	5048	INPP5A	-1.428	-	1.60E-03	1.29E-02
217124_PM_at	IQ motif containing E	57461	IQCE	-0.505	-	4.80E-02	2.10E-02
223429_PM_x_at	ISY1 splicing factor homolog (S. cerevisiae)	60685	ISY1	-0.795	-	1.03E-02	2.49E-02
209743_PM_s_at	itchy E3 ubiquitin protein ligase homolog (mouse)	51719	ITCH	-1.083	-	1.58E-02	2.34E-02
209744_PM_x_at	itchy E3 ubiquitin protein ligase homolog (mouse)	1073	ITCH	-0.812	-	2.50E-02	3.13E-02
204989_PM_s_at	integrin, beta 4	9702	ITGB4	-0.717	-	1.81E-04	7.67E-04
214292_PM_at	integrin, beta 4	6665	ITGB4	-0.400	-	2.55E-03	4.41E-03
211360_PM_s_at	inositol 1,4,5-triphosphate receptor, type 2	146664	ITPR2	-0.285	-	2.39E-02	3.60E-02
1552611_PM_a_at	Janus kinase 1	139324	JAK1	-0.548	-	1.11E-02	1.48E-02
231720_PM_s_at	junctional adhesion molecule 3	---	JAM3	-2.361	-	9.60E-05	2.96E-03
231721_PM_at	junctional adhesion molecule 3	729262	JAM3	-0.850	-	7.34E-03	2.81E-02
225800_PM_at	JAZF zinc finger 1	9125	JAZF1	-1.053	-	3.99E-03	3.86E-02
224933_PM_s_at	jumonji domain containing 1C	387758	JMJD1C	-1.712	-	2.24E-03	2.63E-03
60528_PM_at	JMJD7-PLA2G4B readthrough transcript /// phospholipase A2, group IVB (cytosolic)	6509	JMJD7-PLA2G4B /// PLA2G4B	-0.269	-	3.43E-02	4.65E-02
220188_PM_at	junctophilin 3	24138	JPH3	-1.435	-	9.10E-03	1.89E-02

216309_PM_x_at	jerky homolog (mouse)	79693	JRK	-0.360	-	6.17E-03	2.60E-02
201465_PM_s_at	jun oncogene	7341	JUN	-1.264	-	2.25E-02	4.56E-02
214326_PM_x_at	jun D proto-oncogene	10917	JUND	-0.731	-	3.01E-03	2.27E-02
203751_PM_x_at	jun D proto-oncogene	9665	JUND	-1.442	-	4.94E-03	1.01E-02
201015_PM_s_at	junction plakoglobin	7295	JUP	-0.286	-	4.89E-02	2.87E-02
223585_PM_x_at	kelch repeat and BTB (POZ) domain containing 2	79871	KBTBD2	-2.073	-	9.58E-03	3.88E-02
207237_PM_at	potassium voltage-gated channel, shaker-related subfamily, member 3	11163 /// 440672	KCNA3	-1.317	-	1.25E-02	1.17E-02
208213_PM_s_at	potassium voltage-gated channel, shaker-related subfamily, beta member 1	7170	KCNAB1	-0.972	-	8.67E-03	1.16E-02
210079_PM_x_at	potassium voltage-gated channel, shaker-related subfamily, beta member 1	152007	KCNAB1	-0.717	-	1.51E-02	7.06E-03
211791_PM_s_at	potassium voltage-gated channel, shaker-related subfamily, beta member 2	1995	KCNAB2	-1.741	-	1.13E-02	1.96E-02
1552507_PM_at	potassium voltage-gated channel, Isk-related family, member 4	54715	KCNE4	-0.700	-	1.63E-02	2.00E-02
1555230_PM_a_at	Kv channel interacting protein 2	3945	KCNIP2	-2.389	-	1.61E-03	7.04E-03
221321_PM_s_at	Kv channel interacting protein 2	38	KCNIP2	-1.584	-	3.46E-03	1.34E-02
1555694_PM_a_at	Kv channel interacting protein 3, calsenilin	4714	KCNIP3	-0.346	-	7.74E-03	2.27E-02
224530_PM_s_at	Kv channel interacting protein 4	29883	KCNIP4	-0.550	-	3.45E-03	3.12E-02
231740_PM_at	potassium inwardly-rectifying channel, subfamily J, member 11	63877	KCNJ11	-0.364	-	1.29E-03	1.40E-03
207141_PM_s_at	potassium inwardly-rectifying channel, subfamily J, member 3	56105	KCNJ3	-1.432	-	2.66E-03	1.08E-02
207527_PM_at	potassium inwardly-rectifying channel, subfamily J, member 9	80205	KCNJ9	-0.309	-	2.97E-02	1.52E-02
220448_PM_at	potassium channel, subfamily K, member 12	4548	KCNK12	-1.343	-	2.13E-02	4.26E-02
224552_PM_s_at	potassium channel, subfamily K, member 4	200933	KCNK4	-0.979	-	4.05E-03	1.21E-03
221583_PM_s_at	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	2556	KCNMA1	-1.116	-	3.42E-03	6.81E-03
1563608_PM_a_at	potassium channel, subfamily T, member 1	4087	KCNT1	-0.289	-	4.03E-03	7.78E-03
214849_PM_at	potassium channel tetramerisation domain containing 20	22861 /// 728392	KCTD20	-0.740	-	4.15E-02	2.95E-02

200922_PM_at	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	7267	KDELR1	-1.935	-	1.57E-02	2.56E-02
200700_PM_s_at	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	3674	KDELR2	-1.247	-	7.38E-04	6.98E-03
208987_PM_s_at	lysine (K)-specific demethylase 2A	10169 /// 25764	KDM2A	-1.550	-	1.01E-02	1.62E-02
212492_PM_s_at	lysine (K)-specific demethylase 4B	10559	KDM4B	-1.130	-	1.36E-02	2.33E-02
202040_PM_s_at	lysine (K)-specific demethylase 5A	2885	KDM5A	-0.576	-	1.08E-02	3.15E-03
41386_PM_i_at	lysine (K)-specific demethylase 6B	---	KDM6B	-1.275	-	2.94E-04	3.37E-04
213146_PM_at	lysine (K)-specific demethylase 6B	5627	KDM6B	-0.305	-	4.73E-03	8.74E-04
201488_PM_x_at	KH domain containing, RNA binding, signal transduction associated 1	22848	KHDRBS1	-1.576	-	1.22E-02	3.37E-02
212396_PM_s_at	KIAA0090	6632	KIAA0090	-0.385	-	9.04E-03	4.02E-02
1558697_PM_a_at	KIAA0430	5528	KIAA0430	-0.462	-	3.72E-04	2.13E-03
201775_PM_s_at	KIAA0494	6935	KIAA0494	-0.403	-	4.28E-02	4.85E-02
203363_PM_s_at	KIAA0652	55755	KIAA0652	-0.543	-	8.04E-03	1.90E-02
1554755_PM_a_at	KIAA0774	5720	KIAA0774	-0.352	-	3.60E-03	5.35E-05
216294_PM_s_at	KIAA1109	56254	KIAA1109	-1.524	-	1.18E-03	7.41E-03
223799_PM_at	KIAA1826	55632	KIAA1826	-0.638	-	1.54E-02	4.38E-02
224706_PM_at	KIAA2013	440145	KIAA2013	-0.289	-	4.09E-02	3.61E-02
201992_PM_s_at	kinesin family member 5B	334	KIF5B	-0.523	-	5.32E-04	7.11E-03
203129_PM_s_at	kinesin family member 5C	151887	KIF5C	-1.557	-	7.13E-03	1.02E-02
219878_PM_s_at	Kruppel-like factor 13	5993	KLF13	-2.192	-	3.00E-02	3.98E-02
219657_PM_s_at	Kruppel-like factor 3 (basic)	8932	KLF3	-0.275	-	2.10E-02	4.77E-02
203542_PM_s_at	Kruppel-like factor 9	10634	KLF9	-1.197	-	2.69E-04	4.85E-03
225963_PM_at	kelch domain containing 5	51256	KLHDC5	-2.104	-	1.78E-03	1.34E-02
221837_PM_at	kelch-like 22 (Drosophila)	10026	KLHL22	-1.605	-	6.00E-03	1.80E-02
221986_PM_s_at	kelch-like 24 (Drosophila)	10985	KLHL24	-0.532	-	2.25E-02	1.73E-02
1554145_PM_a_at	KLRAQ motif containing 1	55209	KLRAQ1	-1.466	-	4.26E-03	3.19E-02
202058_PM_s_at	karyopherin alpha 1 (importin alpha 5)	65220	KPNA1	-1.605	-	2.63E-04	6.36E-03

213741_PM_s_at	karyopherin alpha 1 (importin alpha 5)	23001	KPNA1	-0.848	-	3.39E-03	3.19E-02
221503_PM_s_at	karyopherin alpha 3 (importin alpha 4)	23205	KPNA3	-1.632	-	6.18E-04	3.67E-03
212102_PM_s_at	karyopherin alpha 6 (importin alpha 7)	1108	KPNA6	-0.563	-	2.83E-02	4.99E-02
213507_PM_s_at	karyopherin (importin) beta 1	1949	KPNB1	-0.984	-	4.22E-02	2.52E-03
214352_PM_s_at	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	51371	KRAS	-2.330	-	8.02E-03	2.73E-02
224534_PM_at	kringle containing transmembrane protein 1	84918	KREMEN1	-0.480	-	1.27E-02	5.47E-03
204738_PM_s_at	KRIT1, ankyrin repeat containing	6845	KRIT1	-0.483	-	2.10E-02	4.60E-02
230116_PM_at	Keratin 8 pseudogene 12	145748	KRT8P12	-0.269	-	2.52E-03	1.98E-02
200914_PM_x_at	kinectin 1 (kinesin receptor)	5879	KTN1	-2.004	-	4.38E-03	1.72E-02
1555815_PM_a_at	l(3)mbt-like 2 (Drosophila)	9898	L3MBTL2	-0.341	-	1.13E-02	1.36E-02
201551_PM_s_at	lysosomal-associated membrane protein 1	84525	LAMP1	-2.294	-	1.04E-02	2.72E-02
218219_PM_s_at	LanC lantibiotic synthetase component C-like 2 (bacterial)	253558	LANCL2	-0.835	-	5.53E-03	2.74E-02
1554679_PM_a_at	lysosomal protein transmembrane 4 beta	4735	LAPTM4B	-1.130	-	1.05E-02	1.84E-02
223888_PM_s_at	leucyl-tRNA synthetase	51259	LARS	-0.552	-	2.05E-03	1.30E-02
219813_PM_at	LATS, large tumor suppressor, homolog 1 (Drosophila)	5519	LATS1	-0.359	-	9.49E-03	3.84E-02
202595_PM_s_at	leptin receptor overlapping transcript-like 1	27068	LEPROTL1	-0.819	-	1.73E-03	1.59E-02
227821_PM_at	leucine-rich repeat LGI family, member 4	378938	LGI4	-0.290	-	4.48E-02	3.58E-02
212325_PM_at	LIM and calponin homology domains 1	10915	LIMCH1	-0.664	-	2.82E-02	4.41E-02
236156_PM_at	lipase A, lysosomal acid, cholesterol esterase	---	LIPA	-0.345	-	3.25E-03	2.07E-02
235036_PM_at	Lix1 homolog (mouse)-like	3308	LIX1L	-0.489	-	9.66E-05	3.26E-03
31837_PM_at	lipase maturation factor 2	---	LMF2	-0.302	-	4.27E-02	2.18E-02
209204_PM_at	LIM domain only 4	83440	LMO4	-1.322	-	4.36E-05	5.43E-04
209205_PM_s_at	LIM domain only 4	64850	LMO4	-1.257	-	5.64E-04	9.17E-03
1557103_PM_a_at	lemur tyrosine kinase 3	2908	LMTK3	-0.413	-	9.85E-03	3.22E-02
1562022_PM_s_at	similar to hCG1815675 /// RAD9 homolog A (S. pombe)	9551	LOC100130987 /// RAD9A	-0.918	-	5.17E-03	2.44E-02
1557783_PM_at	similar to hCG1995169	158	LOC100133991	-0.287	-	5.14E-03	2.67E-02
232309_PM_at	hypothetical protein LOC202181	83852	LOC202181	-0.463	-	1.44E-02	2.79E-02
241464_PM_s_at	hypothetical LOC400931	84856	LOC400931	-0.731	-	2.96E-02	4.65E-02

1556771_PM_a_at	hypothetical LOC415056	5431	LOC415056	-0.796	-	1.27E-03	1.46E-02
215090_PM_x_at	hypothetical protein FLJ11822	78991	LOC440434	-1.188	-	4.47E-03	4.61E-03
214107_PM_x_at	hypothetical protein FLJ11822	1506	LOC440434	-1.542	-	7.87E-03	1.86E-02
1558688_PM_at	hypothetical LOC441461	6744	LOC441461	-0.421	-	1.87E-02	1.20E-02
212113_PM_at	hypothetical protein LOC552889	10541	LOC552889	-1.873	-	8.13E-04	3.48E-03
227223_PM_at	similar to RNA binding motif protein 39 /// RNA binding motif protein 39	54165	LOC643167 /// RBM39	-1.937	-	2.58E-03	2.59E-03
215812_PM_s_at	similar to solute carrier family 6 member 8 /// solute carrier family 6 (neurotransmitter transporter, creatine), member 10 (pseudogene) /// solute carrier family 6 (neurotransmitter transporter, creatine), member 8	9440	LOC653562 /// SLC6A10P /// SLC6A8	-1.643	-	4.75E-03	1.23E-02
231808_PM_at	hypothetical protein LOC729082	10691	LOC729082	-1.650	-	9.85E-03	2.62E-02
216908_PM_x_at	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene	56987	LOC730092	-0.687	-	3.21E-03	1.33E-02
40472_PM_at	lysophosphatidylcholine acyltransferase 4	285147	LPCAT4	-1.204	-	7.81E-03	2.14E-02
212272_PM_at	lipin 1	1349	LPIN1	-0.616	-	1.04E-02	2.76E-02
218509_PM_at	lipid phosphate phosphatase-related protein type 2	5058	LPPR2	-1.954	-	2.12E-02	3.07E-02
64899_PM_at	lipid phosphate phosphatase-related protein type 2	---	LPPR2	-2.594	-	2.74E-02	4.22E-02
200784_PM_s_at	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	785	LRP1	-0.910	-	1.01E-02	2.58E-03
239320_PM_at	leucine rich repeat containing 4B	92979	LRRC4B	-1.035	-	5.05E-03	1.51E-02
241585_PM_at	leucine rich repeat containing 4C	---	LRRC4C	-0.466	-	9.82E-03	2.17E-02
216164_PM_at	leucine rich repeat neuronal 2	23409	LRRN2	-0.265	-	9.39E-03	9.08E-03
212529_PM_at	LSM12 homolog (S. cerevisiae)	669	LSM12	-2.283	-	6.11E-04	6.23E-03
219653_PM_at	LSM14B, SCD6 homolog B (S. cerevisiae)	11044	LSM14B	-0.462	-	1.75E-02	2.18E-02
1553304_PM_at	LSM14B, SCD6 homolog B (S. cerevisiae)	7072	LSM14B	-0.531	-	3.43E-02	4.71E-02
213176_PM_s_at	latent transforming growth factor beta binding protein 4	6731	LTBP4	-0.546	-	1.89E-02	2.31E-02
208835_PM_s_at	LUC7-like 3 (S. cerevisiae)	4708	LUC7L3	-1.647	-	1.92E-03	1.11E-02
206773_PM_at	lymphocyte antigen 6 complex, locus H	9747	LY6H	-3.120	-	1.28E-02	1.97E-02
210754_PM_s_at	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	84293	LYN	-0.542	-	7.22E-04	6.92E-03
200900_PM_s_at	mannose-6-phosphate receptor (cation dependent)	23499	M6PR	-0.919	-	1.69E-02	3.03E-02

209347_PM_s_at	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	81929	MAF	-0.271	-	1.13E-02	8.98E-03
222670_PM_s_at	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	220594	MAFB	-0.472	-	9.65E-03	2.51E-02
216617_PM_s_at	myelin associated glycoprotein	51258	MAG	-1.848	-	1.00E-02	4.70E-02
220925_PM_at	MAK10 homolog, amino-acid N-acetyltransferase subunit (S. cerevisiae)	8269	MAK10	-1.098	-	3.64E-03	7.81E-03
223940_PM_x_at	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	93974	MALAT1	-2.637	-	1.02E-03	1.42E-03
224568_PM_x_at	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	28996	MALAT1	-2.587	-	3.51E-03	3.85E-03
1558678_PM_s_at	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)	2965	MALAT1	-0.658	-	2.41E-02	3.45E-02
214577_PM_at	microtubule-associated protein 1B	54529	MAP1B	-3.423	-	8.88E-03	1.13E-02
226084_PM_at	microtubule-associated protein 1B	8452	MAP1B	-0.708	-	4.14E-02	3.43E-02
227219_PM_x_at	microtubule-associated protein 1 light chain 3 alpha	51030	MAP1LC3A	-0.969	-	2.12E-02	3.59E-02
232011_PM_s_at	microtubule-associated protein 1 light chain 3 alpha	440556	MAP1LC3A	-3.074	-	2.26E-02	3.67E-02
221697_PM_at	microtubule-associated protein 1 light chain 3 gamma	10130	MAP1LC3C	-0.322	-	6.37E-03	5.14E-03
210015_PM_s_at	microtubule-associated protein 2	85440	MAP2	-2.384	-	5.95E-04	7.90E-03
203265_PM_s_at	mitogen-activated protein kinase kinase 4	10600	MAP2K4	-2.058	-	4.61E-03	1.89E-02
211081_PM_s_at	mitogen-activated protein kinase kinase kinase kinase 5	148252	MAP4K5	-0.326	-	1.39E-02	3.70E-02
208351_PM_s_at	mitogen-activated protein kinase 1	2861	MAPK1	-2.629	-	7.81E-03	2.20E-02
1552264_PM_a_at	mitogen-activated protein kinase 1	5594	MAPK1	-2.508	-	8.19E-03	2.06E-02
211087_PM_x_at	mitogen-activated protein kinase 14	8437	MAPK14	-0.560	-	5.48E-03	7.80E-03
211561_PM_x_at	mitogen-activated protein kinase 14	8623	MAPK14	-0.855	-	6.04E-03	3.42E-02
210449_PM_x_at	mitogen-activated protein kinase 14	6095	MAPK14	-0.666	-	8.51E-03	2.32E-02
213014_PM_at	mitogen-activated protein kinase 8 interacting protein 1	2888	MAPK8IP1	-2.721	-	4.92E-04	3.88E-03
208603_PM_s_at	mitogen-activated protein kinase 8 interacting protein 2	51668	MAPK8IP2	-1.043	-	3.17E-03	7.09E-03
229846_PM_s_at	mitogen-activated protein kinase associated protein 1	29035	MAPKAP1	-1.650	-	5.03E-03	2.16E-02
202501_PM_at	microtubule-associated protein, RP/EB family, member 2	54946	MAPRE2	-0.287	-	2.19E-02	2.51E-02
214270_PM_s_at	microtubule-associated protein, RP/EB family, member 3	9639	MAPRE3	-3.238	-	4.73E-03	1.33E-02
203841_PM_x_at	microtubule-associated protein, RP/EB family, member 3	6418	MAPRE3	-3.191	-	4.76E-03	1.31E-02

206401_PM_s_at	microtubule-associated protein tau	84263	MAPT	-2.201	-	4.67E-03	4.89E-03
201668_PM_x_at	myristoylated alanine-rich protein kinase C substrate	800	MARCKS	-2.391	-	2.56E-03	9.57E-03
203942_PM_s_at	MAP/microtubule affinity-regulating kinase 2	10724	MARK2	-1.126	-	2.45E-02	4.73E-02
200769_PM_s_at	methionine adenosyltransferase II, alpha	9497	MAT2A	-2.621	-	8.19E-03	2.81E-02
210734_PM_x_at	MYC associated factor X	93589	MAX	-1.556	-	1.80E-02	4.62E-02
232138_PM_at	Muscleblind-like 2 (Drosophila)	---	MBNL2	-0.647	-	2.51E-03	8.99E-03
205018_PM_s_at	muscleblind-like 2 (Drosophila)	4925	MBNL2	-2.595	-	5.47E-03	2.18E-02
205017_PM_s_at	muscleblind-like 2 (Drosophila)	10150	MBNL2	-1.140	-	1.63E-02	4.86E-02
1563809_PM_a_at	MCF.2 cell line derived transforming sequence-like	4891	MCF2L	-0.532	-	3.09E-03	2.34E-03
212142_PM_at	minichromosome maintenance complex component 4	55041	MCM4	-0.979	-	2.53E-03	9.97E-03
204059_PM_s_at	malic enzyme 1, NADP(+)-dependent, cytosolic	10054	ME1	-0.703	-	2.40E-02	3.85E-02
221884_PM_at	MDS1 and EVI1 complex locus	10181	MECOM	-0.297	-	1.90E-03	2.06E-02
212208_PM_at	mediator complex subunit 13-like	8615	MED13L	-0.737	-	1.44E-02	1.98E-02
221517_PM_s_at	mediator complex subunit 17	1472	MED17	-0.376	-	1.80E-02	3.38E-02
226293_PM_at	mediator complex subunit 19	9764	MED19	-0.801	-	3.46E-02	3.33E-02
208328_PM_s_at	myocyte enhancer factor 2A	5098	MEF2A	-0.311	-	6.04E-03	1.00E-02
235077_PM_at	maternally expressed 3 (non-protein coding)	4791	MEG3	-1.997	-	1.30E-02	1.75E-02
1569879_PM_a_at	multiple EGF-like-domains 11	8412	MEGF11	-0.641	-	1.06E-02	1.15E-02
211599_PM_x_at	met proto-oncogene (hepatocyte growth factor receptor)	254531	MET	-1.033	-	2.66E-04	5.38E-03
213807_PM_x_at	met proto-oncogene (hepatocyte growth factor receptor)	6272	MET	-0.920	-	5.92E-03	6.54E-04
206468_PM_s_at	methyltransferase like 13	8930	METTL13	-0.436	-	1.11E-02	5.24E-03
222567_PM_s_at	mex-3 homolog C (C. elegans)	6874	MEX3C	-1.077	-	4.27E-03	2.81E-02
216205_PM_s_at	mitofusin 2	80762	MFN2	-1.404	-	1.99E-03	1.09E-02
219858_PM_s_at	major facilitator superfamily domain containing 6	9917	MFSD6	-0.422	-	4.95E-03	2.97E-02
220189_PM_s_at	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B	7915	MGAT4B	-1.476	-	2.20E-02	3.80E-02
200898_PM_s_at	meningioma expressed antigen 5 (hyaluronidase)	23542	MGEA5	-0.709	-	8.95E-03	4.94E-02
223494_PM_at	meningioma expressed antigen 5 (hyaluronidase)	64864	MGEA5	-1.359	-	1.66E-02	2.02E-02
214972_PM_at	Meningioma expressed antigen 5 (hyaluronidase)	57826	MGEA5	-0.336	-	4.98E-02	1.33E-02
228658_PM_at	myocardial infarction associated transcript (non-protein	3696	MIAT	-0.339	-	1.96E-02	2.35E-02

	coding)						
214625_PM_s_at	misshapen-like kinase 1 (zebrafish)	8303	MINK1	-1.132	-	3.28E-02	3.93E-02
222510_PM_s_at	makorin ring finger protein 2	23097	MKRN2	-1.475	-	1.27E-02	2.54E-02
1565436_PM_s_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	6635	MLL	-0.498	-	9.33E-03	2.81E-02
212078_PM_s_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	23451	MLL	-1.240	-	4.63E-02	1.26E-02
222413_PM_s_at	myeloid/lymphoid or mixed-lineage leukemia 3	124801	MLL3	-0.276	-	4.12E-02	3.37E-02
223189_PM_x_at	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	51319	MLL5	-1.996	-	5.29E-03	3.68E-03
223190_PM_s_at	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	55841	MLL5	-1.398	-	6.08E-03	7.91E-03
216506_PM_x_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	55017	MLLT10	-0.626	-	1.54E-02	1.25E-02
216503_PM_s_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	83641	MLLT10	-0.808	-	2.19E-02	2.52E-02
202519_PM_at	MLX interacting protein	5716	MLXIP	-0.932	-	1.65E-02	4.79E-02
221895_PM_at	motile sperm domain containing 2	429	MOSPD2	-0.319	-	3.83E-03	6.79E-05
205079_PM_s_at	multiple PDZ domain protein	51668	MPDZ	-0.458	-	1.18E-02	1.47E-02
225041_PM_at	M-phase phosphoprotein 8	286343	MPHOSPH8	-1.580	-	2.74E-03	1.06E-02
221771_PM_s_at	M-phase phosphoprotein 8	8543	MPHOSPH8	-0.836	-	1.54E-02	4.29E-02
241398_PM_at	Metallophosphoesterase domain containing 1	---	MPPED1	-0.368	-	3.82E-02	1.16E-02
215692_PM_s_at	metallophosphoesterase domain containing 2	81617	MPPED2	-1.162	-	2.22E-02	2.17E-02
225233_PM_at	musashi homolog 2 (Drosophila)	340554	MSI2	-1.033	-	2.54E-03	1.91E-02
1554126_PM_at	methionine sulfoxide reductase B3	57223	MSRB3	-0.931	-	1.11E-02	1.36E-02
212251_PM_at	metadherin	10314	MTDH	-0.955	-	1.41E-02	1.47E-02
205322_PM_s_at	metal-regulatory transcription factor 1	9016	MTF1	-0.485	-	1.08E-02	9.28E-03
214975_PM_s_at	myotubularin related protein 1	57826	MTMR1	-0.351	-	9.97E-03	2.02E-02
202198_PM_s_at	myotubularin related protein 3	889	MTMR3	-0.426	-	4.52E-02	3.87E-02
212095_PM_s_at	mitochondrial tumor suppressor 1	8239	MTUS1	-0.378	-	1.54E-03	1.16E-02
212347_PM_x_at	MAX dimerization protein 4	1739	MXD4	-0.311	-	8.99E-03	3.12E-02

1557370_PM_s_at	MYC binding protein 2	832	MYCBP2	-2.121	-	6.60E-03	9.63E-03
201959_PM_s_at	MYC binding protein 2	9444	MYCBP2	-1.444	-	9.34E-03	1.19E-02
216222_PM_s_at	myosin X	51773	MYO10	-0.287	-	2.10E-02	2.60E-02
1560788_PM_at	myosin IIIB	6921	MYO3B	-0.343	-	1.30E-05	7.10E-04
204527_PM_at	myosin VA (heavy chain 12, myoxin)	9453	MYO5A	-0.744	-	3.79E-02	2.25E-02
203215_PM_s_at	myosin VI	55578	MYO6	-0.421	-	2.80E-02	8.01E-03
219027_PM_s_at	myosin IXA	1762	MYO9A	-0.285	-	2.03E-02	2.14E-02
202423_PM_at	MYST histone acetyltransferase (monocytic leukemia) 3	53343	MYST3	-0.642	-	1.58E-02	9.39E-03
211874_PM_s_at	MYST histone acetyltransferase (monocytic leukemia) 4	285093	MYST4	-1.571	-	3.90E-03	8.85E-03
214496_PM_x_at	MYST histone acetyltransferase (monocytic leukemia) 4	64771	MYST4	-1.491	-	4.64E-03	2.08E-02
212452_PM_x_at	MYST histone acetyltransferase (monocytic leukemia) 4	9197	MYST4	-1.394	-	5.24E-03	1.31E-02
215822_PM_x_at	myelin transcription factor 1	55620	MYT1	-0.497	-	3.01E-02	1.07E-03
1554633_PM_a_at	myelin transcription factor 1-like	5230	MYT1L	-2.474	-	1.93E-03	1.13E-02
216017_PM_s_at	NGFI-A binding protein 2 (EGR1 binding protein 2)	7596	NAB2	-1.626	-	6.03E-03	5.05E-03
215159_PM_s_at	NAD kinase	64783	NADK	-0.504	-	3.09E-03	1.18E-02
213607_PM_x_at	NAD kinase	23244	NADK	-0.945	-	4.32E-03	1.16E-02
208753_PM_s_at	nucleosome assembly protein 1-like 1	51307	NAP1L1	-0.400	-	2.34E-02	2.79E-02
206491_PM_s_at	N-ethylmaleimide-sensitive factor attachment protein, alpha	3298	NAPA	-2.181	-	2.04E-02	2.94E-02
210048_PM_at	N-ethylmaleimide-sensitive factor attachment protein, gamma	122786	NAPG	-0.756	-	4.64E-03	2.65E-02
219158_PM_s_at	NMDA receptor regulated 1	10285	NARG1	-1.516	-	3.83E-04	2.79E-03
235189_PM_at	NMDA receptor regulated 2	---	NARG2	-0.327	-	7.89E-04	2.42E-03
222599_PM_s_at	neuron navigator 2	91	NAV2	-0.673	-	4.57E-02	4.01E-03
201383_PM_s_at	neighbor of BRCA1 gene 1	1837	NBR1	-0.779	-	7.79E-03	3.07E-02
205669_PM_at	neural cell adhesion molecule 2	6886	NCAM2	-0.540	-	2.51E-03	2.63E-02
209557_PM_s_at	neurochondrin	51538	NCDN	-2.469	-	1.43E-03	4.76E-03
209556_PM_at	neurochondrin	11164	NCDN	-0.429	-	1.20E-02	2.40E-02
222206_PM_s_at	nicalin homolog (zebrafish)	79572	NCLN	-0.324	-	6.43E-03	7.04E-03
205732_PM_s_at	nuclear receptor coactivator 2	2322	NCOA2	-0.887	-	5.50E-03	3.51E-02
211352_PM_s_at	nuclear receptor coactivator 3	134218	NCOA3	-0.337	-	4.36E-03	4.02E-02
222422_PM_s_at	Nedd4 family interacting protein 1	23347	NDFIP1	-2.238	-	1.26E-02	3.70E-02

224799_PM_at	Nedd4 family interacting protein 2	285282	NDFIP2	-1.098	-	2.11E-03	1.29E-02
203039_PM_s_at	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	29058	NDUFS1	-0.631	-	9.30E-03	1.20E-02
207279_PM_s_at	nebulette	90411	NEBL	-0.727	-	2.66E-03	5.75E-03
223954_PM_x_at	N-terminal EF-hand calcium binding protein 3	58527	NECAB3	-0.521	-	1.59E-03	4.57E-03
212448_PM_at	neural precursor cell expressed, developmentally down-regulated 4-like	10952	NEDD4L	-0.589	-	1.26E-02	2.14E-02
213328_PM_at	NIMA (never in mitosis gene a)-related kinase 1	5612	NEK1	-0.650	-	3.71E-02	2.64E-02
239267_PM_at	NIMA (never in mitosis gene a)-related kinase 6	---	NEK6	-0.441	-	1.96E-03	1.08E-02
214738_PM_s_at	NIMA (never in mitosis gene a)- related kinase 9	29883	NEK9	-0.853	-	1.99E-02	4.71E-02
222774_PM_s_at	neuropilin (NRP) and tolloid (TLL)-like 2	9271	NETO2	-0.562	-	1.47E-02	3.21E-02
204325_PM_s_at	neurofibromin 1	1163	NF1	-0.324	-	1.39E-02	1.29E-02
211092_PM_s_at	neurofibromin 2 (merlin)	5136	NF2	-0.509	-	1.87E-03	1.60E-02
211091_PM_s_at	neurofibromin 2 (merlin)	26470	NF2	-0.367	-	3.21E-03	4.68E-03
224976_PM_at	nuclear factor I/A	150290	NFIA	-2.043	-	4.78E-03	7.17E-03
224975_PM_at	nuclear factor I/A	7802	NFIA	-1.247	-	7.14E-03	1.43E-02
211524_PM_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)	9749	NFKB2	-0.294	-	1.63E-03	2.75E-03
243556_PM_at	neuronal guanine nucleotide exchange factor	---	NGEF	-1.361	-	5.69E-04	9.90E-03
1564746_PM_at	Na+/H+ exchanger domain containing 2	79096	NHEDC2	-0.745	-	1.66E-03	3.10E-03
242352_PM_at	Nipped-B homolog (Drosophila)	439921	NIPBL	-0.868	-	2.30E-02	2.51E-02
211949_PM_s_at	nucleolar and coiled-body phosphoprotein 1	3337	NOLC1	-0.339	-	1.74E-03	8.29E-03
205895_PM_s_at	nucleolar and coiled-body phosphoprotein 1	6506	NOLC1	-0.733	-	2.83E-03	5.11E-03
221853_PM_s_at	NODAL modulator 1 /// NODAL modulator 2 /// NODAL modulator 3	4863	NOMO1 /// NOMO2 /// NOMO3	-0.303	-	1.97E-02	3.90E-02
214427_PM_at	NOP2 nucleolar protein homolog (yeast)	26073	NOP2	-0.282	-	1.81E-02	4.13E-02
239132_PM_at	Nitric oxide synthase 1 (neuronal)	---	NOS1	-0.511	-	2.86E-05	1.66E-03
205459_PM_s_at	neuronal PAS domain protein 2	3290	NPAS2	-0.393	-	5.86E-04	4.92E-03
220316_PM_at	neuronal PAS domain protein 3	10127	NPAS3	-0.924	-	2.29E-02	4.62E-02
218086_PM_at	neural proliferation, differentiation and control, 1	153339	NPDC1	-0.817	-	1.26E-02	1.96E-02
201454_PM_s_at	aminopeptidase puromycin sensitive	3308	NPEPPS	-0.529	-	3.35E-02	4.49E-02

210730_PM_s_at	neuropeptide Y receptor Y2	90293	NPY2R	-0.708	-	5.07E-03	1.22E-02
217370_PM_x_at	nuclear receptor subfamily 1, group H, member 3	64919	NR1H3	-2.465	-	1.44E-02	2.92E-02
209261_PM_s_at	nuclear receptor subfamily 2, group F, member 6	10776	NR2F6	-0.396	-	1.20E-02	2.81E-02
201866_PM_s_at	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	5786	NR3C1	-0.379	-	3.64E-03	3.28E-03
201865_PM_x_at	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	27332	NR3C1	-0.272	-	5.76E-03	2.01E-02
216959_PM_x_at	neuronal cell adhesion molecule	29761	NRCAM	-2.755	-	1.85E-02	4.39E-02
211279_PM_at	nuclear respiratory factor 1	6546	NRF1	-0.396	-	2.57E-02	2.82E-02
204081_PM_at	neurogranin (protein kinase C substrate, RC3)	6856	NRGN	-2.771	-	2.59E-02	4.86E-02
202600_PM_s_at	nuclear receptor interacting protein 1	55768	NRIP1	-0.950	-	2.06E-03	4.75E-03
210510_PM_s_at	neuropilin 1	256586	NRP1	-0.524	-	2.42E-02	4.09E-02
214632_PM_at	neuropilin 2	28998	NRP2	-0.337	-	1.17E-02	1.94E-03
209914_PM_s_at	neurexin 1	55704	NRXN1	-2.169	-	4.77E-04	4.27E-04
216096_PM_s_at	neurexin 1	63875	NRXN1	-2.737	-	1.38E-02	4.18E-02
209982_PM_s_at	neurexin 2	87178	NRXN2	-1.289	-	1.74E-02	5.40E-03
215021_PM_s_at	neurexin 3	65109	NRXN3	-1.583	-	3.99E-02	3.21E-02
1569354_PM_at	NOL1/NOP2/Sun domain family, member 6	1756	NSUN6	-0.306	-	9.19E-03	3.22E-02
207152_PM_at	neurotrophic tyrosine kinase, receptor, type 2	23215	NTRK2	-1.849	-	7.93E-03	3.97E-03
214680_PM_at	neurotrophic tyrosine kinase, receptor, type 2	55081	NTRK2	-1.316	-	2.88E-02	4.15E-02
215025_PM_at	neurotrophic tyrosine kinase, receptor, type 3	64763	NTRK3	-0.510	-	1.21E-02	3.12E-02
1557795_PM_s_at	neurotrophic tyrosine kinase, receptor, type 3	10381	NTRK3	-0.947	-	4.00E-02	3.57E-02
200646_PM_s_at	nucleobindin 1	486	NUCB1	-0.456	-	2.38E-02	4.72E-03
229353_PM_s_at	nuclear casein kinase and cyclin-dependent kinase substrate 1	285550	NUCKS1	-1.528	-	6.09E-03	5.86E-03
226880_PM_at	Nuclear casein kinase and cyclin-dependent kinase substrate 1	3837	NUCKS1	-1.053	-	2.19E-02	1.95E-03
221579_PM_s_at	nudix (nucleoside diphosphate linked moiety X)-type motif 3	2842	NUDT3	-0.751	-	6.78E-03	1.43E-02
206303_PM_s_at	nudix (nucleoside diphosphate linked moiety X)-type motif 4	8543	NUDT4	-0.398	-	6.51E-04	5.14E-03
206302_PM_s_at	nudix (nucleoside diphosphate linked moiety X)-type motif 4 /// nudix (nucleoside diphosphate linked moiety X)-type motif 4 pseudogene 1	22978	NUDT4 /// NUDT4P1	-0.574	-	3.36E-03	3.75E-02

205134_PM_s_at	nuclear fragile X mental retardation protein interacting protein 1	23387	NUFIP1	-0.414	-	1.36E-02	4.81E-02
214251_PM_s_at	nuclear mitotic apparatus protein 1	2119	NUMA1	-0.941	-	9.69E-03	5.99E-03
214250_PM_at	nuclear mitotic apparatus protein 1	182	NUMA1	-0.364	-	4.58E-02	1.41E-03
211513_PM_s_at	opioid growth factor receptor	9534	OGFR	-0.413	-	4.16E-03	2.29E-02
216408_PM_at	olfactory receptor, family 2, subfamily B, member 2	64919	OR2B2	-0.299	-	2.69E-03	8.13E-03
1555212_PM_at	olfactory receptor, family 8, subfamily B, member 8	301	OR8B8	-0.293	-	9.86E-03	2.44E-02
221237_PM_s_at	oxysterol binding protein 2	8577	OSBP2	-0.518	-	3.67E-02	1.42E-02
201245_PM_s_at	OTU domain, ubiquitin aldehyde binding 1	552900 /// 654483	OTUB1	-2.881	-	3.08E-02	3.67E-02
201246_PM_s_at	OTU domain, ubiquitin aldehyde binding 1	27040 /// 83985	OTUB1	-0.405	-	3.15E-02	2.79E-02
1555426_PM_a_at	OTU domain containing 5	9774	OTUD5	-1.110	-	1.26E-02	3.52E-02
233933_PM_s_at	OTU domain containing 5	---	OTUD5	-1.176	-	1.30E-02	1.73E-02
1553351_PM_at	OTU domain containing 7A	783	OTUD7A	-0.816	-	2.01E-03	2.11E-03
238409_PM_x_at	oxidation resistance 1	---	OXR1	-0.351	-	9.44E-03	4.17E-02
1564494_PM_s_at	prolyl 4-hydroxylase, beta polypeptide	7088	P4HB	-2.154	-	2.21E-03	1.55E-02
215157_PM_x_at	poly(A) binding protein, cytoplasmic 1	79589	PABPC1	-0.313	-	2.57E-02	3.10E-02
1555823_PM_at	phosphofurin acidic cluster sorting protein 2	4077	PACS2	-0.703	-	3.26E-02	2.46E-02
1554385_PM_a_at	peptidyl arginine deiminase, type II	5573	PADI2	-0.337	-	4.96E-02	3.74E-02
200813_PM_s_at	platelet-activating factor acetylhydrolase, isoform Ib, subunit 1 (45kDa)	1453	PAFAH1B1	-0.805	-	1.10E-02	2.90E-02
200815_PM_s_at	platelet-activating factor acetylhydrolase, isoform Ib, subunit 1 (45kDa)	288	PAFAH1B1	-0.563	-	2.33E-02	3.51E-02
211547_PM_s_at	platelet-activating factor acetylhydrolase, isoform Ib, subunit 1 (45kDa)	2110	PAFAH1B1	-0.523	-	3.61E-02	1.12E-02
225626_PM_at	phosphoprotein associated with glycosphingolipid microdomains 1	283554	PAG1	-0.406	-	2.45E-02	3.39E-02
209615_PM_s_at	p21 protein (Cdc42/Rac)-activated kinase 1	55075	PAK1	-0.894	-	2.50E-02	3.20E-02
214607_PM_at	p21 protein (Cdc42/Rac)-activated kinase 3	7570	PAK3	-1.553	-	5.71E-03	6.77E-03
33814_PM_at	p21 protein (Cdc42/Rac)-activated kinase 4	285343	PAK4	-0.342	-	1.64E-02	1.28E-02

202760_PM_s_at	PALM2-AKAP2 readthrough transcript	9939	PALM2-AKAP2	-0.390	-	4.61E-04	5.01E-04
242825_PM_at	phosphatidic acid phosphatase type 2	161882	PAP2D	-0.494	-	3.25E-02	1.60E-02
224427_PM_s_at	poly(A) polymerase gamma	90488	PAPOLG	-0.734	-	1.41E-02	3.20E-02
212858_PM_at	progestin and adipoQ receptor family member IV	10485	PAQR4	-0.356	-	7.70E-03	1.61E-02
226423_PM_at	progestin and adipoQ receptor family member VIII	3084	PAQR8	-0.713	-	5.42E-03	2.69E-02
221526_PM_x_at	par-3 partitioning defective 3 homolog (C. elegans)	6334	PARD3	-0.966	-	2.57E-02	1.08E-02
205245_PM_at	par-6 partitioning defective 6 homolog alpha (C. elegans)	10978	PARD6A	-0.328	-	2.59E-02	2.50E-02
37965_PM_at	parvin, beta	---	PARVB	-1.605	-	1.99E-02	3.20E-02
212151_PM_at	pre-B-cell leukemia homeobox 1	10159	PBX1	-1.244	-	2.10E-03	2.55E-03
213517_PM_at	poly(rC) binding protein 2	8487	PCBP2	-0.931	-	4.10E-02	1.51E-02
219737_PM_s_at	protocadherin 9	2308	PCDH9	-1.146	-	1.60E-02	2.44E-02
224212_PM_s_at	protocadherin alpha 1	7170	PCDHA1	-1.967	-	2.55E-03	2.55E-03
216352_PM_x_at	protocadherin gamma subfamily A, 1	51111	PCDHGA1	-0.392	-	1.56E-02	4.46E-02
211876_PM_x_at	protocadherin gamma subfamily A, 11	23333	PCDHGA11	-0.658	-	6.58E-03	1.18E-02
211879_PM_x_at	protocadherin gamma subfamily A, 3	100130987 /// 5883	PCDHGA3	-0.460	-	1.58E-02	3.25E-02
214564_PM_s_at	protocadherin gamma subfamily C, 3	8649	PCDHGC3	-0.504	-	2.41E-02	4.25E-02
235507_PM_at	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	---	PCMTD1	-0.418	-	8.76E-03	1.27E-02
218952_PM_at	proprotein convertase subtilisin/kexin type 1 inhibitor	23704	PCSK1N	-1.988	-	2.40E-02	3.48E-02
204870_PM_s_at	proprotein convertase subtilisin/kexin type 2	4646	PCSK2	-0.457	-	2.67E-03	1.84E-02
206474_PM_at	PCTAIRE protein kinase 2	4345	PCTK2	-1.570	-	4.10E-03	2.78E-02
1558680_PM_s_at	phosphodiesterase 1A, calmodulin-dependent	8727	PDE1A	-1.700	-	2.90E-03	1.87E-02
233547_PM_x_at	phosphodiesterase 1A, calmodulin-dependent	23033	PDE1A	-0.467	-	3.52E-03	1.92E-02
242789_PM_at	phosphodiesterase 1A, calmodulin-dependent	---	PDE1A	-1.135	-	4.03E-02	4.84E-02
214130_PM_s_at	phosphodiesterase 4D interacting protein	4915	PDE4DIP	-0.818	-	6.85E-04	3.28E-03
213228_PM_at	phosphodiesterase 8B	6751	PDE8B	-1.077	-	2.46E-04	1.34E-03
213724_PM_s_at	pyruvate dehydrogenase kinase, isozyme 2	26036	PDK2	-1.621	-	7.38E-03	1.12E-02
221957_PM_at	pyruvate dehydrogenase kinase, isozyme 3	220988	PDK3	-0.620	-	1.29E-02	3.53E-04
205960_PM_at	pyruvate dehydrogenase kinase, isozyme 4	3030	PDK4	-0.465	-	2.28E-02	1.15E-02

218273_PM_s_at	pyruvate 221eparin221ing221e phosphatase catalytic subunit 1	9185	PDP1	-1.534	-	6.42E-04	4.32E-03
32029_PM_at	3-phosphoinositide dependent protein kinase-1	---	PDPK1	-0.407	-	3.34E-02	2.46E-02
230068_PM_s_at	Paternally expressed 3	57683	PEG3	-0.912	-	3.21E-02	3.04E-02
222910_PM_s_at	peroxisomal biogenesis factor 5-like	57003	PEX5L	-1.047	-	2.49E-03	1.12E-02
201102_PM_s_at	phosphofructokinase, liver	1634	PFKL	-0.485	-	3.70E-02	1.78E-02
201118_PM_at	phosphogluconate dehydrogenase	347733 /// 7280	PGD	-0.398	-	3.48E-02	2.31E-02
229553_PM_at	phosphoglucomutase 2-like 1	7110	PGM2L1	-0.533	-	2.21E-02	2.00E-02
213638_PM_at	phosphatase and actin regulator 1	9444	PHACTR1	-1.010	-	2.16E-03	8.78E-03
244774_PM_at	phosphatase and actin regulator 2	10480	PHACTR2	-1.088	-	4.26E-02	2.11E-02
202928_PM_s_at	PHD finger protein 1	283234	PHF1	-1.192	-	3.90E-02	4.81E-02
210417_PM_s_at	phosphatidylinositol 4-kinase, catalytic, beta	29091	PI4KB	-1.880	-	2.20E-02	4.08E-02
215832_PM_x_at	phosphatidylinositol binding clathrin assembly protein	79081	PICALM	-1.525	-	1.63E-02	4.71E-02
223470_PM_at	phosphatidylinositol glycan anchor biosynthesis, class M	55236	PIGM	-0.728	-	6.01E-03	3.23E-03
1569022_PM_a_at	phosphoinositide-3-kinase, class 2, alpha polypeptide	3909	PIK3C2A	-0.408	-	1.56E-02	4.97E-02
217620_PM_s_at	phosphoinositide-3-kinase, catalytic, beta polypeptide	119504	PIK3CB	-0.473	-	8.13E-04	5.07E-03
209018_PM_s_at	PTEN induced putative kinase 1	79677	PINK1	-1.148	-	1.33E-02	3.67E-02
205570_PM_at	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	25780	PIP4K2A	-1.380	-	5.37E-03	2.91E-02
1568949_PM_at	phosphatidylinositol transfer protein, cytoplasmic 1	4281	PITPNC1	-1.152	-	1.78E-03	4.23E-03
238649_PM_at	phosphatidylinositol transfer protein, cytoplasmic 1	8828	PITPNC1	-0.396	-	2.99E-02	2.20E-02
1552923_PM_a_at	phosphatidylinositol transfer protein, membrane-associated 2	1727	PITPNM2	-0.971	-	1.05E-02	3.78E-02
201927_PM_s_at	plakophilin 4	9659	PKP4	-1.762	-	2.03E-02	4.67E-02
211925_PM_s_at	phospholipase C, beta 1 (phosphoinositide-specific)	8629	PLCB1	-1.864	-	3.41E-04	5.66E-03
215687_PM_x_at	phospholipase C, beta 1 (phosphoinositide-specific)	57105	PLCB1	-1.699	-	2.64E-03	8.65E-03
201050_PM_at	phospholipase D family, member 3	10492	PLD3	-2.264	-	1.86E-02	2.97E-02
201373_PM_at	plectin 1, intermediate filament binding protein 500kDa	8165	PLEC1	-0.417	-	1.88E-02	2.11E-02
219024_PM_at	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	253827	PLEKHA1	-0.861	-	8.86E-05	1.13E-03
217677_PM_at	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2	56990	PLEKHA2	-0.901	-	2.54E-03	1.23E-03

1558407_PM_at	pleckstrin homology domain containing, family G (with RhoGef domain) member 2	3093	PLEKHG2	-0.280	-	1.41E-02	1.53E-02
215807_PM_s_at	plexin B1	9236	PLXNB1	-2.211	-	1.65E-02	3.79E-02
179_PM_at	postmeiotic segregation increased 2-like 11 pseudogene	8732	PMS2L11	-0.310	-	1.80E-02	1.96E-02
222406_PM_s_at	proline-rich nuclear receptor coactivator 2	23131	PNRC2	-0.473	-	2.21E-03	3.63E-03
215357_PM_s_at	polymerase (DNA-directed), delta interacting protein 3	56935	POLDIP3	-1.176	-	4.74E-03	7.01E-03
212178_PM_s_at	POM121 membrane glycoprotein (rat) /// POM121 membrane glycoprotein C	55854	POM121 /// POM121C	-0.771	-	2.42E-02	1.86E-02
233638_PM_s_at	protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase	1024	POMGNT1	-0.713	-	5.32E-03	2.80E-02
208928_PM_at	P450 (cytochrome) oxidoreductase	8409	POR	-0.434	-	2.35E-02	2.06E-02
219483_PM_s_at	porcupine homolog (Drosophila)	3597	PORCN	-0.898	-	1.92E-02	2.94E-02
206789_PM_s_at	POU class 2 homeobox 1	5921	POU2F1	-0.994	-	1.43E-03	6.60E-04
208345_PM_s_at	POU class 3 homeobox 1	6375 /// 6846	POU3F1	-0.786	-	3.09E-02	4.25E-02
207084_PM_at	POU class 3 homeobox 2	3597	POU3F2	-0.389	-	1.47E-02	2.43E-02
208563_PM_x_at	POU class 3 homeobox 3	2558	POU3F3	-0.457	-	9.77E-03	3.63E-02
212226_PM_s_at	phosphatidic acid phosphatase type 2B	11231	PPAP2B	-1.563	-	1.91E-03	8.56E-04
209355_PM_s_at	phosphatidic acid phosphatase type 2B	54800	PPAP2B	-2.898	-	3.02E-03	4.37E-03
210235_PM_s_at	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1	51088	PPFIA1	-0.566	-	3.46E-02	4.97E-02
208993_PM_s_at	peptidylprolyl isomerase G (cyclophilin G)	51651	PPIG	-1.261	-	7.44E-03	9.79E-03
201703_PM_s_at	protein phosphatase 1, regulatory (inhibitor) subunit 10	667	PPP1R10	-0.299	-	1.62E-02	3.31E-02
201602_PM_s_at	protein phosphatase 1, regulatory (inhibitor) subunit 12A	23163	PPP1R12A	-0.783	-	4.38E-02	2.97E-02
205478_PM_at	protein phosphatase 1, regulatory (inhibitor) subunit 1A	1428	PPP1R1A	-0.493	-	2.32E-02	1.40E-02
231966_PM_at	protein phosphatase 1, regulatory (inhibitor) subunit 9A	65986	PPP1R9A	-0.359	-	1.42E-02	1.18E-02
200695_PM_at	protein phosphatase 2 (formerly 2A), regulatory subunit A, alpha isoform	51603	PPP2R1A	-3.202	-	3.45E-02	4.85E-02
223574_PM_x_at	protein phosphatase 2 (formerly 2A), regulatory subunit B, gamma isoform	54665	PPP2R2C	-1.111	-	1.51E-02	7.07E-03
211159_PM_s_at	protein phosphatase 2, regulatory subunit B’, delta isoform	54716	PPP2R5D	-0.945	-	1.54E-03	9.00E-03
202513_PM_s_at	protein phosphatase 2, regulatory subunit B’, delta isoform	29789	PPP2R5D	-0.352	-	3.13E-03	1.94E-02
229322_PM_at	protein phosphatase 2, regulatory subunit B’, epsilon isoform	57482	PPP2R5E	-0.788	-	4.91E-03	9.74E-03
220673_PM_s_at	protein phosphatase 4, regulatory subunit 4	9781	PPP4R4	-1.682	-	4.15E-03	9.58E-03

201979_PM_s_at	protein phosphatase 5, catalytic subunit	118	PPP5C	-1.100	-	3.75E-02	4.03E-02
212527_PM_at	PPPDE peptidase domain containing 2	54726	PPPDE2	-0.390	-	7.79E-03	3.22E-02
203056_PM_s_at	PR domain containing 2, with ZNF domain	284361	PRDM2	-0.762	-	3.94E-03	2.51E-04
212216_PM_at	prolyl endopeptidase-like	567	PREPL	-1.432	-	1.43E-02	3.57E-02
224909_PM_s_at	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1	3920	PREX1	-0.824	-	3.32E-03	6.70E-03
218292_PM_s_at	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	85315	PRKAG2	-1.185	-	1.86E-02	3.66E-02
200604_PM_s_at	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	50855	PRKAR1A	-1.706	-	2.14E-03	2.03E-02
206270_PM_at	protein kinase C, gamma	10548	PRKCG	-1.060	-	8.84E-03	1.80E-02
215707_PM_s_at	prion protein	81609	PRNP	-2.902	-	2.05E-02	4.19E-02
228656_PM_at	prospero homeobox 1	51312	PROX1	-0.521	-	1.56E-02	1.97E-02
209162_PM_s_at	PRP4 pre-mRNA processing factor 4 homolog (yeast)	51104	PRPF4	-0.348	-	7.07E-03	5.25E-03
214941_PM_s_at	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	51696	PRPF40A	-1.318	-	2.18E-03	1.21E-02
213729_PM_at	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	114882	PRPF40A	-1.341	-	1.12E-02	2.39E-02
231739_PM_at	proline-rich transmembrane protein 1	64866	PRRT1	-2.274	-	1.13E-02	3.18E-02
209599_PM_s_at	prune homolog (Drosophila)	29089	PRUNE	-0.429	-	1.39E-02	4.56E-02
212806_PM_at	prune homolog 2 (Drosophila)	22881	PRUNE2	-0.271	-	3.20E-02	1.91E-02
200871_PM_s_at	prosaposin	4205	PSAP	-0.291	-	2.87E-02	1.17E-02
220892_PM_s_at	phosphoserine aminotransferase 1	6018	PSAT1	-2.880	-	2.54E-02	4.69E-02
228204_PM_at	Proteasome (prosome, macropain) subunit, beta type, 4	5611	PSMB4	-1.399	-	3.36E-02	3.43E-02
201198_PM_s_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	6002	PSMD1	-1.498	-	2.12E-02	4.18E-02
222611_PM_s_at	paraspeckle component 1	9881	PSPC1	-1.037	-	6.19E-03	2.75E-02
1554614_PM_a_at	polypyrimidine tract binding protein 2	10956	PTBP2	-0.785	-	3.53E-03	2.21E-02
204054_PM_at	phosphatase and tensin homolog	5878	PTEN	-0.703	-	1.26E-02	2.72E-02
216988_PM_s_at	protein tyrosine phosphatase type IVA, member 2	64801	PTP4A2	-0.987	-	1.23E-02	3.42E-02
208616_PM_s_at	protein tyrosine phosphatase type IVA, member 2	1528	PTP4A2	-0.294	-	2.72E-02	4.75E-02
238841_PM_at	protein tyrosine phosphatase domain containing 1	---	PTPDC1	-0.789	-	1.30E-02	1.25E-02
222404_PM_x_at	protein tyrosine phosphatase-like A domain containing 1	64795	PTPLAD1	-1.786	-	4.37E-03	5.76E-03

234000_PM_s_at	protein tyrosine phosphatase-like A domain containing 1	---	PTPLAD1	-1.885	-	8.01E-03	1.23E-02
227741_PM_at	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	57616	PTPLB	-0.404	-	4.78E-03	1.00E-02
209895_PM_at	protein tyrosine phosphatase, non-receptor type 11	54331	PTPN11	-0.764	-	2.38E-03	3.89E-03
209896_PM_s_at	protein tyrosine phosphatase, non-receptor type 11	93185	PTPN11	-0.854	-	4.95E-03	9.81E-03
205868_PM_s_at	protein tyrosine phosphatase, non-receptor type 11	3055	PTPN11	-0.558	-	1.48E-02	1.85E-02
216915_PM_s_at	protein tyrosine phosphatase, non-receptor type 12	170506	PTPN12	-0.343	-	3.03E-02	3.54E-02
233471_PM_at	protein tyrosine phosphatase, non-receptor type 5 (striatum-enriched)	2743	PTPN5	-1.440	-	6.96E-03	6.35E-03
213799_PM_s_at	protein tyrosine phosphatase, receptor type, A	23271	PTPRA	-1.516	-	1.72E-03	1.07E-02
205712_PM_at	protein tyrosine phosphatase, receptor type, D	25988	PTPRD	-0.552	-	1.49E-02	2.88E-02
203030_PM_s_at	protein tyrosine phosphatase, receptor type, N polypeptide 2	50801	PTPRN2	-1.257	-	8.19E-03	2.37E-02
211534_PM_x_at	protein tyrosine phosphatase, receptor type, N polypeptide 2	51663	PTPRN2	-0.597	-	3.08E-02	2.85E-02
210823_PM_s_at	protein tyrosine phosphatase, receptor type, S	284111	PTPRS	-0.735	-	2.08E-03	9.40E-03
1557938_PM_s_at	polymerase I and transcript release factor	6880	PTRF	-0.326	-	2.23E-02	8.86E-03
227718_PM_at	purine-rich element binding protein B	---	PURB	-1.586	-	3.95E-03	7.41E-04
235711_PM_at	purine-rich element binding protein B	---	PURB	-1.357	-	8.04E-03	1.15E-02
201606_PM_s_at	PWP1 homolog (S. cerevisiae)	51343	PWP1	-1.367	-	2.77E-02	4.70E-02
1552274_PM_at	PX domain containing serine/threonine kinase	54899	PXK	-0.585	-	2.14E-03	6.51E-03
205577_PM_at	phosphorylase, glycogen, muscle	2562	PYGM	-1.420	-	2.90E-02	4.50E-02
225370_PM_at	pygopus homolog 2 (Drosophila)	64147	PYGO2	-0.641	-	2.35E-02	1.88E-02
1555154_PM_a_at	quaking homolog, KH domain RNA binding (mouse)	309	QKI	-2.105	-	2.64E-03	1.73E-02
214543_PM_x_at	quaking homolog, KH domain RNA binding (mouse)	394	QKI	-2.044	-	5.81E-03	2.21E-02
204157_PM_s_at	serine/threonine-protein kinase QSK	10657	QSK	-0.596	-	4.27E-03	5.02E-03
34478_PM_at	RAB11B, member RAS oncogene family	---	RAB11B	-1.368	-	1.45E-02	8.62E-03
214999_PM_s_at	RAB11 family interacting protein 3 (class II)	51098	RAB11FIP3	-0.280	-	2.41E-02	3.19E-02
211503_PM_s_at	RAB14, member RAS oncogene family	2917	RAB14	-1.753	-	3.38E-03	5.50E-03
205461_PM_at	RAB35, member RAS oncogene family	4862	RAB35	-0.437	-	1.58E-02	2.86E-02
208466_PM_at	RAB3D, member RAS oncogene family	26168	RAB3D	-0.456	-	4.02E-03	8.84E-03
203582_PM_s_at	RAB4A, member RAS oncogene family	63827	RAB4A	-1.133	-	2.71E-02	4.64E-02

201156_PM_s_at	RAB5C, member RAS oncogene family	23291	RAB5C	-1.126	-	4.78E-02	2.85E-02
201048_PM_x_at	RAB6A, member RAS oncogene family	10735	RAB6A	-2.858	-	6.05E-03	2.12E-02
210127_PM_at	RAB6B, member RAS oncogene family	554282 /// 653820 /// 729533	RAB6B	-1.141	-	7.61E-03	5.65E-03
225259_PM_at	RAB6B, member RAS oncogene family	219736	RAB6B	-0.356	-	2.18E-02	6.56E-03
214552_PM_s_at	rabaptin, RAB GTPase binding effector protein 1	56993	RABEP1	-0.757	-	1.01E-02	3.89E-02
1567458_PM_s_at	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	9232	RAC1	-0.565	-	7.06E-03	4.30E-02
208641_PM_s_at	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	4651	RAC1	-1.036	-	1.85E-02	3.48E-02
200607_PM_s_at	RAD21 homolog (S. pombe)	23552	RAD21	-2.972	-	4.60E-03	1.84E-02
201039_PM_s_at	RAD23 homolog A (S. cerevisiae)	6774	RAD23A	-0.823	-	3.74E-02	4.36E-02
214435_PM_x_at	v-ral simian leukemia viral oncogene homolog A (ras related)	58190	RALA	-1.299	-	4.06E-04	3.13E-03
202844_PM_s_at	ralA binding protein 1	25912	RALBP1	-1.098	-	4.39E-03	8.45E-03
201711_PM_x_at	RAN binding protein 2	23063	RANBP2	-1.174	-	8.08E-04	8.03E-03
1553535_PM_a_at	Ran GTPase activating protein 1	23157	RANGAP1	-1.736	-	1.58E-02	2.59E-02
212125_PM_at	Ran GTPase activating protein 1	10625	RANGAP1	-0.534	-	5.00E-02	2.36E-02
221830_PM_at	RAP2A, member of RAS oncogene family	64087	RAP2A	-2.074	-	9.36E-04	1.01E-02
214487_PM_s_at	RAP2A, member of RAS oncogene family /// RAP2B, member of RAS oncogene family	60313	RAP2A /// RAP2B	-0.925	-	4.79E-03	2.27E-02
204680_PM_s_at	Rap guanine nucleotide exchange factor (GEF) 5	6433	RAPGEF5	-1.335	-	4.23E-04	4.12E-04
208530_PM_s_at	retinoic acid receptor, beta	154661	RARB	-0.531	-	1.69E-03	4.88E-03
232902_PM_s_at	arginyl-tRNA synthetase 2, mitochondrial	728485	RARS2	-0.389	-	1.50E-03	3.99E-03
233144_PM_s_at	RAS protein activator like 1 (GAP1 like)	3480	RASAL1	-0.882	-	2.14E-02	2.49E-02
234343_PM_s_at	RAS protein activator like 2	---	RASAL2	-1.403	-	6.96E-03	1.05E-02
222810_PM_s_at	RAS protein activator like 2	100272147	RASAL2	-1.110	-	2.24E-02	3.18E-02
1554834_PM_a_at	Ras association (RalGDS/AF-6) domain family member 5	10528	RASSF5	-0.419	-	9.44E-03	3.78E-02
212332_PM_at	retinoblastoma-like 2 (p130)	3423	RBL2	-0.727	-	5.39E-03	2.48E-02
225751_PM_at	RNA binding motif protein 17	124923	RBM17	-1.735	-	1.07E-03	2.70E-03
1557081_PM_at	RNA binding motif protein 25	5327	RBM25	-0.836	-	1.26E-02	1.41E-02

212028_PM_at	RNA binding motif protein 25	8766	RBM25	-0.621	-	2.41E-02	4.32E-03
212030_PM_at	RNA binding motif protein 25	6745	RBM25	-0.285	-	3.42E-02	3.06E-02
205740_PM_s_at	RNA binding motif protein 42	8545	RBM42	-0.570	-	2.65E-02	1.93E-02
209936_PM_at	RNA binding motif protein 5	94056	RBM5	-1.319	-	1.68E-03	5.01E-03
212104_PM_s_at	RNA binding motif protein 9	1488	RBM9	-1.499	-	7.43E-03	1.71E-03
213901_PM_x_at	RNA binding motif protein 9	23299	RBM9	-3.091	-	1.09E-02	1.37E-02
225265_PM_at	RNA binding motif, single stranded interacting protein 1	728855	RBMS1	-0.737	-	1.88E-02	4.20E-02
1556336_PM_at	similar to RNA binding motif protein, X-linked /// hypothetical protein LOC100291994 /// RNA binding motif protein, X-linked /// RNA binding motif protein, X-linked-like 1	8539	RBMXL1	-0.345	-	3.42E-02	7.81E-03
230134_PM_s_at	ring finger and CCCH-type zinc finger domains 2	56704	RC3H2	-0.489	-	1.41E-03	4.83E-03
230133_PM_at	ring finger and CCCH-type zinc finger domains 2	55266	RC3H2	-0.290	-	7.61E-03	6.62E-03
220202_PM_s_at	ring finger and CCCH-type zinc finger domains 2	9896	RC3H2	-1.426	-	8.86E-03	1.19E-02
215253_PM_s_at	regulator of calcineurin 1	79659	RCAN1	-2.280	-	1.15E-02	2.92E-02
212398_PM_at	radixin	2634	RDX	-0.616	-	3.04E-02	2.21E-02
208872_PM_s_at	receptor accessory protein 5	27244	REEP5	-0.912	-	1.59E-02	3.55E-02
1566472_PM_s_at	retinol saturase (all-trans-retinol 13,14-reductase)	51362	RETSAT	-1.137	-	4.04E-03	9.22E-03
1552651_PM_a_at	ring finger and FYVE-like domain containing 1	10771	RFFL	-0.320	-	9.62E-03	6.78E-03
226786_PM_at	regulatory factor X, 1 (influences HLA class II expression)	23158	RFX1	-0.449	-	1.04E-02	2.26E-02
208492_PM_at	regulatory factor X-associated protein	23254	RFXAP	-0.385	-	7.31E-04	1.07E-02
209637_PM_s_at	regulator of G-protein signaling 12	22931	RGS12	-0.630	-	1.46E-02	4.02E-02
211021_PM_s_at	regulator of G-protein signaling 14	54556	RGS14	-1.008	-	1.03E-02	1.08E-02
232053_PM_x_at	rhomboid domain containing 2	6117	RHBDD2	-3.103	-	3.21E-02	4.57E-02
1553962_PM_s_at	ras homolog gene family, member B	7559	RHOB	-2.894	-	1.62E-03	1.05E-02
240111_PM_at	Rho-related BTB domain containing 3	645323	RHOBTB3	-0.450	-	7.80E-04	3.07E-03
216048_PM_s_at	Rho-related BTB domain containing 3	9236	RHOBTB3	-1.915	-	4.59E-03	1.46E-02
202975_PM_s_at	Rho-related BTB domain containing 3	83877	RHOBTB3	-2.064	-	1.28E-02	3.71E-02
221789_PM_x_at	ras homolog gene family, member T2	4664	RHOT2	-0.433	-	4.62E-03	1.16E-02
210791_PM_s_at	Rho GTPase-activating protein	57628	RICS	-1.010	-	5.64E-03	1.46E-03

228248_PM_at	RPTOR independent companion of MTOR, complex 2	2957	RICTOR	-0.800	-	1.89E-02	4.00E-02
216184_PM_s_at	regulating synaptic membrane exocytosis 1	5519	RIMS1	-2.338	-	2.54E-03	1.18E-02
212479_PM_s_at	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	6310	RMND5A	-0.596	-	4.43E-03	1.86E-03
212478_PM_at	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	6310	RMND5A	-0.297	-	4.81E-02	1.16E-02
205748_PM_s_at	ring finger protein 126	2549	RNF126	-1.274	-	2.77E-02	3.82E-02
219104_PM_at	ring finger protein 141	374786	RNF141	-1.285	-	8.20E-03	2.20E-02
1569080_PM_at	ring finger protein 165	6925	RNF165	-0.432	-	3.42E-02	8.66E-03
234461_PM_at	ring finger protein 215	---	RNF215	-0.756	-	7.26E-03	2.10E-02
210706_PM_s_at	ring finger protein 24	10806	RNF24	-0.571	-	2.81E-02	8.64E-03
224338_PM_s_at	ring finger protein 26	84992	RNF26	-0.319	-	1.53E-02	2.80E-02
222660_PM_s_at	ring finger protein 38	8674	RNF38	-1.183	-	4.13E-03	2.01E-02
201961_PM_s_at	ring finger protein 41	5063	RNF41	-0.849	-	5.93E-03	5.48E-03
204207_PM_s_at	RNA guanylyltransferase and 5’-phosphatase	4659	RNGTT	-0.500	-	7.98E-03	7.13E-03
226975_PM_at	RNA-binding region (RNP1, RRM) containing 3	23329	RNPC3	-1.528	-	4.17E-03	3.99E-03
211504_PM_x_at	Rho-associated, coiled-coil containing protein kinase 2	57584	ROCK2	-1.044	-	1.05E-03	5.70E-03
215138_PM_s_at	kazrin	51182	RP1-21O18.1	-0.544	-	5.46E-04	6.57E-03
213478_PM_at	kazrin	4116	RP1-21O18.1	-0.767	-	2.82E-03	2.50E-03
204245_PM_s_at	ribonuclease P/MRP 14kDa subunit	1182	RPP14	-2.049	-	3.28E-03	7.39E-03
1555202_PM_a_at	regulation of nuclear pre-mRNA domain containing 1A	10155	RPRD1A	-1.528	-	1.49E-03	5.93E-03
204906_PM_at	ribosomal protein S6 kinase, 90kDa, polypeptide 2	6416	RPS6KA2	-0.453	-	2.00E-02	4.97E-02
204633_PM_s_at	ribosomal protein S6 kinase, 90kDa, polypeptide 5	8498	RPS6KA5	-0.706	-	3.33E-04	4.06E-04
201476_PM_s_at	ribonucleotide reductase M1	4771	RRM1	-1.350	-	1.30E-02	3.37E-02
222540_PM_s_at	remodeling and spacing factor 1	23507	RSF1	-1.368	-	1.09E-02	3.01E-02
219507_PM_at	arginine/serine-rich coiled-coil 1	1956	RSRC1	-1.335	-	2.88E-02	4.36E-02
210251_PM_s_at	RUN and FYVE domain containing 3	961	RUFY3	-1.072	-	7.02E-03	1.21E-02
215321_PM_at	RUN domain containing 3B	55070	RUNDC3B	-0.524	-	1.53E-02	6.40E-03
205528_PM_s_at	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	51760	RUNX1T1	-0.498	-	4.63E-02	1.74E-02

215099_PM_s_at	retinoid X receptor, beta	80206	RXRB	-0.596	-	1.82E-04	2.54E-03
201846_PM_s_at	RING1 and YY1 binding protein	4141	RYBP	-1.428	-	1.59E-03	1.60E-03
233001_PM_at	sterile alpha motif domain containing 10	4678	SAMD10	-0.276	-	2.02E-03	8.14E-04
210790_PM_s_at	SAR1 homolog A (S. cerevisiae)	64147	SAR1A	-1.880	-	1.91E-03	1.03E-02
201543_PM_s_at	SAR1 homolog A (S. cerevisiae)	491	SAR1A	-0.702	-	4.22E-03	2.34E-02
209127_PM_s_at	squamous cell carcinoma antigen recognized by T cells 3	81545	SART3	-0.887	-	2.21E-03	1.09E-02
1552978_PM_a_at	secretory carrier membrane protein 1	58155	SCAMP1	-1.563	-	2.44E-04	7.44E-03
206667_PM_s_at	secretory carrier membrane protein 1	8774	SCAMP1	-2.310	-	9.97E-04	1.45E-02
206668_PM_s_at	secretory carrier membrane protein 1	6877	SCAMP1	-0.346	-	2.14E-03	2.46E-03
212417_PM_at	secretory carrier membrane protein 1	11329	SCAMP1	-1.457	-	8.64E-03	2.87E-02
235073_PM_at	secretory carrier membrane protein 4	---	SCAMP4	-0.552	-	4.48E-03	3.29E-02
223842_PM_s_at	scavenger receptor class A, member 3	10194	SCARA3	-0.975	-	8.39E-04	6.82E-03
201647_PM_s_at	scavenger receptor class B, member 2	1457 /// 283106	SCARB2	-0.647	-	1.11E-02	1.26E-02
211708_PM_s_at	stearoyl-CoA desaturase (delta-9-desaturase)	55322	SCD	-0.495	-	6.46E-03	2.47E-02
200831_PM_s_at	stearoyl-CoA desaturase (delta-9-desaturase)	10605	SCD	-1.765	-	8.16E-03	2.02E-02
224018_PM_s_at	stearoyl-CoA desaturase 5	6860	SCD5	-3.371	-	5.24E-05	9.19E-04
206381_PM_at	sodium channel, voltage-gated, type II, alpha subunit	4094	SCN2A	-1.573	-	3.88E-03	2.36E-02
210363_PM_s_at	sodium channel, voltage-gated, type II, beta	257415	SCN2B	-1.836	-	5.84E-03	3.62E-03
207049_PM_at	sodium channel, voltage gated, type VIII, alpha subunit	2319	SCN8A	-2.313	-	1.86E-02	3.87E-02
228761_PM_at	scratch homolog 1, zinc finger protein (Drosophila)	---	SCRT1	-1.172	-	5.91E-03	2.49E-02
221026_PM_s_at	scratch homolog 1, zinc finger protein (Drosophila)	23047	SCRT1	-0.309	-	6.07E-03	3.20E-02
221220_PM_s_at	SCY1-like 2 (S. cerevisiae)	27245	SCYL2	-0.924	-	1.06E-02	4.52E-02
228408_PM_s_at	SDA1 domain containing 1	23261	SDAD1	-1.583	-	1.32E-02	1.15E-02
212154_PM_at	syndecan 2	7072	SDC2	-0.750	-	1.68E-02	2.78E-02
1554864_PM_a_at	syndecan 3	5710	SDC3	-0.340	-	3.37E-02	1.75E-02
1557950_PM_at	serologically defined colon cancer antigen 1	50999	SDCCAG1	-1.652	-	4.10E-04	2.05E-03
1569594_PM_a_at	serologically defined colon cancer antigen 1	2011	SDCCAG1	-1.198	-	1.16E-02	9.90E-03
221972_PM_s_at	stromal cell derived factor 4	147179	SDF4	-1.247	-	4.40E-03	1.76E-02
202082_PM_s_at	SEC14-like 1 (S. cerevisiae)	23256	SEC14L1	-0.832	-	6.70E-03	5.36E-03

224470_PM_at	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	9644	SEC22C	-0.344	-	2.18E-02	3.99E-02
204344_PM_s_at	Sec23 homolog A (S. cerevisiae)	2108	SEC23A	-1.303	-	2.14E-02	4.85E-02
244841_PM_at	SEC24 family, member A (S. cerevisiae)	254251	SEC24A	-0.409	-	3.72E-03	4.42E-04
222385_PM_x_at	Sec61 alpha 1 subunit (S. cerevisiae)	11017	SEC61A1	-0.746	-	3.24E-04	3.34E-03
201914_PM_s_at	SEC63 homolog (S. cerevisiae)	2677	SEC63	-1.199	-	6.73E-03	1.64E-02
224250_PM_s_at	SECIS binding protein 2	84302	SECISBP2	-1.528	-	1.90E-03	7.22E-04
212451_PM_at	SECIS binding protein 2-like	9025	SECISBP2L	-0.659	-	4.97E-03	1.01E-02
205405_PM_at	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain I and short cytoplasmic domain, (229eparin229ing) 5A	535	SEMA5A	-0.527	-	3.16E-02	1.05E-02
233801_PM_s_at	sema domain, transmembrane domain I, and cytoplasmic domain, (229eparin229ing) 6D	58517	SEMA6D	-0.564	-	2.59E-03	9.95E-03
233882_PM_s_at	sema domain, transmembrane domain I, and cytoplasmic domain, (229eparin229ing) 6D	---	SEMA6D	-1.421	-	1.90E-02	4.28E-02
218122_PM_s_at	SUMO1/sentrin/SMT3 specific peptidase 2	348180	SENP2	-1.978	-	1.48E-02	3.67E-02
215113_PM_s_at	SUMO1/sentrin/SMT3 specific peptidase 3	50862	SENP3	-0.877	-	2.20E-02	4.11E-02
209669_PM_s_at	SERPINE1 mRNA binding protein 1	84253	SERBP1	-0.741	-	6.04E-03	1.08E-02
211769_PM_x_at	serine incorporator 3	9690	SERINC3	-1.515	-	2.70E-02	2.54E-02
221473_PM_x_at	serine incorporator 3	8846	SERINC3	-1.147	-	3.16E-02	2.45E-02
226763_PM_at	SEC14 and spectrin domains 1	4128	SESTD1	-0.545	-	2.31E-02	2.86E-02
200630_PM_x_at	SET nuclear oncogene	862	SET	-0.455	-	3.09E-02	8.04E-03
1569106_PM_s_at	SET domain containing 5	6636	SETD5	-0.823	-	6.67E-03	1.17E-02
225094_PM_at	SET domain containing (lysine methyltransferase) 8	9852	SETD8	-0.393	-	6.38E-03	2.59E-02
220200_PM_s_at	SET domain containing (lysine methyltransferase) 8	8161	SETD8	-0.398	-	8.00E-03	3.92E-02
232229_PM_at	senataxin	65998	SETX	-0.382	-	2.80E-04	3.93E-03
233337_PM_s_at	seizure related 6 homolog (mouse)-like 2	171023	SEZ6L2	-2.576	-	2.80E-02	4.59E-02
214305_PM_s_at	splicing factor 3b, subunit 1, 155kDa	27292	SF3B1	-1.385	-	4.73E-04	7.59E-03
201070_PM_x_at	splicing factor 3b, subunit 1, 155kDa	23479	SF3B1	-0.969	-	1.77E-03	1.05E-02
237746_PM_at	Splicing factor, arginine/serine-rich 11	---	SFRS11	-0.331	-	2.05E-02	3.47E-02
212177_PM_at	splicing factor, arginine/serine-rich 18	55854	SFRS18	-1.342	-	7.38E-03	1.32E-02
225507_PM_at	splicing factor, arginine/serine-rich 18	1105	SFRS18	-1.177	-	9.42E-03	4.35E-03

209376_PM_x_at	splicing factor, arginine/serine-rich 2, interacting protein	55737	SFRS2IP	-0.767	-	4.20E-02	6.23E-03
239512_PM_at	splicing factor, arginine/serine-rich 4	---	SFRS4	-1.056	-	1.61E-02	1.89E-02
210077_PM_s_at	splicing factor, arginine/serine-rich 5	49854	SFRS5	-0.353	-	6.43E-03	4.32E-02
202774_PM_s_at	splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot homolog, Drosophila)	51111	SFRS8	-1.009	-	2.29E-03	2.02E-03
205120_PM_s_at	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)	10210	SGCB	-1.031	-	7.10E-03	3.63E-02
215519_PM_x_at	small G protein signaling modulator 3	58516	SGSM3	-0.394	-	1.31E-02	1.99E-02
209322_PM_s_at	SH2B adaptor protein 1	54934	SH2B1	-0.324	-	2.57E-02	4.42E-02
205367_PM_at	SH2B adaptor protein 2	6196	SH2B2	-0.368	-	4.80E-02	3.76E-02
1552667_PM_a_at	SH2 domain containing 3C	8672	SH2D3C	-0.391	-	4.77E-03	1.27E-02
1558647_PM_at	SH3 domain containing 19	2965	SH3D19	-0.309	-	1.51E-03	1.31E-02
218813_PM_s_at	SH3-domain GRB2-like endophilin B2	55435	SH3GLB2	-1.892	-	2.59E-02	3.91E-02
1554168_PM_a_at	SH3-domain kinase binding protein 1	6152	SH3KBP1	-0.360	-	3.32E-02	4.23E-02
225590_PM_at	SH3 domain containing ring finger 1	129450	SH3RF1	-0.776	-	3.81E-02	2.58E-02
223744_PM_s_at	sialic acid acetylesterase	84247	SIAE	-1.276	-	1.37E-02	4.06E-02
221705_PM_s_at	suppressor of IKBKE 1	4673	SIKE1	-0.308	-	5.61E-03	4.39E-02
202255_PM_s_at	signal-induced proliferation-associated 1 like 1	6595	SIPA1L1	-1.054	-	1.45E-02	1.89E-02
217024_PM_x_at	signal-regulatory protein alpha	83607	SIRPA	-1.823	-	1.30E-04	2.10E-03
202896_PM_s_at	signal-regulatory protein alpha	51256	SIRPA	-0.896	-	9.11E-03	2.32E-02
200719_PM_at	S-phase kinase-associated protein 1	23266	SKP1	-0.367	-	4.05E-02	3.11E-02
224854_PM_s_at	SLAIN motif family, member 2	114294	SLAIN2	-0.353	-	2.03E-03	4.52E-03
224853_PM_at	SLAIN motif family, member 2	133746	SLAIN2	-0.634	-	5.56E-03	3.43E-03
203125_PM_x_at	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	124540	SLC11A2	-0.923	-	9.24E-03	3.19E-02
223994_PM_s_at	solute carrier family 12 (potassium/chloride transporters), member 9	57002	SLC12A9	-0.417	-	5.46E-03	2.34E-02
204230_PM_s_at	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	9231	SLC17A7	-2.832	-	2.52E-02	3.59E-02
206396_PM_at	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	9181	SLC1A1	-1.472	-	2.70E-02	4.18E-02

208389_PM_s_at	solute carrier family 1 (glial high affinity glutamate transporter), member 2	54470 /// 653354	SLC1A2	-2.050	-	4.19E-04	1.88E-03
1558010_PM_s_at	solute carrier family 1 (glial high affinity glutamate transporter), member 2	10480	SLC1A2	-2.541	-	1.41E-02	3.61E-02
1558009_PM_at	solute carrier family 1 (glial high affinity glutamate transporter), member 2	1398	SLC1A2	-3.328	-	1.70E-02	3.66E-02
209611_PM_s_at	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	83940	SLC1A4	-0.763	-	1.66E-02	2.97E-02
201917_PM_s_at	solute carrier family 25, member 36	5756	SLC25A36	-1.071	-	5.99E-03	6.90E-03
218136_PM_s_at	solute carrier family 25, member 37	2686	SLC25A37	-0.288	-	3.89E-03	8.82E-03
205716_PM_at	solute carrier family 25, member 40	10693	SLC25A40	-0.422	-	8.78E-03	2.45E-02
225881_PM_at	solute carrier family 35, member B4	147670	SLC35B4	-0.443	-	1.13E-02	3.05E-02
209711_PM_at	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	63941	SLC35D1	-0.278	-	2.59E-02	4.63E-02
218237_PM_s_at	solute carrier family 38, member 1	145173	SLC38A1	-0.467	-	1.38E-03	1.57E-02
202089_PM_s_at	solute carrier family 39 (zinc transporter), member 6	2044	SLC39A6	-0.446	-	3.03E-03	2.09E-02
219175_PM_s_at	solute carrier family 41, member 3	3927	SLC41A3	-0.341	-	4.41E-03	2.57E-02
211494_PM_s_at	solute carrier family 4, sodium bicarbonate cotransporter, member 4	79582	SLC4A4	-0.813	-	5.74E-04	9.42E-03
210739_PM_x_at	solute carrier family 4, sodium bicarbonate cotransporter, member 4	285331	SLC4A4	-0.588	-	3.22E-02	4.98E-02
207604_PM_s_at	solute carrier family 4, sodium bicarbonate cotransporter, member 7	51574	SLC4A7	-0.813	-	3.57E-03	2.04E-02
210854_PM_x_at	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	1602	SLC6A8	-1.365	-	2.00E-03	3.73E-03
213843_PM_x_at	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	23276	SLC6A8	-1.277	-	4.83E-03	9.65E-03
205864_PM_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 4	4168	SLC7A4	-0.315	-	3.60E-03	2.42E-02
211557_PM_x_at	solute carrier organic anion transporter family, member 2B1	9230	SLCO2B1	-0.740	-	4.68E-03	1.54E-03
209897_PM_s_at	slit homolog 2 (Drosophila)	91272	SLIT2	-0.671	-	2.20E-02	1.14E-02
232636_PM_at	SLIT and NTRK-like family, member 4	22907	SLITRK4	-1.265	-	9.26E-04	3.68E-03

212257_PM_s_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	5927	SMARCA2	-1.489	-	6.98E-03	2.76E-02
212167_PM_s_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	1845	SMARCB1	-0.873	-	1.88E-02	2.87E-02
201073_PM_s_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	9733	SMARCC1	-0.437	-	1.51E-02	3.92E-03
209257_PM_s_at	structural maintenance of chromosomes 3	51742	SMC3	-1.534	-	1.81E-03	6.31E-03
220368_PM_s_at	SMEK homolog 1, suppressor of mek1 (Dictyostelium)	7764	SMEK1	-0.615	-	8.03E-03	4.34E-02
210057_PM_at	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)	51704	SMG1	-0.269	-	2.37E-04	7.28E-03
1555680_PM_a_at	spermine oxidase	10250	SMOX	-0.809	-	1.15E-02	3.53E-02
1556629_PM_a_at	Synaptosomal-associated protein, 25kDa	79022	SNAP25	-0.310	-	3.30E-02	3.38E-02
207853_PM_s_at	synuclein, beta	10592	SNCB	-2.315	-	2.90E-02	4.81E-02
218033_PM_s_at	stannin	1911	SNN	-0.958	-	7.34E-03	2.51E-02
1554986_PM_a_at	sorting nexin 19	7414	SNX19	-0.574	-	1.68E-03	1.61E-02
1569481_PM_s_at	sorting nexin 22	6880	SNX22	-0.279	-	1.14E-02	2.68E-02
221006_PM_s_at	sorting nexin family member 27	10610	SNX27	-1.343	-	1.70E-02	5.63E-03
201085_PM_s_at	SON DNA binding protein	9128	SON	-0.558	-	2.51E-02	2.54E-02
211819_PM_s_at	sorbin and SH3 domain containing 1	9557	SORBS1	-0.550	-	2.69E-02	1.69E-02
203509_PM_at	sortilin-related receptor, L(DLR class) A repeats-containing	8573	SORL1	-1.160	-	6.25E-03	4.17E-03
212797_PM_at	sortilin 1	29902	SORT1	-0.448	-	5.92E-03	3.87E-02
212807_PM_s_at	sortilin 1	9829	SORT1	-0.577	-	9.80E-03	2.80E-02
213721_PM_at	SRY (sex determining region Y)-box 2	29072	SOX2	-1.575	-	1.65E-03	1.07E-03
213722_PM_at	SRY (sex determining region Y)-box 2	10486	SOX2	-0.868	-	7.94E-03	2.75E-02
207336_PM_at	SRY (sex determining region Y)-box 5	51603	SOX5	-0.419	-	3.24E-02	2.86E-02
202935_PM_s_at	SRY (sex determining region Y)-box 9	57704	SOX9	-0.901	-	1.34E-02	6.62E-03
242668_PM_x_at	sperm associated antigen 4-like	---	SPAG4L	-0.346	-	1.37E-02	2.68E-02
222593_PM_s_at	spermatogenesis associated, serine-rich 2	9857	SPATS2	-0.274	-	2.97E-02	7.92E-03

201996_PM_s_at	spen homolog, transcriptional regulator (Drosophila)	23499	SPEN	-1.633	-	1.92E-02	1.84E-02
230884_PM_s_at	spastic paraplegia 7 (pure and complicated autosomal recessive)	286499	SPG7	-1.212	-	2.35E-03	7.00E-03
217813_PM_s_at	233eparin233i 1	55727	SPIN1	-0.759	-	4.41E-04	5.07E-03
202523_PM_s_at	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	29929	SPOCK2	-0.350	-	3.28E-03	1.61E-02
209437_PM_s_at	spondin 1, extracellular matrix protein	10072 /// 582	SPON1	-0.598	-	1.21E-02	8.96E-03
215833_PM_s_at	signal peptide peptidase-like 2B	57406	SPPL2B	-0.271	-	1.09E-02	1.83E-02
212466_PM_at	233epari-related, EVH1 domain containing 2	6302	SPRED2	-0.494	-	6.29E-05	3.37E-04
200671_PM_s_at	spectrin, beta, non-erythrocytic 1	311	SPTBN1	-1.079	-	9.27E-05	4.53E-03
200672_PM_x_at	spectrin, beta, non-erythrocytic 1	1740	SPTBN1	-2.869	-	2.71E-04	3.69E-03
201471_PM_s_at	sequestosome 1	9874	SQSTM1	-0.297	-	1.14E-02	2.08E-02
208095_PM_s_at	signal recognition particle 72kDa	5303	SRP72	-0.717	-	3.29E-02	4.26E-02
203181_PM_x_at	SFRS protein kinase 2	122704	SRPK2	-1.340	-	2.78E-03	2.35E-03
214931_PM_s_at	SFRS protein kinase 2	10827	SRPK2	-1.336	-	1.75E-02	4.80E-02
200917_PM_s_at	signal recognition particle receptor (docking protein)	7267	SRPR	-1.741	-	1.50E-04	2.46E-03
201224_PM_s_at	serine/arginine repetitive matrix 1	1646	SRRM1	-1.193	-	1.90E-03	8.08E-04
217051_PM_s_at	synovial sarcoma translocation, chromosome 18	84937	SS18	-0.275	-	2.03E-03	1.19E-03
209954_PM_x_at	synovial sarcoma translocation, chromosome 18	54751	SS18	-0.502	-	4.60E-02	4.47E-02
223635_PM_s_at	single stranded DNA binding protein 3	30061	SSBP3	-2.223	-	3.13E-02	4.52E-02
226712_PM_at	signal sequence receptor, alpha	23198	SSR1	-0.307	-	9.56E-03	8.20E-03
200889_PM_s_at	signal sequence receptor, alpha	1837	SSR1	-0.714	-	2.67E-02	4.58E-02
208482_PM_at	somatostatin receptor 1	11340	SSTR1	-0.302	-	2.67E-02	3.38E-02
1555702_PM_a_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	7296	ST3GAL3	-1.694	-	5.14E-03	2.60E-02
207983_PM_s_at	stromal antigen 2	898	STAG2	-1.552	-	3.18E-04	2.92E-03
209023_PM_s_at	stromal antigen 2	80025	STAG2	-0.831	-	3.95E-03	1.83E-02
208194_PM_s_at	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	22924	STAM2	-0.433	-	6.56E-03	5.02E-03
221610_PM_s_at	signal transducing adaptor family member 2	6939	STAP2	-0.278	-	2.12E-02	1.96E-02
208992_PM_s_at	signal transducer and activator of transcription 3 (acute-phase response factor)	55311	STAT3	-0.973	-	1.68E-02	2.42E-02
1553117_PM_a_at	serine/threonine kinase 38	6867	STK38	-0.432	-	2.63E-02	2.96E-02

218207_PM_s_at	stathmin-like 3	29945	STMN3	-2.750	-	3.00E-03	1.21E-02
234317_PM_s_at	storkhead box 2	283933	STOX2	-0.884	-	3.51E-02	4.77E-02
215505_PM_s_at	striatin, calmodulin binding protein 3	51334	STRN3	-1.466	-	2.17E-02	4.39E-02
221638_PM_s_at	syntaxin 16	3567	STX16	-0.886	-	1.94E-03	9.42E-03
1558249_PM_s_at	syntaxin 16	10579	STX16	-1.192	-	2.18E-03	7.69E-03
222708_PM_s_at	syntaxin 17	286527	STX17	-0.408	-	2.53E-02	1.09E-02
214441_PM_at	syntaxin 6	55207	STX6	-0.271	-	2.32E-02	3.14E-02
226462_PM_at	syntaxin binding protein 6 (amisyn)	7204	STXBP6	-0.479	-	6.40E-03	2.57E-02
233555_PM_s_at	sulfatase 2	23135	SULF2	-1.779	-	1.92E-02	2.50E-02
200739_PM_s_at	SMT3 suppressor of mif two 3 homolog 3 (S. cerevisiae)	9536	SUMO3	-0.820	-	2.57E-02	4.82E-02
233827_PM_s_at	suppressor of Ty 16 homolog (S. cerevisiae)	1915	SUPT16H	-1.567	-	1.18E-03	4.35E-03
213971_PM_s_at	suppressor of zeste 12 homolog (Drosophila) /// suppressor of zeste 12 homolog pseudogene	5861	SUZ12 /// SUZ12P	-0.396	-	7.97E-04	8.22E-03
225154_PM_at	synapse associated protein 1, SAP47 homolog (Drosophila)	54813	SYAP1	-1.114	-	2.46E-02	4.11E-02
1553264_PM_a_at	synapsin I	83593	SYN1	-2.803	-	1.70E-02	2.78E-02
210315_PM_at	synapsin II	284252	SYN2	-2.624	-	1.71E-02	3.07E-02
1553037_PM_a_at	synapsin II	23040	SYN2	-2.193	-	1.78E-02	1.65E-02
209024_PM_s_at	synaptotagmin binding, cytoplasmic RNA interacting protein	23411	SYNCRIP	-1.403	-	6.89E-03	1.66E-02
207594_PM_s_at	synaptojanin 1	9804	SYNJ1	-0.564	-	2.52E-03	3.73E-03
232981_PM_s_at	synergin, gamma	57563	SYNRG	-0.313	-	4.22E-02	4.54E-02
209198_PM_s_at	synaptotagmin XI	57728	SYT11	-1.978	-	1.43E-03	2.98E-03
205613_PM_at	synaptotagmin XVII	5166	SYT17	-1.028	-	8.61E-03	7.89E-03
206161_PM_s_at	synaptotagmin V	8669	SYT5	-2.034	-	2.70E-02	3.37E-02
206162_PM_x_at	synaptotagmin V	3189	SYT5	-0.435	-	4.85E-02	4.94E-02
1554690_PM_a_at	transforming, acidic coiled-coil containing protein 1	60	TACC1	-1.256	-	2.11E-02	4.30E-03
222728_PM_s_at	TATA box binding protein (TBP)-associated factor, RNA polymerase I, D, 41kDa	6227	TAF1D	-0.420	-	4.38E-02	6.95E-03
200916_PM_at	transgelin 2	7267	TAGLN2	-0.458	-	2.08E-02	9.81E-04

210978_PM_s_at	transgelin 2	79365	TAGLN2	-0.312	-	2.97E-02	1.47E-02
218466_PM_at	TBC1 domain family, member 17	285193	TBC1D17	-0.480	-	2.18E-02	7.80E-03
226664_PM_at	TBC1 domain family, member 20	3843	TBC1D20	-0.576	-	2.37E-03	4.37E-03
201815_PM_s_at	TBC1 domain family, member 5	5495	TBC1D5	-0.347	-	5.31E-03	1.03E-02
1563839_PM_at	TBC1 domain family, member 7	5925	TBC1D7	-0.283	-	2.74E-04	1.71E-03
222633_PM_at	235eparin235ing (beta)-like 1 X-linked receptor 1	23637	TBL1XR1	-1.492	-	8.11E-03	2.00E-02
230517_PM_at	similar to GLI-Kruppel family member HKR1	51735	tcag7.1196	-0.304	-	3.32E-03	2.51E-02
212931_PM_at	transcription factor 20 (AR1)	10178	TCF20	-0.455	-	9.95E-03	2.87E-03
213311_PM_s_at	transcription factor 25 (basic helix-loop-helix)	27069	TCF25	-1.399	-	1.79E-05	8.66E-05
212382_PM_at	transcription factor 4	27336	TCF4	-2.047	-	2.17E-03	6.76E-03
203753_PM_at	transcription factor 4	57545	TCF4	-1.349	-	2.97E-03	5.39E-03
222146_PM_s_at	transcription factor 4	171023	TCF4	-0.970	-	1.42E-02	1.22E-02
212762_PM_s_at	transcription factor 7-like 2 (T-cell specific, HMG-box)	2801	TCF7L2	-0.848	-	1.57E-03	3.99E-04
231912_PM_s_at	tectonin beta-propeller repeat containing 1	151516	TECPR1	-0.339	-	1.24E-02	2.47E-02
203176_PM_s_at	transcription factor A, mitochondrial	57176	TFAM	-0.323	-	1.57E-02	1.50E-03
1565347_PM_s_at	transcription factor binding to IGHM enhancer 3	8131	TFE3	-0.524	-	9.40E-03	2.58E-02
203833_PM_s_at	trans-golgi network protein 2	808	TGOLN2	-1.042	-	7.52E-03	1.26E-03
213894_PM_at	thrombospondin, type I, domain containing 7A	5771	THSD7A	-0.982	-	1.10E-02	2.00E-02
208850_PM_s_at	Thy-1 cell surface antigen	1939	THY1	-1.207	-	3.13E-02	2.83E-02
208851_PM_s_at	Thy-1 cell surface antigen	51128	THY1	-0.536	-	3.34E-02	2.29E-02
201446_PM_s_at	TIA1 cytotoxic granule-associated RNA binding protein	2260	TIA1	-0.631	-	2.40E-02	1.66E-02
1554890_PM_a_at	TIA1 cytotoxic granule-associated RNA binding protein	694	TIA1	-0.311	-	2.65E-02	1.34E-02
206409_PM_at	T-cell lymphoma invasion and metastasis 1	8767	TIAM1	-0.824	-	2.14E-03	1.24E-02
203167_PM_at	TIMP metallopeptidase inhibitor 2	10059	TIMP2	-1.225	-	1.97E-03	3.55E-03
201149_PM_s_at	TIMP metallopeptidase inhibitor 3	288	TIMP3	-1.195	-	7.60E-04	1.50E-03
208700_PM_s_at	transketolase	3423	TKT	-0.636	-	2.16E-02	2.53E-02
203220_PM_s_at	235eparin235ing-like enhancer of split 1 (E(sp1) homolog, Drosophila)	80031	TLE1	-0.688	-	1.26E-02	2.11E-02
216997_PM_x_at	235eparin235ing-like enhancer of split 4 (E(sp1) homolog, Drosophila)	160	TLE4	-0.318	-	5.00E-02	1.31E-02
211077_PM_s_at	tousled-like kinase 1	55754	TLK1	-0.750	-	8.33E-03	3.85E-02

209149_PM_s_at	transmembrane 9 superfamily member 1	93	TM9SF1	-1.077	-	5.76E-03	1.63E-02
212194_PM_s_at	transmembrane 9 superfamily protein member 4	10289	TM9SF4	-1.605	-	1.71E-03	9.02E-03
200803_PM_s_at	transmembrane BAX inhibitor motif containing 6	7982	TMBIM6	-0.895	-	9.98E-04	8.44E-03
220240_PM_s_at	transmembrane and coiled-coil domains 3	596	TMCO3	-0.789	-	1.86E-02	4.69E-02
204426_PM_at	transmembrane emp24 domain trafficking protein 2	60496	TMED2	-2.619	-	1.73E-02	4.11E-02
204427_PM_s_at	transmembrane emp24 domain trafficking protein 2	5525	TMED2	-2.990	-	2.44E-02	4.69E-02
224676_PM_at	transmembrane emp24 protein transport domain containing 4	246184	TMED4	-1.649	-	2.31E-02	3.97E-02
202195_PM_s_at	transmembrane emp24 protein transport domain containing 5	1595	TMED5	-0.758	-	8.01E-03	3.90E-02
242617_PM_at	Transmembrane emp24 protein transport domain containing 8	---	TMED8	-0.294	-	2.42E-03	2.10E-02
236667_PM_at	transmembrane protein 120B	---	TMEM120B	-0.734	-	3.13E-02	3.77E-02
222914_PM_s_at	transmembrane protein 121	51465	TMEM121	-0.449	-	9.79E-03	4.45E-02
1553479_PM_at	transmembrane protein 145	55593	TMEM145	-0.700	-	1.10E-02	2.41E-02
216315_PM_x_at	TMEM189-UBE2V1 readthrough transcript /// ubiquitin-conjugating enzyme E2 variant 1	51110	TMEM189-UBE2V1 /// UBE2V1	-0.287	-	2.32E-02	6.47E-03
226647_PM_at	transmembrane protein 25	91369	TMEM25	-0.438	-	3.96E-02	3.25E-02
232591_PM_s_at	transmembrane protein 30A	6429	TMEM30A	-1.970	-	1.91E-03	1.44E-02
238831_PM_at	transmembrane protein 33	---	TMEM33	-0.343	-	2.01E-02	2.85E-02
222736_PM_s_at	transmembrane protein 38B	2778	TMEM38B	-0.408	-	1.69E-02	3.42E-02
212202_PM_s_at	transmembrane protein 87A	2192	TMEM87A	-0.321	-	2.38E-02	2.39E-02
207839_PM_s_at	transmembrane protein 8B	10950	TMEM8B	-0.344	-	7.11E-04	1.39E-03
223827_PM_at	tumor necrosis factor receptor superfamily, member 19	51496	TNFRSF19	-0.309	-	4.27E-02	4.21E-02
213109_PM_at	TRAF2 and NCK interacting kinase	27255	TNIK	-1.140	-	8.43E-03	1.46E-02
210585_PM_s_at	transportin 2	57120	TNPO2	-0.715	-	1.54E-02	2.30E-02
214550_PM_s_at	transportin 3	58478	TNPO3	-0.581	-	1.89E-02	1.00E-02
1553346_PM_a_at	trinucleotide repeat containing 6A	57569	TNRC6A	-1.937	-	6.45E-03	1.49E-02
227149_PM_at	trinucleotide repeat containing 6C	10062	TNRC6C	-0.552	-	3.08E-03	2.84E-03
216339_PM_s_at	tenascin XA pseudogene /// tenascin XB	55151	TNXA /// TNXB	-0.437	-	1.89E-02	4.15E-02
217930_PM_s_at	toll interacting protein	5537	TOLLIP	-1.650	-	6.77E-03	1.85E-03
212773_PM_s_at	translocase of outer mitochondrial membrane 20 homolog	5803	TOMM20	-0.828	-	5.90E-03	1.99E-02

	(yeast)						
217960_PM_s_at	translocase of outer mitochondrial membrane 22 homolog (yeast)	255967	TOMM22	-1.936	-	3.44E-02	4.94E-02
208900_PM_s_at	topoisomerase (DNA) I	26273	TOP1	-1.435	-	1.53E-03	5.72E-03
212409_PM_s_at	torsin A interacting protein 1	51406	TOR1AIP1	-1.287	-	2.83E-03	1.07E-02
201683_PM_x_at	TOX high mobility group box family member 4	5905	TOX4	-1.498	-	9.19E-03	1.37E-02
201684_PM_s_at	TOX high mobility group box family member 4	4173	TOX4	-0.456	-	1.31E-02	2.35E-02
1569098_PM_s_at	tumor protein p53 binding protein 1	7164	TP53BP1	-0.423	-	1.55E-02	1.47E-02
225605_PM_at	tumor protein p53 inducible protein 13	154215	TP53I13	-0.296	-	1.44E-02	2.07E-02
206116_PM_s_at	tropomyosin 1 (alpha)	3422	TPM1	-0.721	-	4.58E-03	1.69E-02
214365_PM_at	tropomyosin 3	2590	TPM3	-0.618	-	3.95E-02	4.14E-02
212481_PM_s_at	tropomyosin 4	51020	TPM4	-0.686	-	1.86E-02	3.26E-02
214196_PM_s_at	tripeptidyl peptidase I	2332	TPP1	-2.460	-	9.73E-04	7.24E-03
201730_PM_s_at	translocated promoter region (to activated MET oncogene)	22998	TPR	-1.572	-	1.78E-02	5.57E-03
202079_PM_s_at	trafficking protein, kinesin binding 1	23245	TRAK1	-0.338	-	1.75E-02	1.65E-02
202124_PM_s_at	trafficking protein, kinesin binding 2	8301	TRAK2	-0.755	-	1.23E-03	1.14E-04
201399_PM_s_at	translocation associated membrane protein 1	8671	TRAM1	-1.285	-	1.00E-02	4.19E-02
56829_PM_at	trafficking protein particle complex 9	3181	TRAPPC9	-0.618	-	3.33E-03	2.39E-03
211788_PM_s_at	three prime repair exonuclease 2	9672	TREX2	-0.273	-	2.31E-02	2.70E-02
203147_PM_s_at	tripartite motif-containing 14	9815	TRIM14	-0.422	-	1.01E-02	9.20E-03
214248_PM_s_at	tripartite motif-containing 2	22836	TRIM2	-2.268	-	1.01E-03	7.67E-03
210995_PM_s_at	tripartite motif-containing 23	60680	TRIM23	-2.338	-	1.55E-03	1.18E-02
210994_PM_x_at	tripartite motif-containing 23	8193	TRIM23	-2.464	-	6.02E-03	2.63E-02
210541_PM_s_at	tripartite motif-containing 27	8573	TRIM27	-1.734	-	1.11E-02	1.84E-02
200990_PM_at	tripartite motif-containing 28	10236	TRIM28	-1.016	-	2.87E-02	4.67E-02
210266_PM_s_at	tripartite motif-containing 33	55904	TRIM33	-0.454	-	9.22E-03	1.87E-02
223131_PM_s_at	tripartite motif-containing 8	51691	TRIM8	-1.117	-	2.50E-03	1.96E-02
208178_PM_x_at	triple functional domain (PTPRF interacting)	5432	TRIO	-1.322	-	1.58E-02	3.19E-02
209013_PM_x_at	triple functional domain (PTPRF interacting)	57122	TRIO	-0.774	-	4.09E-02	4.72E-02
216452_PM_at	transient receptor potential cation channel, subfamily M, member 3	23731	TRPM3	-0.627	-	1.35E-02	4.74E-02
234351_PM_x_at	trichorhinophalangeal syndrome I	---	TRPS1	-0.663	-	1.12E-02	2.87E-02

224218_PM_s_at	trichorhinophalangeal syndrome I	8325	TRPS1	-1.003	-	1.18E-02	1.72E-02
214908_PM_s_at	transformation/transcription domain-associated protein	55802	TRRAP	-0.694	-	2.75E-03	4.83E-03
225484_PM_at	testis specific, 14	390980	TSGA14	-0.658	-	2.84E-02	3.19E-02
209890_PM_at	tetraspanin 5	6470	TSPAN5	-1.995	-	2.40E-04	3.20E-03
233617_PM_at	TSPY-like 3 (pseudogene)	57599	TSPYL3	-0.420	-	6.94E-03	3.90E-03
208663_PM_s_at	tetratricopeptide repeat domain 3	10144	TTC3	-1.900	-	1.23E-03	3.11E-03
208661_PM_s_at	tetratricopeptide repeat domain 3	4099	TTC3	-2.734	-	3.75E-03	6.82E-03
208664_PM_s_at	tetratricopeptide repeat domain 3	23288	TTC3	-2.082	-	1.39E-02	2.83E-02
208662_PM_s_at	tetratricopeptide repeat domain 3	8073	TTC3	-0.992	-	1.59E-02	7.76E-03
1554029_PM_a_at	tetratricopeptide repeat domain 37	10062 /// 2521	TTC37	-0.524	-	3.10E-03	2.14E-02
230872_PM_s_at	tubulin tyrosine ligase-like family, member 3	64425	TTLL3	-1.187	-	1.73E-02	3.88E-02
232042_PM_at	tweety homolog 2 (Drosophila)	399959	TTYH2	-1.962	-	1.28E-03	1.14E-02
209372_PM_x_at	tubulin, beta 2A /// tubulin, beta 2B	29927	TUBB2A /// TUBB2B	-3.618	-	3.21E-02	4.91E-02
208977_PM_x_at	tubulin, beta 2C	55268	TUBB2C	-0.432	-	2.85E-02	3.18E-02
202154_PM_x_at	tubulin, beta 3	4216	TUBB3	-0.357	-	2.73E-02	1.36E-02
202476_PM_s_at	tubulin, gamma complex associated protein 2	80155	TUBGCP2	-0.571	-	2.66E-03	2.76E-02
230635_PM_at	taurine upregulated 1 (non-protein coding)	134548	TUG1	-0.341	-	2.03E-03	1.15E-02
203272_PM_s_at	tumor suppressor candidate 2	118491	TUSC2	-1.401	-	3.32E-02	4.17E-02
214007_PM_s_at	twinfilin, actin-binding protein, homolog 1 (Drosophila)	221692	TWF1	-1.517	-	9.41E-03	4.72E-02
201008_PM_s_at	thioredoxin interacting protein	5687	TXNIP	-1.286	-	1.51E-02	3.35E-02
211431_PM_s_at	TYRO3 protein tyrosine kinase	138639	TYRO3	-0.504	-	2.36E-02	4.72E-02
200964_PM_at	ubiquitin-like modifier activating enzyme 1	100130966 /// 387082 /// 6613 /// 728825	UBA1	-0.736	-	3.16E-02	4.99E-02
201378_PM_s_at	ubiquitin associated protein 2-like	4887	UBAP2L	-1.001	-	1.57E-02	4.91E-02
238587_PM_at	ubiquitin associated and SH3 domain containing, B	---	UBASH3B	-0.346	-	2.54E-03	1.23E-02
200669_PM_s_at	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	7168	UBE2D3	-1.327	-	1.04E-02	2.67E-02
200668_PM_s_at	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	3157	UBE2D3	-0.519	-	1.25E-02	2.49E-02
221962_PM_s_at	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	1282	UBE2H	-1.112	-	4.73E-04	4.43E-03
217799_PM_x_at	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	57580	UBE2H	-2.119	-	1.60E-03	8.49E-03

217823_PM_s_at	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	146223	UBE2J1	-0.267	-	6.49E-04	1.19E-03
202347_PM_s_at	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast)	55830	UBE2K	-0.826	-	1.97E-02	3.77E-02
200682_PM_s_at	ubiquitin-conjugating enzyme E2L 3	11163	UBE2L3	-0.501	-	2.81E-02	2.56E-02
223014_PM_at	ubiquitin-conjugating enzyme E2R 2	26060	UBE2R2	-0.542	-	4.73E-02	2.52E-02
202779_PM_s_at	ubiquitin-conjugating enzyme E2S	89797	UBE2S	-2.792	-	2.08E-02	3.46E-02
1554794_PM_a_at	ubiquitin protein ligase E3C	100291837 /// 6227	UBE3C	-0.430	-	8.01E-03	2.88E-02
212756_PM_s_at	ubiquitin protein ligase E3 component n-recognin 2	10484	UBR2	-0.284	-	9.35E-03	3.54E-02
212007_PM_at	UBX domain protein 4	2058	UBXN4	-0.793	-	2.46E-03	5.69E-03
223142_PM_s_at	uridine-cytidine kinase 1	112399	UCK1	-0.600	-	1.11E-02	2.70E-02
1552656_PM_s_at	U2AF homology motif (UHM) kinase 1	30011	UHMK1	-1.760	-	2.88E-03	1.51E-03
235003_PM_at	U2AF homology motif (UHM) kinase 1	9478	UHMK1	-1.455	-	8.08E-03	3.54E-03
227740_PM_at	U2AF homology motif (UHM) kinase 1	55608	UHMK1	-1.306	-	1.01E-02	7.97E-03
1554292_PM_a_at	UHRF1 binding protein 1-like	3326	UHRF1BP1L	-0.537	-	1.19E-04	6.22E-05
231768_PM_at	upstream transcription factor 1	5502	USF1	-0.267	-	2.17E-02	3.79E-02
201831_PM_s_at	USO1 homolog, vesicle docking protein (yeast)	1268	USO1	-1.993	-	4.88E-03	2.26E-02
202412_PM_s_at	ubiquitin specific peptidase 1	51053	USP1	-0.923	-	3.72E-03	3.65E-03
209136_PM_s_at	ubiquitin specific peptidase 10	55733	USP10	-0.499	-	2.86E-03	1.86E-02
208723_PM_at	ubiquitin specific peptidase 11	23588	USP11	-2.478	-	2.81E-02	4.67E-02
201671_PM_x_at	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	4637	USP14	-0.438	-	8.60E-03	4.13E-02
222616_PM_s_at	ubiquitin specific peptidase 16	51663	USP16	-0.702	-	4.34E-03	1.19E-02
1555559_PM_s_at	ubiquitin specific peptidase 25	396	USP25	-0.322	-	1.98E-02	6.24E-03
214843_PM_s_at	ubiquitin specific peptidase 33	29093	USP33	-1.236	-	4.72E-03	1.39E-02
226174_PM_at	ubiquitin specific peptidase 42	25782	USP42	-0.303	-	1.56E-03	3.45E-03
223701_PM_s_at	ubiquitin specific peptidase 47	55122	USP47	-2.400	-	2.61E-02	4.37E-02
230543_PM_at	ubiquitin specific peptidase 9, X-linked	79364	USP9X	-0.694	-	3.90E-02	2.48E-02
201556_PM_s_at	vesicle-associated membrane protein 2 (synaptobrevin 2)	2820	VAMP2	-0.673	-	1.67E-02	2.33E-02
201796_PM_s_at	valyl-tRNA synthetase	79882	VARS	-0.331	-	1.77E-02	6.60E-03

208649_PM_s_at	valosin-containing protein	9404	VCP	-1.304	-	3.46E-02	4.66E-02
217140_PM_s_at	voltage-dependent anion channel 1	79576	VDAC1	-1.186	-	1.95E-02	4.85E-02
210513_PM_s_at	vascular endothelial growth factor A	441951	VEGFA	-0.849	-	2.70E-03	3.90E-03
211527_PM_x_at	vascular endothelial growth factor A	91289	VEGFA	-0.973	-	2.16E-02	2.63E-02
212324_PM_s_at	vacuolar protein sorting 13 homolog D (S. cerevisiae)	10007	VPS13D	-0.316	-	1.75E-02	1.43E-02
230306_PM_at	vacuolar protein sorting 26 homolog B (S. pombe)	84948	VPS26B	-0.463	-	9.39E-03	4.82E-02
222387_PM_s_at	vacuolar protein sorting 35 homolog (S. cerevisiae)	11017	VPS35	-1.990	-	4.22E-05	4.78E-04
233864_PM_s_at	vacuolar protein sorting 35 homolog (S. cerevisiae)	---	VPS35	-1.751	-	1.96E-02	3.61E-02
217727_PM_x_at	vacuolar protein sorting 35 homolog (S. cerevisiae)	84191	VPS35	-1.692	-	3.57E-02	3.99E-02
221707_PM_s_at	vacuolar protein sorting 53 homolog (S. cerevisiae)	51366	VPS53	-0.300	-	1.87E-02	1.56E-02
221998_PM_s_at	vaccinia related kinase 3	23167	VRK3	-0.575	-	1.43E-02	7.83E-03
219679_PM_s_at	WW domain containing adaptor with coiled-coil	9806	WAC	-2.361	-	3.06E-03	1.73E-02
212264_PM_s_at	wings apart-like homolog (Drosophila)	8500	WAPAL	-0.776	-	2.00E-03	1.12E-02
200628_PM_s_at	tryptophanyl-tRNA synthetase	1386	WARS	-0.831	-	6.54E-03	2.14E-02
205810_PM_s_at	Wiskott-Aldrich syndrome-like	7730	WASL	-1.197	-	1.13E-04	1.01E-03
205809_PM_s_at	Wiskott-Aldrich syndrome-like	2911	WASL	-1.714	-	2.82E-03	6.12E-03
209117_PM_at	WW domain binding protein 2	64146 /// 84342	WBP2	-0.878	-	3.35E-02	4.98E-02
1554410_PM_a_at	Williams-Beuren syndrome chromosome region 16	7534	WBSCR16	-0.322	-	1.34E-02	1.55E-02
210935_PM_s_at	WD repeat domain 1	130507	WDR1	-1.245	-	3.82E-03	1.91E-02
200611_PM_s_at	WD repeat domain 1	7804	WDR1	-0.725	-	1.23E-02	2.06E-02
223308_PM_s_at	WD repeat domain 5	665	WDR5	-0.530	-	3.65E-02	3.74E-02
221981_PM_s_at	WD repeat domain 59	57178	WDR59	-0.417	-	5.78E-03	1.04E-02
221248_PM_s_at	Wolf-Hirschhorn syndrome candidate 1-like 1	26747	WHSC1L1	-1.591	-	1.62E-02	4.43E-02
222544_PM_s_at	Wolf-Hirschhorn syndrome candidate 1-like 1	113146	WHSC1L1	-1.321	-	4.29E-02	2.46E-02
202665_PM_s_at	WAS/WASL interacting protein family, member 1	3778	WIPF1	-0.347	-	3.99E-02	3.79E-02
212050_PM_at	WAS/WASL interacting protein family, member 2	10724	WIPF2	-0.425	-	8.36E-04	4.05E-03
221785_PM_at	widely interspaced zinc finger motifs	84516	WIZ	-0.563	-	1.78E-02	7.71E-03
201295_PM_s_at	WD repeat and SOCS box-containing 1	9478	WSB1	-0.478	-	8.01E-04	4.22E-03
201294_PM_s_at	WD repeat and SOCS box-containing 1	10772	WSB1	-1.851	-	2.93E-03	2.54E-03
225273_PM_at	WWC family member 3	120892	WWC3	-2.059	-	4.32E-04	6.21E-03
237802_PM_at	XK, Kell blood group complex subunit-related family, member	---	XKR4	-1.183	-	4.44E-02	2.70E-02

	4						
208459_PM_s_at	exportin 7	50814	XPO7	-1.172	-	3.97E-02	4.80E-02
213342_PM_at	Yes-associated protein 1, 65kDa	9169	YAP1	-0.533	-	5.42E-03	3.99E-03
213996_PM_at	yippee-like 1 (Drosophila)	92342	YPEL1	-0.483	-	3.30E-02	2.11E-02
222703_PM_s_at	yrdC domain containing (E. coli)	221981	YRDC	-0.327	-	3.55E-02	2.46E-02
1564053_PM_a_at	YTH domain family, member 3	10244	YTHDF3	-0.907	-	6.03E-03	3.29E-02
201020_PM_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	6938	YWHAH	-0.297	-	2.41E-02	2.00E-02
200638_PM_s_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	51601	YWHAZ	-0.367	-	1.00E-03	8.96E-03
200641_PM_s_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	5837	YWHAZ	-2.026	-	1.49E-02	3.86E-02
201901_PM_s_at	YY1 transcription factor	3267	YY1	-1.415	-	7.59E-04	4.25E-03
201902_PM_s_at	YY1 transcription factor	6201	YY1	-0.349	-	5.44E-03	8.63E-03
205883_PM_at	zinc finger and BTB domain containing 16	10254	ZBTB16	-1.108	-	3.62E-02	3.06E-02
235308_PM_at	zinc finger and BTB domain containing 20	---	ZBTB20	-1.204	-	2.57E-02	2.32E-02
204180_PM_s_at	zinc finger and BTB domain containing 43	22916	ZBTB43	-1.013	-	3.63E-02	5.40E-03
205787_PM_x_at	zinc finger CCCH-type containing 11A	1009	ZC3H11A	-1.285	-	8.36E-03	3.56E-02
201593_PM_s_at	zinc finger CCCH-type containing 15	11219	ZC3H15	-1.840	-	1.88E-02	2.96E-02
219247_PM_s_at	zinc finger, DHHC-type containing 14	3281	ZDHHC14	-0.328	-	1.99E-03	1.93E-02
217486_PM_s_at	zinc finger, DHHC-type containing 17	10923	ZDHHC17	-0.806	-	9.28E-03	7.55E-03
218077_PM_s_at	zinc finger, DHHC-type containing 3	10009	ZDHHC3	-0.374	-	2.96E-02	4.12E-02
212758_PM_s_at	zinc finger E-box binding homeobox 1	1307	ZEB1	-0.659	-	3.40E-02	4.59E-02
202456_PM_s_at	zer-1 homolog (C. elegans)	80227	ZER1	-0.309	-	5.39E-03	4.44E-02
202448_PM_s_at	zer-1 homolog (C. elegans)	56904	ZER1	-0.362	-	1.20E-02	2.67E-02
222493_PM_s_at	zinc finger, AN1-type domain 3	124222	ZFAND3	-0.722	-	3.15E-02	4.98E-02
217741_PM_s_at	zinc finger, AN1-type domain 5	2113	ZFAND5	-1.324	-	8.39E-03	3.22E-02
219779_PM_at	zinc finger homeobox 4	901	ZFHX4	-0.935	-	2.78E-02	2.10E-02
224631_PM_at	zinc finger protein 91 homolog (mouse)	586	ZFP91	-2.220	-	1.18E-02	2.41E-02
213286_PM_at	zinc finger RNA binding protein	7105	ZFR	-2.223	-	8.90E-04	6.47E-03
33148_PM_at	zinc finger RNA binding protein	338811	ZFR	-1.035	-	6.45E-03	6.59E-03

201856_PM_s_at	zinc finger RNA binding protein	80823	ZFR	-0.724	-	1.20E-02	1.36E-02
223388_PM_s_at	zinc finger, FYVE domain containing 1	199731	ZFYVE1	-0.349	-	2.22E-02	4.24E-02
208446_PM_s_at	zinc finger, FYVE domain containing 9	8776	ZFYVE9	-0.496	-	2.31E-02	4.60E-02
1555609_PM_a_at	zinc finger, matrin type 3	5111	ZMAT3	-1.850	-	6.67E-03	3.39E-02
210281_PM_s_at	zinc finger, MYM-type 2	128439	ZMYM2	-1.548	-	2.25E-03	1.90E-03
1554159_PM_a_at	zinc finger, MYND domain containing 11	84465	ZMYND11	-1.950	-	3.68E-03	1.73E-02
1559881_PM_s_at	zinc finger protein 12	86	ZNF12	-1.158	-	3.36E-03	9.30E-03
207402_PM_at	zinc finger protein 132	8801	ZNF132	-0.301	-	6.71E-03	3.98E-02
207164_PM_s_at	zinc finger protein 238	9221	ZNF238	-2.900	-	1.02E-02	3.39E-02
203247_PM_s_at	zinc finger protein 24	56945	ZNF24	-0.508	-	2.51E-02	4.05E-02
206900_PM_x_at	zinc finger protein 253	51635	ZNF253	-0.330	-	1.22E-02	6.42E-03
242602_PM_x_at	zinc finger protein 254	3192	ZNF254	-0.291	-	3.17E-02	1.72E-02
226260_PM_x_at	zinc finger protein 358	2983	ZNF358	-0.722	-	9.99E-03	4.33E-02
1555015_PM_a_at	zinc finger protein 398	22872	ZNF398	-0.282	-	8.46E-03	4.47E-02
242684_PM_at	zinc finger protein 425	8110	ZNF425	-0.317	-	1.51E-02	5.94E-03
215359_PM_x_at	zinc finger protein 44	54842	ZNF44	-0.432	-	1.61E-02	1.17E-02
232247_PM_at	zinc finger protein 502	84959	ZNF502	-0.498	-	2.37E-02	9.15E-03
230542_PM_at	zinc finger protein 597	11076	ZNF597	-0.437	-	1.40E-02	2.87E-02
1553725_PM_s_at	zinc finger protein 644	64783	ZNF644	-0.362	-	6.46E-03	3.71E-02
235577_PM_at	zinc finger protein 652	7184	ZNF652	-0.291	-	1.16E-02	1.92E-02
220760_PM_x_at	zinc finger protein 665	1036	ZNF665	-0.643	-	5.28E-04	3.19E-03
220215_PM_at	zinc finger protein 669	5116	ZNF669	-0.767	-	4.81E-02	4.87E-02
217547_PM_x_at	zinc finger protein 675	113201	ZNF675	-0.344	-	7.07E-03	8.36E-03
215570_PM_s_at	zinc finger protein 780A /// zinc finger protein 780B	55002	ZNF780A /// ZNF780B	-0.574	-	6.55E-03	3.36E-02
1564362_PM_x_at	zinc finger protein 843	6733	ZNF843	-0.354	-	4.96E-02	3.31E-04

215758_PM_x_at	zinc finger protein 93	54904	ZNF93	-0.417	-	1.73E-02	9.04E-03
223382_PM_s_at	zinc and ring finger 1	2018	ZNRF1	-0.781	-	6.56E-03	2.62E-03
223383_PM_at	zinc and ring finger 1	7328	ZNRF1	-1.840	-	7.72E-03	2.20E-02
225131_PM_at	zinc finger, RAN-binding domain containing 1	5549	ZRANB1	-0.303	-	5.62E-03	3.63E-02
223016_PM_x_at	zinc finger, RAN-binding domain containing 2	55915	ZRANB2	-1.677	-	1.29E-02	2.35E-02
218349_PM_s_at	Zwilch, kinetochore associated, homolog (Drosophila)	144402	ZWILCH	-0.417	-	4.55E-02	4.22E-02
230106_PM_at	ZXD family zinc finger C	339324	ZXDC	-0.918	-	1.08E-02	1.86E-03
229325_PM_at	zinc finger, ZZ-type containing 3	84668	ZZZ3	-0.270	-	2.74E-02	1.58E-02
1562408_PM_at	---	4719	---	0.314	+	1.90E-05	2.04E-05
241769_PM_at	---	54832	---	0.592	+	4.69E-05	3.49E-05
227499_PM_at	---	81566	---	0.683	+	5.72E-05	2.07E-05
227278_PM_at	---	51171	---	0.416	+	7.09E-05	1.30E-05
228548_PM_at	---	80018	---	0.411	+	8.69E-05	3.97E-04
238752_PM_at	---	---	---	0.355	+	1.04E-04	7.87E-05
244349_PM_at	---	---	---	0.434	+	1.29E-04	3.61E-03
1565810_PM_at	---	5000	---	0.280	+	1.90E-04	2.34E-03
225123_PM_at	---	128344	---	0.592	+	1.92E-04	1.92E-05
227306_PM_at	---	54834	---	0.384	+	2.14E-04	1.46E-03
228603_PM_at	---	57586	---	0.404	+	5.07E-04	2.92E-03
1557623_PM_at	---	23476	---	0.272	+	5.76E-04	9.46E-03
226231_PM_at	---	9653	---	0.278	+	5.82E-04	6.11E-03
229640_PM_x_at	---	---	---	0.871	+	6.00E-04	3.79E-04
224769_PM_at	---	284184	---	0.381	+	7.36E-04	2.79E-03
236369_PM_at	---	---	---	0.278	+	7.40E-04	8.34E-03
226282_PM_at	---	27252	---	0.521	+	8.16E-04	1.75E-02
1570301_PM_at	---	902	---	0.916	+	8.74E-04	1.51E-02
232788_PM_at	---	57689	---	0.458	+	9.59E-04	7.37E-03
224691_PM_at	---	116983	---	0.549	+	9.71E-04	3.19E-03
1559535_PM_s_at	---	102	---	0.355	+	1.01E-03	5.54E-03
230446_PM_at	---	258010	---	0.312	+	1.06E-03	1.13E-02
230139_PM_at	---	119504	---	0.942	+	1.13E-03	4.97E-03

235663_PM_at	---	---	---	0.444	+	1.15E-03	8.05E-03
228528_PM_at	---	64841	---	0.646	+	1.15E-03	2.18E-03
226621_PM_at	---	1822	---	0.420	+	1.16E-03	4.02E-03
226742_PM_at	---	---	---	0.497	+	1.20E-03	5.06E-03
230154_PM_at	---	23360	---	0.887	+	1.35E-03	4.08E-03
220452_PM_x_at	---	8850	---	0.366	+	1.35E-03	1.60E-02
231165_PM_at	---	220164	---	0.620	+	1.49E-03	4.54E-03
226773_PM_at	---	6654	---	0.490	+	1.49E-03	6.80E-03
240415_PM_at	---	---	---	0.568	+	1.53E-03	3.12E-03
232903_PM_at	---	5454	---	0.852	+	1.62E-03	1.93E-03
228560_PM_at	---	149041	---	0.316	+	1.66E-03	3.85E-04
1555617_PM_x_at	---	1654	---	0.300	+	1.68E-03	6.99E-04
1567913_PM_at	---	178	---	0.390	+	1.77E-03	1.17E-02
229248_PM_at	---	26524	---	0.339	+	1.78E-03	1.45E-02
217107_PM_at	---	51639	---	0.371	+	1.80E-03	3.49E-03
243023_PM_at	---	---	---	0.839	+	1.83E-03	7.25E-03
1568799_PM_at	---	6502	---	0.264	+	1.85E-03	8.70E-03
240099_PM_at	---	---	---	0.291	+	1.95E-03	5.35E-03
213705_PM_at	---	171546	---	0.264	+	1.99E-03	9.42E-03
1555848_PM_at	---	10159	---	0.382	+	2.07E-03	6.68E-03
1562979_PM_at	---	8050	---	0.326	+	2.10E-03	1.31E-02
228914_PM_at	---	6876	---	0.752	+	2.18E-03	1.08E-02
244008_PM_at	---	---	---	0.874	+	2.33E-03	1.17E-02
230293_PM_at	---	5599	---	0.396	+	2.34E-03	1.36E-02
228692_PM_at	---	79832	---	0.510	+	2.42E-03	4.85E-03
227815_PM_at	---	---	---	0.499	+	2.53E-03	6.80E-03
228070_PM_at	---	80854	---	0.651	+	2.55E-03	8.48E-03
227290_PM_at	---	55295	---	0.632	+	2.63E-03	6.57E-03
243887_PM_at	---	---	---	0.291	+	2.68E-03	2.46E-02
243398_PM_at	---	---	---	0.794	+	2.70E-03	5.06E-03
211976_PM_at	---	10550	---	0.325	+	2.71E-03	8.55E-03

226873_PM_at	---	53844	---	0.759	+	2.80E-03	1.88E-04
229898_PM_at	---	79018	---	0.341	+	2.87E-03	2.18E-03
229885_PM_at	---	79884	---	0.710	+	2.91E-03	3.01E-04
232752_PM_at	---	---	---	0.289	+	2.93E-03	9.96E-03
213549_PM_at	---	83941	---	0.423	+	2.94E-03	1.67E-03
242366_PM_at	---	54554	---	0.629	+	2.97E-03	7.50E-03
229111_PM_at	---	---	---	0.879	+	3.00E-03	1.50E-02
240196_PM_at	---	100129122	---	0.267	+	3.02E-03	8.61E-03
243907_PM_at	---	---	---	0.559	+	3.03E-03	1.32E-02
235227_PM_at	---	8467	---	0.784	+	3.05E-03	3.85E-03
213657_PM_s_at	---	23065	---	0.546	+	3.06E-03	4.23E-03
227682_PM_at	---	64328	---	0.586	+	3.08E-03	5.21E-03
239637_PM_at	---	---	---	0.514	+	3.17E-03	6.24E-03
225880_PM_at	---	114783	---	0.470	+	3.23E-03	5.87E-03
1562194_PM_at	---	5799	---	0.393	+	3.25E-03	1.39E-02
238786_PM_at	---	221981	---	0.558	+	3.28E-03	8.04E-03
227630_PM_at	---	7328	---	0.586	+	3.34E-03	8.60E-03
240433_PM_x_at	---	---	---	0.470	+	3.44E-03	2.33E-02
240095_PM_at	---	---	---	0.792	+	3.50E-03	1.21E-02
239752_PM_at	---	---	---	0.883	+	3.50E-03	2.40E-02
240502_PM_at	---	---	---	0.457	+	3.61E-03	2.94E-02
226532_PM_at	---	22823	---	0.474	+	3.74E-03	1.29E-02
227749_PM_at	---	56985	---	0.277	+	3.74E-03	8.41E-03
235529_PM_x_at	---	388650	---	0.744	+	3.83E-03	2.17E-03
217329_PM_x_at	---	92259	---	0.348	+	3.90E-03	8.00E-04
238209_PM_at	---	---	---	0.294	+	4.20E-03	1.83E-02
225950_PM_at	---	140469	---	0.652	+	4.51E-03	4.99E-03
237931_PM_at	---	1272	---	0.285	+	4.51E-03	1.21E-02
238919_PM_at	---	---	---	0.367	+	4.59E-03	2.84E-02
230171_PM_at	---	---	---	0.398	+	4.60E-03	2.60E-03
226480_PM_at	---	3400	---	0.537	+	4.73E-03	1.71E-02
235611_PM_at	---	---	---	0.623	+	4.79E-03	1.01E-03

235964_PM_x_at	---	79685	---	0.617	+	4.84E-03	1.76E-03
213573_PM_at	---	55573	---	0.367	+	4.97E-03	6.09E-03
235764_PM_at	---	60560	---	0.312	+	5.06E-03	7.00E-03
228240_PM_at	---	51132	---	0.352	+	5.13E-03	1.59E-02
229366_PM_at	---	140685	---	0.501	+	5.21E-03	3.38E-02
226719_PM_at	---	92140	---	0.549	+	5.24E-03	1.51E-02
226280_PM_at	---	6198	---	0.538	+	5.26E-03	9.26E-03
210030_PM_at	---	9117	---	0.280	+	5.29E-03	3.50E-02
238191_PM_at	---	---	---	0.600	+	5.36E-03	1.93E-02
225318_PM_at	---	645323	---	0.312	+	5.63E-03	1.49E-02
228734_PM_at	---	84333	---	0.277	+	5.70E-03	1.19E-02
239923_PM_at	---	157503	---	0.525	+	5.78E-03	2.49E-03
242968_PM_at	---	57085	---	0.528	+	5.81E-03	1.18E-02
241687_PM_at	---	---	---	0.320	+	6.00E-03	1.43E-02
230350_PM_at	---	9201	---	0.661	+	6.11E-03	4.12E-03
236089_PM_at	---	---	---	0.764	+	6.14E-03	2.61E-03
213567_PM_at	---	26099	---	0.873	+	6.29E-03	7.91E-03
235984_PM_at	---	---	---	0.693	+	6.41E-03	1.12E-02
233095_PM_at	---	54467	---	0.454	+	6.45E-03	1.61E-02
230589_PM_at	---	---	---	1.082	+	6.60E-03	2.30E-02
231137_PM_at	---	54014	---	0.368	+	6.64E-03	1.10E-02
241721_PM_at	---	---	---	1.016	+	6.66E-03	3.11E-03
1566221_PM_at	---	5428	---	0.278	+	6.79E-03	1.80E-02
228151_PM_at	---	22836	---	0.605	+	7.26E-03	8.79E-03
238297_PM_at	---	---	---	1.004	+	7.31E-03	2.64E-03
230740_PM_at	---	728743	---	0.355	+	7.33E-03	1.74E-02
1560496_PM_at	---	8881	---	0.270	+	7.44E-03	1.06E-02
234907_PM_x_at	---	11137	---	0.301	+	7.44E-03	1.69E-02
215515_PM_at	---	56172	---	0.294	+	7.45E-03	2.03E-02
226821_PM_at	---	85453	---	0.513	+	7.49E-03	5.80E-03
242967_PM_at	---	---	---	0.298	+	7.54E-03	5.41E-03
227167_PM_s_at	---	51186	---	1.083	+	7.64E-03	1.05E-02

1556444_PM_a_at	---	120	---	0.919	+	7.64E-03	9.86E-03
229786_PM_at	---	60674	---	0.869	+	7.70E-03	1.97E-02
234807_PM_x_at	---	221078	---	0.405	+	7.71E-03	6.84E-03
229072_PM_at	---	5208	---	0.706	+	7.71E-03	1.17E-02
1556744_PM_a_at	---	7407	---	0.832	+	7.78E-03	1.60E-03
241629_PM_at	---	---	---	0.315	+	7.81E-03	3.43E-02
239291_PM_at	---	---	---	0.975	+	8.11E-03	7.82E-04
223366_PM_at	---	84900	---	0.611	+	8.26E-03	1.56E-02
227448_PM_at	---	57084	---	0.553	+	8.29E-03	6.11E-03
1568931_PM_at	---	4281	---	0.300	+	8.36E-03	5.68E-03
1562529_PM_s_at	---	857	---	0.481	+	8.48E-03	2.27E-02
237839_PM_at	---	---	---	0.268	+	8.53E-03	1.06E-02
236031_PM_x_at	---	---	---	0.686	+	8.69E-03	4.32E-02
230605_PM_at	---	127018	---	0.679	+	8.72E-03	3.43E-02
228611_PM_s_at	---	220213	---	0.737	+	8.82E-03	9.39E-03
230411_PM_at	---	11231	---	0.366	+	8.82E-03	3.11E-03
239678_PM_at	---	---	---	0.967	+	8.88E-03	2.15E-02
239277_PM_at	---	---	---	1.069	+	8.92E-03	1.77E-02
1560738_PM_at	---	8974	---	0.291	+	8.92E-03	9.33E-03
235355_PM_at	---	9939	---	0.509	+	8.96E-03	2.75E-02
229824_PM_at	---	29097	---	0.510	+	9.07E-03	2.06E-02
226883_PM_at	---	6868	---	0.547	+	9.12E-03	2.70E-02
226641_PM_at	---	1837	---	0.492	+	9.20E-03	3.98E-03
238879_PM_at	---	26009	---	0.736	+	9.23E-03	1.10E-02
230211_PM_at	---	149563	---	0.301	+	9.25E-03	1.81E-02
224107_PM_at	---	56776	---	0.286	+	9.52E-03	1.79E-02
235750_PM_at	---	79999	---	0.524	+	9.60E-03	1.09E-02
221788_PM_at	---	5178	---	1.388	+	9.64E-03	9.82E-03
1554597_PM_at	---	5518	---	0.503	+	9.64E-03	3.56E-02

244621_PM_x_at	---	---	---	0.643	+	9.67E-03	2.47E-02
236798_PM_at	---	56943	---	0.772	+	9.80E-03	1.49E-02
235065_PM_at	---	51366	---	0.595	+	9.85E-03	6.02E-03
226579_PM_at	---	2273	---	0.461	+	1.00E-02	1.71E-02
231925_PM_at	---	5814	---	1.175	+	1.01E-02	1.30E-02
242303_PM_at	---	5471	---	0.562	+	1.02E-02	3.70E-02
235659_PM_at	---	---	---	0.314	+	1.02E-02	3.10E-02
239673_PM_at	---	---	---	0.422	+	1.03E-02	5.92E-03
234998_PM_at	---	5121	---	0.476	+	1.04E-02	3.13E-02
229383_PM_at	---	23517	---	0.861	+	1.08E-02	1.03E-02
235304_PM_at	---	---	---	0.328	+	1.09E-02	4.07E-02
228991_PM_at	---	401504	---	0.453	+	1.10E-02	2.64E-02
244847_PM_at	---	8476	---	0.301	+	1.10E-02	9.29E-03
226941_PM_at	---	6657	---	0.695	+	1.11E-02	5.21E-03
225227_PM_at	---	196294	---	0.713	+	1.11E-02	4.98E-03
238524_PM_at	---	---	---	0.305	+	1.12E-02	1.11E-02
226399_PM_at	---	3738	---	0.361	+	1.13E-02	2.17E-02
228006_PM_at	---	4302	---	0.463	+	1.13E-02	2.19E-02
235553_PM_at	---	10446	---	0.607	+	1.13E-02	1.53E-02
1557375_PM_at	---	5536	---	0.376	+	1.13E-02	9.15E-03
240922_PM_at	---	---	---	0.306	+	1.13E-02	1.48E-02
232999_PM_at	---	5136	---	0.776	+	1.14E-02	1.34E-02
236282_PM_at	---	---	---	0.335	+	1.14E-02	3.77E-02
227273_PM_at	---	51735 /// 96459	---	0.371	+	1.15E-02	7.76E-03
226546_PM_at	---	3431	---	0.274	+	1.15E-02	3.32E-02
238115_PM_at	---	219899	---	0.479	+	1.16E-02	2.84E-02
233116_PM_at	---	145788	---	0.456	+	1.17E-02	1.27E-02
244884_PM_at	---	---	---	0.272	+	1.17E-02	2.42E-02
1556329_PM_a_at	---	8539	---	0.499	+	1.21E-02	4.14E-02
226203_PM_at	---	445815	---	0.495	+	1.23E-02	1.60E-02
235118_PM_at	---	9581	---	0.310	+	1.24E-02	5.47E-03

239278_PM_at	---	---	---	0.636	+	1.24E-02	2.63E-02
238044_PM_at	---	10983	---	0.271	+	1.27E-02	2.32E-03
239425_PM_at	---	5178	---	1.008	+	1.27E-02	1.79E-03
227623_PM_at	---	100129250	---	0.676	+	1.28E-02	3.95E-02
1554007_PM_at	---	5034	---	0.361	+	1.29E-02	2.58E-02
229602_PM_at	---	55331	---	0.931	+	1.29E-02	3.10E-02
238202_PM_at	---	---	---	0.332	+	1.30E-02	1.77E-02
226560_PM_at	---	23657	---	0.589	+	1.30E-02	2.36E-02
239307_PM_at	---	100134361	---	0.267	+	1.30E-02	1.08E-02
229861_PM_at	---	117583	---	0.462	+	1.31E-02	4.01E-02
236016_PM_at	---	100133130	---	0.334	+	1.31E-02	1.98E-02
226826_PM_at	---	23135	---	0.575	+	1.31E-02	2.77E-02
230794_PM_at	---	9495	---	0.273	+	1.31E-02	2.53E-02
226139_PM_at	---	10217	---	0.395	+	1.33E-02	2.28E-02
224811_PM_at	---	80144	---	1.067	+	1.34E-02	2.14E-02
239355_PM_at	---	---	---	0.516	+	1.40E-02	1.81E-02
236204_PM_at	---	10490	---	0.329	+	1.41E-02	2.82E-02
238739_PM_at	---	---	---	0.419	+	1.43E-02	2.88E-02
225176_PM_at	---	123228	---	0.492	+	1.44E-02	3.78E-02
215450_PM_at	---	58498	---	0.497	+	1.45E-02	1.32E-02
226756_PM_at	---	5291	---	0.545	+	1.47E-02	2.13E-02
226297_PM_at	---	3134	---	0.449	+	1.51E-02	1.70E-02
239819_PM_at	---	7483	---	0.402	+	1.51E-02	2.56E-02
236261_PM_at	---	7029	---	0.573	+	1.53E-02	2.03E-02
230305_PM_at	---	145853	---	0.435	+	1.53E-02	4.31E-02
229118_PM_at	---	253512	---	0.457	+	1.53E-02	6.89E-03
1560747_PM_at	---	7750	---	0.334	+	1.53E-02	3.48E-02
235556_PM_at	---	6191	---	0.649	+	1.58E-02	1.40E-03
233335_PM_at	---	257000	---	0.278	+	1.60E-02	3.79E-02
227754_PM_at	---	56945	---	0.391	+	1.61E-02	3.40E-02
229131_PM_at	---	79627	---	0.694	+	1.69E-02	3.63E-02
227929_PM_at	---	153339	---	0.547	+	1.74E-02	1.66E-02

235570_PM_at	---	90011	---	0.880	+	1.74E-02	3.44E-02
229823_PM_at	---	222658	---	0.571	+	1.75E-02	9.04E-03
1569234_PM_at	---	5095	---	0.298	+	1.77E-02	4.97E-02
227107_PM_at	---	---	---	0.792	+	1.77E-02	3.85E-02
1565830_PM_at	---	4152	---	0.371	+	1.79E-02	3.08E-02
243424_PM_at	---	255488	---	0.268	+	1.79E-02	1.87E-02
1555753_PM_x_at	---	6726	---	0.313	+	1.81E-02	1.71E-02
229828_PM_at	---	53344	---	0.756	+	1.84E-02	1.08E-02
236236_PM_at	---	---	---	0.567	+	1.86E-02	4.22E-02
243134_PM_at	---	---	---	0.319	+	1.86E-02	3.94E-02
230680_PM_at	---	730094	---	0.516	+	1.87E-02	2.63E-02
234881_PM_at	---	5917	---	0.414	+	1.88E-02	1.02E-02
238782_PM_at	---	---	---	0.281	+	1.92E-02	3.48E-03
240892_PM_at	---	---	---	0.364	+	1.92E-02	5.27E-03
237384_PM_x_at	---	---	---	0.868	+	1.96E-02	2.61E-02
228390_PM_at	---	152217	---	0.998	+	1.96E-02	1.81E-02
225159_PM_s_at	---	221302	---	0.371	+	2.00E-02	4.36E-02
229569_PM_at	---	389337	---	0.701	+	2.00E-02	1.35E-02
227052_PM_at	---	100134674 /// 57876	---	0.395	+	2.01E-02	3.53E-02
238133_PM_at	---	---	---	0.745	+	2.02E-02	3.73E-02
236537_PM_at	---	---	---	0.540	+	2.02E-02	1.82E-03
224545_PM_at	---	112495	---	0.471	+	2.03E-02	2.41E-02
228120_PM_at	---	387893	---	0.511	+	2.06E-02	3.60E-02
241114_PM_s_at	---	---	---	0.278	+	2.06E-02	3.91E-02
237026_PM_at	---	1106	---	0.623	+	2.07E-02	2.82E-02
213500_PM_at	---	51780	---	0.369	+	2.09E-02	4.00E-02
241010_PM_x_at	---	---	---	0.372	+	2.09E-02	2.88E-02
229687_PM_s_at	---	137392	---	0.400	+	2.12E-02	7.40E-03
227579_PM_at	---	60559	---	0.915	+	2.16E-02	1.91E-02
226468_PM_at	---	4162	---	0.273	+	2.19E-02	1.30E-02

237250_PM_at	---	64710	---	0.474	+	2.21E-02	1.11E-02
227531_PM_at	---	11160	---	0.335	+	2.22E-02	8.25E-03
1556194_PM_a_at	---	4830	---	0.736	+	2.22E-02	1.87E-02
243974_PM_at	---	---	---	0.334	+	2.22E-02	3.55E-02
212867_PM_at	---	3336	---	0.503	+	2.22E-02	2.58E-03
236402_PM_at	---	---	---	0.658	+	2.23E-02	3.80E-02
232937_PM_at	---	730051	---	0.386	+	2.25E-02	4.02E-02
227200_PM_at	---	4801	---	0.453	+	2.26E-02	1.48E-02
239133_PM_at	---	441027	---	0.461	+	2.27E-02	3.62E-02
241968_PM_at	---	---	---	0.392	+	2.30E-02	3.93E-02
213294_PM_at	---	1207	---	0.362	+	2.31E-02	1.65E-02
226779_PM_at	---	23172	---	0.464	+	2.31E-02	3.88E-02
241618_PM_at	---	10454	---	0.299	+	2.44E-02	3.96E-02
213686_PM_at	---	80273	---	0.544	+	2.45E-02	3.70E-02
232758_PM_s_at	---	56899	---	0.380	+	2.49E-02	3.00E-02
229359_PM_at	---	401264	---	0.307	+	2.52E-02	3.92E-02
229333_PM_at	---	5451	---	0.753	+	2.53E-02	2.10E-02
227492_PM_at	---	79184	---	0.338	+	2.58E-02	4.36E-02
230127_PM_at	---	5494	---	0.621	+	2.60E-02	3.74E-02
1555461_PM_at	---	47	---	0.310	+	2.61E-02	4.59E-02
213411_PM_at	---	10098	---	0.719	+	2.62E-02	4.04E-03
1557813_PM_at	---	10659	---	0.593	+	2.62E-02	4.31E-02
232081_PM_at	---	84676	---	0.459	+	2.63E-02	2.83E-02
226374_PM_at	---	9831	---	0.421	+	2.63E-02	4.26E-02
213808_PM_at	---	23312	---	0.369	+	2.64E-02	2.88E-03
225328_PM_at	---	2047	---	1.031	+	2.65E-02	2.82E-02
212812_PM_at	---	889	---	0.878	+	2.68E-02	2.46E-02
230042_PM_at	---	84817	---	0.347	+	2.69E-02	2.71E-02
1554609_PM_at	---	1933	---	0.677	+	2.70E-02	8.15E-03
1556153_PM_s_at	---	25813	---	0.434	+	2.71E-02	1.68E-02

243856_PM_at	---	---	---	0.541	+	2.72E-02	3.91E-02
225356_PM_at	---	163259	---	0.393	+	2.80E-02	3.82E-02
227095_PM_at	---	22848	---	0.758	+	2.80E-02	2.27E-02
229300_PM_at	---	55526	---	0.451	+	2.83E-02	1.22E-02
235902_PM_at	---	56946	---	0.302	+	2.83E-02	1.63E-02
214809_PM_at	---	114885	---	0.345	+	2.86E-02	3.43E-02
226345_PM_at	---	4685	---	0.320	+	2.87E-02	3.04E-02
222824_PM_at	---	4897	---	0.348	+	2.89E-02	4.48E-02
226102_PM_at	---	3398	---	0.519	+	2.89E-02	3.26E-02
243948_PM_at	---	---	---	0.437	+	2.90E-02	2.34E-02
239368_PM_at	---	220108	---	0.490	+	2.96E-02	2.17E-03
1558102_PM_at	---	26037	---	0.444	+	2.97E-02	3.09E-02
1557487_PM_at	---	6397	---	0.327	+	3.12E-02	4.57E-02
242096_PM_at	---	---	---	0.513	+	3.15E-02	3.83E-02
1557286_PM_at	---	8502	---	0.288	+	3.16E-02	2.12E-02
227772_PM_at	---	79626	---	0.620	+	3.17E-02	2.50E-02
235736_PM_at	---	55299	---	0.594	+	3.18E-02	4.83E-02
240053_PM_x_at	---	57231	---	0.302	+	3.19E-02	3.82E-02
243184_PM_at	---	26207	---	0.323	+	3.32E-02	3.29E-02
233481_PM_at	---	10802	---	0.696	+	3.37E-02	1.53E-02
227665_PM_at	---	55718	---	0.346	+	3.40E-02	3.70E-03
239710_PM_at	---	---	---	0.299	+	3.40E-02	4.24E-02
227004_PM_at	---	10418	---	0.602	+	3.50E-02	1.94E-02
230785_PM_at	---	84978	---	0.324	+	3.57E-02	2.71E-02
232794_PM_at	---	400120	---	0.346	+	3.66E-02	3.29E-02
242610_PM_x_at	---	---	---	0.429	+	3.71E-02	4.56E-02
1561242_PM_at	---	5252	---	0.348	+	3.72E-02	3.81E-02
244707_PM_at	---	---	---	0.367	+	3.73E-02	4.49E-02
235434_PM_at	---	10724	---	0.431	+	3.75E-02	4.12E-02
239744_PM_at	---	---	---	0.788	+	3.76E-02	3.29E-02
237509_PM_at	---	---	---	0.279	+	3.76E-02	3.15E-02
222294_PM_s_at	---	221154	---	0.554	+	3.78E-02	1.06E-02

226594_PM_at	---	3858	---	0.580	+	3.78E-02	6.03E-03
231078_PM_at	---	285590	---	0.268	+	3.88E-02	1.84E-02
239765_PM_at	---	221002	---	0.310	+	3.89E-02	1.98E-02
217191_PM_x_at	---	81602	---	0.348	+	3.90E-02	9.49E-03
226392_PM_at	---	8535	---	0.495	+	3.94E-02	1.17E-02
241756_PM_at	---	---	---	0.477	+	3.95E-02	4.46E-02
230913_PM_at	---	780529	---	0.358	+	4.05E-02	3.67E-02
241970_PM_at	---	---	---	0.359	+	4.10E-02	4.53E-03
229319_PM_at	---	79872	---	0.439	+	4.12E-02	4.03E-02
236433_PM_at	---	---	---	0.278	+	4.13E-02	4.38E-02
234839_PM_at	---	---	---	0.522	+	4.15E-02	1.13E-02
235302_PM_at	---	---	---	0.636	+	4.23E-02	7.24E-03
229504_PM_at	---	10026	---	0.643	+	4.24E-02	3.86E-02
242384_PM_at	---	---	---	0.641	+	4.30E-02	2.12E-02
235015_PM_at	---	8073	---	0.759	+	4.38E-02	4.36E-02
228724_PM_at	---	84897	---	0.565	+	4.45E-02	2.45E-02
226197_PM_at	---	9792	---	0.670	+	4.51E-02	5.00E-02
226348_PM_at	---	55972	---	0.375	+	4.57E-02	4.06E-02
238712_PM_at	---	253842	---	0.695	+	4.59E-02	1.88E-02
216565_PM_x_at	---	84641	---	0.275	+	4.64E-02	4.09E-02
225007_PM_at	---	6426	---	0.313	+	4.65E-02	2.94E-02
238719_PM_at	---	---	---	0.364	+	4.68E-02	2.99E-02
227422_PM_at	---	79906	---	0.400	+	4.84E-02	4.96E-02
235782_PM_at	---	51236	---	0.824	+	4.87E-02	4.90E-02
242481_PM_at	---	55745	---	0.365	+	4.87E-02	4.06E-02
213256_PM_at	membrane-associated ring finger (C3HC4) 3	7070	3-Mar	0.348	+	2.17E-03	1.55E-03
226394_PM_at	membrane-associated ring finger (C3HC4) 5	398	3-Mar	0.572	+	4.28E-03	4.19E-03
200902_PM_at	15 kDa selenoprotein	87	3-Mar	0.394	+	6.86E-03	2.92E-02
202653_PM_s_at	membrane-associated ring finger (C3HC4) 7	3184	3-Mar	0.511	+	1.36E-02	9.51E-03
200015_PM_s_at	septin 2	137492 /// 6834	3-Mar	0.323	+	1.96E-02	1.06E-02
230001_PM_at	membrane-associated ring finger (C3HC4) 9	91750	3-Mar	0.264	+	2.63E-02	1.89E-02
208999_PM_at	septin 8	54873	3-Mar	0.592	+	2.84E-02	4.17E-02

214956_PM_at	AP2 associated kinase 1	6839	AAK1	0.283	+	4.50E-02	4.00E-02
231845_PM_at	alanyl-tRNA synthetase 2, mitochondrial (putative)	9331	AARS2	0.398	+	2.12E-04	3.21E-03
203505_PM_at	ATP-binding cassette, sub-family A (ABC1), member 1	8573	ABCA1	0.998	+	1.15E-02	3.42E-02
242541_PM_at	ATP-binding cassette, sub-family A (ABC1), member 9	---	ABCA9	0.518	+	4.18E-02	3.02E-02
223320_PM_s_at	ATP-binding cassette, sub-family B (MDR/TAP), member 10	3839	ABCB10	0.739	+	4.69E-02	4.31E-02
213485_PM_s_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	9146	ABCC10	0.438	+	6.70E-03	2.89E-02
209380_PM_s_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	58533	ABCC5	0.637	+	3.32E-02	4.03E-02
218633_PM_x_at	abhydrolase domain containing 10	136227	ABHD10	0.449	+	1.92E-02	5.41E-03
235348_PM_at	abhydrolase domain containing 13	---	ABHD13	0.369	+	4.45E-03	1.19E-02
213935_PM_at	abhydrolase domain containing 5	221443	ABHD5	0.421	+	2.96E-02	4.85E-02
225112_PM_at	abl-interactor 2	141	ABI2	0.363	+	2.74E-03	2.64E-03
200965_PM_s_at	actin binding LIM protein 1	10808	ABLIM1	0.470	+	4.06E-03	6.01E-04
202003_PM_s_at	acetyl-Coenzyme A acyltransferase 2	6733	ACAA2	0.409	+	1.76E-04	5.47E-03
49452_PM_at	acetyl-Coenzyme A carboxylase beta	152485	ACACB	0.561	+	1.42E-02	1.71E-02
219986_PM_s_at	acyl-Coenzyme A dehydrogenase family, member 10	10671	ACAD10	0.354	+	3.52E-03	3.06E-02
205412_PM_at	acetyl-Coenzyme A acetyltransferase 1	10458	ACAT1	0.339	+	4.34E-03	1.38E-02
225663_PM_at	acyl-Coenzyme A binding domain containing 5	203069	ACBD5	0.314	+	3.63E-02	2.44E-02
225317_PM_at	acyl-Coenzyme A binding domain containing 6	28985	ACBD6	0.427	+	9.09E-03	1.54E-02
227776_PM_at	alkaline ceramidase 3	4325	ACER3	0.557	+	1.68E-03	1.20E-02
201127_PM_s_at	ATP citrate lyase	9324	ACLY	0.683	+	2.44E-05	1.49E-03
241949_PM_at	acyl-CoA thioesterase 6	---	ACOT6	0.337	+	2.12E-03	8.35E-03
218795_PM_at	acid phosphatase 6, lysophosphatidic	25836	ACP6	0.414	+	2.97E-02	3.21E-02
238825_PM_at	acidic repeat containing	79611	ACRC	0.339	+	6.08E-03	2.83E-03
206465_PM_at	acyl-CoA synthetase bubblegum family member 1	23275	ACSBG1	0.330	+	4.66E-02	3.30E-02
201963_PM_at	acyl-CoA synthetase long-chain family member 1	2138	ACSL1	0.644	+	2.79E-02	7.70E-03
229725_PM_at	Acyl-CoA synthetase long-chain family member 6	9879	ACSL6	0.296	+	6.21E-03	1.49E-02
229222_PM_at	acyl-CoA synthetase short-chain family member 3	81873	ACSS3	0.407	+	1.68E-02	3.08E-02
202666_PM_s_at	actin-like 6A	55863	ACTL6A	0.352	+	2.14E-02	4.29E-02
206014_PM_at	actin-like 6B	8943	ACTL6B	0.502	+	1.12E-02	2.30E-03
203863_PM_at	actinin, alpha 2	6612	ACTN2	0.715	+	1.24E-02	1.91E-02
203862_PM_s_at	actinin, alpha 2	10121	ACTN2	0.271	+	4.05E-02	2.26E-02
218395_PM_at	ARP6 actin-related protein 6 homolog (yeast)	11127	ACTR6	0.393	+	4.03E-03	1.28E-02

213198_PM_at	activin A receptor, type IB	829	ACVR1B	0.391	+	3.36E-02	3.05E-02
228416_PM_at	activin A receptor, type IIA	59345	ACVR2A	0.653	+	3.64E-03	9.87E-03
236126_PM_at	activin A receptor, type IIB	---	ACVR2B	0.689	+	2.91E-02	3.42E-02
205260_PM_s_at	acylphosphatase 1, erythrocyte (common) type	2261	ACYP1	0.481	+	2.54E-04	3.29E-03
202603_PM_at	ADAM metallopeptidase domain 10	51192	ADAM10	0.428	+	1.30E-03	6.85E-03
213532_PM_at	ADAM metallopeptidase domain 17	8671	ADAM17	0.322	+	3.40E-02	3.11E-02
214913_PM_at	ADAM metallopeptidase with thrombospondin type 1 motif, 3	55032	ADAMTS3	0.870	+	5.60E-03	2.24E-02
235649_PM_at	ADAM metallopeptidase with thrombospondin type 1 motif, 8	---	ADAMTS8	0.379	+	4.20E-04	7.13E-04
227213_PM_at	adenosine deaminase, tRNA-specific 2, TAD2 homolog (S. cerevisiae)	56647	ADAT2	0.501	+	2.04E-03	4.93E-03
226690_PM_at	Adenylate cyclase activating polypeptide 1 (pituitary) receptor type I	204	ADCYAP1R1	0.440	+	7.25E-04	5.59E-03
208030_PM_s_at	255eparin255 1 (alpha)	4233	ADD1	0.298	+	2.45E-02	1.26E-02
208848_PM_at	alcohol dehydrogenase 5 (class III), chi polypeptide	9950	ADH5	0.285	+	5.69E-03	1.19E-02
227113_PM_at	alcohol dehydrogenase, iron containing, 1	23236	ADHFE1	0.514	+	4.43E-03	1.46E-02
201346_PM_at	adiponectin receptor 2	9590	ADIPOR2	0.414	+	4.08E-02	2.33E-02
220538_PM_at	adrenomedullin 2	64854	ADM2	0.296	+	3.19E-02	1.51E-02
226426_PM_at	activity-dependent neuroprotector homeobox	5994	ADNP	0.788	+	3.28E-02	2.64E-02
203322_PM_at	ADNP homeobox 2	10717	ADNP2	0.468	+	4.89E-03	1.42E-02
220980_PM_s_at	ADP-dependent glucokinase	2869	ADPGK	0.591	+	2.45E-03	2.12E-02
228042_PM_at	ADP-ribosylarginine hydrolase	90871	ADPRH	0.476	+	3.21E-02	3.40E-02
223097_PM_at	ADP-ribosylhydrolase like 2	79029	ADPRHL2	0.387	+	1.65E-02	1.14E-02
229309_PM_at	adrenergic, beta-1-, receptor	130271	ADRB1	0.796	+	4.25E-02	5.67E-03
202144_PM_s_at	adenylosuccinate lyase	22999	ADSL	0.824	+	6.16E-03	4.76E-03
225889_PM_at	AE binding protein 2	10063	AEBP2	0.495	+	1.16E-02	5.30E-03
212221_PM_x_at	arylformamidase /// iduronate 2-sulfatase	3615	AFMID /// IDS	0.266	+	1.74E-02	2.03E-02
226561_PM_at	ArfGAP with FG repeats 1	2130	AGFG1	0.486	+	4.68E-02	4.01E-02
203566_PM_s_at	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase	57147	AGL	0.298	+	5.46E-03	1.48E-02
223182_PM_s_at	1-acylglycerol-3-phosphate O-acyltransferase 3	79612	AGPAT3	0.278	+	1.80E-03	1.14E-02
225108_PM_at	alkylglycerone phosphate synthase	80143	AGPS	0.602	+	8.08E-03	3.77E-02
238135_PM_at	Angiotensin II receptor-associated protein	64750	AGTRAP	0.310	+	2.92E-03	2.22E-02

221008_PM_s_at	alanine-glyoxylate aminotransferase 2-like 1	5509	AGXT2L1	0.599	+	1.30E-02	3.13E-02
214766_PM_s_at	AT hook containing transcription factor 1	79665	AHCTF1	0.307	+	8.19E-03	2.75E-02
212992_PM_at	AHNAK nucleoprotein 2	6861	AHNAK2	0.615	+	1.11E-02	2.44E-03
226801_PM_s_at	axin interactor, dorsalization associated	57798	AIDA	0.495	+	1.83E-02	7.26E-03
223136_PM_at	androgen-induced 1	10891	AIG1	0.309	+	8.36E-04	4.12E-04
206513_PM_at	absent in melanoma 2	83737	AIM2	0.572	+	2.14E-02	4.18E-02
209971_PM_x_at	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2	5937	AIMP2	0.365	+	2.51E-02	1.92E-02
205996_PM_s_at	adenylate kinase 2	1983	AK2	0.333	+	2.52E-03	1.46E-02
212174_PM_at	adenylate kinase 2	22938	AK2	0.500	+	1.91E-02	4.89E-02
225342_PM_at	adenylate kinase 3-like 1	130026	AK3L1	0.519	+	1.01E-02	8.36E-03
204348_PM_s_at	adenylate kinase 3-like 1	832	AK3L1	0.271	+	1.05E-02	6.06E-03
210517_PM_s_at	A kinase (PRKA) anchor protein 12	81873	AKAP12	0.549	+	3.79E-03	9.29E-03
227530_PM_at	A kinase (PRKA) anchor protein 12	81609	AKAP12	0.899	+	1.49E-02	2.06E-02
226694_PM_at	A kinase (PRKA) anchor protein 2 /// PALM2-AKAP2 readthrough transcript	25957	AKAP2 /// PALM2-AKAP2	0.515	+	4.34E-03	7.89E-03
230846_PM_at	A kinase (PRKA) anchor protein 5	157695	AKAP5	0.596	+	2.21E-02	2.82E-02
205359_PM_at	A kinase (PRKA) anchor protein 6	1102	AKAP6	0.505	+	1.94E-02	1.69E-02
205771_PM_s_at	A kinase (PRKA) anchor protein 7	10472	AKAP7	0.338	+	1.23E-02	4.01E-02
210962_PM_s_at	A kinase (PRKA) anchor protein (yotiao) 9	5926	AKAP9	0.821	+	6.56E-03	2.17E-03
222459_PM_at	akirin 1	23173	AKIRIN1	0.646	+	3.33E-02	3.24E-02
204151_PM_x_at	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)	7072	AKR1C1	0.478	+	2.29E-02	2.68E-02
209699_PM_x_at	aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)	51435	AKR1C2	0.307	+	4.89E-02	4.89E-02
212609_PM_s_at	V-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	9553	AKT3	0.339	+	4.90E-02	2.94E-03
201952_PM_at	activated leukocyte cell adhesion molecule	23522	ALCAM	0.282	+	1.42E-02	1.54E-02
203608_PM_at	aldehyde dehydrogenase 5 family, member A1	27327	ALDH5A1	0.528	+	3.55E-02	3.44E-02

201612_PM_at	aldehyde dehydrogenase 9 family, member A1	50649	ALDH9A1	0.833	+	4.52E-02	3.68E-02
205583_PM_s_at	asparagine-linked glycosylation 13 homolog (S. cerevisiae)	120	ALG13	0.693	+	3.46E-02	3.02E-02
218203_PM_at	asparagine-linked glycosylation 5, dolichyl-phosphate beta-glucosyltransferase homolog (S. cerevisiae)	57539	ALG5	0.769	+	2.39E-03	2.48E-03
219649_PM_at	asparagine-linked glycosylation 6, alpha-1,3-glucosyltransferase homolog (S. cerevisiae)	9663	ALG6	0.485	+	1.39E-03	7.97E-03
203545_PM_at	asparagine-linked glycosylation 8, alpha-1,3-glucosyltransferase homolog (S. cerevisiae)	2810	ALG8	0.556	+	2.19E-02	3.86E-02
228817_PM_at	asparagine-linked glycosylation 9, alpha-1,2-mannosyltransferase homolog (S. cerevisiae)	23394	ALG9	0.678	+	6.96E-03	1.55E-02
205621_PM_at	alkB, alkylation repair homolog 1 (E. coli)	22887	ALKBH1	0.682	+	7.27E-03	1.99E-02
226291_PM_at	amyotrophic lateral sclerosis 2 (juvenile)	9818	ALS2	0.445	+	4.40E-02	4.78E-02
228255_PM_at	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4	254048	ALS2CR4	0.621	+	5.30E-03	9.71E-03
209424_PM_s_at	alpha-methylacyl-CoA racemase	55074	AMACR	0.341	+	1.05E-02	4.14E-02
226421_PM_at	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1	7204	AMMECR1	0.552	+	4.09E-03	5.97E-03
204976_PM_s_at	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1	963	AMMECR1	0.744	+	5.57E-03	2.45E-02
223297_PM_at	AMME chromosomal region gene 1-like	54819	AMMECR1L	0.950	+	4.23E-03	9.75E-03
226258_PM_at	antagonist of mitotic exit network 1 homolog (S. cerevisiae)	6239	AMN1	0.449	+	9.94E-03	6.26E-03
208498_PM_s_at	amylase, alpha 1A (salivary) /// amylase, alpha 1B (salivary) /// amylase, alpha 1C (salivary) /// amylase, alpha 2A (pancreatic) /// amylase, alpha 2B (pancreatic)	26047	AMY1A /// AMY1B /// AMY1C /// AMY2A /// AMY2B	0.736	+	8.26E-03	2.08E-03
207845_PM_s_at	anaphase promoting complex subunit 10	100130175 /// 92482	ANAPC10	0.632	+	4.63E-03	5.50E-04
209001_PM_s_at	anaphase promoting complex subunit 13	5583	ANAPC13	0.436	+	1.05E-03	7.94E-03
232524_PM_x_at	anaphase promoting complex subunit 4	1630	ANAPC4	0.767	+	6.56E-03	6.55E-03
226917_PM_s_at	anaphase promoting complex subunit 4	---	ANAPC4	0.710	+	1.01E-02	1.46E-02
225521_PM_at	anaphase promoting complex subunit 7	6671	ANAPC7	0.671	+	1.16E-02	2.54E-02
221825_PM_at	angel homolog 2 (Drosophila)	5435	ANGEL2	0.322	+	3.14E-02	2.96E-02

220076_PM_at	ankylosis, progressive homolog (mouse)	2591	ANKH	0.357	+	1.67E-02	4.08E-02
208773_PM_s_at	ankyrin repeat and KH domain containing 1 /// ANKHD1-EIF4EBP3 readthrough transcript	26993	ANKHD1 /// ANKHD1-EIF4EBP3	0.728	+	2.60E-02	2.48E-02
214919_PM_s_at	ANKHD1-EIF4EBP3 readthrough transcript /// eukaryotic translation initiation factor 4E binding protein 3	11266	ANKHD1-EIF4EBP3 /// EIF4EBP3	0.414	+	1.08E-03	3.66E-03
243181_PM_at	ankyrin repeat and IBR domain containing 1	---	ANKIB1	0.268	+	1.02E-02	4.57E-02
224682_PM_at	ankyrin repeat and IBR domain containing 1	144363	ANKIB1	0.533	+	3.67E-02	3.95E-02
212798_PM_s_at	ankyrin repeat and MYND domain containing 2	1462	ANKMY2	0.378	+	1.36E-02	2.44E-02
218769_PM_s_at	ankyrin repeat, family A (RFXANK-like), 2	146713	ANKRA2	0.475	+	1.04E-02	7.57E-03
223251_PM_s_at	ankyrin repeat domain 10	63933	ANKRD10	0.599	+	2.30E-02	3.42E-02
213035_PM_at	ankyrin repeat domain 28	9447	ANKRD28	0.499	+	6.92E-03	1.69E-02
223542_PM_at	ankyrin repeat domain 32	55339	ANKRD32	0.740	+	7.29E-03	8.41E-03
231118_PM_at	ankyrin repeat domain 35	253039	ANKRD35	0.485	+	1.11E-03	3.22E-03
230238_PM_at	ankyrin repeat domain 43	257194	ANKRD43	0.437	+	4.49E-02	3.13E-02
212731_PM_at	ankyrin repeat domain 46	27252	ANKRD46	0.307	+	3.10E-02	4.44E-03
219069_PM_at	ankyrin repeat domain 49	6506	ANKRD49	1.170	+	5.58E-03	1.21E-02
225731_PM_at	ankyrin repeat domain 50	23527	ANKRD50	0.536	+	1.33E-02	1.11E-02
204672_PM_s_at	ankyrin repeat domain 6	23518	ANKRD6	0.702	+	3.77E-03	1.12E-02
230972_PM_at	ankyrin repeat domain 9	22871	ANKRD9	0.270	+	2.19E-02	4.20E-02
212747_PM_at	ankyrin repeat and sterile alpha motif domain containing 1A	57030	ANKS1A	0.561	+	2.55E-02	3.52E-02
240292_PM_x_at	ankyrin repeat and sterile alpha motif domain containing 1B	---	ANKS1B	0.346	+	3.12E-03	5.00E-04
218910_PM_at	anoctamin 10	8996	ANO10	0.402	+	1.91E-02	1.25E-02
236420_PM_s_at	anoctamin 4	---	ANO4	0.934	+	3.65E-02	6.87E-03
201306_PM_s_at	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	22902	ANP32B	0.294	+	3.69E-02	2.32E-02
221505_PM_at	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	3741	ANP32E	0.498	+	4.82E-04	1.43E-03
224694_PM_at	anthrax toxin receptor 1	29904	ANTXR1	0.683	+	1.85E-02	1.33E-02
228573_PM_at	anthrax toxin receptor 2	7690	ANTXR2	0.361	+	3.10E-03	1.53E-03
201012_PM_at	annexin A1	821	ANXA1	0.980	+	1.76E-03	5.11E-03
225771_PM_at	adaptor-related protein complex 1, gamma 1 subunit	150622	AP1G1	0.270	+	4.78E-03	3.17E-02

203142_PM_s_at	adaptor-related protein complex 3, beta 1 subunit	25957	AP3B1	0.350	+	1.59E-02	3.04E-02
222517_PM_at	adaptor-related protein complex 3, mu 1 subunit	167227	AP3M1	0.729	+	1.15E-02	3.94E-03
202442_PM_at	adaptor-related protein complex 3, sigma 1 subunit	10161	AP3S1	0.443	+	9.80E-03	1.97E-03
231714_PM_s_at	adaptor-related protein complex 4, beta 1 subunit	22927	AP4B1	0.439	+	7.21E-03	2.24E-02
235647_PM_at	Adaptor-related protein complex 4, sigma 1 subunit	6129	AP4S1	0.536	+	7.29E-03	1.09E-02
215148_PM_s_at	amyloid beta (A4) precursor protein-binding, family A, member 3	55540	APBA3	0.305	+	7.84E-03	6.47E-03
212985_PM_at	amyloid beta (A4) precursor protein-binding, family B, member 2	10538	APBB2	0.342	+	3.96E-02	4.00E-03
203525_PM_s_at	adenomatous polyposis coli	10471	APC	0.387	+	4.70E-02	3.15E-02
225016_PM_at	adenomatosis polyposis coli down-regulated 1	83999	APCDD1	0.406	+	3.75E-02	2.53E-02
201687_PM_s_at	apoptosis inhibitor 5	9777	API5	0.397	+	1.86E-02	1.42E-02
218698_PM_at	APAF1 interacting protein	165545	APIP	0.641	+	1.49E-03	4.85E-04
213553_PM_x_at	apolipoprotein C-I	5441	APOC1	0.429	+	1.78E-02	1.65E-02
221013_PM_s_at	apolipoprotein L, 2	6781	APOL2	0.378	+	1.34E-02	2.56E-02
235433_PM_at	apolipoprotein O-like	---	APOOL	0.598	+	2.35E-03	8.59E-03
202630_PM_at	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	23762	APPBP2	0.556	+	2.12E-02	1.41E-02
218158_PM_s_at	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1	285343	APPL1	0.409	+	1.13E-02	1.52E-02
229526_PM_at	aquaporin 11	199704	AQP11	0.641	+	1.11E-02	2.72E-02
39248_PM_at	aquaporin 3 (Gill blood group)	283578	AQP3	0.368	+	3.37E-02	3.70E-02
226228_PM_at	aquaporin 4	7058	AQP4	0.408	+	4.68E-03	5.62E-03
242039_PM_at	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1	11154	ARAP1	0.303	+	8.00E-03	1.41E-02
201097_PM_s_at	ADP-ribosylation factor 4	490	ARF4	0.370	+	1.80E-02	2.06E-02
224788_PM_at	ADP-ribosylation factor 6	10818	ARF6	0.691	+	3.57E-03	2.37E-03
202211_PM_at	ADP-ribosylation factor GTPase activating protein 3	8751	ARFGAP3	0.435	+	1.52E-02	4.38E-02
202956_PM_at	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	56894	ARFGEF1	0.407	+	5.84E-03	1.23E-02
218230_PM_at	ADP-ribosylation factor interacting protein 1	166929	ARFIP1	0.376	+	1.24E-02	1.81E-02
202117_PM_at	Rho GTPase activating protein 1	386757 /// 6535 /// 653562	ARHGAP1	0.321	+	2.85E-02	3.98E-02

207606_PM_s_at	Rho GTPase activating protein 12	158471	ARHGAP12	0.544	+	3.10E-02	1.98E-02
212738_PM_at	Rho GTPase activating protein 19	1318	ARHGAP19	0.323	+	1.52E-02	1.96E-02
235635_PM_at	Rho GTPase activating protein 5	6760	ARHGAP5	1.388	+	1.60E-03	4.08E-03
217936_PM_at	Rho GTPase activating protein 5	115098	ARHGAP5	0.391	+	3.41E-03	1.37E-03
216620_PM_s_at	Rho guanine nucleotide exchange factor (GEF) 10	56172	ARHGEF10	0.644	+	5.92E-03	7.21E-03
221656_PM_s_at	Rho guanine nucleotide exchange factor (GEF) 10-like	11261	ARHGEF10L	0.617	+	1.16E-02	1.04E-02
201334_PM_s_at	Rho guanine nucleotide exchange factor (GEF) 12	1432	ARHGEF12	0.553	+	2.90E-02	6.80E-03
209435_PM_s_at	Rho/Rac guanine nucleotide exchange factor (GEF) 2	10600	ARHGEF2	0.341	+	1.42E-02	3.42E-02
209539_PM_at	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	51126	ARHGEF6	0.610	+	6.33E-03	1.30E-02
225181_PM_at	AT rich interactive domain 1B (SWI1-like)	55607	ARID1B	0.415	+	2.19E-02	6.01E-03
218964_PM_at	AT rich interactive domain 3B (BRIGHT-like)	161725	ARID3B	0.388	+	3.30E-03	1.57E-02
230141_PM_at	AT rich interactive domain 4A (RBP1-like)	340481	ARID4A	0.549	+	2.19E-02	1.96E-02
221230_PM_s_at	AT rich interactive domain 4B (RBP1-like)	9397	ARID4B	0.449	+	3.26E-02	3.11E-02
201880_PM_at	260eparin homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	1350	ARIH1	0.426	+	2.64E-02	1.79E-02
1554245_PM_x_at	ADP-ribosylation factor-like 17 /// ADP-ribosylation factor-like 17 pseudogene 1	4736	ARL17 /// ARL17P1	0.462	+	5.42E-04	2.77E-03
223735_PM_at	ADP-ribosylation factor-like 6	58480	ARL6	0.372	+	1.94E-03	9.45E-03
235320_PM_at	ADP-ribosylation factor-like 6	---	ARL6	0.395	+	2.77E-02	3.07E-03
200761_PM_s_at	ADP-ribosylation-like factor 6 interacting protein 5	8867	ARL6IP5	0.375	+	1.67E-03	4.54E-04
217852_PM_s_at	ADP-ribosylation factor-like 8B	10152	ARL8B	0.336	+	1.63E-02	1.26E-03
229062_PM_at	ADP-ribosylation factor-like 9	57695	ARL9	0.325	+	1.37E-02	4.93E-02
203487_PM_s_at	armadillo repeat containing 8	283130	ARMC8	0.634	+	5.78E-03	1.94E-02
203404_PM_at	armadillo repeat containing, X-linked 2	55737	ARMCX2	0.463	+	3.12E-02	4.11E-02
227444_PM_at	Armadillo repeat containing, X-linked 4	55777	ARMCX4	0.699	+	1.50E-02	1.83E-02
214749_PM_s_at	armadillo repeat containing, X-linked 6 /// similar to armadillo repeat containing, X-linked 6	79048	ARMCX6 /// LOC653354	0.709	+	1.59E-03	2.78E-03
226914_PM_at	actin related protein 2/3 complex, subunit 5-like	---	ARPC5L	0.760	+	6.07E-03	1.83E-02
226915_PM_s_at	actin related protein 2/3 complex, subunit 5-like	151230	ARPC5L	0.297	+	6.35E-03	2.22E-03
220966_PM_x_at	actin related protein 2/3 complex, subunit 5-like	78988	ARPC5L	0.356	+	1.62E-02	6.20E-03
221483_PM_s_at	cAMP-regulated phosphoprotein, 19kDa	204	ARPP19	0.365	+	1.18E-03	9.13E-03
221482_PM_s_at	cAMP-regulated phosphoprotein, 19kDa	2960	ARPP19	0.419	+	7.11E-03	8.65E-03

220359_PM_s_at	cyclic AMP-regulated phosphoprotein, 21 kD	51096	ARPP-21	0.629	+	1.15E-02	2.47E-02
231935_PM_at	cyclic AMP-regulated phosphoprotein, 21 kD	---	ARPP-21	0.421	+	3.22E-02	5.22E-03
224797_PM_at	arrestin domain containing 3	219854	ARRDC3	0.813	+	3.53E-03	1.86E-03
225283_PM_at	arrestin domain containing 4	125704	ARRDC4	0.329	+	1.43E-02	4.25E-02
225280_PM_x_at	arylsulfatase D	144108	ARSD	0.392	+	5.00E-03	1.79E-02
223223_PM_at	ARV1 homolog (S. cerevisiae)	51274	ARV1	0.461	+	1.51E-03	1.56E-02
224791_PM_at	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	23476	ASAP1	0.540	+	3.01E-02	1.31E-02
206414_PM_s_at	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2	23154	ASAP2	0.466	+	2.55E-02	4.95E-02
224524_PM_s_at	ankyrin repeat and SOCS box-containing 3 /// G protein-coupled receptor 75 /// GPR75-ASB3	81566	ASB3 /// GPR75 /// LOC100302652	0.328	+	1.13E-02	7.51E-03
235503_PM_at	ankyrin repeat and SOCS box-containing 5	---	ASB5	0.279	+	2.04E-03	1.45E-02
226513_PM_at	ankyrin repeat and SOCS box-containing 7	521	ASB7	0.439	+	1.92E-02	7.88E-03
226861_PM_at	ankyrin repeat and SOCS box-containing 8	115123	ASB8	0.400	+	1.78E-02	1.26E-02
1554627_PM_a_at	activating signal cointegrator 1 complex subunit 1	23521	ASCC1	0.598	+	7.05E-03	1.85E-02
209988_PM_s_at	achaete-scute complex homolog 1 (Drosophila)	115106	ASCL1	0.918	+	1.96E-02	4.37E-02
203428_PM_s_at	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	84256	ASF1A	0.525	+	3.34E-02	3.26E-03
203427_PM_at	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	55738	ASF1A	0.511	+	3.83E-02	3.09E-02
36553_PM_at	acetylserotonin O-methyltransferase-like	---	ASMTL	0.455	+	2.07E-03	2.19E-02
217987_PM_at	asparagine synthetase domain containing 1	84991	ASNSD1	0.458	+	2.49E-02	1.74E-02
235514_PM_at	aspartic peptidase, retroviral-like 1	30000	ASPRV1	0.267	+	6.07E-03	1.17E-02
215407_PM_s_at	astrotactin 2	51621	ASTN2	0.374	+	1.70E-02	4.27E-02
212234_PM_at	additional sex combs like 1 (Drosophila)	29889	ASXL1	0.391	+	1.38E-02	4.62E-02
212984_PM_at	activating transcription factor 2	9221	ATF2	0.725	+	5.40E-03	8.65E-03
228830_PM_s_at	activating transcription factor 7	89890	ATF7	0.391	+	2.34E-02	1.21E-02
228829_PM_at	activating transcription factor 7	528	ATF7	0.956	+	3.17E-02	2.62E-02
204833_PM_at	ATG12 autophagy related 12 homolog (S. cerevisiae)	8520	ATG12	0.302	+	4.06E-02	8.37E-03
226684_PM_at	ATG2 autophagy related 2 homolog B (S. cerevisiae)	23433	ATG2B	0.656	+	1.97E-02	2.42E-02
213115_PM_at	ATG4 autophagy related 4 homolog A (S. cerevisiae)	29855	ATG4A	0.473	+	1.64E-02	1.41E-02
202512_PM_s_at	ATG5 autophagy related 5 homolog (S. cerevisiae)	56986	ATG5	0.440	+	1.68E-02	2.06E-02

202511_PM_s_at	ATG5 autophagy related 5 homolog (S. cerevisiae)	29071	ATG5	0.359	+	3.21E-02	1.47E-02
224893_PM_at	atlastin GTPase 3	64145	ATL3	0.745	+	1.69E-02	1.90E-02
213238_PM_at	ATPase, class V, type 10D	7415	ATP10D	0.299	+	2.68E-03	7.21E-03
212297_PM_at	ATPase type 13A3	64746	ATP13A3	0.503	+	3.96E-02	1.55E-02
203296_PM_s_at	ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide	79109	ATP1A2	0.402	+	7.85E-03	1.01E-02
212930_PM_at	ATPase, Ca++ transporting, plasma membrane 1	2675	ATP2B1	0.392	+	2.93E-02	3.04E-02
211137_PM_s_at	ATPase, Ca++ transporting, type 2C, member 1	160	ATP2C1	0.304	+	6.93E-03	1.35E-02
213366_PM_x_at	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	9459	ATP5C1	0.348	+	5.90E-03	8.25E-03
208870_PM_x_at	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	57140	ATP5C1	0.426	+	7.30E-03	4.98E-03
205711_PM_x_at	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	8775	ATP5C1	0.348	+	1.04E-02	6.50E-03
211755_PM_s_at	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1	51326 /// 641522	ATP5F1	0.336	+	6.35E-03	1.78E-02
209492_PM_x_at	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	51247	ATP5I	0.381	+	7.29E-03	2.00E-02
207335_PM_x_at	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	89910	ATP5I	0.340	+	8.78E-03	2.33E-02
202325_PM_s_at	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6	27430	ATP5J	0.428	+	1.41E-03	7.56E-04
202961_PM_s_at	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	23621	ATP5J2	0.334	+	6.19E-03	9.34E-03
216954_PM_x_at	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	84064	ATP5O	0.299	+	2.02E-03	5.41E-03
221677_PM_s_at	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit /// downstream neighbor of SON	2892	ATP5O /// DONSON	0.868	+	2.45E-03	1.99E-03
230132_PM_at	ATP5S-like	23408	ATP5SL	0.598	+	9.66E-03	5.17E-03
201443_PM_s_at	ATPase, H+ transporting, lysosomal accessory protein 2	10142	ATP6AP2	0.396	+	1.80E-02	1.53E-02
214150_PM_x_at	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	26034	ATP6V0E1	0.403	+	6.62E-03	1.10E-02
200096_PM_s_at	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1	10150	ATP6V0E1	0.489	+	1.19E-02	1.38E-02
226463_PM_at	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	7381	ATP6V1C1	0.333	+	1.06E-03	6.99E-03
208898_PM_at	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	55337	ATP6V1D	0.435	+	3.75E-03	6.09E-03

213106_PM_at	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	2787	ATP8A1	0.270	+	1.63E-02	2.02E-02
226302_PM_at	ATPase, class I, type 8B, member 1	357	ATP8B1	0.367	+	2.13E-02	2.20E-02
224728_PM_at	ATP synthase mitochondrial F1 complex assembly factor 1	8935	ATPAF1	0.637	+	1.01E-02	1.58E-02
218671_PM_s_at	ATPase inhibitory factor 1	115294	ATPIF1	0.564	+	3.66E-04	1.59E-03
223338_PM_s_at	ATPase inhibitory factor 1	9367	ATPIF1	0.317	+	1.09E-02	1.44E-03
209902_PM_at	ataxia telangiectasia and Rad3 related	401505	ATR	0.646	+	6.25E-03	8.06E-03
209903_PM_s_at	ataxia telangiectasia and Rad3 related	54737	ATR	0.611	+	2.29E-02	1.61E-02
208861_PM_s_at	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevisiae)	64786	ATRX	0.345	+	3.32E-03	2.17E-02
203232_PM_s_at	ataxin 1	643167 /// 9584	ATXN1	0.426	+	1.40E-02	6.36E-03
226095_PM_s_at	ataxin 1-like	5412	ATXN1L	0.564	+	1.30E-02	2.18E-02
202622_PM_s_at	ataxin 2	54758	ATXN2	0.304	+	1.62E-02	4.56E-02
235240_PM_at	ataxin 3	129642	ATXN3	0.298	+	6.43E-04	2.56E-03
205415_PM_s_at	ataxin 3	10675	ATXN3	0.418	+	4.44E-03	4.73E-03
243259_PM_at	ataxin 7	---	ATXN7	0.457	+	3.01E-02	2.96E-03
205052_PM_at	AU RNA binding protein/enoyl-Coenzyme A hydratase	7703	AUH	0.377	+	1.95E-02	3.77E-02
222498_PM_at	5-azacytidine induced 2	4493	AZI2	0.844	+	8.96E-03	1.03E-02
223846_PM_at	5-azacytidine induced 2	84640	AZI2	0.456	+	9.38E-03	2.83E-02
201891_PM_s_at	beta-2-microglobulin	6613	B2M	0.587	+	1.62E-02	2.12E-02
217452_PM_s_at	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	79877	B3GALT2	0.462	+	4.76E-03	1.07E-03
227100_PM_at	beta 1,3-galactosyltransferase-like	4916	B3GALTL	0.366	+	1.19E-02	2.23E-02
235333_PM_at	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6	5125	B4GALT6	0.536	+	7.96E-03	6.05E-03
218899_PM_s_at	brain and acute leukemia, cytoplasmic	1540	BAALC	0.473	+	2.42E-02	1.45E-02
221234_PM_s_at	BTB and CNC homology 1, basic leucine zipper transcription factor 2	7518	BACH2	0.832	+	1.14E-02	4.54E-03
229720_PM_at	BCL2-associated athanogene	163486	BAG1	0.806	+	2.57E-04	3.69E-03
202387_PM_at	BCL2-associated athanogene	89797	BAG1	0.291	+	8.16E-03	5.47E-03
217911_PM_s_at	BCL2-associated athanogene 3	9043	BAG3	0.404	+	7.50E-03	1.98E-02
211946_PM_s_at	BAT2 domain containing 1	7528	BAT2D1	0.474	+	4.13E-02	3.06E-02
205965_PM_at	basic leucine zipper transcription factor, ATF-like	6767	BATF	0.333	+	6.93E-03	3.97E-03

208445_PM_s_at	bromodomain adjacent to zinc finger domain, 1B	55660	BAZ1B	0.317	+	2.88E-02	4.87E-02
201355_PM_s_at	bromodomain adjacent to zinc finger domain, 2A	658	BAZ2A	0.334	+	1.48E-02	2.21E-02
203080_PM_s_at	bromodomain adjacent to zinc finger domain, 2B	91012	BAZ2B	0.601	+	2.36E-02	1.65E-02
211692_PM_s_at	BCL2 binding component 3	83696	BBC3	0.679	+	1.32E-02	1.71E-02
205363_PM_at	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1	5126	BBOX1	0.939	+	1.51E-03	1.55E-03
218471_PM_s_at	Bardet-Biedl syndrome 1	130733	BBS1	0.669	+	7.03E-03	3.06E-02
230697_PM_at	Bardet-Biedl syndrome 5	401207	BBS5	0.503	+	1.95E-02	1.31E-02
40093_PM_at	basal cell adhesion molecule (Lutheran blood group)	---	BCAM	0.288	+	2.26E-02	1.29E-02
204032_PM_at	breast cancer anti-estrogen resistance 3	5931	BCAR3	0.298	+	7.98E-03	1.93E-02
225285_PM_at	branched chain aminotransferase 1, cytosolic	643008	BCAT1	0.288	+	2.04E-02	2.45E-02
218264_PM_at	BRCA2 and CDKN1A interacting protein	148523	BCCIP	0.718	+	7.28E-04	2.90E-03
227322_PM_s_at	BRCA2 and CDKN1A interacting protein	79686	BCCIP	0.496	+	3.01E-03	1.81E-02
210653_PM_s_at	branched chain keto acid dehydrogenase E1, beta polypeptide	1456	BCKDHB	0.346	+	4.65E-02	3.66E-02
1559078_PM_at	B-cell CLL/lymphoma 11A (zinc finger protein)	2947	BCL11A	0.507	+	1.75E-02	1.85E-02
203685_PM_at	B-cell CLL/lymphoma 2	27125	BCL2	0.774	+	1.91E-02	2.68E-02
225606_PM_at	BCL2-like 11 (apoptosis facilitator)	54556	BCL2L11	0.410	+	2.78E-02	3.23E-02
201084_PM_s_at	BCL2-associated transcription factor 1	9139	BCLAF1	0.336	+	1.31E-02	3.39E-02
226290_PM_at	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	2261	BDP1	1.007	+	1.86E-02	1.04E-02
214068_PM_at	brain expressed, associated with Nedd4	6742	BEAN	0.324	+	1.22E-02	3.17E-02
213709_PM_at	basic helix-loop-helix domain containing, class B, 9	23030	BHLHB9	0.574	+	2.27E-03	1.13E-03
206119_PM_at	betaine-homocysteine methyltransferase	51382	BHMT	1.196	+	4.46E-03	2.04E-03
213154_PM_s_at	bicaudal D homolog 2 (Drosophila)	6620	BICD2	0.727	+	3.13E-02	1.41E-02
233093_PM_s_at	baculoviral IAP repeat-containing 6	---	BIRC6	0.486	+	3.52E-02	2.93E-02
220451_PM_s_at	baculoviral IAP repeat-containing 7	63931	BIRC7	0.339	+	7.04E-03	1.60E-02
222761_PM_at	basic, immunoglobulin-like variable motif containing	259217	BIVM	0.604	+	1.35E-02	8.58E-03
225049_PM_at	biogenesis of lysosomal organelles complex-1, subunit 2	2674	BLOC1S2	0.477	+	7.03E-04	1.70E-03
203773_PM_x_at	biliverdin reductase A	161497	BLVRA	0.645	+	2.93E-03	3.39E-03
211729_PM_x_at	biliverdin reductase A	23299	BLVRA	0.527	+	5.90E-03	8.59E-03
202201_PM_at	biliverdin reductase B (flavin reductase (NADPH))	324	BLVRB	0.346	+	4.46E-02	3.01E-02

32088_PM_at	basic leucine zipper nuclear factor 1	---	BLZF1	0.347	+	1.18E-03	7.12E-04
59644_PM_at	BMP2 inducible kinase	---	BMP2K	0.278	+	3.20E-02	2.18E-02
209590_PM_at	bone morphogenetic protein 7	51313	BMP7	0.492	+	5.22E-03	1.36E-02
213578_PM_at	bone morphogenetic protein receptor, type IA	4000	BMPR1A	0.634	+	2.91E-02	1.03E-02
229975_PM_at	bone morphogenetic protein receptor, type IB	118429	BMPR1B	0.270	+	2.94E-02	4.25E-02
201849_PM_at	BCL2/adenovirus E1B 19kDa interacting protein 3	5378	BNIP3	0.349	+	1.11E-02	3.02E-02
221478_PM_at	BCL2/adenovirus E1B 19kDa interacting protein 3-like	5587	BNIP3L	0.351	+	4.11E-02	1.64E-02
225030_PM_at	biorientation of chromosomes in cell division 1	151195	BOD1	0.282	+	2.69E-03	7.51E-03
225821_PM_s_at	biorientation of chromosomes in cell division 1-like	55735	BOD1L	0.546	+	1.95E-02	1.23E-02
209836_PM_x_at	265epa homolog 2 (E. coli) /// 265epa homolog 2B (E. coli)	84128	BOLA2 /// BOLA2B	0.554	+	3.89E-03	1.31E-02
227291_PM_s_at	265epa homolog 3 (E. coli)	80219	BOLA3	0.527	+	3.06E-02	3.86E-02
203502_PM_at	2,3-bisphosphoglycerate mutase	79712	BPGM	0.762	+	3.79E-03	2.99E-03
209271_PM_at	bromodomain PHD finger transcription factor	3839	BPTF	0.570	+	3.64E-02	3.74E-02
221196_PM_x_at	BRCA1/BRCA2-containing complex, subunit 3	9575	BRCC3	0.498	+	1.02E-02	2.55E-02
229436_PM_x_at	BRCA1/BRCA2-containing complex, subunit 3	651250	BRCC3	0.277	+	4.77E-02	8.25E-03
226052_PM_at	bromodomain containing 4	9167	BRD4	0.448	+	2.14E-02	2.06E-02
226580_PM_at	breast cancer metastasis-suppressor 1-like	8741	BRMS1L	0.368	+	6.93E-03	1.53E-02
202427_PM_s_at	brain protein 44	10600	BRP44	0.346	+	5.58E-03	1.75E-03
218024_PM_at	brain protein 44-like	84058	BRP44L	0.440	+	8.49E-03	7.40E-03
225217_PM_s_at	bromodomain and PHD finger containing, 3	6815	BRPF3	0.802	+	2.53E-02	2.62E-02
231960_PM_at	bromodomain and WD repeat domain containing 1	100113407	BRWD1	0.595	+	9.85E-03	1.35E-02
209430_PM_at	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, 170kDa (Mot1 homolog, S. cerevisiae)	55758	BTAF1	0.695	+	2.10E-02	1.12E-02
224945_PM_at	BTB (POZ) domain containing 7	728568	BTBD7	0.654	+	3.09E-02	1.33E-02
214800_PM_x_at	basic transcription factor 3	723790 /// 8337	BTF3	0.536	+	5.19E-03	4.86E-03
211939_PM_x_at	basic transcription factor 3	441263	BTF3	0.346	+	9.04E-03	7.23E-03
238675_PM_x_at	basic transcription factor 3-like 4	---	BTF3L4	0.474	+	9.74E-03	3.87E-02
201236_PM_s_at	BTG family, member 2	10634	BTG2	0.638	+	3.56E-02	2.41E-02
205548_PM_s_at	BTG family, member 3	79171	BTG3	0.979	+	4.15E-03	1.57E-03
213134_PM_x_at	BTG family, member 3	8544	BTG3	0.692	+	1.37E-02	1.81E-02

204820_PM_s_at	butyrophilin, subfamily 3, member A2 /// butyrophilin, subfamily 3, member A3	4528	BTN3A2 /// BTN3A3	1.088	+	2.28E-02	2.12E-02
217207_PM_s_at	butyrophilin-like 3	25948	BTNL3	0.308	+	3.22E-02	3.16E-02
224504_PM_s_at	BUD13 homolog (S. cerevisiae)	10011	BUD13	0.264	+	3.14E-02	4.19E-02
219177_PM_at	brix domain containing 2	9804	BXDC2	0.287	+	1.51E-02	2.34E-02
218462_PM_at	brix domain containing 5	116835	BXDC5	0.443	+	3.53E-03	5.64E-03
215449_PM_at	266eparin266ing266e266 receptor (peripheral)-like 1	50632	BZRPL1	0.270	+	6.65E-03	1.90E-02
200777_PM_s_at	basic leucine zipper and W2 domains 1	815	BZW1	0.307	+	3.45E-02	2.91E-02
217809_PM_at	basic leucine zipper and W2 domains 2	81555	BZW2	0.674	+	7.43E-03	6.87E-03
229145_PM_at	chromosome 10 open reading frame 104	161742	C10orf104	0.267	+	1.04E-02	3.39E-02
224664_PM_at	chromosome 10 open reading frame 104	57678	C10orf104	0.358	+	1.63E-02	4.16E-03
242660_PM_at	chromosome 10 open reading frame 112	---	C10orf112	0.268	+	1.29E-02	2.18E-02
226892_PM_at	chromosome 10 open reading frame 12	26035	C10orf12	0.567	+	1.26E-02	2.18E-02
218331_PM_s_at	chromosome 10 open reading frame 18	57722	C10orf18	0.502	+	1.15E-02	1.87E-02
226398_PM_s_at	chromosome 10 open reading frame 4	10001	C10orf4	0.475	+	3.83E-04	6.29E-04
228155_PM_at	chromosome 10 open reading frame 58	140688	C10orf58	0.362	+	1.09E-02	7.78E-04
222617_PM_s_at	chromosome 10 open reading frame 84	23116	C10orf84	0.368	+	3.69E-03	5.42E-03
234947_PM_s_at	chromosome 10 open reading frame 84	2775	C10orf84	0.263	+	4.62E-03	2.43E-02
231530_PM_s_at	chromosome 11 open reading frame 1	90342	C11orf1	0.748	+	1.66E-03	9.09E-03
222785_PM_x_at	chromosome 11 open reading frame 1	2926	C11orf1	0.515	+	1.45E-02	1.17E-02
222807_PM_at	chromosome 11 open reading frame 30	81697	C11orf30	0.398	+	7.67E-03	3.35E-02
231045_PM_x_at	chromosome 11 open reading frame 31	64145	C11orf31	0.356	+	1.07E-03	1.99E-03
228332_PM_s_at	chromosome 11 open reading frame 31	641638	C11orf31	0.444	+	8.80E-03	8.11E-03
226383_PM_at	chromosome 11 open reading frame 46	6505	C11orf46	0.485	+	4.03E-02	7.11E-03
221637_PM_s_at	chromosome 11 open reading frame 48	6367	C11orf48	0.660	+	9.74E-03	7.48E-03
203257_PM_s_at	chromosome 11 open reading frame 49	84268	C11orf49	0.314	+	2.78E-03	1.18E-02
204218_PM_at	chromosome 11 open reading frame 51	10175	C11orf51	0.309	+	1.43E-02	1.73E-03
225811_PM_at	chromosome 11 open reading frame 58	153222	C11orf58	0.424	+	1.03E-03	4.66E-04
200084_PM_at	chromosome 11 open reading frame 58	3691	C11orf58	0.401	+	3.28E-03	3.54E-03
201784_PM_s_at	chromosome 11 open reading frame 58	6934	C11orf58	0.340	+	6.22E-03	1.93E-04
221599_PM_at	chromosome 11 open reading frame 67	22878	C11orf67	1.003	+	3.85E-03	1.17E-02
219979_PM_s_at	chromosome 11 open reading frame 73	266655	C11orf73	0.871	+	5.97E-05	4.09E-04

230326_PM_s_at	chromosome 11 open reading frame 73	---	C11orf73	0.462	+	3.81E-03	2.23E-04
219806_PM_s_at	chromosome 11 open reading frame 75	27347	C11orf75	0.579	+	2.63E-02	1.24E-02
224759_PM_s_at	chromosome 12 open reading frame 23	26122	C12orf23	0.317	+	6.96E-03	1.63E-02
204521_PM_at	chromosome 12 open reading frame 24	26054	C12orf24	0.308	+	1.38E-02	1.50E-02
225888_PM_at	chromosome 12 open reading frame 30	284098	C12orf30	0.688	+	1.58E-02	3.46E-03
221821_PM_s_at	chromosome 12 open reading frame 41	11212	C12orf41	0.660	+	1.45E-02	4.49E-03
222767_PM_s_at	chromosome 12 open reading frame 49	145389	C12orf49	0.369	+	2.79E-03	1.87E-02
211034_PM_s_at	chromosome 12 open reading frame 51	56884	C12orf51	0.496	+	3.30E-02	4.32E-02
226943_PM_at	chromosome 12 open reading frame 73	51406	C12orf73	0.283	+	5.91E-03	4.93E-03
225105_PM_at	chromosome 12 open reading frame 75	23099	C12orf75	0.968	+	1.31E-02	7.46E-03
213346_PM_at	chromosome 13 open reading frame 27	5631	C13orf27	0.697	+	2.16E-02	1.03E-02
241672_PM_at	chromosome 13 open reading frame 36	55706	C13orf36	0.524	+	2.70E-02	1.80E-02
225578_PM_at	chromosome 13 open reading frame 37	376940	C13orf37	0.268	+	3.94E-03	9.53E-03
213246_PM_at	chromosome 14 open reading frame 109	8894	C14orf109	0.482	+	1.04E-02	1.20E-03
223060_PM_at	chromosome 14 open reading frame 119	94104	C14orf119	0.290	+	8.38E-03	1.70E-02
227158_PM_at	chromosome 14 open reading frame 126	59339	C14orf126	0.807	+	4.93E-03	1.56E-02
223239_PM_at	chromosome 14 open reading frame 129	54898	C14orf129	0.978	+	1.05E-02	8.59E-03
219563_PM_at	chromosome 14 open reading frame 139	392	C14orf139	0.731	+	2.36E-02	4.02E-02
212460_PM_at	chromosome 14 open reading frame 147	55312	C14orf147	0.528	+	6.18E-03	1.67E-02
221434_PM_s_at	chromosome 14 open reading frame 156	11341	C14orf156	0.313	+	3.16E-03	6.93E-04
217768_PM_at	chromosome 14 open reading frame 166	200185	C14orf166	0.282	+	2.13E-02	4.48E-03
225514_PM_at	chromosome 14 open reading frame 21	7094	C14orf21	0.290	+	3.51E-03	7.76E-03
243061_PM_at	chromosome 14 open reading frame 23	4123	C14orf23	0.630	+	2.02E-02	4.30E-02
238647_PM_at	chromosome 14 open reading frame 28	---	C14orf28	0.441	+	2.40E-02	2.27E-02
225980_PM_at	chromosome 14 open reading frame 43	494470	C14orf43	0.529	+	4.53E-02	3.24E-02
239933_PM_x_at	chromosome 14 open reading frame 45	---	C14orf45	0.549	+	7.26E-03	1.51E-02
215877_PM_at	chromosome 14 open reading frame 56	58525	C14orf56	0.308	+	7.08E-04	3.63E-03
218791_PM_s_at	chromosome 15 open reading frame 29	64130	C15orf29	0.668	+	7.74E-03	2.14E-03
1552310_PM_at	chromosome 15 open reading frame 40	394	C15orf40	1.068	+	1.14E-03	2.49E-03
229742_PM_at	chromosome 15 open reading frame 61	154743	C15orf61	0.407	+	2.89E-02	2.81E-02
233746_PM_x_at	chromosome 15 open reading frame 63 /// small EDRK-rich factor 2	64860	C15orf63 /// SERF2	0.608	+	5.18E-03	7.63E-03

218680_PM_x_at	chromosome 15 open reading frame 63 /// small EDRK-rich factor 2	255919	C15orf63 /// SERF2	0.410	+	7.69E-03	3.30E-02
230721_PM_at	chromosome 16 open reading frame 52	441108	C16orf52	0.619	+	3.62E-03	3.49E-03
227351_PM_at	chromosome 16 open reading frame 52	80095	C16orf52	0.452	+	3.13E-02	2.44E-02
228373_PM_at	chromosome 16 open reading frame 72	388753	C16orf72	0.392	+	1.72E-02	5.16E-04
217957_PM_at	chromosome 16 open reading frame 80	91768	C16orf80	0.437	+	4.78E-03	1.36E-03
228452_PM_at	chromosome 17 open reading frame 39	89970	C17orf39	0.335	+	3.17E-03	1.33E-02
223401_PM_at	chromosome 17 open reading frame 48	79901	C17orf48	0.395	+	7.25E-03	8.61E-04
227668_PM_at	chromosome 17 open reading frame 56	64343	C17orf56	0.287	+	1.29E-03	1.00E-02
225966_PM_at	chromosome 17 open reading frame 89	133308	C17orf89	0.327	+	1.27E-02	1.09E-02
225808_PM_at	chromosome 17 open reading frame 95	155435	C17orf95	0.583	+	1.48E-02	3.01E-02
226406_PM_at	chromosome 18 open reading frame 25	521	C18orf25	0.746	+	1.04E-02	4.65E-03
221190_PM_s_at	chromosome 18 open reading frame 8	8819	C18orf8	0.607	+	4.24E-02	2.14E-02
231901_PM_at	chromosome 19 open reading frame 52	140458	C19orf52	0.445	+	6.22E-03	1.25E-02
218429_PM_s_at	chromosome 19 open reading frame 66	7552	C19orf66	0.479	+	1.67E-02	2.08E-02
53720_PM_at	chromosome 19 open reading frame 66	---	C19orf66	0.445	+	3.42E-02	3.47E-02
238866_PM_at	chromosome 19 open reading frame 68	51477	C19orf68	0.375	+	2.98E-03	1.64E-03
219283_PM_at	C1GALT1-specific chaperone 1	8553	C1GALT1C1	0.618	+	7.88E-04	1.49E-02
206721_PM_at	chromosome 1 open reading frame 114	8450	C1orf114	0.660	+	3.85E-02	9.17E-03
226242_PM_at	chromosome 1 open reading frame 131	19	C1orf131	0.428	+	1.08E-02	2.40E-02
228096_PM_at	chromosome 1 open reading frame 151	2013	C1orf151	0.657	+	7.39E-04	3.33E-04
224867_PM_at	chromosome 1 open reading frame 151	222194	C1orf151	0.361	+	6.94E-03	3.92E-03
213528_PM_at	chromosome 1 open reading frame 156	1272	C1orf156	0.664	+	7.91E-04	2.53E-03
224501_PM_at	chromosome 1 open reading frame 170	1021	C1orf170	0.343	+	2.14E-02	2.83E-02
230608_PM_at	chromosome 1 open reading frame 182	284297	C1orf182	0.495	+	4.82E-04	7.23E-03
229382_PM_at	chromosome 1 open reading frame 183	205717	C1orf183	0.288	+	7.38E-03	2.00E-02
221272_PM_s_at	chromosome 1 open reading frame 21	4520	C1orf21	0.415	+	6.90E-03	4.28E-03
237131_PM_at	chromosome 1 open reading frame 230	5569	C1orf230	0.606	+	2.36E-02	8.91E-03
225638_PM_at	chromosome 1 open reading frame 31	4076	C1orf31	0.364	+	3.13E-02	3.94E-02
223034_PM_s_at	chromosome 1 open reading frame 43	55204	C1orf43	0.469	+	2.11E-03	4.20E-04
219406_PM_at	chromosome 1 open reading frame 50	7175	C1orf50	1.021	+	5.53E-04	2.37E-04
62212_PM_at	chromosome 1 open reading frame 50	388591	C1orf50	0.726	+	3.96E-03	9.31E-03

227285_PM_at	chromosome 1 open reading frame 51	374354	C1orf51	0.381	+	1.09E-02	2.88E-02
228135_PM_at	chromosome 1 open reading frame 52	51274	C1orf52	0.313	+	2.08E-02	4.74E-02
226813_PM_at	chromosome 1 open reading frame 57	5286	C1orf57	0.704	+	4.03E-04	3.00E-04
225841_PM_at	chromosome 1 open reading frame 59	---	C1orf59	0.478	+	1.45E-02	2.73E-02
205103_PM_at	chromosome 1 open reading frame 61	9984	C1orf61	0.523	+	7.61E-03	8.25E-03
229381_PM_at	chromosome 1 open reading frame 64	202018	C1orf64	0.270	+	4.46E-03	3.47E-02
228100_PM_at	chromosome 1 open reading frame 88	283742	C1orf88	0.838	+	2.91E-03	1.34E-02
203429_PM_s_at	chromosome 1 open reading frame 9	8618	C1orf9	0.333	+	3.08E-02	1.30E-02
224690_PM_at	chromosome 20 open reading frame 108	1054	C20orf108	0.395	+	8.82E-03	1.88E-02
225376_PM_at	chromosome 20 open reading frame 11	163404	C20orf11	0.325	+	5.21E-03	1.27E-02
221954_PM_at	Chromosome 20 open reading frame 111	10128	C20orf111	0.384	+	2.10E-02	8.58E-03
225224_PM_at	chromosome 20 open reading frame 112	58492	C20orf112	0.419	+	2.91E-02	4.86E-02
225313_PM_at	chromosome 20 open reading frame 177	2259	C20orf177	0.877	+	4.68E-03	2.84E-02
224915_PM_x_at	chromosome 20 open reading frame 199	112574	C20orf199	0.611	+	5.54E-04	8.09E-03
226835_PM_s_at	chromosome 20 open reading frame 199	10302	C20orf199	0.557	+	5.85E-03	8.47E-03
226227_PM_x_at	chromosome 20 open reading frame 199	9652	C20orf199	0.523	+	6.66E-03	2.35E-02
219706_PM_at	chromosome 20 open reading frame 29	64844	C20orf29	0.279	+	3.56E-03	3.32E-02
224584_PM_at	chromosome 20 open reading frame 30	55691	C20orf30	0.448	+	2.19E-02	4.57E-02
222894_PM_x_at	chromosome 20 open reading frame 7	10135	C20orf7	0.610	+	1.07E-04	1.38E-03
225499_PM_at	chromosome 20 open reading frame 74	11095	C20orf74	0.318	+	5.93E-04	1.27E-03
219004_PM_s_at	chromosome 21 open reading frame 45	10302	C21orf45	0.954	+	6.39E-03	4.05E-03
227188_PM_at	chromosome 21 open reading frame 63	59343	C21orf63	0.488	+	1.25E-02	8.22E-03
218515_PM_at	chromosome 21 open reading frame 66	27115	C21orf66	0.669	+	3.31E-02	1.26E-02
226109_PM_at	chromosome 21 open reading frame 91	56255	C21orf91	0.674	+	3.94E-02	1.25E-02
1558097_PM_at	chromosome 22 open reading frame 30	9129	C22orf30	0.566	+	2.51E-02	3.97E-02
36552_PM_at	C2 calcium-dependent domain containing 3	---	C2CD3	0.741	+	2.86E-02	4.95E-02
219329_PM_s_at	chromosome 2 open reading frame 28	7411	C2orf28	0.373	+	1.95E-02	2.27E-02
219176_PM_at	chromosome 2 open reading frame 47	6282	C2orf47	0.377	+	2.46E-02	2.83E-02
241825_PM_at	chromosome 2 open reading frame 60	---	C2orf60	0.328	+	7.87E-03	2.39E-03
235686_PM_at	chromosome 2 open reading frame 60	1347	C2orf60	0.351	+	3.93E-02	3.58E-02
225409_PM_at	chromosome 2 open reading frame 64	55607	C2orf64	0.300	+	2.04E-03	1.61E-02
238974_PM_at	chromosome 2 open reading frame 69	---	C2orf69	0.485	+	2.15E-02	2.52E-02

236909_PM_at	chromosome 2 open reading frame 77	---	C2orf77	1.061	+	3.61E-03	2.92E-03
228195_PM_at	chromosome 2 open reading frame 88	414	C2orf88	0.402	+	1.99E-03	2.14E-03
223004_PM_s_at	chromosome 3 open reading frame 1	29099	C3orf1	0.342	+	1.64E-02	1.26E-02
219288_PM_at	chromosome 3 open reading frame 14	55611	C3orf14	0.402	+	6.52E-03	7.55E-03
226688_PM_at	chromosome 3 open reading frame 23	5087	C3orf23	0.448	+	2.27E-02	1.60E-02
224523_PM_s_at	chromosome 3 open reading frame 26	389203	C3orf26	0.636	+	3.14E-05	1.28E-03
209285_PM_s_at	chromosome 3 open reading frame 63	84656	C3orf63	0.371	+	8.41E-03	2.80E-02
223204_PM_at	chromosome 4 open reading frame 18	100287515 /// 7574	C4orf18	0.495	+	1.38E-02	1.38E-02
218646_PM_at	chromosome 4 open reading frame 27	8562	C4orf27	0.487	+	1.42E-02	1.49E-02
236240_PM_at	chromosome 4 open reading frame 29	100131801	C4orf29	0.333	+	7.44E-04	6.18E-03
224602_PM_at	chromosome 4 open reading frame 3	54516	C4orf3	0.305	+	1.90E-02	1.30E-02
201812_PM_s_at	chromosome 4 open reading frame 46 /// translocase of outer mitochondrial membrane 7 homolog (yeast)	8425	C4orf46 /// TOMM7	0.273	+	3.51E-02	5.87E-03
224876_PM_at	chromosome 5 open reading frame 24	150864	C5orf24	0.575	+	1.63E-02	1.46E-02
228594_PM_at	chromosome 5 open reading frame 33	11320	C5orf33	0.308	+	1.11E-02	6.09E-03
227267_PM_at	chromosome 5 open reading frame 37	54877	C5orf37	0.912	+	3.95E-03	4.01E-03
218674_PM_at	chromosome 5 open reading frame 44	394	C5orf44	0.432	+	1.22E-03	5.53E-03
226159_PM_at	chromosome 5 open reading frame 51	10480	C5orf51	0.462	+	2.29E-02	4.64E-03
226977_PM_at	chromosome 5 open reading frame 53	5912	C5orf53	0.406	+	4.16E-02	1.10E-02
220770_PM_s_at	chromosome 5 open reading frame 54	4258	C5orf54	0.556	+	2.19E-02	7.69E-03
230405_PM_at	chromosome 5 open reading frame 56	55349	C5orf56	0.416	+	2.15E-02	2.46E-02
223361_PM_at	chromosome 6 open reading frame 115	158747	C6orf115	0.463	+	4.53E-03	4.19E-03
213322_PM_at	chromosome 6 open reading frame 130	9126	C6orf130	0.271	+	9.09E-03	1.63E-02
236178_PM_at	chromosome 6 open reading frame 162	---	C6orf162	0.327	+	6.24E-04	1.09E-03
223576_PM_at	chromosome 6 open reading frame 203	55149	C6orf203	0.350	+	1.97E-02	3.87E-03
222638_PM_s_at	chromosome 6 open reading frame 35	404672	C6orf35	0.387	+	1.28E-02	4.14E-03
243943_PM_x_at	chromosome 6 open reading frame 52	---	C6orf52	0.701	+	1.12E-02	1.77E-02
236504_PM_x_at	chromosome 6 open reading frame 52	---	C6orf52	0.568	+	3.83E-02	8.05E-03
225419_PM_at	chromosome 7 open reading frame 11	139065	C7orf11	0.716	+	5.55E-03	1.92E-03
220231_PM_at	chromosome 7 open reading frame 16	6902	C7orf16	0.593	+	7.97E-04	2.41E-03
226386_PM_at	chromosome 7 open reading frame 30	7504	C7orf30	0.448	+	3.18E-03	2.37E-03

226385_PM_s_at	chromosome 7 open reading frame 30	2745	C7orf30	0.417	+	8.05E-03	1.37E-02
223433_PM_at	chromosome 7 open reading frame 36	51645	C7orf36	0.841	+	1.98E-03	3.57E-03
238609_PM_at	chromosome 7 open reading frame 38	---	C7orf38	0.384	+	2.04E-02	4.41E-02
226780_PM_s_at	chromosome 7 open reading frame 55	6655	C7orf55	0.415	+	6.90E-03	2.00E-02
228149_PM_at	chromosome 7 open reading frame 60	65059	C7orf60	1.106	+	7.85E-03	9.87E-03
218507_PM_at	chromosome 7 open reading frame 68	55425	C7orf68	0.356	+	2.85E-02	2.32E-02
235509_PM_at	chromosome 8 open reading frame 38	---	C8orf38	0.623	+	2.51E-03	4.47E-03
230903_PM_s_at	chromosome 8 open reading frame 42	5136	C8orf42	0.704	+	3.39E-03	5.54E-03
236634_PM_at	chromosome 8 open reading frame 48	---	C8orf48	0.269	+	1.81E-02	2.34E-02
226165_PM_at	chromosome 8 open reading frame 59	5718	C8orf59	0.491	+	2.30E-02	2.90E-03
225702_PM_at	chromosome 8 open reading frame 76	79078	C8orf76	0.371	+	5.45E-03	2.76E-03
226027_PM_at	chromosome 9 open reading frame 119	1964	C9orf119	0.454	+	1.79E-02	4.94E-02
224879_PM_at	chromosome 9 open reading frame 123	375061	C9orf123	0.539	+	1.21E-02	5.01E-03
227443_PM_at	chromosome 9 open reading frame 150	51284	C9orf150	0.670	+	5.25E-03	3.16E-03
223522_PM_at	chromosome 9 open reading frame 45	9419	C9orf45	0.515	+	2.50E-03	1.24E-03
218992_PM_at	chromosome 9 open reading frame 46	388	C9orf46	0.752	+	7.14E-03	1.09E-02
223008_PM_s_at	chromosome 9 open reading frame 5	55745	C9orf5	0.469	+	2.69E-02	3.46E-02
218998_PM_at	chromosome 9 open reading frame 6	158158	C9orf6	0.309	+	2.27E-02	2.37E-03
220050_PM_at	chromosome 9 open reading frame 9	23473	C9orf9	0.389	+	2.71E-02	2.04E-02
219147_PM_s_at	chromosome 9 open reading frame 95	161436	C9orf95	0.575	+	1.62E-02	4.12E-02
223550_PM_s_at	carbonic anhydrase X	81831	CA10	0.516	+	6.73E-03	2.92E-02
214164_PM_x_at	carbonic anhydrase XII	27324	CA12	0.326	+	6.21E-03	2.65E-02
215867_PM_x_at	carbonic anhydrase XII	1290	CA12	0.435	+	1.58E-02	1.69E-02
225532_PM_at	Cdk5 and Abl enzyme substrate 1	134701	CABLES1	0.761	+	2.02E-02	4.52E-02
225627_PM_s_at	cache domain containing 1	6314	CACHD1	0.761	+	2.30E-02	2.26E-02
242973_PM_at	calcium channel, voltage-dependent, L type, alpha 1C subunit	---	CACNA1C	0.640	+	2.70E-02	4.06E-02
1555993_PM_at	calcium channel, voltage-dependent, L type, alpha 1D subunit	3725	CACNA1D	0.413	+	5.60E-03	6.63E-03
228083_PM_at	calcium channel, voltage-dependent, alpha 2/delta subunit 4	4893	CACNA2D4	0.284	+	4.98E-03	2.68E-03
211761_PM_s_at	calcyclin binding protein	285527	CACYBP	0.325	+	2.72E-02	6.46E-03
222293_PM_at	cell adhesion molecule 4	26092	CADM4	0.333	+	3.98E-04	1.46E-03
212077_PM_at	caldesmon 1	3150	CALD1	0.869	+	4.03E-03	1.83E-02
212710_PM_at	calmodulin regulated spectrin-associated protein 1	3176	CAMSAP1	0.352	+	1.03E-02	1.53E-02

212765_PM_at	calmodulin regulated spectrin-associated protein 1-like 1	10959	CAMSAP1L1	0.389	+	2.26E-02	2.18E-02
225693_PM_s_at	calmodulin binding transcription activator 1	55589	CAMTA1	0.570	+	3.55E-03	4.82E-03
225692_PM_at	calmodulin binding transcription activator 1	79959	CAMTA1	0.682	+	8.65E-03	5.89E-03
1555370_PM_a_at	calmodulin binding transcription activator 1	6651	CAMTA1	0.422	+	2.89E-02	3.17E-02
213268_PM_at	calmodulin binding transcription activator 1	6717	CAMTA1	0.344	+	4.21E-02	3.77E-02
213547_PM_at	cullin-associated and neddylation-dissociated 2 (putative)	4233	CAND2	0.702	+	3.08E-02	1.66E-02
238034_PM_at	calnexin	---	CANX	0.489	+	4.49E-02	1.83E-02
208683_PM_at	calpain 2, (m/II) large subunit	2558	CAPN2	0.510	+	3.11E-02	2.79E-02
203356_PM_at	calpain 7	55342	CAPN7	0.670	+	3.27E-03	8.24E-03
243370_PM_at	cell cycle associated protein 1	---	CAPRIN1	0.319	+	3.52E-02	3.57E-02
236085_PM_at	calcyphosine-like	---	CAPSL	0.317	+	3.12E-02	2.55E-02
208374_PM_s_at	capping protein (actin filament) muscle Z-line, alpha 1	283537	CAPZA1	0.576	+	1.25E-03	9.26E-04
1552701_PM_a_at	caspase recruitment domain family, member 16	8904 /// 9054	CARD16	0.985	+	2.08E-02	3.54E-02
224619_PM_at	cancer susceptibility candidate 4	54545	CASC4	0.412	+	1.88E-03	7.65E-03
227156_PM_at	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	7067 /// 9572	CASK	0.526	+	2.23E-02	4.37E-02
219645_PM_at	calsequestrin 1 (fast-twitch, skeletal muscle)	10444	CASQ1	0.324	+	6.86E-03	2.54E-03
202370_PM_s_at	core-binding factor, beta subunit	51422	CBFB	0.758	+	4.20E-02	4.68E-02
225231_PM_at	Cas-Br-M (murine) ecotropic retroviral transforming sequence	132946	CBL	0.539	+	6.19E-04	4.43E-03
225234_PM_at	Cas-Br-M (murine) ecotropic retroviral transforming sequence	148808	CBL	0.661	+	6.86E-03	5.10E-03
227187_PM_at	Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1	55173	CBLL1	0.695	+	2.58E-02	3.99E-02
220175_PM_s_at	COBW domain containing 1 /// COBW domain containing 2 /// COBW domain containing 3 /// COBW domain containing 5 /// COBW domain containing 6 /// COBW domain containing 7	8027	CBWD1 /// CBWD2 /// CBWD3 /// CBWD5 /// CBWD6 /// CBWD7	0.621	+	6.16E-03	1.74E-02
201518_PM_at	chromobox homolog 1 (HP1 beta homolog Drosophila)	1022	CBX1	0.461	+	2.67E-03	1.15E-02
234936_PM_s_at	coiled-coil and C2 domain containing 2A	3416	CC2D2A	0.977	+	4.35E-03	1.63E-02
224968_PM_at	coiled-coil domain containing 104	90874	CCDC104	0.276	+	3.81E-02	1.50E-02

227157_PM_at	coiled-coil domain containing 111	---	CCDC111	1.027	+	7.92E-03	3.09E-02
224946_PM_s_at	coiled-coil domain containing 115	201627	CCDC115	0.559	+	4.68E-03	1.45E-02
228087_PM_at	coiled-coil domain containing 126	8030	CCDC126	0.501	+	6.40E-03	5.58E-04
217845_PM_x_at	coiled-coil domain containing 13 /// HIG1 hypoxia inducible domain family, member 1A /// similar to HIG1 domain family, member 1A	84932	CCDC13 /// HIGD1A /// LOC100130383	0.383	+	4.03E-03	6.24E-03
226723_PM_at	coiled-coil domain containing 23	91754	CCDC23	0.773	+	5.48E-03	6.35E-03
209479_PM_at	coiled-coil domain containing 28A	79982	CCDC28A	0.414	+	6.91E-04	2.64E-03
226287_PM_at	coiled-coil domain containing 34	2313	CCDC34	0.615	+	3.98E-03	7.25E-03
229918_PM_at	coiled-coil domain containing 40	---	CCDC40	0.391	+	3.17E-02	2.84E-02
217814_PM_at	coiled-coil domain containing 47	64951	CCDC47	0.469	+	2.39E-03	1.62E-02
222706_PM_at	coiled-coil domain containing 49	91304	CCDC49	0.624	+	1.27E-02	2.74E-02
218628_PM_at	coiled-coil domain containing 53	81627	CCDC53	0.643	+	8.80E-03	1.04E-03
225010_PM_at	coiled-coil domain containing 6	202052	CCDC6	0.416	+	6.94E-03	2.74E-02
228122_PM_at	coiled-coil domain containing 66	8540	CCDC66	0.939	+	6.55E-03	1.09E-03
225242_PM_s_at	coiled-coil domain containing 80	6299	CCDC80	1.126	+	2.63E-04	2.11E-03
223301_PM_s_at	coiled-coil domain containing 82	81563	CCDC82	0.638	+	1.71E-02	2.15E-02
227208_PM_at	coiled-coil domain containing 84	50861	CCDC84	0.585	+	1.09E-02	1.62E-02
225045_PM_at	coiled-coil domain containing 88A	94234	CCDC88A	0.441	+	2.05E-02	1.78E-03
223663_PM_at	coiled-coil domain containing 88B	51124	CCDC88B	0.336	+	2.43E-02	3.58E-02
227228_PM_s_at	coiled-coil domain containing 88C	79666	CCDC88C	0.265	+	3.50E-02	4.14E-02
220094_PM_s_at	coiled-coil domain containing 90A	10588	CCDC90A	0.761	+	1.50E-02	2.73E-02
218288_PM_s_at	coiled-coil domain containing 90B	143279	CCDC90B	0.446	+	3.57E-03	7.12E-03
221685_PM_s_at	coiled-coil domain containing 99	3621	CCDC99	0.679	+	1.33E-02	3.11E-02
207861_PM_at	chemokine (C-C motif) ligand 22	22980	CCL22	0.316	+	2.16E-02	1.98E-02
201955_PM_at	cyclin C	1385	CCNC	0.640	+	2.51E-02	5.44E-03
213523_PM_at	cyclin E1	27032	CCNE1	0.320	+	3.65E-02	4.94E-02
228081_PM_at	cyclin G2	7112	CCNG2	0.533	+	6.03E-03	5.06E-03
202770_PM_s_at	cyclin G2	54904	CCNG2	0.382	+	2.45E-02	3.06E-02
204093_PM_at	cyclin H	23478	CCNH	0.335	+	1.19E-03	6.21E-03
220046_PM_s_at	cyclin L1	22850	CCNL1	0.842	+	1.13E-02	2.02E-02

204645_PM_at	cyclin T2	5921	CCNT2	0.429	+	3.30E-02	1.29E-02
213743_PM_at	cyclin T2	23376	CCNT2	0.680	+	4.60E-02	4.18E-02
227280_PM_s_at	cyclin Y-like 1	79596	CCNYL1	0.548	+	2.52E-02	1.64E-02
222156_PM_x_at	cell cycle progression 1	27346	CCPG1	0.312	+	3.63E-03	3.17E-02
214152_PM_at	cell cycle progression 1	689	CCPG1	0.820	+	7.18E-03	1.95E-02
221511_PM_x_at	cell cycle progression 1	7087	CCPG1	0.422	+	1.35E-02	2.67E-02
214151_PM_s_at	cell cycle progression 1	25909	CCPG1	0.453	+	1.43E-02	2.66E-02
205271_PM_s_at	cell cycle related kinase	24139	CCRK	0.322	+	2.03E-02	1.60E-02
206587_PM_at	chaperonin containing TCP1, subunit 6B (zeta 2)	8738	CCT6B	0.508	+	1.62E-02	3.04E-02
200873_PM_s_at	chaperonin containing TCP1, subunit 8 (theta)	3631	CCT8	0.352	+	1.63E-02	1.51E-02
209583_PM_s_at	CD200 molecule	56916	CD200	0.322	+	2.48E-02	1.87E-02
203799_PM_at	CD302 molecule	79856	CD302	0.309	+	1.35E-02	3.37E-02
226016_PM_at	CD47 molecule	4035	CD47	0.364	+	6.58E-03	1.16E-02
213857_PM_s_at	CD47 molecule	9527	CD47	0.519	+	2.17E-02	1.42E-02
203416_PM_at	CD53 molecule	80031	CD53	0.343	+	2.80E-02	8.86E-03
204440_PM_at	CD83 molecule	50999	CD83	0.463	+	8.37E-03	4.61E-02
205685_PM_at	CD86 molecule	4094	CD86	0.391	+	2.52E-02	3.57E-02
233647_PM_s_at	cytidine and dCMP deaminase domain containing 1	---	CDADC1	0.642	+	4.42E-03	2.66E-03
223527_PM_s_at	cytidine and dCMP deaminase domain containing 1	64224	CDADC1	0.548	+	4.44E-03	6.20E-03
221556_PM_at	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	7539	CDC14B	0.441	+	3.77E-02	2.91E-02
202717_PM_s_at	cell division cycle 16 homolog (S. cerevisiae)	2122	CDC16	0.435	+	3.33E-03	6.20E-03
209659_PM_s_at	cell division cycle 16 homolog (S. cerevisiae)	57579	CDC16	0.648	+	9.89E-03	5.58E-03
210559_PM_s_at	cell division cycle 2, G1 to S and G2 to M	59271	CDC2	0.306	+	3.67E-03	1.37E-02
225422_PM_at	cell division cycle 26 homolog (S. cerevisiae)	57448	CDC26	0.769	+	1.15E-04	9.23E-04
217880_PM_at	cell division cycle 27 homolog (S. cerevisiae)	27154	CDC27	0.619	+	2.54E-03	1.92E-03
212899_PM_at	cell division cycle 2-like 6 (CDK8-like)	8540	CDC2L6	0.363	+	4.14E-02	1.24E-02
214230_PM_at	cell division cycle 42 (GTP binding protein, 25kDa)	4665	CDC42	0.806	+	4.82E-03	7.39E-03
240735_PM_at	CDC42 binding protein kinase alpha (DMPK-like)	---	CDC42BPA	0.264	+	1.88E-02	2.76E-02
209286_PM_at	CDC42 effector protein (Rho GTPase binding) 3	56994	CDC42EP3	0.432	+	1.40E-02	3.73E-02
224709_PM_s_at	CDC42 small effector 2	54534	CDC42SE2	0.329	+	1.99E-02	7.31E-03
204510_PM_at	cell division cycle 7 homolog (S. cerevisiae)	51567	CDC7	0.823	+	2.16E-02	3.62E-02
234932_PM_s_at	CUB domain containing protein 1	9475	CDCP1	0.278	+	3.24E-03	1.09E-02

201938_PM_at	cyclin-dependent kinase 2 associated protein 1	1200	CDK2AP1	0.293	+	3.68E-02	2.03E-02
204995_PM_at	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	6653	CDK5R1	0.347	+	3.50E-02	9.24E-03
233540_PM_s_at	CDK5 regulatory subunit associated protein 2	26005	CDK5RAP2	0.796	+	6.61E-04	1.23E-02
224847_PM_at	cyclin-dependent kinase 6	129531	CDK6	0.401	+	2.53E-04	8.41E-04
211297_PM_s_at	cyclin-dependent kinase 7	7569	CDK7	0.616	+	6.14E-04	2.02E-03
1553113_PM_s_at	cyclin-dependent kinase 8	9139	CDK8	0.357	+	4.43E-02	3.58E-02
204831_PM_at	cyclin-dependent kinase 8	4891	CDK8	0.458	+	4.57E-02	2.84E-02
1555758_PM_a_at	cyclin-dependent kinase inhibitor 3	5686	CDKN3	0.721	+	1.83E-03	4.25E-03
209714_PM_s_at	cyclin-dependent kinase inhibitor 3	96459	CDKN3	0.760	+	2.35E-03	7.85E-04
204154_PM_at	cysteine dioxygenase, type I	1736	CDO1	0.535	+	2.85E-02	2.42E-02
212010_PM_s_at	CDV3 homolog (mouse)	2058	CDV3	0.495	+	9.81E-03	1.18E-02
203098_PM_at	chromodomain protein, Y-like	51692	CDYL	0.589	+	1.07E-02	1.29E-02
225527_PM_at	CCAAT/enhancer binding protein (C/EBP), gamma	84466	CEBPG	0.379	+	6.62E-03	1.06E-02
226610_PM_at	centromere protein V	6535	CENPV	0.548	+	9.46E-03	2.93E-03
226449_PM_at	centrosomal protein 120kDa	1452	CEP120	0.305	+	1.68E-02	3.43E-02
213165_PM_at	centrosomal protein 350kDa	5467	CEP350	0.420	+	2.92E-02	2.08E-02
203493_PM_s_at	centrosomal protein 57kDa	9627	CEP57	0.848	+	1.09E-02	1.87E-02
224150_PM_s_at	centrosomal protein 70kDa	150274	CEP70	0.315	+	1.96E-02	7.35E-03
52285_PM_f_at	centrosomal protein 76kDa	---	CEP76	0.720	+	1.97E-02	2.79E-02
219375_PM_at	choline/ethanolamine phosphotransferase 1	950	CEPT1	0.296	+	3.14E-02	2.83E-02
209662_PM_at	centrin, EF-hand protein, 3 (CDC31 homolog, yeast)	51250	CETN3	0.668	+	3.10E-03	6.45E-03
203166_PM_at	craniofacial development protein 1	6217	CFDP1	0.275	+	3.97E-02	4.37E-02
224352_PM_s_at	cofilin 2 (muscle)	116151	CFL2	0.655	+	6.38E-03	2.56E-03
224663_PM_s_at	cofilin 2 (muscle)	136647	CFL2	0.400	+	1.09E-02	2.62E-03
209939_PM_x_at	CASP8 and FADD-like apoptosis regulator	57492	CFLAR	0.436	+	6.91E-03	2.08E-02
205387_PM_s_at	chorionic gonadotropin, beta polypeptide /// chorionic gonadotropin, beta polypeptide 5	8505	CGB /// CGB5	0.268	+	2.98E-02	8.07E-03
224599_PM_at	CGG triplet repeat binding protein 1	9218	CGGBP1	0.312	+	2.71E-02	2.96E-02
235117_PM_at	ChaC, cation transport regulator homolog 2 (E. coli)	---	CHAC2	0.424	+	4.29E-03	2.17E-03
217972_PM_at	coiled-coil-helix-coiled-coil-helix domain containing 3	25879	CHCHD3	0.382	+	4.38E-03	4.75E-03

229595_PM_at	coiled-coil-helix-coiled-coil-helix domain containing 4	55628	CHCHD4	0.444	+	1.78E-02	1.15E-02
235791_PM_x_at	chromodomain helicase DNA binding protein 1	51526	CHD1	0.353	+	3.34E-02	1.96E-02
1556988_PM_s_at	chromodomain helicase DNA binding protein 1-like	2202	CHD1L	0.877	+	6.29E-03	1.42E-02
226830_PM_x_at	Chromodomain helicase DNA binding protein 2	23302	CHD2	0.402	+	6.95E-03	6.46E-03
225951_PM_s_at	Chromodomain helicase DNA binding protein 2	---	CHD2	0.422	+	4.28E-02	2.27E-02
213965_PM_s_at	chromodomain helicase DNA binding protein 5	11037	CHD5	0.271	+	3.01E-02	3.77E-02
225031_PM_at	chromodomain helicase DNA binding protein 6	55432	CHD6	0.695	+	4.28E-03	1.14E-02
225026_PM_at	chromodomain helicase DNA binding protein 6	134359	CHD6	0.496	+	3.23E-02	2.26E-02
212616_PM_at	chromodomain helicase DNA binding protein 9	10247	CHD9	0.377	+	4.47E-03	4.36E-03
229954_PM_at	choline dehydrogenase	---	CHDH	0.915	+	1.37E-02	1.38E-02
228345_PM_at	cysteine-rich hydrophobic domain 1	51714	CHIC1	0.663	+	6.16E-03	2.12E-02
204193_PM_at	choline kinase beta	56681	CHKB	0.309	+	1.12E-02	1.58E-02
218085_PM_at	chromatin modifying protein 5	64420	CHMP5	0.691	+	3.05E-03	3.88E-03
219356_PM_s_at	chromatin modifying protein 5	80777	CHMP5	0.338	+	4.16E-03	1.93E-02
221675_PM_s_at	choline phosphotransferase 1	3431	CHPT1	0.419	+	1.50E-02	1.15E-02
230364_PM_at	choline phosphotransferase 1	440957	CHPT1	0.467	+	4.23E-02	3.43E-02
209763_PM_at	chordin-like 1	79038	CHRDL1	0.599	+	1.96E-02	3.64E-02
203044_PM_at	chondroitin sulfate synthase 1	1073	CHSY1	0.417	+	4.78E-02	4.50E-02
226736_PM_at	276eparin276i domain containing 1	253782	CHURC1	0.515	+	7.34E-03	5.97E-03
205008_PM_s_at	calcium and integrin binding family member 2	9839	CIB2	0.601	+	8.15E-03	1.34E-02
221058_PM_s_at	chemokine-like factor	2245	CKLF	0.320	+	2.83E-03	2.05E-02
219161_PM_s_at	chemokine-like factor	5885	CKLF	0.430	+	1.22E-02	3.31E-02
223451_PM_s_at	chemokine-like factor	51320	CKLF	0.383	+	1.46E-02	2.36E-02
201897_PM_s_at	CDC28 protein kinase regulatory subunit 1B	3015	CKS1B	0.725	+	7.11E-03	2.79E-03
212309_PM_at	cytoplasmic linker associated protein 2	2962	CLASP2	0.307	+	8.38E-03	8.87E-03
226274_PM_at	chloride channel 5	9706	CLCN5	0.557	+	2.77E-03	1.72E-03
203950_PM_s_at	chloride channel 6	9403	CLCN6	0.290	+	5.51E-03	1.07E-02
205328_PM_at	claudin 10	7347	CLDN10	0.401	+	3.46E-02	4.90E-02
201769_PM_at	clathrin interactor 1	113251	CLINT1	0.474	+	1.37E-02	1.88E-03
209143_PM_s_at	chloride channel, nucleotide-sensitive, 1A	9946	CLNS1A	0.297	+	4.97E-03	2.54E-03

204370_PM_at	CLP1, cleavage and polyadenylation factor I subunit, homolog (S. cerevisiae)	6251	CLP1	0.369	+	5.26E-03	1.45E-02
227522_PM_at	carboxymethylenebutenolidase homolog (Pseudomonas)	9334	CMBL	0.361	+	2.47E-03	1.72E-02
228283_PM_at	COX assembly mitochondrial protein homolog (S. cerevisiae)	55161	CMC1	0.633	+	1.04E-02	1.08E-02
217870_PM_s_at	cytidine monophosphate (UMP-CMP) kinase 1, cytosolic	151613	CMPK1	0.566	+	4.31E-02	3.95E-02
226702_PM_at	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	25957	CMPK2	0.324	+	2.42E-02	4.60E-02
224998_PM_at	CKLF-like MARVEL transmembrane domain containing 4	221710	CMTM4	0.415	+	3.68E-03	7.83E-04
227731_PM_at	CCHC-type zinc finger, nucleic acid binding protein	80267	CNBP	0.534	+	1.33E-02	2.39E-02
201653_PM_at	cornichon homolog (Drosophila)	1457	CNIH	0.442	+	1.25E-03	1.31E-03
228306_PM_at	cornichon homolog 4 (Drosophila)	253461	CNIH4	0.518	+	1.01E-03	5.14E-04
228437_PM_at	cornichon homolog 4 (Drosophila)	4040	CNIH4	0.467	+	5.24E-03	1.39E-02
218728_PM_s_at	cornichon homolog 4 (Drosophila)	25942	CNIH4	0.397	+	6.67E-03	5.57E-03
223993_PM_s_at	cornichon homolog 4 (Drosophila)	85025	CNIH4	0.291	+	2.82E-02	1.47E-02
218900_PM_at	cyclin M4	26051	CNNM4	0.435	+	3.12E-02	3.92E-02
217798_PM_at	CCR4-NOT transcription complex, subunit 2	55066	CNOT2	0.488	+	1.68E-02	1.81E-02
222476_PM_at	CCR4-NOT transcription complex, subunit 6	8939	CNOT6	0.608	+	1.74E-03	7.79E-03
227119_PM_at	CCR4-NOT transcription complex, subunit 6-like	4661	CNOT6L	0.703	+	1.18E-03	4.38E-03
225053_PM_at	CCR4-NOT transcription complex, subunit 7	54790	CNOT7	0.363	+	2.29E-02	2.95E-03
213436_PM_at	cannabinoid receptor 1 (brain)	6760	CNR1	0.429	+	1.98E-02	2.94E-02
227202_PM_at	Contactin 1	9525	CNTN1	0.537	+	9.48E-03	9.88E-04
207195_PM_at	contactin 6	4297	CNTN6	0.366	+	5.02E-03	1.21E-02
232388_PM_at	contactin associated protein-like 4	374920	CNTNAP4	0.468	+	2.63E-02	9.34E-03
223450_PM_s_at	component of oligomeric golgi complex 3	55197	COG3	0.498	+	1.54E-03	2.70E-03
212189_PM_s_at	component of oligomeric golgi complex 4	5824	COG4	0.603	+	5.62E-05	2.04E-03
227089_PM_at	component of oligomeric golgi complex 5	8502	COG5	0.318	+	9.29E-03	3.24E-02
219575_PM_s_at	component of oligomeric golgi complex 8 /// peptide deformylase (mitochondrial)	10221	COG8 /// PDF	0.352	+	2.09E-02	1.51E-02
204345_PM_at	collagen, type XVI, alpha 1	1362	COL16A1	0.534	+	2.21E-02	3.41E-02
202312_PM_s_at	collagen, type I, alpha 1	8554	COL1A1	0.316	+	9.35E-03	1.21E-02
211980_PM_at	collagen, type IV, alpha 1	4144	COL4A1	0.581	+	9.47E-03	3.35E-02
226277_PM_at	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	2483	COL4A3BP	0.338	+	1.05E-02	1.61E-02

221729_PM_at	collagen, type V, alpha 2	51100	COL5A2	0.791	+	2.78E-02	2.19E-02
221730_PM_at	collagen, type V, alpha 2	7326	COL5A2	0.313	+	4.11E-02	1.84E-02
226024_PM_at	copper metabolism (Murr1) domain containing 1	10527	COMMD1	0.549	+	2.44E-03	1.77E-03
222637_PM_at	COMM domain containing 10	4750	COMMD10	0.462	+	1.36E-02	7.71E-03
218048_PM_at	COMM domain containing 3	54149	COMMD3	0.569	+	5.87E-03	1.31E-02
225312_PM_at	COMM domain containing 6	84630	COMMD6	0.378	+	3.46E-02	2.10E-02
218351_PM_at	COMM domain containing 8	151354	COMMD8	0.764	+	1.86E-03	2.05E-03
218072_PM_at	COMM domain containing 9	361	COMMD9	0.598	+	5.11E-04	1.17E-03
201359_PM_at	coatomer protein complex, subunit beta 1	983	COPB1	0.499	+	1.10E-02	1.17E-02
201358_PM_s_at	coatomer protein complex, subunit beta 1	5987	COPB1	0.441	+	1.50E-02	3.73E-02
201098_PM_at	coatomer protein complex, subunit beta 2 (beta prime)	11321	COPB2	0.408	+	2.75E-02	3.30E-02
213486_PM_at	COPG2 imprinted transcript 1 (non-protein coding)	1006	COPG2IT1	0.343	+	4.77E-02	4.44E-02
209838_PM_at	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis)	3146	COPS2	0.354	+	1.90E-02	2.54E-02
202467_PM_s_at	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis)	51072 /// 84661	COPS2	0.290	+	2.02E-02	5.26E-04
202078_PM_at	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)	79017	COPS3	0.277	+	4.74E-03	2.75E-02
218042_PM_at	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis)	91748	COPS4	0.470	+	8.67E-03	4.72E-03
202141_PM_s_at	COP9 constitutive photomorphogenic homolog subunit 8 (Arabidopsis)	9378	COPS8	0.316	+	1.47E-02	2.20E-02
219561_PM_at	coatomer protein complex, subunit zeta 2	6400	COPZ2	0.277	+	3.37E-02	4.46E-02
219397_PM_at	coenzyme Q10 homolog B (S. cerevisiae)	5903	COQ10B	0.531	+	4.51E-03	1.36E-03
223515_PM_s_at	coenzyme Q3 homolog, methyltransferase (S. cerevisiae)	55284	COQ3	0.395	+	2.37E-02	1.14E-02
223114_PM_at	coenzyme Q5 homolog, methyltransferase (S. cerevisiae)	54069	COQ5	0.330	+	2.90E-02	2.77E-02
223191_PM_at	COX16 cytochrome c oxidase assembly homolog (S. cerevisiae)	79728	COX16	0.439	+	6.81E-03	8.76E-03
1558346_PM_at	COX17 cytochrome c oxidase assembly homolog (S. cerevisiae)	1454	COX17	0.798	+	4.41E-02	3.96E-02
203663_PM_s_at	cytochrome c oxidase subunit Va	26269	COX5A	0.348	+	2.89E-02	2.26E-02
202343_PM_x_at	cytochrome c oxidase subunit Vb	10580	COX5B	0.315	+	3.26E-02	2.28E-02
201441_PM_at	cytochrome c oxidase subunit Vib polypeptide 1 (ubiquitous)	9948	COX6B1	0.297	+	1.65E-02	1.78E-02

201754_PM_at	cytochrome c oxidase subunit Vic	23513	COX6C	0.423	+	2.36E-03	1.49E-03
201597_PM_at	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	2581	COX7A2	0.760	+	3.84E-04	1.58E-03
217249_PM_x_at	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	54675	COX7A2	0.457	+	3.07E-02	9.48E-03
201256_PM_at	cytochrome c oxidase subunit VIIa polypeptide 2 like	9378	COX7A2L	0.413	+	3.92E-05	2.62E-04
202110_PM_at	cytochrome c oxidase subunit VIIb	5364	COX7B	0.432	+	1.03E-03	7.96E-04
217491_PM_x_at	cytochrome c oxidase subunit VIIc	6730	COX7C	0.297	+	1.64E-02	2.17E-03
213846_PM_at	cytochrome c oxidase subunit VIIc	6942	COX7C	0.277	+	4.77E-02	1.04E-04
204662_PM_at	CP110 protein	25804	CP110	0.347	+	4.80E-02	7.20E-03
201941_PM_at	carboxypeptidase D	10979	CPD	0.634	+	1.92E-02	6.71E-03
226939_PM_at	cytoplasmic polyadenylation element binding protein 2	6657	CPEB2	0.641	+	2.91E-02	3.01E-03
202119_PM_s_at	copine III	100294451 /// 2990 /// 91316	CPNE3	0.832	+	7.93E-03	1.76E-02
228365_PM_at	copine VIII	55824	CPNE8	0.673	+	8.70E-03	2.63E-02
225082_PM_at	cleavage and polyadenylation specific factor 3, 73kDa	127933	CPSF3	0.303	+	4.52E-03	8.72E-03
217866_PM_at	cleavage and polyadenylation specific factor 7, 59kDa	85476	CPSF7	0.424	+	3.08E-03	3.80E-03
203633_PM_at	carnitine palmitoyltransferase 1A (liver)	10260	CPT1A	0.331	+	2.69E-04	3.09E-03
209833_PM_at	CASP2 and RIPK1 domain containing adaptor with death domain	219771	CRADD	0.324	+	1.81E-02	4.66E-02
222533_PM_at	cereblon	23119	CRBN	0.326	+	1.21E-02	2.13E-02
225572_PM_at	cAMP responsive element binding protein 1	386618	CREB1	0.454	+	3.42E-02	2.61E-03
228177_PM_at	CREB binding protein	867	CREBBP	0.645	+	2.38E-02	4.04E-02
201990_PM_s_at	cAMP responsive element binding protein-like 2	813	CREBL2	0.314	+	9.58E-03	4.33E-02
225594_PM_at	CREB/ATF bZIP transcription factor	641372	CREBZF	0.840	+	5.42E-03	1.22E-02
202979_PM_s_at	CREB/ATF bZIP transcription factor	25821	CREBZF	0.647	+	1.52E-02	2.60E-02
228092_PM_at	cAMP responsive element modulator	55274	CREM	0.480	+	1.16E-02	1.52E-02
218643_PM_s_at	cysteine-rich PDZ-binding protein	57697	CRIPT	0.507	+	1.10E-02	4.58E-03
222702_PM_x_at	cysteine-rich PDZ-binding protein	28996	CRIPT	0.441	+	2.24E-02	4.34E-02
212180_PM_at	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	1209	CRKL	0.428	+	7.25E-03	7.41E-03
223978_PM_s_at	cardiolipin synthase 1	65977	CRLS1	0.444	+	1.68E-03	5.39E-03
218648_PM_at	CREB regulated transcription coactivator 3	79152	CRTC3	0.648	+	2.18E-02	2.32E-02
209674_PM_at	cryptochrome 1 (photolyase-like)	56853	CRY1	0.645	+	3.16E-02	6.00E-03
206778_PM_at	279eparin279ing, beta B2	224	CRYBB2	0.295	+	5.15E-03	1.44E-03

205489_PM_at	280eparin280ing, mu	2110	CRYM	0.406	+	4.87E-03	9.48E-03
226151_PM_x_at	280eparin280ing, zeta (quinone reductase)-like 1	9354	CRYZL1	0.661	+	7.29E-03	2.33E-03
219767_PM_s_at	280eparin280ing, zeta (quinone reductase)-like 1	2200	CRYZL1	0.528	+	1.96E-02	1.69E-02
201111_PM_at	CSE1 chromosome segregation 1-like (yeast)	8613	CSE1L	0.451	+	1.87E-02	1.28E-02
240228_PM_at	CUB and Sushi multiple domains 3	---	CSMD3	0.756	+	2.00E-02	2.78E-02
208865_PM_at	casein kinase 1, alpha 1	60492	CSNK1A1	0.335	+	8.35E-03	6.41E-03
227767_PM_at	casein kinase 1, gamma 3	51805	CSNK1G3	0.731	+	9.63E-03	7.96E-03
224922_PM_at	casein kinase 2, alpha prime polypeptide	79066	CSNK2A2	0.368	+	4.83E-02	3.96E-02
227105_PM_at	centrosome and spindle pole associated protein 1	---	CSPP1	0.274	+	2.98E-02	2.55E-02
221260_PM_s_at	cysteine-serine-rich nuclear protein 2	2176	CSRNP2	0.422	+	3.20E-02	6.51E-03
207030_PM_s_at	cysteine and glycine-rich protein 2	1209	CSRP2	0.465	+	6.84E-03	2.24E-02
229666_PM_s_at	cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kDa	158586	CSTF3	0.522	+	1.88E-03	6.45E-03
201218_PM_at	C-terminal binding protein 2	26135	CTBP2	0.304	+	8.43E-03	6.06E-03
201220_PM_x_at	C-terminal binding protein 2	11100	CTBP2	0.594	+	9.98E-03	2.20E-02
202521_PM_at	CCCTC-binding factor (zinc finger protein)	51611	CTCF	0.407	+	4.32E-02	1.51E-02
203445_PM_s_at	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	55812	CTDSP2	0.352	+	4.16E-02	1.45E-02
223270_PM_at	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	29951	CTDSPL2	0.725	+	1.91E-02	3.54E-02
202468_PM_s_at	catenin (cadherin-associated protein), alpha-like 1	56947	CTNNAL1	0.464	+	4.52E-03	5.92E-03
209618_PM_at	catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein)	84255	CTNND2	0.443	+	4.69E-02	3.75E-02
222819_PM_at	CTP synthase II	730092	CTPS2	0.524	+	9.63E-03	3.11E-02
202060_PM_at	Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	23499	CTR9	0.654	+	2.07E-02	7.14E-03
214377_PM_s_at	chymotrypsin-like	7328	CTRL	0.281	+	2.99E-02	2.87E-02
201487_PM_at	cathepsin C	5528	CTSC	0.356	+	8.10E-03	1.92E-02
202087_PM_s_at	cathepsin L1	163131 /// 284323	CTSL1	0.601	+	4.85E-03	1.42E-02
232136_PM_s_at	cortactin binding protein 2	344405	CTTNBP2	0.425	+	4.65E-02	1.40E-02
226410_PM_at	cytosolic thiouridylase subunit 2 homolog (S. pombe)	57343	CTU2	0.292	+	7.40E-03	1.72E-02
201370_PM_s_at	cullin 3	2976	CUL3	0.645	+	7.46E-03	7.60E-05

201424_PM_s_at	cullin 4A	8522	CUL4A	0.357	+	6.20E-03	5.08E-03
203531_PM_at	cullin 5	775	CUL5	0.405	+	2.27E-03	1.54E-02
223067_PM_at	CWC15 spliceosome-associated protein homolog (S. cerevisiae)	54463	CWC15	0.330	+	3.54E-02	3.06E-02
232087_PM_at	chromosome X open reading frame 23	---	Cxorf23	0.728	+	9.26E-03	1.61E-02
225216_PM_at	Chromosome X open reading frame 39	96459	Cxorf39	0.715	+	9.34E-03	3.19E-03
214112_PM_s_at	chromosome X open reading frame 40A /// chromosome X open reading frame 40B	23534	Cxorf40A /// Cxorf40B	0.298	+	6.04E-04	2.60E-03
219355_PM_at	chromosome X open reading frame 57	223	Cxorf57	0.466	+	1.74E-02	4.53E-02
215726_PM_s_at	cytochrome b5 type A (microsomal)	81603	CYB5A	0.490	+	2.28E-04	5.96E-03
207843_PM_x_at	cytochrome b5 type A (microsomal)	6670	CYB5A	0.329	+	1.11E-03	1.67E-02
201634_PM_s_at	cytochrome b5 type B (outer mitochondrial membrane)	23236	CYB5B	0.557	+	2.55E-02	8.80E-03
224735_PM_at	cytochrome b, ascorbate dependent 3	57182	CYBASC3	0.457	+	6.18E-03	1.03E-02
222453_PM_at	cytochrome b reductase 1	5781	CYBRD1	0.538	+	1.80E-02	4.39E-02
229415_PM_at	cytochrome c, somatic	113263	CYCS	0.384	+	3.45E-03	2.14E-02
208923_PM_at	cytoplasmic FMR1 interacting protein 1	56943	CYFIP1	0.908	+	1.39E-02	8.24E-03
213295_PM_at	cylindromatosis (turban tumor syndrome)	6307	CYLD	0.601	+	8.55E-03	2.82E-03
39582_PM_at	cylindromatosis (turban tumor syndrome)	---	CYLD	0.315	+	1.94E-02	3.92E-02
219825_PM_at	cytochrome P450, family 26, subfamily B, polypeptide 1	9053	CYP26B1	0.296	+	1.12E-02	3.00E-02
202314_PM_at	cytochrome P450, family 51, subfamily A, polypeptide 1	27249	CYP51A1	0.305	+	9.39E-03	1.61E-02
220813_PM_at	cysteinyl leukotriene receptor 2	23288	CYSLTR2	0.331	+	1.53E-02	3.35E-02
201278_PM_at	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	361	DAB2	1.143	+	2.26E-02	3.94E-02
228915_PM_at	dachshund homolog 1 (Drosophila)	23248	DACH1	0.779	+	3.61E-02	4.84E-02
200046_PM_at	defender against cell death 1	8317	DAD1	0.384	+	7.96E-03	2.37E-02
205417_PM_s_at	dystroglycan 1 (dystrophin-associated glycoprotein 1)	9472	DAG1	0.282	+	1.08E-02	3.56E-02
211070_PM_x_at	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)	860	DBI	0.303	+	3.47E-02	2.62E-02
225676_PM_s_at	DDB1 and CUL4 associated factor 13	4862	DCAF13	0.543	+	1.12E-02	1.36E-02
217908_PM_s_at	DDB1 and CUL4 associated factor 6	84923	DCAF6	0.522	+	2.58E-02	3.36E-02
224522_PM_s_at	dephospho-CoA kinase domain containing	26258	DCAKD	0.401	+	4.38E-03	1.91E-02
239446_PM_x_at	discoidin, CUB and LCCL domain containing 2	90133	DCBLD2	0.300	+	1.78E-02	2.42E-02

238914_PM_at	deleted in colorectal carcinoma	---	DCC	0.715	+	4.31E-02	1.75E-02
229800_PM_at	Doublecortin-like kinase 1	256714	DCLK1	0.483	+	7.56E-03	2.26E-02
209804_PM_at	DNA cross-link repair 1A (PSO2 homolog, S. cerevisiae)	8545	DCLRE1A	0.305	+	8.69E-04	5.60E-03
209335_PM_at	decorin	84861	DCN	0.293	+	8.73E-03	1.12E-02
225443_PM_at	DCP1 decapping enzyme homolog A (S. cerevisiae)	51523	DCP1A	0.753	+	2.65E-02	1.75E-02
212919_PM_at	DCP2 decapping enzyme homolog (S. cerevisiae)	9734	DCP2	0.788	+	8.75E-03	1.86E-02
203261_PM_at	dynactin 6	10914	DCTN6	0.472	+	6.32E-04	1.36E-03
218583_PM_s_at	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	57453	DCUN1D1	0.628	+	1.03E-02	2.69E-03
212855_PM_at	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	10046	DCUN1D4	0.264	+	4.05E-03	3.40E-03
223151_PM_at	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	57415	DCUN1D5	0.787	+	8.13E-04	1.37E-04
204850_PM_s_at	doublecortin	4646	DCX	0.384	+	2.27E-02	4.73E-02
209094_PM_at	dimethylarginine dimethylaminohydrolase 1	10390	DDAH1	0.378	+	5.78E-03	2.18E-02
225971_PM_at	DDHD domain containing 1	26207	DDHD1	0.383	+	1.35E-02	3.57E-03
208718_PM_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	51727	DDX17	0.274	+	3.07E-02	3.40E-02
224654_PM_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	151636	DDX21	0.777	+	1.46E-02	2.89E-02
228039_PM_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	64432	DDX46	0.500	+	1.93E-02	1.02E-02
225549_PM_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	93953	DDX6	0.429	+	4.38E-06	9.29E-05
202447_PM_at	2,4-dienoyl CoA reductase 1, mitochondrial	54778	DECR1	0.439	+	2.07E-03	1.08E-02
228032_PM_s_at	DENN/MADD domain containing 1B	57606	DENND1B	0.364	+	4.14E-02	4.81E-02
230769_PM_at	DENN/MADD domain containing 2C	57495	DENND2C	0.371	+	8.26E-03	1.52E-02
1554352_PM_s_at	DENN/MADD domain containing 4A	8661	DENND4A	0.382	+	1.15E-02	2.26E-02
226867_PM_at	DENN/MADD domain containing 4C	57403	DENND4C	0.683	+	2.76E-02	3.35E-02
212561_PM_at	DENN/MADD domain containing 5A	9057	DENND5A	0.452	+	2.15E-02	1.59E-02
214027_PM_x_at	desmin /// family with sequence similarity 48, member A	3836	DES /// FAM48A	0.283	+	3.34E-02	3.65E-02
219641_PM_at	de-etiolated homolog 1 (Arabidopsis)	6256	DET1	0.392	+	2.45E-02	7.19E-03
221887_PM_s_at	deafness, autosomal recessive 31	8837	DFNB31	0.296	+	9.53E-03	2.84E-02
208072_PM_s_at	diacylglycerol kinase, delta 130kDa	6472	DGKD	0.406	+	1.70E-02	3.97E-02

239093_PM_at	dihydrodipicolinate synthase-like, mitochondrial	---	DHDPSL	0.291	+	3.99E-02	2.63E-02
202534_PM_x_at	dihydrofolate reductase	51322	DHFR	0.591	+	5.46E-03	1.19E-03
210788_PM_s_at	dehydrogenase/reductase (SDR family) member 7	91942	DHRS7	0.509	+	3.60E-02	1.83E-02
227094_PM_at	dehydrogenase E1 and transketolase domain containing 1	9508	DHTKD1	0.385	+	7.78E-04	1.59E-03
239772_PM_x_at	DEAH (Asp-Glu-Ala-His) box polypeptide 30	---	DHX30	0.417	+	1.39E-03	3.87E-03
218277_PM_s_at	DEAH (Asp-Glu-Ala-His) box polypeptide 40	55553	DHX40	0.392	+	2.97E-02	1.69E-02
212888_PM_at	dicer 1, ribonuclease type III	2218	DICER1	0.534	+	3.07E-02	2.29E-03
217106_PM_x_at	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	55646	DIMT1L	0.348	+	8.90E-03	6.18E-03
204405_PM_x_at	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	9337	DIMT1L	0.295	+	3.56E-02	4.34E-02
224872_PM_at	DIP2 disco-interacting protein 2 homolog B (Drosophila)	54708	DIP2B	0.408	+	4.28E-02	9.52E-03
201479_PM_at	dyskeratosis 283eparin283in 1, dyskerin	4849	DKC1	0.424	+	1.36E-02	3.42E-03
213149_PM_at	dihydrolipoamide S-acetyltransferase	10393	DLAT	0.289	+	3.76E-02	2.32E-02
202515_PM_at	discs, large homolog 1 (Drosophila)	51374	DLG1	0.489	+	4.24E-02	8.96E-03
201681_PM_s_at	discs, large homolog 5 (Drosophila)	57509	DLG5	0.654	+	4.06E-03	7.61E-03
235527_PM_at	discs, large (Drosophila) homolog-associated protein 1 /// hypothetical protein LOC284214	100132832 /// 100289811 /// 441259 /// 5379 /// 5380 /// 5383 /// 5387 /// 5395	DLGAP1 /// LOC284214	0.480	+	2.42E-02	7.00E-04
242138_PM_at	distal-less homeobox 1	---	DLX1	0.512	+	3.91E-02	3.80E-02
230882_PM_at	DLX6 antisense RNA (non-protein coding)	280636	DLX6AS	0.354	+	2.28E-02	3.53E-02
203881_PM_s_at	dystrophin	23196	DMD	0.572	+	4.56E-03	9.66E-04
212820_PM_at	Dmx-like 2	4092	DMXL2	0.344	+	9.15E-03	2.14E-02
220125_PM_at	dynein, axonemal, intermediate chain 1	10106	DNAI1	0.413	+	1.67E-02	1.98E-03
226994_PM_at	DnaJ (Hsp40) homolog, subfamily A, member 2	5733	DNAJA2	0.743	+	5.64E-04	3.21E-03
203810_PM_at	DnaJ (Hsp40) homolog, subfamily B, member 4	6727	DNAJB4	0.642	+	3.68E-03	4.86E-03
218976_PM_at	DnaJ (Hsp40) homolog, subfamily C, member 12	114792	DNAJC12	0.843	+	1.64E-03	4.38E-03
225359_PM_at	DnaJ (Hsp40) homolog, subfamily C, member 19	167359	DNAJC19	0.455	+	4.09E-02	2.18E-02
238337_PM_s_at	DnaJ (Hsp40) homolog, subfamily C, member 21	11128	DNAJC21	0.614	+	2.91E-02	1.38E-03
213853_PM_at	DnaJ (Hsp40) homolog, subfamily C, member 24	259230	DNAJC24	0.941	+	2.54E-03	9.44E-04
227859_PM_at	DnaJ (Hsp40) homolog, subfamily C, member 27	1979	DNAJC27	0.356	+	2.15E-02	2.07E-02
225284_PM_at	DnaJ (Hsp40) homolog, subfamily C, member 3	573	DNAJC3	0.292	+	3.69E-02	2.81E-02

204720_PM_s_at	DnaJ (Hsp40) homolog, subfamily C, member 6	5335	DNAJC6	0.391	+	9.72E-03	5.20E-03
212491_PM_s_at	DnaJ (Hsp40) homolog, subfamily C, member 8	477	DNAJC8	0.566	+	1.11E-02	4.53E-02
213088_PM_s_at	DnaJ (Hsp40) homolog, subfamily C, member 9	1021	DNAJC9	0.456	+	1.47E-02	3.07E-02
226309_PM_at	dynein, axonemal, light chain 1	26747	DNAL1	0.547	+	9.13E-03	1.12E-02
227081_PM_at	dynein, axonemal, light intermediate chain 1	23504	DNALI1	0.316	+	4.16E-03	2.08E-02
226154_PM_at	dynamin 1-like	25800	DNM1L	0.346	+	1.48E-02	8.49E-03
209839_PM_at	dynamin 3	55749	DNM3	0.311	+	2.42E-02	1.73E-02
213482_PM_at	dedicator of cytokinesis 3	6323	DOCK3	0.431	+	3.89E-02	2.95E-02
225384_PM_at	dedicator of cytokinesis 7	57505	DOCK7	0.932	+	4.58E-03	3.60E-03
223553_PM_s_at	docking protein 3	64776	DOK3	0.911	+	2.97E-03	4.56E-03
231980_PM_at	docking protein 6	---	DOK6	0.331	+	7.07E-03	5.26E-03
213271_PM_s_at	dopey family member 1	65018	DOPEY1	0.411	+	3.45E-02	3.51E-02
40612_PM_at	dopey family member 1	339500	DOPEY1	0.272	+	4.42E-02	1.33E-02
236442_PM_at	D4, zinc and double PHD fingers, family 3	---	DPF3	0.695	+	2.08E-03	3.43E-03
238532_PM_at	D4, zinc and double PHD fingers, family 3	5692	DPF3	1.048	+	6.54E-03	7.91E-03
202673_PM_at	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	8675	DPM1	0.470	+	2.27E-03	3.01E-04
228598_PM_at	dipeptidyl-peptidase 10	4131	DPP10	0.678	+	2.56E-02	1.82E-02
230158_PM_at	dpy-19-like 2 (C. elegans)	22990	DPY19L2	0.353	+	1.98E-02	3.56E-02
213391_PM_at	dpy-19-like 4 (C. elegans)	49855	DPY19L4	0.387	+	1.93E-02	3.30E-02
224129_PM_s_at	dpy-30 homolog (C. elegans)	7546	DPY30	0.399	+	6.72E-03	1.34E-02
219065_PM_s_at	dpy-30 homolog (C. elegans) /// mediator of cell motility 1	284119	DPY30 /// MEMO1	0.611	+	1.06E-02	6.19E-03
236055_PM_at	DEAQ box RNA-dependent ATPase 1	---	DQX1	0.284	+	1.75E-02	2.22E-02
209187_PM_at	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	79444	DR1	0.385	+	1.14E-02	2.25E-03
206032_PM_at	desmocollin 3	1312	DSC3	0.341	+	1.77E-02	3.12E-02
232059_PM_at	Down syndrome cell adhesion molecule like 1	646113	DSCAML1	0.571	+	4.46E-02	4.81E-02
203635_PM_at	Down syndrome critical region gene 3	81554	DSCR3	0.328	+	2.14E-02	3.01E-02
215016_PM_x_at	dystonin	29097	DST	0.429	+	2.33E-02	2.05E-02
212254_PM_s_at	dystonin	9821	DST	0.469	+	2.48E-02	1.18E-02
205741_PM_s_at	dystrobrevin, alpha	9754	DTNA	0.451	+	1.00E-02	7.08E-03

244142_PM_at	dystrobrevin, alpha	---	DTNA	0.368	+	4.52E-02	2.37E-02
219291_PM_at	DTW domain containing 1	23365	DTWD1	0.371	+	7.61E-03	2.51E-03
225415_PM_at	deltex 3-like (Drosophila)	256643	DTX3L	0.501	+	1.97E-03	8.47E-03
202703_PM_at	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	3134	DUSP11	0.687	+	4.91E-03	1.33E-02
218576_PM_s_at	dual specificity phosphatase 12	57711	DUSP12	0.585	+	1.90E-04	6.38E-05
203367_PM_at	dual specificity phosphatase 14	55624	DUSP14	0.504	+	5.48E-03	2.89E-02
229211_PM_at	dual specificity phosphatase 28	85460	DUSP28	0.299	+	1.23E-02	2.24E-03
216473_PM_x_at	double homeobox, 4 /// double homeobox, 4-like /// double homeobox, 4-like /// double homeobox, 4-like /// double homeobox, 4-like	51534	DUX4 /// LOC653543 /// LOC653544 /// LOC653545 /// LOC728410	0.541	+	1.43E-03	2.12E-03
203230_PM_at	285eparin285in, dsh homolog 1 (Drosophila)	11217 /// 445815	DVL1	0.313	+	1.58E-02	1.87E-02
239733_PM_at	DPY30 domain containing 2	284112	DYDC2	0.598	+	1.79E-02	3.11E-02
219469_PM_at	dynein, cytoplasmic 2, heavy chain 1	664	DYNC2H1	0.568	+	2.41E-02	4.20E-02
203763_PM_at	dynein, cytoplasmic 2, light intermediate chain 1	1131	DYNC2LI1	0.691	+	2.03E-02	1.31E-02
200703_PM_at	dynein, light chain, LC8-type 1	1452	DYNLL1	0.351	+	7.48E-03	6.31E-03
238116_PM_at	dynein, light chain, roadblock-type 2	---	DYNLRB2	0.790	+	8.88E-03	4.03E-03
201999_PM_s_at	dynein, light chain, Tctex-type 1	6046	DYNLT1	0.562	+	4.33E-03	1.07E-02
203303_PM_at	dynein, light chain, Tctex-type 3	51501	DYNLT3	0.298	+	1.77E-02	1.21E-02
209033_PM_s_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A	79675	DYRK1A	0.454	+	9.14E-03	1.27E-02
226952_PM_at	ELL associated factor 1	120526	EAF1	0.312	+	7.51E-03	2.85E-02
204274_PM_at	estrogen receptor binding site associated, antigen, 9	3930	EBAG9	0.429	+	7.15E-03	1.63E-02
201323_PM_at	EBNA1 binding protein 2	1998	EBNA1BP2	0.461	+	1.05E-02	1.95E-02
202735_PM_at	emopamil binding protein (sterol isomerase)	51231	EBP	0.465	+	4.40E-03	2.08E-02
218552_PM_at	enoyl Coenzyme A hydratase domain containing 2	1128	ECHDC2	0.690	+	8.77E-03	8.50E-03
219298_PM_at	enoyl Coenzyme A hydratase domain containing 3	10625	ECHDC3	0.330	+	7.62E-03	3.55E-02
206101_PM_at	extracellular matrix protein 2, female organ and adipocyte	9908	ECM2	0.835	+	2.70E-02	2.41E-02

	specific						
218225_PM_at	ECSIT homolog (Drosophila)	132789	ECSIT	0.315	+	1.53E-03	1.07E-02
225885_PM_at	early endosome antigen 1	---	EEA1	0.769	+	1.03E-02	1.27E-02
209572_PM_s_at	embryonic ectoderm development	83549	EED	0.583	+	1.07E-03	8.79E-05
1557120_PM_at	Eukaryotic translation elongation factor 1 alpha 1	5445	EEF1A1	0.285	+	3.30E-03	1.71E-04
200705_PM_s_at	eukaryotic translation elongation factor 1 beta 2	598	EEF1B2	0.319	+	1.37E-02	1.93E-03
214394_PM_x_at	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	3609	EEF1D	0.398	+	2.12E-02	1.06E-02
204905_PM_s_at	eukaryotic translation elongation factor 1 epsilon 1	6416	EEF1E1	0.481	+	6.11E-04	3.61E-03
225546_PM_at	eukaryotic elongation factor-2 kinase	8715	EEF2K	0.342	+	2.92E-03	2.94E-03
225545_PM_at	eukaryotic elongation factor-2 kinase	125488	EEF2K	0.355	+	6.64E-03	2.95E-02
1558301_PM_a_at	EF-hand calcium binding domain 5	1595	EFCAB5	0.286	+	1.35E-02	2.17E-02
201843_PM_s_at	EGF-containing fibulin-like extracellular matrix protein 1	65220	EFEMP1	0.279	+	5.71E-03	1.58E-02
201842_PM_s_at	EGF-containing fibulin-like extracellular matrix protein 1	9045	EFEMP1	0.392	+	3.32E-02	4.89E-02
212410_PM_at	EF-hand domain family, member A1	4683	EFHA1	0.526	+	1.19E-03	5.22E-03
217992_PM_s_at	EF-hand domain family, member D2	123606	EFHD2	0.421	+	6.33E-03	1.36E-03
202023_PM_at	ephrin-A1	667	EFNA1	0.290	+	4.85E-02	2.03E-02
212149_PM_at	EFR3 homolog A (S. cerevisiae)	1977	EFR3A	0.617	+	7.81E-03	8.68E-04
209826_PM_at	EGF-like-domain, multiple 8 /// palmitoyl-protein thioesterase 2	27248	EGFL8 /// PPT2	0.467	+	4.90E-03	9.04E-03
219232_PM_s_at	egl nine homolog 3 (C. elegans)	7803	EGLN3	0.298	+	5.73E-03	1.22E-02
212653_PM_s_at	EH domain binding protein 1	1185	EHBP1	0.356	+	2.89E-02	4.74E-02
225461_PM_at	euchromatic histone-lysine N-methyltransferase 1	26190	EHMT1	0.308	+	4.63E-02	4.08E-02
208669_PM_s_at	EP300 interacting inhibitor of differentiation 1	9149	EID1	0.332	+	9.70E-03	1.11E-03
201018_PM_at	eukaryotic translation initiation factor 1A, X-linked	23191	EIF1AX	0.373	+	1.50E-02	3.46E-02
201738_PM_at	eukaryotic translation initiation factor 1B	23327	EIF1B	0.370	+	3.61E-02	7.15E-03
223015_PM_at	eukaryotic translation initiation factor 2A, 65kDa	25996	EIF2A	0.332	+	4.20E-02	8.93E-03
217736_PM_s_at	eukaryotic translation initiation factor 2-alpha kinase 1	116228	EIF2AK1	0.556	+	1.56E-02	3.19E-02
201142_PM_at	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	2887	EIF2S1	0.481	+	2.88E-04	1.85E-04
208726_PM_s_at	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	9531	EIF2S2	0.371	+	7.00E-03	3.61E-03

200597_PM_at	eukaryotic translation initiation factor 3, subunit A	5281	EIF3A	0.413	+	2.58E-03	9.93E-03
201592_PM_at	eukaryotic translation initiation factor 3, subunit H	7321	EIF3H	0.540	+	1.02E-03	2.66E-03
208985_PM_s_at	eukaryotic translation initiation factor 3, subunit J	51409	EIF3J	0.377	+	2.04E-02	1.01E-02
217719_PM_at	eukaryotic translation initiation factor 3, subunit L	339287	EIF3L	0.421	+	2.86E-02	2.60E-02
202231_PM_at	eukaryotic translation initiation factor 3, subunit M	2002 /// 652030	EIF3M	0.582	+	2.66E-05	3.54E-04
202232_PM_s_at	eukaryotic translation initiation factor 3, subunit M	9568	EIF3M	0.624	+	6.80E-03	1.55E-03
201303_PM_at	eukaryotic translation initiation factor 4A, isoform 3	274	EIF4A3	0.383	+	2.34E-02	2.83E-02
201437_PM_s_at	eukaryotic translation initiation factor 4E	6624	EIF4E	0.667	+	1.16E-03	2.75E-03
201436_PM_at	eukaryotic translation initiation factor 4E	2969	EIF4E	0.888	+	2.51E-03	5.61E-03
213571_PM_s_at	eukaryotic translation initiation factor 4E family member 2	23190	EIF4E2	0.371	+	9.23E-03	2.81E-02
225941_PM_at	eukaryotic translation initiation factor 4E family member 3	63947 /// 728656	EIF4E3	0.617	+	2.77E-03	5.88E-03
225939_PM_at	eukaryotic translation initiation factor 4E family member 3	6638	EIF4E3	0.587	+	6.08E-03	1.10E-02
224653_PM_at	eukaryotic translation initiation factor 4E binding protein 2	4155	EIF4EBP2	0.417	+	2.04E-02	1.80E-02
208706_PM_s_at	eukaryotic translation initiation factor 5	10927	EIF5	0.342	+	3.38E-02	1.01E-02
201726_PM_at	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	204851	ELAVL1	0.635	+	1.88E-02	2.39E-02
244660_PM_at	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	---	ELAVL1	0.704	+	2.31E-02	4.47E-02
210361_PM_s_at	E74-like factor 2 (ets domain transcription factor)	55814	ELF2	0.393	+	1.32E-04	2.39E-04
203822_PM_s_at	E74-like factor 2 (ets domain transcription factor)	8661	ELF2	0.498	+	2.64E-02	4.67E-02
229581_PM_at	extracellular leucine-rich repeat and fibronectin type III domain containing 1	4093	ELFN1	0.284	+	3.61E-02	2.83E-02
55692_PM_at	engulfment and cell motility 2	---	ELMO2	0.400	+	3.81E-02	1.19E-02
208788_PM_at	ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	9978	ELOVL5	0.384	+	3.60E-02	1.63E-02
227180_PM_at	ELOVL family member 7, elongation of long chain fatty acids (yeast)	51304	ELOVL7	0.735	+	7.81E-03	1.13E-02
234464_PM_s_at	essential meiotic endonuclease 1 homolog 1 (S. pombe)	51231	EME1	0.349	+	1.90E-04	1.18E-03
233894_PM_x_at	EMI domain containing 2	---	EMID2	0.291	+	2.32E-02	2.32E-02
225079_PM_at	epithelial membrane protein 2	5494	EMP2	0.493	+	4.15E-03	2.95E-02
221950_PM_at	empty spiracles homeobox 2	51552	EMX2	0.573	+	9.26E-04	6.60E-03
232531_PM_at	EMX2 opposite strand (non-protein coding)	7707	EMX2OS	0.716	+	4.05E-03	1.89E-02

228310_PM_at	enabled homolog (Drosophila)	161424	ENAH	0.355	+	4.24E-02	3.90E-02
217956_PM_s_at	enolase-phosphatase 1	6542	ENOPH1	0.598	+	5.76E-03	1.38E-02
204844_PM_at	glutamyl aminopeptidase (aminopeptidase A)	2744	ENPEP	0.318	+	5.90E-04	7.90E-04
227803_PM_at	ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function)	84319	ENPP5	0.426	+	8.03E-03	1.27E-02
221486_PM_at	endosulfine alpha	1825	ENSA	0.359	+	1.55E-03	6.11E-03
204076_PM_at	ectonucleoside triphosphate diphosphohydrolase 4	55611	ENTPD4	0.351	+	7.73E-03	1.27E-03
218482_PM_at	enhancer of yellow 2 homolog (Drosophila)	131474	ENY2	0.699	+	1.70E-03	6.18E-03
226776_PM_at	enhancer of yellow 2 homolog (Drosophila)	6272	ENY2	0.263	+	2.19E-03	3.30E-03
225051_PM_at	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	9204	EPB41	0.667	+	6.89E-03	1.36E-02
225855_PM_at	erythrocyte membrane protein band 4.1 like 5	388403	EPB41L5	0.641	+	3.18E-03	1.34E-02
225417_PM_at	enhancer of polycomb homolog 1 (Drosophila)	115399	EPC1	0.584	+	7.16E-04	1.53E-03
225838_PM_at	enhancer of polycomb homolog 2 (Drosophila)	---	EPC2	0.434	+	2.13E-02	1.22E-02
230425_PM_at	EPH receptor B1	658	EPHB1	0.936	+	6.32E-03	1.44E-02
204600_PM_at	EPH receptor B3	8204	EPHB3	0.367	+	9.64E-03	2.11E-02
227847_PM_at	EPM2A (laforin) interacting protein 1	3998	EPM2AIP1	0.474	+	2.04E-02	3.28E-02
200843_PM_s_at	glutamyl-prolyl-tRNA synthetase	7881	EPRS	0.471	+	1.69E-02	2.88E-02
217941_PM_s_at	erbb2 interacting protein	95681	ERBB2IP	0.409	+	1.84E-03	2.67E-06
222473_PM_s_at	erbb2 interacting protein	10228	ERBB2IP	0.330	+	1.93E-03	1.02E-03
214053_PM_at	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	23512 /// 440423	ERBB4	0.617	+	1.77E-02	1.67E-02
228131_PM_at	excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	54764	ERCC1	0.360	+	6.05E-03	1.40E-02
218135_PM_at	ERGIC and golgi 2	84153	ERGIC2	0.461	+	1.35E-02	2.05E-02
226416_PM_at	exoribonuclease 1	4185	ERI1	0.495	+	1.36E-02	1.60E-02
213365_PM_at	exoribonuclease 2	54861	ERI2	0.759	+	2.94E-03	8.27E-03
227017_PM_at	glutamate-rich 1	10690	ERICH1	0.367	+	1.02E-02	7.40E-03
224628_PM_at	endoplasmic reticulum lectin 1	22834	ERLEC1	0.313	+	3.35E-02	3.47E-02
221543_PM_s_at	ER lipid raft associated 2	781	ERLIN2	0.949	+	7.71E-03	5.13E-03
218342_PM_s_at	endoplasmic reticulum metallopeptidase 1	152100	ERMP1	0.359	+	2.27E-02	3.71E-02
208959_PM_s_at	endoplasmic reticulum protein 44	51306	ERP44	0.609	+	4.95E-04	8.48E-04

226866_PM_at	establishment of cohesion 1 homolog 1 (S. cerevisiae)	23211	ESCO1	0.739	+	4.68E-03	6.40E-03
209009_PM_at	esterase D/formylglutathione hydrolase	10352	ESD	0.406	+	1.96E-03	1.16E-02
215096_PM_s_at	esterase D/formylglutathione hydrolase	56521	ESD	0.508	+	1.46E-02	1.06E-02
201931_PM_at	electron-transfer-flavoprotein, alpha polypeptide	113251	ETFA	0.410	+	5.83E-03	8.44E-03
33494_PM_at	electron-transferring-flavoprotein dehydrogenase	---	ETFDH	0.829	+	7.94E-03	1.60E-02
205530_PM_at	electron-transferring-flavoprotein dehydrogenase	942	ETFDH	0.345	+	2.13E-02	3.56E-02
225290_PM_at	ethanolamine kinase 1	55036	ETNK1	0.513	+	3.44E-02	1.11E-02
224833_PM_at	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	140467	ETS1	0.850	+	5.77E-03	9.67E-03
226259_PM_at	exocyst complex component 6	11080	EXOC6	0.575	+	1.70E-02	9.25E-03
227916_PM_x_at	exosome component 3	201595	EXOSC3	0.407	+	3.45E-02	3.53E-02
215136_PM_s_at	exosome component 8	54433	EXOSC8	0.599	+	5.09E-03	1.84E-02
205061_PM_s_at	exosome component 9	22911	EXOSC9	0.454	+	4.73E-03	3.58E-03
214608_PM_s_at	eyes absent homolog 1 (Drosophila)	8303	EYA1	0.617	+	1.88E-03	1.28E-02
226170_PM_at	eyes absent homolog 3 (Drosophila)	5906	EYA3	0.360	+	1.58E-02	9.13E-03
203358_PM_s_at	enhancer of zeste homolog 2 (Drosophila)	404734 /// 54882	EZH2	0.293	+	2.30E-02	3.33E-02
223000_PM_s_at	F11 receptor	23609	F11R	0.580	+	7.70E-03	8.12E-03
205756_PM_s_at	coagulation factor VIII, procoagulant component	4915	F8	0.572	+	3.18E-02	1.43E-02
202345_PM_s_at	fatty acid binding protein 5 (psoriasis-associated)	4718	FABP5	0.631	+	1.91E-03	5.51E-03
205030_PM_at	fatty acid binding protein 7, brain	6905	FABP7	0.532	+	1.46E-03	5.58E-03
220643_PM_s_at	Fas apoptotic inhibitory molecule	5134	FAIM	0.368	+	2.61E-02	3.98E-02
225208_PM_s_at	family with sequence similarity 103, member A1	152137	FAM103A1	0.735	+	2.32E-03	1.07E-03
225210_PM_s_at	family with sequence similarity 103, member A1	113510	FAM103A1	0.742	+	5.94E-03	3.43E-03
225319_PM_s_at	family with sequence similarity 104, member A	112936	FAM104A	0.960	+	6.15E-03	2.33E-02
218248_PM_at	family with sequence similarity 111, member A	51123	FAM111A	0.304	+	2.32E-03	7.15E-03
222682_PM_s_at	family with sequence similarity 114, member A2	402055	FAM114A2	0.402	+	9.92E-03	1.19E-02
218588_PM_s_at	family with sequence similarity 114, member A2	83992	FAM114A2	0.763	+	3.86E-02	1.77E-02
226965_PM_at	family with sequence similarity 116, member A	317662	FAM116A	0.344	+	9.40E-04	2.22E-03
226431_PM_at	family with sequence similarity 117, member B	10284	FAM117B	0.644	+	3.45E-03	7.80E-03
229512_PM_at	family with sequence similarity 120C	---	FAM120C	0.745	+	4.13E-02	4.04E-02
222673_PM_x_at	family with sequence similarity 122B	657	FAM122B	0.590	+	8.55E-03	1.97E-02
225361_PM_x_at	family with sequence similarity 122B	6687	FAM122B	0.574	+	3.09E-02	4.86E-02
230067_PM_at	Family with sequence similarity 124A	54557	FAM124A	0.613	+	3.97E-02	3.79E-02

227239_PM_at	family with sequence similarity 126, member A	51318	FAM126A	0.589	+	1.62E-02	4.33E-02
231131_PM_at	family with sequence similarity 133, member A	84340	FAM133A	0.569	+	2.15E-02	3.02E-02
226332_PM_at	family with sequence similarity 133, member B	1605	FAM133B	0.544	+	3.46E-03	8.05E-03
218532_PM_s_at	family with sequence similarity 134, member B	83700	FAM134B	0.444	+	1.25E-03	2.24E-03
223497_PM_at	family with sequence similarity 135, member A	51397	FAM135A	0.647	+	1.11E-02	3.05E-03
217047_PM_s_at	family with sequence similarity 13, member A	5150	FAM13A	0.490	+	3.57E-02	2.51E-02
218518_PM_at	family with sequence similarity 13, member B	118672	FAM13B	0.456	+	4.04E-02	1.66E-02
213896_PM_x_at	family with sequence similarity 149, member B1	1737	FAM149B1	0.344	+	2.65E-03	1.89E-02
241808_PM_at	family with sequence similarity 164, member A	---	FAM164A	0.337	+	1.23E-02	4.96E-03
226614_PM_s_at	family with sequence similarity 167, member A	361	FAM167A	0.415	+	2.51E-02	2.99E-02
36612_PM_at	family with sequence similarity 168, member A	---	FAM168A	0.416	+	1.49E-02	2.45E-02
212017_PM_at	family with sequence similarity 168, member B	2058	FAM168B	0.283	+	2.17E-02	5.63E-03
227370_PM_at	family with sequence similarity 171, member B	149986	FAM171B	0.287	+	1.79E-02	1.11E-03
226521_PM_s_at	family with sequence similarity 175, member A	1501	FAM175A	0.278	+	3.62E-02	4.60E-02
212837_PM_at	family with sequence similarity 175, member B	7091	FAM175B	0.519	+	4.00E-02	1.32E-02
227029_PM_at	family with sequence similarity 177, member A1	8992	FAM177A1	0.618	+	9.24E-03	3.25E-03
203482_PM_at	family with sequence similarity 178, member A	22854	FAM178A	0.538	+	8.73E-03	8.38E-03
213304_PM_at	family with sequence similarity 179, member B	30851	FAM179B	0.310	+	1.07E-02	5.00E-03
231430_PM_at	family with sequence similarity 181, member B	57718	FAM181B	0.401	+	1.50E-02	1.19E-02
1558523_PM_at	family with sequence similarity 184, member A	4147	FAM184A	0.593	+	1.36E-02	1.17E-02
218446_PM_s_at	family with sequence similarity 18, member B	84324	FAM18B	0.449	+	9.81E-03	2.15E-02
241399_PM_at	family with sequence similarity 19 (chemokine (C-C motif)-like), member A2	26091	FAM19A2	0.509	+	1.03E-02	3.19E-02
202916_PM_s_at	family with sequence similarity 20, member B	5522	FAM20B	0.301	+	1.03E-02	1.91E-02
234414_PM_at	family with sequence similarity 22, member A /// family with sequence similarity 22, member B /// family with sequence similarity 22, member F /// family with sequence similarity 22, member G	---	FAM22A /// FAM22B /// FAM22F /// FAM22G	0.635	+	2.39E-03	1.47E-02
234695_PM_x_at	family with sequence similarity 22, member B	---	FAM22B	0.368	+	5.05E-03	2.52E-02
224824_PM_at	family with sequence similarity 36, member A	57589	FAM36A	0.581	+	5.60E-03	7.40E-03
240062_PM_at	family with sequence similarity 3, member C	283713	FAM3C	0.344	+	1.51E-02	1.81E-02
226330_PM_s_at	family with sequence similarity 48, member A	5203	FAM48A	0.784	+	2.15E-02	3.55E-03

230276_PM_at	family with sequence similarity 49, member A	80205	FAM49A	0.300	+	3.51E-02	1.56E-02
218023_PM_s_at	family with sequence similarity 53, member C	57669	FAM53C	0.363	+	1.00E-02	1.54E-02
217562_PM_at	family with sequence similarity 5, member C	80829	FAM5C	0.680	+	1.72E-02	1.24E-02
220147_PM_s_at	family with sequence similarity 60, member A	27095	FAM60A	0.759	+	2.51E-02	3.16E-02
213689_PM_x_at	family with sequence similarity 69, member A	51592	FAM69A	0.394	+	2.02E-02	4.71E-03
216044_PM_x_at	family with sequence similarity 69, member A	80204	FAM69A	0.329	+	2.50E-02	1.43E-02
229645_PM_at	family with sequence similarity 69, member C	114787	FAM69C	0.276	+	2.05E-02	2.24E-02
225834_PM_at	family with sequence similarity 72, member A /// family with sequence similarity 72, member B /// family with sequence similarity 72, member C	54328	FAM72A /// FAM72B /// FAM72C	0.434	+	1.56E-02	1.80E-02
235125_PM_x_at	family with sequence similarity 73, member A	8301	FAM73A	0.550	+	2.08E-04	1.38E-03
228604_PM_at	family with sequence similarity 76, member A	342371	FAM76A	0.653	+	5.63E-03	1.39E-02
226753_PM_at	family with sequence similarity 76, member B	3987	FAM76B	0.749	+	1.06E-02	1.74E-02
225864_PM_at	family with sequence similarity 84, member B	---	FAM84B	0.708	+	2.72E-02	2.01E-03
226448_PM_at	family with sequence similarity 89, member A	128	FAM89A	0.506	+	6.88E-03	1.93E-02
203420_PM_at	family with sequence similarity 8, member A1	55593	FAM8A1	0.440	+	1.01E-02	8.84E-03
228011_PM_at	family with sequence similarity 92, member A1	382	FAM92A1	0.456	+	1.92E-03	8.24E-03
235391_PM_at	family with sequence similarity 92, member A1	284244	FAM92A1	0.309	+	3.72E-02	3.79E-03
224779_PM_s_at	family with sequence similarity 96, member A	80821	FAM96A	0.540	+	1.87E-02	2.30E-02
225086_PM_at	Family with sequence similarity 98, member B	90390	FAM98B	0.466	+	3.76E-03	2.12E-02
205189_PM_s_at	Fanconi anemia, complementation group C	4329	FANCC	0.310	+	4.54E-02	4.05E-02
234733_PM_s_at	Fanconi anemia, complementation group M	---	FANCM	0.531	+	4.49E-02	3.52E-02
227996_PM_at	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	647087	FARP1	0.870	+	1.63E-02	8.23E-03
204282_PM_s_at	phenylalanyl-tRNA synthetase 2, mitochondrial	201725 /// 54543	FARS2	0.486	+	3.49E-04	4.47E-03
219002_PM_at	FAST kinase domains 1	9652	FASTKD1	0.315	+	2.44E-02	3.37E-02
201579_PM_at	FAT tumor suppressor homolog 1 (Drosophila)	5682	FAT1	0.422	+	4.08E-02	2.41E-02
225258_PM_at	filamin binding LIM protein 1	2043	FBLIM1	0.282	+	1.94E-03	1.72E-02
202766_PM_s_at	fibrillin 1	56997	FBN1	0.910	+	7.86E-03	1.34E-02
222119_PM_s_at	F-box protein 11	23360	FBXO11	0.427	+	1.53E-02	2.50E-02
231472_PM_at	F-box protein 15	730200	FBXO15	0.452	+	3.23E-02	2.26E-02
214891_PM_at	F-box protein 21	55596	FBXO21	0.298	+	4.69E-02	4.31E-02

225736_PM_at	F-box protein 22	157753	FBXO22	0.542	+	1.07E-03	2.45E-03
225737_PM_s_at	F-box protein 22	122773	FBXO22	0.432	+	2.21E-02	3.85E-02
202271_PM_at	F-box protein 28	7763	FBXO28	0.742	+	2.11E-02	2.77E-02
218432_PM_at	F-box protein 3	92482	FBXO3	0.310	+	3.66E-02	3.72E-02
226541_PM_at	F-box protein 30	23169	FBXO30	0.323	+	1.64E-03	1.25E-02
227521_PM_at	F-box protein 33	103910	FBXO33	0.769	+	4.70E-03	1.66E-03
224369_PM_s_at	F-box protein 38	401397	FBXO38	0.574	+	2.02E-02	2.53E-02
47773_PM_at	F-box protein 42	---	FBXO42	0.346	+	3.82E-02	2.70E-02
223240_PM_at	F-box protein 8	80235	FBXO8	0.294	+	1.16E-02	1.84E-02
1554806_PM_a_at	F-box protein 8	5660	FBXO8	0.668	+	3.06E-02	2.94E-02
212987_PM_at	F-box protein 9	51412	FBXO9	0.416	+	1.96E-02	2.39E-02
235195_PM_at	F-box and WD repeat domain containing 2	7779	FBXW2	0.691	+	2.37E-02	4.93E-02
214511_PM_x_at	Fc fragment of IgG, high affinity Ib, receptor (CD64)	28972	FCGR1B	0.278	+	2.47E-02	7.36E-03
210889_PM_s_at	Fc fragment of IgG, low affinity IIb, receptor (CD32)	151126	FCGR2B	0.266	+	1.98E-03	1.81E-03
228220_PM_at	FCH domain only 2	---	FCHO2	0.649	+	1.11E-02	1.34E-02
203115_PM_at	ferrochelatase (protoporphyria)	57231	FECH	0.411	+	3.94E-03	2.32E-02
212367_PM_at	fem-1 homolog b (C. elegans)	2764	FEM1B	0.273	+	1.76E-02	1.66E-02
233353_PM_at	fer-1-like 5 (C. elegans)	1994	FER1L5	0.377	+	1.01E-02	2.64E-02
1553906_PM_s_at	FYVE, RhoGEF and PH domain containing 2	152503	FGD2	1.006	+	2.38E-03	1.24E-02
230231_PM_at	fibroblast growth factor 14	257000	FGF14	0.845	+	5.37E-03	1.11E-02
204379_PM_s_at	fibroblast growth factor receptor 3	57862	FGFR3	0.415	+	1.85E-02	3.16E-02
201540_PM_at	four and a half LIM domains 1	11309	FHL1	0.323	+	4.17E-02	3.11E-02
202949_PM_s_at	four and a half LIM domains 2	56996	FHL2	0.353	+	2.47E-03	2.03E-02
218980_PM_at	formin homology 2 domain containing 3	79842	FHOD3	0.345	+	4.48E-02	7.25E-03
226769_PM_at	fin bud initiation factor homolog (zebrafish)	23294	FIBIN	0.353	+	1.55E-02	1.89E-02
203656_PM_at	FIG4 homolog (S. cerevisiae)	55353	FIG4	0.485	+	3.97E-02	4.38E-02
218003_PM_s_at	FK506 binding protein 3, 25kDa	221895	FKBP3	0.414	+	1.35E-03	1.07E-03
224840_PM_at	FK506 binding protein 5	4084	FKBP5	0.576	+	3.69E-03	2.92E-02
224002_PM_s_at	FK506 binding protein 7	81571	FKBP7	0.471	+	2.91E-03	2.61E-03
205283_PM_at	fukutin	1917	FKTN	0.590	+	2.12E-02	4.42E-02

204236_PM_at	Friend leukemia virus integration 1	9878	FLI1	0.340	+	8.81E-04	3.98E-03
229623_PM_at	Hypothetical LOC441027	162073	FLJ12993	0.745	+	3.38E-02	1.08E-02
1553292_PM_s_at	uncharacterized serine/threonine-protein kinase SgK494	5825	FLJ25006	0.426	+	3.03E-02	8.71E-03
243309_PM_at	hypothetical LOC145788	---	FLJ27352	0.608	+	2.39E-02	1.34E-02
1553446_PM_at	hypothetical protein FLJ37396	30819	FLJ37396	0.295	+	6.73E-03	2.22E-02
227298_PM_at	hypothetical gene supported by AK095117	79078	FLJ37798	0.368	+	1.05E-02	4.71E-02
229914_PM_at	FLJ38717 protein	153572	FLJ38717	0.519	+	1.61E-02	3.66E-02
227717_PM_at	FLJ41603 protein	79794	FLJ41603	0.279	+	1.38E-02	2.18E-02
229014_PM_at	hypothetical LOC441094	64376	FLJ42709	0.605	+	2.62E-03	2.07E-03
236360_PM_at	hypothetical LOC440556	---	FLJ42875	0.265	+	1.37E-02	3.95E-03
236902_PM_at	hypothetical LOC646113	23143	FLJ43390	0.676	+	1.82E-02	1.81E-02
229246_PM_at	hypothetical LOC645460	10294	FLJ44342	0.597	+	1.77E-03	1.34E-03
226419_PM_s_at	hypothetical LOC645460	2260	FLJ44342	0.640	+	6.80E-03	7.12E-03
230404_PM_at	glutaredoxin-like protein YDR286C homolog	401261	FLJ44606	0.501	+	1.44E-03	7.00E-03
204359_PM_at	fibronectin leucine rich transmembrane protein 2	2180	FLRT2	0.420	+	4.29E-02	3.10E-02
226498_PM_at	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	9044	FLT1	0.606	+	5.29E-03	3.09E-03
222033_PM_s_at	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	4502	FLT1	0.922	+	6.31E-03	1.56E-02
206674_PM_at	fms-related tyrosine kinase 3	361	FLT3	0.354	+	3.47E-02	3.90E-02
223618_PM_at	formin 2	54926	FMN2	0.376	+	1.16E-02	2.30E-02
1555471_PM_a_at	formin 2	7078	FMN2	0.439	+	1.73E-02	2.65E-02
215245_PM_x_at	fragile X mental retardation 1	54968	FMR1	0.933	+	7.19E-04	2.29E-03
203689_PM_s_at	fragile X mental retardation 1	253559	FMR1	0.558	+	6.06E-03	3.07E-02
211719_PM_x_at	fibronectin 1	57605	FN1	0.991	+	1.26E-02	1.56E-02
216442_PM_x_at	fibronectin 1	80757	FN1	0.928	+	1.65E-02	2.98E-02
215017_PM_s_at	formin binding protein 1-like	56925	FNBP1L	0.752	+	1.42E-02	2.88E-03
212232_PM_at	formin binding protein 4	8099	FNBP4	0.846	+	2.31E-02	9.23E-03
225032_PM_at	fibronectin type III domain containing 3B	56647	FNDC3B	0.785	+	1.28E-03	1.20E-02
228768_PM_at	folliculin interacting protein 1	84376	FNIP1	0.581	+	2.00E-02	2.98E-02

219112_PM_at	folliculin interacting protein 1 /// Rap guanine nucleotide exchange factor (GEF) 6	253943	FNIP1 /// RAPGEF6	0.447	+	2.24E-02	1.92E-02
206015_PM_s_at	forkhead box J3	8237	FOXJ3	0.304	+	9.57E-03	3.85E-02
226711_PM_at	forkhead box N2	115207	FOXN2	0.558	+	1.11E-02	6.72E-03
202724_PM_s_at	forkhead box O1	25861	FOXO1	0.407	+	3.57E-02	3.10E-02
224891_PM_at	forkhead box O3	84085	FOXO3	0.477	+	3.48E-03	5.42E-03
221333_PM_at	forkhead box P3	9912	FOXP3	0.430	+	3.17E-04	6.37E-03
227475_PM_at	forkhead box Q1	619426	FOXQ1	0.425	+	1.25E-02	2.77E-02
226145_PM_s_at	Fraser syndrome 1	1362	FRAS1	0.742	+	2.36E-02	2.04E-02
219889_PM_at	frequently rearranged in advanced T-cell lymphomas	22836	FRAT1	0.374	+	9.54E-03	7.93E-03
204145_PM_at	FSHD region gene 1	1340	FRG1	0.372	+	1.61E-02	3.56E-02
225163_PM_at	FERM domain containing 4A	280636	FRMD4A	0.613	+	1.37E-02	2.17E-02
230831_PM_at	FERM domain containing 5	285987	FRMD5	0.758	+	3.90E-02	1.78E-03
225464_PM_at	FERM domain containing 6	28962	FRMD6	0.541	+	3.78E-03	8.38E-03
225481_PM_at	FERM domain containing 6	137392	FRMD6	0.601	+	1.01E-02	1.75E-02
226045_PM_at	fibroblast growth factor receptor substrate 2	8125	FRS2	0.783	+	2.53E-02	1.19E-02
212548_PM_s_at	FRY-like	687	FRYL	0.395	+	3.36E-02	6.21E-03
203697_PM_at	frizzled-related protein	30818	FRZB	0.508	+	2.02E-02	3.45E-02
230904_PM_at	fibronectin type III and SPRY domain containing 1-like	137970	FSD1L	0.730	+	1.01E-02	6.83E-03
232010_PM_at	follistatin-like 5	283401	FSTL5	0.837	+	9.40E-03	2.45E-02
214211_PM_at	ferritin, heavy polypeptide 1	81931	FTH1	0.466	+	4.46E-03	2.17E-02
205324_PM_s_at	FtsJ homolog 1 (E. coli)	3422	FTSJ1	0.399	+	6.31E-03	9.25E-03
212847_PM_at	Far upstream element (FUSE) binding protein 1	10518	FUBP1	0.536	+	3.61E-02	2.24E-02
212824_PM_at	far upstream element (FUSE) binding protein 3	9140	FUBP3	0.514	+	6.02E-03	9.86E-03
235346_PM_at	FUN14 domain containing 1	---	FUNDC1	0.932	+	3.29E-04	2.69E-03
223042_PM_s_at	FUN14 domain containing 2	80135	FUNDC2	0.339	+	1.02E-02	1.11E-02
225348_PM_at	FUS interacting protein (serine/arginine-rich) 1	9120	FUSIP1	0.620	+	3.43E-02	1.94E-02
214046_PM_at	fucosyltransferase 9 (alpha (1,3) fucosyltransferase)	83941	FUT9	0.686	+	4.24E-03	7.79E-04
205674_PM_x_at	FXYD domain containing ion transport regulator 2	11163 /// 440672	FXYD2	0.318	+	9.88E-04	4.18E-03
224325_PM_at	frizzled homolog 8 (Drosophila)	80829	FZD8	0.646	+	3.96E-03	6.87E-03
208841_PM_s_at	GTPase activating protein (SH3 domain) binding protein 2	27236	G3BP2	0.422	+	2.07E-02	1.70E-02
44654_PM_at	glucose 6 phosphatase, catalytic, 3	---	G6PC3	0.360	+	1.56E-02	2.69E-02

229114_PM_at	GRB2-associated binding protein 1	154791	GAB1	0.750	+	3.74E-02	9.67E-03
227690_PM_at	gamma-aminobutyric acid (GABA) A receptor, beta 3	51201	GABRB3	0.406	+	3.00E-02	8.31E-03
1568612_PM_at	gamma-aminobutyric acid (GABA) A receptor, gamma 2	4712	GABRG2	0.280	+	2.29E-02	1.49E-02
238123_PM_at	gamma-aminobutyric acid (GABA) receptor, theta	158947	GABRQ	0.438	+	1.43E-02	1.03E-02
207574_PM_s_at	growth arrest and DNA-damage-inducible, beta	23041	GADD45B	0.497	+	2.86E-02	1.65E-02
203397_PM_s_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3)	29989 /// 29991	GALNT3	0.347	+	8.56E-03	1.41E-02
219110_PM_at	GAR1 ribonucleoprotein homolog (yeast)	378938	GAR1	0.336	+	1.36E-02	2.90E-02
213049_PM_at	GTPase activating Rap/RanGAP domain-like 1	1415	GARNL1	0.517	+	4.02E-02	1.08E-02
223604_PM_at	GTPase activating Rap/RanGAP domain-like 3	79896	GARNL3	0.441	+	6.59E-03	8.14E-03
213280_PM_at	GTPase activating Rap/RanGAP domain-like 4	23576	GARNL4	0.311	+	1.87E-02	2.35E-02
31874_PM_at	growth arrest-specific 2 like 1	---	GAS2L1	0.587	+	8.70E-03	2.18E-02
209729_PM_at	growth arrest-specific 2 like 1	51661	GAS2L1	0.308	+	2.22E-02	6.31E-03
228238_PM_at	growth arrest-specific 5 (non-protein coding)	493753	GAS5	0.711	+	1.03E-03	9.25E-03
224841_PM_x_at	growth arrest-specific 5 (non-protein coding)	57679	GAS5	0.278	+	3.14E-02	1.02E-02
213018_PM_at	GATA zinc finger domain containing 1	9211	GATAD1	0.663	+	1.48E-02	2.91E-02
203178_PM_at	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	57223	GATM	0.447	+	3.73E-02	1.31E-02
201816_PM_s_at	glioblastoma amplified sequence	8622	GBAS	0.428	+	1.26E-02	1.66E-02
202748_PM_at	guanylate binding protein 2, interferon-inducible	26010	GBP2	0.284	+	4.37E-03	1.55E-03
202832_PM_at	GRIP and coiled-coil domain containing 2	51300	GCC2	0.499	+	1.75E-02	1.74E-02
203925_PM_at	glutamate-cysteine ligase, modifier subunit	6434	GCLM	0.375	+	2.43E-02	1.20E-02
212139_PM_at	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	156	GCN1L1	0.523	+	5.36E-03	1.08E-02
226269_PM_at	ganglioside-induced differentiation-associated protein 1	5728	GDAP1	0.380	+	1.95E-02	1.60E-02
219473_PM_at	ganglioside induced differentiation associated protein 2	5552	GDAP2	0.327	+	1.75E-03	2.01E-02
226234_PM_at	growth differentiation factor 11	3720	GDF11	0.620	+	1.05E-02	2.23E-02
221314_PM_at	growth differentiation factor 9	53340	GDF9	0.692	+	5.30E-03	1.00E-02
225712_PM_at	gem (nuclear organelle) associated protein 5	11057	GEMIN5	0.342	+	2.22E-02	3.40E-02
225153_PM_at	G elongation factor, mitochondrial 1	96459	GFM1	0.563	+	7.40E-03	1.23E-03
227027_PM_at	glutamine-fructose-6-phosphate transaminase 1	11010	GFPT1	0.509	+	7.71E-03	7.98E-03
227550_PM_at	GDNF family receptor alpha 1	253943	GFRA1	0.340	+	1.16E-02	4.08E-02
215380_PM_s_at	gamma-glutamyl cyclotransferase	55592	GGCT	0.357	+	3.52E-02	1.05E-02

214005_PM_at	gamma-glutamyl carboxylase	5880	GGCX	0.386	+	2.21E-03	3.14E-05
203560_PM_at	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	29780	GGH	0.881	+	3.68E-03	3.03E-03
218079_PM_s_at	gametogenetin binding protein 2	196394	GGNBP2	0.442	+	1.69E-02	1.34E-02
202321_PM_at	geranylgeranyl diphosphate synthase 1	6945	GGPS1	0.624	+	2.74E-02	3.02E-02
209248_PM_at	growth hormone inducible transmembrane protein	55681	GHITM	0.496	+	2.14E-02	3.88E-02
206102_PM_at	GINS complex subunit 1 (Psf1 homolog)	7070	GINS1	0.717	+	6.65E-03	1.70E-02
204982_PM_at	G protein-coupled receptor kinase interacting ArfGAP 2	23480	GIT2	0.594	+	6.81E-03	5.47E-03
225558_PM_at	G protein-coupled receptor kinase interacting ArfGAP 2	326625	GIT2	0.526	+	2.62E-02	1.37E-02
231771_PM_at	gap junction protein, beta 6, 30kDa	57458	GJB6	0.531	+	2.02E-03	2.06E-02
234192_PM_s_at	G kinase anchoring protein 1	---	GKAP1	0.288	+	4.00E-03	4.17E-03
225706_PM_at	glucocorticoid induced transcript 1	27092	GLCCI1	0.648	+	1.38E-02	5.70E-03
227525_PM_at	glucocorticoid induced transcript 1	51271	GLCCI1	0.450	+	3.17E-02	1.98E-02
213552_PM_at	glucuronic acid epimerase	644	GLCE	0.600	+	3.26E-02	2.43E-02
227376_PM_at	GLI family zinc finger 3	80345	GLI3	0.565	+	3.04E-02	3.96E-02
214085_PM_x_at	GLI pathogenesis-related 1	9236	GLIPR1	0.636	+	1.51E-02	3.25E-02
225602_PM_at	GLI pathogenesis-related 2	25831	GLIPR2	0.435	+	2.56E-03	2.64E-02
229435_PM_at	GLIS family zinc finger 3	29078	GLIS3	0.695	+	3.35E-04	1.59E-03
207153_PM_s_at	glomulin, FKBP associated protein	23215	GLMN	0.436	+	9.42E-03	3.99E-04
200681_PM_at	glyoxalase I	5582	GLO1	0.264	+	1.51E-02	4.61E-02
244680_PM_at	glycine receptor, beta	---	GLRB	0.285	+	4.12E-02	1.14E-02
206662_PM_at	glutaredoxin (thioltransferase)	9353	GLRX	0.428	+	4.13E-03	1.44E-02
219933_PM_at	glutaredoxin 2	3800	GLRX2	0.342	+	1.74E-02	2.94E-02
209080_PM_x_at	glutaredoxin 3	11201	GLRX3	0.400	+	1.42E-02	3.35E-02
221932_PM_s_at	glutaredoxin 5	3082	GLRX5	0.533	+	7.27E-03	1.57E-02
221510_PM_s_at	glutaminase	3759	GLS	0.525	+	3.02E-02	2.24E-02
218146_PM_at	glycosyltransferase 8 domain containing 1	7994	GLT8D1	0.469	+	2.44E-02	3.63E-02
212414_PM_s_at	glyoxylate reductase 1 homolog (Arabidopsis) /// septin 6	7525	GLYR1 /// SEPT6	0.551	+	6.88E-03	1.10E-02
235233_PM_s_at	glucocorticoid modulatory element binding protein 1	27229	GMEB1	0.691	+	2.07E-02	4.89E-02
202544_PM_at	glia maturation factor, beta	7812	GMFB	0.444	+	4.13E-03	1.21E-03
218350_PM_s_at	geminin, DNA replication inhibitor	84458	GMNN	0.603	+	6.50E-03	9.09E-03

214431_PM_at	guanine 297eparin297ing297e synthetase	51125	GMPS	0.591	+	3.41E-02	2.52E-02
227539_PM_at	guanine nucleotide binding protein (G protein), alpha 13	28971	GNA13	0.378	+	3.03E-02	3.25E-02
224761_PM_at	guanine nucleotide binding protein (G protein), alpha 13	114990	GNA13	0.387	+	3.18E-02	3.77E-02
201180_PM_s_at	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	58497	GNAI3	0.677	+	3.06E-02	2.15E-02
214157_PM_at	GNAS complex locus	54874	GNAS	0.329	+	2.49E-02	3.10E-02
225710_PM_at	guanine nucleotide binding protein (G protein), beta polypeptide 4	79874	GNB4	0.546	+	9.00E-03	1.13E-02
224964_PM_s_at	guanine nucleotide binding protein (G protein), gamma 2	157697	GNG2	0.450	+	5.34E-03	1.40E-02
207157_PM_s_at	guanine nucleotide binding protein (G protein), gamma 5	23215	GNG5	0.505	+	3.05E-02	2.15E-02
201948_PM_at	guanine nucleotide binding protein-like 2 (nucleolar)	3845	GNL2	0.418	+	2.05E-02	1.14E-02
217850_PM_at	guanine nucleotide binding protein-like 3 (nucleolar)	55239	GNL3	0.350	+	5.69E-03	2.57E-03
202382_PM_s_at	glucosamine-6-phosphate deaminase 1	55288	GNPDA1	0.558	+	1.61E-03	1.09E-02
227022_PM_at	glucosamine-6-phosphate deaminase 2	146227	GNPDA2	0.484	+	3.52E-02	9.86E-03
225853_PM_at	glucosamine-phosphate N-acetyltransferase 1	---	GNPNAT1	0.265	+	2.90E-02	1.98E-02
212334_PM_at	glucosamine (N-acetyl)-6-sulfatase	1176	GNS	0.551	+	1.68E-02	3.61E-02
219876_PM_s_at	golgi autoantigen, golgin subfamily a, 2-like 1	6662	GOLGA2L1	0.294	+	8.04E-04	1.80E-03
201567_PM_s_at	golgi autoantigen, golgin subfamily a, 4	27113	GOLGA4	0.921	+	9.85E-03	7.17E-03
218241_PM_at	golgi autoantigen, golgin subfamily a, 5	79848	GOLGA5	0.478	+	4.44E-02	4.23E-02
217819_PM_at	golgi autoantigen, golgin subfamily a, 7	112942	GOLGA7	0.460	+	3.18E-02	1.29E-02
218361_PM_at	golgi phosphoprotein 3-like	389114	GOLPH3L	0.531	+	2.49E-03	2.74E-03
222552_PM_at	golgi transport 1 homolog B (S. cerevisiae)	112464	GOLT1B	0.680	+	1.12E-02	4.08E-03
213020_PM_at	golgi SNAP receptor complex member 1	8853	GOSR1	0.338	+	3.05E-02	4.90E-02
200708_PM_at	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	2571	GOT2	0.342	+	4.49E-02	4.44E-02
212485_PM_at	G patch domain containing 8	1819	GPATCH8	0.371	+	7.19E-04	4.24E-03
224648_PM_at	GC-rich promoter binding protein 1	90780	GPBP1	0.453	+	4.22E-02	2.36E-02
217877_PM_s_at	GC-rich promoter binding protein 1-like 1	22808	GPBP1L1	0.482	+	1.77E-02	1.25E-02
225447_PM_at	glycerol-3-phosphate dehydrogenase 2 (mitochondrial)	200312	GPD2	0.321	+	1.28E-02	2.11E-02
203776_PM_at	G patch domain and KOW motifs	10419	GPKOW	0.351	+	1.11E-02	6.03E-03
209313_PM_at	GPN-loop GTPase 1	221037	GPN1	0.350	+	3.90E-03	1.32E-02
65718_PM_at	G protein-coupled receptor 124	---	GPR124	0.498	+	1.07E-02	8.73E-03

1556039_PM_s_at	G protein-coupled receptor 173	6240	GPR173	0.622	+	7.82E-03	1.26E-03
228949_PM_at	G protein-coupled receptor 177	84312	GPR177	0.653	+	1.91E-02	1.29E-02
207183_PM_at	G protein-coupled receptor 19	23199	GPR19	0.672	+	7.32E-03	1.56E-02
221288_PM_at	G protein-coupled receptor 22	5203	GPR22	0.576	+	3.69E-02	5.30E-03
214586_PM_at	G protein-coupled receptor 37 (endothelin receptor type B-like)	79180	GPR37	0.619	+	4.10E-03	6.10E-03
229055_PM_at	G protein-coupled receptor 68	6745	GPR68	0.287	+	2.05E-02	4.28E-02
225463_PM_x_at	G protein-coupled receptor 89A /// G protein-coupled receptor 89B /// G protein-coupled receptor 89C	28962	GPR89A /// GPR89B /// GPR89C	0.420	+	1.72E-02	1.06E-02
223582_PM_at	G protein-coupled receptor 98	56952	GPR98	0.584	+	4.31E-03	1.08E-02
225511_PM_at	G protein-coupled receptor, family C, group 5, member B	64805	GPRC5B	0.367	+	3.06E-03	2.66E-03
227975_PM_at	G protein regulated inducer of neurite outgrowth 1	10238	GPRIN1	0.295	+	3.27E-02	3.15E-02
204265_PM_s_at	G-protein signaling modulator 3 (AGS3-like, C. elegans)	9685	GPSM3	0.376	+	5.33E-03	1.33E-02
209409_PM_at	growth factor receptor-bound protein 10	23609	GRB10	0.494	+	3.35E-02	3.44E-02
206204_PM_at	growth factor receptor-bound protein 14	10539	GRB14	1.010	+	1.33E-02	4.10E-02
205862_PM_at	GREB1 protein	1528	GREB1	0.520	+	3.02E-02	1.57E-02
214864_PM_s_at	glyoxylate reductase/hydroxypyruvate reductase	55325	GRHPR	0.423	+	1.47E-04	5.96E-04
230593_PM_at	glutamate receptor, ionotropic, 298eparin 3	---	GRIK3	0.380	+	3.43E-02	4.18E-02
233220_PM_at	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	25791	GRIN3A	0.856	+	2.55E-02	2.66E-02
235957_PM_at	glutamate receptor interacting protein 1	53832	GRIP1	0.595	+	2.58E-02	3.22E-02
204396_PM_s_at	G protein-coupled receptor kinase 5	8899	GRK5	0.765	+	4.16E-03	7.13E-03
207299_PM_s_at	glutamate receptor, metabotropic 1	92140	GRM1	0.582	+	2.32E-03	4.04E-03
241049_PM_at	glutamate receptor, metabotropic 7	---	GRM7	0.357	+	1.91E-02	3.14E-02
206326_PM_at	gastrin-releasing peptide	8473	GRP	0.641	+	2.14E-02	1.79E-02
212434_PM_at	GrpE-like 1, mitochondrial (E. coli)	4594	GRPEL1	0.362	+	1.39E-02	6.75E-03
226881_PM_at	GrpE-like 2, mitochondrial (E. coli)	5094	GRPEL2	0.715	+	1.63E-02	1.90E-03
215030_PM_at	G-rich RNA sequence binding factor 1	57763	GRSF1	0.474	+	5.46E-03	1.82E-02
226183_PM_at	glycogen synthase kinase 3 beta	6782	GSK3B	0.430	+	1.20E-02	7.84E-03
201415_PM_at	glutathione synthetase	9743	GSS	0.352	+	1.07E-02	4.51E-02
235405_PM_at	glutathione S-transferase alpha 4	6136	GSTA4	0.457	+	1.35E-02	4.22E-02

202554_PM_s_at	glutathione S-transferase mu 3 (brain)	57018	GSTM3	0.441	+	4.08E-03	2.30E-02
205752_PM_s_at	glutathione S-transferase mu 5	3760	GSTM5	0.657	+	4.33E-02	3.46E-02
225433_PM_at	General transcription factor IIA, 1, 19/37kDa	11198	GTF2A1	0.514	+	1.68E-02	2.98E-02
202678_PM_at	general transcription factor IIA, 2, 12kDa	55275	GTF2A2	0.631	+	1.59E-03	1.57E-03
208066_PM_s_at	general transcription factor IIB	2017	GTF2B	0.468	+	1.47E-03	1.68E-03
205930_PM_at	general transcription factor IIE, polypeptide 1, alpha 56kDa	7430	GTF2E1	0.635	+	3.11E-02	4.91E-02
202451_PM_at	general transcription factor IIH, polypeptide 1, 62kDa	80150	GTF2H1	0.512	+	1.83E-02	1.22E-02
213357_PM_at	general transcription factor IIH, polypeptide 5	81542	GTF2H5	0.794	+	1.58E-03	9.37E-04
201338_PM_x_at	general transcription factor IIIA	8829	GTF3A	0.631	+	3.30E-03	2.15E-03
215091_PM_s_at	general transcription factor IIIA	10620	GTF3A	0.425	+	2.33E-02	4.77E-03
225083_PM_at	general transcription factor IIIC, polypeptide 6, alpha 35kDa	90390	GTF3C6	0.364	+	3.31E-02	4.24E-02
221050_PM_s_at	GTP binding protein 2	3131	GTPBP2	0.471	+	1.97E-02	2.86E-03
207003_PM_at	guanylate cyclase activator 2A (guanylin)	8487	GUCA2A	0.282	+	1.41E-04	4.07E-03
203817_PM_at	guanylate cyclase 1, soluble, beta 3	3550	GUCY1B3	0.467	+	2.37E-02	1.47E-03
202605_PM_at	glucuronidase, beta	55704	GUSB	0.631	+	1.52E-03	2.66E-03
215816_PM_at	glucuronidase, beta /// similar to hCG1820960 /// glucuronidase, beta/ immunoglobulin lambda-like polypeptide 1 pseudogene	11165	GUSB /// LOC100294451 /// LOC91316	0.337	+	2.74E-02	3.17E-02
211275_PM_s_at	glycogenin 1	137682	GYG1	0.397	+	3.22E-02	4.16E-02
207168_PM_s_at	H2A histone family, member Y	3320	H2AFY	0.294	+	2.11E-02	5.50E-03
213911_PM_s_at	H2A histone family, member Z	5094	H2AFZ	0.284	+	1.78E-04	1.69E-04
200853_PM_at	H2A histone family, member Z	10634	H2AFZ	0.494	+	4.53E-03	4.17E-03
216875_PM_x_at	B1 for mucin	81603	HAB1	0.332	+	9.31E-03	9.44E-03
233919_PM_s_at	hyaluronan binding protein 4	---	HABP4	0.404	+	8.37E-03	2.63E-02
223541_PM_at	hyaluronan synthase 3	54841	HAS3	0.670	+	1.37E-02	3.13E-02
203138_PM_at	histone acetyltransferase 1	51463 /// 653519 /// 728932	HAT1	0.562	+	1.34E-02	3.50E-03
225297_PM_at	HAUS augmin-like complex, subunit 1	1153	HAUS1	0.386	+	1.19E-02	2.99E-03
222685_PM_at	HAUS augmin-like complex, subunit 6	---	HAUS6	0.332	+	2.86E-02	7.37E-03
201145_PM_at	HCLS1 associated protein X-1	23600	HAX1	0.336	+	1.54E-02	5.59E-03
209314_PM_s_at	HBS1-like (S. cerevisiae)	89941	HBS1L	0.539	+	3.48E-02	1.01E-02

202299_PM_s_at	hepatitis B virus x interacting protein	5464	HBXIP	0.530	+	3.39E-03	3.81E-03
203745_PM_at	holocytochrome c synthase (cytochrome c heme-lyase)	10085	HCCS	0.363	+	3.87E-03	2.96E-02
202474_PM_s_at	host cell factor C1 (VP16-accessory protein)	54981	HCFC1	0.497	+	1.01E-02	3.54E-02
241710_PM_at	hCG1645220	---	hCG_1645220	0.591	+	6.25E-03	3.12E-02
200833_PM_s_at	RAP1B, member of RAS oncogene family pseudogene /// RAP1B, member of RAS oncogene family	2959	hCG_1757335 /// RAP1B	0.379	+	1.73E-02	9.78E-03
225577_PM_at	HLA complex group 18	157378	HCG18	0.287	+	1.27E-02	3.55E-02
208018_PM_s_at	hemopoietic cell kinase	3297	HCK	0.269	+	3.47E-03	2.29E-02
201833_PM_at	histone deacetylase 2	341	HDAC2	0.289	+	3.78E-02	3.56E-02
205659_PM_at	histone deacetylase 9	9331	HDAC9	0.574	+	2.90E-02	8.14E-03
203259_PM_s_at	HD domain containing 2	126969	HDDC2	0.608	+	5.89E-03	7.40E-03
227008_PM_at	HD domain containing 3	10418	HDDC3	0.289	+	5.87E-04	8.94E-04
223155_PM_at	haloacid dehalogenase-like hydrolase domain containing 2	79746	HDHD2	0.434	+	4.58E-02	1.30E-02
1553646_PM_at	highly divergent homeobox	6487	HDX	0.510	+	1.41E-02	1.02E-02
218991_PM_at	HEAT repeat containing 6	221472	HEATR6	0.358	+	4.33E-02	2.23E-02
218603_PM_at	headcase homolog (Drosophila)	85445	HECA	0.618	+	2.83E-02	2.91E-03
227568_PM_at	HECT domain containing 2	5911	HECTD2	0.775	+	9.23E-03	4.39E-03
228736_PM_at	helicase, POLQ-like	5478	HELQ	0.592	+	2.22E-03	7.83E-03
225910_PM_at	helicase with zinc finger	728052	HELZ	0.599	+	6.36E-03	1.20E-02
218620_PM_s_at	HemK methyltransferase family member 1	26297	HEMK1	0.305	+	2.65E-02	3.56E-02
218306_PM_s_at	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	91419	HERC1	0.543	+	4.57E-02	4.37E-02
222751_PM_at	HERPUD family member 2	339105	HERPUD2	0.353	+	3.05E-02	3.18E-02
219743_PM_at	hairy/enhancer-of-split related with YRPW motif 2	9452	HEY2	1.063	+	3.55E-02	4.04E-02
210755_PM_at	hepatocyte growth factor (hepapoietin A; scatter factor)	1903	HGF	0.337	+	1.90E-03	1.04E-03
219687_PM_at	hedgehog acyltransferase	10473	HHAT	0.430	+	1.65E-07	1.24E-04
223073_PM_at	hippocampus abundant transcript-like 1	79023	HIATL1	0.552	+	2.18E-02	2.75E-02
224812_PM_at	3-hydroxyisobutyrate dehydrogenase	145567	HIBADH	0.388	+	3.64E-02	4.29E-02
203711_PM_s_at	3-hydroxyisobutyryl-Coenzyme A hydrolase	64399	HIBCH	0.449	+	4.77E-02	3.72E-02
212964_PM_at	hypermethylated in cancer 2	9450	HIC2	0.809	+	2.61E-02	2.03E-02
206495_PM_s_at	histone H4 transcription factor	83737	HINFP	0.273	+	3.94E-03	1.98E-02

226364_PM_at	Huntingtin interacting protein 1	9837	HIP1	0.310	+	1.69E-02	1.04E-02
212293_PM_at	homeodomain interacting protein kinase 1	27258	HIPK1	0.469	+	2.49E-03	6.20E-03
217427_PM_s_at	HIR histone cell cycle regulation defective homolog A (S. cerevisiae)	9117	HIRA	0.521	+	1.33E-02	2.96E-02
204578_PM_at	histidine acid phosphatase domain containing 2A	9474	HISPPD2A	0.401	+	7.76E-04	5.42E-03
218280_PM_x_at	histone cluster 2, H2aa3 /// histone cluster 2, H2aa4	10291	HIST2H2AA3 /// HIST2H2AA4	0.282	+	7.22E-03	2.64E-02
204512_PM_at	human immunodeficiency virus type I enhancer binding protein 1	4694	HIVEP1	0.795	+	1.51E-02	2.16E-02
204754_PM_at	hepatic leukemia factor	10928	HLF	0.325	+	9.08E-03	4.42E-03
218152_PM_at	high-mobility group 20A	57187	HMG20A	0.300	+	5.00E-03	2.21E-02
224731_PM_at	high-mobility group box 1	51776	HMGB1	0.307	+	1.67E-02	1.89E-02
203744_PM_at	high-mobility group box 3	22950	HMGB3	0.618	+	1.48E-02	2.51E-02
202540_PM_s_at	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	5101	HMGCR	0.880	+	1.22E-02	4.45E-02
221750_PM_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble)	1810	HMGCS1	0.369	+	1.29E-02	2.58E-02
200943_PM_at	high-mobility group nucleosome binding domain 1	334	HMGN1	0.405	+	1.37E-02	1.16E-02
209377_PM_s_at	high mobility group nucleosomal binding domain 3	51495	HMGN3	0.447	+	3.71E-03	2.62E-03
202579_PM_x_at	high mobility group nucleosomal binding domain 4	55671	HMGN4	0.542	+	1.21E-02	1.79E-02
204112_PM_s_at	histamine N-methyltransferase	1315	HNMT	0.548	+	1.04E-02	3.82E-02
244131_PM_at	heterogeneous nuclear ribonucleoprotein A2/B1	---	HNRNPA2B1	0.350	+	1.37E-02	1.87E-02
211929_PM_at	heterogeneous nuclear ribonucleoprotein A3	2566	HNRNPA3	0.333	+	4.21E-02	1.84E-02
221480_PM_at	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	2902	HNRNPD	0.344	+	1.54E-02	2.74E-02
208990_PM_s_at	heterogeneous nuclear ribonucleoprotein H3 (2H9)	51074	HNRNPH3	0.441	+	5.15E-03	4.27E-03
232004_PM_at	heterogeneous nuclear ribonucleoprotein R	---	HNRNPR	0.657	+	3.51E-02	1.70E-02
235603_PM_at	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	8028	HNRNPU	0.310	+	6.45E-03	1.06E-02
225385_PM_s_at	heterogeneous nuclear ribonucleoprotein L-like	27143	HNRPLL	0.538	+	1.97E-02	1.49E-02
219976_PM_at	hook homolog 1 (Drosophila)	10428	HOOK1	0.674	+	7.82E-03	3.85E-02
225792_PM_at	hook homolog 1 (Drosophila)	3340	HOOK1	0.377	+	3.22E-02	9.36E-03

226395_PM_at	hook homolog 3 (Drosophila)	9394	HOOK3	0.482	+	6.53E-03	6.76E-03
211597_PM_s_at	HOP homeobox	9786	HOPX	0.391	+	2.24E-04	3.64E-03
202854_PM_at	hypoxanthine phosphoribosyltransferase 1	51742	HPRT1	0.272	+	3.88E-03	6.24E-03
227139_PM_s_at	Hermansky-Pudlak syndrome 3	140885	HPS3	0.490	+	2.16E-02	3.20E-02
203790_PM_s_at	heat-responsive protein 12	5411	HRSP12	0.349	+	3.18E-02	4.28E-02
203284_PM_s_at	302eparin sulfate 2-O-sulfotransferase 1	7068	HS2ST1	0.725	+	1.38E-02	1.52E-02
230030_PM_at	302eparin sulfate 6-O-sulfotransferase 2	57537	HS6ST2	0.555	+	4.98E-02	2.94E-02
200941_PM_at	heat shock factor binding protein 1	7086	HSBP1	0.331	+	2.63E-02	2.29E-02
223647_PM_x_at	HscB iron-sulfur cluster co-chaperone homolog (E. coli)	51503	HSCB	0.319	+	2.05E-02	3.50E-02
205404_PM_at	hydroxysteroid (11-beta) dehydrogenase 1	25950	HSD11B1	0.300	+	4.61E-02	1.91E-02
219113_PM_x_at	hydroxysteroid (17-beta) dehydrogenase 14	374900	HSD17B14	0.386	+	7.35E-04	4.53E-03
228713_PM_s_at	hydroxysteroid (17-beta) dehydrogenase 14	5205	HSD17B14	0.269	+	2.29E-02	2.62E-02
201413_PM_at	hydroxysteroid (17-beta) dehydrogenase 4	56681	HSD17B4	0.642	+	4.36E-03	1.59E-02
209513_PM_s_at	hydroxysteroid dehydrogenase like 2	8907	HSDL2	0.314	+	6.62E-03	1.77E-03
209657_PM_s_at	heat shock transcription factor 2	57129	HSF2	0.652	+	1.20E-02	1.78E-02
214434_PM_at	heat shock 70kDa protein 12A	79811	HSPA12A	0.618	+	4.58E-02	2.36E-02
229172_PM_at	heat shock 70kD protein 12B	26148	HSPA12B	0.581	+	3.45E-02	3.98E-02
202557_PM_at	heat shock protein 70kDa family, member 13	56891	HSPA13	0.576	+	6.44E-03	1.72E-02
219212_PM_at	heat shock 70kDa protein 14	22919	HSPA14	0.635	+	1.43E-02	1.11E-02
210189_PM_at	heat shock 70kDa protein 1-like	94241	HSPA1L	0.352	+	1.25E-02	1.57E-02
203960_PM_s_at	heat shock protein family B (small), member 11	3895	HSPB11	1.357	+	2.52E-03	1.25E-02
215691_PM_x_at	heat shock protein family B (small), member 11	81873	HSPB11	0.873	+	5.15E-03	1.30E-02
226188_PM_at	galectin-related protein	10513	HSPC159	0.657	+	1.45E-02	5.48E-03
205133_PM_s_at	heat shock 10kDa protein 1 (chaperonin 10)	1645	HSPE1	0.353	+	1.80E-02	7.68E-03
209448_PM_at	HIV-1 Tat interactive protein 2, 30kDa	10827	HTATIP2	0.432	+	7.67E-03	2.11E-02
202602_PM_s_at	HIV-1 Tat specific factor 1	29968	HTATSF1	0.327	+	8.90E-03	5.99E-04
207307_PM_at	5-hydroxytryptamine (serotonin) receptor 2C	23028	HTR2C	1.139	+	5.86E-03	2.64E-02
236281_PM_x_at	5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-coupled)	---	HTR7	0.410	+	1.21E-02	4.27E-02
232984_PM_at	hydrocephalus inducing homolog (mouse)	140732	HYDIN	0.473	+	1.51E-02	4.05E-02
227687_PM_at	hydrolethalus syndrome 1	54801	HYLS1	0.663	+	7.41E-03	2.56E-03
230454_PM_at	islet cell autoantigen 1,69kDa-like	116442	ICA1L	0.346	+	1.49E-02	4.51E-02

201566_PM_x_at	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	9568	ID2	0.478	+	1.85E-02	4.63E-03
209292_PM_at	Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	54908	ID4	0.361	+	1.90E-02	5.58E-03
203327_PM_at	insulin-degrading enzyme	80863	IDE	0.783	+	1.94E-02	3.60E-02
208881_PM_x_at	isopentenyl-diphosphate delta isomerase 1	64431	IDI1	0.364	+	5.83E-03	1.43E-02
204615_PM_x_at	isopentenyl-diphosphate delta isomerase 1	2990	IDI1	0.549	+	1.34E-02	1.91E-02
223071_PM_at	immediate early response 3 interacting protein 1	60561	IER3IP1	0.400	+	3.28E-03	5.74E-03
203153_PM_at	interferon-induced protein with tetratricopeptide repeats 1	84897	IFIT1	0.712	+	9.59E-04	2.84E-04
203595_PM_s_at	interferon-induced protein with tetratricopeptide repeats 5	9522	IFIT5	0.272	+	1.52E-02	1.56E-02
210312_PM_s_at	intraflagellar transport 20 homolog (Chlamydomonas)	84678	IFT20	0.354	+	2.67E-02	2.90E-03
218709_PM_s_at	intraflagellar transport 52 homolog (Chlamydomonas)	80167	IFT52	0.601	+	1.71E-02	1.24E-02
218100_PM_s_at	intraflagellar transport 57 homolog (Chlamydomonas)	219541	IFT57	0.541	+	5.05E-03	2.19E-04
202105_PM_at	immunoglobulin (CD79A) binding protein 1	11332	IGBP1	0.426	+	5.72E-03	2.99E-02
227870_PM_at	immunoglobulin superfamily, DCC subclass, member 4	54467	IGDCC4	1.149	+	5.61E-03	9.81E-03
209540_PM_at	insulin-like growth factor 1 (somatomedin C)	65991	IGF1	0.550	+	6.15E-03	1.14E-02
230670_PM_at	immunoglobulin superfamily, member 10	81553	IGSF10	0.495	+	2.57E-02	4.66E-02
200066_PM_at	IK cytokine, down-regulator of HLA II	4291	IK	0.312	+	1.20E-02	1.15E-02
209341_PM_s_at	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	25932	IKBKB	0.612	+	3.70E-02	1.24E-02
231929_PM_at	IKAROS family zinc finger 2 (Helios)	4089	IKZF2	1.073	+	1.20E-02	1.50E-02
226680_PM_at	IKAROS family zinc finger 5 (Pegasus)	151162 /// 4249	IKZF5	0.450	+	1.01E-02	1.89E-02
201887_PM_at	interleukin 13 receptor, alpha 1	961	IL13RA1	0.352	+	3.71E-02	1.12E-02
227401_PM_at	interleukin 17D	23493	IL17D	0.335	+	4.31E-02	2.67E-02
224156_PM_x_at	interleukin 17 receptor B	114900	IL17RB	1.402	+	4.89E-03	7.03E-03
219255_PM_x_at	interleukin 17 receptor B	6224	IL17RB	0.866	+	1.58E-02	3.49E-02
224361_PM_s_at	interleukin 17 receptor B	84168	IL17RB	0.341	+	4.86E-02	3.56E-02
222828_PM_at	interleukin 20 receptor, alpha	8711	IL20RA	0.277	+	1.32E-03	5.19E-03
207952_PM_at	interleukin 5 (colony-stimulating factor, eosinophil)	6907	IL5	0.372	+	3.42E-02	1.07E-02
217804_PM_s_at	interleukin enhancer binding factor 3, 90kDa	441951	ILF3	0.352	+	5.47E-03	6.39E-03
229025_PM_s_at	IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae)	117	IMMP1L	0.441	+	3.65E-03	1.25E-03

230556_PM_at	IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae)	55101	IMMP1L	0.656	+	1.28E-02	3.29E-02
224743_PM_at	inositol monophosphatase domain containing 1	124512	IMPAD1	0.410	+	9.07E-03	8.40E-03
201892_PM_s_at	IMP (inosine monophosphate) dehydrogenase 2	23543	IMPDH2	0.407	+	1.40E-03	7.80E-03
208415_PM_x_at	inhibitor of growth family, member 1	222658	ING1	0.417	+	1.69E-02	1.60E-02
231863_PM_at	inhibitor of growth family, member 3	---	ING3	0.977	+	5.62E-03	3.10E-02
242293_PM_at	inhibitor of growth family, member 3	---	ING3	0.370	+	4.44E-02	4.71E-02
228287_PM_at	inhibitor of growth family, member 5	144438	ING5	0.472	+	1.10E-02	1.93E-02
205376_PM_at	inositol polyphosphate-4-phosphatase, type II, 105kDa	2173	INPP4B	0.368	+	9.76E-03	3.39E-02
218616_PM_at	integrator complex subunit 12	9468	INTS12	0.598	+	1.33E-02	3.21E-03
222239_PM_s_at	integrator complex subunit 6	2799	INTS6	0.554	+	2.53E-02	7.77E-03
218905_PM_at	integrator complex subunit 8	27147	INTS8	0.751	+	1.66E-02	3.01E-03
214735_PM_at	interaction protein for cytohesin exchange factors 1	51118	IPCEF1	0.764	+	1.24E-02	3.57E-03
211952_PM_at	importin 5	754	IPO5	0.266	+	2.17E-02	2.98E-02
200994_PM_at	importin 7	5693	IPO7	0.346	+	3.48E-02	4.93E-02
211707_PM_s_at	IQ motif containing B1	127933	IQCB1	0.373	+	4.54E-03	2.68E-03
204202_PM_at	IQ motif containing E	2803	IQCE	0.437	+	2.66E-02	2.53E-02
213392_PM_at	IQ motif containing K	6683	IQCK	0.515	+	8.85E-03	3.64E-02
201587_PM_s_at	interleukin-1 receptor-associated kinase 1	515	IRAK1	0.678	+	4.28E-03	2.03E-02
224571_PM_at	interferon regulatory factor 2 binding protein 2	93380	IRF2BP2	0.496	+	2.88E-03	7.25E-03
228462_PM_at	304eparin304 homeobox 2	27161	IRX2	0.266	+	1.59E-02	2.83E-02
209274_PM_s_at	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	8555	ISCA1	0.392	+	1.75E-03	1.66E-03
209075_PM_s_at	iron-sulfur cluster scaffold homolog (E. coli)	79683	ISCU	0.406	+	7.02E-05	2.93E-04
205483_PM_s_at	ISG15 ubiquitin-like modifier	11104	ISG15	0.370	+	1.67E-02	3.13E-02
229324_PM_x_at	inositol-3-phosphate synthase 1	100132815	ISYNA1	0.267	+	9.47E-03	1.80E-02
226295_PM_at	integrin alpha FG-GAP repeat containing 2	6461	ITFG2	0.364	+	3.42E-02	3.01E-02
206493_PM_at	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	1407	ITGA2B	0.397	+	5.83E-03	1.34E-02
202351_PM_at	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	51295	ITGAV	0.346	+	1.56E-02	1.22E-02
211945_PM_s_at	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	1603	ITGB1	0.481	+	1.96E-02	7.83E-03

203336_PM_s_at	integrin beta 1 binding protein 1	10777	ITGB1BP1	0.429	+	3.51E-02	4.38E-02
226189_PM_at	integrin, beta 8	5440	ITGB8	0.513	+	3.24E-02	9.65E-03
202746_PM_at	integral membrane protein 2A	29127	ITM2A	0.459	+	2.04E-03	5.16E-03
202661_PM_at	inositol 1,4,5-triphosphate receptor, type 2	51176	ITPR2	0.347	+	1.32E-02	2.75E-02
227792_PM_at	inositol 1,4,5-triphosphate receptor interacting protein-like 2	378938	ITPRIPL2	0.368	+	2.43E-04	5.45E-03
225311_PM_at	isovaleryl Coenzyme A dehydrogenase	283417	IVD	0.427	+	2.90E-03	1.42E-02
201363_PM_s_at	influenza virus NS1A binding protein	6303	IVNS1ABP	0.672	+	1.03E-02	1.75E-03
201362_PM_at	influenza virus NS1A binding protein	30000	IVNS1ABP	0.754	+	4.01E-02	8.89E-03
216268_PM_s_at	jagged 1 (Alagille syndrome)	79047	JAG1	0.548	+	1.82E-02	2.23E-02
203297_PM_s_at	jumonji, AT rich interactive domain 2	641649	JARID2	0.871	+	1.69E-03	4.61E-03
203298_PM_s_at	jumonji, AT rich interactive domain 2	54542	JARID2	0.460	+	3.15E-02	4.89E-02
221778_PM_at	jumonji C domain containing histone demethylase 1 homolog D (S. cerevisiae)	9554	JHDM1D	0.975	+	2.08E-03	1.20E-03
221763_PM_at	jumonji domain containing 1C	23208	JMJD1C	0.656	+	3.99E-02	4.28E-02
226352_PM_at	junction mediating and regulatory protein, p53 cofactor	10499	JMY	0.503	+	2.71E-02	2.11E-02
229139_PM_at	junctophilin 1	57456	JPH1	0.780	+	2.90E-03	1.62E-02
1568605_PM_at	jerky homolog (mouse)	8481	JRK	0.314	+	2.60E-02	4.78E-02
205206_PM_at	Kallmann syndrome 1 sequence	4763	KAL1	0.499	+	2.48E-02	1.78E-02
221068_PM_at	KN motif and ankyrin repeat domains 2	89795	KANK2	0.439	+	9.28E-03	3.49E-02
200840_PM_at	lysyl-tRNA synthetase	81550	KARS	0.402	+	7.88E-03	1.12E-02
203845_PM_at	K(lysine) acetyltransferase 2B	4924	KAT2B	0.754	+	2.36E-02	7.26E-03
205526_PM_s_at	katanin p60 (ATPase-containing) subunit A 1	57147	KATNA1	0.427	+	8.35E-03	1.43E-02
203162_PM_s_at	katanin p80 (WD repeat containing) subunit B 1	317649	KATNB1	0.863	+	7.36E-03	4.01E-03
226479_PM_at	kelch repeat and BTB (POZ) domain containing 6	10602	KBTBD6	0.598	+	1.04E-02	1.45E-02
222471_PM_s_at	potassium channel modulatory factor 1	57037	KCMF1	0.875	+	1.10E-02	1.17E-02
230849_PM_at	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)	83856	KCNA1	0.462	+	2.89E-02	4.57E-02
206762_PM_at	potassium voltage-gated channel, shaker-related subfamily, member 5	6327	KCNA5	0.380	+	1.60E-04	3.51E-03
206765_PM_at	potassium inwardly-rectifying channel, subfamily J, member 2	6328	KCNJ2	0.573	+	4.08E-02	1.65E-02
220629_PM_at	KCNQ1 downstream neighbor	7988	KCNQ1DN	0.431	+	4.19E-04	2.22E-03
244455_PM_at	potassium channel, subfamily T, member 2	---	KCNT2	0.701	+	2.33E-03	1.95E-03

226245_PM_at	potassium channel tetramerisation domain containing 1	8065	KCTD1	0.426	+	4.59E-02	3.08E-02
226518_PM_at	potassium channel tetramerisation domain containing 10	655	KCTD10	0.398	+	9.60E-03	3.09E-02
212192_PM_at	potassium channel tetramerisation domain containing 12	1182	KCTD12	0.574	+	2.67E-02	5.17E-03
222668_PM_at	potassium channel tetramerisation domain containing 15	1795	KCTD15	0.511	+	1.10E-02	4.30E-02
228299_PM_at	potassium channel tetramerisation domain containing 20	57186	KCTD20	0.937	+	4.08E-03	5.62E-03
240512_PM_x_at	potassium channel tetramerisation domain containing 4	80349	KCTD4	0.691	+	1.61E-02	2.19E-02
239787_PM_at	potassium channel tetramerisation domain containing 4	---	KCTD4	0.441	+	2.32E-02	1.33E-02
225128_PM_at	KDEL (Lys-Asp-Glu-Leu) containing 2	115548	KDELC2	0.395	+	1.98E-03	9.47E-03
212348_PM_s_at	lysine (K)-specific demethylase 1	22877	KDM1	0.343	+	3.97E-02	9.19E-03
226215_PM_s_at	lysine (K)-specific demethylase 2B	4938	KDM2B	0.613	+	2.57E-03	7.54E-03
212689_PM_s_at	lysine (K)-specific demethylase 3A	7016	KDM3A	0.605	+	4.78E-02	2.30E-02
210878_PM_s_at	lysine (K)-specific demethylase 3B	203523	KDM3B	0.489	+	1.94E-02	3.74E-03
211202_PM_s_at	lysine (K)-specific demethylase 5B	7227	KDM5B	0.415	+	1.62E-02	1.66E-02
203991_PM_s_at	lysine (K)-specific demethylase 6A	7533	KDM6A	0.963	+	3.11E-02	2.91E-02
229850_PM_at	3-ketodihydrosphingosine reductase	5592	KDSR	0.706	+	4.32E-02	2.49E-03
204371_PM_s_at	KH-type splicing regulatory protein	6993	KHSRP	0.283	+	2.54E-02	1.69E-02
212395_PM_s_at	KIAA0090	11073	KIAA0090	0.622	+	2.90E-03	1.14E-02
212056_PM_at	KIAA0182	4074	KIAA0182	0.493	+	1.67E-02	2.96E-02
206017_PM_at	KIAA0319	404734 /// 54882	KIAA0319	0.541	+	3.30E-03	2.56E-02
212355_PM_at	KIAA0323	3156	KIAA0323	0.784	+	2.95E-02	3.18E-02
214356_PM_s_at	KIAA0368	51109	KIAA0368	0.913	+	2.57E-02	1.84E-02
204546_PM_at	KIAA0513	10237	KIAA0513	0.501	+	8.00E-04	2.85E-03
212946_PM_at	KIAA0564	2949	KIAA0564	0.449	+	2.75E-02	2.76E-02
37232_PM_at	KIAA0586	---	KIAA0586	0.265	+	2.77E-02	5.10E-03
212314_PM_at	KIAA0746 protein	865	KIAA0746	0.431	+	2.43E-02	2.76E-02
212633_PM_at	KIAA0776	10946	KIAA0776	0.643	+	1.47E-02	1.47E-02
204568_PM_at	KIAA0831	10844	KIAA0831	0.422	+	7.20E-03	2.51E-03
227465_PM_at	KIAA0892	55539	KIAA0892	0.387	+	2.93E-02	1.62E-02
207305_PM_s_at	KIAA1012	55187	KIAA1012	0.371	+	4.68E-02	3.56E-02
226816_PM_s_at	KIAA1143	55023	KIAA1143	1.204	+	2.03E-04	4.54E-05
227231_PM_at	KIAA1211	10166	KIAA1211	0.296	+	1.13E-02	4.62E-02
230765_PM_at	KIAA1239	730094	KIAA1239	0.802	+	1.17E-02	2.47E-02

231887_PM_s_at	KIAA1274	---	KIAA1274	0.287	+	1.66E-02	2.73E-02
232358_PM_at	KIAA1328	130752	KIAA1328	0.273	+	3.58E-02	1.53E-02
226221_PM_at	KIAA1432	6147	KIAA1432	0.633	+	2.88E-02	3.74E-02
225506_PM_at	KIAA1468	123263	KIAA1468	0.321	+	1.57E-03	1.12E-02
52837_PM_at	KIAA1644	---	KIAA1644	0.268	+	3.00E-04	5.68E-03
229891_PM_x_at	KIAA1704	29097	KIAA1704	0.908	+	3.77E-03	8.55E-03
225623_PM_at	KIAA1737	10350	KIAA1737	0.269	+	1.07E-02	3.60E-02
218503_PM_at	KIAA1797	5255	KIAA1797	0.463	+	2.42E-02	4.07E-02
238828_PM_at	KIAA1919	---	KIAA1919	0.293	+	1.56E-03	8.66E-04
227433_PM_at	KIAA2018	11092	KIAA2018	0.707	+	1.63E-02	3.14E-02
225878_PM_at	kinesin family member 1B	57709	KIF1B	0.864	+	1.04E-02	1.43E-02
228680_PM_at	kinesin family member 3A	84693	KIF3A	0.420	+	3.82E-03	3.32E-03
231319_PM_x_at	kinesin family member 9	57162	KIF9	0.790	+	6.12E-03	4.27E-03
228429_PM_x_at	kinesin family member 9	171024	KIF9	0.733	+	7.23E-03	2.01E-02
209661_PM_at	kinesin family member C3	84250	KIFC3	0.328	+	1.46E-02	2.53E-02
216428_PM_x_at	killer cell immunoglobulin-like receptor, three domains, X1	51555	KIR3DX1	0.281	+	1.58E-02	1.96E-02
227261_PM_at	Kruppel-like factor 12	59338	KLF12	0.928	+	2.92E-03	8.10E-03
225133_PM_at	Kruppel-like factor 3 (basic)	5828	KLF3	0.539	+	1.51E-02	1.01E-02
203543_PM_s_at	Kruppel-like factor 9	10554	KLF9	0.681	+	7.72E-03	4.15E-03
1552733_PM_at	kelch domain containing 1	113451	KLHDC1	0.328	+	1.93E-02	2.83E-02
217906_PM_at	kelch domain containing 2	57181	KLHDC2	0.282	+	1.89E-02	1.76E-02
221219_PM_s_at	kelch domain containing 4	8851	KLHDC4	0.283	+	3.36E-02	4.26E-02
225961_PM_at	kelch domain containing 5	---	KLHDC5	0.589	+	1.43E-03	2.70E-03
227875_PM_at	kelch-like 13 (Drosophila)	---	KLHL13	0.567	+	3.52E-02	1.00E-03
226370_PM_at	kelch-like 15 (Drosophila)	1399	KLHL15	0.783	+	1.94E-02	2.76E-03
212882_PM_at	kelch-like 18 (Drosophila)	5157	KLHL18	0.565	+	6.98E-03	9.29E-03
204176_PM_at	kelch-like 20 (Drosophila)	10951	KLHL20	0.743	+	3.48E-03	1.57E-03
204177_PM_s_at	kelch-like 20 (Drosophila)	2926	KLHL20	0.517	+	1.44E-02	8.43E-03
203068_PM_at	kelch-like 21 (Drosophila)	4257	KLHL21	0.296	+	3.08E-02	1.94E-02
213610_PM_s_at	kelch-like 23 (Drosophila)	6383	KLHL23	0.400	+	2.30E-02	2.44E-02
219354_PM_at	kelch-like 26 (Drosophila)	2195	KLHL26	0.333	+	1.15E-02	3.25E-02
228328_PM_at	kelch-like 28 (Drosophila)	51434	KLHL28	0.651	+	5.44E-03	9.06E-04

1553765_PM_a_at	kelch-like 32 (Drosophila)	55218	KLHL32	0.297	+	1.75E-02	7.55E-03
226001_PM_at	kelch-like 5 (Drosophila)	7453	KLHL5	0.437	+	1.01E-02	3.49E-03
242648_PM_at	kelch-like 8 (Drosophila)	---	KLHL8	0.541	+	5.63E-03	1.61E-02
213233_PM_s_at	kelch-like 9 (Drosophila)	8073	KLHL9	0.289	+	4.36E-03	6.52E-03
234495_PM_at	kallikrein-related peptidase 15	---	KLK15	0.354	+	1.16E-02	1.13E-02
1553955_PM_at	KLRAQ motif containing 1	5136	KLRAQ1	0.629	+	2.26E-02	1.35E-02
202057_PM_at	karyopherin alpha 1 (importin alpha 5)	26986	KPNA1	0.726	+	9.60E-03	6.25E-03
202056_PM_at	karyopherin alpha 1 (importin alpha 5)	6257	KPNA1	0.541	+	1.36E-02	1.61E-02
221502_PM_at	karyopherin alpha 3 (importin alpha 4)	7074	KPNA3	0.393	+	4.29E-02	3.57E-02
225268_PM_at	karyopherin alpha 4 (importin alpha 3)	283209	KPNA4	0.531	+	8.04E-03	1.62E-03
229317_PM_at	karyopherin alpha 5 (importin alpha 6)	114134	KPNA5	0.535	+	1.90E-02	3.93E-02
204009_PM_s_at	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	5886	KRAS	0.424	+	3.31E-03	7.51E-03
227250_PM_at	kringle containing transmembrane protein 1	55656	KREMEN1	0.298	+	1.08E-02	1.98E-02
216713_PM_at	KRIT1, ankyrin repeat containing	84274	KRIT1	0.641	+	7.61E-03	7.73E-03
213287_PM_s_at	keratin 10	9039	KRT10	0.559	+	2.78E-04	1.60E-03
210633_PM_x_at	keratin 10	4644	KRT10	0.410	+	4.75E-03	9.43E-03
224885_PM_s_at	keratinocyte associated protein 2	84142	KRTCAP2	0.557	+	3.00E-04	5.81E-04
200915_PM_x_at	kinectin 1 (kinesin receptor)	8763	KTN1	0.455	+	4.88E-02	3.59E-02
217388_PM_s_at	kynureninase (L-kynurenine hydrolase)	79102	KYNU	1.136	+	6.18E-03	1.49E-02
229393_PM_at	l(3)mbt-like 3 (Drosophila)	9926	L3MBTL3	0.469	+	1.66E-02	4.16E-02
226354_PM_at	lactamase, beta	8976	LACTB	0.551	+	2.39E-02	1.31E-02
222714_PM_s_at	lactamase, beta 2	2066	LACTB2	0.361	+	2.48E-02	1.91E-02
203726_PM_s_at	laminin, alpha 3	7327	LAMA3	1.068	+	5.91E-04	1.33E-02
202202_PM_s_at	laminin, alpha 4	84268	LAMA4	0.367	+	3.29E-02	4.08E-02
226671_PM_at	lysosomal-associated membrane protein 2	---	LAMP2	0.428	+	4.91E-02	3.35E-02
202020_PM_s_at	LanC lantibiotic synthetase component C-like 1 (bacterial)	9024	LANCL1	0.330	+	2.02E-02	1.60E-02
217933_PM_s_at	leucine aminopeptidase 3	2820	LAP3	0.530	+	2.76E-02	1.93E-02
212714_PM_at	La ribonucleoprotein domain family, member 4	8460	LARP4	0.337	+	5.84E-03	4.87E-02
214155_PM_s_at	La ribonucleoprotein domain family, member 4	8801	LARP4	0.614	+	1.62E-02	3.22E-02
212785_PM_s_at	La ribonucleoprotein domain family, member 7	3096	LARP7	0.425	+	3.82E-02	2.77E-02
200618_PM_at	LIM and SH3 protein 1	24140	LASP1	0.438	+	7.10E-03	2.37E-02

224951_PM_at	LAG1 homolog, ceramide synthase 5	222166	LASS5	0.318	+	2.29E-03	3.41E-03
212446_PM_s_at	LAG1 homolog, ceramide synthase 6	2235	LASS6	0.489	+	2.87E-02	2.24E-02
209881_PM_s_at	linker for activation of T cells /// spinster homolog 1 (Drosophila)	57606	LAT /// SPNS1	0.282	+	1.84E-03	1.73E-03
227013_PM_at	LATS, large tumor suppressor, homolog 2 (Drosophila)	6421	LATS2	1.074	+	1.63E-02	4.68E-02
213261_PM_at	lupus brain antigen 1	7905	LBA1	0.270	+	1.45E-02	3.15E-02
201795_PM_at	lamin B receptor	6137	LBR	0.304	+	4.04E-02	2.75E-02
226996_PM_at	lysocardiolipin acyltransferase 1	51099	LCLAT1	0.813	+	5.80E-03	1.37E-02
204012_PM_s_at	leucine carboxyl methyltransferase 2	5886	LCMT2	0.334	+	3.10E-03	6.28E-03
228454_PM_at	ligand dependent nuclear receptor corepressor	284702	LCOR	0.619	+	3.57E-02	3.98E-02
232293_PM_at	ligand dependent nuclear receptor corepressor-like	51693	LCORL	0.428	+	6.46E-03	1.13E-02
240592_PM_at	ligand dependent nuclear receptor corepressor-like	153346	LCORL	0.579	+	1.93E-02	3.22E-02
200650_PM_s_at	lactate dehydrogenase A	5789	LDHA	0.270	+	1.36E-02	8.32E-03
213564_PM_x_at	lactate dehydrogenase B	10955	LDHB	0.308	+	2.80E-02	2.91E-02
201030_PM_x_at	lactate dehydrogenase B	22992	LDHB	0.427	+	2.83E-02	1.83E-02
223228_PM_at	leucine zipper, down-regulated in cancer 1-like	55317	LDOC1L	0.511	+	1.61E-02	2.89E-02
221558_PM_s_at	lymphoid enhancer-binding factor 1	5454	LEF1	0.465	+	2.20E-02	4.56E-02
202594_PM_at	leptin receptor overlapping transcript-like 1	55179	LEPROTL1	0.407	+	1.21E-02	2.38E-02
220158_PM_at	lectin, galactoside-binding, soluble, 14	24149	LGALS14	0.492	+	1.34E-03	7.15E-03
206349_PM_at	leucine-rich, glioma inactivated 1	2063	LGI1	0.323	+	8.05E-03	3.60E-02
219699_PM_at	leucine-rich repeat LGI family, member 2	23484	LGI2	0.325	+	1.74E-03	1.43E-03
218253_PM_s_at	ligatin	201973	LGTN	0.579	+	1.96E-03	4.66E-03
225575_PM_at	leukemia inhibitory factor receptor alpha	8925	LIFR	0.788	+	2.48E-02	6.75E-03
212327_PM_at	LIM and calponin homology domains 1	7994	LIMCH1	0.303	+	2.88E-02	8.27E-03
222762_PM_x_at	LIM domains containing 1	5898	LIMD1	0.424	+	1.12E-02	4.02E-03
212687_PM_at	LIM and senescent cell antigen-like domains 1	10810	LIMS1	0.529	+	5.93E-03	6.00E-03
213526_PM_s_at	lin-37 homolog (C. elegans)	10765	LIN37	0.797	+	5.56E-03	2.68E-03
228583_PM_at	lin-52 homolog (C. elegans)	1106	LIN52	0.709	+	2.01E-02	2.05E-02
241957_PM_x_at	lin-7 homolog B (C. elegans)	---	LIN7B	0.526	+	3.17E-04	1.94E-03
205571_PM_at	lipoyltransferase 1	8976	LIPT1	0.878	+	4.57E-02	1.65E-02
224629_PM_at	lectin, mannose-binding, 1	91947	LMAN1	0.620	+	1.92E-02	2.69E-02
212089_PM_at	lamin A/C	9276	LMNA	0.385	+	2.13E-02	4.85E-03

204249_PM_s_at	LIM domain only 2 (rhombotin-like 1)	5756	LMO2	0.445	+	2.13E-02	3.42E-02
1565936_PM_a_at	LIM domain only 3 (rhombotin-like 2)	9776	LMO3	0.290	+	8.52E-03	2.58E-02
231062_PM_at	Hypothetical protein LOC100129122	729082	LOC100129122	0.327	+	3.10E-04	8.44E-04
221979_PM_at	similar to hCG1811779	23673	LOC100129250	0.655	+	4.66E-03	1.06E-02
78383_PM_at	similar to hCG1811779	23201	LOC100129250	0.340	+	1.03E-02	8.38E-03
213220_PM_at	hypothetical protein LOC100130175 /// non-protein coding RNA 81	2563	LOC100130175 /// NCRNA00081	0.525	+	1.24E-04	2.11E-04
208738_PM_x_at	similar to SMT3 suppressor of mif two 3 homolog 2 /// similar to SMT3 suppressor of mif two 3 homolog 2 pseudogene /// SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae) /// SMT3 suppressor of mif two 3 homolog 4 (S. cerevisiae)	54472	LOC100130966 /// LOC728825 /// SUMO2 /// SUMO4	0.308	+	1.07E-03	4.04E-03
227074_PM_at	hypothetical protein LOC100131564	91754	LOC100131564	0.391	+	1.74E-02	3.91E-02
226006_PM_at	similar to hCG2036585	2806	LOC100131801	0.336	+	3.80E-02	9.25E-03
227234_PM_at	Hypothetical protein LOC100132815	79768	LOC100132815	0.299	+	8.56E-03	5.68E-03
223766_PM_at	PRO1102	26269	LOC100133130	0.264	+	1.55E-02	4.40E-02
229930_PM_at	similar to hCG1811002	64065	LOC100134361	0.785	+	6.77E-04	1.22E-02
214676_PM_x_at	similar to Mucin-3A precursor (Intestinal mucin-3A) /// mucin 3B, cell surface associated	4201	LOC100134674 /// MUC3B	0.281	+	1.41E-02	1.81E-02
219595_PM_at	similar to zinc finger protein 26 (KOX 20) /// zinc finger protein 26	7979	LOC100287515 /// ZNF26	0.630	+	7.65E-03	3.22E-02
210111_PM_s_at	PNAS-119	26263	LOC100287552	0.526	+	8.54E-03	4.93E-03
200834_PM_s_at	similar to ribosomal protein S21 /// ribosomal protein S21	5980	LOC100291837 /// RPS21	0.265	+	1.26E-02	3.34E-02
230374_PM_at	hypothetical protein LOC100294358	2531	LOC100294358	0.485	+	3.52E-03	1.09E-02
225493_PM_at	hypothetical LOC144438	29942	LOC144438	0.408	+	2.43E-02	2.59E-02
1557430_PM_at	hypothetical protein LOC147670	4700	LOC147670	0.576	+	1.76E-03	4.71E-03

1553797_PM_a_at	hypothetical LOC150622	1495	LOC150622	0.300	+	1.36E-02	4.83E-03
1553796_PM_at	hypothetical LOC150622	4916	LOC150622	0.420	+	2.16E-02	3.33E-02
212098_PM_at	hypothetical LOC151162 /// mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase	1434	LOC151162 /// MGAT5	0.473	+	5.20E-03	1.98E-02
225657_PM_at	hypothetical LOC152217	1837	LOC152217	0.538	+	4.49E-03	1.93E-02
232181_PM_at	hypothetical protein LOC153346	55879	LOC153346	0.796	+	8.37E-03	2.35E-02
230692_PM_at	hypothetical protein LOC157503	56994	LOC157503	0.860	+	1.65E-03	3.94E-03
228051_PM_at	Hypothetical protein LOC202451	25923	LOC202451	0.667	+	5.14E-03	7.04E-03
213510_PM_x_at	TL132 protein	6904	LOC220594	0.444	+	2.68E-02	2.35E-02
227124_PM_at	hypothetical protein LOC221710	5782	LOC221710	0.319	+	3.47E-02	1.07E-02
231828_PM_at	hypothetical LOC253039	84100	LOC253039	0.640	+	5.28E-05	1.21E-03
228894_PM_at	hypothetical protein LOC253842	140460	LOC253842	0.364	+	1.69E-02	1.75E-02
229734_PM_at	hypothetical LOC283174	901	LOC283174	0.555	+	3.16E-02	4.28E-02
230783_PM_at	hypothetical protein LOC283713	7707	LOC283713	0.857	+	3.92E-03	1.17E-02
230353_PM_at	hypothetical protein LOC284112	---	LOC284112	0.412	+	2.88E-02	3.43E-02
214162_PM_at	hypothetical protein LOC284244	2098	LOC284244	0.471	+	4.88E-02	3.94E-02
230228_PM_at	hypothetical LOC284297	55924	LOC284297	0.278	+	3.77E-02	4.73E-04
1560934_PM_at	hypothetical protein LOC284669	287	LOC284669	0.408	+	9.22E-03	2.49E-02
242852_PM_at	hypothetical protein LOC285147	---	LOC285147	0.315	+	1.38E-02	1.41E-02
227270_PM_at	hypothetical protein LOC285550	55751	LOC285550	0.436	+	3.98E-03	2.34E-02
236321_PM_at	hypothetical protein LOC285550	---	LOC285550	0.572	+	4.28E-03	1.16E-02
226236_PM_at	hypothetical LOC388789	10019	LOC388789	0.483	+	1.82E-02	4.15E-02
225014_PM_at	hypothetical protein LOC389203	134637	LOC389203	0.480	+	2.74E-03	9.61E-04
236640_PM_at	Hypothetical gene supported by BX647608	---	LOC399959	0.435	+	7.82E-03	4.64E-04
225381_PM_at	hypothetical LOC399959	27092	LOC399959	0.765	+	1.39E-02	2.53E-03
227887_PM_at	hypothetical LOC400236	116151	LOC400236	0.294	+	1.15E-02	3.70E-03
224723_PM_x_at	hypothetical LOC401397	113174	LOC401397	0.747	+	3.36E-04	1.05E-03
226635_PM_at	Hypothetical gene supported by AK091718	4899	LOC401504	0.293	+	3.09E-02	3.42E-02
1558345_PM_a_at	hypothetical gene supported by NM_194304	522	LOC439911	0.718	+	3.46E-03	1.17E-02
238207_PM_at	similar to CG32736-PA	7024	LOC440957	0.763	+	3.02E-03	9.03E-04

229826_PM_at	similar to CG32736-PA	114825	LOC440957	0.551	+	8.64E-03	9.02E-03
229740_PM_at	hypothetical protein LOC643008	---	LOC643008	0.420	+	2.47E-02	3.62E-02
230388_PM_s_at	hypothetical protein LOC644246	---	LOC644246	0.338	+	2.33E-02	2.49E-02
213754_PM_s_at	similar to poly(A) binding protein interacting protein 1 /// poly(A) binding protein interacting protein 1	1741	LOC645139 /// PAIP1	0.421	+	4.99E-02	1.45E-02
230902_PM_at	Hypothetical LOC645323	23566	LOC645323	0.410	+	3.33E-03	2.78E-02
230272_PM_at	hypothetical LOC645323	392617	LOC645323	0.414	+	1.33E-02	9.61E-03
244268_PM_x_at	p21-activated kinase 2 pseudogene	---	LOC646214	0.467	+	1.57E-02	3.59E-02
227567_PM_at	hypothetical LOC651250	---	LOC651250	0.333	+	2.98E-03	6.18E-05
201240_PM_s_at	signal peptidase complex subunit 2 homolog pseudogene /// signal peptidase complex subunit 2 homolog (S. cerevisiae)	5727	LOC653566 /// SPCS2	0.353	+	1.31E-02	2.03E-02
238152_PM_at	hypothetical protein LOC65998	---	LOC65998	0.318	+	3.65E-02	1.26E-02
214129_PM_at	similar to phosphodiesterase 4D interacting protein isoform 2 /// phosphodiesterase 4D interacting protein	7543	LOC727927 /// PDE4DIP	0.463	+	2.91E-02	4.34E-02
1558796_PM_a_at	Similar to hCG2031213	1719	LOC728052	0.730	+	4.85E-03	2.41E-03
1558795_PM_at	Similar to hCG2031213	1400	LOC728052	0.576	+	4.87E-03	7.76E-03
218380_PM_at	hypothetical protein LOC728392 /// NLR family, pyrin domain containing 1	11011	LOC728392 /// NLRP1	0.344	+	2.66E-03	6.83E-03
242070_PM_at	hypothetical protein LOC728485	---	LOC728485	0.447	+	1.31E-02	3.17E-02
229429_PM_x_at	hypothetical LOC728855	---	LOC728855	0.442	+	6.85E-03	2.31E-02
225225_PM_at	Hypothetical protein LOC729082	441094	LOC729082	0.492	+	2.59E-04	6.40E-03
233249_PM_at	Hypothetical LOC730200	347744	LOC730200	0.292	+	1.87E-04	1.39E-03
231027_PM_at	Hypothetical LOC730631	220382	LOC730631	0.509	+	1.49E-04	2.55E-03
231354_PM_at	hypothetical LOC780529	---	LOC780529	0.289	+	6.53E-03	2.99E-02
220849_PM_at	hypothetical LOC79999	4335	LOC79999	0.275	+	3.42E-03	3.89E-03
233566_PM_at	hypothetical LOC84856	85352	LOC84856	0.329	+	1.84E-03	3.35E-03
231192_PM_at	lysophosphatidic acid receptor 3	10236	LPAR3	0.508	+	2.46E-02	1.95E-02
218589_PM_at	lysophosphatidic acid receptor 6	57536	LPAR6	0.485	+	3.78E-02	4.31E-02
227476_PM_at	lysophosphatidylglycerol acyltransferase 1	79788	LPGAT1	0.468	+	3.85E-02	1.92E-02
206953_PM_s_at	latrophilin 2	8407	LPHN2	0.501	+	4.02E-02	1.33E-02
202460_PM_s_at	lipin 2	51002	LPIN2	0.545	+	8.27E-03	5.66E-03

216250_PM_s_at	leupaxin	55269	LPXN	0.293	+	3.44E-02	2.56E-02
226795_PM_at	leucine-rich repeats and calponin homology (CH) domain containing 1	323	LRCH1	0.620	+	4.84E-02	3.35E-02
227688_PM_at	leucine-rich repeats and calponin homology (CH) domain containing 2	55014	LRCH2	0.552	+	2.55E-02	4.36E-02
228119_PM_at	leucine-rich repeats and calponin homology (CH) domain containing 3	7402	LRCH3	0.353	+	3.63E-03	1.19E-02
225060_PM_at	low density lipoprotein receptor-related protein 11	2562	LRP11	0.474	+	4.05E-02	2.10E-02
219631_PM_at	low density lipoprotein-related protein 12	3423	LRP12	0.329	+	2.80E-02	3.27E-02
212850_PM_s_at	low density lipoprotein receptor-related protein 4	5557	LRP4	0.597	+	1.42E-02	1.57E-02
225745_PM_at	low density lipoprotein receptor-related protein 6	6854	LRP6	0.849	+	1.20E-02	5.59E-03
205282_PM_at	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	4644	LRP8	0.359	+	2.31E-02	7.91E-03
211615_PM_s_at	leucine-rich PPR-motif containing	10826	LRPPRC	0.339	+	1.88E-03	7.70E-03
219573_PM_at	leucine rich repeat containing 16A	5504	LRRC16A	0.445	+	1.38E-02	1.60E-02
205381_PM_at	leucine rich repeat containing 17	973	LRRC17	0.874	+	3.46E-03	1.58E-02
229085_PM_at	leucine rich repeat containing 3B	91612	LRRC3B	0.680	+	4.38E-03	1.97E-02
208140_PM_s_at	leucine rich repeat containing 48	4926	LRRC48	0.388	+	1.18E-02	1.33E-02
219338_PM_s_at	leucine rich repeat containing 49	1075	LRRC49	0.453	+	2.64E-02	2.57E-02
232554_PM_at	leucine rich repeat containing 56	94030	LRRC56	0.415	+	1.77E-04	1.70E-03
212976_PM_at	leucine rich repeat containing 8 family, member B	5781	LRRC8B	0.660	+	4.85E-02	2.52E-02
229584_PM_at	leucine-rich repeat kinase 2	201562	LRRK2	0.803	+	2.81E-03	9.78E-03
202209_PM_at	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)	6627	LSM3	0.738	+	7.42E-03	7.90E-04
202737_PM_s_at	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	4666 /// 83955	LSM4	0.293	+	3.98E-02	4.52E-02
211747_PM_s_at	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	84146	LSM5	0.757	+	5.35E-04	2.27E-03
219119_PM_at	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae)	9147	LSM8	0.581	+	8.28E-03	5.66E-03
215633_PM_x_at	leukocyte specific transcript 1	29954	LST1	0.381	+	1.95E-02	1.18E-02
207339_PM_s_at	lymphotoxin beta (TNF superfamily, member 3)	26092	LTB	0.374	+	7.12E-03	3.67E-02
223295_PM_s_at	LUC7-like (S. cerevisiae)	83482	LUC7L	0.446	+	4.54E-02	1.30E-02

226758_PM_at	LUC7-like 2 (S. cerevisiae)	157922	LUC7L2	0.668	+	3.11E-03	6.09E-03
218729_PM_at	latexin	83657	LXN	0.763	+	4.83E-02	3.10E-02
205859_PM_at	lymphocyte antigen 86	1741	LY86	0.808	+	2.82E-02	7.86E-03
223414_PM_s_at	Ly1 antibody reactive homolog (mouse)	79647	LYAR	0.496	+	8.97E-03	3.63E-02
227764_PM_at	LY6/PLAUR domain containing 6	10724	LYPD6	0.423	+	2.26E-02	3.72E-02
212449_PM_s_at	lysophospholipase I	8546	LYPLA1	0.308	+	2.24E-02	1.59E-03
230174_PM_at	lysophospholipase-like 1	153	LYPLAL1	0.598	+	5.27E-03	8.77E-03
203897_PM_at	LYR motif containing 1	3015	LYRM1	0.438	+	2.60E-02	1.29E-02
225469_PM_at	LYR motif containing 5	139341	LYRM5	0.436	+	9.43E-03	1.15E-02
228841_PM_at	Lyrm7 homolog (mouse)	57224	LYRM7	0.640	+	5.01E-03	4.97E-03
232283_PM_at	LysM, putative peptidoglycan-binding, domain containing 1	84959	LYSMD1	0.282	+	4.59E-03	3.11E-02
226748_PM_at	LysM, putative peptidoglycan-binding, domain containing 2	8723	LYSMD2	0.286	+	8.01E-03	2.71E-02
228954_PM_at	LysM, putative peptidoglycan-binding, domain containing 4	160418	LYSMD4	0.379	+	1.19E-02	1.44E-02
218437_PM_s_at	leucine zipper transcription factor-like 1	64282	LZTFL1	0.536	+	4.25E-02	1.88E-02
214894_PM_x_at	microtubule-actin crosslinking factor 1	29923	MACF1	0.472	+	2.69E-02	4.17E-02
208634_PM_s_at	microtubule-actin crosslinking factor 1	3995	MACF1	0.399	+	2.84E-02	2.85E-02
215222_PM_x_at	microtubule-actin crosslinking factor 1	79139	MACF1	0.519	+	4.51E-02	3.30E-02
209348_PM_s_at	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	196743	MAF	0.866	+	1.88E-02	9.50E-03
206363_PM_at	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	11311	MAF	0.774	+	2.73E-02	2.64E-02
1559256_PM_at	membrane associated guanylate kinase, WW and PDZ domain containing 1	4140	MAGI1	0.500	+	2.06E-02	2.58E-02
225465_PM_at	membrane associated guanylate kinase, WW and PDZ domain containing 1	130589	MAGI1	0.322	+	2.06E-02	3.13E-03
209737_PM_at	membrane associated guanylate kinase, WW and PDZ domain containing 2	79966	MAGI2	0.462	+	1.76E-02	8.08E-03
226770_PM_at	membrane associated guanylate kinase, WW and PDZ domain containing 3	23304	MAGI3	0.563	+	4.51E-02	2.35E-02
218969_PM_at	mitochondria-associated protein involved in granulocyte-macrophage colony-stimulating factor signal transduction	196500	Magmas	0.400	+	1.04E-02	1.34E-02
210093_PM_s_at	mago-nashi homolog, proliferation-associated (Drosophila)	91452	MAGOH	0.657	+	3.35E-04	4.54E-03
210092_PM_at	mago-nashi homolog, proliferation-associated (Drosophila)	10018	MAGOH	0.479	+	3.57E-03	2.69E-02

224899_PM_s_at	magnesium transporter 1	134492	MAGT1	0.562	+	4.14E-02	2.65E-02
202360_PM_at	mastermind-like 1 (Drosophila)	63901	MAML1	0.403	+	2.64E-02	5.57E-03
205088_PM_at	mastermind-like domain containing 1	3845	MAMLD1	0.675	+	4.17E-02	6.55E-03
226538_PM_at	mannosidase, alpha, class 2A, member 1	23169	MAN2A1	0.759	+	1.54E-02	5.01E-03
238230_PM_x_at	mannosidase, alpha, class 2C, member 1	---	MAN2C1	0.281	+	1.97E-02	1.63E-02
224689_PM_at	mannosidase, beta A, lysosomal-like	4289	MANBAL	0.318	+	8.91E-03	4.35E-02
222805_PM_at	mannosidase, endo-alpha	222642	MANEA	0.498	+	1.48E-02	3.33E-02
212741_PM_at	monoamine oxidase A	10465	MAOA	0.363	+	3.36E-03	1.14E-02
204389_PM_at	monoamine oxidase A	9592	MAOA	0.555	+	2.63E-02	1.37E-02
204041_PM_at	monoamine oxidase B	5226	MAOB	0.277	+	1.42E-02	2.41E-02
203266_PM_s_at	mitogen-activated protein kinase kinase 4	11016	MAP2K4	0.399	+	3.76E-02	2.35E-02
226556_PM_at	mitogen-activated protein kinase kinase kinase 13	5781	MAP3K13	0.365	+	1.49E-03	9.86E-03
227131_PM_at	mitogen-activated protein kinase kinase kinase 3	539	MAP3K3	0.534	+	3.21E-03	6.00E-04
216199_PM_s_at	mitogen-activated protein kinase kinase kinase 4	58508	MAP3K4	0.663	+	4.78E-03	2.24E-03
204089_PM_x_at	mitogen-activated protein kinase kinase kinase 4	23608	MAP3K4	0.705	+	1.20E-02	6.49E-03
203837_PM_at	mitogen-activated protein kinase kinase kinase 5	6418	MAP3K5	0.438	+	3.39E-02	1.78E-02
233679_PM_at	Mitogen-activated protein kinase kinase kinase 7 interacting protein 1	---	MAP3K7IP1	0.480	+	9.65E-03	4.63E-02
213927_PM_at	mitogen-activated protein kinase kinase kinase 9	1540	MAP3K9	0.718	+	2.10E-02	8.31E-03
212566_PM_at	microtubule-associated protein 4	9057	MAP4	0.323	+	3.91E-02	2.21E-02
218311_PM_at	mitogen-activated protein kinase kinase kinase kinase 3	284695	MAP4K3	0.431	+	2.79E-02	3.26E-02
222548_PM_s_at	mitogen-activated protein kinase kinase kinase kinase 4	23515	MAP4K4	0.409	+	1.92E-02	2.14E-02
203552_PM_at	mitogen-activated protein kinase kinase kinase kinase 5	10298	MAP4K5	0.563	+	1.22E-02	7.97E-03
221713_PM_s_at	MAP6 domain containing 1	23071	MAP6D1	0.318	+	3.29E-03	4.33E-03
202890_PM_at	microtubule-associated protein 7	55692	MAP7	0.523	+	1.43E-02	4.90E-02
228262_PM_at	MAP7 domain containing 2	9223	MAP7D2	0.435	+	1.93E-02	4.13E-02
228423_PM_at	microtubule-associated protein 9	25929	MAP9	0.287	+	3.91E-02	7.81E-03
207121_PM_s_at	mitogen-activated protein kinase 6	27101	MAPK6	0.439	+	2.37E-02	1.97E-03
229664_PM_at	mitogen-activated protein kinase 8	10160	MAPK8	0.703	+	1.52E-02	8.76E-03
217971_PM_at	MAPK scaffold protein 1	57659	MAPKSP1	0.500	+	3.36E-03	5.96E-04
200712_PM_s_at	microtubule-associated protein, RP/EB family, member 1	2554	MAPRE1	0.326	+	6.43E-03	2.59E-02
200713_PM_s_at	microtubule-associated protein, RP/EB family, member 1	4062	MAPRE1	0.455	+	3.29E-02	2.54E-02

225897_PM_at	myristoylated alanine-rich protein kinase C substrate	79632	MARCKS	0.660	+	7.46E-03	6.07E-04
202569_PM_s_at	MAP/microtubule affinity-regulating kinase 3	150472 /// 220869 /// 445571 /// 55871 /// 644019 /// 728013	MARK3	0.541	+	5.89E-03	8.41E-03
213671_PM_s_at	methionyl-tRNA synthetase	5962	MARS	0.338	+	1.32E-03	4.34E-03
239148_PM_at	MARVEL domain containing 3	---	MARVELD3	0.303	+	1.70E-03	7.28E-03
215903_PM_s_at	microtubule associated serine/threonine kinase 2	84851	MAST2	0.366	+	5.19E-03	4.58E-03
217993_PM_s_at	methionine adenosyltransferase II, beta	3842	MAT2B	0.333	+	9.81E-03	2.82E-02
202350_PM_s_at	matrilin 2	65083	MATN2	0.599	+	7.62E-03	9.47E-03
228798_PM_x_at	MYC-associated zinc finger protein (purine-binding transcription factor)	645460	MAZ	0.319	+	1.52E-02	4.78E-02
203353_PM_s_at	methyl-CpG binding domain protein 1	11276	MBD1	0.398	+	2.55E-02	2.52E-02
202484_PM_s_at	methyl-CpG binding domain protein 2	51192	MBD2	0.685	+	4.30E-02	2.22E-02
214047_PM_s_at	methyl-CpG binding domain protein 4	4603	MBD4	0.590	+	1.43E-02	1.25E-02
209580_PM_s_at	methyl-CpG binding domain protein 4	387521 /// 7335	MBD4	0.594	+	1.93E-02	1.20E-02
220195_PM_at	methyl-CpG binding domain protein 5	9797	MBD5	0.361	+	3.05E-03	1.54E-02
227833_PM_s_at	methyl-CpG binding domain protein 6	401152	MBD6	0.511	+	3.65E-05	8.84E-04
218411_PM_s_at	MAP3K12 binding inhibitory protein 1	51171	MBIP	0.363	+	1.64E-02	4.28E-02
201153_PM_s_at	muscleblind-like (Drosophila)	10553	MBNL1	0.777	+	3.95E-03	5.20E-03
203640_PM_at	muscleblind-like 2 (Drosophila)	79918	MBNL2	0.303	+	3.85E-02	3.10E-04
213288_PM_at	membrane bound O-acyltransferase domain containing 2	9100	MBOAT2	0.695	+	5.06E-03	6.62E-03
225407_PM_at	myelin basic protein	53944	MBP	0.571	+	1.56E-02	2.49E-02
226797_PM_at	mbt domain containing 1	26268	MBTD1	0.592	+	3.23E-02	6.93E-03
209087_PM_x_at	melanoma cell adhesion molecule	55086	MCAM	0.444	+	1.36E-04	4.30E-03
226225_PM_at	mutated in colorectal cancers	9910	MCC	0.890	+	2.05E-02	2.25E-03
218440_PM_at	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	8111	MCCC1	0.306	+	6.74E-03	2.63E-02
209623_PM_at	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	83787	MCCC2	0.738	+	2.29E-02	3.49E-02
226238_PM_at	methylmalonyl CoA epimerase	25842	MCEE	0.695	+	4.73E-03	1.05E-02
208017_PM_s_at	MCF.2 cell line derived transforming sequence	905	MCF2	0.489	+	2.28E-02	3.58E-02
212245_PM_at	multiple coagulation factor deficiency 2	214	MCFD2	0.311	+	2.70E-02	3.25E-02
200797_PM_s_at	myeloid cell leukemia sequence 1 (BCL2-related)	4595	MCL1	0.455	+	2.56E-02	1.99E-02

212269_PM_s_at	minichromosome maintenance complex component 3 associated protein	3476	MCM3AP	0.287	+	1.80E-02	1.06E-02
222036_PM_s_at	minichromosome maintenance complex component 4	25963	MCM4	0.426	+	3.86E-03	1.51E-02
230235_PM_at	malignant T cell amplified sequence 1	54205	MCTS1	0.589	+	2.34E-03	6.25E-03
218163_PM_at	malignant T cell amplified sequence 1	91404	MCTS1	0.365	+	3.60E-02	4.14E-02
203062_PM_s_at	mediator of DNA-damage checkpoint 1	60592	MDC1	0.395	+	2.30E-03	1.33E-03
238721_PM_at	malate dehydrogenase 1B, NAD (soluble)	---	MDH1B	0.546	+	3.00E-02	2.49E-02
225740_PM_x_at	Mdm4 p53 binding protein homolog (mouse)	94032	MDM4	0.539	+	9.21E-03	1.16E-02
218061_PM_at	male-enhanced antigen 1	84132	MEA1	0.275	+	3.88E-03	3.81E-03
226420_PM_at	MDS1 and EVI1 complex locus	1268	MECOM	0.399	+	9.13E-03	5.94E-03
201987_PM_at	mediator complex subunit 13	23032	MED13	0.647	+	6.41E-03	1.98E-03
209362_PM_at	mediator complex subunit 21	23677	MED21	0.657	+	1.72E-03	3.18E-03
227787_PM_s_at	mediator complex subunit 30	64231	MED30	0.565	+	2.51E-03	5.53E-04
227786_PM_at	mediator complex subunit 30	64343	MED30	0.506	+	3.07E-03	4.67E-03
222867_PM_s_at	mediator complex subunit 31	171392	MED31	0.692	+	3.14E-03	1.35E-03
207078_PM_at	mediator complex subunit 6	5048	MED6	0.280	+	8.71E-03	1.52E-02
204350_PM_s_at	mediator complex subunit 7	892	MED7	0.467	+	5.43E-03	5.76E-03
212535_PM_at	myocyte enhancer factor 2A	687	MEF2A	0.421	+	3.53E-02	3.98E-02
236517_PM_at	multiple EGF-like-domains 10	4124	MEGF10	0.338	+	3.31E-02	3.90E-02
224675_PM_at	mesoderm development candidate 2	135293	MESDC2	0.693	+	1.22E-02	1.42E-02
212673_PM_at	methionyl aminopeptidase 1	7403	METAP1	0.658	+	1.68E-02	3.69E-02
226744_PM_at	methyltransferase 10 domain containing	10000	METT10D	0.354	+	8.74E-04	4.57E-03
238773_PM_at	methyltransferase 5 domain containing 1	---	METT5D1	0.404	+	1.35E-02	7.91E-03
223368_PM_s_at	methyltransferase like 11A	5128	METTL11A	0.359	+	2.84E-02	3.73E-02
212407_PM_at	methyltransferase like 13	10427	METTL13	0.520	+	1.23E-02	4.88E-02
222447_PM_at	methyltransferase like 9	10240	METTL9	0.619	+	9.75E-03	4.93E-03
213123_PM_at	microfibrillar-associated protein 3	7691	MFAP3	0.401	+	4.01E-03	1.73E-03
219137_PM_s_at	mitochondrial fission factor	374875	MFF	0.365	+	4.13E-02	2.69E-02
204153_PM_s_at	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	9520	MFNG	0.314	+	1.09E-02	1.05E-02
229254_PM_at	major facilitator superfamily domain containing 4	2673	MFSD4	0.409	+	2.96E-02	4.27E-02
225325_PM_at	major facilitator superfamily domain containing 6	644246	MFSD6	0.526	+	1.88E-02	1.96E-02

226039_PM_at	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	5870	MGAT4A	0.367	+	1.90E-02	3.04E-02
238445_PM_x_at	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isozyme B	152485	MGAT5B	0.353	+	6.79E-03	7.65E-03
228235_PM_at	hypothetical protein MGC16121	54994	MGC16121	0.514	+	4.34E-04	1.44E-03
230864_PM_at	serine/threonine-protein kinase NIM1	---	MGC42105	0.434	+	1.47E-02	8.61E-03
200899_PM_s_at	meningioma expressed antigen 5 (hyaluronidase)	1981	MGEA5	0.415	+	1.86E-02	4.09E-02
224918_PM_x_at	microsomal glutathione S-transferase 1	374969	MGST1	0.443	+	2.21E-02	1.89E-04
204168_PM_at	microsomal glutathione S-transferase 2	5547	MGST2	0.503	+	2.22E-02	4.29E-03
203637_PM_s_at	midline 1 (Opitz/BBB syndrome)	85406	MID1	1.016	+	8.27E-03	3.01E-02
203636_PM_at	midline 1 (Opitz/BBB syndrome)	1499	MID1	0.461	+	8.36E-03	1.69E-02
228961_PM_at	mesoderm induction early response 1, family member 3	83648	MIER3	0.580	+	3.59E-03	3.64E-04
223411_PM_at	MIF4G domain containing	79647	MIF4GD	0.310	+	4.44E-06	1.71E-04
221559_PM_s_at	MIS12, MIND kinetochore complex component, homolog (S. pombe)	4974	MIS12	0.439	+	8.95E-04	3.22E-03
226329_PM_s_at	MIT, microtubule interacting and transport, domain containing 1	6565	MITD1	0.283	+	7.90E-04	2.30E-03
225526_PM_at	muskelin 1, intracellular mediator containing kelch motifs	121601	MKLN1	0.317	+	9.36E-03	8.87E-04
201285_PM_at	makorin ring finger protein 1	20	MKRN1	0.341	+	3.34E-02	3.20E-02
218071_PM_s_at	makorin ring finger protein 2	441951	MKRN2	0.476	+	1.32E-02	1.52E-02
204784_PM_s_at	myeloid leukemia factor 1	25843	MLF1	0.606	+	1.71E-03	6.22E-03
217216_PM_x_at	mutL homolog 3 (E. coli)	84437	MLH3	0.465	+	1.50E-02	3.44E-02
226981_PM_at	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	4293	MLL	0.509	+	6.28E-03	7.61E-03
222415_PM_at	myeloid/lymphoid or mixed-lineage leukemia 3	285527	MLL3	0.547	+	1.39E-02	1.11E-02
226100_PM_at	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	2273	MLL5	0.746	+	2.77E-02	8.70E-03
211071_PM_s_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	91392	MLLT11	0.308	+	9.10E-03	4.98E-02
224784_PM_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	23328	MLLT6	0.379	+	2.40E-03	1.16E-02
217910_PM_x_at	MAX-like protein X	54842	MLX	0.581	+	1.06E-02	1.82E-02
238975_PM_at	methylmalonic aciduria (cobalamin deficiency) cblB type	---	MMAB	0.503	+	2.18E-02	4.33E-02

217883_PM_at	methylmalonic aciduria (cobalamin deficiency) cblD type, with homocystinuria	3840	MMADHC	0.349	+	9.46E-03	6.28E-03
225125_PM_at	membrane magnesium transporter 1	404217	MMGT1	0.297	+	4.09E-02	4.52E-02
223614_PM_at	matrix metallopeptidase 16 (membrane-inserted)	50848	MMP16	0.713	+	8.05E-04	8.82E-04
203565_PM_s_at	319epari a trois homolog 1, cyclin H assembly factor (Xenopus laevis)	23770	MNAT1	0.422	+	2.08E-03	3.26E-03
204206_PM_at	MAX binding protein	9989	MNT	0.411	+	2.39E-02	4.77E-02
201298_PM_s_at	MOB1, Mps One Binder kinase activator-like 1B (yeast)	10396	MOBKL1B	0.529	+	1.32E-02	1.16E-02
214812_PM_s_at	MOB1, Mps One Binder kinase activator-like 1B (yeast)	8491	MOBKL1B	0.495	+	2.09E-02	1.71E-02
219265_PM_at	MOB1, Mps One Binder kinase activator-like 2B (yeast)	6235	MOBKL2B	0.692	+	3.53E-02	2.68E-02
202919_PM_at	MOB1, Mps One Binder kinase activator-like 3 (yeast)	84059	MOBKL3	0.352	+	1.47E-02	1.25E-02
212754_PM_s_at	MON2 homolog (S. cerevisiae)	10667	MON2	0.550	+	5.10E-03	2.13E-03
213000_PM_at	MORC family CW-type zinc finger 3	4356	MORC3	0.323	+	7.59E-03	6.56E-03
219852_PM_s_at	MORN repeat containing 1	4927	MORN1	0.568	+	1.11E-03	2.56E-03
226790_PM_at	MORN repeat containing 2	4673	MORN2	0.634	+	7.95E-03	2.97E-03
218865_PM_at	MOCO sulphurase C-terminal domain containing 1	85004	MOSC1	0.425	+	3.66E-02	1.28E-02
218853_PM_s_at	motile sperm domain containing 1	91120	MOSPD1	0.724	+	1.58E-03	5.03E-03
203740_PM_at	M-phase phosphoprotein 6	221178 /// 338872	MPHOSPH6	0.409	+	2.00E-02	4.85E-02
206186_PM_at	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)	2098	MPP3	0.512	+	9.75E-03	1.57E-02
213924_PM_at	Metallophosphoesterase 1	23108	MPPE1	0.496	+	1.53E-02	3.71E-02
227226_PM_at	melanocortin 2 receptor accessory protein 2	55347	MRAP2	0.695	+	2.74E-02	4.95E-02
225185_PM_at	muscle RAS oncogene homolog	9378	MRAS	0.471	+	9.25E-03	9.99E-03
204386_PM_s_at	mitochondrial ribosomal protein 63	8533	MRP63	0.449	+	2.69E-03	4.47E-03
223154_PM_at	mitochondrial ribosomal protein L1	55145	MRPL1	0.583	+	1.69E-03	3.59E-03
218049_PM_s_at	mitochondrial ribosomal protein L13	146198	MRPL13	0.956	+	1.05E-03	3.88E-03
217980_PM_s_at	mitochondrial ribosomal protein L16	113263	MRPL16	0.614	+	1.14E-02	3.32E-03
222216_PM_s_at	mitochondrial ribosomal protein L17	23168	MRPL17	0.433	+	8.29E-03	1.23E-02
217907_PM_at	mitochondrial ribosomal protein L18	3712	MRPL18	0.333	+	2.82E-02	6.42E-03
203465_PM_at	mitochondrial ribosomal protein L19	132864	MRPL19	0.311	+	1.34E-03	1.67E-03
218339_PM_at	mitochondrial ribosomal protein L22	26090	MRPL22	0.396	+	3.97E-03	1.83E-03

225260_PM_s_at	mitochondrial ribosomal protein L32	146713	MRPL32	0.377	+	1.74E-02	5.39E-03
203781_PM_at	mitochondrial ribosomal protein L33	4297	MRPL33	0.580	+	2.04E-02	2.62E-02
225255_PM_at	mitochondrial ribosomal protein L35	5529	MRPL35	0.582	+	1.14E-02	3.08E-02
218890_PM_x_at	mitochondrial ribosomal protein L35	360	MRPL35	0.511	+	1.44E-02	4.96E-02
203152_PM_at	mitochondrial ribosomal protein L40	26263	MRPL40	0.511	+	1.23E-02	2.61E-02
222466_PM_s_at	mitochondrial ribosomal protein L42	7334	MRPL42	0.317	+	1.34E-02	1.26E-03
219244_PM_s_at	mitochondrial ribosomal protein L46	6745	MRPL46	0.473	+	1.52E-02	2.39E-02
223480_PM_s_at	mitochondrial ribosomal protein L47	63877	MRPL47	0.544	+	2.42E-03	3.19E-03
218281_PM_at	mitochondrial ribosomal protein L48	9590	MRPL48	0.460	+	4.09E-03	6.20E-03
225580_PM_at	mitochondrial ribosomal protein L50	138199	MRPL50	1.024	+	7.74E-04	2.37E-03
223086_PM_x_at	mitochondrial ribosomal protein L51	51575	MRPL51	0.409	+	1.19E-02	1.16E-03
226241_PM_s_at	mitochondrial ribosomal protein L52	25852	MRPL52	0.547	+	1.02E-02	2.23E-03
218106_PM_s_at	mitochondrial ribosomal protein S10	84460	MRPS10	0.550	+	5.14E-03	2.25E-02
203800_PM_s_at	mitochondrial ribosomal protein S14	11315	MRPS14	0.333	+	1.43E-02	3.45E-02
226296_PM_s_at	mitochondrial ribosomal protein S15	2342	MRPS15	0.406	+	9.14E-04	6.72E-04
228019_PM_s_at	mitochondrial ribosomal protein S18C	50807	MRPS18C	0.533	+	3.56E-03	4.49E-03
222997_PM_s_at	mitochondrial ribosomal protein S21	55505	MRPS21	0.385	+	1.40E-03	2.42E-04
226257_PM_x_at	mitochondrial ribosomal protein S22	22909	MRPS22	0.450	+	4.76E-03	1.36E-02
219220_PM_x_at	mitochondrial ribosomal protein S22	22919	MRPS22	0.420	+	8.29E-03	2.71E-02
223448_PM_x_at	mitochondrial ribosomal protein S22	55745	MRPS22	0.482	+	8.57E-03	3.30E-02
228059_PM_x_at	mitochondrial ribosomal protein S22	1459	MRPS22	0.490	+	1.24E-02	2.72E-02
223156_PM_at	mitochondrial ribosomal protein S23	26232	MRPS23	0.540	+	2.42E-03	6.41E-03
224948_PM_at	mitochondrial ribosomal protein S24	492311	MRPS24	0.411	+	3.56E-03	2.02E-03
224873_PM_s_at	mitochondrial ribosomal protein S25	128637	MRPS25	0.402	+	2.22E-04	2.04E-05
212603_PM_at	mitochondrial ribosomal protein S31	3052	MRPS31	0.409	+	2.73E-02	1.11E-02
218654_PM_s_at	mitochondrial ribosomal protein S33	157869	MRPS33	0.329	+	2.11E-02	2.47E-02
224302_PM_s_at	mitochondrial ribosomal protein S36	199692	MRPS36	0.427	+	1.98E-02	1.09E-02
225126_PM_at	mitochondrial ribosome recycling factor	286205	MRRF	0.396	+	1.89E-02	3.99E-02
228542_PM_at	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	84912	MRS2	0.373	+	1.20E-03	6.50E-03
226047_PM_at	murine retrovirus integration site 1 homolog	1965	MRVI1	0.870	+	7.39E-03	1.66E-02
223922_PM_x_at	membrane-spanning 4-domains, subfamily A, member 6A	54822	MS4A6A	0.281	+	3.28E-02	2.51E-02

243010_PM_at	musashi homolog 2 (Drosophila)	---	MSI2	1.388	+	6.60E-03	2.63E-02
224765_PM_at	male-specific lethal 1 homolog (Drosophila)	57542	MSL1	0.334	+	3.06E-02	1.18E-02
212859_PM_x_at	metallothionein 1E	6443	MT1E	0.604	+	6.24E-03	2.95E-02
212185_PM_x_at	metallothionein 2A	5706	MT2A	0.366	+	2.55E-02	3.26E-02
216862_PM_s_at	mature T-cell proliferation 1 neighbor	55031	MTCP1NB	0.544	+	1.16E-02	4.53E-02
210212_PM_x_at	mature T-cell proliferation 1 neighbor	5562	MTCP1NB	0.591	+	1.79E-02	2.56E-02
212248_PM_at	metadherin	10449	MTDH	0.337	+	2.60E-03	1.95E-03
225346_PM_at	MTERF domain containing 3	129880	MTERFD3	0.687	+	4.85E-02	3.43E-02
209705_PM_at	metal response element binding transcription factor 2	81847	MTF2	0.711	+	1.37E-02	1.61E-02
235689_PM_at	mitochondrial methionyl-tRNA formyltransferase	6173	MTFMT	0.774	+	2.46E-02	1.05E-02
203433_PM_at	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)	441457 /// 54754 /// 728118 /// 729262	MTHFS	0.478	+	1.45E-02	4.24E-02
203095_PM_at	mitochondrial translational initiation factor 2	25870	MTIF2	0.409	+	3.38E-02	3.07E-02
36920_PM_at	myotubularin 1	---	MTM1	0.459	+	2.48E-02	4.76E-02
204101_PM_at	myotubularin 1	2971	MTM1	0.365	+	3.75E-02	2.53E-02
225232_PM_at	myotubularin related protein 12	2549	MTMR12	0.459	+	2.35E-03	2.67E-04
203678_PM_at	myotubularin related protein 15	26493	MTMR15	0.280	+	6.44E-03	1.94E-02
203212_PM_s_at	myotubularin related protein 2	56945	MTMR2	0.455	+	1.95E-02	3.89E-02
226956_PM_at	myotubularin related protein 3	81688	MTMR3	0.421	+	3.28E-02	2.23E-02
214429_PM_at	myotubularin related protein 6	57092	MTMR6	0.471	+	2.61E-02	1.05E-02
224430_PM_s_at	mitochondrial translation optimization 1 homolog (S. cerevisiae)	10672	MTO1	0.329	+	4.43E-03	7.83E-03
222794_PM_x_at	mitochondrial poly(A) polymerase	199731	MTPAP	0.503	+	1.97E-02	1.88E-02
203774_PM_at	5-methyltetrahydrofolate-homocysteine methyltransferase	1131	MTR	0.326	+	1.68E-02	4.95E-02
225206_PM_s_at	mitochondrial translational release factor 1-like	126328	MTRF1L	0.506	+	1.99E-02	3.16E-02
210386_PM_s_at	metaxin 1	2122	MTX1	0.545	+	3.74E-04	7.83E-03
203517_PM_at	metaxin 2	114788	MTX2	0.873	+	6.80E-03	1.36E-02
226528_PM_at	metaxin 3	1070	MTX3	0.641	+	1.04E-02	2.52E-02
222531_PM_s_at	MU-2/AP1M2 domain containing, death-inducing	23078	MUDENG	0.589	+	1.49E-03	9.60E-03
218139_PM_s_at	MU-2/AP1M2 domain containing, death-inducing	83892	MUDENG	0.611	+	6.36E-03	3.15E-03
232156_PM_at	MU-2/AP1M2 domain containing, death-inducing	---	MUDENG	0.704	+	2.34E-02	2.09E-02
236004_PM_at	MU-2/AP1M2 domain containing, death-inducing	51128	MUDENG	0.351	+	2.37E-02	4.17E-02

202959_PM_at	methylmalonyl Coenzyme A mutase	10910	MUT	0.349	+	1.45E-02	6.68E-03
207727_PM_s_at	mutY homolog (E. coli)	490	MUTYH	0.479	+	5.85E-04	6.75E-03
226275_PM_at	MAX dimerization protein 1	51634	MXD1	0.573	+	1.15E-02	5.31E-03
235836_PM_at	matrix-remodelling associated 7	---	MXRA7	0.330	+	1.65E-02	2.60E-02
213906_PM_at	v-myb myeloblastosis viral oncogene homolog (avian)-like 1	23405	MYBL1	0.552	+	1.83E-02	4.27E-02
203360_PM_s_at	c-myc binding protein	84867	MYCBP	0.479	+	3.51E-03	4.98E-03
209757_PM_s_at	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	81545	MYCN	0.853	+	9.13E-03	6.02E-03
226845_PM_s_at	myeloma overexpressed 2	10154	MYEOV2	0.319	+	3.22E-02	1.02E-02
221474_PM_at	myosin, light chain 12B, regulatory	1040	MYL12B	0.363	+	1.81E-03	1.20E-04
212082_PM_s_at	myosin, light chain 6, alkali, smooth muscle and non-muscle	6599	MYL6	0.328	+	4.02E-03	1.62E-02
219942_PM_at	myosin, light chain 7, regulatory	3434	MYL7	0.327	+	1.54E-02	2.97E-02
224823_PM_at	myosin light chain kinase	29094	MYLK	0.391	+	1.59E-02	3.58E-02
227761_PM_at	myosin VA (heavy chain 12, myoxin)	83548	MYO5A	0.285	+	2.93E-02	4.50E-03
203216_PM_s_at	myosin VI	80325	MYO6	0.740	+	2.97E-02	1.07E-02
214156_PM_at	myosin VIIA and Rab interacting protein	23014	MYRIP	0.731	+	1.02E-02	2.56E-03
221820_PM_s_at	MYST histone acetyltransferase 1	4094	MYST1	0.515	+	2.88E-02	1.31E-02
226547_PM_at	MYST histone acetyltransferase (monocytic leukemia) 3	10152	MYST3	0.452	+	7.80E-03	1.89E-02
213375_PM_s_at	NEDD4 binding protein 2-like 1	23355	N4BP2L1	0.305	+	4.10E-02	3.90E-02
209272_PM_at	NGFI-A binding protein 1 (EGR1 binding protein 1)	81611	NAB1	0.683	+	1.23E-02	2.09E-02
222018_PM_at	nascent polypeptide-associated complex alpha subunit /// nascent-polypeptide-associated complex alpha polypeptide pseudogene 1	5087	NACA /// NACAP1	0.725	+	6.13E-03	8.79E-03
202268_PM_s_at	NEDD8 activating enzyme E1 subunit 1	27102	NAE1	0.318	+	1.92E-02	1.37E-02
1555041_PM_a_at	N-acetylgalactosaminidase, alpha-	7317	NAGA	0.307	+	7.03E-03	3.03E-02
228608_PM_at	sodium leak channel, non-selective	---	NALCN	0.539	+	2.78E-03	7.36E-03
217738_PM_at	nicotinamide phosphoribosyltransferase	80315	NAMPT	0.621	+	1.93E-02	1.18E-02
217739_PM_s_at	nicotinamide phosphoribosyltransferase	80315	NAMPT	0.496	+	2.49E-02	1.91E-02
218189_PM_s_at	N-acetylneuraminic acid synthase	4774	NANS	0.499	+	7.43E-04	5.35E-03
1556121_PM_at	nucleosome assembly protein 1-like 1	2273	NAP1L1	0.553	+	1.37E-02	7.07E-03
212967_PM_x_at	nucleosome assembly protein 1-like 1	9687	NAP1L1	0.349	+	1.50E-02	1.56E-02
226998_PM_at	NMDA receptor regulated 1	4916	NARG1	1.096	+	5.35E-04	6.01E-03

219378_PM_at	NMDA receptor regulated 1-like	9512	NARG1L	0.474	+	1.60E-02	2.86E-02
200027_PM_at	asparaginyl-tRNA synthetase	4128	NARS	0.343	+	3.58E-02	3.49E-02
242918_PM_at	Nuclear autoantigenic sperm protein (histone-binding)	---	NASP	0.872	+	1.27E-02	1.22E-02
225679_PM_at	N-acetyltransferase 12 (GCN5-related, putative)	4059	NAT12	0.465	+	7.62E-03	3.09E-03
223040_PM_at	N-acetyltransferase 5 (GCN5-related, putative)	54585	NAT5	0.375	+	2.40E-03	1.39E-02
204382_PM_at	N-acetyltransferase 9 (GCN5-related, putative)	3836	NAT9	0.301	+	8.13E-04	3.55E-03
218330_PM_s_at	neuron navigator 2	163175	NAV2	0.598	+	1.65E-02	3.09E-02
204823_PM_at	neuron navigator 3	9425	NAV3	0.418	+	2.03E-02	4.22E-02
202907_PM_s_at	nibrin	56934	NBN	0.524	+	9.79E-03	3.09E-02
201521_PM_s_at	nuclear cap binding protein subunit 2, 20kDa	334	NCBP2	0.706	+	3.50E-03	1.65E-02
207738_PM_s_at	NCK-associated protein 1	127544	NCKAP1	0.269	+	1.57E-02	2.97E-03
209106_PM_at	nuclear receptor coactivator 1	7564	NCOA1	0.395	+	8.14E-03	3.45E-02
209061_PM_at	nuclear receptor coactivator 3	80196	NCOA3	0.307	+	1.41E-02	2.05E-02
210774_PM_s_at	nuclear receptor coactivator 4	389362	NCOA4	0.368	+	4.33E-02	3.42E-02
225344_PM_at	nuclear receptor coactivator 7	196294	NCOA7	0.406	+	4.97E-03	1.32E-03
232910_PM_at	non-protein coding RNA 81	200014	NCRNA00081	0.455	+	1.15E-03	8.65E-03
228993_PM_s_at	non-protein coding RNA 81	84132	NCRNA00081	0.949	+	1.37E-03	2.68E-03
203245_PM_s_at	non-protein coding RNA 94	116154	NCRNA00094	0.354	+	9.67E-03	8.47E-03
237291_PM_at	non-protein coding RNA 117	---	NCRNA00117	0.994	+	1.38E-03	4.61E-03
225786_PM_at	non-protein coding RNA 201	---	NCRNA00201	0.845	+	2.46E-02	3.24E-02
222423_PM_at	Nedd4 family interacting protein 1	23012	NDFIP1	0.317	+	1.93E-02	2.92E-02
224801_PM_at	Nedd4 family interacting protein 2	54887	NDFIP2	0.753	+	2.71E-02	5.87E-03
206022_PM_at	Norrie disease (pseudoglioma)	7514	NDP	0.432	+	1.84E-02	5.46E-03
202607_PM_at	N-deacetylase/N-sulfotransferase (323eparin glucosaminyl) 1	54715	NDST1	0.327	+	9.91E-03	1.11E-02
1554010_PM_at	N-deacetylase/N-sulfotransferase (323eparin glucosaminyl) 1	7030	NDST1	0.362	+	2.27E-02	4.72E-02
202298_PM_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa	5859	NDUFA1	0.316	+	8.37E-03	1.93E-02

228690_PM_s_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa	401548	NDUFA11	0.417	+	1.26E-02	4.78E-02
223244_PM_s_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	64376	NDUFA12	0.543	+	7.14E-04	5.58E-03
201304_PM_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa	1032	NDUFA5	0.487	+	1.23E-02	1.08E-02
202001_PM_s_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa	404734 /// 8637	NDUFA6	0.421	+	8.02E-03	8.77E-03
218160_PM_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8, 19kDa	57544	NDUFA8	0.320	+	4.60E-03	3.49E-03
204125_PM_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1	6173	NDUFAF1	0.536	+	2.82E-03	4.12E-03
228355_PM_s_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2	58487	NDUFAF2	0.885	+	1.66E-03	1.10E-02
227559_PM_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4	100128062	NDUFAF4	0.576	+	8.00E-03	7.90E-03
206790_PM_s_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa	8558	NDUFB1	0.408	+	1.52E-03	1.95E-04
218320_PM_s_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 17.3kDa	219844	NDUFB11	0.264	+	1.08E-02	1.84E-02
218200_PM_s_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa	134266	NDUFB2	0.278	+	1.75E-02	1.15E-03
203613_PM_s_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	23576	NDUFB6	0.346	+	5.63E-03	2.36E-02
201227_PM_s_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa	1033	NDUFB8	0.568	+	2.52E-03	2.48E-03
218101_PM_s_at	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa	64960	NDUFC2	0.339	+	2.06E-03	6.12E-04
232169_PM_x_at	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)	114786	NDUFS8	0.433	+	3.31E-02	3.39E-02
226616_PM_s_at	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kDa	283450	NDUFV3	0.544	+	8.06E-03	2.56E-02
241782_PM_at	nebulette	55384	NEBL	0.321	+	2.97E-02	4.60E-02
203962_PM_s_at	nebulette	473	NEBL	0.280	+	3.44E-02	4.96E-02
229461_PM_x_at	neuronal growth regulator 1	51585	NEGR1	0.411	+	2.81E-03	2.01E-03
213331_PM_s_at	NIMA (never in mitosis gene a)-related kinase 1	3551	NEK1	0.600	+	2.80E-02	2.33E-02

204634_PM_at	NIMA (never in mitosis gene a)-related kinase 4	7456	NEK4	0.392	+	8.18E-03	3.15E-02
212530_PM_at	NIMA (never in mitosis gene a)-related kinase 7	80208	NEK7	0.894	+	1.49E-02	3.18E-03
212299_PM_at	NIMA (never in mitosis gene a)- related kinase 9	1329	NEK9	0.479	+	2.08E-02	2.05E-02
226806_PM_s_at	nuclear factor I/A	6738	NFIA	0.461	+	1.41E-02	3.39E-02
218946_PM_at	NFU1 iron-sulfur cluster scaffold homolog (S. cerevisiae)	54965	NFU1	0.529	+	2.42E-03	1.59E-03
218128_PM_at	nuclear transcription factor Y, beta	5163	NFYB	0.311	+	1.27E-02	1.18E-02
220742_PM_s_at	N-glycanase 1	51103	NGLY1	0.455	+	2.99E-02	2.50E-02
219353_PM_at	NHL repeat containing 2	1845	NHLRC2	0.473	+	1.90E-02	1.63E-02
228933_PM_at	Nance-Horan syndrome (congenital cataracts and dental anomalies)	---	NHS	0.832	+	2.77E-02	3.42E-02
226490_PM_at	NHS-like 1	9412	NHSL1	0.493	+	1.74E-03	8.04E-03
225752_PM_at	non imprinted in Prader-Willi/Angelman syndrome 1	285754	NIPA1	0.511	+	3.81E-02	3.32E-02
219438_PM_at	Na+/K+ transporting ATPase interacting 1	7251	NKAIN1	0.287	+	6.98E-04	2.50E-03
242002_PM_at	Na+/K+ transporting ATPase interacting 2	---	NKAIN2	0.419	+	4.40E-02	1.17E-02
223439_PM_at	NFKB activating protein	11124	NKAP	0.673	+	5.77E-03	6.79E-03
205004_PM_at	NFKB repressing factor	5867	NKRF	0.475	+	3.48E-02	9.53E-03
231361_PM_at	neuroligin 1	29945	NLGN1	0.673	+	7.14E-03	1.79E-02
201577_PM_at	non-metastatic cells 1, protein (NM23A) expressed in	2335	NME1	0.292	+	3.24E-02	9.63E-03
206197_PM_at	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase)	7327	NME5	0.443	+	1.17E-02	1.62E-02
219553_PM_at	non-metastatic cells 7, protein expressed in (nucleoside-diphosphate kinase)	3836	NME7	0.792	+	1.02E-03	2.16E-03
203964_PM_at	N-myc (and STAT) interactor	27230	NMI	0.465	+	2.57E-02	1.79E-02
228090_PM_at	nicotinamide nucleotide adenylyltransferase 3	84181	NMNAT3	0.333	+	1.83E-02	3.39E-02
205006_PM_s_at	N-myristoyltransferase 2	25972	NMT2	0.412	+	6.23E-03	1.09E-02
218889_PM_at	nucleolar complex associated 3 homolog (S. cerevisiae)	1874	NOC3L	0.716	+	4.30E-03	4.21E-03
221970_PM_s_at	nucleolar protein 11	130074	NOL11	0.506	+	3.03E-02	2.58E-02
59625_PM_at	nucleolar protein 3 (apoptosis repressor with CARD domain)	---	NOL3	0.270	+	9.42E-03	4.13E-02
238605_PM_at	nucleolar protein 4	64783	NOL4	0.672	+	1.75E-02	1.70E-02
218199_PM_s_at	nucleolar protein family 6 (RNA-associated)	55667	NOL6	0.292	+	1.70E-02	1.93E-02
213838_PM_at	nucleolar protein 7, 27kDa	4038	NOL7	0.550	+	1.49E-02	5.18E-03
202882_PM_x_at	nucleolar protein 7, 27kDa	55193	NOL7	0.279	+	2.69E-02	1.07E-02

217962_PM_at	NOP10 ribonucleoprotein homolog (yeast)	57685	NOP10	0.307	+	2.02E-02	9.25E-03
200875_PM_s_at	NOP56 ribonucleoprotein homolog (yeast)	1827	NOP56	0.266	+	1.03E-02	4.64E-02
223096_PM_at	NOP58 ribonucleoprotein homolog (yeast)	54680	NOP58	0.464	+	6.95E-04	3.82E-03
39549_PM_at	neuronal PAS domain protein 2	---	NPAS2	0.466	+	4.68E-02	1.92E-02
229281_PM_at	neuronal PAS domain protein 3	---	NPAS3	0.729	+	1.09E-03	7.58E-04
209798_PM_at	nuclear protein, ataxia-telangiectasia locus	83999	NPAT	0.855	+	2.77E-02	3.74E-02
200701_PM_at	Niemann-Pick disease, type C2	6595	NPC2	0.534	+	2.05E-02	2.04E-02
201455_PM_s_at	aminopeptidase puromycin sensitive	10636	NPEPPS	0.326	+	4.36E-02	4.86E-02
221923_PM_s_at	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	28954	NPM1	0.751	+	1.30E-02	1.63E-02
206801_PM_at	natriuretic peptide precursor B	11237	NPPB	0.293	+	1.18E-02	2.18E-02
201468_PM_s_at	NAD(P)H dehydrogenase, quinone 1	1622	NQO1	0.548	+	1.43E-03	1.05E-02
217476_PM_at	nuclear receptor subfamily 1, group D, member 1 /// thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	57222	NR1D1 /// THRA	0.389	+	8.35E-03	1.04E-02
207443_PM_at	nuclear receptor subfamily 2, group E, member 1	1654	NR2E1	0.903	+	1.79E-02	1.58E-02
209262_PM_s_at	nuclear receptor subfamily 2, group F, member 6	2029	NR2F6	0.306	+	2.55E-03	2.16E-02
226499_PM_at	NOTCH-regulated ankyrin repeat protein	10418	NRARP	0.439	+	8.81E-03	2.21E-02
224985_PM_at	neuroblastoma RAS viral (v-ras) oncogene homolog	403341	NRAS	0.864	+	3.35E-03	2.27E-04
208241_PM_at	neuregulin 1	8833	NRG1	0.302	+	2.89E-03	3.20E-02
228699_PM_at	Neuropilin 2	4076	NRP2	0.277	+	6.49E-04	1.50E-03
228547_PM_at	neurexin 1	8411	NRXN1	0.279	+	5.16E-03	1.29E-02
215093_PM_at	NAD(P) dependent steroid dehydrogenase-like	51025	NSDHL	0.281	+	2.28E-03	5.50E-03
203269_PM_at	neutral sphingomyelinase (N-Smase) activation associated factor	116135	NSMAF	0.533	+	2.25E-02	1.42E-02
211376_PM_s_at	non-SMC element 4 homolog A (S. cerevisiae)	317649	NSMCE4A	0.530	+	1.17E-02	1.60E-02
219067_PM_s_at	non-SMC element 4 homolog A (S. cerevisiae)	6506	NSMCE4A	0.645	+	1.85E-02	2.81E-02
236247_PM_at	NOL1/NOP2/Sun domain family, member 4	---	NSUN4	0.284	+	4.54E-03	8.39E-03
209155_PM_s_at	5'-nucleotidase, cytosolic II	387893	NT5C2	0.324	+	5.72E-03	1.13E-02
213061_PM_s_at	N-terminal asparagine amidase	4879	NTAN1	0.300	+	4.06E-04	3.10E-03
223315_PM_at	netrin 4	54583	NTN4	0.729	+	1.19E-02	1.54E-02
236088_PM_at	netrin G1	5576	NTNG1	0.563	+	2.49E-02	5.03E-03
213960_PM_at	neurotrophic tyrosine kinase, receptor, type 3	124152	NTRK3	0.452	+	2.09E-02	2.12E-02

203675_PM_at	nucleobindin 2	57541	NUCB2	0.943	+	5.11E-04	2.46E-03
226642_PM_s_at	NudC domain containing 2	9475	NUDCD2	0.699	+	2.09E-02	2.89E-03
219347_PM_at	nudix (nucleoside diphosphate linked moiety X)-type motif 15	7247	NUDT15	0.338	+	3.12E-02	4.10E-02
212181_PM_s_at	nudix (nucleoside diphosphate linked moiety X)-type motif 4 /// nudix (nucleoside diphosphate linked moiety X)-type motif 4 pseudogene 1	9878	NUDT4 /// NUDT4P1	0.327	+	4.63E-02	4.39E-02
223100_PM_s_at	nudix (nucleoside diphosphate linked moiety X)-type motif 5	27344	NUDT5	0.623	+	1.26E-02	9.46E-04
218375_PM_at	nudix (nucleoside diphosphate linked moiety X)-type motif 9	133686	NUDT9	0.531	+	4.88E-03	2.13E-03
205136_PM_s_at	nuclear fragile X mental retardation protein interacting protein 1	23099	NUFIP1	0.439	+	1.76E-02	4.36E-02
224938_PM_at	nuclear fragile X mental retardation protein interacting protein 2	64853	NUFIP2	0.553	+	2.02E-03	1.25E-02
218768_PM_at	nucleoporin 107kDa	386618	NUP107	0.738	+	4.32E-03	2.78E-02
212247_PM_at	nucleoporin 205kDa	23077	NUP205	0.779	+	2.00E-02	3.94E-02
218622_PM_at	nucleoporin 37kDa	60684	NUP37	0.847	+	5.05E-04	2.78E-03
202900_PM_s_at	nucleoporin 88kDa	117177	NUP88	0.683	+	2.11E-02	2.42E-02
204435_PM_at	nucleoporin like 1	8522	NUPL1	1.009	+	6.26E-03	5.25E-03
232377_PM_at	neurexophilin 1	91749	NXPH1	0.570	+	3.56E-02	7.32E-03
218708_PM_at	NTF2-like export factor 1	57150	NXT1	0.393	+	4.20E-03	1.00E-02
202869_PM_at	2’,5’-oligoadenylate synthetase 1, 40/46kDa	55904	OAS1	0.595	+	5.31E-03	1.00E-02
234841_PM_x_at	odorant binding protein 2A /// odorant binding protein 2B	9295	OBP2A /// OBP2B	0.267	+	2.32E-02	1.09E-02
233860_PM_s_at	odorant binding protein 2A /// odorant binding protein 2B	---	OBP2A /// OBP2B	0.292	+	2.91E-02	1.54E-02
205728_PM_at	odz, odd Oz/ten-m homolog 1(Drosophila)	9522	ODZ1	1.092	+	1.08E-02	3.34E-02
203569_PM_s_at	oral-facial-digital syndrome 1	56834	OFD1	0.594	+	8.34E-03	1.87E-02
221090_PM_s_at	2-oxoglutarate and iron-dependent oxygenase domain containing 1	51367	OGFOD1	0.317	+	1.22E-03	5.87E-03
225106_PM_s_at	2-oxoglutarate and iron-dependent oxygenase domain containing 1	51023	OGFOD1	0.336	+	1.01E-02	4.40E-02
211512_PM_s_at	opioid growth factor receptor	1745	OGFR	0.401	+	2.35E-03	1.30E-02
226810_PM_at	opioid growth factor receptor-like 1	196441	OGFRL1	0.624	+	2.68E-03	6.27E-03
209240_PM_at	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl	140803	OGT	0.265	+	2.35E-03	7.68E-03

	transferase)						
219293_PM_s_at	Obg-like ATPase 1	11176	OLA1	0.326	+	7.37E-03	2.76E-03
207093_PM_s_at	oligodendrocyte myelin glycoprotein	377	OMG	0.462	+	2.64E-02	1.63E-02
212213_PM_x_at	optic atrophy 1 (autosomal dominant)	51663	OPA1	0.312	+	1.36E-02	4.77E-02
203351_PM_s_at	origin recognition complex, subunit 4-like (yeast)	131408	ORC4L	0.264	+	4.06E-03	4.93E-03
204957_PM_at	origin recognition complex, subunit 5-like (yeast)	26292	ORC5L	0.703	+	1.67E-02	1.81E-02
227548_PM_at	ORM1-like 1 (S. cerevisiae)	7503	ORMDL1	0.435	+	1.51E-02	1.53E-03
200714_PM_x_at	osteosarcoma amplified 9, endoplasmic reticulum lectin	5451	OS9	0.272	+	1.35E-02	1.32E-02
218304_PM_s_at	oxysterol binding protein-like 11	146705	OSBPL11	0.545	+	2.90E-02	4.31E-02
212585_PM_at	oxysterol binding protein-like 8	9377	OSBPL8	0.643	+	1.59E-02	5.58E-03
218047_PM_at	oxysterol binding protein-like 9	23468	OSBPL9	0.340	+	1.80E-02	5.58E-03
235198_PM_at	osteopetrosis associated transmembrane protein 1	23503	OSTM1	0.520	+	1.03E-02	1.19E-02
235197_PM_s_at	osteopetrosis associated transmembrane protein 1	---	OSTM1	0.271	+	1.21E-02	3.48E-02
226140_PM_s_at	OTU domain containing 1	10412	OTUD1	0.474	+	3.81E-02	3.96E-02
203480_PM_s_at	OTU domain containing 4	5080	OTUD4	0.421	+	1.77E-02	1.20E-02
222553_PM_x_at	oxidation resistance 1	9479	OXR1	0.459	+	1.81E-02	1.91E-03
235885_PM_at	purinergic receptor P2Y, G-protein coupled, 12	54883	P2RY12	0.978	+	2.80E-02	2.44E-02
202733_PM_at	prolyl 4-hydroxylase, alpha polypeptide II	51150	P4HA2	0.507	+	2.07E-03	2.20E-02
218957_PM_s_at	proteasomal ATPase-associated factor 1	163051	PAAF1	0.315	+	4.82E-02	2.49E-02
214204_PM_at	PARK2 co-regulated	29966	PACRG	0.875	+	5.55E-05	1.72E-03
227354_PM_at	phosphoprotein associated with glycosphingolipid microdomains 1	844	PAG1	0.521	+	6.50E-03	6.50E-03
208051_PM_s_at	poly(A) binding protein interacting protein 1	23215	PAIP1	0.422	+	1.73E-02	2.60E-02
222984_PM_at	poly(A) binding protein interacting protein 2	23469	PAIP2	0.413	+	1.16E-03	3.95E-03
230100_PM_x_at	p21 protein (Cdc42/Rac)-activated kinase 1	90624	PAK1	0.314	+	4.87E-02	4.88E-02
208878_PM_s_at	p21 protein (Cdc42/Rac)-activated kinase 2	55055	PAK2	0.295	+	7.99E-03	2.66E-03
210721_PM_s_at	p21 protein (Cdc42/Rac)-activated kinase 7	100293328 /// 90736	PAK7	0.721	+	7.00E-04	2.68E-03
219530_PM_at	partner and localizer of BRCA2	3799	PALB2	0.341	+	4.89E-02	4.74E-02
200897_PM_s_at	328eparin, cytoskeletal associated protein	5915	PALLD	0.966	+	6.07E-03	1.21E-02
218736_PM_s_at	palmdelphin	8110	PALMD	0.359	+	4.92E-02	3.51E-02
225563_PM_at	PAN3 poly(A) specific ribonuclease subunit homolog (S.	80127	PAN3	0.569	+	8.91E-03	1.17E-02

	cerevisiae)						
218809_PM_at	pantothenate kinase 2	155054	PANK2	0.428	+	8.28E-03	1.43E-04
221941_PM_at	polyamine oxidase (exo-N4-amino)	3709	PAOX	0.417	+	4.58E-02	3.11E-02
231397_PM_at	phosphatidic acid phosphatase type 2	196047	PAP2D	0.731	+	2.26E-02	1.55E-02
229043_PM_at	PAP associated domain containing 5	3344	PAPD5	0.816	+	1.75E-02	1.90E-03
228569_PM_at	poly(A) polymerase alpha	9931	PAPOLA	0.618	+	1.50E-02	1.51E-03
222273_PM_at	poly(A) polymerase gamma	5962	PAPOLG	0.924	+	3.87E-03	6.15E-03
213372_PM_at	progestin and adipoQ receptor family member III	3479	PAQR3	0.709	+	2.76E-02	8.77E-03
227626_PM_at	progestin and adipoQ receptor family member VIII	6925	PAQR8	0.331	+	2.70E-02	1.45E-02
228411_PM_at	par-3 partitioning defective 3 homolog B (C. elegans)	84933	PARD3B	0.512	+	2.47E-02	2.40E-02
205060_PM_at	poly (ADP-ribose) glycohydrolase	10618	PARG	0.302	+	2.72E-02	9.66E-03
200006_PM_at	Parkinson disease (autosomal recessive, early onset) 7	4005	PARK7	0.341	+	5.33E-03	2.65E-03
214086_PM_s_at	poly (ADP-ribose) polymerase 2	771	PARP2	0.460	+	2.06E-02	6.86E-03
215773_PM_x_at	poly (ADP-ribose) polymerase 2	81892	PARP2	0.490	+	2.42E-02	2.10E-02
219033_PM_at	poly (ADP-ribose) polymerase family, member 8	56776	PARP8	0.904	+	6.32E-03	1.77E-02
217890_PM_s_at	parvin, alpha	55841	PARVA	0.577	+	4.81E-02	2.43E-02
206802_PM_at	paired box 5	57144	PAX5	0.286	+	2.06E-02	1.27E-02
235795_PM_at	paired box 6	51333	PAX6	0.665	+	8.92E-04	2.77E-03
219543_PM_at	phenazine biosynthesis-like protein domain containing	23013	PBLD	0.270	+	9.66E-03	2.80E-02
223238_PM_s_at	polybromo 1	80724	PBRM1	0.752	+	2.09E-03	2.92E-03
212148_PM_at	pre-B-cell leukemia homeobox 1	2937	PBX1	0.450	+	5.09E-03	4.30E-02
214177_PM_s_at	pre-B-cell leukemia homeobox interacting protein 1	9546	PBXIP1	0.351	+	2.47E-02	7.62E-04
213264_PM_at	poly(rC) binding protein 2	7150	PCBP2	0.365	+	7.25E-03	2.31E-02
203860_PM_at	propionyl Coenzyme A carboxylase, alpha polypeptide	11014	PCCA	0.559	+	8.44E-03	2.89E-02
228863_PM_at	protocadherin 17	80012	PCDH17	0.716	+	7.15E-03	4.98E-03
227622_PM_at	PCF11, cleavage and polyadenylation factor subunit, homolog (S. cerevisiae)	5165	PCF11	0.398	+	1.36E-02	1.48E-02
203792_PM_x_at	polycomb group ring finger 2	5286	PCGF2	0.360	+	1.16E-02	3.71E-02
226326_PM_at	polycomb group ring finger 5	6038	PCGF5	0.561	+	4.33E-02	1.81E-02
201202_PM_at	proliferating cell nuclear antigen	8881	PCNA	0.412	+	5.33E-03	1.11E-02
217816_PM_s_at	PEST proteolytic signal containing nuclear protein	54331	PCNP	0.384	+	3.10E-03	2.13E-03
203660_PM_s_at	pericentrin	3632	PCNT	0.480	+	1.13E-02	1.01E-02

229287_PM_at	pecanex homolog (Drosophila)	100131564	PCNX	0.533	+	1.38E-02	1.30E-02
205549_PM_at	Purkinje cell protein 4	8448	PCP4	0.599	+	2.80E-02	9.79E-04
213652_PM_at	Proprotein convertase subtilisin/kexin type 5	23122	PCSK5	0.779	+	7.48E-03	1.74E-02
221918_PM_at	PCTAIRE protein kinase 2	100272147	PCTK2	0.364	+	4.05E-02	2.48E-02
218953_PM_s_at	prenylcysteine oxidase 1 like	84984	PCYOX1L	0.345	+	5.42E-03	1.40E-02
232553_PM_at	phosphate cytidylyltransferase 1, choline, beta	23043	PCYT1B	0.362	+	9.32E-03	3.58E-02
210907_PM_s_at	programmed cell death 10	79184	PDCD10	0.690	+	2.82E-03	3.17E-03
204025_PM_s_at	programmed cell death 2	9774	PDCD2	0.756	+	2.15E-03	2.04E-03
224467_PM_s_at	programmed cell death 2-like	11112	PDCD2L	0.436	+	4.97E-03	1.96E-03
231213_PM_at	phosphodiesterase 1A, calmodulin-dependent	57695	PDE1A	0.735	+	1.39E-02	2.57E-02
204491_PM_at	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	3910	PDE4D	0.459	+	2.29E-02	1.29E-02
213388_PM_at	phosphodiesterase 4D interacting protein	9655	PDE4DIP	0.490	+	2.40E-02	4.02E-02
214099_PM_s_at	phosphodiesterase 4D interacting protein	1314	PDE4DIP	0.585	+	2.67E-02	2.25E-02
227088_PM_at	phosphodiesterase 5A, cGMP-specific	55233	PDE5A	0.307	+	5.91E-03	3.62E-02
223358_PM_s_at	phosphodiesterase 7A	90806	PDE7A	0.313	+	1.55E-02	4.20E-02
230109_PM_at	phosphodiesterase 7B	2043	PDE7B	0.271	+	5.26E-03	2.13E-02
212522_PM_at	phosphodiesterase 8A	9801	PDE8A	0.307	+	2.90E-02	8.62E-03
218718_PM_at	platelet derived growth factor C	129881	PDGFC	0.519	+	7.16E-03	2.47E-02
203131_PM_at	platelet-derived growth factor receptor, alpha polypeptide	170622	PDGFRA	0.572	+	1.50E-02	1.19E-02
205226_PM_at	platelet-derived growth factor receptor-like	7188	PDGFRL	0.310	+	4.70E-03	8.43E-03
211023_PM_at	pyruvate dehydrogenase (lipoamide) beta	22807	PDHB	0.380	+	4.36E-03	1.02E-02
203067_PM_at	pyruvate dehydrogenase complex, component X	4638	PDHX	0.570	+	2.94E-02	4.51E-02
208638_PM_at	protein disulfide isomerase family A, member 6	23369	PDIA6	0.313	+	3.30E-02	4.87E-02
226452_PM_at	pyruvate dehydrogenase kinase, isozyme 1	5062	PDK1	0.325	+	1.36E-02	8.46E-03
224904_PM_at	pyruvate dehydrogenase phosphatase regulatory subunit	6198	PDPR	0.304	+	4.96E-03	7.77E-03
212140_PM_at	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	5500	PDS5A	0.588	+	3.04E-02	2.21E-02
204742_PM_s_at	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	10907	PDS5B	0.432	+	1.08E-02	1.12E-02
220865_PM_s_at	prenyl (decaprenyl) diphosphate synthase, subunit 1	25906	PDSS1	0.844	+	7.61E-03	7.99E-03
219307_PM_at	prenyl (decaprenyl) diphosphate synthase, subunit 2	6659	PDSS2	0.434	+	1.05E-03	6.91E-03

220595_PM_at	PDZ domain containing ring finger 4	8504	PDZRN4	0.426	+	2.69E-02	3.38E-02
208982_PM_at	platelet/endothelial cell adhesion molecule	57117	PECAM1	0.473	+	9.31E-03	2.98E-02
209242_PM_at	paternally expressed 3	29919	PEG3	0.439	+	2.30E-03	5.71E-04
232304_PM_at	Pellino homolog 1 (Drosophila)	91408	PELI1	0.808	+	3.14E-02	2.40E-02
218472_PM_s_at	pelota homolog (Drosophila)	64710	PELO	0.349	+	2.70E-02	4.30E-02
205251_PM_at	period homolog 2 (Drosophila)	9857	PER2	0.458	+	2.47E-02	2.33E-02
222392_PM_x_at	PERP, TP53 apoptosis effector	64795	PERP	0.642	+	1.82E-02	3.37E-02
228541_PM_x_at	PERP, TP53 apoptosis effector	84912	PERP	0.294	+	4.52E-02	4.54E-02
201707_PM_at	peroxisomal biogenesis factor 19	6595	PEX19	0.488	+	9.74E-03	2.26E-02
203970_PM_s_at	peroxisomal biogenesis factor 3	5538	PEX3	0.436	+	1.87E-02	2.70E-02
205362_PM_s_at	prefoldin subunit 4	10329	PFDN4	0.300	+	2.81E-03	1.31E-02
205361_PM_s_at	prefoldin subunit 4	11326	PFDN4	0.518	+	1.52E-02	4.25E-03
242048_PM_at	prefoldin subunit 6	---	PFDN6	0.275	+	2.01E-02	3.66E-02
226733_PM_at	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	10116	PFKFB2	0.721	+	1.32E-02	1.17E-02
239725_PM_at	post-GPI attachment to proteins 1	---	PGAP1	0.467	+	3.00E-03	2.28E-03
220576_PM_at	post-GPI attachment to proteins 1	2730	PGAP1	0.414	+	1.24E-02	3.19E-02
200738_PM_s_at	phosphoglycerate kinase 1	4050	PGK1	0.273	+	5.00E-02	4.28E-02
225367_PM_at	phosphoglucomutase 2	58512	PGM2	0.472	+	4.59E-03	2.52E-02
229256_PM_at	phosphoglucomutase 2-like 1	23161	PGM2L1	0.446	+	5.72E-03	6.63E-03
210041_PM_s_at	phosphoglucomutase 3	122786	PGM3	0.467	+	8.78E-03	2.93E-03
227949_PM_at	phosphatase and actin regulator 3	7528	PHACTR3	0.444	+	1.98E-02	1.18E-02
225958_PM_at	polyhomeotic homolog 1 (Drosophila)	---	PHC1	0.559	+	2.89E-02	4.57E-02
226508_PM_at	polyhomeotic homolog 3 (Drosophila)	201254	PHC3	0.666	+	4.43E-03	1.46E-03
225048_PM_at	PHD finger protein 10	254170	PHF10	0.508	+	1.65E-02	1.64E-03
221816_PM_s_at	PHD finger protein 11	5495	PHF11	0.462	+	1.83E-02	1.08E-02
225816_PM_at	PHD finger protein 17	374408	PHF17	0.502	+	1.26E-02	1.01E-02
217954_PM_s_at	PHD finger protein 3	84295	PHF3	0.420	+	1.53E-02	1.16E-02
225501_PM_at	PHD finger protein 6	129450	PHF6	0.386	+	4.88E-02	3.33E-02
213074_PM_at	pleckstrin homology domain interacting protein	9283	PHIP	0.604	+	2.03E-02	4.98E-03
229876_PM_at	phosphorylase kinase, alpha 1 (muscle)	92	PHKA1	0.935	+	3.32E-03	4.28E-03
213407_PM_at	PH domain and leucine rich repeat protein phosphatase 2	6404	PHLPP2	0.635	+	9.59E-03	2.08E-02
230434_PM_at	phosphatase, orphan 2	258010	PHOSPHO2	0.775	+	2.22E-03	2.10E-03

217863_PM_at	protein inhibitor of activated STAT, 1	143888	PIAS1	0.515	+	1.20E-02	1.08E-02
213239_PM_at	progesterone immunomodulatory binding factor 1	23741	PIBF1	0.358	+	2.53E-03	1.00E-02
212511_PM_at	phosphatidylinositol binding clathrin assembly protein	25842	PICALM	1.083	+	2.69E-02	2.67E-02
205452_PM_at	phosphatidylinositol glycan anchor biosynthesis, class B	10234	PIGB	0.802	+	1.55E-03	4.10E-03
202846_PM_s_at	phosphatidylinositol glycan anchor biosynthesis, class C	55591	PIGC	0.696	+	5.76E-03	1.05E-02
205077_PM_s_at	phosphatidylinositol glycan anchor biosynthesis, class F	10479	PIGF	0.696	+	9.42E-04	4.42E-04
209707_PM_at	phosphatidylinositol glycan anchor biosynthesis, class K	51520	PIGK	0.558	+	1.19E-02	1.40E-02
227639_PM_at	phosphatidylinositol glycan anchor biosynthesis, class K	51187	PIGK	0.739	+	2.01E-02	1.13E-02
1558292_PM_s_at	phosphatidylinositol glycan anchor biosynthesis, class W	9637	PIGW	0.638	+	2.33E-04	2.40E-04
1552291_PM_at	phosphatidylinositol glycan anchor biosynthesis, class X	3716	PIGX	0.424	+	3.38E-02	3.76E-02
224660_PM_at	phosphatidylinositol glycan anchor biosynthesis, class Y	80314	PIGY	0.335	+	2.29E-02	4.05E-02
220041_PM_at	phosphatidylinositol glycan anchor biosynthesis, class Z	6990	PIGZ	0.327	+	9.43E-03	3.97E-02
213070_PM_at	phosphoinositide-3-kinase, class 2, alpha polypeptide	2980	PIK3C2A	0.709	+	6.43E-03	8.23E-03
212688_PM_at	phosphoinositide-3-kinase, catalytic, beta polypeptide	4900	PIK3CB	0.573	+	3.22E-02	3.63E-02
203879_PM_at	phosphoinositide-3-kinase, catalytic, delta polypeptide	813	PIK3CD	0.570	+	9.62E-03	1.98E-02
212740_PM_at	phosphoinositide-3-kinase, regulatory subunit 4	8732	PIK3R4	0.322	+	4.74E-02	2.86E-02
214224_PM_s_at	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)	55966	PIN4	0.603	+	5.02E-03	8.19E-03
204571_PM_x_at	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)	10982	PIN4	0.543	+	1.07E-02	2.84E-02
207469_PM_s_at	pirin (iron-binding nuclear protein)	23029	PIR	0.359	+	2.29E-02	3.01E-02
202522_PM_at	phosphatidylinositol transfer protein, beta	51389	PITPNB	0.500	+	2.76E-02	1.02E-02
229414_PM_at	phosphatidylinositol transfer protein, cytoplasmic 1	134147	PITPNC1	0.784	+	2.68E-03	1.34E-02
214868_PM_at	piwi-like 1 (Drosophila)	79887	PIWIL1	0.300	+	4.49E-03	1.06E-02
226864_PM_at	Protein kinase (cAMP-dependent, catalytic) inhibitor alpha	23033	PKIA	0.545	+	2.26E-02	1.28E-02
223551_PM_at	protein kinase (cAMP-dependent, catalytic) inhibitor beta	7468	PKIB	0.576	+	8.31E-03	2.49E-02
214874_PM_at	plakophilin 4	79735	PKP4	0.767	+	1.04E-02	1.41E-02
224751_PM_at	PL-5283 protein	79960	PL-5283	0.557	+	1.29E-02	2.08E-02
224752_PM_at	PL-5283 protein	259282	PL-5283	0.431	+	4.39E-02	2.49E-02
215870_PM_s_at	phospholipase A2, group V	54737	PLA2G5	0.458	+	3.20E-02	9.81E-03
244374_PM_at	placenta-specific 2 (non-protein coding)	---	PLAC2	0.318	+	3.48E-03	2.29E-03

229385_PM_s_at	placenta-specific 2 (non-protein coding)	85439	PLAC2	0.329	+	2.08E-02	4.73E-02
205372_PM_at	pleiomorphic adenoma gene 1	9949	PLAG1	0.274	+	2.63E-02	1.06E-02
201860_PM_s_at	plasminogen activator, tissue	10605 /// 645139	PLAT	0.499	+	2.81E-02	1.13E-02
218454_PM_at	phospholipase B domain containing 1	118491	PLBD1	0.889	+	2.67E-02	3.51E-02
202789_PM_at	phospholipase C, gamma 1	159090	PLCG1	0.341	+	4.51E-04	6.39E-03
204613_PM_at	phospholipase C, gamma 2 (phosphatidylinositol-specific)	27336	PLCG2	0.407	+	3.60E-02	3.82E-02
214745_PM_at	phospholipase C, eta 1	51082	PLCH1	0.672	+	1.73E-02	6.25E-04
213309_PM_at	phospholipase C-like 2	23299	PLCL2	0.689	+	2.28E-02	7.77E-03
224892_PM_at	pallidin homolog (mouse)	147184	PLDN	0.486	+	1.81E-02	1.58E-02
223370_PM_at	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 3	4869	PLEKHA3	0.570	+	2.45E-03	9.19E-03
220952_PM_s_at	pleckstrin homology domain containing, family A member 5	23768	PLEKHA5	0.569	+	1.85E-02	1.32E-02
201410_PM_at	pleckstrin homology domain containing, family B (evectins) member 2	2902	PLEKHB2	0.410	+	1.32E-02	1.98E-02
218640_PM_s_at	pleckstrin homology domain containing, family F (with FYVE domain) member 2	146956	PLEKHF2	0.351	+	2.87E-03	1.83E-02
227148_PM_at	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2	50628	PLEKHH2	0.297	+	1.02E-02	1.52E-02
200827_PM_at	procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	118	PLOD1	0.311	+	3.27E-03	8.47E-03
213241_PM_at	plexin C1	51433	PLXNC1	1.041	+	3.12E-02	1.87E-02
225421_PM_at	peptidase M20 domain containing 2	140700	PM20D2	0.438	+	8.95E-03	2.76E-02
201682_PM_at	peptidase (mitochondrial processing) beta	23543	PMPCB	0.353	+	3.85E-02	4.58E-02
213677_PM_s_at	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	9522	PMS1	1.093	+	2.55E-03	2.08E-03
216039_PM_at	postmeiotic segregation increased 2-like 5-like	83444	PMS2L5	0.713	+	2.56E-02	9.42E-03
212037_PM_at	pinin, desmosome associated protein	23022	PNN	0.492	+	2.70E-02	1.77E-02
1567214_PM_a_at	pinin, desmosome associated protein	26019	PNN	0.304	+	3.29E-02	1.02E-02
225291_PM_at	polyribonucleotide nucleotidyltransferase 1	90161	PNPT1	0.694	+	2.46E-02	2.51E-02
209578_PM_s_at	protein O-fucosyltransferase 2	56894	POFUT2	0.420	+	5.48E-03	2.04E-02
214226_PM_at	polyserase 3	771	POL3S	0.378	+	3.24E-02	3.34E-02
204835_PM_at	polymerase (DNA directed), alpha 1, catalytic subunit	9830	POLA1	0.340	+	4.16E-03	2.16E-03
203616_PM_at	polymerase (DNA directed), beta	253982	POLB	0.563	+	5.92E-04	1.65E-03

217806_PM_s_at	polymerase (DNA-directed), delta interacting protein 2	221037	POLDIP2	0.300	+	2.87E-02	3.04E-02
203366_PM_at	polymerase (DNA directed), gamma	55959	POLG	0.306	+	5.47E-03	8.44E-03
219317_PM_at	polymerase (DNA directed) iota	7265	POLI	0.602	+	4.57E-02	2.17E-02
218258_PM_at	polymerase (RNA) I polypeptide D, 16kDa	112609	POLR1D	0.713	+	1.21E-03	2.43E-03
231041_PM_at	polymerase (RNA) I polypeptide E, 53kDa	3767	POLR1E	0.277	+	4.56E-02	2.77E-02
201803_PM_at	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa	6125	POLR2B	0.353	+	3.58E-02	1.15E-02
1555837_PM_s_at	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa	3295	POLR2B	0.301	+	4.60E-02	4.74E-02
214263_PM_x_at	polymerase (RNA) II (DNA directed) polypeptide C, 33kDa	49855	POLR2C	0.533	+	1.63E-02	7.24E-03
209511_PM_at	polymerase (RNA) II (DNA directed) polypeptide F	9406	POLR2F	0.359	+	5.04E-03	1.89E-02
202306_PM_at	polymerase (RNA) II (DNA directed) polypeptide G	51566	POLR2G	0.496	+	8.01E-03	1.68E-03
202635_PM_s_at	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa	2661	POLR2K	0.377	+	1.98E-03	5.43E-03
202634_PM_at	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa	84991	POLR2K	0.507	+	1.88E-02	2.71E-02
211730_PM_s_at	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa	11329	POLR2L	0.274	+	4.29E-02	4.30E-02
227872_PM_at	polymerase (RNA) III (DNA directed) polypeptide A, 155kDa	54467	POLR3A	0.265	+	3.07E-02	1.88E-02
209382_PM_at	polymerase (RNA) III (DNA directed) polypeptide C (62kD)	58508	POLR3C	0.635	+	4.53E-02	4.76E-02
222490_PM_at	polymerase (RNA) III (DNA directed) polypeptide E (80kD)	23076	POLR3E	0.633	+	2.70E-02	3.11E-02
223269_PM_at	polymerase (RNA) III (DNA directed) polypeptide G (32kD)-like	79924	POLR3GL	0.356	+	1.56E-02	3.94E-02
202466_PM_at	polymerase (DNA directed) sigma	29803	POLS	0.481	+	1.21E-02	3.97E-03
217769_PM_s_at	proteasome maturation protein	10413	POMP	0.543	+	1.39E-03	2.71E-03
220632_PM_s_at	protein-O-mannosyltransferase 2	9836	POMT2	0.420	+	2.73E-03	1.80E-02
201876_PM_at	paraoxonase 2	6535	PON2	0.647	+	1.78E-03	5.89E-03
202868_PM_s_at	processing of precursor 4, ribonuclease P/MRP subunit (S. cerevisiae)	55904	POP4	0.417	+	2.96E-02	1.13E-02
204839_PM_at	processing of precursor 5, ribonuclease P/MRP subunit (S. cerevisiae)	64976	POP5	0.587	+	7.13E-03	6.40E-03
227254_PM_at	POU class 2 homeobox 1	64418	POU2F1	0.495	+	3.62E-02	3.43E-02
242455_PM_at	POU class 3 homeobox 2	---	POU3F2	0.433	+	3.23E-02	1.28E-02
217848_PM_s_at	pyrophosphatase (inorganic) 1	387882	PPA1	0.459	+	3.37E-03	3.75E-03
220741_PM_s_at	pyrophosphatase (inorganic) 2	4199	PPA2	0.619	+	1.08E-03	5.37E-03
208044_PM_s_at	peroxisome proliferator-activated receptor delta	8930	PPARD	0.546	+	1.14E-03	1.29E-03

37152_PM_at	peroxisome proliferator-activated receptor delta	---	PPARD	0.667	+	7.34E-03	1.37E-02
219195_PM_at	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha	10577	PPARGC1A	0.523	+	2.08E-02	2.34E-02
235833_PM_at	Phosphoribosyl pyrophosphate amidotransferase	64895	PPAT	0.306	+	5.21E-03	1.21E-02
218341_PM_at	phosphopantothenoylcysteine synthetase	29796	PPCS	0.339	+	6.04E-03	1.64E-02
202066_PM_at	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1	84271	PPFIA1	0.434	+	3.64E-02	3.81E-02
226336_PM_at	peptidylprolyl isomerase A (cyclophilin A)	5502	PPIA	0.323	+	8.48E-03	2.63E-02
204228_PM_at	peptidylprolyl isomerase H (cyclophilin H)	9097	PPIH	0.540	+	2.43E-03	8.79E-03
222500_PM_at	peptidylprolyl isomerase (cyclophilin)-like 1	10484	PPIL1	0.410	+	1.39E-02	1.91E-02
224364_PM_s_at	peptidylprolyl isomerase (cyclophilin)-like 3	27327	PPIL3	0.561	+	3.05E-03	5.18E-03
227728_PM_at	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	51241	PPM1A	0.653	+	6.78E-03	3.31E-03
229027_PM_at	protein phosphatase 1A (formerly 2C), magnesium-dependent, alpha isoform	129607	PPM1A	0.427	+	1.60E-02	4.51E-02
213225_PM_at	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform	9545	PPM1B	0.762	+	2.97E-02	4.42E-02
209296_PM_at	protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform	3157	PPM1B	0.421	+	3.50E-02	7.46E-04
37384_PM_at	protein phosphatase 1F (PP2C domain containing)	---	PPM1F	0.362	+	9.74E-03	1.51E-02
201408_PM_at	protein phosphatase 1, catalytic subunit, beta isoform	8031	PPP1CB	0.385	+	4.86E-03	1.97E-02
201407_PM_s_at	protein phosphatase 1, catalytic subunit, beta isoform	10395	PPP1CB	0.436	+	6.78E-03	3.41E-03
201603_PM_at	protein phosphatase 1, regulatory (inhibitor) subunit 12A	10580	PPP1R12A	0.333	+	4.36E-02	2.68E-02
41577_PM_at	protein phosphatase 1, regulatory (inhibitor) subunit 16B	387978	PPP1R16B	0.433	+	4.07E-02	1.38E-02
235129_PM_at	protein phosphatase 1, regulatory (inhibitor) subunit 1A	---	PPP1R1A	0.273	+	3.13E-02	3.29E-02
202165_PM_at	protein phosphatase 1, regulatory (inhibitor) subunit 2	387522 /// 7335	PPP1R2	0.349	+	1.05E-02	1.68E-02
204554_PM_at	protein phosphatase 1, regulatory (inhibitor) subunit 3D	9318	PPP1R3D	0.270	+	4.41E-02	1.86E-02
228494_PM_at	protein phosphatase 1, regulatory (inhibitor) subunit 9A	6558	PPP1R9A	0.471	+	3.16E-03	3.07E-03
202883_PM_s_at	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	55967	PPP2R1B	0.610	+	5.51E-04	2.02E-03
222351_PM_at	protein phosphatase 2 (formerly 2A), regulatory subunit A, beta isoform	9522	PPP2R1B	0.282	+	3.00E-02	4.09E-02

218852_PM_at	protein phosphatase 2 (formerly 2A), regulatory subunit B'', gamma	139231	PPP2R3C	0.650	+	5.44E-03	2.20E-03
202187_PM_s_at	protein phosphatase 2, regulatory subunit B', alpha isoform	80036	PPP2R5A	0.480	+	4.28E-02	1.51E-02
201594_PM_s_at	protein phosphatase 4, regulatory subunit 1	8514	PPP4R1	0.623	+	2.17E-02	8.02E-03
233002_PM_at	protein phosphatase 4, regulatory subunit 4	124540	PPP4R4	0.995	+	3.26E-02	2.10E-02
225429_PM_at	protein phosphatase 6, catalytic subunit	116443	PPP6C	0.345	+	3.65E-02	2.91E-02
212371_PM_at	PPPDE peptidase domain containing 1	23484	PPPDE1	0.583	+	3.27E-02	3.65E-02
200975_PM_at	palmitoyl-protein thioesterase 1	7341	PPT1	0.345	+	4.27E-02	1.47E-02
213483_PM_at	peptidylprolyl isomerase domain and WD repeat containing 1	4580	PPWD1	0.414	+	2.81E-03	9.46E-03
201494_PM_at	prolylcarboxypeptidase (angiotensinase C)	8573	PRCP	0.273	+	3.06E-02	4.39E-02
203057_PM_s_at	PR domain containing 2, with ZNF domain	220002	PRDM2	0.427	+	3.49E-02	1.75E-02
218329_PM_at	PR domain containing 4	59084	PRDM4	0.370	+	6.42E-03	2.82E-02
201923_PM_at	peroxiredoxin 4	727927 /// 9659	PRDX4	0.499	+	5.79E-03	6.16E-03
228224_PM_at	proline/arginine-rich end leucine-rich repeat protein	10772	PRELP	0.385	+	9.70E-03	2.39E-02
218233_PM_s_at	prickle homolog 4 (Drosophila) /// translocase of outer mitochondrial membrane 6 homolog (yeast)	201266	PRICKLE4 /// TOMM6	0.282	+	2.32E-02	2.03E-02
205053_PM_at	primase, DNA, polypeptide 1 (49kDa)	1998	PRIM1	0.447	+	9.21E-03	3.37E-02
225985_PM_at	protein kinase, AMP-activated, alpha 1 catalytic subunit	8724	PRKAA1	0.320	+	1.20E-02	4.81E-02
225011_PM_at	Protein kinase, cAMP-dependent, regulatory, type II, alpha	338657	PRKAR2A	0.647	+	4.19E-04	1.19E-03
203680_PM_at	protein kinase, cAMP-dependent, regulatory, type II, beta	23261	PRKAR2B	0.435	+	2.02E-02	1.23E-02
213010_PM_at	protein kinase C, delta binding protein	8382	PRKCDBP	0.275	+	5.47E-03	2.28E-02
218764_PM_at	protein kinase C, eta	83659	PRKCH	0.418	+	2.18E-02	1.23E-02
205880_PM_at	protein kinase D1	8527	PRKD1	0.749	+	1.55E-02	1.97E-02
228396_PM_at	protein kinase, cGMP-dependent, type I	339745	PRKG1	1.395	+	2.95E-03	4.16E-03
209323_PM_at	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)	196403	PRKRIR	0.843	+	7.78E-03	8.00E-03
1564520_PM_s_at	protein arginine methyltransferase 5	1855	PRMT5	0.277	+	1.78E-02	2.95E-02
207808_PM_s_at	protein S (alpha)	7337	PROS1	0.416	+	2.11E-02	1.63E-02
209384_PM_at	proline synthetase co-transcribed homolog (bacterial)	28977	PROSC	0.744	+	7.32E-04	5.18E-03
202251_PM_at	PRP3 pre-mRNA processing factor 3 homolog (S. cerevisiae)	1350	PRPF3	0.683	+	8.03E-03	9.32E-03
202127_PM_at	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	604	PRPF4B	0.504	+	3.54E-03	4.53E-03

202126_PM_at	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	2710	PRPF4B	0.517	+	2.34E-02	9.28E-03
209440_PM_at	phosphoribosyl pyrophosphate synthetase 1	30001	PRPS1	0.285	+	3.15E-02	1.20E-02
220014_PM_at	proline rich 16	8439	PRR16	0.946	+	1.69E-02	1.36E-02
224643_PM_at	proline-rich coiled-coil 1	131118	PRRC1	0.396	+	9.82E-03	1.67E-02
222803_PM_at	phosphoribosyl transferase domain containing 1	51710	PRTFDC1	0.319	+	3.36E-02	1.31E-02
212805_PM_at	prune homolog 2 (Drosophila)	9738	PRUNE2	0.383	+	1.21E-02	1.69E-02
211746_PM_x_at	proteasome (prosome, macropain) subunit, alpha type, 1	64478	PSMA1	0.348	+	1.36E-02	3.35E-02
201317_PM_s_at	proteasome (prosome, macropain) subunit, alpha type, 2	814	PSMA2	0.321	+	1.77E-02	1.23E-02
201316_PM_at	proteasome (prosome, macropain) subunit, alpha type, 2	47	PSMA2	0.341	+	3.50E-02	1.57E-02
201532_PM_at	proteasome (prosome, macropain) subunit, alpha type, 3	5265	PSMA3	0.302	+	3.11E-02	4.18E-02
201274_PM_at	proteasome (prosome, macropain) subunit, alpha type, 5	5238	PSMA5	0.525	+	2.85E-03	5.54E-03
208805_PM_at	proteasome (prosome, macropain) subunit, alpha type, 6	26225	PSMA6	0.274	+	3.10E-03	3.63E-03
214288_PM_s_at	proteasome (prosome, macropain) subunit, beta type, 1	64499 /// 7177	PSMB1	0.554	+	2.25E-04	5.84E-05
202244_PM_at	proteasome (prosome, macropain) subunit, beta type, 4	23390	PSMB4	0.495	+	4.89E-04	2.53E-03
208799_PM_at	proteasome (prosome, macropain) subunit, beta type, 5	10431	PSMB5	0.451	+	2.05E-03	1.01E-02
204279_PM_at	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)	9559	PSMB9	0.385	+	7.36E-03	1.71E-02
201068_PM_s_at	proteasome (prosome, macropain) 26S subunit, ATPase, 2	11170	PSMC2	0.407	+	2.70E-04	6.12E-04
201699_PM_at	proteasome (prosome, macropain) 26S subunit, ATPase, 6	8613	PSMC6	0.364	+	3.40E-03	2.07E-03
219485_PM_s_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	55186	PSMD10	0.395	+	7.88E-03	1.84E-02
202353_PM_s_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	100188893 /// 29964	PSMD12	0.673	+	6.75E-03	8.58E-03
212296_PM_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	10542	PSMD14	0.439	+	4.37E-04	5.24E-04
200882_PM_s_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	1993	PSMD4	0.462	+	1.25E-03	7.85E-03
203447_PM_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	113178	PSMD5	0.624	+	6.50E-04	1.60E-03
200814_PM_at	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	3382	PSME1	0.581	+	1.11E-02	2.58E-02
212222_PM_at	proteasome (prosome, macropain) activator subunit 4	7528	PSME4	0.763	+	1.49E-02	1.41E-02
218467_PM_at	proteasome (prosome, macropain) assembly chaperone 2	64067	PSMG2	0.449	+	2.03E-02	8.42E-03
228217_PM_s_at	proteasome (prosome, macropain) assembly chaperone 4	55500	PSMG4	0.624	+	9.50E-03	9.55E-03

218371_PM_s_at	paraspeckle component 1	129831	PSPC1	0.295	+	7.59E-03	4.02E-02
230129_PM_at	phosphoseryl-tRNA kinase	7473	PSTK	0.566	+	1.29E-03	4.57E-03
226110_PM_at	protein prenyltransferase alpha subunit repeat containing 1	4082	PTAR1	0.414	+	2.10E-02	3.19E-02
209815_PM_at	patched homolog 1 (Drosophila)	57533	PTCH1	0.750	+	1.29E-02	3.58E-02
225363_PM_at	phosphatase and tensin homolog	148741	PTEN	0.382	+	3.61E-03	3.56E-03
213933_PM_at	prostaglandin E receptor 3 (subtype EP3)	23228	PTGER3	0.275	+	2.62E-02	4.26E-02
207388_PM_s_at	prostaglandin E synthase	9522	PTGES	0.284	+	3.17E-02	4.05E-02
200733_PM_s_at	protein tyrosine phosphatase type IVA, member 1	6660	PTP4A1	0.407	+	8.69E-03	2.46E-02
200732_PM_s_at	protein tyrosine phosphatase type IVA, member 1	10529	PTP4A1	0.464	+	1.55E-02	6.68E-03
208617_PM_s_at	protein tyrosine phosphatase type IVA, member 2	56928	PTP4A2	0.421	+	4.26E-03	1.57E-02
208615_PM_s_at	protein tyrosine phosphatase type IVA, member 2	744	PTP4A2	0.303	+	2.62E-02	4.04E-02
219654_PM_at	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member A	3054	PTPLA	0.348	+	1.23E-03	6.62E-03
223808_PM_s_at	protein tyrosine phosphatase, mitochondrial 1	84265	PTPMT1	0.417	+	2.30E-04	4.51E-04
212610_PM_at	protein tyrosine phosphatase, non-receptor type 11	23635	PTPN11	0.311	+	1.99E-02	2.20E-02
202006_PM_at	protein tyrosine phosphatase, non-receptor type 12	8539	PTPN12	0.664	+	2.16E-02	2.17E-02
204201_PM_s_at	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	6624	PTPN13	0.495	+	1.02E-03	1.37E-02
213136_PM_at	protein tyrosine phosphatase, non-receptor type 2	4616	PTPN2	1.061	+	1.91E-03	1.81E-04
207238_PM_s_at	protein tyrosine phosphatase, receptor type, C	25839	PTPRC	0.284	+	4.63E-02	4.41E-02
203329_PM_at	protein tyrosine phosphatase, receptor type, M	10804	PTPRM	0.531	+	1.76E-02	4.10E-02
204469_PM_at	protein tyrosine phosphatase, receptor-type, Z polypeptide 1	8897	PTPRZ1	0.418	+	7.75E-03	8.82E-03
218732_PM_at	peptidyl-tRNA hydrolase 2	55074	PTRH2	0.461	+	6.81E-03	1.10E-02
209694_PM_at	6-pyruvoyltetrahydropterin synthase	84100	PTS	0.616	+	4.12E-03	4.60E-03
203554_PM_x_at	pituitary tumor-transforming 1	816	PTTG1	0.424	+	5.63E-05	3.66E-05
200677_PM_at	pituitary tumor-transforming 1 interacting protein	8187	PTTG1IP	0.374	+	3.82E-02	2.01E-02
201166_PM_s_at	pumilio homolog 1 (Drosophila)	6119	PUM1	0.295	+	2.24E-02	2.69E-02
216221_PM_s_at	pumilio homolog 2 (Drosophila)	51185	PUM2	0.580	+	2.84E-02	2.71E-02
225120_PM_at	purine-rich element binding protein B	90693	PURB	0.353	+	1.36E-02	1.25E-03
235634_PM_at	purine-rich element binding protein G	55547	PURG	0.315	+	3.15E-02	3.02E-02
221025_PM_x_at	pseudouridylate synthase 7 homolog (S. cerevisiae)-like	9771	PUS7L	0.386	+	1.58E-03	2.66E-03
201607_PM_at	PWP1 homolog (S. cerevisiae)	23522	PWP1	0.269	+	3.59E-02	1.79E-02

226720_PM_at	PWWP domain containing 2A	23192	PWWP2A	0.662	+	2.81E-03	1.47E-02
228336_PM_at	PWWP domain containing 2A	1656	PWWP2A	0.907	+	3.22E-02	3.04E-02
228225_PM_at	peroxisomal membrane protein 3, 35kDa	5728	PXMP3	0.280	+	3.20E-02	4.94E-02
217846_PM_at	glutaminyl-tRNA synthetase	9135	QARS	0.330	+	1.03E-02	2.55E-02
1556205_PM_at	Quinoid dihydropteridine reductase	3654	QDPR	0.267	+	1.51E-02	2.98E-02
212265_PM_at	quaking homolog, KH domain RNA binding (mouse)	25800	QKI	0.360	+	1.83E-02	1.82E-03
226265_PM_at	glutamine and serine rich 1	88	QSER1	0.699	+	1.28E-02	3.86E-02
35156_PM_at	R3H domain and coiled-coil containing 1	---	R3HCC1	0.368	+	1.80E-04	1.32E-03
202754_PM_at	R3H domain containing 1	26512	R3HDM1	0.423	+	3.71E-02	2.14E-02
200864_PM_s_at	RAB11A, member RAS oncogene family	9478	RAB11A	0.427	+	4.17E-02	2.51E-02
225177_PM_at	RAB11 family interacting protein 1 (class I)	57619	RAB11FIP1	0.282	+	1.69E-02	4.66E-02
203884_PM_s_at	RAB11 family interacting protein 2 (class I)	9689	RAB11FIP2	0.730	+	1.62E-02	2.22E-02
223336_PM_s_at	RAB18, member RAS oncogene family	1290	RAB18	0.348	+	4.75E-02	4.05E-02
213440_PM_at	RAB1A, member RAS oncogene family	6772	RAB1A	0.440	+	6.75E-03	8.27E-03
226268_PM_at	RAB21, member RAS oncogene family	88	RAB21	0.354	+	4.75E-02	3.90E-02
213405_PM_at	RAB22A, member RAS oncogene family	5889	RAB22A	0.453	+	1.09E-02	1.53E-02
225074_PM_at	RAB2B, member RAS oncogene family	56849	RAB2B	0.556	+	1.84E-03	4.10E-03
221014_PM_s_at	RAB33B, member RAS oncogene family	2049	RAB33B	0.334	+	1.39E-02	4.28E-02
230075_PM_at	RAB39B, member RAS oncogene family	4150	RAB39B	0.726	+	1.39E-02	1.45E-02
202372_PM_at	RAB3 GTPase activating protein subunit 2 (non-catalytic)	54539	RAB3GAP2	0.854	+	3.00E-02	8.32E-03
231399_PM_at	RAB3A interacting protein (rabin3)	---	RAB3IP	0.624	+	2.82E-02	2.16E-02
223471_PM_at	RAB3A interacting protein (rabin3)	55236	RAB3IP	0.396	+	2.85E-02	2.02E-02
226633_PM_at	RAB8B, member RAS oncogene family	27332	RAB8B	0.404	+	1.06E-02	1.41E-02
221808_PM_at	RAB9A, member RAS oncogene family	23272	RAB9A	0.457	+	3.10E-03	7.11E-03
222918_PM_at	RAB9B, member RAS oncogene family	10492	RAB9B	0.508	+	4.24E-03	7.18E-03
225092_PM_at	rabaptin, RAB GTPase binding effector protein 1	4086	RABEP1	0.348	+	1.15E-02	5.50E-04
74694_PM_s_at	rabaptin, RAB GTPase binding effector protein 2	---	RABEP2	0.585	+	1.09E-02	1.30E-03
203150_PM_at	Rab9 effector protein with kelch motifs	414777	RABEPK	0.611	+	3.65E-03	1.35E-02
213313_PM_at	RAB GTPase activating protein 1	9126	RABGAP1	0.358	+	3.06E-02	4.01E-02
203020_PM_at	RAB GTPase activating protein 1-like	80333	RABGAP1L	0.341	+	3.09E-02	3.11E-02
209181_PM_s_at	Rab geranylgeranyltransferase, beta subunit	56996	RABGGTB	0.606	+	2.24E-04	1.21E-03
213970_PM_at	RAB, member of RAS oncogene family-like 3	10799	RABL3	0.593	+	1.74E-03	2.20E-02

226089_PM_at	RAB, member of RAS oncogene family-like 3	9868	RABL3	0.493	+	3.39E-02	4.56E-02
213603_PM_s_at	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	23516	RAC2	0.273	+	5.19E-03	9.20E-03
222077_PM_s_at	Rac GTPase activating protein 1	23389	RACGAP1	0.301	+	1.26E-02	2.51E-02
228535_PM_at	RAD1 homolog (S. pombe)	157638	RAD1	0.632	+	5.27E-03	1.51E-02
207405_PM_s_at	RAD17 homolog (S. pombe)	200734	RAD17	0.512	+	6.76E-03	8.08E-03
201046_PM_s_at	RAD23 homolog A (S. cerevisiae)	10735	RAD23A	0.383	+	2.95E-03	2.00E-02
209849_PM_s_at	RAD51 homolog C (S. cerevisiae)	92912	RAD51C	0.404	+	1.81E-02	4.19E-02
224880_PM_at	v-ral simian leukemia viral oncogene homolog A (ras related)	153241	RALA	0.457	+	1.07E-02	8.23E-03
204199_PM_at	Ral GEF with PH domain and SH3 binding motif 1	3916	RALGPS1	0.574	+	1.69E-02	1.82E-02
201712_PM_s_at	RAN binding protein 2	8888	RANBP2	0.483	+	1.43E-02	3.09E-03
201713_PM_s_at	RAN binding protein 2	23175	RANBP2	0.269	+	2.30E-02	2.14E-02
202640_PM_s_at	RAN binding protein 3	30819	RANBP3	0.352	+	2.17E-02	2.60E-02
218526_PM_s_at	RAN guanine nucleotide release factor	201456	RANGRF	0.565	+	1.44E-03	1.55E-02
202362_PM_at	RAP1A, member of RAS oncogene family	54704	RAP1A	0.653	+	5.61E-03	2.09E-03
213923_PM_at	RAP2B, member of RAS oncogene family	57209	RAP2B	0.506	+	6.50E-03	7.57E-03
218668_PM_s_at	RAP2C, member of RAS oncogene family	25999	RAP2C	0.884	+	1.28E-02	1.90E-02
218669_PM_at	RAP2C, member of RAS oncogene family	83852	RAP2C	0.616	+	1.75E-02	2.98E-02
203097_PM_s_at	Rap guanine nucleotide exchange factor (GEF) 2	2035	RAPGEF2	0.330	+	2.00E-02	3.80E-02
230078_PM_at	Rap guanine nucleotide exchange factor (GEF) 6	11016	RAPGEF6	0.417	+	2.27E-02	3.06E-02
225189_PM_s_at	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	255758	RAPH1	0.294	+	3.10E-02	6.06E-03
201330_PM_at	arginyl-tRNA synthetase	5298	RARS	0.265	+	2.30E-02	3.05E-02
202677_PM_at	RAS p21 protein activator (GTPase activating protein) 1	29980 /// 539	RASA1	0.707	+	1.33E-02	1.30E-02
210621_PM_s_at	RAS p21 protein activator (GTPase activating protein) 1	94101	RASA1	0.392	+	2.04E-02	4.28E-02
1553986_PM_at	RAS and EF-hand domain containing	11325	RASEF	0.299	+	6.94E-03	6.81E-04
230563_PM_at	RasGEF domain family, member 1A	54542	RASGEF1A	0.369	+	1.74E-02	2.90E-02
205801_PM_s_at	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	2186	RASGRP3	0.433	+	9.14E-03	1.33E-02
225946_PM_at	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	---	RASSF8	0.725	+	1.62E-02	1.82E-02
203132_PM_at	retinoblastoma 1	135112	RB1	0.724	+	3.68E-02	3.27E-02
202034_PM_x_at	RB1-inducible coiled-coil 1	598	RB1CC1	0.905	+	3.24E-02	3.96E-03

225396_PM_at	retinoblastoma binding protein 4	90580	RBBP4	0.567	+	1.85E-02	1.64E-02
212781_PM_at	retinoblastoma binding protein 6	29966	RBBP6	0.460	+	1.38E-02	5.94E-03
232044_PM_at	retinoblastoma binding protein 6	144404	RBBP6	0.462	+	2.01E-02	4.33E-02
201092_PM_at	retinoblastoma binding protein 7	488	RBBP7	0.488	+	7.96E-03	7.09E-03
203344_PM_s_at	retinoblastoma binding protein 8	56987	RBBP8	0.737	+	5.56E-03	7.07E-03
57540_PM_at	ribokinase	---	RBKS	0.409	+	2.46E-02	2.22E-02
212168_PM_at	RNA binding motif protein 12	6844	RBM12	0.764	+	2.00E-02	1.13E-02
228455_PM_at	RNA binding motif protein 15	51361	RBM15	0.404	+	1.36E-03	9.30E-03
219286_PM_s_at	RNA binding motif protein 15	7832	RBM15	0.819	+	2.68E-02	1.92E-02
1555762_PM_s_at	RNA binding motif protein 15	5683	RBM15	0.818	+	3.46E-02	2.21E-02
221309_PM_at	RNA binding motif protein 17	9037	RBM17	0.334	+	1.05E-02	4.40E-02
224780_PM_at	RNA binding motif protein 17	2549	RBM17	0.429	+	1.80E-02	1.40E-02
226732_PM_at	RNA binding motif protein 33	23351	RBM33	0.282	+	1.67E-02	5.63E-03
1554095_PM_at	RNA binding motif protein 33	5879	RBM33	0.334	+	4.05E-02	2.15E-02
212591_PM_at	RNA binding motif protein 34	2332	RBM34	0.459	+	1.39E-02	3.04E-02
228578_PM_at	RNA binding motif protein 45	11228	RBM45	0.639	+	3.56E-03	2.54E-03
242516_PM_x_at	RNA binding motif protein 46	---	RBM46	0.270	+	2.02E-02	3.79E-02
222443_PM_s_at	RNA binding motif protein 8A	23347	RBM8A	0.486	+	9.36E-04	1.08E-03
213852_PM_at	RNA binding motif protein 8A	22934	RBM8A	0.623	+	1.44E-02	3.77E-02
225269_PM_s_at	RNA binding motif, single stranded interacting protein 1	8239	RBMS1	0.761	+	9.05E-03	1.09E-02
204098_PM_at	RNA binding motif protein, X-linked 2	10969	RBMX2	0.430	+	2.17E-02	4.34E-02
211974_PM_x_at	recombination signal binding protein for immunoglobulin kappa J region	6612	RBPJ	0.299	+	2.67E-02	4.96E-02
218117_PM_at	ring-box 1	257218	RBX1	0.430	+	1.47E-02	3.92E-02
225893_PM_at	ring finger and CCCH-type zinc finger domains 1	64857	RC3H1	0.521	+	3.01E-02	4.03E-02
225813_PM_at	ring finger and CCCH-type zinc finger domains 2	10097	RC3H2	0.532	+	1.53E-02	2.53E-02
208370_PM_s_at	regulator of calcineurin 1	29	RCAN1	0.497	+	2.19E-02	9.84E-03
204759_PM_at	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	3251	RCBTB2	0.281	+	7.49E-03	3.89E-02
222605_PM_at	REST corepressor 3	26175	RCOR3	0.578	+	2.18E-02	3.37E-02
217776_PM_at	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	10413	RDH11	0.282	+	1.22E-02	6.11E-03

222203_PM_s_at	retinol dehydrogenase 14 (all-trans/9-cis/11-cis)	10213	RDH14	0.351	+	4.29E-03	4.33E-03
212397_PM_at	radixin	10682	RDX	0.756	+	2.94E-03	3.50E-03
244739_PM_at	radixin	---	RDX	0.765	+	4.40E-02	3.21E-02
212918_PM_at	RecQ protein-like (DNA helicase Q1-like)	10950	RECQL	0.408	+	1.02E-02	2.58E-02
204365_PM_s_at	receptor accessory protein 1	523	REEP1	0.362	+	3.25E-02	4.39E-02
226430_PM_at	RELT-like 1	5455	RELL1	0.775	+	1.55E-02	1.10E-02
210300_PM_at	RAS (RAD and GEM)-like GTP-binding 1	401466	REM1	0.333	+	8.89E-04	3.55E-03
219041_PM_s_at	replication initiator 1	4673	REPIN1	0.663	+	1.43E-02	1.90E-02
224366_PM_s_at	RALBP1 associated Eps domain containing 1	90231	REPS1	0.395	+	2.01E-02	2.85E-02
227425_PM_at	RALBP1 associated Eps domain containing 2	10023	REPS2	0.671	+	2.40E-03	2.90E-03
200940_PM_s_at	arginine-glutamic acid dipeptide (RE) repeats	6046	RERE	0.397	+	4.32E-02	3.27E-02
244745_PM_at	RAS-like, estrogen-regulated, growth inhibitor	---	RERG	0.309	+	6.84E-03	1.48E-02
208070_PM_s_at	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	10038	REV3L	0.744	+	9.52E-03	1.20E-02
218194_PM_at	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	114799	REXO2	0.620	+	8.54E-03	6.36E-03
203224_PM_at	riboflavin kinase	4731	RFK	0.341	+	6.42E-03	1.51E-02
223673_PM_at	regulatory factor X, 4 (influences HLA class II expression)	54936	RFX4	1.468	+	8.38E-03	1.10E-02
202963_PM_at	regulatory factor X, 5 (influences HLA class II expression)	53938	RFX5	0.713	+	3.68E-02	3.04E-02
222630_PM_at	regulatory factor X, 7	22941	RFX7	0.382	+	3.25E-02	3.30E-02
210751_PM_s_at	regucalcin (senescence marker protein-30)	221785	RGN	0.348	+	3.59E-03	8.51E-03
220334_PM_at	regulator of G-protein signaling 17	26275	RGS17	0.383	+	2.05E-02	1.11E-02
210138_PM_at	regulator of G-protein signaling 20	113802	RGS20	0.472	+	4.94E-03	1.44E-02
225202_PM_at	Rho-related BTB domain containing 3	414918	RHOBTB3	0.487	+	1.80E-03	1.08E-02
212120_PM_at	ras homolog gene family, member Q	6451	RHOQ	0.667	+	9.23E-03	1.17E-02
212122_PM_at	ras homolog gene family, member Q	5683	RHOQ	0.717	+	1.88E-02	4.08E-02
218323_PM_at	ras homolog gene family, member T1	643836	RHOT1	0.388	+	2.08E-02	6.05E-03
223168_PM_at	ras homolog gene family, member U	55270	RHOU	0.634	+	2.63E-02	2.19E-03
205414_PM_s_at	Rho-type GTPase-activating protein RICH2	9071	RICH2	0.412	+	1.97E-03	4.79E-03
226207_PM_at	Rab interacting lysosomal protein-like 1	6921	RILPL1	0.311	+	4.20E-02	1.24E-02
214811_PM_at	RIMS binding protein 2	8925	RIMBP2	0.456	+	3.83E-02	2.14E-02
226164_PM_x_at	Ribosomal modification protein rimK-like family member B	1277	RIMKLB	0.521	+	1.12E-02	2.51E-02
209684_PM_at	Ras and Rab interactor 2	9406	RIN2	0.511	+	2.82E-02	2.88E-02
218598_PM_at	RAD50 interactor 1	30010	RINT1	0.383	+	2.23E-02	2.33E-02

209545_PM_s_at	receptor-interacting serine-threonine kinase 2	83930	RIPK2	0.883	+	2.04E-02	2.71E-02
236771_PM_at	ripply2 homolog (zebrafish)	51631	RIPPLY2	0.344	+	1.12E-02	2.26E-02
204243_PM_at	rearranged L-myc fusion	5514	RLF	0.623	+	1.78E-02	1.91E-02
225416_PM_at	ring finger protein, LIM domain interacting	388695	RLIM	0.553	+	9.29E-03	1.80E-02
213397_PM_x_at	ribonuclease, Rnase A family, 4	4613	RNASE4	0.366	+	6.19E-03	2.47E-02
205158_PM_at	ribonuclease, Rnase A family, 4	1376	RNASE4	0.602	+	2.36E-02	2.79E-02
213566_PM_at	ribonuclease, Rnase A family, k6	1975	RNASE6	1.392	+	1.27E-02	1.16E-02
226453_PM_at	ribonuclease H2, subunit C	5175	RNASEH2C	0.316	+	1.76E-02	2.05E-03
218761_PM_at	ring finger protein 111	146177	RNF111	0.611	+	1.72E-02	6.77E-03
219263_PM_at	ring finger protein 128	1964	RNF128	0.373	+	1.36E-02	1.30E-02
204040_PM_at	ring finger protein 144A	378	RNF144A	0.671	+	2.28E-02	1.19E-02
239012_PM_at	Ring finger protein 144B	26207	RNF144B	0.277	+	1.24E-02	1.11E-02
223886_PM_s_at	ring finger protein 146	79780	RNF146	0.319	+	3.22E-02	1.69E-02
226739_PM_at	ring finger protein 169	140609	RNF169	0.841	+	2.67E-03	4.48E-03
223085_PM_at	ring finger protein 19A	51121	RNF19A	0.985	+	5.70E-03	1.15E-03
36564_PM_at	ring finger protein 19B	---	RNF19B	0.935	+	7.91E-03	4.79E-02
213038_PM_at	ring finger protein 19B	51276	RNF19B	0.453	+	1.35E-02	3.35E-02
222683_PM_at	ring finger protein 20	10924	RNF20	0.687	+	1.40E-02	2.09E-02
244591_PM_x_at	Ring finger protein 207	22836	RNF207	0.385	+	2.16E-02	1.01E-02
227065_PM_at	ring finger protein 216	9898	RNF216	0.348	+	3.60E-03	2.18E-03
219303_PM_at	ring finger protein 219	9898	RNF219	0.470	+	5.12E-04	4.70E-03
219035_PM_s_at	ring finger protein 34	23241	RNF34	0.414	+	8.62E-03	1.14E-02
218528_PM_s_at	ring finger protein 38	83700	RNF38	0.426	+	4.46E-02	1.70E-02
203160_PM_s_at	ring finger protein 8	221955	RNF8	0.317	+	2.60E-02	9.13E-03
221908_PM_at	ring finger protein, transmembrane 2	51560	RNFT2	0.592	+	2.48E-02	2.76E-02
204208_PM_at	RNA guanylyltransferase and 5’-phosphatase	11137	RNGTT	0.285	+	3.78E-02	3.85E-02
218301_PM_at	arginyl aminopeptidase (aminopeptidase B)-like 1	57570	RNPEPL1	0.357	+	5.90E-03	2.33E-02
202762_PM_at	Rho-associated, coiled-coil containing protein kinase 2	55291	ROCK2	0.438	+	1.29E-02	3.01E-03
224617_PM_at	ROD1 regulator of differentiation 1 (S. pombe)	83640	ROD1	0.667	+	1.19E-02	2.92E-02
226682_PM_at	RAR-related orphan receptor A	552889	RORA	0.543	+	1.48E-02	7.06E-03
219732_PM_at	plasticity related gene 3	8446	RP11-35N6.1	0.724	+	2.31E-03	9.43E-03

224835_PM_at	hypothetical protein KIAA1434	54332	RP5-1022P6.2	0.527	+	1.56E-02	2.49E-02
227035_PM_x_at	retinitis pigmentosa 9 pseudogene	998	RP9P	0.264	+	1.00E-02	1.72E-02
236675_PM_at	replication protein A1, 70kDa	---	RPA1	0.341	+	9.99E-03	2.11E-03
209507_PM_at	replication protein A3, 14kDa	54460	RPA3	0.613	+	8.21E-04	1.51E-03
228183_PM_s_at	RPA interacting protein	51560	RPAIN	0.415	+	1.60E-02	2.87E-02
216961_PM_s_at	RPA interacting protein	79365	RPAIN	0.340	+	1.66E-02	8.17E-03
222893_PM_s_at	RNA polymerase II associated protein 2	2892	RPAP2	0.272	+	1.06E-02	4.07E-02
212973_PM_at	ribose 5-phosphate isomerase A	6545	RPIA	0.595	+	9.77E-03	2.11E-02
200036_PM_s_at	ribosomal protein L10a	8536	RPL10A	0.299	+	1.67E-02	1.41E-02
200088_PM_x_at	ribosomal protein L12	10150	RPL12	0.334	+	6.94E-03	4.85E-03
214271_PM_x_at	ribosomal protein L12	2917	RPL12	0.331	+	2.05E-02	6.27E-03
212933_PM_x_at	ribosomal protein L13	1837	RPL13	0.315	+	3.25E-02	3.90E-02
200715_PM_x_at	ribosomal protein L13a	4707	RPL13A	0.477	+	5.22E-03	3.92E-03
213588_PM_x_at	ribosomal protein L14	23633	RPL14	0.401	+	2.00E-03	1.36E-03
200074_PM_s_at	ribosomal protein L14	5001	RPL14	0.398	+	6.79E-03	1.08E-02
214335_PM_at	ribosomal protein L18	5291	RPL18	0.534	+	1.41E-02	1.18E-02
225541_PM_at	ribosomal protein L22-like 1	54885	RPL22L1	1.157	+	9.59E-04	4.19E-03
203012_PM_x_at	ribosomal protein L23a	100302652 /// 10936 /// 51130	RPL23A	0.270	+	3.07E-03	2.20E-03
200013_PM_at	ribosomal protein L24	5698	RPL24	0.325	+	3.19E-02	2.44E-02
222229_PM_x_at	ribosomal protein L26	23231	RPL26	0.327	+	2.45E-02	8.26E-03
218830_PM_at	ribosomal protein L26-like 1	165215	RPL26L1	0.484	+	5.52E-03	1.54E-02
200025_PM_s_at	ribosomal protein L27	9443	RPL27	0.334	+	1.48E-02	2.10E-03
200062_PM_s_at	ribosomal protein L30	5336	RPL30	0.264	+	1.27E-02	1.19E-02
201406_PM_at	ribosomal protein L36a	4067	RPL36A	0.389	+	4.99E-03	1.88E-03
217256_PM_x_at	ribosomal protein L36a	84661	RPL36A	0.465	+	9.78E-03	7.00E-03
207585_PM_s_at	ribosomal protein L36a-like	23304	RPL36AL	0.417	+	1.51E-02	1.06E-02
213080_PM_x_at	ribosomal protein L5	5597	RPL5	0.352	+	2.04E-03	2.86E-03
217092_PM_x_at	ribosomal protein L7	53349	RPL7	0.366	+	8.12E-04	3.69E-03
224738_PM_x_at	ribosomal protein L7-like 1	164	RPL7L1	0.688	+	2.39E-02	2.82E-02
213427_PM_at	ribonuclease P/MRP 40kDa subunit	57862	RPP40	1.016	+	2.64E-03	1.50E-03

222559_PM_s_at	regulation of nuclear pre-mRNA domain containing 1A	56987	RPRD1A	0.398	+	3.49E-03	4.01E-03
225953_PM_at	regulation of nuclear pre-mRNA domain containing 1A	284669	RPRD1A	0.546	+	6.16E-03	1.70E-03
226527_PM_at	regulation of nuclear pre-mRNA domain containing 2	83604	RPRD2	0.412	+	2.71E-02	2.55E-02
226131_PM_s_at	ribosomal protein S16	9913	RPS16	0.375	+	1.69E-03	4.35E-03
200949_PM_x_at	ribosomal protein S20	54499	RPS20	0.354	+	3.86E-02	3.93E-02
214097_PM_at	ribosomal protein S21	23451	RPS21	0.409	+	1.93E-02	3.46E-02
217753_PM_s_at	ribosomal protein S26	57606	RPS26	0.441	+	1.59E-03	4.92E-03
218007_PM_s_at	ribosomal protein S27-like	113402	RPS27L	0.658	+	1.81E-03	9.63E-04
201094_PM_at	ribosomal protein S29	6713	RPS29	0.297	+	3.08E-02	4.11E-02
216342_PM_x_at	ribosomal protein S4, X-linked	29117	RPS4X	0.493	+	5.12E-03	1.72E-03
213347_PM_x_at	ribosomal protein S4, X-linked	333	RPS4X	0.400	+	1.02E-02	6.97E-03
204171_PM_at	ribosomal protein S6 kinase, 70kDa, polypeptide 1	10146	RPS6KB1	0.592	+	1.32E-02	1.08E-02
226660_PM_at	ribosomal protein S6 kinase, 70kDa, polypeptide 1	56112	RPS6KB1	0.523	+	2.55E-02	3.21E-02
218909_PM_at	ribosomal protein S6 kinase, 52kDa, polypeptide 1	64080	RPS6KC1	0.519	+	1.96E-02	2.45E-02
213941_PM_x_at	ribosomal protein S7	10413	RPS7	0.367	+	1.12E-02	7.60E-03
213179_PM_at	RCD1 required for cell differentiation1 homolog (S. pombe)	5594	RQCD1	0.466	+	2.33E-03	1.73E-02
1554080_PM_at	RCD1 required for cell differentiation1 homolog (S. pombe)	253959	RQCD1	0.821	+	4.64E-03	4.91E-03
222514_PM_at	Ras-related GTP binding C	5965	RRAGC	0.381	+	2.07E-02	2.35E-02
212589_PM_at	related RAS viral (r-ras) oncogene homolog 2	5577	RRAS2	1.162	+	4.88E-03	1.02E-02
203704_PM_s_at	ras responsive element binding protein 1	57488	RREB1	0.362	+	2.06E-02	2.64E-02
219037_PM_at	ribosomal RNA processing 15 homolog (S. cerevisiae)	23235	RRP15	0.404	+	1.94E-03	7.21E-04
212846_PM_at	ribosomal RNA processing 1 homolog B (S. cerevisiae)	8406	RRP1B	0.509	+	3.10E-03	8.75E-03
222791_PM_at	round spermatid basic protein 1	440434	RSBN1	0.884	+	7.62E-03	1.02E-02
213694_PM_at	round spermatid basic protein 1	10434	RSBN1	0.517	+	1.29E-02	1.84E-02
226387_PM_at	round spermatid basic protein 1-like	57821	RSBN1L	0.476	+	2.26E-02	4.92E-02
213750_PM_at	ribosomal L1 domain containing 1	3842	RSL1D1	0.441	+	1.59E-02	2.91E-02
222465_PM_at	ribosomal L24 domain containing 1	84986	RSL24D1	0.500	+	2.91E-04	4.27E-03
225773_PM_at	ring finger and SPRY domain containing 1	150622	RSPRY1	0.782	+	4.71E-03	4.27E-03
201980_PM_s_at	Ras suppressor protein 1	2734	RSU1	0.305	+	1.09E-02	3.50E-02
212301_PM_at	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	2171	RTF1	0.286	+	2.55E-02	1.15E-02
232231_PM_at	runt-related transcription factor 2	7284	RUNX2	0.872	+	9.73E-03	1.75E-02

201459_PM_at	RuvB-like 2 (E. coli)	3551	RUVBL2	0.599	+	2.34E-02	1.61E-02
219598_PM_s_at	RWD domain containing 1	5436	RWDD1	0.591	+	1.04E-02	1.05E-02
205087_PM_at	RWD domain containing 3	9111	RWDD3	0.918	+	2.48E-02	1.84E-02
202449_PM_s_at	retinoid X receptor, alpha	55012	RXRA	0.292	+	3.44E-02	3.16E-02
200660_PM_at	S100 calcium binding protein A11	2157	S100A11	0.365	+	2.59E-03	1.39E-03
228176_PM_at	sphingosine-1-phosphate receptor 3	867	S1PR3	0.282	+	4.07E-03	1.84E-02
225614_PM_at	serum amyloid A-like 1	166863	SAAL1	0.722	+	9.39E-03	2.73E-02
202797_PM_at	SAC1 suppressor of actin mutations 1-like (yeast)	51000	SACM1L	0.427	+	4.41E-02	2.94E-02
229273_PM_at	sal-like 1 (Drosophila)	80110	SALL1	0.736	+	4.09E-02	1.76E-03
229402_PM_at	sterile alpha motif domain containing 13	26040	SAMD13	0.438	+	4.93E-03	1.25E-02
212845_PM_at	sterile alpha motif domain containing 4A	9521	SAMD4A	0.432	+	4.02E-02	7.59E-03
201569_PM_s_at	sorting and assembly machinery component 50 homolog (S. cerevisiae)	474343 /// 54466	SAMM50	0.383	+	1.48E-02	1.16E-02
208741_PM_at	Sin3A-associated protein, 18kDa	55914	SAP18	0.548	+	1.10E-03	1.01E-03
204900_PM_x_at	Sin3A-associated protein, 30kDa	7572	SAP30	0.621	+	1.96E-02	3.36E-02
222831_PM_at	SAP30-like	7290	SAP30L	0.670	+	9.64E-03	1.37E-02
222467_PM_s_at	SAPS domain family, member 3	23271	SAPS3	0.510	+	8.74E-03	2.81E-03
201542_PM_at	SAR1 homolog A (S. cerevisiae)	1432	SAR1A	0.444	+	4.08E-02	3.59E-02
223512_PM_at	SAR1 homolog B (S. cerevisiae)	729515	SAR1B	0.711	+	6.12E-03	1.83E-02
218254_PM_s_at	SAR1 homolog B (S. cerevisiae)	84557	SAR1B	0.511	+	1.05E-02	7.59E-03
229069_PM_at	SAP domain containing ribonucleoprotein	155435	SARNP	0.491	+	1.37E-03	4.56E-03
226022_PM_at	SAM and SH3 domain containing 1	7009	SASH1	0.450	+	9.99E-03	2.69E-02
210592_PM_s_at	spermidine/spermine N1-acetyltransferase 1	57120	SAT1	0.639	+	1.10E-03	1.85E-03
203455_PM_s_at	spermidine/spermine N1-acetyltransferase 1	2941	SAT1	0.549	+	7.03E-03	2.01E-03
226169_PM_at	SET binding factor 2	9794	SBF2	0.666	+	3.05E-02	3.75E-02
209146_PM_at	sterol-C4-methyl oxidase-like	51361	SC4MOL	0.412	+	8.61E-03	4.81E-02
228174_PM_at	suppressor of cancer cell invasion	729082	SCAI	0.681	+	2.27E-03	4.86E-03
212416_PM_at	secretory carrier membrane protein 1	7525	SCAMP1	0.264	+	1.57E-02	1.86E-02
212425_PM_at	secretory carrier membrane protein 1	10565	SCAMP1	0.619	+	1.94E-02	9.88E-03
216399_PM_s_at	S-phase cyclin A-associated protein in the ER	10000	SCAPER	0.574	+	1.28E-02	2.57E-02
209741_PM_x_at	S-phase cyclin A-associated protein in the ER	79048	SCAPER	0.574	+	3.20E-02	4.04E-02
201826_PM_s_at	saccharopine dehydrogenase (putative)	509	SCCPDH	0.384	+	1.79E-02	6.11E-03

215548_PM_s_at	sec1 family domain containing 1	115290 /// 54938	SCFD1	0.502	+	7.94E-03	1.38E-02
203889_PM_at	secretogranin V (7B2 protein)	4170	SCG5	0.417	+	1.95E-02	2.56E-02
206147_PM_x_at	sex comb on midleg-like 2 (Drosophila)	5447	SCML2	0.482	+	4.59E-02	3.27E-02
210383_PM_at	sodium channel, voltage-gated, type I, alpha subunit	118924	SCN1A	0.428	+	3.83E-03	2.87E-04
229057_PM_at	sodium channel, voltage-gated, type II, alpha subunit	114825	SCN2A	0.296	+	1.53E-02	5.48E-04
210432_PM_s_at	sodium channel, voltage-gated, type III, alpha subunit	128637	SCN3A	0.570	+	7.07E-03	2.39E-02
224786_PM_at	short coiled-coil protein	375757	SCOC	0.284	+	1.23E-04	4.68E-04
218217_PM_at	serine carboxypeptidase 1	55599	SCPEP1	0.463	+	1.52E-02	7.66E-03
205475_PM_at	stimulator of chondrogenesis 1	11021	SCRG1	0.586	+	2.25E-02	4.37E-02
212556_PM_at	scribbled homolog (Drosophila)	11183	SCRIB	0.366	+	7.12E-03	2.80E-02
205607_PM_s_at	SCY1-like 3 (S. cerevisiae)	7704	SCYL3	0.501	+	3.89E-03	5.47E-03
41329_PM_at	SCY1-like 3 (S. cerevisiae)	---	SCYL3	0.562	+	2.56E-02	1.71E-02
200958_PM_s_at	syndecan binding protein (syntenin)	10521	SDCBP	0.395	+	3.07E-02	1.50E-02
223337_PM_at	serologically defined colon cancer antigen 10	54915	SDCCAG10	0.397	+	1.80E-02	3.61E-03
227785_PM_at	serologically defined colon cancer antigen 8	55504	SDCCAG8	0.534	+	1.29E-02	1.95E-02
202026_PM_at	succinate dehydrogenase complex, subunit D, integral membrane protein	9369	SDHD	0.357	+	9.25E-03	6.97E-03
201290_PM_at	SEC11 homolog A (S. cerevisiae)	8601	SEC11A	0.537	+	1.31E-02	1.08E-02
209206_PM_at	SEC22 vesicle trafficking protein homolog B (S. cerevisiae)	23780	SEC22B	0.438	+	5.12E-03	8.54E-03
225460_PM_at	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	127933	SEC22C	0.349	+	3.20E-02	4.16E-03
212887_PM_at	Sec23 homolog A (S. cerevisiae)	97	SEC23A	0.432	+	6.54E-03	7.14E-03
209175_PM_at	SEC23 interacting protein	26575	SEC23IP	0.292	+	9.10E-04	3.43E-03
212900_PM_at	SEC24 family, member A (S. cerevisiae)	9488	SEC24A	0.450	+	3.34E-02	4.82E-02
202798_PM_at	SEC24 family, member B (S. cerevisiae)	56658	SEC24B	0.435	+	3.71E-02	1.81E-02
200945_PM_s_at	SEC31 homolog A (S. cerevisiae)	1983	SEC31A	0.538	+	2.10E-02	9.61E-03
209889_PM_at	SEC31 homolog B (S. cerevisiae)	84317	SEC31B	0.295	+	6.53E-03	3.99E-02
203133_PM_at	Sec61 beta subunit	159090	SEC61B	0.298	+	6.48E-04	2.25E-03
203484_PM_at	Sec61 gamma subunit	3363	SEC61G	0.638	+	7.79E-03	9.60E-03
229969_PM_at	SEC63 homolog (S. cerevisiae)	65986	SEC63	0.381	+	2.13E-04	1.67E-04
218265_PM_at	SECIS binding protein 2	388962	SECISBP2	0.722	+	2.70E-03	1.80E-03
221931_PM_s_at	SEH1-like (S. cerevisiae)	6854	SEH1L	0.507	+	9.58E-03	2.18E-02
202061_PM_s_at	sel-1 suppressor of lin-12-like (C. elegans)	1827	SEL1L	0.606	+	3.76E-03	5.23E-03

223070_PM_at	selenoprotein K	55870	SELK	0.485	+	9.23E-04	3.56E-03
209879_PM_at	selectin P ligand	2289	SELPLG	0.383	+	2.79E-03	4.64E-03
223209_PM_s_at	selenoprotein S	9200	SELS	0.373	+	1.08E-02	2.68E-02
225561_PM_at	selenoprotein T	80055	SELT	0.439	+	2.00E-02	1.91E-02
219259_PM_at	sema domain, immunoglobulin domain (Ig), transmembrane domain I and short cytoplasmic domain, (348eparin348ing) 4A	10628	SEMA4A	0.360	+	2.02E-02	2.84E-03
226492_PM_at	sema domain, transmembrane domain I, and cytoplasmic domain, (348eparin348ing) 6D	10623	SEMA6D	0.562	+	3.29E-02	2.08E-02
202318_PM_s_at	SUMO1/sentrin specific peptidase 6	55827	SENP6	0.528	+	3.35E-02	6.25E-03
228398_PM_at	SUMO/sentrin specific peptidase family member 8	122830	SENP8	0.618	+	1.21E-02	3.09E-02
232983_PM_s_at	secretion regulating guanine nucleotide exchange factor	340895	SERGEF	0.303	+	2.53E-02	9.44E-03
221472_PM_at	serine incorporator 3	10570	SERINC3	0.333	+	2.87E-02	3.61E-02
200969_PM_at	stress-associated endoplasmic reticulum protein 1	10211	SERP1	0.569	+	2.62E-02	7.61E-03
228044_PM_at	stress-associated endoplasmic reticulum protein family member 2	154807	SERP2	0.315	+	1.41E-02	7.34E-03
211429_PM_s_at	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1	196074	SERPINA1	0.493	+	1.02E-02	1.47E-02
202657_PM_s_at	SERTA domain containing 2	56288	SERTAD2	0.547	+	4.11E-02	2.83E-02
218346_PM_s_at	sestrin 1	55740	SESN1	0.498	+	2.48E-02	1.29E-02
227041_PM_at	SEC14 and spectrin domains 1	6141	SESTD1	0.650	+	1.04E-02	1.32E-02
200631_PM_s_at	SET nuclear oncogene	5305	SET	0.308	+	3.96E-05	8.04E-04
227478_PM_at	SET binding protein 1	83448	SETBP1	0.622	+	6.65E-03	9.94E-03
212493_PM_s_at	SET domain containing 2	5797	SETD2	0.669	+	7.44E-03	7.04E-03
1554555_PM_a_at	SET domain containing 6	7323	SETD6	0.352	+	2.64E-02	9.63E-03
224928_PM_at	SET domain containing (lysine methyltransferase) 7	143684	SETD7	0.431	+	4.63E-02	3.12E-02
238684_PM_at	SET domain, bifurcated 2	---	SETDB2	0.778	+	6.77E-03	3.75E-02
235339_PM_at	SET domain, bifurcated 2	---	SETDB2	0.799	+	2.46E-02	4.32E-02
227516_PM_at	splicing factor 3a, subunit 1, 120kDa	10955	SF3A1	0.713	+	2.73E-02	3.12E-02
203818_PM_s_at	splicing factor 3a, subunit 3, 60kDa	10944	SF3A3	0.411	+	1.01E-02	2.58E-02
223416_PM_at	splicing factor 3B, 14 kDa subunit	57472	SF3B14	0.479	+	7.31E-03	4.94E-03
33322_PM_i_at	stratifin	400931	SFN	0.606	+	1.15E-03	1.30E-03

33323_PM_r_at	stratifin	---	SFN	0.727	+	5.87E-03	1.28E-02
214016_PM_s_at	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)	7626	SFPQ	0.446	+	7.89E-03	1.77E-02
207468_PM_s_at	secreted frizzled-related protein 5	4205	SFRP5	0.282	+	3.15E-02	3.25E-02
227164_PM_at	splicing factor, arginine/serine-rich 1	10135	SFRS1	0.422	+	2.01E-02	3.60E-02
200685_PM_at	splicing factor, arginine/serine-rich 11	9908	SFRS11	0.743	+	4.33E-03	9.61E-03
200686_PM_s_at	splicing factor, arginine/serine-rich 11	4137	SFRS11	0.431	+	4.11E-02	2.87E-02
212179_PM_at	splicing factor, arginine/serine-rich 18	1347	SFRS18	0.358	+	2.22E-02	3.43E-02
208804_PM_s_at	splicing factor, arginine/serine-rich 6	51290	SFRS6	0.531	+	1.12E-02	4.89E-03
201129_PM_at	splicing factor, arginine/serine-rich 7, 35kDa	2887	SFRS7	0.424	+	3.06E-03	1.15E-03
225849_PM_s_at	SFT2 domain containing 1	5860	SFT2D1	0.382	+	3.45E-03	2.01E-02
227560_PM_at	sideroflexin 2	80853	SFXN2	0.378	+	6.51E-03	2.23E-02
204688_PM_at	sarcoglycan, epsilon	27338	SGCE	0.666	+	3.50E-03	5.81E-03
223672_PM_at	SH3-domain GRB2-like (endophilin) interacting protein 1	51602	SGIP1	0.295	+	2.00E-02	2.94E-02
227627_PM_at	serum/glucocorticoid regulated kinase family, member 3	64065	SGK3	0.546	+	4.66E-03	2.31E-03
212989_PM_at	sphingomyelin synthase 1	10389	SGMS1	0.586	+	4.56E-02	3.51E-03
227038_PM_at	sphingomyelin synthase 2	3727	SGMS2	0.497	+	1.43E-02	5.15E-03
228745_PM_at	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	80311	SGTB	0.566	+	1.46E-03	3.91E-04
203320_PM_at	SH2B adaptor protein 3	117177	SH2B3	0.678	+	2.65E-02	2.72E-02
201312_PM_s_at	SH3 domain binding glutamic acid-rich protein like	7750	SH3BGRL	0.516	+	2.49E-03	1.41E-03
222258_PM_s_at	SH3-domain binding protein 4	51029	SH3BP4	0.794	+	2.32E-02	1.29E-02
209090_PM_s_at	SH3-domain GRB2-like endophilin B1	51510	SH3GLB1	0.672	+	1.65E-02	1.58E-02
224817_PM_at	SH3 and PX domains 2A	2932	SH3PXD2A	0.324	+	2.53E-02	4.40E-02
231823_PM_s_at	SH3 and PX domains 2B	26137	SH3PXD2B	0.298	+	6.01E-03	2.74E-02
213307_PM_at	SH3 and multiple ankyrin repeat domains 2	5876	SHANK2	0.417	+	2.27E-02	2.83E-02
243681_PM_at	SH3 and multiple ankyrin repeat domains 2	---	SHANK2	0.723	+	2.87E-02	1.23E-02
204656_PM_at	Src homology 2 domain containing adaptor protein B	558	SHB	0.470	+	1.27E-02	5.15E-03
202276_PM_at	split hand/foot malformation (ectrodactyly) type 1	6231	SHFM1	0.275	+	4.07E-03	5.31E-03
224954_PM_at	serine hydroxymethyltransferase 1 (soluble)	374659	SHMT1	0.471	+	3.89E-03	1.79E-02
214095_PM_at	serine hydroxymethyltransferase 2 (mitochondrial)	57326	SHMT2	0.582	+	1.16E-03	4.47E-03
226366_PM_at	SNF2 histone linker PHD RING helicase	7693	SHPRH	1.113	+	3.56E-03	2.56E-03

204967_PM_at	shroom family member 2	9823	SHROOM2	0.263	+	3.83E-02	3.70E-02
228400_PM_at	shroom family member 3	23261	SHROOM3	0.328	+	1.08E-02	3.63E-02
1556056_PM_at	salt-inducible kinase 2	5684	SIK2	0.490	+	1.06E-02	1.43E-02
228026_PM_at	suppressor of IKBKE 1	60674	SIKE1	0.849	+	7.18E-03	5.46E-03
238005_PM_s_at	SIN3 homolog A, transcription regulator (yeast)	---	SIN3A	0.445	+	3.99E-02	3.25E-02
211114_PM_x_at	survival of motor neuron protein interacting protein 1	81602	SIP1	0.332	+	3.19E-03	2.15E-03
205063_PM_at	survival of motor neuron protein interacting protein 1	5293	SIP1	0.464	+	4.11E-03	1.85E-02
210779_PM_x_at	survival of motor neuron protein interacting protein 1	51733	SIP1	0.393	+	5.18E-03	7.87E-03
211115_PM_x_at	survival of motor neuron protein interacting protein 1	10169 /// 25764	SIP1	0.549	+	7.17E-03	7.59E-03
218878_PM_s_at	sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)	5467	SIRT1	0.973	+	7.23E-03	7.23E-03
222248_PM_s_at	sirtuin (silent mating type information regulation 2 homolog) 4 (S. cerevisiae)	10608	SIRT4	0.309	+	1.67E-02	2.57E-02
229112_PM_at	sirtuin (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	---	SIRT5	0.329	+	1.94E-02	2.57E-02
225684_PM_at	spindle and kinetochore associated complex subunit 2	32	SKA2	0.635	+	3.39E-02	1.41E-02
225639_PM_at	src kinase associated phosphoprotein 2	22941	SKAP2	0.918	+	1.46E-03	1.13E-02
227447_PM_at	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	57118	SKIV2L2	0.770	+	3.70E-03	1.23E-04
203625_PM_x_at	S-phase kinase-associated protein 2 (p45)	54462	SKP2	0.562	+	3.76E-02	4.50E-02
224844_PM_at	SLAIN motif family, member 2	22847	SLAIN2	0.652	+	1.12E-02	3.47E-03
1553770_PM_a_at	SLAM family member 9	5431	SLAMF9	0.281	+	6.02E-03	1.70E-02
203124_PM_s_at	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	92399	SLC11A2	0.539	+	3.80E-02	4.22E-02
225835_PM_at	solute carrier family 12 (sodium/potassium/chloride transporters), member 2	85302	SLC12A2	0.520	+	3.79E-02	7.15E-03
220371_PM_s_at	solute carrier family 12 (potassium/chloride transporters), member 9	3149	SLC12A9	0.431	+	3.17E-03	7.33E-03
228844_PM_at	solute carrier family 13 (sodium-dependent citrate transporter), member 5	2321	SLC13A5	0.305	+	1.30E-02	3.72E-02
205316_PM_at	solute carrier family 15 (H+/peptide transporter), member 2	5303	SLC15A2	0.600	+	1.46E-03	3.48E-03
230748_PM_at	solute carrier family 16, member 6 (monocarboxylic acid transporter 7)	2899	SLC16A6	0.663	+	1.24E-03	1.58E-02

223441_PM_at	solute carrier family 17 (anion/sugar transporter), member 5	26985	SLC17A5	0.322	+	1.20E-02	9.15E-03
220551_PM_at	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6	22841	SLC17A6	0.517	+	9.32E-04	2.26E-03
244377_PM_at	Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	---	SLC1A4	0.532	+	8.95E-04	6.58E-04
205074_PM_at	solute carrier family 22 (organic cation/carnitine transporter), member 5	57149	SLC22A5	0.316	+	2.04E-02	1.90E-02
204587_PM_at	solute carrier family 25 (mitochondrial carrier, brain), member 14	1455	SLC25A14	0.432	+	1.45E-02	1.67E-02
218653_PM_at	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15	494143	SLC25A15	0.313	+	2.10E-02	2.23E-02
235747_PM_at	Solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16	---	SLC25A16	0.447	+	4.64E-03	3.06E-02
223192_PM_at	solute carrier family 25, member 28	79572	SLC25A28	0.467	+	1.00E-02	3.92E-03
226782_PM_at	solute carrier family 25, member 30	10802	SLC25A30	0.364	+	1.21E-03	4.65E-04
221020_PM_s_at	solute carrier family 25, member 32	6787	SLC25A32	0.487	+	2.39E-02	5.46E-03
223296_PM_at	solute carrier family 25, member 33	55239	SLC25A33	0.426	+	8.29E-03	2.78E-02
201919_PM_at	solute carrier family 25, member 36	2934	SLC25A36	0.497	+	1.57E-02	2.19E-02
226179_PM_at	solute carrier family 25, member 37	573	SLC25A37	0.472	+	3.03E-02	3.06E-02
236436_PM_at	solute carrier family 25, member 45	---	SLC25A45	0.608	+	1.75E-02	3.85E-02
219344_PM_at	solute carrier family 29 (nucleoside transporters), member 3	7247	SLC29A3	0.264	+	2.61E-02	4.09E-02
227176_PM_at	solute carrier family 2 (facilitated glucose transporter), member 13	51065	SLC2A13	0.430	+	1.71E-02	4.03E-02
221751_PM_at	Solute carrier family 2 (facilitated glucose transporter), member 3 pseudogene 1	84617	SLC2A3P1	0.456	+	3.92E-03	1.99E-02
212907_PM_at	Solute carrier family 30 (zinc transporter), member 1	64771	SLC30A1	0.459	+	7.54E-03	8.95E-03
226601_PM_at	solute carrier family 30 (zinc transporter), member 7	54499	SLC30A7	0.267	+	2.57E-02	2.49E-02
204204_PM_at	solute carrier family 31 (copper transporters), member 2	8667	SLC31A2	0.754	+	5.90E-03	3.08E-02
203164_PM_at	solute carrier family 33 (acetyl-CoA transporter), member 1	123016	SLC33A1	0.794	+	1.39E-02	2.75E-03
203306_PM_s_at	solute carrier family 35 (CMP-sialic acid transporter), member A1	26140	SLC35A1	0.445	+	2.19E-02	1.06E-02
218519_PM_at	solute carrier family 35, member A5	132204	SLC35A5	0.495	+	4.14E-02	3.75E-02
202433_PM_at	solute carrier family 35, member B1	56922	SLC35B1	0.294	+	5.73E-03	4.73E-04

222691_PM_at	solute carrier family 35, member B3	54665	SLC35B3	0.268	+	7.75E-03	1.86E-02
225882_PM_at	solute carrier family 35, member B4	100133991	SLC35B4	0.552	+	3.51E-03	3.63E-03
209712_PM_at	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	29097	SLC35D1	0.355	+	3.47E-02	4.59E-02
223304_PM_at	solute carrier family 37 (glycerol-3-phosphate transporter), member 3	2845	SLC37A3	0.567	+	1.11E-02	1.51E-02
214830_PM_at	solute carrier family 38, member 6	11108	SLC38A6	0.485	+	2.20E-02	3.00E-02
225295_PM_at	solute carrier family 39 (zinc transporter), member 10	254263	SLC39A10	0.337	+	2.22E-02	1.90E-02
227046_PM_at	solute carrier family 39 (metal ion transporter), member 11	4131	SLC39A11	0.337	+	9.13E-03	3.79E-02
212110_PM_at	solute carrier family 39 (zinc transporter), member 14	9775	SLC39A14	0.380	+	1.50E-02	1.18E-03
202088_PM_at	solute carrier family 39 (zinc transporter), member 6	7940	SLC39A6	0.508	+	3.54E-02	3.70E-02
222445_PM_at	solute carrier family 39 (zinc transporter), member 9	22800	SLC39A9	0.606	+	1.44E-02	2.50E-02
223044_PM_at	solute carrier family 40 (iron-regulated transporter), member 1	28978	SLC40A1	0.579	+	2.13E-02	3.83E-02
228221_PM_at	solute carrier family 44, member 3	283578	SLC44A3	0.856	+	1.09E-02	2.30E-02
214719_PM_at	solute carrier family 46, member 3	4702	SLC46A3	1.020	+	4.13E-02	4.22E-03
1558201_PM_s_at	solute carrier family 4 (anion exchanger), member 1, adaptor protein	10421	SLC4A1AP	0.325	+	1.08E-02	1.06E-02
234291_PM_s_at	solute carrier family 6 (proline IMINO transporter), member 20	---	SLC6A20	0.282	+	5.71E-03	6.59E-03
209921_PM_at	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	56927	SLC7A11	0.452	+	3.91E-02	4.80E-02
1556641_PM_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 14	10944	SLC7A14	0.399	+	1.76E-02	4.02E-02
225516_PM_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	387338	SLC7A2	0.384	+	1.06E-02	1.63E-02
203578_PM_s_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	54976	SLC7A6	0.338	+	7.96E-03	8.29E-04
203580_PM_s_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	63916	SLC7A6	0.611	+	2.80E-02	3.34E-02
238546_PM_at	solute carrier family 8 (sodium/calcium exchanger), member 1	---	SLC8A1	0.322	+	3.37E-02	3.73E-02
235518_PM_at	solute carrier family 8 (sodium/calcium exchanger), member 1	89919	SLC8A1	0.389	+	4.11E-02	4.35E-02
203909_PM_at	solute carrier family 9 (sodium/hydrogen exchanger), member 6	10694	SLC9A6	0.358	+	4.09E-02	3.88E-02
217828_PM_at	SAFB-like, transcription modulator	147495	SLTM	0.350	+	3.87E-02	3.78E-02

227798_PM_at	SMAD family member 1	80321	SMAD1	0.595	+	1.58E-02	2.68E-02
203077_PM_s_at	SMAD family member 2	81555	SMAD2	0.615	+	7.62E-03	1.21E-02
226563_PM_at	SMAD family member 2	7881	SMAD2	0.660	+	8.42E-03	1.12E-02
235725_PM_at	SMAD family member 4	100130383 /// 152206 /// 25994	SMAD4	0.704	+	2.24E-03	4.04E-03
225223_PM_at	SMAD family member 5	79971	SMAD5	0.537	+	1.33E-02	1.03E-02
204790_PM_at	SMAD family member 7	8445	SMAD7	0.713	+	1.81E-02	3.12E-02
227719_PM_at	SMAD family member 9	51209	SMAD9	0.583	+	6.67E-03	4.42E-03
217707_PM_x_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	64756	SMARCA2	0.699	+	2.17E-02	1.09E-02
206542_PM_s_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	91851	SMARCA2	0.298	+	2.30E-02	2.44E-02
213251_PM_at	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	60481	SMARCA5	0.385	+	3.81E-02	1.75E-03
223197_PM_s_at	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1	51226	SMARCAD1	0.649	+	3.52E-02	7.71E-03
213253_PM_at	structural maintenance of chromosomes 2	9908	SMC2	0.278	+	1.86E-02	2.75E-02
209259_PM_s_at	structural maintenance of chromosomes 3	54332	SMC3	0.620	+	1.10E-02	2.09E-02
218781_PM_at	structural maintenance of chromosomes 6	10529	SMC6	0.426	+	9.57E-03	3.53E-02
212577_PM_at	structural maintenance of chromosomes flexible hinge domain containing 1	10311	SMCHD1	0.425	+	2.77E-03	1.51E-02
212569_PM_at	structural maintenance of chromosomes flexible hinge domain containing 1	9694	SMCHD1	0.289	+	4.87E-02	4.37E-02
222270_PM_at	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	6925	SMEK2	0.664	+	9.41E-05	2.76E-04
1568627_PM_at	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	5423	SMEK2	0.277	+	6.25E-03	9.74E-03
233759_PM_s_at	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	---	SMEK2	0.550	+	7.09E-03	2.54E-03
226230_PM_at	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	9693	SMEK2	0.662	+	1.14E-02	2.55E-02
200071_PM_at	survival motor neuron domain containing 1	1641	SMNDC1	0.491	+	2.25E-02	1.96E-02
213624_PM_at	sphingomyelin phosphodiesterase, acid-like 3A	23165	SMPDL3A	0.508	+	4.53E-03	1.71E-02
227489_PM_at	SMAD specific E3 ubiquitin protein ligase 2	25959	SMURF2	0.591	+	1.45E-02	2.27E-02
219480_PM_at	snail homolog 1 (Drosophila)	25820	SNAI1	0.270	+	1.18E-02	2.94E-02
213203_PM_at	small nuclear RNA activating complex, polypeptide 5, 19kDa	9031	SNAPC5	0.331	+	4.23E-03	1.46E-02

1554093_PM_a_at	small nuclear RNA activating complex, polypeptide 5, 19kDa	26268	SNAPC5	0.400	+	1.80E-02	4.69E-02
237833_PM_s_at	synuclein, alpha interacting protein	---	SNCAIP	0.308	+	2.39E-03	1.09E-02
226149_PM_at	small nucleolar RNA host gene 11 (non-protein coding)	9969	SNHG11	0.365	+	2.12E-02	1.45E-02
225547_PM_at	small nucleolar RNA host gene 6 (non-protein coding)	122525	SNHG6	0.402	+	8.93E-03	1.89E-02
1554759_PM_at	SNAP25-interacting protein	6633	SNIP	0.293	+	1.24E-02	4.24E-03
218032_PM_at	stannin	55197	SNN	0.504	+	1.00E-02	1.21E-02
209481_PM_at	SNF related kinase	79133	SNRK	0.431	+	2.69E-02	7.11E-03
212438_PM_at	small nuclear ribonucleoprotein 27kDa (U4/U6.U5)	58487	SNRNP27	0.452	+	8.61E-03	6.79E-03
212440_PM_at	small nuclear ribonucleoprotein 27kDa (U4/U6.U5)	9903	SNRNP27	0.305	+	1.56E-02	1.06E-02
216977_PM_x_at	small nuclear ribonucleoprotein polypeptide A’	55829	SNRPA1	0.625	+	8.57E-03	1.39E-02
202690_PM_s_at	small nuclear ribonucleoprotein D1 polypeptide 16kDa	84148	SNRPD1	0.585	+	2.12E-03	2.82E-04
200826_PM_at	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa	10735	SNRPD2	0.572	+	6.22E-03	8.92E-03
203316_PM_s_at	small nuclear ribonucleoprotein polypeptide E	116988	SNRPE	0.572	+	1.39E-03	9.15E-04
203832_PM_at	small nuclear ribonucleoprotein polypeptide F	808	SNRPF	0.389	+	3.31E-04	2.77E-03
205644_PM_s_at	small nuclear ribonucleoprotein polypeptide G	2043	SNRPG	0.563	+	2.97E-03	4.39E-04
1559546_PM_s_at	small nuclear ribonucleoprotein polypeptide N	9874	SNRPN	0.657	+	1.12E-02	6.23E-03
226591_PM_at	small nuclear ribonucleoprotein polypeptide N	2904	SNRPN	0.356	+	4.42E-02	2.62E-02
201575_PM_at	SNW domain containing 1	6319	SNW1	0.515	+	1.43E-02	1.46E-02
213364_PM_s_at	sorting nexin 1	25901	SNX1	0.628	+	3.71E-02	3.66E-02
218404_PM_at	sorting nexin 10	254778	SNX10	0.518	+	1.40E-02	4.53E-03
227031_PM_at	sorting nexin 13	7503	SNX13	0.644	+	4.76E-02	4.57E-02
230759_PM_at	Sorting nexin 14	55000	SNX14	0.283	+	6.77E-03	4.61E-03
225101_PM_s_at	sorting nexin 14	153396	SNX14	0.535	+	9.02E-03	1.75E-02
226683_PM_at	sorting nexin 18	23433	SNX18	0.672	+	8.21E-03	1.06E-02
221498_PM_at	sorting nexin family member 27	635	SNX27	0.476	+	3.00E-02	2.74E-03
200067_PM_x_at	sorting nexin 3	10384 /// 11118	SNX3	0.520	+	1.59E-02	5.48E-03
213545_PM_x_at	sorting nexin 3	25778	SNX3	0.359	+	2.29E-02	4.49E-03
226249_PM_at	sorting nexin family member 30	9724	SNX30	0.364	+	7.58E-03	1.38E-03
212652_PM_s_at	sorting nexin 4	6447	SNX4	0.444	+	3.84E-02	2.88E-02
222410_PM_s_at	sorting nexin 6	27351	SNX6	0.275	+	2.85E-02	9.56E-03

205573_PM_s_at	sorting nexin 7	7381	SNX7	0.827	+	2.50E-03	7.31E-03
209648_PM_x_at	suppressor of cytokine signaling 5	28989	SOCS5	0.553	+	1.60E-02	1.13E-02
200642_PM_at	superoxide dismutase 1, soluble	6637	SOD1	0.343	+	8.68E-03	3.79E-03
214988_PM_s_at	SON DNA binding protein	29107	SON	0.343	+	1.22E-02	6.78E-03
218087_PM_s_at	sorbin and SH3 domain containing 1	10087	SORBS1	0.449	+	4.06E-02	7.12E-03
228720_PM_at	sortilin-related VPS10 domain containing receptor 2	83544	SORCS2	0.287	+	1.52E-02	2.23E-02
215522_PM_at	sortilin-related VPS10 domain containing receptor 3	57338	SORCS3	0.473	+	4.68E-02	5.70E-04
212780_PM_at	son of sevenless homolog 1 (Drosophila)	5144	SOS1	0.666	+	4.68E-02	1.19E-02
212870_PM_at	son of sevenless homolog 2 (Drosophila)	1678	SOS2	0.689	+	1.51E-02	1.44E-02
204915_PM_s_at	SRY (sex determining region Y)-box 11	9270	SOX11	0.527	+	1.47E-02	1.44E-02
217040_PM_x_at	SRY (sex determining region Y)-box 15	10283	SOX15	0.572	+	8.29E-04	3.71E-03
228038_PM_at	SRY (sex determining region Y)-box 2	57609	SOX2	0.469	+	1.59E-02	1.73E-03
201417_PM_at	SRY (sex determining region Y)-box 4	4850	SOX4	0.902	+	3.49E-04	1.10E-03
201416_PM_at	SRY (sex determining region Y)-box 4	5802	SOX4	0.669	+	1.67E-02	2.28E-02
227498_PM_at	SRY (sex determining region Y)-box 6	60468	SOX6	0.873	+	2.35E-02	6.86E-03
202864_PM_s_at	SP100 nuclear antigen	56987	SP100	0.349	+	7.70E-04	1.10E-03
208012_PM_x_at	SP110 nuclear body protein	10772	SP110	0.558	+	3.89E-03	3.48E-03
209762_PM_x_at	SP110 nuclear body protein	51534	SP110	0.556	+	3.33E-02	2.71E-02
213168_PM_at	Sp3 transcription factor	81553	SP3	0.626	+	1.53E-02	8.22E-03
236265_PM_at	Sp4 transcription factor	57494	SP4	0.544	+	3.55E-02	3.35E-03
205406_PM_s_at	sperm autoantigenic protein 17	1174	SPA17	0.529	+	6.42E-03	2.20E-02
240898_PM_at	sperm associated antigen 16	---	SPAG16	0.567	+	2.24E-06	1.73E-05
225339_PM_at	sperm associated antigen 9	493911	SPAG9	0.448	+	2.23E-02	1.05E-02
209748_PM_at	spastin	55540	SPAST	0.514	+	7.71E-03	2.90E-03
218933_PM_at	spermatogenesis associated 5-like 1	25960	SPATA5L1	0.364	+	2.82E-02	2.02E-02
234929_PM_s_at	spermatogenesis associated 7	8874	SPATA7	0.465	+	1.29E-02	3.01E-02
222154_PM_s_at	spermatogenesis associated, serine-rich 2-like	27346	SPATS2L	0.519	+	1.87E-02	1.70E-02
217927_PM_at	signal peptidase complex subunit 1 homolog (S. cerevisiae)	5928	SPCS1	0.385	+	1.92E-03	5.44E-04
221844_PM_x_at	signal peptidase complex subunit 3 homolog (S. cerevisiae)	9863	SPCS3	0.374	+	1.91E-02	2.18E-03
203513_PM_at	spastic paraplegia 11 (autosomal recessive)	10447	SPG11	0.886	+	3.32E-02	4.34E-02
211704_PM_s_at	355eparin355i family, member 2A /// 355eparin355i family, member 2B	100137049 /// 8681	SPIN2A /// SPIN2B	0.555	+	2.54E-02	1.94E-02

213994_PM_s_at	spondin 1, extracellular matrix protein	55957	SPON1	0.527	+	1.64E-02	1.45E-02
213993_PM_at	spondin 1, extracellular matrix protein	89845	SPON1	0.987	+	2.85E-02	1.89E-02
225658_PM_at	speckle-type POZ protein-like	5962	SPOPL	0.497	+	3.12E-02	3.44E-03
226837_PM_at	356epari-related, EVH1 domain containing 1	55958	SPRED1	0.605	+	3.05E-02	1.96E-03
229594_PM_at	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae)	130574	SPTY2D1	0.413	+	4.33E-02	4.46E-02
209218_PM_at	squalene epoxidase	54676	SQLE	0.405	+	1.64E-02	4.55E-02
224864_PM_at	steroid receptor RNA activator 1	115416	SRA1	0.327	+	1.60E-02	2.38E-02
201859_PM_at	serglycin	55660	SRGN	0.789	+	1.25E-02	8.31E-03
208921_PM_s_at	sorcin	53918	SRI	0.315	+	4.61E-03	4.35E-03
200007_PM_at	signal recognition particle 14kDa (homologous Alu RNA binding protein)	63940	SRP14	0.423	+	1.82E-03	1.85E-03
205335_PM_s_at	signal recognition particle 19kDa	905	SRP19	0.363	+	6.35E-03	3.38E-04
224607_PM_s_at	signal recognition particle 68kDa	83640	SRP68	0.333	+	4.24E-02	1.84E-02
208801_PM_at	signal recognition particle 72kDa	56683	SRP72	0.588	+	1.21E-02	2.40E-03
201273_PM_s_at	signal recognition particle 9kDa	4133	SRP9	0.680	+	4.26E-04	1.07E-03
204955_PM_at	sushi-repeat-containing protein, X-linked	2146	SRPX	1.103	+	7.52E-03	2.52E-02
213608_PM_s_at	SRR1 domain containing	8289	SRRD	0.379	+	8.84E-04	9.62E-03
218283_PM_at	synovial sarcoma translocation gene on chromosome 18-like 2	118980	SS18L2	0.511	+	3.72E-03	7.81E-03
214060_PM_at	single-stranded DNA binding protein 1	1674 /// 55578	SSBP1	0.266	+	3.89E-03	2.20E-03
202591_PM_s_at	single-stranded DNA binding protein 1	1600	SSBP1	0.501	+	5.81E-03	1.80E-02
203787_PM_at	single-stranded DNA binding protein 2	54884	SSBP2	0.433	+	3.66E-02	8.07E-03
202506_PM_at	sperm specific antigen 2	64218	SSFA2	0.486	+	4.69E-02	2.05E-02
226932_PM_at	sarcospan (Kras oncogene-associated gene)	9204	SSPN	0.881	+	1.79E-02	2.03E-02
200891_PM_s_at	signal sequence receptor, alpha	9372	SSR1	0.514	+	4.23E-02	1.88E-02
223051_PM_at	SSU72 RNA polymerase II CTD phosphatase homolog (S. cerevisiae)	7227	SSU72	0.364	+	2.85E-03	8.69E-03
208666_PM_s_at	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	27030	ST13	0.499	+	2.97E-02	6.43E-03
204542_PM_at	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	25874	ST6GALNAC2	0.291	+	3.74E-02	4.96E-02
207871_PM_s_at	suppression of tumorigenicity 7	6843	ST7	0.644	+	1.59E-02	3.76E-02

230262_PM_at	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	54954	ST8SIA3	0.418	+	3.37E-02	2.37E-02
202294_PM_at	stromal antigen 1	28969	STAG1	0.402	+	2.10E-02	1.16E-02
209022_PM_at	stromal antigen 2	51205	STAG2	0.645	+	2.36E-02	1.97E-03
203544_PM_s_at	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	2810	STAM	0.467	+	2.42E-02	8.65E-03
223065_PM_s_at	STARD3 N-terminal like	29110	STARD3NL	0.582	+	8.65E-04	2.83E-03
206868_PM_at	StAR-related lipid transfer (START) domain containing 8	9229	STARD8	0.306	+	4.85E-02	3.93E-02
209969_PM_s_at	signal transducer and activator of transcription 1, 91kDa	5937	STAT1	0.648	+	8.70E-03	8.65E-03
204597_PM_x_at	stanniocalcin 1	6742	STC1	0.409	+	1.12E-02	1.32E-02
225649_PM_s_at	serine/threonine kinase 35	127254	STK35	0.701	+	1.19E-02	1.60E-02
202951_PM_at	serine/threonine kinase 38	56134	STK38	0.427	+	2.61E-03	3.45E-03
212572_PM_at	serine/threonine kinase 38 like	1783	STK38L	0.503	+	3.13E-02	4.17E-02
202786_PM_at	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)	152006	STK39	0.544	+	3.58E-02	6.57E-03
213413_PM_at	357eparin 1	545	STON1	0.307	+	4.48E-02	1.70E-02
227461_PM_at	357eparin 2	80055	STON2	0.913	+	3.40E-03	1.44E-02
229378_PM_at	storkhead box 1	55824	STOX1	0.317	+	3.87E-04	7.32E-04
209478_PM_at	stimulated by retinoic acid 13 homolog (mouse)	56474	STRA13	0.298	+	1.18E-03	4.82E-03
223266_PM_at	STE20-related kinase adaptor beta	56660	STRADB	0.779	+	2.11E-02	1.55E-02
233251_PM_at	Spermatid perinuclear RNA binding protein	---	STRBP	0.567	+	1.45E-05	3.28E-04
233252_PM_s_at	spermatid perinuclear RNA binding protein	646214	STRBP	0.347	+	2.64E-02	6.62E-03
1561306_PM_s_at	stereocilin	274	STRC	0.521	+	7.55E-03	2.10E-02
204496_PM_at	striatin, calmodulin binding protein 3	26286	STRN3	0.619	+	3.39E-02	4.31E-02
224700_PM_at	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	203547	STT3B	0.469	+	1.74E-02	1.33E-02
212111_PM_at	syntaxin 12	4698	STX12	0.472	+	3.08E-02	3.96E-02
221500_PM_s_at	syntaxin 16	3423	STX16	0.277	+	3.43E-02	3.89E-02
212799_PM_at	syntaxin 6	9252	STX6	0.530	+	6.18E-03	3.29E-02
228853_PM_at	serine/threonine/tyrosine interacting protein	441478	STYX	0.704	+	5.59E-03	5.28E-03
224586_PM_x_at	SUB1 homolog (S. cerevisiae)	757	SUB1	0.356	+	4.14E-03	1.42E-02
202930_PM_s_at	succinate-CoA ligase, ADP-forming, beta subunit	84251	SUCLA2	0.353	+	3.66E-02	2.23E-02
212459_PM_x_at	succinate-CoA ligase, GDP-forming, beta subunit	2628	SUCLG2	0.710	+	1.15E-02	1.60E-02

214835_PM_s_at	succinate-CoA ligase, GDP-forming, beta subunit	54906	SUCLG2	0.713	+	1.94E-02	3.29E-02
215772_PM_x_at	succinate-CoA ligase, GDP-forming, beta subunit	83460	SUCLG2	0.501	+	2.05E-02	2.43E-02
224309_PM_s_at	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	84808	SUGT1	0.348	+	2.44E-03	8.38E-04
223330_PM_s_at	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	440738	SUGT1	0.520	+	6.55E-03	7.64E-03
212354_PM_at	sulfatase 1	23760	SULF1	0.987	+	6.32E-03	1.07E-02
225002_PM_s_at	sulfatase modifying factor 2	57690	SUMF2	0.265	+	2.93E-04	1.52E-03
211069_PM_s_at	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)	23064	SUMO1	0.421	+	2.02E-03	2.81E-03
208761_PM_s_at	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)	51660	SUMO1	0.381	+	7.72E-03	5.95E-03
213881_PM_x_at	SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae)	10396	SUMO2	0.265	+	3.03E-03	1.55E-02
200740_PM_s_at	SMT3 suppressor of mif two 3 homolog 3 (S. cerevisiae)	5884	SUMO3	0.292	+	2.25E-02	1.05E-02
201838_PM_s_at	suppressor of Ty 7 (S. cerevisiae)-like	3945	SUPT7L	0.315	+	8.06E-03	2.40E-02
204295_PM_at	surfeit 1 /// vacuolar protein sorting 37 homolog A (S. cerevisiae)	2202	SURF1 /// VPS37A	0.377	+	7.95E-03	3.34E-03
226264_PM_at	sushi domain containing 1	4217	SUSD1	0.407	+	5.48E-03	1.62E-02
218619_PM_s_at	suppressor of variegation 3-9 homolog 1 (Drosophila)	57038	SUV39H1	0.311	+	1.13E-02	3.46E-02
222566_PM_at	suppressor of variegation 4-20 homolog 1 (Drosophila)	23234	SUV420H1	0.545	+	3.15E-02	4.03E-02
222759_PM_at	suppressor of variegation 4-20 homolog 1 (Drosophila)	23392	SUV420H1	0.453	+	3.69E-02	3.41E-02
230006_PM_s_at	small VCP/p97-interacting protein	5629	SVIP	0.376	+	7.83E-03	6.85E-03
230005_PM_at	small VCP/p97-interacting protein	259232	SVIP	0.651	+	2.25E-02	2.95E-02
217833_PM_at	synaptotagmin binding, cytoplasmic RNA interacting protein	84181	SYNCRIP	0.813	+	1.12E-03	2.26E-03
209025_PM_s_at	synaptotagmin binding, cytoplasmic RNA interacting protein	26750	SYNCRIP	0.577	+	3.02E-02	4.62E-02
225721_PM_at	synaptopodin 2	123207	SYNPO2	0.387	+	1.24E-02	1.98E-02
243313_PM_at	synaptopodin 2-like	---	SYNPO2L	0.325	+	1.59E-02	2.80E-02
230303_PM_at	synaptoporin	414918	SYNPR	0.357	+	1.07E-02	1.72E-02
232387_PM_at	synergin, gamma	55161	SYNRG	0.297	+	7.15E-03	3.21E-03
64418_PM_at	synergin, gamma	---	SYNRG	0.416	+	1.83E-02	2.49E-02
201260_PM_s_at	synaptophysin-like 1	9379	SYPL1	0.263	+	2.79E-02	5.65E-03
226086_PM_at	synaptotagmin XIII	1728	SYT13	0.431	+	6.52E-03	2.18E-02
1554797_PM_at	synaptotagmin XVI	10768	SYT16	0.369	+	3.85E-02	4.44E-02
223529_PM_at	synaptotagmin IV	51095	SYT4	0.448	+	1.36E-02	2.33E-02
202289_PM_s_at	transforming, acidic coiled-coil containing protein 2	51646	TACC2	0.693	+	2.66E-02	3.56E-02

213090_PM_s_at	TAF4 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 135kDa	11146	TAF4	0.762	+	2.63E-02	2.37E-02
210053_PM_at	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100kDa	129787	TAF5	0.972	+	2.50E-02	2.12E-02
203893_PM_at	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	3735	TAF9	0.598	+	2.26E-03	2.07E-03
202168_PM_at	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	7146 /// 7148	TAF9	0.516	+	2.88E-03	4.66E-03
226523_PM_at	transgelin	1174	TAGLN	0.290	+	1.67E-02	2.30E-02
206283_PM_s_at	T-cell acute lymphocytic leukemia 1	10548	TAL1	0.331	+	9.86E-03	6.84E-03
227407_PM_at	transmembrane anterior posterior transformation 1	9113	TAPT1	0.550	+	1.64E-02	1.09E-02
219443_PM_at	taspase, threonine aspartase, 1	9690	TASP1	0.522	+	1.35E-02	8.59E-03
223231_PM_at	TatD Dnase domain containing 1	55088	TATDN1	0.514	+	1.27E-02	4.87E-03
203648_PM_at	TatD Dnase domain containing 2	10659	TATDN2	0.406	+	1.45E-02	4.20E-02
209154_PM_at	Tax1 (human T-cell leukemia virus type I) binding protein 3	11282	TAX1BP3	1.136	+	1.19E-03	1.83E-03
224622_PM_at	TBC1 domain family, member 14	51318	TBC1D14	0.468	+	1.97E-02	1.23E-02
218268_PM_at	TBC1 domain family, member 15	53342	TBC1D15	0.540	+	4.89E-03	7.56E-04
226409_PM_at	TBC1 domain family, member 20	3765	TBC1D20	0.550	+	1.83E-03	3.88E-03
225121_PM_at	TBC1 domain family, member 23	1390	TBC1D23	0.495	+	5.00E-03	4.22E-03
213912_PM_at	TBC1 domain family, member 30	23261	TBC1D30	0.800	+	1.23E-02	5.46E-03
223461_PM_at	TBC1 domain family, member 7	65244	TBC1D7	0.435	+	3.74E-02	4.60E-02
238067_PM_at	TBC1 domain family, member 8B (with GRAM domain)	165215	TBC1D8B	0.298	+	8.19E-04	2.06E-04
212956_PM_at	TBC1 domain family, member 9 (with GRAM domain)	7220	TBC1D9	0.450	+	7.21E-03	5.82E-03
203667_PM_at	tubulin folding cofactor A	399979	TBCA	0.451	+	2.23E-04	1.85E-03
211052_PM_s_at	tubulin folding cofactor D	94015	TBCD	0.264	+	2.86E-02	1.56E-02
203714_PM_s_at	tubulin folding cofactor E	400073	TBCE	0.567	+	5.81E-04	2.99E-03
227395_PM_at	Tubulin folding cofactor E-like	55203	TBCEL	0.494	+	1.78E-02	4.55E-02
218520_PM_at	TANK-binding kinase 1	122416	TBK1	0.640	+	2.11E-02	1.73E-02
213400_PM_s_at	359eparin359ing (beta)-like 1X-linked	9937	TBL1X	0.405	+	7.80E-03	2.20E-02
226318_PM_at	transforming growth factor beta regulator 1	9865	TBRG1	0.322	+	9.22E-04	8.71E-03
225819_PM_at	transforming growth factor beta regulator 1	80725	TBRG1	0.374	+	8.06E-03	5.04E-03
207555_PM_s_at	thromboxane A2 receptor	23301	TBXA2R	0.295	+	1.07E-03	5.05E-04

227705_PM_at	transcription elongation factor A (SII)-like 7	8994	TCEAL7	0.405	+	2.25E-02	1.24E-02
224819_PM_at	transcription elongation factor A (SII)-like 8	29767	TCEAL8	0.464	+	4.71E-04	4.78E-05
202824_PM_s_at	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	7812	TCEB1	0.376	+	1.30E-02	9.55E-03
202823_PM_at	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	26289	TCEB1	0.357	+	4.22E-02	3.81E-02
202396_PM_at	transcription elongation regulator 1	79717	TCERG1	0.577	+	1.17E-02	6.71E-03
208986_PM_at	transcription factor 12	80006	TCF12	0.607	+	2.13E-02	1.03E-02
207306_PM_at	transcription factor 15 (basic helix-loop-helix)	22998	TCF15	0.319	+	1.70E-02	7.33E-05
212761_PM_at	transcription factor 7-like 2 (T-cell specific, HMG-box)	26151	TCF7L2	0.645	+	3.64E-02	9.77E-03
228606_PM_at	Tctex1 domain containing 2	375743	TCTEX1D2	0.525	+	8.79E-03	4.03E-03
203743_PM_s_at	thymine-DNA glycosylase	10097	TDG	0.526	+	1.29E-02	2.26E-03
208089_PM_s_at	tudor domain containing 3	9659	TDRD3	0.501	+	3.03E-02	2.33E-02
236904_PM_x_at	tectorin alpha	84284	TECTA	0.487	+	3.32E-03	1.45E-02
239216_PM_at	tektin 1	23305	TEKT1	0.286	+	2.26E-02	4.23E-02
204106_PM_at	testis-specific kinase 1	8507	TESK1	0.339	+	3.23E-04	4.29E-03
227624_PM_at	tet oncogene family member 2	2321	TET2	0.753	+	2.26E-02	6.20E-03
228075_PM_x_at	transcription factor B1, mitochondrial	57532	TFB1M	0.622	+	1.11E-03	1.51E-02
227637_PM_at	Transcription factor CP2	80762	TFCP2	0.452	+	3.01E-02	1.44E-02
226157_PM_at	Transcription factor Dp-2 (E2F dimerization partner 2)	7716	TFDP2	0.325	+	2.70E-02	3.05E-02
212457_PM_at	transcription factor binding to IGHM enhancer 3	7019	TFE3	0.377	+	5.00E-03	2.14E-03
224793_PM_s_at	transforming growth factor, beta receptor 1	84134	TGFBR1	0.686	+	1.30E-02	2.98E-03
219292_PM_at	THAP domain containing, apoptosis associated protein 1	79602	THAP1	0.436	+	2.25E-02	1.66E-02
212910_PM_at	THAP domain containing 11	9636	THAP11	0.514	+	4.27E-03	8.93E-04
203083_PM_at	thrombospondin 2	4774	THBS2	0.806	+	7.10E-03	1.37E-02
222931_PM_s_at	threonine synthase-like 1 (S. cerevisiae)	996	THNSL1	0.449	+	3.78E-02	4.31E-03
204064_PM_at	THO complex 1	653566 /// 9789	THOC1	0.436	+	3.51E-02	3.11E-02
226628_PM_at	THO complex 2	2902	THOC2	0.272	+	4.15E-03	4.36E-03
226626_PM_at	THO complex 2	1432	THOC2	0.639	+	1.86E-02	8.09E-03
218334_PM_at	THO complex 7 homolog (Drosophila)	51010	THOC7	0.451	+	1.67E-02	5.51E-03
229657_PM_at	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	79692	THRB	0.770	+	1.03E-02	6.87E-04

229159_PM_at	Thrombospondin, type I, domain containing 7A	150678	THSD7A	0.491	+	4.10E-02	3.46E-02
201448_PM_at	TIA1 cytotoxic granule-associated RNA binding protein	3308	TIA1	0.805	+	8.85E-03	1.52E-02
201447_PM_at	TIA1 cytotoxic granule-associated RNA binding protein	373	TIA1	0.618	+	3.87E-02	1.26E-02
228234_PM_at	toll-like receptor adaptor molecule 2 /// TMED7-TICAM2 read-through transcript	55276	TICAM2 /// TMED7-TICAM2	0.383	+	1.61E-02	4.61E-02
229758_PM_at	tigger transposable element derived 5	84848	TIGD5	0.273	+	3.77E-02	3.23E-02
215171_PM_s_at	translocase of inner mitochondrial membrane 17 homolog A (yeast)	57107	TIMM17A	0.619	+	1.01E-02	1.09E-02
219184_PM_x_at	translocase of inner mitochondrial membrane 22 homolog (yeast)	6711	TIMM22	0.291	+	1.05E-02	2.12E-02
218118_PM_s_at	translocase of inner mitochondrial membrane 23 homolog (yeast)	147339	TIMM23	0.404	+	8.95E-03	2.64E-02
225535_PM_s_at	translocase of inner mitochondrial membrane 23 homolog (yeast)	284485	TIMM23	0.294	+	1.57E-02	1.88E-03
205217_PM_at	translocase of inner mitochondrial membrane 8 homolog A (yeast)	205	TIMM8A	0.500	+	4.51E-03	1.02E-02
219058_PM_x_at	tubulointerstitial nephritis antigen-like 1	415056	TINAGL1	0.300	+	9.84E-04	3.99E-03
201922_PM_at	TGF beta-inducible nuclear protein 1	541578 /// 91966	TINP1	0.355	+	2.82E-03	1.32E-03
212665_PM_at	TCDD-inducible poly(ADP-ribose) polymerase	10529	TIPARP	0.692	+	8.88E-03	7.48E-03
204872_PM_at	361eparin361ing-like enhancer of split 4 (E(sp1) homolog, Drosophila)	4849	TLE4	0.648	+	1.88E-02	2.38E-03
202606_PM_s_at	tousled-like kinase 1	54816	TLK1	0.572	+	1.51E-02	3.02E-02
228627_PM_at	tousled-like kinase 2	285636	TLK2	0.378	+	4.73E-03	2.38E-02
212997_PM_s_at	tousled-like kinase 2	6861	TLK2	0.353	+	9.69E-03	1.73E-03
236132_PM_at	talin 1	63939	TLN1	0.290	+	1.56E-02	1.29E-02
220146_PM_at	toll-like receptor 7	9702	TLR7	0.413	+	1.63E-02	2.42E-02
213883_PM_s_at	TM2 domain containing 1	4238	TM2D1	1.105	+	2.27E-03	1.41E-03
211703_PM_s_at	TM2 domain containing 1	114112	TM2D1	0.315	+	2.48E-02	2.35E-02
224413_PM_s_at	TM2 domain containing 2	647087	TM2D2	0.280	+	1.97E-03	9.93E-03
209150_PM_s_at	transmembrane 9 superfamily member 1	27019	TM9SF1	0.301	+	1.74E-02	9.13E-03
235146_PM_at	transmembrane and coiled-coil domain family 3	8880	TMCC3	0.543	+	2.53E-02	2.64E-02
208716_PM_s_at	transmembrane and coiled-coil domains 1	79869	TMCO1	0.348	+	1.69E-03	2.63E-03
210768_PM_x_at	transmembrane and coiled-coil domains 1	84281	TMCO1	0.417	+	2.56E-02	1.42E-02

202194_PM_at	transmembrane emp24 protein transport domain containing 5	8028	TMED5	0.575	+	2.38E-02	1.65E-02
209404_PM_s_at	transmembrane emp24 protein transport domain containing 7	55914	TMED7	0.306	+	1.71E-02	4.49E-03
225343_PM_at	transmembrane emp24 protein transport domain containing 8	146434	TMED8	0.442	+	1.77E-02	7.78E-03
205122_PM_at	transmembrane protein with EGF-like and two follistatin-like domains 1	2309	TMEFF1	0.555	+	4.07E-02	1.62E-03
219230_PM_at	transmembrane protein 100	6500	TMEM100	0.610	+	1.95E-03	1.70E-04
201764_PM_at	transmembrane protein 106C	10042	TMEM106C	0.397	+	7.15E-04	1.10E-03
239824_PM_s_at	transmembrane protein 107	---	TMEM107	0.298	+	2.26E-02	1.82E-02
223334_PM_at	transmembrane protein 126A	79929	TMEM126A	0.426	+	4.48E-03	1.02E-03
221622_PM_s_at	transmembrane protein 126B	23495	TMEM126B	0.620	+	8.02E-04	8.04E-05
218477_PM_at	transmembrane protein 14A	84456	TMEM14A	0.517	+	3.24E-05	4.24E-04
227861_PM_at	transmembrane protein 161B	9188	TMEM161B	0.518	+	2.13E-02	1.06E-02
226276_PM_at	transmembrane protein 167A	4534	TMEM167A	0.674	+	1.96E-03	3.52E-03
224702_PM_at	transmembrane protein 167A	1385	TMEM167A	0.316	+	4.17E-02	2.57E-02
218962_PM_s_at	transmembrane protein 168	6853	TMEM168	0.896	+	1.08E-02	2.27E-02
235798_PM_at	transmembrane protein 170B	4173	TMEM170B	0.686	+	3.37E-03	2.53E-04
229302_PM_at	transmembrane protein 178	246175	TMEM178	0.308	+	3.06E-02	1.77E-02
225489_PM_at	transmembrane protein 18	139322	TMEM18	0.515	+	9.49E-03	4.70E-02
219074_PM_at	transmembrane protein 184C	253143	TMEM184C	0.357	+	2.86E-03	1.48E-02
204340_PM_at	transmembrane protein 187	10549	TMEM187	0.453	+	5.17E-04	1.05E-03
235812_PM_at	transmembrane protein 188	57223	TMEM188	0.425	+	1.33E-04	3.00E-03
223186_PM_at	transmembrane protein 189 /// ubiquitin-conjugating enzyme E2 variant 1	55617	TMEM189 /// UBE2V1	0.501	+	1.57E-02	1.51E-02
229126_PM_at	transmembrane protein 19	5989	TMEM19	1.010	+	4.99E-04	3.08E-04
223305_PM_at	transmembrane protein 216	2850	TMEM216	0.830	+	2.27E-03	3.65E-03
226073_PM_at	transmembrane protein 218	26118	TMEM218	0.590	+	5.36E-03	1.34E-02
219569_PM_s_at	transmembrane protein 22	8895	TMEM22	0.460	+	3.23E-02	5.74E-04
222391_PM_at	transmembrane protein 30A	9728	TMEM30A	0.325	+	2.26E-03	3.69E-03
225492_PM_at	transmembrane protein 33	57118	TMEM33	0.401	+	2.76E-03	7.83E-03
212622_PM_at	transmembrane protein 41B	9936	TMEM41B	0.565	+	1.21E-02	5.06E-03
209656_PM_s_at	transmembrane protein 47	53349	TMEM47	0.433	+	9.78E-03	2.13E-02
234672_PM_s_at	transmembrane protein 48	---	TMEM48	0.582	+	3.45E-02	3.87E-02

204808_PM_s_at	transmembrane protein 5	29994	TMEM5	0.461	+	2.20E-02	3.59E-02
225182_PM_at	transmembrane protein 50B	5810	TMEM50B	0.325	+	2.42E-02	5.60E-03
200620_PM_at	transmembrane protein 59	1082 /// 93659	TMEM59	0.346	+	9.53E-05	6.79E-04
223396_PM_at	transmembrane protein 60	55334	TMEM60	0.527	+	1.55E-03	2.12E-03
241342_PM_at	transmembrane protein 65	55342	TMEM65	0.441	+	1.29E-03	1.10E-02
219449_PM_s_at	transmembrane protein 70	51097	TMEM70	0.440	+	5.43E-03	8.49E-04
1552520_PM_at	transmembrane protein 74	5905	TMEM74	0.693	+	1.54E-02	1.55E-02
229957_PM_at	transmembrane protein 91	---	TMEM91	0.283	+	4.37E-03	4.23E-02
221255_PM_s_at	transmembrane protein 93	10090	TMEM93	0.331	+	4.17E-02	4.88E-02
212282_PM_at	transmembrane protein 97	645	TMEM97	0.715	+	7.48E-03	4.81E-02
212281_PM_s_at	transmembrane protein 97	8899	TMEM97	0.895	+	7.82E-03	2.75E-02
226565_PM_at	transmembrane protein 99	100287552	TMEM99	0.351	+	6.59E-04	4.80E-04
227685_PM_at	TATA element modulatory factor 1	9935	TMF1	0.415	+	3.21E-02	1.31E-02
226186_PM_at	tropomodulin 2 (neuronal)	3340	TMOD2	0.415	+	3.94E-03	1.08E-02
224944_PM_at	thymopoietin	8082	TMPO	0.319	+	3.58E-02	2.25E-03
214051_PM_at	thymosin beta 15B	26038	TMSB15B	0.583	+	9.15E-03	1.77E-02
226604_PM_at	transmembrane and tetratricopeptide repeat containing 3	2902	TMTC3	0.392	+	2.87E-02	2.66E-02
225666_PM_at	transmembrane and tetratricopeptide repeat containing 4	9647	TMTC4	0.345	+	2.06E-02	1.14E-02
209476_PM_at	thioredoxin-related transmembrane protein 1	9462	TMX1	0.420	+	1.19E-02	6.16E-03
225302_PM_at	thioredoxin-related transmembrane protein 3	23413	TMX3	0.603	+	4.69E-03	1.29E-02
201581_PM_at	thioredoxin-related transmembrane protein 4	23658	TMX4	0.336	+	8.73E-03	1.58E-02
223583_PM_at	tumor necrosis factor, alpha-induced protein 8-like 2	51003	TNFAIP8L2	0.264	+	1.67E-02	3.49E-02
207641_PM_at	tumor necrosis factor receptor superfamily, member 13B	23405	TNFRSF13B	0.363	+	9.04E-03	2.17E-02
210314_PM_x_at	tumor necrosis factor (ligand) superfamily, member 13	128061	TNFSF13	0.613	+	1.55E-02	4.12E-02
207426_PM_s_at	tumor necrosis factor (ligand) superfamily, member 4	23032	TNFSF4	0.454	+	4.66E-02	4.80E-02
239288_PM_at	TRAF2 and NCK interacting kinase	---	TNIK	0.731	+	1.72E-02	3.68E-02
217149_PM_x_at	tyrosine kinase, non-receptor, 1	93183	TNK1	0.388	+	3.48E-03	6.46E-04
218228_PM_s_at	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	283635	TNKS2	0.305	+	2.25E-02	7.13E-03
225765_PM_at	transportin 1	284339	TNPO1	0.453	+	9.49E-03	2.45E-02
212635_PM_at	transportin 1	22924	TNPO1	0.490	+	1.92E-02	3.65E-02
215844_PM_at	transportin 2	80143	TNPO2	0.296	+	4.66E-02	4.68E-02

224704_PM_at	trinucleotide repeat containing 6A	3977	TNRC6A	0.591	+	2.37E-03	3.34E-03
217853_PM_at	tensin 3	128866	TNS3	0.591	+	7.50E-03	1.32E-02
200662_PM_s_at	translocase of outer mitochondrial membrane 20 homolog (yeast)	9465	TOMM20	0.282	+	5.30E-03	5.75E-03
226059_PM_at	translocase of outer mitochondrial membrane 40 homolog (yeast)-like	26118	TOMM40L	0.507	+	4.64E-02	1.18E-02
225036_PM_at	translocase of outer mitochondrial membrane 5 homolog (yeast)	2737	TOMM5	0.465	+	4.04E-03	7.84E-03
201519_PM_at	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	8202	TOMM70A	0.290	+	1.35E-02	7.32E-03
211987_PM_at	topoisomerase (DNA) II beta 180kDa	5351	TOP2B	0.415	+	1.97E-02	2.46E-02
202633_PM_at	topoisomerase (DNA) II binding protein 1	81926	TOPBP1	0.624	+	3.64E-02	1.62E-02
204071_PM_s_at	topoisomerase I binding, arginine/serine-rich	481	TOPORS	0.572	+	9.49E-03	1.48E-02
212408_PM_at	torsin A interacting protein 1	9648	TOR1AIP1	0.449	+	1.83E-02	2.21E-02
215108_PM_x_at	TOX high mobility group box family member 3	51018	TOX3	0.804	+	2.66E-02	2.46E-02
225912_PM_at	tumor protein p53 inducible nuclear protein 1	728052	TP53INP1	0.774	+	1.82E-02	1.18E-02
201690_PM_s_at	tumor protein D52	4976	TPD52	0.270	+	1.38E-03	7.88E-04
203786_PM_s_at	tumor protein D52-like 1	55885	TPD52L1	0.489	+	1.76E-02	3.95E-02
224164_PM_at	tropomyosin 3	54414	TPM3	0.383	+	8.20E-04	9.38E-04
230104_PM_s_at	tubulin polymerization promoting protein	27253	TPPP	0.368	+	3.34E-02	1.51E-02
219030_PM_at	TP53RK binding protein	83851	TPRKB	0.991	+	7.16E-03	2.18E-02
217023_PM_x_at	tryptase alpha/beta 1 /// tryptase beta 2	84275	TPSAB1 /// TPSB2	0.299	+	5.70E-03	2.01E-02
204140_PM_at	tyrosylprotein sulfotransferase 1	1977	TPST1	0.324	+	3.43E-02	4.29E-02
200893_PM_at	transformer 2 beta homolog (Drosophila)	276 /// 277 /// 278 /// 279 /// 280	TRA2B	0.341	+	5.84E-03	8.08E-03
1729_PM_at	TNFRSF1A-associated via death domain	5783	TRADD	0.352	+	6.53E-03	6.68E-04
204352_PM_at	TNF receptor-associated factor 5	10193	TRAF5	0.507	+	3.29E-03	1.51E-02
238628_PM_s_at	trafficking protein particle complex 2-like	199870	TRAPPC2L	0.296	+	4.35E-02	3.12E-02
203512_PM_at	trafficking protein particle complex 3	84314	TRAPPC3	0.421	+	2.08E-03	1.34E-02
202241_PM_at	tribbles homolog 1 (Drosophila)	2752	TRIB1	0.327	+	4.66E-02	8.46E-03
205151_PM_s_at	TLR4 interactor with leucine rich repeats	11102	TRIL	0.673	+	2.70E-03	7.63E-03

202702_PM_at	tripartite motif-containing 26	23420 /// 283820 /// 408050	TRIM26	0.281	+	3.58E-02	1.69E-02
212435_PM_at	tripartite motif-containing 33	58487	TRIM33	0.578	+	3.31E-02	1.68E-02
222732_PM_at	tripartite motif-containing 39	25924	TRIM39	0.582	+	6.66E-03	2.49E-02
217760_PM_at	tripartite motif-containing 44	134553	TRIM44	0.397	+	4.25E-02	4.15E-02
221897_PM_at	tripartite motif-containing 52	6430	TRIM52	0.424	+	9.60E-03	1.76E-02
236972_PM_at	tripartite motif-containing 63	---	TRIM63	0.853	+	1.04E-02	1.66E-02
221012_PM_s_at	tripartite motif-containing 8	22863	TRIM8	0.479	+	2.81E-02	1.73E-02
218877_PM_s_at	tRNA methyltransferase 11 homolog (S. cerevisiae)	2801	TRMT11	0.451	+	1.34E-04	1.00E-04
227653_PM_at	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)	56888	TRMT5	0.575	+	8.22E-03	1.21E-02
221229_PM_s_at	tRNA methyltransferase 61 homolog B (S. cerevisiae)	55922	TRMT61B	0.515	+	3.38E-02	2.13E-02
222754_PM_at	tRNA nucleotidyl transferase, CCA-adding, 1	3691	TRNT1	0.329	+	1.39E-02	3.73E-02
213027_PM_at	TROVE domain family, member 2	5128	TROVE2	0.673	+	3.01E-02	4.88E-02
205803_PM_s_at	transient receptor potential cation channel, subfamily C, member 1	2915	TRPC1	0.340	+	1.49E-02	2.12E-02
221102_PM_s_at	transient receptor potential cation channel, subfamily M, member 6	27107	TRPM6	0.294	+	8.38E-03	3.74E-02
223324_PM_s_at	transient receptor potential cation channel, subfamily M, member 7	2744	TRPM7	0.383	+	2.01E-02	4.45E-02
218502_PM_s_at	trichorhinophalangeal syndrome I	2562	TRPS1	0.516	+	2.12E-03	1.00E-02
223109_PM_at	TruB pseudouridine (psi) synthase homolog 2 (E. coli)	55848	TRUB2	0.564	+	1.27E-03	9.46E-05
208763_PM_s_at	TSC22 domain family, member 3	51138	TSC22D3	0.338	+	9.32E-03	8.31E-04
201758_PM_at	tumor susceptibility gene 101	4134	TSG101	0.548	+	1.29E-02	2.27E-02
223282_PM_at	teashirt zinc finger homeobox 1	83452	TSHZ1	0.651	+	1.45E-03	5.16E-03
223393_PM_s_at	teashirt zinc finger homeobox 3	55629	TSHZ3	0.807	+	1.21E-02	2.41E-02
201515_PM_s_at	translin	7337	TSN	0.285	+	8.01E-03	9.08E-03
201513_PM_at	translin	1612	TSN	0.411	+	1.38E-02	5.98E-04
203983_PM_at	translin-associated factor X	3728	TSNAX	0.481	+	2.16E-02	1.70E-02
203227_PM_s_at	tetraspanin 31	84866	TSPAN31	0.454	+	7.01E-03	1.77E-02
209108_PM_at	tetraspanin 6	29922	TSPAN6	0.374	+	4.89E-02	3.58E-02
213122_PM_at	TSPY-like 5	10085	TSPYL5	0.493	+	4.72E-03	1.79E-02
230191_PM_at	tau tubulin kinase 1	3841	TTBK1	0.465	+	2.56E-02	2.38E-02
201434_PM_at	tetratricopeptide repeat domain 1	2213	TTC1	0.580	+	1.24E-03	1.24E-03

225180_PM_at	tetratricopeptide repeat domain 14	55153	TTC14	0.361	+	1.97E-02	1.34E-02
229169_PM_at	tetratricopeptide repeat domain 18	140461	TTC18	0.315	+	9.73E-03	2.63E-02
229170_PM_s_at	tetratricopeptide repeat domain 18	---	TTC18	0.278	+	4.09E-02	1.33E-02
203584_PM_at	tetratricopeptide repeat domain 35	56990	TTC35	0.532	+	5.74E-03	7.73E-03
203049_PM_s_at	tetratricopeptide repeat domain 37	63905	TTC37	0.564	+	9.52E-03	8.66E-03
238480_PM_at	tetratricopeptide repeat domain 39C	440574	TTC39C	0.694	+	2.57E-04	3.47E-03
226152_PM_at	tetratricopeptide repeat domain 7B	22906	TTC7B	0.619	+	3.00E-02	4.10E-02
226120_PM_at	tetratricopeptide repeat domain 8	5903	TTC8	0.513	+	1.64E-02	1.48E-02
224896_PM_s_at	tubulin tyrosine ligase	9213	TTL	0.685	+	2.51E-02	5.82E-03
202266_PM_at	TRAF and TNF receptor associated protein	166	TTRAP	0.497	+	1.80E-03	3.98E-03
209191_PM_at	tubulin, beta 6	57718	TUBB6	0.484	+	3.72E-02	4.12E-02
203690_PM_at	tubulin, gamma complex associated protein 3	29761	TUBGCP3	0.520	+	2.62E-02	1.24E-02
213266_PM_at	Tubulin, gamma complex associated protein 4	23062	TUBGCP4	0.607	+	9.85E-03	2.20E-02
238190_PM_at	Tu translation elongation factor, mitochondrial	---	TUFM	0.305	+	2.47E-02	3.78E-02
201745_PM_at	twinfilin, actin-binding protein, homolog 1 (Drosophila)	23522	TWF1	0.700	+	1.61E-02	1.71E-02
226784_PM_at	TWIST neighbor	137886	TWISTNB	0.471	+	2.55E-02	4.58E-02
208864_PM_s_at	thioredoxin	51642	TXN	0.272	+	2.06E-02	1.56E-02
226747_PM_at	thioredoxin domain containing 16	440026	TXNDC16	0.847	+	7.77E-03	6.92E-03
224511_PM_s_at	thioredoxin domain containing 17	440574	TXNDC17	0.564	+	2.84E-03	5.57E-03
228743_PM_at	thioredoxin domain containing 17	---	TXNDC17	0.344	+	2.49E-02	4.15E-02
202836_PM_s_at	thioredoxin-like 4A	83939	TXNL4A	0.469	+	1.21E-03	3.87E-03
201266_PM_at	thioredoxin reductase 1	9568	TXNRD1	0.402	+	2.21E-02	5.84E-03
59631_PM_at	thioredoxin reductase 3	---	TXNRD3	0.473	+	7.25E-03	8.88E-03
223279_PM_s_at	uveal autoantigen with coiled-coil domains and ankyrin repeats	64388	UACA	0.752	+	3.37E-02	3.86E-02
201177_PM_s_at	ubiquitin-like modifier activating enzyme 2	8726	UBA2	0.520	+	9.60E-03	2.59E-03
209115_PM_at	ubiquitin-like modifier activating enzyme 3	80723	UBA3	0.454	+	3.36E-03	3.24E-03
222602_PM_at	ubiquitin-like modifier activating enzyme 6	10464	UBA6	0.272	+	2.02E-03	6.34E-03
222601_PM_at	ubiquitin-like modifier activating enzyme 6	57205	UBA6	0.446	+	7.57E-03	4.37E-02
46270_PM_at	ubiquitin associated protein 1	---	UBAP1	0.430	+	2.39E-02	1.18E-02
221490_PM_at	ubiquitin associated protein 1	8745	UBAP1	0.526	+	2.55E-02	1.69E-02
214695_PM_at	ubiquitin associated protein 2-like	10363	UBAP2L	0.362	+	3.31E-03	2.59E-02

201377_PM_at	ubiquitin associated protein 2-like	594	UBAP2L	0.760	+	4.34E-02	4.68E-02
238462_PM_at	ubiquitin associated and SH3 domain containing, B	---	UBASH3B	0.660	+	9.51E-03	1.31E-02
202334_PM_s_at	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	51510	UBE2B	0.363	+	3.53E-02	4.19E-02
227790_PM_at	ubiquitin-conjugating enzyme E2C binding protein	84066	UBE2CBP	0.345	+	3.52E-02	3.13E-02
211764_PM_s_at	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	11240	UBE2D1	0.411	+	2.40E-02	2.21E-02
201344_PM_at	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)	7422	UBE2D2	0.696	+	3.08E-03	5.27E-03
209141_PM_at	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast)	54886	UBE2G1	0.338	+	2.10E-02	2.02E-03
1557053_PM_s_at	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	51663	UBE2G2	0.394	+	6.64E-03	3.51E-02
209042_PM_s_at	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	79668	UBE2G2	0.552	+	4.64E-02	4.29E-02
222421_PM_at	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	23258	UBE2H	0.607	+	2.79E-02	2.57E-02
212751_PM_at	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast)	9166	UBE2N	0.281	+	2.10E-02	2.36E-03
224747_PM_at	ubiquitin-conjugating enzyme E2Q family member 2	10944	UBE2Q2	0.513	+	1.39E-02	2.78E-02
223229_PM_at	ubiquitin-conjugating enzyme E2T (putative)	56603	UBE2T	0.408	+	4.19E-02	3.28E-02
209096_PM_at	ubiquitin-conjugating enzyme E2 variant 2	10000	UBE2V2	0.483	+	5.35E-04	8.64E-04
222656_PM_at	ubiquitin-conjugating enzyme E2W (putative)	23035	UBE2W	0.360	+	1.03E-02	5.21E-04
222657_PM_s_at	ubiquitin-conjugating enzyme E2W (putative)	7474	UBE2W	0.571	+	1.13E-02	1.72E-02
213128_PM_s_at	ubiquitin protein ligase E3A	7292	UBE3A	0.477	+	3.93E-03	1.39E-02
211285_PM_s_at	ubiquitin protein ligase E3A	3192	UBE3A	0.401	+	2.44E-02	4.53E-02
212403_PM_at	ubiquitin protein ligase E3B	22908	UBE3B	0.451	+	4.88E-03	3.28E-03
201817_PM_at	ubiquitin protein ligase E3C	1508	UBE3C	0.285	+	7.23E-03	1.12E-02
202038_PM_at	ubiquitination factor E4A (UFD2 homolog, yeast)	23348	UBE4A	0.648	+	2.02E-03	2.91E-03
201535_PM_at	ubiquitin-like 3	11054	UBL3	0.531	+	3.82E-02	2.30E-02
207253_PM_s_at	ubinuclein 1	23014	UBN1	0.351	+	1.69E-02	4.29E-02
225444_PM_at	ubinuclein 2	56977	UBN2	0.714	+	7.27E-03	1.27E-02
224513_PM_s_at	ubiquilin 4	5898	UBQLN4	0.623	+	5.12E-03	2.74E-04
226921_PM_at	ubiquitin protein ligase E3 component n-recognin 1	388650	UBR1	0.757	+	6.45E-03	1.68E-03
212760_PM_at	ubiquitin protein ligase E3 component n-recognin 2	8570	UBR2	0.379	+	1.82E-03	1.84E-02
230029_PM_x_at	ubiquitin protein ligase E3 component n-recognin 3 (putative)	254778	UBR3	0.412	+	3.57E-02	2.28E-02
208883_PM_at	ubiquitin protein ligase E3 component n-recognin 5	51562	UBR5	0.811	+	2.42E-02	2.87E-02
208882_PM_s_at	ubiquitin protein ligase E3 component n-recognin 5	29887	UBR5	0.786	+	2.99E-02	2.88E-02
212934_PM_at	UBX domain protein 2B	55658	UBXN2B	0.271	+	7.66E-03	1.61E-02

204616_PM_at	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	6311	UCHL3	0.432	+	7.52E-03	9.74E-03
228142_PM_at	ubiquinol-cytochrome c reductase complex (7.2 kD)	80223	UCRC	0.265	+	7.21E-03	3.22E-02
218449_PM_at	UFM1-specific peptidase 2	125150	UFSP2	0.348	+	1.59E-02	2.99E-02
231968_PM_at	UDP-glucose glycoprotein glucosyltransferase 1	93	UGGT1	0.448	+	6.65E-03	4.58E-02
226135_PM_at	UHRF1 binding protein 1	7528	UHRF1BP1	0.490	+	8.15E-03	3.87E-03
213118_PM_at	UHRF1 binding protein 1-like	3358	UHRF1BP1L	0.553	+	2.92E-04	4.58E-04
204063_PM_s_at	unc-51-like kinase 2 (C. elegans)	2773	ULK2	0.550	+	2.58E-02	3.07E-02
202893_PM_at	unc-13 homolog B (C. elegans)	51192	UNC13B	0.323	+	3.36E-02	3.03E-02
203583_PM_at	unc-50 homolog (C. elegans)	56990	UNC50	0.353	+	3.92E-03	1.63E-02
231325_PM_at	unc-5 homolog D (C. elegans)	202181	UNC5D	0.475	+	3.82E-02	2.20E-02
243523_PM_at	LMNE6487	---	UNQ6487	0.409	+	2.11E-02	4.11E-02
228219_PM_s_at	ureidopropionase, beta	---	UPB1	0.359	+	2.38E-02	9.99E-03
203519_PM_s_at	UPF2 regulator of nonsense transcripts homolog (yeast)	60412	UPF2	0.353	+	1.44E-02	3.52E-02
218757_PM_s_at	UPF3 regulator of nonsense transcripts homolog B (yeast)	221786	UPF3B	0.389	+	1.34E-02	2.11E-02
205849_PM_s_at	ubiquinol-cytochrome c reductase binding protein	6915	UQCRB	0.335	+	5.55E-04	1.98E-03
209066_PM_x_at	ubiquinol-cytochrome c reductase binding protein	64129	UQCRB	0.300	+	1.60E-02	4.10E-02
244293_PM_at	ubiquinol-cytochrome c reductase binding protein	---	UQCRB	0.539	+	2.02E-02	1.56E-02
212600_PM_s_at	ubiquinol-cytochrome c reductase core protein II	6996	UQCRC2	0.325	+	2.47E-02	2.08E-02
202233_PM_s_at	ubiquinol-cytochrome c reductase hinge protein	7416	UQCRH	0.366	+	1.20E-02	3.57E-03
218386_PM_x_at	ubiquitin specific peptidase 16	440823	USP16	0.678	+	5.14E-03	1.88E-03
228822_PM_s_at	ubiquitin specific peptidase 16	55500	USP16	0.765	+	7.96E-03	6.83E-03
226357_PM_at	ubiquitin specific peptidase 19	9856	USP19	0.643	+	2.83E-03	4.55E-03
223167_PM_s_at	ubiquitin specific peptidase 25	55315	USP25	0.643	+	1.65E-02	1.64E-02
220419_PM_s_at	ubiquitin specific peptidase 25	3727	USP25	0.347	+	2.46E-02	1.35E-02
212513_PM_s_at	ubiquitin specific peptidase 33	1000	USP33	0.427	+	3.49E-02	1.23E-02
212066_PM_s_at	ubiquitin specific peptidase 34	8407	USP34	0.521	+	1.25E-02	2.99E-02
232033_PM_at	ubiquitin specific peptidase 37	---	USP37	0.446	+	1.37E-03	5.26E-03
226730_PM_s_at	ubiquitin specific peptidase 37	286451	USP37	0.475	+	1.60E-02	1.36E-02
223288_PM_at	ubiquitin specific peptidase 38	81034	USP38	0.432	+	1.54E-02	3.08E-02
226669_PM_at	ubiquitin specific peptidase 42	677	USP42	0.560	+	3.86E-02	2.59E-02
238057_PM_at	ubiquitin specific peptidase 45	---	USP45	0.279	+	4.80E-03	6.23E-03

203870_PM_at	ubiquitin specific peptidase 46	2782	USP46	0.476	+	3.15E-02	1.41E-02
223117_PM_s_at	ubiquitin specific peptidase 47	54780	USP47	0.435	+	1.03E-02	3.10E-02
229501_PM_s_at	ubiquitin specific peptidase 8	---	USP8	0.714	+	3.09E-02	2.93E-02
201099_PM_at	ubiquitin specific peptidase 9, X-linked	10767	USP9X	0.813	+	2.51E-02	2.32E-02
229573_PM_at	ubiquitin specific peptidase 9, X-linked	5814	USP9X	0.528	+	3.34E-02	2.88E-02
205139_PM_s_at	uronyl-2-sulfotransferase	1120	UST	0.411	+	1.83E-03	1.35E-02
218235_PM_s_at	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	54476	UTP11L	0.377	+	3.62E-02	3.57E-02
203614_PM_at	UTP14, U3 small nucleolar ribonucleoprotein, homolog C (yeast)	89886	UTP14C	0.286	+	1.28E-02	4.81E-02
203721_PM_s_at	UTP18, small subunit (SSU) processome component, homolog (yeast)	100131735 /// 100291994 /// 27316 /// 494115	UTP18	0.665	+	3.96E-02	3.21E-02
225093_PM_at	utrophin	114785	UTRN	0.517	+	3.98E-02	4.95E-02
218495_PM_at	ubiquitously-expressed transcript	9589	UXT	0.423	+	1.87E-02	9.97E-03
213326_PM_at	vesicle-associated membrane protein 1 (synaptobrevin 1)	81689	VAMP1	0.647	+	2.74E-02	1.02E-02
213480_PM_at	vesicle-associated membrane protein 4	4116	VAMP4	0.869	+	7.82E-03	6.02E-03
202829_PM_s_at	vesicle-associated membrane protein 7	51523	VAMP7	0.742	+	3.36E-02	1.03E-02
225198_PM_at	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	7637	VAPA	0.341	+	1.53E-02	4.67E-02
226200_PM_at	valyl-tRNA synthetase 2, mitochondrial (putative)	3709	VARS2	0.487	+	1.51E-02	4.57E-02
225867_PM_at	vasorin	---	VASN	0.390	+	4.91E-03	1.17E-02
201472_PM_at	von Hippel-Lindau binding protein 1	4771	VBP1	0.367	+	1.60E-03	3.06E-03
204619_PM_s_at	versican	5440	VCAN	0.847	+	1.75E-02	4.91E-03
200931_PM_s_at	vinculin	824	VCL	0.574	+	7.45E-03	9.90E-03
1556228_PM_a_at	valosin containing protein (p97)/p47 complex interacting protein 1	4659	VCPIP1	0.337	+	8.17E-03	2.84E-02
210512_PM_s_at	vascular endothelial growth factor A	729967	VEGFA	0.497	+	2.39E-02	1.89E-02
202172_PM_at	vascular endothelial zinc finger 1	2335	VEZF1	0.429	+	4.04E-02	2.43E-02
223090_PM_x_at	vezatin, adherens junctions transmembrane protein	64318	VEZT	0.585	+	2.49E-02	4.00E-02
223675_PM_s_at	vezatin, adherens junctions transmembrane protein	81563	VEZT	0.670	+	3.09E-02	3.95E-02
224881_PM_at	vitamin K epoxide reductase complex, subunit 1-like 1	84186	VKORC1L1	0.457	+	6.04E-03	8.92E-03
225556_PM_at	VMA21 vacuolar H+-ATPase homolog (S. cerevisiae)	205327	VMA21	0.505	+	7.83E-03	2.03E-02

208091_PM_s_at	vesicular, overexpressed in cancer, prosurvival protein 1	23062	VOPP1	0.384	+	2.73E-03	3.95E-03
235023_PM_at	Vacuolar protein sorting 13 homolog C (S. cerevisiae)	8073	VPS13C	0.471	+	1.76E-04	6.15E-03
201807_PM_at	vacuolar protein sorting 26 homolog A (S. pombe)	23043	VPS26A	0.354	+	3.96E-02	2.50E-02
222478_PM_at	vacuolar protein sorting 36 homolog (S. cerevisiae)	23034	VPS36	0.581	+	2.23E-02	2.97E-02
209268_PM_at	vacuolar protein sorting 45 homolog (S. cerevisiae)	8675	VPS45	0.429	+	5.64E-03	6.67E-03
218171_PM_at	vacuolar protein sorting 4 homolog B (S. cerevisiae)	260425	VPS4B	0.407	+	3.42E-02	1.42E-02
218423_PM_x_at	vacuolar protein sorting 54 homolog (S. cerevisiae)	79796	VPS54	0.756	+	9.97E-03	5.34E-03
233656_PM_s_at	vacuolar protein sorting 54 homolog (S. cerevisiae)	---	VPS54	0.750	+	2.44E-02	1.46E-02
209553_PM_at	vacuolar protein sorting 8 homolog (S. cerevisiae)	112398	VPS8	0.277	+	4.85E-02	2.56E-02
203856_PM_at	vaccinia related kinase 1	9295	VRK1	0.330	+	1.25E-02	1.77E-02
1566701_PM_at	vaccinia related kinase 3	10651	VRK3	0.288	+	1.33E-02	2.58E-02
204787_PM_at	V-set and immunoglobulin domain containing 4	8803	VSIG4	0.366	+	1.71E-04	1.36E-03
223022_PM_s_at	Vps20-associated 1 homolog (S. cerevisiae)	80145	VTA1	0.407	+	1.79E-02	4.00E-02
224437_PM_s_at	Vps20-associated 1 homolog (S. cerevisiae)	283991	VTA1	0.266	+	2.46E-02	9.86E-03
225926_PM_at	vesicle transport through interaction with t-SNAREs homolog 1B (yeast)	---	VTI1B	0.448	+	1.11E-02	1.20E-02
238864_PM_at	von Willebrand factor A domain containing 3A	---	VWA3A	0.318	+	7.12E-03	2.12E-02
218766_PM_s_at	tryptophanyl tRNA synthetase 2, mitochondrial	131566	WARS2	0.393	+	4.16E-03	1.51E-02
205400_PM_at	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	5393	WAS	0.311	+	3.56E-02	3.57E-02
204042_PM_at	WAS protein family, member 3	6432	WASF3	0.433	+	1.01E-02	8.23E-03
217975_PM_at	WW domain binding protein 5	348235	WBP5	0.581	+	4.13E-03	1.20E-02
212606_PM_at	WD repeat and FYVE domain containing 3	51626	WDFY3	0.429	+	4.93E-02	3.29E-02
220917_PM_s_at	WD repeat domain 19	9849	WDR19	0.456	+	8.25E-03	2.53E-02
227541_PM_at	WD repeat domain 20	55160	WDR20	0.674	+	1.44E-02	3.19E-02
222763_PM_s_at	WD repeat domain 33	2210	WDR33	0.542	+	7.70E-03	1.58E-02
226889_PM_at	WD repeat domain 35	8724	WDR35	0.764	+	1.30E-02	5.86E-03
218055_PM_s_at	WD repeat domain 41	81846	WDR41	0.454	+	6.65E-03	1.09E-02
203855_PM_at	WD repeat domain 47	7332	WDR47	0.538	+	8.77E-03	2.31E-03
56919_PM_at	WD repeat domain 48	---	WDR48	0.315	+	2.96E-02	3.98E-02
225898_PM_at	WD repeat domain 54	441461	WDR54	0.283	+	5.49E-03	3.00E-04
235850_PM_at	WD repeat domain 5B	55754	WDR5B	1.031	+	6.14E-03	1.56E-02
217734_PM_s_at	WD repeat domain 6	90843	WDR6	0.348	+	3.95E-02	4.06E-02

232075_PM_at	WD repeat domain 61	7007	WDR61	0.380	+	3.51E-02	1.45E-02
215218_PM_s_at	WD repeat domain 62	54839	WDR62	0.306	+	5.42E-03	9.76E-03
224721_PM_at	WD repeat domain 75	90313	WDR75	0.463	+	1.98E-03	3.13E-03
222777_PM_s_at	Wolf-Hirschhorn syndrome candidate 1	2901	WHSC1	0.303	+	6.43E-03	6.90E-03
229103_PM_at	wingless-type MMTV integration site family, member 3	254225	WNT3	0.334	+	2.14E-02	4.00E-02
213425_PM_at	wingless-type MMTV integration site family, member 5A	659	WNT5A	0.462	+	5.53E-03	5.48E-03
230643_PM_at	wingless-type MMTV integration site family, member 9A	51046	WNT9A	0.680	+	5.49E-04	7.24E-04
213155_PM_at	WSC domain containing 1	23177	WSCD1	0.378	+	3.62E-02	2.73E-02
229630_PM_s_at	Wilms tumor 1 associated protein	400236	WTAP	0.420	+	1.81E-02	2.65E-02
219520_PM_s_at	WWC family member 3	1389	WWC3	0.470	+	1.31E-02	1.09E-02
204022_PM_at	WW domain containing E3 ubiquitin protein ligase 2	5701	WWP2	0.533	+	3.92E-02	1.32E-02
214567_PM_s_at	chemokine (C motif) ligand 1 /// chemokine (C motif) ligand 2	54927	XCL1 /// XCL2	0.422	+	6.23E-03	1.34E-02
214218_PM_s_at	X (inactive)-specific transcript (non-protein coding)	10038	XIST	0.377	+	4.15E-03	5.86E-03
221728_PM_x_at	X (inactive)-specific transcript (non-protein coding)	23705	XIST	0.471	+	9.16E-03	9.13E-03
206698_PM_at	X-linked Kx blood group (McLeod syndrome)	8500	XK	0.870	+	1.74E-02	3.74E-02
228820_PM_at	X-prolyl aminopeptidase (aminopeptidase P) 3, putative	768211	XPNPEP3	0.869	+	7.75E-03	2.10E-02
208775_PM_at	exportin 1 (CRM1 homolog, yeast)	56654	XPO1	0.435	+	3.45E-02	3.64E-02
222649_PM_at	exportin 4	126208	XPO4	0.353	+	2.48E-02	2.93E-02
226615_PM_at	xenotropic and polytropic retrovirus receptor	373	XPR1	0.590	+	2.14E-03	1.15E-02
205071_PM_x_at	X-ray repair complementing defective repair in Chinese hamster cells 4	1613	XRCC4	0.480	+	2.39E-02	3.67E-02
227678_PM_at	XRCC6 binding protein 1	51026	XRCC6BP1	1.103	+	1.55E-03	1.25E-03
225814_PM_at	5’-3’ exoribonuclease 1	---	XRN1	0.997	+	1.84E-02	3.08E-02
224894_PM_at	Yes-associated protein 1, 65kDa	148867	YAP1	0.891	+	6.82E-03	6.83E-03
224895_PM_at	Yes-associated protein 1, 65kDa	201161	YAP1	0.338	+	1.48E-02	1.29E-02
202932_PM_at	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	55591	YES1	0.843	+	4.50E-03	1.12E-02
202933_PM_s_at	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	114971	YES1	0.729	+	6.82E-03	2.65E-03
224934_PM_at	Yip1 domain family, member 5	54799	YIPF5	0.691	+	9.33E-03	1.01E-02
224949_PM_at	Yip1 domain family, member 5	80155	YIPF5	0.285	+	1.89E-02	1.74E-02
212343_PM_at	Yip1 domain family, member 6	9474	YIPF6	0.529	+	2.23E-02	2.09E-02
227309_PM_at	YOD1 OTU deubiquinating enzyme 1 homolog (S. cerevisiae)	6615	YOD1	0.718	+	1.99E-03	4.22E-03

1556420_PM_s_at	yippee-like 2 (Drosophila)	7163	YPEL2	0.664	+	2.45E-02	2.64E-02
217783_PM_s_at	yippee-like 5 (Drosophila)	150465	YPEL5	0.516	+	9.83E-03	7.36E-03
221741_PM_s_at	YTH domain family, member 1	2824	YTHDF1	0.450	+	4.72E-02	3.62E-02
221749_PM_at	YTH domain family, member 3	11196	YTHDF3	0.492	+	8.13E-03	1.93E-03
224711_PM_at	YY1 transcription factor	57630	YY1	0.354	+	4.06E-02	4.99E-02
200047_PM_s_at	YY1 transcription factor	9677	YY1	0.373	+	4.92E-02	3.38E-02
225665_PM_at	sterile alpha motif and leucine zipper containing kinase AZK	4534	ZAK	1.120	+	5.93E-03	2.18E-03
218263_PM_s_at	zinc finger, BED-type containing 5	440193	ZBED5	0.712	+	1.51E-02	1.21E-02
236105_PM_at	zinc finger and BTB domain containing 10	139231	ZBTB10	0.367	+	6.25E-03	1.68E-02
228562_PM_at	zinc finger and BTB domain containing 10	4082	ZBTB10	0.738	+	3.17E-02	7.06E-03
204847_PM_at	zinc finger and BTB domain containing 11	8898	ZBTB11	0.649	+	1.84E-02	8.45E-04
1553858_PM_at	zinc finger and BTB domain containing 3	8675	ZBTB3	0.559	+	2.65E-02	2.08E-02
226255_PM_at	zinc finger and BTB domain containing 33	1374	ZBTB33	0.643	+	6.62E-03	1.78E-02
227111_PM_at	zinc finger and BTB domain containing 34	22986	ZBTB34	0.685	+	9.54E-03	2.60E-03
225512_PM_at	zinc finger and BTB domain containing 38	23426	ZBTB38	0.480	+	2.63E-02	1.38E-02
225629_PM_s_at	zinc finger and BTB domain containing 4	79933	ZBTB4	0.463	+	1.61E-02	8.86E-03
227991_PM_x_at	zinc finger and BTB domain containing 43	54928	ZBTB43	0.398	+	4.28E-02	4.86E-02
227329_PM_at	zinc finger and BTB domain containing 46	55604	ZBTB46	0.454	+	2.00E-03	1.13E-03
229234_PM_at	zinc finger CCCH-type containing 12B	197131	ZC3H12B	0.763	+	1.44E-02	3.92E-02
213063_PM_at	zinc finger CCCH-type containing 14	5079	ZC3H14	0.298	+	1.64E-02	3.45E-02
201595_PM_s_at	zinc finger CCCH-type containing 15	10152	ZC3H15	0.347	+	6.41E-03	7.26E-04
213390_PM_at	zinc finger CCCH-type containing 4	5805	ZC3H4	0.365	+	1.89E-02	1.72E-02
241372_PM_at	zinc finger CCCH-type containing 6	---	ZC3H6	0.478	+	2.79E-02	2.71E-02
221193_PM_s_at	zinc finger, CCHC domain containing 10	6664	ZCCHC10	0.523	+	1.38E-02	2.20E-02
223107_PM_s_at	zinc finger, CCHC domain containing 17	63897	ZCCHC17	0.381	+	2.05E-02	1.32E-02
219062_PM_s_at	zinc finger, CCHC domain containing 2	25831	ZCCHC2	0.661	+	3.26E-02	2.22E-02
236155_PM_at	Zinc finger, CCHC domain containing 6	205	ZCCHC6	0.361	+	3.38E-02	2.69E-02
226496_PM_at	zinc finger, CCHC domain containing 7	51014	ZCCHC7	0.431	+	8.07E-03	1.41E-02
218478_PM_s_at	zinc finger, CCHC domain containing 8	169792	ZCCHC8	0.326	+	1.64E-02	3.14E-02
225538_PM_at	zinc finger, CCHC domain containing 9	821	ZCCHC9	0.433	+	2.54E-02	4.13E-02
228749_PM_at	zinc finger, DBF-type containing 2	115416	ZDBF2	0.524	+	3.03E-02	2.92E-02

222731_PM_at	zinc finger, DHHC-type containing 2	440434	ZDHHC2	0.292	+	2.16E-02	3.92E-03
229240_PM_at	Zinc finger, DHHC-type containing 21	85403	ZDHHC21	0.498	+	4.34E-03	5.08E-03
212764_PM_at	zinc finger E-box binding homeobox 1	10959	ZEB1	0.620	+	4.31E-03	1.22E-02
203603_PM_s_at	zinc finger E-box binding homeobox 2	149986	ZEB2	0.808	+	1.45E-02	3.26E-03
221613_PM_s_at	zinc finger, AN1-type domain 6	6425	ZFAND6	0.397	+	3.28E-03	1.65E-02
213065_PM_at	zinc finger, C3H1-type containing	2977	ZFC3H1	0.561	+	3.39E-02	1.99E-02
211962_PM_s_at	zinc finger protein 36, C3H type-like 1	2739	ZFP36L1	0.440	+	1.67E-02	2.68E-02
207068_PM_at	zinc finger protein 37 homolog (mouse)	11054	ZFP37	0.382	+	3.91E-02	9.99E-03
227796_PM_at	zinc finger protein 62 homolog (mouse)	84278	ZFP62	0.994	+	1.57E-02	1.60E-02
226124_PM_at	zinc finger protein 90 homolog (mouse)	9813	ZFP90	0.410	+	9.32E-03	7.57E-03
224636_PM_at	zinc finger protein 91 homolog (mouse)	84320	ZFP91	0.379	+	1.05E-02	1.00E-02
237463_PM_at	Zinc finger protein, multitype 1	---	ZFPM1	0.450	+	4.89E-03	1.16E-02
201857_PM_at	zinc finger RNA binding protein	5164	ZFR	0.302	+	3.55E-02	3.79E-02
214678_PM_x_at	zinc finger protein, X-linked	79893	ZFX	0.378	+	1.81E-02	3.05E-02
223387_PM_at	zinc finger, FYVE domain containing 1	25926	ZFYVE1	0.446	+	4.31E-02	4.83E-02
226581_PM_at	zinc finger, FYVE domain containing 20	2002	ZFYVE20	0.529	+	8.81E-03	1.03E-02
231765_PM_at	zinc finger, FYVE domain containing 20	374986	ZFYVE20	0.275	+	3.92E-02	3.57E-02
224445_PM_s_at	zinc finger, FYVE domain containing 21	57561	ZFYVE21	0.529	+	2.88E-03	3.47E-03
213073_PM_at	zinc finger, FYVE domain containing 26	1466	ZFYVE26	0.335	+	7.14E-03	1.90E-02
223642_PM_at	Zic family member 2 (odd-paired homolog, Drosophila)	29101	ZIC2	0.816	+	8.54E-03	9.26E-03
226344_PM_at	zinc finger, matrin type 1	79868	ZMAT1	0.904	+	1.10E-02	8.95E-03
212124_PM_at	zinc finger, MIZ-type containing 1	7322	ZMIZ1	0.577	+	1.83E-02	2.29E-02
202778_PM_s_at	zinc finger, MYM-type 2	84146	ZMYM2	0.482	+	3.61E-02	1.65E-02
202051_PM_s_at	zinc finger, MYM-type 4	116986	ZMYM4	0.557	+	2.75E-02	3.03E-02
213698_PM_at	zinc finger, MYM-type 6	7030	ZMYM6	0.989	+	3.18E-03	1.47E-02
227595_PM_at	zinc finger, MYM-type 6	7702	ZMYM6	1.085	+	1.28E-02	2.66E-02
226015_PM_at	zinc finger protein 12	10097	ZNF12	0.306	+	4.98E-02	3.45E-02
225916_PM_at	zinc finger protein 131	9223	ZNF131	0.511	+	3.04E-02	2.36E-02
206182_PM_at	zinc finger protein 134	9360	ZNF134	0.490	+	2.01E-02	4.59E-02
221873_PM_at	zinc finger protein 143	9318	ZNF143	0.736	+	3.22E-02	1.26E-02
230821_PM_at	zinc finger protein 148	3736	ZNF148	1.059	+	2.28E-03	7.65E-04
238711_PM_s_at	zinc finger protein 148	63929	ZNF148	0.433	+	7.84E-03	6.62E-03

239024_PM_at	zinc finger protein 148	---	ZNF148	0.484	+	2.54E-02	1.91E-02
219548_PM_at	zinc finger protein 16	9202	ZNF16	0.443	+	2.96E-02	2.57E-02
207417_PM_s_at	zinc finger protein 177	22826	ZNF177	0.611	+	2.26E-02	4.98E-02
235810_PM_at	zinc finger protein 182	6154	ZNF182	0.368	+	3.51E-02	1.94E-02
205437_PM_at	zinc finger protein 211	5324	ZNF211	0.702	+	1.06E-02	2.28E-02
203985_PM_at	zinc finger protein 212	1964 /// 280661	ZNF212	0.360	+	1.03E-03	4.67E-03
203739_PM_at	zinc finger protein 217	23077	ZNF217	0.385	+	1.26E-02	4.12E-02
218005_PM_at	zinc finger protein 22 (KOX 15)	54464	ZNF22	0.395	+	1.03E-02	1.42E-02
206261_PM_at	zinc finger protein 239	23558	ZNF239	0.278	+	1.26E-02	2.62E-02
213269_PM_at	zinc finger protein 248	25847	ZNF248	0.484	+	2.75E-03	3.70E-03
228920_PM_at	zinc finger protein 260	345778	ZNF260	0.459	+	4.10E-03	2.75E-02
203707_PM_at	zinc finger protein 263	23196	ZNF263	0.469	+	9.11E-03	2.44E-02
221213_PM_s_at	zinc finger protein 280D	9815	ZNF280D	0.805	+	1.13E-02	8.48E-03
228785_PM_at	Zinc finger protein 281	90459	ZNF281	0.650	+	1.56E-02	2.28E-03
225539_PM_at	zinc finger protein 295	85015	ZNF295	0.700	+	3.37E-02	4.55E-02
207753_PM_at	zinc finger protein 304	115201	ZNF304	0.426	+	2.26E-02	4.64E-02
236551_PM_at	zinc finger protein 311	---	ZNF311	0.730	+	9.29E-03	1.65E-02
203521_PM_s_at	zinc finger protein 318	116985	ZNF318	0.454	+	2.07E-02	1.82E-02
227980_PM_at	zinc finger protein 322A	285855	ZNF322A	0.735	+	9.55E-03	1.65E-03
227680_PM_at	zinc finger protein 326	79718	ZNF326	0.371	+	3.43E-03	1.86E-03
229019_PM_at	zinc finger protein 385B	55102	ZNF385B	0.543	+	3.94E-02	4.59E-02
227768_PM_at	zinc finger protein 407	79930	ZNF407	0.377	+	2.33E-03	1.95E-02
209944_PM_at	zinc finger protein 410	4090	ZNF410	0.731	+	8.82E-03	6.05E-04
202010_PM_s_at	zinc finger protein 410	6651	ZNF410	0.371	+	1.56E-02	2.27E-02
218707_PM_at	zinc finger protein 444	133690	ZNF444	0.412	+	1.80E-02	4.86E-02
228968_PM_at	zinc finger protein 449	57187	ZNF449	0.560	+	3.53E-02	4.60E-02
222028_PM_at	zinc finger protein 45	1399	ZNF45	0.387	+	3.16E-02	2.92E-02
212557_PM_at	zinc finger protein 451	8836	ZNF451	0.308	+	9.66E-03	3.21E-02
228138_PM_at	zinc finger protein 498	---	ZNF498	0.265	+	6.47E-03	4.02E-04
226327_PM_at	zinc finger protein 507	3730	ZNF507	0.502	+	3.04E-03	5.61E-03
204291_PM_at	zinc finger protein 518A	2631	ZNF518A	0.648	+	3.79E-02	3.56E-02
226909_PM_at	zinc finger protein 518B	6039	ZNF518B	0.605	+	8.48E-04	1.03E-03

226676_PM_at	zinc finger protein 521	58517	ZNF521	1.020	+	4.04E-03	7.28E-03
226677_PM_at	zinc finger protein 521	5411	ZNF521	0.804	+	1.33E-02	3.75E-02
231940_PM_at	zinc finger protein 529	8034	ZNF529	0.407	+	3.94E-03	1.66E-02
238316_PM_at	zinc finger protein 567	---	ZNF567	0.486	+	1.78E-02	4.27E-02
1568900_PM_a_at	zinc finger protein 568	51704	ZNF568	0.562	+	3.37E-03	2.57E-03
206648_PM_at	zinc finger protein 571	25956	ZNF571	0.361	+	5.68E-03	7.98E-03
218762_PM_at	zinc finger protein 574	112817	ZNF574	0.628	+	7.21E-03	7.91E-03
227674_PM_at	zinc finger protein 585A	64121	ZNF585A	0.424	+	5.76E-03	8.10E-04
227507_PM_at	zinc finger protein 592	50943	ZNF592	0.691	+	4.59E-02	3.51E-02
219635_PM_at	zinc finger protein 606	10444	ZNF606	0.456	+	8.11E-03	3.77E-02
227045_PM_at	zinc finger protein 614	9107	ZNF614	0.455	+	4.15E-02	3.68E-02
225152_PM_at	zinc finger protein 622	253260	ZNF622	0.585	+	1.48E-03	4.39E-03
206188_PM_at	zinc finger protein 623	10938	ZNF623	0.322	+	4.22E-03	9.10E-03
224492_PM_s_at	zinc finger protein 627	56261	ZNF627	0.505	+	1.56E-03	5.48E-03
213775_PM_x_at	zinc finger protein 638	6934	ZNF638	0.458	+	2.75E-02	3.33E-03
211257_PM_x_at	zinc finger protein 638	4287	ZNF638	0.378	+	4.32E-02	4.21E-02
222580_PM_at	zinc finger protein 644	23074	ZNF644	0.806	+	2.13E-02	8.13E-03
225266_PM_at	zinc finger protein 652	282679	ZNF652	0.534	+	7.65E-03	3.56E-03
228538_PM_at	zinc finger protein 662	23095	ZNF662	0.314	+	4.98E-02	2.52E-02
236635_PM_at	zinc finger protein 667	---	ZNF667	0.723	+	2.02E-02	1.80E-02
242923_PM_at	zinc finger protein 678	---	ZNF678	0.290	+	3.17E-02	2.11E-02
242915_PM_at	zinc finger protein 682	---	ZNF682	1.329	+	3.72E-04	2.00E-03
227080_PM_at	zinc finger protein 697	---	ZNF697	0.613	+	1.58E-03	1.13E-03
227132_PM_at	zinc finger protein 706	7091	ZNF706	0.351	+	1.70E-02	5.39E-03
1553247_PM_a_at	zinc finger protein 709	9181	ZNF709	0.682	+	3.03E-03	7.82E-03
228988_PM_at	zinc finger protein 711	51762	ZNF711	0.719	+	1.32E-02	9.45E-03
213659_PM_at	zinc finger protein 75D	23065	ZNF75D	0.453	+	1.50E-02	3.56E-02
229000_PM_at	zinc finger protein 77	25925	ZNF77	0.369	+	5.02E-03	2.02E-02
221968_PM_s_at	Zinc finger protein 771	7155	ZNF771	0.277	+	2.84E-02	4.65E-02
213402_PM_at	zinc finger protein 787	26052	ZNF787	0.279	+	7.71E-03	4.40E-03

235398_PM_at	zinc finger protein 805	4926	ZNF805	0.622	+	2.34E-02	3.09E-02
242564_PM_at	Zinc finger protein 814	79670	ZNF814	0.792	+	2.63E-02	4.30E-02
243618_PM_s_at	Zinc finger protein 827	---	ZNF827	0.819	+	1.98E-03	2.80E-03
243617_PM_at	Zinc finger protein 827	4842	ZNF827	0.859	+	2.64E-03	7.90E-04
228046_PM_at	Zinc finger protein 827	2309	ZNF827	0.730	+	1.58E-02	1.99E-02
228630_PM_at	zinc finger protein 84	2140	ZNF84	0.454	+	1.43E-02	1.34E-02
218932_PM_at	zinc finger, HIT type 6	64748	ZNHIT6	0.383	+	2.83E-03	1.80E-02
223716_PM_s_at	zinc finger, RAN-binding domain containing 2	51649	ZRANB2	0.430	+	1.55E-02	4.68E-03
213876_PM_x_at	zinc finger (CCCH type), RNA-binding motif and serine/arginine rich 2	123803	ZRSR2	0.473	+	2.46E-03	8.27E-03
219676_PM_at	zinc finger and SCAN domain containing 16	10664	ZSCAN16	0.321	+	3.79E-03	1.20E-02
229119_PM_s_at	zinc finger, SWIM-type containing 7	221830	ZSWIM7	0.588	+	1.83E-02	3.99E-02
228330_PM_at	zinc finger with UFM1-specific peptidase domain	29904	ZUFSP	0.378	+	6.90E-03	2.54E-02
228005_PM_at	zinc finger, X-linked, duplicated B	---	ZXDB	0.476	+	2.34E-02	3.67E-02
212893_PM_at	zinc finger, ZZ-type containing 3	8424	ZZZ3	0.636	+	1.46E-02	1.94E-02

Supplementary Table 10. Transcripts correlated (r>0.60 and r <-0.60) with mean total activity in the caudate nucleus. Transcripts are identified by their Affymetrix Probe Set ID, Gene Title, Gene Symbol, and Entrez Gene ID number. The last 2 columns denote Pearson correlations between gene expression and mean total activity in both caudate replicates (R1c and R2c). Positive correlations are indicated in red text and negative correlation is denoted by blue.

SUPPLEMENTARY TABLE 10. Transcripts correlated (r > 0.60 or r < -0.60) with mean total activity in the caudate.

Probe Set ID	Gene Title	Gene Symbol	Entrez Gene ID	ACT R1c r=	ACT R2c r=
215063_PM_x_at	leucine rich repeat containing 40	LRRC40	55631	-0.943	-0.799
218742_PM_at	nuclear prelamin A recognition factor-like	NARFL	64428	-0.942	-0.688
234913_PM_at	testis-specific transcript, Y-linked 4 (non-protein coding) /// testis-specific transcript, Y-linked 4B (non-protein coding) /	TTTY4 /// TTTY4B /// TTTY4C	114761 /// 474149 ///	-0.931	-0.721
201384_PM_s_at	neighbor of BRCA1 gene 1	NBR1	4077	-0.875	-0.937
232547_PM_at	SRC kinase signaling inhibitor 1	SRCIN1	80725	-0.865	-0.792
232566_PM_at	nucleolar protein family 6 (RNA-associated)	NOL6	65083	-0.811	-0.662
243724_PM_at	---	---	---	-0.805	-0.898
243719_PM_at	similar to serine/threonine kinase 19 /// serine/threonine kinase 19	LOC100294221 /// STK19	100294221 /// 8859	-0.801	-0.601
215645_PM_at	folliculin	FLCN	201163	-0.791	-0.661
221404_PM_at	interleukin 1 family, member 6 (epsilon)	IL1F6	27179	-0.768	-0.857
224532_PM_at	ubiquitin specific peptidase 26	USP26	83844	-0.756	-0.684
224211_PM_at	forkhead box P3	FOXP3	50943	-0.743	-0.766
227811_PM_at	FYVE, RhoGEF and PH domain containing 3	FGD3	89846	-0.742	-0.774
213905_PM_x_at	biglycan	BGN	633	-0.730	-0.666
221849_PM_s_at	DDB1 and CUL4 associated factor 15	DCAF15	90379	-0.726	-0.699
236222_PM_at	chromosome 3 open reading frame 15	C3orf15	89876	-0.708	-0.788
214715_PM_x_at	zinc finger protein 160	ZNF160	90338	-0.707	-0.644

1560754_PM_at	CKLF-like MARVEL transmembrane domain containing 7	CMTM7	112616	-0.699	-0.830
224388_PM_s_at	collagen, type XXV, alpha 1	COL25A1	84570	-0.698	-0.793
214778_PM_at	multiple EGF-like-domains 8	MEGF8	1954	-0.680	-0.731
242824_PM_at	---	---	---	-0.677	-0.622
203904_PM_x_at	CD82 molecule	CD82	3732	-0.677	-0.724
1556292_PM_s_at	POM121 membrane glycoprotein-like 12 (rat)	POM121L12	285877	-0.675	-0.776
241020_PM_at	---	---	---	-0.675	-0.623
241924_PM_at	---	---	---	-0.675	-0.774
243971_PM_x_at	hypothetical LOC731789	LOC731789	731789	-0.670	-0.776
204189_PM_at	retinoic acid receptor, gamma	RARG	5916	-0.668	-0.668
221283_PM_at	runt-related transcription factor 2	RUNX2	860	-0.665	-0.811
1557008_PM_at	hypothetical protein LOC340107	LOC340107	340107	-0.664	-0.656
1555135_PM_at	---	---	---	-0.662	-0.817
229471_PM_s_at	---	---	---	-0.658	-0.712
219144_PM_at	dual specificity phosphatase 26 (putative)	DUSP26	78986	-0.653	-0.761
209245_PM_s_at	kinesin family member 1C	KIF1C	10749	-0.652	-0.608
216216_PM_at	slit homolog 3 (Drosophila)	SLIT3	6586	-0.648	-0.814
210413_PM_x_at	serpin peptidase inhibitor, clade B (ovalbumin), member 4	SERPINB4	6318	-0.644	-0.674
1553560_PM_at	vomeronasal 1 receptor 4	VN1R4	317703	-0.640	-0.816
222319_PM_at	---	---	---	-0.639	-0.642
1553328_PM_a_at	solute carrier family 18 (vesicular monoamine), member 2	SLC18A2	6571	-0.631	-0.764
239495_PM_at	---	---	---	-0.627	-0.657
230641_PM_at	---	---	---	-0.621	-0.821
244830_PM_at	Ras interacting protein 1	RASIP1	54922	-0.620	-0.657

1559911_PM_at	---	---	---	-0.616	-0.735
205425_PM_at	huntingtin interacting protein 1	HIP1	3092	-0.614	-0.771
1559166_PM_at	---	---	---	-0.613	-0.720
1557347_PM_at	microcephalin 1	MCPH1	79648	0.615	0.768
236728_PM_at	leucyl/cystinyl aminopeptidase	LNPEP	4012	0.616	0.624
236143_PM_at	---	---	---	0.618	0.645
1565900_PM_at	Methyltransferase 5 domain containing 1	METT5D1	196074	0.621	0.600
224941_PM_at	pregnancy-associated plasma protein A, pappalysin 1	PAPPA	5069	0.625	0.646
203461_PM_at	chromodomain helicase DNA binding protein 2	CHD2	1106	0.648	0.827
229101_PM_at	interleukin 17 receptor A	IL17RA	23765	0.650	0.860
235890_PM_at	379eparin379ing (beta)-like 1 X-linked receptor 1	TBL1XR1	79718	0.660	0.872
216447_PM_at	---	---	---	0.661	0.698
208092_PM_s_at	family with sequence similarity 49, member A	FAM49A	81553	0.676	0.761
228393_PM_s_at	zinc finger protein 302	ZNF302	55900	0.676	0.878
224296_PM_x_at	---	---	---	0.677	0.661
244142_PM_at	dystrobrevin, alpha	DTNA	1837	0.678	0.660
236542_PM_at	---	---	---	0.698	0.704
232462_PM_s_at	non-protein coding RNA 181	NCRNA00181	503538	0.708	0.610
233358_PM_at	---	---	---	0.710	0.605
228685_PM_at	interleukin 17 receptor A	IL17RA	23765	0.732	0.777
215894_PM_at	prostaglandin D2 receptor (DP)	PTGDR	5729	0.744	0.646
236524_PM_at	---	---	---	0.751	0.746
243368_PM_at	---	---	---	0.765	0.698
216209_PM_at	hypothetical gene supported by AK057632; AL137270; BC057846	LOC400084	400084	0.778	0.644
237392_PM_at	hypothetical protein LOC283480	LOC283480	283480	0.782	0.691

202965_PM_s_at	calpain 6	CAPN6	827	0.790	0.713
1558885_PM_at	---	---	---	0.791	0.744
241490_PM_s_at	piggyBac transposable element derived 2	PGBD2	267002	0.792	0.796
205205_PM_at	v-rel reticuloendotheliosis viral oncogene homolog B	RELB	5971	0.797	0.788
230064_PM_at	---	---	---	0.802	0.908
1556162_PM_at	immunoglobulin superfamily, member 3	IGSF3	3321	0.811	0.702
215053_PM_at	Snf2-related CREBBP activator protein	SRCAP	10847	0.816	0.905
214744_PM_s_at	ribosomal protein L23	RPL23	9349	0.825	0.716
216755_PM_at	oxysterol binding protein-like 10	OSBPL10	114884	0.827	0.777
233142_PM_at	---	---	---	0.833	0.721
237745_PM_at	hypothetical LOC641467	LOC641467	641467	0.845	0.661
207823_PM_s_at	allograft inflammatory factor 1	AIF1	199	0.919	0.666

Supplementary Table 11. Transcripts correlated (r>0.60 and r <-0.60) with mean total activity in the putamen. Transcripts are identified by their Affymetrix Probe Set ID, Gene Title, Gene Symbol, and Entrez Gene ID number. The last 2 columns denote Pearson correlations between gene expression and mean total activity in both putamen replicates (R1p and R2p). Positive correlations are indicated in red text and negative correlation is denoted by blue text.

SUPPLEMENTARY TABLE 11. Transcripts correlated (r > 0.60 or r < -0.60) with mean total activity in the putamen.

Probe Set ID	Gene Title	Gene Symbol	Entrez Gene ID	ACT R1p r=	ACT R2p r=
1569020_PM_at	neural precursor cell expressed, developmentally down-regulated 9	NEDD9	4739	-0.964	-0.768
230865_PM_at	Lix1 homolog (chicken)	LIX1	167410	-0.951	-0.826
222458_PM_s_at	akirin 1	AKIRIN1	79647	-0.945	-0.674
239186_PM_at	hypothetical protein MGC39372	MGC39372	221756	-0.945	-0.794
233557_PM_s_at	MON1 homolog B (yeast)	MON1B	22879	-0.933	-0.614
244072_PM_at	---	---	---	-0.913	-0.701
233848_PM_x_at	zinc finger protein 221	ZNF221	7638	-0.903	-0.607
225327_PM_at	KIAA1370	KIAA1370	56204	-0.885	-0.837
210131_PM_x_at	succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa	SDHC	6391	-0.876	-0.733
1556619_PM_at	shisa homolog 9 (Xenopus laevis)	SHISA9	729993	-0.869	-0.665
1555198_PM_x_at	chromosome 21 open reading frame 58	C21orf58	54058	-0.864	-0.657
211385_PM_x_at	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2	SULT1A2	6799	-0.855	-0.880
221569_PM_at	Abelson helper integration site 1	AHI1	54806	-0.849	-0.797
230294_PM_at	---	---	---	-0.847	-0.922
205546_PM_s_at	tyrosine kinase 2	TYK2	7297	-0.830	-0.637
244703_PM_x_at	importin 9	IPO9	55705	-0.826	-0.757
207906_PM_at	interleukin 3 (colony-stimulating factor, multiple)	IL3	3562	-0.825	-0.614
229966_PM_at	Ewing sarcoma breakpoint region 1	EWSR1	2130	-0.819	-0.946
1552585_PM_s_at	general transcription factor IIA, 1-like	GTF2A1L	11036	-0.803	-0.680
226870_PM_at	catechol-O-methyltransferase domain containing 1	COMTD1	118881	-0.803	-0.645

242088_PM_at	kelch-like 24 (Drosophila)	KLHL24	54800	-0.798	-0.834
1568686_PM_at	ATPase, class I, type 8B, member 5, pseudogene	ATP8B5P	158381	-0.796	-0.738
233376_PM_at	---	---	---	-0.794	-0.657
216985_PM_s_at	syntaxin 3	STX3	6809	-0.792	-0.779
237715_PM_at	AT-hook transcription factor	AKNA	80709	-0.789	-0.774
221251_PM_x_at	INO80 complex subunit B	INO80B	83444	-0.782	-0.836
209295_PM_at	tumor necrosis factor receptor superfamily, member 10b	TNFRSF10B	8795	-0.777	-0.627
205308_PM_at	family with sequence similarity 164, member A	FAM164A	51101	-0.775	-0.606
238340_PM_at	DDB1 and CUL4 associated factor 8	DCAF8	50717	-0.774	-0.713
216488_PM_s_at	ATPase, class VI, type 11A	ATP11A	23250	-0.773	-0.726
219470_PM_x_at	cyclin J	CCNJ	54619	-0.771	-0.634
224519_PM_at	similar to hCG1993567	LOC100132167	100132167	-0.770	-0.873
52005_PM_at	widely interspaced zinc finger motifs	WIZ	58525	-0.761	-0.666
212619_PM_at	transmembrane protein 194A	TMEM194A	23306	-0.761	-0.711
1561204_PM_at	---	---	---	-0.752	-0.623
1556395_PM_at	---	---	---	-0.747	-0.743
203715_PM_at	tubulin folding cofactor E	TBCE	6905	-0.747	-0.650
1557944_PM_s_at	catenin (cadherin-associated protein), delta 1	CTNND1	1500	-0.742	-0.684
231230_PM_at	potassium channel, subfamily K, member 10	KCNK10	54207	-0.740	-0.680
218886_PM_at	PAK1 interacting protein 1	PAK1IP1	55003	-0.740	-0.633
235622_PM_at	---	---	---	-0.736	-0.712
237981_PM_at	cardiomyopathy associated 5	CMYA5	202333	-0.734	-0.607
215025_PM_at	neurotrophic tyrosine kinase, receptor, type 3	NTRK3	4916	-0.731	-0.644
214765_PM_s_at	N-acylethanolamine acid amidase	NAAA	27163	-0.719	-0.843
226243_PM_at	chromosome 2 open reading frame 79	C2orf79	391356	-0.716	-0.669
235641_PM_at	Tribbles homolog 1 (Drosophila)	TRIB1	10221	-0.714	-0.669
226403_PM_at	transmembrane channel-like 4	TMC4	147798	-0.709	-0.715
207546_PM_at	ATPase, H+/K+ exchanging, beta polypeptide	ATP4B	496	-0.707	-0.761
231274_PM_s_at	---	---	---	-0.701	-0.803

243686_PM_at	---	---	---	-0.695	-0.864
1562866_PM_at	---	---	---	-0.691	-0.839
225695_PM_at	chromosome 2 open reading frame 18	C2orf18	54978	-0.686	-0.743
203056_PM_s_at	PR domain containing 2, with ZNF domain	PRDM2	7799	-0.680	-0.650
202736_PM_s_at	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	LSM4	25804	-0.679	-0.804
218159_PM_at	DDRGK domain containing 1	DDRGK1	65992	-0.679	-0.731
225009_PM_at	CKLF-like MARVEL transmembrane domain containing 4	CMTM4	146223	-0.671	-0.696
240024_PM_at	SEC14-like 2 (S. cerevisiae)	SEC14L2	23541	-0.671	-0.923
224868_PM_at	zinc finger, DHHC-type containing 5	ZDHHC5	25921	-0.666	-0.613
205424_PM_at	TBK1 binding protein 1	TBKBP1	9755	-0.665	-0.889
217438_PM_at	---	---	---	-0.664	-0.625
214336_PM_s_at	coatomer protein complex, subunit alpha	COPA	1314	-0.662	-0.665
241481_PM_at	Family with sequence similarity 81, member A	FAM81A	145773	-0.661	-0.679
204490_PM_s_at	CD44 molecule (Indian blood group)	CD44	960	-0.661	-0.667
234370_PM_at	V-set and immunoglobulin domain containing 1	VSIG1	340547	-0.660	-0.629
228884_PM_at	leucine rich repeat containing 27	LRRC27	80313	-0.660	-0.880
210813_PM_s_at	X-ray repair complementing defective repair in Chinese hamster cells 4	XRCC4	7518	-0.653	-0.872
202761_PM_s_at	spectrin repeat containing, nuclear envelope 2	SYNE2	23224	-0.642	-0.762
219369_PM_s_at	OTU domain, ubiquitin aldehyde binding 2	OTUB2	78990	-0.641	-0.725
1555495_PM_a_at	CWC27 spliceosome-associated protein homolog (S. cerevisiae)	CWC27	10283	-0.641	-0.621
228124_PM_at	abhydrolase domain containing 12	ABHD12	26090	-0.641	-0.665
1557812_PM_a_at	---	---	---	-0.641	-0.742
214569_PM_at	interferon, alpha 5	IFNA5	3442	-0.639	-0.792
227845_PM_s_at	Src homology 2 domain containing transforming protein D	SHD	56961	-0.639	-0.804
238221_PM_at	---	---	---	-0.639	-0.611
215595_PM_x_at	---	---	---	-0.637	-0.659
218808_PM_at	DALR anticodon binding domain containing 3	DALRD3	55152	-0.636	-0.708

206980_PM_s_at	fms-related tyrosine kinase 3 ligand	FLT3LG	2323	-0.636	-0.805
244378_PM_at	Chromosome 12 open reading frame 51	C12orf51	283450	-0.634	-0.812
55093_PM_at	chondroitin polymerizing factor 2	CHPF2	54480	-0.626	-0.689
214911_PM_s_at	bromodomain containing 2	BRD2	6046	-0.625	-0.838
238047_PM_at	Rho GTPase activating protein 36	ARHGAP36	158763	-0.625	-0.617
211891_PM_s_at	Rho guanine nucleotide exchange factor (GEF) 4	ARHGEF4	50649	-0.622	-0.617
206845_PM_s_at	ring finger protein 40	RNF40	9810	-0.618	-0.605
214196_PM_s_at	tripeptidyl peptidase I	TPP1	1200	-0.617	-0.841
231385_PM_at	developmental pluripotency associated 3	DPPA3	359787	-0.617	-0.791
228275_PM_at	---	---	---	-0.617	-0.785
244644_PM_at	family with sequence similarity 9, member C	FAM9C	171484	-0.614	-0.883
204545_PM_at	peroxisomal biogenesis factor 6	PEX6	5190	-0.610	-0.857
227093_PM_at	Ubiquitin specific peptidase 36	USP36	57602	-0.604	-0.612
239409_PM_at	---	---	---	-0.604	-0.620
202990_PM_at	phosphorylase, glycogen, liver	PYGL	5836	-0.602	-0.782
1555113_PM_at	par-3 partitioning defective 3 homolog B (C. elegans)	PARD3B	117583	0.605	0.752
1562633_PM_at	rhabdomyosarcoma 2 associated transcript (non-protein coding)	RMST	196475	0.605	0.643
1561137_PM_s_at	glycophorin E (MNS blood group)	GYPE	2996	0.607	0.760
1557116_PM_at	apolipoprotein L, 6	APOL6	80830	0.609	0.818
228421_PM_s_at	EGF-containing fibulin-like extracellular matrix protein 1	EFEMP1	2202	0.612	0.857
216766_PM_at	---	---	---	0.615	0.845
215580_PM_at	minichromosome maintenance complex component 3 associated protein	MCM3AP	8888	0.618	0.727
1555492_PM_a_at	bestrophin 3	BEST3	144453	0.619	0.716
230892_PM_at	---	---	---	0.623	0.684
210807_PM_s_at	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	SLC16A7	9194	0.623	0.706
240090_PM_at	---	---	---	0.626	0.883
210530_PM_s_at	nuclear receptor subfamily 2, group C, member 1	NR2C1	7181	0.626	0.796

203627_PM_at	insulin-like growth factor 1 receptor	IGF1R	3480	0.628	0.725
200940_PM_s_at	arginine-glutamic acid dipeptide (RE) repeats	RERE	473	0.629	0.609
1554029_PM_a_at	tetratricopeptide repeat domain 37	TTC37	9652	0.631	0.731
1559891_PM_at	high mobility group AT-hook 2	HMGA2	8091	0.636	0.862
1558430_PM_at	---	---	---	0.636	0.957
219457_PM_s_at	Ras and Rab interactor 3	RIN3	79890	0.639	0.693
240098_PM_at	RAP1 interacting factor homolog (yeast)	RIF1	55183	0.641	0.655
1561224_PM_at	---	---	---	0.642	0.665
233610_PM_at	hypothetical LOC645355	LOC645355	645355	0.645	0.906
1552672_PM_a_at	immunoglobulin superfamily, member 3	IGSF3	3321	0.647	0.822
207208_PM_at	RNA binding motif protein, X-linked-like 2	RBMXL2	27288	0.649	0.711
215742_PM_at	---	---	---	0.657	0.668
1553517_PM_at	Fer3-like (Drosophila)	FERD3L	222894	0.659	0.946
237690_PM_at	G protein-coupled receptor 115	GPR115	221393	0.660	0.754
222100_PM_at	Cytochrome P450, family 2, subfamily E, polypeptide 1	CYP2E1	1571	0.660	0.766
1555185_PM_x_at	telomeric repeat binding factor 2	TERF2	7014	0.665	0.766
209720_PM_s_at	serpin peptidase inhibitor, clade B (ovalbumin), member 3	SERPINB3	6317	0.666	0.674
219701_PM_at	tropomodulin 2 (neuronal)	TMOD2	29767	0.668	0.709
236821_PM_at	---	---	---	0.669	0.899
204302_PM_s_at	KIAA0427	KIAA0427	9811	0.672	0.793
1559042_PM_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	NDUFB6	4712	0.674	0.659
203469_PM_s_at	cyclin-dependent kinase 10	CDK10	8558	0.675	0.651
237392_PM_at	hypothetical protein LOC283480	LOC283480	283480	0.675	0.807
232133_PM_at	ADAM metallopeptidase with thrombospondin type 1 motif, 10	ADAMTS10	81794	0.675	0.630
1560812_PM_at	---	---	---	0.683	0.880
241669_PM_x_at	protein kinase D2	PRKD2	25865	0.684	0.807
221160_PM_s_at	calcium binding protein 5	CABP5	56344	0.685	0.742

220635_PM_at	psoriasis susceptibility 1 candidate 2	PSORS1C2	170680	0.685	0.879
1569345_PM_at	---	---	---	0.689	0.968
220451_PM_s_at	baculoviral IAP repeat-containing 7	BIRC7	79444	0.689	0.763
211480_PM_s_at	solute carrier organic anion transporter family, member 1A2	SLCO1A2	6579	0.689	0.729
215029_PM_at	---	---	---	0.691	0.731
1558546_PM_at	deoxyribonuclease I	DNASE1	1773	0.692	0.844
217152_PM_at	---	---	---	0.693	0.618
1569878_PM_at	cyclin Y-like 2	CCNYL2	414194	0.698	0.778
237431_PM_at	Ubiquitin specific peptidase 32	USP32	84669	0.698	0.783
239542_PM_at	inositol 1,4,5-triphosphate receptor, type 3	ITPR3	3710	0.699	0.651
1552311_PM_a_at	retina and anterior neural fold homeobox 2	RAX2	84839	0.703	0.801
1553560_PM_at	vomeronasal 1 receptor 4	VN1R4	317703	0.708	0.767
1556971_PM_a_at	Hypothetical protein LOC100289312	LOC100289312	100289312	0.710	0.695
218389_PM_s_at	anterior pharynx defective 1 homolog A (C. elegans)	APH1A	51107	0.711	0.762
1557056_PM_at	chromosome 5 open reading frame 47	C5orf47	133491	0.713	0.862
232442_PM_at	breast cancer anti-estrogen resistance 1	BCAR1	9564	0.717	0.904
213907_PM_at	Eukaryotic translation elongation factor 1 epsilon 1	EEF1E1	9521	0.718	0.695
1555100_PM_at	aprataxin and PNKP like factor	APLF	200558	0.720	0.887
231942_PM_at	---	---	---	0.721	0.738
236676_PM_at	---	---	---	0.722	0.703
229085_PM_at	leucine rich repeat containing 3B	LRRC3B	116135	0.726	0.826
203722_PM_at	aldehyde dehydrogenase 4 family, member A1	ALDH4A1	8659	0.728	0.903
223839_PM_s_at	stearoyl-CoA desaturase (delta-9-desaturase)	SCD	6319	0.728	0.683
216879_PM_at	Hr44 antigen	HR44	27251	0.730	0.716
1554222_PM_at	hypothetical LOC284365	MGC45922	284365	0.731	0.679
223153_PM_x_at	transmembrane and ubiquitin-like domain containing 1	TMUB1	83590	0.731	0.872
229920_PM_at	---	---	---	0.735	0.878
219765_PM_at	zinc finger protein 329	ZNF329	79673	0.736	0.631

225497_PM_at	arginyltransferase 1	ATE1	11101	0.737	0.637
222030_PM_at	SIVA1, apoptosis-inducing factor	SIVA1	10572	0.738	0.644
1568745_PM_at	hCG1654703	LOC646268	646268	0.740	0.601
1560818_PM_at	Hypothetical protein LOC100288701	LOC100288701	100288701	0.740	0.895
244151_PM_at	hypothetical LOC285733	LOC285733	285733	0.740	0.692
239049_PM_at	---	---	---	0.741	0.706
226635_PM_at	Hypothetical gene supported by AK091718	LOC401504	401504	0.741	0.893
239111_PM_at	PR domain containing 8	PRDM8	56978	0.741	0.829
1552459_PM_a_at	methyl-CpG binding domain protein 3-like 1	MBD3L1	85509	0.745	0.640
218783_PM_at	integrator complex subunit 7	INTS7	25896	0.748	0.693
233531_PM_at	solute carrier family 46 (folate transporter), member 1	SLC46A1	113235	0.749	0.717
1553321_PM_a_at	sulfotransferase family, cytosolic, 1C, member 4	SULT1C4	27233	0.751	0.706
205044_PM_at	gamma-aminobutyric acid (GABA) A receptor, pi	GABRP	2568	0.751	0.719
1559237_PM_a_at	---	---	---	0.751	0.681
228157_PM_at	zinc finger protein 207	ZNF207	7756	0.751	0.775
238104_PM_at	---	---	---	0.754	0.866
220360_PM_at	THAP domain containing 9	THAP9	79725	0.755	0.603
233644_PM_at	katanin p60 subunit A-like 2	KATNAL2	83473	0.755	0.762
239792_PM_at	---	---	---	0.757	0.804
214155_PM_s_at	La ribonucleoprotein domain family, member 4	LARP4	113251	0.757	0.791
224356_PM_x_at	membrane-spanning 4-domains, subfamily A, member 6A	MS4A6A	64231	0.760	0.789
226231_PM_at	---	---	---	0.762	0.807
236152_PM_at	P antigen family, member 5 (prostate associated)	PAGE5	90737	0.763	0.835
208726_PM_s_at	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	EIF2S2	8894	0.764	0.699
220653_PM_at	zinc finger, imprinted 2	ZIM2	23619	0.766	0.680
1569780_PM_at	---	---	---	0.767	0.970
212321_PM_at	sphingosine-1-phosphate lyase 1	SGPL1	8879	0.768	0.923
227044_PM_at	---	---	---	0.772	0.920

231871_PM_at	G protein-coupled receptor 180	GPR180	160897	0.772	0.852
226850_PM_at	sulfatase modifying factor 1	SUMF1	285362	0.773	0.728
1554739_PM_at	intracisternal A particle-promoted polypeptide	IPP	3652	0.778	0.638
1557480_PM_a_at	dysferlin interacting protein 1	DYSFIP1	116729	0.781	0.869
238703_PM_at	chromosome 21 open reading frame 70 /// hypothetical LOC729535	C21orf70 /// LOC729535	729535 /// 85395	0.781	0.626
207833_PM_s_at	holocarboxylase synthetase (biotin-(proprionyl-CoA-carboxylase (ATP-hydrolysing)) ligase)	HLCS	3141	0.782	0.698
237369_PM_at	---	---	---	0.785	0.777
221864_PM_at	ORAI calcium release-activated calcium modulator 3	ORAI3	93129	0.789	0.601
218690_PM_at	PDZ and LIM domain 4	PDLIM4	8572	0.790	0.674
218300_PM_at	chromosome 16 open reading frame 53	C16orf53	79447	0.791	0.819
1557775_PM_a_at	---	---	---	0.793	0.736
202440_PM_s_at	suppression of tumorigenicity 5	ST5	6764	0.793	0.736
236683_PM_at	---	---	---	0.798	0.941
225409_PM_at	chromosome 2 open reading frame 64	C2orf64	493753	0.799	0.823
233707_PM_at	---	---	---	0.799	0.677
239023_PM_at	---	---	---	0.800	0.838
235811_PM_at	---	---	---	0.801	0.767
1554831_PM_x_at	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 11	ALS2CR11	151254	0.802	0.938
206705_PM_at	tubby like protein 1	TULP1	7287	0.804	0.858
219508_PM_at	glucosaminyl (N-acetyl) transferase 3, mucin type	GCNT3	9245	0.804	0.836
235943_PM_at	---	---	---	0.806	0.712
230758_PM_at	gem (nuclear organelle) associated protein 8	GEMIN8	54960	0.808	0.704
1557683_PM_at	---	---	---	0.810	0.885
220322_PM_at	interleukin 1 family, member 9	IL1F9	56300	0.813	0.853
220652_PM_at	kinesin family member 24	KIF24	347240	0.816	0.864
229059_PM_at	chromosome 9 open reading frame 109 /// chromosome 9 open reading frame 110	C9orf109 /// C9orf110	100128385 /// 286333	0.817	0.753

239790_PM_s_at	---	---	---	0.818	0.856
1560012_PM_at	---	---	---	0.819	0.793
239086_PM_at	---	---	---	0.821	0.784
208902_PM_s_at	ribosomal protein S28	RPS28	6234	0.821	0.710
233031_PM_at	zinc finger E-box binding homeobox 2	ZEB2	9839	0.824	0.858
233267_PM_at	Selenium binding protein 1	SELENBP1	8991	0.825	0.740
219746_PM_at	D4, zinc and double PHD fingers, family 3	DPF3	8110	0.832	0.902
223861_PM_at	HORMA domain containing 1	HORMAD1	84072	0.833	0.676
213759_PM_at	---	---	---	0.840	0.657
1553612_PM_at	zinc finger protein 354B	ZNF354B	117608	0.844	0.747
1562330_PM_s_at	CUB and Sushi multiple domains 1	CSMD1	64478	0.845	0.845
207965_PM_at	neurogenin 3	NEUROG3	50674	0.848	0.853
243966_PM_at	---	---	---	0.850	0.738
1555516_PM_at	forkhead box P2	FOXP2	93986	0.850	0.733
210718_PM_s_at	ADP-ribosylation factor-like 17A /// similar to ADP-ribosylation factor-like 17	ARL17A /// LOC100294341	100294341 /// 51326	0.855	0.781
1570625_PM_at	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	TCEB3	6924	0.857	0.685
237306_PM_at	zinc finger protein 829	ZNF829	374899	0.857	0.878
215274_PM_at	solute carrier family 12 (sodium/chloride transporters), member 3	SLC12A3	6559	0.859	0.761
231712_PM_at	---	---	---	0.860	0.802
1553992_PM_s_at	neighbor of BRCA1 gene 2 (non-protein coding)	NBR2	10230	0.861	0.796
206314_PM_at	zinc finger protein 167	ZNF167	55888	0.862	0.915
242155_PM_x_at	ring finger and FYVE-like domain containing 1	RFFL	117584	0.869	0.807
219697_PM_at	389eparin sulfate (glucosamine) 3-O-sulfotransferase 2	HS3ST2	9956	0.869	0.819
213120_PM_at	UHRF1 binding protein 1-like	UHRF1BP1L	23074	0.869	0.719
242189_PM_at	---	---	---	0.870	0.653
1563868_PM_a_at	chromosome 9 open reading frame 79	C9orf79	286234	0.871	0.690
244864_PM_at	---	---	---	0.872	0.752

239286_PM_at	cadherin 11, type 2, OB-cadherin (osteoblast)	CDH11	1009	0.874	0.751
201487_PM_at	cathepsin C	CTSC	1075	0.877	0.811
233133_PM_at	---	---	---	0.879	0.714
1561148_PM_at	---	---	---	0.883	0.708
240093_PM_x_at	---	---	---	0.901	0.741
212972_PM_x_at	amyloid beta (A4) precursor protein-binding, family B, member 2	APBB2	323	0.902	0.920
206007_PM_at	proteoglycan 4	PRG4	10216	0.915	0.734
202068_PM_s_at	low density lipoprotein receptor	LDLR	3949	0.917	0.836
235890_PM_at	390eparin390ing (beta)-like 1 X-linked receptor 1	TBL1XR1	79718	0.919	0.642
241994_PM_at	xanthine dehydrogenase	XDH	7498	0.922	0.772
234692_PM_at	---	---	---	0.923	0.842
1561061_PM_at	---	---	---	0.925	0.882
219455_PM_at	chromosome 7 open reading frame 63	C7orf63	79846	0.926	0.834
210946_PM_at	phosphatidic acid phosphatase type 2A	PPAP2A	8611	0.927	0.646
228905_PM_at	pericentriolar material 1	PCM1	5108	0.930	0.692
240168_PM_at	exportin 7	XPO7	23039	0.931	0.662
1554895_PM_a_at	rhomboid, veinlet-like 2 (Drosophila)	RHBDL2	54933	0.949	0.659
240309_PM_at	---	---	---	0.966	0.718

Supplementary Table 12. Transcripts correlated (r>0.60 and r <-0.60) with mean total activity, percent loss [^{11}C]DTBZ binding potential (PET), and percent loss tyrosine hydroxylase levels (TH) in the caudate nucleus. Transcripts are identified by their Affymetrix Probe Set ID, Gene Title, Gene Symbol, Entrez Gene ID number. The last six columns denote Pearson correlation between gene expression mean total activity, gene expression and percent loss [^{11}C]DTBZ binding, and gene expression and percent loss TH in both caudate replicates (R1c and R2c). Positive correlations are indicated in red text and negative correlation is denoted by blue text.

SUPPLEMENTARY TABLE 12. Transcripts correlated (r > 0.60 or r < -0.60) with mean total activity, PET, and TH in the caudate.

Probe Set ID	Gene Title	Gene Symbol	Entrez Gene ID	ACT R1c r=	ACT R2c r=	PET R1c r=	PET R2c r=	TH R1c r=	TH R2c r=
215063_PM_x_at	leucine rich repeat containing 40	LRRC40	55631	-0.943	-0.799	-0.652	-0.615	-0.622	-0.655
232566_PM_at	nucleolar protein family 6 (RNA-associated)	NOL6	65083	-0.811	-0.662	-0.791	-0.882	-0.781	-0.806
215645_PM_at	folliculin	FLCN	201163	-0.791	-0.661	-0.661	-0.823	-0.716	-0.824
214778_PM_at	multiple EGF-like-domains 8	MEGF8	1954	-0.680	-0.731	-0.735	-0.897	-0.639	-0.891
242824_PM_at	---	---	---	-0.677	-0.622	-0.857	-0.652	-0.860	-0.650
204189_PM_at	retinoic acid receptor, gamma	RARG	5916	-0.668	-0.668	-0.901	-0.829	-0.894	-0.827
1553328_PM_a_at	solute carrier family 18 (vesicular monoamine), member 2	SLC18A2	6571	-0.631	-0.764	-0.712	-0.708	-0.675	-0.622
230641_PM_at	---	---	---	-0.621	-0.821	-0.744	-0.894	-0.794	-0.881
236143_PM_at	---	---	---	0.618	0.645	0.740	0.813	0.678	0.729
224941_PM_at	pregnancy-associated plasma protein A, pappalysin 1	PAPPA	5069	0.625	0.646	0.890	0.710	0.902	0.653
235890_PM_at	transducin (beta)-like 1 X-linked receptor 1	TBL1XR1	79718	0.660	0.872	0.813	0.611	0.783	0.621
208092_PM_s_at	family with sequence similarity 49, member A	FAM49A	81553	0.676	0.761	0.723	0.771	0.758	0.824

228393_PM_s_at	zinc finger protein 302	ZNF302	55900	0.676	0.878	0.707	0.687	0.749	0.716
233358_PM_at	---	---	---	0.710	0.605	0.955	0.782	0.943	0.715
241490_PM_s_at	piggyBac transposable element derived 2	PGBD2	267002	0.792	0.796	0.818	0.671	0.881	0.630
230064_PM_at	---	---	---	0.802	0.908	0.833	0.828	0.843	0.795
214744_PM_s_at	ribosomal protein L23	RPL23	9349	0.825	0.716	0.888	0.671	0.858	0.699

Supplementary Table 13. Transcripts correlated (r>0.60 and r <-0.60) with mean total activity, percent loss [^{11}C]DTBZ binding potential (PET), and percent loss tyrosine hydroxylase levels (TH) in the putamen. Transcripts are identified by their Affymetrix Probe Set ID, Gene Title, Gene Symbol, Entrez Gene ID number. The last six columns denote Pearson correlation between gene expression mean total activity, gene expression and percent loss [^{11}C]DTBZ binding, and gene expression and percent loss TH in both putamen replicates (R1p and R2p). Positive correlations are indicated in red text and negative correlation is denoted by blue text.

SUPPLEMENTARY TABLE 13. Transcripts correlated (r > 0.60 or r < -0.60) with mean total activity, PET, and TH in the putamen.

Probe Set ID	Gene Title	Gene Symbol	Entrez Gene ID	ACT R1p r=	ACT R2p r=	PET R1p r=	PET R2p r=	TH R1p r=	TH R2p r=
1569020_PM_at	neural precursor cell expressed, developmentally down-regulated 9	NEDD9	4739	-0.964	-0.768	-0.894	-0.706	-0.857	-0.835
230865_PM_at	Lix1 homolog (chicken)	LIX1	167410	-0.951	-0.826	-0.719	-0.645	-0.732	-0.685
244072_PM_at	---	---	---	-0.913	-0.701	-0.756	-0.616	-0.808	-0.670
233848_PM_x_at	zinc finger protein 221	ZNF221	7638	-0.903	-0.607	-0.924	-0.911	-0.870	-0.864
1555198_PM_x_at	chromosome 21 open reading frame 58	C21orf58	54058	-0.864	-0.657	-0.756	-0.761	-0.743	-0.695
211385_PM_x_at	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2	SULT1A2	6799	-0.855	-0.880	-0.783	-0.776	-0.671	-0.712
244703_PM_x_at	importin 9	IPO9	55705	-0.826	-0.757	-0.752	-0.743	-0.752	-0.665
207906_PM_at	interleukin 3 (colony-stimulating factor, multiple)	IL3	3562	-0.825	-0.614	-0.715	-0.735	-0.634	-0.748
229966_PM_at	Ewing sarcoma breakpoint region 1	EWSR1	2130	-0.819	-0.946	-0.927	-0.833	-0.894	-0.748
1552585_PM_s_at	general transcription factor IIA, 1-like	GTF2A1L	11036	-0.803	-0.680	-0.806	-0.809	-0.833	-0.714
1568686_PM_at	ATPase, class I, type 8B, member 5, pseudogene	ATP8B5P	158381	-0.796	-0.738	-0.665	-0.691	-0.747	-0.704
216985_PM_s_at	syntaxin 3	STX3	6809	-0.792	-0.779	-0.636	-0.839	-0.698	-0.826

1556395_PM_at	---	---	---	-0.747	-0.743	-0.755	-0.977	-0.721	-0.927
218886_PM_at	PAK1 interacting protein 1	PAK1IP1	55003	-0.740	-0.633	-0.716	-0.646	-0.668	-0.700
214765_PM_s_at	N-acylethanolamine acid amidase	NAAA	27163	-0.719	-0.843	-0.810	-0.625	-0.889	-0.680
226403_PM_at	transmembrane channel-like 4	TMC4	147798	-0.709	-0.715	-0.702	-0.724	-0.725	-0.725
1562866_PM_at	---	---	---	-0.691	-0.839	-0.857	-0.979	-0.920	-0.937
202736_PM_s_at	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	LSM4	25804	-0.679	-0.804	-0.714	-0.678	-0.685	-0.732
204490_PM_s_at	CD44 molecule (Indian blood group)	CD44	960	-0.661	-0.667	-0.804	-0.907	-0.844	-0.884
214569_PM_at	interferon, alpha 5	IFNA5	3442	-0.639	-0.792	-0.659	-0.774	-0.693	-0.833
206980_PM_s_at	fms-related tyrosine kinase 3 ligand	FLT3LG	2323	-0.636	-0.805	-0.710	-0.669	-0.630	-0.705
244378_PM_at	Chromosome 12 open reading frame 51	C12orf51	283450	-0.634	-0.812	-0.845	-0.866	-0.859	-0.838
214911_PM_s_at	bromodomain containing 2	BRD2	6046	-0.625	-0.838	-0.616	-0.673	-0.664	-0.681
214196_PM_s_at	tripeptidyl peptidase I	TPP1	1200	-0.617	-0.841	-0.749	-0.869	-0.755	-0.929
204545_PM_at	peroxisomal biogenesis factor 6	PEX6	5190	-0.610	-0.857	-0.777	-0.701	-0.737	-0.658
1557116_PM_at	apolipoprotein L, 6	APOL6	80830	0.609	0.818	0.616	0.725	0.678	0.810
210530_PM_s_at	nuclear receptor subfamily 2, group C, member 1	NR2C1	7181	0.626	0.796	0.795	0.826	0.811	0.734
203627_PM_at	insulin-like growth factor 1 receptor	IGF1R	3480	0.628	0.725	0.710	0.828	0.602	0.685
1554029_PM_a_at	tetratricopeptide repeat domain 37	TTC37	9652	0.631	0.731	0.686	0.729	0.765	0.796
1558430_PM_at	---	---	---	0.636	0.957	0.685	0.908	0.605	0.891
219457_PM_s_at	Ras and Rab interactor 3	RIN3	79890	0.639	0.693	0.663	0.732	0.686	0.733

240098_PM_at	RAP1 interacting factor homolog (yeast)	RIF1	55183	0.641	0.655	0.689	0.805	0.684	0.903
1561224_PM_at	---	---	---	0.642	0.665	0.647	0.863	0.635	0.762
1553517_PM_at	Fer3-like (Drosophila)	FERD3L	222894	0.659	0.946	0.813	0.873	0.886	0.883
1555185_PM_x_at	telomeric repeat binding factor 2	TERF2	7014	0.665	0.766	0.639	0.782	0.604	0.684
209720_PM_s_at	serpin peptidase inhibitor, clade B (ovalbumin), member 3	SERPINB3	6317	0.666	0.674	0.743	0.649	0.675	0.677
1560812_PM_at	---	---	---	0.683	0.880	0.737	0.816	0.858	0.856
221160_PM_s_at	calcium binding protein 5	CABP5	56344	0.685	0.742	0.751	0.679	0.845	0.724
239542_PM_at	inositol 1,4,5-triphosphate receptor, type 3	ITPR3	3710	0.699	0.651	0.643	0.712	0.622	0.746
1553560_PM_at	vomeronasal 1 receptor 4	VN1R4	317703	0.708	0.767	0.785	0.978	0.709	0.961
232442_PM_at	breast cancer anti-estrogen resistance 1	BCAR1	9564	0.717	0.904	0.875	0.965	0.938	0.929
223153_PM_x_at	transmembrane and ubiquitin-like domain containing 1	TMUB1	83590	0.731	0.872	0.774	0.827	0.722	0.860
225497_PM_at	arginyltransferase 1	ATE1	11101	0.737	0.637	0.873	0.805	0.895	0.903
1560818_PM_at	Hypothetical protein LOC100288701	LOC100288701	1E+08	0.740	0.895	0.799	0.792	0.877	0.798
226635_PM_at	Hypothetical gene supported by AK091718	LOC401504	401504	0.741	0.893	0.847	0.789	0.850	0.803
1552459_PM_a_at	methyl-CpG binding domain protein 3-like 1	MBD3L1	85509	0.745	0.640	0.708	0.627	0.821	0.760
1553321_PM_a_at	sulfotransferase family, cytosolic, 1C, member 4	SULT1C4	27233	0.751	0.706	0.706	0.605	0.836	0.660
1559237_PM_a_at	---	---	---	0.751	0.681	0.688	0.864	0.798	0.938
228157_PM_at	zinc finger protein 207	ZNF207	7756	0.751	0.775	0.789	0.848	0.691	0.865

238104_PM_at	---	---	---	0.754	0.866	0.875	0.735	0.779	0.669
239792_PM_at	---	---	---	0.757	0.804	0.804	0.742	0.873	0.850
224356_PM_x_at	membrane-spanning 4-domains, subfamily A, member 6A	MS4A6A	64231	0.760	0.789	0.662	0.699	0.671	0.753
236152_PM_at	P antigen family, member 5 (prostate associated)	PAGE5	90737	0.763	0.835	0.832	0.774	0.776	0.803
220653_PM_at	zinc finger, imprinted 2	ZIM2	23619	0.766	0.680	0.687	0.803	0.718	0.777
212321_PM_at	sphingosine-1-phosphate lyase 1	SGPL1	8879	0.768	0.923	0.835	0.832	0.692	0.740
226850_PM_at	sulfatase modifying factor 1	SUMF1	285362	0.773	0.728	0.804	0.931	0.772	0.905
237369_PM_at	---	---	---	0.785	0.777	0.621	0.635	0.639	0.663
221864_PM_at	ORAI calcium release-activated calcium modulator 3	ORAI3	93129	0.789	0.601	0.651	0.766	0.750	0.825
218690_PM_at	PDZ and LIM domain 4	PDLIM4	8572	0.790	0.674	0.664	0.730	0.657	0.847
218300_PM_at	chromosome 16 open reading frame 53	C16orf53	79447	0.791	0.819	0.666	0.611	0.749	0.623
1557775_PM_a_at	---	---	---	0.793	0.736	0.753	0.755	0.815	0.712
202440_PM_s_at	suppression of tumorigenicity 5	ST5	6764	0.793	0.736	0.713	0.937	0.812	0.944
236683_PM_at	---	---	---	0.798	0.941	0.709	0.697	0.805	0.744
239023_PM_at	---	---	---	0.800	0.838	0.776	0.773	0.876	0.847
1554831_PM_x_at	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 11	ALS2CR11	151254	0.802	0.938	0.895	0.708	0.964	0.720
235943_PM_at	---	---	---	0.806	0.712	0.815	0.755	0.835	0.660
1557683_PM_at	---	---	---	0.810	0.885	0.739	0.843	0.851	0.837

229059_PM_at	chromosome 9 open reading frame 109 /// chromosome 9 open reading frame 110	C9orf109 /// C9orf110	100128385 /// 286333	0.817	0.753	0.707	0.660	0.776	0.743
239790_PM_s_at	---	---	---	0.818	0.856	0.731	0.913	0.692	0.894
208902_PM_s_at	ribosomal protein S28	RPS28	6234	0.821	0.710	0.742	0.757	0.800	0.847
233031_PM_at	zinc finger E-box binding homeobox 2	ZEB2	9839	0.824	0.858	0.697	0.666	0.771	0.677
219746_PM_at	D4, zinc and double PHD fingers, family 3	DPF3	8110	0.832	0.902	0.617	0.885	0.669	0.853
1553612_PM_at	zinc finger protein 354B	ZNF354B	117608	0.844	0.747	0.833	0.712	0.765	0.765
1562330_PM_s_at	CUB and Sushi multiple domains 1	CSMD1	64478	0.845	0.845	0.673	0.722	0.742	0.744
207965_PM_at	neurogenin 3	NEUROG3	50674	0.848	0.853	0.822	0.751	0.897	0.804
210718_PM_s_at	ADP-ribosylation factor-like 17A /// similar to ADP-ribosylation factor-like 17	ARL17A /// LOC100294341	100294341 /// 51326	0.855	0.781	0.836	0.712	0.883	0.797
237306_PM_at	zinc finger protein 829	ZNF829	374899	0.857	0.878	0.762	0.778	0.852	0.857
215274_PM_at	solute carrier family 12 (sodium/chloride transporters), member 3	SLC12A3	6559	0.859	0.761	0.749	0.736	0.738	0.836
1553992_PM_s_at	neighbor of BRCA1 gene 2 (non-protein coding)	NBR2	10230	0.861	0.796	0.611	0.791	0.690	0.862
242155_PM_x_at	ring finger and FYVE-like domain containing 1	RFFL	117584	0.869	0.807	0.724	0.679	0.803	0.724
219697_PM_at	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	HS3ST2	9956	0.869	0.819	0.720	0.720	0.721	0.831

213120_PM_at	UHRF1 binding protein 1-like	UHRF1BP1L	23074	0.869	0.719	0.798	0.661	0.766	0.680
1563868_PM_a_at	chromosome 9 open reading frame 79	C9orf79	286234	0.871	0.690	0.661	0.767	0.651	0.793
244864_PM_at	---	---	---	0.872	0.752	0.730	0.692	0.735	0.795
239286_PM_at	cadherin 11, type 2, OB-cadherin (osteoblast)	CDH11	1009	0.874	0.751	0.851	0.636	0.799	0.667
212972_PM_x_at	amyloid beta (A4) precursor protein-binding, family B, member 2	APBB2	323	0.902	0.920	0.915	0.785	0.938	0.717
202068_PM_s_at	low density lipoprotein receptor	LDLR	3949	0.917	0.836	0.821	0.646	0.815	0.752
219455_PM_at	chromosome 7 open reading frame 63	C7orf63	79846	0.926	0.834	0.859	0.788	0.853	0.891
210946_PM_at	phosphatidic acid phosphatase type 2A	PPAP2A	8611	0.927	0.646	0.944	0.870	0.886	0.904
228905_PM_at	pericentriolar material 1	PCM1	5108	0.930	0.692	0.754	0.652	0.822	0.734
240309_PM_at	---	---	---	0.966	0.718	0.916	0.743	0.909	0.712

Supplementary Table 14. Transcripts associated with the lesioned hemisphere. Transcripts are identified by their Affymetrix Probe Set ID, Gene Title, Gene Symbol, and Entrez Gene ID number. Transcripts are differentially expressed between the lesioned and nonlesioned hemispheres with p< 0.05 for a paired t-test and an average log ratio (ALR) > 0.3785 indicated a 30% change in expression. Positive ALRs are indicated in red text and negative ALRs are denoted by blue text.

SUPPLEMENTARY TABLE 14. Transcripts associated with the lesioned hemisphere.

Probe Set ID	Gene Title	Gene Symbol	Entrez Gene	t-test	ALR
203263_PM_s_at	Cdc42 guanine nucleotide exchange factor (GEF) 9	ARHGEF9	23229	0.016	-0.73
219935_PM_at	ADAM metallopeptidase with thrombospondin type 1 motif, 5	ADAMTS5	11096	0.041	-0.68
229824_PM_at	---	---	---	0.005	-0.65
226084_PM_at	microtubule-associated protein 1B	MAP1B	4131	0.023	-0.64
226232_PM_at	growth differentiation factor 11	GDF11	10220	0.047	-0.57
221646_PM_s_at	zinc finger, DHHC-type containing 11	ZDHHC11	79844	0.009	-0.57
232224_PM_at	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	MASP1	5648	0.016	-0.55
206513_PM_at	absent in melanoma 2	AIM2	9447	0.017	-0.55
211383_PM_s_at	WD repeat domain 37	WDR37	22884	0.004	-0.53
204388_PM_s_at	monoamine oxidase A	MAOA	4128	0.033	-0.5
201821_PM_s_at	translocase of inner mitochondrial membrane 17 homolog A (yeast)	TIMM17A	10440	0.025	-0.5
201899_PM_s_at	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	UBE2A	7319	0.016	-0.5
232176_PM_at	SLIT and NTRK-like family, member 6	SLITRK6	84189	0.03	-0.49
213762_PM_x_at	RNA binding motif protein, X-linked	RBMX	27316	0.025	-0.48
235905_PM_at	---	---	---	0.016	-0.48
219810_PM_at	valosin containing protein (p97)/p47 complex interacting protein 1	VCPIP1	80124	0.048	-0.47
244040_PM_at	---	---	---	0.043	-0.47
233422_PM_at	---	---	---	0.036	-0.46
232347_PM_x_at	---	---	---	0.016	-0.45
238604_PM_at	---	---	---	0.038	-0.45
232653_PM_at	---	---	---	0.021	-0.45
233268_PM_s_at	churchill domain containing 1	CHURC1	91612	0.041	-0.45
227217_PM_at	WNK lysine deficient protein kinase 2	WNK2	65268	0.012	-0.44

225317_PM_at	acyl-CoA binding domain containing 6	ACBD6	84320	0.047	-0.44
239036_PM_at	---	---	---	0.024	-0.43
208942_PM_s_at	SEC62 homolog (S. cerevisiae)	SEC62	7095	0.022	-0.43
218457_PM_s_at	DNA (cytosine-5-)-methyltransferase 3 alpha	DNMT3A	1788	0.006	-0.43
203580_PM_s_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	SLC7A6	9057	0.033	-0.43
205592_PM_at	solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)	SLC4A1	6521	0	-0.43
1561192_PM_at	---	---	---	0.002	-0.43
213259_PM_s_at	sterile alpha and TIR motif containing 1	SARM1	23098	0.026	-0.43
232220_PM_at	S100 calcium binding protein A7A	S100A7A	338324	0.042	-0.42
208345_PM_s_at	POU class 3 homeobox 1	POU3F1	5453	0.005	-0.42
226923_PM_at	sec1 family domain containing 2	SCFD2	152579	0.031	-0.42
219566_PM_at	pleckstrin homology domain containing, family F (with FYVE domain) member 1	PLEKHF1	79156	0.044	-0.41
216042_PM_at	tumor necrosis factor receptor superfamily, member 25	TNFRSF25	8718	0.022	-0.41
225830_PM_at	PDZ domain containing 8	PDZD8	118987	0.022	-0.41
233407_PM_at	---	---	---	0.021	-0.4
1568639_PM_a_at	---	---	---	0.032	-0.4
214040_PM_s_at	gelsolin	GSN	2934	0.001	-0.4
243033_PM_at	Twinfilin, actin-binding protein, homolog 1 (Drosophila)	TWF1	5756	0.047	-0.4
222977_PM_at	surfeit 4	SURF4	6836	0.024	-0.4
235603_PM_at	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	HNRNPU	3192	0.014	-0.39
1562381_PM_at	hypothetical LOC285830	LOC285830	285830	0.036	-0.39
1554572_PM_a_at	suppressor of variegation 3-9 homolog 2 (Drosophila)	SUV39H2	79723	0.039	-0.39
236772_PM_s_at	---	---	---	0.047	-0.39
238104_PM_at	---	---	---	0.015	-0.38
201669_PM_s_at	myristoylated alanine-rich protein kinase C substrate	MARCKS	4082	0.036	-0.38
240799_PM_at	solute carrier family 35, member F4	SLC35F4	341880	0.046	-0.38
204290_PM_s_at	aldehyde dehydrogenase 6 family, member A1	ALDH6A1	4329	0.021	-0.38
226347_PM_at	---	---	---	0.041	-0.38

244334_PM_at	translocation associated membrane protein 1-like 1	TRAM1L1	133022	0.011	-0.38
206645_PM_s_at	nuclear receptor subfamily 0, group B, member 1	NR0B1	190	0.01	-0.38
215779_PM_s_at	histone cluster 1, H2bg	HIST1H2BG	8339	0.038	-0.37
204758_PM_s_at	C2CD2-like	C2CD2L	9854	0.03	-0.36
215282_PM_at	anaphase promoting complex subunit 13	ANAPC13	25847	0.041	-0.36
234070_PM_at	---	---	---	0.049	-0.36
217570_PM_x_at	---	---	---	0.012	-0.36
1557185_PM_at	two pore segment channel 1	TPCN1	53373	0.049	-0.36
241218_PM_at	---	---	---	0.045	-0.36
216921_PM_s_at	keratin 35	KRT35	3886	0.049	-0.36
1556771_PM_a_at	hypothetical LOC415056	LOC415056	415056	0.015	-0.35
235497_PM_at	hypothetical LOC643837	LOC643837	643837	0.019	-0.35
234424_PM_at	---	---	---	0.038	-0.35
1569996_PM_at	ankyrin repeat domain 26 pseudogene	LOC100101938	100101938	0.05	-0.35
238334_PM_at	Shadow of prion protein homolog (zebrafish)	SPRN	503542	0.038	-0.35
209605_PM_at	thiosulfate sulfurtransferase (rhodanese)	TST	7263	0.026	-0.35
217296_PM_at	Killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 1	KIR2DL1	3802	0.009	-0.35
234074_PM_at	---	---	---	0.009	-0.35
1560352_PM_at	---	---	---	0.024	-0.35
244457_PM_at	---	---	---	0.046	-0.35
205434_PM_s_at	AP2 associated kinase 1	AAK1	22848	0.003	-0.35
233952_PM_s_at	zinc finger protein 295	ZNF295	49854	0.046	-0.35
1559369_PM_at	chromosome 5 open reading frame 44	C5orf44	80006	0.021	-0.34
237945_PM_at	---	---	---	0.021	-0.34
225303_PM_at	kin of IRRE like (Drosophila)	KIRREL	55243	0.024	-0.34
238184_PM_at	---	---	---	0.029	-0.34
220482_PM_s_at	secretion regulating guanine nucleotide exchange factor	SERGEF	26297	0.02	-0.34
1565544_PM_at	ring finger protein 141	RNF141	50862	0.021	-0.34
1555037_PM_a_at	isocitrate dehydrogenase 1 (NADP+), soluble	IDH1	3417	0.026	-0.34
1555734_PM_x_at	adaptor-related protein complex 1, sigma 3 subunit	AP1S3	130340	0.045	-0.34
218729_PM_at	latexin	LXN	56925	0.018	-0.33

213196_PM_at	zinc finger protein 629	ZNF629	23361	0.024	-0.33
202384_PM_s_at	Treacher Collins-Franceschetti syndrome 1	TCOF1	6949	0.001	-0.33
1557275_PM_a_at	TLC domain containing 2	TLCD2	727910	0.04	-0.33
224954_PM_at	serine hydroxymethyltransferase 1 (soluble)	SHMT1	6470	0.039	-0.33
1553523_PM_at	NLR family, pyrin domain containing 14	NLRP14	338323	0.017	-0.33
220731_PM_s_at	NECAP endocytosis associated 2	NECAP2	55707	0.038	-0.33
210568_PM_s_at	RecQ protein-like (DNA helicase Q1-like)	RECQL	5965	0.002	-0.33
206521_PM_s_at	general transcription factor IIA, 1, 19/37kDa	GTF2A1	2957	0.038	-0.32
234869_PM_at	---	---	---	0.038	-0.32
220573_PM_at	kallikrein-related peptidase 14	KLK14	43847	0.014	-0.32
1557780_PM_at	---	---	---	0.015	-0.32
244763_PM_at	mitochondrial translational release factor 1	MTRF1	9617	0.04	-0.32
228454_PM_at	ligand dependent nuclear receptor corepressor	LCOR	84458	0.047	-0.32
202665_PM_s_at	WAS/WASL interacting protein family, member 1	WIPF1	7456	0.015	-0.32
210620_PM_s_at	general transcription factor IIIC, polypeptide 2, beta 110kDa	GTF3C2	2976	0.015	-0.32
1553405_PM_a_at	CUB and Sushi multiple domains 1	CSMD1	64478	0.034	-0.32
217095_PM_x_at	natural cytotoxicity triggering receptor 1	NCR1	9437	0.049	-0.32
200656_PM_s_at	prolyl 4-hydroxylase, beta polypeptide	P4HB	5034	0.021	-0.32
205809_PM_s_at	Wiskott-Aldrich syndrome-like	WASL	8976	0.008	-0.31
209902_PM_at	ataxia telangiectasia and Rad3 related	ATR	545	0.041	-0.31
206091_PM_at	matrilin 3	MATN3	4148	0.043	-0.31
207823_PM_s_at	allograft inflammatory factor 1	AIF1	199	0.001	-0.31
225943_PM_at	neurolysin (metallopeptidase M3 family)	NLN	57486	0.047	-0.31
227941_PM_at	hypothetical protein LOC339803	LOC339803	339803	0.048	-0.31
1553067_PM_a_at	gonadotropin-releasing hormone (type 2) receptor 2	GNRHR2	114814	0.033	-0.31
1570402_PM_at	kinesin light chain 3	KLC3	147700	0.016	-0.31
241866_PM_at	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)	SLC16A7	9194	0.009	-0.31
225331_PM_at	coiled-coil domain containing 50	CCDC50	152137	0.017	-0.31
208815_PM_x_at	heat shock 70kDa protein 4	HSPA4	3308	0.027	-0.31
215351_PM_at	RNA terminal phosphate cyclase domain 1	RTCD1	8634	0.03	-0.31
206900_PM_x_at	zinc finger protein 253	ZNF253	56242	0.032	-0.31

226298_PM_at	RUN domain containing 1	RUNDC1	146923	0.037	-0.31
222130_PM_s_at	FtsJ homolog 2 (E. coli)	FTSJ2	29960	0.01	-0.31
226572_PM_at	suppressor of cytokine signaling 7	SOCS7	30837	0.021	-0.31
1558602_PM_a_at	hypothetical LOC285194	LOC285194	285194	0.043	-0.31
1561853_PM_a_at	interleukin 23 receptor	IL23R	149233	0.049	-0.31
224029_PM_x_at	sodium channel, voltage-gated, type XI, alpha subunit	SCN11A	11280	0.024	-0.3
243591_PM_at	---	---	---	0.03	-0.3
227765_PM_at	---	---	---	0.012	-0.3
231831_PM_at	COX19 cytochrome c oxidase assembly homolog (S. cerevisiae)	COX19	90639	0.038	-0.3
1564165_PM_at	PRKR interacting protein 1 (IL11 inducible)	PRKRIP1	79706	0.026	-0.3
226787_PM_at	zinc finger protein 18	ZNF18	7566	0.034	-0.3
201310_PM_s_at	chromosome 5 open reading frame 13	C5orf13	9315	0.04	-0.3
221342_PM_at	chromosome 6 open reading frame 25	C6orf25	80739	0.049	-0.3
214316_PM_x_at	---	---	---	0.014	-0.3
223531_PM_x_at	G protein-coupled receptor 89A /// G protein-coupled receptor 89B /// G protein-coupled receptor 89C	GPR89A /// GPR89B /// GPR89C	51463 /// 653519 /// 728932	0.023	-0.3
241163_PM_at	---	---	---	0.049	-0.3
1552803_PM_a_at	stathmin 1	STMN1	3925	0.003	-0.3
240274_PM_at	---	---	---	0.001	-0.3
227270_PM_at	family with sequence similarity 200, member B	FAM200B	285550	0.007	-0.3
209038_PM_s_at	EH-domain containing 1	EHD1	10938	0.008	-0.3
223714_PM_at	zinc finger protein 256	ZNF256	10172	0.019	-0.3
1562947_PM_x_at	---	---	---	0.027	-0.3
207046_PM_at	histone cluster 2, H4a /// histone cluster 2, H4b	HIST2H4A /// HIST2H4B	554313 /// 8370	0.037	-0.3
244372_PM_at	---	---	---	0.045	-0.3
1566487_PM_at	---	---	---	0.014	-0.29
234129_PM_at	Rho guanine nucleotide exchange factor (GEF) 12	ARHGEF12	23365	0.031	-0.29
1561451_PM_a_at	---	---	---	0.032	-0.29
233401_PM_at	---	---	---	0.038	-0.29

238372_PM_s_at	---	---	---	0.007	-0.29
209751_PM_s_at	trafficking protein particle complex 2 /// trafficking protein particle complex 2 pseudogene 1	TRAPPC2 /// TRAPPC2P1	10597 /// 6399	0.023	-0.29
232790_PM_at	---	---	---	0.044	-0.29
230381_PM_at	chromosome 1 open reading frame 186	C1orf186	440712	0.031	-0.29
234260_PM_at	---	---	---	0.044	-0.29
230861_PM_at	Hypothetical LOC26082	DKFZP434L187	26082	0.013	-0.29
215985_PM_at	Non-protein coding RNA 171	NCRNA00171	80862	0.045	-0.29
211442_PM_x_at	cytochrome P450, family 3, subfamily A, polypeptide 43	CYP3A43	64816	0.046	-0.29
243434_PM_at	---	---	---	0.013	-0.29
206962_PM_x_at	---	---	---	0.016	-0.29
243331_PM_at	---	---	---	0.025	-0.29
1564112_PM_at	Family with sequence similarity 71, member A	FAM71A	149647	0.03	-0.29
1561542_PM_at	---	---	---	0.02	-0.29
244669_PM_at	small nucleolar RNA host gene 5 (non-protein coding) /// small nucleolar RNA, C/D box 50A /// small nucleolar RNA, C/D box 50B	SNHG5 /// SNORD50A /// SNORD50B	26799 /// 387066 /// 692088	0.037	-0.29
239483_PM_at	FLJ37035 protein /// hypothetical protein LOC100287412	FLJ37035 /// LOC100287412	100287412 /// 399821	0.029	-0.29
206736_PM_x_at	cholinergic receptor, nicotinic, alpha 4	CHRNA4	1137	0.046	-0.29
233524_PM_at	chromosome 9 open reading frame 44	C9orf44	158314	0.033	-0.28
202523_PM_s_at	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	SPOCK2	9806	0.015	-0.28
215678_PM_at	---	---	---	0.046	-0.28
222501_PM_s_at	replication initiator 1	REPIN1	29803	0.008	-0.28
201011_PM_at	ribophorin I	RPN1	6184	0.021	-0.28
225533_PM_at	PHD finger protein 19	PHF19	26147	0.027	-0.28
221528_PM_s_at	engulfment and cell motility 2	ELMO2	63916	0.032	-0.28
1553859_PM_at	tryptophan hydroxylase 1	TPH1	7166	0.003	-0.28
219095_PM_at	JMJD7-PLA2G4B readthrough /// phospholipase A2, group IVB (cytosolic)	JMJD7-PLA2G4B /// PLA2G4B	100137049 /// 8681	0.048	-0.28
1561016_PM_at	---	---	---	0.034	-0.28

220251_PM_at	chromosome 1 open reading frame 107	C1orf107	27042	0.038	-0.28
232934_PM_at	---	---	---	0.044	-0.28
221034_PM_s_at	testis expressed 13B	TEX13B	56156	0.007	-0.28
204332_PM_s_at	aspartylglucosaminidase	AGA	175	0.047	-0.28
1553482_PM_at	chromosome 15 open reading frame 32	C15orf32	145858	0.006	-0.28
229364_PM_at	---	---	---	0.02	-0.28
233965_PM_at	hypothetical protein LOC255480	LOC255480	255480	0.029	-0.28
1560979_PM_a_at	---	---	---	0.049	-0.28
231375_PM_at	Hypothetical protein LOC202181	LOC202181	202181	0.02	-0.28
205466_PM_s_at	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	HS3ST1	9957	0.035	-0.28
220818_PM_s_at	transient receptor potential cation channel, subfamily C, member 4	TRPC4	7223	0.013	-0.27
201108_PM_s_at	thrombospondin 1	THBS1	7057	0.023	-0.27
209545_PM_s_at	receptor-interacting serine-threonine kinase 2	RIPK2	8767	0.023	-0.27
238058_PM_at	hypothetical LOC150381	LOC150381	150381	0.023	-0.27
210433_PM_at	protein O-fucosyltransferase 1	POFUT1	23509	0.009	-0.27
220494_PM_s_at	---	---	---	0.018	-0.27
237814_PM_at	---	---	---	0.029	-0.27
226725_PM_at	---	---	---	0.009	-0.27
204357_PM_s_at	LIM domain kinase 1	LIMK1	3984	0.048	-0.27
244367_PM_at	---	---	---	0.022	-0.27
223005_PM_s_at	chromosome 9 open reading frame 5	C9orf5	23731	0.038	-0.27
213695_PM_at	paraoxonase 3	PON3	5446	0.044	-0.27
1559249_PM_at	ataxin 1	ATXN1	6310	0.029	-0.27
207274_PM_at	cholinergic receptor, nicotinic, epsilon	CHRNE	1145	0.017	-0.27
232062_PM_at	adenylate cyclase 1 (brain)	ADCY1	107	0.02	-0.27
222057_PM_at	nucleolar protein 12	NOL12	79159	0.017	-0.27
244414_PM_at	---	---	---	0.045	-0.27
225847_PM_at	neutral cholesterol ester hydrolase 1	NCEH1	57552	0.001	-0.27
242391_PM_at	---	---	---	0.046	-0.27
1553672_PM_at	enabled homolog (Drosophila)	ENAH	55740	0.012	-0.26
214742_PM_at	5-azacytidine induced 1	AZI1	22994	0.021	-0.26

1558670_PM_at	---	---	---	0.028	-0.26
38157_PM_at	dom-3 homolog Z (C. elegans)	DOM3Z	1797	0	0.264
240253_PM_at	---	---	---	0.014	0.264
1562245_PM_a_at	Zinc finger protein 578	ZNF578	147660	0.027	0.265
203668_PM_at	mannosidase, alpha, class 2C, member 1	MAN2C1	4123	0.047	0.265
1555613_PM_a_at	zeta-chain (TCR) associated protein kinase 70kDa	ZAP70	7535	0.021	0.266
203393_PM_at	hairy and enhancer of split 1, (Drosophila)	HES1	3280	0.024	0.266
220927_PM_s_at	heparanase 2	HPSE2	60495	0.029	0.266
232592_PM_at	---	---	---	0.01	0.267
220279_PM_at	tripartite motif-containing 17	TRIM17	51127	0.014	0.267
232958_PM_at	---	---	---	0.035	0.267
240327_PM_at	---	---	---	0.005	0.268
207643_PM_s_at	tumor necrosis factor receptor superfamily, member 1A	TNFRSF1A	7132	0.014	0.269
224608_PM_s_at	vacuolar protein sorting 25 homolog (S. cerevisiae)	VPS25	84313	0.049	0.269
235715_PM_at	shadow of prion protein pseudogene	FLJ44653	399833	0.036	0.27
236453_PM_at	---	---	---	0.005	0.271
219187_PM_at	FK506 binding protein like	FKBPL	63943	0.009	0.271
210871_PM_x_at	synovial sarcoma, X breakpoint 2 interacting protein	SSX2IP	117178	0.041	0.271
223406_PM_x_at	family with sequence similarity 192, member A	FAM192A	80011	0.021	0.272
211367_PM_s_at	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	CASP1	834	0.039	0.272
1556865_PM_at	---	---	---	0.003	0.273
231545_PM_at	---	---	---	0.003	0.273
204716_PM_at	coiled-coil domain containing 6	CCDC6	8030	0.005	0.273
234475_PM_x_at	Cholecystokinin B receptor	CCKBR	887	0.025	0.273
1555509_PM_a_at	solute carrier family 25, member 41	SLC25A41	284427	0.002	0.275
210336_PM_x_at	myeloid zinc finger 1	MZF1	7593	0.012	0.276
201638_PM_s_at	cleavage and polyadenylation specific factor 1, 160kDa	CPSF1	29894	0.021	0.277
236716_PM_at	---	---	---	0.037	0.278
241970_PM_at	---	---	---	0.002	0.279
212272_PM_at	lipin 1	LPIN1	23175	0.003	0.279
209508_PM_x_at	CASP8 and FADD-like apoptosis regulator	CFLAR	8837	0.017	0.282

222336_PM_at	chromosome 4 open reading frame 34	C4orf34	201895	0.024	0.282
220694_PM_at	ASAP1 intronic transcript 1 (non-protein coding)	ASAP1IT1	29065	0.028	0.283
41660_PM_at	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	CELSR1	9620	0.003	0.284
213676_PM_at	transmembrane protein 151B	TMEM151B	441151	0.013	0.284
234209_PM_at	---	---	---	0.017	0.285
1566881_PM_at	---	---	---	0.025	0.285
211990_PM_at	major histocompatibility complex, class II, DP alpha 1	HLA-DPA1	3113	0.041	0.285
1561132_PM_at	DEAH (Asp-Glu-Ala-His) box polypeptide 35	DHX35	60625	0.026	0.286
233599_PM_at	hCG2003663	LOC728061	728061	0.039	0.286
237541_PM_at	---	---	---	0.001	0.287
225226_PM_at	family with sequence similarity 40, member A	FAM40A	85369	0.031	0.287
241658_PM_at	---	---	---	0.049	0.287
223632_PM_s_at	brevican	BCAN	63827	0.045	0.288
236240_PM_at	chromosome 4 open reading frame 29	C4orf29	80167	0	0.289
1556354_PM_s_at	ral guanine nucleotide dissociation stimulator-like 3	RGL3	57139	0.014	0.289
AFFX-BioC-5_at	---	---	---	0.015	0.289
234294_PM_x_at	GATA zinc finger domain containing 2A	GATAD2A	54815	0.029	0.289
231900_PM_at	Zinc finger, DHHC-type containing 18	ZDHHC18	84243	0.012	0.29
238950_PM_at	---	---	---	0.028	0.29
241187_PM_at	---	---	---	0.039	0.29
1553107_PM_s_at	chromosome 5 open reading frame 24	C5orf24	134553	0.003	0.291
1554849_PM_at	torsin family 1, member A (torsin A)	TOR1A	1861	0.005	0.291
201767_PM_s_at	elaC homolog 2 (E. coli)	ELAC2	60528	0.048	0.291
241318_PM_at	---	---	---	0.019	0.292
227435_PM_at	KIAA2018	KIAA2018	205717	0.024	0.292
1562863_PM_at	---	---	---	0.008	0.293
200822_PM_x_at	triosephosphate isomerase 1	TPI1	7167	0.034	0.293
1563783_PM_a_at	zinc finger protein 333	ZNF333	84449	0.035	0.294
1557131_PM_at	hypothetical protein LOC254100	LOC254100	254100	0.046	0.294
1557260_PM_a_at	zinc finger protein 382	ZNF382	84911	0.009	0.295
241161_PM_at	---	---	---	0.009	0.295

211982_PM_x_at	exportin 6	XPO6	23214	0.025	0.295
1560274_PM_at	Wilms tumor 1 associated protein	WTAP	9589	0.032	0.295
1563584_PM_at	family with sequence similarity 38, member B	FAM38B	63895	0.047	0.295
213746_PM_s_at	filamin A, alpha	FLNA	2316	0.017	0.298
211030_PM_s_at	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	SLC6A6	6533	0.048	0.298
218699_PM_at	RAB7, member RAS oncogene family-like 1	RAB7L1	8934	0.015	0.299
214643_PM_x_at	bridging integrator 1	BIN1	274	0.022	0.299
225995_PM_x_at	WAS protein family homolog 1 /// WAS protein family homolog 2 pseudogene	WASH1 /// WASH2P	100287171 /// 375260	0.033	0.3
239368_PM_at	---	---	---	0.04	0.3
1565689_PM_at	---	---	---	0.006	0.302
209021_PM_x_at	KIAA0652	KIAA0652	9776	0.012	0.302
226655_PM_at	syntaxin 17	STX17	55014	0	0.303
212892_PM_at	zinc finger protein 282	ZNF282	8427	0.044	0.303
227451_PM_s_at	Coiled-coil domain containing 90A	CCDC90A	63933	0.049	0.303
242057_PM_at	---	---	---	0.015	0.305
218185_PM_s_at	armadillo repeat containing 1	ARMC1	55156	0.015	0.306
1558858_PM_at	---	---	---	0.014	0.307
1558666_PM_at	---	---	---	0.032	0.309
205698_PM_s_at	mitogen-activated protein kinase kinase 6	MAP2K6	5608	0.031	0.311
237239_PM_at	---	---	---	0.037	0.311
1552344_PM_s_at	CCR4-NOT transcription complex, subunit 7	CNOT7	29883	0.043	0.311
220641_PM_at	NADPH oxidase, EF-hand calcium binding domain 5	NOX5	79400	0.004	0.313
1563369_PM_at	non-protein coding RNA 173	NCRNA00173	100287569	0.008	0.313
241547_PM_at	---	---	---	0.011	0.314
244586_PM_x_at	---	---	---	0.003	0.315
236380_PM_at	---	---	---	0.037	0.315
229074_PM_at	EH-domain containing 4	EHD4	30844	0.012	0.316
1556846_PM_at	---	---	---	0.027	0.316
236540_PM_at	---	---	---	0.032	0.316
217230_PM_at	ezrin	EZR	7430	0.04	0.316

221670_PM_s_at	LIM homeobox 3	LHX3	8022	0.019	0.318
224234_PM_at	---	---	---	0.025	0.318
242519_PM_at	coiled-coil domain containing 152	CCDC152	100129792	0.017	0.319
240207_PM_at	---	---	---	0.029	0.32
1559535_PM_s_at	---	---	---	0.038	0.321
238961_PM_s_at	Fibronectin type III domain containing 3A	FNDC3A	22862	0.012	0.322
225192_PM_at	chromosome 10 open reading frame 46	C10orf46	143384	0.042	0.324
243418_PM_at	---	---	---	0.049	0.324
219451_PM_at	methionine sulfoxide reductase B2	MSRB2	22921	0.01	0.325
225296_PM_at	zinc finger protein 317	ZNF317	57693	0.035	0.325
1563894_PM_at	hypothetical LOC441178	LOC441178	441178	0.046	0.325
206169_PM_x_at	zinc finger CCCH-type containing 7B	ZC3H7B	23264	0.029	0.326
204421_PM_s_at	fibroblast growth factor 2 (basic)	FGF2	2247	0.035	0.326
234088_PM_at	---	---	---	0.017	0.328
221893_PM_s_at	aarF domain containing kinase 2	ADCK2	90956	0.009	0.329
213642_PM_at	---	---	---	0.043	0.329
220031_PM_at	OTU domain containing 7B	OTUD7B	56957	0.037	0.33
203287_PM_at	ladinin 1	LAD1	3898	0.016	0.331
202887_PM_s_at	DNA-damage-inducible transcript 4	DDIT4	54541	0.018	0.331
204658_PM_at	transformer 2 alpha homolog (Drosophila)	TRA2A	29896	0.025	0.333
204272_PM_at	lectin, galactoside-binding, soluble, 4	LGALS4	3960	0.012	0.336
227872_PM_at	polymerase (RNA) III (DNA directed) polypeptide A, 155kDa	POLR3A	11128	0.014	0.336
206959_PM_s_at	UPF3 regulator of nonsense transcripts homolog A (yeast)	UPF3A	65110	0.017	0.336
237721_PM_s_at	ankyrin repeat and SOCS box-containing 4	ASB4	51666	0.036	0.337
241662_PM_x_at	---	---	---	0.004	0.339
217580_PM_x_at	---	---	---	0.012	0.339
1569091_PM_at	---	---	---	0.047	0.339
1569034_PM_a_at	hypothetical gene supported by BC040724	LOC440864	440864	0.042	0.34
217843_PM_s_at	mediator complex subunit 4	MED4	29079	0.043	0.34
222676_PM_at	brain protein I3 /// hypothetical protein LOC644975	BRI3 /// FLJ30064	25798 /// 644975	0.036	0.341
244030_PM_at	serine/threonine/tyrosine interacting protein	STYX	6815	0.016	0.342

239318_PM_at	family with sequence similarity 118, member B	FAM118B	79607	0.032	0.342
1557966_PM_x_at	MTERF domain containing 2	MTERFD2	130916	0.04	0.342
222252_PM_x_at	ubiquilin 4	UBQLN4	56893	0.017	0.343
213213_PM_at	death inducer-obliterator 1	DIDO1	11083	0.042	0.343
1563916_PM_at	hypothetical protein LOC283089	LOC283089	283089	0.037	0.345
243178_PM_at	---	---	---	0.041	0.346
223739_PM_at	peptidyl arginine deiminase, type I	PADI1	29943	0.046	0.347
229995_PM_at	syncollin	SYCN	342898	0.04	0.348
1559490_PM_at	leucine-rich repeats and calponin homology (CH) domain containing 3	LRCH3	84859	0.038	0.351
227587_PM_at	KRI1 homolog (S. cerevisiae)	KRI1	65095	0.049	0.352
235086_PM_at	thrombospondin 1	THBS1	7057	0.033	0.356
203090_PM_at	stromal cell-derived factor 2	SDF2	6388	0.015	0.357
213526_PM_s_at	lin-37 homolog (C. elegans)	LIN37	55957	0.022	0.357
239967_PM_at	---	---	---	0.045	0.357
207418_PM_s_at	D-aspartate oxidase	DDO	8528	0.035	0.358
208185_PM_x_at	---	---	---	0.019	0.361
229988_PM_at	---	---	---	0.025	0.361
220934_PM_s_at	transmembrane protein 223	TMEM223	79064	0.029	0.365
1561216_PM_at	---	---	---	0.019	0.366
223765_PM_s_at	kelch repeat and BTB (POZ) domain containing 4	KBTBD4	55709	0.046	0.368
209856_PM_x_at	abl-interactor 2	ABI2	10152	0.011	0.377
209238_PM_at	syntaxin 3	STX3	6809	0.036	0.38
218038_PM_at	ATP5S-like	ATP5SL	55101	0.03	0.381
203766_PM_s_at	leiomodin 1 (smooth muscle)	LMOD1	25802	0.028	0.383
236550_PM_s_at	zinc finger protein 311	ZNF311	282890	0.04	0.383
1567622_PM_at	Actin binding LIM protein family, member 2	ABLIM2	84448	0.046	0.383
202385_PM_s_at	Treacher Collins-Franceschetti syndrome 1	TCOF1	6949	0.039	0.386
237954_PM_x_at	Protein SOLO	FLJ10357	55701	0.006	0.388
209964_PM_s_at	ataxin 7	ATXN7	6314	0.005	0.391
235340_PM_at	glucosidase, alpha; neutral C	GANC	2595	0.02	0.393
203509_PM_at	sortilin-related receptor, L(DLR class) A repeats-containing	SORL1	6653	0.032	0.398

219905_PM_at	erythroblast membrane-associated protein (Scianna blood group)	ERMAP	114625	0.038	0.401
242537_PM_at	---	---	---	0.021	0.404
236397_PM_at	---	---	---	0.024	0.405
209565_PM_at	ring finger protein 113A	RNF113A	7737	0.014	0.406
225671_PM_at	spinster homolog 2 (Drosophila)	SPNS2	124976	0.044	0.414
229776_PM_at	solute carrier organic anion transporter family, member 3A1	SLCO3A1	28232	0.042	0.415
202246_PM_s_at	cyclin-dependent kinase 4	CDK4	1019	0.043	0.42
228874_PM_at	Pleckstrin homology-like domain, family B, member 3	PHLDB3	653583	0.013	0.422
228158_PM_at	lymphocyte-specific protein 1 pseudogene	LOC645166	645166	0.029	0.425
229514_PM_at	chromosome 14 open reading frame 118	C14orf118	55668	0.038	0.426
43511_PM_s_at	---	---	---	0.023	0.432
213748_PM_at	tripartite motif-containing 66	TRIM66	9866	0.04	0.433
243787_PM_at	---	---	---	0.042	0.433
91682_PM_at	---	---	---	0.004	0.434
228620_PM_at	---	---	---	0.006	0.437
210720_PM_s_at	N-terminal EF-hand calcium binding protein 3	NECAB3	63941	0.032	0.442
235292_PM_at	hypothetical protein LOC643977	FLJ32255	643977	0.031	0.444
235480_PM_at	TGF-beta activated kinase 1/MAP3K7 binding protein 1	TAB1	10454	0.046	0.445
204261_PM_s_at	presenilin 2 (Alzheimer disease 4)	PSEN2	5664	0.028	0.455
205645_PM_at	RALBP1 associated Eps domain containing 2	REPS2	9185	0.046	0.455
200696_PM_s_at	gelsolin	GSN	2934	0.04	0.475
1554621_PM_at	diacylglycerol kinase, epsilon 64kDa	DGKE	8526	0.025	0.476
1555554_PM_at	breast cancer and salivary gland expression gene	BASE	317716	0.045	0.483
1554112_PM_a_at	unc-51-like kinase 2 (C. elegans)	ULK2	9706	0.027	0.484
214487_PM_s_at	RAP2A, member of RAS oncogene family /// RAP2B, member of RAS oncogene family	RAP2A /// RAP2B	5911 /// 5912	0.004	0.506
233230_PM_s_at	SLAIN motif family, member 2	SLAIN2	57606	0.006	0.509
213622_PM_at	collagen, type IX, alpha 2	COL9A2	1298	0.031	0.549
226734_PM_at	eukaryotic translation initiation factor 4E family member 2	EIF4E2	9470	0.04	0.567
215700_PM_x_at	copine VI (neuronal)	CPNE6	9362	0.031	0.573
240947_PM_at	anoctamin 6	ANO6	196527	0.026	0.633

201823_PM_s_at	ring finger protein 14	RNF14	9604	0.042	0.725
213793_PM_s_at	homer homolog 1 (Drosophila)	HOMER1	9456	0.038	1.487

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