



**REGULATION OF MUSCLE METABOLISM BY
MYOSTATIN**

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SCHOOL OF BIOLOGICAL SCIENCES

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ABSTRACT

Obesity and type 2 diabetes have become global issues through increased fat accumulation in adipose tissue due to a combination of chronic high calorie food intake and sedentary lifestyle. Interestingly, results presented in this thesis reveal that depletion of myostatin (Mstn), a TGF- β superfamily member, leads to reduced fat accumulation and improved insulin sensitivity in mice even during diet-induced obesity. This thesis includes a general review of literature (Chapter 1), a detailed materials and methods chapter (Chapter 2), followed by 4 results chapters, focusing on delineating the mechanism of how Mstn regulates carbohydrate metabolism (Chapter 3) and lipid metabolism (Chapter 4). Moreover, global gene expression analysis was undertaken to determine the molecular function of Mstn in metabolism (Chapter 5). In addition, there is one chapter discussing a novel role of Mstn in skin regeneration (Chapter 6). Finally, the thesis ends with a prospective chapter (Chapter 7).

In the current thesis, the mechanism through which Mstn regulates muscle metabolism is summarized. Myostatin-null (*Mstn*^{-/-}) mice display an improved carbohydrate metabolism even during high calorie intake. Increased insulin sensitivity is due to up-regulated insulin signaling, as supported through enhanced expression of GLUT4, Akt, p-Akt and IRS-1 in *Mstn*^{-/-} mice. Molecular analysis reveals that the expression of AMPK is up-regulated in skeletal muscle and white adipose tissue (WAT) isolated from *Mstn*^{-/-} mice. Enhanced AMPK expression leads to phosphorylation of ACC, promoting fatty acid oxidation and finally resulting in improved insulin sensitivity in *Mstn*^{-/-} mice. Moreover, in *Mstn*^{-/-} mice, increased expression of the AMPK downstream target genes, *Sirt1* and *Pgc-1 α* , was observed in skeletal muscle; indicating another possible signaling pathway for AMPK. Furthermore, during this

study, treatment with Mstn antagonist, soluble activin type IIB receptor (sActRIIB), also significantly improved carbohydrate metabolism, indicating sActRIIB may serve as a therapy for type 2 diabetes.

In addition to the improved carbohydrate metabolism, *Mstn*^{-/-} mice also exhibit benefits in lipid metabolism, which are regulated by at least two independent mechanisms. One mechanism is that lack of Mstn promotes fatty acid oxidation in peripheral tissues through up-regulating enzymes involved in lipolysis and fatty acid oxidation in mitochondria. Specifically, significantly increased expression of genes involved in fatty acid synthesis (*Fasn*, *Acc1*), lipolysis (*Atgl*, *Hsl*, *Mgl*) and fatty acid oxidation (*Lcad*, *Vlcas*, *Vlcad*) was also observed in WAT from *Mstn*^{-/-} mice. Consistent with the enhanced expression of fatty acid oxidation genes, a dramatically increased fatty acid oxidation in WAT, liver and differentiated myotubes from *Mstn*^{-/-} mice has also been detected. Furthermore, expression of enzymes critical to mitochondrial activity also was measured in *Mstn*^{-/-} WAT. The second mechanism involves the promotion of brown adipose tissue (BAT) like qualities in WAT of *Mstn*^{-/-} mice. Crucial BAT molecular markers, such as *Ucp1*, *PPARα/β/γ* and *Pgc-1α*, are all up-regulated in WAT of *Mstn*^{-/-} mice, implying that in *Mstn*^{-/-} mice, WAT adopts more BAT-like characteristics. Consistent with the gene expression changes, elevated body temperature in high fat diet (HFD) fed *Mstn*^{-/-} mice and a preponderance of BAT phenotype (small size, multilocular adipocytes) in *Mstn*^{-/-} WAT was observed. The BAT-like characteristics were due to enhanced COX-2 induced prostaglandin release, resulting in the conversion of mesenchymal progenitor cells into a BAT phenotype. In agreement with the above results, treatment of WT mice on HFD with sActRIIB, Mstn antagonist, improves insulin sensitivity and protects against the obesity phenotype.

Therefore, these results suggest that either prenatal or postnatal inactivation of Mstn prevents diet-induced obesity and improves insulin sensitivity.

Genome-wide gene expression analysis revealed that lack of Mstn protects against the normal gene profile changes expected as a result of HFD. Specifically, loss of Mstn results in reduced lipid uptake and lipid storage, which could potentially lead to the atrophy observed in WAT isolated from *Mstn*^{-/-} mice.

In addition to characterizing the role of Mstn in regulation of muscle metabolism, this thesis has addressed the function of Mstn during skin wound regeneration. The role of Mstn in muscle regeneration has been well characterized, but little is known about its function in skin regeneration. The results presented in this thesis, for the first time, indicate that Mstn exists in both epidermis and dermis of murine and human skin. Moreover, *Mstn*^{-/-} mice exhibit delayed skin wound healing as a combination of delayed epidermal re-epithelialization and dermal contraction. In the epidermis, slower re-epithelialization results from a delay in epidermal thickness recovery due to reduced keratinocyte migration and protracted keratinocyte proliferation. This observation was further confirmed by an *in vitro* migration and adhesion assay. Flow cytometry and Western blotting analysis also revealed increased proliferation of primary keratinocytes isolated from *Mstn*^{-/-} mice. In the underlying dermis, reduced fibroblast-to-myofibroblast transformation and lower collagen deposition collectively contribute to the delayed dermal wound contraction. Furthermore, topically treatment of TGF- β protein on the wound area rescues the impaired wound healing seen in *Mstn*^{-/-} mice. These observations are due to blockage of TGF- β signalling secondary to an elevation in decorin expression, which is a naturally occurring TGF- β suppressor, in Mstn deficient mice. These results reveal an interaction between TGF- β and Mstn signalling

pathways, through which Mstn regulates decorin levels during the skin wound healing process. Therefore, Mstn agonist might be a potential therapy for skin wound repair.

In summary, the work in this thesis examined the possible mechanisms by which Mstn regulates carbohydrate and lipid metabolism, as well as the role of Mstn in obesity and type 2 diabetes. The results presented here explain the lean and anti-diabetic phenotype in *Mstn*^{-/-} mice, even during HFD feeding. Finally, Mstn was also found to be associated with skin regeneration, pointing out the novel function of Mstn in skin. The research in this thesis also shed light on the Mstn antagonist, sActRIIB, which maybe a potential first-line drug for anti-obesity and anti-diabetes in the future.

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warm, amiable nature inspired and motivated me through the course of my PhD. I am deeply indebted to her and I would like to share a part of my success with her.

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Lastly, I will forever cherish the rich and colorful memories that I had as part of this lab. I am a much better individual than I was when I joined this FMG Lab and NTU. These memories will forever reside in me and make me strive towards a better life, a better future.

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LIST OF ABBREVIATIONS

α -SMA	alpha-smooth muscle actin
β Me	beta-mercaptoethanol
ACC	acetyl-coA carboxylase
ActRIIB	activin type IIB receptor
<i>Adipoq</i>	adiponectin gene
Akt	protein kinase B
ALK5	TGF- β receptor type I
AMPK	AMP-activated protein kinase
Apoc3	Apolipoprotein C3
Ay	agouti lethal yellow
BAT	brown adipose tissue
BMI	body mass index
BSA	bovine serum albumin
COX-2	cyclooxygenase-2
Cox5b	cytochrome c oxidase enzyme subunits Vb
Cox7a1	cytochrome c oxidase enzyme subunits VIIa1
Cox8b	cytochrome c oxidase enzyme subunits VIIIb
CPT1	carnitine palmitoyltransferase I
Crot	Carnitine O-octanoyltransferase
CDK2	cyclin-dependent kinase 2
DAG	diacylglycerol
ECM	extracellular matrix
EDL	<i>M. extensor digitorum longus</i> muscle

Erk	1/2 extracellular signal-regulated kinase 1/2
FBS	fetal bovine serum
FDR	false discovery rate
FFA	free fatty acid
FGF	fibroblast growth factor
FOXO1	forkhead box protein O1
GAS	<i>M. gastrocnemius</i> muscle
GDF-8	growth and differentiation factor-8
GO	gene ontology
GSEA	gene set enrichment analysis
GTT	glucose tolerance test
H&E	haematoxylin and eosin
HFD	high-fat diet
HRP	horseradish peroxidase
IGF-1	insulin-like growth factor 1
IL-1	interleukin-1
IL-6	interleukin-6
IRS	insulin receptor substrate
KRB	Krebs-Ringer bicarbonate
LAP	latency-associated peptide
Lep ^{ob/ob} mice	obese mice
LPL	lipoprotein lipase
MAPK	Mitogen-activated protein kinase
MCP1	monocyte chemotactic protein
MHC	myosin heavy chain
Mstn	myostatin protein

<i>Mstn</i>	myostatin gene
<i>Mstn</i> ^{-/-}	myostatin-null
NFκB	nuclear factor kappa-light-chain-enhancer of activated B cells
NGS	normal goat serum
P21	cyclin-dependent kinase inhibitor 1
PBS	phosphate buffered saline
PDGF	platelet-derived growth factor
PEG	polyethylene glycol
PI3 kinase	phosphatidylinositol 3-kinase
PGC-1α	peroxisome proliferator-activated receptor-gamma coactivator-1 alpha
PPAR	peroxisome proliferator-activated receptor
PVP	polyvinylpyrrolidone
Rb	retinoblastoma
RBC	red blood cell
ROS	reactive oxygen species
RXR	retinoid X receptors
sActRIIB	soluble activin type IIB receptor
SDS	sodium dodecyl sulfate
SIRT1	sirtuin 1
SV	stromal vascular
TAG	triglyceride
TGF-β	transforming growth factor-β
TNF-α	tumor necrosis factor- α
UCP1	uncoupling protein 1
VLDL	very low density lipoprotein

WAT	white adipose tissue
WT	wild-type

This Thesis is dedicated

to

My Parents

and

My Dear Boyfriend

Chapter 1 Review of Literature

1.1 Role of skeletal muscle and adipose tissue in obesity-induced diabetes

Muscle, derived from embryonic germ cells in the mesodermal layer, is a type of contractile tissue and can be categorized into smooth, cardiac, and skeletal muscle. Adipose tissue is a loose connective tissue, which is composed of adipocytes, and can be divided into two groups: white adipose tissue (WAT) and brown adipose tissue (BAT). The following section will focus on reviewing current literature relating to skeletal muscle structure, adipose tissue characteristics, and their roles in obesity-induced diabetes.

1.1.1 Skeletal muscle structure

Smooth and cardiac muscle contraction is involuntary and contributes to body maintenance. However, as the principal function of skeletal muscle is to produce force for body movement, skeletal muscle is under voluntary control.

Skeletal muscle consists of thousands of muscle fibers (Figure 1.1) [1]. Muscle fibers or skeletal muscle cells, are surrounded by connective tissue, nerves, and blood vessels, which together serve to either protect or exert function on muscle fibers (Figure 1.1) [1]. Skeletal muscle is enclosed in a connective tissue layer, termed epimysium, while the perimysium separates muscle fibers into bundles termed fascicles (Figure 1.1) [1]. Individual muscle fibers are further separated by a thin sheath of connective tissue, known as the endomysium (Figure 1.1) [1]. Skeletal muscle fibers, or myofibers, contain thousands of myofibrils, which are bundles of myofilaments (Figure 1.2) [1]. Myofilaments can be divided into thick and thin filaments, which represent myosin

and actin filaments, respectively (Figure 1.2) [1]. Myofilaments are composed of repeated compartments called sarcomeres (Figure 1.2) [1]. Sarcomeres are the fundamental units of myofibrils, and it is the interactions between the thick and thin filaments within the sarcomeres that result in muscle contraction and force generation (Figure 1.2) [1]. Sarcomeres are composed of several distinct, highly ordered regions (Figure 1.2) [1]. An A band, which is a darker centrally localized region, and is the zone of overlap for the thick and thin filaments (Figure 1.2) [1]. The I band, which is near the adjacent areas between two sarcomeres, and contains thin filaments only (Figure 1.2) [1]. In the middle of the A band is an area composed of thick filaments only, termed the H zone (Figure 1.2) [1]. It is in the centre of the H zone that the M protein connects neighbouring thick filaments (Figure 1.2) [1]. Finally the Z line indicates the boundary of two adjacent sarcomeres and plays a role in binding the thin filaments between two sarcomeres (Figure 1.2) [1].

The mechanism for muscle contraction is explained by the “sliding filament theory”. During muscle contraction, the A band maintains the same length while the I band shrinks due to the movement of Z lines towards each other, thus shortening the sarcomeres and pulling the ends of the myofibril toward its center [1].

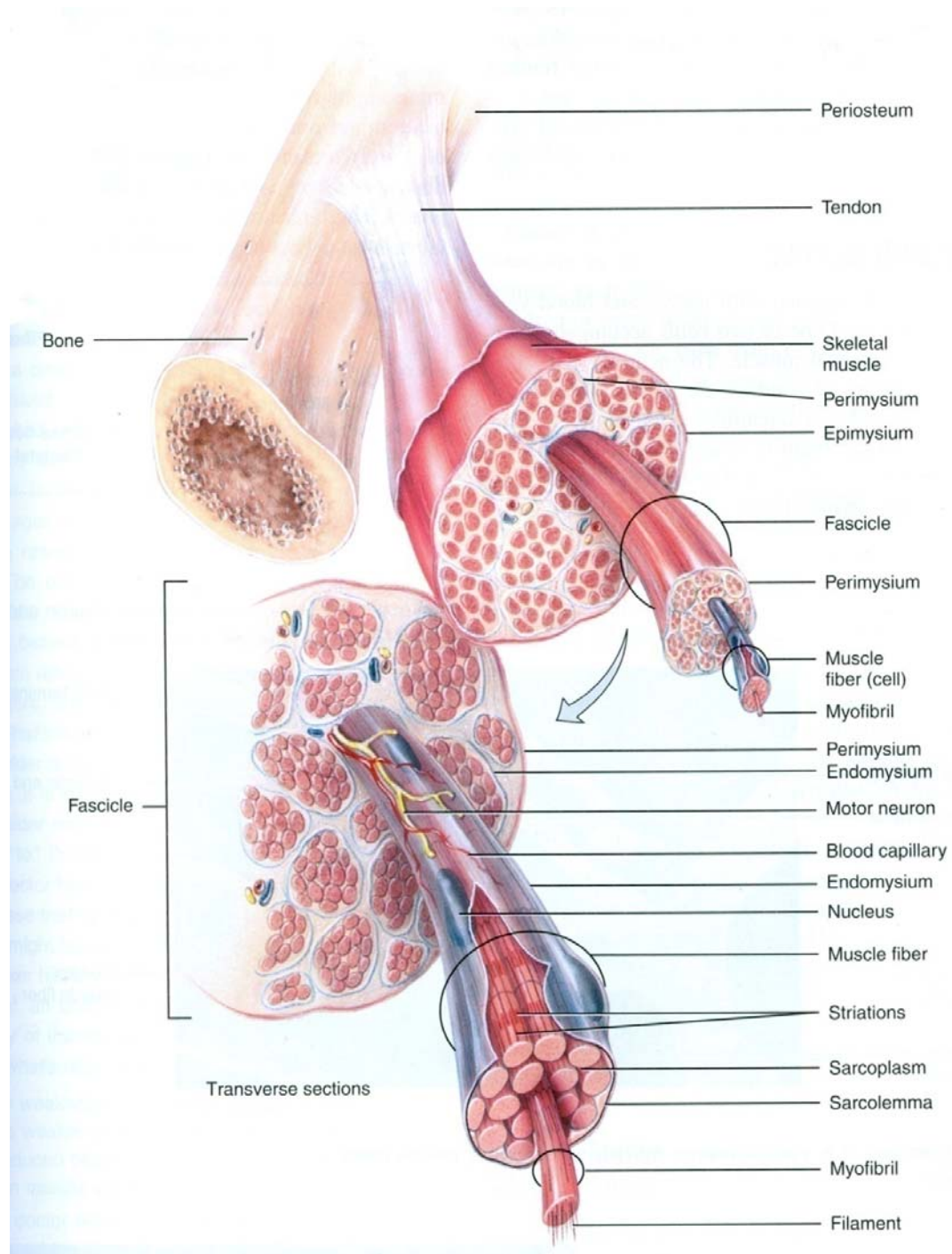


Figure 1.1 *Skeletal muscle structure*

Epimysium, perimysium, and endomysium are all connective tissue. The whole muscle is surrounded by epimysium. Muscle is separated by perimysium into different compartments named fascicles. Fascicles consist of myofibers, which are separated by endomysium. The myofiber encloses myofibrils. Modified from Jenkins *et al* [1].

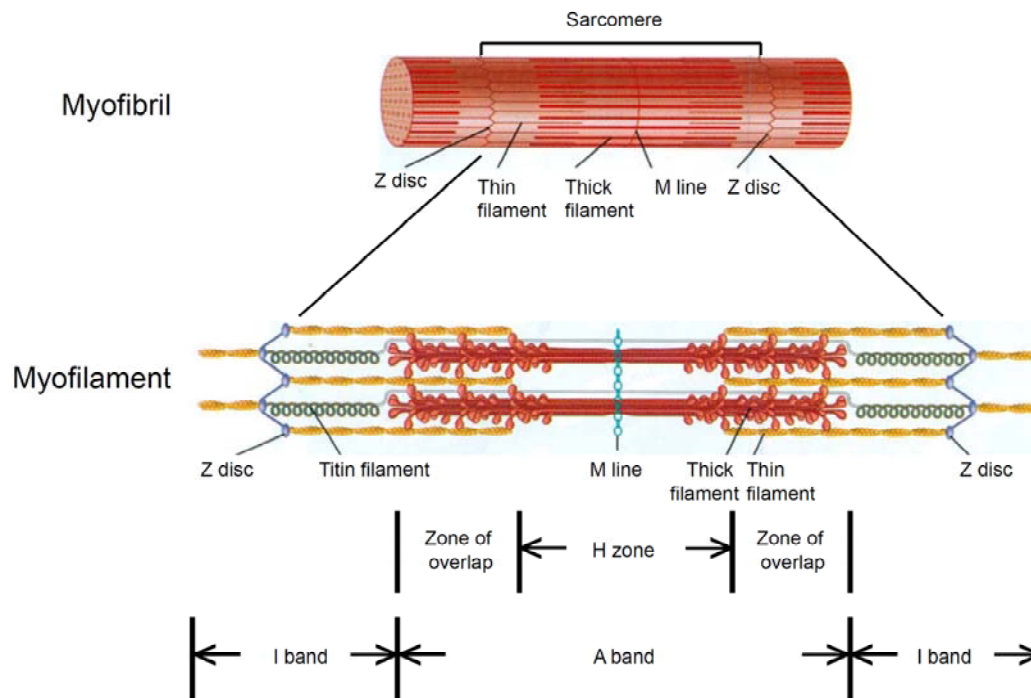


Figure 1.2 *Sarcomere structure*

Myofibrils enclose sarcomeres which are the basic unit for muscle contraction. Sarcomeres consist of thick and thin filaments in a highly structured order. Modified from Jenkins *et al* [1].

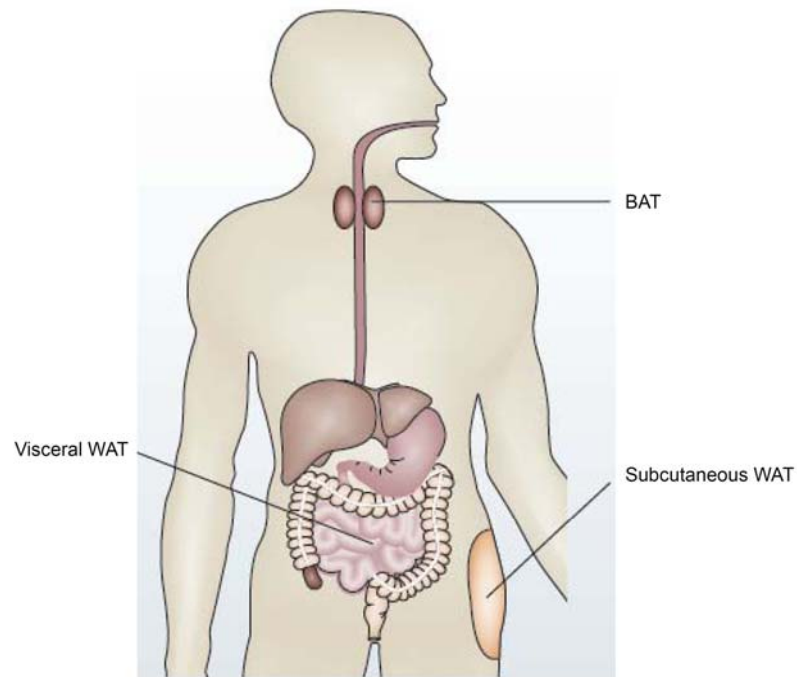
1.1.2 Adipose tissue

Adipose tissue is loose connective tissue composed of adipocytes. Adipose tissue can be divided into two types: white adipose tissue (WAT) and brown adipose tissue (BAT). Both WAT and BAT arise from mesenchymal progenitors, but follow a distinct lineage during preadipocyte differentiation [2]. Adipose tissue is deposited as “fat pads”, which in humans are distributed in 3 locations: subcutaneous WAT (beneath skin), visceral WAT (around the internal organs), and BAT (under the skin, in the paraspinal and interscapular regions) (Figure 1.3A). Previously, BAT was thought to be only present in rodents and infants, however, recent studies have demonstrated that functional BAT is also found in human adults [3-6]. In mice, 8 different types of fat pads are detected: Anterior, flank/inguinal fat pads (subcutaneous WAT), mesenteric, retroperitoneal, perirenal, and perigonadal (epididymal in male or parametrial in female) fat pads (visceral WAT), interscapular and mediastinal fat pads (BAT) (Figure 1.3B). Among them, the most accessible fat pads are the epididymal (or parametrial), retroperitoneal, inguinal and interscapular fat pads; therefore, these four fat pads are generally used in studies.

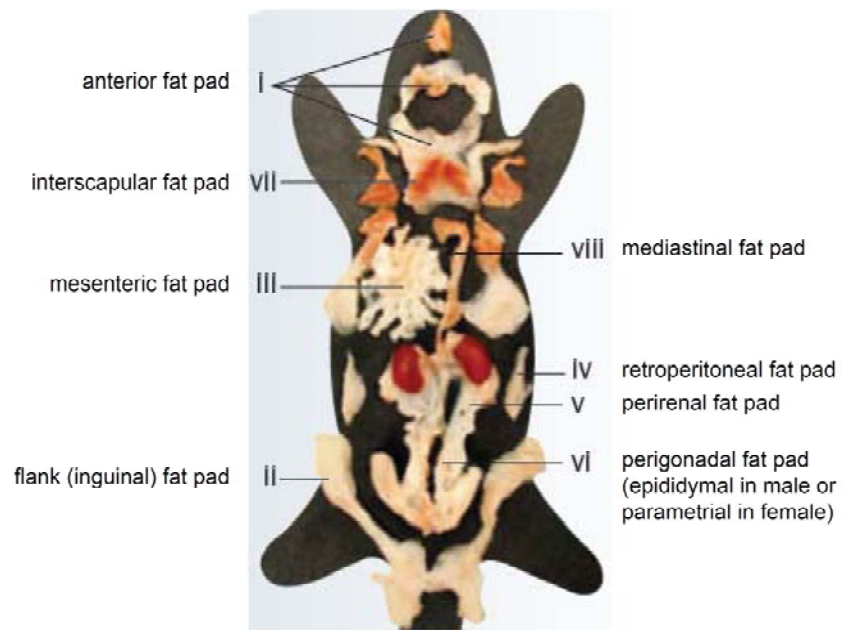
Figure 1.3 *Human and mouse adipose tissue depots*

(A) In human, fat pads include: subcutaneous WAT (beneath skin), visceral WAT (around the internal organs), and BAT (under the skin, in the paraspinal and interscapular regions). (B) In mice, there are 8 different types of fat pads: subcutaneous WAT: anterior fat pad and flank (inguinal) fat pad; visceral WAT: mesenteric fat pad, retroperitoneal fat pad, perirenal fat pad, and perigonadal fat pad (epididymal in male or parametrial in female); BAT: interscapular fat pad and mediastinal fat pad. Modified from Tran *et al* [18]

A.



B.



The main function for WAT is to act as an energy reservoir through storing fat, in the form of triglyceride (TAG). Approximately 90% of the intracellular space in adipocytes is occupied by a large lipid droplet with the cytoplasm and nucleus squeezed into a thin ring around the periphery of the cell. WAT plays a critical role in reducing heat loss through skin. It also functions as a cushion for various organs, and carries out secretory functions, such as secreting fatty acids and prostaglandins [1]. Current research demonstrates that WAT may be involved in cross talk with many other organs to regulate metabolism. Indeed, adipokine production by adipose tissue was found to be linked to obesity and type 2 diabetes [7-8].

While WAT is predominantly utilized for storing fat, BAT is responsible for oxidizing fat to generate heat. BAT is darker in appearance when compared to WAT, which is due to the increased mitochondrial content in BAT [9]. Also unlike the single lipid droplet observed in WAT, BAT has a multilocular appearance, containing multiple smaller lipid droplets [9]. BAT also has increased expression of thermogenesis genes, such as uncoupling protein 1 (*Ucp1*), which promotes uncoupled oxidative phosphorylation and release of excess energy as heat for body temperature maintenance [10]. In addition, the expression of peroxisome proliferator-activated receptor-gamma coactivator-1alpha (*Pgc-1α*) and peroxisome proliferator-activated receptor α , β/δ , γ (*Ppar α, β/δ, γ*) are all elevated in BAT, supporting the increased fatty acid oxidation in BAT [11-13]. Increased fatty acid oxidation in BAT contributes to decreased circulatory FFA resulting in the alleviation of obesity.

Recently, numerous publications describe a phenomenon whereby WAT may acquire BAT-like characteristics. These data reveal that the conversion of WAT into a BAT-like phenotype occurs upon exposure to a cold environment or through stimulation with a β 3-adrenergic agonist [14-16]. Despite the well-documented appearance of

BAT depots in WAT in both human and rodent [4, 17], the signaling mechanism controlling BAT deposition in WAT are yet to be fully understood. However, a recent publication has indicated that cyclooxygenase-2 (COX-2), the downstream target of β -adrenergic signaling may be the key factor involved in the formation of a BAT phenotype in WAT. Specifically, activation of COX-2 signaling up-regulates the expression of critical thermogenic genes, such as *Ucp1*, *Cidea*, *Cpt1b*, shifting mesenchymal progenitor cells towards a BAT phenotype through a prostaglandin-mediated signaling pathway [16].

1.1.3 Obesity

Obesity is termed as excess body fat accumulation [18]. Body mass index (BMI), a parameter defined as the comparison between body weight and height, is widely employed to evaluate human obesity. An individual who is more than 30 kg/m^2 is termed obese. Currently, obesity has become a worldwide issue due to increased high calorie intake, sedentary lifestyle, and genetic defects. To date, therapies to control obesity include dieting and physical exercise. However, in some cases, dietary control and physical activity are not always sufficient to overcome obesity and metabolic syndrome, thus, additional therapeutics are required to alleviate this particular pathology.

TAG can be stored in adipocytes after food consumption, and released during fasting in the form of free fatty acid (FFA). In the lipid droplet of adipocytes, TAG is degraded into FFA and glycerol by lipolysis [19]. Fatty acids can then either be oxidized in the mitochondria or transferred to the blood stream [19]. Conversely, TAG can be synthesized from acetyl-CoA by a process called lipid synthesis. Lipolysis and

lipid synthesis are balanced according to the energy requirement of the body. It is reported that dysfunction in lipolysis leads to adipose tissue overload, which results in obesity and chronic inflammation [20-21].

Lean individuals exhibit normal insulin sensitivity in skeletal muscle. However in obese individuals, the adipocytes are enlarged due to an increase in TAG storage. Prolonged fat accumulation in adipocytes results in macrophage recruitment, due to enhanced production of monocyte chemotactic protein (MCP-1) by adipocytes. Consequentially, this proinflammatory state of adipocytes results in increased secretion of TNF- α , impairing TAG deposition and elevating lipolysis and accumulation of circulating FFA [22-24]. Hypertrophy of adipocytes also leads to increased oxidative stress, resulting in the dysfunction of adipokines, which further promotes the development obesity-induced metabolic syndrome [25].

To aid in the study of obesity, a number of obese animal models have been established, such as diet-induced obesity models, transgenic obese animal models and catch up growth animal models.

Diet-induced obesity animal models are commonly used for accruing fat mass postnatally without genetic perturbation [26-27]. Experimental mice are normally fed on high-fat diet (HFD) (45 % or 60% energy from fat) from the age of 7-8 weeks, for a specific time point [27-29]; while control littermates are fed on chow diet (CD) (10% energy from fat).

Transgenic obesity animal models are animals, such as Zucker rats, Agouti lethal yellow (Ay) mice and obese (Lep^{ob/ob}) mice, which have mutations in obesity-related genes. Specifically, obese Zucker rats have a gene mutation in the leptin receptor (fa/fa), resulting in the dysregulation of body weight [30-31]. Ay mice are agouti locus

(chromosome 2) dominant mutation containing mice [32] and display an obese phenotype. *Lep^{ob/ob}* mice lack the 16 kDa leptin protein, which is specifically expressed in adipose tissue of normal mice. Loss of leptin protein leads to obesity, glucose intolerance and insulin resistance in these mutant mice [33].

Catch up growth is a form of accelerated growth in infants or young children who had a low-birth weight. Children that exhibit catch up growth are at high risk of obesity, type 2 diabetes and other metabolic syndrome as they mature [34]. Although the molecular mechanism(s), relating catch up growth with metabolic syndrome, have yet to be clarified, rapid WAT growth may play a crucial role [35]. In low-birth weight babies, while lean muscle growth is inhibited, WAT accumulation ensues, leading to the development of adult obesity and insulin resistance [35]. Catch up growth experimental rodent models are designed by restricting 40% to 50% of the food intake, followed by re-feeding the same diet [36-38]. In addition, catch up growth can be induced through restricting 50% to 70% of the food intake of pregnant female mice, with litters collected after birth for further study [39-40].

Obesity is normally associated with numerous other diseases and complications, such as heart disease, type 2 diabetes, hypertension, and sleep apnea [18]. Among these secondary disorders, type 2 diabetes is most frequently observed in obese patients. The following section will review current literature on obesity-induced type 2 diabetes.

1.1.4 Type 2 diabetes

Diabetes is defined as a group of metabolic syndromes in which a person has high blood glucose, due to either a failure in insulin production (type 1 diabetes) or insulin

deficiency and insulin resistance (type 2 diabetes) [41]. Gestational diabetes refers to the syndrome of high blood glucose developed only during pregnancy [41]. While daily administration of insulin may be a suitable therapy for type 1 diabetes, therapies that modulate insulin sensitivity may be more valuable in treating type 2 diabetes.

Type 2 diabetes is characterized as a metabolic disorder which results in high blood glucose due to insulin resistance and relative insulin deficiency [41]. Many factors may lead to the development of type 2 diabetes; namely obesity, hypertension, high cholesterol, and metabolic disorders. Among these factors, 55% of all type 2 diabetes cases are reported to be due to obesity [42]. Most certainly, weight gain is associated with an increase in insulin resistance and glucose intolerance, which are the main characteristics of type 2 diabetes [42]. Moreover, weight reduction has been shown to result in improved blood pressure and blood lipid profile, enhanced glucose and insulin sensitivity and increased glycosylated hemoglobin levels [43]. It is noteworthy to mention that abdominal obesity is more closely associated with insulin resistance; it is believed to be due to the higher metabolic activity observed in visceral fat when compared to subcutaneous fat [44].

1.1.5 Role of WAT in obesity-induced type 2 diabetes

The role of WAT in obesity-induced type 2 diabetes may be derived from the following 3 aspects: failure in adipose tissue expansion, increased inflammation and altered adipokine profiles.

Among these, failure in adipose tissue expansion is thought to be the major mechanism behind obesity-induced type 2 diabetes. The main function of WAT is to store fat [1], however, in the obese state, adipose tissue expands to such a point that

the expansion capacity becomes saturated [45]. Therefore, excess lipid is deposited in non-adipose tissues/organs, such as muscle and liver [45]. Such ectopic lipid deposition in non-adipose tissue organs leads to lipotoxicity, altered insulin signaling and insulin resistance [45].

Obesity is considered to be a state of mild inflammation, and as such promotes increased secretion of cytokines, such as TNF- α and IL6, resulting in insulin resistance [22]. Furthermore, expanded adipocytes secrete more pro-inflammatory cytokines and chemoattractants, resulting in enhanced macrophage infiltration [8]. Meanwhile, increased FFA, resulting from failure in adipose tissue expansion, also results in the activation of macrophages [46], endoplasmic reticular stress and reactive oxygen species (ROS) production, further leading to insulin resistance [47-48].

As adipose tissue is an endocrine organ, it is able to secrete multiple hormones, known as adipokines, which include leptin, adiponectin, visfatin and resistin [7-8]. Development of obesity alters the adipokine profile, impairing insulin signaling and promoting insulin resistance [49].

1.1.6 Role of skeletal muscle in obesity-induced type 2 diabetes

As discussed above, failure in adipose tissue expansion leads to excess lipid deposition in skeletal muscle. Therefore, the role of skeletal muscle in obesity-induced type 2 diabetes is closely related to intramyocellular lipid deposition. Skeletal muscle plays a key role in deciding the fate of circulating FFA. FFAs are normally oxidized in skeletal muscles, however; excess levels of FFAs result in increased intramyocellular lipid accumulation, which interferes with normal insulin signaling [50]. This phenomenon plays a critical role in the development of obesity-induced metabolic syndrome. Reasons for this syndrome remain unclear, however, elevated FFA,

increased basal or postprandial TAG, or impaired fatty acid oxidation in muscle may contribute to the metabolic syndrome [50-52]. In addition, metabolic syndrome may be associated with disorders in adipose tissue metabolism and whole body homeostasis [50-52].

Fatty acid oxidation is conducted in mitochondria, therefore mitochondrial dysfunction may contribute to obesity-associated metabolic syndrome [53]. The generation of reactive oxygen species (ROS), and increased intramyocellular lipids interferes with mitochondrial function [54-57]. As a consequence, lipid membranes suffer from peroxidative injury, and mitochondrial membrane-dependent enzymes become inactive, thus leading to oxidative metabolism disorder [54-57].

Increased intramyocellular lipid contributes to reduced muscle insulin sensitivity [50, 58-59]. One hypothesis is that the elevated intramyocellular fatty acid metabolites, such as diacylglycerol (DAG), fatty acyl-CoA or ceramides, phosphorylate insulin receptor substrate (IRS) and activate the serine/threonine kinase cascade. The serine-phosphorylated forms of IRS are unable to activate phosphatidylinositol 3-kinase (PI3 kinase), thus impairing glucose transport and insulin sensitivity [60-61].

1.1.7 Role of AMPK signaling in metabolism

AMPK plays a critical role in whole body carbohydrate and lipid metabolism. AMPK is an energy-sensing enzyme, which is activated by increasing AMP:ATP ratio in the body [62-63]. During exercise or other energy consuming conditions, AMPK is activated and functions by suppressing energy consuming processes, like glycogen, fatty acid and protein synthesis, and enhancing energy producing processes like

glucose uptake and fatty acid oxidation [62]. AMPK is a heterotrimeric serine/threonine kinase that is composed of a catalytic α subunit and two regulatory β and γ subunits [62-64]. In skeletal muscle, the AMPK heterotrimeric complex is composed of $\alpha 2/\beta 2/\gamma 3$ subunits.[65-66]. It is reported that AMPK stimulates glucose uptake by promoting GLUT4 trafficking to the membrane, which improves insulin sensitivity in skeletal muscle [67-69]. AMPK has also been shown to enhance fatty acid oxidation through a acetyl-coA carboxylase (ACC) and sirtuin 1 (SIRT1) signaling pathway. Specifically, activation of AMPK will lead to the phosphorylation of ACC, resulting in reduced malonyl-CoA levels, and increased transfer of long chain fatty acyl-CoA into the mitochondria via carnitine palmitoyltransferase I (CPT1) for β -oxidation (Figure 1.4) [70-71]. AMPK has also been shown to phosphorylate PGC-1 α , which allows for the subsequent deacetylation of PGC-1 α by SIRT-1. Deacetylated, and thus active PGC-1 α , will also contribute to the elevation of fatty acid oxidation (Figure 1.4) [72].

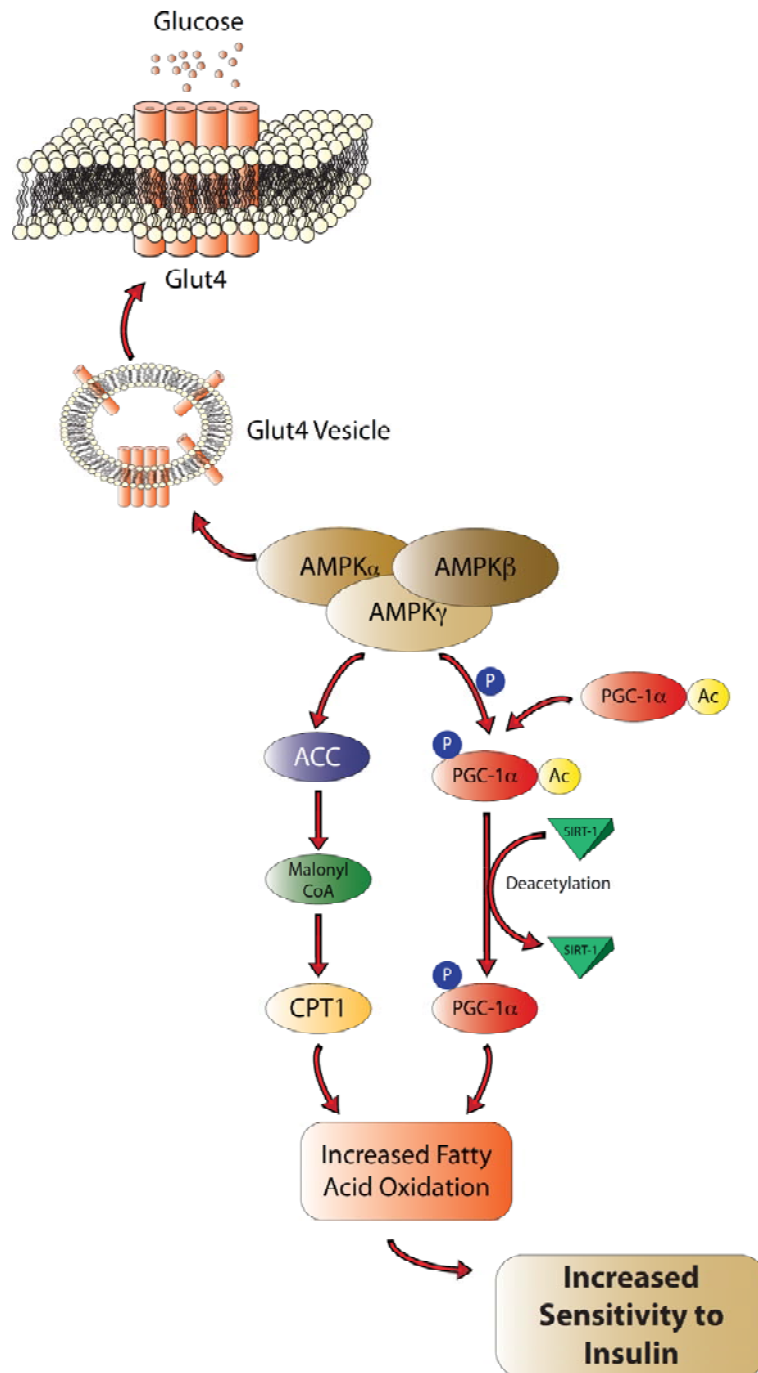


Figure 1.4 AMPK signaling pathway

Activation of AMPK results in the phosphorylation of ACC, leading to the reduction of malonyl-CoA and accelerated long chain fatty acyl CoA influx into mitochondria via CPT1, promoting fatty acid oxidation. Activation of AMPK also phosphorylates PGC-1 α , leading to deacetylation of PGC-1 α by SIRT-1 to further enhance fatty acid oxidation. Increased fatty acid oxidation thus leads to increased insulin sensitivity. Modified from Zhang *et al* [73]

1.1.8 Role of PPAR signaling in metabolism

PPARs are ligand-inducible nucleic transcription factors. PPARs form heterodimers with retinoid X receptors (RXR), and with the assistance of co-activators such as PGC-1 α , regulate gene transcription (Figure 1.5). There are three types of PPARs: PPAR α , PPAR β/δ and PPAR γ , and they have been shown to be key factors in maintaining whole body lipid homeostasis [74-75]. PPAR α activates a transcriptional program in skeletal muscle resulting in increased fatty acid uptake, binding, and oxidation, hence decreasing tissue FFA and improving oxidative capacity [76]. Specific activation of PPAR β/δ in adipose tissue up-regulates the expression of genes involve in fatty acid oxidation and energy dissipation [11]. PPAR γ is believed to be the nuclei receptor for cyclooxygenase-2 (COX-2)-mediated prostaglandin signalling pathway, contributing to the BAT phenotype in WAT, increasing fatty acid oxidation [77].

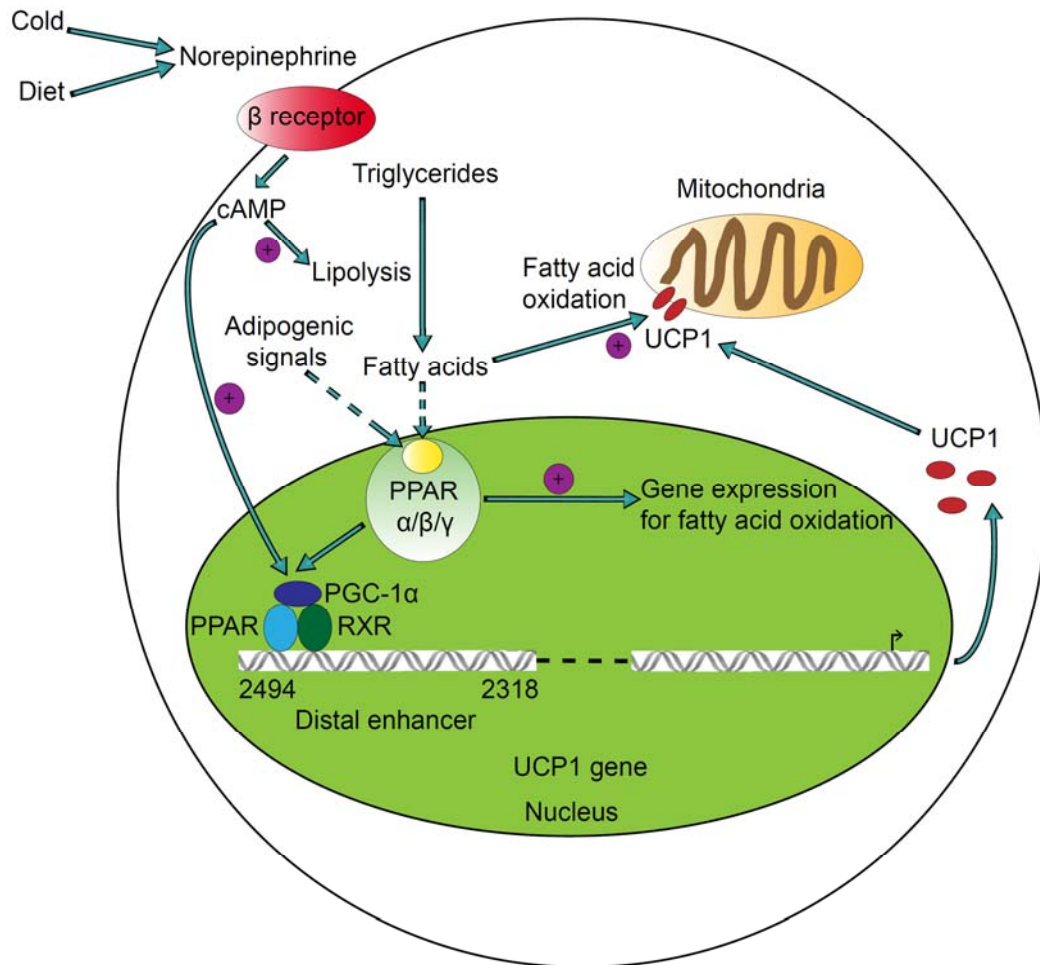


Figure 1.5 PPAR signaling pathway

Exposure to cold or diet induce increased norepinephrine, activating β -adrenergic receptor, leading to the activation of cAMP signaling; contributing to either increased lipolysis of TAG or direct activation of PPAR signaling. PPARs form heterodimers with retinoid X receptors (RXR) and with the assistance of co-activators, such as PGC-1 α , trigger gene transcription. The downstream target genes, such as *Ucp1*, facilitate fatty acid oxidation in mitochondria.

1.2 Skin

Skin, the largest organ in the integumentary system, is the soft outer cover in animals, which protects the body from infection, supplies nerve endings for sensation, regulates body temperature and prevents water evaporation. The following section will specifically provide background knowledge pertaining to skin structure as well as skin regeneration during cutaneous and chronic wound healing.

1.2.1 Skin structure

Skin is composed of two major layers, the epidermis and dermis. The epidermis is the outermost layer that works as a barrier against infection and water evaporation and contains various cell types including keratinocytes, melanocytes, langerhans and merkel cells [1]. The dermis is the inner layer, which is full of connective tissue including collagen and elastic fibers and also contains hairs follicles, blood vessels, and sweat glands (Fig 1.6) [1].

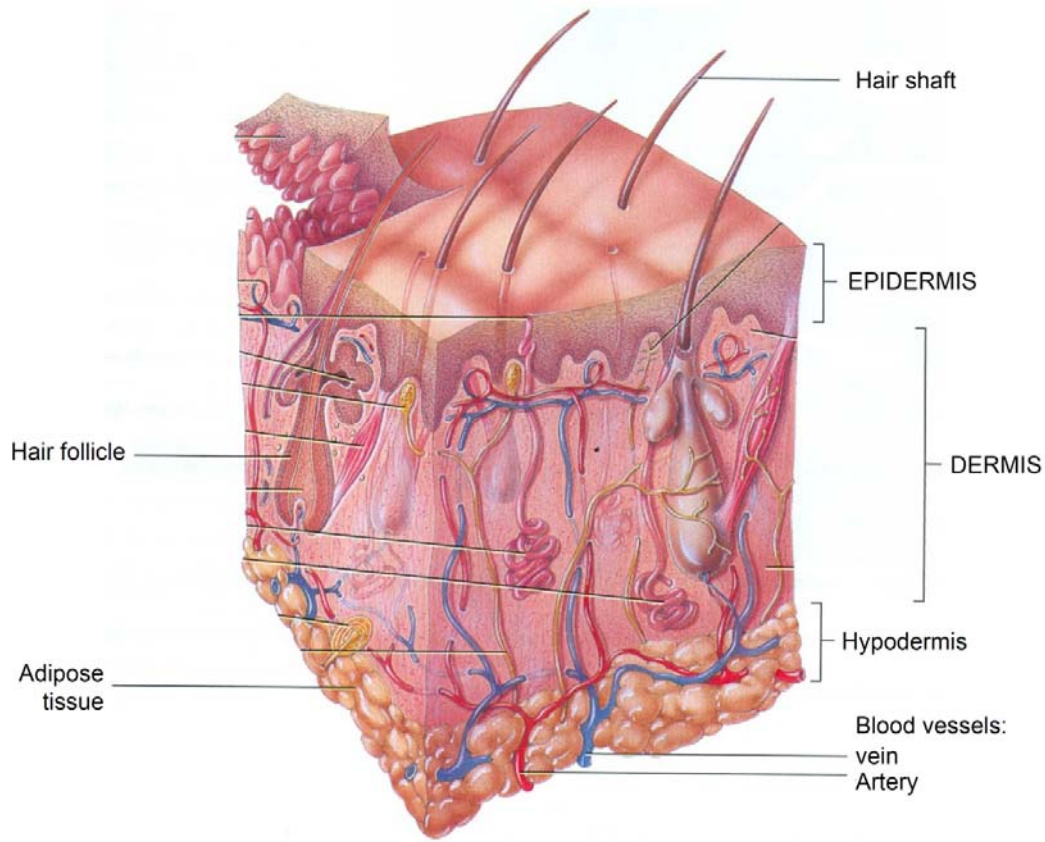


Figure 1.6 *Skin diagram*

Skin is composed of two major layers: the outermost epidermis layer and the inner dermis layer. Skin also contains hair shaft, hair follicle and blood vessels. A layer of adipose tissue is located under the skin. Modified from Jenkins *et al* [1].

1.2.2 Skin regeneration

Skin wound healing is important for maintaining skin homeostasis after acute skin injury. A schematic of skin wound healing process is illustrated in Figure 1.7. For epidermal wound healing, cells from the stratum basale of the wound edges migrate towards each other and merge together [78]. This process is regulated by epidermal growth factor (EGF), transforming growth factor- α (TGF- α) and fibroblast growth factor (FGF), which stimulate basal stem cell proliferation and migration [79-80]. In dermal wound healing, or deep wound healing, the procedure becomes more complicated. There are four main phases of dermal wound healing, specifically: inflammation, migration, proliferation, and maturation [80]. Inflammation proceeds immediately after the wound area is covered by a blood clot. Inflammation is followed closely by vasodilation and secretion of critical growth factors such as transforming growth factor- β (TGF- β), platelet-derived growth factor (PDGF), and FGF from residential inflammation cells [81]. Subsequently, phagocytic neutrophils, macrophages, and mesenchymal stem cells are attracted to the wound site [81]; which further results in activation and migration of keratinocytes (in the epidermis) from each side of the wound edge to form a repair bridge over the wound area [79-80]. In the dermis, the now activated myofibroblasts migrate until granulation tissue is formed to replace the wound bed [78, 80]. In the proliferation and maturation phases, the activated alpha-smooth muscle actin (α -SMA)-expressing myofibroblasts proliferate and together with collagen to fill the wound site [80].

Growth factors and cytokines are critical factors in skin wound healing. PDGF serves as a chemotactic agent, responsible for the influx of cells such as neutrophils, monocytes, and fibroblasts into wound area [82-83]. Moreover, PDGF also promotes fibroblast proliferation, induces the activation of myofibroblasts, and stimulates further

wound contraction [82-83]. FGFs stimulate the proliferation of numerous cells, most notably FGF7, which is specifically responsible for stimulating keratinocyte proliferation during wound healing [84]. Other FGF family members, such as FGF1 and FGF2, are responsible for initiating angiogenesis during wound healing [85]. FGFs also stimulate the migration and differentiation of epithelial cell and fibroblasts [86]. TGF- β is shown to inhibit keratinocyte proliferation [87-88], whereas in contrast, it accelerates keratinocyte migration [89-90]. Therefore, the function of TGF- β in re-epithelialization is still paradoxical. However, TGF- β is responsible for the initiation of extracellular matrix deposition and angiogenesis, fibroblast proliferation, and myofibroblasts formation [81, 91]. Interestingly, loss of Mstn, a TGF- β superfamily member, has been shown to enhance skeletal muscle regeneration in response to injury, resulting from enhanced satellite cell functionality and reduced fibrosis [92]. Please see Section 1.3.3.3, Page 34 for a detailed review of the role of Mstn in skeletal muscle regeneration. Therefore it is interesting to surmise that absence of Mstn may also result in improved skin wound regeneration. However, as loss of Mstn has been shown to result in reduced TGF- β activity and decreased fibrosis during skeletal muscle regeneration, *Mstn*^{-/-} mice may display impaired skin wound healing (The role of Mstn in skin wound healing has been elucidated in this current thesis and is presented in Chapter 6). Interleukin-1 (IL-1) and Interleukin-6 (IL-6) are other key factors in stimulating neutrophil migration into the wound bed [81]. In addition, IL-6 also serves as a stimulator for keratinocyte mitosis [93].

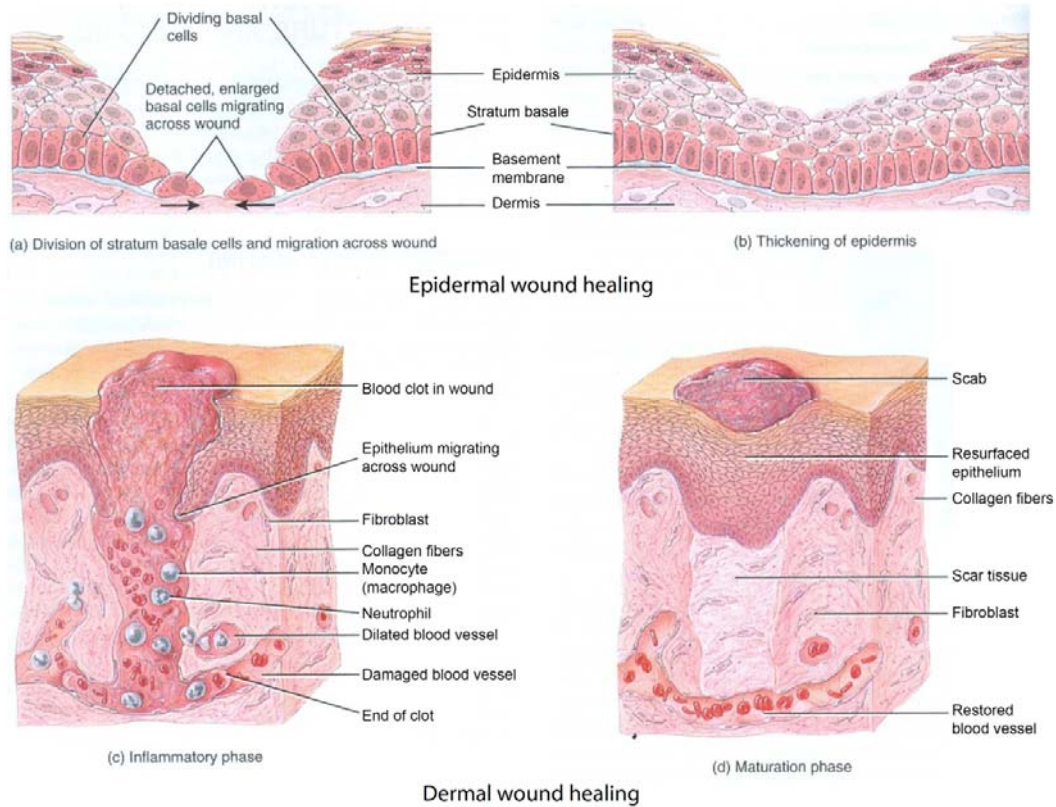


Figure 1.7 Skin wound healing process

For epidermal wound healing, cells from stratum basale of wound edges migrate to merge together. The process of dermal wound healing, or deep wound healing includes four main phases: inflammation, migration, proliferation and maturation. Immediately after injury, a blood clot is formed on the top of the wound site, followed by phagocytic neutrophils, macrophages, and mesenchymal stem cells recruiting into the wound area. Keratinocytes are then activated to migrate to form the new epidermis layer, while fibroblasts are recruited and activated to become myofibroblasts. Myofibroblasts and collagen exert strength to contract wound edges to fulfill the dermal wound healing. Modified from Jenkins *et al* [1].

1.2.3 Diabetic skin wound healing

Diabetic patients may exhibit disrupted skin wound healing [94-96] and increased prevalence of foot ulcers due to neuropathy, vascular disease, and foot deformities [97-98]. Impaired keratinocyte proliferation and migration, as well as narrowing blood vessels, contribute to the delayed wound healing in diabetic patients [99]. In addition, the metabolic disorder during diabetes results in the insufficient migration of neutrophils and macrophages to the wound site. Together with the reduced chemotaxis of leukocytes, diabetes patients have an increased wound infection [100-101].

At the molecular level, several changes induced by diabetes leads to the impaired skin wound healing. Growth factors are important in skin regeneration and regulate keratinocytes migration, inflammation, as well as wound contraction [102]. The majority of studies have addressed the changes in critical growth factors during skin wound healing in diabetic patients. Specifically, insulin-like growth factor 1 (IGF-1) and TGF- β levels are reported to decrease in the skin of diabetic patients and rats [103-104]. Furthermore, in the wounded tissue of diabetic rats and patients, diminished PDGF levels are detected [105-106]. Furthermore, IL-6 is reduced in the wound fluid of diabetic mice [107], and FGF expression is also notably absent in diabetic mice [108]. Keratinocytes and dermal cells are regulated by sensory nerves innervations and releasing neuropeptides [109]. It is reported that a decline in sensory nerves, as well as increased neuropeptide specific peptidase contribute to the attenuated skin wound healing in diabetic patients [110-112]. Extracellular matrix (ECM) plays an important role in skin wound healing, especially in skin wound contraction [113-114]. Decreased collagen (localized in ECM), which is observed in diabetic patients and animals [115-116], results in diminished skin wound contraction [117] and impaired skin wound healing.

1.3 Myostatin (Mstn)

Mstn, or growth and differentiation factor-8 (GDF-8), is a TGF- β superfamily member. Targeted disruption of the myostatin gene (*Mstn*) in mice [118] or naturally occurring mutation of *Mstn* in bovine [119-120], ovine [121] and humans [122] leads to increased skeletal muscle growth. Generally, absence of Mstn results in a ~2 to 3-fold increase in muscle mass and is due to hyperplasia and hypertrophy of muscle fibers (Fig 1.8). Therefore, Mstn is defined as a negative regulator of skeletal muscle growth.

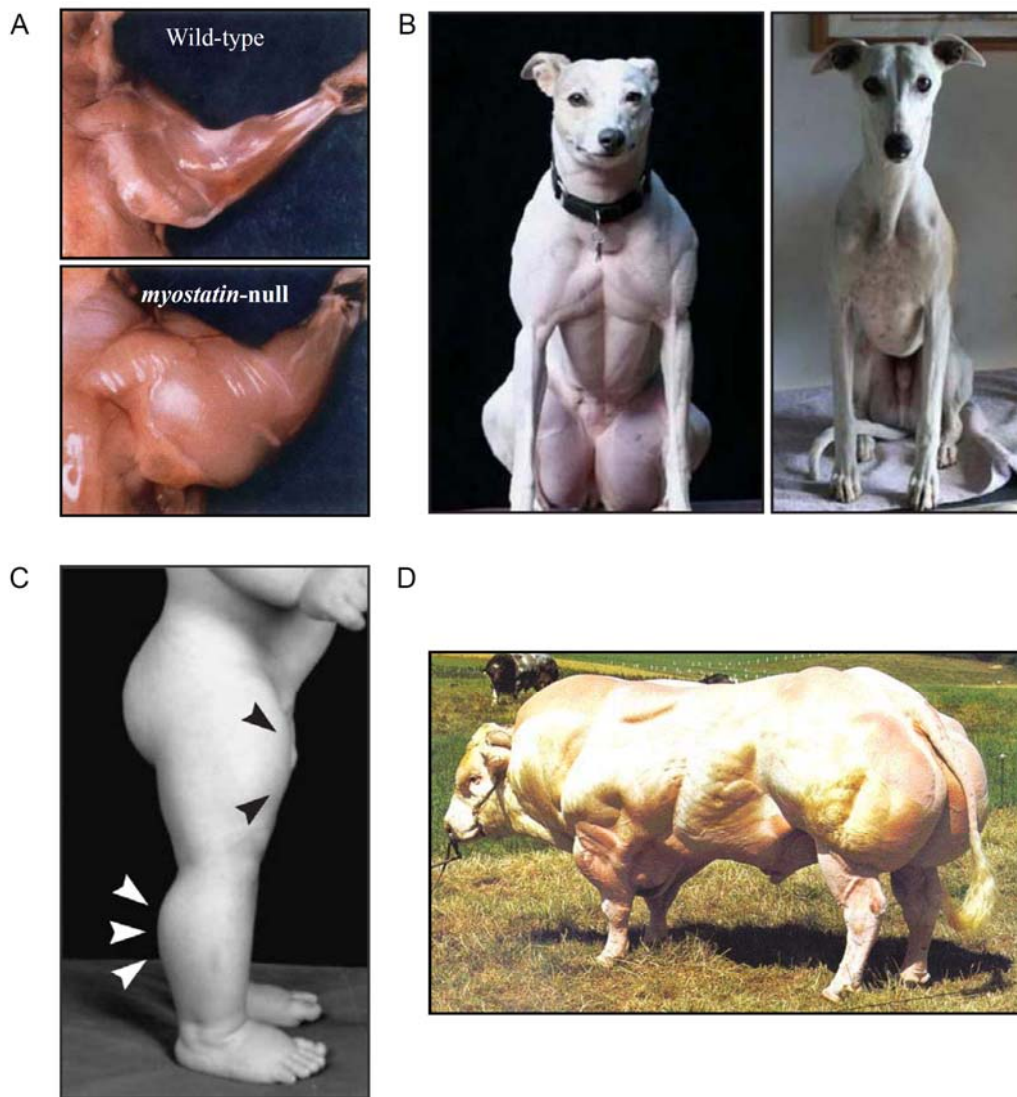


Figure 1.8 *Mutations in Mstn*

Mutations in *Mstn* gene in mouse (A) [118], dog (B) [123], human child at 7 months old (C) [122], Belgian Blue cattle breed (D) (reproduced from Haliba '96 Catalogue) lead to increased musculature.

1.3.1 Structure of Mstn protein

Structurally, the N-terminal region of the precursor Mstn molecule contains a hydrophobic amino acid signaling sequence [118]. Additionally, the C-terminal region of the Mstn protein contains nine highly conserved cysteine residues, which are involved in the formation of a “cysteine knot” structure, critical for homodimerisation of the mature Mstn protein [118, 124]. Mstn is synthesized as a 376 amino acid precursor protein, which is proteolytically cleaved at the RSRR site to release a C-terminal mature Mstn protein fragment and N-terminal Mstn propeptide/latency-associated peptide (LAP) (Fig 1.9) [125-127]. The importance of the RSRR site is clear, as mutation of the consensus RSRR sequence to GLDG has been shown to result in increased muscle growth, consistent with loss of Mstn function [128]. Like other TGF- β superfamily members, maturation of Mstn occurs in the Golgi apparatus, where cleavage of the full-length Mstn protein is facilitated by the serine protease Furin, a member of the proprotein convertase family [118, 126, 129].

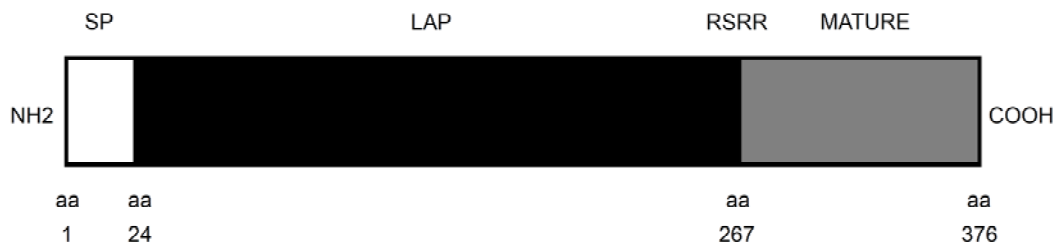


Figure 1.9 *Mstn structure*

Mstn protein is synthesized as a 376 aa protein. Mstn is a secreted growth factor. In support, in the N-terminal region of the Mstn protein, there is a signal peptide (SP) for secretion. Following the proteolytic processing of Mstn, at the RSRR site, Mstn is cleaved into a mature portion and a latency-associated peptide (LAP) portion. Modified from Joulia-Ekaza *et al* [130].

1.3.2 Distribution of Mstn

During embryonic development, Mstn is initially detected in the mouse embryo at day 9.5 post-coitum and is primarily detected in rostral somites [118]. By day 10.5 post-coitum, Mstn expression is detected in all somites, especially in the myotome compartment. Mstn expression has also been detected in other embryos, appearing between day 15 to 29 in cattle [119, 131], day 21 to 35 in pigs [132] and from day 0 onwards in the chicken [133]. During post-natal development, a high level of Mstn expression is still detected in skeletal muscle [118-119], however, low levels of Mstn expression have also been characterized in other tissues, including heart [129], adipose tissue [118], lung, liver, spleen, kidney [134], and skin (Chapter 6).

The distribution of Mstn in skeletal muscle may also be variable between muscle fiber types. It has been reported that Type IIb muscle fibers (fast-twitch fibers) contain more Mstn mRNA and protein when compared to Type I fibers (slow-twitch fibers) [135]. Furthermore, myostatin-null (*Mstn*^{-/-}) mice exhibit more fast-twitch fibers, in the predominantly slow-twitch fiber dominated *M. soleus* muscle. Moreover, there is a transition from slow-twitch fibers to fast-twitch fibers in EDL muscle from *Mstn*^{-/-} mice [136]. Therefore, in *Mstn*^{-/-} mice, muscle appears to adopt a more glycolytic, rather than oxidative, phenotype [137]. Paradoxically, although *Mstn*^{-/-} mice contain more glycolytic fast-twitch fibers, unpublished data from our laboratory indicate that they adopt more oxidative characteristics due to the increased mitochondrial number and activity.

1.3.3 Mstn signaling in skeletal muscle growth

Mstn plays an important role in regulating both the proliferation and differentiation of myoblasts [125, 138], as well as the activation and self-renewal of skeletal muscle stem cells, termed satellite cells [139].

1.3.3.1 Role of Mstn in myoblast proliferation

In the presence of high levels of Mstn, myoblasts can neither proliferate nor differentiate [125, 138]. Mstn regulates myoblast proliferation through a Retinoblastoma (Rb)-dependent signaling pathway. Mstn up-regulates cyclin-dependent kinase inhibitor 1 (P21) [125], and down regulates cyclin-dependent kinase 2 (CDK2) [125], resulting in the accumulation of hypophosphorylated Rb, thus arresting myoblasts in the G1 checkpoint of the cell cycle (Figure 1.10). It is also noted that Mstn may regulate myoblast proliferation through the P38 mitogen activated protein kinase (MAPK) signaling pathway [140]. The activation of P38 MAPK by Mstn has been shown to further elevate Mstn expression and also promote Mstn-mediated P21 transcription and subsequent inhibition of myoblast proliferation [140].

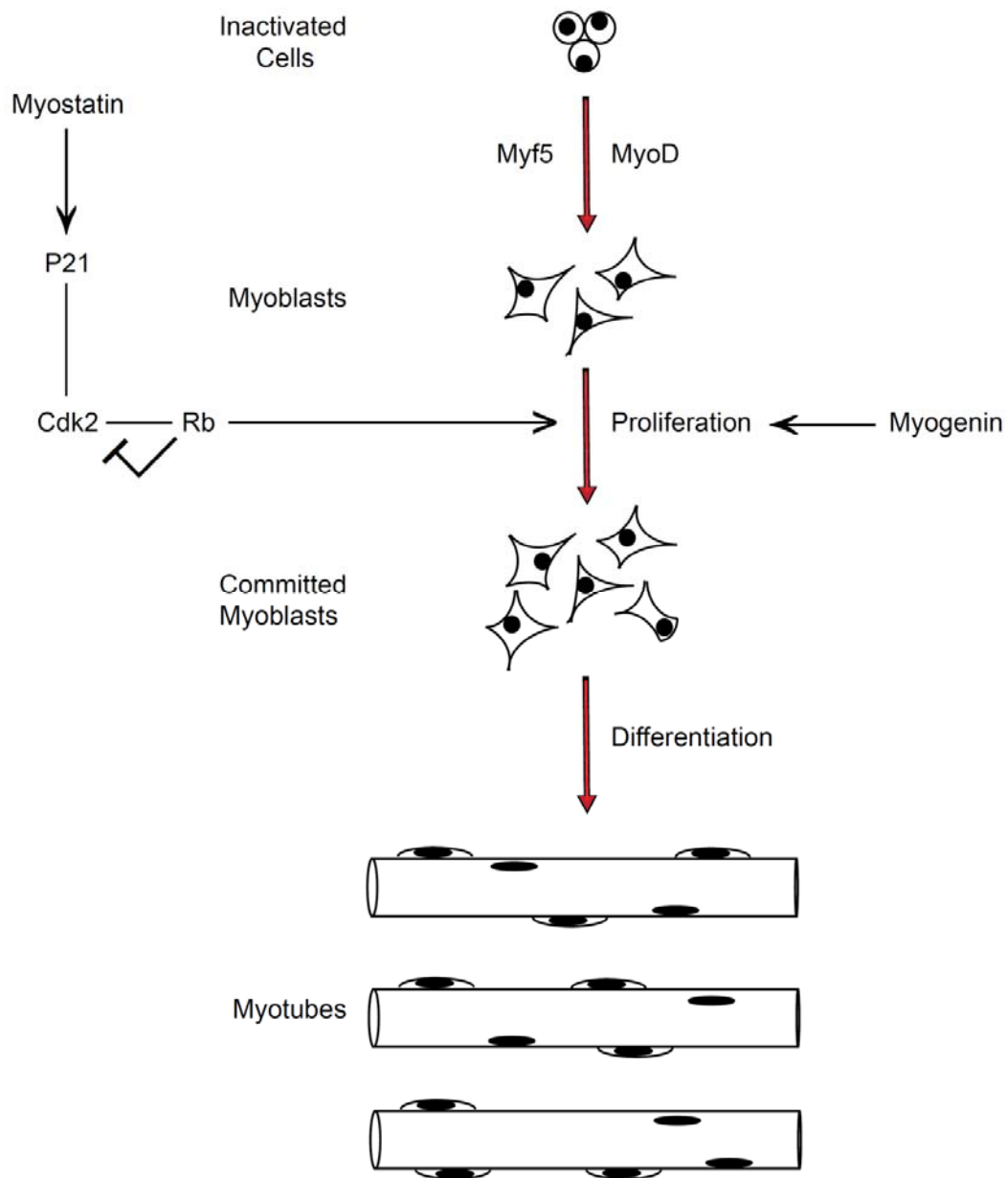


Figure 1.10 Role of *Mstn* in myoblast proliferation

Mstn is able to regulate myoblast proliferation through a retinoblastoma (Rb)-dependent signaling pathway. By up-regulating P21 (one of the cyclin-dependent kinase inhibitors) and down-regulating cdk2, Mstn promotes the accumulation of hypophosphorylated Rb, arresting cells in G1 phase, and blocking of the cell cycle proliferation. Modified from Thomas *et al* [125].

1.3.3.2 Role of Mstn in myoblast differentiation

Mstn, like other TGF- β superfamily members, appears to elicit biological function via the canonical Smad signaling pathway. The schematic Mstn signaling via Smad3 is illustrated in Figure 1.11. Mstn signaling is initiated upon binding of Mstn to its receptor, ActRIIB; which induces the activation of the TGF- β type I receptor (ALK5) and subsequent phosphorylation and activation of Smad proteins, most notably Smad3 [141]. The now active Smad3 is then able to bind to the co-Smad, Smad4, allowing for translocation of the active Smad complex to the nucleus for regulation of gene expression [142]. Functionally, the Smad3 signaling pathway appears to play a major role in Mstn-mediated inhibition of differentiation. Specifically, treatment with Mstn has been shown to promote Smad3-MyoD interaction, which is suggested to prevent MyoD-E protein association, resulting in inhibition of MyoD activity. As MyoD is critical for timely induction of differentiation [143], Mstn inhibition of MyoD activity is proposed to be key for the inhibition of myogenic differentiation observed following treatment with Mstn [138]. In addition, it has recently been shown that extracellular signal-regulated kinase 1/2 (Erk 1/2) MAPK signaling may also be involved in Mstn-mediated inhibition of myogenesis [144]. In particular, suppression of Erk1/2 signaling was shown to rescue Mstn-mediated inhibition of myoblast proliferation and differentiation. Furthermore, blockade of Erk1/2 signaling also prevented Mstn inhibition of myosin heavy chain (MHC), MyoD and myogenin expression [144].

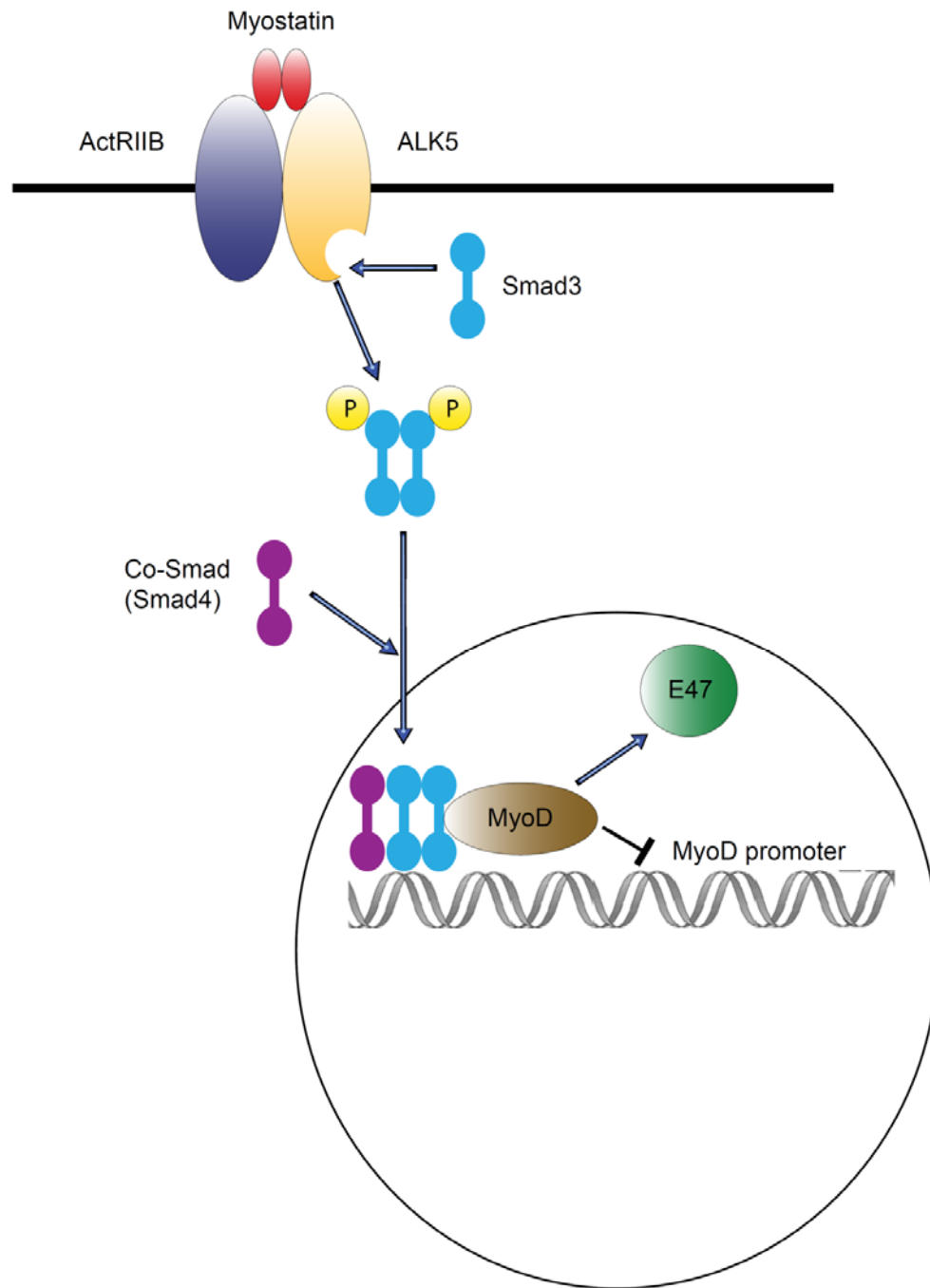


Figure 1.11 *Mstn* signaling

Mstn activates the activin type IIB receptor (ActRIIB), and further triggers ALK5, which phosphorylates either Smad3 or Smad2. The phosphorylated Smad proteins bind to Smad4, leading to translocation into the nucleus. The translocation of Smad3/Smad4 prevents E47 from binding to MyoD, inhibiting the activation of MyoD, resulting in the perturbation of cell differentiation.

1.3.3.3 Role of Mstn in satellite cell activation, self-renewal, and muscle regeneration

In addition to regulating myoblast growth and differentiation, Mstn has also been shown to regulate satellite cell activation and self-renewal as well as post-natal muscle growth and repair.

Satellite cells are the resident stem cell pool in skeletal muscle that function to maintain and repair muscle tissue in response to injury [145-146]. Importantly Mstn has been shown to block satellite cell activation through arresting satellite cells in the G1 phase of the cell cycle [139]. Moreover, BrdU incorporation demonstrates that satellite cells isolated from *Mstn*^{-/-} mice display increased satellite cell activation when compared with WT mice [139, 147].

Pax7 is a transcription factor which is widely used as a satellite cell marker due to its existence both in proliferating and quiescent satellite cells [148-149]. Once activated, satellite cells continue to express Pax7 and MyoD until differentiation, where Pax7 expression declines [149]. Satellite cells with high levels of Pax7 and low levels of MyoD fail to differentiate and adopt a quiescent phenotype [149-150]. Published results from our laboratory demonstrate that Mstn down-regulates Pax7, which results in impaired satellite cell self-renewal [151].

Previous work from our laboratory indicates that Mstn negatively regulates skeletal muscle regeneration [92]. Muscle stem cells, or satellite cells, are critically involved in repairing muscle following injury through the migration of primary myoblasts derived from satellite cells [152]. As described above, Mstn functions through impairing satellite cell function, therefore it follows that Mstn may be involved in the negative regulation of muscle regeneration after injury. In support, absence of Mstn stimulates

increased migration of macrophages, promotes the proliferation myoblasts, and reduces fibrosis [92]. In support, *in vitro* treatment of myoblasts and macrophages with Mstn protein significantly decreases the migration of both cells [92]. Moreover, it has been shown that Mstn stimulates fibrosis during skeletal muscle regeneration [92].

1.3.4 Effect of Mstn antagonists on muscle mass

Mstn antagonists appear to have functions in regulating muscle atrophy, whole body homeostasis, and metabolism (see section 1.3.6 for review of Mstn antagonist and metabolism). Intraperitoneal injections of Mstn antagonists, such as a soluble form of the Mstn receptor, activin type IIB (sActRIIB), a mutated uncleavable Mstn propeptide/LAP and Mstn specific neutralizing monoclonal antibodies, are efficient methods of inhibiting Mstn signaling [153-154]. Specifically, either overexpression of a dominant negative form of ActRIIB in muscle [126] or treatment of mice with sActRIIB [155] results in increased musculature. Follistatin is an active Mstn antagonist due to its binding affinity to the Mstn receptor, ActRIIB, although follistatin has also been shown to bind to other activin receptors [156-157]. Consistent with the role of follistatin in regulating Mstn, follistatin-null mice display growth defects, with associated muscle loss [158]. In addition, inhibition of Mstn function by treatment with specific anti-Mstn antibodies attenuates sarcopenia associated muscle loss, which is muscle wasting associated with ageing [159-160]. Moreover, in the *mdx* mouse model of muscular dystrophy, muscle function is improved by either inhibiting the Mstn receptor, ActRIIB, through RNA interference-mediated knock down, or through treatment with an Mstn neutralizing monoclonal antibody [161-162]. Cachexia is defined as a dramatic weight loss, including loss of muscle and fat mass,

associated with chronic illness, such as cancer [163]. Importantly, postnatal inhibition of Mstn, through treatment with the activin receptor extracellular domain, contributes to reduced muscle wasting during cachexia [164].

1.3.5 Mstn and metabolism

It is well known that genetic inactivation of the Mstn gene in mice, not only induces muscle hypertrophy, but also reduces body fat accumulation [165]. A similar lean phenotype can also be observed in mice that overexpress a dominant negative ActRIIB transgene or following injection of the Mstn propeptide/LAP, which binds to and inhibits the function of Mstn [166-167]. An increase in the prevalence of glycolytic muscle fibers has been observed in *Mstn*^{-/-} mice [137]. It is reported that increased glycolytic muscle fibers, which are induced by Akt overexpression, could promote transcription of respective genes involving in fatty acid metabolism, improving hepatic fatty acid oxidation and further resulting in a decline in fat mass and improved lipid metabolism [168]. These data support the increased hepatic fatty acid oxidation and lean phenotype seen in *Mstn*^{-/-} mice (Chapter 3&4). Consistent with the lean phenotype in *Mstn*^{-/-} mice, muscle-specific inhibition of Mstn leads to reduced fat mass and improved insulin sensitivity [166]. *Mstn*^{-/-} mice also display enhanced insulin sensitivity and improved glucose tolerance when compared to WT mice [73]. In addition, serum and hepatic cholesterol, as well as TAG levels are all reduced in *Mstn*^{-/-} mice when compared to WT mice, which is consistent with the increased insulin sensitivity in *Mstn*^{-/-} mice [165-166]. In agreement with improved insulin sensitivity, insulin signaling is also enhanced in *Mstn*^{-/-} mice, as assessed through up-regulation of protein kinase B (Akt), IRS1, and IGF1, all of which mediate insulin signaling in

skeletal muscle and adipose tissue [73, 166]. However, some contradictory results have been reported, whereby Mstn treatment results in increased glucose uptake in human placental extracts [169]. In addition, it is also reported that adipose tissue atrophy can be induced through ectopic expression of Mstn in adipose tissue [170]. Therefore, the actual function of Mstn in regulating carbohydrate and lipid metabolism remains to be clarified.

Inhibition of Mstn also leads to reduced adiposity and improved insulin sensitivity during obesity. Se-Jin Lee *et al.* reported that crossing Agouti lethal yellow (Ay) mice (details of Ay mice can be found in section 1.1.3) with *Mstn*^{-/-} mice resulted in decreased adipose tissue weight, lower fasting blood glucose level and elevated glucose tolerance when compared to Ay mice alone [165]. Furthermore, crossing of obese mice (*Lep*^{ob/ob}) with *Mstn*^{-/-} mice also resulted in reduced fat pad weight and improved carbohydrate metabolism [165]. Work from our laboratory revealed that severe obesity due to HFD feeding was ameliorated in the absence of *Mstn* [73]. Furthermore, serum insulin, leptin, cholesterol, and TAG are all decreased in *Mstn*^{-/-} mice when compared to WT mice [73, 166, 171-172]. As a consequence of reduced adipose accumulation, improved insulin sensitivity and glucose tolerance are also observed in *Mstn*^{-/-} mice during diet-induced obesity [73, 166-167, 171]. Furthermore, it is reported that there are reduced levels of proinflammatory cytokines, such as TNFα in adipose tissue and skeletal muscle of mice with Mstn function loss. Consistent with this, these mice also exhibit improved insulin sensitivity in liver and skeletal muscle, as well as the improved hepatosteatosis during HFD feeding [171]. In support, treatment of Mstn deficient mice with recombinant Mstn protein contributes to the increased insulin resistance and circulating TNFα level during HFD feeding [171].

As mentioned in section 1.1.4, skeletal muscle is critical in controlling the fate of FFA, and with perturbed fatty acid oxidation and accumulation of FFA in skeletal muscle leading to metabolic syndrome and insulin resistance (Section 1.1.4). Meanwhile, it is noteworthy to mention that *Mstn*^{-/-} mice display a muscle hypertrophy phenotype [118]. Therefore, the improved carbohydrate metabolism, observed in *Mstn*^{-/-} mice, may be due to the increased muscle mass rather than the direct effect of Mstn on carbohydrate metabolism. However, Wilkes *et al* report that short-term injection of recombinant Mstn protein into Mstn deficient mice perturbs insulin sensitivity in these mutant mice, despite no significant alteration in body mass [171]. Moreover, it is reported that *Mstn* gene expression is increased both in skeletal muscle and adipose tissue of WT mice when challenged with HFD [173]. Therefore, although the mechanism has not been fully clarified, the *Mstn* gene itself may play a direct role in regulating metabolism that is independent of its effect on muscle mass.

Previous studies from our laboratory and others demonstrate that *Mstn*^{-/-} mice display reduced fat accumulation during HFD feeding [73, 165]. Also, it is well known that *Mstn*^{-/-} mice display double musculature [118]. As mentioned above, enhanced carbohydrate metabolism in *Mstn*^{-/-} mice is suggested to be due to deletion of the *Mstn* gene itself, rather than as a result of increased musculature. However, whether or not the reduction in adiposity observed in *Mstn*^{-/-} mice is due to a direct effect of Mstn deficiency on adipose tissue, or as a secondary effect due to increased muscle mass, remains to be clarified. Guo *et al* claim that adipose tissue specific deletion of *Mstn* gene could not prevent fat accumulation and insulin resistance [166]. However, due to the relatively low expression of *Mstn* in adipose tissue [118], when compared to skeletal muscle and liver expression [118, 134], the contribution of deletion of the *Mstn* gene in adipose tissue maybe insignificant with respect to total circulatory levels

of Mstn. Therefore, future work needs to be performed to clarify the reason for the reduced adiposity observed in *Mstn*^{-/-} mice.

1.3.6 Potential clinical applications for Mstn antagonists in targeting obesity and type 2 diabetes

Mstn regulates whole body homeostasis both prenatally and postnatally. It is reported that 10 weeks of sActRIIB treatment resulted in reduced fat mass as well as improved insulin sensitivity and increased muscle glucose uptake when compared to control vehicle-treated mice [173]. However, no significant changes were detected upon 4 weeks of sActRIIB treatment, suggesting a cumulative effect for Mstn in the regulation of metabolism [173]. Treatment with sActRIIB for 10 or 12 weeks will further prevent fat mass gain in mice challenged with HFD, as well as improve insulin sensitivity when compared with WT mice [73, 173]. It is important to mention that previously published data has revealed that in addition to Mstn, several ligands are able to bind ActRIIB in circulation [174-175], as such targeting the ActRIIB receptor as a means to repress Mstn function may not be a viable approach. In addition to sActRIIB, treatment with the anti-Mstn neutralizing antibody PF-879 has been shown to reduce fasting blood glucose levels and increase glucose tolerance in *Lep*^{ob/ob} mice, however, PF-879 treatment failed to prevent adipose tissue accumulation [154]. Moreover, treatment with the JA16 antibody Mstn antagonist did not reduce fat pad mass in the *Lep*^{ob/ob} obese mouse model [176]. In summary, although there is evidence to support that antagonizing Mstn has utility in preventing the development of obesity and type 2 diabetes, target specificity of Mstn antagonists needs to be fully clarified before these therapeutics can be utilized.

1.4 Aims and objectives

As the signaling pathways behind Mstn and its role in the regulation of obesity-induced type 2 diabetes are still not fully delineated, here in this thesis, studies were performed to identify the relationship between Mstn, AMPK and PPAR signaling pathways, and their roles in carbohydrate and lipid metabolism. Furthermore, the potential therapeutic benefit of an Mstn antagonist, sActRIIB, in protecting against obesity and type 2 diabetes was assessed.

Although the role of Mstn in skeletal muscle growth is well established, the function of Mstn in skin remains unclear. Data presented in the current thesis characterize for the first time a role for Mstn in the progression of skin wound regeneration. These data may potentially shed new light on therapies to aid in skin wound healing.

The aims of this thesis are addressed in the following objectives:

Objective 1: To characterize the role of Mstn in carbohydrate metabolism.

Objective 2: To study how Mstn regulates lipid metabolism.

Objective 3: To delineate the function of Mstn in regulating diet-induced obesity.

Objective 4: To specify the functional role of Mstn in skin wound healing.

Chapter 2 Materials and Methods

2.1 Materials

2.1.1 Common chemical reagents

Table 2.1 *Common chemical reagents*

All commonly used chemical reagents are listed below unless otherwise stated.

Acetone; Ammonium Chloride [NH ₄ Cl];
Ammonium sulphate; AMP; ATP; Beta-
mercaptoethanol [βMe]; Bovine serum albumin
[BSA]; BSA, FA-free; Bromophenol blue; L-
carnitine; CaCl ₂ , anhydrous; Coenzyme A;
Collagenase, Type I; Cytochalasin B;
Dexamethasone; DMSO; DPBS; DTT; EDTA; Sigma-Aldrich, St. Louis, MO,
Etomoxir; Formaldehyde; Formamide; Glycerol; USA
D-glucose; HEPES; IBMX; IGEPAL [®] CA-630;
Indomethacin; Insulin from bovine pancreas;
KCl; KHCO ₃ ; KH ₂ PO ₄ ; KOH; Krebs-Ringer
bicarbonate [KRB] buffer; Malate; Mannitol;
MgCl ₂ ·6H ₂ O; MOPS; Nicotinamide; Normal
goat serum [NGS]; Palmitic acid;
Paraformaldehyde; Perchloric acid;
Polyvinylpyrrolidone [PVP]; Polyethylene
glycol [PEG]; NaHCO ₃ ; NaF; Na ₂ HPO ₄ ;

NaH₂PO₄; NaCl; Sodium acetate; Sodium

dodecyl sulfate [SDS]; Sodium pyruvate;

Sucrose; Oil Red O; Trichostatin A; Tris base

Hyamine Hydroxide

PerkinElmer Life Sciences,

Waltham, MA, USA

Complete protease inhibitor

Roche Molecular Biochemicals,

Indianapolis, IN, USA

TWEEN® 20

Amresco, Solon, OH, USA

Ethidium bromide

Bio-Rad, Hercules, CA, USA

Glycine

2-propanol

Merck Chemicals, Darmstadt,

DPX mounting medium

Germany

Eosin

Haematoxylin

Hydrochloric acid [HCl]

Methanol

Sodium hydroxide [NaOH]

Milli-Q® water

Millipore, Billerica, MA, USA

Triton® X-100

USB, Cleveland, OH, USA

Chloroform

Fisher Scientific, Pittsburgh, PA,

Phosphoric acid

USA

Phosphate buffered saline [PBS]

OXOID, Thermofisher,

Hampshire, UK

DMEM/ F12

PAA Laboratories GmbH,

Pasching, Austria

AdipoRed™ Lipid Assay Reagent	Cambrex Corporation, East Rutherford, New Jersey, USA
Fetal bovine serum [FBS]	Hyclone, Thermo Scientific, Waltham, MA, USA

2.1.2 Common radioisotopes

Table 2.2 *Common radioisotopes*

All radioisotopes used in this thesis are listed below, and details of the radioisotopes are in each section.

2-[³ H]-deoxy-D-glucose	PerkinElmer Life Sciences, Waltham, MA, USA
D-[¹⁴ C]-mannitol	
Adenosine 5'-Triphosphate, [γ - ³² P]	
Palmitic acid[1- ¹⁴ C]	
Palmitic acid[U- ¹⁴ C]	

2.1.3 Solutions

2.1.3.1 Western blotting analysis

Table 2.3 *Protein lysis buffer (for muscle, WAT and liver)*

1 M Tris pH 7.5	0.5 ml
5 M NaCl	0.5 ml
0.5 M EDTA	0.1 ml
IGEPAL® CA-630	10 μ l

Complete protease inhibitor	½ tablet
Milli-Q [®] water	8.89 ml
Total	10 ml
Store at 4°C	

Table 2.4 *Protein lysis buffer (for skin)*

1M Na ₂ H ₂ PO ₄	5 ml
NaCl	1.461g
Triton [®] X-100	1 ml
SDS	0.1 g
Top up with Milli-Q [®] water to	100 ml
Store at 4°C	

Table 2.5 *Na₂H₂PO₄ solution (1 M, for skin protein lysis buffer)*

1 M Na ₂ HPO ₄	14.196 g powder and top up to 100 ml with Milli-Q [®] water, heat at 40°C to dissolve and do not add all the powder at the same time.
1 M NaH ₂ PO ₄	1.380 g of powder and top up to 10 ml with Milli-Q [®] water.
100 ml of 1M Na ₂ H ₂ PO ₄	93.2 ml of 1 M Na ₂ HPO ₄ + 6.8 ml of 1 M NaH ₂ PO ₄ , pH 8.0

Table 2.6 *Transfer buffer*

Tris	15.1 g
Glycine	75 g

Methanol	1 L
Top up with Milli-Q [®] water to	5 L
Store at 4°C	

Table 2.7 *TBST (Tris-buffered saline with Tween)*

1 M Tris pH 7.5	50 ml
5 M NaCl	30 ml
TWEEN [®] 20	1 ml
Top up with Milli-Q [®] water to	1 L
Store at room temperature	

Table 2.8 *PVP solution*

Polyvinylpyrrolidone [PVP]	1 g
Polyethylene glycol [PEG]	1 g
Bovine serum Albumin [BSA]	0.3 g
top up with TBST to	100 ml
Sterile filter before use, store at 4°C	

2.1.3.2 RNA electrophoresis**Table 2.9** *MOPS buffer (10X)*

MOPS	41.9 g
1 M Sodium acetate	50 ml
0.5 M EDTA	10 ml

Top up with Milli-Q® water to 500 ml, pH 7.0

Sterile filter and store at 4°C, protected from light

Table 2.10 *RNA loading dye (2X)*

MOPS (10X)	10%
deionised formaldehyde	20%
deionised formamide	50%
bromophenol blue	0.02%
glycerol	5%
EDTA (pH 8.0)	1 mM
ethidium bromide	40 µg/ml

2.1.3.3 Glucose transport in muscle

Table 2.11 *Radioisotope*

2-[³ H]-deoxy-D-glucose	1 mCi
	20 Ci/mmol (740 GBq/mmol)
	1 mCi/ml
D-[¹⁴ C]-mannitol	50 µCi
	56.6 mCi/mmol
	0.1 mCi/ml

Table 2.12 *Stock solution*

KRB buffer	9.5 g powder into 1 L water, supplemented with 1.26 g sodium bicarbonate

Insulin	2 mg into 1 ml 0.01M HCl (pH = 2.0)
Cytochalasin B	400 µg into 20 µl ethanol

Table 2.13 *Non-radiolabeled solution*

Final KRB buffer + insulin	Prepare diluted KRB buffer + insulin: 60 µl stock insulin solution into 60 ml KRB buffer.
	500 µl stock insulin solution into 60 ml diluted KRB buffer + insulin
Cytochalasin B	19.2 µl stock solution into 10 ml KRB buffer
KRB buffer + Pyruvate	KRB 49 ml + 100 mM sodium pyruvate 1 ml

Table 2.14 *Radiolabeled solution*

2-[³ H]-deoxy-D-glucose	36 µl
D-[¹⁴ C]-mannitol	72 µl
Final KRB buffer + insulin/KRB buffer	24 ml

2.1.3.4 AMPK assays**Table 2.15** *Radioisotope*

Adenosine 5'-Triphosphate, [γ - ³² P]	250 µCi
	3000 Ci/mmol (111 TBq/mmol)
	10 mCi/ml

Table 2.16 *Stock solutions*

AMP	Dissolve 0.2 g in 10 ml water. Confirm concentration using 1 to 1000 dilution in water at UV = 260 (extinction coefficient = 15400), Dilute with water to give a final concentration of 50 mM. Store at –80°C
ATP	Dissolve 0.4 g in 10 ml water. Confirm concentration using 1 to 1000 dilution in water at UV = 260 (extinction coefficient = 15400), Dilute with water to give a final concentration of 50 mM. Store at –80°C
DTT	Dissolve 0.1542 g into 0.8457 ml of water to give 1M. Store at –80°C
SAMS peptide	Dissolve in water to give 20 mM. Store at –80°C

Table 2.17 *Homogenization buffer*

Mannitol	3.6 g
NaF	0.21 g
Tris Base	0.12 g
EDTA	0.037 g
Beta-mercaptoethanol	75 µl (add after pH adjustment)
[βMe]	
Top up with Milli-Q® water to 100 ml, pH 7.5. Store at 4°C.	
Prior to use add 1 Complete protease inhibitor tablet per 10 ml.	

Table 2.18 *Assay buffer stock solution*

HEPES	2.38 g
NaCl	1.16 g
Glycerol	20 ml

EDTA	0.074 g
MgCl ₂	0.254 g
Top up with Milli-Q [®] water to 100 ml, pH 7.0. Store at 4°C.	

Table 2.19 Working assay mix (cocktail) (Freshly prepared)

50 mM AMP	10 µl
1 M DTT	2 µl
50 mM ATP	10 µl
Assay Buffer Working Solution	978 µl
To 100 µl of required Working Assay Mix add 2 µl of 10 mCi/ml Adenosine 5'-Triphosphate, [γ - ³² P]	

Table 2.20 Working assay mix (others)

Working SAMS peptide solution	5 µl of 20 mM SAMS + 95 µl Milli-Q [®] water
1% Phosphoric acid	16.5 ml phosphoric acid (85%) + 1383.5 ml Milli-Q [®] water

2.1.3.5 Measurement of TAG in white adipose tissue (WAT)**Table 2.21** Ethanol/ KOH solution (500 µl) (freshly prepared)

100% Ethanol	475 µl
80% KOH	25 µl

Table 2.22 HCl (10%, 5 ml) (freshly prepared)

37% HCl	1.35 ml
Milli-Q [®] water	3.65 ml

Table 2.23 *Saturated NaHCO₃ (freshly prepared)*

NaHCO ₃	1.5 g
Top up with Milli-Q [®] water to	10 ml

2.1.3.6 Haematoxylin and eosin (H&E) staining of WAT**Table 2.24** *Scott's tap water*

Sodium Bicarbonate	2 g
Magnesium Sulphate	20 g
Thymol	1 Crystal
Top up with Milli-Q [®] water to	1L

2.1.3.7 Assessment of fatty acid oxidation in tissues

Table 2.25 Reaction mix

Powder	Stock solution		Working solution (100 ml)	
	Conc	Quantity	Conc	Quantity
Sucrose	1 M	17.115 g + 50 ml H ₂ O	100 mM	10 ml
Tris-HCl pH 7.4	1 M		10 mM	1 ml
KH ₂ PO ₄	1 M	6.8 g + 50 ml H ₂ O	5 mM	0.5 ml
EDTA pH8.0	0.5 M		0.2 mM	40 µl
NAM	1 M	6.1 g + 50 ml H ₂ O	5 mM	0.5 ml
TSA	5 mM		1 µM	20 µl
30% FA-free	30%	3 mg + 10 ml H ₂ O	0.3%	1 ml
BSA				
KCl	1 M	3.7 g + 50 ml H ₂ O	80 mM	8 ml
MgCl ₂	1 M		1 mM	0.1 ml
L-carnitine	50 mg/ml (0.25 M)	500 mg + 10 ml H ₂ O	2 mM	0.8 ml
Malatic acid	100 mg/ml (0.75 M)	100 mg + 1 ml H ₂ O	0.1 mM	13.3 µl
Coenzyme A	50 mg/ml (0.065 M)	10 mg + 0.2 ml H ₂ O	0.05mM	76.9 µl
Adjust pH = 8.0, Store at 4°C				

Table 2.26 *Reaction mix (fresh)*

	Stock solution		Working solution(400 µl)		
	Conc	Quantity	Conc	Quantity	Stock Rx
ATP	50 mM		2 mM	16 µl	183.6 µl
DTT	1 M		1 mM	0.4 µl	
Palmitic acid	0.1 M	Bring stock reaction	0 µM	0 µl	176 µl
		buffer to RT. 25.643	100 µM	0.4 µl	175.6 µl
		mg palmitic acid + 1	200 µM	0.8 µl	175.2 µl
		ml H ₂ O, at 70°C to	300 µM	1.2 µl	174.8 µl
		dissolve. Then when	400 µM	1.6 µl	174.4 µl
		it is hot, add to stock	500 µM	2 µl	174 µl
		reaction buffer			
Palmitic acid[1- ¹⁴ C]		50 µCi in 0.5 ml	0.4 µCi/	4 µL (0.1	
		Ethanol	reaction	µCi/µl)	

Table 2.27 *STE buffer (keep in 4°C)*

	Stock solution		Final(100ml)	
		Conc		Quantity
Sucrose	1 M	0.25 M		25 ml
Tris	1 M	10 mM		1 ml
EDTA	0.5 M	1 mM		0.2 ml
TSA	5 mM	1 µM		20 µl
NAM	1 M	5 mM		0.5 ml

Table 2.28 *Inhibitor and activator (add before tissue collection)*

	Stock solution		Working solution(X2)		Homogenate
	Conc	Quantity	Conc	Quantity	
Etomoxir	15 mM	5 mg + 1 ml H ₂ O (4°C)	100 µM	1 µl	149 µl
AICAR	50 mM		500 µM	1 µl	99 µl

1 M Perchloric acid: 5 ml of 70% perchloric acid + 77.8 ml H₂O

2.1.3.8 Assessment of fatty acid oxidation in myotube cultures

Table 2.29 *Incubation medium*

Final concentration	
20 mM HEPES	2 ml of 1 M HEPES
1 µM L-carnitine	Stock solution: 1 mM = 12 mg into 50 ml medium, and keep in -20°C Take out 0.1 ml
Top up with 1 x DPBS to 100 ml, pH = 7.3	Stock solution: 10 x DPBS
Keep non-radiolabeled medium in 4°C	
1 µCi/ml palmitic acid[U- ¹⁴ C]	For 1 ml medium, add 10 µl of 0.1 mCi/ml palmitic acid[U- ¹⁴ C]

2.1.3.9 Van Gieson staining (Skin Biopsy)

Table 2.30 *Van Gieson solution*

1% (g:ml) aqueous acid fuchsin	10 ml
Saturated picric acid	90 ml
Concentrated HCl	0.25 ml

2.1.3.10 Immunohistochemistry (Skin Biopsy)

Immunohistochemistry for Ki67 antibody:

Citrate buffer: 2.94 g Sodium citrate + 1 L Milli-Q[®] water, pH = 6.

Immunohistochemistry for GDF-8 (myostatin, Mstn) antibody:

Table 2.31 *Blocking buffer*

2% Triton X-100	0.1 ml
2% BSA	0.1 ml
NGS	0.05 ml
Top up with PBS to 1 ml	

Table 2.32 *PBS-T*

PBS	900 μ l
1% Tween [®] 20	100 μ l

Table 2.33 *Antibody incubation medium*

2% BSA	100 μ l
NGS	50 μ l

Top up with PBS-T to 1 ml

2.2 Methods

2.2.1 Animals

Wild-type (WT) mice (C57BL/6 background) were bought from the Centre for Animal Resources (National University of Singapore, Singapore). *Mstn*-null (*Mstn*^{-/-}) C57BL/6 mice were kindly given by Se-Jin Lee (Johns Hopkins University, Baltimore, MD). Animal experiments were approved by the Institutional Animal Care and Use Committee (IACUC), Singapore. For high-fat diet (HFD) trial, 7 week old male mice were selected while for skin regeneration project, 6 week old female mice were selected, and all mice were derived from different litters. The detailed description of animals' preparation is listed in each chapter.

2.2.2 Western blotting analysis

M. gastrocnemius (GAS) muscle, WAT (from epididymal fat pad), liver and skin samples were homogenized in 1 ml lysis buffer (50 mg muscle, 100 mg WAT and skin, and 30 mg liver samples). This was followed by centrifugation at 12,000 rpm for 15 min at 4°C. The supernatant was collected and protein concentration was analyzed using Bradford's protein assay reagent (Bio-Rad) against BSA standard (Bio-Rad) detected at 595 nm. Equal amounts of protein lysates (15 µg for muscle and WAT, 10 µg for liver and skin samples) were mixed with 4 x loading dye (Invitrogen, Carlsbad, CA, USA) and Beta-mercaptoethanol (βMe) (loading dye: βMe = 3:1, V:V), and boiled at 100°C for 5 min. While using SeeBlue Plus2 Pre-stained standard (Invitrogen) to indicate the size of protein, samples were resolved by NuPage 4–12% gradient Bis-Tris pre-cast polyacrylamide gels (Invitrogen) for electrophoresis. SDS-

PAGE was run at 50 mA (single gel) or 90 mA (double gels) in Xcell Surelock electrophoresis cell (Invitrogen) and 1 x NuPage MES SDS running buffer were used. Following electrophoresis, SDS-PAGE gels were rinsed in transfer buffer and transferred to Trans-Blot (Bio-Rad) nitrocellulose membrane by electroblotting using Xcell II blot module (Invitrogen) at 30 V for 1.5 h (single gel) or 2 h (double gels). Upon completion of the transfer procedure, the membrane was stained with Ponceau S (Fluka, Sigma-Aldrich) for 1 min and scanned with the GS-800 Calibrated Densitometer (Bio-Rad) to estimate equal protein loading. The membranes were then washed with tap water for 5 min, and subsequently blocked in TBST with 5% (w/v) milk powder overnight at 4°C. The membrane was incubated with the desired primary and secondary antibodies (conjugated to Horseradish Peroxidase, HRP; Bio-Rad) for 3 h and 1 h, respectively, at room temperature, while washing with TBST for 5 min, 5 times, after each antibody incubation. Alternatively, the membranes were blocked in PVP solution for 1h, and incubated with specific primary antibody overnight at 4°C, followed by secondary antibody incubation for 1 h at room temperature. Immunoreactivity was detected using Western Lightning Chemiluminescence Reagent Plus (NEL104; PerkinElmer Life Sciences). Exposed autoradiography films were analyzed by GS-800 Calibrated Densitometer (Bio-Rad). Antibodies used are listed in each chapter.

2.2.3 RNA extraction

Total RNA was extracted using TRIzol reagent (Invitrogen) from *M. gastrocnemius* (GAS) muscle, WAT (from epididymal fat pad), liver according to the manufacturer's protocol. For 1 ml TRIzol, 100 mg muscle, WAT and skin, 30 mg liver were used, and

the sample was homogenized using an Ultra-Turrax[®] (IKA, Wilmington, NC, USA). For WAT, an additional centrifugation step (12,000 x g for 10 min at 4°C) was needed to remove the excess fat (top layer). After 5 min incubation at room temperature, 200 µl of chloroform was added, and the tubes were vigorously shaken by hand for 15 s. Following incubation at room temperature for a further 3 min, the samples were centrifuged at 12,000 x g for 15 min at 4°C. The aqueous phase was removed to a fresh tube, mixed with 0.5 ml of isopropanol, and total RNA was precipitated for 10 min at room temperature. Total RNA was pelleted by centrifugation at 14,000 x g for 10 min. The pellet was washed with 1 ml of 75% ethanol and resuspended in an appropriate volume of DEPC-treated MQ water (~20 µl), followed by an incubation at 55°C for 10 min. For skin RNA, an additional purification using the RNeasy[®] mini kit (QIAGEN, Valencia, CA, USA) was performed (see below). RNA was quantified using the NanoDrop[®] spectrophotometer (ND-1000, NanoDrop Technologies Inc., Wilmington, DE, USA). All RNA samples were stored at -80°C.

2.2.4 RNA purification using the RNeasy[®] mini kit (QIAGEN)

Following RNA isolation, the volume of the RNA solution was adjusted to 100 µl with RNase-free water. 350 µl of Buffer RLT and 250 µl of 100% ethanol were added to the diluted RNA samples. Samples were applied to an RNeasy mini spin column placed in a 2 ml collection tube and centrifuged for 15 s at 8000 x g. The flowthrough was discarded. 500 µl of Buffer RPE was subsequently applied to the column and centrifuged at 8000 x g for 15 s. Another 500 µl of Buffer RPE was applied to column and centrifuged at 8000 x g for 2 min. The RNeasy spin column was placed into a new 2 ml collection tube and centrifuged at 14,000 x g for 1 min. Finally, the RNeasy spin

column was transferred into a fresh 1.5 ml collection tube, where the RNA was eluted by the addition of 30 μ l of RNase-free water and subsequent centrifugation for 1 min at 8000 x g.

2.2.5 RNA electrophoresis

Formaldehyde/Agarose gel was prepared as follows: 0.6 g of UltraPure™ Agarose (Invitrogen) was dissolved in 40 ml Milli-Q® water and 5 ml of 10 x MOPS buffer was added. After cooling down to 40-50°C, 9 ml formaldehyde was added. Total RNA concentration was adjusted to 0.2 μ g/ μ l and the diluted RNA concentration was reestimated. Total RNA (1 μ g) was mixed with an equal volume of RNA 2 x loading dye and incubated at 65°C for 5 min prior to loading. Electrophoresis of RNA was between 40-80 V until the desired separation was achieved using 1 x MOPS as running buffer. The RNA loading dye contained ethidium bromide and allowed the visualization of the RNA by UV illumination. Gel Doc™ XR+ System (Bio-Rad) was used to photograph gels. The integrity of the RNA was evaluated by observing the quality and resolution of the 28S and 18S ribosomal bands.

2.2.6 cDNA synthesis (muscle, WAT, and liver)

Synthesis of cDNA was performed using iScript™ cDNA Synthesis Kit (Bio-Rad). 1 μ g (5 μ l) of total RNA was mixed with 4 μ l of 5 x iScript reaction mixture, 1 μ l of iScript reverse transcriptase and 10 μ l of Nuclease-free water. The reaction mixture was incubated for 5 min at 25°C, followed by 30 min at 42°C, 5 min at 85°C, and finally kept in 4°C. cDNA samples were stored at -20°C until further use.

2.2.7 cDNA synthesis (skin)

First-strand synthesis was performed using the SuperScript First-Strand Synthesis System (Invitrogen). Firstly, 0.5 µg of Oligo(dT)12-18 was added to 1.6 µg of total RNA (8 µl) containing 1 µl dNTPs (10 mM). This reaction was incubated at 65°C for 5 min then placed on ice for 1 min. Secondly, the remaining reaction mixture containing 2 µl of 10 x RT Buffer, 4 µl of 25 mM MgCl₂, 2 µl of 0.1 M DTT and 1 µl RNaseOUT recombinant RNase inhibitor was added to the RNA/primer mixture. The reaction tube mixed and incubated at 42°C for 2 min. Finally, SuperScript II RT (50 U) was added to the mixture and incubated at 42°C for 50 min. The reaction was subsequently terminated by incubation at 70°C for 15 min, followed by treatment with 1 µl of RNase H at 37°C for 20 min. cDNA samples were stored at -20°C until further use.

2.2.8 Real-time PCR (qPCR)

Triplicate qPCR reactions were performed (10 µl reactions, each) using Sso Fast EvaGreen (Bio-Rad). 20 µl of cDNA isolated from muscle, WAT, and liver samples were diluted in 80 µl of sterile Milli-Q[®] water. Primers were diluted from 100 µM to 2 µM. 3 µl of the cDNA solution was mixed with 5 µl of Evagreen (Invitrogen), and 1 µl of forward and reverse primers. The qPCR reaction was conducted on the Bio-Rad CFX96 real-time PCR machine. The program is as follows: 98°C incubation for 3 min, followed by 45 cycles of 98°C incubation for 3 s, 60°C for 10 s, 72°C for 10 s, and the final step of 95°C for 10 s. 60°C was used as annealing temperature for all primers. Gene expression was calculated using $\Delta\Delta CT$ and normalized to GAPDH (a house

keeping gene) for muscle, WAT, and liver, L27 (a house keeping gene) for skin. Primer sequences used are listed in each chapter.

2.2.9 Glucose transport in muscle

M. extensor digitorum longus (EDL) muscles were rapidly removed from euthanized mice and were pre-incubated in KRB buffer containing 2 mmol/l pyruvate for 20 min, followed by a further incubation in KRB buffer containing 3129.3 pmol/l insulin for 30 min. The muscles were then incubated in KRB buffer containing the same concentration of insulin, 1 mmol/l 2- ^3H -deoxy-D-glucose (55500 Bq/ml) and 7 mmol/l D- ^{14}C -mannitol (11100 Bq/ml) at 30°C for a further 10 min. During the incubation period, Cytochalasin B solution was distributed into 6-well plate, 5 ml/well. Glucose transport was terminated by dipping muscles in KRB buffer containing 80 $\mu\text{mol/l}$ cytochalasin B pre-chilled at 4°C. The muscles were transferred to a 1.5 ml lockable Eppendorf tube and subsequently frozen with liquid nitrogen. Muscles were weighed and digested by incubating in 250 μl of 1 M NaOH at 80°C for 10 min, followed by neutralization with 250 μl of 1 M HCl. Particulates were precipitated by centrifugation at 13,000 x g for 5 min. 100 μl supernatant was mixed with 1 ml scintillation cocktail (PerkinElmer) for radioactivity counting with a scintillation counter (1450 LSC & Luminescence counter, PerkinElmer). Counts were normalized to muscle weight.

2.2.10 AMPK assays

GAS muscle (100 mg) was homogenized with 1 ml homogenization buffer, and centrifuged at 12,000 x rpm for 15 min at 4°C. The supernatant containing 1 mg of

muscle protein was centrifuged in a TLA 120.1 rotor (Beckman Coulter, Brea, CA, USA) at 37,000 x rpm (48,000 x g) for 30 min at 4°C. The aspirated supernatant was then transferred to another pre-chilled 1.5 ml centrifuge tube. 80 mg of ammonium sulphate (per 1 mg of protein) was added, and the supernatant was stirred with a magnetic stir bar for 30 min. The sample was centrifuged at 37,000 x rpm for 30 min at 4°C. The supernatant was then discarded and the pellet containing AMPK was resuspended in 100 µl of homogenization buffer.

The SAMS peptide (His-Met-Arg-Ser-Ala-Met-Ser-Gly-Leu-His-Leu-Val-Lys-Arg-Arg) utilized in this study was synthesized commercially (School of Biological Sciences, Nanyang Technological University). 2 µl of the resuspended AMPK pellet was diluted with 8 µl of water. The enzymatic reaction was started by incubating the diluted AMPK sample with the SAMS peptide (5 µl) and cocktail (10 µl) for 10 min at 37°C. The reaction was terminated by pipetting 15 µl of incubation mix onto a 15 x 15 mm piece of P81 Whatman filter paper (Fisher Scientific), allowing at least 20 s for the solution to absorb into paper. 150 µl of 1% phosphoric acid was added to the incubation mixture absorbed to the Whatman filter paper. The filter paper was washed for 5 min, 6 times, with 150 µl of 1% phosphoric acid, followed by a final wash with 50 µl acetone. The dried filter paper was mixed with 3 µl scintillation cocktail (PerkinElmer) and radioactivity was measured with a scintillation counter (1450 LSC & Luminescence counter, PerkinElmer). Counts were normalized to protein concentration.

2.2.11 Serum collection

Cardiac puncture was performed on terminated mice with an 18-gauge needle. Blood was clotted for 30 min at room temperature, followed by centrifugation at 3,000 x g for

15 min at 4°C. Finally, serum (upper layer) was aliquoted and transferred into fresh centrifuge tubes and stored at -80°C.

2.2.12 Serum insulin measurement

Total serum insulin concentrations were measured using the Rat/Mouse Insulin ELISA kit (Millipore). Each well was washed 3 times with 300 µl of diluted Wash Buffer. 10 µl Assay Buffer was added to each well. 10 µl of Matrix solution was aliquoted into blank, standard and quality control wells. 10 µl of insulin standard, quality control, and serum samples were added to the designated wells and each well was incubated with 80 µl of detection antibody. After 2 h incubation at room temperature, wells were washed 3 times with 300 µl of diluted Wash Buffer. 100 µl of Enzyme Solution was added after the wash procedure, and incubated for 30 min at room temperature. Each well was washed 6 times with 300 µl of diluted Wash Buffer. Finally, 100 µl Substrate Solution was added and incubated for approximately 15 min at room temperature with gentle agitation. After addition of 100 µl Stop Solution, the plate was read with xMark™ Microplate Absorbance Spectrophotometer (Bio-Rad) at 450 and 590 nm.

2.2.13 Serum total cholesterol measurement

Total cholesterol concentration was determined using the LabAssay™ cholesterol kit (Wako, Chuo-Ku, Osaka, Japan). 2 µl of serum samples and standard solutions were mixed with 300 µl chromogen reagents, and incubated at 37°C for 5 min. The solutions were read with xMark™ Microplate Absorbance Spectrophotometer (Bio-Rad) at 600 and 700 nm.

2.2.14 Blood triglyceride (TAG) measurement

Blood TAG levels were analyzed using the Accutrend[®] Plus meter (Roche Diagnostics, Indianapolis, IN, USA).

2.2.15 Serum free fatty acid measurement

Serum free fatty acid (FFA) levels were measured using the NEFA C kit (Wako). 50 μ l of serum samples, standard solutions, and distilled water were mixed with 1 ml of R1 solution and incubated for 10 min at 37°C. 2 ml of R2 solution was added and incubated for another 10 min at 37°C. The solutions were read with xMark[™] Microplate Absorbance Spectrophotometer (Bio-Rad) at 550 nm.

2.2.16 Free glycerol measurement

The levels of glycerol were analyzed using the Free glycerol determination kit (Sigma-Aldrich). Free glycerol reagent (0.8 ml) was pipetted into each centrifuge tube, followed by the addition of 10 μ l of water, glycerol standard, and samples. Solutions were mixed by gentle inversion. After incubation at 37°C for 5 min, the solutions were read with xMark[™] Microplate Absorbance Spectrophotometer (Bio-Rad) at 540 nm.

2.2.17 Measurement of TAG (WAT)

Lipids were extracted from peripheral tissues using the Folch extraction method [177-178]. Approximately 400 mg of frozen WAT (from epididymal fat pad) was weighed and homogenized in methanol (1.33 ml), followed by addition of chloroform (2.66 ml). Following an overnight incubation at 4°C with shaking, 12 μ l of 1 M MgCl₂ was

added and the tube was centrifuged at 1000 g for 1 h at 4°C. The upper (aqueous) phase was discarded and the infranatant phase was collected into a fresh tube and evaporated to dryness at 70°C overnight followed by dissolving in 1 ml of 1M NaOH for determination of protein concentration using Bradford assay. The TAG residue was saponified with ethanol/KOH (500 µl/reaction) at 75°C for 20 min. The process was then terminated by adding 10% HCl (500 µl/reaction), cooled down to 0°C and then slowly neutralized with saturated NaHCO₃ (1.5 ml/reaction). The levels of glycerol, which reflect the total TAG content in the WAT, were analyzed using the Free glycerol determination kit (Sigma-Aldrich).

2.2.18 Serum leptin measurement

Serum leptin levels were determined using the Mouse leptin ELISA kit (Millipore). Each well was washed 3 times with 300 µl of diluted Wash Buffer followed by addition of 30 µl Assay Buffer to the background, standard, and quality control wells, and 40 µl Assay Buffer to the serum wells. 10 µl Matrix Solution was supplied to background, standard, and quality control wells. 10 µl of Assay Buffer, Mouse Leptin Standard, Quality Control Buffer, and sample serum was added to the background, standard, quality, and serum wells, respectively. 50 µl of antiserum solution was added to all wells. After 2 h incubation with shaking at 400 rpm in room temperature, each well was washed 3 times with 300 µl of diluted Wash Buffer. Next, all wells were incubated with 100 µl detection antibodies for 1 h at room temperature with shaking at 400 x rpm. Wells were washed 3 times with 300 µl of diluted Wash Buffer, followed by incubation with 100 µl of Enzyme Solution for 30 min at room temperature with gentle agitation. Finally, 100 µl Substrate Solution was added to each wells and incubated for approximately 10-15 min. The procedure was terminated by the addition

of 100 μ l Stop Solution. Solutions were read with xMark™ Microplate Absorbance Spectrophotometer (Bio-Rad) at 450 and 590 nm.

2.2.19 Fat pad embedding

Epididymal fat pads were fixed at room temperature with 10% formalin for 48 h with shaking. Following fixation fat pads were then dehydrated in an automated tissue processor (TP1020, Leica Wetzlar, Germany) using the following program:

Table 2.34 *Fat pad embedding process*

70% Ethanol	1 h
90% Ethanol	1 h
100% Ethanol	1 h x 3 times
Xylene	1 h x 3 times
Paraffin wax	3 h x 2 times

The dehydrated fat pads were then embedded using the modular tissue embedding center (EG 1150, Leica) and sectioned, to give 3-4 μ m thick sections, using a rotary microtome (RM2265, Leica).

2.2.20 Fat pad sections deparaffinization

Table 2.35 *Fat pad sections deparaffinization process*

Fat pad sections were deparaffinized according to the following procedure

Xylene	5 min x 2 times
Xylene + 100% Ethanol	5 min x 2 times
100% Ethanol	5 min x 2 times
95% Ethanol	5 min
90% Ethanol	5 min
70% Ethanol	5 min
50% Ethanol	5 min
PBS	5 min

2.2.21 Haematoxylin and eosin (H&E) staining of WAT

Following deparaffinization, fat pad sections were stained with haematoxylin and eosin (H&E) according to the following procedure:

Table 2.36 *WAT H&E staining process*

Haematoxylin	30 s
Rinse with tap water	Until clear
Stain with Scott's tap water	2 min
Rinse with tap water	1 s
Stain with Eosin	3 min
Rinse with tap water	Until clear
50% Ethanol	3 dips
70% Ethanol	3 dips
95% Ethanol	2 min
100% Ethanol	2 min x 2 times

Xylene	5 min x 2 times
Mount with DPX	

2.2.22 Immunohistochemical (IHC) staining

Immunohistochemical (IHC) staining of fat pad sections was performed using the VECTASTAIN[®] Elite ABC kit (Vector laboratories, Burlingame, CA, USA). Sections were deparaffinized (as stated in above section 2.2.20) and subjected to antigen retrieval for 10 min at 100°C in Tris-EDTA buffer (10 mM Tris, 1 mM EDTA, pH 9.0). After cooling, the sections were washed in PBS for 5 min, and blocked for 20 min in blocking serum (rabbit) followed by incubation with 1:100 dilution of either goat anti-UCP1 (sc-6528; Biotechnology, Santa Cruz, CA, USA) or goat anti-COX-2 (sc-1745; Santa Cruz Biotechnology) for 30 min at room temperature. The sections were washed for 5 min in PBS and incubated with (1:200) rabbit anti-goat biotinylated secondary antibody for 30 min at room temperature. Sections were washed for 5 min in PBS and incubated with VECTASTAIN[®] Elite ABC reagent for 30 min at room temperature. After a 5 min wash, UCP1 and COX-2 immunostaining was visualized by peroxidase substrate solution (DAB; Vector laboratories). Peroxidase substrate solution was incubated on the section for 2-10 min until the desired stain intensity developed. Stained sections were washed for 5 min with tap water, and counterstained with haematoxylin. Slides were mounted with DPX. Haematoxylin staining was performed according to the following procedure:

Table 2.37 *Haematoxylin staining for IHC staining*

Haematoxylin	5 s

Rinse with tap water	Until clear
50% Ethanol	3 dips
70% Ethanol	3 dips
95% Ethanol	2 min
100% Ethanol	2 min x 2 times
Xylene	5 min x 2 times
Mount with DPX	

2.2.23 Assessment of fatty acid oxidation in tissues

Radiolabelled palmitic acid [$1\text{-}^{14}\text{C}$] was dried on a hot plate at 70°C , combined with non-radiolabeled palmitic acid reaction mixture and incubated on a thermo mixer (Eppendorf, Hamburg, Germany) at 60°C for 2 h at maximum speed. Liver (200 mg) or WAT (Epididymal) (>100 mg) were rinsed in cold STE buffer (liver, 200 mg + 1 ml STE buffer; WAT, 200 mg + 0.5 ml STE buffer), homogenized using a glass 2 ml Dounce homogenizer (5 strokes), then centrifuged at 420 g for 10 min at 4°C . A small volume of supernatant was kept on ice to measure protein concentration (1:10-1:100 dilutions for BSA assay). 149 μl and 99 μl tissue homogenate supernatant was added into Etomoxir and AICAR control group, respectively. A portion (20 μl , ~250-500 μg) of the mitochondria containing supernatant was then added to 380 μl of [$1\text{-}^{14}\text{C}$] Palmitic acid reaction mixture (containing ATP and DTT), to commence the reaction. Following incubation at 37°C for 60 min, 200 μl of 1M perchloric acid was supplemented to the reaction mixture. The entire reaction mixture was transferred to a 1.5 ml centrifuge tube containing a Whatman filter paper disc saturated with 20 μl of concentrated hyamine hydroxide placed in the tube cap. The filter paper was incubated for 1 h, dried, and mixed with 1 ml scintillation cocktail (PerkinElmer). Radioactivity

was measured with a scintillation counter (1450 LSC & Luminescence counter, PerkinElmer). Counts were normalized to protein concentration.

2.2.24 Measurement of prostaglandin released from WAT explants.

WAT explants (50 mg) were incubated in 0.5 ml HBSS medium containing 15 mM HEPES, 0.5% BSA, 1% penicillin/streptomycin at 37°C/5% CO₂ for 8 h. Following centrifugation at 5,000 x rpm for 5 min at 4°C, supernatants were collected, snap-frozen with liquid nitrogen, and stored at -80°C. The levels of Prostaglandin E2 and 6-keto-prostaglandin F1 α were measured using the Prostaglandin E2 express kit-Monoclonal and 6-keto-prostaglandin F1 α EIA kits, respectively (Cayman Chemical, Ann Arbor, Michigan, USA).

For measurement of Prostaglandin E2, samples were diluted (1:40 and 1:60) in EIA Buffer; 100 μ l EIA buffer was added to non-specific binding wells and 50 μ l was added to maximum binding wells. 50 μ l of standard solution and samples was added to the designated wells. Finally, 50 μ l of Prostaglandin E2 express AChE tracer was added to each well. Note, total activity and blank wells did not receive Prostaglandin E2 express AChE tracer solution. Prostaglandin E2 express monoclonal antibody was supplied to each well except for the total activity, the non-specific binding, and the blank wells. The plate was then incubated for 60 min at room temperature with gentle shaking. The plate was rinsed 5 times with Wash Buffer, and 200 μ l of Ellman's reagent was added to all wells. Additionally, total activity wells received 5 μ l of AChE tracer. The assay was developed for 60-90 min with shaking in the dark. Plate was read with xMark™ Microplate Absorbance Spectrophotometer (Bio-Rad) at 410 nm. The development time was terminated when the absorbance of maximum binding wells reached a range of 0.3 to 1.0 A.U. (blank subtracted).

For measurement of 6-keto Prostaglandin F1 α samples were diluted 1:200 and 1:250 in EIA Buffer. 100 μ l EIA buffer was added to non-specific binding wells, and 50 μ l was added to maximum binding wells. 50 μ l of standard solution and samples were added to the designated wells. 50 μ l of 6-keto Prostaglandin F1 α AChE tracer was added to each well, with the exception the total activity and blank wells. 50 μ l of 6-keto Prostaglandin F1 α monoclonal antibody was supplied to each well. Note, total activity, non-specific binding, and the blank wells did not receive 6-keto Prostaglandin F1 α monoclonal antibody. The plate was then incubated for 18 h at 4°C. The plate was rinsed 5 times with Wash Buffer, and 200 μ l of Ellman's reagent was added to all wells and total activity wells received 5 μ l of AChE tracer. This assay was developed for 90-120 min with shaking in the dark. Plate was read with at 410 nm. The development time was terminated when the absorbance of maximum binding wells reached a range of 0.3 to 1.0 A.U. (blank subtracted).

2.2.25 Assessment of fatty acid oxidation in myotube cultures

Differentiated (72 h) primary myotubes were grown on a 96-well plate. Before adding incubation medium, protein was extracted from control wells (25 μ l protein lysis buffer/well) and protein concentration was estimated. Each well was supplemented with 50 μ l/well incubation medium. A 96-well filter plate was activated for capturing of CO₂ by the addition of freshly made 1 M NaOH (25 μ l/well). The plate harbouring the cells was clamped together with the filter plate, thus forming a "sandwich". The following is the apparatus set-up (bottom-to-top): cell plate, aluminum foil gasket, parafilm (punctured with holes), inversed filter plate, parafilm. The plate sandwich was placed in a humid incubator at 37°C, and fatty acid oxidation was allowed to proceed for 4 h. After incubation, filter plate was dried and Decon 90 (Decon

Laboratories) was added to each well to terminate the reaction. 25 µl/well of scintillation cocktail (PerkinElmer) was added, and the amount of $^{14}\text{CO}_2$ captured on the filter plate was assessed using a scintillation counter (1450 LSC & Luminescence counter, PerkinElmer Life Sciences).

2.2.26 H&E (Skin Biopsy)

Table 2.38 *H&E staining for skin biopsy*

Fix with 4% paraformaldehyde	10 min
Rinse with running tap water	1 min
Immerse in 0.1% HCl	2 s
Eosin	27 s
Rinse with running tap water	Until clear
Haematoxylin	2 min 30 s
Rinse with running tap water	Until clear
70% Ethanol	5 min
80% Ethanol	5 min
90% Ethanol	5 min
100% Ethanol	5 min
Xylene	5 min x 2 times
Mount with DPX	

Images were captured by MIRAX MIDI slide scanner microscope (Carl Zeiss) with a 10 x objective and MIRAX Scan software.

2.2.27 Van Gieson staining (Skin Biopsy)

Sections were stained with Weigert's iron hematoxylin (Merck Chemicals) (freshly prepared) for 10 min and rinsed with tap water. Sections were then stained with Van Gieson solution for 5 min, and rinse with tap water. The sections were then immersed in 90% ethanol, and 100% ethanol containing 6 drops of saturated picric acid, both for 1 min duration. Finally, sections were immersed in xylene for 5 min, 2 times, and mounted with DPX. Images were captured by MIRAX MIDI slide scanner microscope (Carl Zeiss) with a 10 x objective and MIRAX Scan software.

2.2.28 Immunohistochemistry (Skin Biopsy)

Immunohistochemistry for Ki67 antibody:

Cryosections were fixed in 100% acetone at -20°C for 5 min and then rinsed with 1 x PBS for 5 min. For antigen retrieval, sections were immersed in 95-100°C citrate buffer (pH = 6.0) for 10 min and then cooled for 30 min. Next, sections were washed in 1 x PBS 2 min for 2 times, and blocked with 0.1% BSA (in PBS) for 30 min at room temperature in a humid chamber. Sections were then incubated with rabbit anti-mouse Ki67 antibody (1:100 dilution in 0.1% BSA) overnight at 4°C, and washed with 1 x PBS 5 min for 3 times on the following day. Sections were incubated with AlexaFluor[®] goat anti-rabbit 488 IgG antibody (1:250 dilution in 0.1% BSA) for 1 h at room temperature. Finally, sections were washed with 1 x PBS for 5 min, 2 times and mounted with DAPI-containing mounting medium (Vector Laboratories).

Immunohistochemistry for K6 antibody:

Cryosections were fixed in 100% acetone at -20°C for 5 min, and rinsed with 1 x PBS for 5 min. Sections were then blocked with 15% NGS (in PBS) for 1 h at room temperature in a humid chamber. Sections were then incubated with rabbit anti-mouse K6 antibody (1:700 dilution in 15% NGS) for 1 h at room temperature and washed with 1 x PBS 5 min for 3 times, followed by incubation with AlexaFluor® goat anti rabbit 594 IgG antibody (1:250 dilution in 15% NGS) for 1 h at room temperature. Finally, sections were washed with 1 x PBS 3 times for 5 min, and mounted with DAPI-containing mounting medium (Vector Laboratories).

Immunohistochemistry for F4/80 antibody:

Cryosections were fixed in 100% acetone at -20°C for 5 min, then rinsed with 1 x PBS for 5 min. Sections were then blocked with 15% NGS (in PBS) for 1 h at room temperature in a humid chamber. Sections were then incubated with rat anti-mouse F4/80 antibody (1:500 dilution in 15% NGS) for 1 h at room temperature and washed with 1 x PBS 3 times for 5 min, followed by incubation with AlexaFluor® goat anti-rat 488 IgG antibody (1:500 dilution in 15% NGS) for 1 h at room temperature. Finally, sections were washed with 1 x PBS 3 times for 5 min, and mounted with DAPI-containing mounting medium (Vector Laboratories).

Immunohistochemistry for GDF-8 (Mstn) antibody:

Cryosections were blocked with blocking buffer for 1 h at room temperature in a humid chamber. Sections were then incubated with rabbit anti-mouse GDF-8 (Mstn)

antibody (1:25 dilution in antibody incubation medium) overnight at 4°C and washed with 1 x PBS 5 min for 3 times. Sections were then fixed in 10% buffered formalin for 5 min at room temperature and then rinsed with 1 x PBS for 5 min, 3 times, followed by incubation with biotinylated goat anti-rat IgG antibody (1:300 dilution in antibody incubation medium) for 1 h at room temperature. Sections were first washed with 1 x PBS 3 times for 5 min, and then incubated in streptavidin-conjugated AlexaFluor® 488 antibody (1:400 dilution in 0.2% BSA in PBS-T) for 1 h at room temperature. Finally, sections were washed with 1x PBS 3 times for 5 min each, and mounted with DAPI-containing mounting medium (Vector Laboratories).

2.2.29 Statistical analysis

In this thesis, two-way ANOVA and robust regression analysis were used for multiple comparisons and two-tail Student's-t-tests were performed for single comparisons. P value < 0.05 were defined as significant and data were expressed in the form of mean $\pm$ SEM. Number of replicates were listed in each chapter.

2.2.30 Microarray Analysis

WAT tissue from WT and *Mstn*^{-/-} CD and HFD fed mice was used for Microarray analysis in duplicate followed by gene expression verification using qPCR. RNA quality was confirmed by Agilent RNA 6000 Nano Kit and 2100 Bioanalyzer (Agilent, Santa Clara, CA, USA) and agilent SurePrint G3 Mouse Gene Expression array (Genomax Technologies, Singapore) was used for Microarray experiment. All data analysis and statistics was performed using GenSpring software (v.11.0.2) and the genes showing a P value < 0.05 using two-tailed Student's-t-tests and fold changes $\geq$

1.5 were considered as significant. Differentially regulated genes are listed in tables in each respective chapter.

Chapter 3 Myostatin-deficient mice exhibit reduced insulin resistance through activating the AMP-activated protein kinase signalling pathway

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ARTICLE

Myostatin-deficient mice exhibit reduced insulin resistance through activating the AMP-activated protein kinase signalling pathway

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Abstract

Aims/hypothesis

Myostatin-null (*Mstn*^{-/-}) mice have reduced body fat and increased tolerance to glucose. To date the molecular mechanisms through which myostatin (Mstn) regulates body fat content and insulin sensitivity are not known. Therefore, the aim of the current study was to identify signalling pathways through which Mstn regulates insulin sensitivity.

Methods

Wild-type (WT) mice and *Mstn*^{-/-} mice were fed either a control chow diet or a high fat diet (HFD) for 12 weeks. Glucose tolerance testing and insulin stimulated glucose uptake by M. extensor digitorum longus (EDL) were used as variables to determine insulin sensitivity. Quantitative PCR, Western blotting analysis and enzyme assays were used to monitor AMP-activated protein kinase (AMPK) levels and activity.

Results

Mstn^{-/-} mice exhibited reduced fat accumulation and peripheral insulin resistance when compared with WT mice, even when they were fed an HFD. Furthermore, treatment with a Mstn antagonist also increased insulin sensitivity during HFD. Consistent with increased insulin sensitivity, we also detected elevated levels of GLUT4, AKT, p-AKT and IRS-1 in *Mstn*^{-/-} muscles. Molecular analysis showed that there is increased expression and activity of AMPK in *Mstn*^{-/-} muscles. Furthermore, we also observed an increase in the AMPK downstream target genes, *Sirt1* and *Pgc-1α* (also known as *Ppargc1a*), in skeletal muscle of *Mstn*^{-/-} mice.

Conclusions/interpretation

We conclude that Mstn inactivation leads to increased AMPK levels and activity resulting in increased insulin sensitivity of skeletal muscle. We propose that, by regulating AMPK in skeletal muscle and adipose tissues, Mstn plays a major role in regulating insulin signalling.

Keywords p-AKT, AMPK, Glucose, GLUT4, Insulin, Myostatin, PGC-1α, PRKAB1, SLC2A4, SIRT1

Abbreviations ACC Acetyl-CoA carboxylase; ActRIIB Activin type IIB receptor; sActRIIB Soluble activin type IIB receptor; AMPK AMP-activated protein kinase; CD Chow diet; CPT-1 Carnitine palmitoyl transferase-1; EDL M. extensor digitorum longus; GTT Glucose tolerance test; HFD High fat diet.

3.1 Introduction

Myostatin (Mstn) is a growth and differentiating factor that belongs to the TGF- β superfamily. While a high level of *Mstn* gene expression is detected in skeletal muscle [118], a low level of *Mstn* expression is also detected in other tissues including adipose tissue [118] and heart [129]. Inactivation of the *Mstn* gene in mice [118] or mutations in the bovine [119-120], ovine [121] and human [122] *Mstn* gene result in a similar phenotype of increased muscle growth. Therefore, it is believed that Mstn is a negative regulator of skeletal myogenesis and its function is highly conserved during evolution. Functionally, Mstn not only regulates the proliferation and differentiation phases of myoblast growth [125, 138], but also controls the activation and further proliferation of muscle stem cells, the satellite cells [139]. Mstn has been shown to bind to the activin type IIB receptor (ActRIIB) and, therefore, either overproduction of a dominant negative form of ActRIIB in muscle [126] or treatment of mice with a soluble form of ActRIIB [155] (sActRIIB) have been shown to result in increased musculature.

The physiological effects of *Mstn* deletion are not restricted to skeletal muscle. A number of studies have reported significant decreases in the amount of adipose tissue in association with loss of Mstn function [165-166, 179]. A flurry of recent research also suggests that loss of, or reduction in, Mstn levels leads to increased insulin sensitivity. In fact, suppression of Mstn function in mice, through transgenic overproduction of the Mstn propeptide, results in resistance to high fat dietary-induced obesity and insulin resistance [167]. This finding is further supported by studies on insulin resistant human participants, which show increased levels of Mstn in muscle and plasma [180]. Interestingly, short-term administration of recombinant Mstn

protein has also been shown to induce insulin resistance in mice [180]. In extremely obese human participants it was further discovered that there were elevated levels of Mstn protein in both muscle and plasma samples [181]. In addition, injection of Mstn-specific antibodies along with exercise results in significantly increased insulin sensitivity [154]. Recently, Guo et al. showed that inhibition of Mstn signalling, specifically in adipose tissue, had no effect on glucose and insulin tolerance [166]. Contrary to this, muscle-specific inactivation of Mstn resulted in increased lean mass and improved glucose metabolism on both standard and high fat diets (HFDs) [166]. Although it is clear that lack of Mstn affects glucose uptake and metabolism, the specific mechanisms and signalling events in skeletal muscle and adipose tissue that help overcome insulin resistance in *Mstn*^{-/-} mice are not clearly understood.

Recently, a series of investigations has delineated the role of AMPK (also known as PRKAB1) in insulin sensitivity and resistance. AMPK is a heterotrimeric serine/threonine kinase, which consists of a catalytic α -subunit and regulatory β - and γ -subunits [182-184]. In skeletal muscle, $\alpha 2$ [65-66] is the major catalytic isoform produced, which forms a heterotrimeric complex with $\beta 2$ and $\gamma 3$ subunits. AMPK acts as a metabolic switch, which becomes activated by acute increases in the cellular AMP/ATP ratio, such as occurs following exercise, or during conditions such as hypoxia, ischaemia or osmotic stress [185]. When intracellular ATP levels are low, AMPK switches off ATP-consuming processes, such as glycogen, fatty acid, and protein synthesis pathways, and activates alternative pathways for ATP regeneration, which include glucose transport, glycolysis and fatty acid oxidation. Activation of AMPK has also been shown to improve insulin sensitivity resulting in enhanced insulin-mediated glucose uptake in skeletal muscle [67-69].

In the current manuscript we have identified the molecular mechanisms that are responsible for the increased insulin sensitivity in *Mstn*^{-/-} mice. Here for the first time we show that there is increased abundance of AMPK in skeletal muscle, adipose tissue and liver, leading to an overall increase in glucose uptake and reduced fat accumulation in *Mstn*^{-/-} mice, despite being fed on an HFD. This in turn leads to the increased sensitivity to insulin in *Mstn*^{-/-} mice. We further show that treatment with an Mstn antagonist also reduces insulin resistance in mice fed on an HFD.

3.2 Methods

3.2.1 Animals

Wild-type (WT) C57BL/6 mice were obtained from the Centre for Animal Resources (National University of Singapore, Singapore). *Mstn*^{-/-} mice (C57BL/6 background) were gifted from Se-Jin Lee (Johns Hopkins University, Baltimore, MD). The Institutional Animal Care and Use Committee (IACUC), Singapore, approved all experiments involving animals. Seven-week-old male *Mstn*^{-/-} mice and WT littermates were derived from different litters and were housed in groups and maintained on standard chow diet (CD) at a constant temperature (20°C) under a 12 h/12 h artificial light/dark cycle with unlimited access to water until commencement of the trial. Two groups, consisting of five WT and five *Mstn*^{-/-} mice each, were either fed HFD (45% energy from fat; 58V8, TestDiet, Richmond, IN, USA) or CD (10% energy from fat ;58Y2, TestDiet) for 12 weeks. Please see Table 3.1 for details of diet compositions (Table 3.1).

Table 3.1 *Diet compositions*

WT and *Mstn*^{-/-} mice were fed either CD or HFD with the following compositions.

Nutritional Profile			Energy from:	
Chow Diet (58Y2, TestDiet)	Protein	17.3%	Protein	18.3%
	Fat	4.3%	Fat	10.2%
	Carbohydrates	67.4%	Carbohydrates	71.5%
	Fiber	4.7%		
High-fat Diet (58V8, TestDiet)	Protein	21.3%	Protein	18.3%
	Fat	23.6%	Fat	45.7%

Carbohydrates	41.2%	Carbohydrates	35.5%
Fiber	5.8%		

For Mstn antagonist studies, 7-week-old male WT mice were fed the same CD or HFD (see above) for a period of 12 weeks together with injection (i.p.) of either saline or sActRIIB Mstn antagonist (5 µg/g body weight) three times a week (see section 3.2.4 for details of purification). Body weight and energy intake (energy intake is equal to food consumption multiplied by metabolisable energy content) were measured twice a week in all trial mice. Mice were killed 1 week after GTT and insulin tolerance test (ITT) analysis, and were not fasted prior to death.

3.2.2 RNA extraction, quantitative real-time PCR (qPCR)

RNA extraction and PCR were performed as previously described [186] (see section 2.2.3, 2.2.5, 2.2.6 and 2.2.8 for details). Total RNA was extracted using TRIzol reagent (Invitrogen, Carlsbad, CA, USA) from M. gastrocnemius, epididymal fat pad (gonadal) and liver. Subsequent cDNA synthesis was performed using the Superscript II First strand synthesis system (Invitrogen) from 1 µg of total RNA. qPCR was performed in triplicate in 20 µl reactions using Sso Fast Evagreen (Bio-Rad, Hercules, CA, USA) and the Bio-Rad CFX96 real-time PCR machine. The following PCR primers were used for qPCR: *Ampka2*, 5'-CGC CTC TAG TCC TCC ATC AG-3' and 5'-ATG TCA CAC GCT TTG CTC TG-3'; *Ampkβ2*, 5'-TCC AGA GGG AGA GCA TCA GT-3' and 5'-ACA TGA TTG GGC TCA GGA AG-3'; *Ampkγ3*, 5'-AGA GCC TAG GTG AAG TCA TTG ACA-3' and 5'-AGA TGG CTT GGG TGT GAG GA-3'; *Pgc-1α*, 5'-AAG TGT GGA ACT CTC TGG AAC TG-3' and 5'-GGG TTA TCT

TGG TTG GCT TTA TG-3'; *Glut4*, 5'-CTT CTT TGA GAT TGG CCC TGG-3' and 5'-AGG TGA AGA TGA AGA AGC CAA GC-3'; *Sirt1*, 5'-CAG TGT CAT GGT TCC TTT GC-3' and 5'-GCA CCG AGG AAC TAC CTG AT-3'; *Gapdh*, 5'-AAC TTT GGC ATT GTG GAA GG-3' and 5'-ACA CAT TGG GGG TAG GAA CA-3'.

3.2.3 Western blotting analysis

Western blotting analysis was performed as previously described [186] (see section 2.2.2 for details). The muscle samples were homogenised in lysis buffer (PBS, containing 1% NP40, 1 mmol/l EDTA, 10 mmol/l NaF, and Complete protease inhibitor [Roche Molecular Biochemicals, Indianapolis, IN, USA]) protease inhibitors). Equal amounts of protein lysates were resolved by 4–12% SDS-PAGE (Invitrogen) electrophoresis and transferred to nitrocellulose membrane by electroblotting. The membranes were blocked in TBST with 5% (wt/vol.) milk powder overnight at 4 °C, followed by incubation with specific primary and secondary antibodies for 3 h and 1 h respectively at room temperature. Immunoreactivity was detected using Western Lightning Chemiluminescence Reagent Plus (NEL104; PerkinElmer Life Sciences, Waltham, MA, USA) and exposure to autoradiography film. The following primary antibodies were used for western blotting analysis: anti-p-AMPK α (Cell Signaling, Danvers, MA, USA); anti-AMPK γ 3 (Cell Signaling); anti-GLUT4 (Cell Signaling); anti-IRS-1 (Cell Signaling); anti-p-ACC (Millipore); anti-AKT (Santa Cruz); anti-p-AKT (Ser473) (Santa Cruz); anti-SIRT1 (Santa Cruz); anti-PGC-1 α (Santa Cruz); anti-acetylated-lysine (Cell Signaling) and anti- α -tubulin (Sigma-Aldrich, St Louis, MO, USA).

3.2.4 Recombinant soluble ActRIIB purification

Histidine-tagged soluble ActRIIB (sActRIIB) fusion protein was expressed in bacteria using the pET expression system (Novagen, Madison, WI, USA). sActRIIB cDNA was amplified by PCR as a BamHI fragment and cloned into the pET 16-B vector in frame with the 10 histidine residues, according to the manufacturer's protocol (Novagen). The resulting construct was used to transform the BL21 bacterial strain. An overnight *Escherichia coli* culture harbouring the recombinant sActRIIB expression vector was diluted (1:50) and grown up to an OD of 0.8 (600 nm) in 1 l of Lennox LBroth (LB) medium plus 50 mg/ml ampicillin. sActRIIB fusion protein was induced by adding 0.5 mmol/l isopropyl thio- β -galactoside (IPTG) to the culture and the induction was continued for 2 h. Bacteria were harvested by centrifugation, resuspended in 40 ml of lysis buffer (6 mol/l guanidine hydrochloride, 20 mmol/l Tris [pH 8.1], 5 mmol/l 2-mercaptoethanol), sonicated, and centrifuged at 10,000 x g for 30 min. sActRIIB was purified from the supernatant fraction by Ni-agarose affinity chromatography (Qiagen, Valencia, CA, USA), according to the manufacturer's protocol. Column fractions containing sActRIIB were pooled and dialysed against two changes of 50 mmol/l Tris-HCl (pH 8.0) containing 150 mmol/l NaCl for 6 h. The purity of the recombinant sActRIIB protein was verified by SDS-PAGE.

3.2.5 Insulin and glucose tolerance testing

The ITT and GTT were performed as previously described in [167] and [187] respectively. The insulin tolerance test (ITT) was performed according to the previously described protocol [167]. Initial blood samples were collected from trial mice following a period of 12 h fasting, after which bovine insulin was injected i.p. at

a dose of 0.75 U/kg of body weight. Blood was collected from the tail vein at regular intervals (0, 30, 60 and 120 min) following the injection of insulin and the total level of blood glucose was measured using a glucometer (ACCU-CHEK, Roche). The glucose tolerance test (GTT) was performed according to the protocol described previously [187]. Mice were fasted for 12 h, after which mice were injected with glucose (1 mg/g) i.p. Blood was collected at different intervals (0, 30, 60 and 120 min) and the total level of blood glucose was assessed using a glucometer (ACCU-CHEK, Roche).

3.2.6 Biochemical analysis

Total serum insulin concentrations were measured using the Rat/Mouse Insulin ELISA kit (EZRMI-13K; Millipore, Billerica, MA, USA) as per the manufacturer's guidelines (see section 2.2.11 and 2.2.12 for details). Total cholesterol concentration was determined using the 'LabAssay cholesterol' kit (Wako, Chuo-Ku, Osaka, Japan) (see section 2.2.11 and 2.2.13 for details), triglyceride (TAG) levels were analysed using the AccutrendPlus meter (Cobas Roche) (see section 2.2.14 for details), and serum NEFA levels were measured using the NEFA C kit (Wako) (see section 2.2.11 and 2.2.15 for details) according to the manufacturer's protocols.

3.2.7 Glucose transport in muscle

M. extensor digitorum longus (EDL) were rapidly removed from killed mice and were pre-incubated in Krebs–Ringer bicarbonate (KRB) buffer containing 2 mmol/l pyruvate for 20 min, followed by a further incubation in KRB buffer containing 3,129.3 pmol/l insulin for 30 min. The muscles were then incubated in KRB buffer

containing the same concentration of insulin, 1 mmol/l 2-deoxy-D-[³H]glucose (55,500 Bq/ml) and 7 mmol/l D-[¹⁴C]mannitol (11,100 Bq/ml) at 30°C for a further 10 min. The level of glucose transport was subsequently measured as previously described [187-188] (see section 2.2.9 for details).

3.2.8 AMPK assays

A modified protocol from the Animal Models of Diabetic Complications Consortium [189] was used to measure AMPK activity in protein lysates from muscle tissue (see section 2.2.10 for details). Briefly, after muscle homogenisation, lysates containing 1 mg of muscle protein were centrifuged in a TLA 120.1 rotor (Beckman Coulter, Brea, CA, USA) at 37,000 x rpm (48,000 x g) for 30 min at 4°C. The supernatant fraction was then transferred to another centrifuge tube on ice and stirred together with 144 mg of ammonium sulphate, per ml solution, for an incubation period of 30 min. The sample was then centrifuged at 37,000 x rpm for 30 min at 4°C, the supernatant fraction was discarded, and the pellet resuspended in 100 µl of homogenisation buffer.

The SAMS peptide (His-Met-Arg-Ser-Ala-Met-Ser-Gly-Leu-His-Leu-Val-Lys-Arg-Arg) utilised in this study was synthesised commercially. The reaction was started by incubating the resuspended ammonium sulphate pellet into a mixture of water, SAMS peptide and radioactive ATP (to 100 µl of required working assay mix add 2 µl of 370,000 Bq/ml P³²-γATP) for 10 min at 37°C. The reaction was terminated by pipetting 15 µl of incubation mix onto a 15 × 15 mm piece of P81 Whatman filter paper, allowing at least 20 s for the solution to absorb into paper, then dropping into 150 ml of 1% phosphoric acid. Finally the filter paper was washed six times, 5 min each, in 150 ml of 1% phosphoric acid, followed by a final wash in 50 ml acetone.

After drying, the filter paper was measured on a scintillation counter (1450 LSC and luminescence counter; PerkinElmer Life Sciences, Waltham, MA, USA).

3.2.9 Statistical analysis

The data were analysed using two-way ANOVA and robust regression analysis. Not all the data were normally distributed. Unlike the conventional regression model based on ordinary least square (OLS), the robust model estimates with an iterative reweighted least square (IRWLS) algorithm and generates more reliable estimates about the influence of mouse genotype and diet type on the outcome. The proposed robust model has several advantages over the conventional approach in data analysis. First, it analyses the skewed outcome directly without the need to perform back-transformation for interpretation. This is desirable because arithmetic transformation may not necessarily induce normality in the skewed outcome. Second, it does not discard any observations in the process even if they are confirmed outliers. Finally, it does not impose any strict distributional assumption on the outcome like the generalised linear model (GLM), as there is no precise information about the outcome's probabilistic characteristics [190-191].

3.3 Results

3.3.1 *Mstn*^{-/-} mice exhibit a lean phenotype

Since *Mstn*^{-/-} mice have reduced white adipose tissue (WAT) content, we wanted to investigate the effect of a fat rich diet on muscle metabolism in *Mstn*^{-/-} mice. In order to do this, WT and *Mstn*^{-/-} mice were fed either HFD or regular CD for 12 weeks. During the 12 week diet regimen, no significant difference was noted in the energy intake of WT and *Mstn*^{-/-} mice fed on HFD when compared with their respective CD fed controls, but it is important to mention that both the CD and HFD fed *Mstn*^{-/-} mice had increased energy intake over and above that of both CD and HFD WT mice (Figure 3.1A). The body weights, muscle weights and fat pad weights from WT and *Mstn*^{-/-} mice fed on HFD were compared with their respective CD fed controls. With no change in the amount of food intake, WT mice fed on HFD gained significantly more body weight (~65%) as compared with WT mice fed on regular CD (~35%) during the 12 week period. In contrast, *Mstn*^{-/-} mice fed HFD did not significantly increase body weight as compared with regular CD fed *Mstn*^{-/-} mice (Figure 3.1B). Feeding HFD did not increase muscle weights significantly either in WT or *Mstn*^{-/-} mice (Figure 3.1C). It is noteworthy to mention that 7-week-old *Mstn*^{-/-} mice were very lean and had significantly reduced fat mass as compared with WT mice at the beginning of the HFD trial (Figure 3.1E). Upon HFD feeding, the weights of three types of WAT samples (epididymal, retroperitoneal and inguinal) increased significantly during the 12 week period in WT mice; while an increase in the weight of WAT samples was also observed in *Mstn*^{-/-} mice during the 12 week period, the increase was not statistically significant (Figure 3.1F). Similarly to the findings in

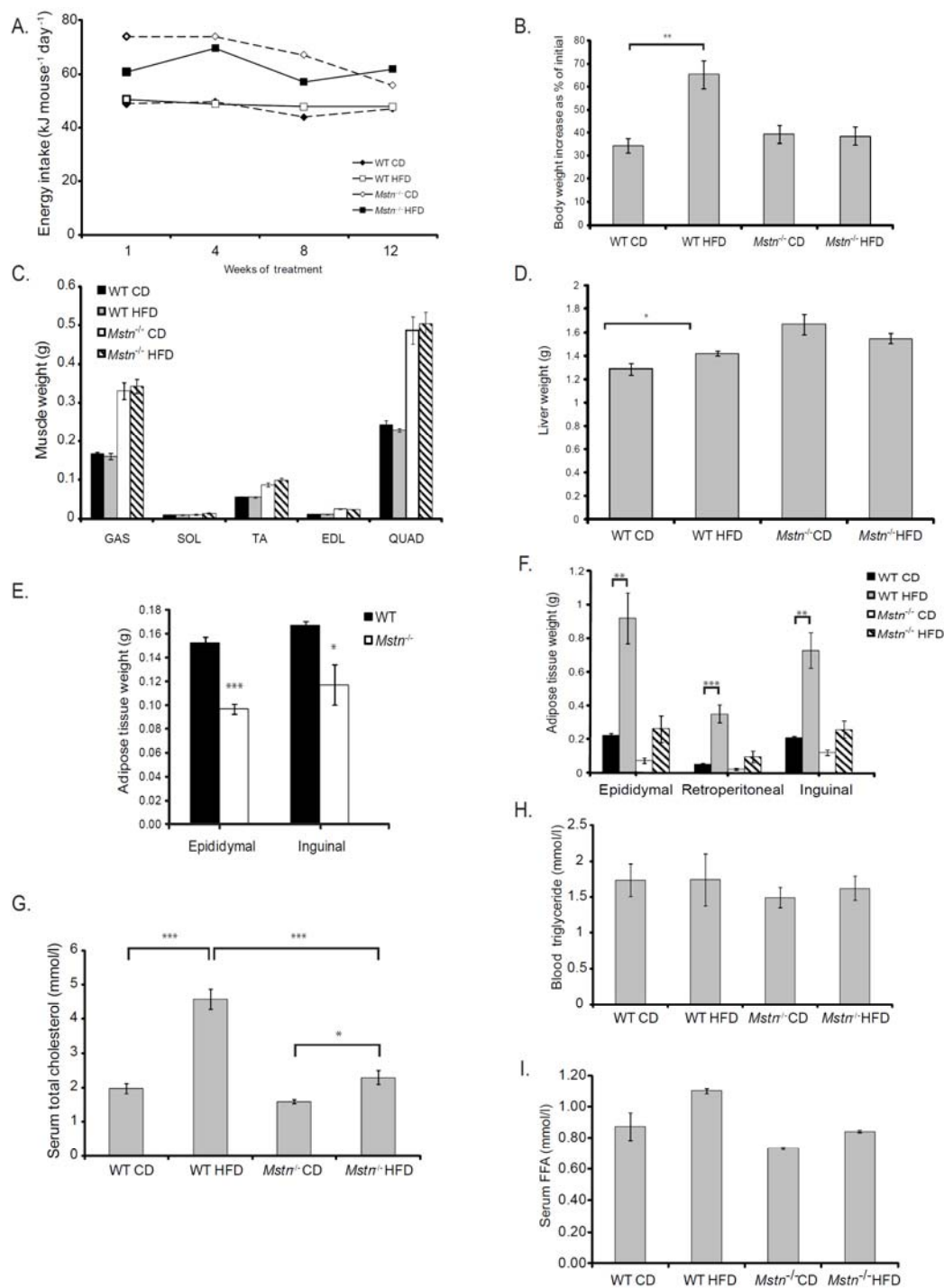
adipose tissue, a significant increase in liver weight was seen in WT mice fed on HFD; however, in contrast, no such increase in liver weight was observed in the *Mstn*^{-/-} mice fed on HFD (Figure 3.1D).

3.3.2 Decreased circulatory cholesterol levels in *Mstn*^{-/-} mice

To determine whether the reduced fat pad weight in *Mstn*^{-/-} mice occurred in conjunction with a decrease in lipid levels, we analysed the circulatory levels of cholesterol, TAG and NEFA. In WT mice fed HFD, there was a 110% increase in circulatory cholesterol levels when compared with WT CD fed controls, while in *Mstn*^{-/-} mice, we observed an increase of 50% in serum cholesterol levels upon HFD feeding when compared with *Mstn*^{-/-} CD fed controls (Figure 3.1G). Therefore, absence of *Mstn* appears to result in reduced circulating cholesterol levels during HFD feeding. In contrast to the reduced cholesterol levels, we observed no significant change in TAG and NEFA levels between WT and *Mstn*^{-/-} mice fed either CD or HFD (Figure 3.1H&3.1I).

Figure 3.1 *Lean phenotype in Mstn deficient mice.*

(A) Energy intake ($\text{kJ mouse}^{-1} \text{ day}^{-1}$) of $Mstn^{-/-}$ mice and WT mice during 12 weeks of CD and HFD treatment (black diamonds, WT CD; white squares, WT HFD; white diamonds, $Mstn^{-/-}$ CD; black squares, $Mstn^{-/-}$ HFD). (B) Body weight increase (expressed as a percentage of initial body weight) observed in $Mstn^{-/-}$ mice and WT littermates after 12 weeks of CD and HFD treatment. (C) M. gastrocnemius (GAS), M. soleus (SOL), M. tibialis anterior (TA), M. EDL and M. quadriceps (QUAD) weights after 12 weeks of CD and HFD treatment (black bars, WT CD; grey bars WT HFD; white bars $Mstn^{-/-}$ CD; hatched bars, $Mstn^{-/-}$ HFD). (D) Liver weights after 12 weeks of CD and HFD treatment. (E) Adipose tissue weights of 7-week-old male $Mstn^{-/-}$ mice and WT littermates (black bars, WT; white bars $Mstn^{-/-}$). (F) Fat pad weights of $Mstn^{-/-}$ mice and WT littermates after 12 weeks of CD and HFD treatment (black bars, WT CD; grey bars WT HFD; white bars $Mstn^{-/-}$ CD; hatched bars, $Mstn^{-/-}$ HFD). (G) Serum total cholesterol, (H) blood TAG and (I) serum NEFA levels of $Mstn^{-/-}$ mice and WT mice after 12 weeks of CD and HFD treatment. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$. Error bars represent $\pm$ SEM ($n = 5$).



3.3.3 Lack of Mstn reduces insulin resistance

The lean phenotype of *Mstn*^{-/-} mice, even when fed a HFD, raised the possibility that insulin sensitivity in *Mstn*^{-/-} mice might be maintained even on an HFD. Therefore, the rate of glucose disposal and insulin sensitivity in the WT and *Mstn*^{-/-} mice was measured. *Mstn*^{-/-} mice had lower fasting blood glucose levels when compared with WT mice (Figure 3.2A). Furthermore, WT mice had significantly elevated levels of fasting plasma glucose following HFD treatment (8 weeks), when compared with that observed at the start of the trial (0 weeks). However, such an increase in fasting plasma glucose levels was not detected in *Mstn*^{-/-} mice fed on HFD (Figure 3.2A). Furthermore, with glucose tolerance testing, a phenotype reflecting insulin resistance, and therefore significantly higher plasma glucose levels, was observed in WT mice when compared with *Mstn*^{-/-} mice fed on HFD (Figure 3.2B). In addition, *Mstn*^{-/-} mice also showed increased glucose disposal in response to insulin as compared with WT mice during ITT (Figure 3.2F).

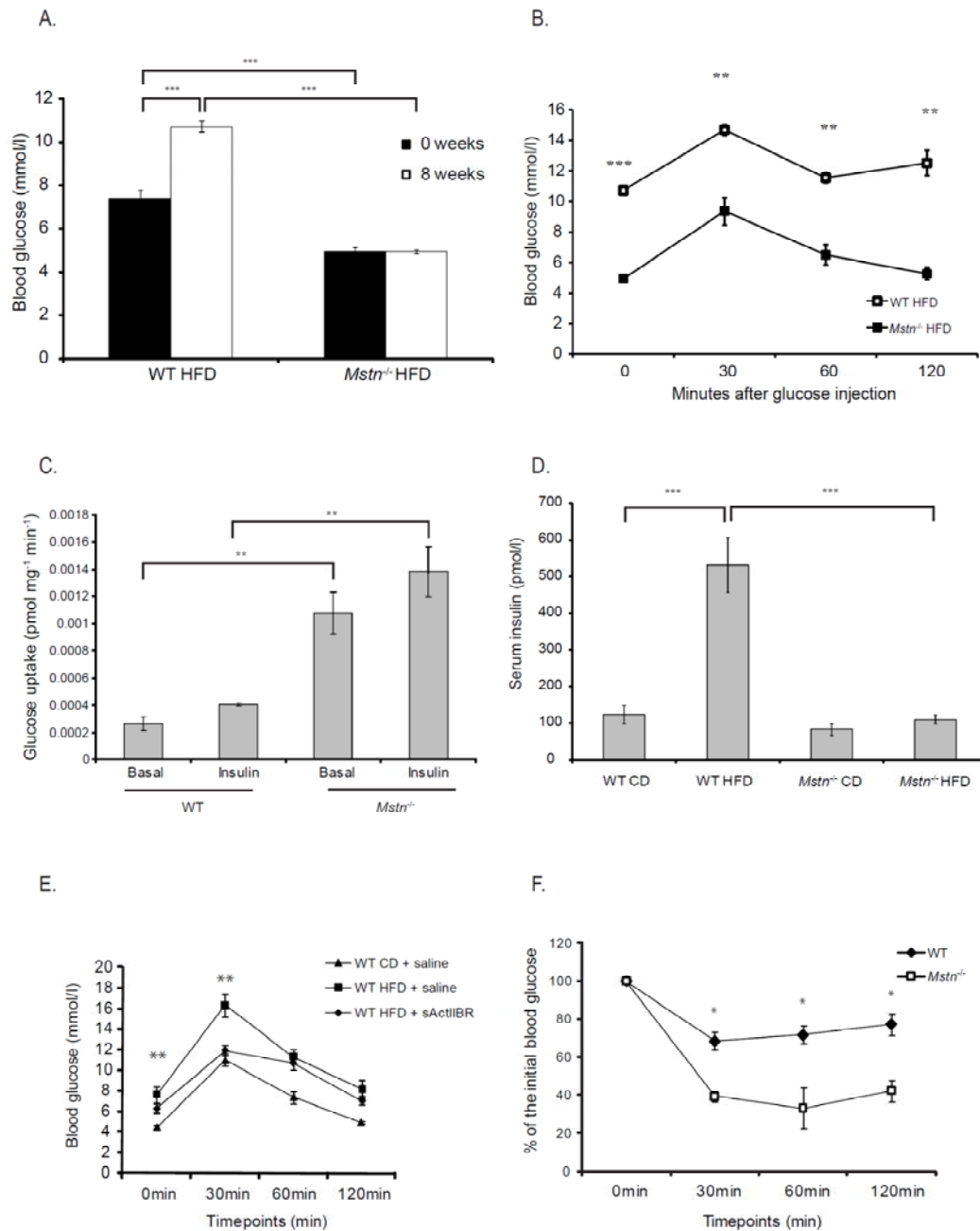
3.3.4 Increased glucose uptake in the absence of Mstn

To determine whether or not disruption of Mstn has a cell autonomous effect on glucose uptake by muscle, we measured glucose uptake in EDL muscle from both WT and *Mstn*^{-/-} mice. The results show that even at the basal level (unstimulated by insulin), there is a 2.7-fold increase in glucose uptake by EDL muscle from *Mstn*^{-/-} mice compared with WT mice. As expected, insulin was able to stimulate glucose uptake twofold in WT EDL muscle, and only to a minor extent in *Mstn*^{-/-} EDL muscle (Figure 3.2C). To determine the molecular basis for the improved glucose uptake in *Mstn*^{-/-} muscle, we next estimated insulin levels using ELISA. ELISA analysis was

performed using serum collected from non-fasted, non-challenged animals at the time of culling. The results show that there was no significant difference in systemic insulin levels between WT and *Mstn*^{-/-} on CD. When challenged with HFD, we observed an increase in circulatory insulin levels in the WT mice; however, in contrast, no significant change in systemic insulin levels was observed in *Mstn*^{-/-} mice fed on HFD (Figure 3.2D).

Figure 3.2 *Lack of Mstn reduces insulin resistance in mice.*

(A) Fasting blood glucose levels in WT and *Mstn*^{-/-} mice at 0 and 8 weeks of HFD treatment (black bar, 0 weeks; white bar, 8 weeks). (B) GTT comparing blood glucose levels between WT and *Mstn*^{-/-} mice fed on HFD (white squares, WT HFD; black squares, *Mstn*^{-/-} HFD). (C) Glucose uptake by muscle following insulin stimulation. (D) Serum insulin levels in WT and *Mstn*^{-/-} mice fed on CD or HFD. (E) Blood glucose levels during GTT on WT mice fed on CD or HFD in the presence of either saline or sActRIIB antagonist (black triangles, WT CD+saline; black squares, WT HFD+saline; black diamonds, WT HFD+sActRIIB). (F) Blood glucose levels during an ITT in WT and *Mstn*^{-/-} mice. The graph displays blood glucose levels expressed as a percentage of the initial blood glucose level following a 12 h period of fasting (black diamonds, WT; white squares, *Mstn*^{-/-}). *P < 0.05, **P < 0.01, ***P < 0.001. Error bars represent $\pm$ SEM ($n = 3$)



3.3.5 Lack of Mstn increases insulin signalling

We next performed qPCR and Western blotting analysis on molecules involved in the insulin-signalling pathway. The results show that there is a significant increase in the expression levels of *Glut4* (also known as *Slc2a4*; Figure 3.3A) in muscle from *Mstn*^{-/-} mice when compared with WT muscles. When challenged with HFD, we observed further upregulation of *Glut4* expression levels in *Mstn*^{-/-} muscle tissue, whereas no such increase is seen in muscles from the WT mice (Figure 3.3A). Western blotting analysis further confirmed this result and showed that indeed there was upregulation of GLUT4 protein content in muscle tissue from *Mstn*^{-/-} fed HFD (Figure 3.3B). Western blotting analysis also demonstrated an increase in total AKT protein in *Mstn*^{-/-} muscles (Figure 3.3B). As a result, increased p-AKT levels were observed in *Mstn*^{-/-} muscles, and when further stimulated with insulin, even greater levels of p-AKT were detected in *Mstn*^{-/-} muscles when compared with WT muscles (Figure 3.3C). Similarly, we also observed an increase in total IRS-1 protein in *Mstn*^{-/-} muscles (Figure 3.3B).

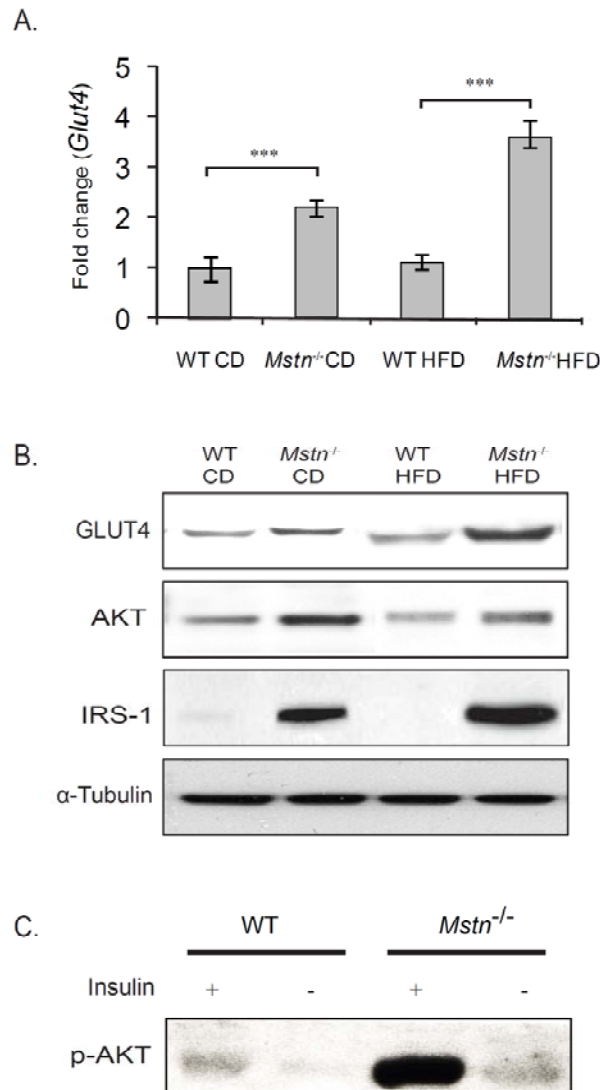


Figure 3.3 Molecules involved in the insulin stimulated glucose uptake pathway are up-regulated in *Mstn*^{-/-} mice.

(A) qPCR analysis of the relative mRNA expression of *Glut4* in muscle from WT and *Mstn*^{-/-} mice fed on CD or HFD. (B) Western blotting analysis of GLUT4, AKT and IRS-1 protein levels in BF muscle from WT and *Mstn*^{-/-} mice fed on CD or HFD. (C) p-AKT protein level in muscle isolated from WT or *Mstn*^{-/-} mice without (-) or with (+) insulin stimulation. All samples were collected from M. gastrocnemius. ***P < 0.001. Error bars represent ±SEM (*n* = 3)

3.3.6 Interfering with Mstn signalling increases tolerance to glucose

To ascertain whether or not interfering with Mstn signalling postnatally has a similar effect to that observed in *Mstn*^{-/-} mice, WT mice fed on HFD were treated with sActRIIB, which has been previously shown to act as a potent antagonist to Mstn activity [192-193]. Treatment with sActRIIB reduced the insulin resistance seen in mice fed on a HFD. In a GTT test, we observed a significant elevation in blood glucose levels in mice fed a HFD; however, treatment with sActRIIB increased insulin sensitivity and enhanced glucose disposal, despite the fact that the mice were fed HFD. Thus, as can be seen in Figure 3.2E, glucose levels were similar between mice fed on regular CD and HFD fed mice treated with sActRIIB (Figure 3.2E).

3.3.7 Increased levels of AMPK in *Mstn*^{-/-} mice

A genome-wide scan for differentially expressed genes revealed that the expression of *Ampk* was up-regulated by several fold in skeletal muscle tissue isolated from *Mstn*^{-/-} mice (data not shown). To study this further, we quantified the expression of *Ampk* ($\alpha 2$, $\beta 2$ and $\gamma 3$ isoforms) in peripheral tissues from WT and *Mstn*^{-/-} mice that had been fed CD or HFD. Subsequent qPCR analysis revealed that mRNA expression of all three isoforms of *Ampk* was significantly up-regulated in *Mstn*^{-/-} muscles, liver and adipose tissues (Figure 3.4). While HFD feeding further up-regulated the mRNA expression of both the catalytic (α) and regulatory (β and γ) subunits of *Ampk* in peripheral tissues of *Mstn*^{-/-} mice, no such increase was observed in the peripheral tissues of WT mice fed an HFD (Figure 3.4). Western blotting analysis further confirmed that there was increased protein production of AMPK $\gamma 3$ in skeletal muscle from *Mstn*^{-/-} mice (Figure 3.5A). Furthermore, there was an increase in the phosphorylation of the α -catalytic

subunit (AMPK α) in skeletal muscle, liver and adipose tissue from *Mstn*^{-/-} mice (Figure 3.5B). It was also observed that there was a significant increase in the levels of the AMPK target protein, p-ACC in *Mstn*^{-/-} skeletal muscle (Figure 3.5A). Consistent with these results, a significant increase in AMPK activity is also detected in *Mstn*^{-/-} skeletal muscle (Figure 3.5C). Recently it has been shown that AMPK functions by regulating the expression of genes involved in energy metabolism by acting in coordination with another metabolic sensor, the NAD-dependent type III deacetylase, SIRT1 [72]. Subsequent qPCR analysis indicates that in *Mstn*^{-/-} muscles there is increased expression of *Sirt1* mRNA (Figure 3.5D) and its downstream target gene *Pgc-1 α* (also known as *Ppargc1a*; Figure 3.5E). Consistent with this result, we also observed an increase in SIRT1 and PGC-1 α protein abundance in *Mstn*^{-/-} muscle collected from mice fed on both CD and HFD when compared with respective WT controls (Figure 3.5F&3.5G). Since increased SIRT1 results in deacetylation of PGC-1 α , we observed lower levels of acetylated PGC-1 α in *Mstn*^{-/-} mice fed on both CD and HFD when compared with respective WT controls. In contrast, there was an increase in acetylation of PGC-1 α in WT mice fed HFD when compared with WT CD fed a control diet (Figure 3.5H).

Figure 3.4 *Increased Ampk mRNA expression is seen in $Mstn^{-/-}$ mice.*

Relative mRNA expression levels of *Ampka2/β2/γ3* in GAS muscle, (A-C) WAT (epididymal fat pad) (D-F) and liver (G-I) as measured by qPCR in WT and *Mstn*^{-/-} mice fed on CD and HFD. *P < 0.05, **P < 0.01, ***P < 0.001. Error bars represent ±SEM (n = 3)

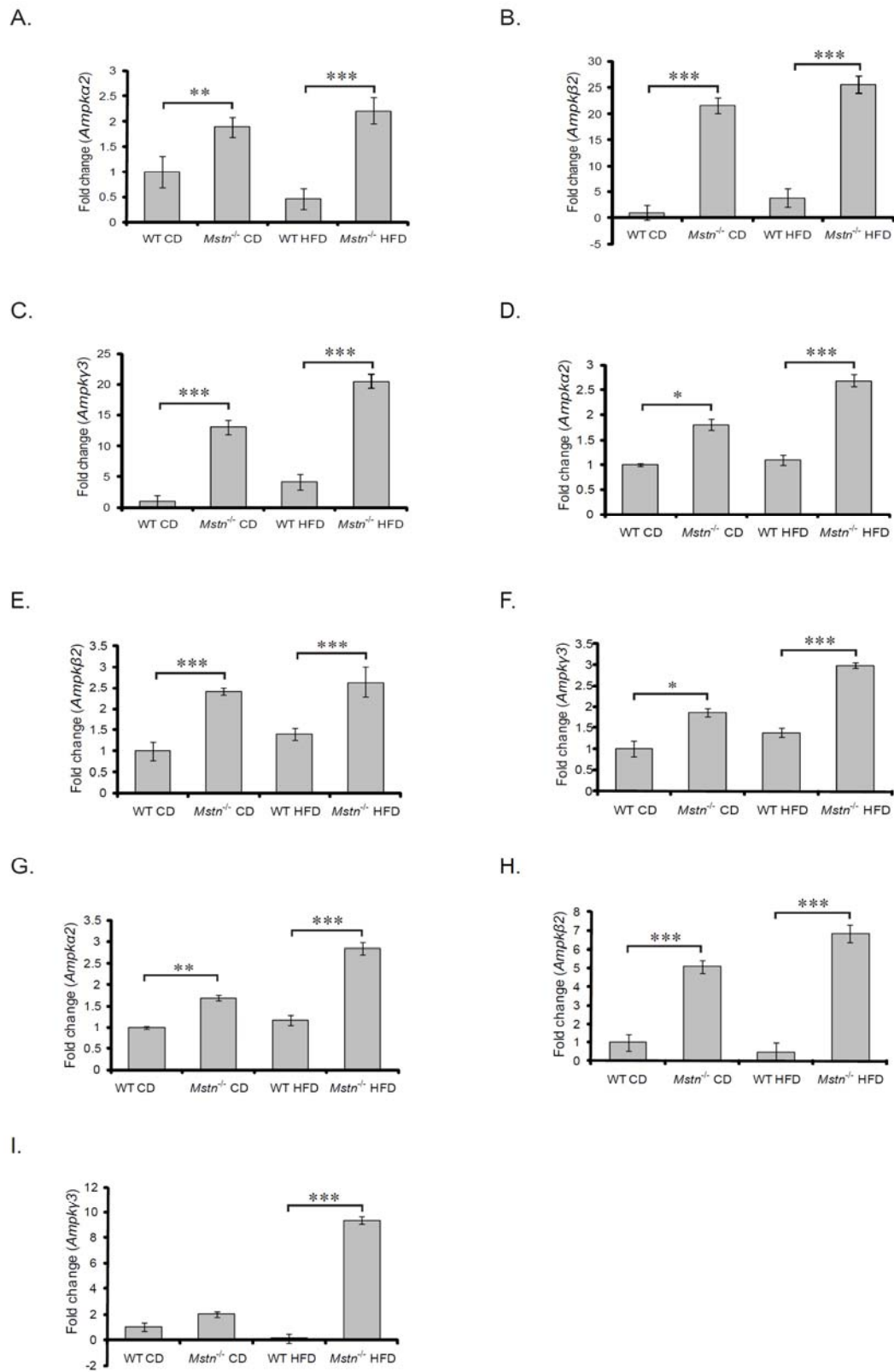
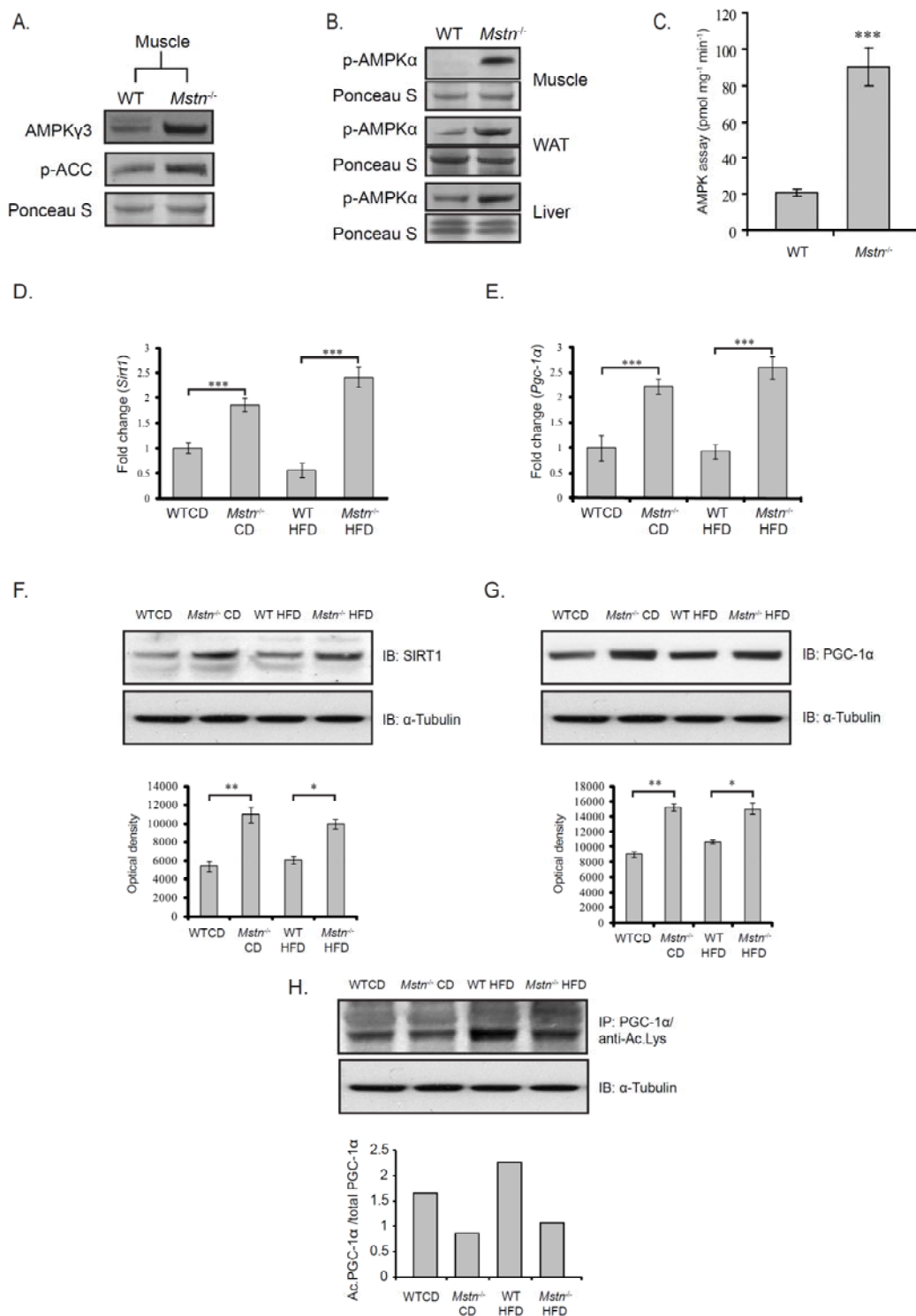


Figure 3.5 *Increased AMPK activity and augmented SIRT1 signalling is observed in $Mstn^{-/-}$ mice.*

(A) AMPK γ 3 and p-ACC protein level in muscle of WT and $Mstn^{-/-}$ mice as measured by Western blotting analysis. (B) p-AMPK α protein level in muscle, WAT and liver of WT and $Mstn^{-/-}$ mice as measured by Western blotting analysis. (C) AMPK activity in skeletal muscle as measured by AMPK assay. Relative mRNA expression levels of *Sirt1* (D) and *Pgc-1 α* (E) in muscle from WT and $Mstn^{-/-}$ mice fed on CD and HFD as measured by qPCR. Western blotting analysis of SIRT1 (F) PGC-1 α (G) and acetyl lysine (Ac.Lys) (H) protein level in muscle isolated from WT and $Mstn^{-/-}$ mice fed on CD or HFD. Graphs for SIRT1 and PGC-1 α represent densitometric analysis of each respective Western blotting analysis normalised to tubulin. The graph for Ac.Lys represents the level of acetylated PGC-1 α expressed as a proportion of total PGC-1 α . All samples were collected from M. gastrocnemius. *P < 0.05, **P < 0.01, ***P < 0.001. Error bars represent $\pm$ SEM ($n = 3$)



3.4 Discussion

The data presented here suggest a mechanism whereby Mstn negatively regulates the levels of AMPK in peripheral tissues, and thus influences insulin sensitivity (Figure 3.6). Increased abundance and activity of AMPK, as observed in *Mstn*^{-/-} mice, will lead to enhanced fatty acid oxidation and decreased lipid storage, which is consistent with both the reduced fat accumulation and reduced insulin resistance observed in *Mstn*^{-/-} mice. These findings reveal Mstn as a novel regulator of fat and glucose metabolism, and suggest that Mstn antagonists may be of benefit in treating obesity and insulin resistance.

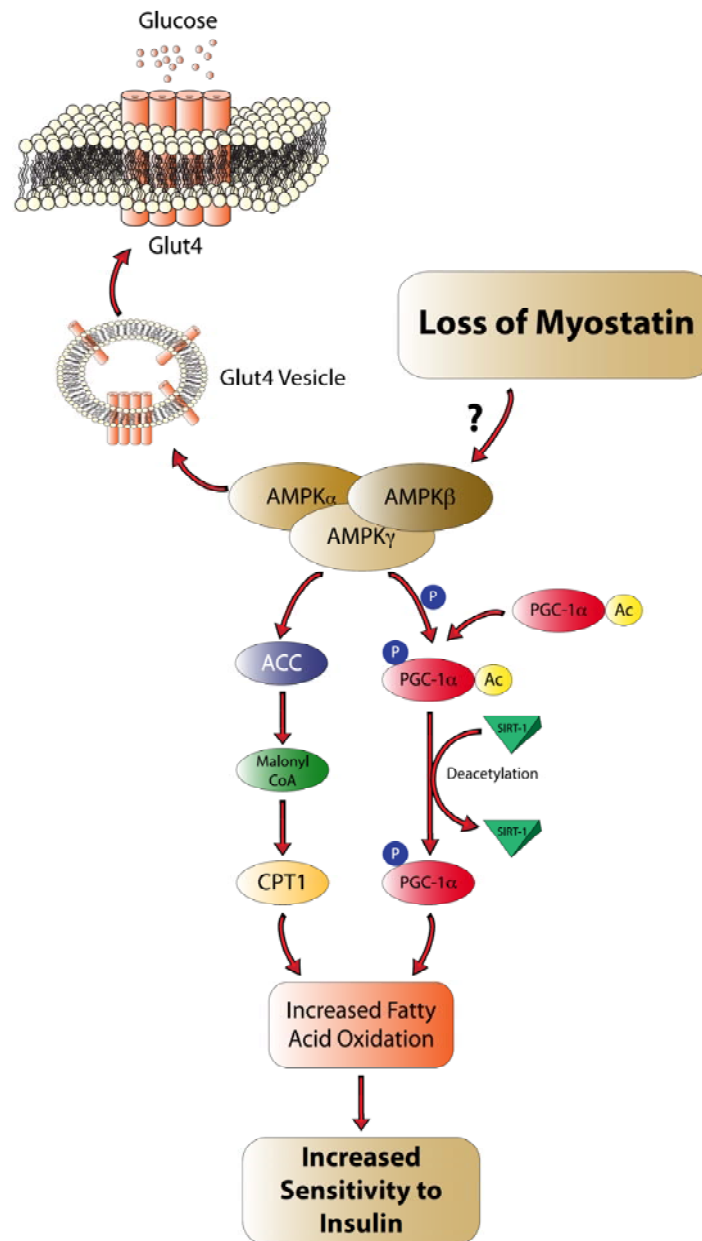


Figure 3.6 *Proposed mechanism.*

Loss of Mstn will lead to the activation of AMPK, resulting in the phosphorylation of ACC, leading to reduced malonyl-CoA and increased long chain fatty acyl CoA flux into mitochondria via carnitine palmitoyl transferase-1 (CPT-1) resulting in increased fatty acid oxidation. Activation of AMPK will also phosphorylate PGC-1α, which is further deacetylated by SIRT1, resulting in increased fatty acid oxidation. Activation of AMPK not only leads to increased fatty acid oxidation, it also promotes glucose uptake by accelerating GLUT4 trafficking to the membrane. Therefore, a combination of increased fatty acid oxidation and enhanced glucose uptake will result in enhanced insulin sensitivity in the absence of *Mstn*.

In contrast to WT mice, *Mstn*^{-/-} mice had reduced adipose tissue and failed to accumulate fat in adipose tissue even on an HFD (Figure 3.1F). Prolonged high caloric intake leads to metabolic overload and increased TAG levels, resulting in adipocyte hypertrophy and increased inflammatory response [23]. Macrophage accumulation in turn leads to secretion of pro-inflammatory cytokines such as TNF- α , resulting in further requirement of macrophages and insulin resistance [23]. It is noteworthy to mention that in *Mstn*^{-/-} mice there are reduced levels of circulating TNF- α during HFD feeding [171], raising the possibility that this may be partly responsible for the increased insulin sensitivity observed in the absence of *Mstn* during HFD feeding (Figure 3.1F).

Absence of *Mstn* results in increased *Ampk* mRNA expression in skeletal muscle, adipose tissue and liver (Figure 3.4). Furthermore, we observed increased protein levels of the AMPK γ subunit in skeletal muscle, and increased phosphorylation of the catalytic AMPK α subunit in skeletal muscle, WAT and liver from *Mstn*^{-/-} mice (Figure 3.5A&3.5B). Consistent with enhanced AMPK production we also observed enhanced activity of AMPK in skeletal muscle (Figure 3.5C). AMPK plays a critical role in energy metabolism. Increased AMPK activation leads to phosphorylation and thus inhibition of ACC enzyme activity (Figure 3.5A). Reduced ACC enzyme activity leads to reduced malonyl-CoA expression, which further limits fatty acid synthesis and increases fatty acid oxidation. In addition to ACC, it has recently been demonstrated that AMPK controls the expression of genes involved in energy metabolism by modulating another metabolic sensor, the NAD⁺-dependent type III deacetylase, SIRT1 [72]. AMPK enhances SIRT1 activity by increasing NAD⁺ levels resulting in deacetylation and further activation of SIRT1 targets including PGC-1 α , leading to increased expression of mitochondrial and lipid metabolism genes [72]. Thus, it is

quite possible that the acute actions of AMPK in lipid metabolism in *Mstn*^{-/-} mice could also be signalled via the decreased acetylation of PGC-1 α observed in *Mstn*^{-/-} mice (Figure 3.5H). However, there is an anomaly; as others and we have shown [136-137, 147], in *Mstn*^{-/-} mice there are a greater proportion of fast twitch glycolytic muscle fibres (type IIB). Therefore, one would expect muscles from *Mstn*^{-/-} mice to be more glycolytic rather than oxidative in nature, as is described here. Interestingly, although predominately fast glycolytic in nature, unpublished data from our lab suggests that there is increased mitochondrial biogenesis, due to fission, in *Mstn*^{-/-} fast twitch fibres from the EDL muscle (S. Lokireddy, C. McFarlane, M. Sharma and R. Kambadur, unpublished data). Furthermore, *Mstn*^{-/-} muscles on average have higher numbers of muscle fibres. Therefore, we speculate that a combination of increased number of mitochondria due to augmented biogenesis and increased muscle fibre number due to hyperplasia are the main driving forces behind the fast glycolytic fibres of *Mstn*^{-/-} muscles adopting a more oxidative nature, in at least as far as ATP generation is concerned. The benefits of increased fast glycolytic muscle fibre content to metabolic syndrome are clear. Specifically, Izumiya et al. have previously demonstrated that overexpression of a constitutively active form of AKT1 in muscle results in dramatic hypertrophy of type IIB fast glycolytic muscle fibres. Moreover, the increased type IIB muscle mass resulted in resistance to diet-induced obesity, improved sensitivity to insulin and enhanced hepatic fatty acid oxidation [168].

In addition to the reduced adiposity, *Mstn*^{-/-} mice and, for that matter, mice treated with sActRIIB, the Mstn antagonist, have improved tolerance to glucose and increased sensitivity to insulin (Figure 3.2). This increased sensitivity to insulin appears to be due to increased insulin signalling rather than increased insulin secretion, since gene expression and Western blotting analysis confirms that there are increased GLUT4

levels and increased phosphorylation of AKT (Figure 3.3). We propose that increased insulin signalling in *Mstn*^{-/-} mice is due to enhanced AMPK levels and activity. Acute activation of AMPK has been previously shown to result in increased insulin-mediated glucose uptake by increasing GLUT4 levels. Also, prior incubation of epitrochlearis muscles with the AMPK agonist 5-aminoimidazole-4-carboxamide ribonucleoside (AICAR) results in a two-fold increase in insulin stimulated glucose transport [67]. Furthermore, AICAR treatment of Zucker rats for 8 weeks improved insulin sensitivity [194]. Moreover, it has been recently shown that ablation of AMPK activity in skeletal muscle exacerbates insulin resistance induced by HFD feeding [188]. Therefore, these prior studies support the hypothesis that enhanced AMPK activity leads to increased insulin signalling in *Mstn*^{-/-} mice.

In contrast to our results, Chen *et al.* recently showed that Mstn treatment increases AMPK abundance in vitro [195]. The inconsistencies between our results and the observations made by Chen *et al.* could be due to the model system used. The addition of Mstn protein (Chen *et al.*) could result in a negative energy balance via Mstn-induced cachexia [186, 196], leading to a high AMP/ATP ratio resulting in AMPK activation. It is important to highlight that we have utilised an HFD model to study the regulation of glucose metabolism by Mstn and, much like previously published reports [166, 171], we find reduced insulin resistance and enhanced glucose uptake, which is consistent with the increase in AMPK activity shown in the present study.

As previously reported, *Mstn*^{-/-} mice are much larger than normal WT mice, which is due to a dramatic increase in skeletal muscle mass [118]. Thus, *Mstn*^{-/-} mice require more energy to maintain this phenotype. In addition, as shown in Chapter 4 of the current thesis, *Mstn*^{-/-} mice display increased thermogenesis with associated energy

uncoupling and increased body temperature when compared to WT mice. Therefore, as described in Chapter 4, the extra energy *Mstn*^{-/-} mice consume is being utilized through oxidation or dissipated as heat.

In summary, the results presented here demonstrate that lack of Mstn increases insulin signalling and enhances insulin sensitivity in skeletal muscle by increasing AMPK signalling. Furthermore, these results suggest that Mstn antagonists would have utility in resisting obesity and, moreover, in increasing insulin sensitivity during obesity (Figure 3.6).

3.5 Acknowledgements

We would like to thank the Agency for Science, Technology and Research (A*STAR) for funding this project. We would also like to thank J. Swain, Singapore Institute for Clinical Sciences, Singapore, for her comments on the manuscript and R. Choo, Singapore Institute for Clinical Sciences, Singapore, for his invaluable help with statistical analysis of the data presented in this manuscript.

3.6 Duality of interest

The authors declare that there is no duality of interest associated with this manuscript.

Chapter 4 Inhibition of myostatin protects against diet-induced obesity through enhancing fatty acid oxidation and promoting brown adipose phenotype

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ARTICLE

Inhibition of myostatin protects against diet-induced obesity by enhancing fatty acid oxidation and promoting a brown adipose phenotype in mice

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Abstract

Aims/hypothesis Although Myostatin-null (*Mstn*^{-/-}) mice fail to accumulate fat in adipose tissue when fed high-fat diet (HFD), little is presently known about the molecular mechanism(s) behind this phenomenon. Therefore the aim of the current study is to identify signaling pathways through which myostatin (Mstn) regulates accumulation/utilization of fat.

Methods Wild-type (WT), *Mstn*^{-/-} and WT mice treated with soluble Activin Type IIB Receptor (sActRIIB) were fed either control chow diet or HFD for 12 weeks. Gene expression changes were measured through Microarray and Quantitative PCR. Histological changes in white adipose tissue were assessed together with peripheral tissue fatty acid oxidation and changes in circulating hormones following HFD feeding.

Results Results presented here demonstrate that inactivation of Mstn, results in reduced fat accumulation in mice HFD. Molecular analysis revealed that metabolic benefits, due to lack of Mstn, are mediated through at least two independent mechanisms. Firstly, lack of Mstn increased fatty acid oxidation in peripheral tissues through induction of enzymes involved in lipolysis and fatty acid oxidation in mitochondria. Secondly, inactivation of Mstn also enhanced brown adipose formation in white adipose tissue of *Mstn*^{-/-} mice. Consistent with above results, treatment of mice on HFD with sActRIIB Mstn antagonist reduced the obesity phenotype.

Conclusions/interpretation We conclude that absence of Mstn results in enhanced peripheral tissue fatty acid oxidation and increased thermogenesis, culminating in increased fat utilization and reduced adipose tissue mass. Collectively our data suggests that anti-Mstn therapeutics would be of great benefit in alleviating obesity.

Keywords: Myostatin, PPAR β , Ucp1, COX-2, Brown Adipose Tissue (BAT), White Adipose Tissue (WAT), Prostaglandin, Fatty Acid Oxidation, sActRIIB.

Abbreviations: ACC, Acetyl-CoA carboxylase; ActRIIB, Activin Type IIB receptor; AMPK, AMP-activated protein kinase; *Atgl*, Adipose triglyceride lipase; BAT, Brown Adipose Tissue; *Cpt*, Carnitine palmitoyltransferase; *Cidea*, Cell death-inducing DFFA-like effector a; CD, Chow Diet; COX-2, Cyclooxygenase-2; *Dio2*, Deiodinase

iodothyronine typeII; EPI, Epididymal; *Fasn*, fatty acid synthase; GAS, M. *gastrocnemius*; HFD, High-fat diet; *Hsl*, Hormone sensitive lipase; INGUI, Inguinal; IACUC, Institutional Animal Care & Use Committee; *Lcad*, Long chain acyl-CoA dehydrogenase; *Lcas*, very long chain acyl-CoA synthetase; *Mgl*, Monoacylglycerol lipase; *Mstn*, Myostatin; *Mstn*^{-/-}, Myostatin-null; PGC-1 α , Peroxisome proliferator-activated receptor-gamma coactivator-1alpha; PPAR, Peroxisome Proliferator-Activated Receptor; PG, Prostaglandin; *Ptges*, Prostaglandin E synthase; qPCR, Quantitative real-time PCR; RETRO, Retroperitoneal; sActRIIB, Soluble Activin Type IIB Receptor; TAG, Triacylglycerol; Ucp1, Uncoupling protein 1; Ucp2, Uncoupling protein 2; Ucp3, Uncoupling protein 3; *Vlcad*, very long chain acyl-CoA Dehydrogenase; WAT, White Adipose Tissue; WT, Wild-type.

4.1 Introduction

Myostatin (Mstn) a secreted growth factor and member of the TGF- β super-family, has recently emerged as an important growth factor that not only regulates levels of lean muscle mass but also body fat content in mice. While high levels of Mstn expression are detected in skeletal muscle [118], low levels of Mstn are also detected in other tissues, including adipose tissue [118] and heart [129]. Inactivation of the *Mstn* gene [118] in mice, or mutations in the bovine [119-120], ovine [121] and human *Mstn* [122] gene result in a similar phenotype of increased muscle growth. In addition murine studies have reported significant decreases in the amount of adipose tissue in association with loss of Mstn function. For example, McPherron and Lee reported that myostatin-null (*Mstn*^{-/-}) mice, despite having a normal food intake, body temperature and a reduced metabolic rate, have significantly less mean total body fat and lower serum leptin levels when compared to wild-type (WT) mice fat-pad [165]. Furthermore, loss of Mstn in genetic models of obesity (agouti lethal yellow and *Leptin*-deficient mice [*Lep*^{ob/ob}]) suppressed body fat accumulation [165]. Similarly, Mstn Prodomain over expressing transgenic mice (in which Mstn function is blocked) also displayed significantly decreased fat-pad weight and moreover were resistant to high-fat diet (HFD)-induced obesity [167]. These results suggest that loss of functional Mstn, while increasing muscle mass, decreases body fat accumulation. However in contrast, Feldman *et al* reported that ectopic expression of Mstn, specifically in adipose tissue, induces adipose wasting [170]. Therefore the exact role of Mstn in regulating adipose tissue growth and functionality remains to be fully understood.

Increased peripheral tissue fatty acid oxidation can lead to increased energy expenditure to protect against obesity. Adipose tissue plays a critical function, in this regard, since white adipose tissue (WAT) acts as energy storing organ and brown adipose tissue (BAT) acts as an energy consuming organ. White adipocytes are characterized by a large unilocular lipid droplet, whereas brown adipocytes contain multiple relatively small lipid droplets, giving it the characteristic multilocular appearance. Brown adipocytes also contain large numbers of mitochondria with densely packed regularly arranged cristae [9], a characteristic of high mitochondrial activity. BAT is an important regulator of thermogenesis, in fact BAT expresses high levels of Uncoupling protein 1 (Ucp1), which functions to uncouple oxidative phosphorylation, resulting in release of excess energy as heat to maintain normal body temperature. Furthermore, genes including Dio2, Cidea, PGC-1 α , as well as members of the peroxisome proliferator-activated receptor (PPAR) family, are also highly enriched in BAT. Interestingly, differentiated WAT has been shown to acquire BAT-like properties, in particular, exposure to cold or stimulation with a β 3-adrenergic agonist can induce the emergence of multilocular, Ucp1 expressing, brown adipocyte depots in WAT [14-16].

Here, we have identified molecular mechanisms which promote leanness in the absence of Mstn. We show that lack of Mstn promotes increased fatty acid oxidation in peripheral tissues as well as increased proportion of Brown-like adipose tissue in WAT. As a result, we show that *Mstn*^{-/-} mice are resistant to obesity even when challenged with HFD. We further show that treatment of mice with a Mstn antagonist, sActRIIB, can also protect mice from diet-induced obesity. These data suggest that novel therapeutics, which increase body energy expenditure, are viable as anti-obesity drugs.

4.2 Methods

4.2.1 Animals.

Animal experiments were conducted under approval from the Institutional Animal Care & Use Committee (IACUC), Singapore. WT mice (C57BL/6 background) were supplied by the Centre for Animal Resources, Singapore (National University of Singapore, Singapore). *Mstn*^{-/-} mice (C57BL/6 background) were gifted by Prof. Se-Jin Lee (Johns Hopkins University, Baltimore, MD). *Mstn*^{-/-} and WT mice were derived from different litters and were housed in groups at a constant temperature (20°C) under a 12h/12h artificial light/dark cycle with *ad libitum* access to water. Two groups of seven-week-old male mice, containing 5xWT and 5x*Mstn*^{-/-} mice each, were either fed HFD (45% energy from fat; 58V8, TestDiet, Richmond, IN, USA) or CD (10% energy from fat; 58Y2, TestDiet) for 12 weeks. Please see Table 3.1 for details of diet compositions (Table 3.1). For sActRIIB antagonist studies, seven-week-old male WT mice were fed CD or HFD (see above) for a period of 12weeks together with intraperitoneal injection of either saline or sActRIIB (5µg/g body weight) 3 times-a-week. Generation and purification of the sActRIIB has been previously described in detail [73]. Body weight and energy intake (energy intake = food consumption x metabolizable energy content) were recorded twice a week in all mice. Rectal temperatures of WT and *Mstn*^{-/-} mice were measured using a rectal thermometer (Thermocouple, Kent Scientific, Torrington, CT, USA). All measurements and analysis were performed on Epididymal WAT (gonadal) and M. *gastrocnemius* (GAS) skeletal muscle unless otherwise stated.

4.2.2 RNA extraction and quantitative real-time PCR (qPCR).

RNA extraction and qPCR were performed as previously described [73] (see section 2.2.3, 2.2.5, 2.2.6 and 2.2.8 for details). RNA was extracted from *M. gastrocnemius* (GAS) muscle, Epididymal fat pad (gonadal) and liver using TRIzol reagent (Invitrogen, Carlsbad, CA, USA) according to the manufacturer's protocol. Synthesis of cDNA was performed using the Superscript II First strand synthesis system (Invitrogen) from 1 µg of total RNA. qPCR was conducted in triplicate using Sso Fast Evagreen and the Bio-Rad CFX96 real-time PCR machine (Bio-Rad, Hercules, CA, USA). The following PCR primers were used for qPCR: *Cpt1 α*, 5'- CTC AGT GGG AGC GAC TCT TCA-3' and 5'- GGC CTC TGT GGT ACA CGA CAA-3'; *Cpt2*, 5'- CAG TGC ACA GAA GCC TCT CTT G-3' and 5'- CTT CCC AAT GCC GTT CTC AA-3'; *Lcad*, 5'- TCT TGC GAT CAG CTC TTT CA-3' and 5'- GGT ACA TGT GGG AGT ACC CG-3'; *Vlcad*, 5'- TCC AGA GGT CAG TCA ACA TGA-3' and 5'- CCT GGT CAA TTT TTC GAG AGT CC-3'; *Lcas*, 5'- TCC GAG ACA GGA CGA TGT G -3' and 5'- AGA CTG GAT CAC TCT CTC AAA CA-3'; *Pgc-1α*, 5'-AAG TGT GGA ACT CTC TGG AAC TG-3' and 5'-GGG TTA TCT TGG TTG GCT TTA TG-3'; *Atgl*, 5'- CTC ATT CGC TGG CTG CGG CT -3' and 5'- CCT GCC GAG GCC CCG TAG AT -3'; *Hsl*, 5'- GCT TGG GGA GCT CCA GTC GGA -3' and 5'- CTC CTG GGC CCT GGC TTG AGA -3'; *Mgl*, 5'- GGG GAT AAA GTG GCG GCG CA-3' and 5'- CTG TCA CGT TCC CCG AGC ACC-3' ; *Fasn*, 5'- CCT CAC GGC GGC AGC AAG AA -3' and 5'- CTG CAG AGC CCG TGC CAG AC -3'; *Acc1*, 5'- CTG AAG GCA GCT GAG GAA GTT GGC-3' and 5'- TCC AGG AAC TTC AGC TTG AAC CTG TCT-3'; *Ucp1*, 5'- AAA CAA GAT TCA TCA ACT CTC TG -3' and 5'- GTC CTT CCT TGG TGT ACA TG -3'; *Ucp2*, 5'- CCG GGG CCT CTG GAA AG -3' and 5'- CCC AAG CGG AGA AAG GA -3'; *Ucp3*, 5'- CGA ATT

GGC CTC TAC GA -3' and 5'- TGT AGG CAT CCA TAG TCC C -3'; *Ptgs2/Cox-2*, 5'- GAC AGT CCA CCT ACT TAC AA -3' and 5'- CTA TGA GTA TGA GTC TGC TG -3'; *Ptges*, 5'- CAG AGC CCA CCG CAA CGA CA-3' and 5'- CCA CGG TGT GTA CCA CAC GGC-3'; *Ppara*, 5'- GCA GCT CGT ACA GGT CAT CA -3' and 5'- CTC TTC ATC CCC AAG CGT AG -3'; *Pparb*, 5'- CGG AGC ATG CGC AGC TCG TAC A -3' and 5'- CCG GTC TCC ACA CAG AAT GAT -3'; *Pparg*, 5'- CAT TCT GGC CCA CCA ACT TC -3' and 5'- TCA AAG GAA TGC GAG TGG TCT T -3'; *Gapdh*, 5'-AAC TTT GGC ATT GTG GAA GG-3' and 5'-ACA CAT TGG GGG TAG GAA CA-3'.

4.2.3 Measurement of triacylglycerol (TAG) in WAT.

Lipid was extracted from peripheral tissues using a modified version of the Folch extraction method, as previously described [177-178] (see section 2.2.17 for details). Frozen WAT (Epididymal) was weighed (~400mg) and homogenized in methanol, followed by addition of chloroform (1:2 v/v). Following an overnight incubation at 4°C, 12µl of 1M MgCl₂ was added and the tube was centrifuged at 1000xg for 1h at 4°C. The upper (aqueous) phase was discarded and the infranatant phase was collected into a fresh tube and evaporated to dryness at 70°C. The TAG residue was saponified with ethanol/KOH at 75°C for 20min. The process was then terminated by adding 10% HCl, cooled down to 0°C and then slowly neutralized with saturated NaHCO₃. The levels of Glycerol, which reflect the total TAG content in the WAT, was analyzed using the Free glycerol determination kit (Sigma-Aldrich, St. Louis, MO, USA). The leftover tissue “cake” which formed at the interface between the two phases was dried and dissolved in 1ml of 1M NaOH for determination of protein concentration using Bradford assay.

4.2.4 Measurement of serum NEFA, leptin and blood TAG.

See section 2.2.11, 2.2.14, 2.2.15 and 2.2.18 for details. Total blood triglyceride (TAG) levels were analyzed using the Accutrend[®] Plus meter (Roche Diagnostics, Indianapolis, IN, USA), serum non-esterified fatty acid (NEFA) was measured using the NEFA-C kit (Wako, Chuo-Ku, Osaka, Japan) and serum leptin levels were determined using the Mouse leptin ELISA kit (Millipore, Billerica, MA, USA), as per the manufacturer's instructions.

4.2.5 H&E staining of WAT.

Epididymal fat-pad was fixed with 10% formalin for 48h then dehydrated in an automated tissue processor (TP1020, Leica Wetzlar, Germany). The fat-pads were paraffin embedded, sectioned using a rotary microtome (RM2265, Leica) and subsequently stained with haematoxylin and eosin as previously described [166] (See section 2.2.19, 2.2.20 and 2.2.21 for details).

4.2.6 Immunohistochemical staining.

Immunohistochemical staining of fat-pad sections was performed using the VECTASTAIN[®] Elite ABC kit (Vector laboratories, Burlingame, CA, USA) according to the manufacturer's instructions with modification (see 2.2.22 for details). Briefly, fat-pad sections were deparaffinized, hydrated and subjected to antigen retrieval for 10min at 100°C in Tris-EDTA buffer (10mM Tris, 1mM EDTA, pH9). After cooling, the sections were blocked for 20min in blocking serum (Rabbit)

followed by incubation with 1:100 dilution of either goat anti-Ucp1 (sc-6528; Biotechnology, Santa Cruz, CA, USA) or goat anti-COX-2 (sc-1745; Santa Cruz Biotechnology) specific primary antibody for 30min at RT. The sections were then incubated with (1:200) diluted anti-goat biotinylated secondary antibody for 30min at RT, followed by incubation with VECTASTAIN® Elite ABC reagent for 30min at RT. Ucp1 and COX-2 immunostaining was visualized using peroxidase substrate solution (DAB; Vector laboratories), prior to counterstaining with hematoxylin and mounting with DPX.

4.2.7 Assessment of fatty acid oxidation in tissues and myotube cultures.

Fatty acid oxidation in liver, WAT [197] and myotube cultures [198] was analyzed as previously described (see 2.1.3.7, 2.1.3.8, 2.2.23 and 2.2.25 for details).

[1-¹⁴C] Palmitic acid was combined with non-radio-labeled Palmitic acid reaction mixture and incubated on a thermo mixer (Eppendorf, Hamburg, Germany) at 60°C for 2h. Liver or WAT (Epididymal) were rinsed in cold STE buffer, homogenized using a Dounce homogenizer then centrifuged at 420xg for 10min at 4°C. A portion (20µl) of the supernatant containing mitochondria was then added to 380ul of the [1-¹⁴C] Palmitic acid reaction mixture, after prior addition of ATP and DTT, to start the reaction. Following incubation at 37°C for 60min, the reaction mixture was added to 200µl of 1M perchloric acid together with a filter paper disc containing 20µl of concentrated hyamine hydroxide placed in the tube cap. After further incubation for 1h the filter paper discs were removed and counted using a liquid scintillation counter (1450 LSC & Luminescence counter; PerkinElmer Life Sciences, Waltham, MA, USA).

Incubation medium was made of DPBS supplemented with 20mM HEPES and 1μM L-Carnitine, adjusted to pH7.3, and added to 100 μM (37000Bq/ml) [U-¹⁴C] Palmitic acid. 72hr differentiated primary myotubes were grown on a 96-well plate supplemented with 50μl/well incubation medium. A 96-well filter plate was activated for capturing of CO₂ by the addition of freshly made 1M NaOH (25μl/well). The plate harboring the cells was clamped together with the filter plate, forming a “sandwich”, with the following bottom-to-top order: cell plate/gasket/inversed filter plate. The plate sandwich was placed in an incubator at 37°C, and fatty acid oxidation was allowed to proceed for 4h. CO₂ produced from cellular respiration during incubation was continuously trapped on the filter plate. After incubation, the amount of ¹⁴CO₂ captured on the filter plate was assessed using a scintillation counter (PerkinElmer Life Sciences).

4.2.8 Measurement of prostaglandin released from WAT explants.

Assessment of the levels of prostaglandins released from WAT explants was performed as previously described [16] (see 2.2.24 for details). WAT explants were incubated in medium (15mM HEPES, 0.5% BSA, 1% Penicillin/Streptomycin) at 37°C/5% CO₂ for 8h. Following centrifugation at 5000rpm for 5min at 4°C, supernatants were collected, snap-frozen and stored in -80°C. The levels of Prostaglandin E2 and 6-keto-prostaglandin F1α were measured using the Prostaglandin E2 express kit-Monoclonal and 6-keto-prostaglandin F1α EIA kits respectively (Cayman Chemical, Ann Arbor, Michigan, USA) according to the manufacturer’s protocol.

4.2.9 Microarray Analysis.

Microarray analysis was performed in duplicate from WAT tissue isolated from WT and *Mstn*^{-/-} mice. Gene expression changes identified by microarray were subsequently verified by qPCR in six different samples per group. RNA from WAT was isolated using TRIzol (Invitrogen, Carlsbad, CA, USA) according to the manufacturer's guidelines. RNA integrity was verified using the Agilent RNA 6000 Nano Kit and 2100 Bioanalyzer (Agilent, Santa Clara, CA, USA). Microarray analysis was performed by Genomax Technologies, Singapore, as per their standardized techniques, using the Agilent SurePrint G3 Mouse Gene Expression array. Normalized data were used for pair-wise comparisons between WT and *Mstn*^{-/-} mice fed on CD. The resulting gene list from the pair-wise comparison included the genes that showed a P value ≤ 0.05 by using a standard two-tailed unequal variance t-test. All statistical analysis on the microarray data was done using GenSpring software (v.11.0.2). Significantly up-regulated genes (≥ 1.5 -fold), were subsequently verified via qPCR.

4.2.10 Statistical analysis.

Multiple comparisons were made using two-way ANOVA and robust regression analysis. Single comparisons were made using two-tail Student's-t-tests. Data are expressed as mean $\pm$ SEM and P values < 0.05 were considered significant. Experimental replicates are described in relevant figure legends.

4.3 Results

4.3.1 *Mstn*^{-/-} mice exhibit reduced adiposity even when fed HFD.

Recently we [73] and others [166, 199] have shown that chronic HFD feeding of *Mstn*^{-/-} mice resulted in significantly less accumulation of visceral adipose tissue mass and improved resistance to diet-induced obesity when compared to WT mice fed HFD. To study this in further detail we fed WT and *Mstn*^{-/-} mice with either HFD or CD for a total period of 12weeks. While no significant difference was observed in the energy intake between WT mice fed either HFD or CD, it was noted that *Mstn*^{-/-} mice fed HFD had increased energy intake over and above that of CD fed *Mstn*^{-/-} mice (Figure 4.1A). As expected, WT mice fed HFD showed a greater increase (~40%) in body weight when compared to WT mice fed CD (~23%) after 12weeks of HFD feeding (Figure 4.1B). In contrast, no significant difference in body weight was observed between *Mstn*^{-/-} mice fed CD or HFD, despite the increased energy intake observed in *Mstn*^{-/-} mice fed HFD (Figure 4.1B). Subsequent quantification of adipocyte area revealed that adipocytes from *Mstn*^{-/-} mice were smaller (< 350 μm^2), when compared to adipocytes in WT mice WAT, where the majority ranged from 350 μm^2 -700 μm^2 or were greater than 700 μm^2 (Figure 4.1D). Furthermore, HFD feeding caused significant hypertrophy of adipocytes in WT mice, while insignificant hypertrophy was observed in *Mstn*^{-/-} adipocytes (Figure 4.1D). Consistent with reduced adipose content, we found significantly lower TAG accumulation in *Mstn*^{-/-} WAT when compared to WT WAT (Figure 4.1E). Furthermore we also observed reduced serum leptin levels in *Mstn*^{-/-} when compared to WT mice (Figure 4.1F). These data suggest

that there is reduced fat accumulation in WAT in *Mstn*^{-/-} mice, which we hypothesized, could result from either reduced TAG synthesis or enhanced fatty acid oxidation.

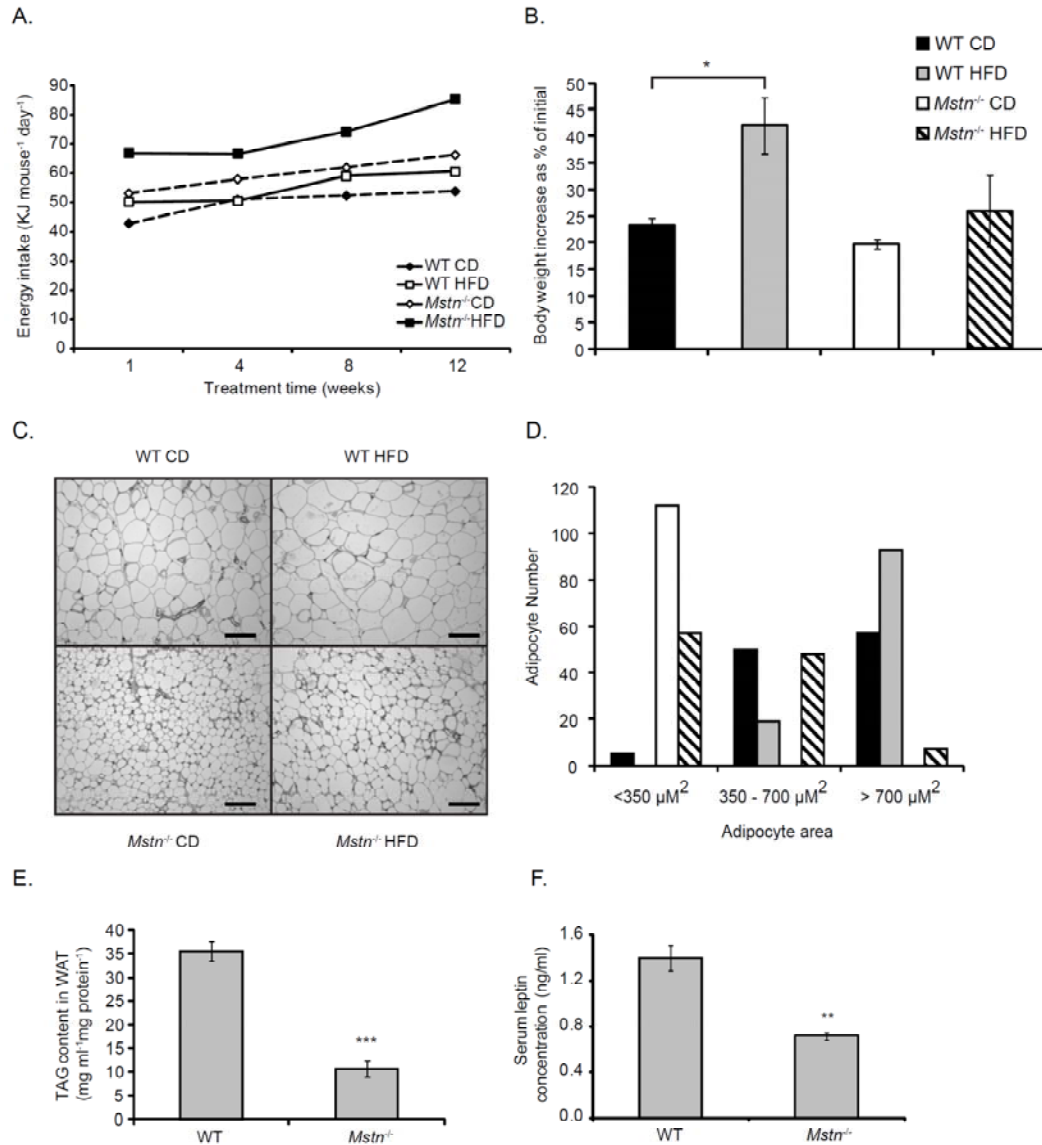


Figure 4.1 Absence of *Mstn* results in a lean phenotype in mice.

(A) Energy intake (kJ mouse⁻¹ day⁻¹) of WT and *Mstn*^{-/-} mice during 12 weeks of CD and HFD treatment. (B) Body weight increase (expressed as a percentage of initial body weight) observed in WT and *Mstn*^{-/-} mice after 12 weeks of CD and HFD treatment. (C) H&E staining and (D) Quantification of Adipocyte size from WAT of WT and *Mstn*^{-/-} mice after 12 weeks of CD and HFD treatment. (E) Total TAG content in WAT (Epididymal) isolated from WT and *Mstn*^{-/-} mice, normalized to protein content. (F) Total serum leptin levels in WT and *Mstn*^{-/-} mice. *P < 0.05, **P < 0.01, ***P < 0.001. Error bars represent ±SEM (n = 5). Scale bar: 100 μm. Magnification: 10X.

4.3.2 Lack of Mstn increases lipolysis and peripheral tissue fatty acid β -oxidation.

Microarray analysis revealed elevated expression of enzymes involved in fatty acid synthesis, including fatty acid synthase (*Fasn*) and acetyl-CoA carboxylase 1 (*Acaca/Acc1*), in WAT tissue isolated from *Mstn*^{-/-} mice, when compared to WT mice WAT (Table 4.1). Subsequent qPCR analysis confirmed up regulation of both *Fasn* and *Acaca* expression in *Mstn*^{-/-} WAT (Figure 4.2A and 4.2B). Several fold up regulation of genes that code for proteins involved in thermogenesis (*Ucp1*, *Ucp2*, *Cidea*, *Cpt1b*, *Dio2*), BAT differentiation (*Cebpb*) and prostaglandin synthesis (*Ptgs2*, *Ptges* and *Ptges2*) (Table 4.1) was also seen in *Mstn*^{-/-} WAT. Furthermore, qPCR analysis revealed that genes encoding for the lipolytic enzymes ATGL, HSL and MGL, critical for catalysing hydrolysis of triacylglycerol, diacylglycerol and monoacylglycerol respectively, were up-regulated in WAT isolated from *Mstn*^{-/-} mice (Figure 4.2C-4.2E). Importantly, the expression of genes involved in fatty acid oxidation (*Ppara*, *Pparg*, *Ppargc1a*, *Ppargc1b*, *Acadvl*, *Acadm*, *Hadha*, *Acadl*, *Hadh*, *Hadhb*, *Acs1l* and *Acs3*) was also enhanced in *Mstn*^{-/-} WAT (Table 4.1). Moreover, qPCR analysis confirmed significant up regulation of Long chain acyl-CoA dehydrogenase (*Lcad*), very long chain acyl-CoA synthetase (*Lcas*) and very long chain acyl-CoA Dehydrogenase (*Vlcad*) in WAT (Figure 4.3A-4.3C), BAT (Figure 4.3D-4.3F) and skeletal muscle (Figure 4.4A-4.4C) from CD fed *Mstn*^{-/-} mice, when compared to WT mice fed CD. Importantly, while increased expression of *Vlcad*, *Lcad* and *Lcas* was maintained in WAT, BAT and skeletal muscle of *Mstn*^{-/-} mice fed HFD, no significant increase occurred in WAT (Figure 4.3A-4.3C), BAT (Figure 4.3D-4.3F) or skeletal muscle (Figure 4.4A-4.4C) tissue from HFD fed WT mice. Consistent with increased fatty acid oxidation enzyme expression (Figure 4.3), we also

observed a large increase in fatty acid oxidation in WAT, liver (Figure 4.3G) and primary myotubes cultures from *Mstn*^{-/-} mice (Figure 4.4F). Furthermore, and consistent with enhanced fatty acid oxidation, we also found significant reduction in NEFA (Figure 4.3H) in *Mstn*^{-/-} mice, as compared to WT controls.

4.3.3 Increased expression of genes involved with mitochondrial activity in peripheral tissues of *Mstn*^{-/-} mice.

Microarray analysis revealed increased expression of genes encoding for mitochondrial cytochrome c oxidase enzyme subunits Vb (*Cox5b*), VIIa1 (*Cox7a1*) and VIIIb (*Cox8b*) (Table 4.1). Furthermore, qPCR analysis identified a ~6-fold and ~10-fold induction in *Cpt1α* and *Cpt2* expression respectively, in WAT from *Mstn*^{-/-} mice fed regular CD when compared to CD fed WT controls (Figure 4.2F and 4.2G). Importantly, HFD feeding resulted in further up regulation of both *Cpt1* and *Cpt2* expression in WAT from *Mstn*^{-/-} mice, however, no such increase was seen in WAT from WT mice fed HFD. A modest, yet significant, increase in *Cpt1α* and *Cpt2* (Figure 4.4D and 4.4E) expression was also observed in skeletal muscle tissue from CD and HFD fed *Mstn*^{-/-} mice, when compared respective WT controls. Taken together, these data suggest that mitochondrial activity is increased in *Mstn*^{-/-} WAT, which we propose may be one mechanism through which lack of Mstn improves lipid metabolism.

Table 4.1 *Global gene expression changes between WAT from WT and $Mstn^{-/-}$ mice fed on CD*

WAT (Epididymal fat pad) was extracted from WT and $Mstn^{-/-}$ mice fed on CD. Genes were separated based on Fatty acid oxidation, Mitochondrial activity, Fatty acid synthesis, Thermogenesis, Prostaglandin synthesis and BAT differentiation function and were at least 1.5-fold up-regulated.

Function	Gene Symbol	Gene Name	Accession No.	Fold up-regulation
Fatty Acid Oxidation	<i>Ppara</i> / <i>Ppara</i>	peroxisome proliferator activated receptor alpha	NM_011144	2.1
	<i>Pparg</i> / <i>Pparg</i>	peroxisome proliferator activated receptor gamma	NM_011146	2.0
	<i>Pparg1a</i> / <i>Pgc-1α</i>	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	NM_008904	2.2
	<i>Ppargc1b</i>	peroxisome proliferative activated receptor, gamma, coactivator 1 beta	NM_133249	4.0
	<i>Acadl</i> / <i>Vlcad</i>	acyl-Coenzyme A dehydrogenase, very long chain	NM_017366	1.7
	<i>Acadm</i>	acyl-Coenzyme A dehydrogenase, medium chain	NM_007382	1.8
	<i>Hadha</i>	hydroxyacyl-Coenzyme A dehydrogenase, alpha subunit	NM_178878	1.9
	<i>Acadl</i> / <i>Lcad</i>	acyl-Coenzyme A dehydrogenase, long-chain	NM_007381	1.8
	<i>Hadh</i>	hydroxyacyl-Coenzyme A dehydrogenase	NM_008212	2.0
	<i>Hadhb</i>	hydroxyacyl-Coenzyme A dehydrogenase, beta subunit	NM_145558	1.7
Mitochondrial Activity	<i>Acs1l</i>	acyl-CoA synthetase long-chain family member 1	NM_007981	1.8
	<i>Acsm3</i>	acyl-CoA synthetase medium-chain family member 3, transcript variant 2	NM_21441	1.9
	<i>Cox5b</i>	cytochrome c oxidase, subunit Vb	NM_009942	2.2
	<i>Cox7a1</i>	cytochrome c oxidase, subunit VIIa 1	NM_009944	2.6
	<i>Cox8b</i>	cytochrome c oxidase, subunit VIIIb	NM_007751	7.2
Fatty Acid Synthesis	<i>Fasn</i>	fatty acid synthase	NM_007988	3.2
	<i>Acaca</i> / <i>Acc1</i>	acetyl-Coenzyme A carboxylase alpha	NM_13336	1.9
Thermogenesis	<i>Ucp1</i>	Uncoupling protein 1	NM_009463	628.8
	<i>Cidea</i>	Cell death-inducing DNA fragmentation factor, alpha subunit-like effector A	NM_007702	18.1
	<i>Cpt1b</i>	Carnitine palmitoyltransferase 1b	NM_009948	4.7
	<i>Ucp2</i>	Uncoupling protein 2	NM_011671	1.7
	<i>Dio2</i>	deiodinase, iodothyronine, type II	NM_010050	3.7
Prostaglandin Synthesis	<i>Pigs2</i> / <i>Cox-2</i>	prostaglandin-endoperoxide synthase 2/Cyclooxygenase-2	NM_011198	4.4
	<i>Piges</i>	prostaglandin E synthase	NM_022415	1.6
	<i>Piges2</i>	prostaglandin E synthase 2	NM_133783	1.7
BAT Differentiation	<i>Cebpb</i>	CCAAT/enhancer binding protein, beta	NM_009883	2.0

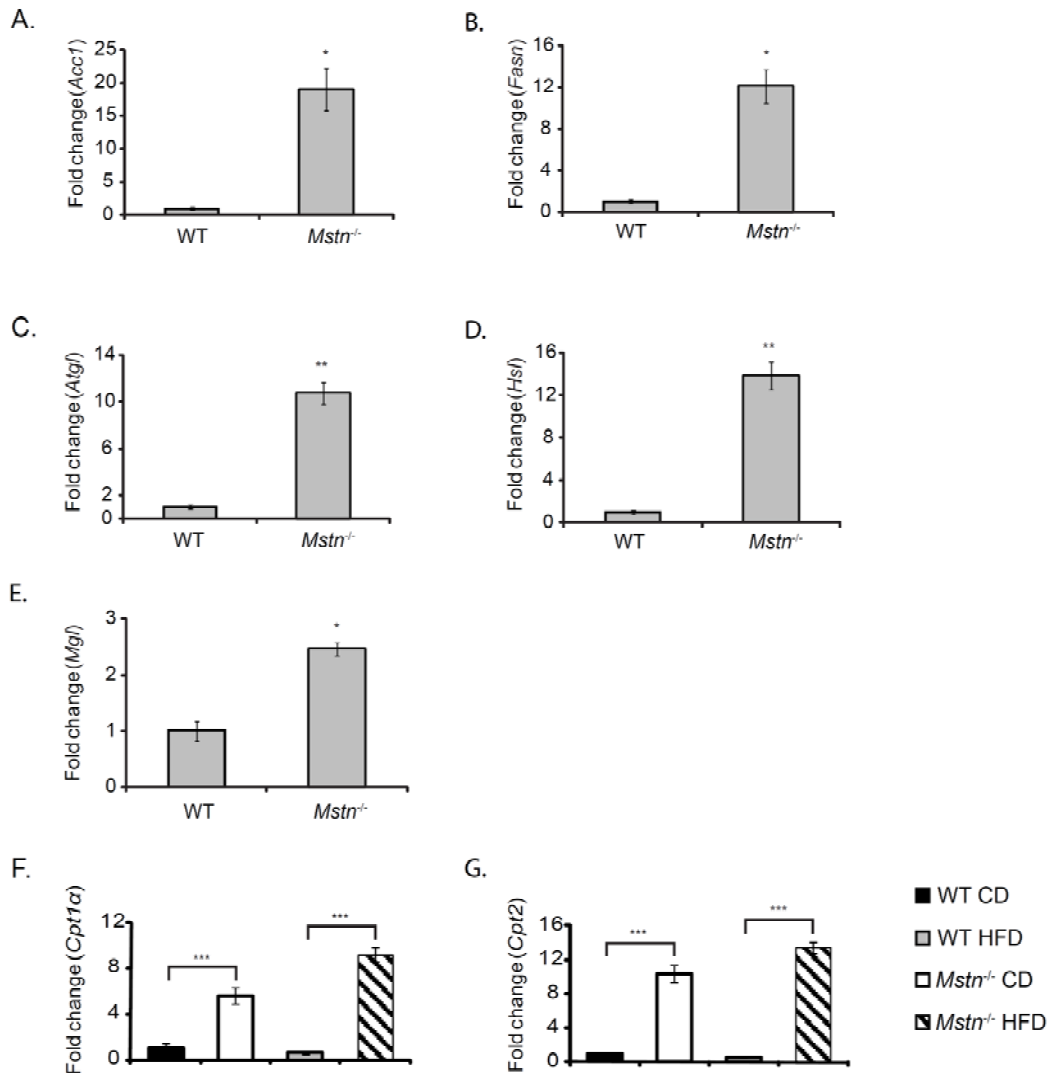


Figure 4.2 Increased expression of genes involved in lipolysis, lipid synthesis and mitochondrial activity in *Mstn*^{-/-} mice.

(A-G) Relative mRNA expression levels of *Acc1*, *Fasn*, *Atgl*, *Hsl*, *Mgl*, *Cpt1 α* , *Cpt2* normalized to GAPDH mRNA expression in WAT (Epididymal) as measured by qPCR in WT and *Mstn*^{-/-} mice after 12 weeks of CD and HFD treatment. *P < 0.05, **P < 0.01, ***P < 0.001. Error bars represent $\pm$ SEM (n = 3).

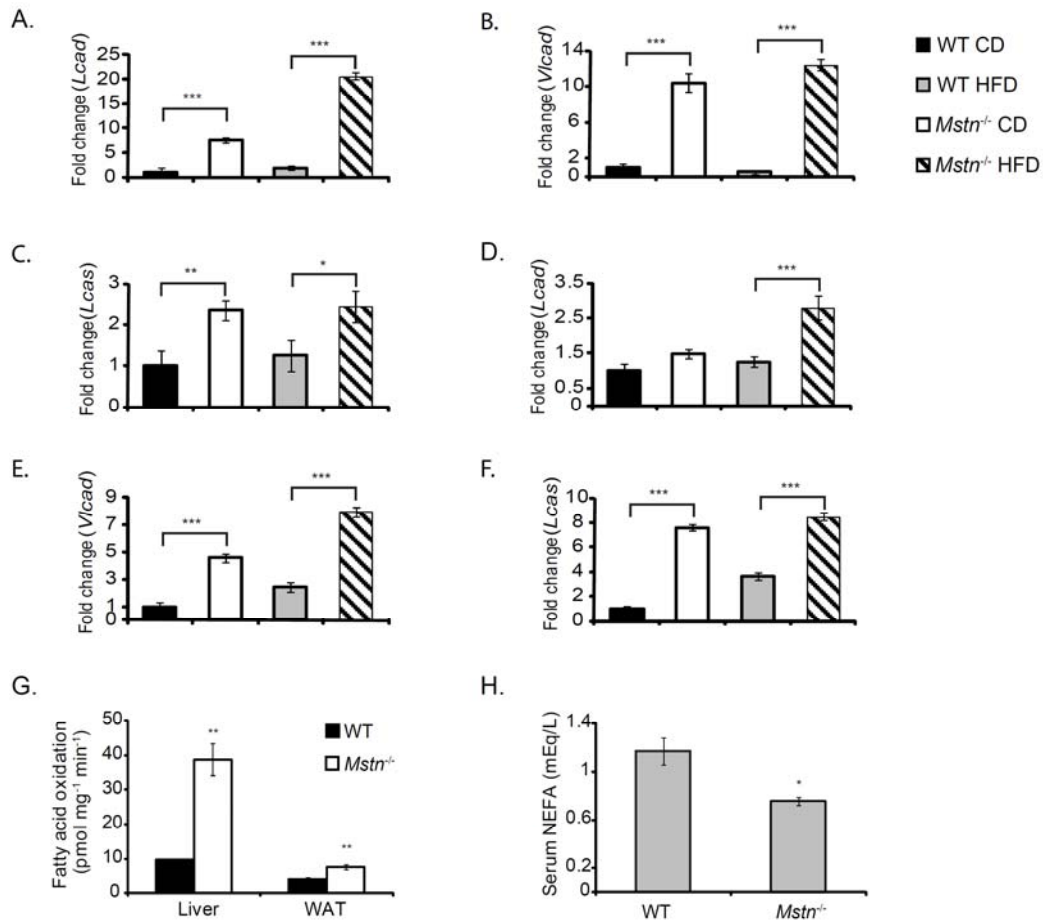


Figure 4.3 Lack of *Mstn* leads to increased Fatty acid oxidation in WAT and Liver.

(A-C) Relative mRNA expression levels of *Lcad*, *Vlcaad*, *Lcas* in WAT (Epididymal fat-pad) and *Lcad*, *Vlcaad*, *Lcas* in BAT (D-F) normalized to GAPDH mRNA expression as measured by qPCR in WT and *Mstn*^{-/-} mice after 12 weeks of CD and HFD treatment. (G) Fatty acid oxidation in liver and WAT (Epididymal) in WT and *Mstn*^{-/-} mice, normalized to protein content. Serum NEFA (H) in WT and *Mstn*^{-/-} mice. *P < 0.05, **P < 0.01, ***P < 0.001. Error bars represent $\pm$ SEM (n = 3).

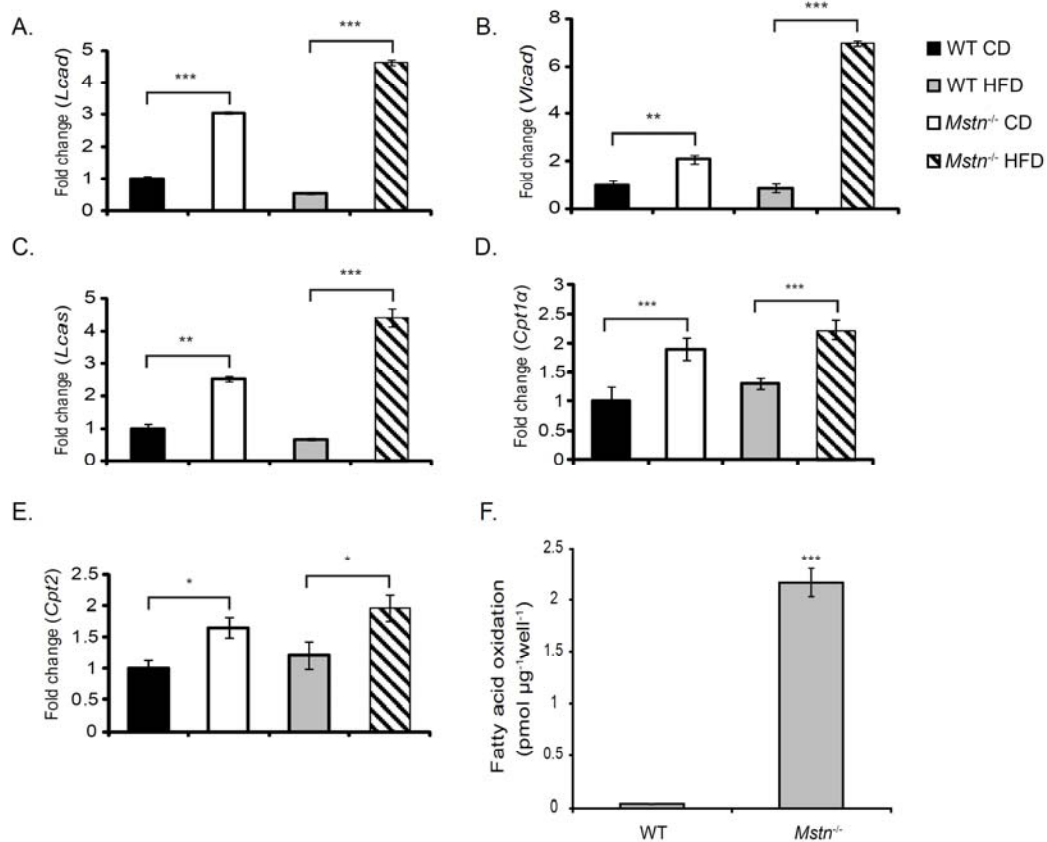


Figure 4.4 Lack of *Mstn* leads to increased Fatty acid oxidation in skeletal muscle.

(A-E) Relative mRNA expression of *Lcad*, *Vlcad*, *Lcas*, *Cpt1a*, *Cpt2* in muscle (GAS) as measured by qPCR in WT and *Mstn*^{-/-} mice after 12 weeks of CD and HFD treatment. (F) Fatty acid oxidation in 72 hr differentiated myotube cultures derived from WT and *Mstn*^{-/-} mice, normalized to total protein content per well. **P* < 0.05, ***P* < 0.01, ****P* < 0.001. Error bars represent $\pm$ SEM (*n* = 3).

4.3.4 Up-regulation of crucial transcriptional factors and BAT-specific proteins in *Mstn*^{-/-} WAT.

BAT is primarily responsible for burning lipids, which via uncoupling proteins (such as Ucp1), results in dissipation of excess energy as heat [200]. Consistent with this, we find significantly elevated (by ~1°C) body temperature in *Mstn*^{-/-} mice when compared to WT mice (Figure 4.5A). Since we observed elevated body temperature, increased expression of fatty acid oxidative enzymes and increased β -oxidation of fatty acids in *Mstn*^{-/-} mice, we next determined if there was increased accumulation of BAT-like cells in *Mstn*^{-/-} WAT. Subsequent immunocytochemistry of WAT revealed a BAT-like phenotype with a predominance of small cells with rich cytoplasmic staining, multilocular lipid droplet appearance (Figure 4.5B) and pronounced Ucp1 expression in *Mstn*^{-/-} WAT (Figure 4.5C). Furthermore qPCR analysis revealed increased expression of *Ucp1*, *Ucp2*, *Ucp3* (Figure 4.5D-4.5F) and genes involved in BAT specification and thermogenesis, including *Ppara*, *Pparb*, *Pparg* and *Pgc-1 α* in *Mstn*^{-/-} WAT, which was further enhanced upon HFD feeding (Figure 4.5G-4.5I). Importantly, we neither observed the multilocular phenotype (Figure 4.5B) nor increased Ucp1 expression (Figure 4.5C) in WAT from WT mice, moreover no increase in *Ucp1*, *Ucp2*, *Ucp3*, *Ppara*, *Pparb*, *Pparg* and *Pgc-1 α* expression was detected upon HFD feeding in WT mice and in fact expression levels of the above genes remained relatively low in WT mice WAT, irrespective of diet regimen (Figure 4.5D-4.5J). Elevated expression of COX-2 (Cyclooxygenase-2), a rate limiting enzyme in prostaglandin synthesis, contributes to the development of a BAT-like or “Beige” phenotype in WAT [16]. Therefore we next analysed COX-2 expression via immunocytochemistry and qPCR in WAT tissue from WT and *Mstn*^{-/-} mice. The results revealed strong induction of COX-2 expression in *Mstn*^{-/-} mice WAT, but not

in the WAT from WT mice (Figure 4.6A and 4.6B). Consistent with elevated *Cox-2* and *Ptges* expression (Figure 4.6B and 4.6E), we also observed enhanced release of PG, PGE2 and PGF1 α , from *Mstn*^{-/-} mice WAT explants when compared to WT controls (Figure 4.6C and 4.6D).

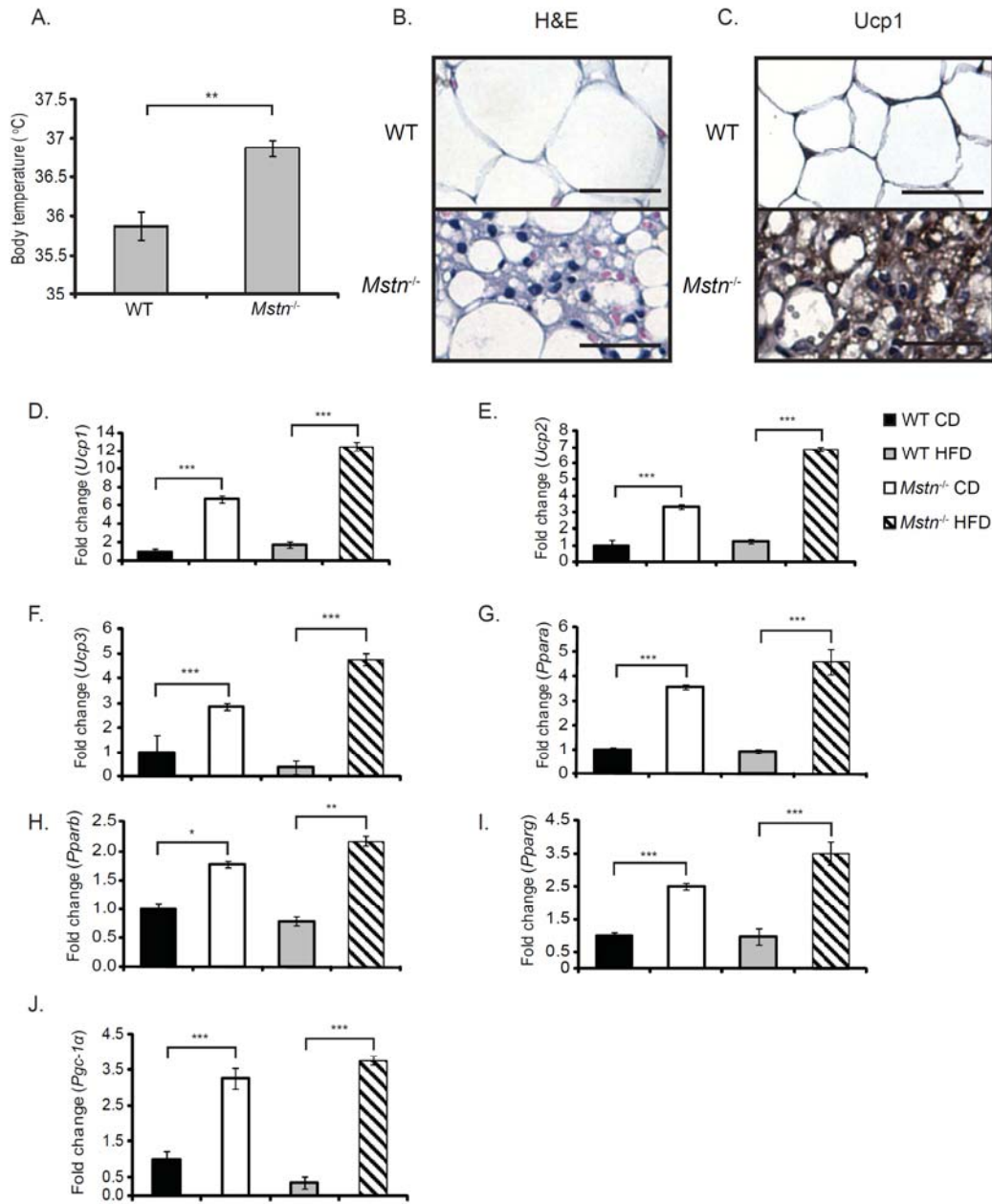


Figure 4.5 Enhanced thermogenesis and energy expenditure in WAT from *Mstn*^{-/-} mice.

(A) Rectal Body temperatures of WT and *Mstn*^{-/-} mice. (B) H&E staining of WAT from WT and *Mstn*^{-/-} mice. (C) Immunohistochemistry analysis of Ucp1 localization in WAT from WT and *Mstn*^{-/-} mice. qPCR analysis of the relative mRNA expression of *Ucp1*, *Ucp2*, *Ucp3* (D-F), *Ppara*, *Pparb*, *Pparg* (G-I) and *Pgc-1α* (J) normalized to GAPDH mRNA expression in WAT (Epididymal) of WT and *Mstn*^{-/-} mice after 12weeks of CD and HFD treatment. *P < 0.05, **P < 0.01, ***P < 0.001. Error bars represent ±SEM (n = 3). Scale bar: 50 μm. Magnification: 20X.

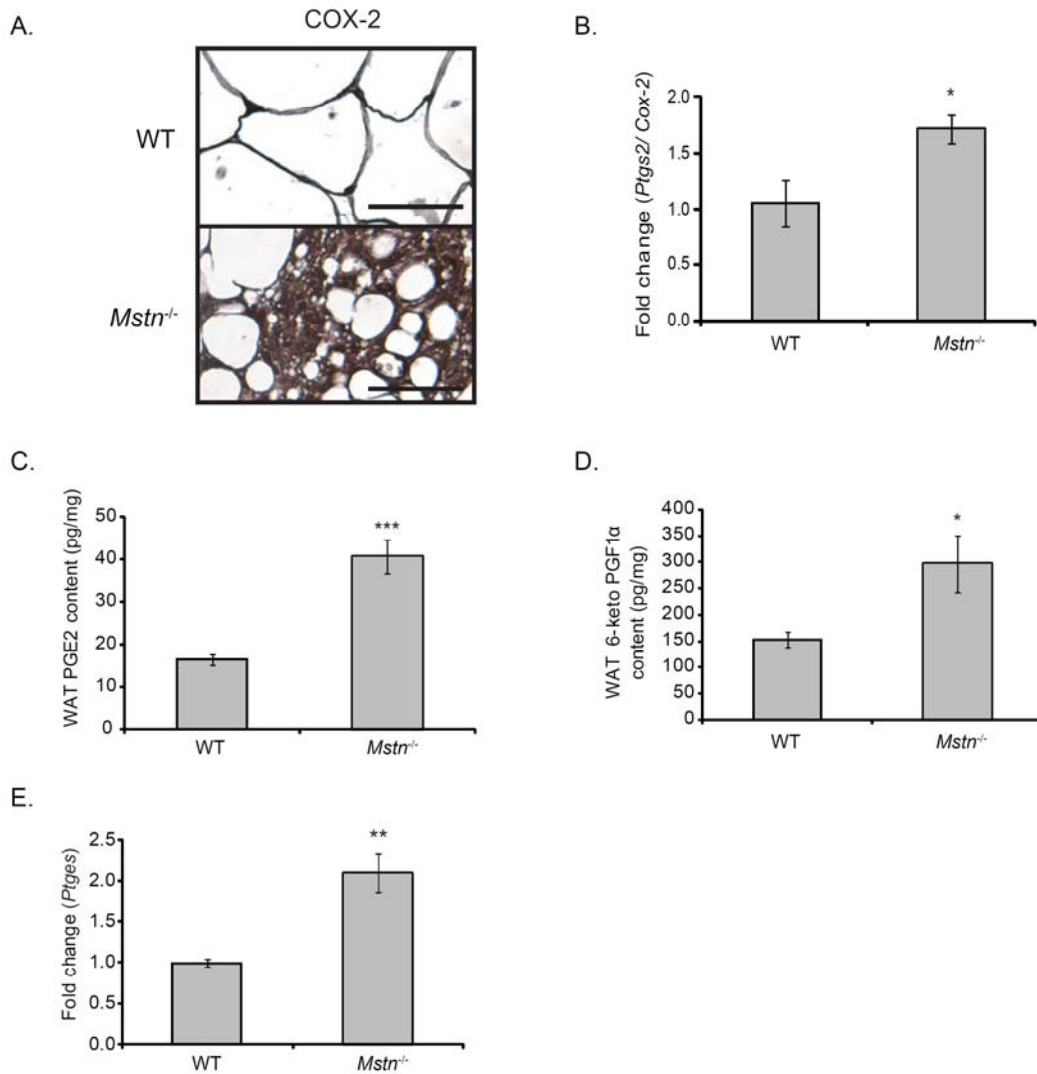


Figure 4.6 Enhanced COX-2-mediated PG signaling in WAT from *Mstn*^{-/-} mice.

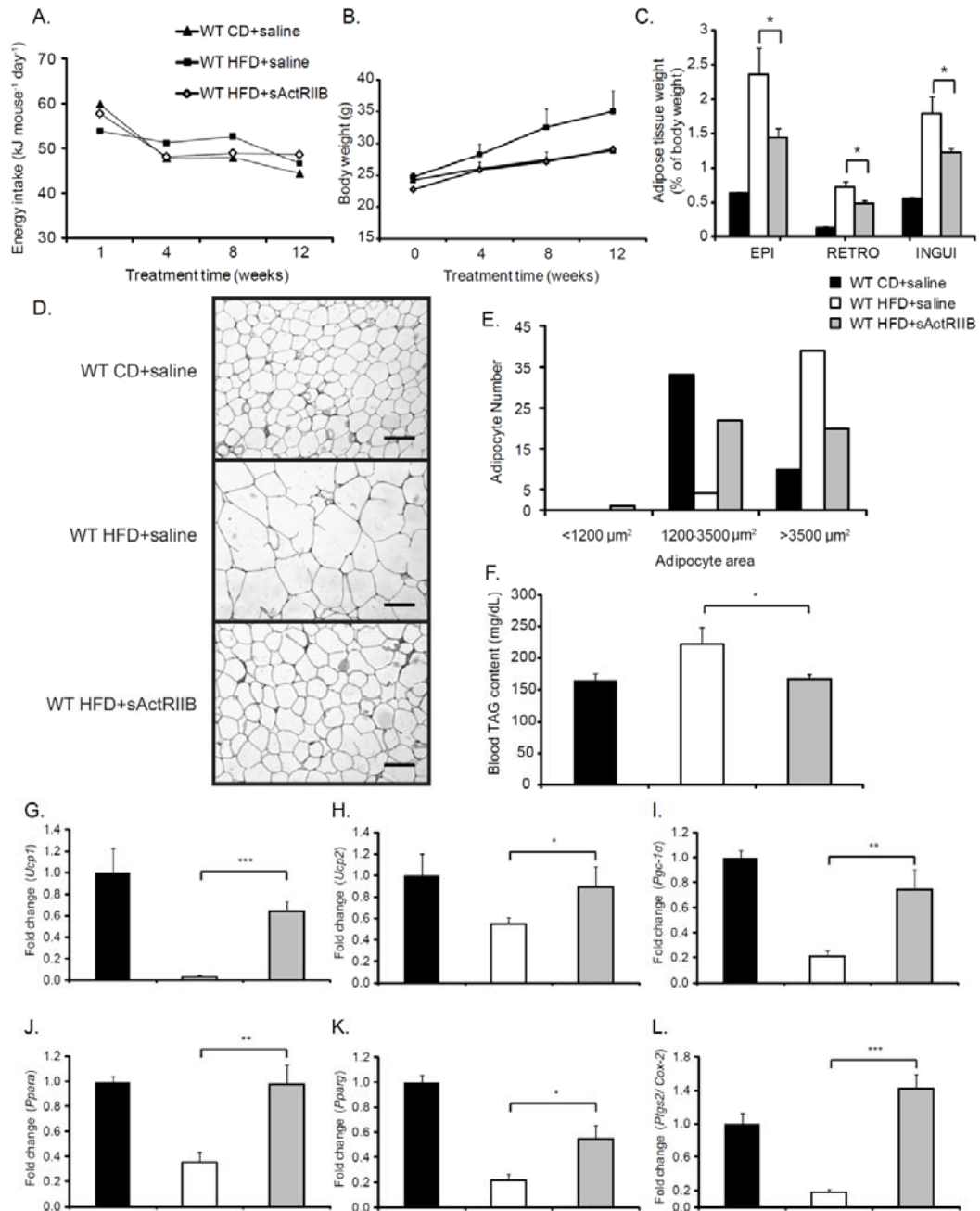
(A) Immunohistochemistry analysis of COX-2 localization in WAT from WT and *Mstn*^{-/-} mice. (B) qPCR analysis of the relative mRNA expression of *Ptgs2/Cox-2* in WAT of *Mstn*^{-/-} and WT mice. The levels of PGE2 (C) and 6-keto PGF1α (D) released from *Mstn*^{-/-} and WT mice WAT explants. (E) qPCR analysis of the relative mRNA expression of *Ptges* normalized to GAPDH mRNA expression in WAT from WT and *Mstn*^{-/-} mice. *P < 0.05, **P < 0.01, ***P < 0.001. Error bars represent ±SEM (n = 3). Scale bar: 50 μm. Magnification: 20X.

4.3.5 Treatment with Mstn antagonist alleviates diet-induced obesity in mice.

To determine whether or not postnatal inactivation of Mstn has therapeutic benefit, WT mice were either fed CD or HFD for a period of 12 weeks in the absence (saline) or presence of sActRIIB, previously shown to block Mstn signaling. Despite similar energy intake (Figure 4.7A), WT mice fed HFD gained more body weight when compared to WT mice fed CD (Figure 4.7B). Moreover, WT mice fed HFD in conjunction with sActRIIB, had reduced body weight gain to that of WT mice fed HFD; in fact the body weight gain observed in WT mice treated with sActRIIB was comparable to control CD-fed WT mice (Figure 4.7B). As expected, WT mice fed HFD had significantly increased WAT tissue weights (Figure 4.7C) and enhanced adipocyte hypertrophy (Figure 4.7D and 4.7E); however, sActRIIB treatment significantly reduced WAT weight gain (Figure 4.7C) and the increased adipocyte size observed following HFD feeding (Figure 4.7D and 4.7E), which is consistent with both reduced body weight gain and smaller WAT weights observed following sActRIIB treatment. As expected, chronic HFD feeding resulted in increased serum TAG content (Figure 4.7F), however in contrast, significant reduction in serum TAG was observed in sActRIIB treated WT mice fed HFD, and in fact, no significant difference in serum TAG level was seen between WT mice fed CD and HFD fed mice treated with sActRIIB (Figure 4.7F).

Figure 4.7 *Postnatal inactivation of Mstn results in an improved metabolic phenotype.*

(A) Energy intake ($\text{kJ mouse}^{-1}\text{day}^{-1}$), (B) Body weight increase and (C) Epididymal (EPI), Retroperitoneal (RETRO) and Inguinal (INGUI) fat-pad weights observed in WT mice fed CD or HFD in the presence of either saline or sActRIIB antagonist. (D) H&E staining and (E) Quantification of individual adipocyte area in WAT isolated from WT mice fed CD or HFD in the presence of either saline or sActRIIB antagonist. (F) Total blood TAG levels of WT mice fed CD or HFD in the presence of either saline or sActRIIB antagonist. (G-L) qPCR analysis of the relative mRNA expression of *Ucp1*, *Ucp2*, *Ppara*, *Pparg*, *Pgc-1 α* and *Ptgs2/Cox-2* normalized to GAPDH mRNA expression in WAT from WT mice fed CD or HFD in the presence of either saline or sActRIIB antagonist. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$. Error bars represent $\pm$ SEM ($n = 3$). Scale bar: 100 μm . Magnification: 10X.



Subsequent qPCR analysis revealed significantly reduced *Ucp1*, *Ucp2*, *Pgc-1 α* , *Ppara*, *Pparg* and *Ptgs2/Cox-2* expression in WAT from HFD fed WT mice when compared to control CD fed WT mice (Figure 4.7G-4.7L). However, we observed significantly elevated expression of *Ucp1*, *Ucp2*, *Pgc-1 α* , *Ppara*, *Pparg* and *Ptgs2/Cox-2*, back to levels comparable to that observed in control CD fed WT mice, in WAT from HFD fed WT mice treated with sActRIIB (Figure 4.7G-4.7L). Therefore post-natal inactivation of *Mstn* results in a similar WAT gene expression profile to that observed in *Mstn*^{-/-} mice fed HFD.

4.4 Discussion

Mstn^{-/-} mice had atrophied adipocytes and failed to accumulate fat in WAT even when fed on HFD (Figure 4.1). Since this does not appear to be due to redistribution of fat in peripheral tissues of *Mstn*^{-/-} mice [73], we reasoned it could be due to increased energy expenditure. Consistent with this hypothesis, we find significantly increased expression of genes critical to mitochondrial activity/function and fatty acid oxidation in the peripheral tissues of *Mstn*^{-/-} mice (Figure 4.3&4.4). In addition, two recent publications also confirmed an increase in total energy expenditure in Mstn-deficient mice [154, 201], suggesting that both increased fatty acid oxidation and total energy expenditure could be pivotal reasons for reduced adiposity in *Mstn*^{-/-} mice. However in a recent study, Guo *et al* [166] showed that deletion of Mstn specifically in adipose tissue had no significant effects on adipose tissue fat accumulation or metabolic homeostasis. Importantly, Mstn expression is low in adipose tissue [118], when compared to skeletal muscle and liver [118, 134], thus conditional deletion of adipose tissue-specific expression of Mstn, may not have a dramatic impact on total circulatory levels of Mstn. Moreover, as Mstn functions in an endocrine fashion, we speculate that Mstn synthesized and secreted by muscle and liver (in the adipose tissue-specific knockout mice) was sufficient to maintain Mstn biological function, which may explain why the authors failed to see increased muscle mass and reduced fat accumulation in these mice [166]. Here we have used a strain of knockout mice, where there is no expression of functional Mstn, and we observed increased mitochondrial activity and fatty acid oxidation consistently in WAT, skeletal muscle and liver. We do not believe that the increased fatty acid oxidation in WAT is a secondary effect of the increased muscle mass observed in *Mstn*^{-/-} mice, since we detected specific up-regulation of genes related to increased mitochondrial activity

both in WAT and skeletal muscle. Furthermore, we also hypothesize that increased AMPK kinase activity [73], and enhanced PPAR pathway signalling (Figure 4.5), in *Mstn*^{-/-} mice are the molecular reason for the increased fatty acid oxidation. Most certainly AMPK activation has been shown to increase fatty acid oxidation [72, 202]. Similarly either over expression of PPAR β or PPAR β agonist treatment results in increased mitochondrial number and activity, as well as enhancement of both fatty acid oxidation enzyme expression and resulting fatty acid oxidation [11]. Consistent with this finding, our unpublished results indicate that although *Mstn*^{-/-} muscle have increased MHC type IIB expressing fast twitch fibers [137], they are metabolically oxidative in nature, since these fibers have increased mitochondrial number and activity (unpublished data, Reddy *et al*). Furthermore, histochemical results indeed point out that *Mstn*^{-/-} MHC IIB muscle fibers possess increased succinate dehydrogenase (SDH) activity, which is consistent with increased oxidative activity in the fast twitch fibers (unpublished data, Reddy *et al*). In addition to WAT and skeletal muscle we also noted increased fatty acid oxidation in liver, which corroborates the recent publication by Wilkes *et al* who showed decreased liver steatosis in *Mstn* deficient mice following HFD feeding [171]. Interestingly, over expression of activated Akt in mice leads to increased fast glycolytic fibers in skeletal muscle and increased fatty acid oxidation [168], much like what is observed in *Mstn*^{-/-} mice. It is noteworthy to mention that these mice have 30% reduction in *Mstn* levels. Hence it is possible that increased fast glycolytic fibers in *Mstn*^{-/-} mice could result in increased liver fatty acid oxidation.

Ucp1 was significantly up-regulated in *Mstn*^{-/-} WAT (Table 4.1 & Figure 4.5). In addition, the expression of PPAR members (*Ppara*, *Pparb* and *Pparg*), *Pgc-1 α* , as well as crucial factors for controlling adipocyte differentiation, lipolysis, fatty acid

oxidation, and thermogenesis was also up-regulated in WAT of *Mstn*^{-/-} mice (Table 4.1, Figure 4.2&4.3). Furthermore, multilocular adipocyte morphology was also observed in the WAT of *Mstn*^{-/-} mice (Figure 4.5). Together these observations strongly suggest that WAT of *Mstn*^{-/-} mice has acquired characteristics of BAT. However, further work will need to be performed to determine whether or not the appearance of BAT in *Mstn*^{-/-} mice WAT is accompanied by increased neural innervation and vascularisation, which would be consistent with the increased metabolic activity observed. Although, published reports have described the transient appearance of BAT in WAT in both human and experimental animal models [4, 17], the growth factor signaling mechanisms that regulate the conversion/formation of brown adipocytes is not known. Our results suggest that Mstn could be one such novel growth factor that can determine BAT content in WAT. Our search for the molecular mechanism(s) behind Mstn regulation of BAT formation in WAT identified that absence of Mstn induces COX-2 expression. Recently, it was shown that COX-2 is a downstream effector of β -adrenergic signaling in WAT and that up-regulation of COX-2 is required and sufficient for *de novo* production of BAT in WAT deposits. Once induced, COX-2 promoted thermogenic gene expression, including *Ucp1*, *Cidea*, *Cpt1b* and *Dio2* and enhanced prostaglandin release from WAT, resulting in conversion of WAT mesenchymal progenitors into a BAT-like or “Beige” phenotype [16]. Similarly, we observed elevated thermogenic gene expression (Table 4.1 & Figure 4.5) and enhanced prostaglandin release from *Mstn*^{-/-} mice WAT explants (Figure 4.6), suggesting that similar mechanisms, to that seen following β -adrenergic stimulation, may be responsible for the development of BAT in *Mstn*^{-/-} WAT. Consistent with enhanced BAT phenotype, we also observed increased expression of uncoupling proteins (*Ucp1*, *Ucp2* and *Ucp3*) in *Mstn*^{-/-} WAT, which are responsible for

uncoupling and dissipation of energy generated in mitochondria as heat resulting in an increase in body temperature (Figure 4.5A). It is important to mention that although we observed an enhanced BAT-like phenotype in *Mstn*^{-/-} mice WAT, we found no significant change in BAT morphology or weights (data not shown).

Further results presented here demonstrate that treatment with an Mstn antagonist (sActRIIB) *in vivo* recapitulates the anti-obesity phenotype observed in *Mstn*^{-/-} mice, which suggests that the blockade of Mstn may be an effective anti-obesity therapy. However it remains unclear at this stage if the effects of sActRIIB on WAT gene expression are primary or secondary to the increased muscle mass observed following sActRIIB treatment [155]. It is noteworthy that in an independent animal trial, treatment with Mstn-specific antibodies had no effect on fat mass accretion in adipose tissue [154]. This result suggests that not all Mstn antagonists have utility in both increasing muscle mass and reducing body fat content. Here we have used sActRIIB, because it has been successfully shown to increase muscle growth in mdx mice [203], increase insulin sensitivity during diet-induced obesity [173] and reduce cachectic muscle wasting [204], much like what is seen in *Mstn*^{-/-} mice. However, sActRIIB can bind to several additional ligands in circulation [174-175], suggesting that sActRIIB could function through inactivating additional ligands other than Mstn. Therefore, before sActRIIB can be employed as an effective anti-obesity therapeutic, there is a further need to determine the target specificity.

The current results demonstrate that inactivation of Mstn leads to increased resistance to HFD-induced obesity in mice. We propose that increased quantities of “brown-like adipose tissue” in WAT together with increased peripheral tissue fatty acid oxidation, through enhanced PPAR signaling, are the two main mechanisms through which mice are protected against HFD-induced obesity in response to lack of, or inhibition of,

Mstn. These findings highlight Mstn antagonists as a novel class of potential anti-obesity drugs which function by increasing energy expenditure, rather than limiting food/fat intake.

4.5 Acknowledgements

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4.6 Duality of interest

The authors declare that there is no duality of interest associated with this manuscript.

Chapter 5 Analysis of Global Gene Expression Changes during Myostatin-Mediated Regulation of Diet-Induced Obesity

This chapter is communicated to the *Journal of Lipid Research*.

Analysis of Global Gene Expression Changes during Myostatin-Mediated Regulation of Diet-Induced Obesity

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Abstract

Myostatin (Mstn), GDF-8, is a secreted growth factor that belongs to the TGF- β superfamily. Our previous results indicate that Myostatin-null (*Mstn*^{-/-}) mice not only have increased myogenesis, but also have a lean phenotype and improved insulin sensitivity even during high-fat diet (HFD) feeding. Although we characterized that such a phenotype is due to the up-regulation of AMPK and PPAR signaling, the molecular basis for the reduced lipid accumulation resulting in the atrophied WAT in

Mstn^{-/-} mice has yet to be analyzed. Microarray analysis has been performed on WAT samples collected from WT and *Mstn*^{-/-} mice fed either HFD or CD. Data has been subsequently analyzed by Volcano, hierarchical, GO, Venn and GSEA analysis. These data reveal that lack of Mstn protects against gene profile changes normally associated with HFD challenge and further suggest that the alterations in lipid metabolism observed in *Mstn*^{-/-} mice are due to reduced lipid uptake and storage. We also highlight an additional signaling pathway (lipid transport) potentially involved in the atrophied WAT phenotype observed in *Mstn*^{-/-} mice, which may become a potential target for further research. Taken together, the current study suggests that therapies designed to target and repress Mstn activity may be beneficial for alleviating obesity and type 2 diabetes.

5.1 Introduction

Mammalian adipose tissue can be divided into two types: white adipose tissue (WAT) and brown adipose tissue (BAT). WAT is mainly used as a fat reservoir, while BAT is primarily involved in oxidizing fats to generate heat. Apolipoprotein C3 (Apoc3) is critically involved in regulating lipid uptake by adipose tissue. Apoc3 facilitates lipid transportation through the bloodstream, in the form of lipoproteins and it is the natural lipoprotein lipase (LPL) inhibitor [205]. Triglyceride (TAG) inside the lipoproteins is hydrolyzed into free fatty acid (FFA) by LPL in peripheral tissue. The hydrolyzed FFA is then taken up into the peripheral tissue and either oxidized in mitochondria or stored in the lipid droplets of adipose tissue.

Although several adipokines, such as adiponectin, leptin and resistin, have been shown to regulate adipose tissue mass [206-208], little is presently known about the function of myokines in adipose tissue. Myostatin (Mstn), a TGF- β superfamily member, is a negative regulator of skeletal muscle growth. Previous publications reveal that lack of Mstn leads to an increased lean phenotype. Specifically, Mstn-null (*Mstn*^{-/-}) mice exhibit a ~2-4-fold reduction in fat pad weight when compared to Wild-type (WT) mice [165]. Recently, it has also been reported that muscle-specific blockade of Mstn results in decreased fat mass and increased insulin sensitivity [166]. Furthermore, loss-of-function mutations in Mstn have been shown to reduce TNF- α production and ameliorate hepatosteatosis, thus improving liver insulin sensitivity [171]. In addition, overexpression of the Mstn prodomain/LAP (an inhibitor of Mstn signaling) also results in decreased fat pad weights [167]. Postnatal inhibition of Mstn through treatment with the PF-879 Mstn neutralizing antibody is also reported to partially reverse obesity and insulin-resistance in mice [154]. Similarly, treatment of WT mice for 10 weeks with the Mstn antagonist, soluble activin type IIB receptor (sActRIIB),

also resulted in reduced glucose production and increased glucose uptake during normal chow diet (CD) feeding [173]. Interestingly, it is reported that the increase in glycolytic muscle mass may potentially promote hepatic fatty acid oxidation and ketone body production, protecting mice from obesity. Consistent with this, *Mstn*^{-/-} mice contain predominantly fast glycolytic muscle fibers [168]. Previous results from our laboratory demonstrate that Mstn deficiency leads to accelerated glucose uptake and enhance fatty acid oxidation in peripheral tissues, leading to increased insulin sensitivity and resistance to diet-induced obesity [73, 209]. It is further suggested that the improved metabolic phenotype is due to up-regulated AMPK and PPAR signaling in *Mstn*^{-/-} mice [73, 209]. Although we observe reduced adipose tissue mass, and for that matter reduced accumulation of adipose in response to high fat diet (HFD) feeding in *Mstn*^{-/-} mice, little is presently known about the mechanism behind this process. Here, through using global gene expression analysis, we show that the atrophied WAT phenotype observed in *Mstn*^{-/-} mice may be due to a combination of decreased lipid uptake and reduced lipid storage.

5.2 Materials and Methods

5.2.1 Animals

All animal experiments were performed according to Institutional Animal Care & Use Committee (IACUC) regulations, Singapore. WT mice (C57BL/6) were supplied by the Centre for Animal Resources, Singapore (National University of Singapore, Singapore). *Mstn*^{-/-} mice were kindly gifted by Prof. Se-Jin Lee (Johns Hopkins University, Baltimore, MD). All *Mstn*^{-/-} and WT mice used in this trial were derived from different litters and were housed in groups fed CD under a 12h/12h artificial light/dark cycle at a constant temperature (20°C), with *Ad libitum* water supply before starting the trial. Seven-week-old male mice were separated into two groups, containing 5xWT and 5x*Mstn*^{-/-} mice each, feed HFD (45% energy from fat; 58V8, TestDiet, Richmond, IN, USA) or CD (10% energy from fat; 58Y2, TestDiet) for 12 weeks. Please see Table 3.1 for details of diet compositions (Table 3.1). All measurements and analysis were performed on Epididymal (gonadal) WAT. Supplementary Tables can be found in attached CD.

5.2.2 Microarray Analysis

For details of RNA extraction and RNA electrophoresis see sections 2.2.3 and 2.2.5 respectively. For microarray, WAT (Epididymal fat pad) tissue was collected in duplicate from 3-4 month old WT and *Mstn*^{-/-} mice. RNA was extracted using TRIzol (Invitrogen, Carlsbad, CA, USA), according to the manufacturer's guidelines. The quantity and quality of the WAT RNA was verified by RNA agarose gel electrophoresis and through using the Agilent RNA 6000 Nano Kit and 2100

Bioanalyzer (Agilent, Santa Clara, CA, USA). All the qualified RNA samples were analyzed using the Agilent SurePrint G3 Mouse Gene Expression array (Genomax Technologies, Singapore), as per their standardized protocol. Hybridization signals were quantified using Feature Extraction Software (Agilent). For normalization of genes, the 75th percentile of all entities within each hybridization panel was selected. Raw data normalization, averaging, transcripts abundance calculations and ratio analysis were analyzed using GeneSpring GX software v.11.5.1 (Agilent) using log transformed data. Normalized data were filtered on expression (20.0th-100.0th) percentile using GeneSpring v.11.5.1 before proceeding to the following functional analysis.

5.2.3 Volcano analysis

Volcano analysis was performed on the normalized data to identify differentially expressed genes between WT and *Mstn*^{-/-} mice fed either CD or HFD. Several pair-wise comparisons between CD and HFD fed WT and *Mstn*^{-/-} mice were made. Specifically: WT group (comparison of WT HFD and CD fed mice), *Mstn*^{-/-} group (comparison of *Mstn*^{-/-} HFD and CD fed mice), HFD group (comparison of WT HFD fed and *Mstn*^{-/-} HFD fed mice) and CD group (comparison of WT CD fed and *Mstn*^{-/-} CD fed mice). Pair-wise comparison was performed on differentially expressed genes which showed a P value ≤ 0.05 and were up- or down-regulated by ≥ 1.5 -fold, as assessed through a standard two-tailed unequal variance *t*-test using the GeneSpring v.11.5.1 software. Some of the significant differentially expressed genes were further validated by real-time PCR (qPCR) in six different samples per group.

5.2.4 Hierarchical clustering analysis

To analyze the similarity of gene expression profiles, unsupervised hierarchical clustering was performed using a standardized Pearson's correlation vector with average linkage for distance measures [210]. Gene Spring v.11.5.1 software was used to visualize the result in the form of a heatmap and dendrogram. The intensity of the gene expression differences were illustrated by changes in color, while the dendrogram depicts relationships between the groups.

5.2.5 Gene ontology (GO) analysis

To analyze differentially expressed genes in WAT between WT and *Mstn*^{-/-} mice fed either CD or HFD, significant overrepresentation analysis through Gene Ontology (GO) was performed, using the online software DAVID gene ontology (GO) tree machine (<http://david.abcc.ncifcrf.gov/>) [211]. GO analysis of differentially expressed genes was conducted using the following GO categories: biological processes, molecular functions and cellular components. The GO analysis was controlled through setting a cut-off threshold for false discovery rate (FDR), with a $P \leq 0.05$ and ≥ 1.5 -fold change considered significant.

5.2.6 Venn analysis

Venn analysis was performed to detect the differentially regulated genes common between different treatment groups. Venn analysis was performed using GeneSpring software v.11.5.1. The analysis was conducted either between different genotypes (WT vs. *Mstn*^{-/-}) or between the different diet regimens (CD vs. HFD). Up- and down-

regulated genes were also been included in the Venn analysis. The cut-off threshold for this analysis was $P \leq 0.05$ and ≥ 1.5 -fold change.

5.2.7 Gene set enrichment analysis (GSEA)

GSEA analysis has been performed using DAVID software (<http://david.abcc.ncifcrf.gov/>). Genes shown to be exclusively differentially regulated in *Mstn*^{-/-} mice were analyzed and separated into different functional annotation clusters.

5.2.8 qPCR analysis

For details of RNA extraction, RNA electrophoresis, cDNA synthesis and qPCR see sections 2.2.3, 2.2.5, 2.2.6 and 2.2.8 respectively. For performing qPCR, cDNA was synthesized using the Superscript II First strand synthesis system (Invitrogen) from 1 µg of total RNA. qPCR was performed using the Bio-Rad CFX96 real-time PCR machine and Sso Fast Evagreen (Bio-Rad, Hercules, CA, USA) in duplicate. PCR primers used were listed as below: *C3 (Apoc3)* 5'- CCG CCA AGA ATC GCT ACT TCC AG-3' and 5'- AGC AGC CTT GAC CTC CAC CTC-3'; *Gapdh*, 5'-AAC TTT GGC ATT GTG GAA GG-3' and 5'-ACA CAT TGG GGG TAG GAA CA-3'. For statistical analysis, multiple comparisons were performed using two-way ANOVA and robust regression analysis. Data were displayed as mean $\pm$ SEM and P values < 0.05 were considered significant. Experimental replicates are indicated in each figure legend.

5.3 Results

Mstn^{-/-} mice are extremely lean and do not accumulate excess body fat even when fed on HFD [165]. Histological analysis indicates that *Mstn*^{-/-} adipocytes are atrophied and do not undergo adipocyte hypertrophy in response to HFD feeding [165]. In order to understand the molecular basis for the reduced adiposity, we performed microarray analysis to identify global gene expression changes in adipose tissue of WT and *Mstn*^{-/-} mice during HFD feeding.

5.3.1 Microarray analysis

Global gene expression analysis was performed on WAT of WT and *Mstn*^{-/-} mice fed either HFD or CD (n = 2, per group) using the 44K probe mouse whole genome oligo array. Differentially regulated genes were indicated by microarray analysis, with a FDR of 0.05 deemed acceptable, so that ~5% of the differentially regulated genes are false positives.

5.3.2 Volcano plots of differentially expressed genes

Genes were filtered based on significance ($P \leq 0.05$) and fold change (≥ 1.5 -fold) (Figure 5.1, Supplementary Table 5.1). Initially we compared the differentially expressed genes between WT mice fed either HFD or CD. Of the 1134 total differentially expressed genes identified, only 818 genes could be analyzed by volcano plot as the remaining 316 genes were either LincRNA or did not have a gene accession number. Among the 818 genes analyzed 282 genes were significantly up-regulated and 536 genes were significantly down-regulated in HFD fed WT mice, when

compared to CD fed WT mice (Figure 5.1A, Supplementary Table 5.1). Similarly, comparison of *Mstn*^{-/-} mice fed either HFD or CD revealed that of the 866 genes analyzed by volcano plot, 354 were significantly up-regulated and 512 were significantly down-regulated in HFD fed *Mstn*^{-/-} mice, when compared to CD fed *Mstn*^{-/-} mice (Figure 5.1B, Supplementary Table 5.1). Much like what was observed during the WT analysis above, 359 differentially regulated genes could not be analyzed by volcano plot as they were either LincRNA or genes that do not have a gene accession number.

Furthermore, we also compared the differentially expressed genes between CD fed WT and *Mstn*^{-/-} mice and HFD fed WT and *Mstn*^{-/-} mice. Similar to the data outlined above a number of the genes could not be analyzed by volcano plot as they were either LincRNA or did not have gene accession numbers. Specifically, of the 1894 differentially regulated genes identified between CD fed WT and *Mstn*^{-/-} mice only 1453 could be analyzed. In addition, of the 1504 differentially regulated genes identified between HFD fed WT and *Mstn*^{-/-} mice only 942 could be analyzed. Upon comparison of CD fed WT and *Mstn*^{-/-} mice, 695 genes were significantly up-regulated, while 758 genes were down-regulated in *Mstn*^{-/-} CD mice (Figure 5.1C, Supplementary Table 5.1). However, comparison of HFD fed WT and *Mstn*^{-/-} mice revealed that 580 genes were significantly up-regulated and 362 genes were significantly down-regulated in *Mstn*^{-/-} HFD mice (Figure 5.1D, Supplementary Table 5.1).

The above data clearly indicated that HFD feeding resulted in a reduction in the total number of differentially regulated genes, when compared to CD feeding, between WT and *Mstn*^{-/-} mice groups. HFD feeding also resulted in a greater number of genes that were up-regulated, as opposed to down-regulated, in *Mstn*^{-/-} mice, when compared to WT mice. However, this trend was reversed upon comparison of differentially

expressed genes between CD fed mice, where we observed a greater number of down-regulated genes in *Mstn*^{-/-} mice, when compared to WT mice (Figure 5.1C&5.1D, Supplementary Table 5.1). We further observed a similar number of differentially expressed genes between WT and *Mstn*^{-/-} mice (fed CD or HFD) groups. In addition, the number of up- and down-regulated genes in both WT and *Mstn*^{-/-} mice, was also similar when compared to their respective CD controls (Figure 5.1A&5.1B, Supplementary Table 5.1).

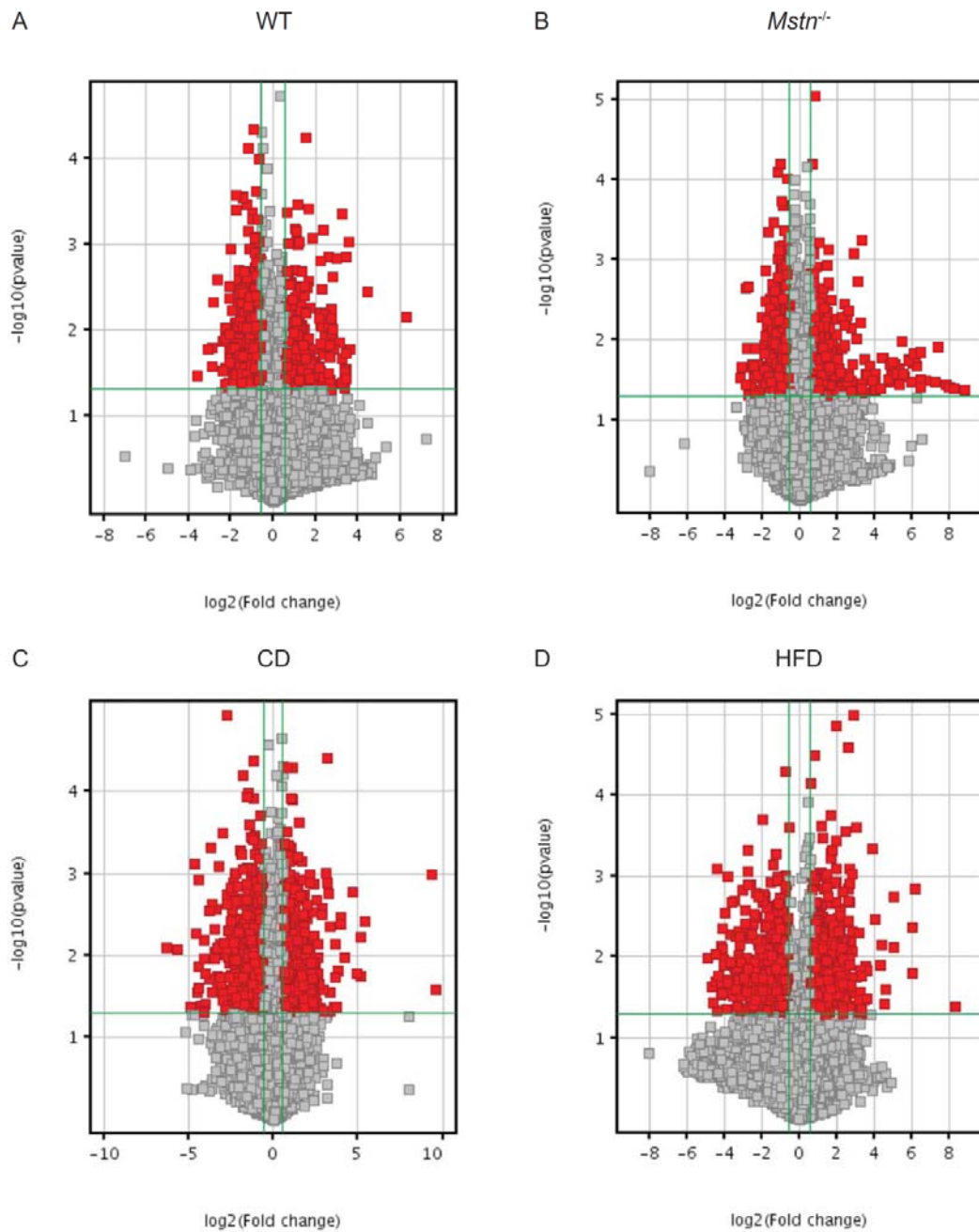


Figure 5.1 Volcano plots of differentially expressed genes

Volcano analysis of differentially regulated genes in (A) WT, (B) *Mstn*^{-/-}, (C) CD and (D) HFD treatment groups. Dots represent genes and the red dots indicate the significantly differentially regulated genes ($P \leq 0.05$ and fold change ≥ 1.5).

5.3.3 Hierarchical clustering analysis

Unsupervised hierarchical clustering analysis was performed on WT CD, WT HFD, *Mstn*^{-/-} CD, *Mstn*^{-/-} HFD groups. The result identified the presence of two main clusters: one consisting of WT CD, *Mstn*^{-/-} CD, *Mstn*^{-/-} HFD treatment groups, and the second consisting only of the WT HFD fed group (Figure 5.2). Importantly, these data suggest that deletion of the *Mstn* gene results in the clustering of the HFD group with the CD fed groups. Therefore, genotype (*Mstn*^{-/-} vs. WT) appears to outweigh the effect of the HFD regimen on gene expression changes.

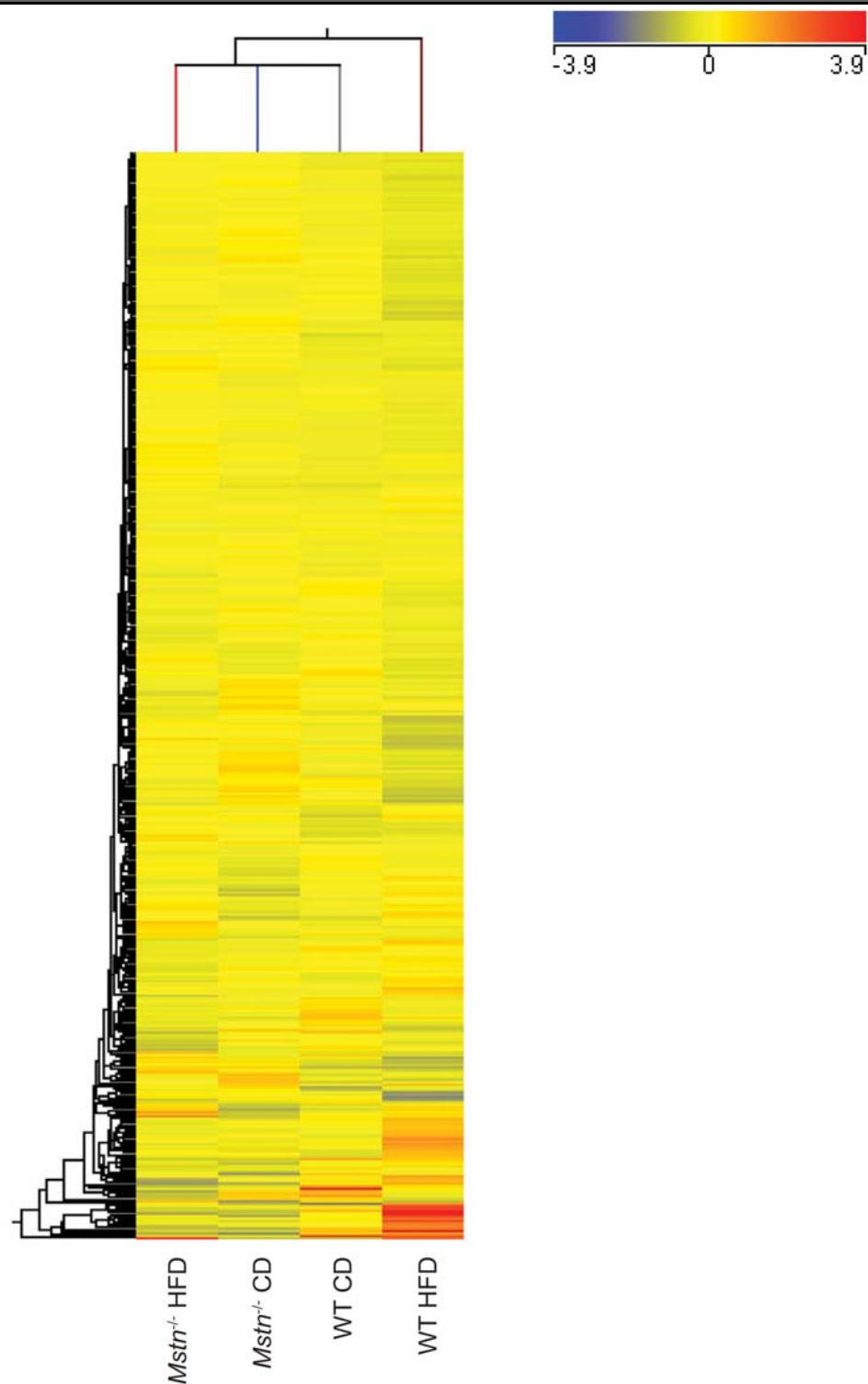


Figure 5.2 Hierarchical analysis of differentially expressed genes

Hierarchical analysis of differentially regulated genes in WT CD, WT HFD, *Mstn*^{-/-} CD and *Mstn*^{-/-} HFD treatment groups. Each band represents one gene, and colors illustrate different fold changes as shown in figure key.

5.3.4 GO analysis

To identify the predominant function of the differentially expressed genes, GO analysis has been performed using the online software DAVID gene ontology (GO) tree machine (<http://david.abcc.ncifcrf.gov/>) [211]. GO analysis resulted in the annotation and grouping of genes into biological process, cellular component and molecular function categories, as summarized in Figure 5.3. The detailed list of gene names, their functional classification and statistical significance can be found in supplementary table 5.2.

In the WT group (comparison of WT HFD and CD fed mice), DAVID GO tree machine allowed 818 genes to be analyzed, and among them, 39% belonged to the biological process category, 15% were associated with the cellular component category, and 46% were linked to the molecular function category (Figure 5.3A, Supplementary Table 5.2). In the *Mstn*^{-/-} group (comparison of *Mstn*^{-/-} HFD and CD fed mice), out of total 866 differentially regulated genes, 31% were associated with the biological process category, 18% were assigned to the cellular component category and 51% belonged to the molecular function category (Figure 5.3B, Supplementary Table 5.2). Out of 1453 differentially regulated genes identified in the CD group (comparison of WT CD fed mice with *Mstn*^{-/-} CD fed mice), 49% belonged to the biological process category, 16% were associated with the cellular component category, and 35% were linked to the molecular function category (Figure 5.3C, Supplementary Table 5.2). However, in the HFD group (comparison of WT HFD fed mice with *Mstn*^{-/-} HFD fed mice) GO analysis only identified 942 differentially expressed genes, out of which 44% were associated with the biological process category, 35% belonged to the cellular component category and 21% were assigned to the molecular function category (Figure 5.3D, Supplementary Table 5.2).

When we compared the differentially expressed genes between WT (CD vs. HFD) and *Mstn*^{-/-} mice (CD vs. HFD) we found similar percentages of differentially expressed genes assigned to biological process (WT vs. *Mstn*^{-/-}; 39% vs. 31% respectively), cellular component (WT vs. *Mstn*^{-/-}; 15% vs. 18% respectively) and molecular function categories (WT vs. *Mstn*^{-/-}; 46% vs. 51% respectively) (Figure 5.3A&5.3B, Supplementary Table 5.2). However, as can be seen in Figure 5.3C&5.3D, HFD treatment resulted in an observable difference in the expression of genes in WT and *Mstn*^{-/-} mice assigned to cellular component and molecular function categories, when compared CD fed mice. Most notably, HFD feeding increased the percentage of differentially expressed genes in the cellular component category (from 16% to 35%), and reduced the percentage of differentially expressed genes associated with the molecular function category (from 35% to 21%), when compared to CD fed mice. However, the majority of differentially expressed genes were assigned to the biological process category between the CD and HFD fed groups, with a similar percentage observed (49% vs. 44%, respectively) (Figure 5.3C&5.3D, Supplementary Table 5.2).

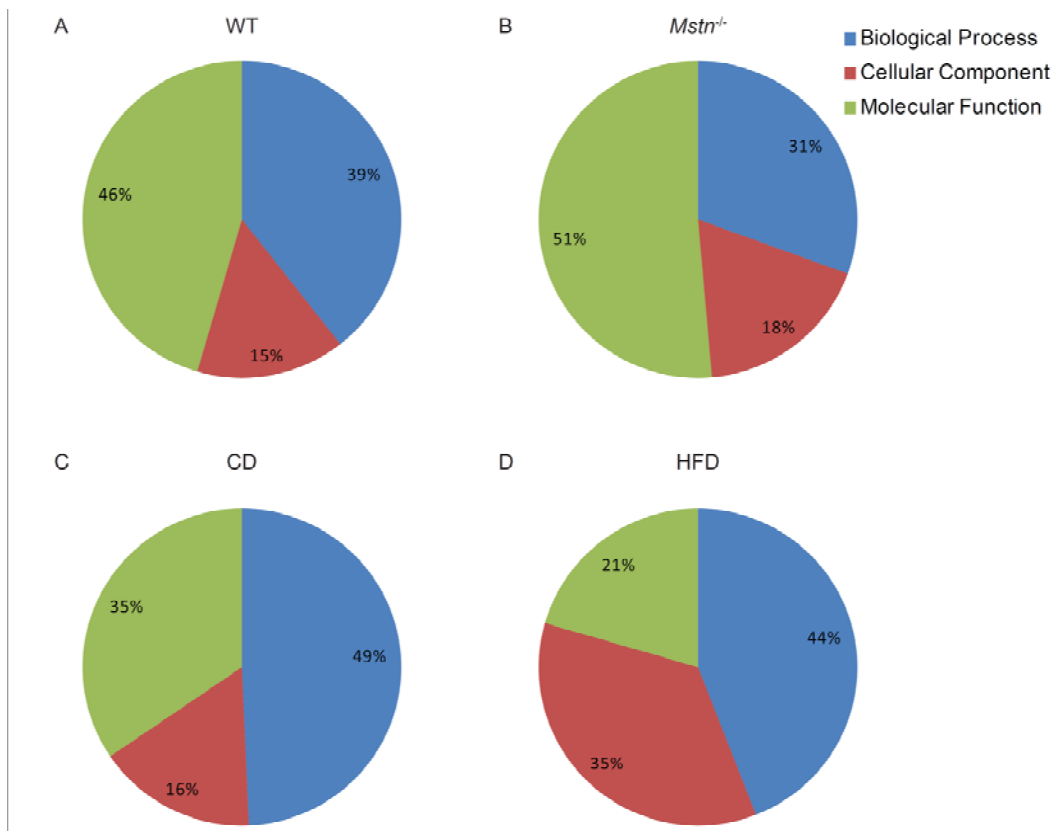


Figure 5.3 *GO Analysis*

Summary of the Gene Ontology (GO) analysis of differentially regulated genes in WAT of WT and *Mstn*^{-/-} mice fed either CD or HFD. Pie charts depict the enriched GO categories, and each slice indicates the percentage of differentially regulated genes in biological process, cellular component and molecular function categories.

5.3.5 Venn analysis

Venn analysis was performed using Genespring software v.11.5.1 (Figure 5.4) to determine the number of differentially expressed genes that were either unique or common to WT CD, WT HFD, *Mstn*^{-/-} CD and *Mstn*^{-/-} HFD treatment groups. The complete list of genes used for Venn analysis is supplied in supplementary Table 5.3.

Initially, we analyzed the differentially expressed genes between WT and *Mstn*^{-/-} mice fed either CD or HFD. As can be seen in Figure 5.4A, Venn analysis identified 73 genes that were common to both *Mstn*^{-/-} and WT mice (CD vs. HFD fed) and 1152 and 1061 genes that were exclusively expressed in *Mstn*^{-/-} and WT treatment groups respectively (Figure 5.4A, Supplementary Table 5.3). In addition, of the 1152 exclusive differentially expressed genes observed in *Mstn*^{-/-} mice, 428 genes were up-regulated and 727 genes were down-regulated in HFD fed mice, when compared to CD fed mice. However, of 1061 exclusively expressed genes in the WT treatment group, 319 genes were up-regulated and 745 genes were down-regulated in HFD fed mice, when compared to CD fed mice. With respect to the 73 genes common to CD and HFD fed *Mstn*^{-/-} and WT mice, 27 genes were up-regulated and 43 genes were down-regulated in response to HFD, when compared to CD regimen (Figure 5.4B&5.4C, Supplementary Table 5.3).

Using Venn analysis we next compared the differentially expressed genes between *Mstn*^{-/-} and WT mice fed the same diet (either HFD or CD). As can be seen in Figure 5.4D, 263 differentially expressed genes were common to either HFD or CD fed (WT vs. *Mstn*^{-/-}) mice, with 1241 and 1631 genes exclusively expressed in HFD and CD fed (WT vs. *Mstn*^{-/-}) groups respectively (Figure 5.4D, Supplementary Table 5.3). Furthermore, of the 1241 differentially expressed genes exclusive to HFD fed mice

(WT vs. *Mstn*^{-/-}), 756 genes were up-regulated and 488 genes were down-regulated in *Mstn*^{-/-} mice when compared to WT mice. Moreover, out of the 1631 differentially expressed genes detected in CD fed mice (WT vs. *Mstn*^{-/-}), 805 genes were up-regulated and 829 genes were down-regulated in *Mstn*^{-/-} mice when compared to WT mice. Lastly we further noted 143 commonly up-regulated genes and 117 commonly down-regulated genes between HFD and CD (WT vs. *Mstn*^{-/-}) fed mice (Figure 5.4E&5.4F, Supplementary Table 5.3).

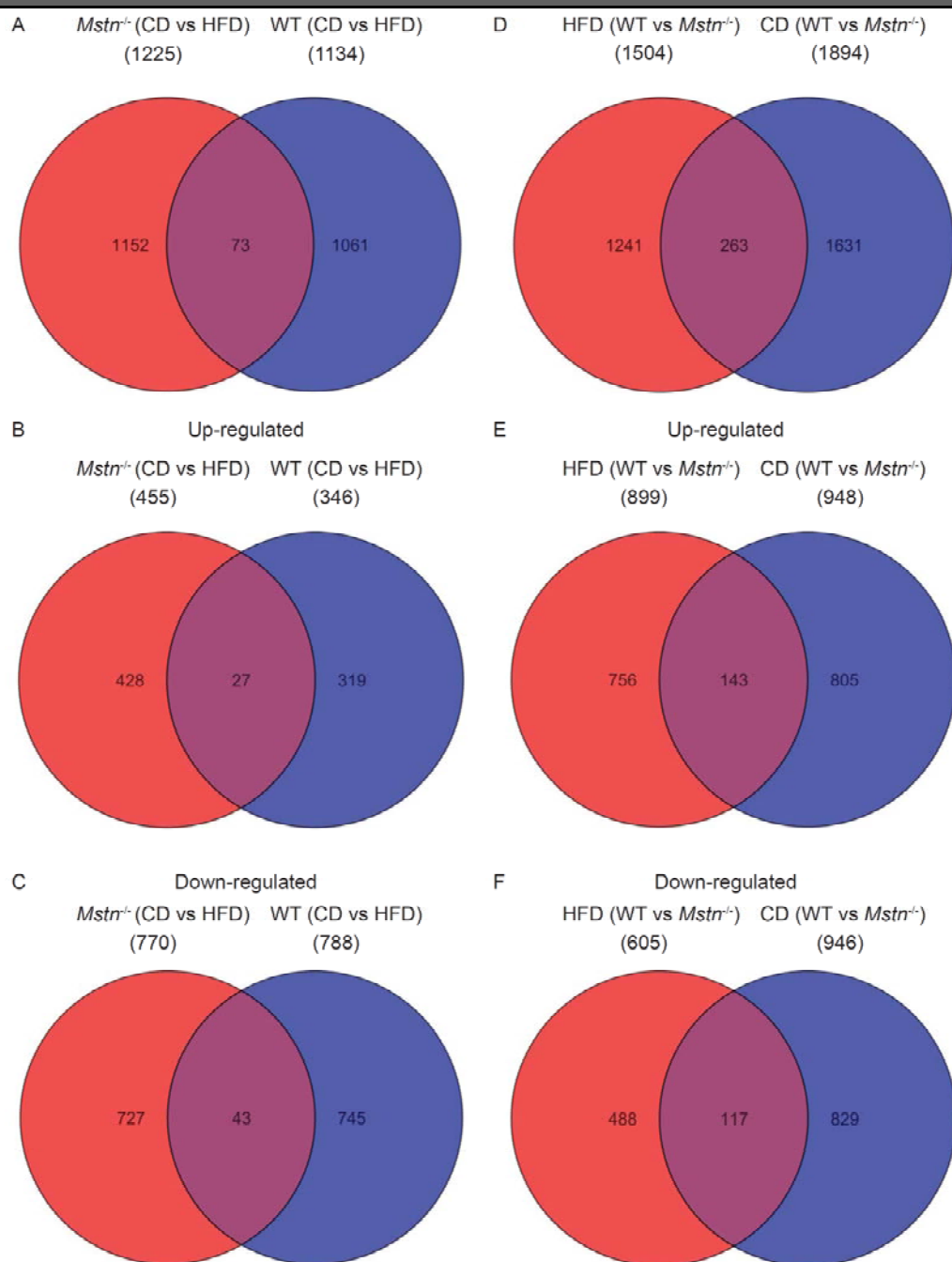


Figure 5.4 Venn analysis

Venn analysis of differentially expressed genes between (A) mice of the same genotype (either *Mstn*^{-/-} or WT mice) fed a different diet (HFD vs. CD) or (D) between mice of different genotypes (*Mstn*^{-/-} vs. WT) fed the same diet (either HFD or CD). Venn diagrams also show the (B) up- and (C) down-regulated genes in each genotype in response to HFD, when compared to CD controls, as well as (E) up- and (F) down-regulated genes in *Mstn*^{-/-} mice fed either HFD or CD, when compared to WT mice.

5.3.6 Gene set enrichment analysis (GSEA)

Next we performed GSEA using DAVID functional annotation clustering software to cluster the differentially expressed gene sets into functional groups. We utilized the differentially expressed genes that were unique to either WT (CD vs. HFD) or *Mstn*^{-/-} mice (CD vs. HFD) for GSEA. GSEA revealed a number of functional groups that were significantly enriched in either WT (CD vs. HFD) or *Mstn*^{-/-} mice (CD vs. HFD). Details of the functional groups and their enrichment scores are listed in supplementary Table 5.4. One particular functional gene group, which had a high enrichment score (2.08) in *Mstn*^{-/-} mice (CD vs. HFD), was the lipid localization and transport functional group. Within this functional group we found that the genes *ATP8A2*, *STARD6*, *Apoa2*, *Apob*, *Apol9b*, *CROT*, *GLTPD2*, *Hexb* and *Slc27a5* were up-regulated, while *OSBP*, *OSBP2* and *ABCG4* were down-regulated in *Mstn*^{-/-} mice (CD vs. HFD) (Table 5.1). These genes were further separated based on function into lipid localization, lipid transport1, lipid transport2 and lipid transporter activity subgroups according to “GOTERM_BP_FAT”, “GOTERM_MF_FAT” and “SP_PIR_KEYWORDS” database assignment (Table 5.1). It is important to mention that while we observed differential expression of genes involved with lipid localization and transport in *Mstn*^{-/-} mice (CD vs. HFD), we did not observe similar changes in WT mice (CD vs. HFD), thus we propose that genes associated with this functional group may play an important role in the prevention of diet-induced obesity in *Mstn*^{-/-} mice.

Table 5.1 GSEA gene cluster subgroups

ID	Gene symbol	Gene Name	Subgroups	Database	regulation
NM_015803	ATP8A2	ATPase, aminophospholipid transporter-like, class I, type 8A, member 2	lipid localization lipid transport1 lipid transporter activity	GOTERM BP FAT GOTERM BP FAT GOTERM MF FAT	up
NM_029019	STARD6	STAR-related lipid transfer (START) domain containing 6	lipid localization lipid transport1 lipid transporter activity lipid transport2	GOTERM BP FAT GOTERM BP FAT GOTERM MF FAT SP_PIR_KEYWORDS	up
NM_013474	Apoa2	apolipoprotein A-II	lipid localization lipid transport1 lipid transport2	GOTERM BP FAT GOTERM BP FAT SP_PIR_KEYWORDS	up
NM_009693	Apob	apolipoprotein B	lipid localization lipid transport1 lipid transporter activity lipid transport2	GOTERM BP FAT GOTERM BP FAT GOTERM MF FAT SP_PIR_KEYWORDS	up
NM_173786	ApoBb;ApoB9a	apolipoprotein L 9b; apolipoprotein L 9a	lipid localization lipid transport1 lipid transporter activity	GOTERM BP FAT GOTERM BP FAT GOTERM BP FAT	up
NM_023733	CROT	carnitine O-octanoyltransferase	lipid localization lipid transport1 lipid transporter activity	GOTERM BP FAT GOTERM BP FAT GOTERM BP FAT	up
NM_146020	GLTPD2	glycolipid transfer protein domain containing 2	lipid localization lipid transport1 lipid transporter activity	GOTERM BP FAT GOTERM BP FAT GOTERM MF FAT	up
NM_010422	Hexb	hexosaminidase B	lipid localization lipid transport1 lipid transporter activity	GOTERM BP FAT GOTERM BP FAT GOTERM MF FAT	up
NM_009512	Slc27a5	solute carrier family 27 (fatty acid transporter), member 5	lipid localization lipid transport1 lipid transporter activity	GOTERM BP FAT GOTERM BP FAT GOTERM MF FAT	up
NM_001033174	OSBP	oxysterol binding protein	lipid localization lipid transport1 lipid transport2	GOTERM BP FAT GOTERM BP FAT SP_PIR_KEYWORDS	down
NM_152818	OSBP2	oxysterol binding protein 2; similar to oxysterol binding protein 2	lipid localization lipid transport1 lipid transport2	GOTERM BP FAT GOTERM BP FAT SP_PIR_KEYWORDS	down
XM_916664	ABCG4	similar to ATP-binding cassette, sub-family G (WHITE), member 4; ATP-binding cassette, sub-family G (WHITE), member 4	lipid localization lipid transport1	GOTERM BP FAT GOTERM BP FAT	down

5.3.7 Up-regulation of genes involved in lipid uptake in *Mstn*^{-/-} WAT

TAG in food is absorbed in the intestine mostly as chylomicron, and transported to peripheral tissues such as liver, adipose tissue and skeletal muscle [212-213]. TAG is broken down into free fatty acids (FFA) at the luminal surface of endothelial cells inside capillaries, with the FFAs subsequently absorbed by the underlying tissue. Therefore, perturbations in the levels of enzymes that are involved in lipid uptake and transport would lead to altered accumulation of fat in adipose tissue. Microarray analysis revealed that during CD feeding, *Mstn*^{-/-} WAT displayed significant up-regulation (4.14-fold) ($P \leq 0.05$) of the lipid uptake inhibitor *Apoc3*, with no significant change in lipid uptake enzymes (*Lpl*, *Ldlr*) ($P > 0.05$ or < 1.5 -fold) (Supplementary Table 5.1). Similarly, during HFD challenging, we also observed an increase (2.64-fold) ($P \leq 0.05$) in *Apoc3* gene expression in *Mstn*^{-/-} WAT, with no significant change in either *Lpl* or *Ldlr* expression ($P > 0.05$ or < 1.5 -fold) (Supplementary Table 5.1). Consistent with the microarray result, qPCR analysis revealed a 2.4-fold ($P < 0.05$) increase in *Apoc3* gene expression in *Mstn*^{-/-} mice during HFD feeding, when compared to relevant WT mice controls (Figure 5.5). Therefore, *Apoc3* gene expression appears to be up-regulated in *Mstn*^{-/-} WAT, which is consistent with reduced lipid uptake in *Mstn*^{-/-} mice during HFD feeding.

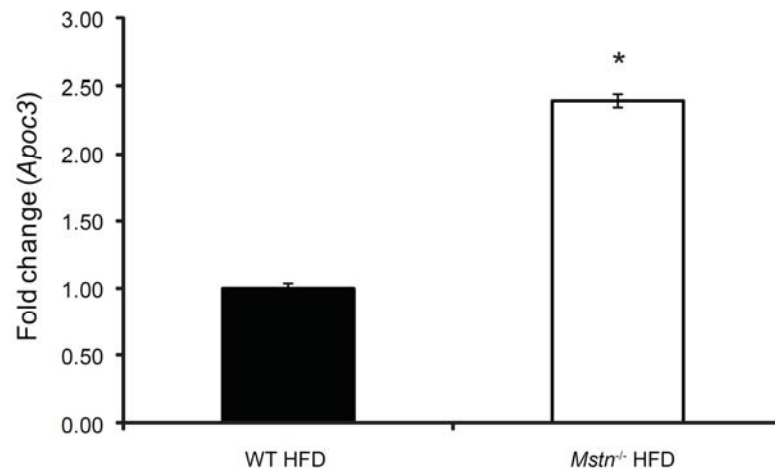


Figure 5.5 Relative mRNA expression levels of *Apoc3*

Relative mRNA expression levels of *Apoc3* normalized to *Gapdh* mRNA expression in WAT (Epididymal) as measured by qPCR in WT and *Mstn*^{-/-} mice after 12weeks of CD and HFD treatment. *P < 0.05. Error bars represent ±SEM (n = 2).

5.4 Discussion

Previous results from our laboratory demonstrate that lack of *Mstn* promotes the development of a lean phenotype and improved insulin sensitivity during HFD feeding via enhanced AMPK and PPAR signaling [73, 209]. However, the exact mechanism(s) through which the atrophied phenotype of *Mstn*^{-/-} WAT is maintained, during HFD feeding, remains unclear. In an attempt to further clarify this, we have employed for the first time global gene expression (microarray) analysis to compare gene expression changes in WAT collected from WT and *Mstn*^{-/-} mice fed either CD or HFD. Microarray data was analyzed using a pathway-based approach with Volcano analysis, Hierarchical clustering analysis, GO analysis, Venn analysis and GSEA analysis performed. Volcano analysis was performed to detect differentially expressed genes between the four treatment groups used in this current study: (i) WT group (comparison of WT HFD and CD fed mice), (ii) *Mstn*^{-/-} group (comparison of *Mstn*^{-/-} HFD and CD fed mice), (iii) HFD group (comparison of WT and *Mstn*^{-/-} HFD fed mice) and (iv) CD group (comparison of WT and *Mstn*^{-/-} CD fed mice). Hierarchical clustering analysis aimed to determine the relationship between the differential gene expression profiles of the four groups; GO analysis revealed the functional categories of the differentially regulated genes; Venn analysis identified differentially expressed genes that were both exclusive and commonly regulated between WT and *Mstn*^{-/-} mice fed either CD or HFD and GSEA further revealed the functional groups of the differentially expressed genes that were unique to *Mstn*^{-/-} and WT mice following HFD feeding.

Subsequent Volcano and Venn analysis revealed that there are a similar number of differentially regulated (Volcano analysis 818 vs. 866 [WT vs. *Mstn*^{-/-}]; Venn analysis 1134 vs. 1225 [WT vs. *Mstn*^{-/-}]), and for that matter up- (Volcano analysis 282 vs. 354 [WT vs. *Mstn*^{-/-}]; Venn analysis 319 vs. 428 [WT vs. *Mstn*^{-/-}]) or down-regulated (Volcano analysis 536 vs. 512 [WT vs. *Mstn*^{-/-}]; Venn analysis 745 vs. 727 [WT vs. *Mstn*^{-/-}]), genes between HFD fed WT and *Mstn*^{-/-} mice, when compared to their respective genotype-specific CD fed controls (Figure 5.1A&5.1B&5.4A-C). In addition, HFD feeding regimen resulted in a reduction in the total number of differentially expressed genes between *Mstn*^{-/-} mice and WT mice, when compared to CD fed *Mstn*^{-/-} mice vs. WT mice (Volcano analysis 1453 vs. 942 [CD vs. HFD]; Venn analysis 1894 vs. 1504 [CD vs. HFD]) (Figure 5.1C&5.1D&5.4D-F). Taken together these data indicate that WT and *Mstn*^{-/-} mice may have a similar gene expression profile upon HFD and that there may be an increase in the number of genes that have a common expression pattern between *Mstn*^{-/-} and WT mice in response to HFD regimen; further suggesting that *Mstn*^{-/-} mice may be adopting a gene expression profile more associated with HFD-induced obesity, as observed in HFD fed WT mice. In agreement with this we do observe an increase in adipose tissue mass in HFD diet fed *Mstn*^{-/-} mice when compared to CD fed *Mstn*^{-/-} mice (Figure 3.1F). However, it is important to mention that the increase in adipose tissue weight observed in *Mstn*^{-/-} mice was not statistically significant (Figure 3.1F). Moreover, as we observed a greater number of up-regulated genes in *Mstn*^{-/-} mice vs. WT mice upon HFD feeding, and a greater number of down-regulated genes in *Mstn*^{-/-} mice vs. WT mice fed normal CD, we suggest that the overall gene expression profile observed in WAT from *Mstn*^{-/-} mice differs from that of WT mice in both HFD and CD fed conditions (Figure 5.1C&5.1D, Supplementary Table 5.1). Consistent with this, Venn analysis revealed

that the vast majority of differentially expressed genes in HFD vs. CD fed *Mstn*^{-/-} mice were different from those detected in HFD vs. CD fed WT mice. In fact, only 73 differentially expressed genes were common to both *Mstn*^{-/-} and WT mice, which further suggests that HFD feeding results in a very distinct differential gene expression profile between WT and *Mstn*^{-/-} mice. These data are also in agreement with the Heirarchical clustering analysis results, which showed that the differentially expressed genes observed in HFD fed *Mstn*^{-/-} mice clustered more closely with the gene expression profiles observed in both CD fed WT and *Mstn*^{-/-} mice, rather than HFD fed WT mice (Figure 5.2). Taken together HFD feeding appears to induce a fundamentally different response between WT and *Mstn*^{-/-} mice, which we propose may form the underlying mechanism through which absence of Mstn protects against diet-induced obesity (See Chapter 3 and Chapter 4).

GO analysis revealed that the majority differentially expressed genes were separated into biological process and molecular function categories, rather than the cellular component category. Interestingly, although almost all of the differentially expressed genes detected in HFD vs. CD fed *Mstn*^{-/-} mice were different from those detected in HFD vs. CD fed WT mice (Figure 5.4A), we find that the percentage of these genes categorized into biological process, cellular component and molecular function are almost identical between *Mstn*^{-/-} (HFD vs. CD fed) and WT (HFD vs. CD fed) mice (Figure 5.3A&5.3B). In addition, when we compare the percentages of the genes separated into the three categories between CD (*Mstn*^{-/-} vs. WT) and HFD (*Mstn*^{-/-} vs. WT) fed mice we observe a noticeable change. Specifically, we observed reduction in the percentage (from 35% to 21%) of genes in the molecular function category and an increase in the percentage (from 16% to 35%) of genes assigned to the cellular

component category in HFD fed mice (*Mstn*^{-/-} vs. WT), when compared to CD fed mice (*Mstn*^{-/-} vs. WT). Therefore it is interesting to surmise that the increased percentage of differentially expressed genes observed in the cellular component category may be indicative of the difference in the response between *Mstn*^{-/-} and WT mice to HFD feeding.

We suggest genes that are exclusively expressed in *Mstn*^{-/-} mice in response to HFD are of particular interest and may be potential targets for further study regarding the role of Mstn in lipid metabolism. As such we selected this exclusive set of genes for further GSEA. Subsequent GSEA revealed a functional group, with a high gene enrichment score (2.08), exclusively expressed in *Mstn*^{-/-} mice. Specifically, genes associated with lipid localization and lipid transport were enriched in *Mstn*^{-/-} mice, which we suggest may play a role in the maintaining the atrophied WAT phenotype in *Mstn*^{-/-} mice challenged with HFD (Table 5.1, Supplementary Table 5.4). Among the genes identified *ATP8A2*, *STARD6*, *Apoa2*, *Apob*, *Apol9b*, *CROT*, *GLTPD2*, *Hexb* and *Slc27a5* were up-regulated, while *OSBP*, *OSBP2*, *ABCG4* were down-regulated exclusively in *Mstn*^{-/-} WAT during HFD challenge. Interestingly, *OSBP*, which is located in cytosol, functions to down-regulate cholesterol synthesis and stimulate cholesterol esterification [214-215]. Therefore, exclusive down-regulation of *OSBP* in *Mstn*^{-/-} WAT during HFD challenge may suggest that there is reduced cholesterol storage in *Mstn*^{-/-} WAT, when compared to WT mice WAT. In addition, Carnitine Octanoyltransferase (Crot) plays an important role in fatty acid degradation. During the obesity state, hyperinsulinemia has been shown to lead to the up-regulation of miR-33b, which represses *Crot* expression, leading to TAG accumulation [216]. Therefore,

it is interesting to surmise that up-regulation of *Crot* in *Mstn*^{-/-} WAT may indicate reduced lipid accumulation.

High calorie intake did not impair the mRNA expression of the enzyme *Apoc3*, which may function to counteract increased lipid consumption (although *Mstn*^{-/-} mice already displayed a significant increase in *Apoc3* gene expression during CD feeding). *Apoc3* is a critical negative regulator of lipid uptake due to its function in inhibiting the key lipid uptake enzyme, LPL. In support, *Apoc3*^{-/-} mice have increased storage of fatty acid in WAT, causing more susceptibility to diet-induced obesity and insulin resistance [217]. Moreover, in humans, a high risk of non-alcoholic fatty liver disease and further liver fibrosis was observed in subjects that express *Apoc3* risk variants [218]. Our global gene expression study clearly showed that *Mstn*^{-/-} WAT displayed significant up-regulation (4.14-fold) of *Apoc3* expression, when compared to WT mice (Supplementary Table 5.1), which was maintained upon HFD feeding (2.64-fold) (Supplementary Table 5.1). Consistent with the microarray result, qPCR analysis revealed a significant 2.4-fold induction of WAT *Apoc3* gene expression (Figure 5.5), in response to high calorie loading in *Mstn*^{-/-} mice when compared with WT controls. Therefore, *Apoc3* may be a potential candidate gene responsible for the atrophied WAT phenotype in *Mstn*^{-/-} mice and may exert its function through down-regulating *Lpl* activity, further limiting lipid uptake in WAT.

In summary, lack of *Mstn* protects against gene profile changes that occur during HFD challenge. Furthermore these data presented in this chapter suggest that the atrophied WAT documented in *Mstn*^{-/-} mice may be explained through a combination of

significantly reduced lipid uptake and decreased lipid storage. We further propose that the excess lipid generated from HFD feeding may be preferentially transported to peripheral tissues to generate energy, which is quite consistent with the significantly increased fatty acid oxidation and BAT phenotype observed in *Mstn*^{-/-} mice (see Chapter 3 and 4).

Chapter 6 Myostatin-null Mice Exhibit Delayed Skin Wound Healing through the Blockage of Transforming Growth Factor- β Signaling by Decorin

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Myostatin-null mice exhibit delayed skin wound healing through the blockade of transforming growth factor- β signaling by decorin

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Abstract

Myostatin (Mstn) is a secreted growth and differentiating factor that belongs to the transforming growth factor- β (TGF- β) superfamily. Mstn has been well characterized as a regulator of myogenesis, and is shown to play a critical role in postnatal muscle regeneration. Herein, we report for the first time that Mstn is expressed in both the epidermis and dermis of murine and human skin. Furthermore, we found that Mstn-null (*Mstn*^{-/-}) mice exhibited delayed skin wound healing due to a combination of effects resulting from delayed epidermal re-epithelialization and dermal contraction. In the epidermis, reduced keratinocyte migration and protracted keratinocyte proliferation were observed, which subsequently led to delayed recovery of epidermal

thickness and slower re-epithelialization. Consistent with this observation, primary keratinocytes derived from *Mstn*^{-/-} mice displayed reduced migration capacity as assessed through *in vitro* migration and adhesion assays. Furthermore, *Mstn*^{-/-} primary keratinocytes also exhibited an increased proliferation rate as indicated by BrdU incorporation and Western blotting analysis. Moreover, in the underlying dermal layer, both fibroblast-to-myofibroblast transformation and collagen deposition were concomitantly reduced, resulting in the delayed dermal wound contraction. These decreases are due to the inhibition of TGF- β signaling as a result of an elevated expression of decorin, a naturally occurring TGF- β suppressor, in the *Mstn*^{-/-} mice. These observations highlight the interplay between TGF- β and Mstn signaling pathways, specifically, through regulation of Mstn-regulated decorin levels during the skin wound healing process. Thus, we propose that Mstn agonist might be beneficial for skin wound repair.

Keywords: Myostatin, Wound healing, Decorin, Skin, TGF- β .

6.1 Introduction

Skin wound healing is critical for the maintenance of skin homeostasis after acute skin injury. The skin consists of two major layers: epidermis, the upper layer consisting of numerous cell types which include keratinocytes, melanocytes, Langerhans, and Merkel cells; and dermis, the lower layer of connective tissue including collagen and elastic fibers. After deep skin injury, wound healing can be categorized into four processes (i.e. inflammation, migration, proliferation, and maturation) which overlap spatio-temporally. During the inflammatory phase, a blood clot is formed at the wounded area to prevent excessive blood loss, followed by vasodilation and secretion of key growth factors such as TGF- β and platelet-derived growth factor (PDGF) from inflammation-responsive cells; which further facilitate the influx of macrophages, neutrophils, and mesenchymal stem cells to the site of injury. Next, peri-wound keratinocytes become activated to form a migratory tongue from each side of the wound edge. This involves the migration of cells from the unwounded area of the stratum basale to form a repair bridge covering the underlying re-generating dermis, where the activated myofibroblasts migrate to, and the formation of granulation tissue takes place to regenerate the wound bed. During the proliferative and maturation phases, the activated and alpha-smooth muscle actin (α -SMA)-expressing myofibroblasts undergo augmented proliferation and increase the production of collagen and vessels that eventually fill the wound area.

Growth factors play a major role in skin wound healing. Several studies have unravelled the important function of TGF- β 1 in skin wound healing. It is reported that TGF- β 1 stimulates collagen deposition and extracellular matrix growth, resulting in the accumulation of fibrotic tissue, suggesting that TGF- β as an important mediator during fibrosis [219]. This is further supported by the observation that Smad3-null

mice (in which TGF- β signaling is perturbed) exhibit accelerated wound healing with reduced scarring [87]. Decorin, a small leucine-rich proteoglycan, is mainly expressed in connective tissue [220]. Being a crucial regulator of extracellular matrix assembly, decorin is able to bind to type I collagen fibrils [221-222], participating in the regulation of collagen fibril formation [223], thus modulating connective tissue formation, skeletal muscle cell differentiation, and migration [224-226]. Decorin has been reported to be a binding partner of TGF- β receptors, thereby it is an important regulator of TGF- β bioavailability and subsequent downstream signaling [227]. It has also been demonstrated that collagen-bound decorin can still interact with TGF- β [228], indicating that TGF- β can be immobilized to the ECM and prevented from interacting with its receptor at the cell membrane. Therefore decorin, by regulating bioavailability of TGF- β , plays a role in skin wound healing. It is noteworthy to mention that in addition to TGF- β , decorin can also sequester, and thus regulate the activity of, another TGF- β super-family member, Myostatin (Mstn) [229]. Mstn, also known as growth and differentiation factor 8 (GDF-8) is primarily expressed in skeletal muscle, but relatively low expression of Mstn has also been detected in adipose tissue [118] and heart [129]. In mice and humans, loss of Mstn leads to increased muscle growth due to both hypertrophy and hyperplasia [118, 122]. Therefore, Mstn functions as a negative regulator for skeletal muscle growth. Functionally, Mstn has been found to regulate not only the proliferation and differentiation of myoblasts [125, 138], but also the activation and proliferation of muscle stem cells, also known as satellite cells [139]. In a muscle regeneration study, Mstn-deficient mice demonstrated accelerated muscle healing accompanied by reduced fibrosis [92] due to enhanced activation of satellite cells, accelerated migration of macrophages and myoblasts into the injured area, and less fibrotic tissue

formation [92]. Although a number of reports have previously demonstrated that Mstn plays an important role in muscle regeneration through TGF- β signaling, its expression and role in skin wound healing is not known.

Herein, we demonstrate for the first time that Mstn is expressed in skin and its deficiency leads to delayed skin closure due to a delay in epidermal re-epithelialization and dermal contraction. We find that the delay in skin wound healing in Mstn-null (*Mstn*^{-/-}) mice is attributed to blockade of TGF- β signaling due to increased decorin expression during skin wound repair. These findings reveal Mstn as a novel regulator of skin wound healing, and suggest that Mstn agonist may be a potential therapeutic solution for the treatment of skin wounds.

6.2 Materials and Methods

6.2.1 Animals and human biopsy

The *Mstn*^{-/-} mice (C57BL/6) were kindly gifted by Dr. Se-Jin Lee (The Johns Hopkins University, Baltimore, MD, USA). Wild-type (WT) mice (C57BL/6) were obtained from the Centre for Animal Resources (National University of Singapore, Singapore). 2 mice per genotype per timepoint and all mice were derived from different litters. All experiments were performed according to the approved protocols of the Institute Animal Ethics Committee (IACUC), Singapore. The human biopsy was kindly provided by Dr. Cleo Choong Swee Neo (Nanyang Technological University, Singapore).

6.2.2 Skin wounding experiment and biopsy procurement

Six-week-old *Mstn*^{-/-} and WT female mice were first anaesthetised and the area assigned for wounding was shaved. Two 0.25 cm² (0.5 cm x 0.5 cm) excisional wounds were generated on the dorsal skin. Prior to the procurement of wound biopsies at specific time points (non-wounded and post-wounding day 1, 3, 5, 7, 10, 12, and 15), the wound area was measured using callipers. Mouse wound biopsies and the human biopsy were embedded in OCT compound before freezing in liquid nitrogen. Sections (6 μ m thickness) were subsequently cut using the Leica CM3050S cryostat microtome. The slides were stored at -20 °C until further use.

6.2.3 Antibodies

Details of the antibodies used in this manuscript are provided below: Anti-Ki67 and anti-cytokeratin 6 (K6) antibodies were purchased from Novocastra; anti- α -smooth muscle actin (α -SMA), anti-GDF8 (Mstn), anti-Phospho-Smad2/3 (p-Smad2/3) and anti-PCNA antibodies were from Santa Cruz Biotechnology; anti-decorin was obtained from Developmental Studies Hybridoma Bank; anti-Cyclin D1 was from Thermo Lab Vision; AlexaFluor[®] 488 goat anti-rabbit IgG, AlexaFluor[®] 594 goat anti-rabbit IgG, AlexaFluor[®] 594 goat anti-mouse IgG and streptavidin-conjugated AlexaFluor[®] 488 antibodies were from Molecular Probes, Invitrogen; biotinylated goat anti-rat IgG was from GE Healthcare Life Sciences; goat anti-rabbit HRP, goat anti-rat HRP and goat anti-mouse HRP were from Santa Cruz Biotechnology.

6.2.4 Histology

Hematoxylin and eosin (H&E) staining was performed as unpublished lab protocol described (details see section 2.2.26). Sections were fixed with 4% paraformaldehyde for 10 min, rinsed with water, and immersed in 0.1% HCl for 2 seconds. The sections were then stained with eosin for 27 seconds and hematoxylin for 150 seconds. Finally, sections were dehydrated and mounted with DPX. Images were captured using MIRAX MIDI slide scanner microscope (Carl Zeiss) with a 10x objective and MIRAX Scan software.

Van Gieson staining was performed as previously described [147] (details see section 2.2.27). Briefly, sections were stained with Weigert's iron hematoxylin and rinsed with water, followed by staining in Van Gieson solution for 5 min. Then the sections were immersed in 90% and 100% ethanol with 6 drops of saturated picric acid for 1 min respectively. Finally, sections were immersed twice in xylene (5 min each) and

mounted with DPX. Images were captured using MIRAX MIDI slide scanner microscope (Carl Zeiss) with a 10x objective and MIRAX Scan software.

6.2.5 Immunohistochemistry

Detailed description of immunohistochemistry was listed in section 2.2.28. Cryosections were fixed in 100% acetone at -20 °C for 5 min and then rinsed with 1x PBS for 5 min. Antigen retrieval was performed only for Ki67 immunostaining. For antigen retrieval, sections were immersed in 95-100 °C citrate buffer (pH = 6.0) for 10 min and then cooled for 30 min. Next, sections were blocked with their respective blocking buffer for a specific incubation time in a humid chamber. Sections were then incubated with the respective primary and secondary antibodies as described above, with exception of Mstn, which was detected using a streptavidin-conjugated tertiary antibody. Finally, sections were mounted with DAPI-containing mounting media (Vector Laboratories).

6.2.6 Isolation and culture of primary mouse keratinocyte

Primary mouse epidermal keratinocytes were isolated from neonates (0–2 days old) according to the protocols previously described with slight modifications [230]. Briefly, pups were decapitated with limbs and tail removed. A ventral cut was made from neck to tail and the whole skin was peeled off. Each skin was then submerged in 3 ml of cold dispase solution (0.5 U/ml) overnight at 4 °C. Epidermis and dermis were separated the next day with fine forceps. Epidermis extracted from 5–8 pups were pooled and transferred to a 50-ml tube containing 10 ml of low-calcium (0.06 mM) SFM keratinocytes medium (Invitrogen) supplemented with recombinant epidermal

growth factor (0.4 ng/ml) and bovine pituitary extract (40 μ g/ml). Epidermal keratinocytes were mechanically separated by vigorous shaking for 20 s. Cell clumps were then removed by passing the cell suspension through a 100- μ m cell strainer. Cultures were maintained in a 5% CO₂ 37°C humidified incubator. Medium was changed every 2 days and cells were subcultured upon reaching 70% confluence. For subculture, medium was removed followed by washing the cells with PBS. Trypsin (0.25%), EDTA (1 mM) in PBS was added to the culture and incubated at 37°C for 10 min, after which the flask was rapped gently to dislodge cells from the surface. To neutralize the action of Trypsin, PBS containing 1% dialyzed fetal bovine serum was added, and the cells were collected by centrifugation at 160 $\times$ g for 5 min. The cell pellet was resuspended with fresh medium and subcultured in a new flask at 2.5×10^3 cells/cm².

6.2.7 *In Vitro* scratch-wound assay

Scratch-wound assay was based on the previous published protocol [231]. When primary cultured keratinocytes reached confluence, a pipette tip was used to scratch a line followed by washing with PBS to remove scratched cells. Mitomycin C was added at the concentration of 2 μ g/ml to inhibit cell proliferation prior to image capture at 5-min intervals over 12 h with a Carl Zeiss live imaging microscope.

6.2.8 Cell proliferation assay

To determine cell proliferation rate of WT and *Mstn*^{-/-} primary keratinocytes, primary keratinocytes were seeded at a density of 2.5×10^3 cells/cm². Cells were pulsed with BrdU (10 μ l of 1 mM BrdU per ml of medium) and the cells were then incubated for a

further 5 consecutive days in the presence of BrdU. Cells were then stained using the FITC BrdU Flow kit and quantified by flow cytometry (FACS), as per the manufacturer's protocol (Becton Dickinson).

6.2.9 Cell adhesion assay

Primary keratinocytes of similar passage number (3-5 passages) were seeded onto a 96-well plate at a density of 2×10^4 cells/well. At the indicated time points, cells that were not adhered to the surface were removed by three washes with $1 \times$ PBS. Attached cells were then fixed with 1% glutaraldehyde for 15 min followed by incubation with 0.05% crystal violet for 10 min at room temperature. After staining, excess dye was removed and the cells were then washed three times with $1 \times$ PBS. The plate was subsequently dried at room temperature overnight, after which, 50 μ l of 1% triton-X/PBS was added to each well to solubilize the dye. The absorbance of the crystal violet was read at OD_{590nm}.

6.2.10 RNA extraction and quantitative real-time PCR (qPCR)

Detailed description of RNA extraction and qPCR were listed in section 2.2.3, 2.2.4, 2.2.5, 2.2.7, and 2.2.8. Total RNA was extracted from the skin wound biopsy using TRIzol reagent, as per the manufacturer's instructions (Invitrogen). RNA was further purified using the RNeasy mini kit (Qiagen) prior to cDNA synthesis using the Superscript II First strand synthesis system (Invitrogen) from 1 μ g of total RNA. qPCR was performed in duplicate in 10 μ l reactions using Sso Fast Evagreen (Bio-Rad) in the CFX96 real-time PCR machine (Bio-Rad). Primer sequences used in this study are listed in Table 6.1.

Table 6.1 Primer sequences used in qPCR

	Forward	Reverse
TGF- β 1	CCGCAACAACGCCATCTATG	CTCTGCACGGGACAGCAAT
Ki67	CTGCCTCAGATGGCTCAAAGA	GAAGACTTCGGTTCCTGTAAAC
FGF2	GCGACCCACACGTCAAATA	TCCCTTGATAGACACAACCTCCTC
Mstn	CATATGGATTTTGGTCTTGACTGT GAT	CATATGTCATGAGCACCCACAGC GGTC

6.2.11 Immunoblotting

Detailed description of immunoblotting was listed in section 2.2.2. Skin wound biopsies were homogenized in protein lysis buffer containing 50 mM Na₂H₂PO₄, 250 mM NaCl, 1% Triton X-100, and 0.1% SDS. This was followed by centrifugation at 12,000 rpm for 15 min. The supernatant was collected and 10 μ g of the extracted proteins were resolved by 4–12% NuPAGE (Invitrogen) followed by transfer onto a nitrocellulose membrane. Membranes were blocked with polyvinylpyrrolidone (PVP) blocker (1% PVP, 1% polyethylene glycol, and 0.3% bovine serum albumin in TBST) for 1 h. Primary and secondary antibodies were both incubated in the PVP blocking solution overnight and for 1 h, respectively. Immunoreactivity was detected through enhanced chemiluminescence.

6.2.12 Statistical analysis

Mann-Whitney test was used for statistical analysis of cell migration and adhesion assay. Two-tailed Student's *t*-test was used for all other statistical significance determinations. $P < 0.05$ was considered statistically significant. Error bars represent $\pm$ SEM.

6.3 Results

6.3.1 Expression of Mstn is restricted to the epidermis, dermis and hair follicles in skin

As a first step towards understanding the role of Mstn in skin wound healing, we determined the expression of Mstn in skin. Our qPCR results showed that Mstn was expressed in skin, and that the expression was relatively lower than in muscle (Figure 6.1A). Immunohistochemical analysis in mouse (Figure 6.1C) and human (Figure 6.1D) showed that Mstn was highly expressed in the epidermal layer while lower levels of Mstn expression were seen in the dermis and hair follicles. Consistent with the result from qPCR and immunohistochemical analysis, western blotting analysis also revealed a detectable level of Mstn protein during skin wound healing (Figure 6.1B). The distribution of Mstn in skin suggests that Mstn may play an important role in epidermis and dermis during skin wound repair.

Figure 6.1 *Expression of Mstn is restricted to the epidermis, dermis and hair follicles in skin.*

(A) Relative fold change of Mstn mRNA expression levels normalized to L27 mRNA expression levels in skin and muscle of WT mice as measured by qPCR. (B) Mstn protein level in skin of WT mice at specific time points during skin wound healing as measured by Western blotting analysis. Both full-length and mature Mstn are expressed in skin during wound healing. Representative images of Mstn immunostaining on WT skin in mouse (C) and human (D). Mstn (green)-immunostained cryosections were counterstained with DAPI (nuclei; blue). Arrows indicate Mstn positive cells are on epidermis, hair follicles and dermis. Negative control (Non-primary antibody control) images indicate non-specific staining. White dashed lines demarcate the epidermis from the dermis. Scale bar: 100 μ m. **P < 0.01. Error bars represent $\pm$ SEM, n = 5.

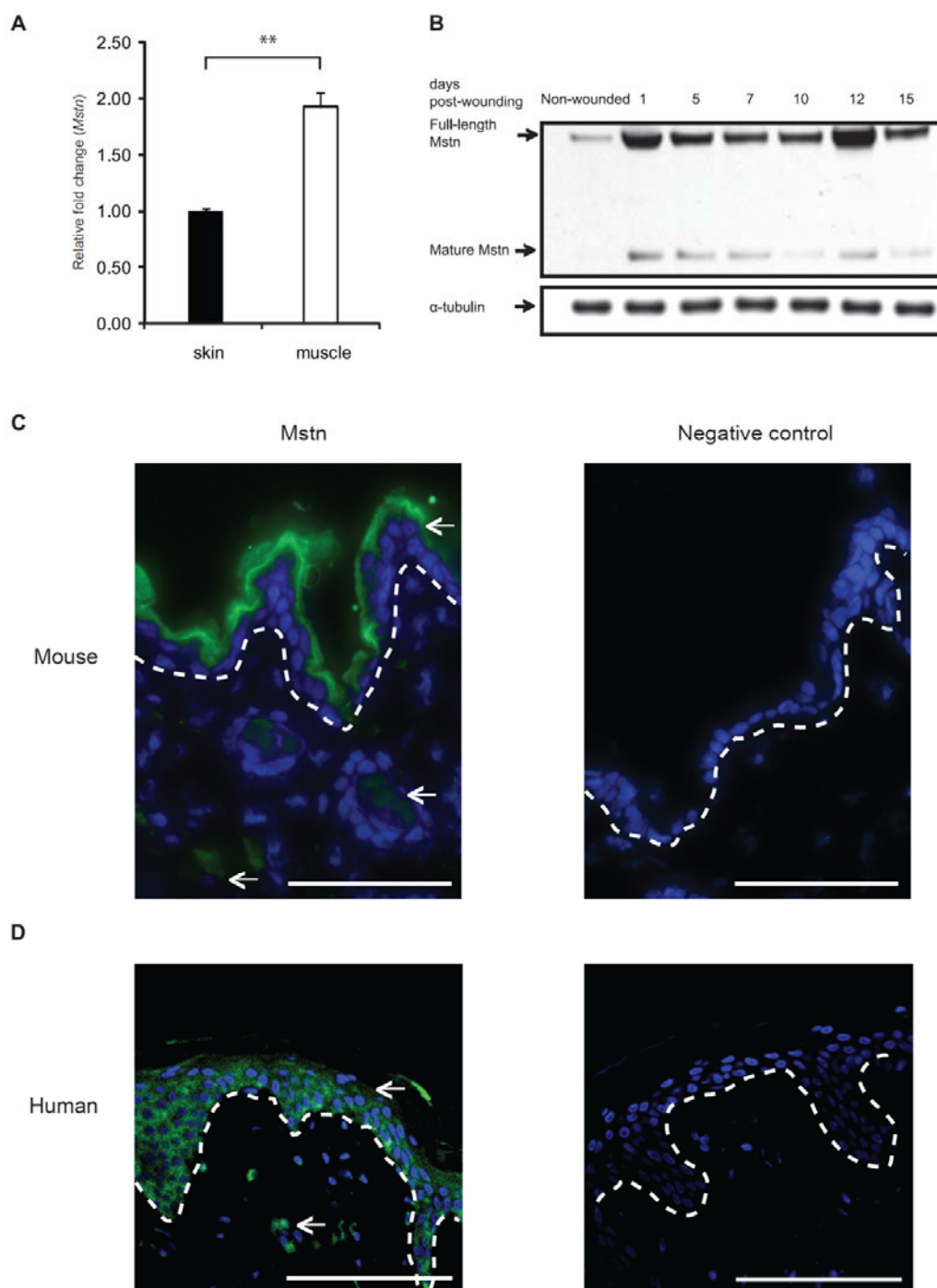
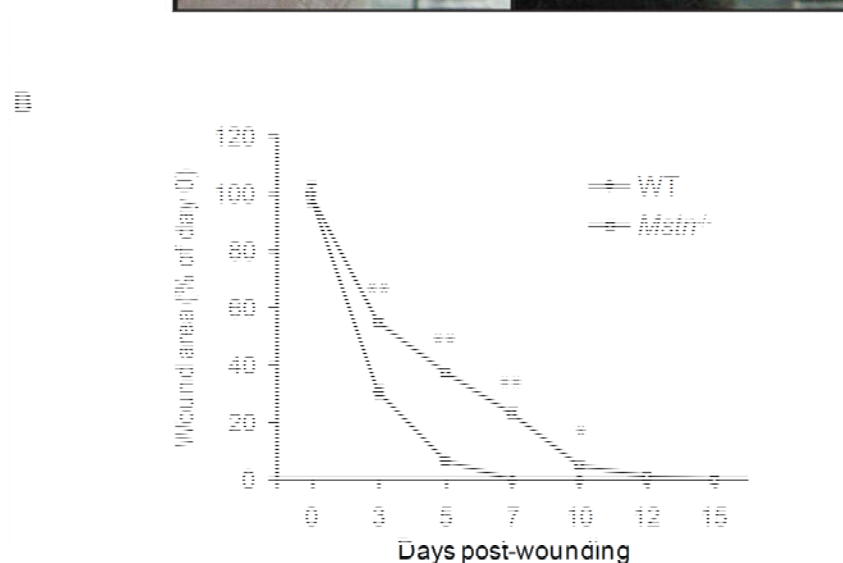
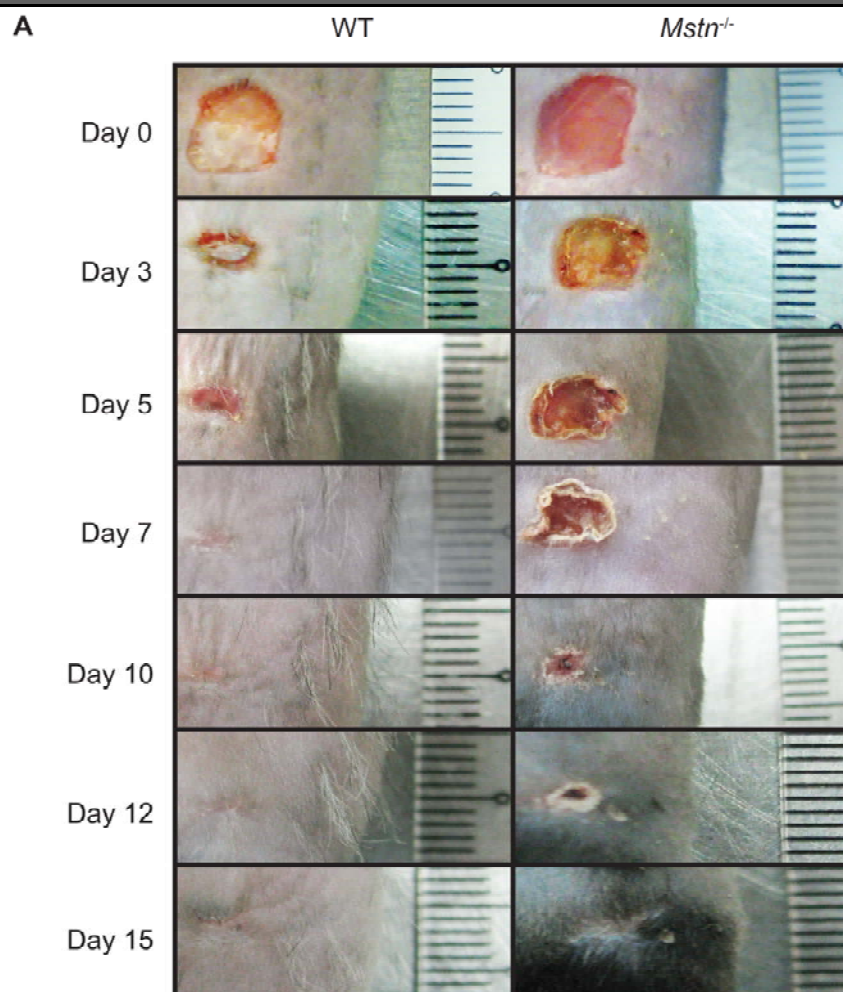


Figure 6.2 *Delayed wound healing in $Mstn^{-/-}$ mice.*

(A) Images of skin wounds at different time points after excisional wounding. $Mstn^{-/-}$ mice exhibited delayed wound healing. Small divisions of ruler =1 mm. (B) Wound healing analysis of $Mstn^{-/-}$ mice and their WT littermates. Average wound area was presented as percentage of the wound area on day 0 (100%). * $P < 0.05$, ** $P < 0.01$. Error bars represent $\pm$ SEM, $n = 5$.



6.3.2 Delayed wound healing in *Mstn*^{-/-} mice

A significant difference in wound healing duration was observed between WT and *Mstn*^{-/-} mice (Figure 6.2A). Following full-thickness excisional wounding, the rate of wound healing was delayed in *Mstn*^{-/-} mice when compared to the WT mice as indicated by the wound area (Figure 6.2B). In particular, the wound area of *Mstn*^{-/-} mice was 1.78, 5.56, 23.39 and 5.13-fold larger than that of the WT mice at post-wounding day 3, 5, 7 and 10 respectively ($P < 0.05$). An approximate delay of 8 days in complete wound closure was observed in the *Mstn*^{-/-} mice as compared to the WT mice, with similar wound healing observed between *Mstn*^{-/-} mice on day 15 and WT controls on day 7 post-wounding.

6.3.3 Slower wound healing in *Mstn*^{-/-} mice is due to delayed re-epithelialization and wound contraction

To determine the reason for delayed wound healing in *Mstn*^{-/-} mice, we performed histomorphometric analysis on the wounded skin biopsies at various time points (Figure 6.3A). As the rate of wound healing is mainly determined by the rate of re-epithelialization and the contractile action of myofibroblasts, we measured several parameters, including area and length of migratory tongues, thickness of epidermis, and the distance between the peri-wound hair follicles. The initial proliferation rate of keratinocytes is indicated by the area of migratory tongues. The area of migratory tongues on day 3 post-wounding in *Mstn*^{-/-} mice was significantly smaller than WT mice (WT vs. *Mstn*^{-/-}: $73752.63 \pm 5542.14 \mu\text{m}^2$ vs. $47978.37 \pm 338.35 \mu\text{m}^2$, $P < 0.05$) (Figure 6.3B), implying slower proliferation of migratory tongues (keratinocytes) at the initial stage of wound healing. The length of migratory tongues in *Mstn*^{-/-} mice was also found to be significantly reduced when compared to WT mice on day 3 post-wounding (WT vs. *Mstn*^{-/-}: $194.03 \pm 21.7 \mu\text{m}$ vs. $70.88 \pm 2.06 \mu\text{m}$, $P < 0.05$) (Figure 6.3C). Smaller area and shorter length of migratory tongues in *Mstn*^{-/-} mice, during the initial stage of wound healing, is indicative of decreased migration of keratinocytes in *Mstn*^{-/-} mice. In addition to reduced keratinocyte proliferation, we also observed that the wounded epidermal region in the *Mstn*^{-/-} mice was significantly thicker than WT mice after 10 days post-wounding (WT vs. *Mstn*^{-/-}: $68.82 \pm 2.39 \mu\text{m}$ vs. $108.72 \pm 4.94 \mu\text{m}$ respectively, $P < 0.01$) (Figure 6.3D). Taken together, these data suggest that there is delayed re-epithelialization in *Mstn*^{-/-} mice during skin wound regeneration. Next we assessed the extent of dermal wound contraction, as quantified by the distance between peri-wound hair follicles. As shown in Figure 6.3E, we observed a significant increase in the distance between peri-wound hair follicles in *Mstn*^{-/-} mice

(WT vs. *Mstn*^{-/-}: $1266.76 \pm 26.59 \mu\text{m}$ vs. $1560.57 \pm 7.03 \mu\text{m}$, $P < 0.01$) at day 10 post-wounding (Figure 6.3E), which is indicative of reduced dermal wound contraction. In summary, we conclude that the slower wound healing observed in *Mstn*^{-/-} mice is a result of delayed re-epithelialization and wound contraction.

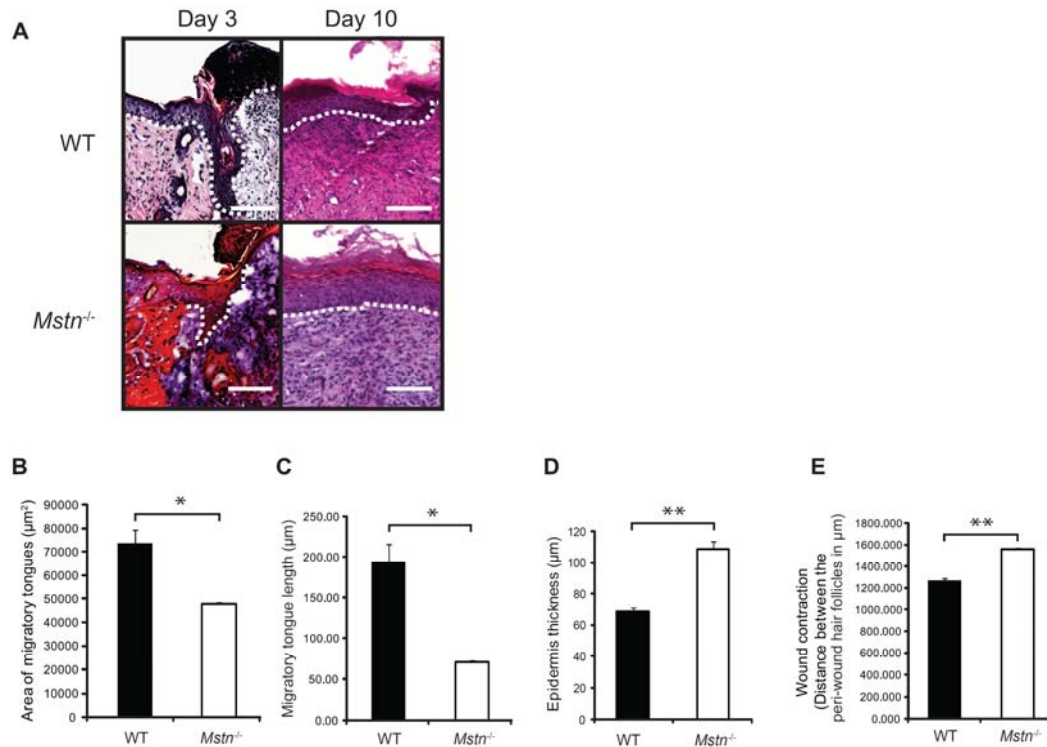


Figure 6.3 Slower wound healing in *Mstn*^{-/-} Mice is due to delayed re-epithelialization and wound contraction.

(A) H&E staining of WT and *Mstn*^{-/-} mice wound biopsies on day 3 and day 10 post-wounding. White dashed lines demarcate the epidermis from the dermis. Scale bar: 100 μ m. (B) Area of migratory tongues on day 3 post-wounding, presented in μ m². (C) Length of migrating tongue on day 3 post-wounding. (D) Epidermis thickness on day 10 post-wounding. (E) Distance between the peri-wound hair follicles on day 10 post-wounding, as a measure of the extent of wound contraction. *P < 0.05, **P < 0.01. Error bars represent $\pm$ SEM, n = 5.

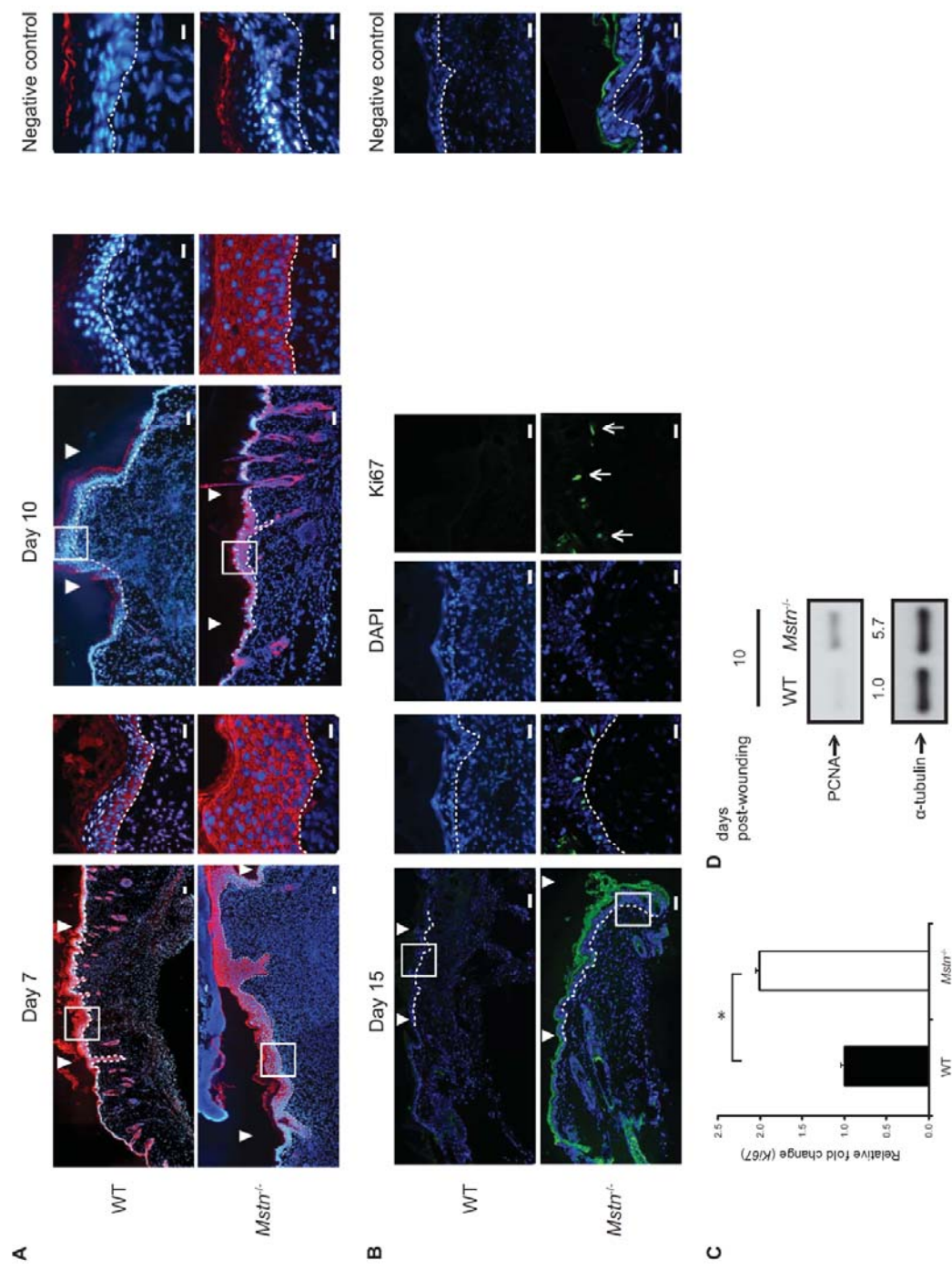
6.3.4 Delayed recovery to normal epidermal thickness is due to protracted keratinocyte proliferation in *Mstn*^{-/-} mice

To determine whether *Mstn* affects the proliferation of keratinocytes, resulting in the observed delay in recovery to normal epidermal thickness, we next stained sections with anti-K6 antibody, which is used as a marker of the hyperproliferative regions of the wound biopsies. On day 7 post-wounding, the enhanced K6 expression coincided with the increase in epidermis thickness in *Mstn*^{-/-} mice. On day 10, K6 expression was dramatically higher in *Mstn*^{-/-} mice compared to WT mice (Figure 6.4A). Ki67 is a molecular marker for proliferating cells, therefore, to detect whether or not there is protracted proliferation of cell populations in the wound site of *Mstn*^{-/-} mice, we performed Ki67 staining. As shown in Figure 6.4B, *Mstn*^{-/-} mice exhibited increased proliferative cells on day 15, whereas few Ki67 positive cells were detected in WT mice (Figure 6.4B). To further strengthen our findings, we performed qPCR analysis of Ki67 mRNA expression. On day 10, nearing the end of the skin wound healing period, we found relatively higher Ki67 expression in *Mstn*^{-/-} mice as compared with WT controls (Figure 6.4C); moreover, increased PCNA protein abundance was also observed in *Mstn*^{-/-} mice on day 10 post-wounding (Figure 6.4D), supporting the presence of increased numbers of proliferating cells in *Mstn*^{-/-} mice. To analyze keratinocyte proliferation *in vitro*, we assessed the proliferation rate of primary keratinocytes extracted from WT and *Mstn*^{-/-} mice through BrdU staining and FACS analysis and also assessed the expression of markers associated with proliferation via Western blotting analysis. Consistent with enhanced proliferation, we observed a significant increase in number of keratinocytes positive for BrdU (81.1% vs. 55.7% of the 20,000 cells sampled using FACS) from *Mstn*^{-/-} mice when compared to WT keratinocytes, indicating that keratinocytes isolated from *Mstn*^{-/-} mice exhibit

prolonged proliferation when compared to WT controls (Figure 6.5A). Furthermore, we also observed more than 2.5-fold increase in both PCNA and Cyclin D1 protein expression in isolated primary keratinocytes from *Mstn*^{-/-} mice when compared to WT (Figure 6.5B). Altogether, *Mstn*^{-/-} keratinocytes displayed protracted proliferation both *in vitro* and *in vivo*, which we suggest attenuates recovery of the epidermal layer to a normal thickness.

Figure 6.4 *Delayed recovery to normal epidermal thickness is due to protracted keratinocyte proliferation in $Mstn^{-/-}$ mice.*

(A) K6 immunofluorescence on WT and $Mstn^{-/-}$ mice wound biopsies on day 7 and day 10 post-wounding. Higher magnification images are listed at the right panel of each day. K6 (red)-immunostained cryosections were counterstained with DAPI (nuclei; blue). Negative control (Non-primary antibody control) images show non-specific staining of the stratum corneum. (B) Ki67 immunofluorescence on WT and $Mstn^{-/-}$ mice wound biopsies on day 15 post-wounding. Higher magnification images are exhibited at the right panel. Unmerged DAPI and Ki67 staining is also displayed respectively in higher magnification images. Ki67-positive cells are indicated by white arrows. Ki67 (green)-immunostained cryosections were counterstained with DAPI (nuclei; blue). Area with non-specific staining is indicated by negative control (Non-primary antibody control). White dashed lines demarcate the epidermis from the dermis. Scale bar: 50 μ m (20 μ m in higher magnification image). White arrows indicate wound edges and regions between arrows represent wounded area. White boxes indicate the regions used in higher magnification images. (C) Relative fold change of Ki67 mRNA expression levels normalized to L27 mRNA expression levels in skin at day 10 post-wounding as measured by qPCR in WT and $Mstn^{-/-}$ mice. (D) PCNA protein expression levels in skin of WT and $Mstn^{-/-}$ mice at day 10 post-wounding as measured by Western blotting analysis. Numbers under images indicate the fold changes of band density normalized to the first band. The levels of α -tubulin were assessed to ensure equal loading of samples. * $P < 0.05$. Error bars represent $\pm$ SEM, $n = 5$.



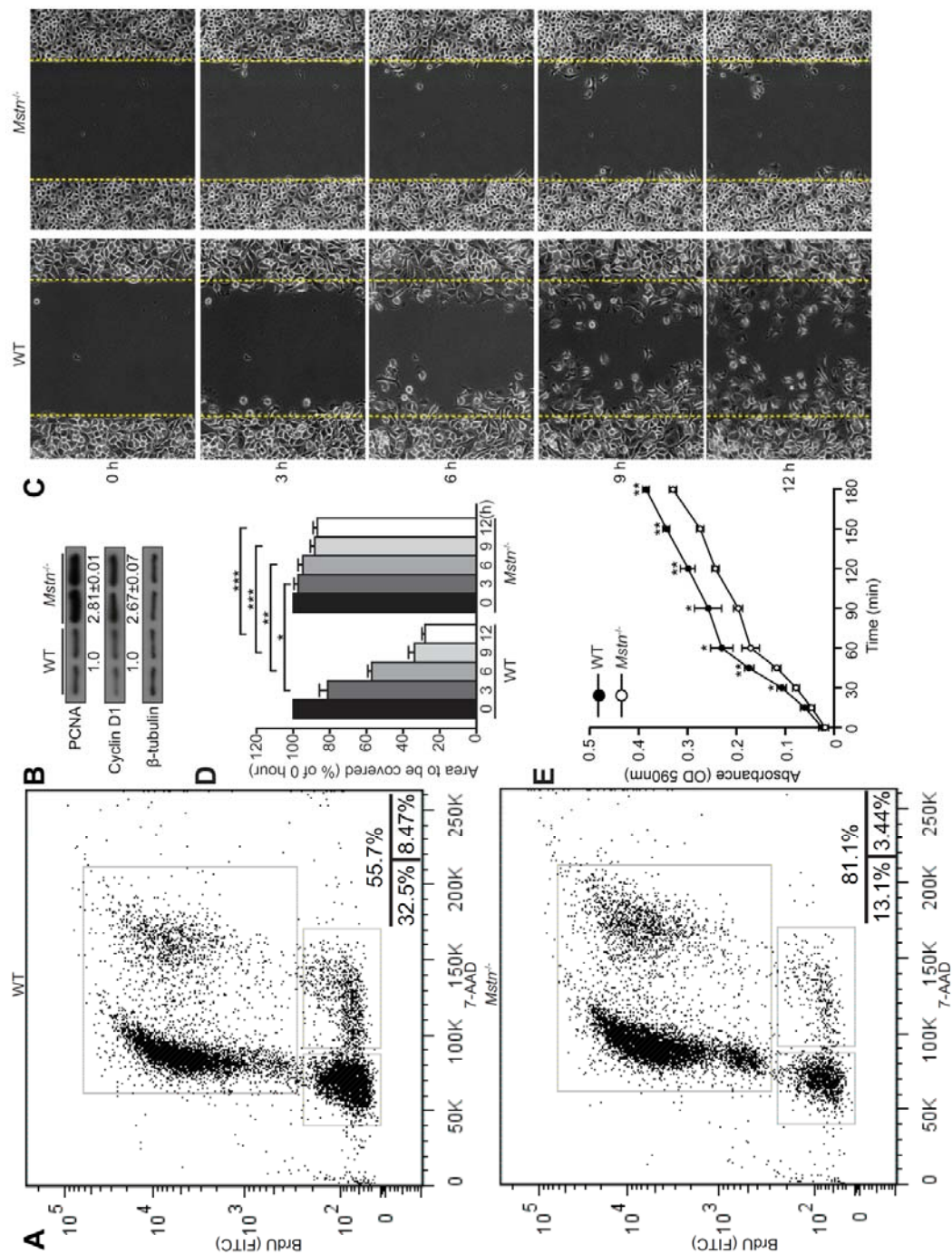
6.3.5 Delayed migration and impaired cell adhesion in keratinocytes isolated from *Mstn*^{-/-} mice

To analyze keratinocyte migration in further detail, we performed an *in vitro* scratch-wound assay [231] which mimics the *in vivo* keratinocyte migration during wound healing. As shown in Figure 6.5C, a significant delay in keratinocyte migration can be seen in *Mstn*^{-/-} cultures when compared to WT cultures. Next we quantified the extent of keratinocyte migration by measuring the area of the cell culture dish remaining uncovered (analogous to the *in vivo* wound gap) at each time point and expressing this as a percentage of 0 h. Subsequent quantification revealed a significant delay in keratinocyte migration in *Mstn*^{-/-} cultures, which was apparent at 3 h post-scratch wounding (with 80% and 95% of the gap area remaining when compared to 0 h for WT and *Mstn*^{-/-} respectively; $P < 0.05$), and further exaggerated at 6, 9 and 12 h post-scratch wounding (Figure 6.5C&6.5D).

Keratinocyte adhesion is an important marker for migration, whereby reduced adhesion is indicative of slower migration and increased apoptosis. Keratinocytes isolated from *Mstn*^{-/-} mice displayed decreased cell adhesion, in an *in vitro* cell adhesion assay, with a significant reduction in cell adhesion initially observed at 30 min ($P < 0.05$), and a sustained comparable reduction in cell adherence observed from 60 min onwards ($P < 0.05$) (Figure 6.5E). Taken together these data suggest that *Mstn*^{-/-} keratinocytes exhibit a decreased migratory rate, which we suggest results in delayed re-epithelialization.

Figure 6.5 *Increased proliferation, delayed migration and impaired adhesion in keratinocytes isolated from $Mstn^{-/-}$ mice*

(A) Cell proliferation analysis as measured through BrdU incorporation and FACS analysis in WT and $Mstn^{-/-}$ primary keratinocytes. (B) Immunoblot analysis of the indicated proliferation markers from WT and $Mstn^{-/-}$ primary keratinocytes. Values below the bands represent mean fold difference in protein expression levels when compared with WT, which was assigned the value 1. β -tubulin was assessed to ensure equal loading of samples. (C) Representative time-lapsed images of scratch-wounded primary keratinocyte cultures treated with mitomycin C (2 μ g/ml) showing the cell migration kinetics of WT and $Mstn^{-/-}$ primary keratinocytes at the indicated time points after scratch-wounding. Yellow dotted lines demarcate the scratch gap at the time of wounding. (D) The graph shows the area remaining to be covered by the migrating keratinocytes expressed as a percentage of 0 h (=100%) *in vitro* wound gap area. (E) Absorbance of crystal violet stain (OD_{590nm}) at the indicated time points after 2×10^4 WT and $Mstn^{-/-}$ primary keratinocytes were seeded. *P < 0.05; **P < 0.01; ***P < 0.001. Error bars represent $\pm$ SEM, n = 4.



6.3.6 Elevated decorin and reduced TGF- β expression in *Mstn*^{-/-} mice

It has been previously shown that TGF- β stimulates collagen deposition and extracellular matrix growth, leading to the accumulation of fibrotic tissue [219], fibroblast activation, and subsequent myofibroblast transformation [91, 232]. Activated myofibroblasts are essential for wound contraction by pulling together the wound edges to complete the skin wound healing process. It has been reported that decorin can compete with TGF- β by binding to the TGF- β receptor or through directly interacting with TGF- β to restrict its bioavailability, therefore inhibiting TGF- β signaling [227-228]. To determine the interplay between TGF- β and decorin proteins and how they regulate wound healing in *Mstn*^{-/-} mice, we examined the mRNA and protein expression profiles of these proteins during wound healing. We found that TGF- β gene expression was reduced in *Mstn*^{-/-} mice at all time points during wound healing (Figure 6.6A), in particular at critical times when extracellular matrix deposition and myofibroblasts activation should normally occur. Moreover, *Mstn*^{-/-} mice showed consistently elevated decorin expression as compared to WT mice throughout the entire healing period, with the exception of day 15 post-wounding, when decorin levels were comparable between WT and *Mstn*^{-/-} mice (Figure 6.6B). Coinciding with the increased expression of decorin, phospho-Smad2/3 (p-Smad2/3) expression decreased in *Mstn*^{-/-} mice during skin wound repair, which is indicative of reduced TGF- β signaling (Figure 6.6B).

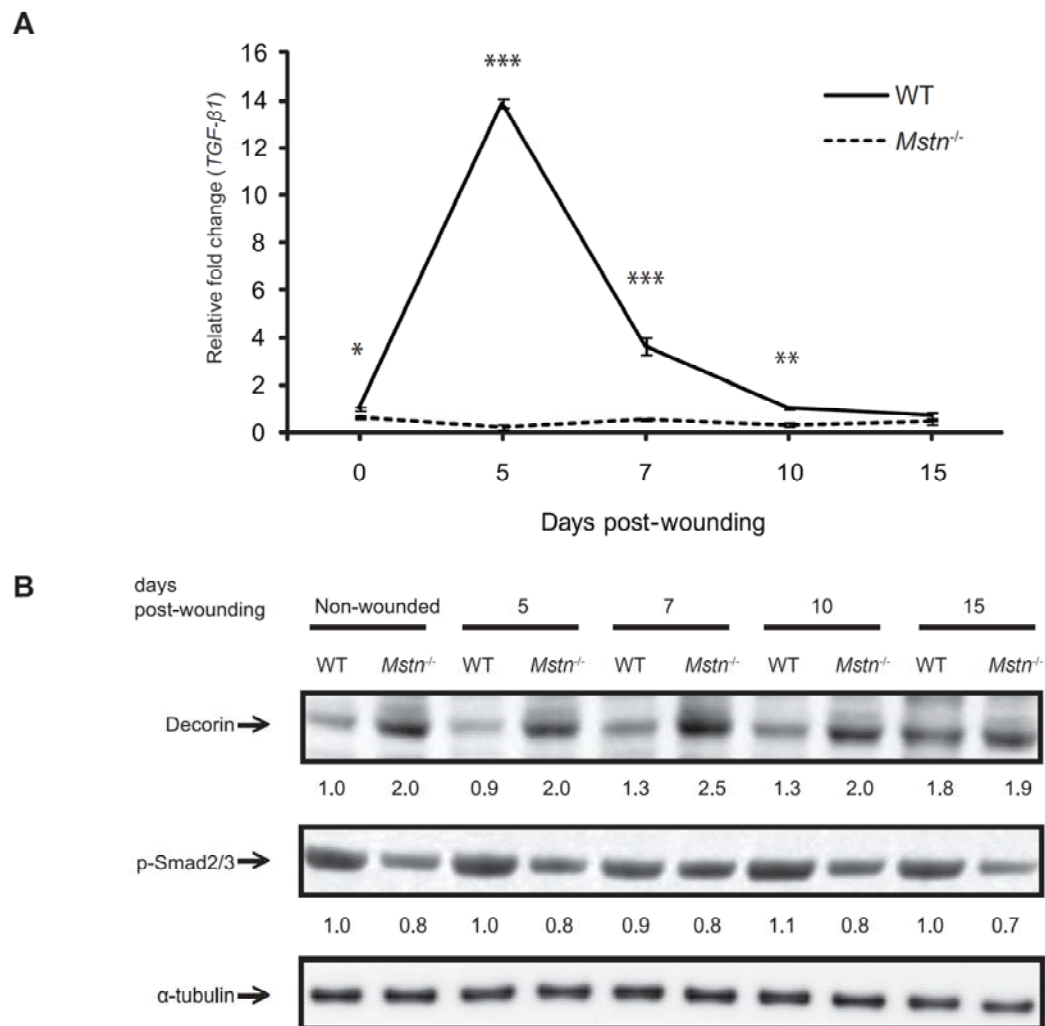


Figure 6.6 Elevated decorin and reduced TGF- β expression in *Mstn*^{-/-} mice.

(A) Relative fold change of TGF- β 1 mRNA expression normalized to L27 mRNA expression in skin at specific time points during skin wound healing as measured by qPCR in WT and *Mstn*^{-/-} mice. (B) Decorin and p-Smad2/3 protein expression levels in skin of WT and *Mstn*^{-/-} mice at specific time points during skin wound healing as measured by Western blotting analysis. Numbers under images indicate the fold changes of band density normalized to the first band. The levels of α -tubulin were assessed to ensure equal loading of samples. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$. Error bars represent $\pm$ SEM, $n = 5$.

6.3.7 Mstn deficiency attenuated dermal contraction and collagen deposition

As described above, *Mstn*^{-/-} mice exhibit impaired dermal contraction during wound healing. To delineate the underlying mechanisms, we performed myofibroblast-specific staining using an antibody against α -smooth muscle actin (α -SMA) as well as Van Geison staining of collagen. During wound healing, fibroblasts are activated and are transformed into α -SMA-expressing myofibroblasts. Myofibroblasts are involved in both wound contraction through intracellular contraction via integrin-mediated collagen fiber alignment [233-235] and extracellular collagen fiber deposition to strengthen wound site [236-237]. As shown in Figure 6.7A, myofibroblasts were readily detected in the skin wound area of WT mice, as indicated by the intense α -SMA staining. However, in contrast, the level of α -SMA staining in the skin wound of *Mstn*^{-/-} mice was greatly reduced (Figure 6.7A).

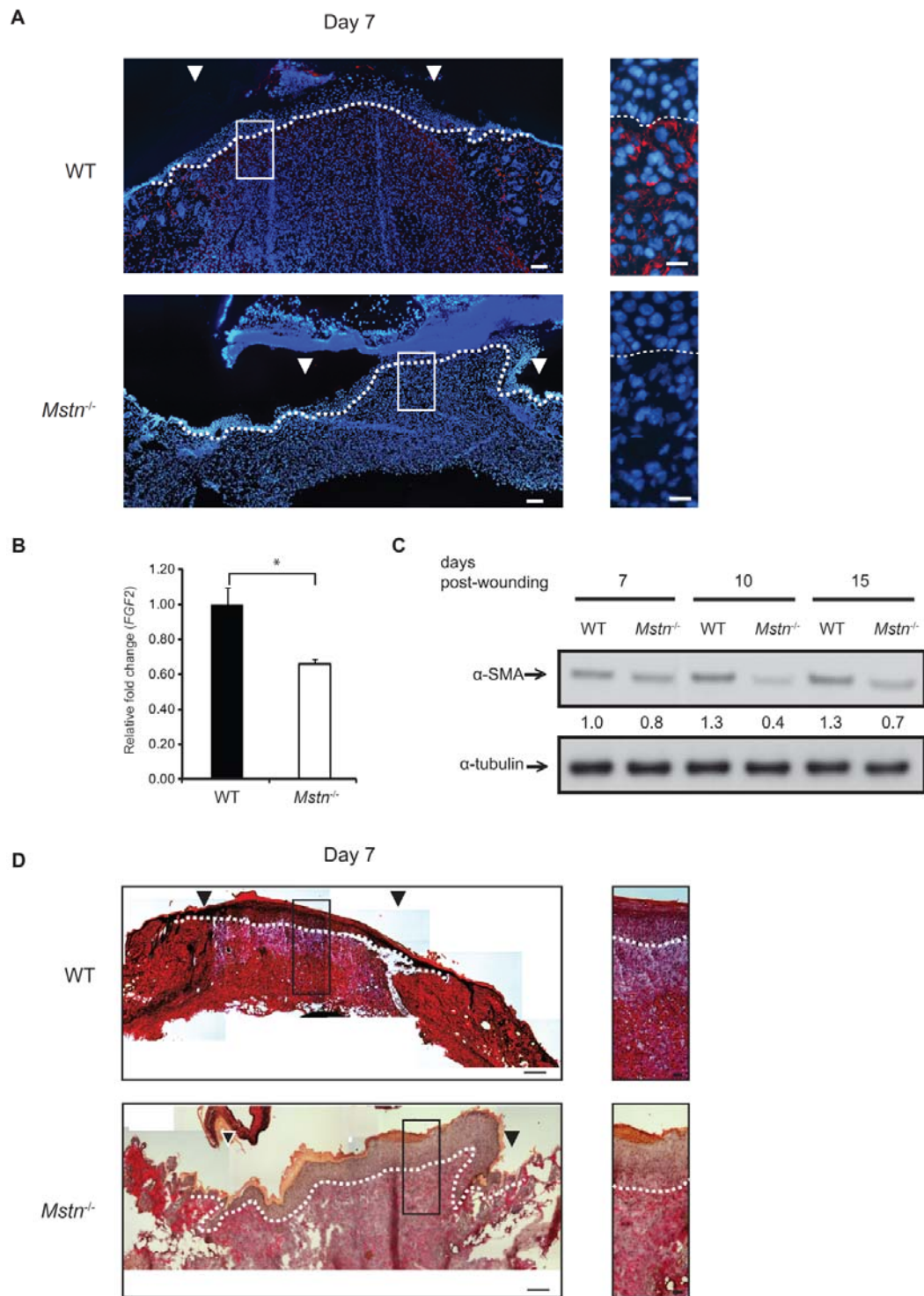
To further confirm the observation of reduced myofibroblast formation in the wound area of *Mstn*^{-/-} mice, mRNA expression of fibroblast growth factor (FGF) was examined during wound healing. The expression of FGF, in particular subtype 2, has been reported to be increased in the acute wound area, correlating with its function in granulation tissue formation, fibroblast migration, myofibroblast transformation, and collagen production [238]. Consistent with impaired myofibroblast formation, we found significantly reduced FGF2 mRNA expression in *Mstn*^{-/-} mice day 7 post-wounding skin biopsies, when compared to WT controls (Figure 6.7B).

In addition to analyzing FGF2 expression we next analysed the protein levels of α -SMA via western blotting analysis, and as shown in Figure 6.7C, reduced α -SMA protein expression was observed in *Mstn*^{-/-} mice at day 7, 10 and 15 post-wounding (Figure 6.7C), which is further consistent with inhibition of FGF2 expression and reduced myofibroblast formation. Next we performed Van Geison staining to detect

the presence of collagen, and consistent with reduced α -SMA staining, reduced myofibroblast number and reduced FGF expression, we also observed reduced collagen (indicated by the decrease in red colour observed in the dermis of the wound area) in *Mstn*^{-/-} mice (Figure 6.7D), implicating reduced wound contraction strength. Considering the crucial roles of myofibroblasts in dermis wound healing, these results may partially explain the delayed wound contraction in *Mstn*^{-/-} mice.

Figure 6.7 *Mstn* deficiency attenuated dermal contraction and collagen deposition.

(A) α -SMA immunofluorescence on WT and *Mstn*^{-/-} mice wound biopsies on day 7 after wounding. Higher magnification images are listed at the right panel. α -SMA (red)-immunostained cryosections were counterstained with DAPI (nuclei; blue). White dashed lines demarcate the epidermis from the dermis. Scale bar: 50 μ m (20 μ m in higher magnification image). White arrows indicate wound edges and regions between arrows represent wounded area. White boxes indicate the regions of higher magnification images. (B) Relative fold change of FGF2 mRNA expression normalized to L27 mRNA expression in skin on day 7 post-wounding as measured by qPCR in WT and *Mstn*^{-/-} mice. (C) α -SMA protein expression levels in skin of WT and *Mstn*^{-/-} mice at specific time points during skin wound healing as measured by Western blotting analysis. Numbers under images indicate the fold changes of band density normalized to the first band. The levels of α -tubulin were assessed to ensure equal loading of samples. (D) Van Geison staining of WT and *Mstn*^{-/-} mice wound biopsies on day 7 after wounding. Higher magnification images are listed at the right panel. White dashed lines demarcate the epidermis from the dermis. Scale bar: 200 μ m (20 μ m in higher magnification image). Black arrows indicate wound edges and regions between arrows represent wounded area. Black boxes indicate the regions of higher magnification images. *P < 0.05. Error bars represent $\pm$ SEM, n = 5.



6.4 Discussion

Here, we show for the first time that mice lacking Mstn exhibit delayed skin wound healing due to impaired epidermal re-epithelialization and dermal contraction. These two events are caused by a decrease in TGF- β signaling through elevated expression of decorin, which can either compete with TGF- β for binding to its receptor or physically bind to TGF- β itself, sequestering it in the ECM and preventing TGF- β /membrane receptor interaction. The present study provides a novel insight into the involvement of Mstn in skin wound healing, thus highlighting Mstn as a potential candidate for further study, to gain greater understanding of the pathology behind delayed wound healing.

We demonstrated that decreased re-epithelialization in *Mstn*^{-/-} mice was due to a reduction in TGF- β signaling. TGF- β 1 has been shown to inhibit keratinocyte proliferation [239-241], which is further supported by the finding that Smad3-null mice exhibit accelerated re-epithelialization due to inactivation of the inhibitory effects of TGF- β /Smad3 signaling on the early keratinocyte proliferative response [242]. Interestingly, *in vitro* and *in vivo* studies have indicated that TGF- β 1 promotes the migration of keratinocytes through upregulation of integrin expression and enhanced integrin-mediated signaling [90]. These observations might account for the apparent paradox that TGF- β 1-dependent stimulation of epidermal wound healing is associated with a growth inhibitory effect on epithelial cells. In agreement with the inhibitory function of TGF- β 1 in keratinocyte proliferation and stimulatory function of TGF- β 1 in keratinocyte migration, we show that by inhibiting TGF- β signaling, (1) *Mstn*^{-/-} mice exhibit delayed epidermal thickness recovery as a result of protracted proliferation of keratinocytes (Figure 6.4). This was further validated by the increased abundance of proliferating cells in *Mstn*^{-/-} primary keratinocyte cultures, as evidenced

through increased BrdU incorporation and enhanced protein levels of the proliferation markers PCNA and Cyclin D1 (Figure 6.5A&6.5B). Consistent with reduced TGF- β signaling, keratinocytes also exhibit a reduced migration rate during the initial stages of wound healing in *Mstn*^{-/-} mice (Figure 6.3B&6.3C); which was further confirmed through *in vitro* migration and adhesion assays performed on primary keratinocytes (Figure 6.5C, 6.5D&6.5E). Activation of TGF- β signaling has previously been shown to lead to increased integrin expression and enhanced integrin-mediated signaling in migrating epithelial tongues at the wound edge [90]. Therefore, we propose that the reduced TGF- β signaling observed in *Mstn*^{-/-} mice may block integrin expression/signaling, resulting in delayed keratinocyte migration in *Mstn*^{-/-} mice during skin wound healing. Importantly, although we observed increased proliferation of keratinocytes in the absence of Mstn, we found impaired keratinocyte migration and subsequent delayed wound healing, suggesting that keratinocyte migration, as opposed to keratinocyte proliferation alone, is critically important for timely skin re-epithelialization.

In *Mstn*^{-/-} mice, increased decorin expression has previously been reported in skeletal muscle [92] and here we show for the first time elevated decorin expression in skin from *Mstn*^{-/-} mice (Figure 6.6). Elevated levels of decorin in *Mstn*^{-/-} mice have been suggested to result in inhibition TGF- β 1 signaling, resulting in reduced fibrosis during skeletal muscle regeneration [243]. Also, increased decorin mRNA expression, as observed in the *Mstn*^{-/-} mice, can sequester the TGF- β latency complex in the ECM, thus preventing TGF- β -mediated signaling [244]. Consistent with this, we observed increased decorin expression concomitant with reduced expression of TGF- β and p-Smad2/3 in *Mstn*^{-/-} mice (Figure 6.6).

Myofibroblasts have been reported to have two main functions during wound healing, firstly, exerting contractile strength and aligning collagen via integrins to contract wound edges [233-235], and secondly, depositing ECM collagen fibers to strengthen the wound [236-237], thus, myofibroblast activation and differentiation is a crucial step in wound contraction. TGF- β has been shown to be a critical factor in myofibroblast activation via its stimulatory action on fibroblast proliferation, myofibroblast differentiation, and matrix deposition [91, 219]. Therefore, reduced TGF- β signaling may be responsible for the diminished myofibroblasts and delayed dermal wound contraction observed in *Mstn*^{-/-} mice. To date, however, the mechanism(s) by which TGF- β 1 regulates myofibroblast activation and differentiation still remain unclear. Nonetheless, it has been proposed that TGF- β 1 regulates myofibroblast activation and differentiation via cell adhesion-dependent integrin signaling-mediated regulation of focal adhesion kinase (FAK). Specifically, it has been reported that TGF- β stimulates the expression of integrin and fibronectin, thus leading to autophosphorylation/activation of FAK, which is essential for myofibroblast activation and differentiation [245]. This further supports our observation of up-regulated α -SMA in WT mice, but not in *Mstn*^{-/-} mice.

While we find that *Mstn*^{-/-} mice show delayed skin wound healing due to slower re-epithelialization and dermal wound contraction, previously published data from our lab revealed that there is enhanced skeletal muscle regeneration in *Mstn*^{-/-} mice [92]. This difference in wound healing between tissues could be due to differences in the underlying mechanism(s). Enhanced skeletal muscle regeneration in *Mstn*^{-/-} mice was found to be due to increased Satellite Cell activation and proliferation and accelerated myoblast and macrophage migration. Furthermore, decreased fibrosis in regenerated *Mstn*^{-/-} muscles was due to increased expression of decorin, which can either bind to

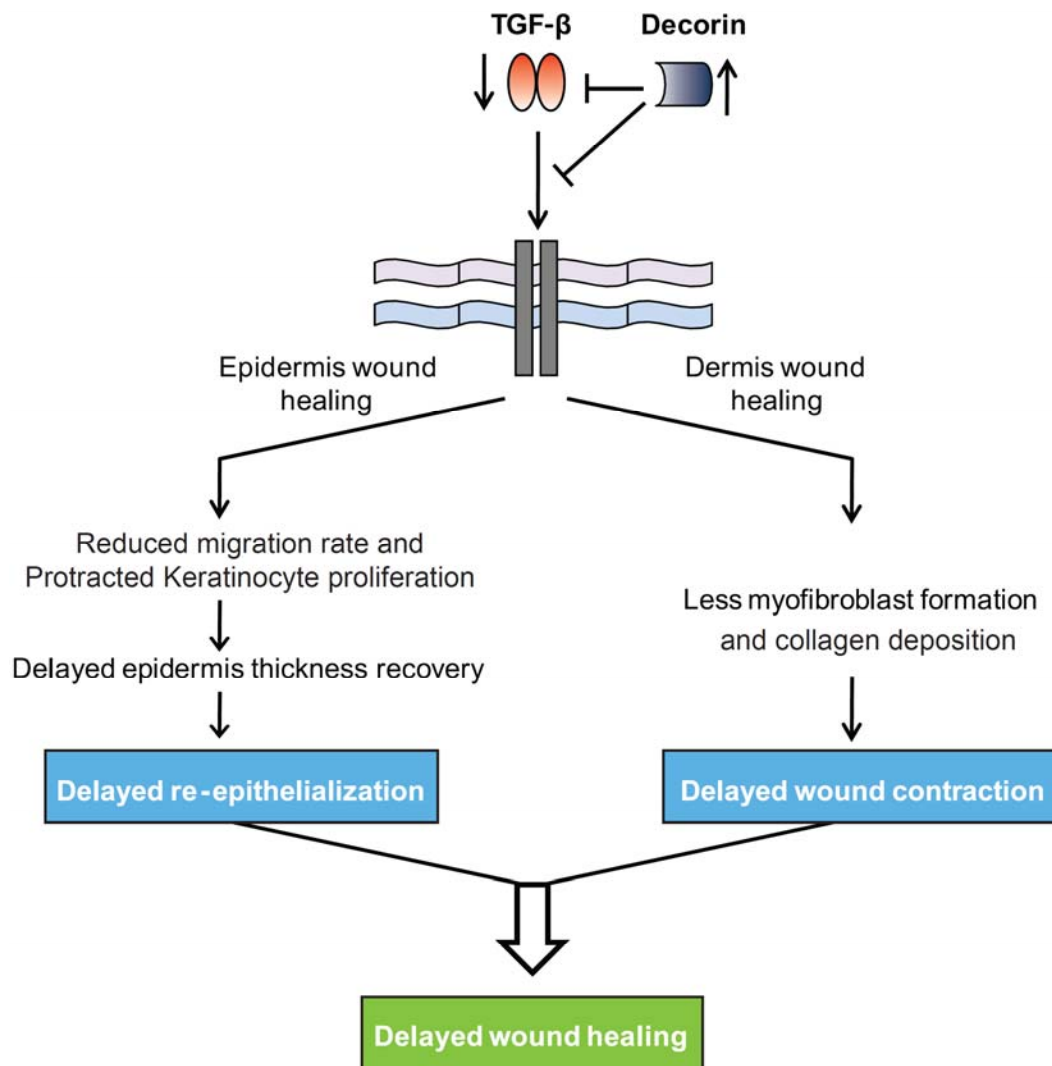
and sequester TGF- β in the ECM [244], or compete with TGF- β for receptor binding [227], thereby blocking TGF- β signaling and reducing skeletal muscle fibrosis. Similar to skeletal muscle, increased decorin levels and reduced TGF- β signaling were also seen in regenerating skin of *Mstn*^{-/-} mice (Figure 6.6). In contrast to skeletal muscle, reduced TGF- β signaling leads to protracted epidermal proliferation resulting in the delayed recovery of the hyperproliferative wound epidermis to normal thickness. In addition, the impaired TGF- β signaling also results in less myofibroblast activation and differentiation as well as reduced collagen deposition, ultimately leading to impaired wound contraction.

Herein, we propose a mechanism that lack of *Mstn* leads to increased decorin expression during skin wound healing. Subsequently, the elevated decorin either binds to TGF- β or competes with TGF- β to bind to its receptor to block TGF- β downstream signaling, resulting in decreased keratinocyte migration, protracted keratinocyte proliferation, delayed re-epithelialization in the epidermis; as well as aberrant myofibroblast formation, reduced collagen protein secretion and finally delayed wound contraction in the dermis. Altogether, we propose that these events result in the delayed wound healing observed in *Mstn*^{-/-} mice (Figure 6.8).

Figure 6.8 *Proposed mechanism.*

In *Mstn*^{-/-} mice, increased levels of decorin bind to TGF- β , either sequestering it in the ECM, preventing TGF- β receptor binding, or compete with TGF- β for binding to its receptor. In the epidermis, reduced TGF- β signaling results in reduced keratinocyte migration, protracted keratinocyte proliferation, and delayed epidermis thickness recovery, leading to delayed re-epithelialization. In the dermis, impaired TGF- β signaling results in less myofibroblast formation and collagen deposition, leading to delayed wound contraction in the dermis. Overall, absence of *Mstn* results in delayed epidermis and dermis wound healing.

Proposed mechanism of skin regeneration in *Mstn*^{-/-} mice



6.5 Acknowledgments

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6.6 Grants

NTU student program

6.7 Disclosures

The authors declare no conflict of interests

Chapter 7 Prospectives

Myostatin (Mstn), a TGF- β superfamily member, is a negative regulator for muscle growth [118-119]. Mutation in the *Mstn* gene is reported to lead to double muscling due to hypertrophy and hyperplasia [118-119]. Although extensive studies have been performed in our lab to understand the role of Mstn in skeletal muscle growth [125, 138, 151, 186, 246], no research has yet been undertaken to study the molecular mechanism behind Mstn regulation of muscle metabolism. It has been previously shown that Mstn deficiency results in a lean phenotype due to reduced fat pad weight [165]. It is also reported that in either Myostatin-null (*Mstn*^{-/-}) mice, or in mice with muscle-specific suppression of Mstn, there is reduced total body fat mass as well as improved insulin sensitivity [73, 166]. However, the exact molecular mechanism through which Mstn regulates skeletal muscle and adipose tissue metabolism remains unclear. Therefore, it is highly relevant to unravel the underlying signaling pathway behind Mstn function in carbohydrate and lipid metabolism. Thus, through utilizing the *Mstn*^{-/-} mouse model, this thesis aimed to delineate the molecular mechanism through which Mstn regulates whole body carbohydrate and lipid metabolism and to further study the efficacy of the Mstn antagonist, soluble activin type IIB receptor (sActRIIB), as a potential therapy for counteracting obesity and type 2 diabetes.

Role of Mstn in regulating AMP-activated protein kinase (AMPK) signaling

Our results reveal that Mstn may regulate muscle and adipose tissue metabolism through AMPK signaling. However, the actual mechanism through which loss of Mstn promotes AMPK remains unclear, as such further studies will be performed to

characterize this in further detail in the future. AMPK is an energy balancing enzyme, which is activated in response to high [AMP]/[ATP] ratio, such as observed during exercise and in conditions of hypoxia [67, 185]. AMPK is a heterotrimeric protein kinase, consisting of a catalytic α subunit and two regulatory β and γ subunits [182-184], with the $\alpha 2$, $\beta 2$ and $\gamma 3$ AMPK subunits specific for skeletal muscle [65-66]. Recently, Fujii *et al* reported that blocking of the AMPK $\alpha 2$ subunit further exacerbates high-fat diet (HFD)-induced insulin resistance [188]. With this in mind, AMPK deficient mice will be crossed with *Mstn*^{-/-} mice, to determine whether or not these double mutant mice have improved insulin sensitivity. Such mutant mice would provide an ideal opportunity to confirm the contribution of AMPK to the anti-diabetic phenotype of *Mstn*^{-/-} mice during HFD feeding. Specifically, if these double mutant mice display an obese phenotype and insulin resistance during HFD feeding, we could propose that AMPK is critically involved in the lean and insulin sensitive phenotype of *Mstn*^{-/-} mice.

It is well known that *Mstn* regulates downstream target genes through Smad3 signaling [138, 246-247]. Recently, Yadav *et al* reported that absence of Smad3 protected against type 2 diabetes and obesity through up-regulating PGC-1 α [248]; moreover, Tan *et al* demonstrated that the improved insulin sensitivity and anti-obesity phenotype seen in Smad3-null (*Smad3*^{-/-}) mice was due to the up-regulation of PPAR β/δ and down-regulation of PPAR γ [249]. Although *Mstn*^{-/-} mice and *Smad3*^{-/-} mice are similarly protected against diet-induced obesity and insulin resistance, no one has yet studied the role of AMPK in *Smad3*^{-/-} mice. Therefore, AMPK expression and activity in *Smad3*^{-/-} mice will be assessed. Furthermore, *Smad3*^{-/-} mice will be crossed with AMPK deficient mice, after which they will be subjected to HFD feeding, to

verify the role of AMPK signaling in the anti-obesity phenotype observed in *Smad3*^{-/-} mice.

Adiponectin is an adipose tissue exclusive secreted protein hormone, and unlike other hormones, the level of adiponectin is inversely correlated with type 2 diabetes and body mass index (BMI). AdipoR1 and AdipoR2 are two well-characterized adiponectin receptors. Importantly, up-regulation of AdipoR1 results in enhanced AMPK, PPAR (especially PPAR α) and COX-2 signaling, triggering fatty acid oxidation, glucose uptake and improving insulin sensitivity in skeletal muscle [250-254]. In addition, activation of AdipoR2 in the liver stimulates AMPK and PPAR α , increasing fatty acid oxidation as well as insulin sensitivity [250-251, 255]. Interestingly, Bernardo *et al* recently reported that blockade of Mstn via addition of a specific anti-Mstn antibody resulted in enhanced circulating levels of adiponectin [154]. In addition, our PCR array data revealed that in *Mstn*^{-/-} mice there is a ~45-fold increase in Adiponectin gene expression in white adipose tissue (WAT) when compared to wild-type (WT) mice during HFD feeding. Therefore, we would like to determine whether or not the increased adiponectin expression in *Mstn*^{-/-} mice is responsible for the enhanced activation of AMPK and resulting improved insulin sensitivity observed in *Mstn*^{-/-} mice fed high-fat diet. To study this, adiponectin-deficient mice [256] will be crossed with *Mstn*^{-/-} mice, to determine whether or not AMPK function is perturbed.

Role of Mstn in metabolism during early postnatal growth

This thesis has mainly focussed on the role of Mstn in carbohydrate and lipid metabolism during later stages of development, especially after sexual maturity (7-8

weeks). However, the metabolic function of Mstn in early stages of postnatal growth and moreover, the difference in metabolic role of Mstn between early and later stages of postnatal growth remains unclear. Therefore, future research will aim to delineate the role of Mstn in regulating catch up growth.

Catch up growth is an accelerated growth in infants or during the early childhood period and it is especially apparent in infants who initially have a low-birth weight. It has been demonstrated that infants with catch up growth are more prone to suffer from obesity, type 2 diabetes and other metabolic syndromes during their childhood and adulthood [34]. In this thesis, it has been proved that lack of Mstn leads to a lean phenotype and improved insulin sensitivity, therefore, it is interesting to analyze whether or not Mstn is involved in catch up growth.

The primary question that needs to be addressed is whether lack of Mstn is able to counteract catch up weight gain. Catch up growth animal models can be set up by restricting food intake in experimental WT and *Mstn*^{-/-} pregnant female mice and giving *ad libitum* access to food to the offspring mice. At specific time intervals the extent of obesity and insulin resistance will be measured.

The second experiment to carry out will be to analyze the role of Mstn in the hypertrophied adipose tissue caused by catch up growth at the molecular level. It is reported that catch up growth results in the enlargement of adipocyte size, but not adipocyte number [39]. However, in chapter 4 & 5 of this thesis, it is demonstrated that *Mstn*^{-/-} mice display reduced lipid uptake and increased fatty acid synthesis, lipolysis, and fatty acid oxidation in WAT, resulting in atrophied adipocytes and a multilocular lipid droplet phenotype. Therefore, it is interesting to investigate the role of Mstn in lipogenesis and adipogenesis during catch up growth. This study may help

us to better understanding the reason for the lean phenotype of *Mstn*^{-/-} mice, especially during later postnatal growth phases.

The final aim is to evaluate the role of Mstn in regulating insulin sensitivity during catch up growth. Surprisingly, human infants with low birth weight have improved insulin sensitivity during catch up growth [257], however, these low birth weight infants are more likely to develop obesity and type 2 diabetes in childhood and adulthood [34, 257-258]. Therefore, insulin sensitivity may not be constant during the whole life time; instead, temporal alterations may occur with aging [259]. Since *Mstn*^{-/-} mice display an insulin sensitive phenotype, it is important to delineate the role of Mstn in regulating carbohydrate metabolism during early postnatal development, to detect whether or not the function of Mstn has temporal variation during aging.

sActRIIB has been shown to be an effective antagonist for Mstn in counteracting obesity and insulin resistance [173]. So treating low birth weight mice with sActRIIB could give us a clearer indication of the effect of postnatal inhibition of Mstn in carbohydrate metabolism.

Conclusion

In summary, this thesis is the first study analyzing the molecular mechanism of Mstn in carbohydrate and lipid metabolism. *Mstn*^{-/-} mice exhibit a lean phenotype and improved insulin sensitivity. The data presented here indicates that the improved insulin sensitivity and lean phenotype are due to accelerated glucose uptake and increased fatty acid oxidation, as well as the adoption of a brown adipose tissue (BAT) phenotype in WAT. In addition, *Mstn*^{-/-} WAT displays reduced adipocyte size, and the

atrophy in adipocyte is due to the reduced lipid uptake and increased fatty acid synthesis, lipolysis, and fatty acid oxidation. Molecularly, lack of Mstn activates AMPK and PPAR signaling, further leading to increased glucose uptake and fatty acid oxidation to enhance insulin sensitivity.

Moreover, in chapter 6, the results demonstrate for the first time that Mstn is detected in skin, in both the epidermis and dermis. Interestingly, skin wound healing in *Mstn*^{-/-} mice is significantly delayed due to delayed re-epithelialization in the epidermis and wound contraction in the dermis. Results reveal that the slower wound contraction is a result of decreased fibroblast-to-myofibroblast transformation and collagen deposition due to impaired TGF- β signaling.

In recent times, obesity and diabetes have become worldwide issues. To date however, no efficient therapy has been developed, thus, research on target-directed first-line drugs is in high demand. Herein, for the first time, we propose Mstn as a potential therapeutic target in obesity, type 2 diabetes and skin wound healing, moreover, the studies done so far have built up a novel and practical relationship between Mstn and metabolic disorder, as well as skin regeneration.

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GeneSymbol	p-value	FCAbsolute	regulation	Description	GenbankAccession
AW125324	0.0159	1.68	up	mp78f05.y1 Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:575361 5'. [AI530666]	AI530666
	0.0011	1.73	up	zinc finger protein 125 Gene [Source:MGI Symbol;Acc:MGI:1336211] [ENSMUST00000079237]	AJ005350
	0.0016	1.73	up	gametogenetin binding protein 1 Gene [Source:MGI (curated);Acc:MGI:3055306] [ENSMUST00000025033]	AK002723
1700023A20Rik	0.0130	1.71	up	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700023A20 product:unclassifiable, full insert sequence. [AK006259]	AK006259
	0.0013	2.06	up	RIKEN cDNA 1700028N14 gene Gene [Source:MGI Symbol;Acc:MGI:1920530] [ENSMUST00000021325]	AK006468
	0.0375	2.02	up	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700064H15 product:unclassifiable, full insert sequence. [AK006881]	AK006881
1700080F18Rik	0.0007	2.07	up	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700080F18 product:unclassifiable, full insert sequence. [AK006954]	AK006954
1810073O08Rik	0.0066	1.76	up	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810073O08 product:unclassifiable, full insert sequence. [AK007978]	AK007978
2210416O15Rik	0.0009	1.53	up	Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210416O15 product:hypothetical protein, full insert sequence. [AK008958]	AK008958

2410024N13Rik	0.0028	1.78	up	Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:2410024N13 product:hypothetical protein, full insert sequence. [AK010586]	AK010586
4122401K19Rik	0.0114	2.34	up	Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:4122401K19 product:unclassifiable, full insert sequence. [AK014465]	AK014465
5830403F22Rik	0.0257	5.09	up	Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone:5830403F22 product:unclassifiable, full insert sequence. [AK017891]	AK017891
	0.0002	2.79	up	Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430403G16 product:weakly similar to zinc finger protein ZNF126 (fragment) [Homo sapiens], full insert sequence. [AK019943]	AK019943
	0.0500	1.62	up	AU RNA binding protein/enoyl-coenzyme A hydratase Gene [Source:MGI (curated);Acc:MGI:1338011] [ENSMUST00000120535]	AK019978
A930009E08Rik	0.0214	1.89	up	Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone:A930009E08 product:unclassifiable, full insert sequence. [AK020836]	AK020836
A930010G16Rik	0.0257	2.00	up	Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone:A930010G16 product:unclassifiable, full insert sequence. [AK020843]	AK020843
4930528J11Rik	0.0379	1.67	up	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4931441A13 product:unclassifiable, full insert sequence. [AK029922]	AK029922

	0.0458	1.53	up	Putative uncharacterized proteinMCG147323 ; [Source:UniProtKB/TrEMBL;Acc:Q8CBV7] [ENSMUST00000064248]	AK034506
9930024M15Rik	0.0267	1.63	up	Mus musculus adult female vagina cDNA, RIKEN full-length enriched library, clone:9930024M15 product:unclassifiable, full insert sequence. [AK036921]	AK036921
Cog5	0.0118	1.76	up	Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630038L12 product:unclassifiable, full insert sequence. [AK041796]	AK041796
A930004J17Rik	0.0217	1.56	up	Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone:A930004J17 product:unclassifiable, full insert sequence. [AK044267]	AK044267
	0.0147	1.66	up	FMS-like tyrosine kinase 3 Gene [Source:MGI (curated);Acc:MGI:95559] [ENSMUST00000110549]	AK045865
B430316J06Rik	0.0010	1.88	up	Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length enriched library, clone:B430316J06 product:unclassifiable, full insert sequence. [AK046698]	AK046698
B630006N21Rik	0.0476	2.18	up	Mus musculus 4 days neonate thymus cDNA, RIKEN full-length enriched library, clone:B630006N21 product:hypothetical protein, full insert sequence. [AK046749]	AK046749
C230076A16Rik	0.0351	1.52	up	Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230076A16 product:unclassifiable, full insert sequence. [AK048857]	AK048857
	0.0129	1.95	up	hepatoma-derived growth factor, related protein 3 Gene [Source:MGI (curated);Acc:MGI:1352760] [ENSMUST00000026094]	AK051401

D430040D24Rik	0.0385	1.68	up	Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched library, clone:D430047J20 product:unclassifiable, full insert sequence. [AK052542]	AK052542
Fitm2	0.0249	1.69	up	fat storage-inducing transmembrane protein 2 Gene [Source:MGI (curated);Acc:MGI:2444508] [ENSMUST00000088333]	AK052945
	0.0340	1.71	up	RIKEN cDNA 4930417O22 gene Gene [Source:MGI Symbol;Acc:MGI:1921137] [ENSMUST00000078285]	AK076700
4.93E+23	0.0406	1.64	up	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932416E17 product:unclassifiable, full insert sequence. [AK077028]	AK077028
	0.0235	2.08	up	RIKEN cDNA 4932441K18 gene Gene [Source:MGI Symbol;Acc:MGI:3590652] [ENSMUST00000112315]	AK078477
	0.0183	1.56	up	cytokine receptor-like factor 3 Gene [Source:MGI (curated);Acc:MGI:1860086] [ENSMUST00000092858]	AK078569
	0.0128	2.41	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q8BJU4] [ENSMUST00000065740]	AK079126
	0.0449	1.88	up	family with sequence similarity 123, member A Gene [Source:MGI Symbol;Acc:MGI:1919375] [ENSMUST00000089421]	AK080717
C130081A10Rik	0.0230	2.69	up	Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130081A10 product:unclassifiable, full insert sequence. [AK081838]	AK081838

D030051J21Rik	0.0005	2.07	up	Mus musculus 9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030051J21 product:unclassifiable, full insert sequence. [AK083595]	AK083595
9030425P06Rik	0.0434	2.00	up	Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130067I06 product:unclassifiable, full insert sequence. [AK083944]	AK083944
	0.0233	2.38	up	phenylalanyl-tRNA synthetase, alpha subunit Gene [Source:MGI (curated);Acc:MGI:1913840] [ENSMUST00000095222]	AK084031
D130095D21Rik	0.0400	1.60	up	Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130095D21 product:unclassifiable, full insert sequence. [AK084110]	AK084110
	0.0372	1.64	up	RIKEN cDNA D630008O14 gene Gene [Source:MGI Symbol;Acc:MGI:3698880] [ENSMUST00000066789]	AK085305
E030042N06Rik	0.0118	1.63	up	Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched library, clone:E030042N06 product:unclassifiable, full insert sequence. [AK087301]	AK087301
E330011O21Rik	0.0072	6.27	up	Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330011O21 product:unclassifiable, full insert sequence. [AK087725]	AK087725
	0.0392	1.71	up	cDNA fis, clone TRACH3037696 [Source:UniProtKB/TrEMBL;Acc:Q6ZQL5] [ENSMUST00000072427]	AK129029
	0.0201	2.34	up	zinc finger protein 407 Gene [Source:MGI (curated);Acc:MGI:2685179] [ENSMUST00000114662]	AK132276

	0.0060	3.35	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3V0M7] [ENSMUST00000098818]	AK133033
Pdyn	0.0420	1.66	up	prodynorphin Gene [Source:MGI (curated);Acc:MGI:97535] [ENSMUST00000028883]	AK133597
	0.0410	4.24	up	Putative uncharacterized protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q3UYL4] [ENSMUST00000098916]	AK134595
A430071A18Rik	0.0075	1.65	up	Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130034B03 product:unclassifiable, full insert sequence. [AK137878]	AK137878
Prrt1	0.0058	1.71	up	proline-rich transmembrane protein 1 Gene [Source:MGI (curated);Acc:MGI:1932118] [ENSMUST00000015620]	AK137892
	0.0081	1.77	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3UTC6] [ENSMUST00000100464]	AK139534
	0.0290	1.52	up	RIKEN cDNA B230314M03 gene Gene [Source:MGI Symbol;Acc:MGI:3588233] [ENSMUST00000097930]	AK140147
C430049E01Rik	0.0176	34.35	up	Mus musculus 7 days embryo whole body cDNA, RIKEN full-length enriched library, clone:C430049E01 product:hypothetical protein, full insert sequence. [AK141396]	AK141396
	0.0040	2.14	up	Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930041O15 product:unclassifiable, full insert sequence. [AK142897]	AK142897
	0.0333	1.90	up	peroxisomal membrane protein 4 Gene [Source:MGI (curated);Acc:MGI:1891701] [ENSMUST00000109703]	AK143785

Gm10776	0.0005	1.56	up	Mus musculus 16 days neonate male medulla oblongata cDNA, RIKEN full-length enriched library, clone:G630043O09 product:hypothetical protein, full insert sequence. [AK144371]	AK144371
	0.0435	1.81	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3UN64] [ENSMUST00000097750]	AK144422
BC062258	0.0019	3.10	up	Mus musculus lung RCB-0558 LLC cDNA, RIKEN full-length enriched library, clone:G730002O11 product:unclassifiable, full insert sequence. [AK144577]	AK144577
BC023969	0.0087	4.20	up	Mus musculus lung RCB-0558 LLC cDNA, RIKEN full-length enriched library, clone:G730014H17 product:unclassifiable, full insert sequence. [AK144629]	AK144629
	0.0166	1.58	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3UMJ3] [ENSMUST00000098867]	AK144859
Ppm1l	0.0356	1.60	up	protein phosphatase 1 (formerly 2C)-like Gene [Source:MGI (curated);Acc:MGI:2139740] [ENSMUST00000029355]	AK147389
5930430L01Rik	0.0389	1.52	up	Mus musculus B16 F10Y cells cDNA, RIKEN full-length enriched library, clone:G370004A16 product:unclassifiable, full insert sequence. [AK148051]	AK148051
	0.0011	2.27	up	homer homolog 3 (Drosophila) Gene [Source:MGI (curated);Acc:MGI:1347359] [ENSMUST00000087467]	AK155463
	0.0331	1.53	up	Novel protein [Source:UniProtKB/TrEMBL;Acc:B1AV28] [ENSMUST00000115553]	AK156771

4931406E20Rik	0.0490	2.23	up	Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230022K22 product:Musashi homolog 2 (Drosophila), full insert sequence. [AK163891]	AK163891
	0.0476	1.68	up	microrchidia 4 Gene [Source:MGI (curated);Acc:MGI:1922996] [ENSMUST00000113014]	AK164017
	0.0327	1.93	up	polymerase (DNA directed), epsilon Gene [Source:MGI (curated);Acc:MGI:1196391] [ENSMUST00000112482]	AK165879
E130304I02Rik	0.0106	1.69	up	Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830113J10 product:hypothetical protein, full insert sequence. [AK172290]	AK172290
	0.0256	1.58	up	MAP kinase-interacting serine/threonine kinase 2 Gene [Source:MGI Symbol;Acc:MGI:894279] [ENSMUST00000105338]	AK177092
1700037C18Rik	0.0349	1.72	up	RIKEN cDNA 1700037C18 gene Gene [Source:MGI Symbol;Acc:MGI:1920511] [ENSMUST00000115859]	AK195538
Trmt5	0.0246	1.73	up	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae) Gene [Source:MGI Symbol;Acc:MGI:1923607] [ENSMUST00000055255]	BC012521
Timm9	0.0218	1.65	up	Mus musculus translocase of inner mitochondrial membrane 9 homolog (yeast), mRNA (cDNA clone IMAGE:1332217), with apparent retained intron. [BC028435]	BC028435
	0.0014	2.04	up	cancer antigen 1 Gene [Source:MGI (curated);Acc:MGI:1918463] [ENSMUST00000089840]	BC082568

D7Ertd661e	0.0120	1.96	up	H3085D11-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3085D11 3', mRNA sequence [BG070263]	BG070263
1700016K05Rik	0.0198	1.70	up	AGENCOURT_10518733 NIH_MGC_169 Mus musculus cDNA clone IMAGE:6706380 5', mRNA sequence [BU938278]	BU938278
Btnl9	0.0150	1.97	up	butyrophilin-like 9 Gene [Source:MGI (curated);Acc:MGI:2442439] [ENSMUST00000046522]	BY730984
Olfr576	0.0088	1.74	up	Mus musculus olfactory receptor 576 (Olfr576), mRNA [NM_001001805]	NM_001001805
Nat8l	0.0297	3.93	up	Mus musculus N-acetyltransferase 8-like (Nat8l), mRNA [NM_001001985]	NM_001001985
Slc25a42	0.0132	2.97	up	Mus musculus solute carrier family 25, member 42 (Slc25a42), mRNA [NM_001007570]	NM_001007570
D8Ertd738e	0.0307	1.67	up	Mus musculus DNA segment, Chr 8, ERATO Doi 738, expressed (D8Ertd738e), mRNA [NM_001007571]	NM_001007571
Olfr1419	0.0366	1.72	up	Mus musculus olfactory receptor 1419 (Olfr1419), mRNA [NM_001011775]	NM_001011775
Cbx6-Nptxr	0.0210	1.60	up	Mus musculus Cbx6-Nptxr readthrough transcripts (Cbx6-Nptxr), transcript variant 2, mRNA [NM_001013362]	NM_001013362
Grm4	0.0393	1.87	up	Mus musculus glutamate receptor, metabotropic 4 (Grm4), mRNA [NM_001013385]	NM_001013385
Vprbp	0.0056	1.54	up	Mus musculus Vpr (HIV-1) binding protein (Vprbp), mRNA [NM_001015507]	NM_001015507
Ddi2	0.0386	1.97	up	Mus musculus DNA-damage inducible protein 2 (Ddi2), mRNA [NM_001017966]	NM_001017966
Ddi2	0.0351	1.65	up	Mus musculus DNA-damage inducible protein 2 (Ddi2), mRNA [NM_001017966]	NM_001017966
Gm414	0.0315	1.58	up	Mus musculus predicted gene 414 (Gm414), mRNA [NM_001018031]	NM_001018031

Ankrd28	0.0214	1.82	up	Mus musculus ankyrin repeat domain 28 (Ankrd28), mRNA [NM_001024604]	NM_001024604
2700007P21Rik	0.0355	1.53	up	Mus musculus RIKEN cDNA 2700007P21 gene (2700007P21Rik), transcript variant 1, mRNA [NM_001025102]	NM_001025102
Brd2	0.0278	1.54	up	Mus musculus bromodomain containing 2 (Brd2), transcript variant 2, mRNA [NM_001025387]	NM_001025387
Usp31	0.0400	1.54	up	Mus musculus ubiquitin specific peptidase 31 (Usp31), mRNA [NM_001033173]	NM_001033173
Tmem181a	0.0364	1.85	up	Mus musculus transmembrane protein 181A (Tmem181a), mRNA [NM_001033178]	NM_001033178
Gm525	0.0272	3.06	up	Mus musculus predicted gene 525 (Gm525), mRNA [NM_001033266]	NM_001033266
Nlrp12	0.0445	1.69	up	Mus musculus NLR family, pyrin domain containing 12 (Nlrp12), mRNA [NM_001033431]	NM_001033431
C330019L16Rik	0.0193	4.98	up	Mus musculus RIKEN cDNA C330019L16 gene (C330019L16Rik), mRNA [NM_001034857]	NM_001034857
EG547347	0.0240	1.67	up	Mus musculus predicted gene, EG547347 (EG547347), mRNA [NM_001034909]	NM_001034909
Fam38a	0.0127	1.88	up	Mus musculus family with sequence similarity 38, member A (Fam38a), mRNA [NM_001037298]	NM_001037298
Xaf1	0.0038	42.07	up	Mus musculus XIAP associated factor 1 (Xaf1), mRNA [NM_001037713]	NM_001037713
Col28a1	0.0372	2.95	up	Mus musculus collagen, type XXVIII, alpha 1 (Col28a1), mRNA [NM_001037865]	NM_001037865
Nolc1	0.0332	1.57	up	Mus musculus nucleolar and coiled-body phosphoprotein 1 (Nolc1), transcript variant 3, mRNA [NM_001039352]	NM_001039352
Slc22a15	0.0392	1.61	up	Mus musculus solute carrier family 22 (organic anion/cation transporter), member 15 (Slc22a15), mRNA [NM_001039371]	NM_001039371

2210404J11Rik	0.0394	2.66	up	Mus musculus RIKEN cDNA 2210404J11 gene (2210404J11Rik), transcript variant 1, mRNA [NM_001039552]	NM_001039552
2210404J11Rik	0.0231	2.64	up	Mus musculus RIKEN cDNA 2210404J11 gene (2210404J11Rik), transcript variant 1, mRNA [NM_001039552]	NM_001039552
Coq10b	0.0487	2.00	up	Mus musculus coenzyme Q10 homolog B (S. cerevisiae) (Coq10b), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA [NM_001039710]	NM_001039710
Sco1	0.0399	1.64	up	Mus musculus SCO cytochrome oxidase deficient homolog 1 (yeast) (Sco1), nuclear gene encoding mitochondrial protein, mRNA [NM_001040026]	NM_001040026
Akap1	0.0310	1.97	up	Mus musculus A kinase (PRKA) anchor protein 1 (Akap1), nuclear gene encoding mitochondrial protein, transcript variant 2, mRNA [NM_001042541]	NM_001042541
Hhip1l	0.0475	1.78	up	Mus musculus hedgehog interacting protein-like 1 (Hhip1l), mRNA [NM_001044380]	NM_001044380
Spata22	0.0376	1.91	up	Mus musculus spermatogenesis associated 22 (Spata22), mRNA [NM_001045531]	NM_001045531
Vmn1r204	0.0332	3.50	up	Mus musculus vomeronasal 1 receptor 204 (Vmn1r204), mRNA [NM_001045544]	NM_001045544
Rbm15	0.0353	1.51	up	Mus musculus RNA binding motif protein 15 (Rbm15), mRNA [NM_001045807]	NM_001045807
Plin5	0.0079	4.38	up	Mus musculus perilipin 5 (Plin5), transcript variant 2, mRNA [NM_001077348]	NM_001077348
Uhrf1bp1	0.0373	2.76	up	Mus musculus UHRF1 (ICBP90) binding protein 1 (Uhrf1bp1), mRNA [NM_001080769]	NM_001080769
Larp4	0.0341	1.72	up	Mus musculus La ribonucleoprotein domain family, member 4 (Larp4), transcript variant 2, mRNA [NM_001080948]	NM_001080948
Ppig	0.0248	1.62	up	Mus musculus peptidyl-prolyl isomerase G (cyclophilin G) (Ppig), mRNA [NM_001081086]	NM_001081086

1300001I01Rik	0.0285	1.54	up	Mus musculus RIKEN cDNA 1300001I01 gene (1300001I01Rik), mRNA [NM_001081158]	NM_001081158
Gpr116	0.0456	1.86	up	Mus musculus G protein-coupled receptor 116 (Gpr116), mRNA [NM_001081178]	NM_001081178
Arid4a	0.0354	1.58	up	Mus musculus AT rich interactive domain 4A (RBP1-like) (Arid4a), mRNA [NM_001081195]	NM_001081195
Fam178a	0.0163	1.54	up	Mus musculus family with sequence similarity 178, member A (Fam178a), mRNA [NM_001081225]	NM_001081225
Fbxo43	0.0488	2.21	up	Mus musculus F-box protein 43 (Fbxo43), mRNA [NM_001081253]	NM_001081253
1600015I10Rik	0.0161	3.39	up	Mus musculus RIKEN cDNA 1600015I10 gene (1600015I10Rik), mRNA [NM_001081273]	NM_001081273
Ibtk	0.0216	1.66	up	Mus musculus inhibitor of Bruton agammaglobulinemia tyrosine kinase (Ibtk), mRNA [NM_001081282]	NM_001081282
Chd2	0.0373	1.73	up	Mus musculus chromodomain helicase DNA binding protein 2 (Chd2), mRNA [NM_001081345]	NM_001081345
Ctcf1	0.0028	2.18	up	Mus musculus CCCTC-binding factor (zinc finger protein)-like (Ctcf1), mRNA [NM_001081387]	NM_001081387
Wdr67	0.0148	1.56	up	Mus musculus WD repeat domain 67 (Wdr67), transcript variant 1, mRNA [NM_001081396]	NM_001081396
Chd7	0.0017	1.60	up	Mus musculus chromodomain helicase DNA binding protein 7 (Chd7), mRNA [NM_001081417]	NM_001081417
Snx27	0.0051	1.67	up	Mus musculus sorting nexin family member 27 (Snx27), transcript variant 1, mRNA [NM_001082484]	NM_001082484
Ptpu	0.0208	1.53	up	Mus musculus protein tyrosine phosphatase, receptor type, U (Ptpu), transcript variant 2, mRNA [NM_001083119]	NM_001083119
Arid1b	0.0368	1.75	up	Mus musculus AT rich interactive domain 1B (SWI-like) (Arid1b), mRNA [NM_001085355]	NM_001085355
Ttll2	0.0158	5.61	up	Mus musculus tubulin tyrosine ligase-like family, member 2 (Ttll2), mRNA [NM_001098267]	NM_001098267

Cdk12	0.0214	1.74	up	Mus musculus cyclin-dependent kinase 12 (Cdk12), transcript variant 1, mRNA [NM_001109626]	NM_001109626
Apold1	0.0106	2.58	up	Mus musculus apolipoprotein L domain containing 1 (Apold1), mRNA [NM_001109914]	NM_001109914
Cym	0.0303	1.84	up	Mus musculus chymosin (Cym), mRNA [NM_001111143]	NM_001111143
Wdfy1	0.0006	2.72	up	Mus musculus WD repeat and FYVE domain containing 1 (Wdfy1), transcript variant 1, mRNA [NM_001111279]	NM_001111279
Uspl1	0.0371	2.30	up	Mus musculus ubiquitin specific peptidase like 1 (Uspl1), transcript variant 1, mRNA [NM_001115153]	NM_001115153
Gm2016	0.0327	1.58	up	Mus musculus predicted gene 2016 (Gm2016), mRNA [NM_001122662]	NM_001122662
Zcchc2	0.0320	1.71	up	Mus musculus zinc finger, CCHC domain containing 2 (Zcchc2), transcript variant A, mRNA [NM_001122676]	NM_001122676
9030025P20Rik	0.0020	2.74	up	Mus musculus RIKEN cDNA 9030025P20 gene (9030025P20Rik), mRNA [NM_001123370]	NM_001123370
Ptpn2	0.0322	1.90	up	Mus musculus protein tyrosine phosphatase, non-receptor type 2 (Ptpn2), transcript variant 2, mRNA [NM_001127177]	NM_001127177
Ace2	0.0122	1.99	up	Mus musculus angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (Ace2), transcript variant 1, mRNA [NM_001130513]	NM_001130513
Gm10220	0.0402	1.53	up	Mus musculus predicted gene 10220 (Gm10220), mRNA [NM_001134299]	NM_001134299
Pitpnm1	0.0221	1.67	up	Mus musculus phosphatidylinositol transfer protein, membrane-associated 1 (Pitpnm1), transcript variant 2, mRNA [NM_001136078]	NM_001136078
Gm9992	0.0482	2.11	up	Mus musculus predicted gene 9992 (Gm9992), mRNA [NM_001142539]	NM_001142539

5730494M16Rik	0.0181	1.60	up	Mus musculus RIKEN cDNA 5730494M16 gene (5730494M16Rik), transcript variant 3, mRNA [NM_001142698]	NM_001142698
Bcl2l15	0.0471	10.00	up	Mus musculus BCL2-like 15 (Bcl2l15), transcript variant 1, mRNA [NM_001142959]	NM_001142959
5730528L13Rik	0.0186	1.51	up	Mus musculus RIKEN cDNA 5730528L13 gene (5730528L13Rik), transcript variant 1, mRNA [NM_001145924]	NM_001145924
5730528L13Rik	0.0323	1.66	up	Mus musculus RIKEN cDNA 5730528L13 gene (5730528L13Rik), transcript variant 1, mRNA [NM_001145924]	NM_001145924
Meis2	0.0126	1.70	up	Mus musculus Meis homeobox 2 (Meis2), transcript variant 5, mRNA [NM_001159569]	NM_001159569
Pum2	0.0043	1.58	up	Mus musculus pumilio 2 (Drosophila) (Pum2), transcript variant 1, mRNA [NM_001160219]	NM_001160219
Myo1b	0.0388	1.90	up	Mus musculus myosin IB (Myo1b), transcript variant 1, mRNA [NM_001161817]	NM_001161817
Mttp	0.0214	2.57	up	Mus musculus microsomal triglyceride transfer protein (Mttp), transcript variant 1, mRNA [NM_001163457]	NM_001163457
Zfp605	0.0100	1.74	up	Mus musculus zinc finger protein 605 (Zfp605), mRNA [NM_001163996]	NM_001163996
Chadl	0.0196	1.55	up	Mus musculus chondroadherin-like (Chadl), mRNA [NM_001164320]	NM_001164320
Dpys	0.0417	4.91	up	Mus musculus dihydropyrimidinase (Dpys), transcript variant 2, mRNA [NM_001164466]	NM_001164466
Trappc9	0.0435	1.52	up	Mus musculus trafficking protein particle complex 9 (Trappc9), transcript variant 5, mRNA [NM_001164643]	NM_001164643
9830001H06Rik	0.0074	1.61	up	Mus musculus RIKEN cDNA 9830001H06 gene (9830001H06Rik), mRNA [NM_001164663]	NM_001164663

Dnaja1	0.0362	1.73	up	Mus musculus DnaJ (Hsp40) homolog, subfamily A, member 1 (Dnaja1), transcript variant 1, mRNA [NM_001164671]	NM_001164671
Ano8	0.0442	1.75	up	Mus musculus anoctamin 8 (Ano8), mRNA [NM_001164679]	NM_001164679
Thsd7a	0.0408	1.58	up	Mus musculus thrombospondin, type I, domain containing 7A (Thsd7a), mRNA [NM_001164805]	NM_001164805
Mgll	0.0370	1.78	up	Mus musculus monoglyceride lipase (Mgll), transcript variant 4, mRNA [NM_001166250]	NM_001166250
Dynlt1c	0.0462	1.95	up	Mus musculus dynein light chain Tctex-type 1C (Dynlt1c), mRNA [NM_001166630]	NM_001166630
Dynlt1c	0.0087	1.88	up	Mus musculus dynein light chain Tctex-type 1C (Dynlt1c), mRNA [NM_001166630]	NM_001166630
Zfp882	0.0279	2.16	up	Mus musculus zinc finger protein 882 (Zfp882), mRNA [NM_001166645]	NM_001166645
Skint5	0.0072	1.89	up	Mus musculus selection and upkeep of intraepithelial T cells 5 (Skint5), transcript variant 2, mRNA [NM_001167878]	NM_001167878
Fcamr	0.0339	1.52	up	Mus musculus Fc receptor, IgA, IgM, high affinity (Fcamr), transcript variant 1, mRNA [NM_001170632]	NM_001170632
Dhrs7b	0.0093	2.11	up	Mus musculus dehydrogenase/reductase (SDR family) member 7B (Dhrs7b), transcript variant 1, mRNA [NM_001172112]	NM_001172112
Krt36	0.0340	3.38	up	Mus musculus keratin 36 (Krt36), mRNA [NM_001174099]	NM_001174099
Gm4340	0.0432	1.61	up	Mus musculus predicted gene 4340 (Gm4340), mRNA [NM_001177535]	NM_001177535
Zfp442	0.0165	1.71	up	Mus musculus zinc finger protein 442 (Zfp442), mRNA [NM_001177550]	NM_001177550
Gm13138	0.0126	2.63	up	Mus musculus predicted gene 13138 (Gm13138), mRNA [NM_001177767]	NM_001177767

Gm10324	0.0087	2.81	up	Mus musculus predicted gene 10324 (Gm10324), mRNA [NM_001177832]	NM_001177832
Acadm	0.0190	1.76	up	Mus musculus acyl-Coenzyme A dehydrogenase, medium chain (Acadm), nuclear gene encoding mitochondrial protein, mRNA [NM_007382]	NM_007382
Plin2	0.0291	2.46	up	Mus musculus perilipin 2 (Plin2), mRNA [NM_007408]	NM_007408
Adrb1	0.0427	2.01	up	Mus musculus adrenergic receptor, beta 1 (Adrb1), mRNA [NM_007419]	NM_007419
Rplp0	0.0394	2.24	up	Mus musculus ribosomal protein, large, P0 (Rplp0), mRNA [NM_007475]	NM_007475
Atf1	0.0453	1.63	up	Mus musculus activating transcription factor 1 (Atf1), mRNA [NM_007497]	NM_007497
Atf3	0.0007	3.16	up	Mus musculus activating transcription factor 3 (Atf3), mRNA [NM_007498]	NM_007498
Atp5k	0.0432	1.60	up	Mus musculus ATP synthase, H ⁺ transporting, mitochondrial F1F0 complex, subunit e (Atp5k), nuclear gene encoding mitochondrial protein, mRNA [NM_007507]	NM_007507
Bard1	0.0112	1.72	up	Mus musculus BRCA1 associated RING domain 1 (Bard1), mRNA [NM_007525]	NM_007525
Cidea	0.0102	18.13	up	Mus musculus cell death-inducing DNA fragmentation factor, alpha subunit-like effector A (Cidea), mRNA [NM_007702]	NM_007702
Socs3	0.0406	1.59	up	Mus musculus suppressor of cytokine signaling 3 (Socs3), mRNA [NM_007707]	NM_007707
Cox8b	0.0031	7.24	up	Mus musculus cytochrome c oxidase, subunit VIIIb (Cox8b), nuclear gene encoding mitochondrial protein, mRNA [NM_007751]	NM_007751
Cycs	0.0357	1.70	up	Mus musculus cytochrome c, somatic (Cycs), nuclear gene encoding mitochondrial protein, mRNA [NM_007808]	NM_007808

Dyrk1a	0.0186	1.70	up	Mus musculus dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a (Dyrk1a), transcript variant 1, mRNA [NM_007890]	NM_007890
Ephx2	0.0041	1.89	up	Mus musculus epoxide hydrolase 2, cytoplasmic (Ephx2), mRNA [NM_007940]	NM_007940
Esr1	0.0063	1.69	up	Mus musculus estrogen receptor 1 (alpha) (Esr1), mRNA [NM_007956]	NM_007956
Mpzl2	0.0071	2.01	up	Mus musculus myelin protein zero-like 2 (Mpzl2), mRNA [NM_007962]	NM_007962
Gh	0.0039	1.81	up	Mus musculus growth hormone (Gh), mRNA [NM_008117]	NM_008117
Gjc1	0.0105	1.76	up	Mus musculus gap junction protein, gamma 1 (Gjc1), transcript variant 1, mRNA [NM_008122]	NM_008122
Glud1	0.0380	1.63	up	Mus musculus glutamate dehydrogenase 1 (Glud1), nuclear gene encoding mitochondrial protein, mRNA [NM_008133]	NM_008133
Cxcl1	0.0159	2.94	up	Mus musculus chemokine (C-X-C motif) ligand 1 (Cxcl1), mRNA [NM_008176]	NM_008176
Has1	0.0134	2.24	up	Mus musculus hyaluronan synthase1 (Has1), mRNA [NM_008215]	NM_008215
Hspe1	0.0414	2.04	up	Mus musculus heat shock protein 1 (chaperonin 10) (Hspe1), mRNA [NM_008303]	NM_008303
Hspe1	0.0452	1.69	up	Mus musculus heat shock protein 1 (chaperonin 10) (Hspe1), mRNA [NM_008303]	NM_008303
Il12rb1	0.0384	1.52	up	Mus musculus interleukin 12 receptor, beta 1 (Il12rb1), mRNA [NM_008353]	NM_008353
Il3ra	0.0486	1.72	up	Mus musculus interleukin 3 receptor, alpha chain (Il3ra), mRNA [NM_008369]	NM_008369
Lrig1	0.0483	1.78	up	Mus musculus leucine-rich repeats and immunoglobulin-like domains 1 (Lrig1), mRNA [NM_008377]	NM_008377
Alad	0.0467	3.29	up	Mus musculus aminolevulinate, delta-, dehydratase (Alad), mRNA [NM_008525]	NM_008525

Ppp1r15a	0.0081	1.79	up	Mus musculus protein phosphatase 1, regulatory (inhibitor) subunit 15A (Ppp1r15a), mRNA [NM_008654]	NM_008654
Gadd45b	0.0152	1.67	up	Mus musculus growth arrest and DNA-damage-inducible 45 beta (Gadd45b), mRNA [NM_008655]	NM_008655
Pick1	0.0451	2.39	up	Mus musculus protein interacting with C kinase 1 (Pick1), transcript variant 1, mRNA [NM_008837]	NM_008837
Pou1f1	0.0445	3.29	up	Mus musculus POU domain, class 1, transcription factor 1 (Pou1f1), mRNA [NM_008849]	NM_008849
Pitx3	0.0153	1.57	up	Mus musculus paired-like homeodomain transcription factor 3 (Pitx3), mRNA [NM_008852]	NM_008852
Ppargc1a	0.0150	2.13	up	Mus musculus peroxisome proliferative activated receptor, gamma, coactivator 1 alpha (Ppargc1a), transcript variant 1, mRNA [NM_008904]	NM_008904
Ppargc1a	0.0135	2.21	up	Mus musculus peroxisome proliferative activated receptor, gamma, coactivator 1 alpha (Ppargc1a), transcript variant 1, mRNA [NM_008904]	NM_008904
Pex5	0.0027	1.76	up	Mus musculus peroxisomal biogenesis factor 5 (Pex5), transcript variant 1, mRNA [NM_008995]	NM_008995
Rab4a	0.0078	1.85	up	Mus musculus RAB4A, member RAS oncogene family (Rab4a), mRNA [NM_009003]	NM_009003
Rad23a	0.0253	2.26	up	Mus musculus RAD23a homolog (S. cerevisiae) (Rad23a), mRNA [NM_009010]	NM_009010
Rfx2	0.0470	1.67	up	Mus musculus regulatory factor X, 2 (influences HLA class II expression) (Rfx2), transcript variant 2, mRNA [NM_009056]	NM_009056
Rxrg	0.0149	2.13	up	Mus musculus retinoid X receptor gamma (Rxrg), transcript variant 1, mRNA [NM_009107]	NM_009107
Tra2b	0.0484	2.65	up	Mus musculus transformer 2 beta homolog (Drosophila) (Tra2b), mRNA [NM_009186]	NM_009186
Sntb2	0.0220	1.90	up	Mus musculus syntrophin, basic 2 (Sntb2), mRNA [NM_009229]	NM_009229

Sephs2	0.0085	2.08	up	Mus musculus selenophosphate synthetase 2 (Sephs2), mRNA [NM_009266]	NM_009266
Svs5	0.0256	775.60	up	Mus musculus seminal vesicle secretory protein 5 (Svs5), mRNA [NM_009301]	NM_009301
Acat2	0.0001	2.18	up	Mus musculus acetyl-Coenzyme A acetyltransferase 2 (Acat2), mRNA [NM_009338]	NM_009338
Phf1	0.0191	1.81	up	Mus musculus PHD finger protein 1 (Phf1), mRNA [NM_009343]	NM_009343
Thrb	0.0041	2.55	up	Mus musculus thyroid hormone receptor beta (Thrb), transcript variant 2, mRNA [NM_009380]	NM_009380
Thrb	0.0435	2.23	up	Mus musculus thyroid hormone receptor beta (Thrb), transcript variant 2, mRNA [NM_009380]	NM_009380
Tnfaip6	0.0360	2.20	up	Mus musculus tumor necrosis factor alpha induced protein 6 (Tnfaip6), mRNA [NM_009398]	NM_009398
Tob1	0.0207	2.31	up	Mus musculus transducer of ErbB-2.1 (Tob1), mRNA [NM_009427]	NM_009427
Ucp1	0.0010	628.75	up	Mus musculus uncoupling protein 1 (mitochondrial, proton carrier) (Ucp1), nuclear gene encoding mitochondrial protein, mRNA [NM_009463]	NM_009463
Pcgf2	0.0117	1.51	up	Mus musculus polycomb group ring finger 2 (Pcgf2), transcript variant 1, mRNA [NM_009545]	NM_009545
Adam17	0.0097	1.64	up	Mus musculus a disintegrin and metallopeptidase domain 17 (Adam17), mRNA [NM_009615]	NM_009615
Adamts1	0.0430	2.13	up	Mus musculus a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1 (Adamts1), mRNA [NM_009621]	NM_009621
Atf4	0.0221	1.90	up	Mus musculus activating transcription factor 4 (Atf4), mRNA [NM_009716]	NM_009716
Bcat2	0.0079	2.04	up	Mus musculus branched chain aminotransferase 2, mitochondrial (Bcat2), nuclear gene encoding mitochondrial protein, mRNA [NM_009737]	NM_009737
Cdc7	0.0477	1.77	up	Mus musculus cell division cycle 7 (S. cerevisiae) (Cdc7), mRNA [NM_009863]	NM_009863

Camp	0.0306	2.14	up	Mus musculus cathelicidin antimicrobial peptide (Camp), mRNA [NM_009921]	NM_009921
Cpt2	0.0242	1.75	up	Mus musculus carnitine palmitoyltransferase 2 (Cpt2), nuclear gene encoding mitochondrial protein, mRNA [NM_009949]	NM_009949
Dbt	0.0110	2.45	up	Mus musculus dihydrolipoamide branched chain transacylase E2 (Dbt), nuclear gene encoding mitochondrial protein, mRNA [NM_010022]	NM_010022
Dffa	0.0088	1.61	up	Mus musculus DNA fragmentation factor, alpha subunit (Dffa), transcript variant 2, mRNA [NM_010044]	NM_010044
Dio2	0.0062	3.69	up	Mus musculus deiodinase, iodothyronine, type II (Dio2), mRNA [NM_010050]	NM_010050
Dlx3	0.0041	1.51	up	Mus musculus distal-less homeobox 3 (Dlx3), mRNA [NM_010055]	NM_010055
Ebf2	0.0112	1.74	up	Mus musculus early B-cell factor 2 (Ebf2), mRNA [NM_010095]	NM_010095
Fmn1	0.0093	1.50	up	Mus musculus formin 1 (Fmn1), transcript variant 1, mRNA [NM_010230]	NM_010230
Gna13	0.0259	1.54	up	Mus musculus guanine nucleotide binding protein, alpha 13 (Gna13), mRNA [NM_010303]	NM_010303
Npbwr1	0.0250	2.25	up	Mus musculus neuropeptides B/W receptor 1 (Npbwr1), mRNA [NM_010342]	NM_010342
Gstt2	0.0332	1.59	up	Mus musculus glutathione S-transferase, theta 2 (Gstt2), mRNA [NM_010361]	NM_010361
Hipk3	0.0380	1.52	up	Mus musculus homeodomain interacting protein kinase 3 (Hipk3), transcript variant 1, mRNA [NM_010434]	NM_010434
Hspa9	0.0168	1.80	up	Mus musculus heat shock protein 9 (Hspa9), nuclear gene encoding mitochondrial protein, mRNA [NM_010481]	NM_010481
Cyr61	0.0410	2.81	up	Mus musculus cysteine rich protein 61 (Cyr61), mRNA [NM_010516]	NM_010516

Kcnab3	0.0016	2.67	up	Mus musculus potassium voltage-gated channel, shaker-related subfamily, beta member 3 (Kcnab3), mRNA [NM_010599]	NM_010599
Kcnk3	0.0294	2.42	up	Mus musculus potassium channel, subfamily K, member 3 (Kcnk3), mRNA [NM_010608]	NM_010608
Klra12	0.0036	3.89	up	Mus musculus killer cell lectin-like receptor subfamily A, member 12 (Klra12), mRNA [NM_010646]	NM_010646
Klra4	0.0032	3.51	up	Mus musculus killer cell lectin-like receptor, subfamily A, member 4 (Klra4), mRNA [NM_010649]	NM_010649
Lama3	0.0427	1.51	up	Mus musculus laminin, alpha 3 (Lama3), mRNA [NM_010680]	NM_010680
Masp2	0.0455	1.73	up	Mus musculus mannan-binding lectin serine peptidase 2 (Masp2), transcript variant 2, mRNA [NM_010767]	NM_010767
Mbp	0.0401	1.85	up	Mus musculus myelin basic protein (Mbp), transcript variant 7, mRNA [NM_010777]	NM_010777
Nkx2-2	0.0128	1.56	up	Mus musculus NK2 transcription factor related, locus 2 (Drosophila) (Nkx2-2), transcript variant 1, mRNA [NM_010919]	NM_010919
Ogdh	0.0185	1.61	up	Mus musculus oxoglutarate dehydrogenase (lipoamide) (Ogdh), nuclear gene encoding mitochondrial protein, mRNA [NM_010956]	NM_010956
P4ha1	0.0196	1.94	up	Mus musculus procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide (P4ha1), mRNA [NM_011030]	NM_011030
Pax7	0.0072	2.32	up	Mus musculus paired box gene 7 (Pax7), mRNA [NM_011039]	NM_011039
Padi3	0.0379	3.30	up	Mus musculus peptidyl arginine deiminase, type III (Padi3), mRNA [NM_011060]	NM_011060
Per2	0.0299	1.72	up	Mus musculus period homolog 2 (Drosophila) (Per2), mRNA [NM_011066]	NM_011066

Pik3c2a	0.0106	1.77	up	Mus musculus phosphatidylinositol 3-kinase, C2 domain containing, alpha polypeptide (Pik3c2a), mRNA [NM_011083]	NM_011083
Psap	0.0442	1.81	up	Mus musculus prosaposin (Psap), transcript variant 2, mRNA [NM_011179]	NM_011179
Ptprd	0.0422	2.56	up	Mus musculus protein tyrosine phosphatase, receptor type, D (Ptprd), transcript variant b, mRNA [NM_011211]	NM_011211
Purb	0.0262	1.53	up	Mus musculus purine rich element binding protein B (Purb), mRNA [NM_011221]	NM_011221
Rad51l3	0.0260	1.91	up	Mus musculus RAD51-like 3 (<i>S. cerevisiae</i>) (Rad51l3), mRNA [NM_011235]	NM_011235
Rarb	0.0267	1.57	up	Mus musculus retinoic acid receptor, beta (Rarb), mRNA [NM_011243]	NM_011243
S100a1	0.0166	1.58	up	Mus musculus S100 calcium binding protein A1 (S100a1), mRNA [NM_011309]	NM_011309
Sema3e	0.0328	1.93	up	Mus musculus sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E (Sema3e), mRNA [NM_011348]	NM_011348
St6galnac1	0.0491	1.54	up	Mus musculus ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 1 (St6galnac1), mRNA [NM_011371]	NM_011371
Spink4	0.0032	1.60	up	Mus musculus serine peptidase inhibitor, Kazal type 4 (Spink4), mRNA [NM_011463]	NM_011463
Stat5a	0.0018	1.54	up	Mus musculus signal transducer and activator of transcription 5A (Stat5a), transcript variant 1, mRNA [NM_011488]	NM_011488
Timm44	0.0229	1.52	up	Mus musculus translocase of inner mitochondrial membrane 44 (Timm44), nuclear gene encoding mitochondrial protein, mRNA [NM_011592]	NM_011592

Trpc1	0.0471	2.14	up	Mus musculus transient receptor potential cation channel, subfamily C, member 1 (Trpc1), mRNA [NM_011643]	NM_011643
Rgs7	0.0382	2.53	up	Mus musculus regulator of G protein signaling 7 (Rgs7), mRNA [NM_011880]	NM_011880
Spry2	0.0010	8.28	up	Mus musculus sprouty homolog 2 (Drosophila) (Spry2), mRNA [NM_011897]	NM_011897
Clcn6	0.0238	1.61	up	Mus musculus chloride channel 6 (Clcn6), mRNA [NM_011929]	NM_011929
Decr2	0.0482	2.28	up	Mus musculus 2-4-dienoyl-Coenzyme A reductase 2, peroxisomal (Decr2), mRNA [NM_011933]	NM_011933
Homer1	0.0116	1.77	up	Mus musculus homer homolog 1 (Drosophila) (Homer1), transcript variant S, mRNA [NM_011982]	NM_011982
Ecsit	0.0135	1.60	up	Mus musculus ECSIT homolog (Drosophila) (Ecsit), nuclear gene encoding mitochondrial protein, mRNA [NM_012029]	NM_012029
Cul1	0.0310	1.50	up	Mus musculus cullin 1 (Cul1), mRNA [NM_012042]	NM_012042
Adra1a	0.0063	3.16	up	Mus musculus adrenergic receptor, alpha 1a (Adra1a), mRNA [NM_013461]	NM_013461
Hsph1	0.0261	3.40	up	Mus musculus heat shock 105kDa/110kDa protein 1 (Hsph1), mRNA [NM_013559]	NM_013559
Hsph1	0.0182	4.12	up	Mus musculus heat shock 105kDa/110kDa protein 1 (Hsph1), mRNA [NM_013559]	NM_013559
Hspb1	0.0333	2.38	up	Mus musculus heat shock protein 1 (Hspb1), mRNA [NM_013560]	NM_013560
Muc1	0.0173	3.48	up	Mus musculus mucin 1, transmembrane (Muc1), mRNA [NM_013605]	NM_013605
Dusp1	0.0164	1.85	up	Mus musculus dual specificity phosphatase 1 (Dusp1), mRNA [NM_013642]	NM_013642
Tnfrsf12a	0.0024	1.61	up	Mus musculus tumor necrosis factor receptor superfamily, member 12a (Tnfrsf12a), transcript variant 1, mRNA [NM_013749]	NM_013749

Klra15	0.0012	3.14	up	Mus musculus killer cell lectin-like receptor, subfamily A, member 15 (Klra15), mRNA [NM_013793]	NM_013793
Klra15	0.0029	5.10	up	Mus musculus killer cell lectin-like receptor, subfamily A, member 15 (Klra15), mRNA [NM_013793]	NM_013793
Barx2	0.0353	1.64	up	Mus musculus BarH-like homeobox 2 (Barx2), mRNA [NM_013800]	NM_013800
Plk3	0.0375	1.91	up	Mus musculus polo-like kinase 3 (Drosophila) (Plk3), mRNA [NM_013807]	NM_013807
Baz1a	0.0278	1.73	up	Mus musculus bromodomain adjacent to zinc finger domain 1A (Baz1a), mRNA [NM_013815]	NM_013815
Bag3	0.0279	2.31	up	Mus musculus BCL2-associated athanogene 3 (Bag3), mRNA [NM_013863]	NM_013863
Timm8a1	0.0455	1.53	up	Mus musculus translocase of inner mitochondrial membrane 8 homolog a1 (yeast) (Timm8a1), nuclear gene encoding mitochondrial protein, mRNA [NM_013898]	NM_013898
Timm10	0.0438	1.65	up	Mus musculus translocase of inner mitochondrial membrane 10 homolog (yeast) (Timm10), nuclear gene encoding mitochondrial protein, mRNA [NM_013899]	NM_013899
Adamts8	0.0112	1.54	up	Mus musculus a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 8 (Adamts8), mRNA [NM_013906]	NM_013906
Adat1	0.0466	1.94	up	Mus musculus adenosine deaminase, tRNA-specific 1 (Adat1), mRNA [NM_013925]	NM_013925
Rgs1	0.0368	2.07	up	Mus musculus regulator of G-protein signaling 1 (Rgs1), mRNA [NM_015811]	NM_015811
Park2	0.0134	1.76	up	Mus musculus Parkinson disease (autosomal recessive, juvenile) 2, parkin (Park2), mRNA [NM_016694]	NM_016694
Hmgn5	0.0026	1.69	up	Mus musculus high-mobility group nucleosome binding domain 5 (Hmgn5), mRNA [NM_016710]	NM_016710

Stip1	0.0437	1.70	up	Mus musculus stress-induced phosphoprotein 1 (Stip1), mRNA [NM_016737]	NM_016737
Tpmt	0.0222	2.41	up	Mus musculus thiopurine methyltransferase (Tpmt), mRNA [NM_016785]	NM_016785
Rbm3	0.0374	1.88	up	Mus musculus RNA binding motif protein 3 (Rbm3), transcript variant 1, mRNA [NM_016809]	NM_016809
Banp	0.0022	1.92	up	Mus musculus BTG3 associated nuclear protein (Banp), transcript variant 2, mRNA [NM_016812]	NM_016812
Ak2	0.0282	1.65	up	Mus musculus adenylate kinase 2 (Ak2), transcript variant 2, mRNA [NM_016895]	NM_016895
Acadvl	0.0074	1.74	up	Mus musculus acyl-Coenzyme A dehydrogenase, very long chain (Acadvl), nuclear gene encoding mitochondrial protein, mRNA [NM_017366]	NM_017366
Slc5a3	0.0228	1.80	up	Mus musculus solute carrier family 5 (inositol transporters), member 3 (Slc5a3), mRNA [NM_017391]	NM_017391
Scn1a	0.0061	2.16	up	Mus musculus sodium channel, voltage-gated, type I, alpha (Scn1a), mRNA [NM_018733]	NM_018733
Apba3	0.0174	1.64	up	Mus musculus amyloid beta (A4) precursor protein-binding, family A, member 3 (Apba3), mRNA [NM_018758]	NM_018758
Apba3	0.0426	1.57	up	Mus musculus amyloid beta (A4) precursor protein-binding, family A, member 3 (Apba3), mRNA [NM_018758]	NM_018758
Dnajb1	0.0443	2.41	up	Mus musculus DnaJ (Hsp40) homolog, subfamily B, member 1 (Dnajb1), mRNA [NM_018808]	NM_018808
Fnbp1	0.0207	1.75	up	Mus musculus formin binding protein 1 (Fnbp1), transcript variant 2, mRNA [NM_019406]	NM_019406
Barhl1	0.0248	1.53	up	Mus musculus BarH-like 1 (Drosophila) (Barhl1), transcript variant 1, mRNA [NM_019446]	NM_019446
Spen	0.0470	1.61	up	Mus musculus SPEN homolog, transcriptional regulator (Drosophila) (Spen), mRNA [NM_019763]	NM_019763

Ptges3	0.0148	1.54	up	Mus musculus prostaglandin E synthase 3 (cytosolic) (Ptges3), mRNA [NM_019766]	NM_019766
Arih1	0.0442	1.74	up	Mus musculus ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila) (Arih1), mRNA [NM_019927]	NM_019927
Fgf21	0.0217	6.35	up	Mus musculus fibroblast growth factor 21 (Fgf21), mRNA [NM_020013]	NM_020013
B3galt2	0.0269	1.61	up	Mus musculus UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2 (B3galt2), mRNA [NM_020025]	NM_020025
Tob2	0.0337	2.42	up	Mus musculus transducer of ERBB2, 2 (Tob2), mRNA [NM_020507]	NM_020507
Psors1c2	0.0399	2.07	up	Mus musculus psoriasis susceptibility 1 candidate 2 (human) (Psors1c2), mRNA [NM_020576]	NM_020576
Abhd1	0.0281	10.04	up	Mus musculus abhydrolase domain containing 1 (Abhd1), mRNA [NM_021304]	NM_021304
Gpr180	0.0080	1.82	up	Mus musculus G protein-coupled receptor 180 (Gpr180), mRNA [NM_021434]	NM_021434
Chst11	0.0112	1.60	up	Mus musculus carbohydrate sulfotransferase 11 (Chst11), mRNA [NM_021439]	NM_021439
Fign	0.0250	1.97	up	Mus musculus fidgetin (Fign), mRNA [NM_021716]	NM_021716
Rbp7	0.0162	6.22	up	Mus musculus retinol binding protein 7, cellular (Rbp7), mRNA [NM_022020]	NM_022020
Ube4b	0.0420	1.68	up	Mus musculus ubiquitination factor E4B, UFD2 homolog (S. cerevisiae) (Ube4b), mRNA [NM_022022]	NM_022022
Slc28a3	0.0434	1.65	up	Mus musculus solute carrier family 28 (sodium-coupled nucleoside transporter), member 3 (Slc28a3), mRNA [NM_022317]	NM_022317
Gprc5b	0.0284	4.31	up	Mus musculus G protein-coupled receptor, family C, group 5, member B (Gprc5b), mRNA [NM_022420]	NM_022420
Apoc3	0.0328	4.14	up	Mus musculus apolipoprotein C-III (Apoc3), mRNA [NM_023114]	NM_023114

Zfp788	0.0070	2.45	up	Mus musculus zinc finger protein 788 (Zfp788), mRNA [NM_023363]	NM_023363
Paqr4	0.0198	5.90	up	Mus musculus progesterin and adipoQ receptor family member IV (Paqr4), mRNA [NM_023824]	NM_023824
Tbc1d20	0.0182	2.01	up	Mus musculus TBC1 domain family, member 20 (Tbc1d20), mRNA [NM_024196]	NM_024196
Hdhd3	0.0470	3.47	up	Mus musculus haloacid dehalogenase-like hydrolase domain containing 3 (Hdhd3), mRNA [NM_024257]	NM_024257
1200011M11Rik	0.0250	1.88	up	Mus musculus RIKEN cDNA 1200011M11 gene (1200011M11Rik), mRNA [NM_024262]	NM_024262
1810037I17Rik	0.0017	9.30	up	Mus musculus RIKEN cDNA 1810037I17 gene (1810037I17Rik), mRNA [NM_024461]	NM_024461
1810037I17Rik	0.0013	9.13	up	Mus musculus RIKEN cDNA 1810037I17 gene (1810037I17Rik), mRNA [NM_024461]	NM_024461
Bhlhe41	0.0013	2.20	up	Mus musculus basic helix-loop-helix family, member e41 (Bhlhe41), mRNA [NM_024469]	NM_024469
Ublcp1	0.0092	2.00	up	Mus musculus ubiquitin-like domain containing CTD phosphatase 1 (Ublcp1), mRNA [NM_024475]	NM_024475
Gng10	0.0179	1.58	up	Mus musculus guanine nucleotide binding protein (G protein), gamma 10 (Gng10), mRNA [NM_025277]	NM_025277
Fmc1	0.0248	1.51	up	Mus musculus formation of mitochondrial complexes 1 homolog (S. cerevisiae) (Fmc1), nuclear gene encoding mitochondrial protein, mRNA [NM_025363]	NM_025363
Tomm7	0.0292	2.17	up	Mus musculus translocase of outer mitochondrial membrane 7 homolog (yeast) (Tomm7), nuclear gene encoding mitochondrial protein, mRNA [NM_025394]	NM_025394
Llph	0.0076	1.60	up	Mus musculus LLP homolog, long-term synaptic facilitation (Aplysia) (Llph), mRNA [NM_025431]	NM_025431
1700001K19Rik	0.0004	1.56	up	Mus musculus RIKEN cDNA 1700001K19 gene (1700001K19Rik), mRNA [NM_025488]	NM_025488

Rwdd3	0.0031	2.46	up	Mus musculus RWD domain containing 3 (Rwdd3), transcript variant 1, mRNA [NM_025637]	NM_025637
Tmigd1	0.0151	1.55	up	Mus musculus transmembrane and immunoglobulin domain containing 1 (Tmigd1), mRNA [NM_025655]	NM_025655
Gpatch4	0.0172	1.57	up	Mus musculus G patch domain containing 4 (Gpatch4), transcript variant 1, mRNA [NM_025663]	NM_025663
Rbm4b	0.0462	1.59	up	Mus musculus RNA binding motif protein 4B (Rbm4b), mRNA [NM_025717]	NM_025717
Mrpl33	0.0079	1.58	up	Mus musculus mitochondrial ribosomal protein L33 (Mrpl33), nuclear gene encoding mitochondrial protein, mRNA [NM_025796]	NM_025796
1200016B10Rik	0.0270	1.72	up	Mus musculus RIKEN cDNA 1200016B10 gene (1200016B10Rik), mRNA [NM_025819]	NM_025819
Chordc1	0.0114	1.90	up	Mus musculus cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1 (Chordc1), mRNA [NM_025844]	NM_025844
Luc7l	0.0426	1.63	up	Mus musculus Luc7 homolog (S. cerevisiae)-like (Luc7l), transcript variant 1, mRNA [NM_025881]	NM_025881
Gtf3c6	0.0384	1.52	up	Mus musculus general transcription factor IIIC, polypeptide 6, alpha (Gtf3c6), mRNA [NM_026113]	NM_026113
Ears2	0.0114	1.66	up	Mus musculus glutamyl-tRNA synthetase 2 (mitochondrial)(putative) (Ears2), nuclear gene encoding mitochondrial protein, mRNA [NM_026140]	NM_026140
Slc48a1	0.0160	1.81	up	Mus musculus solute carrier family 48 (heme transporter), member 1 (Slc48a1), mRNA [NM_026353]	NM_026353
Ddx55	0.0167	1.50	up	Mus musculus DEAD (Asp-Glu-Ala-Asp) box polypeptide 55 (Ddx55), mRNA [NM_026409]	NM_026409
1700021F05Rik	0.0180	1.69	up	Mus musculus RIKEN cDNA 1700021F05 gene (1700021F05Rik), mRNA [NM_026411]	NM_026411

1700020C11Rik	0.0162	2.09	up	Mus musculus RIKEN cDNA 1700020C11 gene (1700020C11Rik), mRNA [NM_026443]	NM_026443
Mak16	0.0045	1.55	up	Mus musculus MAK16 homolog (S. cerevisiae) (Mak16), mRNA [NM_026453]	NM_026453
Fam32a	0.0336	1.80	up	Mus musculus family with sequence similarity 32, member A (Fam32a), mRNA [NM_026455]	NM_026455
Nudt12	0.0311	2.15	up	Mus musculus nudix (nucleoside diphosphate linked moiety X)-type motif 12 (Nudt12), mRNA [NM_026497]	NM_026497
Aen	0.0355	1.52	up	Mus musculus apoptosis enhancing nuclease (Aen), transcript variant 1, mRNA [NM_026531]	NM_026531
Ndufb2	0.0133	3.49	up	Mus musculus NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 (Ndufb2), nuclear gene encoding mitochondrial protein, mRNA [NM_026612]	NM_026612
Ndufa8	0.0114	1.54	up	Mus musculus NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8 (Ndufa8), nuclear gene encoding mitochondrial protein, mRNA [NM_026703]	NM_026703
Hddc3	0.0247	3.66	up	Mus musculus HD domain containing 3 (Hddc3), mRNA [NM_026812]	NM_026812
1190005F20Rik	0.0070	1.82	up	Mus musculus RIKEN cDNA 1190005F20 gene (1190005F20Rik), mRNA [NM_026876]	NM_026876
1810014F10Rik	0.0213	2.02	up	Mus musculus RIKEN cDNA 1810014F10 gene (1810014F10Rik), mRNA [NM_026928]	NM_026928
1810014F10Rik	0.0272	1.95	up	Mus musculus RIKEN cDNA 1810014F10 gene (1810014F10Rik), mRNA [NM_026928]	NM_026928
Comtd1	0.0193	1.54	up	Mus musculus catechol-O-methyltransferase domain containing 1 (Comtd1), mRNA [NM_026965]	NM_026965
Taf1d	0.0491	1.63	up	Mus musculus TATA box binding protein (Tbp)-associated factor, RNA polymerase I, D (Taf1d), transcript variant 3, mRNA [NM_027261]	NM_027261
Mapk6	0.0259	1.68	up	Mus musculus mitogen-activated protein kinase 6 (Mapk6), transcript variant 2, mRNA [NM_027418]	NM_027418

Slc25a33	0.0231	1.94	up	Mus musculus solute carrier family 25, member 33 (Slc25a33), mRNA [NM_027460]	NM_027460
Wars2	0.0017	2.07	up	Mus musculus tryptophanyl tRNA synthetase 2 (mitochondrial) (Wars2), nuclear gene encoding mitochondrial protein, mRNA [NM_027462]	NM_027462
Usp38	0.0356	2.11	up	Mus musculus ubiquitin specific peptidase 38 (Usp38), mRNA [NM_027554]	NM_027554
Katnal2	0.0296	1.91	up	Mus musculus katanin p60 subunit A-like 2 (Katnal2), mRNA [NM_027721]	NM_027721
Trem11	0.0151	13.96	up	Mus musculus triggering receptor expressed on myeloid cells-like 1 (Trem11), mRNA [NM_027763]	NM_027763
Alpk1	0.0100	4.39	up	Mus musculus alpha-kinase 1 (Alpk1), mRNA [NM_027808]	NM_027808
Coasy	0.0130	1.74	up	Mus musculus Coenzyme A synthase (Coasy), nuclear gene encoding mitochondrial protein, mRNA [NM_027896]	NM_027896
Dusp11	0.0484	1.60	up	Mus musculus dual specificity phosphatase 11 (RNA/RNP complex 1-interacting) (Dusp11), mRNA [NM_028099]	NM_028099
Ddhd2	0.0171	1.63	up	Mus musculus DDHD domain containing 2 (Ddhd2), mRNA [NM_028102]	NM_028102
Luc7l	0.0407	1.91	up	Mus musculus Luc7 homolog (S. cerevisiae)-like (Luc7l), transcript variant 2, mRNA [NM_028190]	NM_028190
Ptar1	0.0464	1.63	up	Mus musculus protein prenyltransferase alpha subunit repeat containing 1 (Ptar1), mRNA [NM_028208]	NM_028208
Tmem48	0.0048	1.98	up	Mus musculus transmembrane protein 48 (Tmem48), mRNA [NM_028355]	NM_028355
Rwdd3	0.0056	2.25	up	Mus musculus RWD domain containing 3 (Rwdd3), transcript variant 2, mRNA [NM_028456]	NM_028456
Rassf6	0.0135	5.35	up	Mus musculus Ras association (RalGDS/AF-6) domain family member 6 (Rassf6), mRNA [NM_028478]	NM_028478

2410076I21Rik	0.0425	2.74	up	Mus musculus RIKEN cDNA 2410076I21 gene (2410076I21Rik), mRNA [NM_028598]	NM_028598
Ppp2r1b	0.0357	2.24	up	Mus musculus protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform (Ppp2r1b), transcript variant 2, mRNA [NM_028614]	NM_028614
Nol9	0.0101	1.50	up	Mus musculus nucleolar protein 9 (Nol9), transcript variant 2, mRNA [NM_028727]	NM_028727
1700017B05Rik	0.0082	1.52	up	Mus musculus RIKEN cDNA 1700017B05 gene (1700017B05Rik), mRNA [NM_028820]	NM_028820
2210009G21Rik	0.0071	1.95	up	Mus musculus RIKEN cDNA 2210009G21 gene (2210009G21Rik), transcript variant 1, mRNA [NM_028834]	NM_028834
Xrcc3	0.0034	1.68	up	Mus musculus X-ray repair complementing defective repair in Chinese hamster cells 3 (Xrcc3), mRNA [NM_028875]	NM_028875
Tmem33	0.0104	1.69	up	Mus musculus transmembrane protein 33 (Tmem33), transcript variant 1, mRNA [NM_028975]	NM_028975
8430406I07Rik	0.0120	1.51	up	Mus musculus RIKEN cDNA 8430406I07 gene (8430406I07Rik), mRNA [NM_028984]	NM_028984
Mrpl47	0.0186	1.60	up	Mus musculus mitochondrial ribosomal protein L47 (Mrpl47), nuclear gene encoding mitochondrial protein, mRNA [NM_029017]	NM_029017
Abcb8	0.0024	3.93	up	Mus musculus ATP-binding cassette, sub-family B (MDR/TAP), member 8 (Abcb8), nuclear gene encoding mitochondrial protein, mRNA [NM_029020]	NM_029020
4833422F24Rik	0.0076	1.61	up	Mus musculus RIKEN cDNA 4833422F24 gene (4833422F24Rik), mRNA [NM_029021]	NM_029021
Scpep1	0.0487	1.68	up	Mus musculus serine carboxypeptidase 1 (Scpep1), mRNA [NM_029023]	NM_029023
Ndufs7	0.0386	1.67	up	Mus musculus NADH dehydrogenase (ubiquinone) Fe-S protein 7 (Ndufs7), nuclear gene encoding mitochondrial protein, mRNA [NM_029272]	NM_029272

4930402H24Rik	0.0043	1.91	up	Mus musculus RIKEN cDNA 4930402H24 gene (4930402H24Rik), mRNA [NM_029432]	NM_029432
4930447C04Rik	0.0257	2.27	up	Mus musculus IKEN cDNA 4930447C04 gene (4930447C04Rik), mRNA [NM_029444]	NM_029444
6530401D17Rik	0.0133	2.17	up	Mus musculus RIKEN cDNA 6530401D17 gene (6530401D17Rik), mRNA [NM_029541]	NM_029541
6530401N04Rik	0.0148	1.87	up	Mus musculus RIKEN cDNA 6530401N04 gene (6530401N04Rik), mRNA [NM_029545]	NM_029545
Tsen54	0.0444	1.59	up	Mus musculus tRNA splicing endonuclease 54 homolog (S. cerevisiae) (Tsen54), mRNA [NM_029557]	NM_029557
Klhl25	0.0470	1.63	up	Mus musculus kelch-like 25 (Drosophila) (Klhl25), transcript variant 1, mRNA [NM_029652]	NM_029652
2900062L11Rik	0.0474	1.78	up	Mus musculus RIKEN cDNA 2900062L11 gene (2900062L11Rik), mRNA [NM_029823]	NM_029823
Arsk	0.0497	4.04	up	Mus musculus arylsulfatase K (Arsk), mRNA [NM_029847]	NM_029847
Ocel1	0.0010	4.36	up	Mus musculus occludin/ELL domain containing 1 (Ocel1), mRNA [NM_029865]	NM_029865
Gpbp1l1	0.0127	1.62	up	Mus musculus GC-rich promoter binding protein 1-like 1 (Gpbp1l1), mRNA [NM_029868]	NM_029868
Zfp142	0.0413	1.60	up	Mus musculus zinc finger protein 142 (Zfp142), mRNA [NM_029888]	NM_029888
Apex2	0.0387	1.73	up	Mus musculus apurinic/apyrimidinic endonuclease 2 (Apex2), mRNA [NM_029943]	NM_029943
Snapc3	0.0379	2.47	up	Mus musculus small nuclear RNA activating complex, polypeptide 3 (Snapc3), mRNA [NM_029949]	NM_029949
2700078E11Rik	0.0037	1.57	up	Mus musculus RIKEN cDNA 2700078E11 gene (2700078E11Rik), transcript variant 1, mRNA [NM_030197]	NM_030197
Lsm2	0.0061	1.53	up	Mus musculus LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae) (Lsm2), transcript variant 1, mRNA [NM_030597]	NM_030597

Nr5a2	0.0298	2.00	up	Mus musculus nuclear receptor subfamily 5, group A, member 2 (Nr5a2), transcript variant 1, mRNA [NM_030676]	NM_030676
Mesdc1	0.0489	1.80	up	Mus musculus mesoderm development candidate 1 (Mesdc1), mRNA [NM_030705]	NM_030705
Pum1	0.0245	1.55	up	Mus musculus pumilio 1 (Drosophila) (Pum1), transcript variant 1, mRNA [NM_030722]	NM_030722
Trem2	0.0121	5.22	up	Mus musculus triggering receptor expressed on myeloid cells 2 (Trem2), mRNA [NM_031254]	NM_031254
Nrg4	0.0235	3.39	up	Mus musculus neuregulin 4 (Nrg4), mRNA [NM_032002]	NM_032002
Slmap	0.0042	1.55	up	Mus musculus sarcolemma associated protein (Slmap), mRNA [NM_032008]	NM_032008
P2rx5	0.0475	2.30	up	Mus musculus purinergic receptor P2X, ligand-gated ion channel, 5 (P2rx5), mRNA [NM_033321]	NM_033321
Npnt	0.0394	1.68	up	Mus musculus nephronectin (Npnt), transcript variant 1, mRNA [NM_033525]	NM_033525
Npnt	0.0031	1.90	up	Mus musculus nephronectin (Npnt), transcript variant 1, mRNA [NM_033525]	NM_033525
Hist2h4	0.0000	2.15	up	Mus musculus histone cluster 2, H4 (Hist2h4), mRNA [NM_033596]	NM_033596
Strn3	0.0378	1.51	up	Mus musculus striatin, calmodulin binding protein 3 (Strn3), transcript variant 1, mRNA [NM_052973]	NM_052973
Ophn1	0.0226	1.58	up	Mus musculus oligophrenin 1 (Ophn1), mRNA [NM_052976]	NM_052976
Il24	0.0256	1.56	up	Mus musculus interleukin 24 (Il24), mRNA [NM_053095]	NM_053095
Pcdhb4	0.0144	1.78	up	Mus musculus protocadherin beta 4 (Pcdhb4), mRNA [NM_053129]	NM_053129
Pfkfb3	0.0069	2.45	up	Mus musculus 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 (Pfkfb3), transcript variant 6, mRNA [NM_133232]	NM_133232

Ppargc1b	0.0065	3.95	up	Mus musculus peroxisome proliferative activated receptor, gamma, coactivator 1 beta (Ppargc1b), mRNA [NM_133249]	NM_133249
Vgll1	0.0229	1.87	up	Mus musculus vestigial like 1 homolog (Drosophila) (Vgll1), mRNA [NM_133251]	NM_133251
Prss22	0.0457	1.95	up	Mus musculus protease, serine, 22 (Prss22), mRNA [NM_133731]	NM_133731
4931406C07Rik	0.0162	1.61	up	Mus musculus RIKEN cDNA 4931406C07 gene (4931406C07Rik), mRNA [NM_133732]	NM_133732
Adck4	0.0172	1.74	up	Mus musculus aarF domain containing kinase 4 (Adck4), mRNA [NM_133770]	NM_133770
Ppp1r15b	0.0091	2.33	up	Mus musculus protein phosphatase 1, regulatory (inhibitor) subunit 15b (Ppp1r15b), mRNA [NM_133819]	NM_133819
Rcc1	0.0099	2.16	up	Mus musculus regulator of chromosome condensation 1 (Rcc1), mRNA [NM_133878]	NM_133878
Armc6	0.0301	2.57	up	Mus musculus armadillo repeat containing 6 (Armc6), mRNA [NM_133972]	NM_133972
Acot4	0.0432	2.74	up	Mus musculus acyl-CoA thioesterase 4 (Acot4), mRNA [NM_134247]	NM_134247
Ash1l	0.0265	1.51	up	Mus musculus ash1 (absent, small, or homeotic)-like (Drosophila) (Ash1l), mRNA [NM_138679]	NM_138679
Acer2	0.0218	1.88	up	Mus musculus alkaline ceramidase 2 (Acer2), mRNA [NM_139306]	NM_139306
Eif3j	0.0046	1.55	up	Mus musculus eukaryotic translation initiation factor 3, subunit J (Eif3j), mRNA [NM_144545]	NM_144545
Prdm15	0.0155	1.89	up	Mus musculus PR domain containing 15 (Prdm15), mRNA [NM_144789]	NM_144789
Hnrnpul1	0.0389	1.52	up	Mus musculus heterogeneous nuclear ribonucleoprotein U-like 1 (Hnrnpul1), transcript variant 1, mRNA [NM_144922]	NM_144922
Frs3	0.0013	1.91	up	Mus musculus fibroblast growth factor receptor substrate 3 (Frs3), mRNA [NM_144939]	NM_144939

Uroc1	0.0157	1.78	up	Mus musculus urocanase domain containing 1 (Uroc1), mRNA [NM_144940]	NM_144940
Mgat5	0.0198	1.71	up	Mus musculus mannoside acetylglucosaminyltransferase 5 (Mgat5), mRNA [NM_145128]	NM_145128
Tnpo2	0.0270	2.84	up	Mus musculus transportin 2 (importin 3, karyopherin beta 2b) (Tnpo2), transcript variant 1, mRNA [NM_145390]	NM_145390
Ythdf2	0.0198	1.68	up	Mus musculus YTH domain family 2 (Ythdf2), mRNA [NM_145393]	NM_145393
L2hgdh	0.0316	1.66	up	Mus musculus L-2-hydroxyglutarate dehydrogenase (L2hgdh), nuclear gene encoding mitochondrial protein, mRNA [NM_145443]	NM_145443
L2hgdh	0.0336	1.79	up	Mus musculus L-2-hydroxyglutarate dehydrogenase (L2hgdh), nuclear gene encoding mitochondrial protein, mRNA [NM_145443]	NM_145443
Ifi2712b	0.0012	1.73	up	Mus musculus interferon, alpha-inducible protein 27 like 2B (Ifi2712b), mRNA [NM_145449]	NM_145449
Cplx4	0.0281	2.38	up	Mus musculus complexin 4 (Cplx4), mRNA [NM_145493]	NM_145493
Trub2	0.0481	1.61	up	Mus musculus TruB pseudouridine (psi) synthase homolog 2 (E. coli) (Trub2), transcript variant 1, mRNA [NM_145520]	NM_145520
Efcab7	0.0139	2.12	up	Mus musculus EF-hand calcium binding domain 7 (Efcab7), mRNA [NM_145549]	NM_145549
Agfg2	0.0420	2.30	up	Mus musculus ArfGAP with FG repeats 2 (Agfg2), transcript variant 1, mRNA [NM_145566]	NM_145566
Gys2	0.0491	6.14	up	Mus musculus glycogen synthase 2 (Gys2), mRNA [NM_145572]	NM_145572
Adig	0.0128	1.68	up	Mus musculus adipogenin (Adig), mRNA [NM_145635]	NM_145635
Nlrp3	0.0287	1.63	up	Mus musculus NLR family, pyrin domain containing 3 (Nlrp3), mRNA [NM_145827]	NM_145827

Pphln1	0.0016	2.40	up	Mus musculus periphilin 1 (Pphln1), transcript variant 1, mRNA [NM_146062]	NM_146062
Krt79	0.0001	2.09	up	Mus musculus keratin 79 (Krt79), mRNA [NM_146063]	NM_146063
Ahdc1	0.0479	1.55	up	Mus musculus AT hook, DNA binding motif, containing 1 (Ahdc1), mRNA [NM_146155]	NM_146155
Olfr1396	0.0028	2.35	up	Mus musculus olfactory receptor 1396 (Olfr1396), mRNA [NM_146337]	NM_146337
Olfr905	0.0341	2.22	up	Mus musculus olfactory receptor 905 (Olfr905), mRNA [NM_146804]	NM_146804
Olfr1247	0.0482	2.51	up	Mus musculus olfactory receptor 1247 (Olfr1247), mRNA [NM_146966]	NM_146966
Olfr635	0.0087	1.54	up	Mus musculus olfactory receptor 635 (Olfr635), mRNA [NM_147118]	NM_147118
Homer1	0.0305	1.73	up	Mus musculus homer homolog 1 (Drosophila) (Homer1), transcript variant L, mRNA [NM_147176]	NM_147176
Abca5	0.0239	2.84	up	Mus musculus ATP-binding cassette, sub-family A (ABC1), member 5 (Abca5), mRNA [NM_147219]	NM_147219
Abca5	0.0006	1.92	up	Mus musculus ATP-binding cassette, sub-family A (ABC1), member 5 (Abca5), mRNA [NM_147219]	NM_147219
Glis1	0.0353	2.04	up	Mus musculus GLIS family zinc finger 1 (Glis1), mRNA [NM_147221]	NM_147221
Commd3	0.0406	1.66	up	Mus musculus COMM domain containing 3 (Commd3), mRNA [NM_147778]	NM_147778
Mrgpra2b	0.0139	1.53	up	Mus musculus MAS-related GPR, member A2B (Mrgpra2b), mRNA [NM_153101]	NM_153101
Slc36a1	0.0175	3.24	up	Mus musculus solute carrier family 36 (proton/amino acid symporter), member 1 (Slc36a1), mRNA [NM_153139]	NM_153139
Acat3	0.0053	1.53	up	Mus musculus acetyl-Coenzyme A acetyltransferase 3 (Acat3), mRNA [NM_153151]	NM_153151

Slc36a2	0.0424	1.92	up	Mus musculus solute carrier family 36 (proton/amino acid symporter), member 2 (Slc36a2), mRNA [NM_153170]	NM_153170
Clrn1	0.0321	3.20	up	Mus musculus clarin 1 (Clrn1), transcript variant 1, mRNA [NM_153384]	NM_153384
Atp10d	0.0449	5.10	up	Mus musculus ATPase, class V, type 10D (Atp10d), mRNA [NM_153389]	NM_153389
Clstn3	0.0061	2.54	up	Mus musculus calsyntenin 3 (Clstn3), mRNA [NM_153508]	NM_153508
Insig1	0.0326	3.79	up	Mus musculus insulin induced gene 1 (Insig1), mRNA [NM_153526]	NM_153526
Fam40a	0.0460	1.57	up	Mus musculus family with sequence similarity 40, member A (Fam40a), mRNA [NM_153563]	NM_153563
Cmtm4	0.0453	1.90	up	Mus musculus CKLF-like MARVEL transmembrane domain containing 4 (Cmtm4), mRNA [NM_153582]	NM_153582
Flywch1	0.0497	1.51	up	Mus musculus FLYWCH-type zinc finger 1 (Flywch1), mRNA [NM_153791]	NM_153791
Peo1	0.0073	1.56	up	Mus musculus progressive external ophthalmoplegia 1 (human) (Peo1), mRNA [NM_153796]	NM_153796
Pdxk	0.0309	1.68	up	Mus musculus pyridoxal (pyridoxine, vitamin B6) kinase (Pdxk), mRNA [NM_172134]	NM_172134
Phf17	0.0086	1.55	up	Mus musculus PHD finger protein 17 (Phf17), transcript variant 1, mRNA [NM_172303]	NM_172303
Phf17	0.0050	1.59	up	Mus musculus PHD finger protein 17 (Phf17), transcript variant 1, mRNA [NM_172303]	NM_172303
Tmem120a	0.0238	1.90	up	Mus musculus transmembrane protein 120A (Tmem120a), mRNA [NM_172541]	NM_172541
Hlf	0.0041	1.77	up	Mus musculus hepatic leukemia factor (Hlf), mRNA [NM_172563]	NM_172563
Larp4b	0.0329	1.61	up	Mus musculus La ribonucleoprotein domain family, member 4B (Larp4b), mRNA [NM_172585]	NM_172585
Kctd3	0.0327	1.63	up	Mus musculus potassium channel tetramerisation domain containing 3 (Kctd3), mRNA [NM_172650]	NM_172650

Plaa	0.0035	1.71	up	Mus musculus phospholipase A2, activating protein (Plaa), mRNA [NM_172695]	NM_172695
Naa25	0.0100	1.75	up	Mus musculus N(alpha)-acetyltransferase 25, NatB auxiliary subunit (Naa25), mRNA [NM_172722]	NM_172722
Plekha7	0.0094	2.07	up	Mus musculus pleckstrin homology domain containing, family A member 7 (Plekha7), mRNA [NM_172743]	NM_172743
Zfp868	0.0236	2.65	up	Mus musculus zinc finger protein 868 (Zfp868), transcript variant 1, mRNA [NM_172754]	NM_172754
Gramd1b	0.0300	1.95	up	Mus musculus GRAM domain containing 1B (Gramd1b), mRNA [NM_172768]	NM_172768
Btnl9	0.0095	2.31	up	Mus musculus butyrophilin-like 9 (Btnl9), mRNA [NM_172793]	NM_172793
Zfp454	0.0411	1.87	up	Mus musculus zinc finger protein 454 (Zfp454), mRNA [NM_172794]	NM_172794
Dock4	0.0032	1.61	up	Mus musculus dedicator of cytokinesis 4 (Dock4), mRNA [NM_172803]	NM_172803
Gucy1b2	0.0441	1.53	up	Mus musculus guanylate cyclase 1, soluble, beta 2 (Gucy1b2), mRNA [NM_172810]	NM_172810
Palm2	0.0287	2.45	up	Mus musculus paralectmin 2 (Palm2), mRNA [NM_172868]	NM_172868
Zfp317	0.0326	2.46	up	Mus musculus zinc finger protein 317 (Zfp317), mRNA [NM_172918]	NM_172918
Alkbh5	0.0224	1.53	up	Mus musculus alkB, alkylation repair homolog 5 (E. coli) (Alkbh5), mRNA [NM_172943]	NM_172943
Vat1l	0.0049	2.86	up	Mus musculus vesicle amine transport protein 1 homolog-like (T. californica) (Vat1l), mRNA [NM_173016]	NM_173016
Slc43a2	0.0011	2.20	up	Mus musculus solute carrier family 43, member 2 (Slc43a2), mRNA [NM_173388]	NM_173388
Dcun1d3	0.0124	2.50	up	Mus musculus DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae) (Dcun1d3), transcript variant 1, mRNA [NM_173408]	NM_173408

Arsj	0.0044	2.01	up	Mus musculus arylsulfatase J (Arsj), mRNA [NM_173451]	NM_173451
2310044G17Rik	0.0415	1.98	up	Mus musculus RIKEN cDNA 2310044G17 gene (2310044G17Rik), transcript variant 1, mRNA [NM_173735]	NM_173735
Nudcd3	0.0065	1.57	up	Mus musculus NudC domain containing 3 (Nudcd3), mRNA [NM_173748]	NM_173748
1300010F03Rik	0.0173	1.78	up	Mus musculus RIKEN cDNA 1300010F03 gene (1300010F03Rik), transcript variant 2, mRNA [NM_173758]	NM_173758
Tapt1	0.0360	1.59	up	Mus musculus transmembrane anterior posterior transformation 1 (Tapt1), mRNA [NM_173764]	NM_173764
Rcc2	0.0029	1.71	up	Mus musculus regulator of chromosome condensation 2 (Rcc2), mRNA [NM_173867]	NM_173867
Rcc2	0.0079	1.57	up	Mus musculus regulator of chromosome condensation 2 (Rcc2), mRNA [NM_173867]	NM_173867
Adnp2	0.0069	1.54	up	Mus musculus ADNP homeobox 2 (Adnp2), mRNA [NM_175028]	NM_175028
Tatdn1	0.0354	2.24	up	Mus musculus TatD DNase domain containing 1 (Tatdn1), mRNA [NM_175151]	NM_175151
Srrm2	0.0053	2.09	up	Mus musculus serine/arginine repetitive matrix 2 (Srrm2), mRNA [NM_175229]	NM_175229
2810007J24Rik	0.0157	1.58	up	Mus musculus RIKEN cDNA 2810007J24 gene (2810007J24Rik), mRNA [NM_175250]	NM_175250
D630023F18Rik	0.0420	4.83	up	Mus musculus RIKEN cDNA D630023F18 gene (D630023F18Rik), mRNA [NM_175293]	NM_175293
Chchd10	0.0435	3.19	up	Mus musculus coiled-coil-helix-coiled-coil-helix domain containing 10 (Chchd10), mRNA [NM_175329]	NM_175329
Dcaf12l2	0.0301	2.27	up	Mus musculus DDB1 and CUL4 associated factor 12-like 2 (Dcaf12l2), mRNA [NM_175539]	NM_175539
Acer1	0.0440	1.51	up	Mus musculus alkaline ceramidase 1 (Acer1), mRNA [NM_175731]	NM_175731

Nt5dc1	0.0340	1.81	up	Mus musculus 5'-nucleotidase domain containing 1 (Nt5dc1), mRNA [NM_176968]	NM_176968
Cobll1	0.0368	1.65	up	Mus musculus Cobl-like 1 (Cobll1), transcript variant 1, mRNA [NM_177025]	NM_177025
Adrbk2	0.0014	1.78	up	Mus musculus adrenergic receptor kinase, beta 2 (Adrbk2), transcript variant 1, mRNA [NM_177078]	NM_177078
Msrb3	0.0472	1.55	up	Mus musculus methionine sulfoxide reductase B3 (Msrb3), mRNA [NM_177092]	NM_177092
Senp5	0.0388	3.19	up	Mus musculus SUMO/sentrin specific peptidase 5 (Senp5), mRNA [NM_177103]	NM_177103
Cntn2	0.0278	1.82	up	Mus musculus contactin 2 (Cntn2), mRNA [NM_177129]	NM_177129
A830018L16Rik	0.0071	3.71	up	Mus musculus RIKEN cDNA A830018L16 gene (A830018L16Rik), transcript variant 2, mRNA [NM_177173]	NM_177173
Chd9	0.0194	1.72	up	Mus musculus chromodomain helicase DNA binding protein 9 (Chd9), mRNA [NM_177224]	NM_177224
Pisd	0.0500	1.97	up	Mus musculus phosphatidylserine decarboxylase (Pisd), mRNA [NM_177298]	NM_177298
Taf5	0.0492	1.53	up	Mus musculus TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor (Taf5), mRNA [NM_177342]	NM_177342
A630033E08Rik	0.0148	3.29	up	Mus musculus RIKEN cDNA A630033E08 gene (A630033E08Rik), transcript variant 2, mRNA [NM_177358]	NM_177358
A630033E08Rik	0.0131	2.66	up	Mus musculus RIKEN cDNA A630033E08 gene (A630033E08Rik), transcript variant 2, mRNA [NM_177358]	NM_177358
E2f2	0.0149	1.78	up	Mus musculus E2F transcription factor 2 (E2f2), mRNA [NM_177733]	NM_177733
2700050L05Rik	0.0314	1.53	up	Mus musculus RIKEN cDNA 2700050L05 gene (2700050L05Rik), mRNA [NM_178115]	NM_178115

Hist1h3i	0.0288	1.87	up	Mus musculus histone cluster 1, H3i (Hist1h3i), mRNA [NM_178207]	NM_178207
BC051070	0.0488	2.35	up	Mus musculus cDNA sequence BC051070 (BC051070), mRNA [NM_178412]	NM_178412
Ccdc144b	0.0338	1.52	up	Mus musculus coiled-coil domain containing 144B (Ccdc144b), mRNA [NM_178418]	NM_178418
Rbm47	0.0252	1.61	up	Mus musculus RNA binding motif protein 47 (Rbm47), transcript variant 1, mRNA [NM_178446]	NM_178446
Reep3	0.0408	1.53	up	Mus musculus receptor accessory protein 3 (Reep3), mRNA [NM_178606]	NM_178606
Pde12	0.0322	1.67	up	Mus musculus phosphodiesterase 12 (Pde12), mRNA [NM_178668]	NM_178668
Grsf1	0.0254	1.66	up	Mus musculus G-rich RNA sequence binding factor 1 (Grsf1), transcript variant 1, mRNA [NM_178700]	NM_178700
Rnf214	0.0142	1.71	up	Mus musculus ring finger protein 214 (Rnf214), mRNA [NM_178709]	NM_178709
Sik2	0.0298	1.51	up	Mus musculus salt inducible kinase 2 (Sik2), mRNA [NM_178710]	NM_178710
Slitrk4	0.0479	3.22	up	Mus musculus SLIT and NTRK-like family, member 4 (Slitrk4), mRNA [NM_178740]	NM_178740
Klhl26	0.0141	2.04	up	Mus musculus kelch-like 26 (Drosophila) (Klhl26), transcript variant 2, mRNA [NM_178771]	NM_178771
Trim65	0.0430	1.74	up	Mus musculus tripartite motif-containing 65 (Trim65), mRNA [NM_178802]	NM_178802
Hadha	0.0318	1.93	up	Mus musculus hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit (Hadha), nuclear gene encoding mitochondrial protein, mRNA [NM_178878]	NM_178878
Sfrs15	0.0217	1.62	up	Mus musculus splicing factor, arginine/serine-rich 15 (Sfrs15), mRNA [NM_178923]	NM_178923

Tnfrsf14	0.0287	2.03	up	Mus musculus tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator) (Tnfrsf14), mRNA [NM_178931]	NM_178931
Aoc2	0.0342	1.71	up	Mus musculus amine oxidase, copper containing 2 (retina-specific) (Aoc2), mRNA [NM_178932]	NM_178932
Atad3a	0.0039	1.86	up	Mus musculus ATPase family, AAA domain containing 3A (Atad3a), nuclear gene encoding mitochondrial protein, mRNA [NM_179203]	NM_179203
Gtf2h5	0.0166	4.51	up	Mus musculus general transcription factor IIH, polypeptide 5 (Gtf2h5), mRNA [NM_181392]	NM_181392
Ushbp1	0.0289	2.32	up	Mus musculus Usher syndrome 1C binding protein 1 (Ushbp1), mRNA [NM_181418]	NM_181418
Tppp	0.0484	2.01	up	Mus musculus tubulin polymerization promoting protein (Tppp), mRNA [NM_182839]	NM_182839
Accs	0.0038	1.53	up	Mus musculus 1-aminocyclopropane-1-carboxylate synthase homolog (Arabidopsis)(non-functional) (Accs), mRNA [NM_183220]	NM_183220
Gadd45gip1	0.0234	2.13	up	Mus musculus growth arrest and DNA-damage-inducible, gamma interacting protein 1 (Gadd45gip1), mRNA [NM_183358]	NM_183358
C330019G07Rik	0.0417	1.63	up	Mus musculus RIKEN cDNA C330019G07 gene (C330019G07Rik), mRNA [NM_194340]	NM_194340
Uqcr10	0.0223	1.67	up	Mus musculus ubiquinol-cytochrome c reductase, complex III subunit X (Uqcr10), nuclear gene encoding mitochondrial protein, mRNA [NM_197979]	NM_197979
Adipor2	0.0402	1.57	up	Mus musculus adiponectin receptor 2 (Adipor2), mRNA [NM_197985]	NM_197985
1190005I06Rik	0.0010	1.83	up	Mus musculus RIKEN cDNA 1190005I06 gene (1190005I06Rik), mRNA [NM_197988]	NM_197988
Cuedc1	0.0056	5.05	up	Mus musculus CUE domain containing 1 (Cuedc1), transcript variant 1, mRNA [NM_198013]	NM_198013

Iqcc	0.0034	2.27	up	Mus musculus IQ motif containing C (Iqcc), mRNA [NM_198026]	NM_198026
Tmem63b	0.0013	1.64	up	Mus musculus transmembrane protein 63b (Tmem63b), mRNA [NM_198167]	NM_198167
Cpeb3	0.0228	1.54	up	Mus musculus cytoplasmic polyadenylation element binding protein 3 (Cpeb3), mRNA [NM_198300]	NM_198300
Ppm1m	0.0350	1.57	up	Mus musculus protein phosphatase 1M (Ppm1m), transcript variant 2, mRNA [NM_198931]	NM_198931
C430048L16Rik	0.0321	1.71	up	Mus musculus RIKEN cDNA C430048L16 gene (C430048L16Rik), mRNA [NM_198957]	NM_198957
Ippk	0.0281	1.50	up	Mus musculus inositol 1,3,4,5,6-pentakisphosphate 2-kinase (Ippk), mRNA [NM_199056]	NM_199056
Bckdhb	0.0281	2.18	up	Mus musculus branched chain ketoacid dehydrogenase E1, beta polypeptide (Bckdhb), nuclear gene encoding mitochondrial protein, mRNA [NM_199195]	NM_199195
Olfr372	0.0375	1.99	up	Mus musculus olfactory receptor 372 (Olfr372), mRNA [NM_207555]	NM_207555
Gripap1	0.0450	1.58	up	Mus musculus GRIP1 associated protein 1 (Gripap1), mRNA [NM_207670]	NM_207670
Dedd2	0.0241	2.64	up	Mus musculus death effector domain-containing DNA binding protein 2 (Dedd2), mRNA [NM_207677]	NM_207677
Olfr224	0.0104	6.26	up	Mus musculus olfactory receptor 224 (Olfr224), mRNA [NM_207695]	NM_207695
Acsn3	0.0302	1.94	up	Mus musculus acyl-CoA synthetase medium-chain family member 3 (Acsn3), transcript variant 2, mRNA [NM_212441]	NM_212441
Acsn3	0.0183	1.99	up	Mus musculus acyl-CoA synthetase medium-chain family member 3 (Acsn3), transcript variant 2, mRNA [NM_212441]	NM_212441
Krt73	0.0092	1.60	up	Mus musculus keratin 73 (Krt73), mRNA [NM_212485]	NM_212485

Krt78	0.0241	2.15	up	Mus musculus keratin 78 (Krt78), mRNA [NM_212487]	NM_212487
Malat1	0.0292	1.52	up	Mus musculus metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA) (Malat1), non-coding RNA [NR_002847]	NR_002847
A130040M12Rik	0.0365	1.57	up	Mus musculus RIKEN cDNA A130040M12 gene (A130040M12Rik), non-coding RNA [NR_002860]	NR_002860
BC018473	0.0074	2.33	up	Mus musculus cDNA sequence BC018473 (BC018473), non-coding RNA [NR_003364]	NR_003364
Gm10319	0.0341	1.92	up	Mus musculus predicted pseudogene 10319 (Gm10319), non-coding RNA [NR_003624]	NR_003624
1700096K18Rik	0.0409	1.96	up	Mus musculus RIKEN cDNA 1700096K18 gene (1700096K18Rik), non-coding RNA [NR_027388]	NR_027388
4632415L05Rik	0.0232	1.97	up	Mus musculus RIKEN cDNA 4632415L05 gene (4632415L05Rik), non-coding RNA [NR_027985]	NR_027985
C030016D13Rik	0.0479	2.18	up	Mus musculus RIKEN cDNA C030016D13 gene (C030016D13Rik), non-coding RNA [NR_027987]	NR_027987
Gm10069	0.0295	2.09	up	Mus musculus predicted gene 10069 (Gm10069), transcript variant 1, non-coding RNA [NR_028592]	NR_028592
AA387883	0.0239	1.83	up	Mus musculus expressed sequence AA387883 (AA387883), non-coding RNA [NR_030678]	NR_030678
B330016D10Rik	0.0341	2.54	up	Mus musculus RIKEN cDNA B330016D10 gene (B330016D10Rik), non-coding RNA [NR_030695]	NR_030695
9930014A18Rik	0.0442	1.85	up	Mus musculus RIKEN cDNA 9930014A18 gene (9930014A18Rik), non-coding RNA [NR_030696]	NR_030696
BC065397	0.0200	1.60	up	Mus musculus cDNA sequence BC065397 (BC065397), non-coding RNA [NR_033324]	NR_033324
	0.0246	1.85	up	TFIIi-associated transactivator factor p17 [Source:UniProtKB/TrEMBL;Acc:Q60671] [ENSMUST00000115691]	U11548
Gm9100	0.0404	5.20	up	PREDICTED: Mus musculus predicted gene, EG668313 (EG668313), mRNA [XM_001000832]	XM_001000832

Gm9178	0.0031	3.30	up	PREDICTED: Mus musculus predicted gene, EG668455 (EG668455), mRNA [XM_001004798]	XM_001004798
Gm7044	0.0420	2.22	up	PREDICTED: Mus musculus predicted gene, EG630825 (EG630825), mRNA [XM_001472205]	XM_001472205
Gm13453	0.0044	1.88	up	PREDICTED: Mus musculus similar to vacuolar H ⁺ ATPase G1 (LOC100044530), mRNA [XM_001472372]	XM_001472372
C030010C08Rik	0.0169	1.60	up	PREDICTED: Mus musculus RIKEN cDNA C030010C08 gene (C030010C08Rik), mRNA [XM_001472491]	XM_001472491
Gm2149	0.0056	1.86	up	PREDICTED: Mus musculus hypothetical protein LOC100039307 (LOC100039307), mRNA [XM_001472640]	XM_001472640
LOC100039402	0.0488	1.53	up	PREDICTED: Mus musculus similar to pol protein (LOC100039402), mRNA [XM_001472829]	XM_001472829
Gm1971	0.0095	1.65	up	PREDICTED: Mus musculus predicted gene, ENSMUSG00000072994 (ENSMUSG00000072994), mRNA [XM_001472879]	XM_001472879
LOC100044771	0.0391	1.80	up	PREDICTED: Mus musculus similar to SDA1 domain containing 1 (LOC100044771), mRNA [XM_001473022]	XM_001473022
	0.0129	1.50	up	PREDICTED: Mus musculus hypothetical protein LOC100039686 (LOC100039686), mRNA [XM_001473338]	XM_001473338
LOC100044952	0.0034	2.03	up	PREDICTED: Mus musculus hypothetical protein LOC100044952 (LOC100044952), mRNA [XM_001473387]	XM_001473387
1700094M24Rik	0.0193	1.59	up	PREDICTED: Mus musculus RIKEN cDNA 1700094M24 gene (1700094M24Rik), mRNA [XM_001473576]	XM_001473576

LOC100045251	0.0313	1.77	up	PREDICTED: Mus musculus similar to peptidylprolyl isomerase D (LOC100045251), mRNA [XM_001473933]	XM_001473933
Gm3797	0.0292	1.50	up	PREDICTED: Mus musculus hypothetical protein LOC100045308 (LOC100045308), mRNA [XM_001474029]	XM_001474029
LOC100045319	0.0214	3.71	up	PREDICTED: Mus musculus hypothetical protein LOC100045319 (LOC100045319), mRNA [XM_001474051]	XM_001474051
LOC100045328	0.0456	1.62	up	PREDICTED: Mus musculus hypothetical protein LOC100045328 (LOC100045328), mRNA [XM_001474069]	XM_001474069
	0.0263	2.75	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3URL2] [ENSMUST00000099198]	XM_001474096
Gm9465	0.0117	1.52	up	PREDICTED: Mus musculus hypothetical LOC669675 (LOC669675), mRNA [XM_001474101]	XM_001474101
LOC100043999	0.0410	13.33	up	PREDICTED: Mus musculus hypothetical protein LOC100043999 (LOC100043999), mRNA [XM_001474157]	XM_001474157
Gm2485	0.0292	1.80	up	PREDICTED: Mus musculus hypothetical protein LOC100039902 (LOC100039902), mRNA [XM_001474163]	XM_001474163
Gm9532	0.0054	1.96	up	PREDICTED: Mus musculus hypothetical LOC671399 (LOC671399), mRNA [XM_001474726]	XM_001474726
Gm14635	0.0407	2.06	up	PREDICTED: Mus musculus hypothetical protein LOC100045847 (LOC100045847), mRNA [XM_001475018]	XM_001475018
LOC100045911	0.0357	2.40	up	PREDICTED: Mus musculus similar to TRAV11D (LOC100045911), mRNA [XM_001475159]	XM_001475159

Gm2703	0.0378	1.53	up	PREDICTED: Mus musculus hypothetical protein LOC100040307 (LOC100040307), mRNA [XM_001475212]	XM_001475212
Khdrbs1	0.0173	1.90	up	KH domain containing, RNA binding, signal transduction associated 1 Gene [Source:MGI (curated);Acc:MGI:893579] [ENSMUST00000129342]	XM_001475530
LOC100046121	0.0044	1.83	up	PREDICTED: Mus musculus hypothetical protein LOC100046121 (LOC100046121), mRNA [XM_001475613]	XM_001475613
LOC100046166	0.0272	1.62	up	PREDICTED: Mus musculus similar to Transforming growth factor beta regulated gene 4 (LOC100046166), mRNA [XM_001475720]	XM_001475720
Gm10621	0.0251	1.80	up	Putative uncharacterized protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q3U2L9] [ENSMUST00000098384]	XM_001476249
Gm9471	0.0213	1.94	up	PREDICTED: Mus musculus hypothetical LOC669856 (LOC669856), mRNA [XM_001476382]	XM_001476382
LOC100046567	0.0322	1.62	up	PREDICTED: Mus musculus similar to Transmembrane emp24 protein transport domain containing 5, transcript variant 1 (LOC100046567), mRNA [XM_001476475]	XM_001476475
LOC100046852	0.0397	1.56	up	PREDICTED: Mus musculus hypothetical protein LOC100046852 (LOC100046852), mRNA [XM_001476908]	XM_001476908
LOC100046885	0.0489	2.13	up	PREDICTED: Mus musculus similar to reproductive homeobox on X chromosome 8 (LOC100046885), mRNA [XM_001476995]	XM_001476995
Gm3512	0.0230	3.39	up	PREDICTED: Mus musculus hypothetical protein LOC100041791 (LOC100041791), mRNA [XM_001477011]	XM_001477011

Gm3548	0.0079	1.68	up	PREDICTED: Mus musculus similar to 60S ribosomal protein L36 (LOC100041857), mRNA [XM_001477124]	XM_001477124
Gm9720	0.0026	1.92	up	PREDICTED: Mus musculus similar to CG32602-PA (LOC677603), mRNA [XM_001477594]	XM_001477594
LOC100041719	0.0068	1.61	up	PREDICTED: Mus musculus similar to Sp100 (LOC100041719), mRNA [XM_001477623]	XM_001477623
Gm3730	0.0114	1.66	up	PREDICTED: Mus musculus similar to cyclic nucleotide gated channel beta 1 (LOC100042221), mRNA [XM_001477751]	XM_001477751
LOC100047292	0.0140	1.98	up	PREDICTED: Mus musculus similar to pleckstrin homology domain containing, family A member 7 (LOC100047292), mRNA [XM_001477810]	XM_001477810
LOC100047555	0.0376	1.99	up	PREDICTED: Mus musculus similar to Ubtg protein (LOC100047555), mRNA [XM_001478388]	XM_001478388
Gm9590	0.0057	2.36	up	PREDICTED: Mus musculus similar to crooked legs CG14938-PB (LOC673160), mRNA [XM_001478468]	XM_001478468
	0.0257	7.45	up		XM_001478565
Gm3993	0.0260	4.10	up	PREDICTED: Mus musculus similar to Predicted gene, EG245297 (LOC100042727), mRNA [XM_001478694]	XM_001478694
Gm9306	0.0419	12.01	up	PREDICTED: Mus musculus similar to development and differentiation enhancing factor 2 (LOC668698), mRNA [XM_001478806]	XM_001478806
	0.0106	3.28	up	Putative uncharacterized protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q9CSX2] [ENSMUST00000024228]	XM_001478824
Gm4080	0.0468	1.59	up	PREDICTED: Mus musculus similar to pol protein (LOC100042868), mRNA [XM_001478955]	XM_001478955
	0.0222	1.53	up	PREDICTED: Mus musculus predicted gene, EG668670 (EG668670), mRNA [XM_001478977]	XM_001478977

LOC100047421	0.0430	1.73	up	PREDICTED: Mus musculus similar to activating transcription factor 1 (LOC100047421), mRNA [XM_001479002]	XM_001479002
Gm4092	0.0362	2.09	up	PREDICTED: Mus musculus hypothetical protein LOC100042892 (LOC100042892), mRNA [XM_001479101]	XM_001479101
LOC100047915	0.0356	1.55	up	PREDICTED: Mus musculus similar to Memo1 protein (LOC100047915), mRNA [XM_001479122]	XM_001479122
	0.0303	1.59	up	PREDICTED: Mus musculus hypothetical protein LOC100042808 (LOC100042808), mRNA [XM_001479428]	XM_001479428
LOC100044034	0.0374	4.49	up	PREDICTED: Mus musculus hypothetical protein LOC100044034 (LOC100044034), mRNA [XM_001479541]	XM_001479541
Gm9855	0.0325	1.53	up	PREDICTED: Mus musculus similar to T:G mismatch-specific thymine-DNA glycosylase TDGb, transcript variant 1 (LOC624784), mRNA [XM_001479614]	XM_001479614
	0.0250	1.59	up	T-cell receptor alpha chain V region PHDS58 Precursor [Source:UniProtKB/Swiss-Prot;Acc:P01738] [ENSMUST00000103662]	XM_001479640
Gm4392	0.0201	1.52	up	Putative uncharacterized protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q8CB85] [ENSMUST00000104965]	XM_001480045
Gm4485	0.0422	1.77	up	PREDICTED: Mus musculus hypothetical protein LOC100043505 (LOC100043505), mRNA [XM_001480329]	XM_001480329
Gm11686	0.0410	1.61	up	PREDICTED: Mus musculus similar to ribosomal protein L35a (LOC100043534), mRNA [XM_001480374]	XM_001480374
Gm13997	0.0260	1.65	up	PREDICTED: Mus musculus hypothetical protein LOC100043635 (LOC100043635), mRNA [XM_001480419]	XM_001480419

Gm5953	0.0186	12.39	up	PREDICTED: Mus musculus predicted gene, EG546524 (EG546524), mRNA [XM_001480466]	XM_001480466
LOC100048572	0.0078	1.82	up	PREDICTED: Mus musculus similar to crooked legs CG14938-PB (LOC100048572), mRNA [XM_001480556]	XM_001480556
LOC100048743	0.0135	3.17	up	PREDICTED: Mus musculus similar to FK506 binding protein 4 (LOC100048743), mRNA [XM_001481106]	XM_001481106
LOC436100	0.0247	1.93	up	PREDICTED: Mus musculus similar to hypothetical protein FLJ38281 (LOC436100), mRNA [XM_001481293]	XM_001481293
	0.0226	1.55	up	spectrin beta 5 Gene [Source:MGI (curated);Acc:MGI:2685200] [ENSMUST00000110757]	XM_001481329
Gm13229	0.0088	1.53	up	PREDICTED: Mus musculus similar to acidic ribosomal phosphoprotein P1 (LOC195576), mRNA [XM_112297]	XM_112297
Dcst2	0.0224	1.65	up	PREDICTED: Mus musculus DC-STAMP domain containing 2 (Dcst2), mRNA [XM_283860]	XM_283860
Gm5576	0.0366	2.18	up	PREDICTED: Mus musculus predicted gene, EG434050 (EG434050), mRNA [XM_485792]	XM_485792
Gm5741	0.0262	1.87	up	PREDICTED: Mus musculus predicted gene, EG436049 (EG436049), mRNA [XM_488140]	XM_488140
Gm318	0.0374	2.68	up	PREDICTED: Mus musculus gene model 318, (NCBI) (Gm318), mRNA [XM_619462]	XM_619462
Gm6293	0.0127	1.71	up	PREDICTED: Mus musculus predicted gene, EG622178 (EG622178), mRNA [XM_886587]	XM_886587
Gm6422	0.0472	1.62	up	PREDICTED: Mus musculus predicted gene, EG623370 (EG623370), mRNA [XM_887818]	XM_887818
Hnrnpa112-ps	0.0055	1.66	up	PREDICTED: Mus musculus predicted gene, EG544954, transcript variant 2 (EG544954), mRNA [XM_888940]	XM_888940

Gm13474	0.0454	1.95	up	PREDICTED: Mus musculus similar to golgi autoantigen, golgin subfamily a (LOC624652), mRNA [XM_889201]	XM_889201
Gm13015	0.0176	1.79	up	PREDICTED: Mus musculus similar to RNA polymerase II subunit (LOC625405), mRNA [XM_889972]	XM_889972
Gm6871	0.0249	1.89	up	PREDICTED: Mus musculus predicted gene, EG628359 (EG628359), mRNA [XM_893095]	XM_893095
Gm6611	0.0145	1.73	up	PREDICTED: Mus musculus predicted gene, EG625660 (EG625660), mRNA [XM_894394]	XM_894394
Gm6146	0.0460	1.77	up	PREDICTED: Mus musculus predicted gene, EG620382 (EG620382), mRNA [XM_895806]	XM_895806
Gm6603	0.0031	2.12	up	PREDICTED: Mus musculus predicted gene, EG625586 (EG625586), mRNA [XM_898851]	XM_898851
	0.0411	1.55	up	cytochrome b5 domain containing 1 Gene [Source:MGI (curated);Acc:MGI:2685586] [ENSMUST00000108660]	XM_901734
	0.0441	1.58	up	PREDICTED: Mus musculus predicted gene, EG546797, transcript variant 1 (EG546797), mRNA [XM_902301]	XM_902301
Gm16452	0.0323	1.56	up	PREDICTED: Mus musculus similar to TRAV7-1 (LOC630408), mRNA [XM_903553]	XM_903553
9830167H18Rik	0.0268	4.83	up	zinc finger protein 866 Gene [Source:MGI (curated);Acc:MGI:3584369] [ENSMUST00000130458]	XM_910524
LOC638799	0.0227	1.71	up	PREDICTED: Mus musculus hypothetical LOC638799 (LOC638799), mRNA [XM_914944]	XM_914944
LOC639063	0.0308	2.81	up	PREDICTED: Mus musculus similar to USF2 splicing variant-1 (LOC639063), mRNA [XM_915331]	XM_915331
LOC674340	0.0409	1.89	up	PREDICTED: Mus musculus similar to SLC35D2 protein (LOC674340), mRNA [XM_973875]	XM_973875

5830433I10Rik	0.0233	1.61	up	PREDICTED: Mus musculus RIKEN cDNA 5830433I10 gene (5830433I10Rik), mRNA [XM_974092]	XM_974092
	0.0033	1.50	up	integrator complex subunit 10 Gene [Source:MGI (curated);Acc:MGI:1918135] [ENSMUST00000110242]	XM_977857
	0.0221	1.94	up	microtubule associated monooxygenase, calponin and LIM domain containing 3 Gene [Source:MGI (curated);Acc:MGI:2442733] [ENSMUST00000098457]	XM_979045
LOC100047435	0.0115	3.28	up	myosin light chain kinase 3 Gene [Source:MGI (curated);Acc:MGI:2443063] [ENSMUST00000122452]	XM_987811
LOC676347	0.0013	2.31	up	PREDICTED: Mus musculus similar to Igh protein (LOC676347), mRNA [XM_989290]	XM_989290
Gm7428	0.0393	1.58	up	PREDICTED: Mus musculus predicted gene, EG664965 (EG664965), misc RNA [XR_001700]	XR_001700
Gm9022	0.0221	2.13	up	PREDICTED: Mus musculus predicted gene, EG668177 (EG668177), misc RNA [XR_002153]	XR_002153
A930033H14Rik	0.0329	2.38	up	PREDICTED: Mus musculus RIKEN cDNA A930033H14 gene (A930033H14Rik), misc RNA [XR_002305]	XR_002305
Gm5067	0.0166	30.16	up	PREDICTED: Mus musculus predicted gene, EG272714 (EG272714), misc RNA [XR_002343]	XR_002343
LOC100044376	0.0249	1.62	up	PREDICTED: Mus musculus similar to Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (LOC100044376), misc RNA [XR_030576]	XR_030576
LOC100039037	0.0160	3.07	up	PREDICTED: Mus musculus similar to CG6004-PB (LOC100039037), misc RNA [XR_030580]	XR_030580
Gm6742	0.0278	1.82	up	PREDICTED: Mus musculus similar to Odc1 protein (LOC627245), misc RNA [XR_030600]	XR_030600

Gm3418	0.0437	1.88	up	PREDICTED: Mus musculus similar to DnaJ protein homolog (LOC100044445), misc RNA [XR_030642]	XR_030642
Gm5847	0.0360	2.52	up	PREDICTED: Mus musculus similar to 3-phosphoglycerate dehydrogenase (LOC630761), misc RNA [XR_030672]	XR_030672
Gm12642	0.0456	1.64	up	PREDICTED: Mus musculus similar to protein phosphatase 2A inhibitor-2 I-2PP2A (LOC384125), misc RNA [XR_030692]	XR_030692
Gm7857	0.0473	7.67	up	PREDICTED: Mus musculus similar to 60S ribosomal protein L34 (LOC665941), misc RNA [XR_030849]	XR_030849
Gm2311	0.0104	2.03	up	PREDICTED: Mus musculus similar to histone deacetylase 1 (LOC100039561), misc RNA [XR_031041]	XR_031041
Gm6274	0.0283	4.52	up	PREDICTED: Mus musculus similar to Ribosomal protein L7 (LOC621983), misc RNA [XR_031283]	XR_031283
Gm11826	0.0433	1.63	up	PREDICTED: Mus musculus similar to ribosomal protein L26 (LOC633461), misc RNA [XR_031506]	XR_031506
LOC630077	0.0121	2.35	up	PREDICTED: Mus musculus similar to protein phosphatase 2, regulatory subunit B (B56), alpha isoform (LOC630077), misc RNA [XR_031677]	XR_031677
LOC100045677	0.0107	2.09	up	PREDICTED: Mus musculus similar to DNA replication licensing factor MCM3 (DNA polymerase alpha holoenzyme-associated protein P1) (P1-MCM3) (LOC100045677), misc RNA [XR_031705]	XR_031705
LOC100045517	0.0266	2.94	up	PREDICTED: Mus musculus similar to integrin beta 3 binding protein (LOC100045517), misc RNA [XR_031739]	XR_031739
Gm2903	0.0092	2.48	up	PREDICTED: Mus musculus similar to chaperonin 10 (LOC100040681), misc RNA [XR_031909]	XR_031909

Gm5213	0.0488	4.09	up	PREDICTED: Mus musculus similar to Ferritin light chain 1 (Ferritin L subunit 1) (LOC636666), misc RNA [XR_032412]	XR_032412
Gm5708	0.0145	1.51	up	PREDICTED: Mus musculus similar to Ab1-115 (LOC435727), misc RNA [XR_032419]	XR_032419
Gm8052	0.0426	3.55	up	PREDICTED: Mus musculus hypothetical LOC666336 (LOC666336), misc RNA [XR_032547]	XR_032547
Gm7177	0.0239	1.55	up	PREDICTED: Mus musculus similar to zinc finger protein 91 (LOC636398), misc RNA [XR_032603]	XR_032603
Gm3353	0.0383	2.65	up	PREDICTED: Mus musculus similar to protein phosphatase 2, regulatory subunit B (B56), alpha isoform (LOC100041461), misc RNA [XR_032731]	XR_032731
Gm6651	0.0440	3.15	up	PREDICTED: Mus musculus similar to high mobility group nucleosomal binding domain 2 (LOC626075), misc RNA [XR_032823]	XR_032823
Gm9519	0.0258	4.27	up	PREDICTED: Mus musculus hypothetical LOC676461 (LOC676461), misc RNA [XR_033411]	XR_033411
LOC630233	0.0066	2.29	up	PREDICTED: Mus musculus similar to FUS interacting protein (serine/arginine-rich) 1 (LOC630233), misc RNA [XR_034286]	XR_034286
Gm9108	0.0157	1.82	up	PREDICTED: Mus musculus similar to Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (LOC668327), misc RNA [XR_034404]	XR_034404
LOC100047967	0.0270	1.52	up	PREDICTED: Mus musculus similar to growth arrest-specific 2 like 3 (LOC100047967), misc RNA [XR_034463]	XR_034463
B230317F23Rik	0.0080	1.65	up	PREDICTED: Mus musculus RIKEN cDNA B230317F23 gene (B230317F23Rik), misc RNA [XR_035255]	XR_035255

	0.0397	19.68	down	Ig lambda-3 chain C region [Source:UniProtKB/Swiss-Prot;Acc:P01845] [ENSMUST00000103743]	AF138742
Tsix	0.0280	1.82	down	Mus musculus domesticus antisense RNA from the Xist locus, complete sequence. [AF138745]	AF138745
Cyp4f18	0.0035	4.26	down	Mus musculus cytochrome P450 CYP4F18 mRNA, complete cds. [AF233647]	AF233647
	0.0479	17.08	down	Ig lambda-3 chain C region [Source:UniProtKB/Swiss-Prot;Acc:P01845] [ENSMUST00000103743]	AF290571
	0.0118	1.56	down	RIKEN cDNA 1500002C15 gene Gene [Source:MGI Symbol;Acc:MGI:1916196] [ENSMUST00000097743]	AK005108
	0.0073	2.06	down	RIKEN cDNA 1810013D15 gene Gene [Source:MGI Symbol;Acc:MGI:1916292] [ENSMUST00000029827]	AK007475
2310007J06Rik	0.0316	2.16	down	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310007J06 product:unclassifiable, full insert sequence. [AK009210]	AK009210
2310058N22Rik	0.0368	2.45	down	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310058N22 product:unclassifiable, full insert sequence. [AK009987]	AK009987
Nanog	0.0226	1.58	down	Nanog homeobox Gene [Source:MGI (curated);Acc:MGI:1919200] [ENSMUST00000012540]	AK010332
	0.0119	1.65	down	ubiquitin-conjugating enzyme E2L 6 Gene [Source:MGI (curated);Acc:MGI:1914500] [ENSMUST00000111637]	AK013452
	0.0039	3.27	down	RIKEN cDNA 3110082D06 gene Gene [Source:MGI Symbol;Acc:MGI:1920485] [ENSMUST00000074428]	AK014270

	0.0244	4.05	down	DIX domain containing 1 Gene [Source:MGI (curated);Acc:MGI:2679721] [ENSMUST00000098784]	AK016205
5033403F01Rik	0.0092	1.56	down	Mus musculus 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriched library, clone:5033403F01 product:unclassifiable, full insert sequence. [AK017147]	AK017147
6330407I18Rik	0.0316	1.52	down	Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330407I18 product:unclassifiable, full insert sequence. [AK018137]	AK018137
	0.0274	1.87	down	ADAMTS-like 1 Gene [Source:MGI (curated);Acc:MGI:1924989] [ENSMUST00000120678]	AK020115
	0.0105	2.09	down	RIKEN cDNA 9430002A10 gene Gene [Source:MGI Symbol;Acc:MGI:1924515] [ENSMUST00000074808]	AK020399
5830444B04Rik	0.0222	4.99	down	Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone:5830444B04 product:unclassifiable, full insert sequence. [AK030886]	AK030886
	0.0149	3.58	down	phosphodiesterase 4D, cAMP specific Gene [Source:MGI (curated);Acc:MGI:99555] [ENSMUST00000105096]	AK032648
A930018M24Rik	0.0497	3.05	down	Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330167E06 product:unclassifiable, full insert sequence. [AK034241]	AK034241
	0.0276	1.51	down	Putative uncharacterized protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q8CA46] [ENSMUST00000064090]	AK039657

1700030C10Rik	0.0236	4.87	down	Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630001I11 product:KIAA0400 PROTEIN homolog [Homo sapiens], full insert sequence. [AK041326]	AK041326
A630081D01Rik	0.0101	1.96	down	Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630081D01 product:unclassifiable, full insert sequence. [AK042310]	AK042310
	0.0055	2.87	down	DPH5 homolog (S. cerevisiae) Gene [Source:MGI (curated);Acc:MGI:1916990] [ENSMUST00000106505]	AK046753
B930018H19	0.0026	2.26	down	Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B930018H19 product:unclassifiable, full insert sequence. [AK047086]	AK047086
Gm14762	0.0163	3.70	down	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q8BPW8] [ENSMUST00000105109]	AK052035
A730056A06Rik	0.0065	1.99	down	Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN full-length enriched library, clone:E230007B11 product:unclassifiable, full insert sequence. [AK053954]	AK053954
	0.0072	1.69	down	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3UQ98] [ENSMUST00000099633]	AK082289
	0.0070	2.51	down	RIKEN cDNA 3222401L13 gene Gene [Source:MGI Symbol;Acc:MGI:2444186] [ENSMUST00000097608]	AK086343
F830005D05Rik	0.0225	2.72	down	Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830005D05 product:unclassifiable, full insert sequence. [AK089619]	AK089619

BC064078	0.0064	2.49	down	Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone:5830408J16 product:unclassifiable, full insert sequence. [AK134020]	AK134020
	0.0146	1.55	down	Likely orthologue of H. sapiens chromosome 9 open reading frame 84 [Source:UniProtKB/TrEMBL;Acc:A2ALV5] [ENSMUST00000095066]	AK135748
	0.0104	2.90	down	palmdelphin Gene [Source:MGI (curated);Acc:MGI:2148896] [ENSMUST00000119557]	AK136939
9530036M11Rik	0.0004	1.61	down	Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530029K05 product:unclassifiable, full insert sequence. [AK137178]	AK137178
	0.0271	2.77	down	RIKEN cDNA C130040N14 gene Gene [Source:MGI Symbol;Acc:MGI:3588257] [ENSMUST00000097361]	AK140837
Camk2d	0.0302	1.71	down	calcium/calmodulin-dependent protein kinase II, delta Gene [Source:MGI (curated);Acc:MGI:1341265] [ENSMUST00000066452]	AK142435
D930026N18Rik	0.0076	2.00	down	Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930026N18 product:unclassifiable, full insert sequence. [AK142841]	AK142841
	0.0014	4.40	down	occludin/ELL domain containing 1 Gene [Source:MGI (curated);Acc:MGI:1924340] [ENSMUST00000110052]	AK143433
	0.0370	2.22	down	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3UKC4] [ENSMUST00000099340]	AK146072

Fgd3	0.0303	1.57	down	FYVE, RhoGEF and PH domain containing 3 Gene [Source:MGI (curated);Acc:MGI:1353657] [ENSMUST00000110087]	AK157835
	0.0120	1.60	down	cell division cycle 123 homolog (S. cerevisiae) Gene [Source:MGI (curated);Acc:MGI:2138811] [ENSMUST00000100445]	AK161246
	0.0481	1.72	down	RIKEN cDNA 2900052L18 gene Gene [Source:MGI Symbol;Acc:MGI:1924085] [ENSMUST00000062283]	AK162948
2610507I01Rik	0.0003	8.16	down	Mus musculus adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330105A21 product:unclassifiable, full insert sequence. [AK162965]	AK162965
Ccr11	0.0083	3.39	down	Mus musculus chemokine receptor CCX CKR mRNA, complete cds, alternatively spliced. [AY072938]	AY072938
	0.0389	16.33	down	immunoglobulin lambda chain, variable 1 Gene [Source:MGI Symbol;Acc:MGI:96530] [ENSMUST00000103749]	AY170502
	0.0476	16.92	down	Mus musculus anti-human uPAR immunoglobulin light chain variable region mRNA, partial cds. [AY351698]	AY351698
	0.0421	29.53	down	immunoglobulin lambda chain, variable 1 Gene [Source:MGI Symbol;Acc:MGI:96530] [ENSMUST00000103746]	AY679096
	0.0038	5.93	down	DIX domain containing 1 Gene [Source:MGI (curated);Acc:MGI:2679721] [ENSMUST00000118707]	BC024834
	0.0295	1.74	down	cyclin-dependent kinase-like 5 Gene [Source:MGI (curated);Acc:MGI:1278336] [ENSMUST00000112356]	BC038161
	0.0164	1.61	down	zinc finger protein 420 Gene [Source:MGI (curated);Acc:MGI:2444666] [ENSMUST00000085789]	BC064456

	0.0211	2.01	down	ectonucleotide pyrophosphatase/phosphodiesterase 5 Gene [Source:MGI (curated);Acc:MGI:1933830] [ENSMUST00000087066]	BC089320
C1qtnf7	0.0039	1.84	down	C1q and tumor necrosis factor related protein 7 Gene [Source:MGI (curated);Acc:MGI:1925911] [ENSMUST00000076939]	BC090967
A630012P03Rik	0.0436	1.64	down	Mus musculus cDNA clone IMAGE:6435376. [BC100571]	BC100571
Gm1499	0.0318	1.55	down	AGENCOURT_10123249 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:6530695 5', mRNA sequence [BU523966]	BU523966
	0.0084	5.21	down	Mus musculus clone AiDWTimmB-38 immunoglobulin kappa light chain mRNA, partial cds. [DQ372793]	DQ372793
A430104N18Rik	0.0403	3.25	down	BMSB11367 Hematopoietic stem cells Mus musculus cDNA, mRNA sequence [DT902180]	DT902180
	0.0288	3.58	down	V kappa light chain Precursor; Fragment [Source:UniProtKB/TrEMBL;Acc:A0N8I8] [ENSMUST00000103362]	M61952
	0.0235	1.92	down	Mouse T cell receptor mRNA. [M97158]	M97158
Tpm4	0.0136	1.60	down	Mus musculus tropomyosin 4 (Tpm4), mRNA [NM_001001491]	NM_001001491
Rpl17	0.0021	1.79	down	Mus musculus ribosomal protein L17 (Rpl17), mRNA [NM_001002239]	NM_001002239
Sirpb1a	0.0323	1.69	down	Mus musculus signal-regulatory protein beta 1A (Sirpb1a), transcript variant 3, mRNA [NM_001002898]	NM_001002898
Sirpb1a	0.0054	1.59	down	Mus musculus signal-regulatory protein beta 1A (Sirpb1a), transcript variant 3, mRNA [NM_001002898]	NM_001002898
Cdsn	0.0079	79.22	down	Mus musculus corneodesmosin (Cdsn), mRNA [NM_001008424]	NM_001008424
Olf699	0.0184	1.52	down	Mus musculus olfactory receptor 699 (Olf699), mRNA [NM_001011862]	NM_001011862

D10627	0.0137	2.90	down	Mus musculus cDNA sequence D10627 (D10627), mRNA [NM_001013379]	NM_001013379
Pcdh17	0.0343	1.56	down	Mus musculus protocadherin 17 (Pcdh17), mRNA [NM_001013753]	NM_001013753
Gm13154	0.0233	3.22	down	Mus musculus predicted gene 13154 (Gm13154), mRNA [NM_001014397]	NM_001014397
Pitpnm3	0.0052	2.13	down	Mus musculus PITPNM family member 3 (Pitpnm3), transcript variant 1, mRNA [NM_001024927]	NM_001024927
Pilrb2	0.0477	2.09	down	Mus musculus paired immunoglobulin-like type 2 receptor beta 2 (Pilrb2), mRNA [NM_001024932]	NM_001024932
Gm5797	0.0249	2.70	down	Mus musculus predicted gene 5797 (Gm5797), mRNA [NM_001025085]	NM_001025085
Miip	0.0013	2.21	down	Mus musculus migration and invasion inhibitory protein (Miip), mRNA [NM_001025365]	NM_001025365
Ikzf1	0.0335	1.75	down	Mus musculus IKAROS family zinc finger 1 (Ikzf1), transcript variant 1, mRNA [NM_001025597]	NM_001025597
Il1rl1	0.0164	3.77	down	Mus musculus interleukin 1 receptor-like 1 (Il1rl1), transcript variant 1, mRNA [NM_001025602]	NM_001025602
Tmem231	0.0129	1.64	down	Mus musculus transmembrane protein 231 (Tmem231), mRNA [NM_001033321]	NM_001033321
Nlrc4	0.0431	1.70	down	Mus musculus NLR family, CARD domain containing 4 (Nlrc4), mRNA [NM_001033367]	NM_001033367
Gm1679	0.0489	1.85	down	Mus musculus predicted gene 1679 (Gm1679), mRNA [NM_001033459]	NM_001033459
Ifitm6	0.0247	2.66	down	Mus musculus interferon induced transmembrane protein 6 (Ifitm6), mRNA [NM_001033632]	NM_001033632
Evi2a	0.0320	2.17	down	Mus musculus ecotropic viral integration site 2a (Evi2a), transcript variant 1, mRNA [NM_001033711]	NM_001033711
Cpne8	0.0021	1.95	down	Mus musculus copine VIII (Cpne8), transcript variant 2, mRNA [NM_001033851]	NM_001033851
LOC380994	0.0386	3.37	down	Mus musculus similar to Sycp3 like Y-linked (LOC380994), mRNA [NM_001037748]	NM_001037748

P2rx7	0.0412	1.96	down	Mus musculus purinergic receptor P2X, ligand-gated ion channel, 7 (P2rx7), transcript variant 4, mRNA [NM_001038887]	NM_001038887
Gm13152	0.0403	5.40	down	Mus musculus predicted gene 13152 (Gm13152), mRNA [NM_001039209]	NM_001039209
C230055K05Rik	0.0178	1.92	down	Mus musculus RIKEN cDNA C230055K05 gene (C230055K05Rik), mRNA [NM_001039231]	NM_001039231
Kif21b	0.0369	2.36	down	Mus musculus kinesin family member 21B (Kif21b), mRNA [NM_001039472]	NM_001039472
Oip5	0.0100	2.23	down	Mus musculus Opa interacting protein 5 (Oip5), mRNA [NM_001042653]	NM_001042653
Slc22a18	0.0131	1.71	down	Mus musculus solute carrier family 22 (organic cation transporter), member 18 (Slc22a18), transcript variant 2, mRNA [NM_001042760]	NM_001042760
Timp1	0.0088	1.60	down	Mus musculus tissue inhibitor of metalloproteinase 1 (Timp1), transcript variant 1, mRNA [NM_001044384]	NM_001044384
Akna	0.0233	1.70	down	Mus musculus AT-hook transcription factor (Akna), mRNA [NM_001045514]	NM_001045514
Zfp455	0.0191	2.35	down	Mus musculus zinc finger protein 455 (Zfp455), mRNA [NM_001048204]	NM_001048204
Ptpn6	0.0016	1.60	down	Mus musculus protein tyrosine phosphatase, non-receptor type 6 (Ptpn6), transcript variant 2, mRNA [NM_001077705]	NM_001077705
Ret	0.0418	1.82	down	Mus musculus ret proto-oncogene (Ret), transcript variant 4, mRNA [NM_001080780]	NM_001080780
Cib3	0.0462	3.35	down	Mus musculus calcium and integrin binding family member 3 (Cib3), mRNA [NM_001080812]	NM_001080812
Gipr	0.0042	1.53	down	Mus musculus gastric inhibitory polypeptide receptor (Gipr), mRNA [NM_001080815]	NM_001080815
Slc16a5	0.0195	1.87	down	Mus musculus solute carrier family 16 (monocarboxylic acid transporters), member 5 (Slc16a5), mRNA [NM_001080934]	NM_001080934

Zfp429	0.0039	5.40	down	Mus musculus zinc finger protein 429 (Zfp429), mRNA [NM_001080941]	NM_001080941
Tmsb15b2	0.0119	1.59	down	Mus musculus thymosin beta 15b2 (Tmsb15b2), mRNA [NM_001080967]	NM_001080967
Zfp382	0.0400	1.52	down	Mus musculus zinc finger protein 382 (Zfp382), mRNA [NM_001081007]	NM_001081007
Ankrd35	0.0064	1.93	down	Mus musculus ankyrin repeat domain 35 (Ankrd35), mRNA [NM_001081139]	NM_001081139
Trnp1	0.0407	1.71	down	Mus musculus TMF1-regulated nuclear protein 1 (Trnp1), mRNA [NM_001081156]	NM_001081156
Htra4	0.0311	3.27	down	Mus musculus HtrA serine peptidase 4 (Htra4), mRNA [NM_001081187]	NM_001081187
6330403A02Rik	0.0480	1.80	down	Mus musculus RIKEN cDNA 6330403A02 gene (6330403A02Rik), mRNA [NM_001081227]	NM_001081227
Ttc30a2	0.0464	1.54	down	Mus musculus tetratricopeptide repeat domain 30A2 (Ttc30a2), mRNA [NM_001081228]	NM_001081228
Ccdc88b	0.0016	1.84	down	Mus musculus coiled-coil domain containing 88B (Ccdc88b), mRNA [NM_001081291]	NM_001081291
Fndc1	0.0297	5.39	down	Mus musculus fibronectin type III domain containing 1 (Fndc1), mRNA [NM_001081416]	NM_001081416
Galntl1	0.0413	1.63	down	Mus musculus UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 1 (Galntl1), mRNA [NM_001081421]	NM_001081421
Gm7609	0.0226	2.64	down	Mus musculus predicted pseudogene 7609 (Gm7609), mRNA [NM_001081746]	NM_001081746
Tmsb15b1	0.0040	1.80	down	Mus musculus thymosin beta 15b1 (Tmsb15b1), mRNA [NM_001081983]	NM_001081983
Rnaset2a	0.0267	1.62	down	Mus musculus ribonuclease T2A (Rnaset2a), mRNA [NM_001083938]	NM_001083938
Myom3	0.0087	3.21	down	Mus musculus myomesin family, member 3 (Myom3), mRNA [NM_001085509]	NM_001085509

Gm13298	0.0027	10.62	down	Mus musculus predicted gene 13298 (Gm13298), mRNA [NM_001085530]	NM_001085530
Gm13298	0.0005	13.20	down	Mus musculus predicted gene 13298 (Gm13298), mRNA [NM_001085530]	NM_001085530
Gm13298	0.0045	2.23	down	Mus musculus predicted gene 13298 (Gm13298), mRNA [NM_001085530]	NM_001085530
Duox1	0.0053	1.78	down	Mus musculus dual oxidase 1 (Duox1), mRNA [NM_001099297]	NM_001099297
Fbxo39	0.0336	2.28	down	Mus musculus F-box protein 39 (Fbxo39), mRNA [NM_001099688]	NM_001099688
Pabpc4l	0.0039	2.09	down	Mus musculus poly(A) binding protein, cytoplasmic 4-like (Pabpc4l), mRNA [NM_001101479]	NM_001101479
Ccdc8	0.0312	1.99	down	Mus musculus coiled-coil domain containing 8 (Ccdc8), mRNA [NM_001101535]	NM_001101535
Vmn2r62	0.0250	1.89	down	Mus musculus vomeronasal 2, receptor 62 (Vmn2r62), mRNA [NM_001105059]	NM_001105059
Acp1	0.0283	1.50	down	Mus musculus acid phosphatase 1, soluble (Acp1), transcript variant 1, mRNA [NM_001110239]	NM_001110239
Acp1	0.0231	1.84	down	Mus musculus acid phosphatase 1, soluble (Acp1), transcript variant 1, mRNA [NM_001110239]	NM_001110239
Pclo	0.0340	1.76	down	Mus musculus piccolo (presynaptic cytomatrix protein) (Pclo), transcript variant 2, mRNA [NM_001110796]	NM_001110796
Gria4	0.0419	1.66	down	Mus musculus glutamate receptor, ionotropic, AMPA4 (alpha 4) (Gria4), transcript variant 2, mRNA [NM_001113180]	NM_001113180
Tec	0.0042	1.51	down	Mus musculus tec protein tyrosine kinase (Tec), transcript variant 1, mRNA [NM_001113460]	NM_001113460
Csf1	0.0372	2.08	down	Mus musculus colony stimulating factor 1 (macrophage) (Csf1), transcript variant 3, mRNA [NM_001113530]	NM_001113530
Csf1	0.0275	2.16	down	Mus musculus colony stimulating factor 1 (macrophage) (Csf1), transcript variant 3, mRNA [NM_001113530]	NM_001113530

Chrdl1	0.0066	2.05	down	Mus musculus chordin-like 1 (Chrdl1), transcript variant 1, mRNA [NM_001114385]	NM_001114385
Chrdl1	0.0093	3.95	down	Mus musculus chordin-like 1 (Chrdl1), transcript variant 1, mRNA [NM_001114385]	NM_001114385
Mfsd4	0.0084	4.16	down	Mus musculus major facilitator superfamily domain containing 4 (Mfsd4), transcript variant b, mRNA [NM_001114662]	NM_001114662
Kit	0.0494	1.79	down	Mus musculus kit oncogene (Kit), transcript variant 1, mRNA [NM_001122733]	NM_001122733
Gm13157	0.0056	2.96	down	Mus musculus predicted gene 13157 (Gm13157), mRNA [NM_001127189]	NM_001127189
Klf14	0.0363	2.61	down	Mus musculus Kruppel-like factor 14 (Klf14), mRNA [NM_001135093]	NM_001135093
1190007I07Rik	0.0069	1.88	down	Mus musculus RIKEN cDNA 1190007I07 gene (1190007I07Rik), transcript variant 1, mRNA [NM_001135567]	NM_001135567
Cd82	0.0470	1.60	down	Mus musculus CD82 antigen (Cd82), transcript variant 2, mRNA [NM_001136055]	NM_001136055
Hmha1	0.0026	2.07	down	Mus musculus histocompatibility (minor) HA-1 (Hmha1), transcript variant 1, mRNA [NM_001142701]	NM_001142701
Ppfia4	0.0167	1.84	down	Mus musculus protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4 (Ppfia4), mRNA [NM_001144855]	NM_001144855
Iigp1	0.0352	1.65	down	Mus musculus interferon inducible GTPase 1 (Iigp1), transcript variant 2, mRNA [NM_001146275]	NM_001146275
B3gnt5	0.0166	2.22	down	Mus musculus UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5 (B3gnt5), transcript variant 1, mRNA [NM_001159407]	NM_001159407
Neu2	0.0198	1.74	down	Mus musculus neuraminidase 2 (Neu2), transcript variant 3, mRNA [NM_001160165]	NM_001160165

Fmo5	0.0138	1.85	down	Mus musculus flavin containing monooxygenase 5 (Fmo5), transcript variant 1, mRNA [NM_001161765]	NM_001161765
Fmo5	0.0278	2.31	down	Mus musculus flavin containing monooxygenase 5 (Fmo5), transcript variant 1, mRNA [NM_001161765]	NM_001161765
Fam174b	0.0337	1.66	down	Mus musculus family with sequence similarity 174, member B (Fam174b), mRNA [NM_001162532]	NM_001162532
Gm3604	0.0395	2.18	down	Mus musculus predicted gene 3604 (Gm3604), mRNA [NM_001162910]	NM_001162910
E430029J22Rik	0.0393	2.17	down	Mus musculus RIKEN cDNA E430029J22 gene (E430029J22Rik), mRNA [NM_001162938]	NM_001162938
E430029J22Rik	0.0235	3.71	down	Mus musculus RIKEN cDNA E430029J22 gene (E430029J22Rik), mRNA [NM_001162938]	NM_001162938
Sgsm1	0.0290	2.30	down	Mus musculus small G protein signaling modulator 1 (Sgsm1), transcript variant 3, mRNA [NM_001162965]	NM_001162965
Haus8	0.0143	1.70	down	Mus musculus 4HAUS augmin-like complex, subunit 8 (Haus8), transcript variant 1, mRNA [NM_001163042]	NM_001163042
Fam102b	0.0002	2.63	down	Mus musculus family with sequence similarity 102, member B (Fam102b), mRNA [NM_001163567]	NM_001163567
Fbxo27	0.0015	1.95	down	Mus musculus F-box protein 27 (Fbxo27), transcript variant 1, mRNA [NM_001163702]	NM_001163702
Msl3l2	0.0254	1.90	down	Mus musculus male-specific lethal 3-like 2 (Drosophila) (Msl3l2), mRNA [NM_001163833]	NM_001163833
Gm4902	0.0137	2.02	down	Mus musculus predicted gene 4902 (Gm4902), mRNA [NM_001164327]	NM_001164327
Klhl29	0.0137	3.92	down	Mus musculus kelch-like 29 (Drosophila) (Klhl29), mRNA [NM_001164493]	NM_001164493
Klhl29	0.0410	1.87	down	Mus musculus kelch-like 29 (Drosophila) (Klhl29), mRNA [NM_001164493]	NM_001164493

Il33	0.0360	2.12	down	Mus musculus interleukin 33 (Il33), transcript variant 1, mRNA [NM_001164724]	NM_001164724
Gm10406	0.0412	2.10	down	Mus musculus predicted gene 10406 (Gm10406), mRNA [NM_001164727]	NM_001164727
Gm10406	0.0328	2.09	down	Mus musculus predicted gene 10406 (Gm10406), mRNA [NM_001164727]	NM_001164727
Zfp882	0.0316	1.83	down	Mus musculus zinc finger protein 882 (Zfp882), mRNA [NM_001166645]	NM_001166645
Gpr19	0.0017	1.78	down	Mus musculus G protein-coupled receptor 19 (Gpr19), transcript variant 1, mRNA [NM_001167693]	NM_001167693
Ankrd50	0.0041	2.04	down	Mus musculus ankyrin repeat domain 50 (Ankrd50), mRNA [NM_001167883]	NM_001167883
G2e3	0.0310	2.73	down	Mus musculus G2/M-phase specific E3 ubiquitin ligase (G2e3), transcript variant 2, mRNA [NM_001167963]	NM_001167963
Serpina3f	0.0422	2.12	down	Mus musculus serine (or cysteine) peptidase inhibitor, clade A, member 3F (Serpina3f), transcript variant 1, mRNA [NM_001168294]	NM_001168294
Klra2	0.0424	2.55	down	Mus musculus killer cell lectin-like receptor, subfamily A, member 2 (Klra2), transcript variant 1, mRNA [NM_001170851]	NM_001170851
Kirrel	0.0072	2.05	down	Mus musculus kin of IRRE like (Drosophila) (Kirrel), transcript variant 1, mRNA [NM_001170985]	NM_001170985
Rbms3	0.0238	1.71	down	Mus musculus RNA binding motif, single stranded interacting protein (Rbms3), transcript variant 1, mRNA [NM_001172123]	NM_001172123
Sirpb1b	0.0326	1.77	down	Mus musculus signal-regulatory protein beta 1B (Sirpb1b), mRNA [NM_001173460]	NM_001173460
Camk2b	0.0277	12.24	down	Mus musculus calcium/calmodulin-dependent protein kinase II, beta (Camk2b), transcript variant 1, mRNA [NM_001174053]	NM_001174053

Dbn1	0.0333	2.06	down	Mus musculus drebrin 1 (Dbn1), transcript variant 1, mRNA [NM_001177371]	NM_001177371
Gm15056	0.0497	1.67	down	Mus musculus predicted gene 15056 (Gm15056), mRNA [NM_001177471]	NM_001177471
Ube2i	0.0154	1.74	down	Mus musculus ubiquitin-conjugating enzyme E2I (Ube2i), transcript variant 2, mRNA [NM_001177609]	NM_001177609
Gm7120	0.0271	1.78	down	Mus musculus predicted gene 7120 (Gm7120), transcript variant 2, mRNA [NM_001177666]	NM_001177666
Gm7120	0.0091	1.69	down	Mus musculus predicted gene 7120 (Gm7120), transcript variant 2, mRNA [NM_001177666]	NM_001177666
Clec4b1	0.0465	1.95	down	Mus musculus C-type lectin domain family 4, member b1 (Clec4b1), transcript variant 1, mRNA [NM_001190310]	NM_001190310
Adora2b	0.0141	1.66	down	Mus musculus adenosine A2b receptor (Adora2b), mRNA [NM_007413]	NM_007413
Adra2a	0.0094	2.03	down	Mus musculus adrenergic receptor, alpha 2a (Adra2a), mRNA [NM_007417]	NM_007417
Amy1	0.0167	1.58	down	Mus musculus amylase 1, salivary (Amy1), transcript variant 1, mRNA [NM_007446]	NM_007446
Arhgdib	0.0220	1.60	down	Mus musculus Rho, GDP dissociation inhibitor (GDI) beta (Arhgdib), mRNA [NM_007486]	NM_007486
Arx	0.0458	1.75	down	Mus musculus aristaless related homeobox (Arx), mRNA [NM_007492]	NM_007492
Asgr2	0.0216	2.04	down	Mus musculus asialoglycoprotein receptor 2 (Asgr2), mRNA [NM_007493]	NM_007493
Zfhx3	0.0271	2.73	down	Mus musculus zinc finger homeobox 3 (Zfhx3), mRNA [NM_007496]	NM_007496
Atm	0.0368	2.02	down	Mus musculus ataxia telangiectasia mutated homolog (human) (Atm), mRNA [NM_007499]	NM_007499
Bcl2a1c	0.0243	2.37	down	Mus musculus B-cell leukemia/lymphoma 2 related protein A1c (Bcl2a1c), mRNA [NM_007535]	NM_007535

Bcl2a1d	0.0337	2.38	down	Mus musculus B-cell leukemia/lymphoma 2 related protein A1d (Bcl2a1d), mRNA [NM_007536]	NM_007536
Ccnd1	0.0067	1.66	down	Mus musculus cyclin D1 (Ccnd1), mRNA [NM_007631]	NM_007631
Cd37	0.0481	1.79	down	Mus musculus CD37 antigen (Cd37), mRNA [NM_007645]	NM_007645
Cd48	0.0192	1.61	down	Mus musculus CD48 antigen (Cd48), mRNA [NM_007649]	NM_007649
Cdh2	0.0239	1.93	down	Mus musculus cadherin 2 (Cdh2), mRNA [NM_007664]	NM_007664
Chga	0.0132	3.44	down	Mus musculus chromogranin A (Chga), mRNA [NM_007693]	NM_007693
Cmah	0.0293	1.95	down	Mus musculus cytidine monophospho-N-acetylneuraminic acid hydroxylase (Cmah), transcript variant 1, mRNA [NM_007717]	NM_007717
Ctsh	0.0452	1.56	down	Mus musculus cathepsin H (Ctsh), mRNA [NM_007801]	NM_007801
Cybb	0.0421	2.87	down	Mus musculus cytochrome b-245, beta polypeptide (Cybb), mRNA [NM_007807]	NM_007807
Cyp7b1	0.0305	1.68	down	Mus musculus cytochrome P450, family 7, subfamily b, polypeptide 1 (Cyp7b1), mRNA [NM_007825]	NM_007825
Dlx4	0.0393	2.68	down	Mus musculus distal-less homeobox 4 (Dlx4), mRNA [NM_007867]	NM_007867
Ear2	0.0328	4.44	down	Mus musculus eosinophil-associated, ribonuclease A family, member 2 (Ear2), mRNA [NM_007895]	NM_007895
Fancc	0.0400	2.26	down	Mus musculus Fanconi anemia, complementation group C (Fancc), transcript variant 1, mRNA [NM_007985]	NM_007985
Fgf18	0.0070	2.43	down	Mus musculus fibroblast growth factor 18 (Fgf18), mRNA [NM_008005]	NM_008005
Fgf18	0.0249	1.94	down	Mus musculus fibroblast growth factor 18 (Fgf18), mRNA [NM_008005]	NM_008005

Fmr1	0.0491	1.58	down	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA [NM_008031]	NM_008031
Fmr1	0.0275	1.61	down	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA [NM_008031]	NM_008031
Fstl1	0.0043	1.64	down	Mus musculus follistatin-like 1 (Fstl1), mRNA [NM_008047]	NM_008047
Fzd6	0.0416	4.29	down	Mus musculus frizzled homolog 6 (Drosophila) (Fzd6), transcript variant 1, mRNA [NM_008056]	NM_008056
Gabra3	0.0012	2.02	down	Mus musculus gamma-aminobutyric acid (GABA) A receptor, subunit alpha 3 (Gabra3), mRNA [NM_008067]	NM_008067
Gabrd	0.0133	2.08	down	Mus musculus gamma-aminobutyric acid (GABA) A receptor, subunit delta (Gabrd), mRNA [NM_008072]	NM_008072
Gas1	0.0021	1.62	down	Mus musculus growth arrest specific 1 (Gas1), mRNA [NM_008086]	NM_008086
Gata1	0.0103	1.98	down	Mus musculus GATA binding protein 1 (Gata1), mRNA [NM_008089]	NM_008089
Gfra2	0.0396	2.12	down	Mus musculus glial cell line derived neurotrophic factor family receptor alpha 2 (Gfra2), mRNA [NM_008115]	NM_008115
H2-Oa	0.0157	3.20	down	Mus musculus histocompatibility 2, O region alpha locus (H2-Oa), mRNA [NM_008206]	NM_008206
Hdac1	0.0244	1.61	down	Mus musculus histone deacetylase 1 (Hdac1), mRNA [NM_008228]	NM_008228
Hdac1	0.0296	2.85	down	Mus musculus histone deacetylase 1 (Hdac1), mRNA [NM_008228]	NM_008228
Hdac1	0.0379	4.35	down	Mus musculus histone deacetylase 1 (Hdac1), mRNA [NM_008228]	NM_008228
Hmgcs2	0.0094	1.79	down	Mus musculus 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (Hmgcs2), nuclear gene encoding mitochondrial protein, mRNA [NM_008256]	NM_008256

Hpgd	0.0340	1.51	down	Mus musculus hydroxyprostaglandin dehydrogenase 15 (NAD) (Hpgd), mRNA [NM_008278]	NM_008278
Map4k1	0.0004	2.57	down	Mus musculus mitogen-activated protein kinase kinase kinase 1 (Map4k1), mRNA [NM_008279]	NM_008279
Il18r1	0.0182	2.98	down	Mus musculus interleukin 18 receptor 1 (Il18r1), transcript variant 1, mRNA [NM_008365]	NM_008365
Il2ra	0.0295	1.68	down	Mus musculus interleukin 2 receptor, alpha chain (Il2ra), mRNA [NM_008367]	NM_008367
Rps2	0.0096	2.40	down	Mus musculus ribosomal protein S2 (Rps2), mRNA [NM_008503]	NM_008503
Lrmp	0.0344	1.86	down	Mus musculus lymphoid-restricted membrane protein (Lrmp), mRNA [NM_008511]	NM_008511
Amacr	0.0217	1.97	down	Mus musculus alpha-methylacyl-CoA racemase (Amacr), nuclear gene encoding mitochondrial protein, mRNA [NM_008537]	NM_008537
Mest	0.0466	2.09	down	Mus musculus mesoderm specific transcript (Mest), mRNA [NM_008590]	NM_008590
Foxd2	0.0354	1.51	down	Mus musculus forkhead box D2 (Foxd2), mRNA [NM_008593]	NM_008593
Mgp	0.0092	2.26	down	Mus musculus matrix Gla protein (Mgp), mRNA [NM_008597]	NM_008597
Ncf4	0.0222	1.72	down	Mus musculus neutrophil cytosolic factor 4 (Ncf4), mRNA [NM_008677]	NM_008677
Ppic	0.0020	1.50	down	Mus musculus peptidylprolyl isomerase C (Ppic), mRNA [NM_008908]	NM_008908
Prim2	0.0091	11.29	down	Mus musculus DNA primase, p58 subunit (Prim2), mRNA [NM_008922]	NM_008922
Ptgir	0.0130	2.88	down	Mus musculus prostaglandin I receptor (IP) (Ptgir), mRNA [NM_008967]	NM_008967
Rac2	0.0229	2.08	down	Mus musculus RAS-related C3 botulinum substrate 2 (Rac2), mRNA [NM_009008]	NM_009008

Rbpj	0.0234	1.58	down	Mus musculus recombination signal binding protein for immunoglobulin kappa J region (Rbpj), transcript variant 1, mRNA [NM_009035]	NM_009035
Rpl22	0.0029	1.60	down	Mus musculus ribosomal protein L22 (Rpl22), mRNA [NM_009079]	NM_009079
Rps6	0.0031	2.93	down	Mus musculus ribosomal protein S6 (Rps6), mRNA [NM_009096]	NM_009096
Prrx2	0.0160	2.21	down	Mus musculus paired related homeobox 2 (Prrx2), mRNA [NM_009116]	NM_009116
Sparc	0.0111	2.76	down	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA [NM_009242]	NM_009242
Spn	0.0285	2.05	down	Mus musculus sialophorin (Spn), transcript variant 1, mRNA [NM_009259]	NM_009259
Muc11	0.0192	13.55	down	Mus musculus mucin-like 1 (Muc11), mRNA [NM_009268]	NM_009268
Muc11	0.0166	16.77	down	Mus musculus mucin-like 1 (Muc11), mRNA [NM_009268]	NM_009268
Inmt	0.0357	2.11	down	Mus musculus indolethylamine N-methyltransferase (Inmt), mRNA [NM_009349]	NM_009349
Tgfb2	0.0353	1.67	down	Mus musculus transforming growth factor, beta 2 (Tgfb2), mRNA [NM_009367]	NM_009367
Tnfaip2	0.0285	1.56	down	Mus musculus tumor necrosis factor, alpha-induced protein 2 (Tnfaip2), mRNA [NM_009396]	NM_009396
Wnt10a	0.0146	2.14	down	Mus musculus wingless related MMTV integration site 10a (Wnt10a), mRNA [NM_009518]	NM_009518
Wnt2b	0.0489	1.63	down	Mus musculus wingless related MMTV integration site 2b (Wnt2b), mRNA [NM_009520]	NM_009520
Wnt5b	0.0469	1.91	down	Mus musculus wingless-related MMTV integration site 5B (Wnt5b), mRNA [NM_009525]	NM_009525
Zap70	0.0025	2.00	down	Mus musculus zeta-chain (TCR) associated protein kinase (Zap70), mRNA [NM_009539]	NM_009539
Zap70	0.0083	2.00	down	Mus musculus zeta-chain (TCR) associated protein kinase (Zap70), mRNA [NM_009539]	NM_009539

Zfp105	0.0345	1.63	down	Mus musculus zinc finger protein 105 (Zfp105), mRNA [NM_009544]	NM_009544
Abcg1	0.0053	1.75	down	Mus musculus ATP-binding cassette, sub-family G (WHITE), member 1 (Abcg1), mRNA [NM_009593]	NM_009593
Actg1	0.0497	2.43	down	Mus musculus actin, gamma, cytoplasmic 1 (Actg1), mRNA [NM_009609]	NM_009609
Angpt4	0.0257	2.58	down	Mus musculus angiopoietin 4 (Angpt4), mRNA [NM_009641]	NM_009641
Atp2b2	0.0349	1.66	down	Mus musculus ATPase, Ca ⁺⁺ transporting, plasma membrane 2 (Atp2b2), transcript variant 1, mRNA [NM_009723]	NM_009723
Glb1	0.0458	1.74	down	Mus musculus galactosidase, beta 1 (Glb1), mRNA [NM_009752]	NM_009752
Casp12	0.0002	1.77	down	Mus musculus caspase 12 (Casp12), mRNA [NM_009808]	NM_009808
Cd151	0.0410	1.82	down	Mus musculus CD151 antigen (Cd151), transcript variant 1, mRNA [NM_009842]	NM_009842
Cdkn2a	0.0065	2.50	down	Mus musculus cyclin-dependent kinase inhibitor 2A (Cdkn2a), transcript variant 1, mRNA [NM_009877]	NM_009877
Cfh	0.0289	2.26	down	Mus musculus complement component factor h (Cfh), mRNA [NM_009888]	NM_009888
Coro1a	0.0101	1.82	down	Mus musculus coronin, actin binding protein 1A (Coro1a), mRNA [NM_009898]	NM_009898
Cxcr3	0.0220	2.35	down	Mus musculus chemokine (C-X-C motif) receptor 3 (Cxcr3), mRNA [NM_009910]	NM_009910
Ccr5	0.0189	2.80	down	Mus musculus chemokine (C-C motif) receptor 5 (Ccr5), mRNA [NM_009917]	NM_009917
Cst7	0.0144	2.62	down	Mus musculus cystatin F (leukocystatin) (Cst7), mRNA [NM_009977]	NM_009977
Cx3cr1	0.0145	1.79	down	Mus musculus chemokine (C-X3-C) receptor 1 (Cx3cr1), mRNA [NM_009987]	NM_009987

Dapk2	0.0217	1.56	down	Mus musculus death-associated protein kinase 2 (Dapk2), mRNA [NM_010019]	NM_010019
Dpp4	0.0399	1.68	down	Mus musculus dipeptidylpeptidase 4 (Dpp4), transcript variant 1, mRNA [NM_010074]	NM_010074
Fasl	0.0037	2.50	down	Mus musculus Fas ligand (TNF superfamily, member 6) (Fasl), mRNA [NM_010177]	NM_010177
Fcgr1	0.0133	1.59	down	Mus musculus Fc receptor, IgG, high affinity I (Fcgr1), mRNA [NM_010186]	NM_010186
Pdpn	0.0061	2.81	down	Mus musculus podoplanin (Pdpn), mRNA [NM_010329]	NM_010329
Pdpn	0.0016	5.51	down	Mus musculus podoplanin (Pdpn), mRNA [NM_010329]	NM_010329
Gstm1	0.0319	1.53	down	Mus musculus glutathione S-transferase, mu 1 (Gstm1), mRNA [NM_010358]	NM_010358
Gzma	0.0363	1.83	down	Mus musculus granzyme A (Gzma), mRNA [NM_010370]	NM_010370
H2-DMa	0.0436	2.36	down	Mus musculus histocompatibility 2, class II, locus DMa (H2-DMa), mRNA [NM_010386]	NM_010386
Il16	0.0194	1.68	down	Mus musculus interleukin 16 (Il16), mRNA [NM_010551]	NM_010551
Inha	0.0015	1.90	down	Mus musculus inhibin alpha (Inha), mRNA [NM_010564]	NM_010564
Itga4	0.0409	1.74	down	Mus musculus integrin alpha 4 (Itga4), mRNA [NM_010576]	NM_010576
Klra8	0.0091	2.93	down	Mus musculus killer cell lectin-like receptor, subfamily A, member 8 (Klra8), transcript variant 2, mRNA [NM_010650]	NM_010650
Klra8	0.0164	1.85	down	Mus musculus killer cell lectin-like receptor, subfamily A, member 8 (Klra8), transcript variant 2, mRNA [NM_010650]	NM_010650
Lrrn2	0.0031	3.07	down	Mus musculus leucine rich repeat protein 2, neuronal (Lrrn2), mRNA [NM_010732]	NM_010732

Ly86	0.0135	2.92	down	Mus musculus lymphocyte antigen 86 (Ly86), mRNA [NM_010745]	NM_010745
Ncr1	0.0339	1.80	down	Mus musculus natural cytotoxicity triggering receptor 1 (Ncr1), mRNA [NM_010746]	NM_010746
Meox1	0.0023	2.42	down	Mus musculus mesenchyme homeobox 1 (Meox1), mRNA [NM_010791]	NM_010791
Naip2	0.0326	2.39	down	Mus musculus NLR family, apoptosis inhibitory protein 2 (Naip2), transcript variant 1, mRNA [NM_010872]	NM_010872
Nov	0.0226	2.62	down	Mus musculus nephroblastoma overexpressed gene (Nov), mRNA [NM_010930]	NM_010930
Nsg1	0.0303	2.02	down	Mus musculus neuron specific gene family member 1 (Nsg1), mRNA [NM_010942]	NM_010942
Cdk14	0.0089	2.80	down	Mus musculus cyclin-dependent kinase 14 (Cdk14), mRNA [NM_011074]	NM_011074
Pira11	0.0241	1.63	down	Mus musculus paired-Ig-like receptor A11 (Pira11), mRNA [NM_011088]	NM_011088
Lilra6	0.0490	2.37	down	Mus musculus leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6 (Lilra6), transcript variant 1, mRNA [NM_011090]	NM_011090
Pira7	0.0339	2.15	down	Mus musculus paired-Ig-like receptor A7 (Pira7), mRNA [NM_011094]	NM_011094
Prkca	0.0453	1.74	down	Mus musculus protein kinase C, alpha (Prkca), mRNA [NM_011101]	NM_011101
Prkca	0.0361	2.43	down	Mus musculus protein kinase C, alpha (Prkca), mRNA [NM_011101]	NM_011101
Ccl21a	0.0285	2.93	down	Mus musculus chemokine (C-C motif) ligand 21A (Ccl21a), mRNA [NM_011124]	NM_011124
Prtn3	0.0051	4.11	down	Mus musculus proteinase 3 (Prtn3), mRNA [NM_011178]	NM_011178
Rbp1	0.0419	2.65	down	Mus musculus retinol binding protein 1, cellular (Rbp1), mRNA [NM_011254]	NM_011254

Ccl21b	0.0158	2.33	down	Mus musculus chemokine (C-C motif) ligand 21B (Ccl21b), mRNA [NM_011335]	NM_011335
Frzb	0.0115	2.87	down	Mus musculus frizzled-related protein (Frzb), mRNA [NM_011356]	NM_011356
Slc1a2	0.0240	2.55	down	Mus musculus solute carrier family 1 (glial high affinity glutamate transporter), member 2 (Slc1a2), transcript variant 3, mRNA [NM_011393]	NM_011393
Sykb	0.0427	1.69	down	Mus musculus spleen tyrosine kinase (Sykb), mRNA [NM_011518]	NM_011518
Tfpi	0.0406	2.22	down	Mus musculus tissue factor pathway inhibitor (Tfpi), transcript variant 1, mRNA [NM_011576]	NM_011576
Tfpi	0.0472	1.93	down	Mus musculus tissue factor pathway inhibitor (Tfpi), transcript variant 1, mRNA [NM_011576]	NM_011576
Timp2	0.0282	1.54	down	Mus musculus tissue inhibitor of metalloproteinase 2 (Timp2), mRNA [NM_011594]	NM_011594
Tle1	0.0052	2.67	down	Mus musculus transducin-like enhancer of split 1, homolog of Drosophila E(spl) (Tle1), mRNA [NM_011599]	NM_011599
Tnfrsf17	0.0185	2.74	down	Mus musculus tumor necrosis factor receptor superfamily, member 17 (Tnfrsf17), mRNA [NM_011608]	NM_011608
Tnfrsf1b	0.0359	2.56	down	Mus musculus tumor necrosis factor receptor superfamily, member 1b (Tnfrsf1b), mRNA [NM_011610]	NM_011610
Cd40	0.0205	2.53	down	Mus musculus CD40 antigen (Cd40), transcript variant 1, mRNA [NM_011611]	NM_011611
Uchl1	0.0253	5.56	down	Mus musculus ubiquitin carboxy-terminal hydrolase L1 (Uchl1), mRNA [NM_011670]	NM_011670
Vav1	0.0012	1.60	down	Mus musculus vav 1 oncogene (Vav1), transcript variant 1, mRNA [NM_011691]	NM_011691
Zfp39	0.0229	1.52	down	Mus musculus zinc finger protein 39 (Zfp39), mRNA [NM_011758]	NM_011758

Zfr	0.0458	1.98	down	Mus musculus zinc finger RNA binding protein (Zfr), mRNA [NM_011767]	NM_011767
Ikzf3	0.0006	1.57	down	Mus musculus IKAROS family zinc finger 3 (Ikzf3), mRNA [NM_011771]	NM_011771
Adamts5	0.0423	2.42	down	Mus musculus a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (Adamts5), mRNA [NM_011782]	NM_011782
Cdc6	0.0392	2.50	down	Mus musculus cell division cycle 6 homolog (S. cerevisiae) (Cdc6), transcript variant 1, mRNA [NM_011799]	NM_011799
Cdc6	0.0035	1.78	down	Mus musculus cell division cycle 6 homolog (S. cerevisiae) (Cdc6), transcript variant 1, mRNA [NM_011799]	NM_011799
Rnasel	0.0484	2.23	down	Mus musculus ribonuclease L (2', 5'-oligoadenylate synthetase-dependent) (Rnasel), mRNA [NM_011882]	NM_011882
Dapp1	0.0022	1.89	down	Mus musculus dual adaptor for phosphotyrosine and 3-phosphoinositides 1 (Dapp1), mRNA [NM_011932]	NM_011932
Homer2	0.0034	2.59	down	Mus musculus homer homolog 2 (Drosophila) (Homer2), transcript variant 1, mRNA [NM_011983]	NM_011983
Spag1	0.0156	1.91	down	Mus musculus sperm associated antigen 1 (Spag1), mRNA [NM_012031]	NM_012031
Fkbp9	0.0214	1.51	down	Mus musculus FK506 binding protein 9 (Fkbp9), mRNA [NM_012056]	NM_012056
Btk	0.0160	1.56	down	Mus musculus Bruton agammaglobulinemia tyrosine kinase (Btk), mRNA [NM_013482]	NM_013482
C2	0.0344	1.70	down	Mus musculus complement component 2 (within H-2S) (C2), mRNA [NM_013484]	NM_013484
Cd2	0.0080	3.51	down	Mus musculus CD2 antigen (Cd2), mRNA [NM_013486]	NM_013486
Cd2	0.0337	3.50	down	Mus musculus CD2 antigen (Cd2), mRNA [NM_013486]	NM_013486

Fgf9	0.0277	1.70	down	Mus musculus fibroblast growth factor 9 (Fgf9), mRNA [NM_013518]	NM_013518
Fut7	0.0100	1.78	down	Mus musculus fucosyltransferase 7 (Fut7), transcript variant 1, mRNA [NM_013524]	NM_013524
Gnb4	0.0284	1.68	down	Mus musculus guanine nucleotide binding protein (G protein), beta 4 (Gnb4), mRNA [NM_013531]	NM_013531
Hist2h2aa1	0.0230	1.72	down	Mus musculus histone cluster 2, H2aa1 (Hist2h2aa1), mRNA [NM_013549]	NM_013549
Itgb7	0.0009	2.55	down	Mus musculus integrin beta 7 (Itgb7), mRNA [NM_013566]	NM_013566
Odc1	0.0079	1.68	down	Mus musculus ornithine decarboxylase, structural 1 (Odc1), mRNA [NM_013614]	NM_013614
Rtn2	0.0257	1.79	down	Mus musculus reticulon 2 (Z-band associated protein) (Rtn2), transcript variant B, mRNA [NM_013648]	NM_013648
Ccl5	0.0183	2.18	down	Mus musculus chemokine (C-C motif) ligand 5 (Ccl5), mRNA [NM_013653]	NM_013653
Ccl7	0.0205	2.43	down	Mus musculus chemokine (C-C motif) ligand 7 (Ccl7), mRNA [NM_013654]	NM_013654
Sema4d	0.0297	1.51	down	Mus musculus sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (Sema4d), mRNA [NM_013660]	NM_013660
Thbs3	0.0085	1.95	down	Mus musculus thrombospondin 3 (Thbs3), mRNA [NM_013691]	NM_013691
Clnk	0.0317	1.53	down	Mus musculus cytokine-dependent hematopoietic cell linker (Clnk), mRNA [NM_013748]	NM_013748
Ndrp2	0.0205	2.04	down	Mus musculus N-myc downstream regulated gene 2 (Ndrp2), transcript variant 1, mRNA [NM_013864]	NM_013864
Clic4	0.0063	2.12	down	Mus musculus chloride intracellular channel 4 (mitochondrial) (Clic4), nuclear gene encoding mitochondrial protein, mRNA [NM_013885]	NM_013885
Pttg1	0.0120	1.93	down	Mus musculus pituitary tumor-transforming gene 1 (Pttg1), transcript variant 2, mRNA [NM_013917]	NM_013917

Fgd3	0.0229	1.51	down	Mus musculus FYVE, RhoGEF and PH domain containing 3 (Fgd3), mRNA [NM_015759]	NM_015759
Atp8a2	0.0142	2.47	down	Mus musculus ATPase, aminophospholipid transporter-like, class I, type 8A, member 2 (Atp8a2), mRNA [NM_015803]	NM_015803
Lsm4	0.0479	1.56	down	Mus musculus LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae) (Lsm4), mRNA [NM_015816]	NM_015816
Bcl11a	0.0433	3.36	down	Mus musculus B-cell CLL/lymphoma 11A (zinc finger protein) (Bcl11a), transcript variant 1, mRNA [NM_016707]	NM_016707
Rgs14	0.0227	1.67	down	Mus musculus regulator of G-protein signaling 14 (Rgs14), mRNA [NM_016758]	NM_016758
Matn2	0.0104	2.90	down	Mus musculus matrilin 2 (Matn2), mRNA [NM_016762]	NM_016762
Itgb3	0.0051	2.35	down	Mus musculus integrin beta 3 (Itgb3), mRNA [NM_016780]	NM_016780
Wisp2	0.0305	1.65	down	Mus musculus WNT1 inducible signaling pathway protein 2 (Wisp2), mRNA [NM_016873]	NM_016873
Ptprcap	0.0371	1.98	down	Mus musculus protein tyrosine phosphatase, receptor type, C polypeptide-associated protein (Ptprcap), mRNA [NM_016933]	NM_016933
Sh3gl3	0.0026	2.46	down	Mus musculus SH3-domain GRB2-like 3 (Sh3gl3), mRNA [NM_017400]	NM_017400
Polm	0.0018	1.69	down	Mus musculus polymerase (DNA directed), mu (Polm), mRNA [NM_017401]	NM_017401
Icos	0.0231	1.89	down	Mus musculus inducible T-cell co-stimulator (Icos), mRNA [NM_017480]	NM_017480
Ctnnal1	0.0446	1.50	down	Mus musculus catenin (cadherin associated protein), alpha-like 1 (Ctnnal1), mRNA [NM_018761]	NM_018761
Sfrp5	0.0186	3.32	down	Mus musculus secreted frizzled-related sequence protein 5 (Sfrp5), mRNA [NM_018780]	NM_018780

Cxcl13	0.0109	16.85	down	Mus musculus chemokine (C-X-C motif) ligand 13 (Cxcl13), mRNA [NM_018866]	NM_018866
Cpxm2	0.0246	1.84	down	Mus musculus carboxypeptidase X 2 (M14 family) (Cpxm2), mRNA [NM_018867]	NM_018867
Lsp1	0.0070	2.16	down	Mus musculus lymphocyte specific 1 (Lsp1), transcript variant 2, mRNA [NM_019391]	NM_019391
Tnfsf14	0.0408	1.72	down	Mus musculus tumor necrosis factor (ligand) superfamily, member 14 (Tnfsf14), mRNA [NM_019418]	NM_019418
Irgm2	0.0182	3.44	down	Mus musculus immunity-related GTPase family M member 2 (Irgm2), mRNA [NM_019440]	NM_019440
Mefv	0.0055	3.30	down	Mus musculus Mediterranean fever (Mefv), transcript variant 3, mRNA [NM_019453]	NM_019453
Hebp2	0.0084	3.69	down	Mus musculus heme binding protein 2 (Hebp2), mRNA [NM_019487]	NM_019487
Tbx21	0.0354	2.06	down	Mus musculus T-box 21 (Tbx21), mRNA [NM_019507]	NM_019507
Bace2	0.0425	1.69	down	Mus musculus beta-site APP-cleaving enzyme 2 (Bace2), mRNA [NM_019517]	NM_019517
Plek	0.0163	1.63	down	Mus musculus pleckstrin (Plek), mRNA [NM_019549]	NM_019549
Stk3	0.0077	1.79	down	Mus musculus serine/threonine kinase 3 (Ste20, yeast homolog) (Stk3), mRNA [NM_019635]	NM_019635
Stmn1	0.0429	1.97	down	Mus musculus stathmin 1 (Stmn1), mRNA [NM_019641]	NM_019641
Plcd1	0.0500	1.87	down	Mus musculus phospholipase C, delta 1 (Plcd1), mRNA [NM_019676]	NM_019676
Gria4	0.0405	2.14	down	Mus musculus glutamate receptor, ionotropic, AMPA4 (alpha 4) (Gria4), transcript variant 1, mRNA [NM_019691]	NM_019691
Dusp14	0.0299	1.63	down	Mus musculus dual specificity phosphatase 14 (Dusp14), mRNA [NM_019819]	NM_019819

Mast1	0.0213	2.30	down	Mus musculus microtubule associated serine/threonine kinase 1 (Mast1), mRNA [NM_019945]	NM_019945
Clec4e	0.0028	1.52	down	Mus musculus C-type lectin domain family 4, member e (Clec4e), mRNA [NM_019948]	NM_019948
Rec8	0.0071	3.19	down	Mus musculus REC8 homolog (yeast) (Rec8), mRNA [NM_020002]	NM_020002
Clec7a	0.0309	2.04	down	Mus musculus C-type lectin domain family 7, member a (Clec7a), mRNA [NM_020008]	NM_020008
Hist1h1b	0.0123	2.02	down	Mus musculus histone cluster 1, H1b (Hist1h1b), mRNA [NM_020034]	NM_020034
Tspan32	0.0052	1.80	down	Mus musculus tetraspanin 32 (Tspan32), transcript variant 2, mRNA [NM_020286]	NM_020286
Retnla	0.0269	4.28	down	Mus musculus resistin like alpha (Retnla), mRNA [NM_020509]	NM_020509
Vsig2	0.0304	1.95	down	Mus musculus V-set and immunoglobulin domain containing 2 (Vsig2), mRNA [NM_020518]	NM_020518
Cmpk2	0.0249	2.02	down	Mus musculus cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial (Cmpk2), nuclear gene encoding mitochondrial protein, mRNA [NM_020557]	NM_020557
Cmpk2	0.0058	4.40	down	Mus musculus cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial (Cmpk2), nuclear gene encoding mitochondrial protein, mRNA [NM_020557]	NM_020557
Kcne3	0.0000	2.28	down	Mus musculus potassium voltage-gated channel, Isk-related subfamily, gene 3 (Kcne3), mRNA [NM_020574]	NM_020574
Kcne3	0.0081	1.75	down	Mus musculus potassium voltage-gated channel, Isk-related subfamily, gene 3 (Kcne3), mRNA [NM_020574]	NM_020574
Vstm2b	0.0382	2.41	down	Mus musculus V-set and transmembrane domain containing 2B (Vstm2b), mRNA [NM_021387]	NM_021387

Extl2	0.0411	1.83	down	Mus musculus exostoses (multiple)-like 2 (Extl2), transcript variant 1, mRNA [NM_021388]	NM_021388
Ccl8	0.0262	2.28	down	Mus musculus chemokine (C-C motif) ligand 8 (Ccl8), mRNA [NM_021443]	NM_021443
Cysltr1	0.0426	1.66	down	Mus musculus cysteinyl leukotriene receptor 1 (Cysltr1), mRNA [NM_021476]	NM_021476
Dact1	0.0475	2.47	down	Mus musculus dapper homolog 1, antagonist of beta-catenin (xenopus) (Dact1), transcript variant 2, mRNA [NM_021532]	NM_021532
Ms4a4b	0.0375	2.28	down	Mus musculus membrane-spanning 4-domains, subfamily A, member 4B (Ms4a4b), mRNA [NM_021718]	NM_021718
Gucy1a3	0.0298	1.87	down	Mus musculus guanylate cyclase 1, soluble, alpha 3 (Gucy1a3), mRNA [NM_021896]	NM_021896
Gpr88	0.0196	2.14	down	Mus musculus G-protein coupled receptor 88 (Gpr88), mRNA [NM_022427]	NM_022427
Pmepa1	0.0141	2.10	down	Mus musculus prostate transmembrane protein, androgen induced 1 (Pmepa1), mRNA [NM_022995]	NM_022995
Mcam	0.0167	1.99	down	Mus musculus melanoma cell adhesion molecule (Mcam), mRNA [NM_023061]	NM_023061
Slc30a7	0.0082	6.96	down	Mus musculus solute carrier family 30 (zinc transporter), member 7 (Slc30a7), mRNA [NM_023214]	NM_023214
Jam3	0.0499	1.58	down	Mus musculus junction adhesion molecule 3 (Jam3), mRNA [NM_023277]	NM_023277
Samsn1	0.0154	3.19	down	Mus musculus SAM domain, SH3 domain and nuclear localization signals, 1 (Samsn1), mRNA [NM_023380]	NM_023380
Wfdc1	0.0422	1.64	down	Mus musculus WAP four-disulfide core domain 1 (Wfdc1), mRNA [NM_023395]	NM_023395
Esm1	0.0470	6.17	down	Mus musculus endothelial cell-specific molecule 1 (Esm1), mRNA [NM_023612]	NM_023612

Pi16	0.0078	3.35	down	Mus musculus peptidase inhibitor 16 (Pi16), mRNA [NM_023734]	NM_023734
Pde6h	0.0365	4.00	down	Mus musculus phosphodiesterase 6H, cGMP-specific, cone, gamma (Pde6h), mRNA [NM_023898]	NM_023898
Nkg7	0.0160	3.19	down	Mus musculus natural killer cell group 7 sequence (Nkg7), mRNA [NM_024253]	NM_024253
Cyp4f18	0.0012	5.07	down	Mus musculus cytochrome P450, family 4, subfamily f, polypeptide 18 (Cyp4f18), mRNA [NM_024444]	NM_024444
Klra23	0.0097	3.41	down	Mus musculus killer cell lectin-like receptor subfamily A, member 23 (Klra23), mRNA [NM_024470]	NM_024470
Klra23	0.0165	4.96	down	Mus musculus killer cell lectin-like receptor subfamily A, member 23 (Klra23), mRNA [NM_024470]	NM_024470
Amz2	0.0106	1.54	down	Mus musculus archaelysin family metallopeptidase 2 (Amz2), mRNA [NM_025275]	NM_025275
Mef2c	0.0114	1.79	down	Mus musculus myocyte enhancer factor 2C (Mef2c), transcript variant 2, mRNA [NM_025282]	NM_025282
Spc25	0.0431	1.58	down	Mus musculus SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae) (Spc25), mRNA [NM_025565]	NM_025565
Speer4d	0.0063	17.15	down	Mus musculus spermatogenesis associated glutamate (E)-rich protein 4d (Speer4d), mRNA [NM_025759]	NM_025759
Slc16a9	0.0470	2.21	down	Mus musculus solute carrier family 16 (monocarboxylic acid transporters), member 9 (Slc16a9), mRNA [NM_025807]	NM_025807
Tmem88	0.0355	2.07	down	Mus musculus transmembrane protein 88 (Tmem88), mRNA [NM_025915]	NM_025915
Ssr1	0.0068	1.72	down	Mus musculus signal sequence receptor, alpha (Ssr1), mRNA [NM_025965]	NM_025965
Glod4	0.0164	1.55	down	Mus musculus glyoxalase domain containing 4 (Glod4), mRNA [NM_026029]	NM_026029
Dock7	0.0147	3.51	down	Mus musculus dedicator of cytokinesis 7 (Dock7), mRNA [NM_026082]	NM_026082

Pdlim7	0.0413	1.52	down	Mus musculus PDZ and LIM domain 7 (Pdlim7), transcript variant c, mRNA [NM_026131]	NM_026131
Armxc2	0.0356	1.52	down	Mus musculus armadillo repeat containing, X-linked 2 (Armxc2), transcript variant 1, mRNA [NM_026139]	NM_026139
Eps8l1	0.0487	2.37	down	Mus musculus EPS8-like 1 (Eps8l1), mRNA [NM_026146]	NM_026146
Nudcd1	0.0396	2.40	down	Mus musculus NudC domain containing 1 (Nudcd1), transcript variant 1, mRNA [NM_026149]	NM_026149
Ankrd33b	0.0107	11.22	down	Mus musculus ankyrin repeat domain 33B (Ankrd33b), transcript variant 1, mRNA [NM_026153]	NM_026153
Entpd4	0.0056	2.61	down	Mus musculus ectonucleoside triphosphate diphosphohydrolase 4 (Entpd4), mRNA [NM_026174]	NM_026174
Entpd4	0.0336	1.71	down	Mus musculus ectonucleoside triphosphate diphosphohydrolase 4 (Entpd4), mRNA [NM_026174]	NM_026174
Fam174a	0.0040	1.55	down	Mus musculus family with sequence similarity 174, member A (Fam174a), mRNA [NM_026321]	NM_026321
Rgs10	0.0118	1.83	down	Mus musculus regulator of G-protein signalling 10 (Rgs10), mRNA [NM_026418]	NM_026418
Fam45a	0.0437	1.56	down	Mus musculus family with sequence similarity 45, member A (Fam45a), transcript variant 1, mRNA [NM_026437]	NM_026437
Pef1	0.0377	2.07	down	Mus musculus penta-EF hand domain containing 1 (Pef1), mRNA [NM_026441]	NM_026441
Art4	0.0070	4.33	down	Mus musculus ADP-ribosyltransferase 4 (Art4), mRNA [NM_026639]	NM_026639
Tspan11	0.0384	2.17	down	Mus musculus tetraspanin 11 (Tspan11), mRNA [NM_026743]	NM_026743
Srpx2	0.0412	2.67	down	Mus musculus sushi-repeat-containing protein, X-linked 2 (Srpx2), transcript variant 1, mRNA [NM_026838]	NM_026838

1110059M19Rik	0.0081	9.97	down	Mus musculus RIKEN cDNA 1110059M19 gene (1110059M19Rik), mRNA [NM_026841]	NM_026841
Cd209f	0.0466	2.70	down	Mus musculus CD209f antigen (Cd209f), mRNA [NM_026956]	NM_026956
Wdfy1	0.0133	2.00	down	Mus musculus WD repeat and FYVE domain containing 1 (Wdfy1), transcript variant 2, mRNA [NM_027057]	NM_027057
2310004N24Rik	0.0413	1.67	down	Mus musculus RIKEN cDNA 2310004N24 gene (2310004N24Rik), mRNA [NM_027107]	NM_027107
Cd164l2	0.0206	2.01	down	Mus musculus CD164 sialomucin-like 2 (Cd164l2), mRNA [NM_027152]	NM_027152
Cd164l2	0.0028	5.34	down	Mus musculus CD164 sialomucin-like 2 (Cd164l2), mRNA [NM_027152]	NM_027152
Rnaseh2a	0.0027	1.50	down	Mus musculus ribonuclease H2, large subunit (Rnaseh2a), mRNA [NM_027187]	NM_027187
Nkd1	0.0055	2.09	down	Mus musculus naked cuticle 1 homolog (Drosophila) (Nkd1), transcript variant 1, mRNA [NM_027280]	NM_027280
1700029I01Rik	0.0270	3.32	down	Mus musculus RIKEN cDNA 1700029I01 gene (1700029I01Rik), mRNA [NM_027285]	NM_027285
1700029I01Rik	0.0110	5.20	down	Mus musculus RIKEN cDNA 1700029I01 gene (1700029I01Rik), mRNA [NM_027285]	NM_027285
Prrg1	0.0021	1.66	down	Mus musculus proline rich Gla (G-carboxyglutamic acid) 1 (Prrg1), transcript variant 1, mRNA [NM_027322]	NM_027322
Ly6g6e	0.0085	1.69	down	Mus musculus lymphocyte antigen 6 complex, locus G6E (Ly6g6e), mRNA [NM_027366]	NM_027366
Steap1	0.0273	4.11	down	Mus musculus six transmembrane epithelial antigen of the prostate 1 (Steap1), mRNA [NM_027399]	NM_027399
Mmrn1	0.0164	1.75	down	Mus musculus multimerin 1 (Mmrn1), transcript variant 1, mRNA [NM_027613]	NM_027613
Sntg1	0.0271	3.65	down	Mus musculus syntrophin, gamma 1 (Sntg1), mRNA [NM_027671]	NM_027671

9030607L17Rik	0.0292	1.55	down	Mus musculus RIKEN cDNA 9030607L17 gene (9030607L17Rik), mRNA [NM_027829]	NM_027829
9130008F23Rik	0.0090	2.90	down	Mus musculus RIKEN cDNA 9130008F23 gene (9130008F23Rik), mRNA [NM_027834]	NM_027834
Mettl7b	0.0047	1.58	down	Mus musculus methyltransferase like 7B (Mettl7b), mRNA [NM_027853]	NM_027853
Colec11	0.0418	4.07	down	Mus musculus collectin sub-family member 11 (Colec11), mRNA [NM_027866]	NM_027866
Susd2	0.0296	1.57	down	Mus musculus sushi domain containing 2 (Susd2), transcript variant 1, mRNA [NM_027890]	NM_027890
Mar-08	0.0227	2.07	down	Mus musculus membrane-associated ring finger (C3HC4) 8 (March8), mRNA [NM_027920]	NM_027920
Trnau1ap	0.0185	1.66	down	Mus musculus tRNA selenocysteine 1 associated protein 1 (Trnau1ap), mRNA [NM_027925]	NM_027925
1700026J04Rik	0.0250	1.50	down	Mus musculus RIKEN cDNA 1700026J04 gene (1700026J04Rik), mRNA [NM_027967]	NM_027967
Lypd6b	0.0211	2.47	down	Mus musculus LY6/PLAUR domain containing 6B (Lypd6b), mRNA [NM_027990]	NM_027990
Paqr7	0.0030	1.81	down	Mus musculus progesterin and adipoQ receptor family member VII (Paqr7), mRNA [NM_027995]	NM_027995
Cpsf3l	0.0262	1.68	down	Mus musculus cleavage and polyadenylation specific factor 3-like (Cpsf3l), mRNA [NM_028020]	NM_028020
B3gnt3	0.0320	4.72	down	Mus musculus UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3 (B3gnt3), mRNA [NM_028189]	NM_028189
Angptl1	0.0006	2.14	down	Mus musculus angiopoietin-like 1 (Angptl1), mRNA [NM_028333]	NM_028333
Pot1b	0.0083	2.17	down	Mus musculus protection of telomeres 1B (Pot1b), mRNA [NM_028370]	NM_028370
3110082D06Rik	0.0101	4.51	down	Mus musculus RIKEN cDNA 3110082D06 gene (3110082D06Rik), mRNA [NM_028474]	NM_028474
Btbd11	0.0473	1.83	down	Mus musculus BTB (POZ) domain containing 11 (Btbd11), transcript variant 1, mRNA [NM_028709]	NM_028709

Fcho1	0.0010	2.34	down	Mus musculus FCH domain only 1 (Fcho1), transcript variant 1, mRNA [NM_028715]	NM_028715
Cyp2s1	0.0257	2.43	down	Mus musculus cytochrome P450, family 2, subfamily s, polypeptide 1 (Cyp2s1), mRNA [NM_028775]	NM_028775
P2ry13	0.0063	1.74	down	Mus musculus purinergic receptor P2Y, G-protein coupled 13 (P2ry13), mRNA [NM_028808]	NM_028808
Vit	0.0081	1.61	down	Mus musculus vitrin (Vit), mRNA [NM_028813]	NM_028813
Ctbs	0.0403	1.58	down	Mus musculus chitinase, di-N-acetyl- (Ctbs), mRNA [NM_028836]	NM_028836
Palm3	0.0022	1.69	down	Mus musculus paralemmin 3 (Palm3), mRNA [NM_028877]	NM_028877
Efhd1	0.0235	1.90	down	Mus musculus EF hand domain containing 1 (Efhd1), mRNA [NM_028889]	NM_028889
Nipal3	0.0369	1.88	down	Mus musculus NIPA-like domain containing 3 (Nipal3), mRNA [NM_028995]	NM_028995
Tmem114	0.0035	1.76	down	Mus musculus transmembrane protein 114 (Tmem114), mRNA [NM_029070]	NM_029070
4930528F23Rik	0.0206	3.70	down	Mus musculus RIKEN cDNA 4930528F23 gene (4930528F23Rik), mRNA [NM_029197]	NM_029197
Cklf	0.0203	1.63	down	Mus musculus chemokine-like factor (Cklf), transcript variant 1, mRNA [NM_029295]	NM_029295
Tmem14a	0.0109	1.52	down	Mus musculus transmembrane protein 14A (Tmem14a), mRNA [NM_029398]	NM_029398
Ms4a4c	0.0095	3.92	down	Mus musculus membrane-spanning 4-domains, subfamily A, member 4C (Ms4a4c), mRNA [NM_029499]	NM_029499
Ms4a4c	0.0271	2.56	down	Mus musculus membrane-spanning 4-domains, subfamily A, member 4C (Ms4a4c), mRNA [NM_029499]	NM_029499
Ttc8	0.0026	2.45	down	Mus musculus tetratricopeptide repeat domain 8 (Ttc8), transcript variant 1, mRNA [NM_029553]	NM_029553
Mfap4	0.0011	1.60	down	Mus musculus microfibrillar-associated protein 4 (Mfap4), mRNA [NM_029568]	NM_029568

Ppfia3	0.0347	2.09	down	Mus musculus protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3 (Ppfia3), mRNA [NM_029741]	NM_029741
Adamtsl1	0.0121	1.72	down	Mus musculus ADAMTS-like 1 (Adamtsl1), mRNA [NM_029967]	NM_029967
Batf3	0.0276	1.67	down	Mus musculus basic leucine zipper transcription factor, ATF-like 3 (Batf3), mRNA [NM_030060]	NM_030060
Fam55b	0.0013	2.96	down	Mus musculus family with sequence similarity 55, member B (Fam55b), mRNA [NM_030069]	NM_030069
Rnase6	0.0097	2.41	down	Mus musculus ribonuclease, RNase A family, 6 (Rnase6), mRNA [NM_030098]	NM_030098
Mctp1	0.0460	2.17	down	Mus musculus multiple C2 domains, transmembrane 1 (Mctp1), mRNA [NM_030174]	NM_030174
Rab27b	0.0308	1.89	down	Mus musculus RAB27b, member RAS oncogene family (Rab27b), transcript variant 1, mRNA [NM_030554]	NM_030554
Tmprss5	0.0313	3.19	down	Mus musculus transmembrane protease, serine 5 (spinesin) (Tmprss5), mRNA [NM_030709]	NM_030709
Cxcr6	0.0310	2.53	down	Mus musculus chemokine (C-X-C motif) receptor 6 (Cxcr6), mRNA [NM_030712]	NM_030712
Id4	0.0359	2.18	down	Mus musculus inhibitor of DNA binding 4 (Id4), mRNA [NM_031166]	NM_031166
Gimap3	0.0297	2.45	down	Mus musculus GTPase, IMAP family member 3 (Gimap3), nuclear gene encoding mitochondrial protein, mRNA [NM_031247]	NM_031247
Syt11	0.0220	2.53	down	Mus musculus synaptotagmin-like 1 (Syt11), mRNA [NM_031393]	NM_031393
Syt11	0.0123	1.79	down	Mus musculus synaptotagmin-like 1 (Syt11), mRNA [NM_031393]	NM_031393
Crispld1	0.0382	5.15	down	Mus musculus cysteine-rich secretory protein LCCL domain containing 1 (Crispld1), mRNA [NM_031402]	NM_031402

Actl6b	0.0475	1.81	down	Mus musculus actin-like 6B (Actl6b), mRNA [NM_031404]	NM_031404
Cenpq	0.0321	1.54	down	Mus musculus centromere protein Q (Cenpq), mRNA [NM_031863]	NM_031863
Sucnr1	0.0143	2.22	down	Mus musculus succinate receptor 1 (Sucnr1), mRNA [NM_032400]	NM_032400
Dock2	0.0336	1.87	down	Mus musculus dedicator of cyto-kinesis 2 (Dock2), mRNA [NM_033374]	NM_033374
Pcdhga1	0.0164	1.52	down	Mus musculus protocadherin gamma subfamily A, 1 (Pcdhga1), mRNA [NM_033584]	NM_033584
Csprs	0.0455	2.43	down	Mus musculus component of Sp100-rs (Csprs), mRNA [NM_033616]	NM_033616
Csprs	0.0416	1.72	down	Mus musculus component of Sp100-rs (Csprs), mRNA [NM_033616]	NM_033616
Pard3	0.0059	3.49	down	Mus musculus par-3 (partitioning defective 3) homolog (C. elegans) (Pard3), transcript variant 3, mRNA [NM_033620]	NM_033620
Ear11	0.0401	5.30	down	Mus musculus eosinophil-associated, ribonuclease A family, member 11 (Ear11), mRNA [NM_053113]	NM_053113
Trim16	0.0355	2.53	down	Mus musculus tripartite motif-containing 16 (Trim16), mRNA [NM_053169]	NM_053169
Trim16	0.0278	3.14	down	Mus musculus tripartite motif-containing 16 (Trim16), mRNA [NM_053169]	NM_053169
Kifc1	0.0478	1.65	down	Mus musculus kinesin family member C1 (Kifc1), mRNA [NM_053173]	NM_053173
Col4a6	0.0008	24.98	down	Mus musculus collagen, type IV, alpha 6 (Col4a6), mRNA [NM_053185]	NM_053185
S1pr5	0.0467	1.65	down	Mus musculus sphingosine-1-phosphate receptor 5 (S1pr5), mRNA [NM_053190]	NM_053190
Egln2	0.0130	1.81	down	Mus musculus EGL nine homolog 2 (C. elegans) (Egln2), mRNA [NM_053208]	NM_053208
Myo1f	0.0383	1.78	down	Mus musculus myosin IF (Myo1f), mRNA [NM_053214]	NM_053214

Rpl31	0.0334	1.92	down	Mus musculus ribosomal protein L31 (Rpl31), mRNA [NM_053257]	NM_053257
Osr2	0.0464	2.02	down	Mus musculus odd-skipped related 2 (Drosophila) (Osr2), mRNA [NM_054049]	NM_054049
Slc13a3	0.0285	1.76	down	Mus musculus solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3 (Slc13a3), mRNA [NM_054055]	NM_054055
Alpk3	0.0068	5.11	down	Mus musculus alpha-kinase 3 (Alpk3), mRNA [NM_054085]	NM_054085
Colec12	0.0340	2.73	down	Mus musculus collectin sub-family member 12 (Colec12), mRNA [NM_130449]	NM_130449
Cd209c	0.0296	1.58	down	Mus musculus CD209c antigen (Cd209c), mRNA [NM_130903]	NM_130903
Rogdi	0.0127	1.57	down	Mus musculus rogdi homolog (Drosophila) (Rogdi), mRNA [NM_133185]	NM_133185
Scml2	0.0136	1.66	down	Mus musculus sex comb on midleg-like 2 (Drosophila) (Scml2), mRNA [NM_133194]	NM_133194
Zfp287	0.0013	1.59	down	Mus musculus zinc finger protein 287 (Zfp287), mRNA [NM_133208]	NM_133208
Bco2	0.0020	3.53	down	Mus musculus beta-carotene oxygenase 2 (Bco2), mRNA [NM_133217]	NM_133217
Cd34	0.0088	1.62	down	Mus musculus CD34 antigen (Cd34), transcript variant 2, mRNA [NM_133654]	NM_133654
Olfml3	0.0445	2.13	down	Mus musculus olfactomedin-like 3 (Olfml3), mRNA [NM_133859]	NM_133859
Spon2	0.0106	1.76	down	Mus musculus spondin 2, extracellular matrix protein (Spon2), mRNA [NM_133903]	NM_133903
Il13ra1	0.0123	1.58	down	Mus musculus interleukin 13 receptor, alpha 1 (Il13ra1), mRNA [NM_133990]	NM_133990
Gstt3	0.0381	1.81	down	Mus musculus glutathione S-transferase, theta 3 (Gstt3), mRNA [NM_133994]	NM_133994
4930427A07Rik	0.0098	10.80	down	Mus musculus RIKEN cDNA 4930427A07 gene (4930427A07Rik), mRNA [NM_134041]	NM_134041

Epdr1	0.0040	2.18	down	Mus musculus ependymin related protein 1 (zebrafish) (Epdr1), mRNA [NM_134065]	NM_134065
Sft2d1	0.0203	2.18	down	Mus musculus SFT2 domain containing 1 (Sft2d1), mRNA [NM_134114]	NM_134114
AF251705	0.0178	1.66	down	Mus musculus cDNA sequence AF251705 (AF251705), mRNA [NM_134158]	NM_134158
Abcg4	0.0381	4.22	down	Mus musculus ATP-binding cassette, sub-family G (WHITE), member 4 (Abcg4), mRNA [NM_138955]	NM_138955
Abcg4	0.0454	3.44	down	Mus musculus ATP-binding cassette, sub-family G (WHITE), member 4 (Abcg4), mRNA [NM_138955]	NM_138955
Slc6a13	0.0001	3.02	down	Mus musculus solute carrier family 6 (neurotransmitter transporter, GABA), member 13 (Slc6a13), mRNA [NM_144512]	NM_144512
Stxbp6	0.0336	2.01	down	Mus musculus syntaxin binding protein 6 (amisyn) (Stxbp6), mRNA [NM_144552]	NM_144552
Lgi4	0.0266	1.56	down	Mus musculus leucine-rich repeat LGI family, member 4 (Lgi4), mRNA [NM_144556]	NM_144556
Vash2	0.0026	2.10	down	Mus musculus vasohibin 2 (Vash2), transcript variant 1, mRNA [NM_144879]	NM_144879
Adamtsl4	0.0090	1.70	down	Mus musculus ADAMTS-like 4 (Adamtsl4), mRNA [NM_144899]	NM_144899
Fcrla	0.0186	6.10	down	Mus musculus Fc receptor-like A (Fcrla), transcript variant 2, mRNA [NM_145141]	NM_145141
Chst10	0.0376	1.88	down	Mus musculus carbohydrate sulfotransferase 10 (Chst10), mRNA [NM_145142]	NM_145142
Rasgrp4	0.0144	1.77	down	Mus musculus RAS guanyl releasing protein 4 (Rasgrp4), transcript variant 2, mRNA [NM_145149]	NM_145149
Oas1a	0.0482	1.67	down	Mus musculus 2'-5' oligoadenylate synthetase 1A (Oas1a), mRNA [NM_145211]	NM_145211
Duoxa1	0.0484	2.36	down	Mus musculus dual oxidase maturation factor 1 (Duoxa1), mRNA [NM_145395]	NM_145395

Zfp758	0.0089	2.21	down	Mus musculus zinc finger protein 758 (Zfp758), mRNA [NM_145484]	NM_145484
2310001H12Rik	0.0042	1.53	down	Mus musculus RIKEN cDNA 2310001H12 gene (2310001H12Rik), mRNA [NM_145563]	NM_145563
Siglec5	0.0467	5.99	down	Mus musculus sialic acid binding Ig-like lectin 5 (Siglec5), mRNA [NM_145581]	NM_145581
Gatad2a	0.0225	2.85	down	Mus musculus GATA zinc finger domain containing 2A (Gatad2a), transcript variant 1, mRNA [NM_145596]	NM_145596
Ndr4	0.0278	2.84	down	Mus musculus N-myc downstream regulated gene 4 (Ndr4), mRNA [NM_145602]	NM_145602
Zfp709	0.0211	1.85	down	Mus musculus zinc finger protein 709 (Zfp709), mRNA [NM_145624]	NM_145624
Il17f	0.0184	1.52	down	Mus musculus interleukin 17F (Il17f), mRNA [NM_145856]	NM_145856
Nod2	0.0261	1.50	down	Mus musculus nucleotide-binding oligomerization domain containing 2 (Nod2), mRNA [NM_145857]	NM_145857
Grhl1	0.0020	3.05	down	Mus musculus grainyhead-like 1 (Drosophila) (Grhl1), transcript variant 2, mRNA [NM_145890]	NM_145890
Fanci	0.0074	1.72	down	Mus musculus Fanconi anemia, complementation group I (Fanci), mRNA [NM_145946]	NM_145946
Tagap	0.0316	1.57	down	Mus musculus T-cell activation Rho GTPase-activating protein (Tagap), mRNA [NM_145968]	NM_145968
Arhgap9	0.0112	1.76	down	Mus musculus Rho GTPase activating protein 9 (Arhgap9), mRNA [NM_146011]	NM_146011
Efemp1	0.0069	2.00	down	Mus musculus epidermal growth factor-containing fibulin-like extracellular matrix protein 1 (Efemp1), mRNA [NM_146015]	NM_146015
Eml6	0.0284	1.70	down	Mus musculus echinoderm microtubule associated protein like 6 (Eml6), mRNA [NM_146016]	NM_146016
3830406C13Rik	0.0227	1.57	down	Mus musculus RIKEN cDNA 3830406C13 gene (3830406C13Rik), transcript variant 1, mRNA [NM_146051]	NM_146051

Atf7	0.0364	1.83	down	Mus musculus activating transcription factor 7 (Atf7), mRNA [NM_146065]	NM_146065
Slc16a4	0.0121	2.19	down	Mus musculus solute carrier family 16 (monocarboxylic acid transporters), member 4 (Slc16a4), mRNA [NM_146136]	NM_146136
B3gnt8	0.0215	1.98	down	Mus musculus UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8 (B3gnt8), transcript variant 1, mRNA [NM_146184]	NM_146184
Plekha4	0.0115	1.68	down	Mus musculus pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4 (Plekha4), mRNA [NM_148927]	NM_148927
Ehd2	0.0188	1.69	down	Mus musculus EH-domain containing 2 (Ehd2), mRNA [NM_153068]	NM_153068
Lrrc25	0.0025	2.90	down	Mus musculus leucine rich repeat containing 25 (Lrrc25), mRNA [NM_153074]	NM_153074
Nupl2	0.0077	1.56	down	Mus musculus nucleoporin like 2 (Nupl2), mRNA [NM_153092]	NM_153092
Traf3ip3	0.0191	3.14	down	Mus musculus TRAF3 interacting protein 3 (Traf3ip3), mRNA [NM_153137]	NM_153137
Kctd11	0.0345	1.61	down	Mus musculus potassium channel tetramerisation domain containing 11 (Kctd11), mRNA [NM_153143]	NM_153143
Lars2	0.0223	2.38	down	Mus musculus leucyl-tRNA synthetase, mitochondrial (Lars2), nuclear gene encoding mitochondrial protein, mRNA [NM_153168]	NM_153168
Pilra	0.0135	2.25	down	Mus musculus paired immunoglobulin-like type 2 receptor alpha (Pilra), mRNA [NM_153510]	NM_153510
Pilra	0.0400	2.08	down	Mus musculus paired immunoglobulin-like type 2 receptor alpha (Pilra), mRNA [NM_153510]	NM_153510
BC028528	0.0490	1.79	down	Mus musculus cDNA sequence BC028528 (BC028528), mRNA [NM_153513]	NM_153513
Dennd1c	0.0346	1.70	down	Mus musculus DENN/MADD domain containing 1C (Dennd1c), mRNA [NM_153551]	NM_153551

Klre1	0.0233	1.65	down	Mus musculus killer cell lectin-like receptor family E member 1 (Klre1), mRNA [NM_153590]	NM_153590
Cpt1c	0.0298	1.63	down	Mus musculus carnitine palmitoyltransferase 1c (Cpt1c), mRNA [NM_153679]	NM_153679
Cpt1c	0.0392	1.75	down	Mus musculus carnitine palmitoyltransferase 1c (Cpt1c), mRNA [NM_153679]	NM_153679
Arhgap15	0.0010	1.84	down	Mus musculus Rho GTPase activating protein 15 (Arhgap15), transcript variant 1, mRNA [NM_153820]	NM_153820
Sbsn	0.0234	2.17	down	Mus musculus suprabasin (Sbsn), transcript variant 1, mRNA [NM_172205]	NM_172205
Ddx19b	0.0151	1.88	down	Mus musculus DEAD (Asp-Glu-Ala-Asp) box polypeptide 19b (Ddx19b), mRNA [NM_172284]	NM_172284
Sulf1	0.0385	2.30	down	Mus musculus sulfatase 1 (Sulf1), mRNA [NM_172294]	NM_172294
Zfp536	0.0241	2.01	down	Mus musculus zinc finger protein 536 (Zfp536), mRNA [NM_172385]	NM_172385
Celf3	0.0479	2.47	down	Mus musculus VCUGBP, Elav-like family member 3 (Celf3), mRNA [NM_172434]	NM_172434
Tmc7	0.0034	2.52	down	Mus musculus transmembrane channel-like gene family 7 (Tmc7), mRNA [NM_172476]	NM_172476
A730008H23Rik	0.0010	4.62	down	Mus musculus RIKEN cDNA A730008H23 gene (A730008H23Rik), mRNA [NM_172505]	NM_172505
Gnptg	0.0065	2.58	down	Mus musculus N-acetylglucosamine-1-phosphotransferase, gamma subunit (Gnptg), mRNA [NM_172529]	NM_172529
Txndc16	0.0277	1.82	down	Mus musculus thioredoxin domain containing 16 (Txndc16), mRNA [NM_172597]	NM_172597
Slc2a6	0.0316	3.08	down	Mus musculus solute carrier family 2 (facilitated glucose transporter), member 6 (Slc2a6), transcript variant 1, mRNA [NM_172659]	NM_172659

Slc25a24	0.0012	1.66	down	Mus musculus solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 24 (Slc25a24), nuclear gene encoding mitochondrial protein, mRNA [NM_172685]	NM_172685
Serinc2	0.0488	4.24	down	Mus musculus serine incorporator 2 (Serinc2), mRNA [NM_172702]	NM_172702
Ces5	0.0246	2.46	down	Mus musculus carboxylesterase 5 (Ces5), transcript variant 1, mRNA [NM_172759]	NM_172759
Zc3h12d	0.0345	8.18	down	Mus musculus zinc finger CCCH type containing 12D (Zc3h12d), mRNA [NM_172785]	NM_172785
Slc13a4	0.0432	1.58	down	Mus musculus solute carrier family 13 (sodium/sulfate symporters), member 4 (Slc13a4), mRNA [NM_172892]	NM_172892
Hydin	0.0107	1.76	down	Mus musculus hydrocephalus inducing (Hydin), mRNA [NM_172916]	NM_172916
Fam55d	0.0023	12.12	down	Mus musculus family with sequence similarity 55, member D (Fam55d), mRNA [NM_172921]	NM_172921
Sntg2	0.0059	2.03	down	Mus musculus syntrophin, gamma 2 (Sntg2), mRNA [NM_172951]	NM_172951
Mtap1s	0.0120	1.89	down	Mus musculus microtubule-associated protein 1S (Mtap1s), mRNA [NM_173013]	NM_173013
Cilp	0.0219	2.96	down	Mus musculus cartilage intermediate layer protein, nucleotide pyrophosphohydrolase (Cilp), mRNA [NM_173385]	NM_173385
Xkr6	0.0372	1.93	down	Mus musculus X Kell blood group precursor related family member 6 homolog (Xkr6), mRNA [NM_173393]	NM_173393
Fbxo44	0.0047	3.47	down	Mus musculus F-box protein 44 (Fbxo44), transcript variant 1, mRNA [NM_173401]	NM_173401
Rab6b	0.0381	6.14	down	Mus musculus RAB6B, member RAS oncogene family (Rab6b), mRNA [NM_173781]	NM_173781
Apol9a	0.0359	1.76	down	Mus musculus apolipoprotein L 9a (Apol9a), transcript variant 1, mRNA [NM_173786]	NM_173786

Gm5077	0.0120	1.77	down	Mus musculus predicted gene 5077 (Gm5077), mRNA [NM_173864]	NM_173864
Pyhin1	0.0104	2.08	down	Mus musculus pyrin and HIN domain family, member 1 (Pyhin1), mRNA [NM_175026]	NM_175026
Pyhin1	0.0299	2.36	down	Mus musculus pyrin and HIN domain family, member 1 (Pyhin1), mRNA [NM_175026]	NM_175026
Atg4c	0.0160	3.12	down	Mus musculus autophagy-related 4C (yeast) (Atg4c), transcript variant 1, mRNA [NM_175029]	NM_175029
2300002M23Rik	0.0001	2.33	down	Mus musculus RIKEN cDNA 2300002M23 gene (2300002M23Rik), mRNA [NM_175148]	NM_175148
Dock10	0.0250	1.88	down	Mus musculus dedicator of cytokinesis 10 (Dock10), mRNA [NM_175291]	NM_175291
Slco2b1	0.0240	2.10	down	Mus musculus solute carrier organic anion transporter family, member 2b1 (Slco2b1), mRNA [NM_175316]	NM_175316
Sp110	0.0149	1.56	down	Mus musculus Sp110 nuclear body protein (Sp110), mRNA [NM_175397]	NM_175397
Adamts2	0.0491	1.87	down	Mus musculus a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 2 (Adamts2), mRNA [NM_175643]	NM_175643
Dclre1c	0.0466	2.49	down	Mus musculus DNA cross-link repair 1C, PSO2 homolog (S. cerevisiae) (Dclre1c), transcript variant 2, mRNA [NM_175683]	NM_175683
Ubash3b	0.0004	1.70	down	Mus musculus ubiquitin associated and SH3 domain containing, B (Ubash3b), mRNA [NM_176860]	NM_176860
Ppm1h	0.0214	1.60	down	Mus musculus protein phosphatase 1H (PP2C domain containing) (Ppm1h), transcript variant 2, mRNA [NM_176919]	NM_176919
6030419C18Rik	0.0092	2.84	down	Mus musculus RIKEN cDNA 6030419C18 gene (6030419C18Rik), mRNA [NM_176921]	NM_176921
6330416L07Rik	0.0455	3.94	down	Mus musculus RIKEN cDNA 6330416L07 gene (6330416L07Rik), mRNA [NM_176962]	NM_176962

Rab9b	0.0269	3.91	down	Mus musculus RAB9B, member RAS oncogene family (Rab9b), mRNA [NM_176971]	NM_176971
Fbxl13	0.0477	5.35	down	Mus musculus F-box and leucine-rich repeat protein 13 (Fbxl13), mRNA [NM_177076]	NM_177076
B430306N03Rik	0.0022	2.32	down	Mus musculus RIKEN cDNA B430306N03 gene (B430306N03Rik), mRNA [NM_177083]	NM_177083
Tmem91	0.0068	2.38	down	Mus musculus transmembrane protein 91 (Tmem91), mRNA [NM_177102]	NM_177102
Vps13b	0.0015	1.75	down	Mus musculus vacuolar protein sorting 13B (yeast) (Vps13b), mRNA [NM_177151]	NM_177151
L3mbtl4	0.0217	1.92	down	Mus musculus l(3)mbt-like 4 (Drosophila) (L3mbtl4), mRNA [NM_177278]	NM_177278
Rint1	0.0105	2.19	down	Mus musculus RAD50 interactor 1 (Rint1), mRNA [NM_177323]	NM_177323
Camk1d	0.0382	1.73	down	Mus musculus calcium/calmodulin-dependent protein kinase ID (Camk1d), mRNA [NM_177343]	NM_177343
Rimkla	0.0107	2.65	down	Mus musculus ribosomal modification protein rimK-like family member A (Rimkla), mRNA [NM_177572]	NM_177572
Skint3	0.0069	7.44	down	Mus musculus selection and upkeep of intraepithelial T cells 3 (Skint3), transcript variant 2, mRNA [NM_177578]	NM_177578
Aph1b	0.0255	1.57	down	Mus musculus anterior pharynx defective 1b homolog (C. elegans) (Aph1b), mRNA [NM_177583]	NM_177583
Ldoc1l	0.0389	1.60	down	Mus musculus leucine zipper, down-regulated in cancer 1-like (Ldoc1l), mRNA [NM_177630]	NM_177630
Zfp236	0.0230	1.74	down	Mus musculus zinc finger protein 236 (Zfp236), mRNA [NM_177832]	NM_177832
Pm20d1	0.0106	1.52	down	Mus musculus peptidase M20 domain containing 1 (Pm20d1), mRNA [NM_178079]	NM_178079
Hist1h2ak	0.0331	1.93	down	Mus musculus histone cluster 1, H2ak (Hist1h2ak), mRNA [NM_178183]	NM_178183

Hist1h2an	0.0404	2.04	down	Mus musculus histone cluster 1, H2an (Hist1h2an), mRNA [NM_178184]	NM_178184
Prss34	0.0138	2.80	down	Mus musculus protease, serine, 34 (Prss34), mRNA [NM_178372]	NM_178372
Jakmip1	0.0098	7.39	down	Mus musculus janus kinase and microtubule interacting protein 1 (Jakmip1), mRNA [NM_178394]	NM_178394
Zc3h6	0.0083	1.59	down	Mus musculus zinc finger CCCH type containing 6 (Zc3h6), mRNA [NM_178404]	NM_178404
Zfp867	0.0489	2.11	down	Mus musculus zinc finger protein 867 (Zfp867), mRNA [NM_178417]	NM_178417
Myo1g	0.0059	2.24	down	Mus musculus myosin IG (Myo1g), mRNA [NM_178440]	NM_178440
Unc45b	0.0071	2.10	down	Mus musculus unc-45 homolog B (C. elegans) (Unc45b), mRNA [NM_178680]	NM_178680
E130203B14Rik	0.0092	1.99	down	Mus musculus RIKEN cDNA E130203B14 gene (E130203B14Rik), mRNA [NM_178791]	NM_178791
A530064D06Rik	0.0150	4.86	down	Mus musculus RIKEN cDNA A530064D06 gene (A530064D06Rik), transcript variant 1, mRNA [NM_178796]	NM_178796
Nhedc2	0.0027	13.78	down	Mus musculus Na ⁺ /H ⁺ exchanger domain containing 2 (Nhedc2), nuclear gene encoding mitochondrial protein, mRNA [NM_178877]	NM_178877
AI182371	0.0332	2.42	down	Mus musculus expressed sequence AI182371 (AI182371), mRNA [NM_178885]	NM_178885
Abtb2	0.0263	1.85	down	Mus musculus ankyrin repeat and BTB (POZ) domain containing 2 (Abtb2), mRNA [NM_178890]	NM_178890
AI467606	0.0172	1.55	down	Mus musculus expressed sequence AI467606 (AI467606), mRNA [NM_178901]	NM_178901
Fam26e	0.0320	1.82	down	Mus musculus family with sequence similarity 26, member E (Fam26e), mRNA [NM_178908]	NM_178908
Col14a1	0.0003	2.13	down	Mus musculus collagen, type XIV, alpha 1 (Col14a1), mRNA [NM_181277]	NM_181277

Pxdn	0.0222	2.20	down	Mus musculus peroxidasin homolog (Drosophila) (Pxdn), mRNA [NM_181395]	NM_181395
Me3	0.0252	1.54	down	Mus musculus malic enzyme 3, NADP(+)-dependent, mitochondrial (Me3), nuclear gene encoding mitochondrial protein, mRNA [NM_181407]	NM_181407
Slfn10-ps	0.0053	1.52	down	Mus musculus schlafen 10, pseudogene (Slfn10-ps), mRNA [NM_181542]	NM_181542
Slfn8	0.0054	24.08	down	Mus musculus schlafen 8 (Slfn8), transcript variant 1, mRNA [NM_181545]	NM_181545
Trim46	0.0107	1.81	down	Mus musculus tripartite motif-containing 46 (Trim46), transcript variant 2, mRNA [NM_183037]	NM_183037
Cyp2ab1	0.0108	2.29	down	Mus musculus cytochrome P450, family 2, subfamily ab, polypeptide 1 (Cyp2ab1), mRNA [NM_183158]	NM_183158
AI987944	0.0191	3.52	down	Mus musculus expressed sequence AI987944 (AI987944), mRNA [NM_183167]	NM_183167
5830405N20Rik	0.0485	1.89	down	Mus musculus RIKEN cDNA 5830405N20 gene (5830405N20Rik), mRNA [NM_183264]	NM_183264
Ranbp3l	0.0005	3.97	down	Mus musculus RAN binding protein 3-like (Ranbp3l), mRNA [NM_198024]	NM_198024
Iqcc	0.0391	1.68	down	Mus musculus IQ motif containing C (Iqcc), mRNA [NM_198026]	NM_198026
Bst2	0.0023	1.66	down	Mus musculus bone marrow stromal cell antigen 2 (Bst2), mRNA [NM_198095]	NM_198095
Galnt9	0.0090	3.41	down	Mus musculus UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 9 (Galnt9), transcript variant A, mRNA [NM_198306]	NM_198306
Tspyl3	0.0260	1.67	down	Mus musculus TSPY-like 3 (Tspyl3), mRNA [NM_198617]	NM_198617
2810408P10Rik	0.0106	6.54	down	Mus musculus RIKEN cDNA 2810408P10 gene (2810408P10Rik), mRNA [NM_198619]	NM_198619
Hjurp	0.0023	3.76	down	Mus musculus Holliday junction recognition protein (Hjurp), mRNA [NM_198652]	NM_198652

Hjurp	0.0449	7.05	down	Mus musculus Holliday junction recognition protein (Hjurp), mRNA [NM_198652]	NM_198652
Hn1l	0.0219	2.12	down	Mus musculus hematological and neurological expressed 1-like (Hn1l), mRNA [NM_198937]	NM_198937
Flrt1	0.0489	1.59	down	Mus musculus fibronectin leucine rich transmembrane protein 1 (Flrt1), mRNA [NM_201411]	NM_201411
Flrt2	0.0038	2.12	down	Mus musculus fibronectin leucine rich transmembrane protein 2 (Flrt2), mRNA [NM_201518]	NM_201518
Sly	0.0375	3.23	down	Mus musculus Sycp3 like Y-linked (Sly), mRNA [NM_201530]	NM_201530
Sly	0.0220	2.35	down	Mus musculus Sycp3 like Y-linked (Sly), mRNA [NM_201530]	NM_201530
Tas2r109	0.0430	2.60	down	Mus musculus taste receptor, type 2, member 109 (Tas2r109), mRNA [NM_207017]	NM_207017
H2-Ab1	0.0238	1.63	down	Mus musculus histocompatibility 2, class II antigen A, beta 1 (H2-Ab1), mRNA [NM_207105]	NM_207105
Cebpe	0.0410	6.28	down	Mus musculus CCAAT/enhancer binding protein (C/EBP), epsilon (Cebpe), mRNA [NM_207131]	NM_207131
Olfr1036	0.0342	1.95	down	Mus musculus olfactory receptor 1036 (Olfr1036), mRNA [NM_207142]	NM_207142
Plac9	0.0101	1.96	down	Mus musculus placenta specific 9 (Plac9), mRNA [NM_207229]	NM_207229
A530032D15Rik	0.0378	1.62	down	Mus musculus RIKEN cDNA A530032D15Rik gene (A530032D15Rik), mRNA [NM_213615]	NM_213615
H19	0.0207	4.92	down	Mus musculus H19 fetal liver mRNA (H19), non-coding RNA [NR_001592]	NR_001592
Dnm3os	0.0124	2.61	down	Mus musculus dynamin 3, opposite strand (Dnm3os), non-coding RNA [NR_002870]	NR_002870
Snhg3	0.0342	2.48	down	Mus musculus small nucleolar RNA host gene (non-protein coding) 3 (Snhg3), non-coding RNA [NR_003270]	NR_003270
6330549D23Rik	0.0108	3.86	down	Mus musculus RIKEN cDNA 6330549D23 gene (6330549D23Rik), non-coding RNA [NR_003619]	NR_003619

1700030C10Rik	0.0180	4.44	down	Mus musculus RIKEN cDNA 1700030C10 gene (1700030C10Rik), non-coding RNA [NR_015521]	NR_015521
Snhg6	0.0302	1.62	down	Mus musculus small nucleolar RNA host gene (non-protein coding) 6 (Snhg6), non-coding RNA [NR_024067]	NR_024067
Gm11346	0.0118	2.55	down	Mus musculus predicted gene 11346 (Gm11346), non-coding RNA [NR_024599]	NR_024599
E330013P04Rik	0.0379	1.68	down	Mus musculus RIKEN cDNA E330013P04 gene (E330013P04Rik), non-coding RNA [NR_026942]	NR_026942
Meg3	0.0269	1.85	down	Mus musculus maternally expressed 3 (Meg3), transcript variant 3, non-coding RNA [NR_027652]	NR_027652
Mtag2	0.0008	3.01	down	Mus musculus metastasis associated gene 2 (Mtag2), non-coding RNA [NR_027802]	NR_027802
Nlrp1c-ps	0.0126	1.68	down	Mus musculus NLR family, pyrin domain containing 1C, pseudogene (Nlrp1c-ps), non-coding RNA [NR_027858]	NR_027858
Ncrna00086	0.0031	1.71	down	Mus musculus non-protein coding RNA 86 (Ncrna00086), non-coding RNA [NR_028086]	NR_028086
Gm6524	0.0311	1.95	down	Mus musculus predicted gene 6524 (Gm6524), non-coding RNA [NR_028307]	NR_028307
LOC100303645	0.0001	2.81	down	Mus musculus hypothetical LOC100303645 (LOC100303645), non-coding RNA [NR_028425]	NR_028425
Snord123	0.0041	2.57	down	Mus musculus small nucleolar RNA, C/D box 123 (Snord123), small nucleolar RNA [NR_028575]	NR_028575
A330050B17Rik	0.0093	1.54	down	Mus musculus RIKEN cDNA A330050B17 gene (A330050B17Rik), non-coding RNA [NR_029456]	NR_029456
4933409K07Rik	0.0047	11.29	down	Mus musculus RIKEN cDNA 4933409K07 gene (4933409K07Rik), non-coding RNA [NR_033123]	NR_033123
Gm3893	0.0074	3.02	down	Mus musculus predicted gene 3893 (Gm3893), non-coding RNA [NR_033506]	NR_033506
Gm3893	0.0006	3.76	down	Mus musculus predicted gene 3893 (Gm3893), non-coding RNA [NR_033506]	NR_033506

AY512915	0.0223	1.97	down	Mus musculus cDNA sequence AY512915 (AY512915), non-coding RNA [NR_033559]	NR_033559
Gm15645	0.0078	1.81	down	Mus musculus predicted gene 15645 (Gm15645), non-coding RNA [NR_033578]	NR_033578
	0.0317	2.27	down	T-cell receptor beta, variable 13 Gene [Source:MGI Symbol;Acc:MGI:98587] [ENSMUST00000103299]	U07661
	0.0274	23.05	down	Mus musculus immunoglobulin kappa light chain variable region mRNA, clone MRL1-56, partial cds. [U19317]	U19317
	0.0478	17.16	down		X06519
	0.0082	51.47	down	Mouse mRNA for the V(kappa) region from an anti-phosphatidyl choline producing hybridoma (NC19-F5). [X53355]	X53355
	0.0012	21.85	down	M.musculus BALB/c IgG light chain variable region mRNA. [X79554]	X79554
B230311B06Rik	0.0471	1.74	down	PREDICTED: Mus musculus RIKEN cDNA B230311B06 gene (B230311B06Rik), mRNA [XM_001001884]	XM_001001884
	0.0345	3.41	down	Protein KIAA1045 [Source:UniProtKB/Swiss-Prot;Acc:Q80TL4] [ENSMUST00000107976]	XM_001472112
0610042G04Rik	0.0071	5.48	down	PREDICTED: Mus musculus RIKEN cDNA 0610042G04 gene (0610042G04Rik), mRNA [XM_001472222]	XM_001472222
LOC100044439	0.0285	8.15	down	PREDICTED: Mus musculus similar to cytochrome P450 CYP4F18 (LOC100044439), mRNA [XM_001472253]	XM_001472253
	0.0149	3.23	down	RIKEN cDNA 6720489N17 gene Gene [Source:MGI Symbol;Acc:MGI:2443901] [ENSMUST00000091563]	XM_001472312
	0.0424	2.51	down	placenta specific 9 Gene [Source:MGI Symbol;Acc:MGI:2663998] [ENSMUST00000100820]	XM_001472394

Gm2097	0.0327	3.73	down	PREDICTED: Mus musculus hypothetical protein LOC100039201 (LOC100039201), mRNA [XM_001472439]	XM_001472439
LOC669153	0.0164	1.63	down	PREDICTED: Mus musculus hypothetical LOC669153 (LOC669153), mRNA [XM_001472555]	XM_001472555
LOC100044494	0.0302	1.55	down	PREDICTED: Mus musculus similar to ribosomal protein (LOC100044494), mRNA [XM_001472583]	XM_001472583
Gm9307	0.0084	2.58	down	PREDICTED: Mus musculus similar to Ac2-210 (LOC668699), mRNA [XM_001472674]	XM_001472674
Gm9307	0.0016	2.10	down	PREDICTED: Mus musculus similar to Ac2-210 (LOC668699), mRNA [XM_001472674]	XM_001472674
LOC100044727	0.0164	3.55	down	PREDICTED: Mus musculus hypothetical protein LOC100044727 (LOC100044727), mRNA [XM_001472813]	XM_001472813
	0.0146	2.25	down	PREDICTED: Mus musculus hypothetical protein LOC100044678 (LOC100044678), mRNA [XM_001472893]	XM_001472893
	0.0119	1.83	down	thymocyte selection-associated high mobility group box Gene [Source:MGI (curated);Acc:MGI:2181659] [ENSMUST00000039987]	XM_001473004
Foxn3	0.0186	8.81	down	PREDICTED: Mus musculus hypothetical protein LOC100039892 (LOC100039892), mRNA [XM_001473733]	XM_001473733
Gm2490	0.0114	4.57	down	PREDICTED: Mus musculus similar to 4933409K07Rik protein (LOC100039909), mRNA [XM_001473759]	XM_001473759
Gm2496	0.0004	2.44	down	PREDICTED: Mus musculus hypothetical protein LOC100039923 (LOC100039923), mRNA [XM_001473960]	XM_001473960

LOC100045276	0.0354	2.64	down	PREDICTED: Mus musculus hypothetical protein LOC100045276 (LOC100045276), mRNA [XM_001473983]	XM_001473983
Gm11223	0.0122	6.07	down	PREDICTED: Mus musculus similar to Pr22, transcript variant 1 (LOC100039888), mRNA [XM_001474074]	XM_001474074
	0.0123	1.79	down	predicted gene 2545 Gene [Source:MGI Symbol;Acc:MGI:3780713] [ENSMUST00000104980]	XM_001474090
LOC100040235	0.0424	2.57	down	PREDICTED: Mus musculus similar to spermiogenesis specific transcript on the Y 1 (LOC100040235), mRNA [XM_001474135]	XM_001474135
LOC100045268	0.0421	2.45	down	PREDICTED: Mus musculus similar to precursor (AA - 28 to 232) (LOC100045268), mRNA [XM_001474162]	XM_001474162
LOC100045508	0.0252	2.41	down	PREDICTED: Mus musculus hypothetical protein LOC100045508 (LOC100045508), mRNA [XM_001474311]	XM_001474311
LOC100045501	0.0086	2.20	down	PREDICTED: Mus musculus hypothetical protein LOC100045501 (LOC100045501), mRNA [XM_001474411]	XM_001474411
LOC100045546	0.0334	2.14	down	PREDICTED: Mus musculus similar to Id4 (LOC100045546), mRNA [XM_001474498]	XM_001474498
1810062G17Rik	0.0353	2.07	down	RIKEN cDNA 1810062G17 gene Gene [Source:MGI Symbol;Acc:MGI:1919532] [ENSMUST00000029268]	XM_001475130
LOC100045922	0.0230	1.52	down	PREDICTED: Mus musculus similar to vacuolar protein sorting 52 (LOC100045922), mRNA [XM_001475183]	XM_001475183
Gm3065	0.0045	3.00	down	PREDICTED: Mus musculus hypothetical protein LOC100040962 (LOC100040962), mRNA [XM_001475302]	XM_001475302

	0.0248	1.70	down	PREDICTED: Mus musculus similar to RIKEN cDNA 5830484A20 gene (LOC100041081), mRNA [XM_001475751]	XM_001475751
Gm3115	0.0223	2.20	down	PREDICTED: Mus musculus similar to Predicted gene, EG545013, transcript variant 3 (LOC100041054), mRNA [XM_001476009]	XM_001476009
LOC100046350	0.0243	21.73	down	PREDICTED: Mus musculus similar to immunoglobulin kappa chain (LOC100046350), mRNA [XM_001476057]	XM_001476057
Gm4619	0.0365	2.41	down	PREDICTED: Mus musculus hypothetical protein LOC100046466 (LOC100046466), mRNA [XM_001476246]	XM_001476246
	0.0088	2.11	down	predicted gene, ENSMUSG00000068790 (ENSMUSG00000068790), mRNA [Source:RefSeq DNA;Acc:NM_001029930] [ENSMUST00000112728]	XM_001476394
3300005D01Rik	0.0270	1.55	down	PREDICTED: Mus musculus RIKEN cDNA 3300005D01 gene (3300005D01Rik), mRNA [XM_001476467]	XM_001476467
LOC100047316	0.0165	4.82	down	predicted gene 1502 Gene [Source:MGI Symbol;Acc:MGI:2686348] [ENSMUST00000103348]	XM_001476590
	0.0224	8.67	down	PREDICTED: Mus musculus hypothetical protein LOC100041156 (LOC100041156), mRNA [XM_001476722]	XM_001476722
Gm3380	0.0266	1.75	down	PREDICTED: Mus musculus similar to ribonuclease T2 (LOC100041510), mRNA [XM_001476937]	XM_001476937
Gm3819	0.0022	1.89	down	PREDICTED: Mus musculus hypothetical protein LOC100046872 (LOC100046872), mRNA [XM_001477163]	XM_001477163
LOC100047175	0.0159	2.45	down	PREDICTED: Mus musculus hypothetical protein LOC100047175 (LOC100047175), mRNA [XM_001477580]	XM_001477580

A530001N23Rik	0.0252	2.88	down	PREDICTED: Mus musculus RIKEN cDNA A530001N23 gene (A530001N23Rik), mRNA [XM_001477625]	XM_001477625
Gm3642	0.0286	2.68	down	PREDICTED: Mus musculus similar to Predicted gene, EG432825, transcript variant 2 (LOC100042054), mRNA [XM_001477672]	XM_001477672
Gm3586	0.0429	2.51	down	PREDICTED: Mus musculus hypothetical protein LOC100041950 (LOC100041950), mRNA [XM_001477872]	XM_001477872
	0.0254	1.98	down	neuron navigator 1 Gene [Source:MGI Symbol;Acc:MGI:2183683] [ENSMUST00000112103]	XM_001478191
Gm3648	0.0317	1.79	down	PREDICTED: Mus musculus hypothetical protein LOC100042070 (LOC100042070), mRNA [XM_001478508]	XM_001478508
	0.0452	2.58	down	PREDICTED: Mus musculus hypothetical protein LOC100047576 (LOC100047576), mRNA [XM_001478645]	XM_001478645
Gm9296	0.0047	3.78	down	PREDICTED: Mus musculus predicted gene, EG668670 (EG668670), mRNA [XM_001478977]	XM_001478977
LOC100048152	0.0187	1.62	down	PREDICTED: Mus musculus hypothetical protein LOC100048152 (LOC100048152), mRNA [XM_001479897]	XM_001479897
LOC100048332	0.0075	2.18	down	PREDICTED: Mus musculus similar to a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 5 (aggrecanase-2) (LOC100048332), mRNA [XM_001480027]	XM_001480027
Gm6936	0.0238	1.80	down	PREDICTED: Mus musculus hypothetical protein LOC628951 (LOC628951), mRNA [XM_001480183]	XM_001480183
LOC100048543	0.0254	3.29	down	PREDICTED: Mus musculus similar to glutamine repeat protein-1 (LOC100048543), mRNA [XM_001480480]	XM_001480480

Gm4494	0.0368	4.57	down	PREDICTED: Mus musculus hypothetical protein LOC100043519 (LOC100043519), mRNA [XM_001480485]	XM_001480485
1190002F15Rik	0.0027	1.71	down	PREDICTED: Mus musculus RIKEN cDNA 1190002F15 gene (1190002F15Rik), mRNA [XM_001481164]	XM_001481164
	0.0334	2.05	down	PREDICTED: Mus musculus predicted gene, EG240921 (EG240921), mRNA [XM_136331]	XM_136331
Gm4938	0.0434	1.75	down	PREDICTED: Mus musculus predicted gene, EG238836 (EG238836), mRNA [XM_138832]	XM_138832
	0.0269	1.67	down	RIKEN cDNA 4933413J09 gene Gene [Source:MGI Symbol;Acc:MGI:1918356] [ENSMUST00000022427]	XM_354798
Gm5316	0.0273	2.40	down	PREDICTED: Mus musculus predicted gene, EG384482 (EG384482), mRNA [XM_357669]	XM_357669
Gm1667	0.0100	2.42	down	PREDICTED: Mus musculus gene model 1667, (NCBI) (Gm1667), mRNA [XM_358618]	XM_358618
Gm5834	0.0125	1.97	down	PREDICTED: Mus musculus predicted gene, EG545367 (EG545367), mRNA [XM_619677]	XM_619677
Gm5858	0.0391	4.10	down	PREDICTED: Mus musculus predicted gene, EG545578, transcript variant 1 (EG545578), mRNA [XM_619973]	XM_619973
Gm6970	0.0004	2.32	down	PREDICTED: Mus musculus predicted gene, EG629389 (EG629389), mRNA [XM_894271]	XM_894271
Gm7146	0.0049	6.45	down	PREDICTED: Mus musculus predicted gene, EG634881 (EG634881), mRNA [XM_909745]	XM_909745
	0.0138	21.48	down	Ig heavy chain V region BCL1 Precursor [Source:UniProtKB/Swiss-Prot;Acc:P01759] [ENSMUST00000103538]	XM_919047
LOC674050	0.0171	3.02	down	PREDICTED: Mus musculus similar to adaptor protein Gads (LOC674050), mRNA [XM_972673]	XM_972673
Gm8013	0.0138	3.31	down	PREDICTED: Mus musculus hypothetical LOC674832 (LOC674832), mRNA [XM_977358]	XM_977358

	0.0115	2.90	down	LOC380994 protein [Source:UniProtKB/TrEMBL;Acc:Q4KL07] [ENSMUST00000115920]	XM_979799
Gm8172	0.0017	2.39	down	PREDICTED: Mus musculus predicted gene, EG666577 (EG666577), mRNA [XM_984280]	XM_984280
Gm8272	0.0114	2.63	down	PREDICTED: Mus musculus predicted gene, EG666751 (EG666751), mRNA [XM_985780]	XM_985780
Gm9000	0.0432	1.54	down	PREDICTED: Mus musculus predicted gene, EG668144 (EG668144), mRNA [XM_994545]	XM_994545
LOC630896	0.0470	2.00	down	PREDICTED: Mus musculus similar to 3- phosphoglycerate dehydrogenase (LOC630896), misc RNA [XR_030502]	XR_030502
Gm7172	0.0054	3.50	down	PREDICTED: Mus musculus similar to hCG1992406 (LOC636070), misc RNA [XR_030785]	XR_030785
Gm2367	0.0164	1.55	down	PREDICTED: Mus musculus similar to hCG1789691 (LOC100039677), misc RNA [XR_031150]	XR_031150
Ncf2-rs	0.0103	1.53	down	PREDICTED: Mus musculus similar to neutrophil cytosolic factor 2 (LOC674577), misc RNA [XR_031347]	XR_031347
EG545385	0.0006	1.81	down	PREDICTED: Mus musculus predicted gene, EG545385 (EG545385), misc RNA [XR_031493]	XR_031493
Gm6705	0.0202	2.47	down	PREDICTED: Mus musculus similar to Lysosomal- associated protein transmembrane 4B (LOC626785), misc RNA [XR_031767]	XR_031767
Gm7638	0.0405	2.17	down	PREDICTED: Mus musculus similar to MGC27348 protein (LOC665450), misc RNA [XR_031801]	XR_031801
Gm8681	0.0128	1.53	down	PREDICTED: Mus musculus similar to high mobility group protein B2 (LOC667519), misc RNA [XR_032130]	XR_032130
Gm3252	0.0141	2.65	down	PREDICTED: Mus musculus similar to 1700001E04Rik protein (LOC100041283), misc RNA [XR_032767]	XR_032767

Gm9487	0.0110	1.90	down	PREDICTED: Mus musculus similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (LOC675823), misc RNA [XR_032777]	XR_032777
Gm4864	0.0151	2.32	down	PREDICTED: Mus musculus similar to histone deacetylase (LOC230765), misc RNA [XR_032827]	XR_032827
Gm3667	0.0475	2.32	down	PREDICTED: Mus musculus similar to 1700001E04Rik protein (LOC100042100), misc RNA [XR_033371]	XR_033371
LOC638183	0.0453	1.51	down	PREDICTED: Mus musculus similar to High mobility group box 2 (LOC638183), misc RNA [XR_034120]	XR_034120
Gm9224	0.0181	1.60	down	PREDICTED: Mus musculus similar to Armadillo repeat containing, X-linked 3 (LOC668529), misc RNA [XR_034597]	XR_034597
	0.0273	1.72	down	RIKEN cDNA A530040E14 gene Gene [Source:MGI Symbol;Acc:MGI:3612703] [ENSMUST00000093501]	XR_035200
	0.0033	1.98	down	RIKEN cDNA B130024G19 gene Gene [Source:MGI Symbol;Acc:MGI:3604353] [ENSMUST00000080024]	XR_035339
	0.0176	3.23	down	RIKEN cDNA 4930522L14 gene Gene [Source:MGI Symbol;Acc:MGI:1925270] [ENSMUST00000100937]	XR_035728
	0.0289	2.00	up	lincRNA:chr8:108153471-108159346 reverse strand	
	0.0122	1.57	up	lincRNA:chr19:5795689-5802671 reverse strand	
	0.0432	2.70	up	lincRNA:chr4:15233302-15233632 reverse strand	
	0.0184	2.11	up	lincRNA:chrX:146827709-146913398 reverse strand	
	0.0366	1.55	up	lincRNA:chr10:39659425-39674200 forward strand	
	0.0347	2.04	up	lincRNA:chr12:33604247-33638654 reverse strand	
	0.0343	1.52	up	lincRNA:chr4:129497990-129515290 forward strand	
	0.0334	1.60	up	lincRNA:chr7:66562376-66579519 forward strand	
	0.0493	1.96	up	lincRNA:chr15:59059450-59070576 reverse strand	

	0.0403	1.57	up	lincRNA:chr7:99879368-99889978 reverse strand	
	0.0284	1.64	up	lincRNA:chr12:110003268-110030953 reverse strand	
	0.0059	1.68	up	lincRNA:chr15:101084597-101095097 forward strand	
	0.0438	2.76	up	lincRNA:chr14:99729955-99730583 forward strand	
	0.0360	2.04	up	lincRNA:chr7:129294998-129295498 forward strand	
	0.0321	3.13	up	lincRNA:chr5:22058025-22072475 forward strand	
	0.0466	1.73	up	lincRNA:chr10:60473030-60535340 forward strand	
	0.0054	1.88	up	lincRNA:chr6:116092274-116144199 reverse strand	
	0.0119	1.71	up	lincRNA:chr6:128393530-128394127 forward strand	
	0.0363	4.43	up	lincRNA:chr12:20240893-20435318 reverse strand	
	0.0125	3.23	up	lincRNA:chr12:74135916-74142780 reverse strand	
	0.0200	4.49	up	lincRNA:chr14:27176059-27202735 forward strand	
	0.0052	1.51	up	lincRNA:chr6:116092274-116144199 reverse strand	
	0.0458	3.00	up	lincRNA:chr8:85609155-85615170 forward strand	
	0.0144	1.58	up	lincRNA:chr5:22801058-22939737 reverse strand	
	0.0017	25.85	up	lincRNA:chr3:96074625-96086375 forward strand	
	0.0306	1.55	up	lincRNA:chr19:5795689-5802671 reverse strand	
	0.0164	5.94	up	lincRNA:chr12:74135916-74142780 reverse strand	
	0.0345	3.56	up	lincRNA:chr13:60524145-60528559 reverse strand	
	0.0325	2.20	up	lincRNA:chr10:3231337-3231802 forward strand	
	0.0247	1.85	up	lincRNA:chr10:69669025-69686275 reverse strand	
	0.0319	3.64	up	lincRNA:chr19:5834117-5835940 reverse strand	
	0.0291	1.58	up	lincRNA:chr12:82495575-82516300 reverse strand	
	0.0468	1.53	up	lincRNA:chr1:195327945-195336595 reverse strand	
	0.0482	1.55	up	lincRNA:chr11:96111499-96126224 forward strand	
	0.0214	3.11	up	lincRNA:chr5:22058025-22072475 forward strand	
	0.0065	2.53	up	lincRNA:chr7:140081171-140123058 reverse strand	
	0.0197	1.62	up	lincRNA:chrX:148819227-148844227 forward strand	
	0.0309	3.09	up	lincRNA:chr4:135896689-135918414 forward strand	
	0.0205	1.55	up		

	0.0354	1.63	up	lincRNA:chr1:44915250-44944125 forward strand	
	0.0403	1.68	up	lincRNA:chr6:86476240-86513483 forward strand	
	0.0247	1.73	up	lincRNA:chr6:47687025-47728525 forward strand	
	0.0401	3.60	up	lincRNA:chr11:87872568-87880978 reverse strand	
	0.0000	9.16	up	lincRNA:chr1:58443698-58449898 reverse strand	
	0.0308	2.68	up	lincRNA:chr1:58443698-58449898 forward strand	
	0.0194	1.79	up	lincRNA:chr11:50994911-51050704 reverse strand	
	0.0261	1.79	up	lincRNA:chr17:6830756-6832322 reverse strand	
	0.0018	3.44	up	lincRNA:chr8:85952719-85958369 reverse strand	
	0.0003	1.75	up	lincRNA:chr17:24152225-24169870 reverse strand	
	0.0260	1.62	up	lincRNA:chr15:62090565-62091770 forward strand	
	0.0378	1.57	up	lincRNA:chr6:86776350-86799450 forward strand	
	0.0151	4.84	up	lincRNA:chr5:23195569-23218551 reverse strand	
	0.0121	1.57	up	lincRNA:chr4:82156098-82196298 reverse strand	
	0.0122	1.69	up	lincRNA:chr7:99879368-99889978 reverse strand	
	0.0151	1.54	up	lincRNA:chr9:41137539-41353289 forward strand	
	0.0125	2.18	up	lincRNA:chr17:6830756-6832322 reverse strand	
	0.0026	7.35	up	lincRNA:chr1:58443698-58449898 reverse strand	
	0.0117	2.18	up	lincRNA:chr10:118385588-118439338 reverse strand	
	0.0339	1.96	up	lincRNA:chr14:19295319-19310619 reverse strand	
	0.0342	1.87	up	lincRNA:chr12:33604247-33638654 reverse strand	
	0.0455	1.57	up	lincRNA:chr3:62727150-62758225 forward strand	
	0.0056	1.54	up	lincRNA:chr4:89032648-89133273 forward strand	
	0.0220	1.64	up	lincRNA:chr15:61870759-61938796 forward strand	
	0.0416	1.86	up	lincRNA:chr4:141100989-141106639 reverse strand	
	0.0048	1.65	up	lincRNA:chr8:91569369-91594119 reverse strand	
	0.0038	1.67	up	lincRNA:chr7:6108350-6119600 reverse strand	
	0.0249	2.65	up	lincRNA:chr4:86267450-86277650 forward strand	
	0.0433	6.80	up	lincRNA:chr3:96074625-96086375 forward strand	
	0.0457	3.32	up	lincRNA:chr14:65206167-65206949 forward strand	
	0.0071	12.39	up	lincRNA:chr5:23195569-23218551 reverse strand	
	0.0472	2.39	up	lincRNA:chr19:12079745-12088620 reverse strand	

	0.0191	2.48	up	lincRNA:chr17:56687541-56694616 reverse strand	
	0.0357	2.00	up	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 Gene [Source:MGI (curated);Acc:MGI:1913296] [ENSMUST00000121778]	
	0.0331	1.72	up	lincRNA:chr1:138528250-138538250 forward strand	
	0.0409	1.52	up	lincRNA:chr8:48485495-48485865 reverse strand	
	0.0013	5.12	up	lincRNA:chr1:58443698-58449898 reverse strand	
	0.0171	3.22	up	lincRNA:chr5:22928221-22939127 reverse strand	
	0.0079	1.65	up	lincRNA:chr13:9818700-9824125 reverse strand	
	0.0328	1.51	up	lincRNA:chr7:88668948-88678046 reverse strand	
	0.0108	2.41	up	lincRNA:chr5:35975265-35982561 reverse strand	
	0.0085	1.71	up	lincRNA:chr9:121256738-121257487 forward strand	
	0.0199	2.58	up	lincRNA:chr12:112223388-112223755 forward strand	
	0.0338	2.29	up	lincRNA:chr1:58440355-58449627 reverse strand	
	0.0496	1.52	up	lincRNA:chr6:99472981-99484210 forward strand	
	0.0123	1.54	up	lincRNA:chr4:3746573-3746891 forward strand	
	0.0100	1.73	up	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 9 Gene [Source:MGI (curated);Acc:MGI:1916320] [ENSMUST00000095675]	
	0.0158	2.19	up	lincRNA:chr7:6302922-6306477 forward strand	
	0.0226	1.53	up	lincRNA:chr17:33426488-33444184 forward strand	
	0.0177	1.60	up	lincRNA:chr3:90427029-90427674 forward strand	
	0.0098	1.91	up	lincRNA:chr12:17888352-17907493 forward strand	
	0.0074	3.11	up	lincRNA:chr4:135896689-135918414 forward strand	
	0.0066	1.83	up	lincRNA:chr9:114412295-114418384 reverse strand	
	0.0441	2.15	up	lincRNA:chr15:83181291-83197750 reverse strand	
	0.0449	2.03	up	lincRNA:chr16:46384974-46391331 forward strand	
	0.0399	1.58	up	lincRNA:chr4:105035450-105059250 forward strand	
	0.0425	1.89	up	lincRNA:chr4:86267450-86277650 forward strand	
	0.0312	2.14	up	lincRNA:chr2:94008913-94019798 reverse strand	

	0.0354	1.68	up	lincRNA:chr6:116092274-116144199 reverse strand	
	0.0406	1.56	up	lincRNA:chr1:137482591-137625604 forward strand	
	0.0362	1.72	up	lincRNA:chr6:128393530-128394127 forward strand	
	0.0456	1.68	up	lincRNA:chr15:79764481-79809909 reverse strand	
	0.0456	1.51	up	lincRNA:chr14:73729977-73751877 forward strand	
	0.0081	1.80	up	lincRNA:chr14:77104770-77105392 forward strand	
	0.0044	9.80	up	lincRNA:chr3:96074625-96086375 forward strand	
	0.0248	3.30	up	lincRNA:chr1:58440355-58449627 reverse strand	
	0.0331	1.53	up	lincRNA:chr15:68170864-68171544 reverse strand	
	0.0189	1.74	up	lincRNA:chrX:20374930-20375402 forward strand	
	0.0425	1.75	up	lincRNA:chr7:80762708-80763274 reverse strand	
	0.0463	1.77	up	lincRNA:chrX:93154123-93164481 forward strand	
	0.0088	1.60	up	lincRNA:chr11:31648453-31648952 reverse strand	
	0.0105	2.23	up	lincRNA:chr3:19211659-19213735 forward strand	
	0.0145	1.77	up	lincRNA:chr14:79311982-79334451 forward strand	
	0.0067	2.72	up	lincRNA:chr1:58443698-58449898 reverse strand	
	0.0323	1.84	up	lincRNA:chr7:80762708-80763274 reverse strand	
	0.0269	1.51	up	lincRNA:chr17:22420025-22457650 reverse strand	
	0.0317	3.21	up	lincRNA:chr5:22058025-22072475 forward strand	
	0.0081	1.96	up	lincRNA:chr10:3227840-3233588 forward strand	
	0.0198	1.58	up	lincRNA:chr11:79531768-79532127 forward strand	
	0.0365	1.93	up	lincRNA:chr8:72663625-72673010 reverse strand	
	0.0124	1.61	up	lincRNA:chr5:33186508-33196882 reverse strand	
	0.0024	1.54	up	lincRNA:chr4:155560296-155564642 forward strand	
	0.0466	2.09	up	lincRNA:chr9:114412295-114418384 forward strand	
	0.0035	1.63	up	lincRNA:chr1:92546371-92551596 forward strand	
	0.0176	1.69	up	lincRNA:chr5:125078875-125098525 reverse strand	
	0.0257	3.64	up	lincRNA:chrX:146945573-146950036 reverse strand	
	0.0023	1.52	up	lincRNA:chr2:119412770-119435110 reverse strand	
	0.0449	3.06	up	lincRNA:chr5:107503800-107515575 forward strand	
	0.0329	1.55	up	lincRNA:chr18:61781410-61788685 forward strand	
	0.0162	2.08	up	lincRNA:chr13:49488457-49493732 forward strand	
	0.0331	1.58	up	lincRNA:chr17:22090757-22099418 reverse strand	

	0.0007	1.91	up	lincRNA:chr2:60531602-60543635 reverse strand	
	0.0013	4.47	up	lincRNA:chr1:58443698-58449898 reverse strand	
	0.0110	1.90	up	lincRNA:chr4:128727331-128735227 reverse strand	
	0.0155	1.62	up	ATP synthase, H ⁺ transporting, mitochondrial F1F0 complex, subunit e Gene [Source:MGI (curated);Acc:MGI:106636] [ENSMUST00000118632]	
	0.0010	1.65	up	lincRNA:chr1:173254292-173257445 reverse strand	
	0.0333	2.36	up	lincRNA:chr17:15111725-15139800 forward strand	
	0.0139	1.53	up	lincRNA:chr7:99879368-99889978 reverse strand	
	0.0347	1.80	up	lincRNA:chr1:33965074-34060850 forward strand	
	0.0050	1.54	up	protein kinase, cAMP dependent regulatory, type I, alpha Gene [Source:MGI (curated);Acc:MGI:104878] [ENSMUST00000106676]	
	0.0172	1.86	up	lincRNA:chr6:122725638-122752828 forward strand	
	0.0197	1.93	up	lincRNA:chr11:79529699-79530564 forward strand	
	0.0028	2.09	up	lincRNA:chr2:176583825-176714400 forward strand	
	0.0288	1.87	up	lincRNA:chr10:59385064-59385436 forward strand	
	0.0009	1.62	up	lincRNA:chr3:131153358-131154061 forward strand	
	0.0070	2.73	up	lincRNA:chr5:26374425-26393675 forward strand	
	0.0339	2.53	up	lincRNA:chr17:56687541-56694616 reverse strand	
	0.0365	1.64	up	lincRNA:chrX:146827709-146913398 forward strand	
	0.0114	1.82	up	lincRNA:chrX:148819227-148844227 reverse strand	
	0.0089	1.70	up	Novel zinc finger protein Fragment [Source:UniProtKB/TrEMBL;Acc:B1ATP3] [ENSMUST00000078257]	
	0.0452	1.66	up	lincRNA:chr17:88993214-89025839 forward strand	
	0.0097	2.09	up	lincRNA:chr10:24269165-24276690 forward strand	
	0.0153	2.40	up	lincRNA:chr13:65716675-65765575 forward strand	
	0.0086	1.64	up	lincRNA:chr14:73757550-73758159 reverse strand	
	0.0224	1.65	up	lincRNA:chrX:47893703-47996700 forward strand	

	0.0256	1.82	up	lincRNA:chr13:41337973-41379821 reverse strand	
	0.0316	1.76	up	lincRNA:chr8:122807653-122823000 forward strand	
	0.0329	5.40	up	lincRNA:chr12:74135916-74142780 reverse strand	
	0.0051	2.03	up	lincRNA:chr9:96964067-96973567 forward strand	
	0.0251	2.18	up	lincRNA:chr6:135294099-135300310 forward strand	
	0.0133	1.94	up	lincRNA:chr14:61240427-61325677 reverse strand	
	0.0130	2.49	up	lincRNA:chr8:12535648-12544923 forward strand	
	0.0367	2.34	up	lincRNA:chr5:92548501-92566401 forward strand	
	0.0438	2.04	up	lincRNA:chr8:26869173-26869823 reverse strand	
	0.0372	2.04	up	connector enhancer of kinase suppressor of Ras 2 Gene [Source:MGI (curated);Acc:MGI:2661175] [ENSMUST00000112513]	
	0.0133	1.83	up	lincRNA:chr13:34693404-34717987 forward strand	
	0.0263	1.52	up	lincRNA:chr18:84735774-84760824 forward strand	
	0.0178	2.14	up	lincRNA:chr2:75447542-75448025 reverse strand	
	0.0411	1.60	up	lincRNA:chr1:121982840-121983386 reverse strand	
	0.0401	3.27	up	lincRNA:chr10:6480075-6603900 reverse strand	
	0.0284	1.52	up	lincRNA:chr1:6181200-6204300 forward strand	
	0.0132	1.80	up	lincRNA:chr4:101010948-101032148 forward strand	
	0.0357	2.83	up	lincRNA:chr17:56687541-56694616 reverse strand	
	0.0080	4.28	up	lincRNA:chr6:134838675-134847075 forward strand	
	0.0354	1.72	up	lincRNA:chr5:124694137-124695689 reverse strand	
	0.0034	15.83	up	lincRNA:chr5:23195569-23218551 reverse strand	
	0.0239	2.32	up	lincRNA:chr5:35975265-35982561 reverse strand	
	0.0186	1.51	up	lincRNA:chr15:92197603-92208534 forward strand	
	0.0053	2.51	up	lincRNA:chr11:117835849-117842574 forward strand	
	0.0176	2.42	up	lincRNA:chr3:127039311-127201919 reverse strand	
	0.0014	1.51	up	lincRNA:chr17:26911397-26917047 reverse strand	
	0.0482	2.02	up	lincRNA:chr2:65240793-65292293 reverse strand	
	0.0097	2.43	up	lincRNA:chr17:6514179-6517720 reverse strand	
	0.0301	1.98	up	lincRNA:chr10:39383665-39442690 forward strand	
	0.0267	1.94	up	lincRNA:chr5:15184252-15184923 forward strand	

	0.0124	1.77	up	lincRNA:chr6:135294099-135300310 forward strand	
	0.0214	1.54	up	lincRNA:chr7:77481448-77495548 reverse strand	
	0.0109	3.94	up	lincRNA:chr4:59306575-59317850 reverse strand	
	0.0402	1.54	up	lincRNA:chr4:59264275-59287850 forward strand	
	0.0312	1.74	up	lincRNA:chr14:79725080-79725434 reverse strand	
	0.0092	3.04	up	lincRNA:chr5:22928221-22939127 reverse strand	
	0.0347	2.50	up	lincRNA:chr4:3745783-3746383 reverse strand	
	0.0386	1.86	up	lincRNA:chr2:94008913-94019798 forward strand	
	0.0221	2.05	up	lincRNA:chr17:6830756-6832322 reverse strand	
	0.0027	1.57	up	lincRNA:chr9:41184479-41240162 forward strand	
	0.0346	1.65	up	lincRNA:chr11:79531768-79532127 forward strand	
	0.0191	2.28	up	lincRNA:chr1:155219662-155231912 reverse strand	
	0.0121	1.67	up	lincRNA:chr1:134167181-134181386 reverse strand	
	0.0219	1.59	up	lincRNA:chr6:47928244-47928681 reverse strand	
	0.0318	2.46	up	lincRNA:chr2:25774411-25783757 forward strand	
	0.0447	1.62	up	lincRNA:chr4:11899775-11931875 reverse strand	
	0.0124	1.57	up	lincRNA:chr9:58301467-58323783 reverse strand	
	0.0190	2.07	up	lincRNA:chr4:88604248-88645948 forward strand	
	0.0280	1.78	up	lincRNA:chr19:57426515-57435165 forward strand	
	0.0085	1.99	up	lincRNA:chr17:6306310-6311805 forward strand	
	0.0044	3.62	up	lincRNA:chr5:92548501-92566401 forward strand	
	0.0342	1.69	up	lincRNA:chr1:90508551-90508788 reverse strand	
	0.0037	1.66	up	lincRNA:chr4:129376440-129391690 reverse strand	
	0.0054	2.12	up	lincRNA:chr14:67585234-67596823 forward strand	
	0.0041	15.39	up	lincRNA:chr5:23195569-23218551 reverse strand	
	0.0088	1.65	up	lincRNA:chr3:131128972-131163308 forward strand	
	0.0133	2.48	up	lincRNA:chr5:35975265-35982561 reverse strand	
	0.0182	1.79	up	lincRNA:chr2:157236070-157249445 reverse strand	
	0.0337	3.19	up	lincRNA:chr5:22058025-22072475 forward strand	
	0.0004	1.82	up	lincRNA:chr1:87419050-87452625 forward strand	
	0.0044	1.68	up	lincRNA:chr14:43929100-43945100 forward strand	
	0.0302	1.71	up	lincRNA:chr4:128727331-128735227 reverse strand	

	0.0014	1.87	up	lincRNA:chr11:103005375-103020800 forward strand	
	0.0115	3.21	up	lincRNA:chr5:22928221-22939127 reverse strand	
	0.0323	1.60	up	lincRNA:chr12:81217572-81233910 forward strand	
	0.0243	3.07	up	lincRNA:chr12:110003268-110030953 forward strand	
	0.0063	1.85	up	lincRNA:chr15:74461988-74466728 reverse strand	
	0.0000	1.77	up	lincRNA:chr2:60038543-60046318 forward strand	
	0.0079	1.75	up	lincRNA:chr13:72906878-72923790 forward strand	
	0.0427	2.05	up	lincRNA:chr13:67211950-67217199 reverse strand	
	0.0369	5.93	up	lincRNA:chr17:88890039-88905680 forward strand	
	0.0060	34.30	up	lincRNA:chr3:96074625-96086375 forward strand	
	0.0256	1.64	up	lincRNA:chr7:66562376-66579519 forward strand	
	0.0216	2.57	up	lincRNA:chr19:5834117-5835940 reverse strand	
	0.0438	1.65	up	lincRNA:chr19:23264899-23268776 reverse strand	
	0.0467	1.61	up	lincRNA:chrX:20570399-20571162 forward strand	
	0.0185	1.92	up	lincRNA:chr8:12873805-12880007 forward strand	
	0.0490	1.76	up	lincRNA:chr5:14988715-14989311 forward strand	
	0.0364	3.68	up	lincRNA:chr14:101834175-102005450 forward strand	
	0.0095	3.72	up	lincRNA:chr13:112337405-112356455 reverse strand	
	0.0169	1.58	up	lincRNA:chr18:38542830-38544720 reverse strand	
	0.0452	1.87	up	lincRNA:chr3:34003359-34537330 forward strand	
	0.0463	2.52	up	lincRNA:chr17:15111725-15139800 reverse strand	
	0.0141	3.07	up	lincRNA:chr2:33496712-33501183 forward strand	
	0.0021	5.82	up	lincRNA:chr4:3745750-3756200 forward strand	
	0.0152	3.29	up	lincRNA:chr7:140081171-140123058 reverse strand	
	0.0463	1.90	up	lincRNA:chr3:127039311-127201919 reverse strand	
	0.0377	2.17	up	lincRNA:chr6:31267612-31293337 reverse strand	
	0.0065	2.64	up	lincRNA:chr15:79764481-79809909 forward strand	
	0.0051	3.49	up	lincRNA:chr5:119945358-119962612 forward strand	
	0.0119	4.52	up	lincRNA:chr1:134867906-134885481 reverse strand	

	0.0357	2.17	up	lincRNA:chr14:65431652-65437902 reverse strand	
	0.0330	4.24	up	lincRNA:chr4:13369325-13456750 forward strand	
	0.0083	3.93	up	lincRNA:chr3:34643323-34682773 reverse strand	
	0.0373	4.85	up	lincRNA:chr7:112934153-112943178 forward strand	
	0.0198	5.20	up	lincRNA:chr12:21381390-21381723 forward strand	
	0.0018	2.96	up	lincRNA:chr7:134620707-134626739 reverse strand	
	0.0158	1.54	up	lincRNA:chr15:68161768-68193518 reverse strand	
	0.0031	7.14	up	lincRNA:chr3:10081893-10094218 reverse strand	
	0.0354	2.12	down	lincRNA:chr12:53669892-53710742 forward strand	
	0.0314	1.56	down	lincRNA:chr7:49715933-49771497 reverse strand	
	0.0290	1.80	down	lincRNA:chr18:63525907-63526504 reverse strand	
	0.0082	1.66	down	lincRNA:chr2:128211990-128215223 reverse strand	
	0.0261	2.12	down	lincRNA:chr5:110182844-110228345 reverse strand	
	0.0306	2.37	down	lincRNA:chr17:36131460-36136694 forward strand	
	0.0270	2.61	down	lincRNA:chr7:150399015-150482452 forward strand	
	0.0418	2.22	down	Unknown	
	0.0480	2.03	down	lincRNA:chr2:143991240-143991597 forward strand	
	0.0032	1.91	down	lincRNA:chr10:24269165-24276690 reverse strand	
	0.0175	9.78	down	lincRNA:chr17:32035750-32056000 reverse strand	
	0.0072	9.13	down	lincRNA:chr17:32044823-32045974 reverse strand	
	0.0039	2.52	down	lincRNA:chr18:63525907-63526504 reverse strand	
	0.0195	1.57	down	lincRNA:chr1:135956616-135957485 reverse strand	
	0.0086	1.83	down	lincRNA:chr1:74084292-74138492 reverse strand	
	0.0139	2.88	down	lincRNA:chr3:36280098-36347798 reverse strand	
	0.0203	2.47	down	lincRNA:chr15:32167516-32174427 reverse strand	
	0.0391	2.20	down	lincRNA:chr12:110842154-110883594 forward strand	
	0.0426	1.96	down	lincRNA:chr8:89996710-90049453 forward strand	
	0.0474	2.47	down	lincRNA:chr6:47595238-47601893 reverse strand	
	0.0068	2.01	down	lincRNA:chr11:69106907-69112857 forward strand	
	0.0067	3.64	down	lincRNA:chr17:22420025-22457650 reverse strand	
	0.0246	8.84	down	lincRNA:chr17:32035750-32056000 reverse strand	
	0.0427	5.83	down	lincRNA:chr12:15735906-15798506 reverse strand	

	0.0008	9.63	down	lincRNA:chr3:127037711-127111912 reverse strand	
	0.0135	1.68	down	lincRNA:chr16:21794415-21815365 reverse strand	
	0.0156	5.03	down	lincRNA:chr3:79069438-79073704 reverse strand	
	0.0261	2.14	down	lincRNA:chr5:53931541-53945241 reverse strand	
	0.0060	3.80	down	lincRNA:chr17:22335458-22466521 reverse strand	
	0.0065	5.86	down	lincRNA:chr14:103751075-103769725 forward strand	
	0.0245	2.08	down	lincRNA:chr6:115468025-115489250 forward strand	
	0.0006	2.20	down	lincRNA:chr8:90048940-90049461 forward strand	
	0.0207	5.22	down	lincRNA:chr8:94849929-94870274 reverse strand	
	0.0010	2.26	down	lincRNA:chr3:113296823-113298691 reverse strand	
	0.0207	1.94	down	lincRNA:chr2:143992000-143992611 forward strand	
	0.0027	2.26	down	lincRNA:chr18:46646048-46659873 reverse strand	
	0.0469	3.08	down	lincRNA:chr16:59557120-59602070 reverse strand	
	0.0467	2.23	down	lincRNA:chr5:23195569-23218551 reverse strand	
	0.0022	1.93	down	lincRNA:chr14:77511189-77522852 forward strand	
	0.0084	1.63	down	lincRNA:chr5:110261075-110376700 reverse strand	
	0.0387	2.31	down	lincRNA:chr1:134245856-134246607 forward strand	
	0.0054	3.04	down	lincRNA:chr3:36280098-36347798 reverse strand	
	0.0446	3.03	down	lincRNA:chr17:36136010-36136696 forward strand	
	0.0188	2.39	down	lincRNA:chr4:149445201-149445902 forward strand	
	0.0326	1.57	down	lincRNA:chrX:90997595-91009570 forward strand	
	0.0417	3.43	down	lincRNA:chr1:167219841-167220505 forward strand	
	0.0382	1.52	down	lincRNA:chr6:100518251-100519726 reverse strand	
	0.0016	1.62	down	lincRNA:chr16:90008636-90015586 reverse strand	
	0.0483	2.40	down	lincRNA:chr10:83185606-83225506 forward strand	
	0.0111	1.67	down	lincRNA:chr12:110896603-110940553 forward strand	
	0.0207	4.10	down	lincRNA:chr3:127037711-127111912 reverse strand	
	0.0265	2.00	down	lincRNA:chr8:60132300-60146830 forward strand	
	0.0440	1.50	down	lincRNA:chr5:54053882-54054174 forward strand	
	0.0036	1.58	down	lincRNA:chr3:84609788-84618062 reverse strand	
	0.0421	1.52	down	lincRNA:chr4:11899775-11931875 forward strand	

	0.0285	1.52	down	lincRNA:chr5:53931541-53945241 forward strand	
	0.0208	2.70	down	lincRNA:chr11:95644899-95658549 forward strand	
	0.0398	2.18	down	lincRNA:chr11:87841800-87858725 reverse strand	
	0.0141	1.54	down	lincRNA:chr6:112552041-112560067 forward strand	
	0.0214	9.97	down	lincRNA:chr4:146890596-146891297 forward strand	
	0.0010	2.52	down	lincRNA:chr15:32167516-32174417 reverse strand	
	0.0145	1.58	down	lincRNA:chr9:71687805-71689542 reverse strand	
	0.0325	1.75	down	lincRNA:chr7:77555482-77634858 forward strand	
	0.0312	1.64	down	lincRNA:chr1:85117750-85129200 forward strand	
	0.0338	2.10	down	lincRNA:chr13:112717680-112733330 reverse strand	
	0.0217	3.20	down	lincRNA:chr8:94841965-94881130 reverse strand	
	0.0154	1.96	down	Q61491_MOUSE (Q61491) DNA-binding protein, partial (70%) [TC1607062]	
	0.0319	2.32	down	lincRNA:chr10:83181374-83249774 forward strand	
	0.0202	2.62	down	lincRNA:chr13:62734450-62785325 reverse strand	
	0.0344	1.60	down	lincRNA:chr11:120041124-120052299 reverse strand	
	0.0001	3.51	down	lincRNA:chr15:32167516-32174427 reverse strand	
	0.0167	2.68	down	lincRNA:chr9:96632664-96653249 reverse strand	
	0.0131	1.55	down	lincRNA:chr6:3283191-3284581 reverse strand	
	0.0432	1.69	down	lincRNA:chr1:135956616-135957485 reverse strand	
	0.0310	1.74	down	lincRNA:chr2:72818943-72826893 forward strand	
	0.0058	1.74	down	lincRNA:chr7:88668948-88678046 forward strand	
	0.0008	2.35	down	lincRNA:chr12:73860757-73862034 reverse strand	
	0.0387	1.57	down	lincRNA:chr10:3227840-3233588 reverse strand	
	0.0490	1.88	down	lincRNA:chr17:87674225-87682154 reverse strand	
	0.0157	1.62	down	lincRNA:chr6:146495766-146496419 reverse strand	
	0.0018	6.85	down	lincRNA:chr14:103751075-103769725 forward strand	
	0.0324	1.73	down	lincRNA:chr17:12990484-13018375 forward strand	
	0.0189	1.93	down	lincRNA:chr10:62267317-62269871 reverse strand	
	0.0000	6.81	down	lincRNA:chr17:22420025-22457650 reverse strand	

	0.0124	2.41	down	lincRNA:chr12:72103832-72116875 reverse strand	
	0.0180	2.32	down	lincRNA:chr10:24269165-24276690 reverse strand	
	0.0010	4.90	down	lincRNA:chr17:22420025-22457650 reverse strand	
	0.0139	1.54	down	lincRNA:chr19:53517903-53540753 reverse strand	
	0.0370	1.67	down	lincRNA:chr17:32075308-32075792 reverse strand	
	0.0391	1.69	down	lincRNA:chr1:85036677-85038530 reverse strand	
	0.0489	1.86	down	lincRNA:chr5:23195569-23218551 reverse strand	
	0.0161	1.64	down	lincRNA:chr10:62267317-62269871 reverse strand	
	0.0040	3.48	down	lincRNA:chr4:146149125-146155054 forward strand	
	0.0468	1.68	down	lincRNA:chr2:157361470-157379813 reverse strand	
	0.0357	2.15	down	lincRNA:chr18:63355660-63369610 reverse strand	
	0.0084	2.30	down	lincRNA:chr12:53669892-53710742 forward strand	
	0.0047	1.96	down	lincRNA:chr12:32781477-32808567 reverse strand	
	0.0134	1.61	down	lincRNA:chr3:30099759-30133959 reverse strand	
	0.0106	1.52	down	lincRNA:chr4:114585803-114588898 forward strand	
	0.0418	1.93	down	lincRNA:chr13:28551902-28975446 reverse strand	
	0.0259	1.78	down	lincRNA:chr12:32781477-32808567 reverse strand	
	0.0069	1.68	down	lincRNA:chr2:143992000-143992611 forward strand	
	0.0495	1.54	down	lincRNA:chr13:107822042-107823753 forward strand	
	0.0071	2.62	down	lincRNA:chr15:32167516-32174417 reverse strand	
	0.0245	1.58	down	lincRNA:chr2:128137419-128141735 reverse strand	
	0.0004	1.89	down	lincRNA:chr5:105072936-105074001 forward strand	
	0.0468	2.25	down	lincRNA:chr2:127988295-128194920 reverse strand	
	0.0467	1.81	down	lincRNA:chr8:35652473-35703370 reverse strand	
	0.0466	1.61	down	lincRNA:chr11:120046656-120050065 forward strand	
	0.0153	1.53	down	lincRNA:chr18:35970772-35971449 forward strand	
	0.0022	4.95	down	lincRNA:chr17:32044823-32045974 reverse strand	
	0.0486	1.59	down	lincRNA:chr2:128211990-128215223 reverse strand	
	0.0113	1.66	down	lincRNA:chr10:93774693-93893616 forward strand	
	0.0133	2.21	down	lincRNA:chr5:105072936-105074001 forward strand	
	0.0113	1.76	down	lincRNA:chr5:105032961-105037248 forward strand	

	0.0334	4.23	down	lincRNA:chr7:149761435-149764019 reverse strand	
	0.0074	1.56	down	lincRNA:chr11:120041124-120052299 reverse strand	
	0.0217	2.72	down	lincRNA:chr6:112552041-112560067 forward strand	
	0.0478	2.22	down	lincRNA:chr1:85304494-85305390 reverse strand	
	0.0239	1.63	down	lincRNA:chr17:22422837-22451777 reverse strand	
	0.0192	1.61	down	lincRNA:chr10:6480075-6603900 reverse strand	
	0.0028	2.95	down	lincRNA:chr17:22335458-22466521 reverse strand	
	0.0443	1.71	down	lincRNA:chr9:14460976-14488051 forward strand	
	0.0452	1.64	down	lincRNA:chr3:58730418-58742493 forward strand	
	0.0180	1.57	down	lincRNA:chr13:76326228-76332632 reverse strand	
	0.0330	1.52	down	lincRNA:chr19:61177675-61219875 reverse strand	
	0.0038	1.79	down	lincRNA:chr13:62734450-62785325 reverse strand	
	0.0396	3.54	down	lincRNA:chr8:122712014-122732520 reverse strand	
	0.0105	1.54	down	lincRNA:chr2:92582386-92599365 forward strand	
	0.0374	4.71	down	lincRNA:chr3:79069438-79073704 reverse strand	
	0.0170	5.93	down	lincRNA:chr15:36800254-36809571 reverse strand	
	0.0118	1.61	down	lincRNA:chr8:74439200-74441363 forward strand	
	0.0014	1.70	down	lincRNA:chr13:28947034-28949166 reverse strand	
	0.0349	3.13	down	lincRNA:chrX:120324027-120326909 reverse strand	
	0.0188	1.75	down	lincRNA:chr17:7002731-7032535 reverse strand	
	0.0184	2.18	down	lincRNA:chr14:26834450-26847000 reverse strand	
	0.0016	2.91	down	lincRNA:chr8:94841965-94881130 reverse strand	
	0.0430	1.70	down	lincRNA:chr6:4841700-4847400 reverse strand	
	0.0431	2.42	down	lincRNA:chr14:33923944-34003394 reverse strand	
	0.0147	1.59	down	lincRNA:chr9:43926204-43928496 forward strand	
	0.0057	4.68	down	lincRNA:chr4:147105275-147171025 reverse strand	
	0.0178	2.05	down	lincRNA:chr11:120041124-120052299 reverse strand	
	0.0106	1.74	down	aryl hydrocarbon receptor nuclear translocator Gene [Source:MGI (curated);Acc:MGI:88071] [ENSMUST00000107160]	
	0.0040	5.86	down	lincRNA:chr4:146890596-146891297 forward strand	

	0.0161	1.55	down	lincRNA:chr4:11899775-11931875 forward strand	
	0.0113	1.81	down	lincRNA:chr1:85036677-85038530 reverse strand	
	0.0302	1.99	down	lincRNA:chr17:25990279-25998670 forward strand	
	0.0345	1.91	down	lincRNA:chr9:14460976-14488051 forward strand	
	0.0445	1.76	down	lincRNA:chr6:4841700-4847400 reverse strand	
	0.0137	1.72	down	lincRNA:chr9:14460976-14488051 forward strand	
	0.0153	1.91	down	lincRNA:chr4:11899775-11931875 forward strand	
	0.0062	2.86	down	lincRNA:chr5:33174092-33200792 reverse strand	
	0.0162	1.71	down	lincRNA:chr1:137503023-137625604 reverse strand	
	0.0154	2.07	down	lincRNA:chr4:3437474-3438228 reverse strand	
	0.0396	3.13	down	lincRNA:chr1:85304494-85305390 reverse strand	
	0.0103	6.34	down	lincRNA:chr3:127037711-127111912 reverse strand	
	0.0256	1.74	down	lincRNA:chr8:35652473-35703370 reverse strand	
	0.0383	1.58	down	lincRNA:chr4:11926618-11936190 reverse strand	
	0.0043	2.21	down	lincRNA:chr15:32167516-32174427 reverse strand	
	0.0444	3.21	down	lincRNA:chr15:32708654-32725622 forward strand	
	0.0266	2.31	down	lincRNA:chr2:143988645-143993945 reverse strand	
	0.0093	1.59	down	lincRNA:chr12:117623500-117643575 reverse strand	
	0.0447	1.79	down	lincRNA:chr15:85412264-85549139 reverse strand	
	0.0470	1.65	down	lincRNA:chr17:87674225-87682154 reverse strand	
	0.0023	6.91	down	lincRNA:chr14:103751075-103769725 forward strand	
	0.0113	2.00	down	lincRNA:chr19:57426515-57435165 reverse strand	
	0.0015	5.89	down	lincRNA:chr17:22335458-22466521 reverse strand	
6330545A04Rik	0.0041	1.66	down	RIKEN cDNA 6330545A04 gene Gene [Source:MGI Symbol;Acc:MGI:1923416] [ENSMUST00000097813]	
	0.0165	2.31	down	lincRNA:chr1:137503023-137625604 reverse strand	
	0.0021	3.39	down	lincRNA:chr15:32167516-32174427 reverse strand	
	0.0345	1.93	down	lincRNA:chr8:89996710-90049453 forward strand	
	0.0288	1.80	down	lincRNA:chr5:31856417-31916414 forward strand	
	0.0495	1.94	down	lincRNA:chr13:62734450-62785325 reverse strand	

	0.0351	4.75	down	lincRNA:chr3:79069438-79073704 reverse strand	
	0.0460	2.63	down	lincRNA:chr17:13008796-13023201 forward strand	
	0.0225	2.27	down	lincRNA:chr3:84609788-84618062 reverse strand	
	0.0311	1.90	down	lincRNA:chr10:83181374-83249774 forward strand	
	0.0009	3.46	down	lincRNA:chr1:85304494-85305390 reverse strand	
	0.0072	2.42	down	lincRNA:chr15:32167516-32174427 reverse strand	
	0.0086	2.22	down	lincRNA:chr17:7002731-7032535 reverse strand	
	0.0167	2.18	down	lincRNA:chr1:137503023-137625604 reverse strand	
	0.0068	2.46	down	lincRNA:chr13:24615451-24615973 forward strand	
	0.0211	1.68	down	lincRNA:chr6:149232359-149235295 reverse strand	
	0.0246	1.80	down	lincRNA:chr17:36131460-36136694 forward strand	
	0.0368	1.65	down	lincRNA:chr7:149761435-149764019 reverse strand	
	0.0295	3.47	down	lincRNA:chr15:32167516-32174417 reverse strand	
	0.0174	1.75	down	lincRNA:chr3:146629425-146649125 forward strand	
	0.0423	1.58	down	lincRNA:chr9:13349094-13352732 forward strand	

GeneSymbol	p-value	FCAbsolute	regulation	Description
Gorasp1	0.0183	1.88	up	Ig lambda-3 chain C region [Source:UniProtKB/Swiss-Prot;Acc:P01845] [ENSMUST00000103743]
Zfp868	0.0351	3.66	up	Mus musculus cytochrome P450 CYP4F18 mRNA, complete cds. [AF233647]
	0.0134	3.03	up	Ig lambda-3 chain C region [Source:UniProtKB/Swiss-Prot;Acc:P01845] [ENSMUST00000103743]
	0.0114	2.76	up	immunoglobulin heavy chain (J558 family) Complex/Cluster/Region [Source:MGI Symbol;Acc:MGI:96486] [ENSMUST00000103531]
	0.0320	3.28	up	vv70h06.x1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:1227803 3'. [AI604347]
	0.0166	9.71	up	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700102J08 product:unclassifiable, full insert sequence. [AK007112]
	0.0229	3.12	up	Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010012P19 product:unclassifiable, full insert sequence. [AK008218]
Ocel1	0.0035	4.06	up	Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610312K03 product:unclassifiable, full insert sequence. [AK012020]
2210404J11Rik	0.0062	2.88	up	Mus musculus 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2700068H02 product:unclassifiable, full insert sequence. [AK012503]
4932412D23Rik	0.0354	2.74	up	Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:2900001G08 product:unclassifiable, full insert sequence. [AK013461]
Gm5968	0.0491	1.79	up	RNA binding motif protein 33 Gene [Source:MGI (curated);Acc:MGI:1919670] [ENSMUST00000090355]
	0.0284	3.01	up	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4921515L22 product:unclassifiable, full insert sequence. [AK014901]

Angpt4	0.0182	2.07	up	RIKEN cDNA 4930408O17 gene Gene [Source:MGI Symbol;Acc:MGI:1921178] [ENSMUST00000021520]
Gm7464	0.0144	1.62	up	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930445G23 product:unclassifiable, full insert sequence. [AK015390]
	0.0149	1.75	up	Putative uncharacterized protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q9CUK7] [ENSMUST00000015856]
Thbs2	0.0220	6.57	up	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930529I22 product:unclassifiable, full insert sequence. [AK015936]
Ing5	0.0075	1.82	up	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932434L04 product:hypothetical protein, full insert sequence. [AK016549]
Gm8667	0.0046	1.89	up	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933430A20 product:unclassifiable, full insert sequence. [AK016987]
Kctd18	0.0390	1.62	up	Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130022E09 product:hypothetical Microbodies C-terminal targeting signal/Phenylalanine-rich region containing protein, full insert sequence. [AK018644]
LOC100047703	0.0494	5.08	up	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930414F18 product:unclassifiable, full insert sequence. [AK019576]
Ntrk3	0.0118	2.35	up	Putative uncharacterized protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q9CTX5] [ENSMUST00000059184]
	0.0135	2.41	up	Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430403G16 product:weakly similar to zinc finger protein ZNF126 (fragment) [Homo sapiens], full insert sequence. [AK019943]

Ssbp2	0.0432	1.69	up	staufen (RNA binding protein) homolog 2 (Drosophila) Gene [Source:MGI (curated);Acc:MGI:1352508] [ENSMUST00000115359]
C430049E01Rik	0.0058	3.92	up	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932418C03 product:unclassifiable, full insert sequence. [AK030052]
2900079G21Rik	0.0184	1.94	up	Putative uncharacterized protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q8BSU0] [ENSMUST00000087544]
Rapgef6	0.0393	1.50	up	RIKEN cDNA 6720416L17 gene Gene [Source:MGI Symbol;Acc:MGI:3026978] [ENSMUST00000100000]
	0.0091	1.55	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q8CB95] [ENSMUST00000068730]
	0.0326	2.29	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q8C4T9] [ENSMUST00000069594]
Tmem154	0.0255	1.77	up	Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130010C18 product:unclassifiable, full insert sequence. [AK037357]
	0.0160	1.86	up	poly (ADP-ribose) polymerase family, member 9 Gene [Source:MGI (curated);Acc:MGI:1933117] [ENSMUST00000114877]
LOC100046898	0.0375	1.56	up	phospholipase C, delta 4 Gene [Source:MGI (curated);Acc:MGI:107469] [ENSMUST00000113745]
Tpsb2	0.0369	3.88	up	midline 2 Gene [Source:MGI (curated);Acc:MGI:1344333] [ENSMUST00000112988]
	0.0152	3.80	up	Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630042D17 product:unclassifiable, full insert sequence. [AK041852]
	0.0260	3.00	up	Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730028G07 product:unclassifiable, full insert sequence. [AK042831]

	0.0493	1.89	up	CDC23 (cell division cycle 23, yeast, homolog) Gene [Source:MGI (curated);Acc:MGI:1098815] [ENSMUST00000055365]
	0.0127	1.94	up	integrator complex subunit 10 Gene [Source:MGI (curated);Acc:MGI:1918135] [ENSMUST00000110241]
1300002K09Rik	0.0472	4.26	up	Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:C330016E12 product:unclassifiable, full insert sequence. [AK049241]
	0.0034	3.15	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q8BKS1] [ENSMUST00000072014]
Gdf1	0.0277	3.19	up	hepatoma-derived growth factor, related protein 3 Gene [Source:MGI (curated);Acc:MGI:1352760] [ENSMUST00000026094]
Neurog3	0.0440	2.31	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:B0G0X9] [ENSMUST00000061914]
	0.0436	2.73	up	Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched library, clone:E030046B03 product:unclassifiable, full insert sequence. [AK053225]
2310010J17Rik	0.0069	1.68	up	Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310051F07 product:unclassifiable, full insert sequence. [AK075904]
	0.0427	1.95	up	protein kinase C, eta Gene [Source:MGI (curated);Acc:MGI:97600] [ENSMUST00000119092]
	0.0182	2.38	up	lin-7 homolog A (C. elegans) Gene [Source:MGI Symbol;Acc:MGI:2135609] [ENSMUST00000099302]
	0.0050	4.49	up	Rho-related BTB domain containing 3 Gene [Source:MGI (curated);Acc:MGI:1920546] [ENSMUST00000109606]
	0.0225	1.86	up	Mus musculus 9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030051F04 product:unclassifiable, full insert sequence. [AK083592]

Lypd1	0.0498	7.76	up	Mus musculus 9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030051J21 product:unclassifiable, full insert sequence. [AK083595]
	0.0220	2.94	up	phenylalanyl-tRNA synthetase, alpha subunit Gene [Source:MGI (curated);Acc:MGI:1913840] [ENSMUST00000095222]
Snapc3	0.0051	1.99	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q8BNC0] [ENSMUST00000090647]
	0.0387	1.74	up	a disintegrin and metallopeptidase domain 33 Gene [Source:MGI (curated);Acc:MGI:1341813] [ENSMUST00000110229]
LOC100045816	0.0014	2.43	up	Mus musculus 15 days embryo brain cDNA, RIKEN full-length enriched library, clone:G630055G22 product:unclassifiable, full insert sequence. [AK090337]
	0.0414	1.96	up	cDNA fis, clone TRACH3037696 [Source:UniProtKB/TrEMBL;Acc:Q6ZQL5] [ENSMUST00000072427]
Gpnmb	0.0468	9.67	up	Eph receptor A10 Gene [Source:MGI (curated);Acc:MGI:3586824] [ENSMUST00000106185]
Rwdd1	0.0248	1.82	up	S100P binding protein Gene [Source:MGI (curated);Acc:MGI:1921898] [ENSMUST00000117350]
	0.0405	1.63	up	Putative uncharacterized protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q3UTF5] [ENSMUST00000099365]
Gm4475	0.0265	1.89	up	Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230104I21 product:hypothetical protein, full insert sequence. [AK140029]
2810433D01Rik	0.0281	2.02	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3TR65] [ENSMUST00000104924]

Loxhd1	0.0450	1.58	up	Mus musculus 7 days embryo whole body cDNA, RIKEN full-length enriched library, clone:C430049E01 product:hypothetical protein, full insert sequence. [AK141396]
	0.0121	3.79	up	Mus musculus 9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030012B19 product:unclassifiable, full insert sequence. [AK141659]
2900073C17Rik	0.0118	2.46	up	Mus musculus lung RCB-0558 LLC cDNA, RIKEN full-length enriched library, clone:G730014H17 product:unclassifiable, full insert sequence. [AK144629]
Pcdh11x	0.0271	2.40	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3UEB9] [ENSMUST00000097783]
B230216G23Rik	0.0471	1.65	up	tumor necrosis factor, alpha-induced protein 8-like 3 Gene [Source:MGI Symbol;Acc:MGI:2685363] [ENSMUST00000098760]
Gm6553	0.0298	1.51	up	fibroblast growth factor 20 Gene [Source:MGI (curated);Acc:MGI:1891346] [ENSMUST00000118639]
Olf128	0.0064	3.27	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3TUQ9] [ENSMUST00000114029]
Sms	0.0335	1.79	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q9D1Y2] [ENSMUST00000097692]
	0.0453	2.20	up	Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530069H21 product:unclassifiable, full insert sequence. [AK163097]
	0.0228	5.61	up	Mus musculus 2 cells egg cDNA, RIKEN full-length enriched library, clone:B020017L01 product:unclassifiable, full insert sequence. [AK163349]
	0.0131	1.67	up	topoisomerase (DNA) III alpha Gene [Source:MGI (curated);Acc:MGI:1197527] [ENSMUST00000120417]

	0.0199	3.60	up	RIKEN cDNA 2010111I01 gene Gene [Source:MGI Symbol;Acc:MGI:1919311] [ENSMUST00000021911]
B430316J06Rik	0.0199	2.75	up	myotubularin related protein 15 Gene [Source:MGI (curated);Acc:MGI:3045266] [ENSMUST00000107514]
Ccr8	0.0235	2.01	up	immunoglobulin lambda chain, variable 1 Gene [Source:MGI Symbol;Acc:MGI:96530] [ENSMUST00000103749]
	0.0060	3.38	up	immunoglobulin lambda chain, variable 1 Gene [Source:MGI Symbol;Acc:MGI:96530] [ENSMUST00000103741]
Atp6v0d2	0.0327	5.64	up	immunoglobulin lambda chain, variable 1 Gene [Source:MGI Symbol;Acc:MGI:96530] [ENSMUST00000103746]
Med16	0.0231	4.34	up	rabaptin, RAB GTPase binding effector protein 1 Gene [Source:MGI (curated);Acc:MGI:1860236] [ENSMUST00000108533]
Tmem181a	0.0337	1.98	up	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast) Gene [Source:MGI (curated);Acc:MGI:1916241] [ENSMUST00000105595]
Gjc2	0.0334	1.87	up	transmembrane protein 181B Gene [Source:MGI Symbol;Acc:MGI:3779544] [ENSMUST00000115767]
	0.0180	5.00	up	olfactory receptor 537, pseudogene 1 Pseudogene [Source:MGI Symbol;Acc:MGI:3030371] [ENSMUST00000097963]
	0.0211	3.60	up	fetal and adult testis expressed 1 Gene [Source:MGI (curated);Acc:MGI:1925155] [ENSMUST00000114568]
Gm2285	0.0011	1.75	up	NACHT and WD repeat domain containing 1 Gene [Source:MGI Symbol;Acc:MGI:2442268] [ENSMUST00000093427]
Zfp352	0.0336	2.48	up	GPI anchored molecule like protein Gene [Source:MGI Symbol;Acc:MGI:3644767] [ENSMUST00000089693]

	0.0054	1.68	up	H3058B07-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3058B07 5', mRNA sequence [BG080844]
	0.0034	1.99	up	AGENCOURT_8954237 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:6479116 5', mRNA sequence [BQ938751]
	0.0225	1.73	up	UI-M-FY0-cdb-a-22-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone IMAGE: 6827135 5', mRNA sequence [CA328248]
2010111I01Rik	0.0467	1.66	up	AGENCOURT_14709166 NIH_MGC_190 Mus musculus cDNA clone IMAGE:30505922 5', mRNA sequence [CD772809]
Neb	0.0203	1.96	up	AGENCOURT_24959256 NIH_MGC_169 Mus musculus cDNA clone IMAGE:30916952 5', mRNA sequence [CN840722]
Dhrsx	0.0021	1.81	up	AGENCOURT_24953057 NIH_MGC_169 Mus musculus cDNA clone IMAGE:30917506 5', mRNA sequence [CN842534]
Plekha7	0.0161	1.84	up	VP01_04_A17.x1 FH VP01 Mus musculus cDNA clone VP01_04_A17, mRNA sequence [DV070132]
	0.0165	2.66	up	Mouse Ig rearranged kappa-chain mRNA, clone AN09K. [M19912]
Zfp868	0.0051	3.14	up	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 Gene [Source:MGI Symbol;Acc:MGI:103296] [ENSMUST00000034376]
	0.0058	3.24	up	Ig heavy chain V region MOPC 21 Precursor; Fragment [Source:UniProtKB/Swiss-Prot;Acc:P01783] [ENSMUST00000103459]
	0.0217	5.55	up	T-cell receptor beta chain V region C5 Precursor; Fragment [Source:UniProtKB/Swiss-Prot;Acc:P04213] [ENSMUST00000103271]

Car14	0.0293	4.82	up	V kappa light chain Precursor; Fragment [Source:UniProtKB/TrEMBL;Acc:A0N8I8] [ENSMUST00000103362]
Klra15	0.0271	7.73	up	Mus musculus zinc finger protein 58 (Zfp58), mRNA [NM_001007575]
	0.0308	2.76	up	Mus musculus adenosine A1 receptor (Adora1), transcript variant 1, mRNA [NM_001008533]
	0.0009	2.63	up	Mus musculus interleukin 19 (Il19), mRNA [NM_001009940]
Agrr	0.0005	3.17	up	Mus musculus olfactory receptor 1415 (Olfr1415), mRNA [NM_001011525]
	0.0330	3.69	up	Mus musculus olfactory receptor 332 (Olfr332), mRNA [NM_001011770]
	0.0351	1.67	up	Mus musculus olfactory receptor 312 (Olfr312), mRNA [NM_001011819]
Rnf39	0.0190	3.20	up	Mus musculus heparan sulfate (glucosamine) 3-O- sulfotransferase 6 (Hs3st6), mRNA [NM_001012402]
Cd300c	0.0220	3.60	up	Mus musculus ankyrin repeat domain 34A (Ankrd34a), mRNA [NM_001024851]
LOC630293	0.0429	3.59	up	Mus musculus predicted gene, ENSMUSG00000068790 (ENSMUSG00000068790), mRNA [NM_001029930]
Alpk1	0.0071	3.56	up	Mus musculus transmembrane protein 181A (Tmem181a), mRNA [NM_001033178]
1700061I17Rik	0.0290	3.70	up	Mus musculus YEATS domain containing 2 (Yeats2), transcript variant 2, mRNA [NM_001033237]
	0.0117	1.58	up	Mus musculus dehydrogenase/reductase (SDR family) X chromosome (Dhrsx), mRNA [NM_001033326]
	0.0319	2.51	up	Mus musculus headcase homolog (Drosophila) (Heca), mRNA [NM_001033432]
	0.0012	3.06	up	Mus musculus low density lipoprotein receptor A domain containing 2 (Ldlrad2), mRNA [NM_001033979]
	0.0077	3.92	up	Mus musculus XIAP associated factor 1 (Xaf1), mRNA [NM_001037713]

	0.0238	3.23	up	Mus musculus olfactomedin 1 (Olfm1), transcript variant 2, mRNA [NM_001038612]
	0.0200	1.94	up	Mus musculus RIKEN cDNA 2210404J11 gene (2210404J11Rik), transcript variant 1, mRNA [NM_001039552]
	0.0108	4.92	up	Mus musculus RIKEN cDNA 2210404J11 gene (2210404J11Rik), transcript variant 1, mRNA [NM_001039552]
	0.0163	2.62	up	Mus musculus UHRF1 (ICBP90) binding protein 1 (Uhrf1bp1), mRNA [NM_001080769]
Acss3	0.0115	1.94	up	Mus musculus calcium and integrin binding family member 3 (Cib3), mRNA [NM_001080812]
Gm6686	0.0078	1.58	up	Mus musculus calcium channel, voltage-dependent, L type, alpha 1S subunit (Cacna1s), transcript variant 2, mRNA [NM_001081023]
1810037I17Rik	0.0143	11.97	up	Mus musculus phosphodiesterase 11A (Pde11a), mRNA [NM_001081033]
	0.0063	1.50	up	Mus musculus oxoglutarate dehydrogenase-like (Ogdhl), nuclear gene encoding mitochondrial protein, mRNA [NM_001081130]
Wdr75	0.0029	1.69	up	Mus musculus Rap1 GTPase-activating protein (Rap1gap), mRNA [NM_001081155]
Fam160b2	0.0141	2.42	up	Mus musculus AT rich interactive domain 4A (RBP1-like) (Arid4a), mRNA [NM_001081195]
LOC100044107	0.0223	1.66	up	Mus musculus zinc finger with KRAB and SCAN domains 2 (Zkscan2), mRNA [NM_001081329]
Guk1	0.0296	1.58	up	Mus musculus CCCTC-binding factor (zinc finger protein)-like (Ctcf1), mRNA [NM_001081387]
Srprb	0.0072	1.63	up	Mus musculus pappalysin 2 (Pappa2), mRNA [NM_001085376]
Mfsd4	0.0377	2.60	up	Mus musculus myomesin family, member 3 (Myom3), mRNA [NM_001085509]

2410076I21Rik	0.0173	2.72	up	Mus musculus RIKEN cDNA E030025P04 gene (E030025P04Rik), mRNA [NM_001085512]
	0.0202	1.50	up	Mus musculus ring finger protein 39 (Rnf39), mRNA [NM_001099632]
Map3k7	0.0002	2.24	up	Mus musculus forkhead box I3 (Foxi3), mRNA [NM_001101464]
Snx33	0.0222	1.74	up	Mus musculus core-binding factor, runt domain, alpha subunit 2, translocated to, 3 (human) (Cbfa2t3), transcript variant 2, mRNA [NM_001109873]
Fam129c	0.0190	2.52	up	Mus musculus major facilitator superfamily domain containing 4 (Mfsd4), transcript variant b, mRNA [NM_001114662]
	0.0110	1.71	up	Mus musculus kit oncogene (Kit), transcript variant 1, mRNA [NM_001122733]
Agtr1b	0.0300	2.35	up	Mus musculus patatin-like phospholipase domain containing 6 (Pnpla6), transcript variant 1, mRNA [NM_001122818]
Paqr6	0.0133	2.87	up	Mus musculus RIKEN cDNA 9030025P20 gene (9030025P20Rik), mRNA [NM_001123370]
	0.0064	2.00	up	Mus musculus solute carrier family 39 (metal ion transporter), member 8 (Slc39a8), transcript variant 1, mRNA [NM_001135150]
Synpo2	0.0150	2.41	up	Mus musculus predicted gene 14124 (Gm14124), mRNA [NM_001142410]
Rhbdl2	0.0451	1.91	up	Mus musculus F-box protein 34 (Fbxo34), transcript variant 2, mRNA [NM_001146085]
Gm5459	0.0330	1.67	up	Mus musculus potassium channel tetramerisation domain containing 18 (Kctd18), transcript variant 1, mRNA [NM_001159864]
Scn1b	0.0357	1.95	up	Mus musculus hypothetical protein LOC100041256 (LOC100041256), mRNA [NM_001160142]
	0.0316	5.12	up	Mus musculus RIKEN cDNA E430029J22 gene (E430029J22Rik), mRNA [NM_001162938]

Med1	0.0389	1.69	up	Mus musculus prolactin family 3, subfamily c, member 1 (Prl3c1), transcript variant 2, mRNA [NM_001163218]
	0.0047	4.09	up	Mus musculus POU domain, class 2, transcription factor 2 (Pou2f2), transcript variant 4, mRNA [NM_001163554]
Egr2	0.0096	2.51	up	Mus musculus keratin associated protein 20-2 (Krtap20-2), mRNA [NM_001163615]
LOC433461	0.0361	2.84	up	Mus musculus zinc finger protein 605 (Zfp605), mRNA [NM_001163996]
	0.0141	2.15	up	Mus musculus dihydropyrimidinase (Dpys), transcript variant 2, mRNA [NM_001164466]
Epn2	0.0386	2.71	up	Mus musculus cDNA sequence BC049349 (BC049349), mRNA [NM_001164581]
	0.0459	1.52	up	Mus musculus predicted gene 10406 (Gm10406), mRNA [NM_001164727]
Myoz1	0.0261	2.92	up	Mus musculus family with sequence similarity 129, member C (Fam129c), mRNA [NM_001166213]
Rbm8a	0.0227	1.59	up	Mus musculus G2/M-phase specific E3 ubiquitin ligase (G2e3), transcript variant 2, mRNA [NM_001167963]
Ascl1	0.0198	1.72	up	Mus musculus C-type lectin domain family 4, member a2 (Clec4a2), transcript variant 1, mRNA [NM_001170333]
	0.0195	3.81	up	Mus musculus RIKEN cDNA 3110009E18 gene (3110009E18Rik), transcript variant 2, mRNA [NM_001172074]
	0.0093	2.36	up	Mus musculus RNA binding motif protein 41 (Rbm41), transcript variant 1, mRNA [NM_001172147]
	0.0437	2.32	up	Mus musculus calcium/calmodulin-dependent protein kinase II, beta (Camk2b), transcript variant 1, mRNA [NM_001174053]
	0.0162	1.65	up	Mus musculus chloride channel CLIC-like 1 (Clcc1), transcript variant 1, mRNA [NM_001177770]
	0.0227	3.50	up	Mus musculus activin receptor IIA (Acvr2a), mRNA [NM_007396]

	0.0340	1.75	up	Mus musculus angiogenin, ribonuclease A family, member 2 (Ang2), mRNA [NM_007449]
A930005H10Rik	0.0282	3.62	up	Mus musculus baculoviral IAP repeat-containing 2 (Birc2), mRNA [NM_007465]
Cyp2d13	0.0318	2.26	up	Mus musculus branched chain aminotransferase 1, cytosolic (Bcat1), transcript variant 2, mRNA [NM_007532]
A430017K17	0.0460	3.03	up	Mus musculus branched chain aminotransferase 1, cytosolic (Bcat1), transcript variant 2, mRNA [NM_007532]
Clec4d	0.0491	4.93	up	Mus musculus Bloom syndrome homolog (human) (Blm), transcript variant 1, mRNA [NM_007550]
	0.0289	3.30	up	Mus musculus cyclin D1 (Ccnd1), mRNA [NM_007631]
Stk32a	0.0141	2.00	up	Mus musculus membrane-spanning 4-domains, subfamily A, member 1 (Ms4a1), mRNA [NM_007641]
Decr2	0.0403	2.85	up	Mus musculus cadherin 15 (Cdh15), mRNA [NM_007662]
C920025E04Rik	0.0158	1.56	up	Mus musculus cell death-inducing DNA fragmentation factor, alpha subunit-like effector A (Cidea), mRNA [NM_007702]
	0.0251	1.80	up	Mus musculus coagulation factor II (thrombin) receptor-like 3 (F2rl3), mRNA [NM_007975]
Crybb3	0.0242	1.71	up	Mus musculus coagulation factor II (thrombin) receptor-like 3 (F2rl3), mRNA [NM_007975]
Spry2	0.0176	7.04	up	Mus musculus folate receptor 1 (adult) (Folr1), mRNA [NM_008034]
	0.0499	2.60	up	Mus musculus formyl peptide receptor, related sequence 3 (Fpr-rs3), mRNA [NM_008040]
Pabpc5	0.0335	4.19	up	Mus musculus gamma-aminobutyric acid (GABA) A receptor, subunit delta (Gabrd), mRNA [NM_008072]
	0.0439	2.71	up	Mus musculus Rho GDP dissociation inhibitor (GDI) gamma (Arhgdig), mRNA [NM_008113]
A530083I20Rik	0.0006	3.17	up	Mus musculus histocompatibility 2, T region locus 24 (H2-T24), mRNA [NM_008207]

	0.0298	2.37	up	Mus musculus hemoglobin Y, beta-like embryonic chain (Hbb-y), mRNA [NM_008221]
	0.0127	5.21	up	Mus musculus histone deacetylase 1 (Hdac1), mRNA [NM_008228]
Trem1	0.0247	23.99	up	Mus musculus interleukin 12 receptor, beta 2 (Il12rb2), mRNA [NM_008354]
Lhpp	0.0335	1.58	up	Mus musculus killer cell lectin-like receptor, subfamily A, member 5 (Klra5), mRNA [NM_008463]
	0.0329	1.97	up	Mus musculus killer cell lectin-like receptor, subfamily A, member 5 (Klra5), mRNA [NM_008463]
	0.0049	3.65	up	Mus musculus achaete-scute complex homolog 1 (Drosophila) (Ascl1), mRNA [NM_008553]
	0.0000	3.74	up	Mus musculus myeloblastosis oncogene-like 2 (Mybl2), mRNA [NM_008652]
	0.0244	1.69	up	Mus musculus nuclear factor, erythroid derived 2 (Nfe2), mRNA [NM_008685]
	0.0264	2.36	up	Mus musculus nicotinamide nucleotide transhydrogenase (Nnt), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA [NM_008710]
Gm9465	0.0222	1.77	up	Mus musculus neurotrophic tyrosine kinase, receptor, type 3 (Ntrk3), transcript variant 1, mRNA [NM_008746]
Mmp24	0.0317	2.13	up	Mus musculus neurotrophic tyrosine kinase, receptor, type 3 (Ntrk3), transcript variant 1, mRNA [NM_008746]
	0.0242	1.89	up	Mus musculus peptidyl arginine deiminase, type II (Padi2), mRNA [NM_008812]
	0.0247	4.79	up	Mus musculus phosphatidylinositol transfer protein, alpha (Pitpna), mRNA [NM_008850]
Gm5067	0.0034	15.97	up	Mus musculus inositol polyphosphate 5-phosphatase K (Inpp5k), mRNA [NM_008916]
	0.0312	2.01	up	Mus musculus DNA primase, p58 subunit (Prim2), mRNA [NM_008922]
	0.0012	3.77	up	Mus musculus regulator of G-protein signaling 2 (Rgs2), mRNA [NM_009061]

Gm7575	0.0131	1.65	up	Mus musculus ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2 (St8sia2), mRNA [NM_009181]
1810037I17Rik	0.0130	11.44	up	Mus musculus solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (Slc1a6), mRNA [NM_009200]
	0.0050	1.61	up	Mus musculus spermine synthase (Sms), mRNA [NM_009214]
Gadd45gip1	0.0161	3.25	up	Mus musculus sterol O-acyltransferase 1 (Soat1), mRNA [NM_009230]
	0.0308	3.20	up	Mus musculus synaptotagmin I (Syt1), mRNA [NM_009306]
9030025P20Rik	0.0271	4.07	up	Mus musculus thyroid hormone receptor beta (Thrb), transcript variant 2, mRNA [NM_009380]
	0.0195	1.72	up	Mus musculus uncoupling protein 1 (mitochondrial, proton carrier) (Ucp1), nuclear gene encoding mitochondrial protein, mRNA [NM_009463]
Efcab4a	0.0440	1.94	up	Mus musculus ring finger protein 112 (Rnf112), mRNA [NM_009548]
	0.0448	2.84	up	Mus musculus adenylate cyclase 1 (Adcy1), mRNA [NM_009622]
Ucp1	0.0402	304.79	up	Mus musculus angiopoietin 4 (Angpt4), mRNA [NM_009641]
Zbtb5	0.0255	2.14	up	Mus musculus calcium/calmodulin-dependent serine protein kinase (MAGUK family) (Cask), mRNA [NM_009806]
	0.0369	1.71	up	Mus musculus CD6 antigen (Cd6), transcript variant 2, mRNA [NM_009852]
Ppp4r2	0.0379	1.62	up	Mus musculus early growth response 2 (Egr2), mRNA [NM_010118]
	0.0008	6.07	up	Mus musculus glutathione S-transferase, theta 2 (Gstt2), mRNA [NM_010361]
	0.0467	1.87	up	Mus musculus granzyme A (Gzma), mRNA [NM_010370]
Macrod1	0.0325	1.88	up	Mus musculus histocompatibility 2, class II, locus Mb2 (H2-DMb2), mRNA [NM_010388]

	0.0005	14.49	up	Mus musculus histidine ammonia lyase (Hal), mRNA [NM_010401]
	0.0054	2.32	up	Mus musculus homeodomain interacting protein kinase 1 (Hipk1), mRNA [NM_010432]
Btbd3	0.0403	1.60	up	Mus musculus solute carrier family 6 (neurotransmitter transporter, serotonin), member 4 (Slc6a4), mRNA [NM_010484]
LOC100045168	0.0121	2.38	up	Mus musculus inhibitor of DNA binding 1 (Id1), mRNA [NM_010495]
Gm8618	0.0480	1.82	up	Mus musculus killer cell lectin-like receptor subfamily A, member 12 (Klra12), mRNA [NM_010646]
	0.0416	5.38	up	Mus musculus lamin B1 (Lmnb1), mRNA [NM_010721]
9130019O22Rik	0.0175	1.72	up	Mus musculus lymphotoxin A (Lta), mRNA [NM_010735]
	0.0180	3.08	up	Mus musculus melanoma antigen, family B, 1 (Mageb1), mRNA [NM_010759]
Lypd6	0.0012	3.65	up	Mus musculus mesenchyme homeobox 1 (Meox1), mRNA [NM_010791]
Fnbp1	0.0337	3.45	up	Mus musculus C-type lectin domain family 4, member d (Clec4d), transcript variant 1, mRNA [NM_010819]
Gm1123	0.0464	3.09	up	Mus musculus Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 (Cited2), mRNA [NM_010828]
BC049349	0.0062	3.16	up	Mus musculus nebulin (Neb), mRNA [NM_010889]
Rcc2	0.0049	1.75	up	Mus musculus oxoglutarate dehydrogenase (lipoamide) (Ogdh), nuclear gene encoding mitochondrial protein, mRNA [NM_010956]
	0.0199	3.59	up	Mus musculus opioid receptor-like 1 (Oprl1), mRNA [NM_011012]
Inpp5k	0.0092	1.67	up	Mus musculus phosphatidylinositol 3-kinase, C2 domain containing, alpha polypeptide (Pik3c2a), mRNA [NM_011083]
Ogdh	0.0113	2.05	up	Mus musculus regulator of G-protein signaling 16 (Rgs16), mRNA [NM_011267]

2410024N18Rik	0.0374	2.37	up	Mus musculus secretin (Sct), mRNA [NM_011328]
Pglyrp2	0.0279	2.27	up	Mus musculus chemokine (C-C motif) ligand 3 (Ccl3), mRNA [NM_011337]
Trim65	0.0358	1.96	up	Mus musculus SRY-box containing gene 7 (Sox7), mRNA [NM_011446]
Olfr656	0.0074	3.46	up	Mus musculus syntaxin binding protein 4 (Stxbp4), mRNA [NM_011505]
	0.0050	2.30	up	Mus musculus tight junction protein 2 (Tjp2), mRNA [NM_011597]
Syt10	0.0377	22.66	up	Mus musculus vascular endothelial growth factor B (Vegfb), transcript variant 1, mRNA [NM_011697]
Zfp397	0.0089	1.51	up	Mus musculus zinc finger protein 259 (Zfp259), mRNA [NM_011752]
Tsc2	0.0305	1.53	up	Mus musculus sodium channel, voltage-gated, type XI, alpha (Scn11a), mRNA [NM_011887]
Gm14231	0.0152	2.13	up	Mus musculus 2-4-dienoyl-Coenzyme A reductase 2, peroxisomal (Decr2), mRNA [NM_011933]
Arih1	0.0384	2.18	up	Mus musculus metallothionein 1 (Mt1), mRNA [NM_013602]
Arm6c	0.0157	2.26	up	Mus musculus otogelin (Otog), mRNA [NM_013624]
Bcl11a	0.0152	3.53	up	Mus musculus mediator complex subunit 1 (Med1), transcript variant 1, mRNA [NM_013634]
Ugt3a1	0.0174	3.44	up	Mus musculus cytokine-dependent hematopoietic cell linker (Clnk), mRNA [NM_013748]
	0.0199	1.85	up	Mus musculus killer cell lectin-like receptor, subfamily A, member 15 (Klra15), mRNA [NM_013793]
	0.0289	2.47	up	Mus musculus killer cell lectin-like receptor, subfamily A, member 15 (Klra15), mRNA [NM_013793]
Rgs2	0.0117	1.89	up	Mus musculus killer cell lectin-like receptor, subfamily A, member 16 (Klra16), mRNA [NM_013794]
Ppp1r2	0.0206	1.76	up	Mus musculus regulator of G-protein signaling 1 (Rgs1), mRNA [NM_015811]

Alkbh5	0.0468	1.53	up	Mus musculus hypoxia inducible factor 3, alpha subunit (Hif3a), transcript variant 2, mRNA [NM_016868]
	0.0079	1.70	up	Mus musculus septin 1 (Sept1), mRNA [NM_017461]
	0.0398	1.80	up	Mus musculus synaptotagmin X (Syt10), mRNA [NM_018803]
AI852580	0.0297	4.23	up	Mus musculus B-cell translocation gene 4 (Btg4), mRNA [NM_019493]
	0.0433	3.26	up	Mus musculus WW domain-containing oxidoreductase (Wwox), mRNA [NM_019573]
Arhgap42	0.0328	1.57	up	Mus musculus Ras-related associated with diabetes (Rrad), mRNA [NM_019662]
Abhd1	0.0086	6.88	up	Mus musculus SPEN homolog, transcriptional regulator (Drosophila) (Spen), mRNA [NM_019763]
Raver1	0.0371	2.29	up	Mus musculus prostaglandin E synthase 3 (cytosolic) (Ptges3), mRNA [NM_019766]
	0.0409	1.85	up	Mus musculus ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila) (Arih1), mRNA [NM_019927]
Scpep1	0.0330	2.43	up	Mus musculus melanoma antigen, family A, 1 (Magea1), mRNA [NM_020015]
	0.0471	4.64	up	Mus musculus phosphoinositide-3-kinase, catalytic, gamma polypeptide (Pik3cg), transcript variant 1, mRNA [NM_020272]
Hcrtr1	0.0183	3.33	up	Mus musculus olfactory receptor 690 (Olfr690), mRNA [NM_020290]
Olfr139	0.0263	1.52	up	Mus musculus leukotriene B4 receptor 2 (Ltb4r2), mRNA [NM_020490]
	0.0388	1.73	up	Mus musculus cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial (Cmpk2), nuclear gene encoding mitochondrial protein, mRNA [NM_020557]
	0.0298	1.51	up	Mus musculus X-ray repair complementing defective repair in Chinese hamster cells 2 (Xrcc2), mRNA [NM_020570]

Zfp259	0.0082	1.51	up	Mus musculus abhydrolase domain containing 1 (Abhd1), mRNA [NM_021304]
	0.0443	1.82	up	Mus musculus family with sequence similarity 181, member B (Fam181b), mRNA [NM_021427]
Susd5	0.0036	1.90	up	Mus musculus nucleosome assembly protein 1-like 5 (Nap115), mRNA [NM_021432]
	0.0050	7.28	up	Mus musculus chemokine (C-C motif) ligand 8 (Ccl8), mRNA [NM_021443]
	0.0119	3.30	up	Mus musculus potassium voltage-gated channel, Isk-related family, member 1-like, pseudogene (Kcne1l), mRNA [NM_021487]
	0.0351	1.94	up	Mus musculus dapper homolog 1, antagonist of beta-catenin (xenopus) (Dact1), transcript variant 2, mRNA [NM_021532]
	0.0235	4.18	up	Mus musculus prostate transmembrane protein, androgen induced 1 (Pmepa1), mRNA [NM_022995]
Gm7302	0.0116	1.80	up	Mus musculus growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration) (Gfer), mRNA [NM_023040]
Renbp	0.0473	1.59	up	Mus musculus mucin 2 (Muc2), mRNA [NM_023566]
	0.0199	2.56	up	Mus musculus seryl-aminoacyl-tRNA synthetase 2 (Sars2), mRNA [NM_023637]
	0.0034	1.64	up	Mus musculus nuclear transcription factor, X-box binding 1 (Nfx1), mRNA [NM_023739]
	0.0368	2.24	up	Mus musculus cardiomyopathy associated 5 (Cmya5), mRNA [NM_023821]
Gm5509	0.0372	1.59	up	Mus musculus NOP56 ribonucleoprotein homolog (yeast) (Nop56), mRNA [NM_024193]
	0.0210	1.78	up	Mus musculus cytochrome b5 reductase 4 (Cyb5r4), mRNA [NM_024195]
	0.0115	2.14	up	Mus musculus kinesin family member 24 (Kif24), mRNA [NM_024241]

	0.0109	1.58	up	Mus musculus cytochrome P450, family 4, subfamily f, polypeptide 18 (Cyp4f18), mRNA [NM_024444]
Cdk9	0.0228	1.54	up	Mus musculus RIKEN cDNA 1810037I17 gene (1810037I17Rik), mRNA [NM_024461]
LOC627096	0.0036	5.78	up	Mus musculus RIKEN cDNA 1810037I17 gene (1810037I17Rik), mRNA [NM_024461]
	0.0310	1.71	up	Mus musculus inhibitor of growth family, member 5 (Ing5), mRNA [NM_025454]
Ttc15	0.0083	1.79	up	Mus musculus spermatogenesis associated glutamate (E)-rich protein 4d (Speer4d), mRNA [NM_025759]
Gm9100	0.0481	4.83	up	Mus musculus histidine triad nucleotide binding protein 3 (Hint3), mRNA [NM_025798]
	0.0171	1.78	up	Mus musculus RNA binding motif protein 8a (Rbm8a), transcript variant 2, mRNA [NM_025875]
	0.0283	1.68	up	Mus musculus RIKEN cDNA 2810474O19 gene (2810474O19Rik), mRNA [NM_026054]
Uhrf1bp1	0.0041	1.72	up	Mus musculus dedicator of cytokinesis 7 (Dock7), mRNA [NM_026082]
Gm7372	0.0268	2.89	up	Mus musculus ankyrin repeat domain 33B (Ankrd33b), transcript variant 1, mRNA [NM_026153]
	0.0403	2.59	up	Mus musculus ectonucleoside triphosphate diphosphohydrolase 4 (Entpd4), mRNA [NM_026174]
Olfr460	0.0087	1.74	up	Mus musculus solute carrier family 25, member 37 (Slc25a37), nuclear gene encoding mitochondrial protein, mRNA [NM_026331]
	0.0466	2.80	up	Mus musculus RNA (guanine-7-) methyltransferase (Rnmt), transcript variant 1, mRNA [NM_026440]
Hif3a	0.0416	1.58	up	Mus musculus M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein) (Mphosph10), mRNA [NM_026483]
LOC547349	0.0270	2.39	up	Mus musculus HD domain containing 3 (Hddc3), mRNA [NM_026812]

Fam181b	0.0210	1.72	up	Mus musculus zinc finger protein 397 (Zfp397), mRNA [NM_027007]
	0.0282	2.02	up	Mus musculus WD repeat and FYVE domain containing 1 (Wdfy1), transcript variant 2, mRNA [NM_027057]
Bcat1	0.0052	1.88	up	Mus musculus CD164 sialomucin-like 2 (Cd164l2), mRNA [NM_027152]
	0.0403	1.72	up	Mus musculus mediator of RNA polymerase II transcription, subunit 6 homolog (yeast) (Med6), mRNA [NM_027213]
Hipk1	0.0087	1.54	up	Mus musculus RIKEN cDNA 2010001M09 gene (2010001M09Rik), mRNA [NM_027222]
Narg2	0.0217	1.58	up	Mus musculus DNA segment, Chr 3, ERATO Doi 751, expressed (D3ErtD751e), transcript variant 3, mRNA [NM_027271]
Pltp	0.0377	2.01	up	Mus musculus tryptophanyl tRNA synthetase 2 (mitochondrial) (Wars2), nuclear gene encoding mitochondrial protein, mRNA [NM_027462]
Apoc3	0.0107	2.64	up	Mus musculus triggering receptor expressed on myeloid cells-like 1 (Trem1), mRNA [NM_027763]
	0.0416	1.65	up	Mus musculus gamma-glutamyltransferase 6 (Ggt6), mRNA [NM_027819]
	0.0037	4.55	up	Mus musculus VRho GTPase activating protein 42 (Arhgap42), mRNA [NM_027823]
2500002B13Rik	0.0145	1.82	up	Mus musculus UbiA prenyltransferase domain containing 1 (Ubiad1), mRNA [NM_027873]
Icmt	0.0168	1.56	up	Mus musculus von Willebrand factor C and EGF domains (Vwce), mRNA [NM_027913]
Sars2	0.0233	1.52	up	Mus musculus myeloid leukemia factor 1 interacting protein (Mlfl1p), mRNA [NM_027973]
Kcna7	0.0273	1.84	up	Mus musculus tumor necrosis factor receptor superfamily, member 13c (Tnfrsf13c), mRNA [NM_028075]
	0.0376	1.76	up	Mus musculus transmembrane protein 68 (Tmem68), mRNA [NM_028097]

	0.0274	2.19	up	Mus musculus spindle assembly 6 homolog (C. elegans) (Sass6), mRNA [NM_028349]
Prss29	0.0346	2.11	up	Mus musculus RIKEN cDNA 3110082D06 gene (3110082D06Rik), mRNA [NM_028474]
	0.0245	1.60	up	Mus musculus RIKEN cDNA 2410076I21 gene (2410076I21Rik), mRNA [NM_028598]
Med6	0.0432	1.59	up	Mus musculus WD repeat domain 75 (Wdr75), mRNA [NM_028599]
	0.0009	6.74	up	Mus musculus FCH domain only 1 (Fcho1), transcript variant 1, mRNA [NM_028715]
Pycr1	0.0278	5.43	up	Mus musculus dedicator of cytokinesis 8 (Dock8), mRNA [NM_028785]
Soat1	0.0269	1.50	up	Mus musculus golgi reassembly stacking protein 1 (Gorasp1), mRNA [NM_028976]
Vmn1r204	0.0373	2.62	up	Mus musculus serine carboxypeptidase 1 (Scpep1), mRNA [NM_029023]
	0.0035	1.59	up	Mus musculus RIKEN cDNA 6530401N04 gene (6530401N04Rik), mRNA [NM_029545]
	0.0116	2.57	up	Mus musculus thioredoxin domain containing 11 (Txndc11), transcript variant 1, mRNA [NM_029582]
Stxbp4	0.0119	1.65	up	Mus musculus phospholysine phosphohistidine inorganic pyrophosphate phosphatase (Lhpp), mRNA [NM_029609]
LOC100047869	0.0108	2.02	up	Mus musculus gasdermin A2 (Gsdma2), mRNA [NM_029727]
	0.0090	2.97	up	Mus musculus solute carrier family 10 (sodium/bile acid cotransporter family), member 7 (Slc10a7), mRNA [NM_029736]
Hdhd3	0.0313	2.29	up	Mus musculus collagen, type XXV, alpha 1 (Col25a1), transcript variant 1, mRNA [NM_029838]
	0.0392	3.09	up	Mus musculus arylsulfatase K (Arsk), mRNA [NM_029847]

H1foo	0.0061	1.97	up	Mus musculus occludin/ELL domain containing 1 (Ocel1), mRNA [NM_029865]
	0.0446	2.85	up	Mus musculus microtubule associated tumor suppressor candidate 2 (Mtus2), mRNA [NM_029920]
	0.0085	4.22	up	Mus musculus microtubule associated tumor suppressor candidate 2 (Mtus2), mRNA [NM_029920]
Gm3985	0.0052	2.11	up	Mus musculus small nuclear RNA activating complex, polypeptide 3 (Snapc3), mRNA [NM_029949]
	0.0200	1.67	up	Mus musculus trophinin associated protein (Troap), transcript variant 1, mRNA [NM_030159]
Heca	0.0195	1.87	up	Mus musculus CAP-GLY domain containing linker protein family, member 4 (Clip4), transcript variant 1, mRNA [NM_030179]
	0.0235	1.99	up	Mus musculus Sfi1 homolog, spindle assembly associated (yeast) (Sfi1), mRNA [NM_030207]
	0.0057	2.28	up	Mus musculus RIKEN cDNA 9130019O22 gene (9130019O22Rik), mRNA [NM_030226]
Arid4a	0.0125	1.91	up	Mus musculus WD repeat domain 76 (Wdr76), mRNA [NM_030234]
	0.0394	1.62	up	Mus musculus NEDD4 binding protein 1 (N4bp1), mRNA [NM_030563]
Ptges3	0.0001	1.51	up	Mus musculus solute carrier organic anion transporter family, member 1a4 (Slco1a4), mRNA [NM_030687]
Gm6343	0.0497	2.59	up	Mus musculus phosphoinositide-3-kinase adaptor protein 1 (Pik3ap1), mRNA [NM_031376]
	0.0164	1.53	up	Mus musculus vang-like 2 (van gogh, Drosophila) (Vangl2), mRNA [NM_033509]
Sos1	0.0356	1.63	up	Mus musculus glycoprotein (transmembrane) nmb (Gpnmb), mRNA [NM_053110]
Spen	0.0196	1.65	up	Mus musculus killer cell lectin-like receptor subfamily A, member 22 (Klra22), mRNA [NM_053152]
Muc2	0.0491	1.69	up	Mus musculus tripartite motif-containing 16 (Trim16), mRNA [NM_053169]

	0.0401	1.92	up	Mus musculus tripartite motif-containing 16 (Trim16), mRNA [NM_053169]
Cited2	0.0031	2.14	up	Mus musculus collagen, type IV, alpha 6 (Col4a6), mRNA [NM_053185]
2900052N01Rik	0.0012	6.30	up	Mus musculus regulating synaptic membrane exocytosis 1 (Rims1), transcript variant 1, mRNA [NM_053270]
Wdr76	0.0322	1.92	up	Mus musculus forkhead box P3 (Foxp3), mRNA [NM_054039]
LOC100048869	0.0386	5.71	up	Mus musculus synaptopodin 2 (Synpo2), mRNA [NM_080451]
	0.0338	1.84	up	Mus musculus keratin associated protein 16-8 (Krtap16-8), mRNA [NM_130856]
Faf1	0.0295	1.57	up	Mus musculus diencephalon/mesencephalon homeobox 1 (Dmbx1), transcript variant 1, mRNA [NM_130865]
	0.0381	1.67	up	Mus musculus isoprenylcysteine carboxyl methyltransferase (Icmt), mRNA [NM_133788]
	0.0073	2.01	up	Mus musculus armadillo repeat containing 6 (Armc6), mRNA [NM_133972]
Upk3b	0.0237	2.53	up	Mus musculus MACRO domain containing 1 (Macro1), mRNA [NM_134147]
	0.0226	2.07	up	Mus musculus ATPase, H ⁺ /K ⁺ transporting, nongastric, alpha polypeptide (Atp12a), mRNA [NM_138652]
	0.0351	4.36	up	Mus musculus cat eye syndrome chromosome region, candidate 5 homolog (human) (Cecr5), mRNA [NM_144815]
	0.0422	6.11	up	Mus musculus seizure related 6 homolog like 2 (Sez6l2), mRNA [NM_144926]
	0.0404	2.47	up	Mus musculus Ly6/Plaur domain containing 1 (Lypd1), mRNA [NM_145100]
LOC630233	0.0358	2.81	up	Mus musculus transportin 2 (importin 3, karyopherin beta 2b) (Tnp2), transcript variant 1, mRNA [NM_145390]
	0.0080	4.48	up	Mus musculus nuclear receptor subfamily 1, group D, member 1 (Nr1d1), mRNA [NM_145434]

2010320M18Rik	0.0352	3.66	up	Mus musculus GATA zinc finger domain containing 2A (Gatad2a), transcript variant 1, mRNA [NM_145596]
	0.0432	1.91	up	Mus musculus NMDA receptor-regulated gene 2 (Narg2), mRNA [NM_145618]
Gm2115	0.0308	1.85	up	Mus musculus RasGEF domain family, member 1B (Rasgef1b), transcript variant 1, mRNA [NM_145839]
	0.0270	2.69	up	Mus musculus mannoside acetylglucosaminyltransferase 2 (Mgat2), mRNA [NM_146035]
	0.0190	2.83	up	Mus musculus potassium channel, subfamily K, member 13 (Kcnk13), transcript variant 3, mRNA [NM_146037]
	0.0002	3.05	up	Mus musculus ring finger protein 144B (Rnf144b), transcript variant 1, mRNA [NM_146042]
	0.0136	2.39	up	Mus musculus consortin, connexin sorting protein (Cnst), mRNA [NM_146105]
Ccl3	0.0436	3.18	up	Mus musculus alanyl-tRNA synthetase (Aars), mRNA [NM_146217]
Hal	0.0014	67.90	up	Mus musculus olfactory receptor 122 (Olfr122), mRNA [NM_146288]
Trem2	0.0316	11.64	up	Mus musculus olfactory receptor 460 (Olfr460), mRNA [NM_146383]
D030051J21Rik	0.0405	2.92	up	Mus musculus olfactory receptor 18 (Olfr18), mRNA [NM_146563]
Klra5	0.0102	2.12	up	Mus musculus olfactory receptor 700 (Olfr700), mRNA [NM_146600]
Adcy1	0.0086	3.96	up	Mus musculus olfactory receptor 1441 (Olfr1441), mRNA [NM_146683]
Syt7	0.0238	1.77	up	Mus musculus olfactory receptor 39 (Olfr39), mRNA [NM_146825]
	0.0014	6.04	up	Mus musculus olfactory receptor 476 (Olfr476), mRNA [NM_146924]
	0.0366	1.93	up	Mus musculus olfactory receptor 353 (Olfr353), mRNA [NM_146941]

Ssbp2	0.0361	3.34	up	Mus musculus olfactory receptor 139 (Olfr139), mRNA [NM_147003]
	0.0029	1.64	up	Mus musculus ATP-binding cassette, sub-family A (ABC1), member 5 (Abca5), mRNA [NM_147219]
	0.0039	1.57	up	Mus musculus ATP-binding cassette, sub-family A (ABC1), member 5 (Abca5), mRNA [NM_147219]
2610019E17Rik	0.0109	1.50	up	Mus musculus E2F transcription factor 4 (E2f4), mRNA [NM_148952]
	0.0312	2.98	up	Mus musculus ATPase, class V, type 10D (Atp10d), mRNA [NM_153389]
	0.0335	2.17	up	Mus musculus beta-1,3-glucuronyltransferase 2 (glucuronosyltransferase S) (B3gat2), mRNA [NM_172124]
	0.0431	2.00	up	Mus musculus RIKEN cDNA 2810021J22 gene (2810021J22Rik), mRNA [NM_172403]
Id1	0.0240	1.54	up	Mus musculus benzodiazapine receptor associated protein 1 (Bzrap1), mRNA [NM_172449]
	0.0436	5.66	up	Mus musculus proline-rich transmembrane protein 3 (Prpt3), mRNA [NM_172487]
	0.0459	1.69	up	Mus musculus pleckstrin homology domain containing, family A member 7 (Plekha7), mRNA [NM_172743]
	0.0244	1.87	up	Mus musculus zinc finger protein 868 (Zfp868), transcript variant 1, mRNA [NM_172754]
Gm4125	0.0171	4.45	up	Mus musculus zinc finger protein 454 (Zfp454), mRNA [NM_172794]
	0.0226	2.94	up	Mus musculus dapper homolog 2, antagonist of beta-catenin (xenopus) (Dact2), mRNA [NM_172826]
	0.0079	2.22	up	Mus musculus lipoxygenase homology domains 1 (Loxhd1), mRNA [NM_172834]
Gm6404	0.0041	2.10	up	Mus musculus KN motif and ankyrin repeat domains 4 (Kank4), mRNA [NM_172872]
AW987390	0.0248	2.19	up	Mus musculus regulator of chromosome condensation 2 (Rcc2), mRNA [NM_173867]

Rexo1	0.0425	1.76	up	Mus musculus fragile X mental retardation 1 neighbor (Fmr1nb), transcript variant 1, mRNA [NM_174993]
	0.0165	2.49	up	Mus musculus autophagy-related 4C (yeast) (Atg4c), transcript variant 1, mRNA [NM_175029]
Tmem200b	0.0251	1.92	up	Mus musculus angiotensin II receptor, type 1b (Agtr1b), mRNA [NM_175086]
Wdfy1	0.0335	3.61	up	Mus musculus Rap guanine nucleotide exchange factor (GEF) 6 (Rapgef6), mRNA [NM_175258]
Depdc5	0.0305	2.10	up	Mus musculus choline dehydrogenase (Chdh), transcript variant 2, mRNA [NM_175343]
	0.0254	1.52	up	Mus musculus RIKEN cDNA 4930555G01 gene (4930555G01Rik), mRNA [NM_175393]
	0.0226	3.21	up	Mus musculus ATPase, H ⁺ transporting, lysosomal V0 subunit D2 (Atp6v0d2), mRNA [NM_175406]
	0.0109	1.66	up	Mus musculus ATPase, H ⁺ transporting, lysosomal V0 subunit D2 (Atp6v0d2), mRNA [NM_175406]
	0.0076	3.00	up	Mus musculus gap junction protein, gamma 2 (Gjc2), transcript variant 2, mRNA [NM_175452]
H2-T24	0.0254	3.11	up	Mus musculus Smith-Magenis syndrome chromosome region, candidate 8 homolog (human) (Smcr8), transcript variant 2, mRNA [NM_175491]
Klk10	0.0097	3.25	up	Mus musculus G protein-coupled receptor 68 (Gpr68), transcript variant 1, mRNA [NM_175493]
LOC100047591	0.0036	1.94	up	Mus musculus RIKEN cDNA C530028O21 gene (C530028O21Rik), transcript variant 1, mRNA [NM_175696]
Iqcc	0.0379	3.13	up	Mus musculus RIKEN cDNA 6330416L07 gene (6330416L07Rik), mRNA [NM_176962]
	0.0248	1.52	up	Mus musculus sperm flagellar 2 (Spef2), mRNA [NM_177123]
	0.0119	2.60	up	Mus musculus vacuolar protein sorting 13B (yeast) (Vps13b), mRNA [NM_177151]

	0.0277	1.81	up	Mus musculus procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide III (P4ha3), mRNA [NM_177161]
Snapc3	0.0464	2.60	up	Mus musculus kinase non-catalytic C-lobe domain (KIND) containing 1 (Kndc1), mRNA [NM_177261]
Gm7928	0.0292	1.94	up	Mus musculus vasohibin 1 (Vash1), mRNA [NM_177354]
Tmem29	0.0487	1.57	up	Mus musculus ribosomal modification protein rimK-like family member A (Rimkla), mRNA [NM_177572]
Ctcf1	0.0253	2.80	up	Mus musculus DNA segment, Chr 3, Brigham & Women's Genetics 0562 expressed (D3Bwg0562e), mRNA [NM_177664]
Rgs1	0.0437	9.64	up	Mus musculus DEP domain containing 5 (Depdc5), transcript variant 2, mRNA [NM_177786]
	0.0462	1.63	up	Mus musculus histone cluster 1, H2ak (Hist1h2ak), mRNA [NM_178183]
9830167H18Rik	0.0329	10.62	up	Mus musculus centromere protein M (Cenpm), transcript variant 2, mRNA [NM_178269]
	0.0439	1.53	up	Mus musculus mitogen-activated protein kinase 1 interacting protein 1-like (Mapk1ip1l), mRNA [NM_178684]
Tars2	0.0221	2.28	up	Mus musculus collagen and calcium binding EGF domains 1 (Ccbe1), mRNA [NM_178793]
Ntrk3	0.0147	1.77	up	Mus musculus tetratricopeptide repeat domain 15 (Ttc15), transcript variant 1, mRNA [NM_178811]
	0.0074	4.60	up	Mus musculus Na ⁺ /H ⁺ exchanger domain containing 2 (Nhedc2), nuclear gene encoding mitochondrial protein, mRNA [NM_178877]
Adora1	0.0060	1.61	up	Mus musculus schlafen 8 (Slfn8), transcript variant 1, mRNA [NM_181545]
	0.0037	3.34	up	Mus musculus SHQ1 homolog (S. cerevisiae) (Shq1), mRNA [NM_181590]

Acvr2a	0.0461	1.55	up	Mus musculus WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2 (Wfikkn2), mRNA [NM_181819]
Gm5491	0.0069	1.65	up	Mus musculus elastin microfibril interfacer 3 (Emilin3), mRNA [NM_182840]
C530028O21Rik	0.0348	3.14	up	Mus musculus protein phosphatase 4, regulatory subunit 2 (Ppp4r2), mRNA [NM_182939]
	0.0114	2.41	up	Mus musculus forkhead box I2 (Foxi2), mRNA [NM_183193]
	0.0475	3.06	up	Mus musculus family with sequence similarity 19, member A3 (Fam19a3), mRNA [NM_183224]
Sox7	0.0373	2.75	up	Mus musculus growth arrest and DNA-damage-inducible, gamma interacting protein 1 (Gadd45gip1), mRNA [NM_183358]
LOC670356	0.0277	2.73	up	Mus musculus TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae) (Trmt1), transcript variant 1, mRNA [NM_198020]
	0.0499	2.69	up	Mus musculus SCY1-like 2 (S. cerevisiae) (Scyl2), mRNA [NM_198021]
Wbp2	0.0194	2.10	up	Mus musculus progesterone and adiponectin receptor family member VI (Paqr6), mRNA [NM_198410]
2610018G03Rik	0.0080	1.62	up	Mus musculus pleckstrin homology domain containing, family G (with RhoGef domain) member 6 (Plekhg6), mRNA [NM_198604]
	0.0412	1.81	up	Mus musculus H1 histone family, member X (H1fx), mRNA [NM_198622]
Hist2h2bb	0.0327	2.45	up	Mus musculus Holliday junction recognition protein (Hjrp), mRNA [NM_198652]
LOC100047152	0.0239	5.94	up	Mus musculus Holliday junction recognition protein (Hjrp), mRNA [NM_198652]
Capn12	0.0190	2.57	up	Mus musculus RIKEN cDNA B930007M17 gene (B930007M17Rik), mRNA [NM_198659]

Cnst	0.0458	1.52	up	Mus musculus synovial sarcoma, X member B, breakpoint 9 (Ssxb9), mRNA [NM_199066]
Bcat1	0.0031	2.36	up	Mus musculus leucine zipper, putative tumor suppressor 1 (Lzts1), mRNA [NM_199364]
	0.0344	2.29	up	Mus musculus eukaryotic translation initiation factor 4E binding protein 3 (Eif4ebp3), mRNA [NM_201256]
Dffa	0.0271	1.79	up	Mus musculus Sycp3 like Y-linked (Sly), mRNA [NM_201530]
Cdhr2	0.0469	2.50	up	Mus musculus Sycp3 like Y-linked (Sly), mRNA [NM_201530]
	0.0130	2.85	up	Mus musculus vomeronasal 1 receptor 183 (Vmn1r183), mRNA [NM_203489]
Birc2	0.0288	1.52	up	Mus musculus expressed sequence AI314976 (AI314976), mRNA [NM_207219]
	0.0351	2.95	up	Mus musculus RIKEN cDNA 9430008C03 gene (9430008C03Rik), transcript variant 1, non-coding RNA [NR_015463]
	0.0436	1.78	up	Mus musculus RIKEN cDNA 2410018L13 gene (2410018L13Rik), non-coding RNA [NR_015504]
Bnip2	0.0461	2.31	up	Mus musculus RIKEN cDNA 2610035D17 gene (2610035D17Rik), non-coding RNA [NR_015556]
	0.0044	3.24	up	Mus musculus RIKEN cDNA A430093F15 gene (A430093F15Rik), non-coding RNA [NR_027805]
Cecr2	0.0467	1.85	up	Mus musculus RIKEN cDNA 4930429B21 gene (4930429B21Rik), non-coding RNA [NR_027966]
H2-T18	0.0300	4.69	up	Mus musculus zinc finger protein 672 (Zfp672), transcript variant 2, non-coding RNA [NR_028331]
LOC100047590	0.0108	4.04	up	Mus musculus predicted gene 3002 (Gm3002), non-coding RNA [NR_033388]
LOC100044375	0.0413	2.09	up	Mus musculus RIKEN cDNA 2900079G21 gene (2900079G21Rik), transcript variant 2, non-coding RNA [NR_033431]

	0.0371	2.01	up	Mus musculus predicted gene 6225 (Gm6225), non-coding RNA [NR_033457]
Tnfaip6	0.0480	2.84	up	Mus musculus predicted gene 10389 (Gm10389), non-coding RNA [NR_033541]
	0.0127	2.66	up	Mus musculus predicted gene 3230 (Gm3230), non-coding RNA [NR_033642]
A630033E08Rik	0.0405	4.76	up	Igk protein [Source:UniProtKB/TrEMBL;Acc:Q58EU8] [ENSMUST00000103304]
	0.0179	3.55	up	T-cell receptor beta, variable 13 Gene [Source:MGI Symbol;Acc:MGI:98587] [ENSMUST00000103299]
Shoc2	0.0216	3.58	up	Mus musculus immunoglobulin kappa light chain, variable region mRNA, clone BALB/c-26, partial cds. [U18569]
	0.0225	2.08	up	Mus musculus immunoglobulin kappa light chain, variable region mRNA, clone BALB/c-51, partial cds. [U18577]
E2f4	0.0299	1.57	up	Mus musculus immunoglobulin kappa light chain variable region mRNA, clone MRL1-56, partial cds. [U19317]
	0.0304	3.29	up	Mus musculus epidermal growth factor receptor antibody MR1scFv mRNA, partial cds. [U76382]
	0.0454	3.28	up	Mouse mRNA for the V(kappa) region from an anti-phosphatidyl choline producing hybridoma (NC19-F5). [X53355]
Aqp5	0.0347	2.37	up	Igk protein [Source:UniProtKB/TrEMBL;Acc:A1A540] [ENSMUST00000103328]
	0.0421	2.86	up	PREDICTED: Mus musculus predicted gene, EG668310 (EG668310), mRNA [XM_001000795]
	0.0072	4.33	up	PREDICTED: Mus musculus predicted gene, EG665574 (EG665574), mRNA [XM_001001448]
	0.0070	5.18	up	PREDICTED: Mus musculus similar to Ig heavy chain V region VH558 A1/A4 precursor (LOC677563), mRNA [XM_001004859]
	0.0113	2.10	up	PREDICTED: Mus musculus RIKEN cDNA 0610042G04 gene (0610042G04Rik), mRNA [XM_001472222]

	0.0336	2.66	up	PREDICTED: Mus musculus similar to cytochrome P450 CYP4F18 (LOC100044439), mRNA [XM_001472253]
4933407K13Rik	0.0091	2.19	up	PREDICTED: Mus musculus predicted gene, EG666415 (EG666415), mRNA [XM_001472293]
	0.0431	2.88	up	PREDICTED: Mus musculus similar to vacuolar H ⁺ ATPase G1 (LOC100044530), mRNA [XM_001472372]
	0.0088	1.71	up	PREDICTED: Mus musculus similar to Ubtg protein (LOC100044473), mRNA [XM_001472387]
LOC100048070	0.0478	1.59	up	PREDICTED: Mus musculus hypothetical protein LOC100039148 (LOC100039148), mRNA [XM_001472488]
Gm7606	0.0401	1.70	up	PREDICTED: Mus musculus similar to CDNA sequence BC061237 (LOC100044625), mRNA [XM_001472731]
LOC100045068	0.0399	4.71	up	PREDICTED: Mus musculus hypothetical protein LOC100039461 (LOC100039461), mRNA [XM_001472925]
Gm4121	0.0388	2.31	up	PREDICTED: Mus musculus similar to cyclic nucleotide gated channel beta 1 (LOC100044816), mRNA [XM_001473112]
	0.0295	2.70	up	PREDICTED: Mus musculus similar to MHC class Ib antigen Qa-1c (LOC100046736), mRNA [XM_001473226]
	0.0467	5.76	up	Novel protein [Source:UniProtKB/TrEMBL;Acc:B1AX05] [ENSMUST00000116362]
Gm7684	0.0037	3.32	up	PREDICTED: Mus musculus similar to Ubtg protein (LOC100044930), mRNA [XM_001473350]
	0.0351	3.71	up	RIKEN cDNA 1700066J24 gene Gene [Source:MGI Symbol;Acc:MGI:1924242] [ENSMUST00000038960]
	0.0217	4.72	up	PREDICTED: Mus musculus similar to Sycp3 like Y-linked (LOC100039839), mRNA [XM_001473640]

	0.0239	1.91	up	PREDICTED: Mus musculus hypothetical protein LOC100039844 (LOC100039844), mRNA [XM_001473654]
	0.0275	2.58	up	PREDICTED: Mus musculus similar to KIAA1731 protein (LOC100045054), mRNA [XM_001473884]
	0.0075	3.48	up	PREDICTED: Mus musculus hypothetical protein LOC100040047 (LOC100040047), mRNA [XM_001473997]
	0.0243	3.98	up	PREDICTED: Mus musculus similar to Pr22, transcript variant 1 (LOC100039888), mRNA [XM_001474074]
Xpnpep3	0.0448	1.87	up	PREDICTED: Mus musculus similar to Ubtg protein (LOC100040097), mRNA [XM_001474084]
Gtf2h5	0.0243	3.17	up	PREDICTED: Mus musculus hypothetical LOC669675 (LOC669675), mRNA [XM_001474101]
	0.0138	5.04	up	PREDICTED: Mus musculus hypothetical protein LOC100040101 (LOC100040101), mRNA [XM_001474106]
Sgsm2	0.0450	1.91	up	PREDICTED: Mus musculus similar to spermiogenesis specific transcript on the Y 1 (LOC100040235), mRNA [XM_001474135]
BC023969	0.0370	2.97	up	PREDICTED: Mus musculus similar to prostatic steroid binding protein (LOC623688), mRNA [XM_001474206]
Ppyr1	0.0083	1.95	up	PREDICTED: Mus musculus RIKEN cDNA 4933424M12 gene (4933424M12Rik), mRNA [XM_001474219]
Gm8840	0.0098	2.04	up	keratin associated protein 20-2 [Source:RefSeq peptide;Acc:NP_001157087] [ENSMUST00000073111]
	0.0120	1.71	up	PREDICTED: Mus musculus hypothetical protein LOC100045515 (LOC100045515), mRNA [XM_001474431]
	0.0172	2.07	up	PREDICTED: Mus musculus similar to Dmn protein (LOC100045537), mRNA [XM_001474483]

	0.0135	2.92	up	PREDICTED: Mus musculus hypothetical protein LOC100040327 (LOC100040327), mRNA [XM_001474506]
LOC100044674	0.0190	2.32	up	PREDICTED: Mus musculus similar to ribosomal protein L30 (LOC100045378), mRNA [XM_001474827]
D3Ertd751e	0.0293	1.80	up	PREDICTED: Mus musculus RIKEN cDNA 4921534A09 gene (4921534A09Rik), mRNA [XM_001474893]
	0.0092	1.84	up	PREDICTED: Mus musculus hypothetical protein LOC100040715 (LOC100040715), mRNA [XM_001475122]
	0.0495	1.96	up	PREDICTED: Mus musculus hypothetical protein LOC100040747 (LOC100040747), mRNA [XM_001475175]
	0.0288	2.27	up	ligand dependent nuclear receptor corepressor-like Gene [Source:MGI (curated);Acc:MGI:2651932] [ENSMUST00000045586]
	0.0486	2.26	up	PREDICTED: Mus musculus hypothetical LOC672763 (LOC672763), mRNA [XM_001475504]
	0.0208	2.11	up	PREDICTED: Mus musculus similar to zinc finger, DHHC domain containing 6 (LOC433204), mRNA [XM_001475540]
Grsf1	0.0281	1.89	up	PREDICTED: Mus musculus predicted gene, EG623230 (EG623230), mRNA [XM_001475812]
Uhrf1bp1l	0.0044	1.65	up	PREDICTED: Mus musculus RIKEN cDNA 5033425G24 gene (5033425G24Rik), mRNA [XM_001475910]
	0.0086	5.66	up	
	0.0440	2.13	up	PREDICTED: Mus musculus hypothetical protein LOC100046257 (LOC100046257), mRNA [XM_001476052]
	0.0046	2.06	up	PREDICTED: Mus musculus hypothetical protein LOC100041239 (LOC100041239), mRNA [XM_001476062]

Kdm3b	0.0202	1.52	up	cyclic nucleotide gated channel beta 1 Gene [Source:MGI (curated);Acc:MGI:2664102] [ENSMUST00000121162]
	0.0187	2.22	up	Putative uncharacterized protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q3U2L9] [ENSMUST00000098384]
Aph1a	0.0075	1.61	up	PREDICTED: Mus musculus hypothetical LOC636082 (LOC636082), mRNA [XM_001476250]
	0.0003	5.48	up	PREDICTED: Mus musculus similar to membrane-associated ring finger (C3HC4) 5 (LOC665553), mRNA [XM_001476311]
LOC100048866	0.0132	1.80	up	predicted gene 1502 Gene [Source:MGI Symbol;Acc:MGI:2686348] [ENSMUST00000103348]
	0.0498	1.62	up	PREDICTED: Mus musculus hypothetical protein LOC100041569 (LOC100041569), mRNA [XM_001476596]
Nap1l5	0.0470	3.96	up	PREDICTED: Mus musculus hypothetical LOC672511 (LOC672511), mRNA [XM_001476651]
	0.0293	2.40	up	PREDICTED: Mus musculus similar to High mobility group protein B2 (High mobility group protein 2) (HMG-2) (LOC546590), mRNA [XM_001476729]
Gm13453	0.0132	1.78	up	PREDICTED: Mus musculus RIKEN cDNA 4930547M16 gene, transcript variant 1 (4930547M16Rik), mRNA [XM_001476789]
	0.0345	3.01	up	PREDICTED: Mus musculus hypothetical protein LOC100046382 (LOC100046382), mRNA [XM_001476831]
	0.0313	2.09	up	PREDICTED: Mus musculus hypothetical protein LOC100041575 (LOC100041575), mRNA [XM_001477132]
Nfx1	0.0332	1.63	up	PREDICTED: Mus musculus gene model 831, (NCBI) (Gm831), mRNA [XM_001477145]

Rbm4b	0.0486	1.57	up	PREDICTED: Mus musculus similar to [Human Ig rearranged gamma chain mRNA, V-J-C region and complete cds.], gene product (LOC100046973), mRNA [XM_001477170]
Clcc1	0.0391	2.43	up	PREDICTED: Mus musculus similar to [Human Ig rearranged gamma chain mRNA, V-J-C region and complete cds.], gene product (LOC100047070), mRNA [XM_001477334]
	0.0138	2.26	up	PREDICTED: Mus musculus predicted gene, EG666257 (EG666257), mRNA [XM_001477516]
	0.0301	1.66	up	PREDICTED: Mus musculus similar to Predicted gene, EG432825, transcript variant 2 (LOC100042054), mRNA [XM_001477672]
	0.0461	4.20	up	PREDICTED: Mus musculus hypothetical protein LOC100042207 (LOC100042207), mRNA [XM_001477897]
Sfi1	0.0324	1.91	up	Ig heavy chain V region 5-84 Precursor [Source:UniProtKB/Swiss-Prot;Acc:P18525] [ENSMUST00000103450]
	0.0181	2.97	up	PREDICTED: Mus musculus similar to Cell division cycle 34 homolog (S. cerevisiae) (LOC100046898), mRNA [XM_001478127]
	0.0156	61.46	up	PREDICTED: Mus musculus hypothetical LOC433894 (LOC433894), mRNA [XM_001478331]
	0.0110	2.71	up	PREDICTED: Mus musculus hypothetical protein LOC100042554 (LOC100042554), mRNA [XM_001478420]
Fam32a	0.0064	2.25	up	PREDICTED: Mus musculus similar to crooked legs CG14938-PB (LOC673160), mRNA [XM_001478468]
	0.0322	2.10	up	nudix (nucleotide diphosphate linked moiety X)-type motif 3 Gene [Source:MGI (curated);Acc:MGI:1928484] [ENSMUST00000114886]

	0.0044	2.69	up	PREDICTED: Mus musculus similar to development and differentiation enhancing factor 2 (LOC668698), mRNA [XM_001478806]
Gm6211	0.0228	1.59	up	PREDICTED: Mus musculus hypothetical protein LOC100047775 (LOC100047775), mRNA [XM_001478833]
Drp2	0.0200	2.45	up	PREDICTED: Mus musculus predicted gene, EG668670 (EG668670), mRNA [XM_001478977]
	0.0158	4.08	up	PREDICTED: Mus musculus predicted gene, EG667414 (EG667414), mRNA [XM_001479170]
	0.0038	1.66	up	PREDICTED: Mus musculus hypothetical protein LOC100042858 (LOC100042858), mRNA [XM_001479342]
4930597O21Rik	0.0230	3.48	up	PREDICTED: Mus musculus similar to allergen dI chain C2C (LOC100048016), mRNA [XM_001479348]
Cyb5r4	0.0265	1.58	up	PREDICTED: Mus musculus similar to thioredoxin family Trp26 (LOC100047869), mRNA [XM_001479479]
	0.0461	1.73	up	PREDICTED: Mus musculus hypothetical protein LOC100044034 (LOC100044034), mRNA [XM_001479541]
Scyl2	0.0344	2.54	up	PREDICTED: Mus musculus hypothetical protein LOC100042951 (LOC100042951), mRNA [XM_001479696]
	0.0123	3.37	up	PREDICTED: Mus musculus similar to thioredoxin peroxidase II (LOC100048277), mRNA [XM_001479909]
Mtus2	0.0321	2.36	up	PREDICTED: Mus musculus hypothetical LOC669185 (LOC669185), mRNA [XM_001479912]
2310051F07Rik	0.0253	1.53	up	PREDICTED: Mus musculus similar to 4930529M08Rik protein (LOC100048288), mRNA [XM_001479936]
	0.0368	2.76	up	PREDICTED: Mus musculus similar to mKIAA0328 protein (LOC100043493), mRNA [XM_001480026]

	0.0305	1.84	up	PREDICTED: Mus musculus predicted gene, EG622645 (EG622645), mRNA [XM_001480132]
	0.0023	2.17	up	PREDICTED: Mus musculus similar to MGC58416 protein (LOC100048568), mRNA [XM_001480694]
Rnf144b	0.0469	1.61	up	PREDICTED: Mus musculus RIKEN cDNA 4933406C10 gene (4933406C10Rik), mRNA [XM_001480777]
N4bp1	0.0468	1.68	up	PREDICTED: Mus musculus hypothetical protein LOC100043874 (LOC100043874), mRNA [XM_001481156]
Kank4	0.0262	5.10	up	PREDICTED: Mus musculus similar to hypothetical protein FLJ38281 (LOC436100), mRNA [XM_001481293]
	0.0251	2.64	up	PREDICTED: Mus musculus similar to T-cell receptor alpha chain V region CTL-F3 precursor (LOC328483), mRNA [XM_283255]
	0.0094	1.86	up	PREDICTED: Mus musculus gene model 1667, (NCBI) (Gm1667), mRNA [XM_358618]
Gpbar1	0.0350	2.14	up	PREDICTED: Mus musculus similar to 60S ribosomal protein L9 (LOC433546), mRNA [XM_485172]
	0.0296	2.88	up	PREDICTED: Mus musculus predicted gene, EG434279 (EG434279), mRNA [XM_489223]
Baiap2l2	0.0212	4.78	up	PREDICTED: Mus musculus predicted gene, EG623174 (EG623174), mRNA [XM_887605]
	0.0434	2.92	up	PREDICTED: Mus musculus predicted gene, EG627915 (EG627915), mRNA [XM_892615]
	0.0284	1.67	up	PREDICTED: Mus musculus predicted gene, EG627924 (EG627924), mRNA [XM_892630]
	0.0288	3.66	up	PREDICTED: Mus musculus RIKEN cDNA 2310010J17 gene (2310010J17Rik), mRNA [XM_896611]
Vegfb	0.0173	1.56	up	PREDICTED: Mus musculus predicted gene, EG625276 (EG625276), mRNA [XM_898698]
Gm9590	0.0427	2.59	up	PREDICTED: Mus musculus similar to peptidylprolyl isomerase H (LOC629952), mRNA [XM_905767]

	0.0089	1.75	up	PREDICTED: Mus musculus similar to zinc finger protein 533 (LOC634745), mRNA [XM_909565]
	0.0354	2.85	up	PREDICTED: Mus musculus predicted gene, EG634881 (EG634881), mRNA [XM_909745]
Ankrd34a	0.0401	1.67	up	PREDICTED: Mus musculus hypothetical LOC635339 (LOC635339), mRNA [XM_910366]
	0.0351	1.81	up	PREDICTED: Mus musculus similar to monoclonal antibody heavy chain (LOC636441), mRNA [XM_911832]
E230006M18Rik	0.0202	2.52	up	PREDICTED: Mus musculus similar to monoclonal antibody heavy chain (LOC636441), mRNA [XM_911832]
	0.0126	5.24	up	PREDICTED: Mus musculus similar to Guanine nucleotide-binding protein G(i), alpha-2 subunit (Adenylate cyclase-inhibiting G alpha protein) (LOC637747), mRNA [XM_913514]
	0.0114	2.88	up	VDJ complex Fragment [Source:UniProtKB/TrEMBL;Acc:A0NA69] [ENSMUST00000103469]
	0.0427	2.21	up	predicted gene 5751 Gene [Source:MGI Symbol;Acc:MGI:3642927] [ENSMUST00000115561]
	0.0081	1.67	up	PREDICTED: Mus musculus similar to paired immunoglobulin-like type 2 receptor alpha (LOC640067), mRNA [XM_916809]
Nudc	0.0151	1.60	up	PREDICTED: Mus musculus similar to Ig H-chain (LOC640614), mRNA [XM_917662]
Vwce	0.0050	1.57	up	killer cell lectin-like receptor subfamily A, member 11 Gene [Source:MGI Symbol;Acc:MGI:1321092] [ENSMUST00000112029]
Wars2	0.0464	3.18	up	Ig heavy chain V region BCL1 Precursor [Source:UniProtKB/Swiss-Prot;Acc:P01759] [ENSMUST00000103538]

H2-M10.3	0.0412	3.24	up	PREDICTED: Mus musculus predicted gene, EG640636 (EG640636), mRNA [XM_925112]
Pik3c2a	0.0205	1.86	up	PREDICTED: Mus musculus predicted gene, EG664821 (EG664821), mRNA [XM_972876]
Klra4	0.0071	20.68	up	PREDICTED: Mus musculus similar to keratin associated protein 5-2 (LOC665225), mRNA [XM_975463]
Prkrir	0.0058	2.06	up	PREDICTED: Mus musculus predicted gene, EG666293 (EG666293), mRNA [XM_977531]
	0.0444	1.52	up	PREDICTED: Mus musculus predicted gene, EG665619 (EG665619), mRNA [XM_978208]
LOC674543	0.0486	1.56	up	LOC380994 protein [Source:UniProtKB/TrEMBL;Acc:Q4KL07] [ENSMUST00000115920]
D330038O06Rik	0.0212	1.56	up	PREDICTED: Mus musculus RIKEN cDNA C430049B03 gene (C430049B03Rik), mRNA [XM_980571]
Eif4ebp3	0.0390	1.51	up	PREDICTED: Mus musculus predicted gene, EG666668 (EG666668), mRNA [XM_985281]
Lcorl	0.0000	1.72	up	PREDICTED: Mus musculus predicted gene, EG666892 (EG666892), mRNA [XM_986833]
Rnf112	0.0022	1.88	up	PREDICTED: Mus musculus RIKEN cDNA A830035A12 gene (A830035A12Rik), mRNA [XM_986896]
Ubiad1	0.0222	2.99	up	PREDICTED: Mus musculus predicted gene, EG621312 (EG621312), misc RNA [XR_002190]
	0.0176	3.37	up	PREDICTED: Mus musculus similar to CDK105 (LOC675063), misc RNA [XR_004753]
	0.0310	2.98	up	PREDICTED: Mus musculus similar to ADP-ribosylation factor (LOC666676), misc RNA [XR_030655]
	0.0348	3.79	up	PREDICTED: Mus musculus similar to ribosomal protein L13 (LOC666226), misc RNA [XR_030829]

	0.0095	1.95	up	PREDICTED: Mus musculus similar to ubiquitin-like domain containing CTD phosphatase 1 (LOC667807), misc RNA [XR_030888]
	0.0463	6.28	up	PREDICTED: Mus musculus similar to bromodomain adjacent to zinc finger domain, 2A (LOC622082), misc RNA [XR_030892]
	0.0365	1.53	up	PREDICTED: Mus musculus similar to ribosomal protein L26 (LOC665373), misc RNA [XR_031541]
5430417L22Rik	0.0151	1.78	up	PREDICTED: Mus musculus similar to PHD finger protein 14 (LOC665296), misc RNA [XR_031580]
LOC640965	0.0190	3.72	up	PREDICTED: Mus musculus similar to Sycp3 like Y-linked (LOC100040245), misc RNA [XR_031612]
	0.0418	3.99	up	PREDICTED: Mus musculus similar to mKIAA1116 protein (LOC668270), misc RNA [XR_031680]
	0.0106	2.58	up	PREDICTED: Mus musculus similar to SCIRP10-related protein (LOC100045816), misc RNA [XR_032019]
	0.0099	1.87	up	PREDICTED: Mus musculus similar to ribosomal protein L27a (LOC667497), misc RNA [XR_032610]
Gm3902	0.0362	1.96	up	PREDICTED: Mus musculus similar to ribosomal protein L21 (LOC675609), misc RNA [XR_032645]
	0.0286	3.30	up	PREDICTED: Mus musculus similar to high mobility group nucleosomal binding domain 2 (LOC626075), misc RNA [XR_032823]
	0.0358	1.86	up	PREDICTED: Mus musculus similar to histone deacetylase (LOC230765), misc RNA [XR_032827]
Olfr332	0.0349	3.50	up	PREDICTED: Mus musculus similar to RIKEN cDNA C130026I21 gene (LOC100041746), misc RNA [XR_033326]
Rce1	0.0395	1.72	up	PREDICTED: Mus musculus similar to High mobility group box 1 (LOC674543), misc RNA [XR_033362]
	0.0012	2.73	up	PREDICTED: Mus musculus similar to ribosomal protein L11 (LOC627317), misc RNA [XR_033591]

LOC100045220	0.0260	4.04	up	PREDICTED: Mus musculus similar to PA28 beta subunit (LOC666098), misc RNA [XR_033855]
Gm2922	0.0123	19.59	up	PREDICTED: Mus musculus similar to hCG1997137 (LOC226574), misc RNA [XR_034285]
	0.0384	3.11	up	PREDICTED: Mus musculus similar to FUS interacting protein (serine/arginine-rich) 1 (LOC630233), misc RNA [XR_034286]
	0.0050	8.55	up	PREDICTED: Mus musculus similar to replication factor C 5 (LOC100048070), misc RNA [XR_034330]
	0.0165	1.58	up	PREDICTED: Mus musculus RIKEN cDNA C330011M18 gene (C330011M18Rik), misc RNA [XR_035219]
Padi2	0.0086	1.66	up	PREDICTED: Mus musculus predicted gene, EG667728 (EG667728), misc RNA [XR_035232]
	0.0166	2.66	up	PREDICTED: Mus musculus RIKEN cDNA 5330426L24 gene (5330426L24Rik), misc RNA [XR_035439]
B930007M17Rik	0.0058	2.13	down	Brain cDNA, clone MNCb-2457Novel proteinMCG140451 ;; [Source:UniProtKB/TrEMBL;Acc:Q9JJ83] [ENSMUST00000062902]
Steap1	0.0101	2.57	down	Mus musculus 6E6 monoclonal antibody heavy chain variable region, (IgH) mRNA, partial cds. [AF045501]
AI450886	0.0069	4.71	down	Mus musculus JNK interacting protein-3b (Jip3) mRNA, complete cds. [AF178637]
Gm5606	0.0351	2.51	down	mj69c10.y1 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:481362 5' similar to gb:X53176 Mouse integrin alpha-4 mRNA (MOUSE);. [AI595487]
Cd19	0.0195	2.17	down	UI-M-BH0-aiu-a-10-0-UI.s1 NIH_BMAP_M_S1 Mus musculus cDNA clone UI-M-BH0-aiu-a-10-0-UI 3'. [AI852580]
	0.0050	1.50	down	anthrax toxin receptor 1 Gene [Source:MGI Symbol;Acc:MGI:1916788] [ENSMUST00000113646]

BB217526	0.0176	3.63	down	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930557J02 product:unclassifiable, full insert sequence. [AK016164]
B230104I21Rik	0.0027	2.47	down	DIX domain containing 1 Gene [Source:MGI (curated);Acc:MGI:2679721] [ENSMUST00000098784]
	0.0203	3.90	down	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932412D23 product:unclassifiable, full insert sequence. [AK016521]
LOC100048288	0.0033	2.27	down	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933438K21 product:weakly similar to ORF4 PROTEIN [Rattus norvegicus], full insert sequence. [AK017111]
	0.0202	5.21	down	RIKEN cDNA 6530402F18 gene Gene [Source:MGI Symbol;Acc:MGI:1923470] [ENSMUST00000028141]
Hdac1	0.0018	4.71	down	Mus musculus adult male colon cDNA, RIKEN full-length enriched library, clone:9030625G05 product:unclassifiable, full insert sequence. [AK018576]
A730028G07Rik	0.0423	1.83	down	Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130214F15 product:unclassifiable, full insert sequence. [AK020279]
Gm16525	0.0276	2.97	down	phosphodiesterase 5A, cGMP-specific Gene [Source:MGI Symbol;Acc:MGI:2651499] [ENSMUST00000073213]
	0.0063	2.46	down	tyrosyl-DNA phosphodiesterase 1 Gene [Source:MGI (curated);Acc:MGI:1920036] [ENSMUST00000095477]
2010002M12Rik	0.0046	1.75	down	Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430011C21 product:unclassifiable, full insert sequence. [AK034586]
LOC100047647	0.0036	2.07	down	Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530073H14 product:unclassifiable, full insert sequence. [AK035593]
	0.0123	2.33	down	tribbles homolog 1 (Drosophila) Gene [Source:MGI (curated);Acc:MGI:2443397] [ENSMUST00000118228]

	0.0111	3.36	down	paired immunoglobulin-like type 2 receptor alpha Gene [Source:MGI (curated);Acc:MGI:2450529] [ENSMUST00000110980]
Cd164l2	0.0274	2.07	down	Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length enriched library, clone:B430316J06 product:unclassifiable, full insert sequence. [AK046698]
C430049B03Rik	0.0062	1.86	down	protein tyrosine phosphatase, receptor type, U Gene [Source:MGI (curated);Acc:MGI:1321151] [ENSMUST00000097860]
Bcl2l14	0.0114	2.12	down	Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D230021J12 product:unclassifiable, full insert sequence. [AK051942]
Iqcf4	0.0425	5.22	down	transmembrane protein 161B Gene [Source:MGI Symbol;Acc:MGI:1919995] [ENSMUST00000050885]
Col25a1	0.0137	3.35	down	enhancer trap locus 4 Gene [Source:MGI (curated);Acc:MGI:95454] [ENSMUST00000114610]
0610042G04Rik	0.0115	3.99	down	Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN full-length enriched library, clone:E230006M18 product:unclassifiable, full insert sequence. [AK053951]
2810408P10Rik	0.0209	4.35	down	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932416E17 product:unclassifiable, full insert sequence. [AK077028]
	0.0215	1.60	down	Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430017K17 product:unclassifiable, full insert sequence. [AK079696]
	0.0461	1.87	down	Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230098O21 product:unclassifiable, full insert sequence. [AK082735]
4930555G01Rik	0.0256	3.52	down	Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone:5830419E12 product:hypothetical protein, full insert sequence. [AK134048]

	0.0423	2.32	down	Putative uncharacterized protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q3UYL4] [ENSMUST00000098916]
Atg4c	0.0116	5.32	down	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3UX89] [ENSMUST00000099388]
5830419E12Rik	0.0391	2.98	down	Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330151M24 product:unclassifiable, full insert sequence. [AK136855]
	0.0137	6.72	down	Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530027F24 product:unclassifiable, full insert sequence. [AK137174]
	0.0080	2.69	down	Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430087N04 product:hypothetical protein, full insert sequence. [AK138828]
	0.0093	3.69	down	Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530083O18 product:unclassifiable, full insert sequence. [AK139027]
Troap	0.0142	5.03	down	Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B930011K17 product:unclassifiable, full insert sequence. [AK140493]
	0.0211	2.28	down	Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930032C08 product:unclassifiable, full insert sequence. [AK142864]
Slc30a7	0.0259	5.83	down	Mus musculus mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched library, clone:G830029J16 product:unclassifiable, full insert sequence. [AK145039]
Gml	0.0446	5.95	down	Mus musculus melanocyte cDNA, RIKEN full-length enriched library, clone:G270073A20 product:unclassifiable, full insert sequence. [AK147870]

Gm3642	0.0111	4.26	down	Mus musculus adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330105A21 product:unclassifiable, full insert sequence. [AK162965]
Olf312	0.0016	5.00	down	peroxiredoxin 4 Gene [Source:MGI (curated);Acc:MGI:1859815] [ENSMUST00000038776]
	0.0090	3.67	down	B-cell CLL/lymphoma 11A (zinc finger protein) Gene [Source:MGI (curated);Acc:MGI:106190] [ENSMUST00000109514]
	0.0069	1.87	down	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3TD87] [ENSMUST00000087655]
4921534A09Rik	0.0481	2.10	down	Mus musculus anti-human uPAR immunoglobulin light chain variable region mRNA, partial cds. [AY351698]
	0.0119	2.88	down	NLR family, pyrin domain containing 9C Gene [Source:MGI Symbol;Acc:MGI:3028627] [ENSMUST00000041845]
Syt1	0.0364	2.21	down	TATA box binding protein-like 1 Gene [Source:MGI (curated);Acc:MGI:1339946] [ENSMUST00000092668]
LOC100039005	0.0097	3.44	down	myosin, heavy polypeptide 9, non-muscle Gene [Source:MGI (curated);Acc:MGI:107717] [ENSMUST00000065458]
Sly	0.0202	18.29	down	Mus musculus cDNA clone IMAGE:40046733. [BC125023]
Apln	0.0092	3.99	down	602091706F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4206096 5'. [BF531481]
	0.0219	1.69	down	Mus musculus clone AiDWTimmB-38 immunoglobulin kappa light chain mRNA, partial cds. [DQ372793]
Hist1h2ak	0.0321	1.67	down	Mus musculus clone AIDWTmB-11 immunoglobulin kappa light chain mRNA, partial cds. [DQ372800]
Emilin3	0.0288	1.54	down	Mus musculus developing brain homeobox 1 (Dbx1), mRNA [NM_001005232]
	0.0395	1.86	down	Mus musculus ArfGAP with SH3 domain, ankyrin repeat and PH domain 3 (Asap3), mRNA [NM_001008232]

	0.0471	2.13	down	Mus musculus BCL2/adenovirus E1B interacting protein 2 (Bnip2), transcript variant alpha, mRNA [NM_001008238]
	0.0361	2.91	down	Mus musculus olfactory receptor 314 (Olfr314), mRNA [NM_001011760]
Kit	0.0221	2.07	down	Mus musculus cDNA sequence D10627 (D10627), mRNA [NM_001013379]
Btg4	0.0009	6.90	down	Mus musculus protocadherin 17 (Pcdh17), mRNA [NM_001013753]
	0.0077	2.07	down	Mus musculus growth arrest-specific 2 like 2 (Gas2l2), mRNA [NM_001013759]
	0.0414	1.55	down	Mus musculus similar to MHC class I antigen precursor (LOC547349), mRNA [NM_001025208]
	0.0278	2.43	down	Mus musculus DNA fragmentation factor, alpha subunit (Dffa), transcript variant 1, mRNA [NM_001025296]
	0.0106	1.62	down	Mus musculus cadherin-related family member 2 (Cdhr2), mRNA [NM_001033364]
	0.0486	3.27	down	Mus musculus predicted gene 826 (Gm826), mRNA [NM_001033411]
LOC664934	0.0355	25.24	down	Mus musculus XIAP associated factor 1 (Xaf1), mRNA [NM_001037713]
Pdia2	0.0199	1.56	down	Mus musculus similar to Sycp3 like Y-linked (LOC380994), mRNA [NM_001037748]
D3Bwg0562e	0.0422	5.64	down	Mus musculus predicted gene 13152 (Gm13152), mRNA [NM_001039209]
Foxn3	0.0268	7.06	down	Mus musculus vomeronasal 1 receptor 204 (Vmn1r204), mRNA [NM_001045544]
	0.0278	3.50	down	Mus musculus predicted gene 1123 (Gm1123), mRNA [NM_001080776]
	0.0276	2.37	down	Mus musculus protein disulfide isomerase associated 2 (Pdia2), mRNA [NM_001081070]
Gm9296	0.0476	2.46	down	Mus musculus ankyrin repeat domain 35 (Ankrd35), mRNA [NM_001081139]

Gpn2	0.0001	1.73	down	Mus musculus KDM3B lysine (K)-specific demethylase 3B (Kdm3b), mRNA [NM_001081256]
	0.0260	4.02	down	Mus musculus RIKEN cDNA 1600015I10 gene (1600015I10Rik), mRNA [NM_001081273]
Cd3g	0.0270	1.81	down	Mus musculus membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7) (Mpp7), transcript variant 1, mRNA [NM_001081287]
Nrarp	0.0256	2.82	down	Mus musculus protease, serine, 33 (Prss33), mRNA [NM_001081399]
Gm10621	0.0321	1.79	down	Mus musculus neuropeptide W (Npw), mRNA [NM_001099664]
ENSMUSG0000006879	0.0325	4.09	down	Mus musculus sushi domain containing 5 (Sud5), mRNA [NM_001101510]
	0.0442	1.61	down	Mus musculus G protein-coupled receptor 25 (Gpr25), mRNA [NM_001101516]
	0.0459	3.08	down	Mus musculus calpain 12 (Capn12), mRNA [NM_001110807]
	0.0327	3.53	down	Mus musculus cyclin-dependent kinase inhibitor 1A (P21) (Cdkn1a), transcript variant 2, mRNA [NM_001111099]
6330416L07Rik	0.0018	4.48	down	Mus musculus WD repeat and FYVE domain containing 1 (Wdly1), transcript variant 1, mRNA [NM_001111279]
Rnf213	0.0218	1.74	down	Mus musculus cat eye syndrome chromosome region, candidate 2 homolog (human) (Cecr2), mRNA [NM_001128151]
Vash1	0.0252	1.85	down	Mus musculus dachsous 1 (Drosophila) (Dchs1), mRNA [NM_001162943]
Nwd1	0.0306	2.45	down	Mus musculus zinc finger and BTB domain containing 5 (Zbtb5), transcript variant 1, mRNA [NM_001163284]
Gm6811	0.0447	2.87	down	Mus musculus selectin, lymphocyte (Sell), transcript variant 2, mRNA [NM_001164059]
	0.0088	2.58	down	Mus musculus dehydrogenase/reductase (SDR family) member 7B (Dhrs7b), transcript variant 1, mRNA [NM_001172112]

LOC100041256	0.0411	6.78	down	Mus musculus predicted gene 10394 (Gm10394), mRNA [NM_001177538]
Krtap20-2	0.0481	1.99	down	Mus musculus predicted gene 3985 (Gm3985), mRNA [NM_001177589]
E030025P04Rik	0.0235	2.19	down	Mus musculus predicted gene 2897 (Gm2897), transcript variant 2, mRNA [NM_001177715]
	0.0230	1.72	down	Mus musculus B-cell CLL/lymphoma 6, member B (Bcl6b), mRNA [NM_007528]
	0.0033	1.55	down	Mus musculus cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4) (Cdkn2b), mRNA [NM_007670]
	0.0038	1.59	down	Mus musculus chemokine (C-C motif) receptor 8 (Ccr8), mRNA [NM_007720]
Cd6	0.0211	1.96	down	Mus musculus defensin, alpha, related sequence 2 (Defa-rs2), mRNA [NM_007847]
Pou2f2	0.0323	1.94	down	Mus musculus epidermal growth factor receptor (Egfr), transcript variant 2, mRNA [NM_007912]
Gm14124	0.0393	2.36	down	Mus musculus Fas-associated factor 1 (Faf1), mRNA [NM_007983]
	0.0071	9.31	down	Mus musculus growth differentiation factor 1 (Gdf1), transcript variant 2, mRNA [NM_008107]
Gm2598	0.0317	1.60	down	Mus musculus guanylate kinase 1 (Guk1), transcript variant 1, mRNA [NM_008193]
Gm4864	0.0061	2.67	down	Mus musculus histocompatibility 2, O region alpha locus (H2-Oa), mRNA [NM_008206]
Gm2897	0.0246	4.02	down	Mus musculus histone deacetylase 1 (Hdac1), mRNA [NM_008228]
LOC100046544	0.0388	1.64	down	Mus musculus histone deacetylase 1 (Hdac1), mRNA [NM_008228]
LOC100046350	0.0309	6.14	down	Mus musculus insulin-like growth factor binding protein, acid labile subunit (Igfb1), mRNA [NM_008340]
Fmr1nb	0.0409	5.16	down	Mus musculus interleukin 12 receptor, beta 1 (Il12rb1), mRNA [NM_008353]

Hs3st6	0.0472	8.14	down	Mus musculus integrin alpha L (Itgal), mRNA [NM_008400]
Olfm1	0.0096	2.03	down	Mus musculus lymphotoxin B (Ltb), mRNA [NM_008518]
A430093F15Rik	0.0185	2.32	down	Mus musculus peptidyl arginine deiminase, type II (Padi2), mRNA [NM_008812]
	0.0318	1.91	down	Mus musculus pancreatic polypeptide receptor 1 (Ppyr1), mRNA [NM_008919]
	0.0034	1.62	down	Mus musculus solute carrier family 4 (anion exchanger), member 1, adaptor protein (Slc4a1ap), mRNA [NM_009206]
	0.0010	2.31	down	Mus musculus somatostatin receptor 4 (Sstr4), mRNA [NM_009219]
Pappa2	0.0382	1.50	down	Mus musculus son of sevenless homolog 1 (Drosophila) (Sos1), mRNA [NM_009231]
	0.0247	1.84	down	Mus musculus signal recognition particle receptor, B subunit (Srprb), mRNA [NM_009275]
Dact1	0.0494	2.08	down	Mus musculus mitogen-activated protein kinase kinase kinase 7 (Map3k7), transcript variant B, mRNA [NM_009316]
D10627	0.0276	3.04	down	Mus musculus tumor necrosis factor alpha induced protein 6 (Tnfaip6), mRNA [NM_009398]
4933430A20Rik	0.0416	4.29	down	Mus musculus wingless-related MMTV integration site 5B (Wnt5b), mRNA [NM_009525]
Sct	0.0103	1.82	down	Mus musculus pleiomorphic adenoma gene-like 1 (Plagl1), mRNA [NM_009538]
Ogdhl	0.0041	1.98	down	Mus musculus aquaporin 5 (Aqp5), mRNA [NM_009701]
Sez6l2	0.0331	2.84	down	Mus musculus neurogenin 3 (Neurog3), mRNA [NM_009719]
	0.0030	1.95	down	Mus musculus CD19 antigen (Cd19), mRNA [NM_009844]
	0.0414	3.18	down	Mus musculus CD3 antigen, gamma polypeptide (Cd3g), mRNA [NM_009850]

Rrad	0.0109	2.05	down	Mus musculus cyclin-dependent kinase 4 (Cdk4), mRNA [NM_009870]
	0.0073	1.65	down	Mus musculus chemokine (C-C motif) receptor 3 (Ccr3), mRNA [NM_009914]
	0.0240	2.91	down	Mus musculus cathelicidin antimicrobial peptide (Camp), mRNA [NM_009921]
LOC640614	0.0061	4.78	down	Mus musculus cathepsin W (Ctsw), mRNA [NM_009985]
	0.0407	2.25	down	Mus musculus delta-like 1 homolog (Drosophila) (Dlk1), transcript variant 1, mRNA [NM_010052]
	0.0126	16.64	down	Mus musculus dystrophin related protein 2 (Drp2), mRNA [NM_010078]
Gm13948	0.0312	1.50	down	Mus musculus epsin 2 (Epn2), mRNA [NM_010148]
Cd164l2	0.0219	4.77	down	Mus musculus potassium voltage-gated channel, shaker-related subfamily, member 7 (Kcna7), mRNA [NM_010596]
Clip4	0.0451	1.56	down	Mus musculus killer cell lectin-like receptor, subfamily A, member 4 (Klra4), mRNA [NM_010649]
	0.0113	8.91	down	Mus musculus tryptase beta 2 (Tpsb2), mRNA [NM_010781]
Gm4434	0.0208	2.97	down	Mus musculus matrix metalloproteinase 24 (Mmp24), mRNA [NM_010808]
Speer4d	0.0202	7.87	down	Mus musculus mucin 5, subtypes A and C, tracheobronchial/gastric (Muc5ac), mRNA [NM_010844]
	0.0096	2.43	down	Mus musculus neural cell adhesion molecule 1 (Ncam1), transcript variant 2, mRNA [NM_010875]
Ccl8	0.0127	2.06	down	Mus musculus nuclear distribution gene C homolog (Aspergillus) (Nudc), mRNA [NM_010948]
G630055G22Rik	0.0299	1.87	down	Mus musculus oxytocin (Oxt), mRNA [NM_011025]
	0.0420	2.49	down	Mus musculus procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide (P4ha2), transcript variant 2, mRNA [NM_011031]
LOC629952	0.0059	1.78	down	Mus musculus phospholipid transfer protein (Pltp), mRNA [NM_011125]

	0.0388	3.11	down	Mus musculus regulatory factor X-associated ankyrin-containing protein (Rfxank), transcript variant 1, mRNA [NM_011266]
Prim2	0.0135	9.96	down	Mus musculus sodium channel, voltage-gated, type I, beta (Scn1b), mRNA [NM_011322]
9430008C03Rik	0.0125	2.39	down	Mus musculus SRY-box containing gene 10 (Sox10), mRNA [NM_011437]
	0.0020	4.04	down	Mus musculus SRY-box containing gene 14 (Sox14), mRNA [NM_011440]
	0.0023	2.55	down	Mus musculus thrombospondin 2 (Thbs2), mRNA [NM_011581]
Gm5957	0.0020	11.36	down	Mus musculus tuberous sclerosis 2 (Tsc2), transcript variant 1, mRNA [NM_011647]
	0.0411	2.85	down	Mus musculus carbonic anhydrase 14 (Car14), mRNA [NM_011797]
2700068H02Rik	0.0166	2.84	down	Mus musculus protein kinase C and casein kinase substrate in neurons 1 (Pacsin1), transcript variant 1, mRNA [NM_011861]
P4ha3	0.0410	3.08	down	Mus musculus sprouty homolog 2 (Drosophila) (Spry2), mRNA [NM_011897]
Meox1	0.0303	3.20	down	Mus musculus sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (Sema3c), mRNA [NM_013657]
	0.0473	2.80	down	Mus musculus HRAS-like suppressor (Hrasls), mRNA [NM_013751]
	0.0298	8.66	down	Mus musculus T-cell leukemia/lymphoma 1B, 2 (Tcl1b2), mRNA [NM_013775]
	0.0341	2.62	down	Mus musculus regenerating islet-derived 3 delta (Reg3d), transcript variant 1, mRNA [NM_013893]
Slfn8	0.0106	16.24	down	Mus musculus apelin (Apln), mRNA [NM_013912]
Gm16462	0.0152	3.03	down	Mus musculus tocopherol (alpha) transfer protein (Ttpa), mRNA [NM_015767]

	0.0122	2.39	down	Mus musculus complement component 6 (C6), mRNA [NM_016704]
Trib2	0.0013	1.73	down	Mus musculus WW domain binding protein 2 (Wbp2), mRNA [NM_016852]
	0.0101	29.74	down	Mus musculus MAGI family member, X-linked (Magix), mRNA [NM_018832]
Gm13710	0.0035	1.52	down	Mus musculus formin binding protein 1 (Fnbp1), transcript variant 2, mRNA [NM_019406]
Prima1	0.0444	2.09	down	Mus musculus immunity-related GTPase family M member 2 (Irgm2), mRNA [NM_019440]
Cyp4f18	0.0161	4.03	down	Mus musculus soc-2 (suppressor of clear) homolog (C. elegans) (Shoc2), transcript variant 1, mRNA [NM_019658]
	0.0194	1.90	down	Mus musculus neurexin I (Nrxn1), transcript variant 1, mRNA [NM_020252]
LOC100041746	0.0153	1.88	down	Mus musculus LanC (bacterial lantibiotic synthetase component C)-like 1 (Lanc1), mRNA [NM_021295]
4930547M16Rik	0.0256	3.70	down	Mus musculus zinc finger protein 112 (Zfp112), mRNA [NM_021307]
	0.0164	1.64	down	Mus musculus peptidoglycan recognition protein 2 (Pglyrp2), mRNA [NM_021319]
Gabrd	0.0366	2.40	down	Mus musculus crystallin, beta B3 (Crybb3), transcript variant 1, mRNA [NM_021352]
Ccdc99	0.0021	2.20	down	Mus musculus neuro-oncological ventral antigen 1 (Nova1), mRNA [NM_021361]
Clnk	0.0432	3.59	down	Mus musculus myozenin 1 (Myoz1), mRNA [NM_021508]
Cbfa2t3	0.0316	1.85	down	Mus musculus dapper homolog 1, antagonist of beta-catenin (xenopus) (Dact1), transcript variant 2, mRNA [NM_021532]
LOC637747	0.0395	5.11	down	Mus musculus agrin (Agn), mRNA [NM_021604]
Hdac1	0.0032	3.13	down	Mus musculus RCE1 homolog, prenyl protein peptidase (S. cerevisiae) (Rce1), mRNA [NM_023131]

Fam19a3	0.0012	2.97	down	Mus musculus renin binding protein (Renbp), transcript variant 1, mRNA [NM_023132]
	0.0258	1.67	down	Mus musculus solute carrier family 30 (zinc transporter), member 7 (Slc30a7), mRNA [NM_023214]
	0.0045	2.12	down	Mus musculus haloacid dehalogenase-like hydrolase domain containing 3 (Hdhd3), mRNA [NM_024257]
	0.0168	5.45	down	Mus musculus single-stranded DNA binding protein 2 (Ssbp2), transcript variant 2, mRNA [NM_024272]
Gm2715	0.0445	7.25	down	Mus musculus single-stranded DNA binding protein 2 (Ssbp2), transcript variant 2, mRNA [NM_024272]
LOC636441	0.0214	14.60	down	Mus musculus RWD domain containing 1 (Rwdd1), mRNA [NM_025614]
Rap1gap	0.0361	1.66	down	Mus musculus RNA binding motif protein 4B (Rbm4b), mRNA [NM_025717]
	0.0146	10.80	down	Mus musculus BCL2-like 14 (apoptosis facilitator) (Bcl2l14), mRNA [NM_025778]
Igfals	0.0455	9.33	down	Mus musculus protein phosphatase 1, regulatory (inhibitor) subunit 2 (Ppp1r2), mRNA [NM_025800]
Gm2571	0.0122	2.98	down	Mus musculus REX1, RNA exonuclease 1 homolog (S. cerevisiae) (Rexo1), transcript variant 1, mRNA [NM_025852]
LOC100048016	0.0116	2.26	down	Mus musculus Notch-regulated ankyrin repeat protein (Nrarp), mRNA [NM_025980]
	0.0228	25.88	down	Mus musculus IQ motif containing F4 (Iqcf4), mRNA [NM_026090]
Gpr68	0.0415	1.68	down	Mus musculus family with sequence similarity 32, member A (Fam32a), mRNA [NM_026455]
Gm4590	0.0444	2.70	down	Mus musculus CD164 sialomucin-like 2 (Cd164l2), mRNA [NM_027152]
	0.0323	2.27	down	Mus musculus six transmembrane epithelial antigen of the prostate 1 (Steap1), mRNA [NM_027399]
Sly	0.0171	20.14	down	Mus musculus coiled-coil domain containing 99 (Ccdc99), mRNA [NM_027411]

	0.0163	2.89	down	Mus musculus CWF19-like 2, cell cycle control (S. pombe) (Cwf19l2), mRNA [NM_027545]
	0.0260	1.96	down	Mus musculus PWWP domain containing 2A (Pwwp2a), transcript variant 2, mRNA [NM_027557]
	0.0290	4.01	down	Mus musculus alpha-kinase 1 (Alpk1), mRNA [NM_027808]
Sell	0.0465	2.11	down	Mus musculus ribonucleoprotein, PTB-binding 1 (Raver1), mRNA [NM_027911]
	0.0075	1.77	down	Mus musculus threonyl-tRNA synthetase 2, mitochondrial (putative) (Tars2), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA [NM_027931]
4930455J16Rik	0.0479	7.67	down	Mus musculus protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor) (Prkrir), mRNA [NM_028410]
	0.0011	2.27	down	Mus musculus family with sequence similarity 101, member A (Fam101a), mRNA [NM_028443]
	0.0002	1.51	down	Mus musculus RIKEN cDNA 1300002K09 gene (1300002K09Rik), mRNA [NM_028788]
	0.0110	1.96	down	Mus musculus UHRF1 (ICBP90) binding protein 1-like (Uhrf1bp1l), mRNA [NM_029166]
	0.0444	2.05	down	Mus musculus small nuclear RNA activating complex, polypeptide 3 (Snapc3), mRNA [NM_029949]
Ankrd35	0.0242	1.68	down	Mus musculus family with sequence similarity 55, member B (Fam55b), mRNA [NM_030069]
	0.0374	2.55	down	Mus musculus zinc finger homeodomain 4 (Zfhx4), mRNA [NM_030708]
Magea1	0.0071	3.28	down	Mus musculus SLAM family member 6 (Slamf6), mRNA [NM_030710]
Gatad2a	0.0228	2.57	down	Mus musculus triggering receptor expressed on myeloid cells 2 (Trem2), mRNA [NM_031254]
Gm12128	0.0007	2.69	down	Mus musculus glutaredoxin (Glrx), mRNA [NM_053108]
Gm1667	0.0188	2.30	down	Mus musculus poly(A) binding protein, cytoplasmic 5 (Pabpc5), mRNA [NM_053114]

	0.0110	3.72	down	Mus musculus RIKEN cDNA 2010002M12 gene (2010002M12Rik), mRNA [NM_053217]
Hist1h2al	0.0178	2.43	down	Mus musculus protease, serine, 29 (Prss29), mRNA [NM_053260]
	0.0432	15.14	down	Mus musculus cyclin-dependent kinase 9 (CDC2-related kinase) (Cdk9), mRNA [NM_130860]
	0.0010	1.69	down	Mus musculus proline rich membrane anchor 1 (Prima1), mRNA [NM_133364]
	0.0134	2.02	down	Mus musculus kallikrein related-peptidase 10 (Klk10), mRNA [NM_133712]
Slco1a4	0.0159	2.13	down	Mus musculus integrin alpha 9 (Itga9), transcript variant 1, mRNA [NM_133721]
AA060545	0.0295	1.91	down	Mus musculus RIKEN cDNA 2610018G03 gene (2610018G03Rik), mRNA [NM_133729]
	0.0367	1.55	down	Mus musculus GPN-loop GTPase 2 (Gpn2), mRNA [NM_133884]
Gm13152	0.0384	4.64	down	Mus musculus adenylate cyclase 3 (Adcy3), transcript variant 1, mRNA [NM_138305]
	0.0013	6.84	down	Mus musculus H1 histone family, member O, oocyte-specific (H1foo), mRNA [NM_138311]
Ltb	0.0189	1.91	down	Mus musculus tribbles homolog 2 (Drosophila) (Trib2), mRNA [NM_144551]
Col4a6	0.0136	11.40	down	Mus musculus pyrroline-5-carboxylate reductase 1 (Pycr1), mRNA [NM_144795]
Dchs1	0.0274	1.94	down	Mus musculus Fc receptor-like A (Fcrla), transcript variant 2, mRNA [NM_145141]
1700092C02Rik	0.0442	2.41	down	Mus musculus BTB (POZ) domain containing 3 (Btbd3), transcript variant 1, mRNA [NM_145534]
Fam101a	0.0247	1.69	down	Mus musculus RAS-related protein-1a (Rap1a), mRNA [NM_145541]
C330011M18Rik	0.0236	1.88	down	Mus musculus anterior pharynx defective 1a homolog (C. elegans) (Aph1a), transcript variant 1, mRNA [NM_146104]

Plagl1	0.0092	1.56	down	Mus musculus gelsolin (Gsn), mRNA [NM_146120]
	0.0280	3.24	down	Mus musculus olfactory receptor 1410 (Olfr1410), mRNA [NM_146491]
4930529I22Rik	0.0450	2.77	down	Mus musculus olfactory receptor 870 (Olfr870), mRNA [NM_146904]
	0.0028	15.66	down	Mus musculus olfactory receptor 1348 (Olfr1348), mRNA [NM_146913]
	0.0251	10.22	down	Mus musculus olfactory receptor 791 (Olfr791), mRNA [NM_146930]
	0.0038	5.54	down	Mus musculus olfactory receptor 531 (Olfr531), mRNA [NM_146953]
	0.0277	2.11	down	Mus musculus olfactory receptor 656 (Olfr656), mRNA [NM_147075]
Kif24	0.0318	1.77	down	Mus musculus zinc finger protein 352 (Zfp352), mRNA [NM_153102]
LOC380994	0.0276	17.33	down	Mus musculus solute carrier family 36 (proton/amino acid symporter), member 1 (Slc36a1), mRNA [NM_153139]
Cacna1s	0.0477	3.91	down	Mus musculus RIKEN cDNA A730008H23 gene (A730008H23Rik), mRNA [NM_172505]
Olfr700	0.0289	3.23	down	Mus musculus zinc finger protein 868 (Zfp868), transcript variant 1, mRNA [NM_172754]
Prl3c1	0.0128	2.39	down	Mus musculus zinc finger CCCH type containing 12D (Zc3h12d), mRNA [NM_172785]
Gm6445	0.0013	6.07	down	Mus musculus kelch-like 31 (Drosophila) (Klhl31), mRNA [NM_172925]
Fam165b	0.0308	2.80	down	Mus musculus alkB, alkylation repair homolog 5 (E. coli) (Alkbh5), mRNA [NM_172943]
	0.0103	1.99	down	Mus musculus 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 (Pfkfb4), mRNA [NM_173019]
	0.0029	5.41	down	Mus musculus synaptotagmin VII (Syt7), transcript variant 3, mRNA [NM_173068]
Mybl2	0.0313	1.81	down	Mus musculus brain-specific angiogenesis inhibitor 2 (Bai2), mRNA [NM_173071]

C230098O21Rik	0.0150	1.71	down	Mus musculus Eph receptor B1 (Ephb1), transcript variant 1, mRNA [NM_173447]
Ggt6	0.0126	1.97	down	Mus musculus G protein-coupled bile acid receptor 1 (Gpbar1), mRNA [NM_174985]
Pfkfb4	0.0259	2.39	down	Mus musculus uroplakin 3B (Upk3b), mRNA [NM_175309]
Cmya5	0.0372	1.61	down	Mus musculus myosin light chain kinase 3 (Mylk3), mRNA [NM_175441]
	0.0203	2.85	down	Mus musculus sorting nexin 33 (Snx33), mRNA [NM_175483]
Gm7694	0.0157	2.06	down	Mus musculus histone cluster 2, H2bb (Hist2h2bb), mRNA [NM_175666]
	0.0376	3.13	down	Mus musculus LY6/PLAUR domain containing 6 (Lypd6), transcript variant 1, mRNA [NM_177139]
Trav3n-3	0.0366	2.34	down	Mus musculus transmembrane protein 154 (Tmem154), mRNA [NM_177260]
	0.0024	3.39	down	Mus musculus X-prolyl aminopeptidase (aminopeptidase P) 3, putative (Xpnpep3), mRNA [NM_177310]
	0.0398	3.75	down	Mus musculus RIKEN cDNA A630033E08 gene (A630033E08Rik), transcript variant 2, mRNA [NM_177358]
Sep-01	0.0444	1.89	down	Mus musculus RIKEN cDNA A630033E08 gene (A630033E08Rik), transcript variant 2, mRNA [NM_177358]
2610035D17Rik	0.0068	1.50	down	Mus musculus selection and upkeep of intraepithelial T cells 3 (Skint3), transcript variant 2, mRNA [NM_177578]
Fam55b	0.0410	2.15	down	Mus musculus BAI1-associated protein 2-like 2 (Baiap2l2), mRNA [NM_177580]
Zfp672	0.0216	2.73	down	Mus musculus F-box and WD-40 domain protein 13 (Fbxw13), mRNA [NM_177598]
C130079G13Rik	0.0328	5.20	down	Mus musculus RIKEN cDNA C130079G13 gene (C130079G13Rik), mRNA [NM_177661]

	0.0400	4.01	down	Mus musculus splicing factor, arginine/serine-rich 13B (Sfrs13b), mRNA [NM_177774]
Arhgap11a	0.0368	1.54	down	Mus musculus RIKEN cDNA D330038O06 gene (D330038O06Rik), mRNA [NM_177899]
9430011C21Rik	0.0390	2.17	down	Mus musculus G-rich RNA sequence binding factor 1 (Grsf1), transcript variant 1, mRNA [NM_178700]
	0.0076	2.08	down	Mus musculus serine/threonine kinase 32A (Stk32a), mRNA [NM_178749]
	0.0457	1.81	down	Mus musculus RIKEN cDNA D330012F22 gene (D330012F22Rik), mRNA [NM_178752]
	0.0043	7.01	down	Mus musculus tripartite motif-containing 65 (Trim65), mRNA [NM_178802]
Atrnl1	0.0412	1.62	down	Mus musculus general transcription factor IIH, polypeptide 5 (Gtf2h5), mRNA [NM_181392]
H2-Oa	0.0176	2.38	down	Mus musculus attractin like 1 (Atrnl1), mRNA [NM_181415]
F2rl3	0.0369	2.94	down	Mus musculus Rho GTPase activating protein 11A (Arhgap11a), mRNA [NM_181416]
	0.0054	2.68	down	Mus musculus rhomboid, veinlet-like 2 (Drosophila) (Rhbdl2), mRNA [NM_183163]
	0.0323	5.81	down	Mus musculus nanos homolog 3 (Drosophila) (Nanos3), mRNA [NM_194059]
St8sia2	0.0304	4.20	down	Mus musculus family with sequence similarity 160, member B2 (Fam160b2), mRNA [NM_194345]
LOC677484	0.0056	9.07	down	Mus musculus small G protein signaling modulator 2 (Sgsm2), mRNA [NM_197943]
	0.0447	2.22	down	Mus musculus CUE domain containing 1 (Cuedc1), transcript variant 1, mRNA [NM_198013]
	0.0297	4.59	down	Mus musculus IQ motif containing C (Iqcc), mRNA [NM_198026]
Cdkn2b	0.0044	2.14	down	Mus musculus mediator complex subunit 16 (Med16), transcript variant 1, mRNA [NM_198107]

B3gat2	0.0396	1.57	down	Mus musculus RIKEN cDNA 2810408P10 gene (2810408P10Rik), mRNA [NM_198619]
Olfr18	0.0433	3.08	down	Mus musculus acyl-CoA synthetase short-chain family member 3 (Acss3), transcript variant 2, mRNA [NM_198636]
Zc3h12d	0.0052	2.74	down	Mus musculus Holliday junction recognition protein (Hjrp), mRNA [NM_198652]
Olfr122	0.0275	2.34	down	Mus musculus hypocretin (orexin) receptor 1 (Hcrtr1), transcript variant 1, mRNA [NM_198959]
	0.0300	2.09	down	Mus musculus CD300C antigen (Cd300c), mRNA [NM_199225]
	0.0426	1.84	down	Mus musculus histocompatibility 2, M region locus 10.3 (H2-M10.3), mRNA [NM_201608]
LOC100046257	0.0251	2.61	down	Mus musculus olfactory receptor 128 (Olfr128), mRNA [NM_206816]
	0.0453	1.59	down	Mus musculus taste receptor, type 2, member 117 (Tas2r117), mRNA [NM_207021]
	0.0051	13.19	down	Mus musculus taste receptor, type 2, member 118 (Tas2r118), mRNA [NM_207022]
	0.0056	2.68	down	Mus musculus UDP glycosyltransferases 3 family, polypeptide A1 (Ugt3a1), mRNA [NM_207216]
LOC100039839	0.0191	14.51	down	Mus musculus small nucleolar RNA host gene (non-protein coding) 3 (Snhg3), non-coding RNA [NR_003270]
Gm7677	0.0446	1.65	down	Mus musculus phosphatidylserine decarboxylase, pseudogene 3 (Pisd-ps3), non-coding RNA [NR_003518]
5330426L24Rik	0.0200	1.99	down	Mus musculus cytochrome P450, family 2, subfamily d, polypeptide 13 (Cyp2d13), non-coding RNA [NR_003552]
LOC100048277	0.0136	3.36	down	Mus musculus RIKEN cDNA A930005H10 gene (A930005H10Rik), transcript variant 2, non-coding RNA [NR_015487]
	0.0316	1.60	down	Mus musculus RIKEN cDNA 1700030C10 gene (1700030C10Rik), non-coding RNA [NR_015521]

1700066J03Rik	0.0324	2.87	down	Mus musculus RIKEN cDNA 2900052N01 gene (2900052N01Rik), non-coding RNA [NR_015605]
	0.0273	2.24	down	Mus musculus hypothetical LOC100303645 (LOC100303645), non-coding RNA [NR_028425]
	0.0246	1.62	down	Mus musculus RIKEN cDNA 5430417L22 gene (5430417L22Rik), non-coding RNA [NR_030716]
	0.0245	5.49	down	Mus musculus predicted gene 3002 (Gm3002), non-coding RNA [NR_033388]
	0.0055	10.82	down	Mus musculus RIKEN cDNA 2810433D01 gene (2810433D01Rik), non-coding RNA [NR_033474]
	0.0114	2.58	down	TFIIi-associated transactivator factor p17 [Source:UniProtKB/TrEMBL;Acc:Q60671] [ENSMUST00000115691]
Cyp4f18	0.0295	2.98	down	Mus musculus immunoglobulin kappa light chain, variable region mRNA, clone BALB/c-54, partial cds. [U18580]
AI451458	0.0262	2.48	down	
	0.0226	3.20	down	Ig kappa chain V-III region MOPC 63 Precursor [Source:UniProtKB/Swiss-Prot;Acc:P01661] [ENSMUST00000103397]
	0.0139	1.75	down	M.musculus BALB/c IgG light chain variable region mRNA. [X79554]
Irgm2	0.0472	1.80	down	PREDICTED: Mus musculus predicted gene, EG668313 (EG668313), mRNA [XM_001000832]
	0.0409	2.42	down	PREDICTED: Mus musculus similar to sterile alpha motif domain containing 1 (LOC668408), mRNA [XM_001001317]
	0.0424	4.88	down	PREDICTED: Mus musculus similar to Igh-6 protein (LOC677484), mRNA [XM_001003989]
Pde11a	0.0296	1.57	down	PREDICTED: Mus musculus similar to pol protein (LOC100039005), mRNA [XM_001472072]
Gm3230	0.0176	1.80	down	PREDICTED: Mus musculus hypothetical protein LOC100044458 (LOC100044458), mRNA [XM_001472111]

4930429B21Rik	0.0499	2.27	down	PREDICTED: Mus musculus hypothetical protein LOC100044375 (LOC100044375), mRNA [XM_001472211]
Xrcc2	0.0420	1.72	down	PREDICTED: Mus musculus similar to Guanine nucleotide binding protein, alpha z subunit (LOC100044107), mRNA [XM_001472591]
Gas2l2	0.0175	5.06	down	PREDICTED: Mus musculus hypothetical protein LOC100044674, transcript variant 1 (LOC100044674), mRNA [XM_001472633]
Gm16525	0.0448	3.26	down	PREDICTED: Mus musculus similar to nuclear factor, interleukin 3 regulated (LOC100044670), mRNA [XM_001472807]
Trmt1	0.0081	1.57	down	predicted gene 5785 Gene [Source:MGI Symbol;Acc:MGI:3643232] [ENSMUST00000077293]
Myom3	0.0107	5.91	down	PREDICTED: Mus musculus hypothetical protein LOC100039518 (LOC100039518), mRNA [XM_001473039]
Gm2453	0.0147	2.33	down	
	0.0268	1.83	down	PREDICTED: Mus musculus hypothetical protein LOC100045220 (LOC100045220), mRNA [XM_001473489]
Hdac1	0.0392	1.82	down	PREDICTED: Mus musculus hypothetical protein LOC100045012 (LOC100045012), mRNA [XM_001473504]
Gm4072	0.0432	1.58	down	PREDICTED: Mus musculus hypothetical protein LOC100045056 (LOC100045056), mRNA [XM_001473591]
Dact1	0.0415	2.47	down	PREDICTED: Mus musculus similar to reproductive homeobox on X chromosome 8 (LOC100045068), mRNA [XM_001473610]
	0.0248	3.93	down	PREDICTED: Mus musculus RIKEN cDNA 2900073C17 gene (2900073C17Rik), mRNA [XM_001473664]

Tdrd5	0.0455	2.95	down	PREDICTED: Mus musculus hypothetical protein LOC100039892 (LOC100039892), mRNA [XM_001473733]
	0.0199	2.81	down	PREDICTED: Mus musculus hypothetical protein LOC100045168 (LOC100045168), mRNA [XM_001473785]
	0.0249	10.57	down	RIKEN cDNA 1700045I11 gene Gene [Source:MGI Symbol;Acc:MGI:1920600] [ENSMUST00000068970]
	0.0005	2.48	down	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3URL2] [ENSMUST00000099198]
	0.0429	4.38	down	PREDICTED: Mus musculus similar to CDNA sequence BC025446 (LOC100045879), mRNA [XM_001475080]
	0.0022	2.32	down	PREDICTED: Mus musculus RIKEN cDNA 5430410E06 gene (5430410E06Rik), mRNA [XM_001475205]
Vps13b	0.0386	1.54	down	PREDICTED: Mus musculus similar to Ubtg protein (LOC100040816), mRNA [XM_001475326]
	0.0472	1.82	down	PREDICTED: Mus musculus hypothetical protein LOC100040850 (LOC100040850), mRNA [XM_001475388]
	0.0250	16.68	down	PREDICTED: Mus musculus hypothetical protein LOC100046159 (LOC100046159), mRNA [XM_001475676]
LOC100044473	0.0441	1.52	down	PREDICTED: Mus musculus similar to Sek-3 (LOC100046245), mRNA [XM_001475860]
Gm7144	0.0002	3.96	down	PREDICTED: Mus musculus similar to immunoglobulin kappa chain (LOC100046350), mRNA [XM_001476057]
Slc10a7	0.0079	2.12	down	PREDICTED: Mus musculus similar to gag (LOC100046544), mRNA [XM_001476392]
Dlk1	0.0317	2.12	down	PREDICTED: Mus musculus hypothetical LOC670356 (LOC670356), mRNA [XM_001476496]

	0.0366	1.77	down	PREDICTED: Mus musculus hypothetical protein LOC100041919 (LOC100041919), mRNA [XM_001477525]
	0.0440	2.06	down	PREDICTED: Mus musculus hypothetical protein LOC100047152 (LOC100047152), mRNA [XM_001477532]
Folr1	0.0374	2.01	down	PREDICTED: Mus musculus similar to pleckstrin homology domain containing, family A member 7 (LOC100047292), mRNA [XM_001477810]
Cib3	0.0409	2.61	down	PREDICTED: Mus musculus hypothetical protein LOC100042207 (LOC100042207), mRNA [XM_001477897]
	0.0061	3.09	down	PREDICTED: Mus musculus similar to monoclonal anti-alpha-1,3-galactosyltransferase IgM heavy chain (LOC100047336), mRNA [XM_001477926]
	0.0365	3.59	down	PREDICTED: Mus musculus similar to Inositol polyphosphate-5-phosphatase B (LOC100048869), mRNA [XM_001478120]
	0.0405	2.93	down	PREDICTED: Mus musculus similar to mitochondrial ribosome recycling factor (LOC100047590), mRNA [XM_001478469]
Gm11223	0.0430	7.00	down	PREDICTED: Mus musculus hypothetical protein LOC100047591 (LOC100047591), mRNA [XM_001478470]
Olfr1441	0.0276	2.75	down	PREDICTED: Mus musculus hypothetical protein LOC100047703 (LOC100047703), mRNA [XM_001478711]
	0.0072	3.34	down	PREDICTED: Mus musculus predicted gene, EG546524 (EG546524), mRNA [XM_001480466]
	0.0332	2.64	down	PREDICTED: Mus musculus predicted gene, EG432834 (EG432834), mRNA [XM_484358]
LOC435333	0.0052	5.98	down	PREDICTED: Mus musculus predicted gene, EG433251 (EG433251), mRNA [XM_484811]

	0.0332	1.98	down	RIKEN cDNA 1700061I17 gene Gene [Source:MGI Symbol;Acc:MGI:1920612] [ENSMUST00000029642]
Pacsin1	0.0059	2.42	down	PREDICTED: Mus musculus similar to Cdv3 protein (LOC433790), mRNA [XM_485486]
Hjrp	0.0179	8.10	down	PREDICTED: Mus musculus predicted gene, EG434050 (EG434050), mRNA [XM_485792]
	0.0191	2.57	down	PREDICTED: Mus musculus RIKEN cDNA B230216G23 gene (B230216G23Rik), mRNA [XM_620381]
	0.0363	4.95	down	PREDICTED: Mus musculus predicted gene, EG624023 (EG624023), mRNA [XM_888549]
Itgal	0.0172	1.65	down	PREDICTED: Mus musculus similar to MS4A4A protein (LOC624461), mRNA [XM_889011]
LOC100045054	0.0345	1.81	down	PREDICTED: Mus musculus predicted gene, EG626573 (EG626573), mRNA [XM_891173]
Sema3c	0.0402	1.67	down	PREDICTED: Mus musculus similar to H prechain (AA -19 to 98) (LOC630293), mRNA [XM_903418]
Olf1415	0.0039	3.10	down	zinc finger protein 866 Gene [Source:MGI (curated);Acc:MGI:3584369] [ENSMUST00000130458]
Fbxo34	0.0350	1.66	down	PREDICTED: Mus musculus histocompatibility 2, T region locus 18 (H2-T18), mRNA [XM_912024]
	0.0179	3.91	down	PREDICTED: Mus musculus similar to monoclonal antibody heavy chain (LOC435333), mRNA [XM_917510]
	0.0403	3.69	down	PREDICTED: Mus musculus predicted gene, EG640554 (EG640554), mRNA [XM_917569]
Rims1	0.0099	2.93	down	PREDICTED: Mus musculus similar to E225 (LOC640979), mRNA [XM_918237]
Gm8028	0.0489	3.65	down	PREDICTED: Mus musculus hypothetical LOC665174 (LOC665174), mRNA [XM_975056]
	0.0227	3.44	down	PREDICTED: Mus musculus predicted gene, EG665540 (EG665540), mRNA [XM_977642]

C6	0.0441	3.06	down	Putative uncharacterized protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q8BW36] [ENSMUST00000042610]
LOC100048568	0.0178	2.06	down	myosin light chain kinase 3 Gene [Source:MGI (curated);Acc:MGI:2443063] [ENSMUST00000122452]
1700003G18Rik	0.0022	2.06	down	RIKEN cDNA 4930597O21 gene Gene [Source:MGI Symbol;Acc:MGI:1922623] [ENSMUST00000065878]
Gm3411	0.0183	2.89	down	PREDICTED: Mus musculus predicted gene, EG666560 (EG666560), misc RNA [XR_001891]
Gm6745	0.0450	3.37	down	PREDICTED: Mus musculus predicted gene, EG667483 (EG667483), misc RNA [XR_002032]
Gm8090	0.0486	8.77	down	PREDICTED: Mus musculus predicted gene, EG272714 (EG272714), misc RNA [XR_002343]
	0.0344	2.18	down	PREDICTED: Mus musculus similar to CG6004-PB (LOC100039037), misc RNA [XR_030580]
Gm4703	0.0438	1.91	down	PREDICTED: Mus musculus similar to Ribosomal protein SA (LOC546708), misc RNA [XR_030900]
Gm8350	0.0459	2.22	down	PREDICTED: Mus musculus similar to neuroendocrine differentiation factor (LOC665047), misc RNA [XR_031091]
LOC100044930	0.0202	2.33	down	PREDICTED: Mus musculus similar to spermiogenesis specific transcript on the Y 1 (LOC664934), misc RNA [XR_031164]
Fcrla	0.0191	3.10	down	PREDICTED: Mus musculus similar to GC-rich promoter binding protein 1-like 1 (LOC622701), misc RNA [XR_031357]
Xaf1	0.0445	2.05	down	PREDICTED: Mus musculus similar to ribosomal protein L26 (LOC633461), misc RNA [XR_031506]
	0.0013	1.62	down	PREDICTED: Mus musculus similar to ribosomal protein (LOC664856), misc RNA [XR_031550]
	0.0005	6.80	down	PREDICTED: Mus musculus similar to guanosine monophosphate reductase (LOC100045393), misc RNA [XR_031783]

	0.0183	1.59	down	PREDICTED: Mus musculus similar to Ribosomal protein S6 (LOC100048866), misc RNA [XR_031900]
	0.0411	2.19	down	PREDICTED: Mus musculus similar to ribosomal protein L7a (LOC100040805), misc RNA [XR_032174]
	0.0223	2.50	down	PREDICTED: Mus musculus similar to G protein-coupled receptor 31, D17Leh66c region (LOC625102), misc RNA [XR_032598]
Lta	0.0114	1.71	down	PREDICTED: Mus musculus similar to ribosomal protein L15 (LOC433063), misc RNA [XR_032837]
	0.0477	2.04	down	PREDICTED: Mus musculus RIKEN cDNA D830039M14 gene (D830039M14Rik), misc RNA [XR_035204]
Dact2	0.0037	2.18	down	RIKEN cDNA C330011M18 gene Gene [Source:MGI Symbol;Acc:MGI:3045248] [ENSMUST00000071067]
Zfp58	0.0087	1.57	up	family with sequence similarity 165, member B Gene [Source:MGI (curated);Acc:MGI:1916186] [ENSMUST00000118064]
	0.0267	1.98	up	glutathione S-transferase, mu 6 Gene [Source:MGI (curated);Acc:MGI:1309467] [ENSMUST00000106680]
	0.0406	1.67	up	lincRNA:chr1:13058312-13099826 forward strand
Kcnk13	0.0305	1.94	up	lincRNA:chr1:137482591-137625604 reverse strand
	0.0390	1.99	up	lincRNA:chr1:139814266-139817889 reverse strand
	0.0244	3.07	up	lincRNA:chr1:183783306-183834531 reverse strand
Mgat2	0.0011	1.68	up	lincRNA:chr1:196843592-196865102 forward strand
	0.0340	1.50	up	lincRNA:chr1:58440355-58449627 reverse strand
Hint3	0.0300	1.64	up	lincRNA:chr1:58443698-58449898 reverse strand
	0.0280	3.43	up	lincRNA:chr1:58443698-58449898 reverse strand
Itga9	0.0394	2.73	up	lincRNA:chr1:58443698-58449898 reverse strand
P4ha2	0.0284	1.96	up	lincRNA:chr1:58443698-58449898 reverse strand
	0.0457	3.91	up	lincRNA:chr1:58443698-58449898 reverse strand
	0.0021	1.78	up	lincRNA:chr1:73437958-73451628 reverse strand
	0.0152	4.03	up	lincRNA:chr1:87374975-87412500 reverse strand

Gm8230	0.0405	2.28	up	lincRNA:chr1:94077221-94091396 reverse strand
	0.0452	3.01	up	lincRNA:chr1:95871175-95886625 forward strand
Olfr1348	0.0301	1.58	up	lincRNA:chr1:95871175-95886625 reverse strand
Olfr1410	0.0090	2.90	up	lincRNA:chr10:118385588-118439338 forward strand
	0.0223	2.15	up	lincRNA:chr10:126151060-126156450 reverse strand
	0.0073	2.28	up	lincRNA:chr10:126818382-126856582 forward strand
Nova1	0.0155	2.76	up	lincRNA:chr10:21688115-21710890 reverse strand
Dock8	0.0469	2.42	up	lincRNA:chr10:3227840-3233588 forward strand
Cdk4	0.0312	1.67	up	lincRNA:chr10:39659425-39674200 forward strand
	0.0139	1.98	up	lincRNA:chr10:41368681-41393645 reverse strand
Tmem68	0.0180	1.59	up	lincRNA:chr10:60473030-60535340 forward strand
Ttpa	0.0065	3.20	up	lincRNA:chr10:60473030-60535340 forward strand
Sox10	0.0337	1.53	up	lincRNA:chr10:6081900-6105500 forward strand
Klra12	0.0018	31.98	up	lincRNA:chr10:6497224-6497863 reverse strand
	0.0463	1.97	up	lincRNA:chr10:81165750-81236400 forward strand
	0.0179	2.44	up	lincRNA:chr10:81816994-81863610 forward strand
Zfp605	0.0116	2.11	up	lincRNA:chr10:95144321-95202671 reverse strand
Mapk8ip3	0.0145	1.73	up	lincRNA:chr11:102878974-102888924 forward strand
	0.0316	1.78	up	lincRNA:chr11:112898724-113062945 forward strand
4933424M12Rik	0.0250	1.69	up	lincRNA:chr11:112898724-113062945 reverse strand
	0.0340	1.91	up	lincRNA:chr11:120041124-120052299 forward strand
Bai2	0.0333	2.54	up	lincRNA:chr11:16838587-16850933 reverse strand
LOC100047435	0.0153	4.93	up	lincRNA:chr11:31647436-31647791 reverse strand
	0.0067	2.76	up	lincRNA:chr11:3538125-3554450 reverse strand
	0.0412	4.09	up	lincRNA:chr11:53592946-53637922 forward strand
	0.0017	2.80	up	lincRNA:chr11:58136882-58143829 reverse strand
	0.0013	1.72	up	lincRNA:chr11:6421951-6429173 forward strand
Tcl1b2	0.0126	6.13	up	lincRNA:chr11:87841800-87858725 reverse strand
	0.0058	1.52	up	lincRNA:chr11:87872568-87880978 reverse strand
	0.0385	3.60	up	lincRNA:chr11:95483973-95490751 forward strand
	0.0127	1.56	up	lincRNA:chr11:95644899-95658549 forward strand
Gpr25	0.0233	2.89	up	lincRNA:chr11:97457180-97487074 reverse strand
Mylk3	0.0037	1.97	up	lincRNA:chr12:103151385-103157735 forward strand

Mtus2	0.0406	2.52	up	lincRNA:chr12:110973190-110987668 forward strand
Npw	0.0285	2.96	up	lincRNA:chr12:111824094-111838478 forward strand
Tas2r117	0.0104	3.69	up	lincRNA:chr12:12876192-12918398 forward strand
	0.0245	1.62	up	lincRNA:chr12:21548850-21568550 reverse strand
	0.0014	2.67	up	lincRNA:chr12:21548850-21568550 reverse strand
	0.0411	3.37	up	lincRNA:chr12:33808493-33829143 forward strand
Cecr5	0.0272	1.57	up	lincRNA:chr12:53700970-53703612 reverse strand
	0.0082	2.56	up	lincRNA:chr12:73789535-73799787 forward strand
Tas2r118	0.0003	8.06	up	lincRNA:chr12:73838608-73862621 reverse strand
D330012F22Rik	0.0392	1.50	up	lincRNA:chr12:73860757-73862034 reverse strand
	0.0322	1.93	up	lincRNA:chr12:74135916-74142780 reverse strand
	0.0431	1.76	up	lincRNA:chr12:74135916-74142780 reverse strand
	0.0111	4.88	up	lincRNA:chr12:76771424-76772158 forward strand
Rnmt	0.0013	1.65	up	lincRNA:chr12:77544397-77564122 reverse strand
	0.0395	1.75	up	lincRNA:chr12:81719382-81731865 forward strand
Dbx1	0.0409	2.02	up	lincRNA:chr12:82500406-82501102 forward strand
	0.0215	3.63	up	lincRNA:chr12:82500406-82501102 forward strand
Reg3d	0.0250	1.89	up	lincRNA:chr12:88235624-88264465 reverse strand
Pik3ap1	0.0155	1.54	up	lincRNA:chr13:103101941-103102362 forward strand
Klra16	0.0401	3.43	up	lincRNA:chr13:104591573-104599048 forward strand
Aars	0.0329	1.55	up	lincRNA:chr13:104591573-104599048 reverse strand
Olfr690	0.0199	1.67	up	lincRNA:chr13:104591573-104599048 reverse strand
Rfxank	0.0273	1.54	up	lincRNA:chr13:108577843-108679708 reverse strand
	0.0015	1.53	up	lincRNA:chr13:112717680-112733330 forward strand
Foxi2	0.0010	1.61	up	lincRNA:chr13:114111261-114117957 forward strand
Mphosph10	0.0304	1.60	up	lincRNA:chr13:19618491-19618836 reverse strand
	0.0371	1.92	up	lincRNA:chr13:31736054-31781679 reverse strand
4.93E+23	0.0290	2.21	up	lincRNA:chr13:49488457-49493732 forward strand
	0.0449	1.96	up	lincRNA:chr13:51248372-51259297 forward strand
Klra22	0.0342	4.48	up	lincRNA:chr13:53100475-53113850 reverse strand
Txndc11	0.0346	1.72	up	lincRNA:chr13:56286339-56298089 forward strand
Nnt	0.0398	2.53	up	lincRNA:chr13:62734450-62785325 reverse strand
	0.0164	2.28	up	lincRNA:chr13:62734450-62785325 reverse strand

	0.0336	8.65	up	lincRNA:chr13:62734450-62785325 reverse strand
Gm10389	0.0171	3.16	up	lincRNA:chr13:66381200-66410200 reverse strand
	0.0015	4.90	up	lincRNA:chr13:74712775-74728450 reverse strand
Mt1	0.0480	2.07	up	lincRNA:chr13:94193230-94193710 forward strand
9130214F15Rik	0.0000	6.00	up	lincRNA:chr13:9818700-9824125 reverse strand
	0.0349	4.14	up	lincRNA:chr14:103751075-103769725 forward strand
	0.0030	4.44	up	lincRNA:chr14:103751075-103769725 forward strand
LOC436100	0.0299	1.97	up	lincRNA:chr14:115423660-115463160 reverse strand
Cidea	0.0321	9.19	up	lincRNA:chr14:115423660-115463160 reverse strand
	0.0302	1.58	up	lincRNA:chr14:27176059-27202735 forward strand
	0.0099	2.04	up	lincRNA:chr14:33901152-33976129 reverse strand
Cask	0.0359	1.59	up	lincRNA:chr14:43408099-43415349 forward strand
LOC100045393	0.0498	2.47	up	lincRNA:chr14:67585234-67596823 reverse strand
	0.0179	2.04	up	lincRNA:chr14:77258025-77278750 forward strand
	0.0143	2.56	up	lincRNA:chr15:100888823-100889131 forward strand
Cuedc1	0.0048	6.84	up	lincRNA:chr15:101084597-101095097 forward strand
Olf870	0.0293	4.74	up	lincRNA:chr15:66685663-66686113 reverse strand
LOC100047292	0.0227	1.63	up	lincRNA:chr15:73455424-73477275 reverse strand
	0.0300	1.68	up	lincRNA:chr15:77575125-77585575 forward strand
	0.0135	1.58	up	lincRNA:chr15:79709500-79714700 forward strand
Gm5576	0.0404	2.06	up	lincRNA:chr15:79764481-79809909 forward strand
LOC100047336	0.0432	4.61	up	lincRNA:chr15:85412264-85549139 reverse strand
	0.0288	3.23	up	lincRNA:chr15:85476512-85498105 forward strand
Cdkn1a	0.0243	3.10	up	lincRNA:chr15:85534202-85537090 forward strand
	0.0099	2.93	up	lincRNA:chr15:96032592-96116907 forward strand
	0.0193	3.11	up	lincRNA:chr15:96091428-96115684 forward strand
2810021J22Rik	0.0465	1.94	up	lincRNA:chr16:50715231-50841124 reverse strand
LOC226574	0.0129	1.74	up	lincRNA:chr16:64758224-64765700 forward strand
Padi2	0.0171	1.79	up	lincRNA:chr16:7947710-7948066 reverse strand
Prnt3	0.0112	3.17	up	lincRNA:chr16:9249688-9275013 reverse strand
	0.0253	1.83	up	lincRNA:chr17:13020750-13033750 forward strand
Sox14	0.0020	5.96	up	lincRNA:chr17:13806767-13824342 reverse strand
	0.0039	3.48	up	lincRNA:chr17:15111725-15139800 forward strand

Asap3	0.0079	2.28	up	lincRNA:chr17:15111725-15139800 forward strand
Il12rb1	0.0058	3.72	up	lincRNA:chr17:15111725-15139800 reverse strand
Xaf1	0.0042	62.22	up	lincRNA:chr17:15111725-15139800 reverse strand
Lanc1	0.0130	1.71	up	lincRNA:chr17:15226181-15250333 reverse strand
LOC100044034	0.0009	2.06	up	lincRNA:chr17:17492400-17507525 reverse strand
Gsn	0.0347	2.79	up	lincRNA:chr17:21785442-21801542 forward strand
	0.0394	2.57	up	lincRNA:chr17:22420025-22457650 reverse strand
	0.0347	2.03	up	lincRNA:chr17:26911397-26917047 forward strand
D830039M14Rik	0.0267	2.29	up	lincRNA:chr17:26911397-26917047 reverse strand
	0.0254	3.65	up	lincRNA:chr17:32044823-32045974 reverse strand
	0.0258	2.57	up	lincRNA:chr17:33426488-33444184 forward strand
2810474O19Rik	0.0270	2.43	up	lincRNA:chr17:36131460-36136694 forward strand
	0.0092	1.90	up	lincRNA:chr17:36136010-36136696 forward strand
Chdh	0.0486	3.20	up	lincRNA:chr17:38132217-38157667 reverse strand
	0.0126	1.89	up	lincRNA:chr17:45524689-45525320 reverse strand
	0.0257	1.67	up	lincRNA:chr17:6265275-6362150 reverse strand
Gm13032	0.0021	3.87	up	lincRNA:chr17:6265275-6362150 reverse strand
	0.0352	3.60	up	lincRNA:chr17:6455677-6476228 forward strand
5430410E06Rik	0.0072	1.64	up	lincRNA:chr17:6455677-6476228 forward strand
	0.0037	2.28	up	lincRNA:chr17:6830756-6832322 reverse strand
4930557J02Rik	0.0133	1.58	up	lincRNA:chr17:6830756-6832322 reverse strand
	0.0177	2.16	up	lincRNA:chr17:79042382-79051807 reverse strand
	0.0136	1.69	up	lincRNA:chr17:79042382-79051807 reverse strand
Gm826	0.0358	2.58	up	lincRNA:chr17:86219507-86220112 forward strand
	0.0396	1.58	up	lincRNA:chr17:87483814-87493039 forward strand
Sstr4	0.0191	3.54	up	lincRNA:chr17:88466300-88495175 reverse strand
	0.0010	2.50	up	lincRNA:chr18:32389816-32394927 forward strand
	0.0415	3.03	up	lincRNA:chr18:36470130-36489110 forward strand
	0.0202	1.85	up	lincRNA:chr18:38836368-38935650 forward strand
Gm2982	0.0130	1.92	up	lincRNA:chr18:47327300-47333819 forward strand
Zfx4	0.0100	1.77	up	lincRNA:chr18:60812427-60819775 reverse strand
Atp6v0d2	0.0392	6.44	up	lincRNA:chr18:60906766-60920702 forward strand
Dhrs7b	0.0005	3.10	up	lincRNA:chr18:73870981-73877247 forward strand

Rasgef1b	0.0238	2.16	up	lincRNA:chr19:4209657-4210475 reverse strand
	0.0243	3.27	up	lincRNA:chr19:4994325-4994537 reverse strand
	0.0428	4.95	up	lincRNA:chr19:4994325-4994537 reverse strand
Gm8164	0.0293	1.83	up	lincRNA:chr19:61226425-61270975 reverse strand
LOC100045012	0.0064	2.38	up	lincRNA:chr19:9060613-9060851 forward strand
	0.0244	2.40	up	lincRNA:chr2:118408095-118415745 forward strand
	0.0278	2.19	up	lincRNA:chr2:143963320-143984245 forward strand
	0.0398	3.96	up	lincRNA:chr2:155269145-155303251 forward strand
	0.0046	2.14	up	lincRNA:chr2:155298877-155303251 forward strand
Foxi3	0.0310	2.15	up	lincRNA:chr2:172343878-172344212 reverse strand
Ms4a4a	0.0239	3.70	up	lincRNA:chr2:22782700-22801900 forward strand
Defa-rs2	0.0333	2.61	up	lincRNA:chr2:25774411-25783757 reverse strand
Zfp454	0.0115	1.66	up	lincRNA:chr2:35828611-35838083 forward strand
Magix	0.0139	2.35	up	lincRNA:chr2:52241435-52245307 forward strand
	0.0320	1.81	up	lincRNA:chr2:67834535-67834914 forward strand
Pwwp2a	0.0498	1.56	up	lincRNA:chr2:75489436-75490163 reverse strand
	0.0253	1.85	up	lincRNA:chr2:84344350-84370075 reverse strand
Dpys	0.0439	3.26	up	lincRNA:chr3:126989696-127112471 reverse strand
	0.0411	1.54	up	lincRNA:chr3:127037711-127111912 reverse strand
	0.0213	1.65	up	lincRNA:chr3:127037711-127111912 reverse strand
	0.0161	3.00	up	lincRNA:chr3:145269449-145298239 forward strand
	0.0072	1.59	up	lincRNA:chr3:145390505-145398253 forward strand
Slc4a1ap	0.0036	1.56	up	lincRNA:chr3:27760757-27761151 forward strand
	0.0137	2.51	up	lincRNA:chr3:27837825-27880925 forward strand
	0.0000	7.18	up	lincRNA:chr3:30032959-30079659 forward strand
	0.0061	4.84	up	lincRNA:chr3:34793853-34800591 forward strand
	0.0378	1.86	up	lincRNA:chr3:35236023-35241498 reverse strand
Shq1	0.0345	1.59	up	lincRNA:chr3:37547973-37548436 reverse strand
	0.0287	1.96	up	lincRNA:chr3:41325168-41332366 reverse strand
Ang2	0.0495	1.56	up	lincRNA:chr3:60292527-60292880 reverse strand
LOC100045537	0.0173	2.27	up	lincRNA:chr3:79069438-79073704 reverse strand
	0.0399	2.28	up	lincRNA:chr3:79069438-79073704 reverse strand
Slc39a8	0.0230	2.40	up	lincRNA:chr3:90425270-90435820 forward strand

Gm8225	0.0254	1.72	up	lincRNA:chr3:95443575-95462543 reverse strand
	0.0130	3.06	up	lincRNA:chr4:101075685-101080461 reverse strand
AU015791	0.0424	1.86	up	lincRNA:chr4:11102287-11118421 reverse strand
Olfr314	0.0283	3.29	up	lincRNA:chr4:114585803-114588898 forward strand
	0.0287	2.30	up	lincRNA:chr4:128060015-128075590 forward strand
	0.0144	9.25	up	lincRNA:chr4:129497990-129515290 forward strand
LOC100039037	0.0313	2.23	up	lincRNA:chr4:131734714-131742542 reverse strand
	0.0289	1.60	up	lincRNA:chr4:131737612-131738100 reverse strand
	0.0345	2.25	up	lincRNA:chr4:135896689-135918414 forward strand
	0.0264	3.12	up	lincRNA:chr4:135896689-135918414 forward strand
Gm8826	0.0408	2.10	up	lincRNA:chr4:135896689-135918414 reverse strand
Prss33	0.0391	3.63	up	lincRNA:chr4:146156575-146175425 reverse strand
	0.0037	1.77	up	lincRNA:chr4:146890596-146891297 forward strand
	0.0361	2.28	up	lincRNA:chr4:3406175-3443875 forward strand
Fbxw13	0.0104	6.30	up	lincRNA:chr4:35106125-35127700 forward strand
Pitpna	0.0450	1.50	up	lincRNA:chr4:54851872-54866706 reverse strand
2900057C01Rik	0.0010	1.60	up	lincRNA:chr4:88582120-88582754 forward strand
Olfr791	0.0253	1.94	up	lincRNA:chr4:88604248-88645948 forward strand
	0.0051	3.50	up	lincRNA:chr4:8865575-8899400 reverse strand
Gm3001	0.0355	1.76	up	lincRNA:chr5:110158475-110223700 forward strand
Gm11543	0.0449	1.83	up	lincRNA:chr5:113594167-113645342 forward strand
Gm3142	0.0093	3.16	up	lincRNA:chr5:113609906-113622032 reverse strand
Rbm41	0.0219	1.82	up	lincRNA:chr5:122047900-122065325 forward strand
Gm6284	0.0176	3.64	up	lincRNA:chr5:123440192-123451767 reverse strand
Slc6a4	0.0124	4.30	up	lincRNA:chr5:124667541-124700029 forward strand
Hddc3	0.0062	6.59	up	lincRNA:chr5:125078875-125098525 reverse strand
	0.0482	2.18	up	lincRNA:chr5:125078875-125098525 reverse strand
	0.0065	1.81	up	lincRNA:chr5:136371885-136372424 reverse strand
Slc36a1	0.0087	1.80	up	lincRNA:chr5:143676800-143704125 reverse strand
	0.0459	2.86	up	lincRNA:chr5:149751979-149808240 reverse strand
Mtmr15	0.0219	2.09	up	lincRNA:chr5:22058025-22072475 forward strand
Olfr353	0.0004	3.70	up	lincRNA:chr5:22058025-22072475 forward strand
	0.0352	1.60	up	lincRNA:chr5:22058025-22072475 forward strand

Rap1a	0.0436	3.97	up	lincRNA:chr5:22801058-22939737 reverse strand
Klra5	0.0037	3.65	up	lincRNA:chr5:22890322-22939119 reverse strand
	0.0054	3.67	up	lincRNA:chr5:22890322-22939119 reverse strand
	0.0036	1.60	up	lincRNA:chr5:22890322-22939119 reverse strand
	0.0318	2.67	up	lincRNA:chr5:22928221-22939127 reverse strand
	0.0355	3.92	up	lincRNA:chr5:23195569-23218551 reverse strand
Olfir531	0.0033	4.07	up	lincRNA:chr5:23195569-23218551 reverse strand
GlrX	0.0079	4.05	up	lincRNA:chr5:23195569-23218551 reverse strand
LOC100046245	0.0113	2.40	up	lincRNA:chr5:23195569-23218551 reverse strand
Gm6466	0.0263	1.62	up	lincRNA:chr5:31856417-31916317 forward strand
Zfp112	0.0069	3.91	up	lincRNA:chr5:31856417-31916414 forward strand
	0.0073	1.98	up	lincRNA:chr5:33186508-33196882 reverse strand
	0.0021	6.35	up	lincRNA:chr5:34696192-34722842 reverse strand
Gm5953	0.0262	9.38	up	lincRNA:chr5:52584616-52595441 reverse strand
Nop56	0.0240	1.81	up	lincRNA:chr5:92563184-92566678 reverse strand
	0.0307	1.95	up	lincRNA:chr5:92563184-92566678 reverse strand
Gm2976	0.0133	2.36	up	lincRNA:chr6:12062275-12075800 reverse strand
	0.0076	1.62	up	lincRNA:chr6:121035524-121061074 forward strand
Tnpo2	0.0106	2.55	up	lincRNA:chr6:126766225-126771309 forward strand
	0.0413	1.85	up	lincRNA:chr6:133054025-133069850 reverse strand
	0.0057	2.26	up	lincRNA:chr6:133054025-133069850 reverse strand
Gstt2	0.0031	2.25	up	lincRNA:chr6:13801450-13853450 forward strand
	0.0126	1.79	up	lincRNA:chr6:148162552-148176577 forward strand
	0.0104	5.05	up	lincRNA:chr6:31001656-31002219 reverse strand
	0.0366	1.83	up	lincRNA:chr6:40693617-40720167 forward strand
Plekhg6	0.0186	3.76	up	lincRNA:chr6:50339188-50409363 forward strand
Pisd-ps3	0.0046	1.81	up	lincRNA:chr6:50361567-50406200 reverse strand
Adcy3	0.0435	1.84	up	lincRNA:chr6:86425510-86450160 forward strand
	0.0308	1.58	up	lincRNA:chr6:86477309-86537554 reverse strand
Camp	0.0086	1.52	up	lincRNA:chr6:90848183-90861277 reverse strand
	0.0032	2.01	up	lincRNA:chr7:126872550-126886125 reverse strand
	0.0266	2.02	up	lincRNA:chr7:132218864-132329172 forward strand
	0.0388	2.47	up	lincRNA:chr7:134620707-134626739 forward strand

Gm9306	0.0487	9.87	up	lincRNA:chr7:140011140-140018815 reverse strand
	0.0277	1.72	up	lincRNA:chr7:140081171-140123058 reverse strand
	0.0359	1.55	up	lincRNA:chr7:149108190-149123890 forward strand
	0.0008	3.71	up	lincRNA:chr7:16584852-16657252 forward strand
	0.0251	1.55	up	lincRNA:chr7:30645026-30667034 reverse strand
Thrb	0.0298	2.95	up	lincRNA:chr7:3338500-3360725 reverse strand
Egfr	0.0465	1.72	up	lincRNA:chr7:4827340-4863315 reverse strand
	0.0048	3.72	up	lincRNA:chr7:6296401-6311486 forward strand
4933406C10Rik	0.0472	1.58	up	lincRNA:chr7:71093563-71095094 forward strand
	0.0346	3.53	up	lincRNA:chr7:80763588-80764230 forward strand
	0.0449	2.44	up	lincRNA:chr8:108153471-108159672 forward strand
	0.0396	1.82	up	lincRNA:chr8:10886200-10905925 reverse strand
1600015I10Rik	0.0005	3.19	up	lincRNA:chr8:110196655-110390197 forward strand
Pik3cg	0.0408	2.68	up	lincRNA:chr8:110197171-110206546 reverse strand
	0.0209	1.62	up	lincRNA:chr8:114477602-114488627 reverse strand
Mpp7	0.0195	1.97	up	lincRNA:chr8:114477602-114488627 reverse strand
Gm11826	0.0384	2.80	up	lincRNA:chr8:122712014-122732520 reverse strand
A630033E08Rik	0.0339	4.54	up	lincRNA:chr8:122920901-123008463 reverse strand
	0.0219	3.26	up	lincRNA:chr8:122945743-122946192 forward strand
Ccbe1	0.0123	1.71	up	lincRNA:chr8:126396600-126407275 forward strand
	0.0226	1.79	up	lincRNA:chr8:129336539-129400338 reverse strand
	0.0450	1.87	up	lincRNA:chr8:13200727-13207714 forward strand
	0.0454	1.73	up	lincRNA:chr8:13507348-13543773 reverse strand
Tnfaip8l3	0.0228	2.90	up	lincRNA:chr8:41941084-41947630 reverse strand
2410018L13Rik	0.0042	1.95	up	lincRNA:chr8:49853937-49874087 reverse strand
	0.0361	1.60	up	lincRNA:chr8:57977383-57985712 forward strand
Nanos3	0.0147	1.51	up	lincRNA:chr8:72663625-72673010 reverse strand
	0.0243	1.51	up	lincRNA:chr8:74431707-74442440 forward strand
Tjp2	0.0248	1.58	up	lincRNA:chr8:74820025-74833350 forward strand
	0.0122	3.54	up	lincRNA:chr8:85609155-85615170 forward strand
Abca5	0.0305	2.76	up	lincRNA:chr8:86705694-86711244 forward strand
Ctsv	0.0301	1.69	up	lincRNA:chr8:91569369-91594119 forward strand
	0.0022	2.50	up	lincRNA:chr9:113648970-113715170 reverse strand

	0.0192	4.05	up	lincRNA:chr9:121207045-121269020 forward strand
Slamf6	0.0248	2.35	up	lincRNA:chr9:13224147-13424397 reverse strand
Gm9634	0.0135	1.58	up	lincRNA:chr9:37071677-37072244 reverse strand
	0.0003	2.29	up	lincRNA:chr9:41408354-41420812 forward strand
	0.0009	2.16	up	lincRNA:chr9:61881173-61881351 reverse strand
	0.0413	1.88	up	lincRNA:chr9:65089730-65091897 reverse strand
	0.0399	2.30	up	lincRNA:chr9:67414463-67483185 reverse strand
Yeats2	0.0433	1.51	up	lincRNA:chr9:88575075-88611650 forward strand
	0.0025	4.49	up	lincRNA:chr9:96664617-96683617 forward strand
	0.0131	5.37	up	lincRNA:chrX:11671167-11700242 reverse strand
	0.0121	2.95	up	lincRNA:chrX:120134722-120138152 reverse strand
Ncam1	0.0042	2.13	up	lincRNA:chrX:120590872-120598071 reverse strand
2210404J11Rik	0.0009	2.48	up	lincRNA:chrX:120812236-121038407 reverse strand
Abca5	0.0212	2.51	up	lincRNA:chrX:121970356-121970881 reverse strand
	0.0345	1.99	up	lincRNA:chrX:146832315-146875680 reverse strand
	0.0143	2.87	up	lincRNA:chrX:146945573-146950036 reverse strand
	0.0308	1.91	up	lincRNA:chrX:146945573-146950036 reverse strand
	0.0495	2.95	up	lincRNA:chrX:148732853-148761972 reverse strand
Pnpla6	0.0012	1.64	up	lincRNA:chrX:20389063-20389702 forward strand
Muc5ac	0.0112	2.11	up	lincRNA:chrX:20555593-20591971 forward strand
	0.0196	1.62	up	lincRNA:chrX:35825525-35877700 reverse strand
	0.0096	2.12	up	lincRNA:chrX:45814752-45816313 reverse strand
Atp10d	0.0175	7.75	up	lincRNA:chrX:47890565-47915775 forward strand
	0.0468	1.51	up	lincRNA:chrX:47893703-47996700 forward strand
Cwf19l2	0.0329	1.86	up	lincRNA:chrX:50407969-50410370 reverse strand
	0.0094	2.30	up	lincRNA:chrX:73008593-73009966 reverse strand
Ccr3	0.0477	2.62	up	lincRNA:chrX:75813213-75829323 forward strand
	0.0278	2.65	up	lincRNA:chrX:90997595-91009570 forward strand
	0.0088	1.54	up	lincRNA:chrX:90997595-91009570 reverse strand
Gfer	0.0493	2.61	up	MDIGGVBC immunoglobulin variable region {Mus musculus domesticus} (exp=-1; wgp=0; cg=0), complete [TC1725107]

Arsk	0.0095	3.59	up	MMU231226 immunoglobulin light chain variable region {Mus musculus} (exp=-1; wgp=0; cg=0), complete [TC1706422]
Klra15	0.0077	31.70	up	Novel member of the keratin associated protein 3 (Krtap3) family [Source:UniProtKB/TrEMBL;Acc:A2A592] [ENSMUST00000104931]
	0.0326	2.28	up	peroxisomal biogenesis factor 5-like Gene [Source:MGI (curated);Acc:MGI:1916672] [ENSMUST00000108219]
	0.0022	3.18	up	plastin 1 (I-isoform) Gene [Source:MGI (curated);Acc:MGI:104809] [ENSMUST00000119760]
	0.0178	1.61	up	Unknown
Wwox	0.0232	1.51	up	Unknown
Gm6651	0.0377	4.11	up	Unknown
AI314976	0.0319	2.21	up	
1700102J08Rik	0.0125	1.64	up	
	0.0478	1.88	up	
4921515L22Rik	0.0283	9.06	down	apolipoprotein C-III Gene [Source:MGI (curated);Acc:MGI:88055] [ENSMUST00000118649]
Zkscan2	0.0320	2.37	down	B-cell CLL/lymphoma 11A (zinc finger protein) Gene [Source:MGI (curated);Acc:MGI:106190] [ENSMUST00000109516]
Gm13241	0.0383	5.56	down	Ets2 repressor factor Gene [Source:MGI (curated);Acc:MGI:109637] [ENSMUST00000116343]
Snhg3	0.0131	1.93	down	lincRNA:chr1:134237581-134248506 reverse strand
	0.0234	2.13	down	lincRNA:chr1:137482591-137625604 forward strand
	0.0423	2.57	down	lincRNA:chr1:137503023-137625604 reverse strand
Gm6225	0.0331	1.79	down	lincRNA:chr1:139713316-139913366 reverse strand
Gm3002	0.0099	3.19	down	lincRNA:chr1:155219662-155231912 reverse strand
Slc25a37	0.0367	4.81	down	lincRNA:chr1:167797581-167803031 forward strand
	0.0256	3.22	down	lincRNA:chr1:196843592-196865102 forward strand
	0.0387	4.37	down	lincRNA:chr1:36012298-36020311 reverse strand
	0.0073	18.10	down	lincRNA:chr1:71718767-71719614 forward strand
Gm8008	0.0446	2.25	down	lincRNA:chr1:71730139-71730720 forward strand

	0.0334	2.64	down	lincRNA:chr1:71939741-71947891 forward strand
	0.0144	2.59	down	lincRNA:chr1:81632600-81644175 forward strand
Atp12a	0.0388	2.21	down	lincRNA:chr1:82892851-82943201 reverse strand
Cmpk2	0.0031	5.16	down	lincRNA:chr1:85300475-85331475 reverse strand
Blm	0.0138	1.85	down	lincRNA:chr1:94077196-94077860 forward strand
Hbb-y	0.0369	1.62	down	lincRNA:chr1:94611439-94613779 reverse strand
	0.0264	2.19	down	lincRNA:chr10:117021051-117038683 reverse strand
LOC432958	0.0203	2.60	down	lincRNA:chr10:18036490-18059965 reverse strand
	0.0026	7.58	down	lincRNA:chr10:24269165-24276690 reverse strand
	0.0243	3.01	down	lincRNA:chr10:24269317-24270145 reverse strand
Pmepa1	0.0389	3.40	down	lincRNA:chr10:39607282-39619520 forward strand
Ccnd1	0.0240	2.11	down	lincRNA:chr10:83364590-83364873 forward strand
LOC100040235	0.0458	21.65	down	lincRNA:chr10:84005221-84022896 reverse strand
Wnt5b	0.0027	1.93	down	lincRNA:chr10:94900849-94928059 reverse strand
Gm7544	0.0148	2.78	down	lincRNA:chr11:112898724-113062945 reverse strand
	0.0331	4.42	down	lincRNA:chr11:112905201-113062945 reverse strand
	0.0154	2.22	down	lincRNA:chr11:112905201-113062945 reverse strand
Bzap1	0.0404	2.11	down	lincRNA:chr11:117768049-117807949 reverse strand
Slc1a6	0.0197	1.53	down	lincRNA:chr11:19960515-19961093 reverse strand
	0.0115	13.12	down	lincRNA:chr11:33414450-33450750 reverse strand
Hjurp	0.0409	5.52	down	lincRNA:chr11:3538125-3554450 forward strand
	0.0057	2.97	down	lincRNA:chr11:3538125-3554450 reverse strand
	0.0045	2.94	down	lincRNA:chr11:50994911-51050704 forward strand
	0.0238	4.78	down	lincRNA:chr11:6748267-6818192 forward strand
Spef2	0.0327	2.04	down	lincRNA:chr11:69184157-69201732 reverse strand
	0.0399	4.13	down	lincRNA:chr11:69196530-69197001 forward strand
	0.0466	2.41	down	lincRNA:chr11:79549532-79575807 forward strand
3110009E18Rik	0.0123	2.98	down	lincRNA:chr11:82588507-82594501 forward strand
Wfikn2	0.0243	2.53	down	lincRNA:chr11:87872568-87880978 reverse strand
	0.0322	1.56	down	lincRNA:chr11:97505439-97522274 forward strand
Gm10394	0.0234	2.22	down	lincRNA:chr12:110944403-110988678 forward strand
Entpd4	0.0111	1.69	down	lincRNA:chr12:116850878-116855932 reverse strand
	0.0386	1.92	down	lincRNA:chr12:117623500-117643575 reverse strand

Gm2942	0.0139	3.79	down	lincRNA:chr12:3173375-3203075 reverse strand
	0.0354	1.77	down	lincRNA:chr12:53669892-53710742 reverse strand
	0.0461	2.50	down	lincRNA:chr12:74135916-74142780 forward strand
Gm7146	0.0015	8.33	down	lincRNA:chr12:74135916-74142780 reverse strand
	0.0297	11.52	down	lincRNA:chr12:74883691-74893323 reverse strand
2610507I01Rik	0.0199	6.69	down	lincRNA:chr12:76771424-76772158 forward strand
	0.0316	3.11	down	lincRNA:chr13:108825897-108833335 reverse strand
	0.0279	5.30	down	lincRNA:chr13:19618491-19618836 reverse strand
Hrasls	0.0448	2.66	down	lincRNA:chr13:24833082-24838462 forward strand
Gm5222	0.0172	2.20	down	lincRNA:chr13:28918991-28919231 forward strand
Krtap16-8	0.0268	1.90	down	lincRNA:chr13:34186976-34210579 forward strand
Gm7356	0.0136	4.44	down	lincRNA:chr13:48620882-48643532 reverse strand
LOC640979	0.0079	4.48	down	lincRNA:chr13:64044376-64045368 reverse strand
	0.0078	17.46	down	lincRNA:chr13:67211950-67217199 reverse strand
Tnfrsf13c	0.0103	7.37	down	lincRNA:chr13:67802775-67829550 forward strand
	0.0196	22.40	down	lincRNA:chr13:67806242-67830110 reverse strand
	0.0041	3.51	down	lincRNA:chr13:97700327-97700876 forward strand
4930445G23Rik	0.0125	8.33	down	lincRNA:chr14:101834175-102005450 forward strand
	0.0111	3.25	down	lincRNA:chr14:101834175-102005450 forward strand
	0.0151	1.96	down	lincRNA:chr14:103751075-103769725 forward strand
Fcho1	0.0407	1.66	down	lincRNA:chr14:21437920-21464655 reverse strand
	0.0253	11.59	down	lincRNA:chr14:55317199-55317670 reverse strand
	0.0206	3.08	down	lincRNA:chr14:61321789-61325711 forward strand
	0.0322	2.08	down	lincRNA:chr14:62263564-62307496 forward strand
Scn11a	0.0423	1.72	down	lincRNA:chr14:65433420-65434061 reverse strand
5033425G24Rik	0.0200	2.38	down	lincRNA:chr14:79724027-79729152 forward strand
3110082D06Rik	0.0247	8.47	down	lincRNA:chr15:102100964-102104552 forward strand
	0.0008	21.62	down	lincRNA:chr15:102947390-102971082 reverse strand
	0.0371	2.46	down	lincRNA:chr15:77575125-77585575 forward strand
	0.0305	1.96	down	lincRNA:chr15:82036791-82037660 reverse strand
	0.0039	3.69	down	lincRNA:chr15:97495641-97503721 forward strand
Gm9444	0.0015	1.69	down	lincRNA:chr16:11024315-11055740 forward strand
Ltb4r2	0.0043	3.67	down	lincRNA:chr16:11024315-11055740 forward strand

Clec4a2	0.0257	4.68	down	lincRNA:chr16:13752215-13764390 reverse strand
LOC635339	0.0294	2.26	down	lincRNA:chr16:29711373-29712035 reverse strand
	0.0020	4.06	down	lincRNA:chr16:43623581-43642715 forward strand
2900001G08Rik	0.0047	2.18	down	lincRNA:chr16:4867322-4874772 reverse strand
	0.0056	2.56	down	lincRNA:chr16:8738782-8830148 reverse strand
G2e3	0.0318	1.72	down	lincRNA:chr17:15111725-15139800 reverse strand
LOC100045515	0.0096	1.66	down	lincRNA:chr17:15226181-15250333 reverse strand
1700030C10Rik	0.0164	3.81	down	lincRNA:chr17:21177225-21187525 reverse strand
	0.0096	1.62	down	lincRNA:chr17:21785442-21801542 reverse strand
Ssxb9	0.0224	1.77	down	lincRNA:chr17:33368400-33393525 forward strand
Bcl6b	0.0146	1.97	down	lincRNA:chr17:36131460-36136694 forward strand
H2-DMb2	0.0048	2.61	down	lincRNA:chr17:46972160-46997919 reverse strand
	0.0250	1.72	down	lincRNA:chr17:5795893-5835243 reverse strand
	0.0082	2.74	down	lincRNA:chr17:6602100-6615425 forward strand
	0.0247	2.38	down	lincRNA:chr17:6830756-6832322 reverse strand
Gm5556	0.0187	2.79	down	lincRNA:chr17:8088950-8106700 reverse strand
	0.0060	2.18	down	lincRNA:chr17:88466300-88495175 forward strand
	0.0018	3.61	down	lincRNA:chr17:88469443-88470068 forward strand
Gsdma2	0.0299	3.12	down	lincRNA:chr17:95150800-95180650 reverse strand
	0.0096	1.52	down	lincRNA:chr18:35204950-35216650 forward strand
	0.0483	1.77	down	lincRNA:chr18:35974770-35975091 forward strand
	0.0190	1.52	down	lincRNA:chr18:35976163-35976530 forward strand
Nrxn1	0.0094	2.86	down	lincRNA:chr18:38542830-38544720 reverse strand
	0.0104	9.46	down	lincRNA:chr18:4415233-4415995 forward strand
	0.0047	9.80	down	lincRNA:chr18:46954653-46955671 forward strand
C87490	0.0359	2.21	down	lincRNA:chr18:57124435-57134910 reverse strand
	0.0215	1.99	down	lincRNA:chr18:75513062-75523889 forward strand
Klhl31	0.0438	2.40	down	lincRNA:chr18:78190463-78235438 forward strand
Mlf1ip	0.0145	5.84	down	lincRNA:chr19:14911511-14911831 reverse strand
Kndc1	0.0232	3.39	down	lincRNA:chr19:4207767-4208004 forward strand
Gm7303	0.0487	2.00	down	lincRNA:chr19:54011403-54019143 reverse strand
Sfrs13b	0.0141	2.22	down	lincRNA:chr19:57426515-57435165 reverse strand
4933438K21Rik	0.0010	14.57	down	lincRNA:chr19:61226425-61270975 reverse strand

Gm7716	0.0321	1.97	down	lincRNA:chr2:108456668-108532418 reverse strand
Gm3225	0.0287	2.84	down	lincRNA:chr2:117024098-117025009 reverse strand
A730008H23Rik	0.0016	3.72	down	lincRNA:chr2:117781720-117937595 forward strand
Gm8659	0.0444	1.59	down	lincRNA:chr2:132079092-132087069 reverse strand
Ldlrad2	0.0490	1.62	down	lincRNA:chr2:132722530-132726802 forward strand
	0.0405	3.28	down	lincRNA:chr2:156654675-156665430 reverse strand
	0.0125	3.21	down	lincRNA:chr2:165780133-165800663 reverse strand
4933437N03Rik	0.0123	3.66	down	lincRNA:chr2:170029045-170034220 forward strand
Lmnb1	0.0228	1.56	down	lincRNA:chr2:22753100-22780375 reverse strand
Dmbx1	0.0314	2.01	down	lincRNA:chr2:25774411-25783757 forward strand
LOC100036523	0.0062	3.02	down	lincRNA:chr2:36112429-36112792 forward strand
	0.0219	2.31	down	lincRNA:chr2:60038543-60046318 forward strand
F2rl3	0.0079	2.21	down	lincRNA:chr2:75447542-75448025 reverse strand
Gm831	0.0446	2.34	down	lincRNA:chr2:77807600-77836075 forward strand
9030625G05Rik	0.0408	10.37	down	lincRNA:chr3:10081893-10094218 reverse strand
	0.0459	1.97	down	lincRNA:chr3:108763862-108772151 forward strand
Gm4123	0.0316	1.94	down	lincRNA:chr3:127037711-127111912 reverse strand
Vangl2	0.0397	2.28	down	lincRNA:chr3:145269449-145298239 forward strand
Il12rb2	0.0411	3.42	down	lincRNA:chr3:21964899-21974885 forward strand
Dock7	0.0216	2.59	down	lincRNA:chr3:27837825-27880925 forward strand
Trim16	0.0064	3.77	down	lincRNA:chr3:35782698-35789932 forward strand
	0.0077	1.91	down	lincRNA:chr3:35831966-35841638 forward strand
LOC640067	0.0426	2.99	down	lincRNA:chr3:37797734-37891650 forward strand
Sass6	0.0212	1.97	down	lincRNA:chr3:41143423-41359623 forward strand
Gm6810	0.0434	2.53	down	lincRNA:chr3:60292527-60292880 reverse strand
	0.0318	2.29	down	lincRNA:chr3:63673371-63703295 reverse strand
Gm7990	0.0388	3.10	down	lincRNA:chr3:79069438-79073704 reverse strand
E030046B03Rik	0.0136	1.54	down	lincRNA:chr3:85571525-85645700 reverse strand
	0.0211	2.11	down	lincRNA:chr3:88009045-88036270 reverse strand
LOC100303645	0.0470	4.32	down	lincRNA:chr3:96074625-96086375 forward strand
Oxt	0.0107	1.87	down	lincRNA:chr3:96289850-96301078 forward strand
Ephb1	0.0187	1.69	down	lincRNA:chr4:101010948-101032148 forward strand
Nr1d1	0.0267	1.60	down	lincRNA:chr4:116790373-116797823 forward strand

	0.0261	2.46	down	lincRNA:chr4:124202159-124202824 forward strand
Vmn1r183	0.0491	1.90	down	lincRNA:chr4:124206166-124334412 reverse strand
	0.0427	2.10	down	lincRNA:chr4:129376440-129391690 reverse strand
	0.0290	2.95	down	lincRNA:chr4:129479254-129480362 reverse strand
C130009A20Rik	0.0453	1.74	down	lincRNA:chr4:129497990-129515290 forward strand
	0.0275	2.59	down	lincRNA:chr4:136856064-136875614 reverse strand
Mageb1	0.0280	2.18	down	lincRNA:chr4:140609589-140614789 forward strand
	0.0347	1.66	down	lincRNA:chr4:146507925-146532650 forward strand
Kcne1l	0.0459	2.65	down	lincRNA:chr4:155560050-155570900 reverse strand
2010001M09Rik	0.0060	3.28	down	lincRNA:chr4:155585650-155608700 forward strand
1700084K02Rik	0.0140	6.98	down	lincRNA:chr4:3169583-3180017 forward strand
A830035A12Rik	0.0142	1.97	down	lincRNA:chr4:3406175-3443875 forward strand
	0.0277	4.11	down	lincRNA:chr4:35106125-35127700 forward strand
	0.0058	6.27	down	lincRNA:chr4:82156098-82196298 forward strand
Gm3002	0.0250	4.39	down	lincRNA:chr4:88563206-88563835 reverse strand
Il19	0.0438	1.82	down	lincRNA:chr4:98943050-98959998 reverse strand
	0.0138	2.46	down	lincRNA:chr5:106121842-106127192 reverse strand
Hjurp	0.0019	3.89	down	lincRNA:chr5:112205091-112240992 forward strand
Skint3	0.0191	9.67	down	lincRNA:chr5:119945358-119962612 forward strand
BB557941	0.0060	3.45	down	lincRNA:chr5:121759042-121789992 reverse strand
LOC100040245	0.0283	18.54	down	lincRNA:chr5:123582742-123588202 forward strand
Nfe2	0.0316	2.28	down	lincRNA:chr5:124694137-124695689 reverse strand
LOC100044439	0.0106	4.83	down	lincRNA:chr5:15033568-15033987 forward strand
Olfir39	0.0492	5.54	down	lincRNA:chr5:22058025-22072475 forward strand
	0.0115	7.78	down	lincRNA:chr5:22801058-22939737 reverse strand
	0.0139	2.32	down	lincRNA:chr5:22887983-22939658 reverse strand
Lzts1	0.0295	2.74	down	lincRNA:chr5:22887983-22939658 reverse strand
Arhgdig	0.0269	2.28	down	lincRNA:chr5:22928221-22939127 reverse strand
Nhedc2	0.0203	14.29	down	lincRNA:chr5:22928221-22939127 reverse strand
	0.0166	1.55	down	lincRNA:chr5:23195569-23218551 reverse strand
Ankrd33b	0.0177	9.38	down	lincRNA:chr5:23195569-23218551 reverse strand
	0.0335	4.43	down	lincRNA:chr5:30550467-30559008 reverse strand
	0.0413	3.40	down	lincRNA:chr5:30550467-30559008 reverse strand

	0.0228	4.07	down	lincRNA:chr5:31856417-31916414 forward strand
	0.0299	1.66	down	lincRNA:chr5:33174092-33200792 forward strand
	0.0251	7.85	down	lincRNA:chr5:33174092-33200792 reverse strand
	0.0363	4.68	down	lincRNA:chr5:33773842-33942967 reverse strand
Fpr-rs3	0.0082	2.98	down	lincRNA:chr5:52581905-52637135 forward strand
Rimkla	0.0205	2.20	down	lincRNA:chr5:54053882-54054174 forward strand
Foxp3	0.0180	3.40	down	lincRNA:chr5:74487385-74497428 forward strand
Gm10406	0.0315	3.49	down	lincRNA:chr5:92548501-92566401 reverse strand
	0.0038	7.69	down	lincRNA:chr6:120670699-120677449 forward strand
	0.0336	1.87	down	lincRNA:chr6:126445920-126446242 reverse strand
LOC544904	0.0425	5.59	down	lincRNA:chr6:126766225-126771309 reverse strand
	0.0300	2.83	down	lincRNA:chr6:127588224-127609749 reverse strand
Mapk1ip1l	0.0158	2.46	down	lincRNA:chr6:128389484-128403407 reverse strand
	0.0371	4.19	down	lincRNA:chr6:31017987-31174287 reverse strand
Camk2b	0.0187	10.39	down	lincRNA:chr6:39205913-39248468 forward strand
Otog	0.0227	2.64	down	lincRNA:chr6:47915489-47916089 forward strand
	0.0435	4.35	down	lincRNA:chr6:5311375-5328075 forward strand
	0.0128	3.18	down	lincRNA:chr6:82608223-82669023 forward strand
Pcdh17	0.0151	2.99	down	lincRNA:chr6:90745692-90777977 reverse strand
Tmem200c	0.0177	2.79	down	lincRNA:chr6:90937606-90938335 reverse strand
H1fx	0.0229	2.36	down	lincRNA:chr6:91928958-91936887 reverse strand
Cdh15	0.0230	1.60	down	lincRNA:chr6:93029101-93031007 forward strand
	0.0044	17.41	down	lincRNA:chr7:112934153-112943178 forward strand
Ms4a1	0.0493	5.51	down	lincRNA:chr7:114369337-114407862 reverse strand
	0.0308	2.32	down	lincRNA:chr7:129294166-129301366 forward strand
LOC100046973	0.0495	3.89	down	lincRNA:chr7:129294998-129295498 forward strand
	0.0021	12.22	down	lincRNA:chr7:134779841-134840591 forward strand
Gm3705	0.0462	3.64	down	lincRNA:chr7:16584852-16657252 reverse strand
	0.0032	4.76	down	lincRNA:chr7:26054813-26063725 forward strand
LOC100047070	0.0094	9.70	down	lincRNA:chr7:3309825-3331151 reverse strand
	0.0289	1.70	down	lincRNA:chr7:66562376-66579519 forward strand
E430029J22Rik	0.0390	1.54	down	lincRNA:chr7:71093563-71095094 forward strand
Cc2d2b	0.0467	3.44	down	lincRNA:chr7:88131123-88136898 reverse strand

	0.0222	1.68	down	lincRNA:chr8:108153471-108159672 reverse strand
	0.0199	1.62	down	lincRNA:chr8:122712014-122732520 forward strand
9.13E+15	0.0389	1.72	down	lincRNA:chr8:122963590-122964126 forward strand
	0.0050	1.69	down	lincRNA:chr8:124355710-124401160 forward strand
Smcr8	0.0365	3.55	down	lincRNA:chr8:126396600-126407275 forward strand
	0.0191	2.71	down	lincRNA:chr8:128933150-128943375 forward strand
	0.0370	1.81	down	lincRNA:chr8:131178212-131180657 forward strand
Trim16	0.0441	2.49	down	lincRNA:chr8:18587198-18592948 forward strand
	0.0019	2.09	down	lincRNA:chr8:18895366-18925423 forward strand
4930414F18Rik	0.0180	2.95	down	lincRNA:chr8:26343277-26352902 reverse strand
Rgs16	0.0094	1.64	down	lincRNA:chr8:37582187-37621987 forward strand
LOC100047316	0.0176	2.42	down	lincRNA:chr8:41934312-41945487 reverse strand
	0.0090	22.79	down	lincRNA:chr8:42462791-42466106 reverse strand
	0.0462	2.20	down	lincRNA:chr8:90000619-90061169 forward strand
LOC100044816	0.0312	2.24	down	lincRNA:chr9:106170918-106177894 reverse strand
6530401N04Rik	0.0468	1.75	down	lincRNA:chr9:111214181-111260465 forward strand
	0.0328	2.06	down	lincRNA:chr9:118060025-118085050 forward strand
Gzma	0.0248	2.16	down	lincRNA:chr9:118060025-118085050 forward strand
	0.0356	2.05	down	lincRNA:chr9:14480441-14483362 forward strand
	0.0243	12.47	down	lincRNA:chr9:20784567-20799942 reverse strand
Wdfy1	0.0272	3.72	down	lincRNA:chr9:34192364-34192810 reverse strand
	0.0187	2.09	down	lincRNA:chr9:41488229-41545481 reverse strand
2010012P19Rik	0.0357	3.04	down	lincRNA:chr9:43738583-43757007 forward strand
Olfr476	0.0291	2.62	down	lincRNA:chr9:56379670-56429822 reverse strand
Oprl1	0.0211	2.54	down	lincRNA:chr9:58301467-58323783 reverse strand
Cenpm	0.0079	3.28	down	lincRNA:chr9:66981366-67061725 forward strand
	0.0261	1.87	down	lincRNA:chr9:96664617-96683617 forward strand
	0.0083	2.82	down	lincRNA:chrX:146827709-146913398 forward strand
	0.0251	5.80	down	lincRNA:chrX:90997595-91009570 reverse strand
Gm9077	0.0335	1.57	down	lincRNA:chrX:98680220-98718445 reverse strand
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1300015D01Rik	0.0480	1.82	up	Mus musculus adult male liver cDNA, RIKEN full-length enriched library, clone:1300015D01 product:unclassifiable, full insert sequence. [AK005014]	AK005014
4933438K21Rik	0.0021	2.77	up	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933438K21 product:weakly similar to ORF4 PROTEIN [Rattus norvegicus], full insert sequence. [AK017111]	AK017111
A930018M24Rik	0.0227	1.98	up	Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330167E06 product:unclassifiable, full insert sequence. [AK034241]	AK034241
Asb16	0.0353	3.05	up	ankyrin repeat and SOCS box-containing 16 Gene [Source:MGI (curated);Acc:MGI:2654437] [ENSMUST00000036467]	AK038411
	0.0457	1.56	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q8BR28] [ENSMUST00000099590]	AK045810
	0.0068	1.98	up	Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230343F10 product:unclassifiable, full insert sequence. [AK046125]	AK046125
Zdhhc2	0.0054	3.72	up	zinc finger, DHHC domain containing 2 Gene [Source:MGI (curated);Acc:MGI:1923452] [ENSMUST00000049389]	AK046533
B930018H19	0.0090	2.29	up	Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B930018H19 product:unclassifiable, full insert sequence. [AK047086]	AK047086
1500004A13Rik	0.0466	1.60	up	Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500004A13 product:unclassifiable, full insert sequence. [AK075724]	AK075724
	0.0200	1.90	up	RIKEN cDNA D630004N19 gene Gene [Source:MGI Symbol;Acc:MGI:3028054] [ENSMUST00000064334]	AK085283
	0.0332	1.55	up	RIKEN cDNA 3222401L13 gene Gene [Source:MGI Symbol;Acc:MGI:2444186] [ENSMUST00000097608]	AK086343

	0.0274	2.43	up	cDNA sequence BC027344 (BC027344), mRNA [Source:RefSeq DNA;Acc:NM_173738] [ENSMUST00000108223]	AK137204
	0.0473	3.43	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3UKC4] [ENSMUST00000099340]	AK146072
	0.0358	1.61	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3UF18] [ENSMUST00000098770]	AK149124
	0.0170	1.96	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3U0D0] [ENSMUST00000100702]	AK156988
Fgd3	0.0019	1.61	up	FYVE, RhoGEF and PH domain containing 3 Gene [Source:MGI (curated);Acc:MGI:1353657] [ENSMUST00000110087]	AK157835
	0.0428	1.61	up	demethyl-Q 7 Gene [Source:MGI (curated);Acc:MGI:107207] [ENSMUST00000098090]	AK158380
	0.0054	1.70	up	cell division cycle 123 homolog (S. cerevisiae) Gene [Source:MGI (curated);Acc:MGI:2138811] [ENSMUST00000100445]	AK161246
	0.0132	2.64	up	coiled-coil domain containing 64 Gene [Source:MGI (curated);Acc:MGI:1922915] [ENSMUST00000118576]	AK170295
Ccr11	0.0262	5.84	up	Mus musculus chemokine receptor CCX CKR mRNA, complete cds, alternatively spliced. [AY072938]	AY072938
MacroD2	0.0134	3.06	up	MACRO domain containing 2 Gene [Source:MGI (curated);Acc:MGI:1920149] [ENSMUST00000110064]	BC076574
C79777	0.0029	2.18	up	H3045B01-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3045B01 3', mRNA sequence [BG066537]	BG066537
Masp2	0.0019	2.76	up	Mus musculus mannan-binding lectin serine peptidase 2 (Masp2), transcript variant 1, mRNA [NM_001003893]	NM_001003893
BB014433	0.0260	3.68	up	Mus musculus expressed sequence BB014433 (BB014433), mRNA [NM_001007591]	NM_001007591

Mup21	0.0260	16.20	up	Mus musculus major urinary protein 21 (Mup21), mRNA [NM_001009550]	NM_001009550
Mup20	0.0414	431.57	up	Mus musculus major urinary protein 20 (Mup20), mRNA [NM_001012323]	NM_001012323
Mup20	0.0124	162.69	up	Mus musculus major urinary protein 20 (Mup20), mRNA [NM_001012323]	NM_001012323
Ntrk2	0.0442	1.75	up	Mus musculus neurotrophic tyrosine kinase, receptor, type 2 (Ntrk2), transcript variant 1, mRNA [NM_001025074]	NM_001025074
Ikzf1	0.0215	1.64	up	Mus musculus IKAROS family zinc finger 1 (Ikzf1), transcript variant 1, mRNA [NM_001025597]	NM_001025597
Gm5168	0.0069	2.48	up	Mus musculus predicted gene 5168 (Gm5168), mRNA [NM_001025607]	NM_001025607
D17Wsu92e	0.0317	1.59	up	Mus musculus DNA segment, Chr 17, Wayne State University 92, expressed (D17Wsu92e), transcript variant 1, mRNA [NM_001033279]	NM_001033279
Cpne8	0.0007	2.77	up	Mus musculus copine VIII (Cpne8), transcript variant 2, mRNA [NM_001033851]	NM_001033851
Gm5460	0.0489	2.87	up	Mus musculus predicted gene 5460 (Gm5460), mRNA [NM_001034880]	NM_001034880
Adcy7	0.0169	2.00	up	Mus musculus adenylate cyclase 7 (Adcy7), transcript variant 3, mRNA [NM_001037724]	NM_001037724
Ric3	0.0248	3.25	up	Mus musculus resistance to inhibitors of cholinesterase 3 homolog (C. elegans) (Ric3), transcript variant 1, mRNA [NM_001038624]	NM_001038624
Mup3	0.0306	84.28	up	Mus musculus major urinary protein 3 (Mup3), mRNA [NM_001039544]	NM_001039544
Mup2	0.0199	32.95	up	Mus musculus major urinary protein 2 (Mup2), transcript variant 2, mRNA [NM_001045550]	NM_001045550
Gm9733	0.0158	2.79	up	Mus musculus predicted gene 9733 (Gm9733), mRNA [NM_001076679]	NM_001076679
Ptpn6	0.0001	1.55	up	Mus musculus protein tyrosine phosphatase, non-receptor type 6 (Ptpn6), transcript variant 2, mRNA [NM_001077705]	NM_001077705

Zfp429	0.0032	3.08	up	Mus musculus zinc finger protein 429 (Zfp429), mRNA [NM_001080941]	NM_001080941
Tmsb15b2	0.0213	2.32	up	Mus musculus thymosin beta 15b2 (Tmsb15b2), mRNA [NM_001080967]	NM_001080967
Unc79	0.0496	2.58	up	Mus musculus unc-79 homolog (C. elegans) (Unc79), mRNA [NM_001081017]	NM_001081017
Tsc22d2	0.0271	2.22	up	Mus musculus TSC22 domain family, member 2 (Tsc22d2), mRNA [NM_001081229]	NM_001081229
Ctcf1	0.0100	2.21	up	Mus musculus CCCTC-binding factor (zinc finger protein)-like (Ctcf1), mRNA [NM_001081387]	NM_001081387
Tbc1d8b	0.0321	1.50	up	Mus musculus TBC1 domain family, member 8B (Tbc1d8b), mRNA [NM_001081499]	NM_001081499
Tmsb15b1	0.0332	2.90	up	Mus musculus thymosin beta 15b1 (Tmsb15b1), mRNA [NM_001081983]	NM_001081983
Duox1	0.0298	3.41	up	Mus musculus dual oxidase 1 (Duox1), mRNA [NM_001099297]	NM_001099297
Klra7	0.0290	2.39	up	Mus musculus killer cell lectin-like receptor, subfamily A, member 7 (Klra7), transcript variant 1, mRNA [NM_001110323]	NM_001110323
Phf8	0.0409	1.95	up	Mus musculus PHD finger protein 8 (Phf8), transcript variant 2, mRNA [NM_001113354]	NM_001113354
Lifr	0.0390	1.66	up	Mus musculus leukemia inhibitory factor receptor (Lifr), transcript variant 2, mRNA [NM_001113386]	NM_001113386
Chrdl1	0.0307	1.52	up	Mus musculus chordin-like 1 (Chrdl1), transcript variant 1, mRNA [NM_001114385]	NM_001114385
Mfsd4	0.0313	3.00	up	Mus musculus major facilitator superfamily domain containing 4 (Mfsd4), transcript variant b, mRNA [NM_001114662]	NM_001114662
Pde7a	0.0292	1.76	up	Mus musculus phosphodiesterase 7A (Pde7a), transcript variant 2, mRNA [NM_001122759]	NM_001122759
Ang3	0.0296	1.58	up	Mus musculus angiogenin, ribonuclease A family, member 3 (Ang3), mRNA [NM_001123394]	NM_001123394
Ang3	0.0234	2.47	up	Mus musculus angiogenin, ribonuclease A family, member 3 (Ang3), mRNA [NM_001123394]	NM_001123394

Mup9	0.0389	254.40	up	Mus musculus major urinary protein 9 (Mup9), mRNA [NM_001126319]	NM_001126319
Gm2382	0.0411	1.66	up	Mus musculus predicted gene 2382 (Gm2382), mRNA [NM_001128601]	NM_001128601
LOC100048885	0.0398	294.22	up	Mus musculus major urinary protein LOC100048885 (LOC100048885), mRNA [NM_001134644]	NM_001134644
Klf14	0.0271	11.57	up	Mus musculus Kruppel-like factor 14 (Klf14), mRNA [NM_001135093]	NM_001135093
LOC100189605	0.0363	214.65	up	Mus musculus major urinary protein 17 (LOC100189605), mRNA [NM_001135127]	NM_001135127
LOC100189605	0.0393	243.09	up	Mus musculus major urinary protein 17 (LOC100189605), mRNA [NM_001135127]	NM_001135127
Slx	0.0331	2.40	up	Mus musculus Sycp3 like X-linked (Slx), mRNA [NM_001136476]	NM_001136476
Slc25a44	0.0434	1.51	up	Mus musculus solute carrier family 25, member 44 (Slc25a44), transcript variant 3, mRNA [NM_001145877]	NM_001145877
Hk1	0.0054	1.52	up	Mus musculus hexokinase 1 (Hk1), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA [NM_001146100]	NM_001146100
Rdh7	0.0264	45.29	up	Mus musculus retinol dehydrogenase 7 (Rdh7), transcript variant 1, mRNA [NM_001150749]	NM_001150749
Fmo5	0.0441	1.73	up	Mus musculus flavin containing monooxygenase 5 (Fmo5), transcript variant 1, mRNA [NM_001161765]	NM_001161765
Fmo5	0.0248	2.40	up	Mus musculus flavin containing monooxygenase 5 (Fmo5), transcript variant 1, mRNA [NM_001161765]	NM_001161765
E430029J22Rik	0.0098	1.73	up	Mus musculus RIKEN cDNA E430029J22 gene (E430029J22Rik), mRNA [NM_001162938]	NM_001162938
Sgsm1	0.0073	1.99	up	Mus musculus small G protein signaling modulator 1 (Sgsm1), transcript variant 3, mRNA [NM_001162965]	NM_001162965
Lym5	0.0350	1.85	up	Mus musculus LYR motif containing 5 (Lym5), transcript variant 1, mRNA [NM_001163628]	NM_001163628
Fbxo27	0.0267	2.38	up	Mus musculus F-box protein 27 (Fbxo27), transcript variant 1, mRNA [NM_001163702]	NM_001163702

Tsr2	0.0015	1.50	up	Mus musculus TSR2, 20S rRNA accumulation, homolog (S. cerevisiae) (Tsr2), transcript variant 1, mRNA [NM_001164578]	NM_001164578
Slc39a11	0.0361	1.61	up	Mus musculus solute carrier family 39 (metal ion transporter), member 11 (Slc39a11), transcript variant 1, mRNA [NM_001166503]	NM_001166503
Gm16430	0.0113	2.09	up	Mus musculus predicted gene 16430 (Gm16430), mRNA [NM_001166601]	NM_001166601
Gml	0.0325	2.05	up	Mus musculus GPI anchored molecule like protein (Gml), mRNA [NM_001177524]	NM_001177524
Ankrd29	0.0280	6.04	up	Mus musculus ankyrin repeat domain 29 (Ankrd29), mRNA [NM_001190371]	NM_001190371
Ankrd29	0.0367	5.66	up	Mus musculus ankyrin repeat domain 29 (Ankrd29), mRNA [NM_001190371]	NM_001190371
Pzp	0.0288	46.43	up	Mus musculus pregnancy zone protein (Pzp), mRNA [NM_007376]	NM_007376
Adora2b	0.0054	1.83	up	Mus musculus adenosine A2b receptor (Adora2b), mRNA [NM_007413]	NM_007413
Afp	0.0098	7.99	up	Mus musculus alpha fetoprotein (Afp), mRNA [NM_007423]	NM_007423
Ambp	0.0229	38.00	up	Mus musculus alpha 1 microglobulin/bikunin (Ambp), mRNA [NM_007443]	NM_007443
Ang2	0.0487	2.24	up	Mus musculus angiogenin, ribonuclease A family, member 2 (Ang2), mRNA [NM_007449]	NM_007449
Arg1	0.0346	9.80	up	Mus musculus arginase, liver (Arg1), mRNA [NM_007482]	NM_007482
Fcna	0.0264	2.61	up	Mus musculus ficolin A (Fcna), mRNA [NM_007995]	NM_007995
Gc	0.0411	14.84	up	Mus musculus group specific component (Gc), mRNA [NM_008096]	NM_008096
Gjc1	0.0400	1.56	up	Mus musculus gap junction protein, gamma 1 (Gjc1), transcript variant 1, mRNA [NM_008122]	NM_008122
Hpgd	0.0119	1.86	up	Mus musculus hydroxyprostaglandin dehydrogenase 15 (NAD) (Hpgd), mRNA [NM_008278]	NM_008278

Hpgd	0.0399	2.15	up	Mus musculus hydroxyprostaglandin dehydrogenase 15 (NAD) (Hpgd), mRNA [NM_008278]	NM_008278
Ifit1	0.0008	1.62	up	Mus musculus interferon-induced protein with tetratricopeptide repeats 1 (Ifit1), mRNA [NM_008331]	NM_008331
Klra5	0.0062	2.01	up	Mus musculus killer cell lectin-like receptor, subfamily A, member 5 (Klra5), mRNA [NM_008463]	NM_008463
Lamb3	0.0440	2.16	up	Mus musculus laminin, beta 3 (Lamb3), mRNA [NM_008484]	NM_008484
Mest	0.0476	9.54	up	Mus musculus mesoderm specific transcript (Mest), mRNA [NM_008590]	NM_008590
Mest	0.0396	9.65	up	Mus musculus mesoderm specific transcript (Mest), mRNA [NM_008590]	NM_008590
Cpamd8	0.0194	62.95	up	Mus musculus C3 and PZP-like, alpha-2-macroglobulin domain containing 8 (Cpamd8), mRNA [NM_008646]	NM_008646
Mup4	0.0140	85.40	up	Mus musculus major urinary protein 4 (Mup4), mRNA [NM_008648]	NM_008648
Mup5	0.0328	61.33	up	Mus musculus major urinary protein 5 (Mup5), mRNA [NM_008649]	NM_008649
Pla2g4a	0.0368	1.69	up	Mus musculus phospholipase A2, group IVA (cytosolic, calcium-dependent) (Pla2g4a), mRNA [NM_008869]	NM_008869
Ptgfr	0.0212	13.03	up	Mus musculus prostaglandin F receptor (Ptgfr), mRNA [NM_008966]	NM_008966
Saa1	0.0173	3.91	up	Mus musculus serum amyloid A 1 (Saa1), mRNA [NM_009117]	NM_009117
Ssty1	0.0457	1.91	up	Mus musculus spermiogenesis specific transcript on the Y 1 (Ssty1), mRNA [NM_009220]	NM_009220
Sts	0.0459	1.84	up	Mus musculus steroid sulfatase (Sts), mRNA [NM_009293]	NM_009293
Slc27a5	0.0337	28.59	up	Mus musculus solute carrier family 27 (fatty acid transporter), member 5 (Slc27a5), mRNA [NM_009512]	NM_009512
Slc27a5	0.0458	10.64	up	Mus musculus solute carrier family 27 (fatty acid transporter), member 5 (Slc27a5), mRNA [NM_009512]	NM_009512
Apob	0.0163	19.94	up	Mus musculus apolipoprotein B (Apob), mRNA [NM_009693]	NM_009693

Glb1	0.0237	1.91	up	Mus musculus galactosidase, beta 1 (Glb1), mRNA [NM_009752]	NM_009752
Bnip3l	0.0249	1.61	up	Mus musculus BCL2/adenovirus E1B interacting protein 3-like (Bnip3l), mRNA [NM_009761]	NM_009761
Calm1	0.0449	1.82	up	Mus musculus calmodulin 1 (Calm1), mRNA [NM_009790]	NM_009790
Dnm1	0.0027	2.02	up	Mus musculus dynamin 1 (Dnm1), mRNA [NM_010065]	NM_010065
Gamt	0.0409	3.26	up	Mus musculus guanidinoacetate methyltransferase (Gamt), mRNA [NM_010255]	NM_010255
Gstm1	0.0474	1.79	up	Mus musculus glutathione S-transferase, mu 1 (Gstm1), mRNA [NM_010358]	NM_010358
Hexb	0.0378	1.60	up	Mus musculus hexosaminidase B (Hexb), mRNA [NM_010422]	NM_010422
Klra12	0.0058	5.28	up	Mus musculus killer cell lectin-like receptor subfamily A, member 12 (Klra12), mRNA [NM_010646]	NM_010646
Klra4	0.0065	5.16	up	Mus musculus killer cell lectin-like receptor, subfamily A, member 4 (Klra4), mRNA [NM_010649]	NM_010649
Clec4d	0.0271	3.60	up	Mus musculus C-type lectin domain family 4, member d (Clec4d), transcript variant 1, mRNA [NM_010819]	NM_010819
Nek2	0.0356	1.81	up	Mus musculus NIMA (never in mitosis gene a)-related expressed kinase 2 (Nek2), mRNA [NM_010892]	NM_010892
Sqstm1	0.0012	1.80	up	Mus musculus sequestosome 1 (Sqstm1), mRNA [NM_011018]	NM_011018
Prkcd	0.0358	1.53	up	Mus musculus protein kinase C, delta (Prkcd), mRNA [NM_011103]	NM_011103
Prkcd	0.0097	1.64	up	Mus musculus protein kinase C, delta (Prkcd), mRNA [NM_011103]	NM_011103
Saa2	0.0408	19.40	up	Mus musculus serum amyloid A 2 (Saa2), mRNA [NM_011314]	NM_011314
Ccl17	0.0198	2.44	up	Mus musculus chemokine (C-C motif) ligand 17 (Ccl17), mRNA [NM_011332]	NM_011332
Sema3e	0.0249	1.96	up	Mus musculus sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E (Sema3e), mRNA [NM_011348]	NM_011348

Serf2	0.0124	1.64	up	Mus musculus small EDRK-rich factor 2 (Serf2), mRNA [NM_011354]	NM_011354
Sox14	0.0417	2.04	up	Mus musculus SRY-box containing gene 14 (Sox14), mRNA [NM_011440]	NM_011440
Ube1y1	0.0432	2.53	up	Mus musculus ubiquitin-activating enzyme E1, Chr Y 1 (Ube1y1), mRNA [NM_011667]	NM_011667
Usp18	0.0126	1.54	up	Mus musculus ubiquitin specific peptidase 18 (Usp18), mRNA [NM_011909]	NM_011909
Cd97	0.0343	2.28	up	Mus musculus CD97 antigen (Cd97), transcript variant 1, mRNA [NM_011925]	NM_011925
Adh4	0.0006	9.55	up	Mus musculus alcohol dehydrogenase 4 (class II), pi polypeptide (Adh4), mRNA [NM_011996]	NM_011996
Ahsg	0.0175	54.50	up	Mus musculus alpha-2-HS-glycoprotein (Ahsg), mRNA [NM_013465]	NM_013465
Apoa2	0.0264	39.52	up	Mus musculus apolipoprotein A-II (Apoa2), mRNA [NM_013474]	NM_013474
Apoh	0.0302	25.35	up	Mus musculus apolipoprotein H (Apoh), mRNA [NM_013475]	NM_013475
Fgf9	0.0129	2.33	up	Mus musculus fibroblast growth factor 9 (Fgf9), mRNA [NM_013518]	NM_013518
Gfpt2	0.0296	1.92	up	Mus musculus glutamine fructose-6-phosphate transaminase 2 (Gfpt2), mRNA [NM_013529]	NM_013529
Gnb3	0.0271	2.41	up	Mus musculus guanine nucleotide binding protein (G protein), beta 3 (Gnb3), mRNA [NM_013530]	NM_013530
Hist2h2aa1	0.0045	2.72	up	Mus musculus histone cluster 2, H2aa1 (Hist2h2aa1), mRNA [NM_013549]	NM_013549
Ttr	0.0213	72.94	up	Mus musculus transthyretin (Ttr), mRNA [NM_013697]	NM_013697
Akr1c13	0.0176	2.24	up	Mus musculus aldo-keto reductase family 1, member C13 (Akr1c13), mRNA [NM_013778]	NM_013778
Klra15	0.0070	6.36	up	Mus musculus killer cell lectin-like receptor, subfamily A, member 15 (Klra15), mRNA [NM_013793]	NM_013793

Galnt1	0.0037	1.80	up	Mus musculus UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglactosaminyltransferase 1 (Galnt1), transcript variant 1, mRNA [NM_013814]	NM_013814
Ulk2	0.0006	1.96	up	Mus musculus Unc-51 like kinase 2 (C. elegans) (Ulk2), mRNA [NM_013881]	NM_013881
Zpbp	0.0000	1.71	up	Mus musculus zona pellucida binding protein (Zpbp), transcript variant 1, mRNA [NM_015785]	NM_015785
Atp8a2	0.0213	2.22	up	Mus musculus ATPase, aminophospholipid transporter-like, class I, type 8A, member 2 (Atp8a2), mRNA [NM_015803]	NM_015803
Agxt	0.0423	15.95	up	Mus musculus alanine-glyoxylate aminotransferase (Agxt), mRNA [NM_016702]	NM_016702
Ly96	0.0124	1.56	up	Mus musculus lymphocyte antigen 96 (Ly96), transcript variant 1, mRNA [NM_016923]	NM_016923
Krt14	0.0052	4.71	up	Mus musculus keratin 14 (Krt14), mRNA [NM_016958]	NM_016958
St6galnac6	0.0096	1.54	up	Mus musculus ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylglactosaminide alpha-2,6-sialyltransferase 6 (St6galnac6), transcript variant 1, mRNA [NM_016973]	NM_016973
Hpx	0.0275	28.57	up	Mus musculus hemopexin (Hpx), mRNA [NM_017371]	NM_017371
Sfrp5	0.0189	30.17	up	Mus musculus secreted frizzled-related sequence protein 5 (Sfrp5), mRNA [NM_018780]	NM_018780
Foxo4	0.0491	1.91	up	Mus musculus forkhead box O4 (Foxo4), mRNA [NM_018789]	NM_018789
Robo1	0.0126	2.29	up	Mus musculus roundabout homolog 1 (Drosophila) (Robo1), mRNA [NM_019413]	NM_019413
Dnmt3l	0.0462	2.40	up	Mus musculus DNA (cytosine-5-)-methyltransferase 3-like (Dnmt3l), transcript variant 1, mRNA [NM_019448]	NM_019448
Olfm1	0.0312	2.27	up	Mus musculus olfactomedin 1 (Olfm1), transcript variant 1, mRNA [NM_019498]	NM_019498
Dstn	0.0497	1.53	up	Mus musculus destrin (Dstn), mRNA [NM_019771]	NM_019771
Dclk1	0.0221	2.58	up	Mus musculus doublecortin-like kinase 1 (Dclk1), transcript variant 1, mRNA [NM_019978]	NM_019978

Vsig2	0.0366	2.30	up	Mus musculus V-set and immunoglobulin domain containing 2 (Vsig2), mRNA [NM_020518]	NM_020518
Smpdl3a	0.0332	2.18	up	Mus musculus sphingomyelin phosphodiesterase, acid-like 3A (Smpdl3a), mRNA [NM_020561]	NM_020561
Ehd3	0.0444	4.66	up	Mus musculus EH-domain containing 3 (Ehd3), mRNA [NM_020578]	NM_020578
Nova1	0.0076	1.61	up	Mus musculus neuro-oncological ventral antigen 1 (Nova1), mRNA [NM_021361]	NM_021361
Gpr180	0.0479	1.60	up	Mus musculus G protein-coupled receptor 180 (Gpr180), mRNA [NM_021434]	NM_021434
Fzd1	0.0433	1.71	up	Mus musculus frizzled homolog 1 (Drosophila) (Fzd1), mRNA [NM_021457]	NM_021457
F12	0.0320	14.64	up	Mus musculus coagulation factor XII (Hageman factor) (F12), mRNA [NM_021489]	NM_021489
Oca2	0.0399	2.03	up	Mus musculus oculocutaneous albinism II (Oca2), mRNA [NM_021879]	NM_021879
Slc5a7	0.0105	42.82	up	Mus musculus solute carrier family 5 (choline transporter), member 7 (Slc5a7), mRNA [NM_022025]	NM_022025
Knng1	0.0202	26.57	up	Mus musculus kininogen 1 (Knng1), transcript variant 2, mRNA [NM_023125]	NM_023125
Ccnh	0.0362	1.55	up	Mus musculus cyclin H (Ccnh), mRNA [NM_023243]	NM_023243
Ssty2	0.0073	1.60	up	Mus musculus spermiogenesis specific transcript on the Y 2 (Ssty2), mRNA [NM_023546]	NM_023546
Crot	0.0140	1.99	up	Mus musculus carnitine O-octanoyltransferase (Crot), mRNA [NM_023733]	NM_023733
Ormdl2	0.0150	1.84	up	Mus musculus ORM1-like 2 (S. cerevisiae) (Ormdl2), mRNA [NM_024180]	NM_024180
Cyb5r4	0.0131	1.64	up	Mus musculus cytochrome b5 reductase 4 (Cyb5r4), mRNA [NM_024195]	NM_024195
Hsdl2	0.0110	1.66	up	Mus musculus hydroxysteroid dehydrogenase like 2 (Hsdl2), mRNA [NM_024255]	NM_024255
Scd3	0.0068	2.64	up	Mus musculus stearoyl-coenzyme A desaturase 3 (Scd3), mRNA [NM_024450]	NM_024450

Klra23	0.0019	8.27	up	Mus musculus killer cell lectin-like receptor subfamily A, member 23 (Klra23), mRNA [NM_024470]	NM_024470
Klra23	0.0158	2.60	up	Mus musculus killer cell lectin-like receptor subfamily A, member 23 (Klra23), mRNA [NM_024470]	NM_024470
Tbfg1	0.0050	1.74	up	Mus musculus transforming growth factor beta regulated gene 1 (Tbfg1), mRNA [NM_025289]	NM_025289
Txnl4a	0.0205	1.60	up	Mus musculus thioredoxin-like 4A (Txnl4a), transcript variant 1, mRNA [NM_025299]	NM_025299
Zdhhc12	0.0195	1.57	up	Mus musculus zinc finger, DHHC domain containing 12 (Zdhhc12), transcript variant 1, mRNA [NM_025428]	NM_025428
Speer4d	0.0174	2.96	up	Mus musculus spermatogenesis associated glutamate (E)-rich protein 4d (Speer4d), mRNA [NM_025759]	NM_025759
Pcyox1	0.0331	1.96	up	Mus musculus prenylcysteine oxidase 1 (Pcyox1), mRNA [NM_025823]	NM_025823
1300014I06Rik	0.0429	2.41	up	Mus musculus RIKEN cDNA 1300014I06 gene (1300014I06Rik), mRNA [NM_025831]	NM_025831
Herc5	0.0286	1.85	up	Mus musculus hect domain and RLD 5 (Herc5), mRNA [NM_025992]	NM_025992
Nudcd1	0.0379	3.09	up	Mus musculus NudC domain containing 1 (Nudcd1), transcript variant 1, mRNA [NM_026149]	NM_026149
Entpd4	0.0286	1.54	up	Mus musculus ectonucleoside triphosphate diphosphohydrolase 4 (Entpd4), mRNA [NM_026174]	NM_026174
Fam174a	0.0082	1.95	up	Mus musculus family with sequence similarity 174, member A (Fam174a), mRNA [NM_026321]	NM_026321
1110059M19Rik	0.0263	34.22	up	Mus musculus RIKEN cDNA 1110059M19 gene (1110059M19Rik), mRNA [NM_026841]	NM_026841
Enho	0.0233	1.82	up	Mus musculus energy homeostasis associated (Enho), mRNA [NM_027147]	NM_027147
Casz1	0.0199	1.73	up	Mus musculus castor homolog 1, zinc finger (Drosophila) (Casz1), transcript variant 2, mRNA [NM_027195]	NM_027195
Ms4a6b	0.0135	2.28	up	Mus musculus membrane-spanning 4-domains, subfamily A, member 6B (Ms4a6b), mRNA [NM_027209]	NM_027209

Cdc42ep1	0.0439	2.06	up	Mus musculus CDC42 effector protein (Rho GTPase binding) 1 (Cdc42ep1), mRNA [NM_027219]	NM_027219
Nkd1	0.0238	2.19	up	Mus musculus naked cuticle 1 homolog (Drosophila) (Nkd1), transcript variant 1, mRNA [NM_027280]	NM_027280
Prrg1	0.0045	2.00	up	Mus musculus proline rich Gla (G-carboxyglutamic acid) 1 (Prrg1), transcript variant 1, mRNA [NM_027322]	NM_027322
3830403N18Rik	0.0236	2.18	up	Mus musculus RIKEN cDNA 3830403N18 gene (3830403N18Rik), mRNA [NM_027510]	NM_027510
4921507P07Rik	0.0419	1.77	up	Mus musculus RIKEN cDNA 4921507P07 gene (4921507P07Rik), mRNA [NM_027564]	NM_027564
Ifih1	0.0413	1.81	up	Mus musculus interferon induced with helicase C domain 1 (Ifih1), transcript variant 1, mRNA [NM_027835]	NM_027835
Acsl5	0.0338	1.70	up	Mus musculus acyl-CoA synthetase long-chain family member 5 (Acsl5), mRNA [NM_027976]	NM_027976
Tmem106b	0.0221	1.53	up	Mus musculus transmembrane protein 106B (Tmem106b), mRNA [NM_027992]	NM_027992
Ugt2a3	0.0448	9.52	up	Mus musculus UDP glucuronosyltransferase 2 family, polypeptide A3 (Ugt2a3), mRNA [NM_028094]	NM_028094
Ccpg1	0.0079	1.68	up	Mus musculus cell cycle progression 1 (Ccpg1), transcript variant 2, mRNA [NM_028181]	NM_028181
Cxx1c	0.0310	3.05	up	Mus musculus CAAX box 1 homolog C (human) (Cxx1c), mRNA [NM_028375]	NM_028375
Cib4	0.0082	1.91	up	Mus musculus calcium and integrin binding family member 4 (Cib4), mRNA [NM_028483]	NM_028483
1700057K13Rik	0.0236	2.06	up	Mus musculus RIKEN cDNA 1700057K13 gene (1700057K13Rik), mRNA [NM_028540]	NM_028540
Sdr42e1	0.0466	1.70	up	Mus musculus short chain dehydrogenase/reductase family 42E, member 1 (Sdr42e1), mRNA [NM_028725]	NM_028725
Cyp2s1	0.0392	2.09	up	Mus musculus cytochrome P450, family 2, subfamily s, polypeptide 1 (Cyp2s1), mRNA [NM_028775]	NM_028775
Dock8	0.0050	5.58	up	Mus musculus dedicator of cytokinesis 8 (Dock8), mRNA [NM_028785]	NM_028785

Ctbs	0.0233	2.90	up	Mus musculus chitobiase, di-N-acetyl- (Ctbs), mRNA [NM_028836]	NM_028836
Dnajc14	0.0220	1.55	up	Mus musculus DnaJ (Hsp40) homolog, subfamily C, member 14 (Dnajc14), mRNA [NM_028873]	NM_028873
Stard6	0.0298	2.59	up	Mus musculus StAR-related lipid transfer (START) domain containing 6 (Stard6), mRNA [NM_029019]	NM_029019
Stard6	0.0034	2.00	up	Mus musculus StAR-related lipid transfer (START) domain containing 6 (Stard6), mRNA [NM_029019]	NM_029019
Stx11	0.0379	1.96	up	Mus musculus syntaxin 11 (Stx11), transcript variant 1, mRNA [NM_029075]	NM_029075
Pramef12	0.0427	3.86	up	Mus musculus PRAME family member 12 (Pramef12), mRNA [NM_029948]	NM_029948
Rnase6	0.0324	1.77	up	Mus musculus ribonuclease, RNase A family, 6 (Rnase6), mRNA [NM_030098]	NM_030098
Akr1c6	0.0178	53.94	up	Mus musculus aldo-keto reductase family 1, member C6 (Akr1c6), mRNA [NM_030611]	NM_030611
Tsga14	0.0129	2.02	up	Mus musculus testis specific gene A14 (Tsga14), mRNA [NM_031998]	NM_031998
Csprs	0.0441	5.07	up	Mus musculus component of Sp100-rs (Csprs), mRNA [NM_033616]	NM_033616
Wnt16	0.0242	1.54	up	Mus musculus wingless-related MMTV integration site 16 (Wnt16), mRNA [NM_053116]	NM_053116
Trim16	0.0186	1.62	up	Mus musculus tripartite motif-containing 16 (Trim16), mRNA [NM_053169]	NM_053169
Nans	0.0071	1.86	up	Mus musculus N-acetylneuraminic acid synthase (sialic acid synthase) (Nans), mRNA [NM_053179]	NM_053179
Cadm3	0.0271	1.56	up	Mus musculus cell adhesion molecule 3 (Cadm3), mRNA [NM_053199]	NM_053199
Egln2	0.0266	1.92	up	Mus musculus EGL nine homolog 2 (C. elegans) (Egln2), mRNA [NM_053208]	NM_053208
Kiss1r	0.0170	2.43	up	Mus musculus KISS1 receptor (Kiss1r), mRNA [NM_053244]	NM_053244

Synpo2	0.0435	1.76	up	Mus musculus synaptopodin 2 (Synpo2), mRNA [NM_080451]	NM_080451
Synpo2	0.0204	7.00	up	Mus musculus synaptopodin 2 (Synpo2), mRNA [NM_080451]	NM_080451
Slc2a10	0.0280	2.22	up	Mus musculus solute carrier family 2 (facilitated glucose transporter), member 10 (Slc2a10), mRNA [NM_130451]	NM_130451
Parvb	0.0063	1.56	up	Mus musculus parvin, beta (Parvb), mRNA [NM_133167]	NM_133167
D1Ert622e	0.0243	1.71	up	Mus musculus DNA segment, Chr 1, ERATO Doi 622, expressed (D1Ert622e), mRNA [NM_133825]	NM_133825
Fgg	0.0165	68.82	up	Mus musculus fibrinogen gamma chain (Fgg), mRNA [NM_133862]	NM_133862
Ifi44	0.0403	1.70	up	Mus musculus interferon-induced protein 44 (Ifi44), mRNA [NM_133871]	NM_133871
Ugt2b38	0.0347	16.05	up	Mus musculus UDP glucuronosyltransferase 2 family, polypeptide B38 (Ugt2b38), mRNA [NM_133894]	NM_133894
Cyp4v3	0.0137	3.11	up	Mus musculus cytochrome P450, family 4, subfamily v, polypeptide 3 (Cyp4v3), mRNA [NM_133969]	NM_133969
Apon	0.0347	7.38	up	Mus musculus apolipoprotein N (Apon), mRNA [NM_133996]	NM_133996
4930427A07Rik	0.0289	1.98	up	Mus musculus RIKEN cDNA 4930427A07 gene (4930427A07Rik), mRNA [NM_134041]	NM_134041
Epdr1	0.0420	2.34	up	Mus musculus ependymin related protein 1 (zebrafish) (Epdr1), mRNA [NM_134065]	NM_134065
Flnb	0.0313	1.56	up	Mus musculus filamin, beta (Flnb), mRNA [NM_134080]	NM_134080
Slc6a13	0.0370	2.40	up	Mus musculus solute carrier family 6 (neurotransmitter transporter, GABA), member 13 (Slc6a13), mRNA [NM_144512]	NM_144512
Gas2l1	0.0499	1.54	up	Mus musculus growth arrest-specific 2 like 1 (Gas2l1), transcript variant beta, mRNA [NM_144560]	NM_144560
Oas1f	0.0469	2.44	up	Mus musculus 2'-5' oligoadenylate synthetase 1F (Oas1f), mRNA [NM_145153]	NM_145153
Oas1l	0.0303	1.83	up	Mus musculus 2'-5' oligoadenylate synthetase-like 1 (Oas1l), mRNA [NM_145209]	NM_145209

Oas2	0.0276	2.22	up	Mus musculus 2'-5' oligoadenylate synthetase 2 (Oas2), mRNA [NM_145227]	NM_145227
Creb3l3	0.0397	3.35	up	Mus musculus cAMP responsive element binding protein 3-like 3 (Creb3l3), mRNA [NM_145365]	NM_145365
Duoxa1	0.0268	11.26	up	Mus musculus dual oxidase maturation factor 1 (Duoxa1), mRNA [NM_145395]	NM_145395
Cd300ld	0.0321	6.37	up	Mus musculus CD300 molecule-like family member d (Cd300ld), mRNA [NM_145437]	NM_145437
AI661453	0.0460	2.22	up	Mus musculus expressed sequence AI661453 (AI661453), mRNA [NM_145489]	NM_145489
Lctl	0.0174	10.57	up	Mus musculus lactase-like (Lctl), mRNA [NM_145835]	NM_145835
St8sia6	0.0304	1.79	up	Mus musculus ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6 (St8sia6), mRNA [NM_145838]	NM_145838
Gltpd2	0.0374	2.96	up	Mus musculus glycolipid transfer protein domain containing 2 (Gltpd2), mRNA [NM_146020]	NM_146020
Kcnk13	0.0341	1.94	up	Mus musculus potassium channel, subfamily K, member 13 (Kcnk13), transcript variant 3, mRNA [NM_146037]	NM_146037
Olfr187	0.0323	1.56	up	Mus musculus olfactory receptor 187 (Olfr187), mRNA [NM_146322]	NM_146322
Olfr720	0.0031	1.93	up	Mus musculus olfactory receptor 720 (Olfr720), mRNA [NM_146392]	NM_146392
Olfr531	0.0117	2.14	up	Mus musculus olfactory receptor 531 (Olfr531), mRNA [NM_146953]	NM_146953
Hpse	0.0168	1.98	up	Mus musculus heparanase (Hpse), mRNA [NM_152803]	NM_152803
Mapre2	0.0110	1.58	up	Mus musculus microtubule-associated protein, RP/EB family, member 2 (Mapre2), transcript variant 1, mRNA [NM_153058]	NM_153058
Tmem5	0.0157	1.94	up	Mus musculus transmembrane protein 5 (Tmem5), mRNA [NM_153059]	NM_153059
Adap2	0.0068	1.66	up	Mus musculus ArfGAP with dual PH domains 2 (Adap2), mRNA [NM_172133]	NM_172133
Irak2	0.0329	1.74	up	Mus musculus interleukin-1 receptor-associated kinase 2 (Irak2), transcript variant 1, mRNA [NM_172161]	NM_172161

Kdm1b	0.0355	1.50	up	Mus musculus lysine (K)-specific demethylase 1B (Kdm1b), mRNA [NM_172262]	NM_172262
Plcg2	0.0231	1.81	up	Mus musculus phospholipase C, gamma 2 (Plcg2), mRNA [NM_172285]	NM_172285
Aim1	0.0271	1.55	up	Mus musculus absent in melanoma 1 (Aim1), mRNA [NM_172393]	NM_172393
Ostm1	0.0198	1.84	up	Mus musculus osteopetrosis associated transmembrane protein 1 (Ostm1), mRNA [NM_172416]	NM_172416
Itih5	0.0461	3.26	up	Mus musculus inter-alpha (globulin) inhibitor H5 (Itih5), mRNA [NM_172471]	NM_172471
Lgr4	0.0427	2.08	up	Mus musculus leucine-rich repeat-containing G protein-coupled receptor 4 (Lgr4), mRNA [NM_172671]	NM_172671
Sntg2	0.0057	2.59	up	Mus musculus syntrophin, gamma 2 (Sntg2), mRNA [NM_172951]	NM_172951
Bmp3	0.0281	4.18	up	Mus musculus bone morphogenetic protein 3 (Bmp3), mRNA [NM_173404]	NM_173404
Insc	0.0463	2.68	up	Mus musculus inscuteable homolog (Drosophila) (Insc), mRNA [NM_173767]	NM_173767
Apol9a	0.0132	2.52	up	Mus musculus apolipoprotein L 9a (Apol9a), transcript variant 1, mRNA [NM_173786]	NM_173786
Fam83a	0.0272	3.89	up	Mus musculus family with sequence similarity 83, member A (Fam83a), mRNA [NM_173862]	NM_173862
Gm5077	0.0280	2.16	up	Mus musculus predicted gene 5077 (Gm5077), mRNA [NM_173864]	NM_173864
Chst8	0.0012	2.69	up	Mus musculus carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8 (Chst8), mRNA [NM_175140]	NM_175140
Sec24a	0.0180	2.01	up	Mus musculus Sec24 related gene family, member A (S. cerevisiae) (Sec24a), mRNA [NM_175255]	NM_175255
Wtap	0.0492	1.57	up	Mus musculus Wilms' tumour 1-associating protein (Wtap), transcript variant 2, mRNA [NM_175394]	NM_175394
9530008L14Rik	0.0160	2.11	up	Mus musculus RIKEN cDNA 9530008L14 gene (9530008L14Rik), transcript variant 1, mRNA [NM_175417]	NM_175417

E130304F04Rik	0.0316	1.72	up	Mus musculus RIKEN cDNA E130304F04 gene (E130304F04Rik), mRNA [NM_175538]	NM_175538
Itga11	0.0452	2.94	up	Mus musculus integrin alpha 11 (Itga11), mRNA [NM_176922]	NM_176922
Defb20	0.0301	13.74	up	Mus musculus defensin beta 20 (Defb20), mRNA [NM_176950]	NM_176950
Tmem91	0.0114	3.21	up	Mus musculus transmembrane protein 91 (Tmem91), mRNA [NM_177102]	NM_177102
Agtr1a	0.0021	1.62	up	Mus musculus angiotensin II receptor, type 1a (Agtr1a), mRNA [NM_177322]	NM_177322
Aph1b	0.0014	1.66	up	Mus musculus anterior pharynx defective 1b homolog (C. elegans) (Aph1b), mRNA [NM_177583]	NM_177583
Gm4922	0.0374	1.82	up	Mus musculus predicted gene 4922 (Gm4922), mRNA [NM_177706]	NM_177706
Hbp1	0.0362	1.51	up	Mus musculus high mobility group box transcription factor 1 (Hbp1), transcript variant 2, mRNA [NM_177993]	NM_177993
Hist1h2ak	0.0114	2.19	up	Mus musculus histone cluster 1, H2ak (Hist1h2ak), mRNA [NM_178183]	NM_178183
Hist1h2an	0.0352	2.51	up	Mus musculus histone cluster 1, H2an (Hist1h2an), mRNA [NM_178184]	NM_178184
Zdhhc2	0.0087	3.82	up	Mus musculus zinc finger, DHHC domain containing 2 (Zdhhc2), mRNA [NM_178395]	NM_178395
Tagln2	0.0062	1.65	up	Mus musculus transgelin 2 (Tagln2), mRNA [NM_178598]	NM_178598
AI182371	0.0249	4.35	up	Mus musculus expressed sequence AI182371 (AI182371), mRNA [NM_178885]	NM_178885
Reep4	0.0290	1.52	up	Mus musculus receptor accessory protein 4 (Reep4), mRNA [NM_180588]	NM_180588
Me3	0.0403	1.89	up	Mus musculus malic enzyme 3, NADP(+)-dependent, mitochondrial (Me3), nuclear gene encoding mitochondrial protein, mRNA [NM_181407]	NM_181407
Me3	0.0141	1.90	up	Mus musculus malic enzyme 3, NADP(+)-dependent, mitochondrial (Me3), nuclear gene encoding mitochondrial protein, mRNA [NM_181407]	NM_181407

Arhgap11a	0.0034	1.96	up	Mus musculus Rho GTPase activating protein 11A (Arhgap11a), mRNA [NM_181416]	NM_181416
Arhgap11a	0.0208	1.89	up	Mus musculus Rho GTPase activating protein 11A (Arhgap11a), mRNA [NM_181416]	NM_181416
Arhgap11a	0.0072	2.99	up	Mus musculus Rho GTPase activating protein 11A (Arhgap11a), mRNA [NM_181416]	NM_181416
Optn	0.0207	1.66	up	Mus musculus optineurin (Optn), mRNA [NM_181848]	NM_181848
Ggn	0.0094	1.95	up	Mus musculus gametogenetin (Ggn), transcript variant 3, mRNA [NM_182696]	NM_182696
AI987944	0.0128	4.60	up	Mus musculus expressed sequence AI987944 (AI987944), mRNA [NM_183167]	NM_183167
BC055111	0.0039	2.45	up	Mus musculus cDNA sequence BC055111 (BC055111), mRNA [NM_183182]	NM_183182
Ccdc72	0.0217	1.54	up	Mus musculus coiled-coil domain containing 72 (Ccdc72), mRNA [NM_183250]	NM_183250
Ranbp3l	0.0008	7.29	up	Mus musculus RAN binding protein 3-like (Ranbp3l), mRNA [NM_198024]	NM_198024
Paqr6	0.0155	2.00	up	Mus musculus progesterin and adipoQ receptor family member VI (Paqr6), mRNA [NM_198410]	NM_198410
Plekhg6	0.0035	5.03	up	Mus musculus pleckstrin homology domain containing, family G (with RhoGef domain) member 6 (Plekhg6), mRNA [NM_198604]	NM_198604
Hn1l	0.0276	2.20	up	Mus musculus hematological and neurological expressed 1-like (Hn1l), mRNA [NM_198937]	NM_198937
Vmn1r183	0.0285	2.25	up	Mus musculus vomeronasal 1 receptor 183 (Vmn1r183), mRNA [NM_203489]	NM_203489
Yipf6	0.0436	1.61	up	Mus musculus Yip1 domain family, member 6 (Yipf6), mRNA [NM_207633]	NM_207633
Yipf6	0.0420	1.55	up	Mus musculus Yip1 domain family, member 6 (Yipf6), mRNA [NM_207633]	NM_207633
6430411K18Rik	0.0386	2.73	up	Mus musculus RIKEN cDNA 6430411K18 gen (6430411K18Rik), non-coding RNA [NR_002848]	NR_002848

LOC100042049	0.0072	1.93	up	Mus musculus ribosomal protein L22 like 1 pseudogene (LOC100042049), non-coding RNA [NR_004442]	NR_004442
1700030C10Rik	0.0130	2.25	up	Mus musculus RIKEN cDNA 1700030C10 gene (1700030C10Rik), non-coding RNA [NR_015521]	NR_015521
1700001L05Rik	0.0278	1.86	up	Mus musculus RIKEN cDNA 1700001L05 gene (1700001L05Rik), non-coding RNA [NR_027980]	NR_027980
5330426P16Rik	0.0413	1.68	up	Mus musculus RIKEN cDNA 5330426P16 gene (5330426P16Rik), non-coding RNA [NR_028300]	NR_028300
Gm5627	0.0165	21.43	up	Mus musculus predicted gene 5627 (Gm5627), non-coding RNA [NR_033301]	NR_033301
2810433D01Rik	0.0044	1.86	up	Mus musculus RIKEN cDNA 2810433D01 gene (2810433D01Rik), non-coding RNA [NR_033474]	NR_033474
Gm8221	0.0433	2.83	up	Mus musculus predicted gene 8221 (Gm8221), non-coding RNA [NR_033577]	NR_033577
Gm9054	0.0468	5.09	up	PREDICTED: Mus musculus predicted gene, EG668224 (EG668224), mRNA [XM_001001089]	XM_001001089
	0.0057	1.68	up	RIKEN cDNA 6720489N17 gene Gene [Source:MGI Symbol;Acc:MGI:2443901] [ENSMUST00000091563]	XM_001472312
LOC100044494	0.0427	1.53	up	PREDICTED: Mus musculus similar to ribosomal protein (LOC100044494), mRNA [XM_001472583]	XM_001472583
Gm15452	0.0094	2.49	up	PREDICTED: Mus musculus similar to Cyclin-dependent kinases regulatory subunit 2 (CKS-2) (LOC100044764), mRNA [XM_001472867]	XM_001472867
Pcdh11x	0.0164	1.65	up	PREDICTED: Mus musculus hypothetical protein LOC100039461 (LOC100039461), mRNA [XM_001472925]	XM_001472925
LOC100044852	0.0328	1.66	up	PREDICTED: Mus musculus similar to G protein gamma-5 subunit (LOC100044852), mRNA [XM_001473001]	XM_001473001
Gm8954	0.0489	3.77	up	PREDICTED: Mus musculus predicted gene, EG668061 (EG668061), mRNA [XM_001473041]	XM_001473041
LOC100045185	0.0322	2.02	up	PREDICTED: Mus musculus hypothetical protein LOC100045185 (LOC100045185), mRNA [XM_001473814]	XM_001473814

AW822252	0.0060	9.23	up	PREDICTED: Mus musculus expressed sequence AW822252 (AW822252), mRNA [XM_001474711]	XM_001474711
LOC100045691	0.0042	6.00	up	PREDICTED: Mus musculus similar to keratin associated protein 10-7 (LOC100045691), mRNA [XM_001474758]	XM_001474758
LOC100045922	0.0015	1.54	up	PREDICTED: Mus musculus similar to vacuolar protein sorting 52 (LOC100045922), mRNA [XM_001475183]	XM_001475183
	0.0048	1.69	up	PREDICTED: Mus musculus similar to RIKEN cDNA 5830484A20 gene (LOC100041081), mRNA [XM_001475751]	XM_001475751
Gm4619	0.0208	1.83	up	PREDICTED: Mus musculus hypothetical protein LOC100046466 (LOC100046466), mRNA [XM_001476246]	XM_001476246
Gm3293	0.0350	2.17	up	PREDICTED: Mus musculus similar to Ubtg protein (LOC100041366), mRNA [XM_001476247]	XM_001476247
	0.0485	1.51	up	PREDICTED: Mus musculus similar to Sycp3 like Y-linked, transcript variant 2 (LOC100042050), mRNA [XM_001476868]	XM_001476868
Gm3819	0.0051	2.04	up	PREDICTED: Mus musculus hypothetical protein LOC100046872 (LOC100046872), mRNA [XM_001477163]	XM_001477163
	0.0333	1.79	up	PREDICTED: Mus musculus hypothetical protein LOC100041919 (LOC100041919), mRNA [XM_001477525]	XM_001477525
	0.0492	2.11	up	AHNAK nucleoprotein 2 Gene [Source:MGI (curated);Acc:MGI:2144831] [ENSMUST00000101009]	XM_001477593
LOC100042197	0.0294	2.22	up	PREDICTED: Mus musculus similar to cyclic nucleotide gated channel beta 1 (LOC100042197), mRNA [XM_001477710]	XM_001477710
LOC100042664	0.0178	2.21	up	PREDICTED: Mus musculus similar to polyprotein (LOC100042664), mRNA [XM_001477951]	XM_001477951
Gm9629	0.0026	1.98	up	PREDICTED: Mus musculus similar to CG32602-PA (LOC674779), mRNA [XM_001478781]	XM_001478781

Gm9296	0.0053	2.53	up	PREDICTED: Mus musculus predicted gene, EG668670 (EG668670), mRNA [XM_001478977]	XM_001478977
EG640142	0.0329	1.70	up	PREDICTED: Mus musculus predicted gene, EG640142 (EG640142), mRNA [XM_001479924]	XM_001479924
LOC100048366	0.0387	1.55	up	PREDICTED: Mus musculus similar to G protein gamma-5 subunit (LOC100048366), mRNA [XM_001479988]	XM_001479988
LOC100048303	0.0285	1.59	up	PREDICTED: Mus musculus hypothetical protein LOC100048303 (LOC100048303), mRNA [XM_001480037]	XM_001480037
Gm4452	0.0429	1.73	up	PREDICTED: Mus musculus hypothetical protein LOC100043465 (LOC100043465), mRNA [XM_001480050]	XM_001480050
Gm6936	0.0150	1.72	up	PREDICTED: Mus musculus hypothetical protein LOC628951 (LOC628951), mRNA [XM_001480183]	XM_001480183
4933427G17Rik	0.0240	1.97	up	RIKEN cDNA 4933427G17 gene Gene [Source:MGI Symbol;Acc:MGI:1921716] [ENSMUST00000033166]	XM_133717
Gm4862	0.0308	1.99	up	PREDICTED: Mus musculus predicted gene, EG229879 (EG229879), mRNA [XM_143595]	XM_143595
	0.0461	1.58	up	RIKEN cDNA 4933413J09 gene Gene [Source:MGI Symbol;Acc:MGI:1918356] [ENSMUST00000022427]	XM_354798
LOC630442	0.0058	1.74	up	PREDICTED: Mus musculus hypothetical LOC630442 (LOC630442), mRNA [XM_903593]	XM_903593
LOC640502	0.0050	1.77	up	PREDICTED: Mus musculus similar to UDP-N-acetylglucosamine pyrophosphorylase 1 (LOC640502), mRNA [XM_917484]	XM_917484
LOC640965	0.0116	5.00	up	killer cell lectin-like receptor subfamily A, member 11 Gene [Source:MGI Symbol;Acc:MGI:1321092] [ENSMUST00000112029]	XM_918210
Gm8212	0.0163	1.56	up	PREDICTED: Mus musculus predicted gene, EG666647 (EG666647), mRNA [XM_985174]	XM_985174
	0.0185	1.83	up	PREDICTED: Mus musculus predicted gene, EG666678 (EG666678), mRNA [XM_985370]	XM_985370

Mup-ps10	0.0187	69.91	up	PREDICTED: Mus musculus similar to novel member of the major urinary protein (Mup) gene family (LOC667239), misc RNA [XR_001996]	XR_001996
	0.0327	146.14	up	major urinary protein, pseudogene 8 Pseudogene [Source:MGI (curated);Acc:MGI:3780197] [ENSMUST00000107490]	XR_030536
Mup-ps12	0.0317	104.68	up	PREDICTED: Mus musculus similar to Predicted gene, OTTMUSG00000007485 (LOC100039019), misc RNA [XR_030567]	XR_030567
	0.0356	39.31	up	PREDICTED: Mus musculus similar to Predicted gene, OTTMUSG00000007485 (LOC100039019), misc RNA [XR_030567]	XR_030567
Mup-ps13	0.0390	84.66	up	PREDICTED: Mus musculus similar to novel member of the major urinary protein (Mup) gene family (LOC621093), misc RNA [XR_030662]	XR_030662
Gm13089	0.0493	1.66	up	PREDICTED: Mus musculus predicted gene, OTTMUSG00000010333 (OTTMUSG00000010333), misc RNA [XR_030771]	XR_030771
Gm7660	0.0473	2.09	up	PREDICTED: Mus musculus similar to UDP glucuronosyltransferase 2 family, polypeptide B36 (LOC665494), misc RNA [XR_031289]	XR_031289
Rpl19-ps5	0.0492	4.63	up	PREDICTED: Mus musculus similar to Ribosomal protein L19 (LOC668835), misc RNA [XR_031444]	XR_031444
Gm9435	0.0479	2.33	up	PREDICTED: Mus musculus similar to ribosomal protein L6 (LOC668991), misc RNA [XR_031978]	XR_031978
Gm15442	0.0167	1.56	up	PREDICTED: Mus musculus similar to zinc finger protein ZFP114 (LOC100041691), misc RNA [XR_032938]	XR_032938
LOC100048070	0.0201	1.63	up	PREDICTED: Mus musculus similar to replication factor C 5 (LOC100048070), misc RNA [XR_034330]	XR_034330
Mup-ps3	0.0150	66.61	up	PREDICTED: Mus musculus similar to novel member of the major urinary protein (Mup) gene family (LOC667221), misc RNA [XR_035681]	XR_035681

	0.0133	2.33	down	caveolin 2 Gene [Source:MGI (curated);Acc:MGI:107571] [ENSMUST00000115459]	AB049605
	0.0151	2.81	down	RIKEN cDNA 1110020C17 gene Gene [Source:MGI Symbol;Acc:MGI:1915834] [ENSMUST00000050338]	AK003851
	0.0095	1.99	down	RIKEN cDNA 1700028N14 gene Gene [Source:MGI Symbol;Acc:MGI:1920530] [ENSMUST00000021325]	AK006468
2210416O15Rik	0.0115	2.37	down	Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210416O15 product:hypothetical protein, full insert sequence. [AK008958]	AK008958
3300002A11Rik	0.0011	1.57	down	Mus musculus 11 days embryo whole body cDNA, RIKEN full length enriched library, clone:2700016B18 product:unclassifiable, full insert sequence. [AK012244]	AK012244
	0.0483	2.12	down	glucan (1,4-alpha-), branching enzyme 1 Gene [Source:MGI Symbol;Acc:MGI:1921435] [ENSMUST00000099628]	AK013167
	0.0158	1.65	down	RIKEN cDNA 4930449E01 gene Gene [Source:MGI Symbol;Acc:MGI:1922114] [ENSMUST00000022711]	AK015429
4930474N09Rik	0.0142	1.55	down	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930474N09 product:unclassifiable, full insert sequence. [AK015577]	AK015577
4930488N15Rik	0.0471	2.06	down	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930488N15 product:unclassifiable, full insert sequence. [AK015648]	AK015648
4930506C21Rik	0.0291	1.68	down	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930506C21 product:unclassifiable, full insert sequence. [AK015714]	AK015714
LOC100036523	0.0434	1.86	down	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932434L04 product:hypothetical protein, full insert sequence. [AK016549]	AK016549
4933415J04Rik	0.0481	1.60	down	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933415J04 product:unclassifiable, full insert sequence. [AK016822]	AK016822

4933416A02Rik	0.0342	1.93	down	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933416A02 product:unclassifiable, full insert sequence. [AK016828]	AK016828
4933417C20Rik	0.0461	2.10	down	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933417C20 product:RIKEN cDNA 4933417C20 gene, full insert sequence. [AK016840]	AK016840
4933428C20Rik	0.0307	1.83	down	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933428C20 product:unclassifiable, full insert sequence. [AK016962]	AK016962
6230400D17Rik	0.0306	1.60	down	Mus musculus 11 days embryo head cDNA, RIKEN full-length enriched library, clone:6230400D17 product:hypothetical protein, full insert sequence. [AK018074]	AK018074
	0.0483	1.84	down	RIKEN cDNA D930007J09 gene Gene [Source:MGI Symbol;Acc:MGI:3686989] [ENSMUST00000057911]	AK019527
	0.0452	1.61	down	AU RNA binding protein/enoyl-coenzyme A hydratase Gene [Source:MGI (curated);Acc:MGI:1338011] [ENSMUST00000120535]	AK019978
9430063H18Rik	0.0435	1.82	down	Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430063H18 product:unclassifiable, full insert sequence. [AK020472]	AK020472
Rbm12	0.0024	1.53	down	copine I Gene [Source:MGI (curated);Acc:MGI:2386621] [ENSMUST00000109604]	AK020481
9530003O04Rik	0.0043	1.97	down	Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530003O04 product:unclassifiable, full insert sequence. [AK020539]	AK020539
5230400M03Rik	0.0201	1.61	down	Mus musculus adult male xiphoid cartilage cDNA, RIKEN full-length enriched library, clone:5230400M03 product:unclassifiable, full insert sequence. [AK030345]	AK030345
	0.0317	1.56	down	RIKEN cDNA 6720416L17 gene Gene [Source:MGI Symbol;Acc:MGI:3026978] [ENSMUST00000100000]	AK032721

9330175E14Rik	0.0057	1.84	down	Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330175E14 product:HYPOTHETICAL 4.5 KDA PROTEIN homolog [Homo sapiens], full insert sequence. [AK034303]	AK034303
4930458D05Rik	0.0048	2.60	down	Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:9830138L07 product:unclassifiable, full insert sequence. [AK036594]	AK036594
D9Wsu90e	0.0002	1.98	down	Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130091A19 product:unclassifiable, full insert sequence. [AK038263]	AK038263
	0.0318	1.57	down	B-cell CLL/lymphoma 7C Gene [Source:MGI (curated);Acc:MGI:1332237] [ENSMUST00000106282]	AK038789
	0.0222	3.45	down	phospholipase C, delta 4 Gene [Source:MGI (curated);Acc:MGI:107469] [ENSMUST00000113745]	AK039149
	0.0307	1.71	down	Ellis van Creveld gene homolog (human) Gene [Source:MGI (curated);Acc:MGI:1890596] [ENSMUST00000114154]	AK039759
	0.0079	1.96	down	RIKEN cDNA A530013C23 gene Gene [Source:MGI Symbol;Acc:MGI:3041178] [ENSMUST00000021742]	AK040674
A530020G20Rik	0.0029	2.60	down	Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530051K04 product:unclassifiable, full insert sequence. [AK040960]	AK040960
	0.0014	1.79	down	ribosomal protein S6 kinase polypeptide 3 Gene [Source:MGI (curated);Acc:MGI:104557] [ENSMUST00000112491]	AK041476
LOC432958	0.0432	1.63	down	Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630042D17 product:unclassifiable, full insert sequence. [AK041852]	AK041852
Svil	0.0258	1.75	down	supervillin Gene [Source:MGI (curated);Acc:MGI:2147319] [ENSMUST00000115871]	AK041925
	0.0396	1.55	down	RIKEN cDNA C230012O17 gene Gene [Source:MGI Symbol;Acc:MGI:2442283] [ENSMUST00000108207]	AK044654
	0.0402	1.60	down	PHD finger protein 3 Gene [Source:MGI Symbol;Acc:MGI:2446126] [ENSMUST00000046443]	AK045780

	0.0271	1.60	down	sacsin Gene [Source:MGI (curated);Acc:MGI:1354724] [ENSMUST00000119509]	AK046501
	0.0287	1.70	down	Putative uncharacterized protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q8BQM5] [ENSMUST00000070164]	AK047780
Ncrna00085	0.0053	1.66	down	Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230078D19 product:unclassifiable, full insert sequence. [AK048874]	AK048874
C530014P21Rik	0.0256	1.51	down	Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530014P21 product:unclassifiable, full insert sequence. [AK049648]	AK049648
	0.0419	2.41	down	RIKEN cDNA A730069N07 gene Gene [Source:MGI Symbol;Acc:MGI:2442088] [ENSMUST00000036104]	AK053142
E230012P03	0.0046	1.57	down	Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN full-length enriched library, clone:E230012P03 product:hypothetical protein, full insert sequence. [AK054025]	AK054025
E230024E03Rik	0.0027	2.82	down	Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN full-length enriched library, clone:E230024E03 product:similar to L1MD-9 REPETITIVE SEQUENCE [Mus musculus], full insert sequence. [AK054157]	AK054157
	0.0100	3.48	down	WD repeat domain 61 Gene [Source:MGI (curated);Acc:MGI:1917493] [ENSMUST00000118771]	AK077037
	0.0075	2.78	down	lin-7 homolog A (C. elegans) Gene [Source:MGI Symbol;Acc:MGI:2135609] [ENSMUST00000099302]	AK077191
D4Ertd681e	0.0047	2.41	down	Mus musculus 11 days embryo gonad cDNA, RIKEN full-length enriched library, clone:7030402E17 product:DNA segment, Chr 4, ERATO Doi 681, expressed, full insert sequence. [AK078562]	AK078562
	0.0227	2.45	down	cytokine receptor-like factor 3 Gene [Source:MGI (curated);Acc:MGI:1860086] [ENSMUST00000092858]	AK078569

A530064N14Rik	0.0298	1.76	down	Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530064N14 product:unclassifiable, full insert sequence. [AK080119]	AK080119
	0.0029	2.17	down	Novel proteinPutative uncharacterized proteinMCG147019 ;; [Source:UniProtKB/TrEMBL;Acc:Q8BUP2] [ENSMUST00000070502]	AK083112
D130095D21Rik	0.0286	1.59	down	Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130095D21 product:unclassifiable, full insert sequence. [AK084110]	AK084110
D230040J21Rik	0.0419	1.66	down	Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D230040J21 product:unclassifiable, full insert sequence. [AK084413]	AK084413
	0.0067	2.99	down	RIKEN cDNA 4931415C17 gene Gene [Source:MGI Symbol;Acc:MGI:1918216] [ENSMUST00000068194]	AK088235
BC035044	0.0344	1.76	down	Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430008K23 product:unclassifiable, full insert sequence. [AK088258]	AK088258
ATP8	0.0231	1.58	down	mitochondrially encoded ATP synthase 8 Gene [Source:MGI Symbol;Acc:MGI:99926] [ENSMUST00000082407]	AK131577
Gm10638	0.0419	1.79	down	Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330411O07 product:unclassifiable, full insert sequence. [AK133595]	AK133595
5830419E12Rik	0.0442	2.05	down	Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone:5830419E12 product:hypothetical protein, full insert sequence. [AK134048]	AK134048
6820445E23Rik	0.0349	2.82	down	Mus musculus 12 days embryo female mullerian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:6820445E23 product:hypothetical protein, full insert sequence. [AK135532]	AK135532
	0.0012	1.69	down	Putative uncharacterized protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q3UW30] [ENSMUST00000098928]	AK136654

A430071A18Rik	0.0036	1.65	down	Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130034B03 product:unclassifiable, full insert sequence. [AK137878]	AK137878
Prrt1	0.0020	2.88	down	proline-rich transmembrane protein 1 Gene [Source:MGI (curated);Acc:MGI:1932118] [ENSMUST00000015620]	AK137892
2610019N06Rik	0.0202	1.63	down	Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430078C09 product:unclassifiable, full insert sequence. [AK138804]	AK138804
	0.0073	1.57	down	SET domain containing 1B Gene [Source:MGI Symbol;Acc:MGI:2652820] [ENSMUST00000100731]	AK141316
8030453O22Rik	0.0131	1.74	down	Mus musculus 9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030044L12 product:unclassifiable, full insert sequence. [AK141726]	AK141726
	0.0144	2.19	down	Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930041O15 product:unclassifiable, full insert sequence. [AK142897]	AK142897
BC062258	0.0485	1.85	down	Mus musculus lung RCB-0558 LLC cDNA, RIKEN full-length enriched library, clone:G730002O11 product:unclassifiable, full insert sequence. [AK144577]	AK144577
BC023969	0.0255	2.00	down	Mus musculus lung RCB-0558 LLC cDNA, RIKEN full-length enriched library, clone:G730014H17 product:unclassifiable, full insert sequence. [AK144629]	AK144629
	0.0395	1.53	down	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3ULS7] [ENSMUST00000099221]	AK145331
5930430L01Rik	0.0145	2.04	down	Mus musculus B16 F10Y cells cDNA, RIKEN full-length enriched library, clone:G370004A16 product:unclassifiable, full insert sequence. [AK148051]	AK148051
	0.0263	1.54	down	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3UEV0] [ENSMUST00000101619]	AK149319
	0.0058	2.46	down	cathepsin C Gene [Source:MGI (curated);Acc:MGI:109553] [ENSMUST00000098313]	AK152524

	0.0218	1.78	down	Putative uncharacterized proteinMCG147364 ; [Source:UniProtKB/TrEMBL;Acc:Q8CAT9] [ENSMUST00000093178]	AK155400
	0.0103	2.43	down	Ral GTPase activating protein, alpha subunit 2 (catalytic) Gene [Source:MGI (curated);Acc:MGI:3036245] [ENSMUST00000048349]	AK157932
	0.0094	1.62	down	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3TZ85] [ENSMUST00000098619]	AK158028
C81189	0.0074	1.96	down	Mus musculus visual cortex cDNA, RIKEN full-length enriched library, clone:K430332D03 product:hypothetical protein, full insert sequence. [AK158814]	AK158814
	0.0469	1.74	down	importin 11 Gene [Source:MGI Symbol;Acc:MGI:2442377] [ENSMUST00000091253]	AK164311
Gm10419	0.0163	2.21	down	Mus musculus lung RCB-0558 LLC cDNA, RIKEN full-length enriched library, clone:G730014J15 product:hypothetical protein, full insert sequence. [AK165889]	AK165889
	0.0298	1.62	down	MAP kinase-interacting serine/threonine kinase 2 Gene [Source:MGI Symbol;Acc:MGI:894279] [ENSMUST00000105338]	AK177092
AU015584	0.0278	1.58	down	AU015584 Mouse two-cell stage embryo cDNA Mus musculus cDNA clone J0713G11 3'. [AU015584]	AU015584
D7Ertd595e	0.0327	1.54	down	AU023048 Mouse unfertilized egg cDNA Mus musculus cDNA clone J0425A06 3'. [AU023048]	AU023048
	0.0131	1.52	down	kinesin light chain 4 Gene [Source:MGI Symbol;Acc:MGI:1922014] [ENSMUST00000003641]	BC005746
	0.0028	1.50	down	mitochondrially encoded ATP synthase 6 Gene [Source:MGI Symbol;Acc:MGI:99927] [ENSMUST00000105091]	BC012020
	0.0054	1.69	down	RIKEN cDNA 0610007P22 gene Gene [Source:MGI Symbol;Acc:MGI:1915577] [ENSMUST00000015270]	BC038884

	0.0104	1.72	down	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B Gene [Source:MGI (curated);Acc:MGI:1914878] [ENSMUST00000072244]	BC093506
	0.0067	3.37	down	olfactory receptor 537, pseudogene 1 Pseudogene [Source:MGI Symbol;Acc:MGI:3030371] [ENSMUST00000097963]	BC108946
AI451458	0.0234	2.41	down	UI-M-FY0-cdb-a-22-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone IMAGE: 6827135 5', mRNA sequence [CA328248]	CA328248
1700092C02Rik	0.0055	3.15	down	AGENCOURT_14709166 NIH_MGC_190 Mus musculus cDNA clone IMAGE:30505922 5', mRNA sequence [CD772809]	CD772809
1700066J03Rik	0.0248	4.38	down	AGENCOURT_24959256 NIH_MGC_169 Mus musculus cDNA clone IMAGE:30916952 5', mRNA sequence [CN840722]	CN840722
	0.0224	2.42	down	Mouse T-cell receptor active bet- chain V-region (V15-D-J2.2) mRNA. [M11859]	M11859
Lca5l	0.0313	2.14	down	Mus musculus Leber congenital amaurosis 5-like (Lca5l), mRNA [NM_001001492]	NM_001001492
Lca5l	0.0088	1.74	down	Mus musculus Leber congenital amaurosis 5-like (Lca5l), mRNA [NM_001001492]	NM_001001492
Sohlh1	0.0451	1.66	down	Mus musculus spermatogenesis and oogenesis specific basic helix-loop-helix 1 (Sohlh1), mRNA [NM_001001714]	NM_001001714
Megf10	0.0125	4.87	down	Mus musculus multiple EGF-like-domains 10 (Megf10), mRNA [NM_001001979]	NM_001001979
Rtp1	0.0306	3.04	down	Mus musculus receptor transporter protein 1 (Rtp1), mRNA [NM_001004151]	NM_001004151
Slc25a42	0.0322	1.54	down	Mus musculus solute carrier family 25, member 42 (Slc25a42), mRNA [NM_001007570]	NM_001007570
Tceanc	0.0160	2.47	down	Mus musculus transcription elongation factor A (SII) N- terminal and central domain containing (Tceanc), mRNA [NM_001007577]	NM_001007577

Grm4	0.0052	1.67	down	Mus musculus glutamate receptor, metabotropic 4 (Grm4), mRNA [NM_001013385]	NM_001013385
Ttll4	0.0329	1.66	down	Mus musculus tubulin tyrosine ligase-like family, member 4 (Ttll4), mRNA [NM_001014974]	NM_001014974
Ddi2	0.0046	1.83	down	Mus musculus DNA-damage inducible protein 2 (Ddi2), mRNA [NM_001017966]	NM_001017966
Lrp3	0.0367	2.28	down	Mus musculus low density lipoprotein receptor-related protein 3 (Lrp3), mRNA [NM_001024707]	NM_001024707
Brd2	0.0198	1.56	down	Mus musculus bromodomain containing 2 (Brd2), transcript variant 2, mRNA [NM_001025387]	NM_001025387
Osbp	0.0283	1.80	down	Mus musculus oxysterol binding protein (Osbp), mRNA [NM_001033174]	NM_001033174
Mll2	0.0319	1.68	down	Mus musculus myeloid/lymphoid or mixed-lineage leukemia 2 (Mll2), mRNA [NM_001033276]	NM_001033276
Gm129	0.0395	2.76	down	Mus musculus predicted gene 129 (Gm129), mRNA [NM_001033302]	NM_001033302
Ffar3	0.0229	2.76	down	Mus musculus free fatty acid receptor 3 (Ffar3), mRNA [NM_001033316]	NM_001033316
Usp36	0.0383	1.63	down	Mus musculus ubiquitin specific peptidase 36 (Usp36), mRNA [NM_001033528]	NM_001033528
Pnpla1	0.0357	1.60	down	Mus musculus patatin-like phospholipase domain containing 1 (Pnpla1), mRNA [NM_001034885]	NM_001034885
Gm4925	0.0168	2.51	down	Mus musculus predicted gene 4925 (Gm4925), mRNA [NM_001037166]	NM_001037166
Tomm40l	0.0396	2.63	down	Mus musculus translocase of outer mitochondrial membrane 40 homolog-like (yeast) (Tomm40l), nuclear gene encoding mitochondrial protein, mRNA [NM_001037170]	NM_001037170
Fam40b	0.0411	1.57	down	Mus musculus family with sequence similarity 40, member B (Fam40b), transcript variant 2, mRNA [NM_001037740]	NM_001037740
Pde4dip	0.0031	1.62	down	Mus musculus phosphodiesterase 4D interacting protein (myomegalin) (Pde4dip), transcript variant 1, mRNA [NM_001039376]	NM_001039376

Pde4dip	0.0019	1.66	down	Mus musculus phosphodiesterase 4D interacting protein (myomegalin) (Pde4dip), transcript variant 1, mRNA [NM_001039376]	NM_001039376
Angptl7	0.0464	1.86	down	Mus musculus angiopoietin-like 7 (Angptl7), mRNA [NM_001039554]	NM_001039554
Zfp606	0.0283	1.71	down	Mus musculus zinc finger protein 606 (Zfp606), transcript variant 2, mRNA [NM_001039951]	NM_001039951
Spata22	0.0148	1.88	down	Mus musculus spermatogenesis associated 22 (Spata22), mRNA [NM_001045531]	NM_001045531
Pde11a	0.0151	3.08	down	Mus musculus phosphodiesterase 11A (Pde11a), mRNA [NM_001081033]	NM_001081033
1700081L11Rik	0.0435	1.59	down	Mus musculus RIKEN cDNA 1700081L11 gene (1700081L11Rik), mRNA [NM_001081045]	NM_001081045
Whsc1	0.0113	1.64	down	Mus musculus Wolf-Hirschhorn syndrome candidate 1 (human) (Whsc1), transcript variant 1, mRNA [NM_001081102]	NM_001081102
Ogdhl	0.0225	2.51	down	Mus musculus oxoglutarate dehydrogenase-like (Ogdhl), nuclear gene encoding mitochondrial protein, mRNA [NM_001081130]	NM_001081130
Mamdc4	0.0333	1.70	down	Mus musculus MAM domain containing 4 (Mamdc4), mRNA [NM_001081199]	NM_001081199
Mamdc4	0.0480	1.88	down	Mus musculus MAM domain containing 4 (Mamdc4), mRNA [NM_001081199]	NM_001081199
C2cd4b	0.0418	4.46	down	Mus musculus C2 calcium-dependent domain containing 4B (C2cd4b), mRNA [NM_001081314]	NM_001081314
Wdr67	0.0013	1.86	down	Mus musculus WD repeat domain 67 (Wdr67), transcript variant 1, mRNA [NM_001081396]	NM_001081396
Phf20l1	0.0131	1.78	down	Mus musculus PHD finger protein 20-like 1 (Phf20l1), mRNA [NM_001081409]	NM_001081409
Chd7	0.0282	1.81	down	Mus musculus chromodomain helicase DNA binding protein 7 (Chd7), mRNA [NM_001081417]	NM_001081417
Stfa2	0.0285	2.21	down	Mus musculus stefin A2 (Stfa2), mRNA [NM_001082545]	NM_001082545

Pappa2	0.0099	2.21	down	Mus musculus pappalysin 2 (Pappa2), mRNA [NM_001085376]	NM_001085376
Zfp467	0.0309	1.56	down	Mus musculus zinc finger protein 467 (Zfp467), transcript variant 4, mRNA [NM_001085417]	NM_001085417
Smcr8	0.0339	1.71	down	Mus musculus Smith-Magenis syndrome chromosome region, candidate 8 homolog (human) (Smcr8), transcript variant 1, mRNA [NM_001085440]	NM_001085440
Gm13271	0.0148	2.02	down	Mus musculus predicted gene 13271 (Gm13271), mRNA [NM_001085528]	NM_001085528
Gm13271	0.0306	1.90	down	Mus musculus predicted gene 13271 (Gm13271), mRNA [NM_001085528]	NM_001085528
Sh2d5	0.0483	1.57	down	Mus musculus SH2 domain containing 5 (Sh2d5), mRNA [NM_001099631]	NM_001099631
BC032203	0.0340	1.60	down	Mus musculus cDNA sequence BC032203 (BC032203), mRNA [NM_001100452]	NM_001100452
Vmn2r114	0.0121	1.62	down	Mus musculus vomeronasal 2, receptor 114 (Vmn2r114), mRNA [NM_001102584]	NM_001102584
Zfp703	0.0006	1.57	down	Mus musculus zinc finger protein 703 (Zfp703), transcript variant 2, mRNA [NM_001110508]	NM_001110508
Capn12	0.0220	1.72	down	Mus musculus calpain 12 (Capn12), mRNA [NM_001110807]	NM_001110807
Krtap11-1	0.0357	1.65	down	Mus musculus keratin associated protein 11-1 (Krtap11-1), mRNA [NM_001113406]	NM_001113406
Zmym4	0.0235	1.96	down	Mus musculus zinc finger, MYM-type 4 (Zmym4), mRNA [NM_001114399]	NM_001114399
Gm101	0.0292	2.53	down	Mus musculus predicted gene 101 (Gm101), mRNA [NM_001115074]	NM_001115074
Zbtb44	0.0055	1.78	down	Mus musculus zinc finger and BTB domain containing 44 (Zbtb44), transcript variant a, mRNA [NM_001115130]	NM_001115130
Nfia	0.0041	1.94	down	Mus musculus nuclear factor I/A (Nfia), transcript variant 3, mRNA [NM_001122953]	NM_001122953
Gm5736	0.0395	1.73	down	Mus musculus predicted gene 5736 (Gm5736), mRNA [NM_001127686]	NM_001127686

Hpca	0.0299	9.21	down	Mus musculus hippocalcin (Hpca), mRNA [NM_001130419]	NM_001130419
Il9r	0.0019	2.07	down	Mus musculus interleukin 9 receptor (Il9r), transcript variant 1, mRNA [NM_001134458]	NM_001134458
CK137956	0.0257	2.17	down	Mus musculus cDNA sequence CK137956 (CK137956), mRNA [NM_001134733]	NM_001134733
Tom1	0.0146	1.88	down	Mus musculus target of myb1 homolog (chicken) (Tom1), transcript variant 2, mRNA [NM_001136259]	NM_001136259
Gm9992	0.0314	2.43	down	Mus musculus predicted gene 9992 (Gm9992), mRNA [NM_001142539]	NM_001142539
Gm9992	0.0322	2.39	down	Mus musculus predicted gene 9992 (Gm9992), mRNA [NM_001142539]	NM_001142539
Grm5	0.0344	1.55	down	Mus musculus glutamate receptor, metabotropic 5 (Grm5), transcript variant b, mRNA [NM_001143834]	NM_001143834
2810459M11Rik	0.0009	1.99	down	Mus musculus RIKEN cDNA 2810459M11 gene (2810459M11Rik), transcript variant 1, mRNA [NM_001144992]	NM_001144992
Ncrna00085	0.0124	1.76	down	Mus musculus non-protein coding RNA 85 (Ncrna00085), mRNA [NM_001162909]	NM_001162909
Safb	0.0494	1.59	down	Mus musculus scaffold attachment factor B (Safb), mRNA [NM_001163300]	NM_001163300
C130039O16Rik	0.0370	1.52	down	Mus musculus RIKEN cDNA C130039O16 gene (C130039O16Rik), transcript variant 1, mRNA [NM_001163502]	NM_001163502
Rffl	0.0445	2.17	down	Mus musculus ring finger and FYVE like domain containing protein (Rffl), transcript variant 3, mRNA [NM_001164569]	NM_001164569
Erv3	0.0017	2.02	down	Mus musculus endogenous retroviral sequence 3 (Erv3), mRNA [NM_001166206]	NM_001166206
Mgll	0.0072	1.89	down	Mus musculus monoglyceride lipase (Mgll), transcript variant 4, mRNA [NM_001166250]	NM_001166250
Rad18	0.0398	1.64	down	Mus musculus RAD18 homolog (S. cerevisiae) (Rad18), transcript variant 1, mRNA [NM_001167730]	NM_001167730

Wipf3	0.0009	1.63	down	Mus musculus WAS/WASL interacting protein family, member 3 (Wipf3), transcript variant 1, mRNA [NM_001167860]	NM_001167860
Zfp568	0.0049	1.57	down	Mus musculus zinc finger protein 568 (Zfp568), transcript variant 1, mRNA [NM_001167872]	NM_001167872
Skint5	0.0084	1.63	down	Mus musculus selection and upkeep of intraepithelial T cells 5 (Skint5), transcript variant 2, mRNA [NM_001167878]	NM_001167878
Asb14	0.0363	7.45	down	Mus musculus ankyrin repeat and SOCS box-containing 14 (Asb14), transcript variant 1, mRNA [NM_001170748]	NM_001170748
Trim43b	0.0185	2.06	down	Mus musculus tripartite motif-containing 43B (Trim43b), mRNA [NM_001170884]	NM_001170884
3110009E18Rik	0.0172	3.08	down	Mus musculus RIKEN cDNA 3110009E18 gene (3110009E18Rik), transcript variant 2, mRNA [NM_001172074]	NM_001172074
Cdc14a	0.0305	2.53	down	Mus musculus CDC14 cell division cycle 14 homolog A (S. cerevisiae) (Cdc14a), transcript variant 2, mRNA [NM_001173553]	NM_001173553
Sep-06	0.0394	2.30	down	Mus musculus septin 6 (Sept6), transcript variant 1, mRNA [NM_001177324]	NM_001177324
Snap23	0.0388	1.56	down	Mus musculus synaptosomal-associated protein 23 (Snap23), transcript variant 1, mRNA [NM_001177792]	NM_001177792
Bcl6b	0.0194	2.45	down	Mus musculus B-cell CLL/lymphoma 6, member B (Bcl6b), mRNA [NM_007528]	NM_007528
Hrk	0.0240	1.95	down	Mus musculus harakiri, BCL2 interacting protein (contains only BH3 domain) (Hrk), mRNA [NM_007545]	NM_007545
Cdh15	0.0474	1.55	down	Mus musculus cadherin 15 (Cdh15), mRNA [NM_007662]	NM_007662
Cdkn2c	0.0441	2.46	down	Mus musculus cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4) (Cdkn2c), mRNA [NM_007671]	NM_007671
Socs2	0.0023	1.52	down	Mus musculus suppressor of cytokine signaling 2 (Socs2), transcript variant 1, mRNA [NM_007706]	NM_007706
Socs3	0.0251	1.83	down	Mus musculus suppressor of cytokine signaling 3 (Socs3), mRNA [NM_007707]	NM_007707

Ccr10	0.0044	2.05	down	Mus musculus chemokine (C-C motif) receptor 10 (Ccr10), mRNA [NM_007721]	NM_007721
Col4a3	0.0189	1.84	down	Mus musculus collagen, type IV, alpha 3 (Col4a3), mRNA [NM_007734]	NM_007734
Epyc	0.0249	1.95	down	Mus musculus epiphykan (Epyc), mRNA [NM_007884]	NM_007884
Efnb3	0.0456	2.27	down	Mus musculus ephrin B3 (Efnb3), mRNA [NM_007911]	NM_007911
Fgd1	0.0071	1.58	down	Mus musculus FYVE, RhoGEF and PH domain containing 1 (Fgd1), mRNA [NM_008001]	NM_008001
Has1	0.0013	2.05	down	Mus musculus hyaluronan synthase1 (Has1), mRNA [NM_008215]	NM_008215
Hells	0.0082	1.84	down	Mus musculus helicase, lymphoid specific (Hells), mRNA [NM_008234]	NM_008234
Lrig1	0.0130	1.76	down	Mus musculus leucine-rich repeats and immunoglobulin-like domains 1 (Lrig1), mRNA [NM_008377]	NM_008377
Ppp1r15a	0.0107	1.81	down	Mus musculus protein phosphatase 1, regulatory (inhibitor) subunit 15A (Ppp1r15a), mRNA [NM_008654]	NM_008654
Nfyc	0.0263	1.64	down	Mus musculus nuclear transcription factor-Y gamma (Nfyc), transcript variant 1, mRNA [NM_008692]	NM_008692
Pou1f1	0.0214	8.06	down	Mus musculus POU domain, class 1, transcription factor 1 (Pou1f1), mRNA [NM_008849]	NM_008849
Ptma	0.0173	1.59	down	Mus musculus prothymosin alpha (Ptma), mRNA [NM_008972]	NM_008972
Pex5	0.0330	1.51	down	Mus musculus peroxisomal biogenesis factor 5 (Pex5), transcript variant 1, mRNA [NM_008995]	NM_008995
Rab4a	0.0127	1.62	down	Mus musculus RAB4A, member RAS oncogene family (Rab4a), mRNA [NM_009003]	NM_009003
Rbpjl	0.0450	2.31	down	Mus musculus recombination signal binding protein for immunoglobulin kappa J region-like (Rbpjl), mRNA [NM_009036]	NM_009036
Rfx2	0.0371	1.82	down	Mus musculus regulatory factor X, 2 (influences HLA class II expression) (Rfx2), transcript variant 2, mRNA [NM_009056]	NM_009056

Rgs2	0.0004	3.27	down	Mus musculus regulator of G-protein signaling 2 (Rgs2), mRNA [NM_009061]	NM_009061
Rgs2	0.0014	3.55	down	Mus musculus regulator of G-protein signaling 2 (Rgs2), mRNA [NM_009061]	NM_009061
St8sia2	0.0253	2.52	down	Mus musculus ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2 (St8sia2), mRNA [NM_009181]	NM_009181
Thrb	0.0124	1.52	down	Mus musculus thyroid hormone receptor beta (Thrb), transcript variant 2, mRNA [NM_009380]	NM_009380
Tst	0.0486	5.46	down	Mus musculus thiosulfate sulfurtransferase, mitochondrial (Tst), nuclear gene encoding mitochondrial protein, mRNA [NM_009437]	NM_009437
Pcgf2	0.0172	1.98	down	Mus musculus polycomb group ring finger 2 (Pcgf2), transcript variant 1, mRNA [NM_009545]	NM_009545
Adora3	0.0377	1.67	down	Mus musculus adenosine A3 receptor (Adora3), transcript variant 1, mRNA [NM_009631]	NM_009631
Angpt1	0.0329	2.89	down	Mus musculus angiopoietin 1 (Angpt1), mRNA [NM_009640]	NM_009640
Atf4	0.0328	1.65	down	Mus musculus activating transcription factor 4 (Atf4), mRNA [NM_009716]	NM_009716
Bcat2	0.0160	2.33	down	Mus musculus branched chain aminotransferase 2, mitochondrial (Bcat2), nuclear gene encoding mitochondrial protein, mRNA [NM_009737]	NM_009737
Socs1	0.0333	1.62	down	Mus musculus suppressor of cytokine signaling 1 (Socs1), mRNA [NM_009896]	NM_009896
Camp	0.0040	3.05	down	Mus musculus cathelicidin antimicrobial peptide (Camp), mRNA [NM_009921]	NM_009921
Camp	0.0343	3.61	down	Mus musculus cathelicidin antimicrobial peptide (Camp), mRNA [NM_009921]	NM_009921
Col11a2	0.0067	1.59	down	Mus musculus collagen, type XI, alpha 2 (Col11a2), mRNA [NM_009926]	NM_009926
Cpne6	0.0094	1.65	down	Mus musculus copine VI (Cpne6), transcript variant 2, mRNA [NM_009947]	NM_009947

Dlk1	0.0275	2.23	down	Mus musculus delta-like 1 homolog (Drosophila) (Dlk1), transcript variant 1, mRNA [NM_010052]	NM_010052
Dmc1	0.0060	2.30	down	Mus musculus DMC1 dosage suppressor of mck1 homolog, meiosis-specific homologous recombination (yeast) (Dmc1), mRNA [NM_010059]	NM_010059
Ebf2	0.0235	1.82	down	Mus musculus early B-cell factor 2 (Ebf2), mRNA [NM_010095]	NM_010095
Nr2f1	0.0206	1.61	down	Mus musculus nuclear receptor subfamily 2, group F, member 1 (Nr2f1), mRNA [NM_010151]	NM_010151
Gem	0.0465	1.55	down	Mus musculus GTP binding protein (gene overexpressed in skeletal muscle) (Gem), mRNA [NM_010276]	NM_010276
Nr4a1	0.0230	4.01	down	Mus musculus nuclear receptor subfamily 4, group A, member 1 (Nr4a1), mRNA [NM_010444]	NM_010444
Cyr61	0.0217	3.10	down	Mus musculus cysteine rich protein 61 (Cyr61), mRNA [NM_010516]	NM_010516
Irs1	0.0161	1.81	down	Mus musculus insulin receptor substrate 1 (Irs1), mRNA [NM_010570]	NM_010570
Itsn1	0.0349	1.65	down	Mus musculus intersectin 1 (SH3 domain protein 1A) (Itsn1), transcript variant 1, mRNA [NM_010587]	NM_010587
Jun	0.0336	2.76	down	Mus musculus Jun oncogene (Jun), mRNA [NM_010591]	NM_010591
Myh4	0.0220	8.93	down	Mus musculus myosin, heavy polypeptide 4, skeletal muscle (Myh4), mRNA [NM_010855]	NM_010855
Nos2	0.0419	1.69	down	Mus musculus nitric oxide synthase 2, inducible (Nos2), mRNA [NM_010927]	NM_010927
Oc90	0.0069	1.90	down	Mus musculus otoconin 90 (Oc90), mRNA [NM_010953]	NM_010953
Pla2g2d	0.0353	2.06	down	Mus musculus phospholipase A2, group IID (Pla2g2d), mRNA [NM_011109]	NM_011109
Pla2g2d	0.0296	1.96	down	Mus musculus phospholipase A2, group IID (Pla2g2d), mRNA [NM_011109]	NM_011109
Prodh	0.0230	2.07	down	Mus musculus proline dehydrogenase (Prodh), nuclear gene encoding mitochondrial protein, mRNA [NM_011172]	NM_011172
Purb	0.0253	1.51	down	Mus musculus purine rich element binding protein B (Purb), mRNA [NM_011221]	NM_011221

Rbmy1a1	0.0031	3.13	down	Mus musculus RNA binding motif protein, Y chromosome, family 1, member A1 (Rbmy1a1), transcript variant 1, mRNA [NM_011253]	NM_011253
Rfx3	0.0212	2.02	down	Mus musculus regulatory factor X, 3 (influences HLA class II expression) (Rfx3), transcript variant 1, mRNA [NM_011265]	NM_011265
Snap25	0.0211	1.71	down	Mus musculus synaptosomal-associated protein 25 (Snap25), mRNA [NM_011428]	NM_011428
Tbx6	0.0132	1.58	down	Mus musculus T-box 6 (Tbx6), mRNA [NM_011538]	NM_011538
Ldb3	0.0192	1.60	down	Mus musculus LIM domain binding 3 (Ldb3), transcript variant 1, mRNA [NM_011918]	NM_011918
Psg18	0.0327	1.67	down	Mus musculus pregnancy specific glycoprotein 18 (Psg18), transcript variant 1, mRNA [NM_011963]	NM_011963
Homer1	0.0153	1.61	down	Mus musculus homer homolog 1 (Drosophila) (Homer1), transcript variant S, mRNA [NM_011982]	NM_011982
Madcam1	0.0001	2.36	down	Mus musculus mucosal vascular addressin cell adhesion molecule 1 (Madcam1), mRNA [NM_013591]	NM_013591
Mc5r	0.0216	1.50	down	Mus musculus melanocortin 5 receptor (Mc5r), mRNA [NM_013596]	NM_013596
Mmp9	0.0357	2.29	down	Mus musculus matrix metalloproteinase 9 (Mmp9), mRNA [NM_013599]	NM_013599
Plekhb1	0.0224	3.44	down	Mus musculus pleckstrin homology domain containing, family B (evectins) member 1 (Plekhb1), transcript variant 1, mRNA [NM_013746]	NM_013746
Plekhb1	0.0198	3.05	down	Mus musculus pleckstrin homology domain containing, family B (evectins) member 1 (Plekhb1), transcript variant 1, mRNA [NM_013746]	NM_013746
Clnk	0.0417	1.66	down	Mus musculus cytokine-dependent hematopoietic cell linker (Clnk), mRNA [NM_013748]	NM_013748
Tcl1b4	0.0031	1.93	down	Mus musculus T-cell leukemia/lymphoma 1B, 4 (Tcl1b4), mRNA [NM_013774]	NM_013774

Mfi2	0.0115	2.49	down	Mus musculus antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5 (Mfi2), mRNA [NM_013900]	NM_013900
Axin2	0.0142	3.13	down	Mus musculus axin2 (Axin2), mRNA [NM_015732]	NM_015732
Srpx	0.0343	1.54	down	Mus musculus sushi-repeat-containing protein (Srpx), mRNA [NM_016911]	NM_016911
Zfp316	0.0258	1.51	down	Mus musculus zinc finger protein 316 (Zfp316), mRNA [NM_017467]	NM_017467
Agpat6	0.0098	1.72	down	Mus musculus 1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta) (Agpat6), mRNA [NM_018743]	NM_018743
Pde3a	0.0459	2.88	down	Mus musculus phosphodiesterase 3A, cGMP inhibited (Pde3a), mRNA [NM_018779]	NM_018779
Prpf40b	0.0285	1.61	down	Mus musculus PRP40 pre-mRNA processing factor 40 homolog B (yeast) (Prpf40b), mRNA [NM_018786]	NM_018786
Arc	0.0080	2.91	down	Mus musculus activity regulated cytoskeletal-associated protein (Arc), mRNA [NM_018790]	NM_018790
Dnahc10	0.0470	1.89	down	Mus musculus dynein, axonemal, heavy chain 10 (Dnahc10), mRNA [NM_019536]	NM_019536
Elf4	0.0002	1.87	down	Mus musculus E74-like factor 4 (ets domain transcription factor) (Elf4), mRNA [NM_019680]	NM_019680
Nat6	0.0138	1.63	down	Mus musculus N-acetyltransferase 6 (Nat6), mRNA [NM_019750]	NM_019750
Tgm1	0.0412	2.34	down	Mus musculus transglutaminase 1, K polypeptide (Tgm1), transcript variant 2, mRNA [NM_019984]	NM_019984
Magea1	0.0003	2.69	down	Mus musculus melanoma antigen, family A, 1 (Magea1), mRNA [NM_020015]	NM_020015
Nrxn1	0.0481	1.99	down	Mus musculus neurexin I (Nrxn1), transcript variant 1, mRNA [NM_020252]	NM_020252
Ltb4r2	0.0390	1.62	down	Mus musculus leukotriene B4 receptor 2 (Ltb4r2), mRNA [NM_020490]	NM_020490
Tob2	0.0484	2.11	down	Mus musculus transducer of ERBB2, 2 (Tob2), mRNA [NM_020507]	NM_020507

Cmpk2	0.0186	1.51	down	Mus musculus cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial (Cmpk2), nuclear gene encoding mitochondrial protein, mRNA [NM_020557]	NM_020557
Terf2ip	0.0301	1.76	down	Mus musculus telomeric repeat binding factor 2, interacting protein (Terf2ip), mRNA [NM_020584]	NM_020584
Srrm3	0.0151	1.62	down	Mus musculus serine/arginine repetitive matrix 3 (Srrm3), mRNA [NM_021403]	NM_021403
Doc2g	0.0247	1.70	down	Mus musculus double C2, gamma (Doc2g), mRNA [NM_021791]	NM_021791
Ube4b	0.0416	1.62	down	Mus musculus ubiquitination factor E4B, UFD2 homolog (S. cerevisiae) (Ube4b), mRNA [NM_022022]	NM_022022
Tcte2	0.0083	1.56	down	Mus musculus t-complex-associated testis expressed 2 (Tcte2), mRNA [NM_022311]	NM_022311
Fgf23	0.0301	1.73	down	Mus musculus fibroblast growth factor 23 (Fgf23), mRNA [NM_022657]	NM_022657
Ms4a10	0.0173	1.75	down	Mus musculus membrane-spanning 4-domains, subfamily A, member 10 (Ms4a10), mRNA [NM_023529]	NM_023529
Tbc1d20	0.0151	1.56	down	Mus musculus TBC1 domain family, member 20 (Tbc1d20), mRNA [NM_024196]	NM_024196
Bhlhe41	0.0057	3.37	down	Mus musculus basic helix-loop-helix family, member e41 (Bhlhe41), mRNA [NM_024469]	NM_024469
Ublcp1	0.0019	2.21	down	Mus musculus ubiquitin-like domain containing CTD phosphatase 1 (Ublcp1), mRNA [NM_024475]	NM_024475
Col27a1	0.0354	2.00	down	Mus musculus collagen, type XXVII, alpha 1 (Col27a1), mRNA [NM_025685]	NM_025685
Rbm4b	0.0271	1.74	down	Mus musculus RNA binding motif protein 4B (Rbm4b), mRNA [NM_025717]	NM_025717
Bcl2l14	0.0247	1.84	down	Mus musculus BCL2-like 14 (apoptosis facilitator) (Bcl2l14), mRNA [NM_025778]	NM_025778
1200014J11Rik	0.0426	1.70	down	Mus musculus RIKEN cDNA 1200014J11 gene (1200014J11Rik), mRNA [NM_025818]	NM_025818
2410004A20Rik	0.0162	2.05	down	Mus musculus RIKEN cDNA 2410004A20 gene (2410004A20Rik), mRNA [NM_025890]	NM_025890

Mettl6	0.0171	1.74	down	Mus musculus methyltransferase like 6 (Mettl6), mRNA [NM_025907]	NM_025907
Pgc	0.0481	1.78	down	Mus musculus progastricsin (pepsinogen C) (Pgc), mRNA [NM_025973]	NM_025973
Dhdpsl	0.0487	1.96	down	Mus musculus dihydrodipicolinate synthase-like, mitochondria (Dhdpsl), nuclear gene encoding mitochondrial protein, mRNA [NM_026152]	NM_026152
4921517D21Rik	0.0170	2.69	down	Mus musculus RIKEN cDNA 4921517D21 gene (4921517D21Rik), mRNA [NM_026338]	NM_026338
2610027L16Rik	0.0010	1.58	down	Mus musculus RIKEN cDNA 2610027L16 gene (2610027L16Rik), mRNA [NM_026403]	NM_026403
Nmb	0.0328	1.53	down	Mus musculus neuromedin B (Nmb), mRNA [NM_026523]	NM_026523
Chd1l	0.0129	1.53	down	Mus musculus chromodomain helicase DNA binding protein 1-like (Chd1l), mRNA [NM_026539]	NM_026539
3110057O12Rik	0.0062	1.62	down	Mus musculus RIKEN cDNA 3110057O12 gene (3110057O12Rik), mRNA [NM_026622]	NM_026622
Tspan11	0.0010	2.28	down	Mus musculus tetraspanin 11 (Tspan11), mRNA [NM_026743]	NM_026743
Tmem53	0.0169	1.69	down	Mus musculus transmembrane protein 53 (Tmem53), mRNA [NM_026837]	NM_026837
1190005F20Rik	0.0451	1.51	down	Mus musculus RIKEN cDNA 1190005F20 gene (1190005F20Rik), mRNA [NM_026876]	NM_026876
1500011H22Rik	0.0093	1.55	down	Mus musculus RIKEN cDNA 1500011H22 gene (1500011H22Rik), mRNA [NM_026883]	NM_026883
1810014F10Rik	0.0396	1.90	down	Mus musculus RIKEN cDNA 1810014F10 gene (1810014F10Rik), mRNA [NM_026928]	NM_026928
1810014F10Rik	0.0274	1.87	down	Mus musculus RIKEN cDNA 1810014F10 gene (1810014F10Rik), mRNA [NM_026928]	NM_026928
Gon4l	0.0498	1.51	down	Mus musculus gon-4-like (C.elegans) (Gon4l), mRNA [NM_027389]	NM_027389
Ddo	0.0460	1.58	down	Mus musculus D-aspartate oxidase (Ddo), mRNA [NM_027442]	NM_027442

Ddo	0.0417	2.15	down	Mus musculus D-aspartate oxidase (Ddo), mRNA [NM_027442]	NM_027442
4931408A02Rik	0.0481	1.64	down	Mus musculus RIKEN cDNA 4931408A02 gene (4931408A02Rik), mRNA [NM_027627]	NM_027627
Hexim2	0.0350	1.69	down	Mus musculus hexamethylene bis-acetamide inducible 2 (Hexim2), transcript variant 1, mRNA [NM_027658]	NM_027658
Kctd6	0.0432	1.84	down	Mus musculus potassium channel tetramerisation domain containing 6 (Kctd6), mRNA [NM_027782]	NM_027782
Zbtb43	0.0029	1.58	down	Mus musculus zinc finger and BTB domain containing 43 (Zbtb43), transcript variant 1, mRNA [NM_027947]	NM_027947
1600014K23Rik	0.0012	1.65	down	Mus musculus RIKEN cDNA 1600014K23 gene (1600014K23Rik), mRNA [NM_028046]	NM_028046
Ddhd2	0.0141	1.85	down	Mus musculus DDHD domain containing 2 (Ddhd2), mRNA [NM_028102]	NM_028102
Dennd2d	0.0163	2.92	down	Mus musculus DENN/MADD domain containing 2D (Dennd2d), transcript variant 1, mRNA [NM_028110]	NM_028110
Ptar1	0.0114	1.55	down	Mus musculus protein prenyltransferase alpha subunit repeat containing 1 (Ptar1), mRNA [NM_028208]	NM_028208
Zcchc12	0.0299	5.59	down	Mus musculus zinc finger, CCHC domain containing 12 (Zcchc12), mRNA [NM_028325]	NM_028325
2900006K08Rik	0.0020	1.75	down	Mus musculus RIKEN cDNA 2900006K08 gene (2900006K08Rik), mRNA [NM_028377]	NM_028377
Rwdd3	0.0310	2.71	down	Mus musculus RWD domain containing 3 (Rwdd3), transcript variant 2, mRNA [NM_028456]	NM_028456
1600027N09Rik	0.0474	1.63	down	Mus musculus RIKEN cDNA 1600027N09 gene (1600027N09Rik), mRNA [NM_028479]	NM_028479
Nol9	0.0010	1.59	down	Mus musculus nucleolar protein 9 (Nol9), transcript variant 2, mRNA [NM_028727]	NM_028727
Palm3	0.0099	1.71	down	Mus musculus paralemmi 3 (Palm3), mRNA [NM_028877]	NM_028877
Zfp558-ps	0.0282	1.70	down	Mus musculus zinc finger protein 558, pseudogene (Zfp558-ps), mRNA [NM_028935]	NM_028935
Tmem33	0.0327	1.66	down	Mus musculus transmembrane protein 33 (Tmem33), transcript variant 1, mRNA [NM_028975]	NM_028975

Mrpl47	0.0277	1.51	down	Mus musculus mitochondrial ribosomal protein L47 (Mrpl47), nuclear gene encoding mitochondrial protein, mRNA [NM_029017]	NM_029017
Tmem114	0.0017	2.36	down	Mus musculus transmembrane protein 114 (Tmem114), mRNA [NM_029070]	NM_029070
Ccdc30	0.0210	3.30	down	Mus musculus coiled-coil domain containing 30 (Ccdc30), mRNA [NM_029286]	NM_029286
Tmem49	0.0289	1.51	down	Mus musculus transmembrane protein 49 (Tmem49), mRNA [NM_029478]	NM_029478
Atxn3	0.0476	1.66	down	Mus musculus ataxin 3 (Atxn3), transcript variant 1, mRNA [NM_029705]	NM_029705
Unc5b	0.0235	1.54	down	Mus musculus unc-5 homolog B (C. elegans) (Unc5b), mRNA [NM_029770]	NM_029770
Zfp142	0.0452	1.63	down	Mus musculus zinc finger protein 142 (Zfp142), mRNA [NM_029888]	NM_029888
Grifin	0.0250	2.25	down	Mus musculus galectin-related inter-fiber protein (Grifin), mRNA [NM_030022]	NM_030022
Kctd18	0.0442	1.95	down	Mus musculus potassium channel tetramerisation domain containing 18 (Kctd18), transcript variant 3, mRNA [NM_030211]	NM_030211
Agbl4	0.0346	3.00	down	Mus musculus ATP/GTP binding protein-like 4 (Agbl4), transcript variant 1, mRNA [NM_030231]	NM_030231
Nr5a2	0.0087	1.97	down	Mus musculus nuclear receptor subfamily 5, group A, member 2 (Nr5a2), transcript variant 1, mRNA [NM_030676]	NM_030676
Zfhx4	0.0082	2.39	down	Mus musculus zinc finger homeodomain 4 (Zfhx4), mRNA [NM_030708]	NM_030708
Pum1	0.0136	1.58	down	Mus musculus pumilio 1 (Drosophila) (Pum1), transcript variant 1, mRNA [NM_030722]	NM_030722
Sorcs2	0.0046	1.89	down	Mus musculus sortilin-related VPS10 domain containing receptor 2 (Sorcs2), mRNA [NM_030889]	NM_030889
Npnt	0.0441	1.86	down	Mus musculus nephronectin (Npnt), transcript variant 1, mRNA [NM_033525]	NM_033525

Hist2h4	0.0264	1.76	down	Mus musculus histone cluster 2, H4 (Hist2h4), mRNA [NM_033596]	NM_033596
Pard6g	0.0248	1.58	down	Mus musculus par-6 partitioning defective 6 homolog gamma (C. elegans) (Pard6g), mRNA [NM_053117]	NM_053117
Pcdhb10	0.0042	1.76	down	Mus musculus protocadherin beta 10 (Pcdhb10), mRNA [NM_053135]	NM_053135
Mepe	0.0009	1.63	down	Mus musculus matrix extracellular phosphoglycoprotein with ASARM motif (bone) (Mepe), mRNA [NM_053172]	NM_053172
Crip3	0.0457	1.72	down	Mus musculus cysteine-rich protein 3 (Crip3), transcript variant TLP-B, mRNA [NM_053250]	NM_053250
Tshz2	0.0046	1.50	down	Mus musculus teashirt zinc finger family member 2 (Tshz2), mRNA [NM_080455]	NM_080455
Papln	0.0378	1.64	down	Mus musculus papilin, proteoglycan-like sulfated glycoprotein (Papln), mRNA [NM_130887]	NM_130887
Papln	0.0244	1.82	down	Mus musculus papilin, proteoglycan-like sulfated glycoprotein (Papln), mRNA [NM_130887]	NM_130887
Ppargc1b	0.0202	5.88	down	Mus musculus peroxisome proliferative activated receptor, gamma, coactivator 1 beta (Ppargc1b), mRNA [NM_133249]	NM_133249
Erdr1	0.0130	1.93	down	Mus musculus erythroid differentiation regulator 1 (Erdr1), mRNA [NM_133362]	NM_133362
Ier3	0.0314	2.25	down	Mus musculus immediate early response 3 (Ier3), mRNA [NM_133662]	NM_133662
Cxxc5	0.0305	1.82	down	Mus musculus CXXC finger 5 (Cxxc5), mRNA [NM_133687]	NM_133687
Errfi1	0.0374	1.53	down	Mus musculus ERBB receptor feedback inhibitor 1 (Errfi1), mRNA [NM_133753]	NM_133753
Fbxo31	0.0142	1.58	down	Mus musculus F-box protein 31 (Fbxo31), mRNA [NM_133765]	NM_133765
Adck4	0.0341	1.62	down	Mus musculus aarF domain containing kinase 4 (Adck4), mRNA [NM_133770]	NM_133770
Fam131a	0.0192	1.66	down	Mus musculus family with sequence similarity 131, member A (Fam131a), mRNA [NM_133778]	NM_133778

Pkdcc	0.0179	1.66	down	Mus musculus protein kinase domain containing, cytoplasmic (Pkdcc), mRNA [NM_134117]	NM_134117
2010002N04Rik	0.0445	2.02	down	Mus musculus RIKEN cDNA 2010002N04 gene (2010002N04Rik), mRNA [NM_134133]	NM_134133
Acot4	0.0476	1.65	down	Mus musculus acyl-CoA thioesterase 4 (Acot4), mRNA [NM_134247]	NM_134247
Hps4	0.0255	1.72	down	Mus musculus Hermansky-Pudlak syndrome 4 homolog (human) (Hps4), mRNA [NM_138646]	NM_138646
Cabp4	0.0229	2.11	down	Mus musculus calcium binding protein 4 (Cabp4), mRNA [NM_144532]	NM_144532
Nrbp2	0.0082	1.55	down	Mus musculus nuclear receptor binding protein 2 (Nrbp2), mRNA [NM_144847]	NM_144847
Hhat	0.0097	1.63	down	Mus musculus hedgehog acyltransferase (Hhat), mRNA [NM_144881]	NM_144881
Lypd1	0.0089	3.57	down	Mus musculus Ly6/Plaur domain containing 1 (Lypd1), mRNA [NM_145100]	NM_145100
L2hgdh	0.0007	1.54	down	Mus musculus L-2-hydroxyglutarate dehydrogenase (L2hgdh), nuclear gene encoding mitochondrial protein, mRNA [NM_145443]	NM_145443
L2hgdh	0.0145	1.56	down	Mus musculus L-2-hydroxyglutarate dehydrogenase (L2hgdh), nuclear gene encoding mitochondrial protein, mRNA [NM_145443]	NM_145443
A2ld1	0.0105	1.53	down	Mus musculus AIG2-like domain 1 (A2ld1), mRNA [NM_145466]	NM_145466
Rnf144b	0.0072	1.69	down	Mus musculus ring finger protein 144B (Rnf144b), transcript variant 1, mRNA [NM_146042]	NM_146042
Cpped1	0.0220	1.81	down	Mus musculus calcineurin-like phosphoesterase domain containing 1 (Cpped1), mRNA [NM_146067]	NM_146067
Zadh2	0.0339	1.64	down	Mus musculus zinc binding alcohol dehydrogenase, domain containing 2 (Zadh2), mRNA [NM_146090]	NM_146090
Ppp1r8	0.0016	1.52	down	Mus musculus protein phosphatase 1, regulatory (inhibitor) subunit 8 (Ppp1r8), mRNA [NM_146154]	NM_146154

Zfp768	0.0266	1.73	down	Mus musculus zinc finger protein 768 (Zfp768), mRNA [NM_146202]	NM_146202
Olfr469	0.0120	1.93	down	Mus musculus olfactory receptor 469 (Olfr469), mRNA [NM_146426]	NM_146426
Olfr1262	0.0176	2.64	down	Mus musculus olfactory receptor 1262 (Olfr1262), mRNA [NM_146974]	NM_146974
Osbp2	0.0085	1.54	down	Mus musculus oxysterol binding protein 2 (Osbp2), mRNA [NM_152818]	NM_152818
Fam40a	0.0159	2.03	down	Mus musculus family with sequence similarity 40, member A (Fam40a), mRNA [NM_153563]	NM_153563
AI428936	0.0212	1.67	down	Mus musculus expressed sequence AI428936 (AI428936), mRNA [NM_153577]	NM_153577
Tmem121	0.0346	2.63	down	Mus musculus transmembrane protein 121 (Tmem121), mRNA [NM_153776]	NM_153776
Tmem121	0.0172	1.77	down	Mus musculus transmembrane protein 121 (Tmem121), mRNA [NM_153776]	NM_153776
Cdkl3	0.0205	1.67	down	Mus musculus cyclin-dependent kinase-like 3 (Cdkl3), transcript variant 2, mRNA [NM_153785]	NM_153785
Flywch1	0.0145	1.58	down	Mus musculus FLYWCH-type zinc finger 1 (Flywch1), mRNA [NM_153791]	NM_153791
Peo1	0.0331	1.66	down	Mus musculus progressive external ophthalmoplegia 1 (human) (Peo1), mRNA [NM_153796]	NM_153796
Pdxk	0.0135	1.53	down	Mus musculus pyridoxal (pyridoxine, vitamin B6) kinase (Pdxk), mRNA [NM_172134]	NM_172134
Nup214	0.0205	2.28	down	Mus musculus nucleoporin 214 (Nup214), mRNA [NM_172268]	NM_172268
Ntm	0.0374	2.24	down	Mus musculus neurotrimin (Ntm), mRNA [NM_172290]	NM_172290
Pogz	0.0320	1.50	down	Mus musculus pogo transposable element with ZNF domain (Pogz), transcript variant 1, mRNA [NM_172683]	NM_172683
Oscp1	0.0209	1.90	down	Mus musculus organic solute carrier partner 1 (Oscp1), mRNA [NM_172701]	NM_172701
Stk38l	0.0128	1.90	down	Mus musculus serine/threonine kinase 38 like (Stk38l), mRNA [NM_172734]	NM_172734

Slc17a5	0.0413	1.63	down	Mus musculus solute carrier family 17 (anion/sugar transporter), member 5 (Slc17a5), mRNA [NM_172773]	NM_172773
Palm2	0.0192	2.38	down	Mus musculus paralemmin 2 (Palm2), mRNA [NM_172868]	NM_172868
Palm2	0.0454	2.10	down	Mus musculus paralemmin 2 (Palm2), mRNA [NM_172868]	NM_172868
Hydin	0.0061	2.46	down	Mus musculus hydrocephalus inducing (Hydin), mRNA [NM_172916]	NM_172916
Zfp317	0.0027	1.60	down	Mus musculus zinc finger protein 317 (Zfp317), mRNA [NM_172918]	NM_172918
Zbtb11	0.0237	1.71	down	Mus musculus zinc finger and BTB domain containing 11 (Zbtb11), mRNA [NM_173026]	NM_173026
Zbtb11	0.0086	1.57	down	Mus musculus zinc finger and BTB domain containing 11 (Zbtb11), mRNA [NM_173026]	NM_173026
Vps13a	0.0183	1.73	down	Mus musculus vacuolar protein sorting 13A (yeast) (Vps13a), mRNA [NM_173028]	NM_173028
Sprr4	0.0210	2.10	down	Mus musculus small proline-rich protein 4 (Sprr4), mRNA [NM_173070]	NM_173070
Zfp879	0.0017	1.52	down	Mus musculus zinc finger protein 879 (Zfp879), mRNA [NM_173387]	NM_173387
Fbxo44	0.0141	2.05	down	Mus musculus F-box protein 44 (Fbxo44), transcript variant 1, mRNA [NM_173401]	NM_173401
Atg4c	0.0049	1.89	down	Mus musculus autophagy-related 4C (yeast) (Atg4c), transcript variant 1, mRNA [NM_175029]	NM_175029
Mmd2	0.0393	6.21	down	Mus musculus monocyte to macrophage differentiation-associated 2 (Mmd2), mRNA [NM_175217]	NM_175217
Arid2	0.0411	1.68	down	Mus musculus AT rich interactive domain 2 (ARID, RFX-like) (Arid2), mRNA [NM_175251]	NM_175251
Pi4kb	0.0165	1.91	down	Mus musculus phosphatidylinositol 4-kinase, catalytic, beta polypeptide (Pi4kb), mRNA [NM_175356]	NM_175356
Sobp	0.0370	1.56	down	Mus musculus sine oculis-binding protein homolog (Drosophila) (Sobp), mRNA [NM_175407]	NM_175407
Glis3	0.0120	1.78	down	Mus musculus GLIS family zinc finger 3 (Glis3), mRNA [NM_175459]	NM_175459

E330009J07Rik	0.0167	1.95	down	Mus musculus RIKEN cDNA E330009J07 gene (E330009J07Rik), mRNA [NM_175528]	NM_175528
Ankrd5	0.0369	1.53	down	Mus musculus ankyrin repeat domain 5 (Ankrd5), mRNA [NM_175667]	NM_175667
Acer1	0.0117	2.26	down	Mus musculus alkaline ceramidase 1 (Acer1), mRNA [NM_175731]	NM_175731
Lrtm1	0.0023	7.38	down	Mus musculus leucine-rich repeats and transmembrane domain 1 (Lrtm1), mRNA [NM_176920]	NM_176920
6330416L07Rik	0.0458	1.54	down	Mus musculus RIKEN cDNA 6330416L07 gene (6330416L07Rik), mRNA [NM_176962]	NM_176962
Adrbk2	0.0438	2.10	down	Mus musculus adrenergic receptor kinase, beta 2 (Adrbk2), transcript variant 1, mRNA [NM_177078]	NM_177078
A830018L16Rik	0.0267	3.77	down	Mus musculus RIKEN cDNA A830018L16 gene (A830018L16Rik), transcript variant 2, mRNA [NM_177173]	NM_177173
Chd9	0.0351	1.56	down	Mus musculus chromodomain helicase DNA binding protein 9 (Chd9), mRNA [NM_177224]	NM_177224
Slc26a9	0.0259	1.81	down	Mus musculus solute carrier family 26, member 9 (Slc26a9), mRNA [NM_177243]	NM_177243
Kndc1	0.0289	1.72	down	Mus musculus kinase non-catalytic C-lobe domain (KIND) containing 1 (Kndc1), mRNA [NM_177261]	NM_177261
Hmbox1	0.0371	1.51	down	Mus musculus homeobox containing 1 (Hmbox1), mRNA [NM_177338]	NM_177338
Arhgap32	0.0464	1.68	down	Mus musculus Rho GTPase activating protein 32 (Arhgap32), mRNA [NM_177379]	NM_177379
1110028C15Rik	0.0243	1.89	down	Mus musculus RIKEN cDNA 1110028C15 gene (1110028C15Rik), transcript variant 2, mRNA [NM_177645]	NM_177645
4933408B17Rik	0.0044	1.64	down	Mus musculus RIKEN cDNA 4933408B17 gene (4933408B17Rik), transcript variant hypothetical protein LOC271508, mRNA [NM_177773]	NM_177773
D330038O06Rik	0.0152	1.80	down	Mus musculus RIKEN cDNA D330038O06 gene (D330038O06Rik), mRNA [NM_177899]	NM_177899

Mobkl2b	0.0051	1.94	down	Mus musculus MOB1, Mps One Binder kinase activator-like 2B (yeast) (Mobkl2b), mRNA [NM_178061]	NM_178061
Arap2	0.0437	1.50	down	Mus musculus ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2 (Arap2), mRNA [NM_178407]	NM_178407
BC051070	0.0221	5.40	down	Mus musculus cDNA sequence BC051070 (BC051070), mRNA [NM_178412]	NM_178412
Rbm47	0.0482	1.82	down	Mus musculus RNA binding motif protein 47 (Rbm47), transcript variant 1, mRNA [NM_178446]	NM_178446
Egflam	0.0336	1.67	down	Mus musculus EGF-like, fibronectin type III and laminin G domains (Egflam), mRNA [NM_178748]	NM_178748
Ppip5k1	0.0414	1.54	down	Mus musculus diphosphoinositol pentakisphosphate kinase 1 (Ppip5k1), mRNA [NM_178795]	NM_178795
Atad3a	0.0459	1.84	down	Mus musculus ATPase family, AAA domain containing 3A (Atad3a), nuclear gene encoding mitochondrial protein, mRNA [NM_179203]	NM_179203
Clec18a	0.0493	6.79	down	Mus musculus C-type lectin domain family 18, member A (Clec18a), mRNA [NM_181549]	NM_181549
Dsg1c	0.0259	1.75	down	Mus musculus desmoglein 1 gamma (Dsg1c), mRNA [NM_181680]	NM_181680
Ccdc67	0.0344	2.93	down	Mus musculus coiled-coil domain containing 67 (Ccdc67), mRNA [NM_181816]	NM_181816
Emilin3	0.0373	1.53	down	Mus musculus elastin microfibril interfacer 3 (Emilin3), mRNA [NM_182840]	NM_182840
A430033K04Rik	0.0428	1.63	down	Mus musculus RIKEN cDNA A430033K04 gene (A430033K04Rik), mRNA [NM_183025]	NM_183025
Zfp691	0.0111	1.56	down	Mus musculus zinc finger protein 691 (Zfp691), transcript variant 1, mRNA [NM_183140]	NM_183140
Accs	0.0062	1.80	down	Mus musculus 1-aminocyclopropane-1-carboxylate synthase homolog (Arabidopsis)(non-functional) (Accs), mRNA [NM_183220]	NM_183220
Cdkl1	0.0262	1.83	down	Mus musculus cyclin-dependent kinase-like 1 (CDC2-related kinase) (Cdkl1), mRNA [NM_183294]	NM_183294

Foxo6	0.0243	2.74	down	Mus musculus forkhead box O6 (Foxo6), mRNA [NM_194060]	NM_194060
1190005I06Rik	0.0088	1.75	down	Mus musculus RIKEN cDNA 1190005I06 gene (1190005I06Rik), mRNA [NM_197988]	NM_197988
Cachd1	0.0267	2.20	down	Mus musculus cache domain containing 1 (Cachd1), mRNA [NM_198037]	NM_198037
Pip5kl1	0.0447	1.69	down	Mus musculus phosphatidylinositol-4-phosphate 5-kinase-like 1 (Pip5kl1), mRNA [NM_198191]	NM_198191
C430048L16Rik	0.0078	1.68	down	Mus musculus RIKEN cDNA C430048L16 gene (C430048L16Rik), mRNA [NM_198957]	NM_198957
Nol4	0.0305	2.58	down	Mus musculus nucleolar protein 4 (Nol4), transcript variant 2, mRNA [NM_199024]	NM_199024
Unc93a	0.0442	3.14	down	Mus musculus unc-93 homolog A (C. elegans) (Unc93a), mRNA [NM_199252]	NM_199252
Col8a2	0.0456	1.72	down	Mus musculus collagen, type VIII, alpha 2 (Col8a2), mRNA [NM_199473]	NM_199473
Dand5	0.0350	1.69	down	Mus musculus DAN domain family, member 5 (Dand5), transcript variant 1, mRNA [NM_201227]	NM_201227
Fam71f1	0.0081	1.98	down	Mus musculus family with sequence similarity 71, member F1 (Fam71f1), mRNA [NM_207258]	NM_207258
Olfr220	0.0163	2.99	down	Mus musculus olfactory receptor 220 (Olfr220), mRNA [NM_207694]	NM_207694
Olfr224	0.0022	7.00	down	Mus musculus olfactory receptor 224 (Olfr224), mRNA [NM_207695]	NM_207695
Malat1	0.0080	2.34	down	Mus musculus metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA) (Malat1), non-coding RNA [NR_002847]	NR_002847
BC018473	0.0049	2.12	down	Mus musculus cDNA sequence BC018473 (BC018473), non-coding RNA [NR_003364]	NR_003364
Pisd-ps2	0.0035	1.50	down	Mus musculus phosphatidylserine decarboxylase, pseudogene 2 (Pisd-ps2), non-coding RNA [NR_003519]	NR_003519
Gm6578	0.0372	1.78	down	Mus musculus predicted gene 6578 (Gm6578), non-coding RNA [NR_003631]	NR_003631

5730522E02Rik	0.0143	1.86	down	Mus musculus RIKEN cDNA 5730522E02 gene (5730522E02Rik), non-coding RNA [NR_027973]	NR_027973
Gm9767	0.0430	2.33	down	Mus musculus predicted gene 9767 (Gm9767), non-coding RNA [NR_028030]	NR_028030
2610306M01Rik	0.0319	1.53	down	Mus musculus RIKEN cDNA 2610306M01 gene (2610306M01Rik), non-coding RNA [NR_028298]	NR_028298
AU015836	0.0035	1.80	down	Mus musculus expressed sequence AU015836 (AU015836), non-coding RNA [NR_028320]	NR_028320
4930528A17Rik	0.0272	2.07	down	Mus musculus RIKEN cDNA 4930528A17 gene (4930528A17Rik), non-coding RNA [NR_028384]	NR_028384
D930016D06Rik	0.0380	1.78	down	Mus musculus RIKEN cDNA D930016D06 gene (D930016D06Rik), non-coding RNA [NR_030673]	NR_030673
B330016D10Rik	0.0396	2.00	down	Mus musculus RIKEN cDNA B330016D10 gene (B330016D10Rik), non-coding RNA [NR_030695]	NR_030695
3110021A11Rik	0.0109	1.67	down	Mus musculus RIKEN cDNA 3110021A11 gene (3110021A11Rik), non-coding RNA [NR_030776]	NR_030776
Gm3230	0.0007	1.92	down	Mus musculus predicted gene 3230 (Gm3230), non-coding RNA [NR_033642]	NR_033642
6030408B16Rik	0.0033	2.53	down	Mus musculus RIKEN cDNA 6030408B16 gene (6030408B16Rik), non-coding RNA [NR_033803]	NR_033803
	0.0337	1.89	down	Ig kappa chain V-III region MOPC 63 Precursor [Source:UniProtKB/Swiss-Prot;Acc:P01661] [ENSMUST00000103397]	X67625
	0.0129	7.05	down	immunoglobulin heavy constant gamma 1 (G1m marker) Gene [Source:MGI Symbol;Acc:MGI:96446] [ENSMUST00000103420]	X87228
Gm5294	0.0414	1.76	down	PREDICTED: Mus musculus predicted gene, EG384244 (EG384244), mRNA [XM_001000706]	XM_001000706
	0.0053	4.19	down	Immunoglobulin heavy chain (gamma polypeptide) Gene [Source:MGI Symbol;Acc:MGI:2144967] [ENSMUST00000103418]	XM_001001076
Gm8273	0.0370	1.91	down	PREDICTED: Mus musculus hypothetical LOC677552 (LOC677552), mRNA [XM_001004569]	XM_001004569

LOC100044227	0.0213	1.88	down	PREDICTED: Mus musculus hypothetical protein LOC100044227 (LOC100044227), mRNA [XM_001471788]	XM_001471788
	0.0143	1.84	down	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q8C9Z4] [ENSMUST000000067768]	XM_001472329
LOC100044493	0.0206	1.61	down	PREDICTED: Mus musculus hypothetical protein LOC100044493 (LOC100044493), mRNA [XM_001472353]	XM_001472353
Gm12128	0.0355	1.87	down	PREDICTED: Mus musculus hypothetical protein LOC100039148 (LOC100039148), mRNA [XM_001472488]	XM_001472488
C030010C08Rik	0.0199	1.63	down	PREDICTED: Mus musculus RIKEN cDNA C030010C08 gene (C030010C08Rik), mRNA [XM_001472491]	XM_001472491
Gm2154	0.0148	3.83	down	PREDICTED: Mus musculus hypothetical protein LOC100039312 (LOC100039312), mRNA [XM_001472648]	XM_001472648
Gm2204	0.0252	1.69	down	PREDICTED: Mus musculus similar to retinitis pigmentosa GTPase regulator interacting protein 1 (LOC100039391), mRNA [XM_001472809]	XM_001472809
Gm1971	0.0121	2.79	down	PREDICTED: Mus musculus predicted gene, ENSMUSG00000072994 (ENSMUSG00000072994), mRNA [XM_001472879]	XM_001472879
Gm2262	0.0304	1.64	down	PREDICTED: Mus musculus similar to keratin associated protein 6-2 (LOC100039486), mRNA [XM_001472967]	XM_001472967
LOC100043989	0.0043	1.61	down	PREDICTED: Mus musculus similar to monoclonal anti-alpha- 1,3-galactosyltransferase IgM heavy chain (LOC100043989), mRNA [XM_001473588]	XM_001473588
Gm2453	0.0079	1.93	down	PREDICTED: Mus musculus hypothetical protein LOC100039844 (LOC100039844), mRNA [XM_001473654]	XM_001473654

LOC100045191	0.0303	1.77	down	PREDICTED: Mus musculus similar to heterogeneous nuclear ribonucleoprotein A2/B1 (LOC100045191), mRNA [XM_001473825]	XM_001473825
Gm9908	0.0210	1.97	down	PREDICTED: Mus musculus hypothetical protein LOC100045396 (LOC100045396), mRNA [XM_001473828]	XM_001473828
Hmcn2	0.0467	1.67	down	PREDICTED: Mus musculus hypothetical LOC670182 (LOC670182), mRNA [XM_001473893]	XM_001473893
	0.0256	1.64	down	PREDICTED: Mus musculus similar to CG2861-PB (LOC100045557), mRNA [XM_001473956]	XM_001473956
Gm2559	0.0074	1.55	down	PREDICTED: Mus musculus similar to Crx opposite strand transcript 1 (LOC100040027), mRNA [XM_001474103]	XM_001474103
Gm2485	0.0398	2.49	down	PREDICTED: Mus musculus hypothetical protein LOC100039902 (LOC100039902), mRNA [XM_001474163]	XM_001474163
	0.0056	2.10	down	RIKEN cDNA 2810416G20 gene Gene [Source:MGI Symbol;Acc:MGI:1914374] [ENSMUST00000057404]	XM_001474539
2810416G20Rik	0.0371	2.02	down	PREDICTED: Mus musculus similar to splicing coactivator subunit SRm300 (LOC100040353), mRNA [XM_001474539]	XM_001474539
1700012I11Rik	0.0208	2.35	down	PREDICTED: Mus musculus RIKEN cDNA 1700012I11 gene (1700012I11Rik), mRNA [XM_001474730]	XM_001474730
Gm13017	0.0254	2.21	down	PREDICTED: Mus musculus hypothetical protein LOC100040728 (LOC100040728), mRNA [XM_001475143]	XM_001475143
LOC100046121	0.0106	1.78	down	PREDICTED: Mus musculus hypothetical protein LOC100046121 (LOC100046121), mRNA [XM_001475613]	XM_001475613
Gm3099	0.0439	1.73	down		XM_001475922
Gm3268	0.0286	1.72	down	PREDICTED: Mus musculus hypothetical protein LOC100041314 (LOC100041314), mRNA [XM_001476140]	XM_001476140

Gm10621	0.0472	1.86	down	Putative uncharacterized protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q3U2L9] [ENSMUST00000098384]	XM_001476249
	0.0122	1.58	down	PREDICTED: Mus musculus hypothetical protein LOC100046332 (LOC100046332), mRNA [XM_001476348]	XM_001476348
Mrpl47	0.0311	1.56	down	mitochondrial ribosomal protein L47 Gene [Source:MGI (curated);Acc:MGI:1921850] [ENSMUST00000043966]	XM_001476597
Gm3622	0.0348	1.51	down	PREDICTED: Mus musculus similar to tau tubulin kinase 1 (LOC100042007), mRNA [XM_001477370]	XM_001477370
Gm3718	0.0419	1.91	down	PREDICTED: Mus musculus hypothetical protein LOC100042202 (LOC100042202), mRNA [XM_001477716]	XM_001477716
LOC100047292	0.0030	1.60	down	PREDICTED: Mus musculus similar to pleckstrin homology domain containing, family A member 7 (LOC100047292), mRNA [XM_001477810]	XM_001477810
Gm3939	0.0171	1.60	down	PREDICTED: Mus musculus hypothetical protein LOC100042633 (LOC100042633), mRNA [XM_001478549]	XM_001478549
LOC100047552	0.0084	1.58	down	PREDICTED: Mus musculus hypothetical protein LOC100047552 (LOC100047552), mRNA [XM_001478625]	XM_001478625
	0.0221	2.27	down	Putative uncharacterized protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q9CSX2] [ENSMUST00000024228]	XM_001478824
Gm4590	0.0042	2.67	down	PREDICTED: Mus musculus hypothetical protein LOC100047775 (LOC100047775), mRNA [XM_001478833]	XM_001478833
Gm4092	0.0321	2.26	down	PREDICTED: Mus musculus hypothetical protein LOC100042892 (LOC100042892), mRNA [XM_001479101]	XM_001479101

Gm4428	0.0139	1.57	down	PREDICTED: Mus musculus hypothetical protein LOC100048135 (LOC100048135), mRNA [XM_001479159]	XM_001479159
	0.0138	2.05	down	PREDICTED: Mus musculus hypothetical protein LOC100042808 (LOC100042808), mRNA [XM_001479428]	XM_001479428
Gm4385	0.0017	2.15	down	PREDICTED: Mus musculus similar to cyclic nucleotide gated channel beta 1 (LOC100043356), mRNA [XM_001480022]	XM_001480022
Tmem200c	0.0283	2.18	down	PREDICTED: Mus musculus predicted gene, EG622645 (EG622645), mRNA [XM_001480132]	XM_001480132
Gm11686	0.0468	1.78	down	PREDICTED: Mus musculus similar to ribosomal protein L35a (LOC100043534), mRNA [XM_001480374]	XM_001480374
Gm5488	0.0204	1.60	down	PREDICTED: Mus musculus similar to zinc finger protein 654 (LOC433036), mRNA [XM_001480385]	XM_001480385
C7	0.0249	2.06	down	PREDICTED: Mus musculus complement component 7 (C7), mRNA [XM_356827]	XM_356827
	0.0252	2.12	down		XM_356827
Gm6420	0.0050	1.72	down	predicted gene 6420 Gene [Source:MGI Symbol;Acc:MGI:3644588] [ENSMUST00000097807]	XM_887803
H2afb3-ps	0.0269	1.84	down	PREDICTED: Mus musculus H2A histone family, member B3 (H2afb3), mRNA [XM_889501]	XM_889501
Gm6328	0.0356	2.92	down	PREDICTED: Mus musculus predicted gene, EG622512 (EG622512), mRNA [XM_897144]	XM_897144
Gm6603	0.0016	1.94	down	PREDICTED: Mus musculus predicted gene, EG625586 (EG625586), mRNA [XM_898851]	XM_898851
Syngap1	0.0461	1.61	down	PREDICTED: Mus musculus synaptic Ras GTPase activating protein 1 homolog (rat) (Syngap1), mRNA [XM_915205]	XM_915205
LOC639986	0.0260	2.11	down	PREDICTED: Mus musculus similar to putative white family ATP-binding cassette transporter (LOC639986), mRNA [XM_916664]	XM_916664
LOC641192	0.0356	2.14	down	PREDICTED: Mus musculus similar to heat shock protein 70 cognate (LOC641192), mRNA [XM_918536]	XM_918536

LOC636328	0.0215	1.70	down	PREDICTED: Mus musculus hypothetical LOC636328 (LOC636328), mRNA [XM_922121]	XM_922121
LOC674218	0.0099	1.57	down	PREDICTED: Mus musculus similar to 2900083I11Rik protein (LOC674218), mRNA [XM_972872]	XM_972872
5830433I10Rik	0.0021	1.82	down	PREDICTED: Mus musculus RIKEN cDNA 5830433I10 gene (5830433I10Rik), mRNA [XM_974092]	XM_974092
Gm7716	0.0011	2.03	down	PREDICTED: Mus musculus predicted gene, EG665619 (EG665619), mRNA [XM_978208]	XM_978208
Olf1358	0.0292	1.52	down	olfactory receptor 1358 Gene [Source:MGI Symbol;Acc:MGI:3031192] [ENSMUST00000095474]	XM_981298
Gm8639	0.0262	2.12	down	PREDICTED: Mus musculus predicted gene, EG667449 (EG667449), mRNA [XM_990610]	XM_990610
	0.0287	2.04	down	PREDICTED: Mus musculus hypothetical LOC675508 (LOC675508), mRNA [XM_990953]	XM_990953
Gm7957	0.0356	1.62	down	PREDICTED: Mus musculus predicted gene, EG666160 (EG666160), misc RNA [XR_001840]	XR_001840
A930033H14Rik	0.0440	1.66	down	PREDICTED: Mus musculus RIKEN cDNA A930033H14 gene (A930033H14Rik), misc RNA [XR_002305]	XR_002305
LOC100044400	0.0047	2.07	down	PREDICTED: Mus musculus similar to pyruvate dehydrogenase (lipoamide) beta (LOC100044400), misc RNA [XR_030659]	XR_030659
Ccdc158	0.0456	2.43	down	coiled-coil domain containing 158 Gene [Source:MGI (curated);Acc:MGI:2444555] [ENSMUST00000060930]	XR_031282
LOC100040974	0.0155	1.74	down	PREDICTED: Mus musculus similar to RIKEN cDNA 5830484A20 gene (LOC100040974), misc RNA [XR_032320]	XR_032320
Gm5050	0.0061	1.51	down	PREDICTED: Mus musculus similar to ribosomal protein L7a (LOC269718), misc RNA [XR_032332]	XR_032332
Gm454	0.0407	2.92	down	PREDICTED: Mus musculus gene model 454, (NCBI) (Gm454), misc RNA [XR_032409]	XR_032409
Gm5937	0.0474	1.57	down	PREDICTED: Mus musculus similar to Hmgbl protein (LOC546331), misc RNA [XR_032803]	XR_032803

Trp53tg5	0.0080	1.91	down	PREDICTED: Mus musculus RIKEN cDNA 1700126L10 gene (1700126L10Rik), misc RNA [XR_033202]	XR_033202
LOC100047121	0.0136	1.58	down	PREDICTED: Mus musculus similar to cyclin T1 (LOC100047121), misc RNA [XR_033752]	XR_033752
LOC100047788	0.0460	2.78	down	PREDICTED: Mus musculus similar to gamma-2a immunoglobulin heavy chain (LOC100047788), misc RNA [XR_033948]	XR_033948
LOC100048634	0.0244	1.60	down	PREDICTED: Mus musculus similar to Interferon activated gene 205 (LOC100048634), misc RNA [XR_034828]	XR_034828
9430078G10Rik	0.0456	2.58	down	PREDICTED: Mus musculus RIKEN cDNA 9430078G10 gene (9430078G10Rik), misc RNA [XR_035208]	XR_035208
C330011M18Rik	0.0208	1.80	down	PREDICTED: Mus musculus RIKEN cDNA C330011M18 gene (C330011M18Rik), misc RNA [XR_035219]	XR_035219
1810059H22Rik	0.0238	3.77	down	PREDICTED: Mus musculus RIKEN cDNA 1810059H22 gene (1810059H22Rik), misc RNA [XR_035221]	XR_035221
BC050254	0.0031	1.93	down	PREDICTED: Mus musculus cDNA sequence BC050254 (BC050254), misc RNA [XR_035237]	XR_035237
	0.0179	3.06	up	lincRNA:chr12:110909258-110913909 forward strand	
	0.0088	1.62	up	mitochondrial ribosomal protein S14 Gene [Source:MGI (curated);Acc:MGI:1928141] [ENSMUST00000097193]	
	0.0123	2.21	up	lincRNA:chr18:5119300-5181600 reverse strand	
	0.0389	4.70	up	lincRNA:chr4:149445201-149445902 forward strand	
	0.0217	1.56	up	lincRNA:chr10:83399729-83399790 forward strand	
	0.0224	2.12	up	lincRNA:chr6:13801450-13853450 forward strand	
	0.0441	2.47	up	lincRNA:chr1:135956616-135957485 reverse strand	
	0.0115	1.83	up	lincRNA:chr5:107504871-107507830 forward strand	
	0.0476	1.88	up	lincRNA:chr6:47595238-47601893 reverse strand	
	0.0103	1.66	up	lincRNA:chr4:44181997-44249172 forward strand	
	0.0277	1.84	up	lincRNA:chr2:143963320-143984245 forward strand	
	0.0497	1.81	up	lincRNA:chr13:48576557-48581632 reverse strand	
	0.0495	1.67	up	lincRNA:chr1:87343550-87362900 forward strand	
	0.0071	1.77	up	lincRNA:chr15:12119755-12127230 forward strand	

	0.0125	1.68	up	lincRNA:chrX:90997595-91009570 reverse strand	
	0.0232	1.58	up	lincRNA:chr2:172343878-172344212 reverse strand	
	0.0281	1.60	up	lincRNA:chr14:77511189-77522852 forward strand	
	0.0372	1.91	up	lincRNA:chr2:128217275-128217972 reverse strand	
	0.0356	1.54	up	lincRNA:chr7:140081171-140123058 reverse strand	
	0.0225	4.18	up	lincRNA:chr4:149445201-149445902 forward strand	
	0.0437	1.62	up	lincRNA:chrX:90997595-91009570 forward strand	
	0.0279	1.62	up	lincRNA:chr14:44284425-44300475 reverse strand	
	0.0476	2.47	up	lincRNA:chr1:167219841-167220505 forward strand	
	0.0416	1.51	up	lincRNA:chr6:100518251-100519726 reverse strand	
	0.0354	2.01	up	lincRNA:chr13:48576557-48581836 forward strand	
	0.0072	1.87	up	lincRNA:chr1:85117750-85129200 forward strand	
	0.0431	1.90	up	lincRNA:chr18:36481237-36481819 forward strand	
	0.0178	2.03	up	lincRNA:chr18:3003075-3016150 reverse strand	
	0.0208	2.83	up	lincRNA:chr18:3003075-3016150 reverse strand	
	0.0372	1.71	up	lincRNA:chr6:112552041-112560067 forward strand	
	0.0141	1.76	up	lincRNA:chr4:16144314-16144967 forward strand	
	0.0071	1.71	up	lincRNA:chr1:85117750-85129200 forward strand	
	0.0080	1.58	up	lincRNA:chr1:183783306-183834531 reverse strand	
	0.0364	1.63	up	lincRNA:chr13:48576557-48581632 forward strand	
	0.0069	1.80	up	lincRNA:chrX:50087925-50101700 forward strand	
	0.0205	1.63	up	lincRNA:chr10:3227840-3233588 reverse strand	
	0.0406	1.74	up	lincRNA:chr1:85117750-85129200 forward strand	
	0.0028	1.60	up	lincRNA:chrX:91000651-91005855 reverse strand	
	0.0201	1.79	up	lincRNA:chr6:99472981-99484210 reverse strand	
	0.0149	2.10	up	lincRNA:chr10:24269165-24276690 reverse strand	
	0.0322	1.96	up	lincRNA:chr3:86827945-86886695 forward strand	
	0.0366	2.30	up	lincRNA:chr11:120041124-120052299 forward strand	
	0.0497	2.46	up	lincRNA:chr15:83181291-83197750 reverse strand	
	0.0500	2.29	up	lincRNA:chr9:14460976-14488051 forward strand	
	0.0351	2.06	up	lincRNA:chr2:127988295-128194920 reverse strand	
	0.0323	1.51	up	lincRNA:chr8:35652473-35703370 reverse strand	
	0.0040	1.81	up	lincRNA:chr13:94180737-94182912 forward strand	

	0.0143	1.55	up	lincRNA:chr18:35970772-35971449 forward strand	
	0.0331	2.22	up	lincRNA:chr6:120670699-120677449 reverse strand	
	0.0081	1.55	up	lincRNA:chr10:62347876-62374346 reverse strand	
	0.0425	1.57	up	lincRNA:chr11:6796679-6797670 forward strand	
	0.0484	1.91	up	lincRNA:chr2:92582386-92599365 forward strand	
	0.0102	1.62	up	lincRNA:chr6:129151512-129208737 forward strand	
	0.0197	2.36	up	lincRNA:chr9:14460976-14488051 forward strand	
	0.0044	1.56	up	lincRNA:chr4:35106125-35127700 forward strand	
	0.0187	1.63	up	lincRNA:chr2:36112819-36114110 forward strand	
	0.0233	1.99	up	lincRNA:chr14:26834450-26847000 reverse strand	
	0.0396	2.01	up	lincRNA:chr6:112552041-112560067 forward strand	
	0.0314	1.91	up	lincRNA:chr15:97856041-97867907 reverse strand	
	0.0478	1.69	up	lincRNA:chr9:100977450-100989325 reverse strand	
	0.0300	2.19	up	lincRNA:chrX:120324027-120326909 reverse strand	
	0.0500	2.40	up	lincRNA:chr5:15033568-15033987 forward strand	
	0.0134	1.60	up	lincRNA:chr14:77258025-77278750 forward strand	
	0.0325	1.94	up	lincRNA:chr12:77544397-77564122 forward strand	
	0.0485	1.99	up	lincRNA:chr8:86705694-86711244 forward strand	
	0.0181	2.61	up	lincRNA:chr9:14460976-14488051 forward strand	
	0.0291	1.64	up	lincRNA:chr9:118291593-118324230 reverse strand	
	0.0135	2.18	up	lincRNA:chr13:24833082-24838462 reverse strand	
	0.0122	1.82	up	lincRNA:chr4:155560050-155570900 reverse strand	
	0.0163	1.98	up	lincRNA:chr8:59966759-59989065 reverse strand	
	0.0022	2.30	up	lincRNA:chr3:96074625-96086375 reverse strand	
	0.0253	2.31	up	lincRNA:chr9:58301467-58323783 reverse strand	
	0.0422	1.70	up	lincRNA:chr10:117021051-117038683 forward strand	
	0.0426	1.97	up	lincRNA:chr19:23068397-23190256 reverse strand	
	0.0453	2.24	up	lincRNA:chr5:79860066-79860625 forward strand	
	0.0092	2.39	up	lincRNA:chr9:14460976-14488051 forward strand	
	0.0281	1.94	up	lincRNA:chr3:131153358-131154061 forward strand	
	0.0112	2.84	up	lincRNA:chr10:95729303-95755173 forward strand	
	0.0212	2.06	up	lincRNA:chr8:37582187-37621987 reverse strand	
	0.0096	2.06	up	lincRNA:chr16:11024315-11055740 forward strand	

	0.0113	1.56	up	lincRNA:chrX:90997595-91009570 reverse strand	
	0.0251	1.81	up	lincRNA:chr13:74712775-74728450 forward strand	
	0.0217	1.92	up	lincRNA:chr2:156654675-156665430 reverse strand	
	0.0319	1.61	up	lincRNA:chr2:77146893-77155643 reverse strand	
	0.0400	1.58	up	lincRNA:chr8:35652473-35703370 reverse strand	
	0.0432	4.40	up	lincRNA:chr4:149445201-149445902 forward strand	
	0.0496	1.61	up	lincRNA:chr14:65785477-65815777 reverse strand	
	0.0292	1.98	up	lincRNA:chr11:69184157-69201732 reverse strand	
	0.0406	2.58	up	lincRNA:chr17:38132217-38157667 forward strand	
	0.0324	1.87	up	lincRNA:chr2:143988645-143993945 reverse strand	
	0.0093	1.73	up	lincRNA:chr18:46646048-46659873 reverse strand	
	0.0313	1.80	up	lincRNA:chr1:175705225-175717250 forward strand	
	0.0170	1.99	up	lincRNA:chr17:38132217-38157667 forward strand	
	0.0207	1.54	up	lincRNA:chrX:98658045-98677545 forward strand	
	0.0462	2.39	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q6R5E0] [ENSMUST00000105030]	
	0.0440	6.42	up	lincRNA:chr1:85304494-85305390 reverse strand	
	0.0333	1.81	up	lincRNA:chr1:163508244-163586072 forward strand	
	0.0175	1.92	up	lincRNA:chr19:5001448-5001810 reverse strand	
	0.0215	2.98	up	lincRNA:chr4:21683562-21694344 reverse strand	
	0.0158	1.50	up	lincRNA:chr6:99472981-99484210 reverse strand	
	0.0483	2.62	up	lincRNA:chr12:111617728-111665403 forward strand	
	0.0443	1.92	down	lincRNA:chr2:35828611-35838083 forward strand	
	0.0496	1.95	down	lincRNA:chr15:82769917-82770296 reverse strand	
	0.0183	1.55	down	lincRNA:chr7:118248833-118267766 reverse strand	
	0.0177	1.71	down	lincRNA:chr9:118291593-118324230 forward strand	
	0.0124	2.52	down	lincRNA:chr3:93564825-93576725 reverse strand	
	0.0053	2.16	down	lincRNA:chr19:54011403-54018978 forward strand	
	0.0315	1.52	down	lincRNA:chr1:63163019-63164281 forward strand	
Fam165b	0.0086	2.99	down	family with sequence similarity 165, member B Gene [Source:MGI (curated);Acc:MGI:1916186] [ENSMUST00000118064]	

	0.0374	4.07	down	lincRNA:chr7:71093563-71095094 forward strand	
	0.0030	2.30	down	lincRNA:chr14:76237150-76237464 reverse strand	
	0.0051	1.81	down	lincRNA:chr17:15226181-15250333 reverse strand	
	0.0106	3.17	down	lincRNA:chr11:58659807-58676282 reverse strand	
	0.0048	1.60	down	lincRNA:chr7:134620707-134626739 reverse strand	
	0.0421	2.59	down	lincRNA:chrX:34360500-34388500 reverse strand	
	0.0227	1.83	down	lincRNA:chr8:108153471-108159346 reverse strand	
	0.0231	1.63	down	lincRNA:chr15:76193801-76194225 forward strand	
	0.0457	3.60	down	lincRNA:chr16:23992037-24001037 forward strand	
	0.0084	1.58	down	lincRNA:chr4:138657728-138687028 reverse strand	
	0.0498	1.55	down	Unknown	
	0.0480	2.13	down	lincRNA:chr15:86035939-86042539 forward strand	
	0.0075	2.13	down	lincRNA:chr19:5795689-5802671 reverse strand	
	0.0007	2.23	down	lincRNA:chr16:64758224-64765700 forward strand	
	0.0178	2.19	down	lincRNA:chr15:73227424-73257474 forward strand	
	0.0490	2.19	down	lincRNA:chr13:28760289-28977218 reverse strand	
	0.0046	1.58	down	lincRNA:chr13:98062189-98066613 forward strand	
	0.0384	2.07	down		
	0.0369	2.08	down	lincRNA:chr9:65376063-65390480 forward strand	
	0.0452	2.00	down	lincRNA:chr15:59059450-59070576 reverse strand	
	0.0177	1.63	down	lincRNA:chr15:84737071-84753513 reverse strand	
	0.0106	2.39	down	lincRNA:chr7:99879368-99889978 reverse strand	
	0.0350	1.60	down	lincRNA:chr9:65651848-65652920 reverse strand	
	0.0414	3.34	down	lincRNA:chrX:11671167-11700242 forward strand	
	0.0189	1.78	down	lincRNA:chr13:74642700-74701900 forward strand	
	0.0277	3.92	down	lincRNA:chrX:45814752-45816313 reverse strand	
	0.0068	1.89	down	lincRNA:chr1:94077221-94091396 reverse strand	
	0.0383	1.68	down	lincRNA:chr8:106592650-106603525 reverse strand	
	0.0266	3.86	down	lincRNA:chr5:124667541-124700029 forward strand	
	0.0252	1.74	down	lincRNA:chr9:41184479-41240162 forward strand	
	0.0223	1.88	down	lincRNA:chr15:100906946-100907748 reverse strand	
	0.0349	1.77	down	lincRNA:chr8:47813487-47824869 forward strand	
	0.0463	2.40	down	lincRNA:chr11:119794849-119803349 forward strand	

	0.0403	1.71	down	lincRNA:chr8:26345571-26346095 reverse strand	
	0.0033	3.63	down	lincRNA:chr12:12768528-12849976 forward strand	
	0.0051	3.48	down	lincRNA:chr10:98718526-98719169 reverse strand	
	0.0401	1.86	down	lincRNA:chr5:33174092-33200792 reverse strand	
	0.0088	1.65	down	lincRNA:chr14:43408099-43415349 forward strand	
	0.0232	3.13	down	lincRNA:chr3:127037711-127111912 reverse strand	
	0.0268	1.83	down	lincRNA:chr10:119960546-119979696 reverse strand	
	0.0023	1.90	down	lincRNA:chr9:121256738-121257487 forward strand	
	0.0457	1.55	down	lincRNA:chr6:86776350-86799379 reverse strand	
	0.0100	2.05	down	lincRNA:chr19:5795689-5802671 reverse strand	
	0.0322	1.97	down	lincRNA:chr13:112210279-112212150 reverse strand	
	0.0219	1.65	down	lincRNA:chr9:81536195-81538236 forward strand	
	0.0282	2.85	down	lincRNA:chr16:30936314-30954449 reverse strand	
	0.0131	2.16	down	lincRNA:chr9:41300137-41301556 forward strand	
	0.0027	1.57	down	lincRNA:chr18:84735774-84760824 reverse strand	
	0.0271	1.69	down	lincRNA:chr8:44232164-44267061 reverse strand	
	0.0246	3.65	down	lincRNA:chr9:61881173-61881351 reverse strand	
	0.0316	2.12	down	lincRNA:chr17:36136010-36136696 forward strand	
	0.0013	1.66	down	lincRNA:chr9:89167172-89168980 forward strand	
	0.0089	2.20	down	lincRNA:chr8:119732348-119749198 reverse strand	
	0.0372	1.53	down	lincRNA:chr2:157838320-157853495 reverse strand	
	0.0131	1.53	down	lincRNA:chr7:134643558-134644056 forward strand	
	0.0118	3.70	down	lincRNA:chr17:32035750-32056000 forward strand	
	0.0131	2.73	down		
	0.0001	2.07	down	lincRNA:chr2:77146893-77155643 forward strand	
	0.0399	1.57	down	lincRNA:chr3:96205368-96217943 forward strand	
	0.0293	1.54	down	lincRNA:chrX:148819227-148844227 forward strand	
	0.0374	1.88	down	lincRNA:chr7:88126007-88138301 reverse strand	
	0.0154	2.34	down	lincRNA:chr1:45800000-45834825 reverse strand	
	0.0036	2.31	down	lincRNA:chr7:77323753-77482708 reverse strand	
	0.0012	1.76	down	lincRNA:chr2:67836003-67836461 forward strand	
	0.0462	1.61	down	lincRNA:chr1:196802568-196847687 forward strand	
	0.0434	1.68	down	lincRNA:chr1:63264155-63345773 forward strand	

	0.0260	4.19	down	lincRNA:chr2:35828611-35838083 forward strand	
	0.0238	1.64	down		
	0.0229	2.16	down	lincRNA:chr6:86476240-86513483 forward strand	
	0.0001	1.62	down	lincRNA:chr13:112207480-112213280 reverse strand	
	0.0036	1.92	down	lincRNA:chr16:90116006-90119297 reverse strand	
	0.0213	1.79	down	lincRNA:chr1:34735032-34781146 forward strand	
	0.0290	4.65	down	lincRNA:chr17:32229024-32229663 forward strand	
	0.0117	1.97	down	lincRNA:chrX:75813213-75829323 forward strand	
	0.0485	1.85	down	lincRNA:chr2:71575871-71583454 reverse strand	
	0.0443	1.80	down	lincRNA:chr15:5975553-5994636 reverse strand	
	0.0010	1.51	down	lincRNA:chr1:58443698-58449898 reverse strand	
	0.0427	1.53	down	lincRNA:chr8:18895366-18925423 reverse strand	
	0.0091	2.41	down	lincRNA:chr3:88323145-88335770 reverse strand	
	0.0490	1.54	down	lincRNA:chrX:54627918-54638568 reverse strand	
	0.0134	1.70	down	lincRNA:chr10:60473030-60535340 forward strand	
	0.0231	1.60	down	lincRNA:chr19:56820850-56837925 forward strand	
	0.0456	1.80	down	lincRNA:chr14:33115110-33131171 forward strand	
	0.0454	1.91	down	lincRNA:chr7:6210340-6229115 forward strand	
	0.0039	1.73	down	lincRNA:chr3:84609788-84618062 reverse strand	
	0.0271	1.77	down	lincRNA:chr2:94017095-94019092 reverse strand	
	0.0447	2.39	down	lincRNA:chr1:95871175-95886625 reverse strand	
	0.0418	1.69	down	lincRNA:chr8:48476637-48492537 reverse strand	
	0.0228	2.17	down	lincRNA:chr11:120097758-120098581 forward strand	
	0.0104	1.65	down	lincRNA:chr14:21461716-21462270 forward strand	
	0.0036	1.90	down	lincRNA:chr7:77555482-77634858 forward strand	
	0.0185	1.75	down	lincRNA:chr9:65376063-65390480 reverse strand	
	0.0393	1.64	down	lincRNA:chr18:84760623-84761084 forward strand	
	0.0036	2.45	down	lincRNA:chr9:41300137-41301556 forward strand	
	0.0389	1.76	down	lincRNA:chr2:155269145-155303251 reverse strand	
	0.0198	4.83	down	lincRNA:chr11:102878974-102888924 forward strand	
	0.0339	1.94	down	lincRNA:chr12:72103832-72116875 reverse strand	
	0.0117	1.74	down	lincRNA:chr5:35492530-35492959 reverse strand	
	0.0151	1.55	down	lincRNA:chr12:52950465-52950990 reverse strand	

	0.0481	2.34	down	lincRNA:chr2:173121033-173124485 forward strand	
	0.0286	2.24	down	lincRNA:chr7:99879368-99889978 reverse strand	
	0.0283	1.52	down	lincRNA:chr14:118774481-118873242 reverse strand	
	0.0013	2.01	down	lincRNA:chr2:22782700-22801900 reverse strand	
	0.0481	1.74	down	lincRNA:chr5:149947200-149979950 forward strand	
	0.0071	1.62	down	lincRNA:chr2:25182970-25188091 reverse strand	
	0.0166	2.24	down	lincRNA:chr5:125713450-125735500 reverse strand	
	0.0388	1.57	down	lincRNA:chr1:58443698-58449898 reverse strand	
	0.0409	1.91	down	lincRNA:chr18:60812427-60819775 reverse strand	
	0.0229	1.66	down	lincRNA:chr5:74487385-74497428 reverse strand	
	0.0257	2.46	down	lincRNA:chr8:67213300-67271700 forward strand	
	0.0261	1.51	down	lincRNA:chr11:60728207-60745369 forward strand	
	0.0026	1.57	down	POGZ_MOUSE (Q8BZH4) Pogo transposable element with ZNF domain, partial (4%) [TC1612650]	
	0.0493	1.70	down	lincRNA:chr1:36012298-36020311 reverse strand	
	0.0093	1.93	down	lincRNA:chr10:5950116-5958250 reverse strand	
	0.0127	2.13	down	lincRNA:chr5:149751979-149808240 reverse strand	
	0.0380	1.56	down	lincRNA:chr11:19778600-19815950 forward strand	
	0.0451	1.87	down	lincRNA:chr5:149751979-149808240 reverse strand	
	0.0033	1.95	down	lincRNA:chr12:103151385-103157735 forward strand	
	0.0481	1.62	down	lincRNA:chr2:174088550-174109425 forward strand	
	0.0197	1.86	down	lincRNA:chr17:3103174-3114885 reverse strand	
	0.0284	1.85	down	lincRNA:chr7:6108350-6119600 reverse strand	
	0.0480	1.66	down	lincRNA:chr2:32950586-32984936 reverse strand	
	0.0448	4.57	down	lincRNA:chr9:40266027-40266460 reverse strand	
	0.0365	1.50	down	lincRNA:chr8:4325209-4348788 forward strand	
	0.0167	1.86	down	lincRNA:chr3:93564825-93576725 forward strand	
	0.0327	1.87	down	lincRNA:chr2:60038543-60046318 reverse strand	
	0.0054	1.95	down	lincRNA:chr19:12079745-12088620 reverse strand	
	0.0211	1.83	down	lincRNA:chr17:35080914-35090009 forward strand	
	0.0317	1.62	down	lincRNA:chr15:96091428-96115684 reverse strand	
	0.0292	1.76	down	lincRNA:chr18:84735774-84760824 reverse strand	
	0.0407	1.88	down	lincRNA:chr4:136856064-136877219 forward strand	

	0.0451	1.85	down	lincRNA:chr19:59001589-59006474 reverse strand	
	0.0479	2.65	down	lincRNA:chr5:149751979-149808240 reverse strand	
	0.0452	1.50	down	lincRNA:chr4:138657728-138687028 reverse strand	
	0.0127	5.23	down	lincRNA:chr9:40266027-40266460 reverse strand	
	0.0378	2.45	down	lincRNA:chr9:41368823-41369514 forward strand	
	0.0085	1.69	down	lincRNA:chr9:56910620-56919667 reverse strand	
	0.0043	2.10	down	lincRNA:chr5:35975265-35982561 reverse strand	
	0.0026	2.04	down	lincRNA:chr9:121256738-121257487 forward strand	
	0.0272	1.76	down	lincRNA:chr17:9943615-9967953 reverse strand	
	0.0350	2.67	down	lincRNA:chr13:70745306-70837331 reverse strand	
	0.0277	4.94	down	lincRNA:chr9:40268246-40268441 reverse strand	
	0.0380	2.02	down	lincRNA:chrX:100688896-100701764 forward strand	
	0.0170	1.80	down	lincRNA:chr10:16603950-16794075 forward strand	
	0.0346	2.34	down	lincRNA:chr19:5795689-5802671 reverse strand	
	0.0231	1.57	down	lincRNA:chr17:21787577-21828406 forward strand	
	0.0271	1.51	down	lincRNA:chr1:63163023-63180223 forward strand	
	0.0193	2.05	down	lincRNA:chr12:110842149-110845695 forward strand	
	0.0052	1.68	down	lincRNA:chr1:63163023-63180223 forward strand	
	0.0394	2.21	down	lincRNA:chr5:113594167-113645342 forward strand	
	0.0442	1.50	down	lincRNA:chr12:85252300-85253597 reverse strand	
	0.0180	1.68	down	lincRNA:chr1:87343550-87362900 reverse strand	
	0.0175	1.96	down	lincRNA:chr11:18367482-18393258 reverse strand	
	0.0377	1.58	down	lincRNA:chr10:66559716-66647841 reverse strand	
	0.0481	1.52	down	lincRNA:chr15:59059450-59070576 reverse strand	
	0.0010	1.67	down	lincRNA:chr10:110980223-110980667 reverse strand	
	0.0458	1.67	down	lincRNA:chr4:40720362-40729687 forward strand	
	0.0289	2.18	down	lincRNA:chr12:72103832-72116875 reverse strand	
	0.0043	1.78	down	lincRNA:chr15:83281223-83284791 reverse strand	
	0.0138	2.35	down	lincRNA:chr12:3173375-3203075 reverse strand	
	0.0095	1.83	down	lincRNA:chr2:94008913-94019798 reverse strand	
	0.0108	1.64	down	lincRNA:chr12:21548850-21568550 reverse strand	
	0.0004	1.83	down	lincRNA:chr8:125031410-125075960 reverse strand	
	0.0196	2.09	down	lincRNA:chr15:100909469-100910253 forward strand	

	0.0072	2.39	down	lincRNA:chr9:41300137-41301556 forward strand	
	0.0375	1.53	down	lincRNA:chrX:11671249-11671715 reverse strand	
	0.0348	2.02	down	lincRNA:chr15:100905367-100905654 reverse strand	
	0.0460	1.72	down	lincRNA:chr9:75316023-75344401 forward strand	
	0.0254	1.78	down	lincRNA:chr3:21973306-21974266 reverse strand	
	0.0210	5.70	down	lincRNA:chr9:40268246-40268441 reverse strand	
	0.0177	2.81	down	lincRNA:chrX:50400250-50410825 reverse strand	
	0.0174	2.00	down	lincRNA:chr14:73729977-73751877 forward strand	
	0.0374	1.52	down	lincRNA:chr15:68170864-68171544 reverse strand	
	0.0475	1.88	down	lincRNA:chr3:151746091-151753763 reverse strand	
	0.0283	1.89	down	lincRNA:chr2:35829956-35830757 reverse strand	
	0.0074	1.72	down	lincRNA:chr1:167797581-167803031 reverse strand	
	0.0132	1.64	down	lincRNA:chr2:72818943-72826893 reverse strand	
	0.0262	2.27	down	lincRNA:chr16:64758224-64765700 forward strand	
	0.0062	1.58	down	lincRNA:chr18:84760623-84761084 forward strand	
	0.0190	1.91	down	lincRNA:chr1:92546371-92551596 forward strand	
	0.0289	2.37	down	lincRNA:chr10:118385588-118439338 reverse strand	
	0.0132	2.22	down	lincRNA:chr2:60531602-60543635 reverse strand	
	0.0186	1.56	down	lincRNA:chr17:17462450-17488725 forward strand	
	0.0251	1.62	down	lincRNA:chr1:58443698-58449898 reverse strand	
	0.0182	1.67	down	lincRNA:chr18:84757475-84757969 reverse strand	
	0.0024	2.51	down	lincRNA:chr2:168136389-168136560 reverse strand	
	0.0088	1.74	down	lincRNA:chr1:94077196-94077860 forward strand	
	0.0240	1.74	down	lincRNA:chr12:25852471-25852681 forward strand	
	0.0049	1.96	down	lincRNA:chr1:173254292-173257445 reverse strand	
	0.0328	1.77	down	lincRNA:chr7:118248833-118267766 reverse strand	
	0.0427	2.01	down	lincRNA:chr7:99879368-99889978 reverse strand	
	0.0135	1.54	down	lincRNA:chr17:15357376-15385701 forward strand	
	0.0483	1.55	down	lincRNA:chr7:134595900-134610975 forward strand	
	0.0173	1.64	down	RAR-related orphan receptor alpha Gene [Source:MGI (curated);Acc:MGI:104661] [ENSMUST00000064920]	
	0.0112	2.17	down	lincRNA:chr4:82156098-82196298 reverse strand	
	0.0015	1.56	down	lincRNA:chr2:176583825-176714400 forward strand	

	0.0219	2.31	down	lincRNA:chr10:59385064-59385436 forward strand	
	0.0431	1.65	down	lincRNA:chr17:88993214-89025839 forward strand	
	0.0012	1.51	down	lincRNA:chrX:54627918-54638568 reverse strand	
	0.0205	1.63	down	lincRNA:chr14:73757550-73758159 reverse strand	
	0.0291	3.05	down	lincRNA:chr3:127037711-127111912 reverse strand	
	0.0204	1.66	down	lincRNA:chr15:96091428-96115684 reverse strand	
	0.0034	1.76	down	lincRNA:chr7:137669440-137672712 forward strand	
	0.0462	1.70	down	lincRNA:chr8:26869173-26869823 reverse strand	
	0.0429	1.56	down	lincRNA:chr15:68161768-68193518 reverse strand	
	0.0042	1.75	down	lincRNA:chr12:117623500-117643575 reverse strand	
	0.0211	2.33	down	lincRNA:chr6:86476240-86513483 forward strand	
	0.0103	2.77	down	lincRNA:chr5:92548501-92566401 forward strand	
	0.0222	1.62	down	lincRNA:chr15:102032892-102033838 reverse strand	
	0.0496	1.72	down	lincRNA:chr19:16078625-16110246 reverse strand	
	0.0118	1.64	down	lincRNA:chr18:84735774-84760824 forward strand	
	0.0176	1.96	down	lincRNA:chr2:80338640-80339980 reverse strand	
	0.0104	1.84	down	lincRNA:chr18:84760623-84761084 forward strand	
	0.0447	2.57	down	lincRNA:chr6:134838675-134847075 forward strand	
	0.0008	2.18	down	lincRNA:chr5:35975265-35982561 reverse strand	
	0.0191	2.42	down	lincRNA:chr8:91569369-91594119 forward strand	
	0.0295	2.33	down	lincRNA:chr15:83281223-83284791 reverse strand	
	0.0110	1.81	down	lincRNA:chr11:117835849-117842574 forward strand	
	0.0389	2.43	down	lincRNA:chr3:60292527-60292880 reverse strand	
	0.0454	1.58	down	lincRNA:chr10:39383665-39442690 forward strand	
	0.0380	1.76	down	lincRNA:chr4:59306575-59317850 reverse strand	
	0.0208	2.09	down	lincRNA:chr6:47595238-47601893 forward strand	
	0.0349	1.51	down	lincRNA:chr5:22928221-22939127 reverse strand	
	0.0160	1.52	down	lincRNA:chr6:86776350-86799379 reverse strand	
	0.0431	2.13	down	lincRNA:chr11:116562925-116574575 reverse strand	
	0.0335	1.64	down	lincRNA:chr18:46954653-46955671 forward strand	
	0.0255	1.80	down	lincRNA:chr2:67836003-67836461 forward strand	
	0.0373	1.65	down	lincRNA:chr15:102026122-102033725 reverse strand	
	0.0174	1.77	down	lincRNA:chrX:54636915-54638388 reverse strand	

	0.0285	3.22	down	lincRNA:chr11:79531768-79532127 forward strand	
	0.0045	1.54	down	lincRNA:chr3:95457337-95458070 reverse strand	
	0.0304	2.13	down	lincRNA:chr9:41184479-41240162 forward strand	
	0.0409	1.59	down	lincRNA:chr4:88604248-88645948 forward strand	
	0.0308	1.58	down	lincRNA:chr17:39960567-39992817 reverse strand	
	0.0405	1.54	down	lincRNA:chr1:6199946-6200603 reverse strand	
	0.0077	1.50	down	lincRNA:chrX:54627918-54638568 reverse strand	
	0.0477	1.51	down	lincRNA:chr1:63168439-63172297 forward strand	
	0.0326	1.81	down	lincRNA:chr18:54115625-54123729 forward strand	
	0.0114	2.57	down	lincRNA:chr12:115365529-115379374 reverse strand	
	0.0224	2.13	down	lincRNA:chr19:5771425-5848475 reverse strand	
	0.0424	1.55	down	lincRNA:chr15:68161768-68193518 reverse strand	
	0.0031	1.93	down	lincRNA:chr5:35975265-35982561 reverse strand	
	0.0295	1.81	down	lincRNA:chr2:126501651-126510026 forward strand	
	0.0381	1.52	down	lincRNA:chr6:122741562-122743423 reverse strand	
	0.0394	1.78	down	lincRNA:chrX:54636915-54638388 reverse strand	
	0.0057	2.21	down	lincRNA:chr7:134779841-134840591 forward strand	
	0.0162	1.75	down	lincRNA:chr2:67836003-67836461 forward strand	
	0.0462	2.17	down	lincRNA:chr14:65431652-65437902 reverse strand	
	0.0015	1.67	down	lincRNA:chr1:6199946-6200603 reverse strand	
	0.0294	1.53	down	lincRNA:chr15:68161768-68193518 reverse strand	

GeneSymbol	p-value	FCAbsolute	regulation	Description	GenbankAccession
1700003G18Rik	0.0087	1.54	up	Mus musculus 10 days embryo whole body cDNA, RIKEN full length enriched library, clone:2610312K03 product:unclassifiable full insert sequence. [AK012020]	AK012020
2700068H02Rik	0.0361	2.78	up	Mus musculus 11 days embryo whole body cDNA, RIKEN full length enriched library, clone:2700068H02 product:unclassifiable full insert sequence. [AK012503]	AK012503
4930445G23Rik	0.0154	5.06	up	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930445G23 product:unclassifiable, full insert sequence. [AK015390]	AK015390
4930572J10Rik	0.0396	1.75	up	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930572J10 product:unclassifiable, full insert sequence. [AK016280]	AK016280
4933438K21Rik	0.0035	21.85	up	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933438K21 product:weakly similar to ORF4 PROTEIN [Rattus norvegicus], full insert sequence. [AK017111]	AK017111
2810032G03Rik	0.0083	1.91	up	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930463A03 product:hypothetical protein, full insert sequence. [AK029678]	AK029678
LOC432958	0.0236	2.03	up	Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630042D17 product:unclassifiable, full insert sequence. [AK041852]	AK041852
4930588A03Rik	0.0091	2.41	up	Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230363O11 product:unclassifiable, full insert sequence. [AK046275]	AK046275
9430041J12Rik	0.0098	2.50	up	Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130050D15 product:unclassifiable, full insert sequence. [AK051461]	AK051461
Tmem128	0.0078	1.54	up	transmembrane protein 128 Gene [Source:MGI (curated);Acc:MGI:1913559] [ENSMUST00000119047]	AK076679

C230029M16	0.0395	2.12	up	Mus musculus 0 day neonate cerebellum cDNA, RIKEN full length enriched library, clone:C230029M16 product:unclassifiable, full insert sequence. [AK082258]	AK082258
C230098O21Rik	0.0030	1.72	up	Mus musculus 0 day neonate cerebellum cDNA, RIKEN full length enriched library, clone:C230098O21 product:unclassifiable, full insert sequence. [AK082735]	AK082735
C730029A08Rik	0.0077	5.92	up	Mus musculus adult male hippocampus cDNA, RIKEN full length enriched library, clone:C630024D06 product:unclassifiable, full insert sequence. [AK083183]	AK083183
E330011O21Rik	0.0153	6.21	up	Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330011O21 product:unclassifiable, full insert sequence. [AK087725]	AK087725
	0.0098	1.80	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3UV43] [ENSMUST00000097824]	AK137609
C430049E01Rik	0.0391	2.02	up	Mus musculus 7 days embryo whole body cDNA, RIKEN full length enriched library, clone:C430049E01 product:hypothetical protein, full insert sequence. [AK141396]	AK141396
	0.0149	2.32	up	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3U256] [ENSMUST00000100512]	AK155479
	0.0363	2.07	up	Putative uncharacterized protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q3TXX5] [ENSMUST00000097320]	AK159059
	0.0401	2.04	up	topoisomerase (DNA) III alpha Gene [Source:MGI (curated);Acc:MGI:1197527] [ENSMUST00000120417]	AK164443
Mutyh	0.0071	1.77	up	Mus musculus adenine-DNA glycosylase mRNA, complete cds [AY007717]	AY007717
Gprin3	0.0101	1.78	up	GPRIN family member 3 Gene [Source:MGI Symbol;Acc:MGI:1924785] [ENSMUST00000051065]	BC040234
	0.0215	1.59	up	centrosomal protein 110 Gene [Source:MGI (curated);Acc:MGI:1889576] [ENSMUST00000113037]	BC060146

	0.0134	1.62	up	strawberry notch homolog 2 (Drosophila) Gene [Source:MGI Symbol;Acc:MGI:2448490] [ENSMUST00000092316]	BC064113
	0.0203	2.36	up	sideroflexin 5 Gene [Source:MGI (curated);Acc:MGI:2137681] [ENSMUST00000113788]	BC089588
Gm11520	0.0248	2.89	up	UI-M-BH1-amc-g-06-0-UI.r1 NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BH1-amc-g-06-0-UI 5'. [BE647330]	BE647330
D7Ert661e	0.0483	2.35	up	H3085D11-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3085D11 3', mRNA sequence [BG070263]	BG070263
2700081L22Rik	0.0398	2.86	up	BX515870 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGp998E04751 ; IMAGE:330603, mRNA sequence [BX515870]	BX515870
Tnip3	0.0066	1.62	up	Mus musculus TNFAIP3 interacting protein 3 (Tnip3), mRNA [NM_001001495]	NM_001001495
Olf312	0.0027	3.07	up	Mus musculus olfactory receptor 312 (Olf312), mRNA [NM_001011819]	NM_001011819
Defa23	0.0448	2.32	up	Mus musculus defensin, alpha, 23 (Defa23), mRNA [NM_001012307]	NM_001012307
Zfyve28	0.0033	2.95	up	Mus musculus zinc finger, FYVE domain containing 28 (Zfyve28), mRNA [NM_001015039]	NM_001015039
Cpa2	0.0056	6.45	up	Mus musculus carboxypeptidase A2, pancreatic (Cpa2), mRNA [NM_001024698]	NM_001024698
Adamts17	0.0366	3.22	up	Mus musculus a disintegrin-like and metalloproteinase (reprolysin type) with thrombospondin type 1 motif, 17 (Adamts17), mRNA [NM_001033877]	NM_001033877
LOC380994	0.0370	10.86	up	Mus musculus similar to Sycp3 like Y-linked (LOC380994), mRNA [NM_001037748]	NM_001037748
Olfm1	0.0325	2.51	up	Mus musculus olfactomedin 1 (Olfm1), transcript variant 2, mRNA [NM_001038612]	NM_001038612
Spag11b	0.0235	3.49	up	Mus musculus sperm associated antigen 11B (Spag11b), transcript variant c, mRNA [NM_001039563]	NM_001039563

Gm14316	0.0298	4.66	up	Mus musculus predicted gene 14316 (Gm14316), mRNA [NM_001040055]	NM_001040055
Larp1b	0.0425	1.51	up	Mus musculus La ribonucleoprotein domain family, member 1E (Larp1b), mRNA [NM_001040399]	NM_001040399
Unc79	0.0047	1.67	up	Mus musculus unc-79 homolog (C. elegans) (Unc79), mRNA [NM_001081017]	NM_001081017
2010317E24Rik	0.0109	1.92	up	Mus musculus RIKEN cDNA 2010317E24 gene (2010317E24Rik), mRNA [NM_001081085]	NM_001081085
Mki67	0.0010	2.23	up	Mus musculus antigen identified by monoclonal antibody Ki 67 (Mki67), mRNA [NM_001081117]	NM_001081117
Mki67	0.0007	2.06	up	Mus musculus antigen identified by monoclonal antibody Ki 67 (Mki67), mRNA [NM_001081117]	NM_001081117
Fam89a	0.0347	1.52	up	Mus musculus family with sequence similarity 89, member A (Fam89a), mRNA [NM_001081120]	NM_001081120
Polr3g	0.0155	1.88	up	Mus musculus polymerase (RNA) III (DNA directed) polypeptide G (Polr3g), mRNA [NM_001081176]	NM_001081176
Dgki	0.0462	2.95	up	Mus musculus diacylglycerol kinase, iota (Dgki), mRNA [NM_001081206]	NM_001081206
Tsc22d2	0.0126	2.43	up	Mus musculus TSC22 domain family, member 2 (Tsc22d2), mRNA [NM_001081229]	NM_001081229
Mosc1	0.0082	5.92	up	Mus musculus MOCO sulphurase C-terminal domain containing 1 (Mosc1), nuclear gene encoding mitochondrial protein, mRNA [NM_001081361]	NM_001081361
Mosc1	0.0081	6.14	up	Mus musculus MOCO sulphurase C-terminal domain containing 1 (Mosc1), nuclear gene encoding mitochondrial protein, mRNA [NM_001081361]	NM_001081361
Palld	0.0249	1.66	up	Mus musculus palladin, cytoskeletal associated protein (Palld), mRNA [NM_001081390]	NM_001081390
Osbp17	0.0435	1.52	up	Mus musculus oxysterol binding protein-like 7 (Osbp17), mRNA [NM_001081434]	NM_001081434
Gm7609	0.0334	2.36	up	Mus musculus predicted pseudogene 7609 (Gm7609), mRNA [NM_001081746]	NM_001081746

Dusp5	0.0168	1.53	up	Mus musculus dual specificity phosphatase 5 (Dusp5), mRNA [NM_001085390]	NM_001085390
Duox1	0.0357	1.81	up	Mus musculus dual oxidase 1 (Duox1), mRNA [NM_001099297]	NM_001099297
Lin9	0.0411	1.81	up	Mus musculus lin-9 homolog (C. elegans) (Lin9), transcript variant 1, mRNA [NM_001103182]	NM_001103182
Ppih	0.0187	2.09	up	Mus musculus peptidyl prolyl isomerase H (Ppih), transcript variant 3, mRNA [NM_001110130]	NM_001110130
Sep-09	0.0275	1.62	up	Mus musculus septin 9 (Sept9), transcript variant 2, mRNA [NM_001113487]	NM_001113487
Gm13011	0.0365	1.69	up	Mus musculus predicted gene 13011 (Gm13011), mRNA [NM_001126318]	NM_001126318
Fam55c	0.0180	2.21	up	Mus musculus family with sequence similarity 55, member C (Fam55c), mRNA [NM_001134494]	NM_001134494
Klf14	0.0065	5.27	up	Mus musculus Kruppel-like factor 14 (Klf14), mRNA [NM_001135093]	NM_001135093
Hipk2	0.0486	1.53	up	Mus musculus homeodomain interacting protein kinase 2 (Hipk2) transcript variant 1, mRNA [NM_001136065]	NM_001136065
Golga7b	0.0089	6.39	up	Mus musculus golgi autoantigen, golgin subfamily a, 7B (Golga7b), transcript variant 1, mRNA [NM_001141983]	NM_001141983
Arhgap40	0.0048	2.15	up	Mus musculus Rho GTPase activating protein 40 (Arhgap40), mRNA [NM_001145015]	NM_001145015
Mutyh	0.0439	1.51	up	Mus musculus mutY homolog (E. coli) (Mutyh), transcript variant 1, mRNA [NM_001159581]	NM_001159581
Prl3c1	0.0110	2.47	up	Mus musculus prolactin family 3, subfamily c, member 1 (Prl3c1), transcript variant 2, mRNA [NM_001163218]	NM_001163218
Krtap20-2	0.0054	1.53	up	Mus musculus keratin associated protein 20-2 (Krtap20-2), mRNA [NM_001163615]	NM_001163615
Fbxo27	0.0004	1.58	up	Mus musculus F-box protein 27 (Fbxo27), transcript variant 1, mRNA [NM_001163702]	NM_001163702

Plekha8	0.0208	1.53	up	Mus musculus pleckstrin homology domain containing, family 8 (phosphoinositide binding specific) member 8 (Plekha8), transcript variant 1, mRNA [NM_001164361]	NM_001164361
Mum111	0.0422	6.40	up	Mus musculus melanoma associated antigen (mutated) 1-like 1 (Mum111), transcript variant 1, mRNA [NM_001164630]	NM_001164630
LOC100038947	0.0361	1.72	up	Mus musculus signal-regulatory protein beta 1-like (LOC100038947), mRNA [NM_001173459]	NM_001173459
Gm13138	0.0150	2.61	up	Mus musculus predicted gene 13138 (Gm13138), mRNA [NM_001177767]	NM_001177767
Chrna1	0.0042	2.04	up	Mus musculus cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle) (Chrna1), mRNA [NM_007389]	NM_007389
Ccne1	0.0038	2.35	up	Mus musculus cyclin E1 (Ccne1), mRNA [NM_007633]	NM_007633
Ncan	0.0390	6.36	up	Mus musculus neurocan (Ncan), mRNA [NM_007789]	NM_007789
Dhcr7	0.0140	1.62	up	Mus musculus 7-dehydrocholesterol reductase (Dhcr7), mRNA [NM_007856]	NM_007856
F2rl3	0.0128	1.91	up	Mus musculus coagulation factor II (thrombin) receptor-like 3 (F2rl3), mRNA [NM_007975]	NM_007975
Golga3	0.0354	1.61	up	Mus musculus golgi autoantigen, golgin subfamily a, 3 (Golga3), mRNA [NM_008146]	NM_008146
Igfals	0.0285	2.26	up	Mus musculus insulin-like growth factor binding protein, acidic labile subunit (Igfals), mRNA [NM_008340]	NM_008340
Lep	0.0199	3.03	up	Mus musculus leptin (Lep), mRNA [NM_008493]	NM_008493
Mest	0.0169	7.04	up	Mus musculus mesoderm specific transcript (Mest), mRNA [NM_008590]	NM_008590
Mest	0.0111	6.85	up	Mus musculus mesoderm specific transcript (Mest), mRNA [NM_008590]	NM_008590
Mest	0.0093	6.10	up	Mus musculus mesoderm specific transcript (Mest), mRNA [NM_008590]	NM_008590
Orm1	0.0378	4.17	up	Mus musculus orosomucoid 1 (Orm1), mRNA [NM_008768]	NM_008768
Pde7a	0.0007	2.09	up	Mus musculus phosphodiesterase 7A (Pde7a), transcript variant 1, mRNA [NM_008802]	NM_008802

Rrm2	0.0365	1.83	up	Mus musculus ribonucleotide reductase M2 (Rrm2), mRNA [NM_009104]	NM_009104
Sag	0.0412	2.62	up	Mus musculus retinal S-antigen (Sag), mRNA [NM_009118]	NM_009118
Shc3	0.0383	2.06	up	Mus musculus src homology 2 domain-containing transforming protein C3 (Shc3), mRNA [NM_009167]	NM_009167
Tg	0.0186	2.73	up	Mus musculus thyroglobulin (Tg), mRNA [NM_009375]	NM_009375
Tk1	0.0213	2.16	up	Mus musculus thymidine kinase 1 (Tk1), mRNA [NM_009387]	NM_009387
Tubb4	0.0262	1.55	up	Mus musculus tubulin, beta 4 (Tubb4), mRNA [NM_009451]	NM_009451
Neurog3	0.0178	2.73	up	Mus musculus neurogenin 3 (Neurog3), mRNA [NM_009719]	NM_009719
Dio2	0.0021	2.47	up	Mus musculus deiodinase, iodothyronine, type II (Dio2), mRNA [NM_010050]	NM_010050
Fgf13	0.0142	6.26	up	Mus musculus fibroblast growth factor 13 (Fgf13), mRNA [NM_010200]	NM_010200
Ghrh	0.0138	2.55	up	Mus musculus growth hormone releasing hormone (Ghrh) mRNA [NM_010285]	NM_010285
Kcnk3	0.0494	2.01	up	Mus musculus potassium channel, subfamily K, member 3 (Kcnk3), mRNA [NM_010608]	NM_010608
Melk	0.0032	2.37	up	Mus musculus maternal embryonic leucine zipper kinase (Melk) mRNA [NM_010790]	NM_010790
Myl4	0.0114	2.30	up	Mus musculus myosin, light polypeptide 4 (Myl4), mRNA [NM_010858]	NM_010858
Tnfrsf9	0.0358	1.79	up	Mus musculus tumor necrosis factor receptor superfamily, member 9 (Tnfrsf9), transcript variant 1, mRNA [NM_011612]	NM_011612
Traip	0.0061	2.84	up	Mus musculus TRAF-interacting protein (Traip), mRNA [NM_011634]	NM_011634
Tuba1b	0.0257	1.96	up	Mus musculus tubulin, alpha 1B (Tuba1b), mRNA [NM_011654]	NM_011654
Wnt8b	0.0379	2.27	up	Mus musculus wingless related MMTV integration site 8b (Wnt8b), mRNA [NM_011720]	NM_011720
Cdc6	0.0287	1.57	up	Mus musculus cell division cycle 6 homolog (S. cerevisiae) (Cdc6), transcript variant 1, mRNA [NM_011799]	NM_011799

Pla2g2e	0.0357	5.07	up	Mus musculus phospholipase A2, group IIE (Pla2g2e), mRNA [NM_012044]	NM_012044
Pla2g2e	0.0277	4.53	up	Mus musculus phospholipase A2, group IIE (Pla2g2e), mRNA [NM_012044]	NM_012044
Apoh	0.0186	10.62	up	Mus musculus apolipoprotein H (Apoh), mRNA [NM_013475]	NM_013475
Htr3a	0.0113	2.15	up	Mus musculus 5-hydroxytryptamine (serotonin) receptor 3A (Htr3a), transcript variant 1, mRNA [NM_013561]	NM_013561
Kcnh2	0.0131	2.22	up	Mus musculus potassium voltage-gated channel, subfamily H (eag-related), member 2 (Kcnh2), mRNA [NM_013569]	NM_013569
Rtn2	0.0404	1.66	up	Mus musculus reticulon 2 (Z-band associated protein) (Rtn2), transcript variant B, mRNA [NM_013648]	NM_013648
S100a8	0.0143	4.73	up	Mus musculus S100 calcium binding protein A8 (calgranulin A) (S100a8), mRNA [NM_013650]	NM_013650
Sema3c	0.0293	1.82	up	Mus musculus sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C (Sema3c), mRNA [NM_013657]	NM_013657
Gtse1	0.0326	6.11	up	Mus musculus G two S phase expressed protein 1 (Gtse1), transcript variant 2, mRNA [NM_013882]	NM_013882
Apln	0.0087	2.25	up	Mus musculus apelin (Apln), mRNA [NM_013912]	NM_013912
Bhmt	0.0426	8.80	up	Mus musculus betaine-homocysteine methyltransferase (Bhmt) mRNA [NM_016668]	NM_016668
Bhmt	0.0411	9.15	up	Mus musculus betaine-homocysteine methyltransferase (Bhmt) mRNA [NM_016668]	NM_016668
Fanca	0.0266	2.52	up	Mus musculus Fanconi anemia, complementation group A (Fanca), mRNA [NM_016925]	NM_016925
Pcdh12	0.0245	1.55	up	Mus musculus protocadherin 12 (Pcdh12), mRNA [NM_017378]	NM_017378
Dfna5	0.0351	3.79	up	Mus musculus deafness, autosomal dominant 5 (human) (Dfna5), mRNA [NM_018769]	NM_018769
Sfrp5	0.0024	6.86	up	Mus musculus secreted frizzled-related sequence protein 5 (Sfrp5), mRNA [NM_018780]	NM_018780

Nup210	0.0245	2.14	up	Mus musculus nucleoporin 210 (Nup210), mRNA [NM_018815]	NM_018815
Olfm1	0.0491	2.47	up	Mus musculus olfactomedin 1 (Olfm1), transcript variant 1, mRNA [NM_019498]	NM_019498
Acss2	0.0256	3.88	up	Mus musculus acyl-CoA synthetase short-chain family member 2 (Acss2), mRNA [NM_019811]	NM_019811
Fgf21	0.0109	6.09	up	Mus musculus fibroblast growth factor 21 (Fgf21), mRNA [NM_020013]	NM_020013
Nqo2	0.0273	1.57	up	Mus musculus NAD(P)H dehydrogenase, quinone 2 (Nqo2), transcript variant 1, mRNA [NM_020282]	NM_020282
Fzd3	0.0354	1.61	up	Mus musculus frizzled homolog 3 (Drosophila) (Fzd3), mRNA [NM_021458]	NM_021458
F12	0.0154	5.51	up	Mus musculus coagulation factor XII (Hageman factor) (F12), mRNA [NM_021489]	NM_021489
Slc5a7	0.0071	76.21	up	Mus musculus solute carrier family 5 (choline transporter), member 7 (Slc5a7), mRNA [NM_022025]	NM_022025
Cyp4f14	0.0189	1.53	up	Mus musculus cytochrome P450, family 4, subfamily f, polypeptide 14 (Cyp4f14), mRNA [NM_022434]	NM_022434
2310016C08Rik	0.0205	2.69	up	Mus musculus RIKEN cDNA 2310016C08 gene (2310016C08Rik), transcript variant 2, mRNA [NM_023516]	NM_023516
2310016C08Rik	0.0212	2.69	up	Mus musculus RIKEN cDNA 2310016C08 gene (2310016C08Rik), transcript variant 2, mRNA [NM_023516]	NM_023516
Capn9	0.0164	1.83	up	Mus musculus calpain 9 (Capn9), mRNA [NM_023709]	NM_023709
Kif23	0.0261	3.18	up	Mus musculus kinesin family member 23 (Kif23), mRNA [NM_024245]	NM_024245
Spc25	0.0338	3.28	up	Mus musculus SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae) (Spc25), mRNA [NM_025565]	NM_025565
Ptgr1	0.0352	1.66	up	Mus musculus prostaglandin reductase 1 (Ptgr1), mRNA [NM_025968]	NM_025968
Nrarp	0.0153	2.49	up	Mus musculus Notch-regulated ankyrin repeat protein (Nrarp), mRNA [NM_025980]	NM_025980

Qpctl	0.0354	1.92	up	Mus musculus glutaminyl-peptide cyclotransferase-like (Qpctl) mRNA [NM_026111]	NM_026111
Pdlim7	0.0358	1.68	up	Mus musculus PDZ and LIM domain 7 (Pdlim7), transcript variant c, mRNA [NM_026131]	NM_026131
Lipf	0.0014	10.77	up	Mus musculus lipase, gastric (Lipf), mRNA [NM_026334]	NM_026334
Ndufb2	0.0365	3.27	up	Mus musculus NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 (Ndufb2), nuclear gene encoding mitochondrial protein, mRNA [NM_026612]	NM_026612
Mcoln2	0.0093	1.58	up	Mus musculus mucolipin 2 (Mcoln2), transcript variant 1, mRNA [NM_026656]	NM_026656
Ube2c	0.0300	2.60	up	Mus musculus ubiquitin-conjugating enzyme E2C (Ube2c), mRNA [NM_026785]	NM_026785
1110059M19Rik	0.0246	3.48	up	Mus musculus RIKEN cDNA 1110059M19 gene (1110059M19Rik), mRNA [NM_026841]	NM_026841
1700113I22Rik	0.0044	1.85	up	Mus musculus RIKEN cDNA 1700113I22 gene (1700113I22Rik), mRNA [NM_026865]	NM_026865
Ubap2	0.0306	1.56	up	Mus musculus ubiquitin-associated protein 2 (Ubap2), mRNA [NM_026872]	NM_026872
Ccdc99	0.0398	2.16	up	Mus musculus coiled-coil domain containing 99 (Ccdc99), mRNA [NM_027411]	NM_027411
Tmem144	0.0182	1.55	up	Mus musculus transmembrane protein 144 (Tmem144), mRNA [NM_027495]	NM_027495
Mlf1ip	0.0267	4.53	up	Mus musculus myeloid leukemia factor 1 interacting protein (Mlf1ip), mRNA [NM_027973]	NM_027973
Fam83d	0.0015	4.63	up	Mus musculus family with sequence similarity 83, member E (Fam83d), mRNA [NM_027975]	NM_027975
Paqr7	0.0029	1.65	up	Mus musculus progesterone and adipoQ receptor family member VII (Paqr7), mRNA [NM_027995]	NM_027995
3110082D06Rik	0.0090	4.82	up	Mus musculus RIKEN cDNA 3110082D06 gene (3110082D06Rik), mRNA [NM_028474]	NM_028474
2410076I21Rik	0.0009	2.33	up	Mus musculus RIKEN cDNA 2410076I21 gene (2410076I21Rik), mRNA [NM_028598]	NM_028598

Acox1	0.0272	3.29	up	Mus musculus acyl-Coenzyme A oxidase-like (Acox1), mRNA [NM_028765]	NM_028765
Acox1	0.0007	5.03	up	Mus musculus acyl-Coenzyme A oxidase-like (Acox1), mRNA [NM_028765]	NM_028765
Spinlw1	0.0284	10.85	up	Mus musculus serine protease inhibitor-like, with Kunitz and WAP domains 1 (eppin) (Spinlw1), mRNA [NM_029325]	NM_029325
Dapl1	0.0431	9.03	up	Mus musculus death associated protein-like 1 (Dapl1), mRNA [NM_029723]	NM_029723
Gsdma2	0.0098	2.80	up	Mus musculus gasdermin A2 (Gsdma2), mRNA [NM_029727]	NM_029727
Slc10a7	0.0300	1.97	up	Mus musculus solute carrier family 10 (sodium/bile acid cotransporter family), member 7 (Slc10a7), mRNA [NM_029736]	NM_029736
Pramef12	0.0373	2.39	up	Mus musculus PRAME family member 12 (Pramef12), mRNA [NM_029948]	NM_029948
Ulbp1	0.0160	1.59	up	Mus musculus UL16 binding protein 1 (Ulbp1), mRNA [NM_029975]	NM_029975
Snrnp25	0.0090	1.76	up	Mus musculus small nuclear ribonucleoprotein 25 (U11/U12) (Snrnp25), mRNA [NM_030093]	NM_030093
Snrnp25	0.0105	1.74	up	Mus musculus small nuclear ribonucleoprotein 25 (U11/U12) (Snrnp25), mRNA [NM_030093]	NM_030093
Troap	0.0175	2.27	up	Mus musculus trophinin associated protein (Troap), transcript variant 1, mRNA [NM_030159]	NM_030159
Fam20c	0.0299	2.74	up	Mus musculus family with sequence similarity 20, member C (Fam20c), mRNA [NM_030565]	NM_030565
Slco1a4	0.0314	1.50	up	Mus musculus solute carrier organic anion transporter family, member 1a4 (Slco1a4), mRNA [NM_030687]	NM_030687
Fstl3	0.0089	1.51	up	Mus musculus follistatin-like 3 (Fstl3), mRNA [NM_031380]	NM_031380
Cela1	0.0008	3.61	up	Mus musculus chymotrypsin-like elastase family, member 1 (Cela1), mRNA [NM_033612]	NM_033612
Csprs	0.0347	1.75	up	Mus musculus component of Sp100-rs (Csprs), mRNA [NM_033616]	NM_033616

Trim16	0.0122	1.54	up	Mus musculus tripartite motif-containing 16 (Trim16), mRNA [NM_053169]	NM_053169
Tle6	0.0448	1.51	up	Mus musculus transducin-like enhancer of split 6, homolog of Drosophila E(spl) (Tle6), mRNA [NM_053254]	NM_053254
Dhcr24	0.0213	1.65	up	Mus musculus 24-dehydrocholesterol reductase (Dhcr24), mRNA [NM_053272]	NM_053272
Hist2h3c2-ps	0.0238	3.06	up	Mus musculus histone cluster 2, H3c2, pseudogene (Hist2h3c2 ps), mRNA [NM_054045]	NM_054045
Synpo2	0.0064	2.84	up	Mus musculus synaptopodin 2 (Synpo2), mRNA [NM_080451]	NM_080451
Metrn	0.0277	1.66	up	Mus musculus meteorin, glial cell differentiation regulator (Metrn), mRNA [NM_133719]	NM_133719
Hrh3	0.0406	1.85	up	Mus musculus histamine receptor H3 (Hrh3), mRNA [NM_133849]	NM_133849
Sdsl	0.0403	2.39	up	Mus musculus serine dehydratase-like (Sdsl), mRNA [NM_133902]	NM_133902
Fam64a	0.0334	3.66	up	Mus musculus family with sequence similarity 64, member A (Fam64a), mRNA [NM_144526]	NM_144526
Ncaph	0.0496	1.58	up	Mus musculus non-SMC condensin I complex, subunit H (Ncaph), mRNA [NM_144818]	NM_144818
Crtac1	0.0034	4.84	up	Mus musculus cartilage acidic protein 1 (Crtac1), mRNA [NM_145123]	NM_145123
Duoxa1	0.0014	5.99	up	Mus musculus dual oxidase maturation factor 1 (Duoxa1), mRNA [NM_145395]	NM_145395
Duoxa1	0.0124	3.10	up	Mus musculus dual oxidase maturation factor 1 (Duoxa1), mRNA [NM_145395]	NM_145395
Lctl	0.0088	4.65	up	Mus musculus lactase-like (Lctl), mRNA [NM_145835]	NM_145835
Cenpi	0.0054	3.33	up	Mus musculus centromere protein I (Cenpi), mRNA [NM_145924]	NM_145924
Kcnj14	0.0208	6.43	up	Mus musculus potassium inwardly-rectifying channel, subfamily J, member 14 (Kcnj14), mRNA [NM_145963]	NM_145963
Krt79	0.0001	2.84	up	Mus musculus keratin 79 (Krt79), mRNA [NM_146063]	NM_146063

Tdrd7	0.0164	1.53	up	Mus musculus tudor domain containing 7 (Tdrd7), mRNA [NM_146142]	NM_146142
Olfr532	0.0226	1.51	up	Mus musculus olfactory receptor 532 (Olfr532), mRNA [NM_147026]	NM_147026
Unc5a	0.0350	1.89	up	Mus musculus unc-5 homolog A (C. elegans) (Unc5a), mRNA [NM_153131]	NM_153131
Slc36a1	0.0021	1.55	up	Mus musculus solute carrier family 36 (proton/amino acid symporter), member 1 (Slc36a1), mRNA [NM_153139]	NM_153139
Insig1	0.0154	2.37	up	Mus musculus insulin induced gene 1 (Insig1), mRNA [NM_153526]	NM_153526
Lrrc66	0.0495	1.77	up	Mus musculus leucine rich repeat containing 66 (Lrrc66), mRNA [NM_153568]	NM_153568
BC030307	0.0048	2.40	up	Mus musculus cDNA sequence BC030307 (BC030307), transcript variant 2, mRNA [NM_153595]	NM_153595
Mapk4	0.0418	4.70	up	Mus musculus mitogen-activated protein kinase 4 (Mapk4), mRNA [NM_172632]	NM_172632
Coq3	0.0346	1.65	up	Mus musculus coenzyme Q3 homolog, methyltransferase (yeast) (Coq3), mRNA [NM_172687]	NM_172687
Otop1	0.0318	3.19	up	Mus musculus otopenin 1 (Otop1), mRNA [NM_172709]	NM_172709
Adap1	0.0484	1.79	up	Mus musculus ArfGAP with dual PH domains 1 (Adap1), mRNA [NM_172723]	NM_172723
Ankle1	0.0301	2.25	up	Mus musculus ankyrin repeat and LEM domain containing 1 (Ankle1), mRNA [NM_172756]	NM_172756
Malt1	0.0297	1.52	up	Mus musculus mucosa associated lymphoid tissue lymphoma translocation gene 1 (Malt1), mRNA [NM_172833]	NM_172833
Rgp1	0.0069	1.78	up	Mus musculus RGP1 retrograde golgi transport homolog (S. cerevisiae) (Rgp1), mRNA [NM_172866]	NM_172866
Pfkfb4	0.0170	2.14	up	Mus musculus 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 (Pfkfb4), mRNA [NM_173019]	NM_173019
Insc	0.0452	2.26	up	Mus musculus inscuteable homolog (Drosophila) (Insc), mRNA [NM_173767]	NM_173767

6720463M24Rik	0.0382	2.30	up	Mus musculus RIKEN cDNA 6720463M24 gene (6720463M24Rik), mRNA [NM_175265]	NM_175265
Als2cr12	0.0048	1.73	up	Mus musculus amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 12 (human) (Als2cr12), mRNA [NM_175370]	NM_175370
Hist1h2ab	0.0447	1.55	up	Mus musculus histone cluster 1, H2ab (Hist1h2ab), mRNA [NM_175660]	NM_175660
Tmem91	0.0195	1.74	up	Mus musculus transmembrane protein 91 (Tmem91), mRNA [NM_177102]	NM_177102
Senp5	0.0336	1.52	up	Mus musculus SUMO/sentrin specific peptidase 5 (Senp5), mRNA [NM_177103]	NM_177103
Cyp2r1	0.0156	1.73	up	Mus musculus cytochrome P450, family 2, subfamily r, polypeptide 1 (Cyp2r1), mRNA [NM_177382]	NM_177382
Slc41a2	0.0496	1.96	up	Mus musculus solute carrier family 41, member 2 (Slc41a2), mRNA [NM_177388]	NM_177388
Mogat2	0.0004	9.47	up	Mus musculus monoacylglycerol O-acyltransferase 2 (Mogat2), mRNA [NM_177448]	NM_177448
Ryr3	0.0304	2.25	up	Mus musculus ryanodine receptor 3 (Ryr3), mRNA [NM_177652]	NM_177652
C130079G13Rik	0.0098	6.80	up	Mus musculus RIKEN cDNA C130079G13 gene (C130079G13Rik), mRNA [NM_177661]	NM_177661
D3Bwg0562e	0.0106	6.26	up	Mus musculus DNA segment, Chr 3, Brigham & Women's Genetics 0562 expressed (D3Bwg0562e), mRNA [NM_177664]	NM_177664
Hist1h2ak	0.0392	1.89	up	Mus musculus histone cluster 1, H2ak (Hist1h2ak), mRNA [NM_178183]	NM_178183
Hist1h2ag	0.0488	1.77	up	Mus musculus histone cluster 1, H2ag (Hist1h2ag), mRNA [NM_178186]	NM_178186
Hist2h3c1	0.0088	2.55	up	Mus musculus histone cluster 2, H3c1 (Hist2h3c1), mRNA [NM_178216]	NM_178216
Cenpm	0.0201	2.39	up	Mus musculus centromere protein M (Cenpm), transcript variant 2, mRNA [NM_178269]	NM_178269

Car12	0.0168	3.72	up	Mus musculus carbonic anhydrase 12 (Car12), mRNA [NM_178396]	NM_178396
Ints7	0.0207	1.57	up	Mus musculus integrator complex subunit 7 (Ints7), mRNA [NM_178632]	NM_178632
Mapk1ip1l	0.0004	3.11	up	Mus musculus mitogen-activated protein kinase 1 interacting protein 1-like (Mapk1ip1l), mRNA [NM_178684]	NM_178684
Prune2	0.0418	1.81	up	Mus musculus prune homolog 2 (Drosophila) (Prune2), mRNA [NM_181348]	NM_181348
Optn	0.0275	3.30	up	Mus musculus optineurin (Optn), mRNA [NM_181848]	NM_181848
Poln	0.0236	3.57	up	Mus musculus DNA polymerase N (Poln), mRNA [NM_181857]	NM_181857
Poln	0.0128	3.15	up	Mus musculus DNA polymerase N (Poln), mRNA [NM_181857]	NM_181857
Defb14	0.0010	11.80	up	Mus musculus defensin beta 14 (Defb14), mRNA [NM_183026]	NM_183026
Fam19a3	0.0130	2.54	up	Mus musculus family with sequence similarity 19, member A3 (Fam19a3), mRNA [NM_183224]	NM_183224
Paqr9	0.0075	6.71	up	Mus musculus progesterone and adipoQ receptor family member IX (Paqr9), mRNA [NM_198414]	NM_198414
Gse1	0.0275	1.65	up	Mus musculus genetic suppressor element 1 (Gse1), transcript variant 1, mRNA [NM_198671]	NM_198671
Hn1l	0.0468	1.83	up	Mus musculus hematological and neurological expressed 1-like (Hn1l), mRNA [NM_198937]	NM_198937
Ssxb9	0.0073	1.68	up	Mus musculus synovial sarcoma, X member B, breakpoint 9 (Ssxb9), mRNA [NM_199066]	NM_199066
Bpil3	0.0087	5.49	up	Mus musculus bactericidal/permeability-increasing protein-like 3 (Bpil3), mRNA [NM_199303]	NM_199303
Sly	0.0310	10.41	up	Mus musculus Sycp3 like Y-linked (Sly), mRNA [NM_201530]	NM_201530
Sly	0.0218	9.39	up	Mus musculus Sycp3 like Y-linked (Sly), mRNA [NM_201530]	NM_201530

Gm7337	0.0465	1.97	up	Mus musculus predicted gene 7337 (Gm7337), non-coding RNA [NR_003652]	NR_003652
9430008C03Rik	0.0053	1.59	up	Mus musculus RIKEN cDNA 9430008C03 gene (9430008C03Rik), transcript variant 1, non-coding RNA [NR_015463]	NR_015463
Gm5627	0.0015	8.01	up	Mus musculus predicted gene 5627 (Gm5627), non-coding RNA [NR_033301]	NR_033301
Gm6225	0.0419	1.58	up	Mus musculus predicted gene 6225 (Gm6225), non-coding RNA [NR_033457]	NR_033457
LOC100039005	0.0073	4.47	up	PREDICTED: Mus musculus similar to pol protein (LOC100039005), mRNA [XM_001472072]	XM_001472072
Gm2305	0.0062	4.73	up	PREDICTED: Mus musculus hypothetical protein LOC100039548 (LOC100039548), mRNA [XM_001473102]	XM_001473102
Gm2312	0.0124	1.58	up	PREDICTED: Mus musculus similar to ZK84.1 (LOC100039562), mRNA [XM_001473116]	XM_001473116
Gm2366	0.0091	2.17	up	PREDICTED: Mus musculus hypothetical protein LOC100039673 (LOC100039673), mRNA [XM_001473124]	XM_001473124
Gm7969	0.0199	2.35	up	PREDICTED: Mus musculus hypothetical LOC666185 (LOC666185), mRNA [XM_001473218]	XM_001473218
Gm7969	0.0289	1.84	up	PREDICTED: Mus musculus hypothetical LOC666185 (LOC666185), mRNA [XM_001473218]	XM_001473218
	0.0494	6.71	up	RIKEN cDNA 1700066J24 gene Gene [Source:MGI Symbol;Acc:MGI:1924242] [ENSMUST00000038960]	XM_001473370
LOC100039839	0.0477	10.19	up	PREDICTED: Mus musculus similar to Syp3 like Y-linked (LOC100039839), mRNA [XM_001473640]	XM_001473640
Gm2379	0.0492	1.76	up	PREDICTED: Mus musculus similar to F36H12.3 (LOC100039704), mRNA [XM_001473765]	XM_001473765
LOC100045319	0.0040	2.80	up	PREDICTED: Mus musculus hypothetical protein LOC100045319 (LOC100045319), mRNA [XM_001474051]	XM_001474051

LOC100043999	0.0323	3.05	up	PREDICTED: Mus musculus hypothetical protein LOC100043999 (LOC100043999), mRNA [XM_001474157]	XM_001474157
Gm2650	0.0367	3.28	up	PREDICTED: Mus musculus hypothetical protein LOC100040184 (LOC100040184), mRNA [XM_001474283]	XM_001474283
LOC100045638	0.0089	1.84	up	PREDICTED: Mus musculus hypothetical protein LOC100045638 (LOC100045638), mRNA [XM_001474652]	XM_001474652
Gm14635	0.0381	3.75	up	PREDICTED: Mus musculus hypothetical protein LOC100045847 (LOC100045847), mRNA [XM_001475018]	XM_001475018
Gm2942	0.0115	2.18	up	PREDICTED: Mus musculus hypothetical protein LOC100040747 (LOC100040747), mRNA [XM_001475175]	XM_001475175
	0.0339	1.52	up	RIKEN cDNA 1700036A12 gene Gene [Source:MGI Symbol;Acc:MGI:1920548] [ENSMUST00000064351]	XM_001475271
Gm3014	0.0008	2.09	up	PREDICTED: Mus musculus similar to CG2839-PA (LOC100040872), mRNA [XM_001475360]	XM_001475360
	0.0228	1.88	up	RIKEN cDNA 5830477G23 gene Gene [Source:MGI Symbol;Acc:MGI:1923366] [ENSMUST00000115745]	XM_001476159
Gm10621	0.0027	1.73	up	Putative uncharacterized protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q3U2L9] [ENSMUST00000098384]	XM_001476249
Gm3367	0.0324	3.65	up	PREDICTED: Mus musculus hypothetical protein LOC100041489 (LOC100041489), mRNA [XM_001476471]	XM_001476471
LOC100047220	0.0374	2.39	up	PREDICTED: Mus musculus similar to kappa immunoglobulin (subgroup V kappa I) (LOC100047220), mRNA [XM_001476561]	XM_001476561

Gm5957	0.0196	2.99	up	PREDICTED: Mus musculus similar to High mobility group protein B2 (High mobility group protein 2) (HMG-2) (LOC546590), mRNA [XM_001476729]	XM_001476729
Gm3586	0.0169	12.22	up	PREDICTED: Mus musculus hypothetical protein LOC100041950 (LOC100041950), mRNA [XM_001477872]	XM_001477872
Gm5556	0.0076	2.29	up	PREDICTED: Mus musculus hypothetical LOC433894 (LOC433894), mRNA [XM_001478331]	XM_001478331
Gm3983	0.0446	3.57	up	PREDICTED: Mus musculus hypothetical protein LOC100042713 (LOC100042713), mRNA [XM_001478663]	XM_001478663
LOC100047647	0.0021	1.59	up	nudix (nucleotide diphosphate linked moiety X)-type motif 3 Gene [Source:MGI (curated);Acc:MGI:1928484] [ENSMUST00000114886]	XM_001478680
LOC100047746	0.0382	3.15	up	PREDICTED: Mus musculus hypothetical protein LOC100047746 (LOC100047746), mRNA [XM_001478751]	XM_001478751
Gm6567	0.0233	1.99	up	PREDICTED: Mus musculus hypothetical protein LOC625243 (LOC625243), mRNA [XM_001479033]	XM_001479033
LOC100048016	0.0128	2.83	up	PREDICTED: Mus musculus similar to allergen dI chain C2C (LOC100048016), mRNA [XM_001479348]	XM_001479348
	0.0201	1.78	up	predicted gene 11046 Gene [Source:MGI Symbol;Acc:MGI:3782477] [ENSMUST00000103587]	XM_001479512
LOC546233	0.0409	1.66	up	PREDICTED: Mus musculus hypothetical LOC546233 (LOC546233), mRNA [XM_001479766]	XM_001479766
LOC100048615	0.0382	1.80	up	PREDICTED: Mus musculus hypothetical protein LOC100048615 (LOC100048615), mRNA [XM_001480399]	XM_001480399
Gm4641	0.0477	3.09	up	PREDICTED: Mus musculus hypothetical protein LOC100043778 (LOC100043778), mRNA [XM_001480938]	XM_001480938

Gm4703	0.0365	2.04	up	PREDICTED: Mus musculus hypothetical protein LOC100043874 (LOC100043874), mRNA [XM_001481156]	XM_001481156
LOC620515	0.0193	2.05	up	PREDICTED: Mus musculus similar to secretory protein (LOC620515), mRNA [XM_884904]	XM_884904
Gm6611	0.0351	3.60	up	PREDICTED: Mus musculus predicted gene, EG625660 (EG625660), mRNA [XM_894394]	XM_894394
	0.0319	1.54	up	Putative uncharacterized proteinMGC58416 protein ; [Source:UniProtKB/TrEMBL;Acc:Q8BIG3] [ENSMUST00000062524]	XM_897445
Gm7000	0.0362	2.04	up	PREDICTED: Mus musculus predicted gene, EG629739 (EG629739), mRNA [XM_901778]	XM_901778
Gm7303	0.0313	1.75	up	PREDICTED: Mus musculus predicted gene, EG640636 (EG640636), mRNA [XM_925112]	XM_925112
Gm8028	0.0193	5.01	up	PREDICTED: Mus musculus predicted gene, EG666293 (EG666293), mRNA [XM_977531]	XM_977531
	0.0285	10.29	up	LOC380994 protein [Source:UniProtKB/TrEMBL;Acc:Q4KL07] [ENSMUST00000115920]	XM_979799
A830035A12Rik	0.0308	1.56	up	PREDICTED: Mus musculus RIKEN cDNA A830035A12 gene (A830035A12Rik), mRNA [XM_986896]	XM_986896
LOC675962	0.0450	1.87	up	PREDICTED: Mus musculus similar to Tdpz5 protein (LOC675962), misc RNA [XR_004857]	XR_004857
Gm8956	0.0172	2.61	up	PREDICTED: Mus musculus similar to ubiquitin-conjugating enzyme E2C (LOC668063), misc RNA [XR_030853]	XR_030853
LOC100040245	0.0413	10.29	up	PREDICTED: Mus musculus similar to Sycp3 like Y-linked (LOC100040245), misc RNA [XR_031612]	XR_031612
Gm12813	0.0401	2.38	up	PREDICTED: Mus musculus hypothetical protein LOC100040607 (LOC100040607), misc RNA [XR_032022]	XR_032022
Gm9643	0.0107	1.52	up	PREDICTED: Mus musculus similar to TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa (LOC675463), misc RNA [XR_032212]	XR_032212

Gm3711	0.0255	1.77	up	PREDICTED: Mus musculus similar to Zbed4 protein (LOC100042188), misc RNA [XR_033357]	XR_033357
Gm8126	0.0357	3.47	up	PREDICTED: Mus musculus hypothetical LOC666481 (LOC666481), misc RNA [XR_033489]	XR_033489
AI852580	0.0356	3.68	down	UI-M-BH0-aiu-a-10-0-UI.s1 NIH_BMAP_M_S1 Mus musculus cDNA clone UI-M-BH0-aiu-a-10-0-UI 3'. [AI852580]	AI852580
Sned1	0.0264	2.11	down	sushi, nidogen and EGF-like domains 1 Gene [Source:MGI;Symbol;Acc:MGI:3045960] [ENSMUST00000062202]	AJ584850
1300014J16Rik	0.0259	1.99	down	Mus musculus adult male liver cDNA, RIKEN full-length enriched library, clone:1300014J16 product:unclassifiable, full insert sequence. [AK005005]	AK005005
2210416O15Rik	0.0367	1.84	down	Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210416O15 product:hypothetical protein, full insert sequence. [AK008958]	AK008958
	0.0289	2.37	down	RIKEN cDNA 6530402F18 gene Gene [Source:MGI;Symbol;Acc:MGI:1923470] [ENSMUST00000028141]	AK018312
D330022H12Rik	0.0472	1.72	down	Mus musculus 13 days embryo heart cDNA, RIKEN full-length enriched library, clone:D330022H12 product:unclassifiable, full insert sequence. [AK021285]	AK021285
	0.0003	2.41	down	RIKEN cDNA D730003I15 gene Gene [Source:MGI;Symbol;Acc:MGI:1925971] [ENSMUST00000097438]	AK021325
Usp27x	0.0043	1.60	down	ubiquitin specific peptidase 27, X chromosome Gene [Source:MGI (curated);Acc:MGI:1859645] [ENSMUST00000066557]	AK028249
9530048J24Rik	0.0459	1.96	down	Mus musculus 15 days embryo male testis cDNA, RIKEN full-length enriched library, clone:8030444H24 product:unclassifiable, full insert sequence. [AK033136]	AK033136
	0.0302	2.04	down	tyrosyl-DNA phosphodiesterase 1 Gene [Source:MGI (curated);Acc:MGI:1920036] [ENSMUST00000095477]	AK033868

9530009M10Rik	0.0404	2.04	down	Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530009M10 product:unclassifiable, full insert sequence. [AK035285]	AK035285
2410024N18Rik	0.0350	2.81	down	Mus musculus adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530073H14 product:unclassifiable full insert sequence. [AK035593]	AK035593
A130033P14	0.0367	1.83	down	Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130033P14 product:unclassifiable, full insert sequence. [AK037654]	AK037654
	0.0094	2.40	down	Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130071C16 product:hypothetical protein, full insert sequence. [AK038006]	AK038006
A330062J17Rik	0.0350	1.68	down	Mus musculus adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330062J17 product:unclassifiable, full insert sequence. [AK039561]	AK039561
A330106F07Rik	0.0267	1.57	down	Mus musculus adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330106F07 product:unclassifiable, full insert sequence. [AK039774]	AK039774
A530020G20Rik	0.0433	3.86	down	Mus musculus adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A530051K04 product:unclassifiable, full insert sequence. [AK040960]	AK040960
	0.0356	1.60	down	paired immunoglobulin-like type 2 receptor alpha Gene [Source:MGI (curated);Acc:MGI:2450529] [ENSMUST00000110980]	AK041413
	0.0160	1.67	down	CDC23 (cell division cycle 23, yeast, homolog) Gene [Source:MGI (curated);Acc:MGI:1098815] [ENSMUST00000055365]	AK044478
9630028H03Rik	0.0492	2.46	down	Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230095N21 product:unclassifiable, full insert sequence. [AK049057]	AK049057

Gm13032	0.0041	2.48	down	Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:C330016E12 product:unclassifiable, full insert sequence. [AK049241]	AK049241
Slc16a14	0.0382	1.92	down	solute carrier family 16 (monocarboxylic acid transporters), member 14 Gene [Source:MGI Symbol;Acc:MGI:1919031] [ENSMUST00000027422]	AK049846
	0.0394	1.68	down	ankyrin repeat and SOCS box-containing 7 Gene [Source:MGI (curated);Acc:MGI:2152835] [ENSMUST00000068980]	AK051017
LOC433461	0.0273	1.86	down	Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D230021J12 product:unclassifiable, full insert sequence. [AK051942]	AK051942
	0.0112	1.65	down	transmembrane protein 161B Gene [Source:MGI Symbol;Acc:MGI:1919995] [ENSMUST00000050885]	AK051974
	0.0072	2.90	down	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:B0G0X9] [ENSMUST00000061914]	AK052046
E030046B03Rik	0.0233	4.13	down	Mus musculus 0 day neonate lung cDNA, RIKEN full-length enriched library, clone:E030046B03 product:unclassifiable, full insert sequence. [AK053225]	AK053225
E230006M18Rik	0.0423	1.56	down	Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN full-length enriched library, clone:E230006M18 product:unclassifiable, full insert sequence. [AK053951]	AK053951
	0.0075	1.66	down	RIKEN cDNA 4930417O22 gene Gene [Source:MGI Symbol;Acc:MGI:1921137] [ENSMUST00000078285]	AK076700
Wdr38	0.0179	1.79	down	WD repeat domain 38 Gene [Source:MGI (curated);Acc:MGI:1923896] [ENSMUST00000039535]	AK077027
	0.0210	2.19	down	WD repeat domain 61 Gene [Source:MGI (curated);Acc:MGI:1917493] [ENSMUST00000118771]	AK077037
LOC100038759	0.0345	1.68	down	Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130018J17 product:hypothetical protein, full insert sequence. [AK081449]	AK081449

	0.0043	2.77	down	dynein, axonemal, heavy chain 9 Gene [Source:MGI (curated);Acc:MGI:1289279] [ENSMUST00000108691]	AK082443
Vangl2	0.0190	1.58	down	vang-like 2 (van gogh, Drosophila) Gene [Source:MGI (curated);Acc:MGI:2135272] [ENSMUST00000111263]	AK082938
	0.0411	1.94	down	a disintegrin and metallopeptidase domain 33 Gene [Source:MGI (curated);Acc:MGI:1341813] [ENSMUST00000110229]	AK086734
	0.0017	1.68	down	RIKEN cDNA 5031434C07 gene Gene [Source:MGI Symbol;Acc:MGI:2442810] [ENSMUST00000053559]	AK087115
Myo15b	0.0188	2.99	down	myosin XVB Gene [Source:MGI (curated);Acc:MGI:2685534] [ENSMUST00000093911]	AK087906
Fbxl2	0.0180	2.00	down	F-box and leucine-rich repeat protein 2 Gene [Source:MGI (curated);Acc:MGI:1919429] [ENSMUST00000117537]	AK089994
	0.0342	2.02	down	spondin 1, (f-spondin) extracellular matrix protein Gene [Source:MGI (curated);Acc:MGI:2385287] [ENSMUST00000084696]	AK134774
A530083I20Rik	0.0161	3.55	down	Mus musculus adult male diencephalon cDNA, RIKEN full length enriched library, clone:9330151M24 product:unclassifiable, full insert sequence. [AK136855]	AK136855
Zdhhc23	0.0360	1.85	down	zinc finger, DHHC domain containing 23 Gene [Source:MGI Symbol;Acc:MGI:2685625] [ENSMUST00000036321]	AK137472
Prrt1	0.0410	3.63	down	proline-rich transmembrane protein 1 Gene [Source:MGI (curated);Acc:MGI:1932118] [ENSMUST00000015620]	AK137892
	0.0384	1.69	down	Putative uncharacterized protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q3UP94] [ENSMUST00000100684]	AK143696
	0.0355	2.23	down	predicted gene 867 Gene [Source:MGI Symbol;Acc:MGI:2685713] [ENSMUST00000059658]	AK144847
Rab11fip4	0.0034	1.85	down	RAB11 family interacting protein 4 (class II) Gene [Source:MGI (curated);Acc:MGI:2442920] [ENSMUST00000017783]	AK147344

LOC627096	0.0031	4.33	down	Mus musculus melanocyte cDNA, RIKEN full-length enriched library, clone:G270073A20 product:unclassifiable, full insert sequence. [AK147870]	AK147870
	0.0090	2.79	down	cathepsin C Gene [Source:MGI (curated);Acc:MGI:109553] [ENSMUST00000098313]	AK152524
Tnfaip8l3	0.0158	2.52	down	tumor necrosis factor, alpha-induced protein 8-like 3 Gene [Source:MGI Symbol;Acc:MGI:2685363] [ENSMUST00000098760]	AK154109
F830034J09Rik	0.0324	1.88	down	Mus musculus activated spleen cDNA, RIKEN full-length enriched library, clone:F830034J09 product:hypothetical protein, full insert sequence. [AK156640]	AK156640
	0.0347	2.04	down	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q9D1Y2] [ENSMUST00000097692]	AK161240
Cryba4	0.0216	3.30	down	crystallin, beta A4 Gene [Source:MGI (curated);Acc:MGI:102716] [ENSMUST00000112385]	AK161601
9130219A07Rik	0.0225	2.77	down	Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130219A07 product:hypothetical protein, full insert sequence. [AK162333]	AK162333
	0.0215	1.53	down	importin 11 Gene [Source:MGI Symbol;Acc:MGI:2442377] [ENSMUST00000091253]	AK164311
COX1	0.0355	1.70	down	mitochondrially encoded cytochrome c oxidase I Gene [Source:MGI Symbol;Acc:MGI:102504] [ENSMUST00000082402]	AK165865
	0.0339	1.67	down	zinc finger protein 740 Gene [Source:MGI (curated);Acc:MGI:1915994] [ENSMUST00000121206]	AK170207
	0.0048	2.82	down	Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q3TD87] [ENSMUST00000087655]	AK170322
	0.0296	3.28	down	docking protein 7 Gene [Source:MGI (curated);Acc:MGI:3584043] [ENSMUST00000114270]	AK170454

Mtmr15	0.0436	2.66	down	myotubularin related protein 15 Gene [Source:MGI (curated);Acc:MGI:3045266] [ENSMUST00000107514]	AK173087
AW050000	0.0266	2.54	down	UI-M-BH1-ant-g-09-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BH1-ant-g-09-0-UI 3'. [AW050000]	AW050000
LOC541456	0.0150	1.64	down	BB161756 RIKEN full-length enriched, 16 days neonate thymus Mus musculus cDNA clone A130062C20 3'. [BB161756]	BB161756
	0.0155	1.61	down	kinesin light chain 4 Gene [Source:MGI Symbol;Acc:MGI:1922014] [ENSMUST00000003641]	BC005746
	0.0481	1.59	down	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast) Gene [Source:MGI (curated);Acc:MGI:1916241] [ENSMUST00000105595]	BC016544
AI790276	0.0315	2.25	down	Mus musculus cDNA clone IMAGE:1067550. [BC028446]	BC028446
	0.0316	1.63	down	anaphase promoting complex subunit 1 Gene [Source:MGI (curated);Acc:MGI:103097] [ENSMUST00000110332]	BC057201
	0.0102	2.88	down	fetal and adult testis expressed 1 Gene [Source:MGI (curated);Acc:MGI:1925155] [ENSMUST00000114568]	BC115805
2010320M18Rik	0.0255	2.09	down	602091706F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4206096 5'. [BF531481]	BF531481
AU020147	0.0063	1.59	down	H3078F05-3 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3078F05 3', mRNA sequence [BG069650]	BG069650
AI853106	0.0215	1.51	down	603356119F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5363333 5', mRNA sequence [BI734998]	BI734998
	0.0012	1.83	down	BY201563 RIKEN full-length enriched, B6-derived CD11 +ve dendritic cells Mus musculus cDNA clone F730107H14 5', mRNA sequence [BY201563]	BY201563
AI956758	0.0449	1.54	down	UI-M-GV0-chs-b-03-0-UI.r1 NIH_BMAP_GV0 Mus musculus cDNA clone IMAGE:30542906 5', mRNA sequence [CV883746]	CV883746

	0.0409	1.72	down	Mus musculus clone AiDWTimmB-38 immunoglobulin kappa light chain mRNA, partial cds. [DQ372793]	DQ372793
	0.0317	1.76	down	Mouse T cell receptor mRNA. [M97158]	M97158
Penk	0.0173	2.64	down	Mus musculus preproenkephalin (Penk), mRNA [NM_001002927]	NM_001002927
Crtc1	0.0335	1.71	down	Mus musculus CREB regulated transcription coactivator 1 (Crtc1), mRNA [NM_001004062]	NM_001004062
Dbx1	0.0164	2.66	down	Mus musculus developing brain homeobox 1 (Dbx1), mRNA [NM_001005232]	NM_001005232
Gm1574	0.0427	3.87	down	Mus musculus predicted gene 1574 (Gm1574), mRNA [NM_001005422]	NM_001005422
Inadl	0.0498	1.72	down	Mus musculus InaD-like (Drosophila) (Inadl), transcript variant 2, mRNA [NM_001005784]	NM_001005784
Asap3	0.0389	1.63	down	Mus musculus ArfGAP with SH3 domain, ankyrin repeat and PH domain 3 (Asap3), mRNA [NM_001008232]	NM_001008232
Gm5595	0.0222	1.55	down	Mus musculus predicted gene 5595 (Gm5595), mRNA [NM_001008427]	NM_001008427
Gm5595	0.0184	1.74	down	Mus musculus predicted gene 5595 (Gm5595), mRNA [NM_001008427]	NM_001008427
Gm606	0.0268	3.26	down	Mus musculus predicted gene 606 (Gm606), mRNA [NM_001013761]	NM_001013761
Slc25a34	0.0485	1.95	down	Mus musculus solute carrier family 25, member 34 (Slc25a34), mRNA [NM_001013780]	NM_001013780
Scn2b	0.0404	2.30	down	Mus musculus sodium channel, voltage-gated, type II, beta (Scn2b), mRNA [NM_001014761]	NM_001014761
Lrp3	0.0483	2.10	down	Mus musculus low density lipoprotein receptor-related protein 3 (Lrp3), mRNA [NM_001024707]	NM_001024707
Ankrd34a	0.0472	1.84	down	Mus musculus ankyrin repeat domain 34A (Ankrd34a), mRNA [NM_001024851]	NM_001024851
D11Bwg0517e	0.0172	4.20	down	Mus musculus DNA segment, Chr 11, Brigham & Women's Genetics 0517 expressed (D11Bwg0517e), transcript variant 3, mRNA [NM_001024931]	NM_001024931

LOC547349	0.0062	2.12	down	Mus musculus similar to MHC class I antigen precursor (LOC547349), mRNA [NM_001025208]	NM_001025208
Tmem171	0.0382	2.08	down	Mus musculus transmembrane protein 171 (Tmem171), mRNA [NM_001025606]	NM_001025606
Pdzd4	0.0246	2.24	down	Mus musculus PDZ domain containing 4 (Pdzd4), mRNA [NM_001029868]	NM_001029868
Tceal3	0.0160	2.52	down	Mus musculus transcription elongation factor A (SII)-like 3 (Tceal3), mRNA [NM_001029978]	NM_001029978
Mett11d1	0.0302	1.65	down	Mus musculus methyltransferase 11 domain containing 1 (Mett11d1), mRNA [NM_001029990]	NM_001029990
Gm14288	0.0140	1.56	down	Mus musculus predicted gene 14288 (Gm14288), mRNA [NM_001033123]	NM_001033123
Cd27	0.0305	1.59	down	Mus musculus CD27 antigen (Cd27), transcript variant 1, mRNA [NM_001033126]	NM_001033126
Yeats2	0.0111	1.55	down	Mus musculus YEATS domain containing 2 (Yeats2), transcript variant 2, mRNA [NM_001033237]	NM_001033237
Gm826	0.0495	2.25	down	Mus musculus predicted gene 826 (Gm826), mRNA [NM_001033411]	NM_001033411
Il20rb	0.0097	2.07	down	Mus musculus interleukin 20 receptor beta (Il20rb), mRNA [NM_001033543]	NM_001033543
Pm20d2	0.0496	2.02	down	Mus musculus peptidase M20 domain containing 2 (Pm20d2), mRNA [NM_001034867]	NM_001034867
D11Bwg0517e	0.0286	4.09	down	Mus musculus DNA segment, Chr 11, Brigham & Women's Genetics 0517 expressed (D11Bwg0517e), transcript variant 1, mRNA [NM_001039167]	NM_001039167
Kcnd3	0.0201	1.98	down	Mus musculus potassium voltage-gated channel, Shal-related family, member 3 (Kcnd3), transcript variant 1, mRNA [NM_001039347]	NM_001039347
Kcnj10	0.0236	2.80	down	Mus musculus potassium inwardly-rectifying channel, subfamily J, member 10 (Kcnj10), mRNA [NM_001039484]	NM_001039484
Ivns1abp	0.0261	1.82	down	Mus musculus influenza virus NS1A binding protein (Ivns1abp), transcript variant 1, mRNA [NM_001039511]	NM_001039511

Myo6	0.0470	1.67	down	Mus musculus myosin VI (Myo6), mRNA [NM_001039546]	NM_001039546
Lhx3	0.0103	2.17	down	Mus musculus LIM homeobox protein 3 (Lhx3), mRNA [NM_001039653]	NM_001039653
Mtmt7	0.0019	1.88	down	Mus musculus myotubularin related protein 7 (Mtmt7), mRNA [NM_001040699]	NM_001040699
Ccnj1	0.0145	1.70	down	Mus musculus cyclin J-like (Ccnj1), mRNA [NM_001045530]	NM_001045530
9630025I21Rik	0.0469	1.52	down	Mus musculus RIKEN cDNA 9630025I21 gene (9630025I21Rik), mRNA [NM_001076791]	NM_001076791
Rapgef1	0.0221	2.02	down	Mus musculus Rap guanine nucleotide exchange factor (GEF) like 1 (Rapgef1), mRNA [NM_001080925]	NM_001080925
Rgs11	0.0252	2.01	down	Mus musculus regulator of G-protein signaling 11 (Rgs11), mRNA [NM_001081069]	NM_001081069
Cytl1	0.0186	3.57	down	Mus musculus cytokine-like 1 (Cytl1), mRNA [NM_001081106]	NM_001081106
Ankrd35	0.0087	1.51	down	Mus musculus ankyrin repeat domain 35 (Ankrd35), mRNA [NM_001081139]	NM_001081139
Rap1gap	0.0059	2.97	down	Mus musculus Rap1 GTPase-activating protein (Rap1gap), mRNA [NM_001081155]	NM_001081155
Rap1gap	0.0499	2.69	down	Mus musculus Rap1 GTPase-activating protein (Rap1gap), mRNA [NM_001081155]	NM_001081155
Fam178a	0.0165	1.52	down	Mus musculus family with sequence similarity 178, member A (Fam178a), mRNA [NM_001081225]	NM_001081225
Greb1	0.0055	1.82	down	Mus musculus growth regulation by estrogen in breast cancer-like (Greb1), mRNA [NM_001083628]	NM_001083628
Pappa2	0.0225	2.98	down	Mus musculus pappalysin 2 (Pappa2), mRNA [NM_001085376]	NM_001085376
Fam159a	0.0096	2.88	down	Mus musculus family with sequence similarity 159, member A (Fam159a), mRNA [NM_001099303]	NM_001099303
Gm12776	0.0332	1.81	down	Mus musculus predicted gene 12776 (Gm12776), mRNA [NM_001099330]	NM_001099330
Scgb1c1	0.0297	5.24	down	Mus musculus secretoglobin, family 1C, member 1 (Scgb1c1), mRNA [NM_001099742]	NM_001099742

Phldb3	0.0311	1.54	down	Mus musculus pleckstrin homology-like domain, family B member 3 (Phldb3), mRNA [NM_001102613]	NM_001102613
Acp1	0.0276	1.68	down	Mus musculus acid phosphatase 1, soluble (Acp1), transcript variant 1, mRNA [NM_001110239]	NM_001110239
Adam11	0.0200	1.66	down	Mus musculus a disintegrin and metallopeptidase domain 11 (Adam11), transcript variant 1, mRNA [NM_001110778]	NM_001110778
Cdkn1a	0.0318	2.65	down	Mus musculus cyclin-dependent kinase inhibitor 1A (P21) (Cdkn1a), transcript variant 2, mRNA [NM_001111099]	NM_001111099
Lrrc10b	0.0132	2.29	down	Mus musculus leucine rich repeat containing 10B (Lrrc10b), mRNA [NM_001111140]	NM_001111140
BC019943	0.0173	1.56	down	Mus musculus cDNA sequence BC019943 (BC019943), transcript variant 1, mRNA [NM_001112729]	NM_001112729
Gria1	0.0346	3.54	down	Mus musculus glutamate receptor, ionotropic, AMPA1 (alpha 1) (Gria1), transcript variant 1, mRNA [NM_001113325]	NM_001113325
Mfsd4	0.0085	3.61	down	Mus musculus major facilitator superfamily domain containing 4 (Mfsd4), transcript variant b, mRNA [NM_001114662]	NM_001114662
Pnpla6	0.0030	1.63	down	Mus musculus patatin-like phospholipase domain containing 6 (Pnpla6), transcript variant 1, mRNA [NM_001122818]	NM_001122818
Gm5736	0.0209	1.98	down	Mus musculus predicted gene 5736 (Gm5736), mRNA [NM_001127686]	NM_001127686
Hpca	0.0267	7.42	down	Mus musculus hippocalcin (Hpca), mRNA [NM_001130419]	NM_001130419
Tgtp2	0.0027	1.66	down	Mus musculus T-cell specific GTPase 2 (Tgtp2), mRNA [NM_001145164]	NM_001145164
Zkscan3	0.0011	2.22	down	Mus musculus zinc finger with KRAB and SCAN domains 3 (Zkscan3), transcript variant 1, mRNA [NM_001145778]	NM_001145778
Zfp444	0.0362	1.59	down	Mus musculus zinc finger protein 444 (Zfp444), transcript variant 1, mRNA [NM_001146024]	NM_001146024
F8	0.0289	2.42	down	Mus musculus coagulation factor VIII (F8), transcript variant 3, mRNA [NM_001161374]	NM_001161374
Sgsm1	0.0384	1.94	down	Mus musculus small G protein signaling modulator 1 (Sgsm1), transcript variant 3, mRNA [NM_001162965]	NM_001162965

Krtap20-2	0.0097	1.89	down	Mus musculus keratin associated protein 20-2 (Krtap20-2), mRNA [NM_001163615]	NM_001163615
Ush1c	0.0028	2.61	down	Mus musculus Usher syndrome 1C homolog (human) (Ush1c) transcript variant b4, mRNA [NM_001163733]	NM_001163733
Zfp605	0.0151	1.61	down	Mus musculus zinc finger protein 605 (Zfp605), mRNA [NM_001163996]	NM_001163996
Rarres1	0.0285	2.47	down	Mus musculus retinoic acid receptor responder (tazarotene induced) 1 (Rarres1), mRNA [NM_001164763]	NM_001164763
Thsd7a	0.0005	1.73	down	Mus musculus thrombospondin, type I, domain containing 7A (Thsd7a), mRNA [NM_001164805]	NM_001164805
Txndc6	0.0489	3.53	down	Mus musculus thioredoxin domain containing 6 (Txndc6), mRNA [NM_001165957]	NM_001165957
Vmn1r168	0.0274	1.72	down	Mus musculus vomeronasal 1 receptor 168 (Vmn1r168), mRNA [NM_001166842]	NM_001166842
Nrg2	0.0308	2.46	down	Mus musculus neuregulin 2 (Nrg2), mRNA [NM_001167891]	NM_001167891
Gm7455	0.0281	4.88	down	Mus musculus predicted gene 7455 (Gm7455), mRNA [NM_001167923]	NM_001167923
A330049M08Ri	0.0240	2.59	down	Mus musculus RIKEN cDNA A330049M08 gene (A330049M08Rik), transcript variant 2, mRNA [NM_001168500]	NM_001168500
Klra2	0.0199	1.60	down	Mus musculus killer cell lectin-like receptor, subfamily A, member 2 (Klra2), transcript variant 1, mRNA [NM_001170851]	NM_001170851
Gm3985	0.0091	1.79	down	Mus musculus predicted gene 3985 (Gm3985), mRNA [NM_001177589]	NM_001177589
Tmem132b	0.0472	1.88	down	Mus musculus transmembrane protein 132B (Tmem132b), mRNA [NM_001190352]	NM_001190352
Agrp	0.0158	1.71	down	Mus musculus agouti related protein (Agrp), mRNA [NM_007427]	NM_007427
Alox12	0.0080	3.03	down	Mus musculus arachidonate 12-lipoxygenase (Alox12), mRNA [NM_007440]	NM_007440

Bcl2a1d	0.0429	1.56	down	Mus musculus B-cell leukemia/lymphoma 2 related protein A1c (Bcl2a1d), mRNA [NM_007536]	NM_007536
Bmp7	0.0137	2.70	down	Mus musculus bone morphogenetic protein 7 (Bmp7), mRNA [NM_007557]	NM_007557
Btg1	0.0318	2.26	down	Mus musculus B-cell translocation gene 1, anti-proliferative (Btg1), mRNA [NM_007569]	NM_007569
Col4a3	0.0497	1.70	down	Mus musculus collagen, type IV, alpha 3 (Col4a3), mRNA [NM_007734]	NM_007734
Cyba	0.0344	1.60	down	Mus musculus cytochrome b-245, alpha polypeptide (Cyba), mRNA [NM_007806]	NM_007806
Cyp2f2	0.0345	12.18	down	Mus musculus cytochrome P450, family 2, subfamily f, polypeptide 2 (Cyp2f2), mRNA [NM_007817]	NM_007817
Efnb3	0.0214	2.06	down	Mus musculus ephrin B3 (Efnb3), mRNA [NM_007911]	NM_007911
Fgf2	0.0334	2.10	down	Mus musculus fibroblast growth factor 2 (Fgf2), mRNA [NM_008006]	NM_008006
Gas1	0.0126	2.78	down	Mus musculus growth arrest specific 1 (Gas1), mRNA [NM_008086]	NM_008086
Gdf1	0.0320	2.92	down	Mus musculus growth differentiation factor 1 (Gdf1), transcript variant 2, mRNA [NM_008107]	NM_008107
Arhgdig	0.0192	2.65	down	Mus musculus Rho GDP dissociation inhibitor (GDI) gamma (Arhgdig), mRNA [NM_008113]	NM_008113
Arhgdig	0.0235	2.68	down	Mus musculus Rho GDP dissociation inhibitor (GDI) gamma (Arhgdig), mRNA [NM_008113]	NM_008113
Gh	0.0173	1.88	down	Mus musculus growth hormone (Gh), mRNA [NM_008117]	NM_008117
H2-T24	0.0105	1.59	down	Mus musculus histocompatibility 2, T region locus 24 (H2-T24), mRNA [NM_008207]	NM_008207
Hccs	0.0204	1.69	down	Mus musculus holocytochrome c synthetase (Hccs), mRNA [NM_008222]	NM_008222
Hdc	0.0306	2.58	down	Mus musculus histidine decarboxylase (Hdc), mRNA [NM_008230]	NM_008230
Foxj1	0.0093	3.03	down	Mus musculus forkhead box J1 (Foxj1), mRNA [NM_008240]	NM_008240

Igfbp2	0.0402	3.38	down	Mus musculus insulin-like growth factor binding protein 2 (Igfbp2), mRNA [NM_008342]	NM_008342
Igfbp2	0.0427	2.90	down	Mus musculus insulin-like growth factor binding protein 2 (Igfbp2), mRNA [NM_008342]	NM_008342
Il12rb1	0.0407	1.63	down	Mus musculus interleukin 12 receptor, beta 1 (Il12rb1), mRNA [NM_008353]	NM_008353
Il18r1	0.0198	1.91	down	Mus musculus interleukin 18 receptor 1 (Il18r1), transcript variant 1, mRNA [NM_008365]	NM_008365
Il2rb	0.0061	2.52	down	Mus musculus interleukin 2 receptor, beta chain (Il2rb), mRNA [NM_008368]	NM_008368
Inhba	0.0461	4.07	down	Mus musculus inhibin beta-A (Inhba), mRNA [NM_008380]	NM_008380
Itm2a	0.0394	3.38	down	Mus musculus integral membrane protein 2A (Itm2a), mRNA [NM_008409]	NM_008409
Krt19	0.0367	3.77	down	Mus musculus keratin 19 (Krt19), mRNA [NM_008471]	NM_008471
Lcn2	0.0464	2.37	down	Mus musculus lipocalin 2 (Lcn2), mRNA [NM_008491]	NM_008491
Ascl1	0.0214	1.69	down	Mus musculus achaete-scute complex homolog 1 (Drosophila) (Ascl1), mRNA [NM_008553]	NM_008553
Mgp	0.0123	2.16	down	Mus musculus matrix Gla protein (Mgp), mRNA [NM_008597]	NM_008597
Mt2	0.0444	2.17	down	Mus musculus metallothionein 2 (Mt2), mRNA [NM_008630]	NM_008630
Mtap1b	0.0488	2.25	down	Mus musculus microtubule-associated protein 1B (Mtap1b), mRNA [NM_008634]	NM_008634
Mtap1b	0.0076	2.09	down	Mus musculus microtubule-associated protein 1B (Mtap1b), mRNA [NM_008634]	NM_008634
Nrtn	0.0339	1.71	down	Mus musculus neurturin (Nrtn), mRNA [NM_008738]	NM_008738
Pdcd1	0.0188	2.45	down	Mus musculus programmed cell death 1 (Pdcd1), mRNA [NM_008798]	NM_008798
Padi2	0.0041	2.23	down	Mus musculus peptidyl arginine deiminase, type II (Padi2), mRNA [NM_008812]	NM_008812
Padi2	0.0054	2.22	down	Mus musculus peptidyl arginine deiminase, type II (Padi2), mRNA [NM_008812]	NM_008812
Rab17	0.0414	2.78	down	Mus musculus RAB17, member RAS oncogene family (Rab17), transcript variant 1, mRNA [NM_008998]	NM_008998

Bex1	0.0374	2.90	down	Mus musculus brain expressed gene 1 (Bex1), mRNA [NM_009052]	NM_009052
Scn7a	0.0425	2.05	down	Mus musculus sodium channel, voltage-gated, type VII, alpha (Scn7a), mRNA [NM_009135]	NM_009135
Sstr4	0.0222	3.02	down	Mus musculus somatostatin receptor 4 (Sstr4), mRNA [NM_009219]	NM_009219
Tcf7	0.0426	2.67	down	Mus musculus transcription factor 7, T-cell specific (Tcf7), mRNA [NM_009331]	NM_009331
Tpm2	0.0433	3.10	down	Mus musculus tropomyosin 2, beta (Tpm2), mRNA [NM_009416]	NM_009416
Tst	0.0272	3.99	down	Mus musculus thiosulfate sulfurtransferase, mitochondrial (Tst), nuclear gene encoding mitochondrial protein, mRNA [NM_009437]	NM_009437
Tst	0.0205	4.03	down	Mus musculus thiosulfate sulfurtransferase, mitochondrial (Tst), nuclear gene encoding mitochondrial protein, mRNA [NM_009437]	NM_009437
Vil1	0.0497	3.35	down	Mus musculus villin 1 (Vil1), mRNA [NM_009509]	NM_009509
Wnt5b	0.0340	1.55	down	Mus musculus wingless-related MMTV integration site 5B (Wnt5b), mRNA [NM_009525]	NM_009525
Rnf112	0.0026	2.49	down	Mus musculus ring finger protein 112 (Rnf112), mRNA [NM_009548]	NM_009548
Adcy1	0.0207	2.31	down	Mus musculus adenylylate cyclase 1 (Adcy1), mRNA [NM_009622]	NM_009622
Angpt4	0.0048	7.11	down	Mus musculus angiopoietin 4 (Angpt4), mRNA [NM_009641]	NM_009641
Aldoc	0.0400	2.86	down	Mus musculus aldolase C, fructose-bisphosphate (Aldoc), mRNA [NM_009657]	NM_009657
Aqp5	0.0271	2.76	down	Mus musculus aquaporin 5 (Aqp5), mRNA [NM_009701]	NM_009701
Aqp5	0.0135	3.79	down	Mus musculus aquaporin 5 (Aqp5), mRNA [NM_009701]	NM_009701
Bcl2l1	0.0256	1.65	down	Mus musculus BCL2-like 1 (Bcl2l1), nuclear gene encoding mitochondrial protein, mRNA [NM_009743]	NM_009743
C3	0.0234	2.49	down	Mus musculus complement component 3 (C3), mRNA [NM_009778]	NM_009778

Cask	0.0269	1.79	down	Mus musculus calcium/calmodulin-dependent serine protein kinase (MAGUK family) (Cask), mRNA [NM_009806]	NM_009806
Cd14	0.0358	2.54	down	Mus musculus CD14 antigen (Cd14), mRNA [NM_009841]	NM_009841
Cdk4	0.0386	1.66	down	Mus musculus cyclin-dependent kinase 4 (Cdk4), mRNA [NM_009870]	NM_009870
Celsr1	0.0496	3.47	down	Mus musculus cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila) (Celsr1), mRNA [NM_009886]	NM_009886
Cxcr3	0.0161	1.97	down	Mus musculus chemokine (C-X-C motif) receptor 3 (Cxcr3), mRNA [NM_009910]	NM_009910
Cradd	0.0411	1.67	down	Mus musculus CASP2 and RIPK1 domain containing adaptor with death domain (Cradd), mRNA [NM_009950]	NM_009950
Cst7	0.0134	2.50	down	Mus musculus cystatin F (leukocystatin) (Cst7), mRNA [NM_009977]	NM_009977
Ctsw	0.0146	1.81	down	Mus musculus cathepsin W (Ctsw), mRNA [NM_009985]	NM_009985
Dao	0.0183	4.09	down	Mus musculus D-amino acid oxidase (Dao), mRNA [NM_010018]	NM_010018
Enah	0.0231	1.91	down	Mus musculus enabled homolog (Drosophila) (Enah), transcript variant 1, mRNA [NM_010135]	NM_010135
Gem	0.0369	1.58	down	Mus musculus GTP binding protein (gene overexpressed in skeletal muscle) (Gem), mRNA [NM_010276]	NM_010276
Gli1	0.0492	1.97	down	Mus musculus GLI-Kruppel family member GLI1 (Gli1), mRNA [NM_010296]	NM_010296
Gnaz	0.0289	2.21	down	Mus musculus guanine nucleotide binding protein, alpha z subunit (Gnaz), mRNA [NM_010311]	NM_010311
Pdpn	0.0484	1.79	down	Mus musculus podoplanin (Pdpn), mRNA [NM_010329]	NM_010329
Gstt2	0.0201	1.63	down	Mus musculus glutathione S-transferase, theta 2 (Gstt2), mRNA [NM_010361]	NM_010361
H2-DMb2	0.0139	1.95	down	Mus musculus histocompatibility 2, class II, locus Mb2 (H2-DMb2), mRNA [NM_010388]	NM_010388
Id1	0.0149	1.62	down	Mus musculus inhibitor of DNA binding 1 (Id1), mRNA [NM_010495]	NM_010495

Igf2	0.0016	1.79	down	Mus musculus insulin-like growth factor 2 (Igf2), transcript variant 1, mRNA [NM_010514]	NM_010514
Itga4	0.0207	1.76	down	Mus musculus integrin alpha 4 (Itga4), mRNA [NM_010576]	NM_010576
Lbx2	0.0340	1.97	down	Mus musculus ladybird homeobox homolog 2 (Drosophila) (Lbx2), mRNA [NM_010692]	NM_010692
Mdk	0.0267	2.63	down	Mus musculus midkine (Mdk), transcript variant 1, mRNA [NM_010784]	NM_010784
Cited2	0.0033	2.73	down	Mus musculus Cbp/p300-interacting transactivator, with Glu/Asp rich carboxy-terminal domain, 2 (Cited2), mRNA [NM_010828]	NM_010828
Cited2	0.0271	2.95	down	Mus musculus Cbp/p300-interacting transactivator, with Glu/Asp rich carboxy-terminal domain, 2 (Cited2), mRNA [NM_010828]	NM_010828
Ncam1	0.0147	3.25	down	Mus musculus neural cell adhesion molecule 1 (Ncam1), transcript variant 2, mRNA [NM_010875]	NM_010875
Nfe2l3	0.0442	1.51	down	Mus musculus nuclear factor, erythroid derived 2, like 3 (Nfe2l3), mRNA [NM_010903]	NM_010903
Pak1	0.0354	2.07	down	Mus musculus p21 protein (Cdc42/Rac)-activated kinase 1 (Pak1), mRNA [NM_011035]	NM_011035
Per3	0.0324	1.58	down	Mus musculus period homolog 3 (Drosophila) (Per3), mRNA [NM_011067]	NM_011067
Pla2g2d	0.0039	2.37	down	Mus musculus phospholipase A2, group IID (Pla2g2d), mRNA [NM_011109]	NM_011109
Pla2g2d	0.0121	2.27	down	Mus musculus phospholipase A2, group IID (Pla2g2d), mRNA [NM_011109]	NM_011109
Plp1	0.0409	1.63	down	Mus musculus proteolipid protein (myelin) 1 (Plp1), mRNA [NM_011123]	NM_011123
Ccl21a	0.0098	4.57	down	Mus musculus chemokine (C-C motif) ligand 21A (Ccl21a), mRNA [NM_011124]	NM_011124
Prtn3	0.0125	4.87	down	Mus musculus proteinase 3 (Prtn3), mRNA [NM_011178]	NM_011178
Rarg	0.0445	1.75	down	Mus musculus retinoic acid receptor, gamma (Rarg), transcript variant 1, mRNA [NM_011244]	NM_011244

Rorc	0.0477	4.35	down	Mus musculus RAR-related orphan receptor gamma (Rorc), mRNA [NM_011281]	NM_011281
S100a5	0.0219	1.53	down	Mus musculus S100 calcium binding protein A5 (S100a5), mRNA [NM_011312]	NM_011312
Scnn1b	0.0126	2.66	down	Mus musculus sodium channel, nonvoltage-gated 1 beta (Scnn1b), mRNA [NM_011325]	NM_011325
Ccl21b	0.0047	3.24	down	Mus musculus chemokine (C-C motif) ligand 21B (Ccl21b), mRNA [NM_011335]	NM_011335
Sftpc	0.0336	1.80	down	Mus musculus surfactant associated protein C (Sftpc), mRNA [NM_011359]	NM_011359
Sox9	0.0081	3.00	down	Mus musculus SRY-box containing gene 9 (Sox9), mRNA [NM_011448]	NM_011448
Trpc2	0.0009	1.59	down	Mus musculus transient receptor potential cation channel, subfamily C, member 2 (Trpc2), transcript variant 1, mRNA [NM_011644]	NM_011644
Tsc2	0.0437	1.57	down	Mus musculus tuberous sclerosis 2 (Tsc2), transcript variant 1, mRNA [NM_011647]	NM_011647
Vcam1	0.0454	1.75	down	Mus musculus vascular cell adhesion molecule 1 (Vcam1), mRNA [NM_011693]	NM_011693
Zfpm2	0.0370	1.56	down	Mus musculus zinc finger protein, multitype 2 (Zfpm2), mRNA [NM_011766]	NM_011766
Ikzf4	0.0231	2.92	down	Mus musculus IKAROS family zinc finger 4 (Ikzf4), mRNA [NM_011772]	NM_011772
Ikzf4	0.0243	3.10	down	Mus musculus IKAROS family zinc finger 4 (Ikzf4), mRNA [NM_011772]	NM_011772
Adam23	0.0208	2.13	down	Mus musculus a disintegrin and metallopeptidase domain 23 (Adam23), transcript variant 2, mRNA [NM_011780]	NM_011780
Lamc3	0.0008	1.82	down	Mus musculus laminin gamma 3 (Lamc3), mRNA [NM_011836]	NM_011836
Pacsin1	0.0067	2.30	down	Mus musculus protein kinase C and casein kinase substrate in neurons 1 (Pacsin1), transcript variant 1, mRNA [NM_011861]	NM_011861

Ccl19	0.0367	2.22	down	Mus musculus chemokine (C-C motif) ligand 19 (Ccl19), mRNA [NM_011888]	NM_011888
Cpe	0.0004	1.98	down	Mus musculus carboxypeptidase E (Cpe), mRNA [NM_013494]	NM_013494
Cpe	0.0110	1.88	down	Mus musculus carboxypeptidase E (Cpe), mRNA [NM_013494]	NM_013494
Crabp1	0.0196	2.74	down	Mus musculus cellular retinoic acid binding protein I (Crabp1), mRNA [NM_013496]	NM_013496
Itgb7	0.0279	1.79	down	Mus musculus integrin beta 7 (Itgb7), mRNA [NM_013566]	NM_013566
Kcna6	0.0429	2.01	down	Mus musculus potassium voltage-gated channel, shaker-related, subfamily, member 6 (Kcna6), mRNA [NM_013568]	NM_013568
Mt1	0.0380	1.93	down	Mus musculus metallothionein 1 (Mt1), mRNA [NM_013602]	NM_013602
Pklr	0.0241	4.28	down	Mus musculus pyruvate kinase liver and red blood cell (Pklr), nuclear gene encoding mitochondrial protein, transcript variant 1, mRNA [NM_013631]	NM_013631
Sema4d	0.0207	1.90	down	Mus musculus sema domain, immunoglobulin domain (Ig) transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (Sema4d), mRNA [NM_013660]	NM_013660
Plek2	0.0242	1.87	down	Mus musculus pleckstrin 2 (Plek2), mRNA [NM_013738]	NM_013738
Plekhb1	0.0397	3.15	down	Mus musculus pleckstrin homology domain containing, family F (evectins) member 1 (Plekhb1), transcript variant 1, mRNA [NM_013746]	NM_013746
Rpl3	0.0339	1.73	down	Mus musculus ribosomal protein L3 (Rpl3), mRNA [NM_013762]	NM_013762
Sfrp1	0.0415	2.86	down	Mus musculus secreted frizzled-related protein 1 (Sfrp1), mRNA [NM_013834]	NM_013834
Reg3d	0.0218	2.00	down	Mus musculus regenerating islet-derived 3 delta (Reg3d), transcript variant 1, mRNA [NM_013893]	NM_013893
Usp21	0.0494	1.52	down	Mus musculus ubiquitin specific peptidase 21 (Usp21), mRNA [NM_013919]	NM_013919
Zfp354c	0.0212	1.99	down	Mus musculus zinc finger protein 354C (Zfp354c), mRNA [NM_013922]	NM_013922

Siva1	0.0134	1.67	down	Mus musculus SIVA1, apoptosis-inducing factor (Siva1), transcript variant 1, mRNA [NM_013929]	NM_013929
Ttpa	0.0239	3.19	down	Mus musculus tocopherol (alpha) transfer protein (Ttpa), mRNA [NM_015767]	NM_015767
Cldn2	0.0218	3.25	down	Mus musculus claudin 2 (Cldn2), mRNA [NM_016675]	NM_016675
Chst3	0.0163	2.12	down	Mus musculus carbohydrate (chondroitin 6/keratan) sulfotransferase 3 (Chst3), mRNA [NM_016803]	NM_016803
Stac	0.0166	3.96	down	Mus musculus src homology three (SH3) and cysteine rich domain (Stac), mRNA [NM_016853]	NM_016853
Sart1	0.0281	1.62	down	Mus musculus squamous cell carcinoma antigen recognized by T cells 1 (Sart1), mRNA [NM_016882]	NM_016882
Gria3	0.0210	2.23	down	Mus musculus glutamate receptor, ionotropic, AMPA3 (alpha 3) (Gria3), mRNA [NM_016886]	NM_016886
Celsr2	0.0033	2.14	down	Mus musculus cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila) (Celsr2), transcript variant 1, mRNA [NM_017392]	NM_017392
Icos	0.0115	1.86	down	Mus musculus inducible T-cell co-stimulator (Icos), mRNA [NM_017480]	NM_017480
Igtp	0.0373	1.64	down	Mus musculus interferon gamma induced GTPase (Igtp), mRNA [NM_018738]	NM_018738
Syt6	0.0350	1.67	down	Mus musculus synaptotagmin VI (Syt6), mRNA [NM_018800]	NM_018800
Wisp1	0.0321	2.97	down	Mus musculus WNT1 inducible signaling pathway protein 1 (Wisp1), mRNA [NM_018865]	NM_018865
Srcin1	0.0143	2.17	down	Mus musculus SRC kinase signaling inhibitor 1 (Srcin1), mRNA [NM_018873]	NM_018873
Fmn2	0.0173	1.75	down	Mus musculus formin 2 (Fmn2), mRNA [NM_019445]	NM_019445
Ensa	0.0450	1.51	down	Mus musculus endosulfine alpha (Ensa), transcript variant 1, mRNA [NM_019561]	NM_019561
Il17rb	0.0207	2.39	down	Mus musculus interleukin 17 receptor B (Il17rb), mRNA [NM_019583]	NM_019583
Ncs1	0.0208	1.57	down	Mus musculus neuronal calcium sensor 1 (Ncs1), mRNA [NM_019681]	NM_019681

Cpxm1	0.0180	2.09	down	Mus musculus carboxypeptidase X 1 (M14 family) (Cpxm1), mRNA [NM_019696]	NM_019696
Anapc7	0.0110	1.51	down	Mus musculus anaphase promoting complex subunit 7 (Anapc7), mRNA [NM_019805]	NM_019805
Dusp14	0.0275	2.59	down	Mus musculus dual specificity phosphatase 14 (Dusp14), mRNA [NM_019819]	NM_019819
Tgm1	0.0464	2.73	down	Mus musculus transglutaminase 1, K polypeptide (Tgm1), transcript variant 2, mRNA [NM_019984]	NM_019984
Ckb	0.0499	2.53	down	Mus musculus creatine kinase, brain (Ckb), mRNA [NM_021273]	NM_021273
Zfp112	0.0114	2.46	down	Mus musculus zinc finger protein 112 (Zfp112), mRNA [NM_021307]	NM_021307
Crybb3	0.0436	1.71	down	Mus musculus crystallin, beta B3 (Crybb3), transcript variant 1, mRNA [NM_021352]	NM_021352
Neurl1a	0.0384	2.39	down	Mus musculus neuralized homolog 1A (Drosophila) (Neurl1a), transcript variant 1, mRNA [NM_021360]	NM_021360
Neurl1a	0.0415	2.29	down	Mus musculus neuralized homolog 1A (Drosophila) (Neurl1a), transcript variant 1, mRNA [NM_021360]	NM_021360
Bcl11b	0.0217	2.06	down	Mus musculus B-cell leukemia/lymphoma 11B (Bcl11b), transcript variant 2, mRNA [NM_021399]	NM_021399
Trem1	0.0200	1.78	down	Mus musculus triggering receptor expressed on myeloid cells 1 (Trem1), mRNA [NM_021406]	NM_021406
Agrn	0.0114	3.32	down	Mus musculus agrin (Agrn), mRNA [NM_021604]	NM_021604
Fxyd7	0.0350	1.96	down	Mus musculus FXYD domain-containing ion transport regulator 7 (Fxyd7), mRNA [NM_022007]	NM_022007
Gmfg	0.0234	1.63	down	Mus musculus glia maturation factor, gamma (Gmfg), transcript variant 1, mRNA [NM_022024]	NM_022024
Ngb	0.0421	2.00	down	Mus musculus neuroglobin (Ngb), mRNA [NM_022414]	NM_022414
Gpr88	0.0158	3.70	down	Mus musculus G-protein coupled receptor 88 (Gpr88), mRNA [NM_022427]	NM_022427
Scube1	0.0447	3.44	down	Mus musculus signal peptide, CUB domain, EGF-like 1 (Scube1), mRNA [NM_022723]	NM_022723

Cxcl16	0.0413	1.61	down	Mus musculus chemokine (C-X-C motif) ligand 16 (Cxcl16), mRNA [NM_023158]	NM_023158
Chia	0.0347	1.96	down	Mus musculus chitinase, acidic (Chia), mRNA [NM_023186]	NM_023186
Wfdc1	0.0080	2.56	down	Mus musculus WAP four-disulfide core domain 1 (Wfdc1), mRNA [NM_023395]	NM_023395
Gdpd2	0.0202	2.72	down	Mus musculus glycerophosphodiester phosphodiesterase domain containing 2 (Gdpd2), mRNA [NM_023608]	NM_023608
Crybb1	0.0316	2.09	down	Mus musculus crystallin, beta B1 (Crybb1), mRNA [NM_023695]	NM_023695
Nkg7	0.0090	1.72	down	Mus musculus natural killer cell group 7 sequence (Nkg7), mRNA [NM_024253]	NM_024253
1500015O10Rik	0.0397	3.74	down	Mus musculus RIKEN cDNA 1500015O10 gene (1500015O10Rik), mRNA [NM_024283]	NM_024283
Haao	0.0137	2.12	down	Mus musculus 3-hydroxyanthranilate 3,4-dioxygenase (Haao), mRNA [NM_025325]	NM_025325
Tceal6	0.0244	2.50	down	Mus musculus transcription elongation factor A (SII)-like 6 (Tceal6), mRNA [NM_025355]	NM_025355
Camk2n1	0.0039	1.80	down	Mus musculus calcium/calmodulin-dependent protein kinase I inhibitor 1 (Camk2n1), mRNA [NM_025451]	NM_025451
Ing5	0.0041	1.57	down	Mus musculus inhibitor of growth family, member 5 (Ing5), mRNA [NM_025454]	NM_025454
Col27a1	0.0079	1.51	down	Mus musculus collagen, type XXVII, alpha 1 (Col27a1), mRNA [NM_025685]	NM_025685
Rbm4b	0.0396	1.73	down	Mus musculus RNA binding motif protein 4B (Rbm4b), mRNA [NM_025717]	NM_025717
Cmtm5	0.0132	1.55	down	Mus musculus CKLF-like MARVEL transmembrane domain containing 5 (Cmtm5), mRNA [NM_026066]	NM_026066
Gprasp1	0.0260	2.05	down	Mus musculus G protein-coupled receptor associated sorting protein 1 (Gprasp1), transcript variant 1, mRNA [NM_026081]	NM_026081
Bend5	0.0275	2.12	down	Mus musculus BEN domain containing 5 (Bend5), transcript variant 1, mRNA [NM_026279]	NM_026279

2610027L16Rik	0.0381	1.66	down	Mus musculus RIKEN cDNA 2610027L16 gene (2610027L16Rik), mRNA [NM_026403]	NM_026403
Tspan11	0.0245	3.44	down	Mus musculus tetraspanin 11 (Tspan11), mRNA [NM_026743]	NM_026743
Glod5	0.0296	4.46	down	Mus musculus glyoxalase domain containing 5 (Glod5), mRNA [NM_027227]	NM_027227
2810422O20Rik	0.0132	1.53	down	Mus musculus RIKEN cDNA 2810422O20 gene (2810422O20Rik), mRNA [NM_027279]	NM_027279
2810422O20Rik	0.0252	1.53	down	Mus musculus RIKEN cDNA 2810422O20 gene (2810422O20Rik), mRNA [NM_027279]	NM_027279
Steap1	0.0037	2.71	down	Mus musculus six transmembrane epithelial antigen of the prostate 1 (Steap1), mRNA [NM_027399]	NM_027399
Lrfn2	0.0268	1.79	down	Mus musculus leucine rich repeat and fibronectin type III domain containing 2 (Lrfn2), mRNA [NM_027452]	NM_027452
Cwf19l2	0.0332	1.60	down	Mus musculus CWF19-like 2, cell cycle control (S. pombe) (Cwf19l2), mRNA [NM_027545]	NM_027545
Galnt14	0.0126	2.68	down	Mus musculus UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (Galnt14), mRNA [NM_027864]	NM_027864
Tmem25	0.0428	2.68	down	Mus musculus transmembrane protein 25 (Tmem25), mRNA [NM_027865]	NM_027865
Vwce	0.0075	1.75	down	Mus musculus von Willebrand factor C and EGF domains (Vwce), mRNA [NM_027913]	NM_027913
Bbs10	0.0127	1.60	down	Mus musculus Bardet-Biedl syndrome 10 (human) (Bbs10), mRNA [NM_027914]	NM_027914
Slc39a4	0.0316	2.38	down	Mus musculus solute carrier family 39 (zinc transporter), member 4 (Slc39a4), mRNA [NM_028064]	NM_028064
Ddb2	0.0349	1.67	down	Mus musculus damage specific DNA binding protein 2 (Ddb2), mRNA [NM_028119]	NM_028119
Cda	0.0374	3.42	down	Mus musculus cytidine deaminase (Cda), mRNA [NM_028176]	NM_028176

Ppp2r2b	0.0375	2.23	down	Mus musculus protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform (Ppp2r2b), transcript variant 2, mRNA [NM_028392]	NM_028392
Prkrir	0.0127	1.86	down	Mus musculus protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor) (Prkrir), mRNA [NM_028410]	NM_028410
Glpr1	0.0102	1.61	down	Mus musculus GLI pathogenesis-related 1 (glioma) (Glpr1), mRNA [NM_028608]	NM_028608
Paqr5	0.0323	3.65	down	Mus musculus progesterone and adiponectin receptor family member V (Paqr5), mRNA [NM_028748]	NM_028748
P2ry13	0.0111	1.65	down	Mus musculus purinergic receptor P2Y, G-protein coupled 13 (P2ry13), mRNA [NM_028808]	NM_028808
Vit	0.0420	2.16	down	Mus musculus vitronectin (Vit), mRNA [NM_028813]	NM_028813
Palm3	0.0096	2.33	down	Mus musculus paralemmin 3 (Palm3), mRNA [NM_028877]	NM_028877
Sepn1	0.0191	1.53	down	Mus musculus selenoprotein N, 1 (Sepn1), mRNA [NM_029100]	NM_029100
Rasd2	0.0320	1.70	down	Mus musculus RASD family, member 2 (Rasd2), mRNA [NM_029182]	NM_029182
4930434E21Rik	0.0210	1.58	down	Mus musculus RIKEN cDNA 4930434E21 gene (4930434E21Rik), mRNA [NM_029440]	NM_029440
Gbp8	0.0245	2.26	down	Mus musculus guanylate-binding protein 8 (Gbp8), mRNA [NM_029509]	NM_029509
Txndc11	0.0067	1.63	down	Mus musculus thioredoxin domain containing 11 (Txndc11), transcript variant 1, mRNA [NM_029582]	NM_029582
Abp1	0.0403	2.17	down	Mus musculus amiloride binding protein 1 (amine oxidase, copper containing) (Abp1), transcript variant 3, mRNA [NM_029638]	NM_029638
1600029D21Rik	0.0168	3.88	down	Mus musculus RIKEN cDNA 1600029D21 gene (1600029D21Rik), mRNA [NM_029639]	NM_029639
Mtus2	0.0158	2.05	down	Mus musculus microtubule associated tumor suppressor candidate 2 (Mtus2), mRNA [NM_029920]	NM_029920

Mtus2	0.0066	2.58	down	Mus musculus microtubule associated tumor suppressor candidate 2 (Mtus2), mRNA [NM_029920]	NM_029920
Tmem213	0.0123	3.21	down	Mus musculus transmembrane protein 213 (Tmem213), mRNA [NM_029921]	NM_029921
Ddit4l	0.0132	3.38	down	Mus musculus DNA-damage-inducible transcript 4-like (Ddit4l), mRNA [NM_030143]	NM_030143
Sp2	0.0447	1.52	down	Mus musculus Sp2 transcription factor (Sp2), transcript variant 1, mRNA [NM_030220]	NM_030220
Slc16a3	0.0462	2.38	down	Mus musculus solute carrier family 16 (monocarboxylic acid transporters), member 3 (Slc16a3), mRNA [NM_030696]	NM_030696
Slc16a3	0.0345	2.29	down	Mus musculus solute carrier family 16 (monocarboxylic acid transporters), member 3 (Slc16a3), mRNA [NM_030696]	NM_030696
Zfhx4	0.0034	3.01	down	Mus musculus zinc finger homeodomain 4 (Zfhx4), mRNA [NM_030708]	NM_030708
Slamf6	0.0258	2.01	down	Mus musculus SLAM family member 6 (Slamf6), mRNA [NM_030710]	NM_030710
Syt13	0.0095	2.19	down	Mus musculus synaptotagmin XIII (Syt13), mRNA [NM_030725]	NM_030725
Sorcs2	0.0301	2.79	down	Mus musculus sortilin-related VPS10 domain containing receptor 2 (Sorcs2), mRNA [NM_030889]	NM_030889
Glis2	0.0468	2.30	down	Mus musculus GLIS family zinc finger 2 (Glis2), mRNA [NM_031184]	NM_031184
Gimap3	0.0249	1.79	down	Mus musculus GTPase, IMAP family member 3 (Gimap3), nuclear gene encoding mitochondrial protein, mRNA [NM_031247]	NM_031247
Syt11	0.0235	1.65	down	Mus musculus synaptotagmin-like 1 (Syt11), mRNA [NM_031393]	NM_031393
Srebf2	0.0374	1.64	down	Mus musculus sterol regulatory element binding factor 2 (Srebf2), mRNA [NM_033218]	NM_033218
Pabpc5	0.0477	3.31	down	Mus musculus poly(A) binding protein, cytoplasmic 5 (Pabpc5), mRNA [NM_053114]	NM_053114

Prss29	0.0265	2.80	down	Mus musculus protease, serine, 29 (Prss29), mRNA [NM_053260]	NM_053260
Alpk3	0.0330	3.43	down	Mus musculus alpha-kinase 3 (Alpk3), mRNA [NM_054085]	NM_054085
Tshz2	0.0268	1.82	down	Mus musculus teashirt zinc finger family member 2 (Tshz2), mRNA [NM_080455]	NM_080455
Slc17a6	0.0405	2.10	down	Mus musculus solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6 (Slc17a6), mRNA [NM_080853]	NM_080853
Card14	0.0400	2.74	down	Mus musculus caspase recruitment domain family, member 14 (Card14), mRNA [NM_130886]	NM_130886
Eps8l2	0.0439	3.11	down	Mus musculus EPS8-like 2 (Eps8l2), mRNA [NM_133191]	NM_133191
Rtkn	0.0252	1.86	down	Mus musculus rhotekin (Rtkn), transcript variant 3, mRNA [NM_133641]	NM_133641
Asph	0.0232	1.86	down	Mus musculus aspartate-beta-hydroxylase (Asph), transcript variant 2, mRNA [NM_133723]	NM_133723
Gstt3	0.0061	2.25	down	Mus musculus glutathione S-transferase, theta 3 (Gstt3), mRNA [NM_133994]	NM_133994
Slc38a1	0.0480	1.95	down	Mus musculus solute carrier family 38, member 1 (Slc38a1), transcript variant 1, mRNA [NM_134086]	NM_134086
Pkdcc	0.0491	2.16	down	Mus musculus protein kinase domain containing, cytoplasmic (Pkdcc), mRNA [NM_134117]	NM_134117
2010002N04Rik	0.0193	2.98	down	Mus musculus RIKEN cDNA 2010002N04 gene (2010002N04Rik), mRNA [NM_134133]	NM_134133
Macrocl1	0.0131	1.80	down	Mus musculus MACRO domain containing 1 (Macrocl1), mRNA [NM_134147]	NM_134147
Lrrc4	0.0331	2.23	down	Mus musculus leucine rich repeat containing 4 (Lrrc4), mRNA [NM_138682]	NM_138682
Pycr1	0.0159	7.54	down	Mus musculus pyrroline-5-carboxylate reductase 1 (Pycr1), mRNA [NM_144795]	NM_144795
Cbx7	0.0228	2.38	down	Mus musculus chromobox homolog 7 (Cbx7), mRNA [NM_144811]	NM_144811

Ppp1r1b	0.0424	4.65	down	Mus musculus protein phosphatase 1, regulatory (inhibitor) subunit 1B (Ppp1r1b), mRNA [NM_144828]	NM_144828
Crebzf	0.0143	1.78	down	Mus musculus CREB/ATF bZIP transcription factor (Crebzf), mRNA [NM_145151]	NM_145151
Lgi3	0.0310	1.96	down	Mus musculus leucine-rich repeat LGI family, member 3 (Lgi3), mRNA [NM_145219]	NM_145219
Sectm1a	0.0322	1.85	down	Mus musculus secreted and transmembrane 1A (Sectm1a), mRNA [NM_145373]	NM_145373
Btbd3	0.0237	1.94	down	Mus musculus BTB (POZ) domain containing 3 (Btbd3), transcript variant 1, mRNA [NM_145534]	NM_145534
Spon1	0.0430	2.26	down	Mus musculus spondin 1, (f-spondin) extracellular matrix protein (Spon1), mRNA [NM_145584]	NM_145584
Narg2	0.0231	1.56	down	Mus musculus NMDA receptor-regulated gene 2 (Narg2), mRNA [NM_145618]	NM_145618
Usp11	0.0335	2.07	down	Mus musculus ubiquitin specific peptidase 11 (Usp11), mRNA [NM_145628]	NM_145628
Grhl1	0.0319	2.29	down	Mus musculus grainyhead-like 1 (Drosophila) (Grhl1), transcript variant 2, mRNA [NM_145890]	NM_145890
Slc45a3	0.0484	2.78	down	Mus musculus solute carrier family 45, member 3 (Slc45a3), mRNA [NM_145977]	NM_145977
Aph1a	0.0056	1.52	down	Mus musculus anterior pharynx defective 1a homolog (C. elegans) (Aph1a), transcript variant 1, mRNA [NM_146104]	NM_146104
Tspan33	0.0363	2.10	down	Mus musculus tetraspanin 33 (Tspan33), mRNA [NM_146173]	NM_146173
B3gnt8	0.0216	2.41	down	Mus musculus UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8 (B3gnt8), transcript variant 1, mRNA [NM_146184]	NM_146184
Zfp553	0.0236	1.52	down	Mus musculus zinc finger protein 553 (Zfp553), mRNA [NM_146201]	NM_146201
Olfr460	0.0169	1.54	down	Mus musculus olfactory receptor 460 (Olfr460), mRNA [NM_146383]	NM_146383

Olf1410	0.0020	3.08	down	Mus musculus olfactory receptor 1410 (Olf1410), mRNA [NM_146491]	NM_146491
Olf791	0.0342	1.64	down	Mus musculus olfactory receptor 791 (Olf791), mRNA [NM_146930]	NM_146930
Vwa1	0.0274	2.11	down	Mus musculus von Willebrand factor A domain containing 1 (Vwa1), mRNA [NM_147776]	NM_147776
Dner	0.0135	5.36	down	Mus musculus delta/notch-like EGF-related receptor (Dner), mRNA [NM_152915]	NM_152915
Traf3ip3	0.0212	1.78	down	Mus musculus TRAF3 interacting protein 3 (Traf3ip3), mRNA [NM_153137]	NM_153137
Peo1	0.0378	1.61	down	Mus musculus progressive external ophthalmoplegia 1 (human) (Peo1), mRNA [NM_153796]	NM_153796
Igsf11	0.0289	2.04	down	Mus musculus immunoglobulin superfamily, member 11 (Igsf11) mRNA [NM_170599]	NM_170599
Crocc	0.0110	2.27	down	Mus musculus ciliary rootlet coiled-coil, rootletin (Crocc), transcript variant 1, mRNA [NM_172122]	NM_172122
Slc6a17	0.0097	3.03	down	Mus musculus solute carrier family 6 (neurotransmitter transporter), member 17 (Slc6a17), mRNA [NM_172271]	NM_172271
Ahsa2	0.0274	3.24	down	Mus musculus AHA1, activator of heat shock protein ATPase homolog 2 (yeast) (Ahsa2), mRNA [NM_172391]	NM_172391
2310007B03Rik	0.0468	3.21	down	Mus musculus RIKEN cDNA 2310007B03 gene (2310007B03Rik), transcript variant 1, mRNA [NM_172411]	NM_172411
Inpp5j	0.0350	2.28	down	Mus musculus inositol polyphosphate 5-phosphatase J (Inpp5j), mRNA [NM_172439]	NM_172439
Bzrap1	0.0284	1.83	down	Mus musculus benzodiazapine receptor associated protein 1 (Bzrap1), mRNA [NM_172449]	NM_172449
Arhgef19	0.0436	2.38	down	Mus musculus Rho guanine nucleotide exchange factor (GEF) 19 (Arhgef19), mRNA [NM_172520]	NM_172520
Dok7	0.0402	3.25	down	Mus musculus docking protein 7 (Dok7), mRNA [NM_172708]	NM_172708
Sgsm1	0.0268	2.98	down	Mus musculus small G protein signaling modulator 1 (Sgsm1), transcript variant 1, mRNA [NM_172718]	NM_172718

Clec9a	0.0401	2.11	down	Mus musculus C-type lectin domain family 9, member a (Clec9a) mRNA [NM_172732]	NM_172732
Plxnb1	0.0191	2.58	down	Mus musculus plexin B1 (Plxnb1), mRNA [NM_172775]	NM_172775
E230025N22Rik	0.0229	1.68	down	Mus musculus Riken cDNA E230025N22 gene (E230025N22Rik), mRNA [NM_172831]	NM_172831
Bnc2	0.0391	2.18	down	Mus musculus basenuclin 2 (Bnc2), mRNA [NM_172870]	NM_172870
Vat1l	0.0070	2.12	down	Mus musculus vesicle amine transport protein 1 homolog-like (T californica) (Vat1l), mRNA [NM_173016]	NM_173016
Zfp879	0.0142	1.63	down	Mus musculus zinc finger protein 879 (Zfp879), mRNA [NM_173387]	NM_173387
Gpr171	0.0290	1.70	down	Mus musculus G protein-coupled receptor 171 (Gpr171), mRNA [NM_173398]	NM_173398
Lancl3	0.0409	2.63	down	Mus musculus LanC lantibiotic synthetase component C-like 3 (bacterial) (Lancl3), mRNA [NM_173414]	NM_173414
Pgm5	0.0387	2.77	down	Mus musculus phosphoglucomutase 5 (Pgm5), mRNA [NM_175013]	NM_175013
Zcchc3	0.0137	1.66	down	Mus musculus zinc finger, CCHC domain containing 3 (Zcchc3), mRNA [NM_175126]	NM_175126
Aifm3	0.0050	1.75	down	Mus musculus apoptosis-inducing factor, mitochondrion associated 3 (Aifm3), nuclear gene encoding mitochondrial protein, mRNA [NM_175178]	NM_175178
Fbxl22	0.0343	2.69	down	Mus musculus F-box and leucine-rich repeat protein 22 (Fbxl22), mRNA [NM_175206]	NM_175206
Gjc2	0.0212	1.65	down	Mus musculus gap junction protein, gamma 2 (Gjc2), transcript variant 2, mRNA [NM_175452]	NM_175452
Snx33	0.0090	1.74	down	Mus musculus sorting nexin 33 (Snx33), mRNA [NM_175483]	NM_175483
Rab39	0.0383	1.73	down	Mus musculus RAB39, member RAS oncogene family (Rab39), mRNA [NM_175562]	NM_175562
Hopx	0.0447	1.65	down	Mus musculus HOP homeobox (Hopx), transcript variant 1, mRNA [NM_175606]	NM_175606
Dnajc22	0.0349	2.63	down	Mus musculus DnaJ (Hsp40) homolog, subfamily C, member 22 (Dnajc22), mRNA [NM_176835]	NM_176835

Fam179a	0.0325	2.68	down	Mus musculus family with sequence similarity 179, member A (Fam179a), mRNA [NM_177087]	NM_177087
Lypd6	0.0092	3.22	down	Mus musculus LY6/PLAUR domain containing 6 (Lypd6), transcript variant 1, mRNA [NM_177139]	NM_177139
Plcxd3	0.0310	3.36	down	Mus musculus phosphatidylinositol-specific phospholipase C, X domain containing 3 (Plcxd3), mRNA [NM_177355]	NM_177355
Igsf1	0.0003	3.41	down	Mus musculus immunoglobulin superfamily, member 1 (Igsf1) transcript variant 1, mRNA [NM_177591]	NM_177591
Mkx	0.0327	3.46	down	Mus musculus mohawk homeobox (Mkx), mRNA [NM_177595]	NM_177595
Fbxw13	0.0112	4.32	down	Mus musculus F-box and WD-40 domain protein 13 (Fbxw13), mRNA [NM_177598]	NM_177598
AU021034	0.0209	3.13	down	Mus musculus expressed sequence AU021034 (AU021034), mRNA [NM_177629]	NM_177629
1110028C15Rik	0.0409	2.08	down	Mus musculus RIKEN cDNA 1110028C15 gene (1110028C15Rik), transcript variant 2, mRNA [NM_177645]	NM_177645
Gapt	0.0375	1.67	down	Mus musculus Grb2-binding adaptor, transmembrane (Gapt), mRNA [NM_177713]	NM_177713
Fam198a	0.0349	1.95	down	Mus musculus family with sequence similarity 198, member A (Fam198a), mRNA [NM_177743]	NM_177743
Apol10b	0.0300	1.63	down	Mus musculus apolipoprotein L 10b (Apol10b), mRNA [NM_177820]	NM_177820
Mttr15	0.0337	1.85	down	Mus musculus myotubularin related protein 15 (Mttr15), mRNA [NM_177893]	NM_177893
Hyal3	0.0054	1.71	down	Mus musculus hyaluronoglucosaminidase 3 (Hyal3), mRNA [NM_178020]	NM_178020
Hist2h2be	0.0125	1.76	down	Mus musculus histone cluster 2, H2be (Hist2h2be), mRNA [NM_178214]	NM_178214
Cpsf4	0.0161	1.55	down	Mus musculus cleavage and polyadenylation specific factor 4 (Cpsf4), mRNA [NM_178576]	NM_178576
Ano1	0.0368	2.06	down	Mus musculus anoctamin 1, calcium activated chloride channel (Ano1), mRNA [NM_178642]	NM_178642

B930041F14Rik	0.0307	2.62	down	Mus musculus RIKEN cDNA B930041F14 gene (B930041F14Rik), mRNA [NM_178699]	NM_178699
B930041F14Rik	0.0391	2.90	down	Mus musculus RIKEN cDNA B930041F14 gene (B930041F14Rik), mRNA [NM_178699]	NM_178699
Egflam	0.0001	2.30	down	Mus musculus EGF-like, fibronectin type III and laminin G domains (Egflam), mRNA [NM_178748]	NM_178748
Ccbe1	0.0314	2.09	down	Mus musculus collagen and calcium binding EGF domains 1 (Ccbe1), mRNA [NM_178793]	NM_178793
Trim65	0.0433	1.78	down	Mus musculus tripartite motif-containing 65 (Trim65), mRNA [NM_178802]	NM_178802
AI467606	0.0091	1.53	down	Mus musculus expressed sequence AI467606 (AI467606), mRNA [NM_178901]	NM_178901
BC005764	0.0303	3.28	down	Mus musculus cDNA sequence BC005764 (BC005764), transcript variant 1, mRNA [NM_181681]	NM_181681
Wfikkn2	0.0378	2.04	down	Mus musculus WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2 (Wfikkn2), mRNA [NM_181819]	NM_181819
Wfikkn2	0.0374	3.02	down	Mus musculus WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2 (Wfikkn2), mRNA [NM_181819]	NM_181819
Ankrd43	0.0319	1.93	down	Mus musculus ankyrin repeat domain 43 (Ankrd43), mRNA [NM_183173]	NM_183173
5830405N20Rik	0.0330	2.40	down	Mus musculus RIKEN cDNA 5830405N20 gene (5830405N20Rik), mRNA [NM_183264]	NM_183264
Gadd45gip1	0.0260	1.81	down	Mus musculus growth arrest and DNA-damage-inducible, gamma interacting protein 1 (Gadd45gip1), mRNA [NM_183358]	NM_183358
Slc23a3	0.0473	2.24	down	Mus musculus solute carrier family 23 (nucleobase transporters), member 3 (Slc23a3), mRNA [NM_194333]	NM_194333
1700025G04Rik	0.0329	1.59	down	Mus musculus RIKEN cDNA 1700025G04 gene (1700025G04Rik), mRNA [NM_197990]	NM_197990

Paqr6	0.0186	1.64	down	Mus musculus progesterin and adipoQ receptor family member VI (Paqr6), mRNA [NM_198410]	NM_198410
Acss3	0.0083	2.44	down	Mus musculus acyl-CoA synthetase short-chain family member 3 (Acss3), transcript variant 2, mRNA [NM_198636]	NM_198636
Hcrtr1	0.0351	2.90	down	Mus musculus hypocretin (orexin) receptor 1 (Hcrtr1), transcript variant 1, mRNA [NM_198959]	NM_198959
Cd300c	0.0221	2.43	down	Mus musculus CD300C antigen (Cd300c), mRNA [NM_199225]	NM_199225
Eif4ebp3	0.0238	1.60	down	Mus musculus eukaryotic translation initiation factor 4E binding protein 3 (Eif4ebp3), mRNA [NM_201256]	NM_201256
Flrt2	0.0306	1.64	down	Mus musculus fibronectin leucine rich transmembrane protein 2 (Flrt2), mRNA [NM_201518]	NM_201518
Tas2r117	0.0426	2.21	down	Mus musculus taste receptor, type 2, member 117 (Tas2r117), mRNA [NM_207021]	NM_207021
Cebpe	0.0418	1.66	down	Mus musculus CCAAT/enhancer binding protein (C/EBP), epsilon (Cebpe), mRNA [NM_207131]	NM_207131
BC068157	0.0499	3.01	down	Mus musculus cDNA sequence BC068157 (BC068157), mRNA [NM_207203]	NM_207203
Igsf3	0.0251	1.56	down	Mus musculus immunoglobulin superfamily, member 3 (Igsf3) mRNA [NM_207205]	NM_207205
Krt42	0.0346	3.41	down	Mus musculus keratin 42 (Krt42), mRNA [NM_212483]	NM_212483
H19	0.0244	3.54	down	Mus musculus H19 fetal liver mRNA (H19), non-coding RNA [NR_001592]	NR_001592
Malat1	0.0052	1.67	down	Mus musculus metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA) (Malat1), non-coding RNA [NR_002847]	NR_002847
Dio3os	0.0473	2.66	down	Mus musculus deiodinase, iodothyronine type III, opposite strand (Dio3os), non-coding RNA [NR_002866]	NR_002866
Dnm3os	0.0229	1.96	down	Mus musculus dynamin 3, opposite strand (Dnm3os), non-coding RNA [NR_002870]	NR_002870
Has2as	0.0385	1.90	down	Mus musculus HAS2 antisense RNA (non-protein coding) (Has2as), non-coding RNA [NR_002874]	NR_002874

H2afy3	0.0490	1.62	down	Mus musculus H2A histone family, member Y3 (H2afy3), non coding RNA [NR_003523]	NR_003523
Cyp2d13	0.0364	2.16	down	Mus musculus cytochrome P450, family 2, subfamily d, polypeptide 13 (Cyp2d13), non-coding RNA [NR_003552]	NR_003552
6330549D23Rik	0.0431	2.05	down	Mus musculus RIKEN cDNA 6330549D23 gene (6330549D23Rik), non-coding RNA [NR_003619]	NR_003619
Gm10653	0.0490	1.88	down	Mus musculus predicted gene 10653 (Gm10653), non-coding RNA [NR_003965]	NR_003965
Zfhx2as	0.0317	1.59	down	Mus musculus zinc finger homeobox 2, antisense (Zfhx2as), antisense RNA [NR_004444]	NR_004444
2610203C20Rik	0.0180	1.60	down	Mus musculus RIKEN cDNA 2610203C20 gene (2610203C20Rik), non-coding RNA [NR_015483]	NR_015483
2610035D17Rik	0.0228	1.55	down	Mus musculus RIKEN cDNA 2610035D17 gene (2610035D17Rik), non-coding RNA [NR_015556]	NR_015556
AI854703	0.0224	2.92	down	Mus musculus expressed sequence AI854703 (AI854703), non coding RNA [NR_027236]	NR_027236
1810032O08Rik	0.0462	1.60	down	Mus musculus RIKEN cDNA 1810032O08 gene (1810032O08Rik), transcript variant 3, non-coding RNA [NR_027821]	NR_027821
Gm5607	0.0071	1.83	down	Mus musculus predicted gene 5607 (Gm5607), non-coding RNA [NR_027975]	NR_027975
B230319C09Rik	0.0334	2.33	down	Mus musculus RIKEN cDNA B230319C09 gene (B230319C09Rik), non-coding RNA [NR_028382]	NR_028382
2900079G21Rik	0.0027	1.53	down	Mus musculus RIKEN cDNA 2900079G21 gene (2900079G21Rik), transcript variant 2, non-coding RNA [NR_033431]	NR_033431
Gm11517	0.0207	1.74	down	Mus musculus predicted gene 11517 (Gm11517), non-coding RNA [NR_033523]	NR_033523
	0.0097	1.80	down	M.musculus BALB/c IgG light chain variable region mRNA. [X79554]	X79554
Gm1998	0.0408	1.58	down	PREDICTED: Mus musculus similar to crooked legs CG14938-PB (LOC100038985), mRNA [XM_001472042]	XM_001472042

Gm2054	0.0437	1.98	down	PREDICTED: Mus musculus hypothetical protein LOC100039125 (LOC100039125), mRNA [XM_001472317]	XM_001472317
LOC100044107	0.0162	1.80	down	PREDICTED: Mus musculus similar to Guanine nucleotide binding protein, alpha z subunit (LOC100044107), mRNA [XM_001472591]	XM_001472591
Gm4125	0.0380	2.09	down	PREDICTED: Mus musculus similar to nuclear factor, interleukin 3 regulated (LOC100044670), mRNA [XM_001472807]	XM_001472807
LOC100039416	0.0374	2.15	down	PREDICTED: Mus musculus similar to OBOX4 (LOC100039416), mRNA [XM_001472845]	XM_001472845
	0.0339	1.94	down	thymocyte selection-associated high mobility group box Gen [Source:MGI (curated);Acc:MGI:2181659] [ENSMUST00000039987]	XM_001473004
Gm2285	0.0255	1.92	down	PREDICTED: Mus musculus hypothetical protein LOC100039518 (LOC100039518), mRNA [XM_001473039]	XM_001473039
	0.0189	1.52	down	PREDICTED: Mus musculus hypothetical protein LOC100045056 (LOC100045056), mRNA [XM_001473591]	XM_001473591
LOC100045292	0.0037	2.42	down	PREDICTED: Mus musculus similar to granulocyte-macrophage colony stimulating factor receptor low-affinity subunit (LOC100045292), mRNA [XM_001474011]	XM_001474011
Gm9465	0.0257	1.53	down	PREDICTED: Mus musculus hypothetical LOC669675 (LOC669675), mRNA [XM_001474101]	XM_001474101
LOC100045546	0.0025	2.41	down	PREDICTED: Mus musculus similar to Id4 (LOC100045546), mRNA [XM_001474498]	XM_001474498
LOC100045683	0.0455	2.21	down	PREDICTED: Mus musculus hypothetical protein LOC100045683 (LOC100045683), mRNA [XM_001474741]	XM_001474741
	0.0428	1.74	down	PREDICTED: Mus musculus similar to ribosomal protein L30 (LOC100045378), mRNA [XM_001474827]	XM_001474827

LOC100046071	0.0142	1.74	down	PREDICTED: Mus musculus similar to Ubtg protein (LOC100046071), mRNA [XM_001475526]	XM_001475526
LOC100046245	0.0086	2.02	down	PREDICTED: Mus musculus similar to Sek-3 (LOC100046245), mRNA [XM_001475860]	XM_001475860
Gm3218	0.0148	1.93	down	PREDICTED: Mus musculus hypothetical protein LOC100041229 (LOC100041229), mRNA [XM_001476005]	XM_001476005
	0.0140	1.76	down	cyclic nucleotide gated channel beta 1 Gene [Source:MGI (curated);Acc:MGI:2664102] [ENSMUST00000121162]	XM_001476198
Gm7684	0.0401	1.65	down	PREDICTED: Mus musculus similar to membrane-associated ring finger (C3HC4) 5 (LOC665553), mRNA [XM_001476311]	XM_001476311
LOC100046616	0.0159	2.46	down	PREDICTED: Mus musculus similar to aquaporin 5 (LOC100046616), mRNA [XM_001476512]	XM_001476512
LOC100047316	0.0410	2.66	down	predicted gene 1502 Gene [Source:MGI Symbol;Acc:MGI:2686348] [ENSMUST00000103348]	XM_001476590
A530001N23Rik	0.0420	4.52	down	PREDICTED: Mus musculus RIKEN cDNA A530001N23 gene (A530001N23Rik), mRNA [XM_001477625]	XM_001477625
4930480K23Rik	0.0348	1.51	down	PREDICTED: Mus musculus RIKEN cDNA 4930480K23 gene (4930480K23Rik), mRNA [XM_001477965]	XM_001477965
LOC100048869	0.0435	4.78	down	PREDICTED: Mus musculus similar to Inositol polyphosphate-5 phosphatase B (LOC100048869), mRNA [XM_001478120]	XM_001478120
LOC100047516	0.0410	1.66	down	PREDICTED: Mus musculus similar to casein kinase 1, gamma 3, transcript variant 1 (LOC100047516), mRNA [XM_001478504]	XM_001478504
Gm4662	0.0033	1.81	down	PREDICTED: Mus musculus hypothetical protein LOC100047500 (LOC100047500), mRNA [XM_001479134]	XM_001479134
2310047K21Rik	0.0415	1.80	down	PREDICTED: Mus musculus RIKEN cDNA 2310047K21 gene (2310047K21Rik), mRNA [XM_001479258]	XM_001479258

LOC100048079	0.0320	2.37	down	PREDICTED: Mus musculus similar to Zinc finger and BTB domain containing 1 (LOC100048079), mRNA [XM_001479478]	XM_001479478
Gm4368	0.0422	2.56	down	PREDICTED: Mus musculus similar to hCG2042411 (LOC100043332), mRNA [XM_001479985]	XM_001479985
Gm9647	0.0379	2.51	down	PREDICTED: Mus musculus hypothetical LOC675572 (LOC675572), mRNA [XM_001481199]	XM_001481199
LOC100048780	0.0046	1.71	down	PREDICTED: Mus musculus similar to MRC OX-2 antigen homolog (LOC100048780), mRNA [XM_001481225]	XM_001481225
BC034090	0.0107	2.13	down	MKIAA1614 protein Fragment [Source:UniProtKB/TrEMBL;Acc:Q6ZPL5]	XM_148974
	0.0254	4.12	down	[ENSMUST00000035914]	XM_356827
Gm6404	0.0286	1.82	down	PREDICTED: Mus musculus predicted gene, EG623174 (EG623174), mRNA [XM_887605]	XM_887605
2310010J17Rik	0.0122	1.98	down	PREDICTED: Mus musculus RIKEN cDNA 2310010J17 gene (2310010J17Rik), mRNA [XM_896611]	XM_896611
LOC631980	0.0331	2.52	down	PREDICTED: Mus musculus similar to AV320801 protein (LOC631980), mRNA [XM_905950]	XM_905950
H2-T18	0.0409	2.86	down	PREDICTED: Mus musculus histocompatibility 2, T region locus 18 (H2-T18), mRNA [XM_912024]	XM_912024
Gm7302	0.0023	1.74	down	PREDICTED: Mus musculus predicted gene, EG640554 (EG640554), mRNA [XM_917569]	XM_917569
LOC674050	0.0395	1.67	down	PREDICTED: Mus musculus similar to adaptor protein Gads (LOC674050), mRNA [XM_972673]	XM_972673
LOC674218	0.0284	1.57	down	PREDICTED: Mus musculus similar to 2900083I11Rik protein (LOC674218), mRNA [XM_972872]	XM_972872
LOC675087	0.0039	1.52	down	PREDICTED: Mus musculus hypothetical LOC675087 (LOC675087), mRNA [XM_979388]	XM_979388
Gm11787	0.0109	1.56	down	PREDICTED: Mus musculus similar to Yamaguchi sarcoma viral (v-yes-1) oncogene homolog (LOC666513), mRNA [XM_984338]	XM_984338

Gm8225	0.0490	1.64	down	PREDICTED: Mus musculus predicted gene, EG666668 (EG666668), mRNA [XM_985281]	XM_985281
4930597O21Rik	0.0298	3.36	down	RIKEN cDNA 4930597O21 gene Gene [Source:MGI Symbol;Acc:MGI:1922623] [ENSMUST00000065878]	XM_989547
Gm9634	0.0102	1.67	down	PREDICTED: Mus musculus similar to CDK105 (LOC675063), misc RNA [XR_004753]	XR_004753
Gm7078	0.0029	2.51	down	PREDICTED: Mus musculus similar to CG4090-PA (LOC632000), misc RNA [XR_031221]	XR_031221
Gm11826	0.0461	1.68	down	PREDICTED: Mus musculus similar to ribosomal protein L26 (LOC633461), misc RNA [XR_031506]	XR_031506
Gm4815	0.0244	1.51	down	PREDICTED: Mus musculus similar to calponin 3, acidic (LOC218501), misc RNA [XR_031538]	XR_031538
Gm4804	0.0461	1.67	down	PREDICTED: Mus musculus similar to Glyceraldehyde-3 phosphate dehydrogenase (GAPDH) (LOC633944), misc RNA [XR_032386]	XR_032386
Gm6483	0.0110	1.57	down	PREDICTED: Mus musculus similar to cadherin 11 (LOC624198), misc RNA [XR_032846]	XR_032846
Gm7693	0.0252	2.48	down	PREDICTED: Mus musculus similar to LOC654472 protein (LOC665570), misc RNA [XR_033989]	XR_033989
Gm9735	0.0220	1.52	down	PREDICTED: Mus musculus similar to neural visinin-like Ca ²⁺ -binding protein type 3 (LOC77114), misc RNA [XR_035629]	XR_035629
	0.0020	2.02	up	lincRNA:chr15:12126433-12126745 reverse strand	
	0.0221	2.16	up	lincRNA:chr2:128217275-128217972 reverse strand	
	0.0192	1.87	up	lincRNA:chr6:67155508-67216941 forward strand	
	0.0199	1.91	up	lincRNA:chr2:128211990-128215223 reverse strand	
	0.0257	1.99	up	lincRNA:chr17:38132217-38157667 reverse strand	
	0.0245	2.24	up	lincRNA:chr14:115423660-115463160 reverse strand	
	0.0352	1.78	up	lincRNA:chrX:146827709-146913398 reverse strand	
	0.0139	8.73	up	lincRNA:chr14:43418592-43428090 forward strand	
	0.0487	2.31	up	lincRNA:chr2:157361470-157379813 forward strand	
	0.0060	2.13	up	lincRNA:chr11:69106907-69112857 forward strand	

	0.0461	1.58	up	lincRNA:chr13:62734450-62785325 reverse strand	
	0.0301	2.64	up	lincRNA:chr10:81165750-81236400 forward strand	
	0.0223	2.55	up	lincRNA:chr7:132218864-132329172 forward strand	
	0.0192	2.40	up	lincRNA:chr8:87504644-87513694 forward strand	
	0.0144	2.66	up	lincRNA:chr15:60656586-60685333 reverse strand	
	0.0010	1.65	up	lincRNA:chr7:6296401-6311486 forward strand	
	0.0123	1.69	up	lincRNA:chr9:96664617-96683617 forward strand	
	0.0003	2.21	up	lincRNA:chr10:60473030-60535340 forward strand	
	0.0079	2.25	up	lincRNA:chrX:148732853-148761972 reverse strand	
	0.0137	1.70	up	lincRNA:chr6:127111250-127142925 forward strand	
	0.0385	1.67	up	lincRNA:chr14:103751075-103769725 forward strand	
	0.0365	1.52	up	lincRNA:chr12:110973190-110987668 forward strand	
	0.0268	1.70	up	lincRNA:chrX:35825525-35877700 reverse strand	
	0.0084	1.90	up	lincRNA:chr8:110197171-110206546 reverse strand	
	0.0485	1.81	up	lincRNA:chr4:149445201-149445902 forward strand	
	0.0139	1.82	up	lincRNA:chr8:129336539-129400338 reverse strand	
	0.0031	2.18	up	lincRNA:chr5:14923900-15062725 forward strand	
	0.0394	1.66	up	lincRNA:chr5:125190100-125209625 reverse strand	
	0.0168	1.87	up	lincRNA:chr1:90149027-90152254 forward strand	
	0.0162	2.29	up	lincRNA:chr6:145647711-145756861 reverse strand	
	0.0038	2.15	up	lincRNA:chr10:118385588-118439338 reverse strand	
	0.0379	1.57	up	lincRNA:chr13:62734450-62785325 reverse strand	
	0.0193	3.33	up	lincRNA:chr18:77968421-77972209 reverse strand	
	0.0378	1.55	up	lincRNA:chr17:95150800-95180650 reverse strand	
	0.0121	1.75	up	lincRNA:chr14:103751075-103769725 forward strand	
	0.0353	1.94	up	lincRNA:chr15:99765243-99783300 forward strand	
	0.0174	2.47	up	lincRNA:chr1:139814266-139817889 reverse strand	
	0.0472	2.17	up	lincRNA:chr7:48794017-48815817 reverse strand	
	0.0102	1.65	up	lincRNA:chr8:82836971-82849309 reverse strand	
	0.0374	2.24	up	lincRNA:chr1:85036677-85038530 reverse strand	
	0.0431	1.51	up	lincRNA:chr4:15233302-15233632 reverse strand	
	0.0096	2.44	up	lincRNA:chr7:6302922-6306477 forward strand	

	0.0447	1.67	up	lincRNA:chr12:111617728-111665403 reverse strand	
	0.0496	1.82	up	lincRNA:chr13:112337405-112356455 reverse strand	
	0.0152	2.03	up	lincRNA:chr4:146156575-146175425 reverse strand	
	0.0477	1.87	up	lincRNA:chr12:25866632-25874507 forward strand	
	0.0222	1.80	up	lincRNA:chr5:14923900-15062725 forward strand	
	0.0031	2.69	up	lincRNA:chr3:131153358-131154061 forward strand	
	0.0237	1.82	up	lincRNA:chr4:149445201-149445902 forward strand	
	0.0051	1.77	up	lincRNA:chr2:127988295-128194920 reverse strand	
	0.0115	5.21	up	lincRNA:chr17:38132217-38157667 forward strand	
	0.0054	1.51	up	lincRNA:chr4:146507925-146532650 forward strand	
	0.0302	1.81	up	lincRNA:chr6:117329899-117516899 forward strand	
	0.0348	1.60	up	lincRNA:chr4:124127144-124334840 reverse strand	
	0.0377	2.15	up		
	0.0498	1.89	up	lincRNA:chr1:138570107-138632310 forward strand	
	0.0117	2.19	up	lincRNA:chr5:92548501-92566401 forward strand	
	0.0220	2.82	up	lincRNA:chr17:88890039-88905680 forward strand	
	0.0080	2.10	up	lincRNA:chr3:34497447-34501170 reverse strand	
	0.0108	6.59	up	lincRNA:chr9:96670035-96682896 forward strand	
	0.0383	3.04	up	lincRNA:chr11:117835849-117842574 reverse strand	
	0.0355	1.62	up	WD repeat domain 67 Gene [Source:MGI Symbol;Acc:MGI:2684931] [ENSMUST00000110178]	
	0.0320	1.79	up	lincRNA:chr17:21177225-21187525 reverse strand	
	0.0373	1.51	up	lincRNA:chr15:79764481-79809909 forward strand	
	0.0214	2.53	down	lincRNA:chr1:160888257-160910594 reverse strand	
	0.0098	1.75	down	lincRNA:chr13:70762342-70776512 reverse strand	
	0.0368	2.10	down	lincRNA:chr1:196843592-196865102 forward strand	
	0.0399	1.52	down	lincRNA:chr13:34872696-34906407 reverse strand	
	0.0423	1.56	down	lincRNA:chr2:153163620-153170845 reverse strand	
	0.0235	2.30	down	lincRNA:chr6:117827499-117851478 reverse strand	
	0.0059	1.70	down	lincRNA:chr19:5795689-5802671 reverse strand	
	0.0413	2.18	down	lincRNA:chr15:83091086-83093818 reverse strand	

	0.0311	1.84	down	RNA binding motif protein 39 Gene [Source:MGI (curated);Acc:MGI:2157953] [ENSMUST00000109584]	
	0.0282	1.98	down	lincRNA:chr7:144563845-144603732 forward strand	
	0.0282	1.90	down	lincRNA:chr11:116936834-116948799 reverse strand	
	0.0414	1.84	down	lincRNA:chr3:85806420-85889300 reverse strand	
	0.0322	1.70	down	lincRNA:chr2:174088550-174109425 forward strand	
	0.0062	2.30	down	lincRNA:chrX:47890565-47915775 forward strand	
	0.0039	1.76	down	lincRNA:chr17:15357376-15385701 forward strand	
	0.0171	2.85	down	lincRNA:chr17:46972160-46997919 reverse strand	
	0.0192	1.80	down	lincRNA:chr16:7947710-7948066 reverse strand	
	0.0286	1.62	down	lincRNA:chr8:47813487-47824869 forward strand	
	0.0370	1.76	down	lincRNA:chr17:26911397-26917047 forward strand	
	0.0425	2.02	down	lincRNA:chr6:121035524-121061074 forward strand	
	0.0305	2.12	down	lincRNA:chr1:183783306-183834531 reverse strand	
	0.0328	1.60	down	lincRNA:chr4:133212951-133214017 reverse strand	
	0.0350	1.73	down	lincRNA:chr11:87872568-87880978 reverse strand	
	0.0427	1.84	down	lincRNA:chr17:79042382-79051807 reverse strand	
	0.0251	1.68	down	CDK5 regulatory subunit associated protein 1-like 1 Gene [Source:MGI (curated);Acc:MGI:1921765] [ENSMUST00000110323]	
	0.0042	2.79	down	lincRNA:chr2:75484041-75484815 reverse strand	
	0.0065	1.76	down	lincRNA:chr19:5795689-5802671 reverse strand	
	0.0279	2.35	down	lincRNA:chr11:112898724-113062945 reverse strand	
	0.0440	1.82	down	lincRNA:chr7:88131123-88136898 forward strand	
	0.0180	1.73	down	lincRNA:chr4:126710640-126721240 reverse strand	
	0.0322	1.85	down	lincRNA:chr9:41422319-41425855 forward strand	
	0.0025	3.09	down	lincRNA:chr3:35236023-35241498 reverse strand	
	0.0478	1.98	down	lincRNA:chr8:13200727-13207714 forward strand	
	0.0051	1.61	down	lincRNA:chr10:96098058-96098623 forward strand	
	0.0056	1.70	down	lincRNA:chr13:94182877-94203935 forward strand	
	0.0321	1.70	down	lincRNA:chr4:33375464-33377138 reverse strand	
	0.0379	3.61	down	lincRNA:chr3:95502970-95503399 reverse strand	

	0.0172	1.70	down	lincRNA:chr11:87872568-87880978 reverse strand	
	0.0256	2.80	down	lincRNA:chr8:93337794-93348869 reverse strand	
	0.0103	1.90	down	lincRNA:chr2:158169020-158191295 forward strand	
	0.0133	2.39	down	lincRNA:chr7:77555482-77634858 forward strand	
	0.0186	2.86	down	lincRNA:chr8:93337794-93348869 reverse strand	
	0.0328	1.73	down	lincRNA:chr5:122982442-123000053 reverse strand	
	0.0123	2.30	down	lincRNA:chr10:41368681-41393645 reverse strand	
	0.0403	1.76	down	lincRNA:chr8:41941084-41947630 reverse strand	
	0.0337	1.86	down	lincRNA:chr3:85784436-85784624 reverse strand	
	0.0103	1.54	down	lincRNA:chr10:81816994-81863610 forward strand	
	0.0348	1.63	down	POGZ_MOUSE (Q8BZH4) Pogo transposable element with ZNF domain, partial (4%) [TC1612650]	
	0.0295	1.58	down	lincRNA:chr17:26911397-26917047 reverse strand	
	0.0490	2.29	down	lincRNA:chr15:101084597-101095097 forward strand	
	0.0167	1.70	down	lincRNA:chr12:86415200-86415483 forward strand	
	0.0333	2.29	down	lincRNA:chr1:183783306-183834531 reverse strand	
	0.0040	2.49	down	lincRNA:chr9:118059348-118079494 forward strand	
	0.0206	1.80	down	lincRNA:chr8:87504644-87513694 reverse strand	
	0.0036	2.60	down	lincRNA:chr4:11102287-11118421 reverse strand	
	0.0466	1.72	down	lincRNA:chr17:21177225-21187525 reverse strand	
	0.0202	1.82	down	lincRNA:chr4:8566129-8568514 reverse strand	
	0.0119	2.68	down	lincRNA:chr18:36449530-36456800 reverse strand	
	0.0193	1.72	down	lincRNA:chr1:63163023-63180223 forward strand	
	0.0234	1.95	down	lincRNA:chr4:40194362-40202712 reverse strand	
	0.0423	1.57	down	lincRNA:chr5:100845342-100869667 reverse strand	
	0.0048	1.58	down	lincRNA:chr1:88524037-88540731 reverse strand	
	0.0450	2.21	down	lincRNA:chrX:133315875-133338600 forward strand	
	0.0143	2.33	down	lincRNA:chr3:127170996-127201096 forward strand	
	0.0478	3.49	down	lincRNA:chr6:93029101-93031007 forward strand	
	0.0069	1.61	down	lincRNA:chr15:100905367-100905654 reverse strand	
	0.0005	2.04	down	lincRNA:chr7:111530578-111539097 reverse strand	
	0.0077	1.56	down	lincRNA:chr10:39383665-39442690 reverse strand	

	0.0500	1.89	down	lincRNA:chr10:62267317-62269871 reverse strand	
	0.0160	1.76	down	lincRNA:chr11:112898724-113062945 forward strand	
	0.0465	1.74	down	lincRNA:chr16:4592919-4594230 reverse strand	
	0.0230	3.39	down	lincRNA:chr2:115900355-115900904 forward strand	
	0.0229	1.80	down	lincRNA:chr2:67834535-67834914 forward strand	
	0.0308	1.54	down	lincRNA:chr7:118248833-118267766 reverse strand	
	0.0101	1.89	down	lincRNA:chr19:5795689-5802671 reverse strand	
	0.0464	1.85	down	lincRNA:chr5:122982442-123000053 reverse strand	
	0.0118	1.56	down	lincRNA:chr11:3538125-3554450 forward strand	
	0.0046	2.60	down	lincRNA:chrX:148803114-148851243 forward strand	
	0.0427	1.76	down	lincRNA:chr1:95871175-95886625 forward strand	
	0.0020	1.62	down	lincRNA:chr15:96032592-96116907 forward strand	
	0.0167	3.38	down	lincRNA:chr2:115900355-115900904 forward strand	
	0.0437	1.77	down	lincRNA:chr2:75489436-75490163 reverse strand	
	0.0491	1.85	down	lincRNA:chr9:41408354-41420812 forward strand	
	0.0190	1.73	down	lincRNA:chr3:145269449-145298239 forward strand	
	0.0300	1.78	down	lincRNA:chr11:120046656-120050065 forward strand	
	0.0042	4.19	down	lincRNA:chr2:32950586-32984936 forward strand	
	0.0357	1.53	down	lincRNA:chr3:65729664-65731697 reverse strand	
	0.0186	2.76	down	lincRNA:chr7:134620707-134626739 forward strand	
	0.0022	1.55	down	lincRNA:chr7:77481448-77495548 forward strand	
	0.0249	1.65	down	lincRNA:chr6:12062275-12075800 reverse strand	
	0.0330	2.26	down	lincRNA:chr8:13200727-13207714 forward strand	
	0.0002	1.77	down	lincRNA:chr13:74712775-74728450 reverse strand	
	0.0360	1.58	down	lincRNA:chr10:93774693-93893616 forward strand	
	0.0184	1.73	down	lincRNA:chr15:96111929-96114921 reverse strand	
	0.0080	3.41	down	lincRNA:chr7:149761435-149764019 reverse strand	
	0.0087	2.11	down	lincRNA:chr11:120041124-120052299 reverse strand	
	0.0470	1.78	down	lincRNA:chr12:81217572-81233910 reverse strand	
	0.0014	1.58	down	lincRNA:chr11:53592946-53637922 forward strand	
	0.0259	2.53	down	lincRNA:chr2:155298877-155303251 forward strand	

	0.0073	1.60	down	non-metastatic cells 1, protein (NM23A) expressed in Gene [Source:MGI (curated);Acc:MGI:97355] [ENSMUST00000107844]	
	0.0478	2.80	down	lincRNA:chr3:27837825-27880925 reverse strand	
	0.0073	1.84	down	lincRNA:chr11:112905201-113062945 reverse strand	
	0.0248	1.84	down	lincRNA:chr4:135896689-135918414 forward strand	
	0.0466	1.56	down	lincRNA:chr12:81217572-81233910 reverse strand	
	0.0066	1.70	down	lincRNA:chr2:92582386-92599365 forward strand	
	0.0045	1.89	down	lincRNA:chr16:4585697-4594022 reverse strand	
	0.0100	2.32	down	lincRNA:chrX:120134722-120138152 reverse strand	
	0.0424	1.78	down	lincRNA:chr9:100977450-100989325 forward strand	
	0.0092	1.89	down	lincRNA:chr8:57977383-57985712 forward strand	
	0.0309	1.58	down	lincRNA:chr5:106126051-106128392 reverse strand	
	0.0115	1.61	down	lincRNA:chr8:74439200-74441363 forward strand	
	0.0173	1.76	down	lincRNA:chr4:88604248-88645948 forward strand	
	0.0196	1.60	down	lincRNA:chr2:116796887-116797441 forward strand	
	0.0132	1.95	down	lincRNA:chr5:125078875-125098525 reverse strand	
	0.0327	1.51	down	lincRNA:chr15:77575125-77585575 forward strand	
	0.0303	1.59	down	lincRNA:chr6:31017987-31174287 reverse strand	
	0.0127	2.50	down	lincRNA:chr7:16584852-16657252 forward strand	
	0.0438	1.61	down	lincRNA:chr16:13752215-13764390 forward strand	
	0.0056	1.55	down	lincRNA:chr10:126818382-126856582 forward strand	
	0.0108	1.94	down	lincRNA:chr2:155269145-155303251 forward strand	
	0.0220	2.03	down	lincRNA:chr5:113594167-113645342 reverse strand	
	0.0161	1.60	down	lincRNA:chr4:56480568-56658018 forward strand	
	0.0205	2.64	down	lincRNA:chr5:110158475-110223700 forward strand	
	0.0064	2.60	down	lincRNA:chrX:45814752-45816313 reverse strand	
	0.0134	1.89	down	lincRNA:chr8:96983590-96994419 forward strand	
	0.0424	1.73	down	lincRNA:chr11:97457180-97487074 reverse strand	
	0.0303	3.41	down	lincRNA:chr11:95483973-95490751 forward strand	
	0.0403	1.96	down	lincRNA:chr11:87841800-87858725 reverse strand	
	0.0218	3.28	down	lincRNA:chr13:51248372-51259297 forward strand	

	0.0399	1.82	down	lincRNA:chr8:114477602-114488627 reverse strand	
	0.0001	1.61	down	lincRNA:chr14:67585234-67596823 reverse strand	
	0.0163	2.55	down	lincRNA:chr15:85476512-85498105 forward strand	
	0.0340	1.77	down	aryl hydrocarbon receptor nuclear translocator Gene [Source:MG (curated);Acc:MGI:88071] [ENSMUST00000107160]	
	0.0488	1.73	down	lincRNA:chr16:43623581-43642715 reverse strand	
	0.0137	2.68	down	lincRNA:chr8:93337794-93348869 reverse strand	
	0.0499	4.50	down	lincRNA:chr13:94198298-94198965 reverse strand	
	0.0426	2.78	down	lincRNA:chrX:47890565-47915775 forward strand	
	0.0059	3.88	down	lincRNA:chr15:96091428-96115684 forward strand	
	0.0089	2.16	down	lincRNA:chr1:160888257-160910594 reverse strand	
	0.0376	2.48	down	lincRNA:chr6:50361567-50406200 reverse strand	
	0.0319	2.28	down	lincRNA:chr17:13806767-13824342 reverse strand	
	0.0213	1.60	down	lincRNA:chr15:61870759-61938796 forward strand	
	0.0311	1.70	down	lincRNA:chr12:117623500-117643575 reverse strand	
	0.0122	1.81	down	lincRNA:chr17:21785442-21801542 forward strand	
	0.0255	2.37	down	lincRNA:chr10:21688115-21710890 reverse strand	
	0.0487	2.42	down	lincRNA:chr19:46422690-46423478 reverse strand	
	0.0182	4.17	down	lincRNA:chr8:110196655-110390197 forward strand	
	0.0377	2.50	down	lincRNA:chr3:96289850-96301078 forward strand	
	0.0036	1.54	down	lincRNA:chr12:86415200-86415483 forward strand	
	0.0107	1.96	down	lincRNA:chr2:75444518-75497268 reverse strand	
	0.0340	3.66	down	lincRNA:chr1:82892851-82943201 reverse strand	
	0.0189	1.59	down	lincRNA:chr3:19211659-19213735 forward strand	
	0.0388	2.91	down	lincRNA:chr8:122997422-122998001 forward strand	
	0.0094	4.92	down	lincRNA:chr13:108825897-108833335 reverse strand	
	0.0147	1.79	down	lincRNA:chr11:112905201-113062945 reverse strand	
	0.0339	2.53	down	lincRNA:chr8:37582187-37621987 forward strand	
	0.0040	1.75	down	lincRNA:chr5:123582742-123588202 forward strand	
	0.0374	1.96	down	lincRNA:chr10:21855725-21867925 reverse strand	
	0.0465	2.13	down	lincRNA:chr2:175432867-175469471 reverse strand	

	0.0195	1.97	down	lincRNA:chr13:48620882-48643532 reverse strand	
	0.0007	2.30	down	lincRNA:chr5:74487385-74497428 forward strand	
	0.0246	4.05	down	lincRNA:chr6:93029101-93031007 forward strand	
	0.0232	1.74	down	lincRNA:chr14:76912477-76931702 forward strand	
	0.0094	1.57	down	lincRNA:chr15:102100397-102105872 reverse strand	
	0.0011	3.98	down	lincRNA:chr2:22753100-22780375 reverse strand	
	0.0284	1.76	down	lincRNA:chr13:61703445-62094670 forward strand	
	0.0294	2.56	down	lincRNA:chr5:121759042-121789992 reverse strand	
	0.0219	1.91	down	lincRNA:chr4:135896689-135918414 reverse strand	
	0.0201	3.46	down	lincRNA:chr5:30550467-30559008 reverse strand	
	0.0038	2.47	down	lincRNA:chr11:19960515-19961093 reverse strand	
	0.0190	3.13	down	lincRNA:chr6:47915489-47916089 forward strand	
	0.0122	1.53	down	lincRNA:chr12:117623500-117643575 reverse strand	
	0.0327	1.64	down	lincRNA:chr4:11102287-11118421 reverse strand	
	0.0003	2.76	down	lincRNA:chr7:129294166-129301366 forward strand	
	0.0405	1.68	down	lincRNA:chr7:140016236-140016772 reverse strand	
	0.0038	3.24	down	lincRNA:chr10:117021051-117038683 reverse strand	
	0.0129	1.53	down	lincRNA:chr17:27703181-27716306 forward strand	
	0.0377	2.87	down	lincRNA:chr3:37797734-37891650 forward strand	
	0.0440	2.07	down	lincRNA:chr11:112898724-113062945 reverse strand	
	0.0037	2.97	down	lincRNA:chr6:127588224-127609749 reverse strand	
	0.0162	3.56	down	lincRNA:chr17:33368400-33393525 forward strand	
	0.0381	2.80	down	lincRNA:chr5:92548501-92566401 reverse strand	
	0.0212	2.99	down	lincRNA:chr9:41488229-41545481 reverse strand	
	0.0451	2.80	down	lincRNA:chr4:155560050-155570900 reverse strand	
	0.0192	2.61	down	lincRNA:chr12:74135916-74142780 forward strand	
Dnajc5	0.0284	1.75	down	DnaJ (Hsp40) homolog, subfamily C, member 5 Gene [Source:MGI (curated);Acc:MGI:892995] [ENSMUST00000108796]	
	0.0450	1.78	down	lincRNA:chr12:72103832-72116875 reverse strand	
	0.0225	2.78	down	lincRNA:chr1:167797581-167803031 forward strand	
	0.0406	2.62	down	lincRNA:chr1:85300475-85331475 reverse strand	

	0.0072	2.08	down	lincRNA:chr11:112905201-113062945 reverse strand	
	0.0191	1.64	down	lincRNA:chr8:126396600-126407275 forward strand	
	0.0151	2.00	down	lincRNA:chr5:137392195-137426421 reverse strand	
	0.0194	2.22	down	lincRNA:chr11:112898724-113062945 reverse strand	
	0.0091	2.60	down	lincRNA:chr2:170029045-170034220 forward strand	
	0.0073	1.98	down	lincRNA:chr17:46972160-46997919 reverse strand	
	0.0332	1.60	down	lincRNA:chr5:124694137-124695689 reverse strand	
	0.0084	1.64	down	lincRNA:chr15:83281223-83284791 reverse strand	
	0.0205	2.07	down	lincRNA:chr8:124355710-124401160 forward strand	
	0.0140	2.18	down	lincRNA:chr9:118060025-118085050 forward strand	
	0.0041	2.18	down	lincRNA:chr1:183783306-183834531 reverse strand	
	0.0430	1.89	down	lincRNA:chr11:120041124-120052299 reverse strand	
	0.0281	3.42	down	lincRNA:chr18:57124435-57134910 reverse strand	
	0.0235	2.53	down	lincRNA:chr14:55317199-55317670 reverse strand	
	0.0318	3.53	down	lincRNA:chr14:79724027-79729152 forward strand	
	0.0193	2.51	down	lincRNA:chr17:88466300-88495175 forward strand	
	0.0128	3.12	down	lincRNA:chrX:47890565-47915775 forward strand	
	0.0004	3.37	down	lincRNA:chr2:108456668-108532418 reverse strand	
	0.0379	2.24	down	lincRNA:chr11:112898724-113062945 reverse strand	
	0.0433	1.62	down	lincRNA:chr1:59773381-59775888 forward strand	
	0.0303	1.70	down	lincRNA:chr9:43738583-43757007 reverse strand	
	0.0244	1.63	down	lincRNA:chr1:36012298-36020311 reverse strand	
	0.0373	1.55	down	lincRNA:chr8:26343277-26352902 reverse strand	
	0.0267	3.32	down	lincRNA:chr9:106170918-106177894 reverse strand	
	0.0305	2.67	down	lincRNA:chr10:24269165-24276690 reverse strand	
	0.0126	1.68	down	lincRNA:chr11:6421951-6429173 forward strand	
	0.0021	2.64	down	lincRNA:chr3:108763862-108772151 forward strand	
	0.0138	2.93	down	lincRNA:chr1:137482591-137625604 forward strand	
	0.0222	1.51	down	lincRNA:chr10:83364590-83364873 forward strand	
	0.0366	1.86	down	lincRNA:chr16:43623581-43642715 reverse strand	
	0.0161	1.88	down	lincRNA:chr12:74883691-74893323 reverse strand	
	0.0215	1.72	down	lincRNA:chr10:39383665-39442690 reverse strand	

	0.0178	1.57	down	lincRNA:chr3:51890691-51891781 reverse strand	
	0.0303	2.16	down	lincRNA:chrX:20539200-20563428 forward strand	
	0.0326	1.70	down	lincRNA:chr9:66981366-67061725 forward strand	
	0.0348	1.88	down	lincRNA:chr5:122047900-122065325 forward strand	
	0.0101	1.79	down	lincRNA:chr4:129376440-129391690 reverse strand	
	0.0026	6.30	down	lincRNA:chr4:116790373-116797823 forward strand	
	0.0008	1.73	down	lincRNA:chr19:5771425-5848475 reverse strand	
	0.0003	2.73	down	lincRNA:chr13:70745306-70837331 forward strand	
	0.0285	1.64	down	lincRNA:chr11:59206727-59207172 reverse strand	
	0.0119	1.62	down	lincRNA:chr9:20784567-20799942 reverse strand	
	0.0437	1.92	down	lincRNA:chr15:102100964-102104552 forward strand	
	0.0371	1.94	down	lincRNA:chr6:31017987-31174287 reverse strand	
	0.0198	1.93	down	lincRNA:chr2:126501651-126510026 forward strand	
	0.0211	1.88	down	lincRNA:chr11:6748267-6818192 forward strand	
	0.0160	2.25	down	lincRNA:chr17:8088950-8106700 reverse strand	
	0.0115	2.03	down	lincRNA:chr12:81217572-81233910 reverse strand	
	0.0365	2.58	down	lincRNA:chr2:60038543-60046318 forward strand	
	0.0052	2.30	down	lincRNA:chr13:67211950-67217199 reverse strand	
	0.0166	8.74	down	lincRNA:chr13:97700327-97700876 forward strand	
	0.0073	1.51	down	lincRNA:chr18:84735774-84760824 reverse strand	
	0.0409	3.65	down	lincRNA:chr12:76771424-76772158 forward strand	
	0.0483	2.01	down	MTERF domain containing 2 Gene [Source:MGI (curated);Acc:MGI:1918355] [ENSMUST00000112942]	
	0.0114	2.24	down	lincRNA:chr18:35976163-35976530 forward strand	
	0.0220	2.19	down	lincRNA:chr19:57426515-57435165 reverse strand	
	0.0000	1.94	down	lincRNA:chr5:29779847-29784383 forward strand	
	0.0321	2.92	down	lincRNA:chr6:5311375-5328075 forward strand	
	0.0148	1.55	down	lincRNA:chr15:83266264-83294664 reverse strand	
	0.0432	2.29	down	lincRNA:chr3:96289850-96301078 forward strand	
	0.0339	2.39	down	lincRNA:chr7:16584852-16657252 reverse strand	
	0.0408	2.11	down	lincRNA:chr4:3745750-3756200 forward strand	
	0.0374	1.68	down	lincRNA:chr8:19682258-19700836 forward strand	

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM	GO:00423	20	1.5625	4.09E-06	NM_0333	722	109	13588	3.453201	0.010753	0.010753	0.007269
GOTERM	GO:00069	20	1.5625	4.09E-06	NM_0333	722	109	13588	3.453201	0.010753	0.010753	0.007269
GOTERM	GO:00069	47	3.671875	4.57E-05	NM_0083	722	471	13588	1.877999	0.113556	0.058488	0.081012
GOTERM	GO:00026	26	2.03125	9.47E-05	NM_0134	722	206	13588	2.375333	0.221151	0.079937	0.167908
GOTERM	GO:00300	18	1.40625	1.02E-04	NM_0333	722	114	13588	2.97157	0.237066	0.065409	0.181765
GOTERM	GO:00302	14	1.09375	1.63E-04	NM_0333	722	76	13588	3.466832	0.350231	0.082615	0.289461
GOTERM	GO:00025	20	1.5625	1.81E-04	NM_0333	722	142	13588	2.650696	0.379101	0.076358	0.319926
GOTERM	GO:00017	28	2.1875	2.76E-04	NM_0333	722	246	13588	2.142108	0.517058	0.098756	0.488189
GOTERM	GO:00099	22	1.71875	2.85E-04	NM_0158	722	171	13588	2.421279	0.528615	0.089726	0.504394
GOTERM	GO:00125	44	3.4375	3.93E-04	NM_1722	722	473	13588	1.750693	0.645749	0.108906	0.695314
GOTERM	GO:00076	27	2.109375	4.08E-04	NM_0333	722	239	13588	2.126103	0.659389	0.102104	0.721527
GOTERM	GO:00082	46	3.59375	4.88E-04	NM_1722	722	507	13588	1.707529	0.724233	0.110512	0.862395
GOTERM	GO:00162	46	3.59375	8.01E-04	NM_1722	722	519	13588	1.668049	0.879356	0.161585	1.411921
GOTERM	GO:00485	22	1.71875	8.79E-04	NM_0200	722	186	13588	2.226015	0.901779	0.163478	1.54813
GOTERM	GO:00106	22	1.71875	8.79E-04	NM_0158	722	186	13588	2.226015	0.901779	0.163478	1.54813
GOTERM	GO:00069	25	1.953125	8.83E-04	NM_0134	722	225	13588	2.091105	0.902866	0.153418	1.555499
GOTERM	GO:00421	16	1.25	0.001197	NM_0333	722	116	13588	2.595854	0.957684	0.190095	2.103951
GOTERM	GO:00466	22	1.71875	0.001235	NM_0333	722	191	13588	2.167742	0.961704	0.184456	2.169635
GOTERM	GO:00453	24	1.875	0.00138	NM_0333	722	219	13588	2.06246	0.973886	0.192998	2.421169
GOTERM	GO:00096	33	2.578125	0.001681	NM_0110	722	347	13588	1.789793	0.988235	0.218712	2.942862
GOTERM	GO:00069	41	3.203125	0.001774	NM_1722	722	465	13588	1.659393	0.990786	0.218614	3.102238
GOTERM	GO:00063	15	1.171875	0.001838	NM_1986	722	109	13588	2.589901	0.992228	0.215621	3.21308
GOTERM	GO:00430	6	0.46875	0.001993	NM_0098	722	18	13588	6.273315	0.994837	0.2218	3.478833
GOTERM	GO:00507	17	1.328125	0.002278	NM_0200	722	136	13588	2.352493	0.99757	0.239391	3.966783
GOTERM	GO:00026	13	1.015625	0.002288	NM_1458	722	88	13588	2.780219	0.997635	0.231185	3.984098
GOTERM	GO:00400	7	0.546875	0.00248	NM_0088	722	27	13588	4.879245	0.998579	0.239046	4.312513
GOTERM	GO:00512	19	1.484375	0.002549	NM_0200	722	163	13588	2.193736	0.998815	0.236258	4.429372
GOTERM	GO:00459	10	0.78125	0.002551	NM_0088	722	56	13588	3.360704	0.99882	0.228434	4.432271
GOTERM	GO:00027	11	0.859375	0.003677	NM_1458	722	70	13588	2.95742	0.99994	0.302456	6.329595
GOTERM	GO:00508	18	1.40625	0.003798	NM_0083	722	156	13588	2.171532	0.999957	0.301486	6.531728
GOTERM	GO:00022	12	0.9375	0.005636	NM_0200	722	86	13588	2.626039	1	0.402189	9.544833
GOTERM	GO:00330	7	0.546875	0.006062	XM_9842	722	32	13588	4.116863	1	0.414358	10.23037

GOTERM	GO:00508	13	1.015625	0.007113	NM_0083	722	101	13588	2.422369	1	0.455505	11.90066
GOTERM	GO:00026	17	1.328125	0.007721	NM_0083	722	154	13588	2.077526	1	0.472411	12.85341
GOTERM	GO:00485	26	2.03125	0.008022	NM_1331	722	281	13588	1.741347	1	0.475005	13.32215
GOTERM	GO:00082	26	2.03125	0.009098	NM_1331	722	284	13588	1.722953	1	0.508194	14.97566
GOTERM	GO:00430	44	3.4375	0.009424	NM_0083	722	560	13588	1.47871	1	0.510438	15.47145
GOTERM	GO:00512	16	1.25	0.009488	NM_0083	722	144	13588	2.091105	1	0.502967	15.56744
GOTERM	GO:00400	24	1.875	0.009536	NM_0236	722	256	13588	1.76437	1	0.495235	15.64003
GOTERM	GO:00026	8	0.625	0.010106	NM_1458	722	46	13588	3.273034	1	0.506215	16.49744
GOTERM	GO:00109	44	3.4375	0.010339	NM_0083	722	563	13588	1.47083	1	0.505155	16.84596
GOTERM	GO:00456	9	0.703125	0.011052	NM_0010	722	58	13588	2.920336	1	0.519779	17.90339
GOTERM	GO:00508	13	1.015625	0.011909	NM_0083	722	108	13588	2.265364	1	0.537639	19.15634
GOTERM	GO:00429	43	3.359375	0.012193	NM_0083	722	553	13588	1.463395	1	0.537515	19.56845
GOTERM	GO:00421	9	0.703125	0.01221	NM_0098	722	59	13588	2.870839	1	0.529628	19.59227
GOTERM	GO:00182	7	0.546875	0.012431	NM_0083	722	37	13588	3.56053	1	0.527883	19.91134
GOTERM	GO:00181	7	0.546875	0.012431	NM_0083	722	37	13588	3.56053	1	0.527883	19.91134
GOTERM	GO:00430	23	1.796875	0.012776	NM_0083	722	248	13588	1.745398	1	0.529681	20.40639
GOTERM	GO:00430	23	1.796875	0.013822	NM_0083	722	250	13588	1.731435	1	0.550117	21.88966
GOTERM	GO:00025	26	2.03125	0.014259	NM_1331	722	295	13588	1.658707	1	0.553674	22.50269
GOTERM	GO:00300	23	1.796875	0.014532	NM_1331	722	251	13588	1.724537	1	0.55297	22.88267
GOTERM	GO:00069	36	2.8125	0.014535	NM_0083	722	448	13588	1.512317	1	0.545626	22.88615
GOTERM	GO:00063	10	0.78125	0.014745	NM_1725	722	73	13588	2.578075	1	0.543575	23.17786
GOTERM	GO:00109	23	1.796875	0.014996	NM_0083	722	252	13588	1.717693	1	0.54258	23.52482
GOTERM	GO:00026	12	0.9375	0.015666	NM_0010	722	99	13588	2.281205	1	0.5514	24.44205
GOTERM	GO:00017	7	0.546875	0.015957	NM_0098	722	39	13588	3.377939	1	0.55124	24.83865
GOTERM	GO:00314	10	0.78125	0.017382	NM_1725	722	75	13588	2.509326	1	0.575676	26.74686
GOTERM	GO:00347	10	0.78125	0.018822	NM_1725	722	76	13588	2.476308	1	0.598312	28.62954
GOTERM	GO:00650	10	0.78125	0.018822	NM_1725	722	76	13588	2.476308	1	0.598312	28.62954
GOTERM	GO:00027	8	0.625	0.019237	NM_0200	722	52	13588	2.895376	1	0.599767	29.16269
GOTERM	GO:00022	6	0.46875	0.019605	NM_0098	722	30	13588	3.763989	1	0.60029	29.63282
GOTERM	GO:00421	41	3.203125	0.019663	NM_1331	722	538	13588	1.434234	1	0.595029	29.70781
GOTERM	GO:00321	12	0.9375	0.020521	NM_0098	722	103	13588	2.192615	1	0.604577	30.79184
GOTERM	GO:00099	17	1.328125	0.020616	NM_1458	722	172	13588	1.860111	1	0.60012	30.91058
GOTERM	GO:00027	9	0.703125	0.021092	NM_1458	722	65	13588	2.605838	1	0.602523	31.50458

GOTERM	GO:00512	10	0.78125	0.021959	NM_0085	722	78	13588	2.412813	1	0.611498	32.57318
GOTERM	GO:00509	4	0.3125	0.022842	NM_0111	722	12	13588	6.273315	1	0.620268	33.6453
GOTERM	GO:00029	4	0.3125	0.022842	NM_0098	722	12	13588	6.273315	1	0.620268	33.6453
GOTERM	GO:00020	5	0.390625	0.02286	NM_0111	722	21	13588	4.480939	1	0.614778	33.66742
GOTERM	GO:00450	5	0.390625	0.02286	NM_0333	722	21	13588	4.480939	1	0.614778	33.66742
GOTERM	GO:00508	9	0.703125	0.022927	NM_0010	722	66	13588	2.566356	1	0.610162	33.74753
GOTERM	GO:00071	42	3.28125	0.023501	NM_0106	722	561	13588	1.40898	1	0.613754	34.43568
GOTERM	GO:00015	11	0.859375	0.023719	NM_0236	722	92	13588	2.250211	1	0.611654	34.69437
GOTERM	GO:00226	42	3.28125	0.024091	NM_0106	722	562	13588	1.406473	1	0.611997	35.13462
GOTERM	GO:00072	3	0.234375	0.025258	NM_0119	722	5	13588	11.29197	1	0.624247	36.49841
GOTERM	GO:00434	11	0.859375	0.025364	NM_0111	722	93	13588	2.226015	1	0.620505	36.62003
GOTERM	GO:00506	10	0.78125	0.025454	NM_0098	722	80	13588	2.352493	1	0.61662	36.72464
GOTERM	GO:00329	10	0.78125	0.025454	NM_0098	722	80	13588	2.352493	1	0.61662	36.72464
GOTERM	GO:00450	12	0.9375	0.026405	NM_0010	722	107	13588	2.110648	1	0.62514	37.81153
GOTERM	GO:00512	11	0.859375	0.027089	NM_0010	722	94	13588	2.202334	1	0.629596	38.58203
GOTERM	GO:00027	7	0.546875	0.027655	NM_0200	722	44	13588	2.994082	1	0.632309	39.21348
GOTERM	GO:00400	7	0.546875	0.027655	NM_0111	722	44	13588	2.994082	1	0.632309	39.21348
GOTERM	GO:00706	10	0.78125	0.029326	NM_0098	722	82	13588	2.295115	1	0.649267	41.04172
GOTERM	GO:00507	8	0.625	0.030338	NM_0098	722	57	13588	2.641396	1	0.657047	42.12278
GOTERM	GO:00400	12	0.9375	0.031555	NM_0106	722	110	13588	2.053085	1	0.666909	43.39926
GOTERM	GO:00301	7	0.546875	0.033594	NM_0088	722	46	13588	2.863905	1	0.685432	45.47694
GOTERM	GO:00066	17	1.328125	0.035677	NM_1342	722	184	13588	1.738799	1	0.703	47.52573
GOTERM	GO:00193	5	0.390625	0.035824	NM_1979	722	24	13588	3.920822	1	0.699973	47.66761
GOTERM	GO:00344	5	0.390625	0.035824	NM_1979	722	24	13588	3.920822	1	0.699973	47.66761
GOTERM	GO:00510	19	1.484375	0.035959	NM_0205	722	214	13588	1.67093	1	0.696867	47.79761
GOTERM	GO:00421	6	0.46875	0.035991	NM_0098	722	35	13588	3.226276	1	0.692752	47.82839
GOTERM	GO:00069	3	0.234375	0.036569	XM_9842	722	6	13588	9.409972	1	0.694243	48.38106
GOTERM	GO:00702	3	0.234375	0.036569	XM_9842	722	6	13588	9.409972	1	0.694243	48.38106
GOTERM	GO:00455	7	0.546875	0.040301	NM_0010	722	48	13588	2.744575	1	0.725504	51.8169
GOTERM	GO:00027	7	0.546875	0.040301	NM_0200	722	48	13588	2.744575	1	0.725504	51.8169
GOTERM	GO:00076	31	2.421875	0.040913	NM_0333	722	405	13588	1.440539	1	0.726764	52.35943
GOTERM	GO:00450	4	0.3125	0.041989	NM_0333	722	15	13588	5.018652	1	0.732011	53.29967
GOTERM	GO:00090	4	0.3125	0.041989	NM_0097	722	15	13588	5.018652	1	0.732011	53.29967

GOTERM	GO:00106	17	1.328125	0.043878	NM_1458	722	189	13588	1.692799	1	0.743739	54.90729
GOTERM	GO:00019	21	1.640625	0.04404	NM_0196	722	250	13588	1.580875	1	0.741067	55.0432
GOTERM	GO:00072	20	1.5625	0.046294	NM_0103	722	236	13588	1.594911	1	0.754879	56.88741
GOTERM	GO:00070	5	0.390625	0.046398	BC028435	722	26	13588	3.61922	1	0.75182	56.97135
GOTERM	GO:00072	9	0.703125	0.047721	NM_0167	722	76	13588	2.228678	1	0.757936	58.01845
GOTERM	GO:00329	7	0.546875	0.047798	NM_0098	722	50	13588	2.634792	1	0.754747	58.07898
GOTERM	GO:00506	7	0.546875	0.047798	NM_0098	722	50	13588	2.634792	1	0.754747	58.07898
GOTERM	GO:00510	13	1.015625	0.047817	NM_0200	722	132	13588	1.853479	1	0.751152	58.09361
GOTERM	GO:00063	25	1.953125	0.048136	NM_0010	722	315	13588	1.493646	1	0.749808	58.34214
GOTERM	GO:00507	3	0.234375	0.049424	NM_1458	722	7	13588	8.065691	1	0.755504	59.33106
GOTERM	GO:00458	3	0.234375	0.049424	NM_0091	722	7	13588	8.065691	1	0.755504	59.33106
GOTERM	GO:00327	3	0.234375	0.049424	NM_1458	722	7	13588	8.065691	1	0.755504	59.33106
GOTERM	GO:00327	3	0.234375	0.049424	NM_1458	722	7	13588	8.065691	1	0.755504	59.33106
GOTERM	GO:00507	3	0.234375	0.049424	NM_1458	722	7	13588	8.065691	1	0.755504	59.33106
GOTERM	GO:00507	3	0.234375	0.049424	NM_1458	722	7	13588	8.065691	1	0.755504	59.33106
GOTERM	GO:00507	3	0.234375	0.049424	NM_1458	722	7	13588	8.065691	1	0.755504	59.33106
GOTERM	GO:00507	3	0.234375	0.049424	NM_1458	722	7	13588	8.065691	1	0.755504	59.33106
GOTERM	GO:00450	3	0.234375	0.049424	BC028435	722	7	13588	8.065691	1	0.755504	59.33106
GOTERM	GO:00066	4	0.3125	0.0497	NM_0089	722	16	13588	4.704986	1	0.753866	59.54045
GOTERM	GO:00455	4	0.3125	0.0497	NM_0115	722	16	13588	4.704986	1	0.753866	59.54045
GOTERM	GO:00603	5	0.390625	0.052267	NM_0111	722	27	13588	3.485175	1	0.768008	61.4373
GOTERM	GO:00305	5	0.390625	0.052267	NM_0111	722	27	13588	3.485175	1	0.768008	61.4373
GOTERM	GO:00321	6	0.46875	0.053784	NM_0111	722	39	13588	2.895376	1	0.774467	62.51819
GOTERM	GO:00706	7	0.546875	0.056103	NM_0098	722	52	13588	2.533454	1	0.78555	64.11563
GOTERM	GO:00512	11	0.859375	0.057575	NM_0106	722	107	13588	1.934761	1	0.791015	65.09634
GOTERM	GO:00421	5	0.390625	0.058521	NM_0083	722	28	13588	3.360704	1	0.793247	65.71266
GOTERM	GO:00015	20	1.5625	0.061174	NM_0196	722	244	13588	1.542618	1	0.804818	67.38796
GOTERM	GO:00090	3	0.234375	0.063626	NM_0097	722	8	13588	7.057479	1	0.814556	68.86754
GOTERM	GO:00070	3	0.234375	0.063626	BC028435	722	8	13588	7.057479	1	0.814556	68.86754
GOTERM	GO:00450	3	0.234375	0.063626	NM_0333	722	8	13588	7.057479	1	0.814556	68.86754
GOTERM	GO:00512	6	0.46875	0.064288	NM_0103	722	41	13588	2.754138	1	0.814881	69.25599
GOTERM	GO:00024	6	0.46875	0.064288	NM_0200	722	41	13588	2.754138	1	0.814881	69.25599
GOTERM	GO:00463	9	0.703125	0.064932	NM_0097	722	81	13588	2.091105	1	0.815108	69.62903
GOTERM	GO:00160	9	0.703125	0.064932	NM_0097	722	81	13588	2.091105	1	0.815108	69.62903

GOTERM	GO:00606	4	0.3125	0.067005	NM_0196	722	18	13588	4.18221	1	0.822243	70.80227
GOTERM	GO:00109	4	0.3125	0.067005	NM_0079	722	18	13588	4.18221	1	0.822243	70.80227
GOTERM	GO:00507	4	0.3125	0.067005	NM_0111	722	18	13588	4.18221	1	0.822243	70.80227
GOTERM	GO:00508	7	0.546875	0.070089	NM_0098	722	55	13588	2.395266	1	0.833521	72.4688
GOTERM	GO:00022	12	0.9375	0.071259	NM_0098	722	126	13588	1.792376	1	0.835865	73.07729
GOTERM	GO:00065	13	1.015625	0.071584	NM_0110	722	141	13588	1.735172	1	0.834528	73.24389
GOTERM	GO:00028	5	0.390625	0.072162	NM_1458	722	30	13588	3.136657	1	0.834295	73.53798
GOTERM	GO:00027	5	0.390625	0.072162	NM_1458	722	30	13588	3.136657	1	0.834295	73.53798
GOTERM	GO:00160	9	0.703125	0.072767	NM_1455	722	83	13588	2.040717	1	0.834185	73.84294
GOTERM	GO:00028	7	0.546875	0.075159	NM_1458	722	56	13588	2.352493	1	0.841455	75.01501
GOTERM	GO:00028	7	0.546875	0.075159	NM_1458	722	56	13588	2.352493	1	0.841455	75.01501
GOTERM	GO:00442	7	0.546875	0.075159	NM_0231	722	56	13588	2.352493	1	0.841455	75.01501
GOTERM	GO:00509	6	0.46875	0.07586	NM_0111	722	43	13588	2.626039	1	0.841678	75.3489
GOTERM	GO:00457	6	0.46875	0.07586	NM_0082	722	43	13588	2.626039	1	0.841678	75.3489
GOTERM	GO:00108	12	0.9375	0.077794	NM_0231	722	128	13588	1.76437	1	0.846717	76.24873
GOTERM	GO:00457	3	0.234375	0.078999	NM_0205	722	9	13588	6.273315	1	0.848804	76.79364
GOTERM	GO:00509	3	0.234375	0.078999	NM_0111	722	9	13588	6.273315	1	0.848804	76.79364
GOTERM	GO:00450	3	0.234375	0.078999	NM_0333	722	9	13588	6.273315	1	0.848804	76.79364
GOTERM	GO:00313	7	0.546875	0.080432	NM_0200	722	57	13588	2.311221	1	0.851674	77.42642
GOTERM	GO:00064	11	0.859375	0.080796	NM_0010	722	114	13588	1.81596	1	0.850575	77.58448
GOTERM	GO:00487	12	0.9375	0.084693	NM_0138	722	130	13588	1.737226	1	0.861918	79.21276
GOTERM	GO:00192	7	0.546875	0.085907	NM_0095	722	58	13588	2.271373	1	0.863674	79.69662
GOTERM	GO:00434	4	0.3125	0.086654	NM_0111	722	20	13588	3.763989	1	0.863862	79.98912
GOTERM	GO:00455	5	0.390625	0.087269	NM_0010	722	32	13588	2.940616	1	0.863619	80.227
GOTERM	GO:00063	10	0.78125	0.087568	NM_1725	722	101	13588	1.863361	1	0.862352	80.3416
GOTERM	GO:00512	29	2.265625	0.090724	NM_0010	722	404	13588	1.350937	1	0.870142	81.51432
GOTERM	GO:00071	21	1.640625	0.091034	NM_0082	722	273	13588	1.447688	1	0.868942	81.62601
GOTERM	GO:00509	3	0.234375	0.095377	NM_0111	722	10	13588	5.645983	1	0.879608	83.12336
GOTERM	GO:00171	3	0.234375	0.095377	AK01033	722	10	13588	5.645983	1	0.879608	83.12336
GOTERM	GO:00433	3	0.234375	0.095377	NM_0333	722	10	13588	5.645983	1	0.879608	83.12336
GOTERM	GO:00509	3	0.234375	0.095377	NM_0111	722	10	13588	5.645983	1	0.879608	83.12336
GOTERM	GO:00458	3	0.234375	0.095377	NM_0074	722	10	13588	5.645983	1	0.879608	83.12336
GOTERM	GO:00466	3	0.234375	0.095377	NM_0111	722	10	13588	5.645983	1	0.879608	83.12336

GOTERM	GO:00433	3	0.234375	0.095377	NM_0333	722	10	13588	5.645983	1	0.879608	83.12336
GOTERM	GO:00507	3	0.234375	0.095377	NM_1458	722	10	13588	5.645983	1	0.879608	83.12336
GOTERM	GO:00105	4	0.3125	0.097286	NM_0010	722	21	13588	3.584751	1	0.882869	83.74448
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferron	Benjamini	FDR
GOTERM	GO:00099	34	2.65625	1.08E-04	NM_1722	676	305	12504	2.061965	0.040149	0.040149	0.149847
GOTERM	GO:00055	122	9.53125	4.11E-04	NM_0106	676	1680	12504	1.343238	0.143903	0.074745	0.56698
GOTERM	GO:00098	24	1.875	7.49E-04	NM_0200	676	206	12504	2.154995	0.246526	0.090039	1.030537
GOTERM	GO:00444	44	3.4375	0.004006	NM_0094	676	524	12504	1.553187	0.780698	0.315678	5.401341
GOTERM	GO:00319	32	2.5	0.009287	NM_0094	676	368	12504	1.608438	0.9706	0.506065	12.10827
GOTERM	GO:00057	27	2.109375	0.009908	NM_0094	676	296	12504	1.68723	0.976806	0.465975	12.86764
GOTERM	GO:00057	33	2.578125	0.012386	NM_0094	676	391	12504	1.561131	0.991005	0.489834	15.83638
GOTERM	GO:00007	17	1.328125	0.016662	NM_0010	676	165	12504	1.905756	0.998256	0.54793	20.73964
GOTERM	GO:00198	27	2.109375	0.018555	NM_0094	676	312	12504	1.600706	0.999158	0.54463	22.82468
GOTERM	GO:00329	10	0.78125	0.019197	NM_0089	676	75	12504	2.466272	0.999342	0.519389	23.5196
GOTERM	GO:00444	27	2.109375	0.022978	NM_0010	676	318	12504	1.570504	0.999847	0.550139	27.49873
GOTERM	GO:00310	26	2.03125	0.028553	NM_0106	676	309	12504	1.556385	0.999982	0.598481	33.01645
GOTERM	GO:00058	4	0.3125	0.029846	NM_0074	676	13	12504	5.691397	0.999989	0.58565	34.23955
GOTERM	GO:00319	16	1.25	0.03034	NM_0274	676	163	12504	1.815661	0.999991	0.564759	34.701
GOTERM	GO:00057	16	1.25	0.03034	NM_0274	676	163	12504	1.815661	0.999991	0.564759	34.701
GOTERM	GO:00444	55	4.296875	0.030421	NM_1722	676	774	12504	1.314389	0.999992	0.540915	34.77698
GOTERM	GO:00055	25	1.953125	0.031737	NM_0106	676	297	12504	1.55699	0.999995	0.533242	35.99073
GOTERM	GO:00056	30	2.34375	0.035964	NM_0010	676	378	12504	1.468019	0.999999	0.557096	39.7497
GOTERM	GO:00430	3	0.234375	0.037753	NM_0119	676	6	12504	9.248521	1	0.554324	41.27804
GOTERM	GO:00056	9	0.703125	0.04242	NM_0106	676	73	12504	2.280457	1	0.57783	45.09728
GOTERM	GO:00319	4	0.3125	0.043841	NM_0010	676	15	12504	4.932544	1	0.571435	46.2142
GOTERM	GO:00427	3	0.234375	0.050992	BC028433	676	7	12504	7.927303	1	0.610189	51.51954
GOTERM	GO:00057	85	6.640625	0.062639	NM_0138	676	1322	12504	1.189295	1	0.670914	59.13203
GOTERM	GO:00198	34	2.65625	0.077394	NM_0333	676	472	12504	1.332414	1	0.733898	67.18576
GOTERM	GO:00432	9	0.703125	0.078609	NM_0167	676	83	12504	2.005703	1	0.724584	67.77865
GOTERM	GO:00426	3	0.234375	0.09823	NM_2071	676	10	12504	5.549112	1	0.790565	76.07608
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferron	Benjamini	FDR

GOTERM	GO:00302	32	2.5	0.001228	NM_0269	727	317	13288	1.845083	0.616887	0.616887	1.862176
GOTERM	GO:00080	9	0.703125	0.001464	NM_0097	727	41	13288	4.012212	0.681474	0.435619	2.216521
GOTERM	GO:00018	17	1.328125	0.001627	NM_0200	727	128	13288	2.427528	0.719606	0.34548	2.460498
GOTERM	GO:00302	17	1.328125	0.001627	NM_0200	727	128	13288	2.427528	0.719606	0.34548	2.460498
GOTERM	GO:00055	15	1.171875	0.003652	NM_1458	727	114	13288	2.404981	0.942591	0.510508	5.444746
GOTERM	GO:00082	12	0.9375	0.005332	NM_0214	727	83	13288	2.642581	0.984632	0.566167	7.855038
GOTERM	GO:00199	12	0.9375	0.008273	NM_1339	727	88	13288	2.492435	0.998479	0.660861	11.93684
GOTERM	GO:00054	4	0.3125	0.014599	NM_1531	727	10	13288	7.311142	0.99999	0.80618	20.15097
GOTERM	GO:00018	105	8.203125	0.016083	NM_0134	727	1558	13288	1.231819	0.999997	0.794615	21.9715
GOTERM	GO:00080	7	0.546875	0.016113	NM_0214	727	38	13288	3.366973	0.999997	0.755761	22.00743
GOTERM	GO:00423	7	0.546875	0.018189	NM_0214	727	39	13288	3.28064	0.999999	0.761557	24.48809
GOTERM	GO:00018	104	8.125	0.018825	NM_0134	727	1548	13288	1.22797	1	0.740589	25.23374
GOTERM	GO:00001	140	10.9375	0.024899	NM_0257	727	2183	13288	1.172194	1	0.806214	32.01009
GOTERM	GO:00305	102	7.96875	0.025286	NM_0134	727	1535	13288	1.214554	1	0.785322	32.4218
GOTERM	GO:00055	60	4.6875	0.027446	NM_1722	727	840	13288	1.305561	1	0.788278	34.67744
GOTERM	GO:00049	5	0.390625	0.029447	NM_0307	727	22	13288	4.154058	1	0.789076	36.70473
GOTERM	GO:00055	5	0.390625	0.029447	NM_0236	727	22	13288	4.154058	1	0.789076	36.70473
GOTERM	GO:00055	96	7.5	0.030072	NM_0134	727	1443	13288	1.21599	1	0.774721	37.32513
GOTERM	GO:00199	5	0.390625	0.034153	NM_0307	727	23	13288	3.973447	1	0.797382	41.24072
GOTERM	GO:00325	96	7.5	0.038592	NM_0134	727	1460	13288	1.201832	1	0.818707	45.24043
GOTERM	GO:00480	5	0.390625	0.050739	NM_0269	727	26	13288	3.514972	1	0.882395	54.9221
GOTERM	GO:00045	11	0.859375	0.054673	NM_0531	727	103	13288	1.952004	1	0.888703	57.69723
GOTERM	GO:00170	118	9.21875	0.057384	XR_0307	727	1871	13288	1.152745	1	0.888955	59.51603
GOTERM	GO:00164	4	0.3125	0.062332	NM_0307	727	17	13288	4.300672	1	0.898203	62.64877
GOTERM	GO:00199	4	0.3125	0.062332	NM_0307	727	17	13288	4.300672	1	0.898203	62.64877
GOTERM	GO:00434	3	0.234375	0.067031	NM_0098	727	8	13288	6.854195	1	0.905202	65.41214
GOTERM	GO:00017	3	0.234375	0.067031	NM_0010	727	8	13288	6.854195	1	0.905202	65.41214
GOTERM	GO:00051	16	1.25	0.068115	NM_0113	727	180	13288	1.624698	1	0.899308	66.02234
GOTERM	GO:00055	16	1.25	0.07072	NM_0200	727	181	13288	1.615722	1	0.898866	67.447
GOTERM	GO:00151	5	0.390625	0.070998	NM_1531	727	29	13288	3.151354	1	0.890538	67.59576
GOTERM	GO:00048	7	0.546875	0.0783	NM_1339	727	55	13288	2.326272	1	0.905437	71.28122
GOTERM	GO:00036	14	1.09375	0.0819	NM_0010	727	155	13288	1.650903	1	0.907766	72.95068
GOTERM	GO:00049	3	0.234375	0.08314	NM_0074	727	9	13288	6.092618	1	0.903445	73.50438

GOTERM	GO:00166	3	0.234375	0.08314	NM_1991	727	9	13288	6.092618	1	0.903445	73.50438
GOTERM	GO:00480	3	0.234375	0.08314	NM_0010	727	9	13288	6.092618	1	0.903445	73.50438
GOTERM	GO:00325	112	8.75	0.085011	XR_0307	727	1796	13288	1.139822	1	0.901026	74.31972
GOTERM	GO:00325	112	8.75	0.085011	XR_0307	727	1796	13288	1.139822	1	0.901026	74.31972
GOTERM	GO:00431	232	18.125	0.094158	NM_0257	727	3934	13288	1.077901	1	0.917206	77.97904
GOTERM	GO:00037	8	0.625	0.097427	NM_0088	727	72	13288	2.030873	1	0.918061	79.16422

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM	GO:004269	7	0.84848	0.00379	NM_2016	364	52	12504	4.62426	0.6954	0.6954	4.97976
GOTERM	GO:000588	106	12.8485	0.00642	NM_0110	364	2906	12504	1.25302	0.86667	0.63485	8.29367
GOTERM	GO:000981	14	1.69697	0.00714	NM_0083	364	206	12504	2.33458	0.8938	0.52644	9.18588
GOTERM	GO:000031	3	0.36364	0.02644	NM_0098	364	9	12504	11.4505	0.99977	0.87711	30.2555
GOTERM	GO:004444	61	7.39394	0.03175	NM_0188	364	1633	12504	1.28319	0.99996	0.86729	35.2026
GOTERM	GO:000998	16	1.93939	0.03264	NM_0083	364	305	12504	1.80205	0.99997	0.82295	36.0049
GOTERM	GO:004269	5	0.60606	0.03287	NM_2016	364	42	12504	4.08948	0.99997	0.77563	36.2062
GOTERM	GO:003122	3	0.36364	0.03888	AK01300	364	11	12504	9.36863	1	0.78804	41.333
GOTERM	GO:004444	16	1.93939	0.04478	NM_1725	364	318	12504	1.72838	1	0.79674	45.9984
GOTERM	GO:004522	16	1.93939	0.04545	BC116417	364	319	12504	1.72297	1	0.76678	46.5026
GOTERM	GO:004271	4	0.48485	0.04651	NM_0010	364	28	12504	4.90738	1	0.74212	47.3015
GOTERM	GO:000561	18	2.18182	0.04939	NM_1725	364	378	12504	1.63579	1	0.73319	49.4021
GOTERM	GO:003011	8	0.9697	0.06936	NM_0101	364	124	12504	2.21624	1	0.82282	61.9671
GOTERM	GO:003011	7	0.84848	0.08203	NM_0101	364	104	12504	2.31213	1	0.85245	68.3731
GOTERM	GO:004444	11	1.33333	0.08961	NM_0092	364	212	12504	1.7824	1	0.85902	71.712
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM	GO:000558	10	1.21212	0.00769	NM_0214	403	114	13288	2.89234	0.98917	0.98917	10.7463
GOTERM	GO:003021	19	2.30303	0.00789	NM_0115	403	317	13288	1.97628	0.99034	0.90169	11.0015
GOTERM	GO:000822	8	0.9697	0.01273	NM_0214	403	83	13288	3.17809	0.99945	0.91813	17.1891
GOTERM	GO:000188	10	1.21212	0.0157	NM_0214	403	128	13288	2.57599	0.99991	0.9015	20.7767
GOTERM	GO:003021	10	1.21212	0.0157	NM_0214	403	128	13288	2.57599	0.99991	0.9015	20.7767
GOTERM	GO:000855	9	1.09091	0.01842	NM_0092	403	110	13288	2.69777	0.99998	0.88678	23.9387
GOTERM	GO:000168	9	1.09091	0.01842	NM_0092	403	110	13288	2.69777	0.99998	0.88678	23.9387
GOTERM	GO:003061	19	2.30303	0.02651	NM_0158	403	361	13288	1.73541	1	0.92752	32.6718
GOTERM	GO:006051	19	2.30303	0.03044	NM_0158	403	367	13288	1.70703	1	0.92481	36.5592
GOTERM	GO:000500	12	1.45455	0.03185	NM_0158	403	192	13288	2.06079	1	0.90662	37.9069
GOTERM	GO:000481	5	0.60606	0.0566	AK08403	403	48	13288	3.43466	1	0.97748	57.5852
GOTERM	GO:001688	5	0.60606	0.0566	AK08403	403	48	13288	3.43466	1	0.97748	57.5852
GOTERM	GO:001688	5	0.60606	0.0566	AK08403	403	48	13288	3.43466	1	0.97748	57.5852
GOTERM	GO:004343	2	0.24242	0.05959	BC116417	403	2	13288	32.9727	1	0.97269	59.5265
GOTERM	GO:000801	13	1.57576	0.07599	NM_0158	403	249	13288	1.72147	1	0.98515	68.7579

GOTERM	GO:00037	9	1.09091	0.08792	XR_03264	403	151	13288	1.96526	1	0.98883	74.2003
GOTERM	GO:00045	2	0.24242	0.08805	NM_0010	403	3	13288	21.9818	1	0.98431	74.2526
GOTERM	GO:00047	5	0.60606	0.08889	AK13467	403	56	13288	2.94399	1	0.97969	74.6005

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferron	Benjamini	FDR
GOTERM	GO:00466	4	0.515464	9.22E-04	NM_0098	419	7	13588	18.5312	0.808138	0.808138	1.553819
GOTERM	GO:00108	12	1.546392	0.001979	NM_0096	419	128	13588	3.040274	0.971106	0.830016	3.30584
GOTERM	GO:00160	12	1.546392	0.002839	NM_0088	419	134	13588	2.904143	0.993819	0.816482	4.710036
GOTERM	GO:00466	4	0.515464	0.002952	NM_0098	419	10	13588	12.97184	0.994951	0.733431	4.892585
GOTERM	GO:00068	11	1.417526	0.003674	NM_0096	419	119	13588	2.997694	0.99862	0.732101	6.055691
GOTERM	GO:00082	13	1.675258	0.004127	NM_0280	419	161	13588	2.618539	0.999388	0.708607	6.77717
GOTERM	GO:00442	7	0.902062	0.007245	NM_0088	419	56	13588	4.053699	0.999998	0.844066	11.60794
GOTERM	GO:00025	8	1.030928	0.012222	NM_0096	419	81	13588	3.202923	1	0.936067	18.83385
GOTERM	GO:00302	6	0.773196	0.023031	NM_0531	419	53	13588	3.671275	1	0.990261	32.65856
GOTERM	GO:00507	3	0.386598	0.023377	NM_0098	419	8	13588	12.1611	1	0.985475	33.06246
GOTERM	GO:00400	7	0.902062	0.027718	NM_0088	419	75	13588	3.026762	1	0.989659	37.93578
GOTERM	GO:00486	21	2.706186	0.028133	NM_0097	419	409	13588	1.665089	1	0.985797	38.38394
GOTERM	GO:00325	21	2.706186	0.028133	NM_0097	419	409	13588	1.665089	1	0.985797	38.38394
GOTERM	GO:00019	4	0.515464	0.03243	NM_0098	419	23	13588	5.639929	1	0.989292	42.84661
GOTERM	GO:00071	26	3.350515	0.041167	NM_1340	419	561	13588	1.502976	1	0.995355	51.00047
GOTERM	GO:00226	26	3.350515	0.041538	NM_1340	419	562	13588	1.500302	1	0.993654	51.32117
GOTERM	GO:00160	7	0.902062	0.042482	AK01316	419	83	13588	2.735026	1	0.992202	52.12898
GOTERM	GO:00030	7	0.902062	0.044617	NM_0010	419	84	13588	2.702466	1	0.991797	53.90826
GOTERM	GO:00423	4	0.515464	0.048976	NM_0098	419	27	13588	4.804384	1	0.9932	57.34926
GOTERM	GO:00400	4	0.515464	0.048976	NM_0088	419	27	13588	4.804384	1	0.9932	57.34926
GOTERM	GO:00106	10	1.28866	0.050158	NM_0098	419	155	13588	2.092232	1	0.992135	58.24007
GOTERM	GO:00072	17	2.190722	0.050461	NM_0218	419	331	13588	1.665568	1	0.990261	58.4658
GOTERM	GO:00063	8	1.030928	0.050988	NM_0335	419	109	13588	2.380154	1	0.988419	58.8553
GOTERM	GO:00199	19	2.448454	0.052429	NM_0218	419	386	13588	1.596275	1	0.987465	59.90228
GOTERM	GO:00400	14	1.804124	0.053412	NM_0105	419	256	13588	1.773493	1	0.986013	60.60277
GOTERM	GO:00459	4	0.515464	0.058518	NM_0098	419	29	13588	4.473047	1	0.988834	64.05772
GOTERM	GO:00105	4	0.515464	0.058518	NM_0098	419	29	13588	4.473047	1	0.988834	64.05772
GOTERM	GO:00323	3	0.386598	0.058869	NM_1537	419	13	13588	7.483753	1	0.986986	64.28422
GOTERM	GO:00301	3	0.386598	0.058869	NM_1757	419	13	13588	7.483753	1	0.986986	64.28422
GOTERM	GO:00464	3	0.386598	0.058869	NM_1757	419	13	13588	7.483753	1	0.986986	64.28422
GOTERM	GO:00063	16	2.061856	0.063563	AK14131	419	315	13588	1.647217	1	0.989098	67.18949
GOTERM	GO:00066	10	1.28866	0.064794	NM_0088	419	163	13588	1.989546	1	0.988188	67.91396

GOTERM	GO:00096	17	2.190722	0.069987	NM_0074	419	347	13588	1.58877	1	0.990302	70.80677
GOTERM	GO:00060	5	0.64433	0.075357	NM_1787	419	52	13588	3.11823	1	0.992039	73.53908
GOTERM	GO:00516	7	0.902062	0.075435	NM_0074	419	96	13588	2.364658	1	0.990695	73.57707
GOTERM	GO:00028	3	0.386598	0.076139	NM_0096	419	15	13588	6.485919	1	0.989645	73.91657
GOTERM	GO:00305	3	0.386598	0.0853	NM_0531	419	16	13588	6.080549	1	0.993157	77.97475
GOTERM	GO:00701	3	0.386598	0.0853	NM_0531	419	16	13588	6.080549	1	0.993157	77.97475
GOTERM	GO:00072	5	0.64433	0.093142	NM_0100	419	56	13588	2.895499	1	0.99501	80.96872
GOTERM	GO:00196	10	1.28866	0.093826	NM_0088	419	176	13588	1.842591	1	0.994395	81.21072
GOTERM	GO:00022	8	1.030928	0.093943	NM_0096	419	126	13588	2.059022	1	0.993543	81.25181
GOTERM	GO:00063	65	8.376289	0.093944	NM_1461	419	1772	13588	1.189573	1	0.992572	81.25221
GOTERM	GO:00510	12	1.546392	0.094526	NM_0011	419	228	13588	1.706821	1	0.991779	81.45538
GOTERM	GO:00093	3	0.386598	0.094773	NM_0088	419	17	13588	5.72287	1	0.990791	81.54117
GOTERM	GO:00321	7	0.902062	0.097847	NM_0096	419	103	13588	2.203953	1	0.991116	82.57648
GOTERM	GO:00069	4	0.515464	0.097975	NM_0010	419	36	13588	3.603288	1	0.990065	82.61839
GOTERM	GO:00025	4	0.515464	0.097975	NM_0010	419	36	13588	3.603288	1	0.990065	82.61839
GOTERM	GO:00323	6	0.773196	0.099913	NM_0011	419	80	13588	2.43222	1	0.989879	83.24152
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferron	Benjamini	FDR
GOTERM	GO:00055	76	9.793814	2.96E-04	NM_0074	380	1680	12504	1.488571	0.088522	0.088522	0.397482
GOTERM	GO:00444	40	5.154639	0.001215	NM_0074	380	774	12504	1.70053	0.316497	0.173258	1.621796
GOTERM	GO:00444	9	1.159794	0.006722	NM_1787	380	92	12504	3.218993	0.878893	0.505245	8.671915
GOTERM	GO:00007	12	1.546392	0.011804	NM_0335	380	165	12504	2.39311	0.975683	0.605109	14.76
GOTERM	GO:00057	3	0.386598	0.017395	NM_0010	380	7	12504	14.10226	0.995882	0.666622	21.02233
GOTERM	GO:00007	6	0.773196	0.018687	NM_0010	380	51	12504	3.871207	0.997272	0.62621	22.40809
GOTERM	GO:00056	25	3.221649	0.022601	NM_0135	380	511	12504	1.609847	0.999219	0.640187	26.46837
GOTERM	GO:00056	7	0.902062	0.023093	NM_1787	380	73	12504	3.155299	0.999333	0.599133	26.96534
GOTERM	GO:00310	17	2.190722	0.026025	NM_0135	380	309	12504	1.810322	0.99974	0.600318	29.85884
GOTERM	GO:00055	16	2.061856	0.036772	NM_0135	380	297	12504	1.772674	0.999992	0.690453	39.58179
GOTERM	GO:00057	8	1.030928	0.03857	NM_1342	380	104	12504	2.531174	0.999995	0.673465	41.0814
GOTERM	GO:00425	8	1.030928	0.03857	NM_1342	380	104	12504	2.531174	0.999995	0.673465	41.0814
GOTERM	GO:00444	16	2.061856	0.060455	NM_0194	380	318	12504	1.655611	1	0.803394	56.77301
GOTERM	GO:00056	18	2.319588	0.067322	NM_0108	380	378	12504	1.566917	1	0.813264	60.8343
GOTERM	GO:00002	8	1.030928	0.074902	NM_0095	380	121	12504	2.175555	1	0.82459	64.90508

GOTERM	GO:00343	3	0.386598	0.083145	NM_0091	380	16	12504	6.169737	1	0.836568	68.88548
GOTERM	GO:00059	8	1.030928	0.088458	NM_1340	380	126	12504	2.089223	1	0.836647	71.22494
GOTERM	GO:00057	4	0.515464	0.088714	NM_0095	380	35	12504	3.760602	1	0.81921	71.33311
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferron	Benjamini	FDR
GOTERM	GO:00431	148	19.07216	0.002962	NM_0257	415	3885	13288	1.219782	0.815597	0.815597	4.256586
GOTERM	GO:00431	149	19.20103	0.003601	NM_0257	415	3934	13288	1.212728	0.872088	0.642352	5.153409
GOTERM	GO:00302	19	2.448454	0.010696	NM_0269	415	317	13288	1.919136	0.997822	0.870385	14.59005
GOTERM	GO:00055	13	1.675258	0.01122	NM_0269	415	181	13288	2.299727	0.99839	0.799696	15.25136
GOTERM	GO:00468	142	18.29897	0.012707	NM_0257	415	3850	13288	1.180971	0.999317	0.767277	17.10142
GOTERM	GO:00055	39	5.025773	0.013132	NM_0199	415	840	13288	1.486609	0.999466	0.715156	17.62309
GOTERM	GO:00080	15	1.93299	0.024274	NM_1986	415	249	13288	1.928872	0.999999	0.864795	30.25889
GOTERM	GO:00050	12	1.546392	0.038159	NM_0011	415	192	13288	2.001205	1	0.937467	43.48014
GOTERM	GO:00050	5	0.64433	0.044121	NM_0011	415	43	13288	3.723172	1	0.942607	48.40585
GOTERM	GO:00046	6	0.773196	0.046152	NM_0088	415	63	13288	3.049455	1	0.932342	49.99041
GOTERM	GO:00162	7	0.902062	0.046943	NM_0088	415	84	13288	2.668273	1	0.917212	50.59582
GOTERM	GO:00053	5	0.64433	0.047386	NM_0096	415	44	13288	3.638554	1	0.900334	50.93139
GOTERM	GO:00036	68	8.762887	0.056045	NM_1752	415	1781	13288	1.222522	1	0.920255	57.08145
GOTERM	GO:00306	18	2.319588	0.059826	NM_1986	415	361	13288	1.596529	1	0.918868	59.53464
GOTERM	GO:00469	17	2.190722	0.066753	NM_0105	415	340	13288	1.600964	1	0.927577	63.69343
GOTERM	GO:00605	18	2.319588	0.067456	NM_1986	415	367	13288	1.570428	1	0.916924	64.09243
GOTERM	GO:00421	3	0.386598	0.068837	NM_0110	415	14	13288	6.861274	1	0.908494	64.86452
GOTERM	GO:00082	78	10.05155	0.070804	NM_0257	415	2105	13288	1.186463	1	0.90226	65.93725
GOTERM	GO:00080	6	0.773196	0.073594	NM_0010	415	72	13288	2.668273	1	0.899065	67.40706
GOTERM	GO:00167	4	0.515464	0.076575	NM_0097	415	32	13288	4.00241	1	0.896735	68.91154
GOTERM	GO:00192	6	0.773196	0.077092	NM_0098	415	73	13288	2.631721	1	0.886682	69.16613
GOTERM	GO:00036	4	0.515464	0.082371	NM_0100	415	33	13288	3.881124	1	0.89217	71.65385
GOTERM	GO:00435	6	0.773196	0.088113	NM_0100	415	76	13288	2.527838	1	0.898321	74.14696
GOTERM	GO:00050	12	1.546392	0.089696	NM_0011	415	223	13288	1.72301	1	0.892682	74.79749
GOTERM	GO:00048	5	0.64433	0.096476	NM_0104	415	56	13288	2.858864	1	0.901048	77.41441
GOTERM	GO:00040	3	0.386598	0.096839	NM_0137	415	17	13288	5.650461	1	0.892789	77.54698

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM	GO:00485	18	2.45566	0.001621	NM_0117	428	241	13588	2.37119	0.945458	0.945458	2.716092
GOTERM	GO:00605	11	1.50068	0.005704	NM_0085	428	124	13588	2.81632	0.999965	0.994071	9.252573
GOTERM	GO:00017	3	0.40928	0.009251	NM_0098	428	5	13588	19.0486	1	0.99613	14.59364
GOTERM	GO:00513	17	2.31924	0.016263	XR_0308	428	281	13588	1.92068	1	0.999357	24.29461
GOTERM	GO:00487	5	0.68213	0.017244	AK17045	428	32	13588	4.96057	1	0.998046	25.56588
GOTERM	GO:00068	3	0.40928	0.018632	NM_0280	428	7	13588	13.6061	1	0.996377	27.32964
GOTERM	GO:00071	3	0.40928	0.018632	NM_0098	428	7	13588	13.6061	1	0.996377	27.32964
GOTERM	GO:00002	9	1.22783	0.023661	NM_0116	428	111	13588	2.57413	1	0.997831	33.39868
GOTERM	GO:00550	3	0.40928	0.024331	NM_0280	428	8	13588	11.9054	1	0.995997	34.17038
GOTERM	GO:00487	5	0.68213	0.030582	AK17045	428	38	13588	4.17732	1	0.997945	40.97393
GOTERM	GO:00485	11	1.50068	0.030818	NM_0098	428	161	13588	2.1691	1	0.996348	41.21763
GOTERM	GO:00424	7	0.95498	0.032095	NM_0098	428	76	13588	2.92413	1	0.995094	42.51827
GOTERM	GO:00018	5	0.68213	0.03326	NM_0098	428	39	13588	4.07021	1	0.993617	43.68153
GOTERM	GO:00606	5	0.68213	0.03326	NM_0098	428	39	13588	4.07021	1	0.993617	43.68153
GOTERM	GO:00075	4	0.5457	0.034236	AK17045	428	23	13588	5.52133	1	0.991809	44.63927
GOTERM	GO:00070	13	1.77353	0.034918	NM_0094	428	211	13588	1.95602	1	0.989454	45.29913
GOTERM	GO:00507	5	0.68213	0.039014	NM_0136	428	41	13588	3.87167	1	0.991408	49.10903
GOTERM	GO:00140	5	0.68213	0.042091	NM_0098	428	42	13588	3.77948	1	0.991925	51.80525
GOTERM	GO:00018	6	0.81855	0.042344	NM_0108	428	61	13588	3.12272	1	0.989573	52.02075
GOTERM	GO:00321	8	1.09141	0.043494	NM_0111	428	103	13588	2.46584	1	0.988079	52.98901
GOTERM	GO:00519	10	1.36426	0.043984	NM_0136	428	148	13588	2.14511	1	0.98566	53.39627
GOTERM	GO:00300	17	2.31924	0.044741	NM_0094	428	319	13588	1.69188	1	0.983486	54.01907
GOTERM	GO:00017	3	0.40928	0.044918	NM_0098	428	11	13588	8.65845	1	0.980237	54.16342
GOTERM	GO:00435	8	1.09141	0.045431	NM_0098	428	104	13588	2.44213	1	0.977391	54.57954
GOTERM	GO:00219	7	0.95498	0.046295	NM_0098	428	83	13588	2.67751	1	0.975159	55.27252
GOTERM	GO:00487	12	1.63711	0.046924	NM_0114	428	197	13588	1.93387	1	0.972416	55.77024
GOTERM	GO:00431	4	0.5457	0.04693	AK17045	428	26	13588	4.88426	1	0.96817	55.77467
GOTERM	GO:00455	11	1.50068	0.049715	NM_0136	428	175	13588	1.99557	1	0.9703	57.91825
GOTERM	GO:00160	9	1.22783	0.052563	NM_0214	428	130	13588	2.19792	1	0.972282	60.00856
GOTERM	GO:00421	25	3.41064	0.053287	NM_0082	428	538	13588	1.47526	1	0.970001	60.5242
GOTERM	GO:00076	20	2.72851	0.053921	NM_0074	428	405	13588	1.56779	1	0.967518	60.9705
GOTERM	GO:00488	7	0.95498	0.058498	NM_0098	428	88	13588	2.52538	1	0.972749	64.05453

GOTERM	GO:00424	6	0.81855	0.059185	NM_0098	428	67	13588	2.84307	1	0.970657	64.4972
GOTERM	GO:00107	5	0.68213	0.059467	NM_0136	428	47	13588	3.37741	1	0.96778	64.67702
GOTERM	GO:00303	8	1.09141	0.060539	NM_0085	428	111	13588	2.28812	1	0.966395	65.35463
GOTERM	GO:00431	3	0.40928	0.061139	AK17045	428	13	13588	7.32638	1	0.964097	65.72773
GOTERM	GO:00068	31	4.2292	0.061555	NM_0168	428	712	13588	1.38227	1	0.961404	65.98481
GOTERM	GO:00072	2	0.27285	0.061864	NM_0136	428	2	13588	31.7477	1	0.95844	66.17465
GOTERM	GO:00100	5	0.68213	0.063336	NM_0111	428	48	13588	3.30705	1	0.958027	67.06401
GOTERM	GO:00602	10	1.36426	0.063616	NM_0136	428	159	13588	1.99671	1	0.955014	67.23096
GOTERM	GO:00303	8	1.09141	0.06536	NM_0085	428	113	13588	2.24762	1	0.955291	68.25139
GOTERM	GO:00508	5	0.68213	0.067334	AK17045	428	49	13588	3.23956	1	0.956048	69.37058
GOTERM	GO:00065	42	5.72988	0.072433	NM_0196	428	1034	13588	1.28956	1	0.96268	72.09242
GOTERM	GO:00352	14	1.90996	0.073792	NM_0117	428	264	13588	1.68359	1	0.962088	72.778
GOTERM	GO:00072	15	2.04638	0.074153	NM_0073	428	290	13588	1.64212	1	0.95975	72.95768
GOTERM	GO:00018	5	0.68213	0.075711	NM_0098	428	51	13588	3.11252	1	0.959574	73.72004
GOTERM	GO:00430	25	3.41064	0.076427	NM_1751	428	560	13588	1.41731	1	0.957907	74.06343
GOTERM	GO:00002	11	1.50068	0.077208	NM_0198	428	190	13588	1.83802	1	0.956368	74.43307
GOTERM	GO:00070	11	1.50068	0.077208	NM_0198	428	190	13588	1.83802	1	0.956368	74.43307
GOTERM	GO:00071	3	0.40928	0.079008	AK17045	428	15	13588	6.34953	1	0.956709	75.26655
GOTERM	GO:00507	3	0.40928	0.079008	NM_0136	428	15	13588	6.34953	1	0.956709	75.26655
GOTERM	GO:00071	25	3.41064	0.079376	NM_0196	428	561	13588	1.41478	1	0.954466	75.43352
GOTERM	GO:00420	5	0.68213	0.080088	NM_0111	428	52	13588	3.05266	1	0.952857	75.75415
GOTERM	GO:00226	25	3.41064	0.080504	NM_0196	428	562	13588	1.41226	1	0.950695	75.9398
GOTERM	GO:00109	25	3.41064	0.081053	NM_1751	428	563	13588	1.40975	1	0.948783	76.18226
GOTERM	GO:00000	11	1.50068	0.085872	NM_0198	428	194	13588	1.80013	1	0.954764	78.21605
GOTERM	GO:00604	14	1.90996	0.08642	NM_0199	428	271	13588	1.6401	1	0.953006	78.43661
GOTERM	GO:00018	5	0.68213	0.089207	NM_0098	428	54	13588	2.9396	1	0.955066	79.52638
GOTERM	GO:00550	5	0.68213	0.089207	AK17045	428	54	13588	2.9396	1	0.955066	79.52638
GOTERM	GO:00062	4	0.5457	0.090119	NM_0076	428	34	13588	3.73502	1	0.953985	79.87151
GOTERM	GO:00106	22	3.00136	0.090464	NM_0117	428	488	13588	1.43125	1	0.951972	80.00082
GOTERM	GO:00072	6	0.81855	0.090616	NM_0111	428	76	13588	2.50639	1	0.94961	80.05734
GOTERM	GO:00601	2	0.27285	0.091349	NM_0116	428	3	13588	21.1651	1	0.948252	80.32852
GOTERM	GO:00019	2	0.27285	0.091349	NM_0103	428	3	13588	21.1651	1	0.948252	80.32852
GOTERM	GO:00102	2	0.27285	0.091349	NM_0136	428	3	13588	21.1651	1	0.948252	80.32852

GOTERM	GO:00482	11	1.50068	0.092743	NM_0196	428	197	13588	1.77271	1	0.948068	80.83434
GOTERM	GO:00082	12	1.63711	0.096043	NR_0015	428	224	13588	1.70077	1	0.951074	81.98408
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferron	Benjamini	FDR
GOTERM	GO:00055	93	12.6876	3.12E-08	NM_0196	393	1680	12504	1.76129	8.91E-06	8.91E-06	4.14E-05
GOTERM	GO:00444	44	6.00273	1.78E-04	NM_0196	393	774	12504	1.80871	0.049552	0.025091	0.236146
GOTERM	GO:00056	30	4.09277	0.00149	NM_0196	393	511	12504	1.86791	0.346233	0.132091	1.957739
GOTERM	GO:00003	3	0.40928	0.030501	NM_0076	393	9	12504	10.6056	0.999853	0.889976	33.68117
GOTERM	GO:00430	14	1.90996	0.044779	NM_0094	393	245	12504	1.8181	0.999998	0.926561	45.52346
GOTERM	GO:00017	5	0.68213	0.059021	NM_0103	393	47	12504	3.38477	1	0.944402	55.36109
GOTERM	GO:00429	26	3.54707	0.060525	NM_0168	393	575	12504	1.43867	1	0.921289	56.29836
GOTERM	GO:00056	3	0.40928	0.069585	NM_1787	393	14	12504	6.81788	1	0.923423	61.56752
GOTERM	GO:00430	8	1.09141	0.07486	NM_0094	393	117	12504	2.17551	1	0.914906	64.35814
GOTERM	GO:00452	16	2.18281	0.076969	NM_0188	393	319	12504	1.59583	1	0.897986	65.42042
GOTERM	GO:00055	15	2.04638	0.084035	AK13477	393	297	12504	1.60691	1	0.897124	68.77007
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferron	Benjamini	FDR
GOTERM	GO:00152	22	3.00136	0.003533	NM_0103	401	365	13288	1.99731	0.85264	0.85264	5.022966
GOTERM	GO:00228	22	3.00136	0.003533	NM_0103	401	365	13288	1.99731	0.85264	0.85264	5.022966
GOTERM	GO:00080	12	1.63711	0.003563	NM_0107	401	141	13288	2.82018	0.854991	0.6192	5.064068
GOTERM	GO:00228	10	1.36426	0.004655	NM_1776	401	106	13288	3.12615	0.919871	0.568881	6.567549
GOTERM	GO:00152	10	1.36426	0.004655	NM_1776	401	106	13288	3.12615	0.919871	0.568881	6.567549
GOTERM	GO:00018	11	1.50068	0.005292	NM_0296	401	128	13288	2.84772	0.943321	0.512072	7.434128
GOTERM	GO:00302	11	1.50068	0.005292	NM_0296	401	128	13288	2.84772	0.943321	0.512072	7.434128
GOTERM	GO:00228	21	2.86494	0.006392	NM_0103	401	360	13288	1.933	0.968863	0.500361	8.914413
GOTERM	GO:00055	7	0.95498	0.009862	NM_0296	401	61	13288	3.80262	0.995307	0.590824	13.43704
GOTERM	GO:00052	19	2.59209	0.018761	NM_0168	401	349	13288	1.80403	0.999965	0.768633	24.10028
GOTERM	GO:00051	9	1.22783	0.020738	NM_0074	401	113	13288	2.63924	0.999988	0.757602	26.29677
GOTERM	GO:00055	9	1.22783	0.021741	NM_0296	401	114	13288	2.61609	0.999993	0.733205	27.38766
GOTERM	GO:00314	13	1.77353	0.022177	NM_0113	401	206	13288	2.09118	0.999995	0.702779	27.85771
GOTERM	GO:00228	16	2.18281	0.023065	NM_0168	401	281	13288	1.88681	0.999997	0.682627	28.80603
GOTERM	GO:00082	29	3.95634	0.025113	NM_0196	401	629	13288	1.52779	0.999999	0.682293	30.94796
GOTERM	GO:00082	10	1.36426	0.03245	AK02824	401	146	13288	2.26967	1	0.746603	38.14021

GOTERM	GO:00700	27	3.68349	0.041864	NM_0196	401	603	13288	1.48375	1	0.808442	46.34825
GOTERM	GO:00430	3	0.40928	0.048875	NM_1751	401	12	13288	8.28429	1	0.8359	51.78928
GOTERM	GO:00050	2	0.27285	0.059301	NM_1336	401	2	13288	33.1372	1	0.873437	58.93748
GOTERM	GO:00048	13	1.77353	0.064064	NM_1818	401	243	13288	1.77277	1	0.878396	61.8632
GOTERM	GO:00198	3	0.40928	0.064793	NM_0078	401	14	13288	7.10082	1	0.86646	62.29351
GOTERM	GO:00431	132	18.0082	0.066281	NM_0257	401	3885	13288	1.1259	1	0.858111	63.15724
GOTERM	GO:00052	13	1.77353	0.071961	NM_0091	401	248	13288	1.73703	1	0.867363	66.28939
GOTERM	GO:00166	3	0.40928	0.073314	NM_0259	401	15	13288	6.62743	1	0.859357	66.99807
GOTERM	GO:00431	133	18.1446	0.073942	NM_0257	401	3934	13288	1.1203	1	0.848784	67.32228
GOTERM	GO:00052	3	0.40928	0.08217	NM_0010	401	16	13288	6.21322	1	0.866923	71.30401
GOTERM	GO:00468	129	17.5989	0.097793	NM_0257	401	3850	13288	1.11031	1	0.901706	77.6508
GOTERM	GO:00055	16	2.18281	0.097807	NM_1751	401	343	13288	1.54576	1	0.892185	77.65595
GOTERM	GO:00302	15	2.04638	0.098632	NM_0296	401	317	13288	1.568	1	0.884756	77.95144
GOTERM	GO:00468	14	1.90996	0.099814	NM_0091	401	290	13288	1.59972	1	0.878395	78.36883
GOTERM	GO:00055	33	4.50205	0.099817	NM_0188	401	840	13288	1.30182	1	0.868898	78.36973

p-value (T)	FCAbsolute	regulation	GeneSymbol	Description	GenbankAccession
0.036466	2.406906	down	Gm4619	PREDICT	XM_001476246
0.038134	4.221683	down	Abcg4	Mus musc	NM_138955
0.008761	1.623043	down	Cd34	Mus musc	NM_133654
0.010287	1.980838	down	Gata1	Mus musc	NM_008089
3.37E-04	2.131485	down	Col14a1	Mus musc	NM_181277
0.040341	3.24516	down	A430104N	BMSB113	DT902180
0.043443	1.747825	down	Gm4938	PREDICT	XM_138832
0.033622	2.282073	down	Fbxo39	Mus musc	NM_001099688
0.045953	1.766309	up	Gm6146	PREDICT	XM_895806
0.03543	2.241203	up	Tatdn1	Mus musc	NM_175151
0.03543	2.119122	down		lincRNA:chr12:53669892-53710742 forward strand	
0.02028	2.176905	down	Sft2d1	Mus musc	NM_134114
0.031432	1.556446	down		lincRNA:chr7:49715933-49771497 reverse strand	
0.046516	1.952008	down	Clec4b1	Mus musc	NM_001190310
0.016614	1.579422	up	S100a1	Mus musc	NM_011309
0.005288	1.781043	down	Duox1	Mus musc	NM_001099297
0.002111	1.951406	down	Cpne8	Mus musc	NM_001033851
0.037716	2.068424	down	Pef1	Mus musc	NM_026441
0.027319	2.404481	down	Gm5316	PREDICT	XM_357669
0.042096	2.45103	down	LOC1000	PREDICT	XM_001474162
0.004292	1.914019	up	4930402H	Mus musc	NM_029432
0.00803	3.50707	down	Cd2	Mus musc	NM_013486
0.006344	2.118714	down	Clic4	Mus musc	NM_013885
0.003929	5.395391	down	Zfp429	Mus musc	NM_001080941
0.024784	1.511252	up	Fmc1	Mus musc	NM_025363
0.019099	3.516091	down	AI987944	Mus musc	NM_183167
0.038914	1.520406	up	Hnrnpul1	Mus musc	NM_144922
0.012983	1.808432	down	Egln2	Mus musc	NM_053208
0.006769	2.375031	down	Tmem91	Mus musc	NM_177102
0.008346	2.17306	down	Pot1b	Mus musc	NM_028370
0.011401	2.336689	up	4122401K	Mus musc	AK014465
0.048022	1.796509	down	6330403A	Mus musc	NM_001081227

0.029034	1.803054	down		lincRNA:chr18:63525907-63526504 reverse strand
0.008182	1.658878	down		lincRNA:chr2:128211990-128215223 reverse strand
0.026243	1.525007	up	Purb	Mus musc NM_011221
0.0074	1.7437	up	Acadvl	Mus musc NM_017366
0.038891	1.522708	up	5930430L	Mus musc AK148051
0.003265	1.980721	down		RIKEN cl XR_035339
0.008281	3.394252	down	Ccrl1	Mus musc AY072938
0.010518	2.091006	down		RIKEN cl AK020399
0.026114	2.11655	down		lincRNA:chr5:110182844-110228345 reverse strand
0.042633	1.658797	down	Cysltr1	Mus musc NM_021476
0.019092	2.34882	down	Zfp455	Mus musc NM_001048204
0.026978	2.608249	down		lincRNA:chr7:150399015-150482452 forward strand
0.035893	1.757691	down	Apol9a	Mus musc NM_173786
0.028887	1.999636	up		lincRNA:chr8:108153471-108159346 reverse strand
0.0211	2.47275	down	Lypd6b	Mus musc NM_027990
0.011469	2.874222	down	Frzb	Mus musc NM_011356
0.01068	1.762215	down	Hydin	Mus musc NM_172916
0.016236	2.092032	up	1700020C	Mus musc NM_026443
0.013684	3.917218	down	Klhl29	Mus musc NM_001164493
0.047965	2.03482	down		lincRNA:chr2:143991240-143991597 forward strand
0.007815	1.847237	up	Rab4a	Mus musc NM_009003
0.027804	1.734142	up	Baz1a	Mus musc NM_013815
0.033966	2.733679	down	Colec12	Mus musc NM_130449
0.041705	1.627885	up	C330019C	Mus musc NM_194340
0.040611	1.587243	up	Socs3	Mus musc NM_007707
0.032103	1.536019	down	Cenpq	Mus musc NM_031863
0.003846	2.124395	down	Flrt2	Mus musc NM_201518
0.029533	1.735812	down		cyclin-dep BC038161
0.04808	1.610977	up	Trub2	Mus musc NM_145520
0.003188	1.914394	down		lincRNA:chr10:24269165-24276690 reverse strand
0.025234	2.883195	down	A530001N	PREDICT XM_001477625
0.022887	2.07759	down	Rac2	Mus musc NM_009008
0.019829	1.738355	down	Neu2	Mus musc NM_001160165

0.027055	1.783151	down	Gm7120	Mus musc	NM_001177666
0.01936	1.683955	down	Il16	Mus musc	NM_010551
0.034461	1.633599	down	Zfp105	Mus musc	NM_009544
0.026931	1.845373	down	Meg3	Mus musc	NR_027652
0.045152	2.577739	down		PREDICT	XM_001478645
0.01747	9.779908	down		lincRNA:chr17:32035750-32056000 reverse strand	
0.040049	2.260997	down	Fancc	Mus musc	NM_007985
0.012188	1.566269	up		lincRNA:chr19:5795689-5802671 reverse strand	
0.032193	1.618249	up	LOC1000	PREDICT	XM_001476475
0.018319	2.182541	down	Ccl5	Mus musc	NM_013653
0.01044	1.686399	up	Tmem33	Mus musc	NM_028975
0.048828	4.236336	down	Serinc2	Mus musc	NM_172702
0.04316	2.701226	up		lincRNA:chr4:15233302-15233632 reverse strand	
0.016369	1.850389	up	Dusp1	Mus musc	NM_013642
0.029792	2.004931	up	Nr5a2	Mus musc	NM_030676
0.024865	2.702386	down	Gm5797	Mus musc	NM_001025085
0.018433	2.113299	up		lincRNA:chrX:146827709-146913398 reverse strand	
0.013293	3.489028	up	Ndufb2	Mus musc	NM_026612
0.036626	1.547626	up		lincRNA:chr10:39659425-39674200 forward strand	
0.04907	1.578775	down	Fmr1	Mus musc	NM_008031
0.00444	2.013015	up	Arsj	Mus musc	NM_173451
0.023508	3.38806	up	Nrg4	Mus musc	NM_032002
0.043019	1.741514	up	Trim65	Mus musc	NM_178802
0.035516	1.532629	up	2700007P	Mus musc	NM_001025102
0.034733	2.041428	up		lincRNA:chr12:33604247-33638654 reverse strand	
0.034348	1.517325	up		lincRNA:chr4:129497990-129515290 forward strand	
0.043572	2.356636	down	H2-DMa	Mus musc	NM_010386
0.027289	1.717166	down		RIKEN cl	XR_035200
0.033873	1.523279	up	Fcamr	Mus musc	NM_001170632
0.033363	1.600569	up		lincRNA:chr7:66562376-66579519 forward strand	
0.016447	1.754095	down	Mmrn1	Mus musc	NM_027613
0.014307	2.222336	down	Sucnr1	Mus musc	NM_032400
0.047451	2.296973	up	P2rx5	Mus musc	NM_033321

0.038356	1.51633	up	Il12rb1	Mus musc	NM_008353
0.019759	1.714824	up	Mgat5	Mus musc	NM_145128
0.003865	2.518407	down		lincRNA:chr18:63525907-63526504 reverse strand	
0.004244	1.549889	up	Slmap	Mus musc	NM_032008
0.006956	1.823342	up	1190005F	Mus musc	NM_026876
0.035371	1.509154	down	Foxd2	Mus musc	NM_008593
0.020063	1.524777	up	Gm4392	Putative u	XM_001480045
0.028469	1.755297	down	Slc13a3	Mus musc	NM_054055
0.00713	1.949708	up	2210009G	Mus musc	NM_028834
0.007765	1.807912	down	Gm15645	Mus musc	NR_033578
0.037861	1.673761	up	4930528J	Mus musc	AK029922
0.0195	1.571231	down		lincRNA:chr1:135956616-135957485 reverse strand	
0.003299	1.502249	up		integrator	XM_977857
0.00859	1.833351	down		lincRNA:chr1:74084292-74138492 reverse strand	
0.03884	1.901902	up	Myo1b	Mus musc	NM_001161817
0.013873	2.882241	down		lincRNA:chr3:36280098-36347798 reverse strand	
0.049282	1.960841	up		lincRNA:chr15:59059450-59070576 reverse strand	
0.048354	1.602219	up	Dusp11	Mus musc	NM_028099
0.020273	2.472615	down		lincRNA:chr15:32167516-32174427 reverse strand	
0.001212	1.725102	up	Ifi2712b	Mus musc	NM_145449
0.002493	1.999131	down	Zap70	Mus musc	NM_009539
0.040312	1.567689	up		lincRNA:chr7:99879368-99889978 reverse strand	
0.028065	1.503834	up	Ippk	Mus musc	NM_199056
0.013488	1.600981	up	Ecsit	Mus musc	NM_012029
0.023516	1.903361	down	Efhd1	Mus musc	NM_028889
0.014778	1.874604	up	6530401N	Mus musc	NM_029545
0.019142	3.140167	down	Traf3ip3	Mus musc	NM_153137
0.011434	1.89956	up	Chordc1	Mus musc	NM_025844
0.033269	1.902897	up		peroxisom	AK143785
0.001583	1.725074	up		gametoge	AK002723
0.02166	1.972973	down	Amacr	Mus musc	NM_008537
0.023882	1.931922	down	Cdh2	Mus musc	NM_007664
0.005872	3.487955	down	Pard3	Mus musc	NM_033620

0.022271	1.970602	down	AY512911	Mus musc	NR_033559
0.040666	1.710179	down	Trnp1	Mus musc	NM_001081156
0.037547	1.905872	up	Plk3	Mus musc	NM_013807
0.032745	3.725292	down	Gm2097	PREDICT	XM_001472439
0.005576	2.964073	down	Gm13157	Mus musc	NM_001127189
0.029715	1.51424	down	Sema4d	Mus musc	NM_013660
0.011717	1.506353	up	Pcgf2	Mus musc	NM_009545
0.011402	1.535394	up	Ndufa8	Mus musc	NM_026703
0.041528	1.976219	up	2310044G	Mus musc	NM_173735
0.03909	2.202271	down		lincRNA:chr12:110842154-110883594 forward strand	
0.043472	1.519257	up	Trappc9	Mus musc	NM_001164643
0.014549	1.513357	up	Gm5708	PREDICT	XR_032419
0.001587	1.604583	down	Ptpn6	Mus musc	NM_001077705
0.003976	1.804369	down	Tmsb15b1	Mus musc	NM_001081983
0.049993	1.868476	down	Plcd1	Mus musc	NM_019676
0.028403	1.639621	up		lincRNA:chr12:110003268-110030953 reverse strand	
0.039291	2.172013	down	E430029J	Mus musc	NM_001162938
0.048877	2.132601	up	LOC1000	PREDICT	XM_001476995
0.045618	1.86226	up	Gpr116	Mus musc	NM_001081178
0.003895	1.86225	up	Atad3a	Mus musc	NM_179203
0.016211	1.609168	up	4931406C	Mus musc	NM_133732
0.009825	7.390895	down	Jakmip1	Mus musc	NM_178394
0.001408	1.784869	up	Adrbk2	Mus musc	NM_177078
0.0114	1.786724	down	Mef2c	Mus musc	NM_025282
0.026036	1.645237	up	Gm13997	PREDICT	XM_001480419
0.042639	1.958948	down		lincRNA:chr8:89996710-90049453 forward strand	
0.047391	2.474102	down		lincRNA:chr6:47595238-47601893 reverse strand	
0.005856	1.675534	up		lincRNA:chr15:101084597-101095097 forward strand	
0.021056	2.009051	down		ectonucle	BC089320
0.024181	1.749448	up	Cpt2	Mus musc	NM_009949
0.006758	2.00674	down		lincRNA:chr11:69106907-69112857 forward strand	
0.028343	1.50468	down	Acp1	Mus musc	NM_001110239
0.043792	2.764222	up		lincRNA:chr14:99729955-99730583 forward strand	

0.007028	4.331739	down	Art4	Mus musc	NM_026639
0.048847	2.345544	up	BC051070	Mus musc	NM_178412
0.006701	3.639615	down		lincRNA:chr17:22420025-22457650 reverse strand	
0.049213	1.526895	up	Taf5	Mus musc	NM_177342
0.024566	8.844008	down		lincRNA:chr17:32035750-32056000 reverse strand	
0.022839	1.804781	up	Slc5a3	Mus musc	NM_017391
0.00409	1.773459	up	Hlf	Mus musc	NM_172563
0.042255	2.415387	down	Adamts5	Mus musc	NM_011782
0.035993	2.04067	up		lincRNA:chr7:129294998-129295498 forward strand	
0.047949	2.468665	down	Celf3	Mus musc	NM_172434
0.030174	1.549771	down	LOC1000	PREDICT	XM_001472583
0.01092	1.521931	down	Tmem14a	Mus musc	NM_029398
0.001319	1.642553	up	Tmem63b	Mus musc	NM_198167
0.016041	1.564843	down	Btk	Mus musc	NM_013482
0.005614	2.608799	down	Entpd4	Mus musc	NM_026174
0.03861	1.969716	up	Ddi2	Mus musc	NM_001017966
0.032102	3.201083	up	Clrn1	Mus musc	NM_153384
0.046987	1.603783	down	Cd82	Mus musc	NM_001136055
0.023093	1.842592	down	Acp1	Mus musc	NM_001110239
0.044012	1.509734	up	Acer1	Mus musc	NM_175731
0.048821	1.532079	up	LOC1000	PREDICT	XM_001472829
0.028744	2.450609	up	Palm2	Mus musc	NM_172868
0.001014	1.844207	down	Arhgap15	Mus musc	NM_153820
0.005474	3.299293	down	Mefv	Mus musc	NM_019453
0.039925	1.639798	up	Sco1	Mus musc	NM_001040026
0.009484	3.922723	down	Ms4a4c	Mus musc	NM_029499
0.03181	1.927116	up	Hadha	Mus musc	NM_178878
0.022637	1.548722	up		spectrin b	XM_001481329
0.009553	2.401716	down	Rps2	Mus musc	NM_008503
0.009105	1.688063	down	Gm7120	Mus musc	NM_001177666
0.022248	1.525132	up		PREDICT	XM_001478977
0.027158	3.064009	up	Gm525	Mus musc	NM_001033266
0.00716	1.690273	down		Putative u	AK082289

0.048261	1.780584	up	Lrig1	Mus musc	NM_008377
0.044116	1.577911	up		PREDICT	XM_902301
0.022687	2.073447	down	Mar-08	Mus musc	NM_027920
0.039892	2.066568	up	Psors1c2	Mus musc	NM_020576
0.047149	1.735845	down	B230311E	PREDICT	XM_001001884
0.039055	1.795345	up	LOC1000	PREDICT	XM_001473022
0.047717	2.089397	down	Pilrb2	Mus musc	NM_001024932
0.040722	2.056846	up	Gm14635	PREDICT	XM_001475018
0.012616	1.701768	up	Meis2	Mus musc	NM_001159569
0.046597	1.729723	up		lincRNA:chr10:60473030-60535340 forward strand	
0.039222	1.612087	up	Slc22a15	Mus musc	NM_001039371
0.014575	2.249113	down		PREDICT	XM_001472893
0.022635	2.615236	down	Nov	Mus musc	NM_010930
0.005356	1.875927	up		lincRNA:chr6:116092274-116144199 reverse strand	
0.010597	2.583092	up	Apold1	Mus musc	NM_001109914
0.018242	2.008048	up	Tbc1d20	Mus musc	NM_024196
0.02839	1.679735	down	Gnb4	Mus musc	NM_013531
0.004174	1.530766	down	2310001H	Mus musc	NM_145563
0.030728	1.669895	up	D8Ert73	Mus musc	NM_001007571
0.001111	2.198428	up	Slc43a2	Mus musc	NM_173388
0.043787	1.648343	up	Timm10	Mus musc	NM_013899
0.010634	1.764521	down	Spon2	Mus musc	NM_133903
0.011914	1.712178	up		lincRNA:chr6:128393530-128394127 forward strand	
0.023829	1.610178	up	Clcn6	Mus musc	NM_011929
0.012851	1.643772	down	Tmem231	Mus musc	NM_001033321
0.042665	5.830209	down		lincRNA:chr12:15735906-15798506 reverse strand	
0.036343	4.431109	up		lincRNA:chr12:20240893-20435318 reverse strand	
0.016441	3.548777	down	LOC1000	PREDICT	XM_001472813
0.037574	1.914519	up	Spata22	Mus musc	NM_001045531
0.019788	1.676538	up	Ythdf2	Mus musc	NM_145393
0.031586	1.663005	up	L2hgdh	Mus musc	NM_145443
0.008485	1.945248	down	Thbs3	Mus musc	NM_013691
0.007268	1.562983	up	Peo1	Mus musc	NM_153796

0.028011	1.821381	down	Tsix	Mus musc	AF138745
0.016727	1.500379	up	Ddx55	Mus musc	NM_026409
0.01721	1.742704	up	Adck4	Mus musc	NM_133770
0.010692	2.089083	up	LOC1000	PREDICT	XR_031705
0.02212	1.94343	up		microtubu	XM_979045
0.013457	1.675111	down		lincRNA:chr16:21794415-21815365 reverse strand	
0.013844	1.852532	down	Fmo5	Mus musc	NM_001161765
0.036456	1.570976	up	A130040M	Mus musc	NR_002860
0.009817	10.80452	down	4930427A	Mus musc	NM_134041
0.038201	5.152228	down	Crispld1	Mus musc	NM_031402
0.039189	2.497912	down	Cdc6	Mus musc	NM_011799
0.00922	1.985953	down	E130203B	Mus musc	NM_178791
0.012265	2.0154	down	Hist1h1b	Mus musc	NM_020034
0.01478	1.539439	up	Ptges3	Mus musc	NM_019766
0.049718	1.665599	down	Gm15056	Mus musc	NM_001177471
0.0489	1.85091	down	Gm1679	Mus musc	NM_001033459
0.010054	1.963705	down	Plac9	Mus musc	NM_207229
0.021028	1.601492	up	Cbx6-Npt	Mus musc	NM_001013362
0.005152	1.51414	up		lincRNA:chr6:116092274-116144199 reverse strand	
0.013455	2.248897	down	Pilra	Mus musc	NM_153510
0.037089	2.298055	up	Uspl1	Mus musc	NM_001115153
0.003507	1.709933	up	Plaa	Mus musc	NM_172695
0.01445	1.58163	up		lincRNA:chr5:22801058-22939737 reverse strand	
0.01012	1.962783	down	A630081I	Mus musc	AK042310
0.009328	1.537394	down	A330050B	Mus musc	NR_029456
0.020495	2.533125	down	Cd40	Mus musc	NM_011611
0.026142	2.142403	down		lincRNA:chr5:53931541-53945241 reverse strand	
0.027153	1.619274	up	LOC1000	PREDICT	XM_001475720
0.005974	3.799392	down		lincRNA:chr17:22335458-22466521 reverse strand	
0.003475	1.777187	down	Cdc6	Mus musc	NM_011799
0.045489	2.431475	down	Csprs	Mus musc	NM_033616
0.015605	1.912047	down	Spag1	Mus musc	NM_012031
0.046661	3.291886	up	Alad	Mus musc	NM_008525

0.029813	1.512766	up	Sik2	Mus musc	NM_178710
0.001669	25.84664	up		lincRNA:chr3:96074625-96086375 forward strand	
0.029177	1.548322	down	9030607L	Mus musc	NM_027829
0.024512	2.081025	down		lincRNA:chr6:115468025-115489250 forward strand	
5.71E-04	2.202761	down		lincRNA:chr8:90048940-90049461 forward strand	
0.030596	1.549216	up		lincRNA:chr19:5795689-5802671 reverse strand	
0.029153	1.795343	up	Gm2485	PREDICT	XM_001474163
0.043128	1.579876	down	Spc25	Mus musc	NM_025565
0.039268	2.676793	down	Dlx4	Mus musc	NM_007867
0.046581	2.697051	down	Cd209f	Mus musc	NM_026956
0.021438	1.604024	down	Ppm1h	Mus musc	NM_176919
0.020705	5.217876	down		lincRNA:chr8:94849929-94870274 reverse strand	
0.021288	2.298749	down	Mast1	Mus musc	NM_019945
0.039367	1.675474	up	Npnt	Mus musc	NM_033525
0.027432	1.874932	down		ADAMTS	AK020115
0.030469	1.681734	down	Cyp7b1	Mus musc	NM_007825
0.008572	2.197446	down	LOC1000	PREDICT	XM_001474411
9.50E-04	2.260829	down		lincRNA:chr3:113296823-113298691 reverse strand	
0.0303	2.015822	down	Nsg1	Mus musc	NM_010942
0.034518	3.563131	up		lincRNA:chr13:60524145-60528559 reverse strand	
0.02065	1.938608	down		lincRNA:chr2:143992000-143992611 forward strand	
0.032519	2.202463	up		lincRNA:chr10:3231337-3231802 forward strand	
0.011913	1.588518	down	Tmsb15b2	Mus musc	NM_001080967
0.024691	1.849832	up		lincRNA:chr10:69669025-69686275 reverse strand	
0.024826	1.619792	up	Ppig	Mus musc	NM_001081086
0.031873	3.635688	up		lincRNA:chr19:5834117-5835940 reverse strand	
0.04788	1.564769	down	Lsm4	Mus musc	NM_015816
0.024932	2.015676	down	Cmpk2	Mus musc	NM_020557
0.012024	1.889661	down	Mtap1s	Mus musc	NM_173013
0.029075	1.579089	up		lincRNA:chr12:82495575-82516300 reverse strand	
0.002736	2.26052	down		lincRNA:chr18:46646048-46659873 reverse strand	
0.024025	2.550757	down	Slc1a2	Mus musc	NM_011393
0.004023	2.183436	down	Epdr1	Mus musc	NM_134065

0.035318	1.671659	down	Tgfb2	Mus musc	NM_009367
0.046949	3.08326	down		lincRNA:chr16:59557120-59602070 reverse strand	
0.036771	4.571909	down	Gm4494	PREDICT	XM_001480485
0.041309	1.596463	up	Zfp142	Mus musc	NM_029888
0.019619	1.549952	up	Chadl	Mus musc	NM_001164320
0.014137	2.035108	up	Klhl26	Mus musc	NM_178771
0.046829	1.52802	up		lincRNA:chr1:195327945-195336595 reverse strand	
0.048174	1.547148	up		lincRNA:chr11:96111499-96126224 forward strand	
0.040038	1.539368	up	Usp31	Mus musc	NM_001033173
0.043198	2.737716	up	Acot4	Mus musc	NM_134247
6.23E-04	1.572739	down	Ikzf3	Mus musc	NM_011771
0.035666	2.236344	up	Ppp2r1b	Mus musc	NM_028614
0.021738	1.918909	down	L3mbtl4	Mus musc	NM_177278
0.002201	1.934528	down		lincRNA:chr14:77511189-77522852 forward strand	
0.009732	2.414979	down	Rnase6	Mus musc	NM_030098
0.023776	1.900574	up	Tmem120	Mus musc	NM_172541
0.048981	2.227569	up	4931406E	Mus musc	AK163891
0.006614	2.046292	down	Chrdl1	Mus musc	NM_001114385
0.022912	1.522036	up	Timm44	Mus musc	NM_011592
0.005395	3.500372	down	Gm7172	PREDICT	XR_030785
0.031558	1.570327	down	Tagap	Mus musc	NM_145968
0.008373	1.630857	down		lincRNA:chr5:110261075-110376700 reverse strand	
0.038681	2.309387	down		lincRNA:chr1:134245856-134246607 forward strand	
0.004329	1.644074	down	Fstl1	Mus musc	NM_008047
0.005361	3.04453	down		lincRNA:chr3:36280098-36347798 reverse strand	
0.027768	2.314792	down	Fmo5	Mus musc	NM_001161765
0.022209	2.406642	up	Tpmt	Mus musc	NM_016785
0.047235	1.550872	up	Msrb3	Mus musc	NM_177092
0.008598	1.552308	up	Phf17	Mus musc	NM_172303
0.014571	2.141487	down	Wnt10a	Mus musc	NM_009518
0.007691	1.790318	down	Stk3	Mus musc	NM_019635
0.010371	2.030589	up	Gm2311	PREDICT	XR_031041
0.044529	2.126696	down	Olfml3	Mus musc	NM_133859

0.022597	1.581469	up	Ophn1	Mus musc	NM_052976
0.001497	1.90062	down	Inha	Mus musc	NM_010564
0.03133	1.765999	up	LOC1000	PREDICT	XM_001473933
0.024779	1.529552	up	Barhl1	Mus musc	NM_019446
0.016033	2.205992	down	Prrx2	Mus musc	NM_009116
0.035902	2.563633	down	Tnfrsf1b	Mus musc	NM_011610
0.024948	1.617752	up	LOC1000	PREDICT	XR_030576
0.016628	2.223295	down	B3gnt5	Mus musc	NM_001159407
0.038186	2.407281	down	Vstm2b	Mus musc	NM_021387
0.041938	1.66028	down	Gria4	Mus musc	NM_001113180
0.011828	2.55475	down	Gm11346	Mus musc	NR_024599
0.032752	4.139513	up	Apoc3	Mus musc	NM_023114
0.016654	1.84421	down	Ppfia4	Mus musc	NM_001144855
0.019664	1.618791	up		lincRNA:chrX:148819227-148844227 forward strand	
0.001118	1.729625	up		zinc finge	AJ005350
0.02164	2.042563	down	Asgr2	Mus musc	NM_007493
0.01882	2.387695	down		lincRNA:chr4:149445201-149445902 forward strand	
0.032627	1.569765	down		lincRNA:chrX:90997595-91009570 forward strand	
0.042987	2.598067	down	Tas2r109	Mus musc	NM_207017
0.035181	1.645701	down	Iigp1	Mus musc	NM_001146275
0.027581	1.510314	down		Putative u	AK039657
0.014899	1.777337	up	E2f2	Mus musc	NM_177733
0.005922	2.238277	down	Myo1g	Mus musc	NM_178440
0.011849	1.564591	down		RIKEN cl	AK005108
0.023047	1.522972	down	LOC1000	PREDICT	XM_001475183
0.016819	1.80365	up	Hspa9	Mus musc	NM_010481
0.021794	1.880481	up	Acer2	Mus musc	NM_139306
0.007881	1.573541	up	Rcc2	Mus musc	NM_173867
0.043653	1.879448	up	Gm3418	PREDICT	XR_030642
0.020537	2.036445	down	Ndrg2	Mus musc	NM_013864
0.016671	1.576996	down	Amy1	Mus musc	NM_007446
0.007034	2.427634	down	Fgf18	Mus musc	NM_008005
0.036908	2.359872	down	Kif21b	Mus musc	NM_001039472

0.04374	1.562086	down	Fam45a	Mus musc	NM_026437
0.010635	3.279812	up		Putative u	XM_001478824
0.041666	3.432345	down		lincRNA:chr1:167219841-167220505 forward strand	
0.046565	1.941822	up	Adat1	Mus musc	NM_013925
0.041071	1.828719	down	Extl2	Mus musc	NM_021388
0.01635	1.632805	down	Plek	Mus musc	NM_019549
0.015963	3.19448	down	Nkg7	Mus musc	NM_024253
0.013393	2.237622	up	Has1	Mus musc	NM_008215
0.001958	3.526002	down	Bco2	Mus musc	NM_133217
0.026074	1.504432	down	Nod2	Mus musc	NM_145857
0.020469	1.545018	up			
0.035432	1.634522	up		lincRNA:chr1:44915250-44944125 forward strand	
0.045641	1.643807	up	Gm12642	PREDICT	XR_030692
0.048154	2.113072	up	Gm9992	Mus musc	NM_001142539
0.034034	1.50843	down	Hpgd	Mus musc	NM_008278
0.038183	1.517888	down		lincRNA:chr6:100518251-100519726 reverse strand	
0.045178	1.564581	down	Ctsh	Mus musc	NM_007801
0.004677	11.28923	down	4933409K	Mus musc	NR_033123
0.040319	1.682198	up		lincRNA:chr6:86476240-86513483 forward strand	
0.022864	1.507839	down	Fgd3	Mus musc	NM_015759
0.007897	1.679453	down	Odc1	Mus musc	NM_013614
0.02468	1.73204	up		lincRNA:chr6:47687025-47728525 forward strand	
0.012721	1.712225	up	Gm6293	PREDICT	XM_886587
0.019773	5.897644	up	Paqr4	Mus musc	NM_023824
0.014261	1.699588	down	Haus8	Mus musc	NM_001163042
0.001644	1.621475	down		lincRNA:chr16:90008636-90015586 reverse strand	
0.022938	1.519104	down	Zfp39	Mus musc	NM_011758
0.04286	1.971202	down	Stmn1	Mus musc	NM_019641
0.011775	1.627073	up	E030042N	Mus musc	AK087301
0.006189	3.69118	up	Dio2	Mus musc	NM_010050
0.041916	2.645777	down	Rbp1	Mus musc	NM_011254
0.01571	1.576327	up	2810007J2	Mus musc	NM_175250
0.040853	1.742586	down	Itga4	Mus musc	NM_010576

0.037872	3.297836	up	Padi3	Mus musc	NM_011060
1.25E-04	2.176887	up	Acat2	Mus musc	NM_009338
0.048308	2.399275	down		lincRNA:chr10:83185606-83225506 forward strand	
0.046705	1.653735	down	S1pr5	Mus musc	NM_053190
0.014519	1.725329	up	Gm6611	PREDICT	XM_894394
0.04008	3.603988	up		lincRNA:chr11:87872568-87880978 reverse strand	
0.012397	2.612728	down	Dnm3os	Mus musc	NR_002870
0.013595	1.595127	down	Tpm4	Mus musc	NM_001001491
0.030995	1.970711	up	Akap1	Mus musc	NM_001042541
0.04891	1.626533	down	Wnt2b	Mus musc	NM_009520
0.011082	1.671581	down		lincRNA:chr12:110896603-110940553 forward strand	
0.027078	3.650285	down	Sntg1	Mus musc	NM_027671
0.014353	1.782075	up	Pcdhb4	Mus musc	NM_053129
0.029532	1.68051	down	Il2ra	Mus musc	NM_008367
0.038399	2.170182	down	Tspan11	Mus musc	NM_026743
0.014153	1.707764	up	Rnf214	Mus musc	NM_178709
0.005452	2.088381	down	Nkd1	Mus musc	NM_027280
0.010036	1.754074	up	Naa25	Mus musc	NM_172722
0.020833	1.525801	up	Ptpru	Mus musc	NM_001083119
0.032257	1.691593	down	Sirpb1a	Mus musc	NM_001002898
0.008355	2.579032	down	Gm9307	PREDICT	XM_001472674
0.043232	1.536112	down	Gm9000	PREDICT	XM_994545
0.027843	1.819124	up	Gm6742	PREDICT	XR_030600
0.032581	3.785257	up	Insig1	Mus musc	NM_153526
0.026852	3.907492	down	Rab9b	Mus musc	NM_176971
0.039551	2.402818	down	Nudcd1	Mus musc	NM_026149
0.007451	2.184385	down	LOC1000	PREDICT	XM_001480027
0.030787	2.681676	up		lincRNA:chr1:58443698-58449898 forward strand	
0.044535	3.291527	up	Pou1f1	Mus musc	NM_008849
0.019356	1.791661	up		lincRNA:chr11:50994911-51050704 reverse strand	
0.02129	2.022499	up	1810014F	Mus musc	NM_026928
0.026503	1.995644	down		lincRNA:chr8:60132300-60146830 forward strand	
0.010829	3.864827	down	6330549D	Mus musc	NR_003619

0.00269	10.61709	down	Gm13298	Mus musc	NM_001085530
0.034224	1.709784	up	Aoc2	Mus musc	NM_178932
0.008207	1.52283	up	1700017B	Mus musc	NM_028820
0.043983	1.501186	down			lincRNA:chr5:54053882-54054174 forward strand
0.011979	1.513616	up	8430406I	Mus musc	NM_028984
0.033741	3.496798	down	Cd2	Mus musc	NM_013486
0.030425	1.953468	down	Vsig2	Mus musc	NM_020518
0.036528	3.995564	down	Pde6h	Mus musc	NM_023898
0.031023	2.534766	down	Cxcr6	Mus musc	NM_030712
0.009293	1.502142	up	Fmn1	Mus musc	NM_010230
0.003588	1.58151	down			lincRNA:chr3:84609788-84618062 reverse strand
0.031708	1.789419	down	Gm3648	PREDICT	XM_001478508
0.042062	1.516745	down			lincRNA:chr4:11899775-11931875 forward strand
0.02845	1.520616	down			lincRNA:chr5:53931541-53945241 forward strand
0.048443	2.364233	down	Duoxa1	Mus musc	NM_145395
1.92E-04	1.773123	down	Casp12	Mus musc	NM_009808
0.047707	5.351806	down	Fbxl13	Mus musc	NM_177076
0.008062	1.786247	up	Ppp1r15a	Mus musc	NM_008654
0.024783	1.700433	down		PREDICT	XM_001475751
0.018541	1.660775	down	Trnau1ap	Mus musc	NM_027925
0.047414	1.779825	up	2900062L	Mus musc	NM_029823
0.023246	1.965689	up	4632415L	Mus musc	NR_027985
0.03975	2.181842	down			lincRNA:chr11:87841800-87858725 reverse strand
4.45E-04	1.700281	down	Ubash3b	Mus musc	NM_176860
0.045268	1.903706	up	Cmtm4	Mus musc	NM_153582
0.009224	2.484113	up	Gm2903	PREDICT	XR_031909
0.006544	1.574988	up	Nudcd3	Mus musc	NM_173748
0.001806	3.436216	up			lincRNA:chr8:85952719-85958369 reverse strand
0.014051	1.541708	down			lincRNA:chr6:112552041-112560067 forward strand
0.042248	2.557383	up	Ptprd	Mus musc	NM_011211
0.046651	5.986563	down	Siglec5	Mus musc	NM_145581
0.021427	9.970615	down			lincRNA:chr4:146890596-146891297 forward strand
3.01E-04	1.746103	up			lincRNA:chr17:24152225-24169870 reverse strand

0.039148	1.677153	down	Iqcc	Mus musc	NM_198026
0.02998	1.948043	up	Gramd1b	Mus musc	NM_172768
0.026039	1.624222	up		lincRNA:chr15:62090565-62091770 forward strand	
0.001041	2.522852	down		lincRNA:chr15:32167516-32174417 reverse strand	
0.00909	2.930618	down	Klra8	Mus musc	NM_010650
0.048928	1.585963	down	Flrt1	Mus musc	NM_201411
0.031426	1.533521	up	2700050L	Mus musc	NM_178115
0.048858	2.1074	down	Zfp867	Mus musc	NM_178417
0.044892	1.881944	up		family wit	AK080717
0.014469	1.581393	down		lincRNA:chr9:71687805-71689542 reverse strand	
0.032456	1.746182	down		lincRNA:chr7:77555482-77634858 forward strand	
0.008848	2.10581	down		predicted	XM_001476394
0.024575	2.459187	down	Ces5	Mus musc	NM_172759
0.022324	2.375337	down	Lars2	Mus musc	NM_153168
0.027786	2.844588	down	Ndr4	Mus musc	NM_145602
0.047807	1.649399	down	Kifc1	Mus musc	NM_053173
0.011989	1.773617	down	Gm5077	Mus musc	NM_173864
0.033665	1.662786	down	Fam174b	Mus musc	NM_001162532
0.048687	2.371507	down	Eps8l1	Mus musc	NM_026146
0.005221	2.125716	down	Pitpnm3	Mus musc	NM_001024927
0.031591	1.828139	down	Zfp882	Mus musc	NM_001166645
0.021867	2.120536	down	Hn1l	Mus musc	NM_198937
0.042351	1.915999	up	Slc36a2	Mus musc	NM_153170
0.012655	1.623355	up	Gpbp1l1	Mus musc	NM_029868
0.031172	1.644199	down		lincRNA:chr1:85117750-85129200 forward strand	
0.005889	2.033024	down	Sntg2	Mus musc	NM_172951
0.03775	1.568868	up		lincRNA:chr6:86776350-86799450 forward strand	
0.033794	2.098211	down		lincRNA:chr13:112717680-112733330 reverse strand	
0.014383	2.624969	down	Cst7	Mus musc	NM_009977
0.046432	1.54335	down	Ttc30a2	Mus musc	NM_001081228
0.035614	2.110605	up	Usp38	Mus musc	NM_027554
0.021655	3.201674	down		lincRNA:chr8:94841965-94881130 reverse strand	
0.008758	1.604114	down	Timp1	Mus musc	NM_001044384

0.011051	2.75938	down	Sparc	Mus musc	NM_009242
0.007873	4.3757	up	Plin5	Mus musc	NM_001077348
0.014901	1.556435	down	Sp110	Mus musc	NM_175397
0.0266	1.748533	down	Gm3380	PREDICT	XM_001476937
0.028654	2.026496	up	Tnfrsf14	Mus musc	NM_178931
0.027654	1.696075	down	Fgf9	Mus musc	NM_013518
0.043497	3.187073	up	Chchd10	Mus musc	NM_175329
0.010814	2.293557	down	Cyp2ab1	Mus musc	NM_183158
0.014878	3.580231	down		phosphodi	AK032648
0.023318	1.653158	down	Klre1	Mus musc	NM_153590
0.036049	1.594946	up	Tapt1	Mus musc	NM_173764
0.017767	1.660889	down	AF251705	Mus musc	NM_134158
0.002796	1.520069	down	Clec4e	Mus musc	NM_019948
0.00258	2.074335	down	Hmha1	Mus musc	NM_001142701
0.012109	1.565911	up		lincRNA:chr4:82156098-82196298 reverse strand	
0.018878	2.795842	down	Ccr5	Mus musc	NM_009917
0.005186	1.801324	down	Tspan32	Mus musc	NM_020286
0.012196	1.693549	up		lincRNA:chr7:99879368-99889978 reverse strand	
0.043551	1.635483	down	A630012P	Mus musc	BC100571
0.015444	1.964014	down		Q61491_MOUSE (Q61491) DNA-binding protein, partial (70%) [TC1607062]	
0.002123	1.793089	down	Rpl17	Mus musc	NM_001002239
0.003074	1.712546	down	Ncrna0008	Mus musc	NR_028086
0.032251	1.564506	up	Gm16452	PREDICT	XM_903553
0.015066	1.538652	up		lincRNA:chr9:41137539-41353289 forward strand	
0.024627	1.733613	up	Trmt5	TRM5 tRNA	BC012521
0.016513	1.714815	up	Zfp442	Mus musc	NM_001177550
0.016627	1.582785	up		Putative u	AK144859
0.007354	1.718472	down	Fanci	Mus musc	NM_145946
0.001194	1.659075	down	Slc25a24	Mus musc	NM_172685
0.009679	1.640105	up	Adam17	Mus musc	NM_009615
0.040426	2.043835	down	Hist1h2an	Mus musc	NM_178184
0.042038	2.300282	up	Agfg2	Mus musc	NM_145566
0.011688	2.175589	up		lincRNA:chr10:118385588-118439338 reverse strand	

0.033888	1.963329	up		lincRNA:chr14:19295319-19310619 reverse strand
0.031936	2.320854	down		lincRNA:chr10:83181374-83249774 forward strand
0.02895	2.319873	up	Ushbp1	Mus musc NM_181418
0.029811	1.628339	down	Cpt1c	Mus musc NM_153679
0.034199	1.871003	up		lincRNA:chr12:33604247-33638654 reverse strand
0.007367	3.021256	down	Gm3893	Mus musc NR_033506
0.048986	2.36845	down	Lilra6	Mus musc NM_011090
0.007125	3.710476	up	A830018I	Mus musc NM_177173
0.007161	1.894758	up	Skint5	Mus musc NM_001167878
0.029949	1.721322	up	Per2	Mus musc NM_011066
0.009724	3.411124	down	Klra23	Mus musc NM_024470
0.003706	2.502026	down	Fasl	Mus musc NM_010177
0.033525	1.754483	down	Ikzf1	Mus musc NM_001025597
0.025415	1.89932	down	Msl3l2	Mus musc NM_001163833
0.049979	1.619645	up		AU RNA AK019978
0.024678	2.660686	down	Ifitm6	Mus musc NM_001033632
0.007061	2.098699	down	Unc45b	Mus musc NM_178680
0.026689	1.619119	down	Rnaset2a	Mus musc NM_001083938
0.034358	1.602283	down		lincRNA:chr11:120041124-120052299 reverse strand
0.008469	2.08452	up	Sephs2	Mus musc NM_009266
4.83E-04	13.19949	down	Gm13298	Mus musc NM_001085530
0.045488	1.568004	up		lincRNA:chr3:62727150-62758225 forward strand
0.03114	3.271499	down	Htra4	Mus musc NM_001081187
0.04528	1.627573	up	Atf1	Mus musc NM_007497
0.026912	1.610065	up	B3galt2	Mus musc NM_020025
0.031037	2.734514	down	G2e3	Mus musc NM_001167963
0.047497	1.808766	down	Actl6b	Mus musc NM_031404
0.017099	3.01878	down	LOC6740	PREDICT XM_972673
6.31E-05	3.506591	down		lincRNA:chr15:32167516-32174427 reverse strand
0.043688	1.701214	up	Stip1	Mus musc NM_016737
0.005567	1.536826	up		lincRNA:chr4:89032648-89133273 forward strand
0.010137	1.815183	down	Coro1a	Mus musc NM_009898
0.016388	1.523946	down	Pcdhga1	Mus musc NM_033584

0.024123	2.150115	up	Krt78	Mus musc	NM_212487
0.022574	2.635434	down	Gm7609	Mus musc	NM_001081746
0.004208	1.512022	down	Tec	Mus musc	NM_001113460
0.0089	2.796476	down	Cdk14	Mus musc	NM_011074
0.016702	2.676489	down			lincRNA:chr9:96632664-96653249 reverse strand
0.013112	1.550048	down			lincRNA:chr6:3283191-3284581 reverse strand
0.008744	2.814875	up	Gm10324	Mus musc	NM_001177832
0.009483	1.648988	up	Gm1971	PREDICT	XM_001472879
0.002735	1.709562	down	1190002F	PREDICT	XM_001481164
0.047033	1.66967	up	Rfx2	Mus musc	NM_009056
0.043193	1.689056	down			lincRNA:chr1:135956616-135957485 reverse strand
0.010962	1.90116	down	Gm9487	PREDICT	XR_032777
0.015483	1.890601	up	Prdm15	Mus musc	NM_144789
0.024973	1.878579	down	Dock10	Mus musc	NM_175291
0.021952	1.641324	up			lincRNA:chr15:61870759-61938796 forward strand
0.018555	1.509766	up	5730528L	Mus musc	NM_001145924
0.04158	1.864175	up			lincRNA:chr4:141100989-141106639 reverse strand
0.00483	1.64559	up			lincRNA:chr8:91569369-91594119 reverse strand
0.024999	1.892431	down	Vmn2r62	Mus musc	NM_001105059
0.00323	1.607122	up	Dock4	Mus musc	NM_172803
0.031146	1.949789	down	Gm6524	Mus musc	NR_028307
0.007058	3.191231	down	Rec8	Mus musc	NM_020002
0.030972	1.744267	down			lincRNA:chr2:72818943-72826893 forward strand
0.032323	1.655551	up	5730528L	Mus musc	NM_001145924
0.034528	3.414973	down		Protein K	XM_001472112
0.00307	3.074687	down	Lrrn2	Mus musc	NM_010732
0.004731	1.580197	down	Mettl7b	Mus musc	NM_027853
0.007296	2.061908	down		RIKEN cl	AK007475
0.008956	1.699287	down	Adamtsl4	Mus musc	NM_144899
0.018494	1.609873	up	Ogdh	Mus musc	NM_010956
0.012124	2.349457	up	LOC6300	PREDICT	XR_031677
0.005793	1.741829	down			lincRNA:chr7:88668948-88678046 forward strand
0.039491	2.176342	down	Gm3604	Mus musc	NM_001162910

0.010361	2.083389	down	Pyhin1	Mus musc	NM_175026
0.012999	2.875714	down	Ptgir	Mus musc	NM_008967
0.013508	2.916797	down	Ly86	Mus musc	NM_010745
0.031962	1.822295	down	Fam26e	Mus musc	NM_178908
0.035918	2.179575	down	Id4	Mus musc	NM_031166
0.029283	1.945851	down	Cmah	Mus musc	NM_007717
1.18E-04	2.33067	down	2300002M	Mus musc	NM_175148
0.034361	1.856618	down	Lrmp	Mus musc	NM_008511
0.006992	2.157433	down	Lsp1	Mus musc	NM_019391
0.04531	1.508054	down	LOC6381	PREDICT	XR_034120
0.034531	1.612212	down	Kctd11	Mus musc	NM_153143
0.041441	2.039379	up	Hspe1	Mus musc	NM_008303
0.013623	1.65896	down	Scml2	Mus musc	NM_133194
0.028129	2.184615	up	Bckdhh	Mus musc	NM_199195
0.00383	1.670105	up		lincRNA:chr7:6108350-6119600 reverse strand	
0.00198	1.502111	down	Ppic	Mus musc	NM_008908
0.003403	2.515108	down	Tmc7	Mus musc	NM_172476
0.037522	1.985965	up	Olfr372	Mus musc	NM_207555
0.024905	2.65256	up		lincRNA:chr4:86267450-86277650 forward strand	
0.02303	1.738557	down	Zfp236	Mus musc	NM_177832
0.027081	2.768699	down		RIKEN cl	AK140837
0.025666	2.271395	up	4930447C	Mus musc	NM_029444
0.037894	1.680506	down	E330013P	Mus musc	NR_026942
0.00718	2.053962	down	Kirrel	Mus musc	NM_001170985
0.010396	2.900648	down	Matn2	Mus musc	NM_016762
0.019583	1.940217	up	P4ha1	Mus musc	NM_011030
0.030298	1.592104	up		PREDICT	XM_001479428
0.038713	1.573902	down		lincRNA:chr10:3227840-3233588 reverse strand	
0.009	2.895524	down	9130008F	Mus musc	NM_027834
0.043232	1.581629	down	Slc13a4	Mus musc	NM_172892
0.049021	1.881391	down		lincRNA:chr17:87674225-87682154 reverse strand	
0.009416	2.032014	down	Adra2a	Mus musc	NM_007417
0.014977	2.125767	up	Ppargc1a	Mus musc	NM_008904

0.04788	3.217567	up	Slitrk4	Mus musc	NM_178740
0.025566	1.57993	up		MAP kina	AK177092
0.015673	1.615085	down		lincRNA:chr6:146495766-146496419 reverse strand	
0.04254	1.693881	down	Bace2	Mus musc	NM_019517
0.043332	6.797938	up		lincRNA:chr3:96074625-96086375 forward strand	
0.004243	1.528314	down	Gipr	Mus musc	NM_001080815
0.03528	1.640954	up	Barx2	Mus musc	NM_013800
0.022729	1.573171	down	3830406C	Mus musc	NM_146051
0.038351	1.521939	up	Gtf3c6	Mus musc	NM_026113
0.038072	1.811718	down	Gstt3	Mus musc	NM_133994
0.04103	1.865712	down	Klhl29	Mus musc	NM_001164493
0.023774	1.796248	down	Gm6936	PREDICT	XM_001480183
0.045741	3.321764	up		lincRNA:chr14:65206167-65206949 forward strand	
0.007919	79.224	down	Cdsn	Mus musc	NM_001008424
0.015037	1.967827	up	Btnl9	butyrophil	BY730984
0.011537	1.675521	down	Plekha4	Mus musc	NM_148927
0.01784	1.915208	down	C230055k	Mus musc	NM_001039231
0.032361	1.725771	down		lincRNA:chr17:12990484-13018375 forward strand	
0.032019	1.712717	up	Zcchc2	Mus musc	NM_001122676
0.025991	1.674289	down	Tspyl3	Mus musc	NM_198617
0.003387	2.031189	up	LOC1000	PREDICT	XM_001473387
0.016415	1.626209	down	LOC6691	PREDICT	XM_001472555
1.21E-04	2.092441	up	Krt79	Mus musc	NM_146063
0.018935	1.932195	down		lincRNA:chr10:62267317-62269871 reverse strand	
0.038576	1.665159	up	Ndufs7	Mus musc	NM_029272
0.033909	1.796588	down	Ncr1	Mus musc	NM_010746
0.016252	1.544144	up	Fam178a	Mus musc	NM_001081225
0.002154	1.885834	down	Gm3819	PREDICT	XM_001477163
0.012381	2.410317	down		lincRNA:chr12:72103832-72116875 reverse strand	
0.005101	2.35226	down	Itgb3	Mus musc	NM_016780
6.80E-04	2.069044	up	1700080F	Mus musc	AK006954
0.008073	1.768292	up		Putative u	AK139534
0.0472	2.393227	up		lincRNA:chr19:12079745-12088620 reverse strand	

0.003982	2.135149	up		Mus musc	AK142897
0.03711	1.977604	down	Ptpnrcap	Mus musc	NM_016933
9.13E-04	1.532676	up	22104160	Mus musc	AK008958
0.040015	1.598561	up	D130095I	Mus musc	AK084110
0.008816	1.527735	up	Gm13229	PREDICT	XM_112297
0.019057	2.476705	up		lincRNA:chr17:56687541-56694616 reverse strand	
0.004397	1.834963	up	LOC1000	PREDICT	XM_001475613
0.02069	2.313088	up	Tob1	Mus musc	NM_009427
0.049651	3.046934	down	A930018N	Mus musc	AK034241
0.021458	1.982914	down	B3gnt8	Mus musc	NM_146184
0.017345	1.899507	up	Khdrbs1	KH doma	XM_001475530
0.025285	2.263613	up	Rad23a	Mus musc	NM_009010
0.027699	1.815501	down	Txndc16	Mus musc	NM_172597
0.035665	1.99929	up		NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 Gene [Source:MGI (curated);Acc:M	
0.004713	3.474165	down	Fbxo44	Mus musc	NM_173401
0.018009	2.318356	down		lincRNA:chr10:24269165-24276690 reverse strand	
0.045659	1.945239	up	Prss22	Mus musc	NM_133731
9.59E-04	4.900343	down		lincRNA:chr17:22420025-22457650 reverse strand	
0.02141	1.893419	up	A930009E	Mus musc	AK020836
0.013882	1.544842	down		lincRNA:chr19:53517903-53540753 reverse strand	
0.03312	1.724201	up		lincRNA:chr1:138528250-138538250 forward strand	
0.027112	2.561074	down	Ms4a4c	Mus musc	NM_029499
0.040934	1.515169	up		lincRNA:chr8:48485495-48485865 reverse strand	
0.0027	1.757653	up	Pex5	Mus musc	NM_008995
0.0041	1.513623	up	Dlx3	Mus musc	NM_010055
0.030872	1.680209	up	Pdxk	Mus musc	NM_172134
0.047675	1.770269	up	Cdc7	Mus musc	NM_009863
0.005286	1.517174	down	Slfn10-ps	Mus musc	NM_181542
0.049967	1.970793	up	Pisd	Mus musc	NM_177298
0.039109	4.098978	down	Gm5858	PREDICT	XM_619973
0.006908	1.87954	down	119000710	Mus musc	NM_001135567
0.044647	1.503096	down	Cttnal1	Mus musc	NM_018761
0.02566	7.451304	up			XM_001478565

0.045313	1.739852	down	Prkca	Mus musc	NM_011101
0.010013	1.784472	down	Fut7	Mus musc	NM_013524
0.035367	2.644321	down	LOC1000	PREDICT	XM_001473983
0.026143	3.400029	up	Hsph1	Mus musc	NM_013559
0.028523	1.56065	down	Tnfaip2	Mus musc	NM_009396
0.03018	1.941208	up	Acsm3	Mus musc	NM_212441
0.01583	5.613798	up	Tll2	Mus musc	NM_001098267
0.038178	2.533838	up	Rgs7	Mus musc	NM_011880
0.012256	1.583261	down	Il13ra1	Mus musc	NM_133990
0.01901	1.755886	up	Acadm	Mus musc	NM_007382
0.023978	1.67141	up	EG547347	Mus musc	NM_001034909
0.024921	1.943873	down	Fgf18	Mus musc	NM_008005
0.037017	1.67168	down		lincRNA:chr17:32075308-32075792 reverse strand	
0.039143	1.693267	down		lincRNA:chr1:85036677-85038530 reverse strand	
0.02893	2.259036	down	Cfh	Mus musc	NM_009888
0.003063	2.118858	up	Gm6603	PREDICT	XM_898851
0.047017	1.995621	down	LOC6308	PREDICT	XR_030502
0.010069	1.500633	up	Nol9	Mus musc	NM_028727
0.018644	1.697158	up	Dyrk1a	Mus musc	NM_007890
0.022227	4.98698	down	5830444B	Mus musc	AK030886
0.015922	1.676468	up	AW12532	mp78f05.y	AI530666
0.007616	2.001573	down	D930026N	Mus musc	AK142841
0.043311	3.361615	down	Bcl11a	Mus musc	NM_016707
0.023557	4.874306	down	1700030C	Mus musc	AK041326
0.037821	1.616545	down	A530032I	Mus musc	NM_213615
0.041649	1.720282	down	Csprs	Mus musc	NM_033616
0.008467	1.694115	down	Ly6g6e	Mus musc	NM_027366
0.00692	1.536015	up	Adnp2	Mus musc	NM_175028
0.001324	2.310227	up	LOC6763	PREDICT	XM_989290
0.035607	1.551135	up	LOC1000	PREDICT	XM_001479122
0.032831	1.51358	up		lincRNA:chr7:88668948-88678046 reverse strand	
0.021683	1.557879	down	Dapk2	Mus musc	NM_010019
0.032011	2.17097	down	Evi2a	Mus musc	NM_001033711

0.010803	2.407396	up		lincRNA:chr5:35975265-35982561 reverse strand
0.009469	2.305579	up	Btnl9	Mus musc NM_172793
0.008456	1.713081	up		lincRNA:chr9:121256738-121257487 forward strand
0.035715	2.113455	down	Inmt	Mus musc NM_009349
0.019902	2.576128	up		lincRNA:chr12:112223388-112223755 forward strand
0.016421	3.772941	down	Il1rl1	Mus musc NM_001025602
0.033778	2.289058	up		lincRNA:chr1:58440355-58449627 reverse strand
0.016054	1.635641	down		lincRNA:chr10:62267317-62269871 reverse strand
0.040912	1.886694	up	LOC6743	PREDICT XM_973875
0.049636	1.515468	up		lincRNA:chr6:99472981-99484210 forward strand
0.002748	1.501731	down	Rnaseh2a	Mus musc NM_027187
0.029675	2.452502	down	Gimap3	Mus musc NM_031247
0.049077	6.135358	up	Gys2	Mus musc NM_145572
0.036929	1.875754	down	Nipal3	Mus musc NM_028995
0.00403	3.476117	down		lincRNA:chr4:146149125-146155054 forward strand
0.046818	1.683754	down		lincRNA:chr2:157361470-157379813 reverse strand
0.044198	1.850879	up	9930014A	Mus musc NR_030696
0.012773	1.528945	down	Gm8681	PREDICT XR_032130
0.031188	1.988125	down	Ccdc8	Mus musc NM_001101535
0.028495	1.539375	up	1300001I0	Mus musc NM_001081158
0.028457	2.927613	down	Ccl21a	Mus musc NM_011124
0.001039	1.82983	up	1190005I0	Mus musc NM_197988
0.030562	2.141213	up	Camp	Mus musc NM_009921
0.048733	1.999181	up	Coq10b	Mus musc NM_001039710
0.022233	1.720356	down	Ncf4	Mus musc NM_008677
3.72E-04	2.441363	down	Gm2496	PREDICT XM_001473960
0.028981	2.300277	down	Sgsm1	Mus musc NM_001162965
0.04308	1.697465	down	Nlrc4	Mus musc NM_001033367
0.003947	3.270321	down		RIKEN cl AK014270
0.034159	1.948693	down	Olfr1036	Mus musc NM_207142
0.024945	1.891619	up	Gm6871	PREDICT XM_893095
0.044371	1.591489	up	Tsen54	Mus musc NM_029557
0.023278	1.695028	down	Akna	Mus musc NM_001045514

0.007134	2.005536	up	Mpzl2	Mus musc	NM_007962
0.011755	1.828251	down	Rgs10	Mus musc	NM_026418
0.035666	2.145269	down		lincRNA:chr18:63355660-63369610 reverse strand	
0.012798	1.677411	up	Adig	Mus musc	NM_145635
0.005272	1.747201	down	Abcg1	Mus musc	NM_009593
0.033265	2.062465	down	Dbn1	Mus musc	NM_001177371
0.02661	2.940796	up	LOC1000	PREDICT	XR_031739
0.009188	1.995898	up	Ublcp1	Mus musc	NM_024475
0.008418	2.303463	down		lincRNA:chr12:53669892-53710742 forward strand	
0.015077	1.880931	down	Ddx19b	Mus musc	NM_172284
0.029013	1.517037	up		RIKEN cl	AK140147
0.004142	1.894079	up	Ephx2	Mus musc	NM_007940
0.014657	1.659489	up		FMS-like	AK045865
0.00475	1.95878	down		lincRNA:chr12:32781477-32808567 reverse strand	
0.007747	1.564374	down	Nupl2	Mus musc	NM_153092
0.013364	1.614025	down		lincRNA:chr3:30099759-30133959 reverse strand	
0.031575	2.1602	down	2310007J0	Mus musc	AK009210
0.010586	1.523251	down		lincRNA:chr4:114585803-114588898 forward strand	
0.012287	1.53842	up		lincRNA:chr4:3746573-3746891 forward strand	
0.041752	1.931433	down		lincRNA:chr13:28551902-28975446 reverse strand	
0.005757	1.708165	up	Prrt1	proline-rid	AK137892
0.025904	1.775856	down		lincRNA:chr12:32781477-32808567 reverse strand	
0.028378	1.703885	down	Eml6	Mus musc	NM_146016
0.019451	1.865889	down	Slc16a5	Mus musc	NM_001080934
0.005428	1.957608	up	Gm9532	PREDICT	XM_001474726
0.015845	2.330966	down	Ccl21b	Mus musc	NM_011335
0.006947	1.676958	down		lincRNA:chr2:143992000-143992611 forward strand	
0.017377	1.643287	up	Apba3	Mus musc	NM_018758
0.014415	1.771894	down	Rasgrp4	Mus musc	NM_145149
5.83E-04	2.141308	down	Angptl1	Mus musc	NM_028333
0.031624	3.078136	down	Slc2a6	Mus musc	NM_172659
0.022881	1.871564	up	Vgll1	Mus musc	NM_133251
0.043401	1.996865	up	9030425P	Mus musc	AK083944

0.015911	2.445511	down	LOC1000	PREDICT	XM_001477580
0.009969	1.726184	up		a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 9 C	
0.044212	1.753523	up	Ano8	Mus musc	NM_001164679
0.035057	1.648628	up	Ddi2	Mus musc	NM_001017966
0.021968	2.529246	down	Syt11	Mus musc	NM_031393
0.026154	1.677718	down	Cpsf3l	Mus musc	NM_028020
0.040552	2.220439	down	Tfpi	Mus musc	NM_011576
0.037241	1.638048	up		RIKEN cl	AK085305
0.003074	7.239178	up	Cox8b	Mus musc	NM_007751
0.023759	1.62818	down	H2-Ab1	Mus musc	NM_207105
0.035261	1.509206	up	Rbm15	Mus musc	NM_001045807
0.007624	1.598411	up	Llph	Mus musc	NM_025431
0.024982	2.252906	up	Npbwr1	Mus musc	NM_010342
0.03869	1.72703	up	Apex2	Mus musc	NM_029943
0.026617	1.563124	down	Lgi4	Mus musc	NM_144556
0.04954	1.544608	down		lincRNA:chr13:107822042-107823753 forward strand	
0.006464	2.580889	down	Gnptg	Mus musc	NM_172529
0.019249	13.54838	down	Muc11	Mus musc	NM_009268
0.031825	1.554531	down	Gm1499	AGENCO	BU523966
0.001666	1.597362	up	Chd7	Mus musc	NM_001081417
0.014939	2.134986	up	Rxrg	Mus musc	NM_009107
0.015837	2.188465	up		lincRNA:chr7:6302922-6306477 forward strand	
0.033951	1.809594	up	Nt5dc1	Mus musc	NM_176968
5.07E-04	3.965272	down	Ranbp3l	Mus musc	NM_198024
0.00156	2.673449	up	Kcnab3	Mus musc	NM_010599
0.026494	1.514931	up	Ash1l	Mus musc	NM_138679
0.011996	1.962123	up	D7Ert66	H3085D1	BG070263
0.021391	3.707074	up	LOC1000	PREDICT	XM_001474051
0.039298	1.579118	up	Gm7428	PREDICT	XR_001700
0.006883	2.445399	up	Pfkfb3	Mus musc	NM_133232
0.03752	2.020239	up		Mus musc	AK006881
0.007142	2.623225	down		lincRNA:chr15:32167516-32174417 reverse strand	
0.025905	1.684217	up	Mapk6	Mus musc	NM_027418

0.029853	2.358573	down	Pyhin1	Mus musc	NM_175026
0.017696	1.597181	up		lincRNA:chr3:90427029-90427674 forward strand	
0.00786	2.038261	up	Bcat2	Mus musc	NM_009737
0.03321	2.417558	down	AI182371	Mus musc	NM_178885
0.041008	2.812629	up	Cyr61	Mus musc	NM_010516
0.00976	1.910758	up		lincRNA:chr12:17888352-17907493 forward strand	
0.04835	2.650807	up	Tra2b	Mus musc	NM_009186
0.024532	1.576775	down		lincRNA:chr2:128137419-128141735 reverse strand	
0.036796	2.020799	down	Atm	Mus musc	NM_007499
0.003653	1.572707	up	2700078E	Mus musc	NM_030197
0.026163	1.867016	up	Gm5741	PREDICT	XM_488140
4.25E-04	1.885767	down		lincRNA:chr5:105072936-105074001 forward strand	
0.033834	1.517834	up	Ccdc144b	Mus musc	NM_178418
0.007982	1.651644	up	B230317F	PREDICT	XR_035255
0.04684	2.248776	down		lincRNA:chr2:127988295-128194920 reverse strand	
0.006494	3.952469	up	Ppargc1b	Mus musc	NM_133249
0.046745	1.812058	down		lincRNA:chr8:35652473-35703370 reverse strand	
0.046601	1.614144	down		lincRNA:chr11:120046656-120050065 forward strand	
0.012575	1.682912	down	Nlrp1c-ps	Mus musc	NR_027858
0.034609	1.700244	down	Dennd1c	Mus musc	NM_153551
0.032819	2.094147	down	Gm10406	Mus musc	NM_001164727
0.015328	1.530471	down		lincRNA:chr18:35970772-35971449 forward strand	
0.015316	1.570516	up	Pitx3	Mus musc	NM_008852
0.033615	2.013924	down	Stxbp6	Mus musc	NM_144552
0.013067	1.707122	down	Slc22a18	Mus musc	NM_001042760
0.006296	1.686185	up	Esr1	Mus musc	NM_007956
0.029179	2.171122	up	Tomm7	Mus musc	NM_025394
0.006627	1.826418	up		lincRNA:chr9:114412295-114418384 reverse strand	
0.039575	2.118511	down	Gfra2	Mus musc	NM_008115
0.035493	2.067801	down	Tmem88	Mus musc	NM_025915
0.013033	1.742738	up	Coasy	Mus musc	NM_027896
0.01842	1.522533	down	Il17f	Mus musc	NM_145856
0.01855	2.736188	down	Tnfrsf17	Mus musc	NM_011608

0.043233	1.608607	up	Gm4340	Mus musc	NM_001177535
0.024563	1.836563	down	Cpxm2	Mus musc	NM_018867
0.044066	2.152546	up			lincRNA:chr15:83181291-83197750 reverse strand
4.23E-05	2.281027	down	Kcne3	Mus musc	NM_020574
0.046752	1.590089	up	Gm4080	PREDICT	XM_001478955
0.033142	1.530521	up		Novel pro	AK156771
0.014895	3.225149	down		RIKEN cl	XM_001472312
0.02591	1.538312	up	Gna13	Mus musc	NM_010303
0.002187	4.952762	down			lincRNA:chr17:32044823-32045974 reverse strand
0.029721	3.930969	up	Nat8l	Mus musc	NM_001001985
0.034051	1.919842	up	Gm10319	Mus musc	NR_003624
0.010741	1.806414	down	Trim46	Mus musc	NM_183037
0.025699	1.999553	up	A930010C	Mus musc	AK020843
0.015021	4.860908	down	A530064D	Mus musc	NM_178796
0.044853	2.027167	up			lincRNA:chr16:46384974-46391331 forward strand
0.048569	1.588252	down			lincRNA:chr2:128211990-128215223 reverse strand
0.005535	2.87377	down		DPH5 hor	AK046753
0.002541	2.90195	down	Lrrc25	Mus musc	NM_153074
0.027575	1.669773	down	Batf3	Mus musc	NM_030060
0.02172	6.348887	up	Fgf21	Mus musc	NM_020013
0.042365	2.554402	down	Klra2	Mus musc	NM_001170851
0.039867	1.575452	up			lincRNA:chr4:105035450-105059250 forward strand
0.010322	1.528715	down	Ncf2-rs	PREDICT	XR_031347
0.0219	2.960309	down	Cilp	Mus musc	NM_173385
0.025215	2.409435	down	LOC1000	PREDICT	XM_001474311
0.042491	1.889195	up			lincRNA:chr4:86267450-86277650 forward strand
0.01126	1.6614	down			lincRNA:chr10:93774693-93893616 forward strand
0.045809	1.753775	down	Arx	Mus musc	NM_007492
0.031233	2.139815	up			lincRNA:chr2:94008913-94019798 reverse strand
6.86E-04	3.155505	up	Atf3	Mus musc	NM_007498
0.035398	1.680459	up			lincRNA:chr6:116092274-116144199 reverse strand
0.0302	1.61803	down	Snhg6	Mus musc	NR_024067
0.039973	1.51501	down	Zfp382	Mus musc	NM_001081007

0.002359	1.605942	up	Tnfrsf12a	Mus musc	NM_013749
0.013325	2.20843	down		lincRNA:chr5:105072936-105074001 forward strand	
0.015686	1.77709	up	Uroc1	Mus musc	NM_144940
0.001687	2.385749	down	Gm8172	PREDICT	XM_984280
0.033558	1.79003	up	L2hgdh	Mus musc	NM_145443
0.042656	1.689055	down	Sykb	Mus musc	NM_011518
0.034142	2.544778	up	B330016D	Mus musc	NR_030695
3.59E-04	2.574395	down	Map4k1	Mus musc	NM_008279
0.011154	1.598373	up	Chst11	Mus musc	NM_021439
2.49E-04	2.627943	down	Fam102b	Mus musc	NM_001163567
0.003949	2.085212	down	Pabpc4l	Mus musc	NM_001101479
0.042937	2.506566	down	Gm3586	PREDICT	XM_001477872
0.011277	1.759333	down		lincRNA:chr5:105032961-105037248 forward strand	
0.026966	1.719611	up	1200016B	Mus musc	NM_025819
0.00644	2.488925	down	BC064078	Mus musc	AK134020
0.040866	1.957702	up	1700096K	Mus musc	NR_027388
0.003098	1.89723	up	Npnt	Mus musc	NM_033525
0.017114	1.628382	up	Ddhd2	Mus musc	NM_028102
0.040604	1.557032	up		lincRNA:chr1:137482591-137625604 forward strand	
0.004807	1.975669	up	Tmem48	Mus musc	NM_028355
0.031126	2.151163	up	Nudt12	Mus musc	NM_026497
0.017628	3.225206	down		RIKEN cl	XR_035728
0.033419	4.23106	down		lincRNA:chr7:149761435-149764019 reverse strand	
0.006093	2.808851	down	Pdpm	Mus musc	NM_010329
0.007431	1.558155	down		lincRNA:chr11:120041124-120052299 reverse strand	
0.011218	1.736267	up	Ebf2	Mus musc	NM_010095
0.036183	1.715302	up		lincRNA:chr6:128393530-128394127 forward strand	
4.23E-04	1.609778	down	9530036M	Mus musc	AK137178
0.041753	4.073793	down	Colec11	Mus musc	NM_027866
0.021679	2.719044	down		lincRNA:chr6:112552041-112560067 forward strand	
0.045646	1.68113	up		lincRNA:chr15:79764481-79809909 reverse strand	
0.032777	4.443601	down	Ear2	Mus musc	NM_007895
0.047845	2.220848	down		lincRNA:chr1:85304494-85305390 reverse strand	

0.014119	2.646554	down	Gm3252	PREDICT	XR_032767
0.023926	1.634836	down		lincRNA:chr17:22422837-22451777	reverse strand
0.023402	2.170279	down	Sbsn	Mus musc	NM_172205
0.01237	2.502827	up	Dcun1d3	Mus musc	NM_173408
0.00233	12.11627	down	Fam55d	Mus musc	NM_172921
0.015443	1.742752	down	Ube2i	Mus musc	NM_001177609
0.019229	1.611651	down		lincRNA:chr10:6480075-6603900	reverse strand
0.002767	2.949607	down		lincRNA:chr17:22335458-22466521	reverse strand
0.025651	2.43067	down	Cyp2s1	Mus musc	NM_028775
0.044294	1.7082	down		lincRNA:chr9:14460976-14488051	forward strand
0.045558	1.506359	up		lincRNA:chr14:73729977-73751877	forward strand
0.008115	1.79757	up		lincRNA:chr14:77104770-77105392	forward strand
0.004442	9.798311	up		lincRNA:chr3:96074625-96086375	forward strand
0.022513	2.718634	down	F830005D	Mus musc	AK089619
0.041026	1.820337	down	Cd151	Mus musc	NM_009842
0.021725	1.624376	up	Sfrs15	Mus musc	NM_178923
0.033069	1.534255	up		lincRNA:chr15:68170864-68171544	reverse strand
0.038114	6.140123	down	Rab6b	Mus musc	NM_173781
0.00111	2.274162	up		homer hor	AK155463
0.012	1.926768	down	Pttg1	Mus musc	NM_013917
0.024095	2.644978	up	Dedd2	Mus musc	NM_207677
0.019293	1.537168	up	Comtd1	Mus musc	NM_026965
0.033219	1.569768	up	Nolc1	Mus musc	NM_001039352
0.018885	1.736988	up		lincRNA:chrX:20374930-20375402	forward strand
0.047869	2.177715	up	C030016D	Mus musc	NR_027987
0.033565	1.867003	down	Dock2	Mus musc	NM_033374
0.042455	1.751049	up		lincRNA:chr7:80762708-80763274	reverse strand
6.45E-04	1.805239	down	EG545385	PREDICT	XR_031493
0.024458	1.545829	up	Pum1	Mus musc	NM_030722
0.046255	1.769794	up		lincRNA:chrX:93154123-93164481	forward strand
0.029485	2.086247	up	Gm10069	Mus musc	NR_028592
0.037502	2.277977	down	Ms4a4b	Mus musc	NM_021718
0.045178	1.642438	down		lincRNA:chr3:58730418-58742493	forward strand

0.008905	2.208764	down	Zfp758	Mus musc	NM_145484
0.006866	1.99934	down	Efemp1	Mus musc	NM_146015
0.034053	2.216681	up	Olfr905	Mus musc	NM_146804
0.020143	2.339872	up		zinc finge	AK132276
0.032599	2.387617	down	Naip2	Mus musc	NM_010872
0.022726	1.666972	down	Rgs14	Mus musc	NM_016758
0.018016	1.565824	down		lincRNA:chr13:76326228-76332632 reverse strand	
0.006026	3.353167	up		Putative u	AK133033
0.041989	4.831159	up	D630023F	Mus musc	NM_175293
0.033046	1.516517	down		lincRNA:chr19:61177675-61219875 reverse strand	
0.039322	1.865296	up	Grm4	Mus musc	NM_001013385
0.040687	1.909764	up	Luc7l	Mus musc	NM_028190
0.037201	2.076013	down	Csf1	Mus musc	NM_001113530
0.022985	1.715736	down	Hist2h2aa	Mus musc	NM_013549
0.012346	1.789696	down	Syt11	Mus musc	NM_031393
0.028375	4.313131	up	Gprc5b	Mus musc	NM_022420
0.002873	1.596607	down	Rpl22	Mus musc	NM_009079
0.018399	1.520539	down	Olfr699	Mus musc	NM_001011862
0.008847	1.596549	up		lincRNA:chr11:31648453-31648952 reverse strand	
0.016436	1.614578	down		zinc finge	BC064456
0.042141	2.874911	down	Cybb	Mus musc	NM_007807
0.022959	2.68806	up	C130081A	Mus musc	AK081838
0.010502	2.225743	up		lincRNA:chr3:19211659-19213735 forward strand	
0.005629	1.537191	up	Vprbp	Mus musc	NM_001015507
0.013881	1.527147	up	Mrgpra2b	Mus musc	NM_153101
0.030758	1.885446	down	Rab27b	Mus musc	NM_030554
0.039229	1.74529	down	Cpt1c	Mus musc	NM_153679
0.009151	2.256907	down	Mgp	Mus musc	NM_008597
0.006957	2.449275	up	Zfp788	Mus musc	NM_023363
0.002635	2.259801	down	B930018F	Mus musc	AK047086
0.010517	1.54127	down		lincRNA:chr2:92582386-92599365 forward strand	
0.014537	1.767232	up		lincRNA:chr14:79311982-79334451 forward strand	
0.002617	2.450198	down	Ttc8	Mus musc	NM_029553

0.03234	1.840747	up		lincRNA:chr7:80762708-80763274 reverse strand
0.026871	1.509683	up		lincRNA:chr17:22420025-22457650 reverse strand
0.036827	1.651172	up	Cobll1	Mus musc NM_177025
0.012109	1.722705	down	Adamtsl1	Mus musc NM_029967
0.008141	1.964544	up		lincRNA:chr10:3227840-3233588 forward strand
0.016958	5.925129	down		lincRNA:chr15:36800254-36809571 reverse strand
0.036186	2.086619	up	Gm4092	PREDICT XM_001479101
0.043468	1.811426	up		Putative u AK144422
0.019838	1.579311	up		lincRNA:chr11:79531768-79532127 forward strand
0.038022	1.634293	up	Glud1	Mus musc NM_008133
0.008804	1.743275	up	Olfr576	Mus musc NM_001001805
0.009894	2.159199	up	Rcc1	Mus musc NM_133878
0.017998	1.688044	up	1700021F	Mus musc NM_026411
0.003874	1.814253	up	Gh	Mus musc NM_008117
0.046951	1.627708	up	Klhl25	Mus musc NM_029652
0.036538	1.933862	up		lincRNA:chr8:72663625-72673010 reverse strand
0.00279	1.784626	up	2410024N	Mus musc AK010586
0.019791	1.700355	up	1700016K	AGENC0 BU938278
0.022155	2.202163	down	Pxdn	Mus musc NM_181395
0.040805	1.583464	up	Thsd7a	Mus musc NM_001164805
0.014551	1.554587	down		Likely ort AK135748
0.011411	1.66412	up	Ears2	Mus musc NM_026140
0.033369	1.923812	down	Rpl31	Mus musc NM_053257
0.026986	1.515597	up	LOC1000	PREDICT XR_034463
0.033701	2.380783	down	Bcl2a1d	Mus musc NM_007536
0.048445	2.010631	up	Tppp	Mus musc NM_182839
0.042592	1.565265	up	Apba3	Mus musc NM_018758
0.033327	2.376938	up	Hspb1	Mus musc NM_013560
0.011812	1.611195	down		lincRNA:chr8:74439200-74441363 forward strand
0.022411	1.651301	up	Dcst2	PREDICT XM_283860
0.012909	1.502876	up		PREDICT XM_001473338
0.041176	2.673416	down	Srpx2	Mus musc NM_026838
0.03852	2.301417	down	Sulf1	Mus musc NM_172294

0.032465	1.527437	up	Gm9855	PREDICT	XM_001479614
0.00212	1.62498	down	Gas1	Mus musc	NM_008086
0.002358	1.536889	up			lincRNA:chr4:155560296-155564642 forward strand
0.023259	3.220304	down	Gm13154	Mus musc	NM_001014397
0.046572	2.091097	up			lincRNA:chr9:114412295-114418384 forward strand
0.006547	1.993888	down	A730056A	Mus musc	AK053954
0.007811	3.352518	down	Pi16	Mus musc	NM_023734
0.022434	8.666546	down		PREDICT	XM_001476722
0.003528	1.627895	up			lincRNA:chr1:92546371-92551596 forward strand
0.013334	2.168133	up	6530401D	Mus musc	NM_029541
0.005015	1.586085	up	Phf17	Mus musc	NM_172303
0.001354	1.704015	down			lincRNA:chr13:28947034-28949166 reverse strand
0.03489	3.131016	down			lincRNA:chrX:120324027-120326909 reverse strand
0.007469	1.646139	up	A430071A	Mus musc	AK137878
0.006286	1.7435	down	P2ry13	Mus musc	NM_028808
0.045838	1.737963	down	Glb1	Mus musc	NM_009752
0.003352	2.594199	down	Homer2	Mus musc	NM_011983
0.021837	1.654735	up	Timm9	Mus musc	BC028435
0.018795	1.751691	down			lincRNA:chr17:7002731-7032535 reverse strand
0.018432	2.180487	down			lincRNA:chr14:26834450-26847000 reverse strand
0.006136	1.532729	up	Lsm2	Mus musc	NM_030597
0.021366	1.816666	up	Ankrd28	Mus musc	NM_001024604
0.0016	2.90754	down			lincRNA:chr8:94841965-94881130 reverse strand
0.042998	1.704385	down			lincRNA:chr6:4841700-4847400 reverse strand
0.046421	2.020072	down	Osr2	Mus musc	NM_054049
0.018204	4.123707	up	Hsph1	Mus musc	NM_013559
0.023534	1.919063	down		Mouse T d	M97158
0.034001	1.757732	down	Pclo	Mus musc	NM_001110796
0.043065	2.416051	down			lincRNA:chr14:33923944-34003394 reverse strand
0.035069	1.524943	up	C230076A	Mus musc	AK048857
0.042156	2.124153	down	Serpina3f	Mus musc	NM_001168294
0.008003	1.820291	up	Gpr180	Mus musc	NM_021434
0.046372	1.625843	up	Ptar1	Mus musc	NM_028208

0.002272	1.516275	up		lincRNA:chr2:119412770-119435110 reverse strand
0.026981	1.546365	down	3300005D	PREDICT XM_001476467
0.018276	1.562615	up		cytokine r AK078569
0.004098	2.574844	down	Snord123	Mus musc NR_028575
0.023282	1.606581	up	5830433I	PREDICT XM_974092
0.013223	3.435111	down	Chga	Mus musc NM_007693
0.026743	1.6297	up	9930024M	Mus musc AK036921
0.010492	2.186641	down	Rint1	Mus musc NM_177323
0.014838	1.562755	up	Wdr67	Mus musc NM_001081396
0.007435	2.326977	up	BC018473	Mus musc NR_003364
0.014731	1.589824	down		lincRNA:chr9:43926204-43928496 forward strand
0.002207	2.323617	down	B430306N	Mus musc NM_177083
0.044942	3.057492	up		lincRNA:chr5:107503800-107515575 forward strand
0.001327	2.214637	down	Miip	Mus musc NM_001025365
0.008073	1.608795	down	Vit	Mus musc NM_028813
0.018343	1.992347	up	Acsn3	Mus musc NM_212441
0.011776	1.756665	up	Cog5	Mus musc AK041796
0.01813	1.595454	down	Gm9224	PREDICT XR_034597
0.041294	1.634663	down	Galnt1	Mus musc NM_001081421
0.032895	1.553367	up		lincRNA:chr18:61781410-61788685 forward strand
0.044128	1.526113	up	Gucy1b2	Mus musc NM_172810
0.001266	2.058783	up		RIKEN cl AK006468
0.035255	2.066773	down	1810062G	RIKEN cl XM_001475130
0.025735	1.792721	down	Rtn2	Mus musc NM_013648
0.010537	1.757984	up	Gjc1	Mus musc NM_008122
0.03306	1.584051	up		lincRNA:chr17:22090757-22099418 reverse strand
0.026698	1.568022	up	Rarb	Mus musc NM_011243
0.049126	1.629567	up	Taf1d	Mus musc NM_027261
0.033421	2.05408	down		PREDICT XM_136331
0.018176	2.976296	down	Il18r1	Mus musc NM_008365
0.023534	2.080821	up		RIKEN cl AK078477
7.05E-04	1.91376	up		lincRNA:chr2:60531602-60543635 reverse strand
0.001252	1.588395	down	Zfp287	Mus musc NM_133208

0.005709	4.684787	down		lincRNA:chr4:147105275-147171025 reverse strand
0.002574	1.688543	up	Hmgn5	Mus musc NM_016710
0.042012	1.678575	up	Ube4b	Mus musc NM_022022
0.011049	2.449136	up	Dbt	Mus musc NM_010022
0.001333	2.196748	up	Bhlhe41	Mus musc NM_024469
0.029614	1.574262	down	Susd2	Mus musc NM_027890
0.044455	1.690923	up	Nlrp12	Mus musc NM_001033431
0.038338	1.77716	down	Myo1f	Mus musc NM_053214
9.06E-04	2.545582	down	Itgb7	Mus musc NM_013566
0.017813	2.052442	down		lincRNA:chr11:120041124-120052299 reverse strand
0.00794	1.582457	up	Mrpl33	Mus musc NM_025796
0.008322	2.000147	down	Zap70	Mus musc NM_009539
0.00234	1.662988	down	Bst2	Mus musc NM_198095
0.010552	1.521858	down	Pm20d1	Mus musc NM_178079
0.00786	1.680503	up	Gm3548	PREDICT XM_001477124
0.010593	1.740511	down		aryl hydrocarbon receptor nuclear translocator Gene [Source:MGI (curated);Acc:MGI:88071] [
0.0243	2.368345	down	Bcl2a1c	Mus musc NM_007535
0.002583	2.46289	down	Sh3gl3	Mus musc NM_017400
0.027902	2.162276	up	Zfp882	Mus musc NM_001166645
0.034867	1.720145	up	1700037C	RIKEN cl AK195538
0.043363	1.646472	up	Slc28a3	Mus musc NM_022317
0.043521	2.228384	up	Thrb	Mus musc NM_009380
0.036378	1.828209	down	Atf7	Mus musc NM_146065
0.001826	1.692082	down	Polm	Mus musc NM_017401
0.012333	1.787384	down		predicted XM_001474090
0.032758	1.927796	up	Sema3e	Mus musc NM_011348
0.008812	1.614303	up	Dffa	Mus musc NM_010044
0.022261	2.198743	down	Gm3115	PREDICT XM_001476009
0.019057	1.811016	up	Phf1	Mus musc NM_009343
0.022614	1.583074	down	Nanog	Nanog ho AK010332
0.038316	2.653683	up	Gm3353	PREDICT XR_032731
0.016087	1.547002	down		lincRNA:chr4:11899775-11931875 forward strand
0.027177	1.954544	up	1810014F	Mus musc NM_026928

0.010956	1.902344	up		lincRNA:chr4:128727331-128735227 reverse strand
0.025016	1.876766	up	1200011M	Mus musc NM_024262
0.030969	1.500818	up	Cul1	Mus musc NM_012042
0.008448	3.688254	down	Hebp2	Mus musc NM_019487
0.016367	1.847758	down	Klra8	Mus musc NM_010650
0.049124	1.872151	down	Adamts2	Mus musc NM_175643
0.015488	1.620483	up		ATP synthase, H ⁺ transporting, mitochondrial F1F0 complex, subunit e Gene [Source:MGI (cu
0.036595	1.715003	up	Olfr1419	Mus musc NM_001011775
0.040518	2.167238	down	Gm7638	PREDICT XR_031801
0.029228	1.520438	up	Malat1	Mus musc NR_002847
0.002571	2.097247	down	Vash2	Mus musc NM_144879
0.022278	1.673743	up	Uqcr10	Mus musc NM_197979
0.047185	1.929012	down	Tfpi	Mus musc NM_011576
0.02389	1.546367	up	Gm7177	PREDICT XR_032603
0.021292	1.938662	up	Gm9471	PREDICT XM_001476382
0.02141	2.574687	up	Mttp	Mus musc NM_001163457
0.011399	1.658569	up	Gm3730	PREDICT XM_001477751
0.011286	1.812586	down		lincRNA:chr1:85036677-85038530 reverse strand
9.59E-04	1.646663	up		lincRNA:chr1:173254292-173257445 reverse strand
0.030188	1.988201	down		lincRNA:chr17:25990279-25998670 forward strand
0.039706	1.557862	up	LOC1000	PREDICT XM_001476908
0.034479	1.908836	down		lincRNA:chr9:14460976-14488051 forward strand
0.044488	1.756259	down		lincRNA:chr6:4841700-4847400 reverse strand
0.025203	1.60839	up	Rbm47	Mus musc NM_178446
0.033359	2.14073	down	LOC1000	PREDICT XM_001474498
0.013919	1.525602	up		lincRNA:chr7:99879368-99889978 reverse strand
0.044265	2.407797	up	Dnajb1	Mus musc NM_018808
0.017201	1.565763	up	Gpatch4	Mus musc NM_025663
0.034745	1.797139	up		lincRNA:chr1:33965074-34060850 forward strand
0.036974	2.22007	down		Putative u AK146072
0.030225	1.711625	down	Camk2d	calcium/c AK142435
0.005303	1.530134	up	Acat3	Mus musc NM_153151
0.005	1.537793	up		protein kinase, cAMP dependent regulatory, type I, alpha Gene [Source:MGI (curated);Acc:MC

0.048814	2.21351	up	Fbxo43	Mus musc	NM_001081253
0.025622	775.6025	up	Svs5	Mus musc	NM_009301
0.004477	1.553351	up	Mak16	Mus musc	NM_026453
0.017155	1.855541	up		lincRNA:chr6:122725638-122752828 forward strand	
0.020594	3.700236	down	4930528F	Mus musc	NM_029197
0.029707	5.387078	down	Fndc1	Mus musc	NM_001081416
0.027871	2.313328	up	Bag3	Mus musc	NM_013863
0.047065	9.998684	up	Bcl2l15	Mus musc	NM_001142959
0.010566	1.68962	up	E130304I	Mus musc	AK172290
0.041262	1.524842	down	Pdlim7	Mus musc	NM_026131
0.032576	2.456929	up	Zfp317	Mus musc	NM_172918
0.018704	1.616225	down	LOC1000	PREDICT	XM_001479897
0.046952	2.2115	down	Slc16a9	Mus musc	NM_025807
0.027842	1.542872	up	Brd2	Mus musc	NM_001025387
0.011202	1.536674	up	Adamts8	Mus musc	NM_013906
0.026948	1.666842	down		RIKEN cl	XM_354798
0.019705	1.932712	up		lincRNA:chr11:79529699-79530564 forward strand	
0.005519	1.655468	up	Hnrnpa112	PREDICT	XM_888940
0.025496	1.572913	down	Aph1b	Mus musc	NM_177583
0.001906	3.099672	up	BC062258	Mus musc	AK144577
0.013848	3.311819	down	Gm8013	PREDICT	XM_977358
0.047265	1.829817	down	Btbd11	Mus musc	NM_028709
0.049699	1.508035	up	Flywch1	Mus musc	NM_153791
0.029573	1.905345	up	Katnal2	Mus musc	NM_027721
0.01662	16.76892	down	Muc11	Mus musc	NM_009268
0.002812	2.091274	up		lincRNA:chr2:176583825-176714400 forward strand	
0.03401	1.714444	up		RIKEN cl	AK076700
0.025353	1.977764	down		neuron na	XM_001478191
0.046189	1.948192	up	Dynlt1c	Mus musc	NM_001166630
0.011172	1.757052	down	Arhgap9	Mus musc	NM_146011
0.012538	1.96855	down	Gm5834	PREDICT	XM_619677
0.001602	5.513228	down	Pdpn	Mus musc	NM_010329
0.047876	1.547629	up	Ahdc1	Mus musc	NM_146155

0.016314	3.700327	down	Gm14762	Putative u	AK052035
0.01156	1.765829	up	Homer1	Mus musc	NM_011982
0.013727	1.715614	down		lincRNA:chr9:14460976-14488051 forward strand	
0.040845	1.527175	up	Reep3	Mus musc	NM_178606
0.028778	1.872997	up		lincRNA:chr10:59385064-59385436 forward strand	
0.016692	1.985162	down	Mcam	Mus musc	NM_023061
9.48E-04	1.622299	up		lincRNA:chr3:131153358-131154061 forward strand	
0.005327	2.091559	up	Srrm2	Mus musc	NM_175229
0.036313	2.607719	down	Klf14	Mus musc	NM_001135093
0.020508	2.427777	down	Ccl7	Mus musc	NM_013654
0.002243	1.688092	down	Palm3	Mus musc	NM_028877
0.006985	2.732469	up		lincRNA:chr5:26374425-26393675 forward strand	
0.027067	2.730232	down	Zfhx3	Mus musc	NM_007496
0.004099	2.037374	down	Ankrd50	Mus musc	NM_001167883
0.026022	1.909223	up	Rad51l3	Mus musc	NM_011235
0.015346	1.909665	down		lincRNA:chr4:11899775-11931875 forward strand	
0.004265	1.578165	up	Pum2	Mus musc	NM_001160219
0.01507	1.550831	up	Tmigd1	Mus musc	NM_025655
0.025398	3.289604	down	LOC1000	PREDICT	XM_001480480
0.033884	2.529388	up		lincRNA:chr17:56687541-56694616 reverse strand	
0.043035	2.129271	up	Adamts1	Mus musc	NM_009621
0.036209	1.725115	up	Dnaja1	Mus musc	NM_001164671
0.009418	1.787939	down	Hmgcs2	Mus musc	NM_008256
0.01139	1.819192	up		lincRNA:chrX:148819227-148844227 reverse strand	
0.009289	3.948799	down	Chrdl1	Mus musc	NM_001114385
0.035993	2.124986	down	Il33	Mus musc	NM_001164724
0.034385	1.696428	down	C2	Mus musc	NM_013484
0.008948	1.70215	up		Novel zinc finger protein Fragment [Source:UniProtKB/TrEMBL;Acc:B1ATP3] [ENSMUSTO	
0.045206	1.656838	up		lincRNA:chr17:88993214-89025839 forward strand	
0.012989	1.710251	up	1700023A	Mus musc	AK006259
0.009718	2.09168	up		lincRNA:chr10:24269165-24276690 forward strand	
0.032074	1.714495	up	C430048L	Mus musc	NM_198957
0.046011	1.573733	up	Fam40a	Mus musc	NM_153563

0.015933	2.942286	up	Cxcl1	Mus musc	NM_008176
0.003875	1.844574	down	C1qtnf7	C1q and t	BC090967
0.016196	1.711664	down		lincRNA:chr1:137503023-137625604	reverse strand
0.022144	1.900374	up	Atf4	Mus musc	NM_009716
0.013185	2.968507	up	Slc25a42	Mus musc	NM_001007570
0.040455	2.144774	down	Gria4	Mus musc	NM_019691
0.015365	2.067376	down		lincRNA:chr4:3437474-3438228	reverse strand
0.004032	1.550558	down	Fam174a	Mus musc	NM_026321
0.039594	3.130056	down		lincRNA:chr1:85304494-85305390	reverse strand
0.01415	1.655366	down	Adora2b	Mus musc	NM_007413
0.002245	1.891379	down	Dapp1	Mus musc	NM_011932
0.015303	2.398336	up		lincRNA:chr13:65716675-65765575	forward strand
0.025711	5.0876	up	5830403F	Mus musc	AK017891
0.006063	2.539764	up	Clstn3	Mus musc	NM_153508
0.008629	1.639484	up		lincRNA:chr14:73757550-73758159	reverse strand
0.013315	1.586599	down	Fcgr1	Mus musc	NM_010186
0.001578	2.101739	down	Gm9307	PREDICT	XM_001472674
0.021988	1.597459	down	Arhgdib	Mus musc	NM_007486
0.045223	1.691944	up	Hspe1	Mus musc	NM_008303
0.01418	2.469938	down	Atp8a2	Mus musc	NM_015803
0.008672	1.883428	up	Dynlt1c	Mus musc	NM_001166630
0.046964	6.165962	down	Esm1	Mus musc	NM_023612
0.022367	1.653607	up		lincRNA:chrX:47893703-47996700	forward strand
0.040184	1.566782	up	Adipor2	Mus musc	NM_197985
0.038902	1.598745	down	Ldoc1l	Mus musc	NM_177630
0.005385	1.586129	down	Sirpb1a	Mus musc	NM_001002898
0.025568	1.743704	down		lincRNA:chr8:35652473-35703370	reverse strand
0.03191	1.526125	down	Gstm1	Mus musc	NM_010358
0.003815	5.931838	down		DIX doma	BC024834
0.029424	2.420116	up	Kcnk3	Mus musc	NM_010608
0.016404	1.552608	down	Glod4	Mus musc	NM_026029
0.025595	1.821546	up		lincRNA:chr13:41337973-41379821	reverse strand
0.017212	1.550092	down	AI467606	Mus musc	NM_178901

0.038342	1.579578	down		lincRNA:chr4:11926618-11936190 reverse strand
0.031458	1.583616	up	Gm414	Mus musc NM_001018031
0.045439	3.438469	down	Abcg4	Mus musc NM_138955
0.045829	1.530452	up		Putative u AK034506
0.006127	2.160331	up	Scn1a	Mus musc NM_018733
0.037649	1.884932	down	Chst10	Mus musc NM_145142
0.047517	2.317117	down	Gm3667	PREDICT XR_033371
0.031571	1.756872	up		lincRNA:chr8:122807653-122823000 forward strand
0.001633	1.840093	down	Ccdc88b	Mus musc NM_001081291
0.034143	1.720563	up	Larp4	Mus musc NM_001080948
0.048474	1.887976	down	5830405N	Mus musc NM_183264
0.005102	2.032795	up		lincRNA:chr9:96964067-96973567 forward strand
0.018088	1.603815	up	5730494M	Mus musc NM_001142698
0.025139	2.184076	up		lincRNA:chr6:135294099-135300310 forward strand
0.043183	1.601174	up	Atp5k	Mus musc NM_007507
0.003139	2.458402	up	Rwdd3	Mus musc NM_025637
0.001171	1.599853	down	Vav1	Mus musc NM_011691
0.013268	1.943204	up		lincRNA:chr14:61240427-61325677 reverse strand
0.047505	1.777975	up	Hhipl1	Mus musc NM_001044380
0.028801	1.867204	up	Hist1h3i	Mus musc NM_178207
0.004288	2.210751	down		lincRNA:chr15:32167516-32174427 reverse strand
0.021658	1.555639	up	A930004J	Mus musc AK044267
0.013503	5.35397	up	Rassf6	Mus musc NM_028478
0.048591	1.716576	up	Il3ra	Mus musc NM_008369
0.042	2.22407	up	Gm7044	PREDICT XM_001472205
0.001362	2.044923	up		cancer ant BC082568
0.003224	1.595454	up	Spink4	Mus musc NM_011463
0.003137	2.929378	down	Rps6	Mus musc NM_009096
0.044431	3.205872	down		lincRNA:chr15:32708654-32725622 forward strand
0.026649	2.308187	down		lincRNA:chr2:143988645-143993945 reverse strand
0.04876	4.094317	up	Gm5213	PREDICT XR_032412
0.016439	1.550324	down	Gm2367	PREDICT XR_031150
0.049883	1.582562	down	Jam3	Mus musc NM_023277

0.012998	2.486561	up		lincRNA:chr8:12535648-12544923 forward strand
0.024951	1.50217	down	1700026J	Mus musc NM_027967
1.13E-04	3.023413	down	Slc6a13	Mus musc NM_144512
0.008138	9.973941	down	1110059M	Mus musc NM_026841
0.033958	3.378789	up	Krt36	Mus musc NM_001174099
0.006316	3.159902	up	Adra1a	Mus musc NM_013461
0.035568	1.518623	down	Armcx2	Mus musc NM_026139
0.033693	2.418107	up	Tob2	Mus musc NM_020507
0.009349	1.593131	down		lincRNA:chr12:117623500-117643575 reverse strand
4.59E-04	1.560883	up	Gm10776	Mus musc AK144371
0.00829	1.59001	down	Zc3h6	Mus musc NM_178404
0.036665	2.344202	up		lincRNA:chr5:92548501-92566401 forward strand
0.023942	1.825162	up	AA38788	Mus musc NR_030678
0.029848	1.870533	down	Gucy1a3	Mus musc NM_021896
0.035473	1.519114	up	Aen	Mus musc NM_026531
0.012746	1.881712	up	Fam38a	Mus musc NM_001037298
0.049142	1.538003	up	St6galnac	Mus musc NM_011371
0.018643	1.598594	up	Mrpl47	Mus musc NM_029017
0.008123	1.750949	down	Kcne3	Mus musc NM_020574
0.032862	2.377849	up	A930033F	PREDICT XR_002305
0.043785	2.040789	up		lincRNA:chr8:26869173-26869823 reverse strand
0.012229	1.990688	up	Ace2	Mus musc NM_001130513
0.03715	2.03679	up		connector enhancer of kinase suppressor of Ras 2 Gene [Source:MGI (curated);Acc:MGI:2661]
0.025598	1.556137	up	Il24	Mus musc NM_053095
0.009183	1.556396	down	5033403F	Mus musc AK017147
0.004486	3.002816	down	Gm3065	PREDICT XM_001475302
0.013337	1.829798	up		lincRNA:chr13:34693404-34717987 forward strand
0.005124	1.674265	up	Snx27	Mus musc NM_001082484
0.026297	1.517146	up		lincRNA:chr18:84735774-84760824 forward strand
0.009114	2.330338	up	Ppp1r15b	Mus musc NM_133819
0.047069	2.138524	up	Trpc1	Mus musc NM_011643
0.042739	2.013486	up	Adrb1	Mus musc NM_007419
0.011445	2.631605	down	Gm8272	PREDICT XM_985780

0.001224	2.015137	down	Gabra3	Mus musc	NM_008067
0.022783	1.536403	up	Cpeb3	Mus musc	NM_198300
4.93E-05	2.152995	up	Hist2h4	Mus musc	NM_033596
0.04219	1.635577	down	Wfdc1	Mus musc	NM_023395
0.037158	2.954936	up	Col28a1	Mus musc	NM_001037865
0.045608	1.615253	up	LOC1000	PREDICT	XM_001474069
0.032177	1.668803	up	Pde12	Mus musc	NM_178668
0.010924	16.84631	down	Cxcl13	Mus musc	NM_018866
3.84E-04	2.323098	down	Gm6970	PREDICT	XM_894271
0.028095	2.384313	up	Cplx4	Mus musc	NM_145493
0.002752	2.348907	up	Olfr1396	Mus musc	NM_146337
0.041059	1.596163	up		lincRNA:chr1:121982840-121983386 reverse strand	
0.04185	1.815696	down	Ret	Mus musc	NM_001080780
0.003358	1.677223	up	Xrcc3	Mus musc	NM_028875
0.027026	3.323252	down	170002910	Mus musc	NM_027285
0.017935	1.576051	up	Gng10	Mus musc	NM_025277
0.040975	6.276382	down	Cebpe	Mus musc	NM_207131
0.04885	1.796662	up	Mesdc1	Mus musc	NM_030705
0.044709	1.792158	down		lincRNA:chr15:85412264-85549139 reverse strand	
0.001786	1.537423	up	Stat5a	Mus musc	NM_011488
0.040093	3.272413	up		lincRNA:chr10:6480075-6603900 reverse strand	
0.047004	1.648977	down		lincRNA:chr17:87674225-87682154 reverse strand	
0.028358	1.524049	up		lincRNA:chr1:6181200-6204300 forward strand	
0.048124	1.792728	down	Cd37	Mus musc	NM_007645
0.01132	1.995108	down		lincRNA:chr19:57426515-57435165 reverse strand	
0.013401	1.755863	up	Park2	Mus musc	NM_016694
0.030286	1.568616	down	Fgd3	FYVE, Rf	AK157835
0.034687	2.090629	down	Ppfia3	Mus musc	NM_029741
0.013237	1.799177	up		lincRNA:chr4:101010948-101032148 forward strand	
0.035658	2.830313	up		lincRNA:chr17:56687541-56694616 reverse strand	
0.006844	1.71567	down	Ssr1	Mus musc	NM_025965
0.008048	4.277311	up		lincRNA:chr6:134838675-134847075 forward strand	
0.048137	1.715344	down		RIKEN cl	AK162948

0.023864	2.315959	up		lincRNA:chr5:35975265-35982561 reverse strand
0.035383	2.055883	down	Tbx21	Mus musc NM_019507
0.015707	1.824451	up	Gm9108	PREDICT XR_034404
0.02961	1.578013	down	Cd209c	Mus musc NM_130903
0.018558	1.506931	up		lincRNA:chr15:92197603-92208534 forward strand
0.019164	1.605812	down	Cd48	Mus musc NM_007649
0.001454	5.894779	down		lincRNA:chr17:22335458-22466521 reverse strand
0.003035	1.809793	down	Paqr7	Mus musc NM_027995
0.028162	1.652494	up	Ak2	Mus musc NM_016895
0.005608	2.25186	up	Rwdd3	Mus musc NM_028456
0.005255	2.510125	up		lincRNA:chr11:117835849-117842574 forward strand
0.010592	1.543514	down	Amz2	Mus musc NM_025275
0.027468	1.606551	down	Fmr1	Mus musc NM_008031
0.045538	1.529677	up	Timm8a1	Mus musc NM_013898
0.036832	1.745432	up	Arid1b	Mus musc NM_001085355
0.017588	2.420423	up		lincRNA:chr3:127039311-127201919 reverse strand
0.005565	1.855376	up	Gm2149	PREDICT XM_001472640
0.019285	1.590867	up	1700094M	PREDICT XM_001473576
0.001386	1.510772	up		lincRNA:chr17:26911397-26917047 reverse strand
0.01652	4.959016	down	Klra23	Mus musc NM_024470
0.04821	2.018911	up		lincRNA:chr2:65240793-65292293 reverse strand
0.004056	1.657174	down	6330545A	RIKEN cDNA 6330545A04 gene Gene [Source:MGI Symbol;Acc:MGI:1923416] [ENSMUST
0.016491	2.308415	down		lincRNA:chr1:137503023-137625604 reverse strand
0.009718	2.430224	up		lincRNA:chr17:6514179-6517720 reverse strand
0.00215	3.387622	down		lincRNA:chr15:32167516-32174427 reverse strand
0.047637	2.182672	up	B630006N	Mus musc AK046749
0.001142	1.601944	down	Mfap4	Mus musc NM_029568
0.030085	1.977607	up		lincRNA:chr10:39383665-39442690 forward strand
0.026744	1.940846	up		lincRNA:chr5:15184252-15184923 forward strand
0.035304	2.041809	up	Glis1	Mus musc NM_147221
0.012363	1.772762	up		lincRNA:chr6:135294099-135300310 forward strand
0.030459	1.653289	down	Wisp2	Mus musc NM_016873
0.021352	1.53904	up		lincRNA:chr7:77481448-77495548 reverse strand

0.010922	3.941212	up		lincRNA:chr4:59306575-59317850 reverse strand
0.045969	2.170051	down	Mctp1	Mus musc NM_030174
0.038163	1.729919	down	Camk1d	Mus musc NM_177343
0.037994	1.522357	up	Hipk3	Mus musc NM_010434
0.040234	1.540507	up		lincRNA:chr4:59264275-59287850 forward strand
0.025225	1.54114	down	Me3	Mus musc NM_181407
0.040152	1.52871	up	Gm10220	Mus musc NM_001134299
0.001721	1.781208	down	Gpr19	Mus musc NM_001167693
0.023772	1.711641	down	Rbms3	Mus musc NM_001172123
0.030836	2.805887	up	LOC6390	PREDICT XM_915331
0.032732	1.932778	up		polymeras AK165879
0.034861	1.658566	down	Atp2b2	Mus musc NM_009723
0.026339	1.852044	down	Abtb2	Mus musc NM_178890
0.021636	1.661626	up	Ibtk	Mus musc NM_001081282
0.040145	5.304133	down	Ear11	Mus musc NM_053113
0.031639	1.524842	down	63304071	Mus musc AK018137
0.007236	2.324547	up	Pax7	Mus musc NM_011039
0.031154	1.743053	up		lincRNA:chr14:79725080-79725434 reverse strand
0.03449	1.929862	down		lincRNA:chr8:89996710-90049453 forward strand
0.002564	1.915652	up	Gm9720	PREDICT XM_001477594
0.036142	2.433676	down	Prkca	Mus musc NM_011101
0.030458	1.731055	up	Homer1	Mus musc NM_147176
0.004477	2.23226	down	Gm13298	Mus musc NM_001085530
0.04165	4.289815	down	Fzd6	Mus musc NM_008056
0.038766	3.191492	up	Senp5	Mus musc NM_177103
0.013528	2.208465	up	Ppargc1a	Mus musc NM_008904
0.034746	2.503844	up		lincRNA:chr4:3745783-3746383 reverse strand
0.026884	4.277648	down	Retnla	Mus musc NM_020509
0.025975	4.09705	up	Gm3993	PREDICT XM_001478694
0.038619	1.860385	up		lincRNA:chr2:94008913-94019798 forward strand
0.006826	1.613792	up	LOC1000	PREDICT XM_001477623
0.001493	1.947641	down	Fbxo27	Mus musc NM_001163702
0.035622	1.602532	up	Ppm1l	protein ph AK147389

0.036997	1.780214	up	Mgll	Mus musc	NM_001166250
0.028225	1.535032	down	Timp2	Mus musc	NM_011594
0.015367	3.194775	down	Samsn1	Mus musc	NM_023380
0.028805	1.804048	down		lincRNA:chr5:31856417-31916414 forward strand	
0.007645	1.609634	up	4833422F	Mus musc	NM_029021
0.028539	2.047809	down	Spn	Mus musc	NM_009259
0.037401	1.875047	up	Rbm3	Mus musc	NM_016809
0.005233	2.674845	down	Tle1	Mus musc	NM_011599
0.040976	1.614481	up	Gm11686	PREDICT	XM_001480374
0.002747	1.574549	up		lincRNA:chr9:41184479-41240162 forward strand	
0.00487	2.855777	up	Vat1l	Mus musc	NM_173016
0.002247	1.916374	up	Banp	Mus musc	NM_016812
0.011994	1.598106	down		cell divisi	AK161246
0.032624	1.76794	down	Sirpb1b	Mus musc	NM_001173460
0.049529	1.943224	down		lincRNA:chr13:62734450-62785325 reverse strand	
0.006628	1.757366	up	1810073O	Mus musc	AK007978
0.036029	2.522721	up	Gm5847	PREDICT	XR_030672
0.021955	1.903505	up	Sntb2	Mus musc	NM_009229
0.037605	1.990508	up	LOC1000	PREDICT	XM_001478388
0.034561	1.648015	up		lincRNA:chr11:79531768-79532127 forward strand	
0.001402	4.402484	down		occludin/E	AK143433
0.046647	2.086304	down	Mest	Mus musc	NM_008590
0.037762	1.508432	up	Strn3	Mus musc	NM_052973
0.047215	1.624884	up	Gm6422	PREDICT	XM_887818
0.046001	2.630777	down		lincRNA:chr17:13008796-13023201 forward strand	
0.040015	2.075262	down	Pilra	Mus musc	NM_153510
0.024127	2.014418	down	Zfp536	Mus musc	NM_172385
0.022502	2.273416	down		lincRNA:chr3:84609788-84618062 reverse strand	
0.045421	1.947885	up	Gm13474	PREDICT	XM_889201
0.012146	1.667357	up		lincRNA:chr1:134167181-134181386 reverse strand	
0.023085	1.937217	up	Slc25a33	Mus musc	NM_027460
0.021888	1.593332	up		lincRNA:chr6:47928244-47928681 reverse strand	
0.020319	1.628876	down	Cklf	Mus musc	NM_029295

0.006798	5.107418	down	Alpk3	Mus musc	NM_054085
0.027454	2.16481	down	Csf1	Mus musc	NM_001113530
0.044687	1.621075	up		lincRNA:chr4:11899775-11931875 reverse strand	
0.008972	3.414254	down	Galnt9	Mus musc	NM_198306
0.042559	1.62792	up	Luc7l	Mus musc	NM_025881
0.048197	1.674145	down	Oas1a	Mus musc	NM_145211
0.036788	2.451662	down	2310058N	Mus musc	AK009987
0.025298	5.56388	down	Uchl1	Mus musc	NM_011670
0.023057	1.890223	down	Icos	Mus musc	NM_017480
0.005093	4.108232	down	Prtn3	Mus musc	NM_011178
0.018954	2.073067	up		lincRNA:chr4:88604248-88645948 forward strand	
0.042977	1.729817	up	LOC1000	PREDICT	XM_001479002
0.022072	2.131938	up	Gm9022	PREDICT	XR_002153
0.020679	4.921981	down	H19	Mus musc	NR_001592
0.030301	1.838874	up	Cym	Mus musc	NM_001111143
0.019987	1.598995	up	BC065397	Mus musc	NR_033324
0.007388	1.614274	up	9830001H	Mus musc	NM_001164663
0.020222	2.474986	down	Gm6705	PREDICT	XR_031767
0.012792	1.558183	up	Nkx2-2	Mus musc	NM_010919
0.022676	1.714395	up	LOC6387	PREDICT	XM_914944
0.041277	1.671778	down	2310004N	Mus musc	NM_027107
0.011157	1.720508	up	Bard1	Mus musc	NM_007525
0.015218	1.667351	up	Gadd45b	Mus musc	NM_008655
0.013829	2.800006	down	Prss34	Mus musc	NM_178372
0.04238	2.507458	down		placenta s	XM_001472394
0.028013	1.777332	up		lincRNA:chr19:57426515-57435165 forward strand	
0.008483	1.989775	up		lincRNA:chr17:6306310-6311805 forward strand	
0.004394	3.616443	up		lincRNA:chr5:92548501-92566401 forward strand	
0.034158	1.690592	up		lincRNA:chr1:90508551-90508788 reverse strand	
0.049019	1.787898	down	BC028528	Mus musc	NM_153513
0.024124	1.630916	down	Pira11	Mus musc	NM_011088
0.023984	2.103628	down	Slco2b1	Mus musc	NM_175316
0.021103	1.848962	down	Zfp709	Mus musc	NM_145624

0.011864	1.831716	down		thymocyte	XM_001473004
0.009175	1.604163	up	Krt73	Mus musc	NM_212485
0.001281	1.907891	up	Frs3	Mus musc	NM_144939
0.019621	2.13794	down	Gpr88	Mus musc	NM_022427
0.021362	1.737813	up	Cdk12	Mus musc	NM_001109626
0.033863	2.151054	down	Pira7	Mus musc	NM_011094
0.005387	2.119736	up		lincRNA:chr14:67585234-67596823 forward strand	
0.030104	2.269018	up	Dcaf12l2	Mus musc	NM_175539
0.029087	2.463205	up	Plin2	Mus musc	NM_007408
8.27E-04	3.006157	down	Mtag2	Mus musc	NR_027802
0.00353	1.75644	down	Tmem114	Mus musc	NM_029070
0.031076	1.903643	down		lincRNA:chr10:83181374-83249774 forward strand	
0.039939	1.680173	down	Dpp4	Mus musc	NM_010074
0.042011	1.664627	up	Pdyn	prodynorp	AK133597
0.009178	2.842783	down	6030419C	Mus musc	NM_176921
0.008758	1.64638	up		lincRNA:chr3:131128972-131163308 forward strand	
0.03574	2.397513	up	LOC1000	PREDICT	XM_001475159
0.019382	1.715509	up	Chd9	Mus musc	NM_177224
0.013283	2.478459	up		lincRNA:chr5:35975265-35982561 reverse strand	
0.01816	1.787774	up		lincRNA:chr2:157236070-157249445 reverse strand	
0.045786	1.982158	down	Zfr	Mus musc	NM_011767
0.032193	1.895652	up	Ptpn2	Mus musc	NM_001127177
8.68E-04	3.461406	down		lincRNA:chr1:85304494-85305390 reverse strand	
0.011037	5.197929	down	170002910	Mus musc	NM_027285
0.013909	2.122245	up	Efcab7	Mus musc	NM_145549
0.011382	4.567067	down	Gm2490	PREDICT	XM_001473759
4.42E-04	1.822972	up		lincRNA:chr1:87419050-87452625 forward strand	
0.023442	1.580399	down	Rbpj	Mus musc	NM_009035
0.018554	3.322148	down	Sfrp5	Mus musc	NM_018780
0.002047	3.054648	down	Grhl1	Mus musc	NM_145890
0.029157	1.503643	up	Gm3797	PREDICT	XM_001474029
0.002085	1.663386	down	Prrg1	Mus musc	NM_027322
0.013688	2.015151	down	Gm4902	Mus musc	NM_001164327

0.007184	2.420841	down		lincRNA:chr15:32167516-32174427 reverse strand
4.31E-04	1.559621	up	1700001K	Mus musc NM_025488
0.030887	2.041686	down	Clec7a	Mus musc NM_020008
0.007012	2.508296	down		RIKEN cl AK086343
0.010411	6.260525	up	Olfr224	Mus musc NM_207695
0.04553	1.734324	up	Masp2	Mus musc NM_010767
0.04117	1.957322	down	P2rx7	Mus musc NM_001038887
0.004414	1.67672	up		lincRNA:chr14:43929100-43945100 forward strand
0.01353	3.165575	up	LOC1000	PREDICT XM_001481106
0.016945	1.596603	up	C030010C	PREDICT XM_001472491
0.030207	1.705289	up		lincRNA:chr4:128727331-128735227 reverse strand
0.037297	1.73326	up	Chd2	Mus musc NM_001081345
0.008567	2.223904	down		lincRNA:chr17:7002731-7032535 reverse strand
0.028698	1.629631	up	Nlrp3	Mus musc NM_145827
0.001442	1.871029	up		lincRNA:chr11:103005375-103020800 forward strand
0.040808	1.722307	down	Tnfsf14	Mus musc NM_019418
0.021382	1.511868	down	Fkbp9	Mus musc NM_012056
0.04271	1.511972	up	Lama3	Mus musc NM_010680
0.046626	2.486461	down	Dclre1c	Mus musc NM_175683
0.012846	2.410201	up		Putative u AK079126
0.032293	1.597793	up		lincRNA:chr12:81217572-81233910 forward strand
0.031337	3.191103	down	Tmprss5	Mus musc NM_030709
0.029912	1.629456	down	Dusp14	Mus musc NM_019819
0.006765	2.462829	down		lincRNA:chr13:24615451-24615973 forward strand
0.024255	3.06544	up		lincRNA:chr12:110003268-110030953 forward strand
0.006292	1.850926	up		lincRNA:chr15:74461988-74466728 reverse strand
5.84E-04	3.759892	down	Gm3893	Mus musc NR_033506
0.01726	3.481951	up	Muc1	Mus musc NM_013605
0.01193	1.648547	down		ubiquitin- AK013452
0.040255	1.576836	down	Ctbs	Mus musc NM_028836
0.024865	1.685719	up	Fitm2	fat storage AK052945
0.007927	1.745011	up		lincRNA:chr13:72906878-72923790 forward strand
0.021079	1.676038	down		lincRNA:chr6:149232359-149235295 reverse strand

0.007766	1.823233	up	LOC1000	PREDICT	XM_001480556
0.032894	1.607831	up	Larp4b	Mus musc	NM_172585
0.03695	5.9326	up		lincRNA:chr17:88890039-88905680	forward strand
0.025579	1.638532	up		lincRNA:chr7:66562376-66579519	forward strand
0.037433	2.678424	up	Gm318	PREDICT	XM_619462
0.007161	6.266217	up	E330011C	Mus musc	AK087725
0.012636	2.632808	up	Gm13138	Mus musc	NM_001177767
0.021556	2.574776	up		lincRNA:chr19:5834117-5835940	reverse strand
0.018829	1.693478	down	Ehd2	Mus musc	NM_153068
0.010449	2.900349	down		palmdelph	AK136939
0.043787	1.651009	up		lincRNA:chr19:23264899-23268776	reverse strand
0.048398	2.233601	down	Rnasel	Mus musc	NM_011882
0.046722	1.607366	up		lincRNA:chrX:20570399-20571162	forward strand
0.003835	1.533074	up	Accs	Mus musc	NM_183220
0.016209	6.21916	up	Rbp7	Mus musc	NM_022020
0.04764	1.679899	up		microrchic	AK164017
0.036757	1.65067	down		lincRNA:chr7:149761435-149764019	reverse strand
0.049721	2.434315	down	Actg1	Mus musc	NM_009609
0.008728	1.538392	up	Olfr635	Mus musc	NM_147118
0.01268	1.572847	down	Rogdi	Mus musc	NM_133185
0.042181	1.772548	up	Gm4485	PREDICT	XM_001480329
0.025012	1.590418	up		T-cell rec	XM_001479640
0.048208	2.510268	up	Olfr1247	Mus musc	NM_146966
0.029538	3.466462	down		lincRNA:chr15:32167516-32174417	reverse strand
0.010007	2.233946	down	Oip5	Mus musc	NM_001042653
0.032726	1.627916	up	Kctd3	Mus musc	NM_172650
0.018453	1.920355	up		lincRNA:chr8:12873805-12880007	forward strand
0.031959	4.721194	down	B3gnt3	Mus musc	NM_028189
0.04104	13.32892	up	LOC1000	PREDICT	XM_001474157
0.049045	1.763265	up		lincRNA:chr5:14988715-14989311	forward strand
0.035008	1.566735	up	Ppm1m	Mus musc	NM_198931
0.017325	1.77997	up	1300010F	Mus musc	NM_173758
0.017388	1.746534	down		lincRNA:chr3:146629425-146649125	forward strand

0.03722	1.93328	down	Xkr6	Mus musc	NM_173393
0.027825	1.823767	up	Cntn2	Mus musc	NM_177129
0.042313	1.583461	down		lincRNA:chr9:13349094-13352732 forward strand	
0.032743	1.577144	up	Gm2016	Mus musc	NM_001122662
0.004605	1.545708	up	Eif3j	Mus musc	NM_144545
0.006488	2.49708	down	Cdkn2a	Mus musc	NM_009877
0.037846	1.527952	up	Gm2703	PREDICT	XM_001475212
0.014475	1.788187	down	Cx3cr1	Mus musc	NM_009987
0.009519	3.718303	up		lincRNA:chr13:112337405-112356455 reverse strand	
0.045088	2.385798	up	Pick1	Mus musc	NM_008837
0.041096	1.547676	up		cytochrom	XM_901734
0.045185	1.86756	up		lincRNA:chr3:34003359-34537330 forward strand	
0.012075	2.189478	down	Slc16a4	Mus musc	NM_146136
0.046286	2.520472	up		lincRNA:chr17:15111725-15139800 reverse strand	
0.025755	4.274176	up	Gm9519	PREDICT	XR_033411
0.039364	2.240014	up	Rplp0	Mus musc	NM_007475
0.014117	3.07375	up		lincRNA:chr2:33496712-33501183 forward strand	
0.040055	1.850859	up	Mbp	Mus musc	NM_010777
0.028261	4.522206	up	Gm6274	PREDICT	XR_031283
0.002102	5.815084	up		lincRNA:chr4:3745750-3756200 forward strand	
0.017602	1.788622	up	Gm13015	PREDICT	XM_889972
0.044967	1.575522	up	Gripap1	Mus musc	NM_207670
0.01522	3.290845	up		lincRNA:chr7:140081171-140123058 reverse strand	
0.046324	1.895981	up		lincRNA:chr3:127039311-127201919 reverse strand	
0.022053	1.669954	up	Pitpnm1	Mus musc	NM_001136078
0.037663	2.171726	up		lincRNA:chr6:31267612-31293337 reverse strand	
0.038499	1.677851	up	D430040I	Mus musc	AK052542
0.006503	2.636396	up		lincRNA:chr15:79764481-79809909 forward strand	
0.025027	1.972742	up	Fig	Mus musc	NM_021716
0.011921	4.516372	up		lincRNA:chr1:134867906-134885481 reverse strand	
0.035697	2.173226	up		lincRNA:chr14:65431652-65437902 reverse strand	
0.022985	3.39037	up	Gm3512	PREDICT	XM_001477011
0.035661	1.699896	up	Cycs	Mus musc	NM_007808

0.032995	4.238995	up		lincRNA:chr4:13369325-13456750 forward strand
0.047288	7.668763	up	Gm7857	PREDICT XR_030849
0.008283	3.929955	up		lincRNA:chr3:34643323-34682773 reverse strand
0.015981	1.809515	up	Slc48a1	Mus musc NM_026353
0.003141	3.295848	up	Gm9178	PREDICT XM_001004798
0.022043	2.351959	down	Cxcr3	Mus musc NM_009910
0.019834	5.195141	up		lincRNA:chr12:21381390-21381723 forward strand
0.044177	1.805655	up	Psap	Mus musc NM_011179
0.001552	2.397984	up	Pphln1	Mus musc NM_146062
0.040614	1.662925	up	Commd3	Mus musc NM_147778
0.001837	2.956471	up		lincRNA:chr7:134620707-134626739 reverse strand
0.015767	1.542866	up		lincRNA:chr15:68161768-68193518 reverse strand
0.002389	3.925129	up	Abcb8	Mus musc NM_029020
0.019323	4.975677	up	C330019L	Mus musc NM_001034857
0.042622	3.546519	up	Gm8052	PREDICT XR_032547

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ProbeName	p-value (T)	FCAbsolute	regulation	p-value (T)	FCAbsolute	regulation	GeneSymbol	Description	GenbankAccession
A_30_P01	0.018966	2.832845	up	0.003135	7.144857	up		lincRNA:chr3:10081893-10094218 reverse strand	
A_51_P20	0.028149	1.894998	up	0.025368	1.659838	up	Grsf1	Mus musc	NM_178700
A_55_P20	0.008677	1.798938	up	0.017492	3.238295	up	Slc36a1	Mus musc	NM_153139
A_30_P01	0.042837	4.945733	up	0.037257	4.853063	up		lincRNA:chr7:112934153-112943178 forward strand	
A_55_P20	0.024302	3.166251	up	0.016648	4.514853	up	Gtf2h5	Mus musc	NM_181392
A_55_P20	0.04037	2.056918	up	0.036577	2.180308	up	Gm5576	PREDICT	XM_485792
A_55_P21	0.048098	4.832912	up	0.040434	5.198926	up	Gm9100	PREDICT	XM_001000832
A_51_P51	4.74E-04	3.186878	up	0.016077	3.391375	up	1600015I1	Mus musc	NM_001081273
A_55_P19	0.037289	2.624801	up	0.033213	3.50124	up	Vmn1r204	Mus musc	NM_001045544
A_30_P01	0.043132	2.876661	up	0.005087	3.493438	up		lincRNA:chr5:119945358-119962612 forward strand	
A_66_P12	0.042181	6.109162	up	0.040964	4.244948	up		Putative u	AK134595
A_55_P20	0.019188	4.053568	up	0.026305	2.747749	up		Putative u	XM_001474096
A_30_P01	0.011738	1.584068	up	0.016858	1.582475	up		lincRNA:chr18:38542830-38544720 reverse strand	
A_30_P01	0.018113	2.974762	up	0.036406	3.684835	up		lincRNA:chr14:101834175-102005450 forward strand	
A_55_P20	0.047972	2.842904	up	0.036049	2.20079	up	Tnfaip6	Mus musc	NM_009398
A_55_P23	0.029025	2.214082	up	0.040644	1.641105	up	4.93E+23	Mus musc	AK077028
A_55_P19	0.00422	62.22009	up	0.003751	42.07141	up	Xaf1	Mus musc	NM_001037713
A_30_P01	0.015643	61.4572	up	0.005952	34.29746	up		lincRNA:chr3:96074625-96086375 forward strand	
A_30_P01	8.14E-04	3.714335	up	0.042683	2.048402	up		lincRNA:chr13:67211950-67217199 reverse strand	
A_30_P01	0.024331	3.270147	up	5.00E-05	1.765283	up		lincRNA:chr2:60038543-60046318 forward strand	
A_30_P01	0.033017	3.69073	up	0.011527	3.209353	up		lincRNA:chr5:22928221-22939127 reverse strand	
A_55_P21	0.007103	3.556507	up	0.009961	4.390499	up	Alpk1	Mus musc	NM_027808
A_55_P19	0.031602	11.64356	up	0.012103	5.223036	up	Trem2	Mus musc	NM_031254
A_66_P13	0.036135	1.599894	up	0.024583	1.85106	up		TFIIfi-asso	U11548
A_30_P01	0.012114	2.95065	up	0.03373	3.194699	up		lincRNA:chr5:22058025-22072475 forward strand	
A_55_P21	0.038405	2.795814	up	0.043306	1.630715	up	Gm11826	PREDICT	XR_031506
A_30_P01	0.033576	8.647636	up	0.004097	15.38849	up		lincRNA:chr5:23195569-23218551 reverse strand	
A_30_P01	0.005687	2.261406	up	0.003702	1.658367	up		lincRNA:chr4:129376440-129391690 reverse strand	
A_52_P54	0.00645	2.249861	up	0.033585	1.800416	up	Fam32a	Mus musc	NM_026455
A_30_P01	0.046839	1.50713	up	0.012398	1.566649	up		lincRNA:chr9:58301467-58323783 reverse strand	
A_30_P01	0.033617	2.656195	up	0.031774	2.463284	up		lincRNA:chr2:25774411-25783757 forward strand	
A_30_P01	0.036949	1.712087	up	0.019135	2.275621	up		lincRNA:chr1:155219662-155231912 reverse strand	

A_55_P21	0.022724	1.632641	up	0.014016	1.983441	up	LOC10004	PREDICT	XM_001477810
A_30_P01	0.016117	3.004838	up	0.022138	2.05022	up		lincRNA:chr17:6830756-6832322	reverse strand
A_55_P21	0.033737	3.454033	up	0.020684	1.754242	up	Fnbp1	Mus musc	NM_019406
A_30_P01	0.045232	3.008316	up	0.00919	3.03967	up		lincRNA:chr5:22928221-22939127	reverse strand
A_66_P13	0.032896	10.61904	up	0.026789	4.82864	up	9830167H	zinc finger	XM_910524
A_55_P20	0.033534	3.605742	up	6.17E-04	2.716568	up	Wdfy1	Mus musc	NM_001111279
A_30_P01	0.014404	9.252948	up	0.003414	15.82806	up		lincRNA:chr5:23195569-23218551	reverse strand
A_30_P01	0.031624	1.784714	up	0.035443	1.724569	up		lincRNA:chr5:124694137-124695689	reverse strand
A_55_P19	0.033869	4.543783	up	0.013075	2.659126	up	A630033E	Mus musc	NM_177358
A_30_P01	0.040505	1.632768	up	0.017831	2.141128	up		lincRNA:chr2:75447542-75448025	reverse strand
A_51_P46	0.031294	2.285057	up	0.047014	3.470929	up	Hdhd3	Mus musc	NM_024257
A_55_P20	0.040528	4.75815	up	0.014846	3.289833	up	A630033E	Mus musc	NM_177358
A_55_P23	0.019949	2.746197	up	0.001022	1.878885	up	B430316J0	Mus musc	AK046698
A_55_P20	0.031287	2.230068	up	0.016023	3.072154	up	LOC10003	PREDICT	XR_030580
A_30_P01	0.010428	5.053158	up	0.032875	5.397167	up		lincRNA:chr12:74135916-74142780	reverse strand
A_55_P19	0.017612	7.044909	up	9.89E-04	8.28053	up	Spry2	Mus musc	NM_011897
A_51_P37	0.004819	6.838865	up	0.005611	5.048256	up	Cuedc1	Mus musc	NM_198013
A_55_P20	5.33E-04	3.100534	up	0.009342	2.11243	up	Dhrs7b	Mus musc	NM_001172112
A_55_P20	0.007111	20.68299	up	0.003199	3.51433	up	Klra4	Mus musc	NM_010649
A_30_P01	0.005382	1.677001	up	0.036489	1.643799	up		lincRNA:chrX:146827709-146913398	forward strand
A_55_P19	0.026152	9.383508	up	0.018561	12.39306	up	Gm5953	PREDICT	XM_001480466
A_55_P19	0.015272	4.926915	up	0.011474	3.284807	up	LOC10004	myosin lig	XM_987811
A_52_P37	0.037887	3.134206	up	0.003373	2.266648	up	Iqcc	Mus musc	NM_198026
A_51_P10	0.046829	1.534278	up	0.022374	1.529156	up	Alkbh5	Mus musc	NM_172943
A_55_P19	0.003404	15.97252	up	0.016643	30.15917	up	Gm5067	PREDICT	XR_002343
A_66_P13	0.048636	1.574328	up	0.046237	1.587595	up	Rbm4b	Mus musc	NM_025717
A_55_P19	0.035068	3.662584	up	0.023623	2.648258	up	Zfp868	Mus musc	NM_172754
A_30_P01	0.027759	2.64984	up	0.033297	2.360252	up		lincRNA:chr17:15111725-15139800	forward strand
A_51_P26	0.04371	9.642191	up	0.036838	2.068762	up	Rgs1	Mus musc	NM_015811
A_55_P21	0.022189	1.767493	up	0.011665	1.52299	up	Gm9465	PREDICT	XM_001474101
A_55_P19	0.033013	2.429815	up	0.048694	1.679545	up	Scpep1	Mus musc	NM_029023
A_52_P32	0.024426	1.693538	up	0.023255	2.377402	up		phenylalanine	AK084031
A_66_P10	0.013225	1.775574	up	0.004438	1.883511	up	Gm13453	PREDICT	XM_001472372

A_55_P20	0.01155	1.660226	up	0.041073	1.870012	up	Zfp454	Mus musc	NM_172794
A_30_P01	0.004357	3.239158	up	0.001289	4.470739	up		lincRNA:chr1:58443698-58449898	reverse strand
A_55_P20	0.011593	2.106484	up	0.010041	1.736743	up	Zfp605	Mus musc	NM_001163996
A_52_P30	0.030493	2.761126	up	5.96E-04	1.922457	up	Abca5	Mus musc	NM_147219
A_30_P01	0.038664	1.737216	up	0.016232	2.075811	up		lincRNA:chr13:49488457-49493732	forward strand
A_52_P49	0.006171	2.877121	up	0.023056	2.63817	up	2210404J1	Mus musc	NM_001039552
A_52_P53	9.38E-04	2.476965	up	0.039365	2.660814	up	2210404J1	Mus musc	NM_001039552
A_30_P01	0.012707	5.207031	up	0.02566	3.636102	up		lincRNA:chrX:146945573-146950036	reverse strand
A_30_P01	0.004353	2.690021	up	0.017579	1.692779	up		lincRNA:chr5:125078875-125098525	reverse strand
A_55_P20	0.033673	1.981988	up	0.036376	1.847237	up	Tmem181a	Mus musc	NM_001033178
A_55_P21	0.038801	1.726408	up	0.012922	1.949351	up		hepatoma	AK051401
A_30_P01	0.019579	1.616587	up	0.012444	1.609395	up		lincRNA:chr5:33186508-33196882	reverse strand
A_55_P21	0.016108	1.838127	up	0.009425	2.074619	up	Plekha7	Mus musc	NM_172743
A_52_P30	0.01427	11.97396	up	0.001275	9.134551	up	1810037I1	Mus musc	NM_024461
A_30_P01	0.011886	3.297983	up	0.031693	3.20505	up		lincRNA:chr5:22058025-22072475	forward strand
A_30_P01	0.001231	2.729323	up	0.00665	2.722798	up		lincRNA:chr1:58443698-58449898	reverse strand
A_55_P19	0.025335	2.798554	up	0.002806	2.179434	up	Ctcf1	Mus musc	NM_001081387
A_51_P24	0.043904	3.259659	up	0.04174	4.907675	up	Dpys	Mus musc	NM_001164466
A_30_P01	0.04746	3.062498	up	0.024789	3.298713	up		lincRNA:chr1:58440355-58449627	reverse strand
A_55_P20	0.042743	2.58775	up	0.00571	2.361034	up	Gm9590	PREDICT	XM_001478468
A_51_P27	0.024722	23.99104	up	0.015083	13.96454	up	Trem1	Mus musc	NM_027763
A_55_P20	0.028665	2.302007	up	0.039158	1.708726	up		cDNA fis	AK129029
A_52_P67	0.038413	2.183429	up	0.044161	1.738728	up	Arih1	Mus musc	NM_019927
A_30_P01	0.022719	3.501282	up	0.007396	3.114373	up		lincRNA:chr4:135896689-135918414	forward strand
A_52_P51	0.007674	31.70236	up	0.002933	5.100905	up	Klra15	Mus musc	NM_013793
A_30_P01	0.013648	1.687903	up	0.022624	1.52724	up		lincRNA:chr17:33426488-33444184	forward strand
A_30_P01	0.028375	1.672947	up	0.007906	1.651853	up		lincRNA:chr13:9818700-9824125	reverse strand
A_55_P21	0.037032	2.967886	up	0.008654	4.200232	up	BC023969	Mus musc	AK144629
A_30_P01	0.041071	3.365849	up	0.017119	3.22259	up		lincRNA:chr5:22928221-22939127	reverse strand
A_30_P01	0.004775	3.716656	up	0.001325	5.119646	up		lincRNA:chr1:58443698-58449898	reverse strand
A_30_P01	0.004988	7.277856	up	0.007056	12.39066	up		lincRNA:chr5:23195569-23218551	reverse strand
A_52_P64	0.046391	3.178938	up	0.001696	2.069241	up	Wars2	Mus musc	NM_027462
A_52_P47	0.009523	3.590385	up	0.049718	4.039875	up	Arsk	Mus musc	NM_029847

A_55_P21	0.003484	4.062946	up	0.001033	4.361283	up	Ocel1	Mus musc	NM_029865
A_55_P21	0.012496	1.905427	up	0.035441	1.577529	up	Arid4a	Mus musc	NM_001081195
A_30_P01	0.001426	6.042164	up	0.002576	7.354909	up			lincRNA:chr1:58443698-58449898 reverse strand
A_30_P01	0.035085	2.952247	up	0.012452	2.181707	up			lincRNA:chr17:6830756-6832322 reverse strand
A_52_P52	0.006158	6.59129	up	0.024725	3.664912	up	Hddc3	Mus musc	NM_026812
A_30_P01	0.043302	3.260518	up	0.015099	4.840094	up			lincRNA:chr5:23195569-23218551 reverse strand
A_55_P21	0.035786	2.809726	up	0.006559	2.286794	up	LOC63023	PREDICT	XR_034286
A_51_P16	0.041837	3.989497	up	2.36E-04	2.793993	up		Mus musc	AK019943
A_51_P47	0.015675	2.26054	up	0.030141	2.565228	up	Armc6	Mus musc	NM_133972
A_30_P01	0.026966	2.691917	up	0.026074	1.790179	up			lincRNA:chr17:6830756-6832322 reverse strand
A_52_P21	0.046439	2.59974	up	0.037899	2.472588	up	Snapc3	Mus musc	NM_029949
A_55_P21	0.037694	4.108275	up	0.044027	3.153479	up	Gm6651	PREDICT	XR_032823
A_55_P21	0.013025	11.43694	up	0.00174	9.302982	up	1810037I1	Mus musc	NM_024461
A_55_P21	0.027111	4.071159	up	0.002035	2.741104	up	9030025P2	Mus musc	NM_001123370
A_30_P01	9.93E-06	7.176156	up	3.89E-05	9.160327	up			lincRNA:chr1:58443698-58449898 reverse strand
A_55_P19	0.004139	1.723962	up	0.037273	2.759902	up	Uhrf1bp1	Mus musc	NM_001080769
A_52_P61	0.017539	7.751353	up	0.044901	5.096278	up	Atp10d	Mus musc	NM_153389
A_30_P01	0.028816	3.657035	up	0.030893	3.089138	up			lincRNA:chr4:135896689-135918414 forward strand
A_51_P35	0.003114	2.247878	up	0.03316	1.585368	up	Gstt2	Mus musc	NM_010361
A_30_P01	0.022789	5.609847	up	0.00653	2.533586	up			lincRNA:chr7:140081171-140123058 reverse strand
A_52_P25	0.048662	9.873706	up	0.041922	12.00852	up	Gm9306	PREDICT	XM_001478806
A_55_P21	0.027132	7.733062	up	0.001157	3.138886	up	Klra15	Mus musc	NM_013793
A_55_P23	0.00581	3.919129	up	0.017584	34.34704	up	C430049E	Mus musc	AK141396
A_52_P87	0.037744	2.600261	up	0.008395	4.15902	down	Mfsd4	Mus musc	NM_001114662
A_30_P01	0.034524	3.013552	up	0.021443	3.105041	up			lincRNA:chr5:22058025-22072475 forward strand
A_51_P12	0.017306	2.719089	up	0.042495	2.743553	up	2410076I2	Mus musc	NM_028598
A_30_P01	0.041622	5.375247	up	0.016358	5.937396	up			lincRNA:chr12:74135916-74142780 reverse strand
A_30_P01	0.012552	5.240364	up	0.045768	2.995823	up			lincRNA:chr8:85609155-85615170 forward strand
A_30_P01	0.025442	3.653459	up	0.020027	4.487266	up			lincRNA:chr14:27176059-27202735 forward strand
A_30_P01	0.023498	4.176063	up	0.012523	3.230874	up			lincRNA:chr12:74135916-74142780 reverse strand
A_51_P19	0.032099	9.190989	up	0.010236	18.12927	up	Cidea	Mus musc	NM_007702
A_55_P21	0.004852	1.751701	up	0.002922	1.711854	up	Rcc2	Mus musc	NM_173867
A_55_P23	0.040502	2.91875	up	4.86E-04	2.06807	up	D030051J2	Mus musc	AK083595

A_51_P42	0.040229	304.7876	up	0.001001	628.7509	up	Ucp1	Mus musc	NM_009463
A_51_P44	0.040343	2.849479	up	0.048231	2.280663	up	Decr2	Mus musc	NM_011933
A_30_P01	0.019544	3.80504	up	0.032052	3.13406	up		lincRNA:chr5:22058025-22072475 forward strand	
A_55_P21	0.001752	31.97837	up	0.003563	3.890606	up	Klra12	Mus musc	NM_010646
A_52_P48	0.01058	2.55182	up	0.026955	2.83863	up	Tnpo2	Mus musc	NM_145390
A_52_P36	0.02053	1.863046	up	0.010617	1.767876	up	Pik3c2a	Mus musc	NM_011083
A_52_P85	0.016079	3.245336	up	0.023412	2.132067	up	Gadd45gip	Mus musc	NM_183358
A_55_P20	0.029879	1.966467	up	0.024703	1.928193	up	LOC43610	PREDICT	XM_001481293
A_52_P87	0.029847	2.954257	up	0.004137	2.545775	up	Thrb	Mus musc	NM_009380
A_51_P37	0.018219	2.070471	up	0.025688	2.575404	down	Angpt4	Mus musc	NM_009641
A_55_P20	9.09E-04	2.0602	up	0.037441	4.485392	up	LOC10004	PREDICT	XM_001479541
A_52_P51	0.021166	2.507497	up	0.023876	2.844961	up	Abca5	Mus musc	NM_147219
A_52_P15	0.008577	6.881311	up	0.028134	10.03973	up	Abhd1	Mus musc	NM_021304
A_55_P20	0.019607	1.646776	up	0.046957	1.609927	up	Spen	Mus musc	NM_019763
A_51_P40	0.040987	2.145053	down	0.001329	2.961029	down	Fam55b	Mus musc	NM_030069
A_55_P19	0.027596	17.33264	down	0.03856	3.37006	down	LOC38099	Mus musc	NM_001037748
A_66_P12	0.001769	4.709233	down	0.037898	4.347203	down	Hdac1	Mus musc	NM_008228
A_65_P01	0.017942	8.095184	down	0.04494	7.045506	down	Hjurp	Mus musc	NM_198652
A_55_P21	0.047223	1.803233	down	0.018192	3.435551	down	Irgm2	Mus musc	NM_019440
A_51_P15	0.019149	3.100833	down	0.018624	6.095089	down	Fcrla	Mus musc	NM_145141
A_30_P01	0.020305	2.852276	down	0.024627	1.802851	down		lincRNA:chr17:36131460-36136694 forward strand	
A_55_P20	0.003189	3.125783	down	0.029599	2.851618	down	Hdac1	Mus musc	NM_008228
A_55_P19	0.026768	7.063517	down	0.018609	8.810267	down	Foxn3	PREDICT	XM_001473733
A_30_P01	0.048291	1.773312	down	0.016739	2.179686	down		lincRNA:chr1:137503023-137625604 reverse strand	
A_51_P17	0.041475	2.467532	down	0.047514	2.469616	down	Dact1	Mus musc	NM_021532
A_52_P11	0.015071	2.987567	down	0.03431	1.557507	down	Pcdh17	Mus musc	NM_001013753
A_55_P19	0.0191	9.668268	down	0.006861	7.441421	down	Skint3	Mus musc	NM_177578
A_51_P40	0.024171	1.681392	down	0.006396	1.934136	down	Ankrd35	Mus musc	NM_001081139
A_55_P20	0.016418	3.805974	down	0.017971	4.436787	down	1700030C	Mus musc	NR_015521
A_30_P01	0.001974	4.040733	down	0.035136	4.745823	down		lincRNA:chr3:79069438-79073704 reverse strand	
A_55_P22	0.025861	5.826146	down	0.008178	6.957576	down	Slc30a7	Mus musc	NM_023214
A_55_P20	0.001628	3.716223	down	9.82E-04	4.61923	down	A730008H	Mus musc	NM_172505
A_30_P01	4.71E-04	6.803904	down	0.002284	6.90831	down		lincRNA:chr14:103751075-103769725 forward strand	

A_52_P66	0.013098	1.926739	down	0.034188	2.480345	down	Snhg3	Mus musc	NR_003270
A_55_P19	0.030925	6.137235	down	0.024263	21.73128	down	LOC10004	PREDICT	XM_001476057
A_55_P19	0.027628	3.037451	down	0.013663	2.897669	down	D10627	Mus musc	NM_001013379
A_55_P21	0.029806	8.661532	down	0.02439	4.045424	down		DIX dom	AK016205
A_55_P20	7.88E-04	21.62067	down	0.04783	17.1632	down			X06519
A_55_P21	0.038438	4.63809	down	0.040252	5.404726	down	Gm13152	Mus musc	NM_001039209
A_55_P20	0.009006	22.78883	down	0.001171	21.85014	down		M.muscul	X79554
A_51_P48	0.010115	2.569262	down	0.027281	4.110998	down	Steap1	Mus musc	NM_027399
A_52_P88	0.020875	4.347057	down	0.010581	6.544955	down	2810408P1	Mus musc	NM_198619
A_51_P44	0.017633	2.380685	down	0.01575	3.199302	down	H2-Oa	Mus musc	NM_008206
A_55_P19	0.002713	1.931302	down	0.04692	1.914429	down	Wnt5b	Mus musc	NM_009525
A_52_P64	0.005153	2.739535	down	0.034477	8.176316	down	Zc3h12d	Mus musc	NM_172785
A_55_P22	0.019947	6.691667	down	3.13E-04	8.159998	down	2610507I0	Mus musc	AK162965
A_66_P11	0.004089	3.514072	down	0.008442	5.21304	down		Mus musc	DQ372793
A_55_P22	0.046995	4.324065	down	1.04E-04	2.812568	down	LOC10030	Mus musc	NR_028425
A_30_P01	0.00777	17.4621	down	0.010254	6.339055	down		lincRNA:chr3:127037711-127111912 reverse strand	
A_30_P01	0.021918	2.31233	down	0.006188	2.855439	down		lincRNA:chr5:33174092-33200792 reverse strand	
A_55_P19	0.007267	18.10284	down	0.047575	16.9229	down		Mus musc	AY351698
A_55_P19	0.021858	4.771759	down	0.002813	5.341802	down	Cd164l2	Mus musc	NM_027152
A_51_P42	0.020316	14.29079	down	0.002748	13.7772	down	Nhedc2	Mus musc	NM_178877
A_66_P14	0.017554	2.422831	down	0.016494	4.819108	down	LOC10004	predicted	XM_001476590
A_30_P01	0.028976	4.008152	down	0.004024	5.855618	down		lincRNA:chr4:146890596-146891297 forward strand	
A_51_P12	0.022799	2.569659	down	0.022543	2.849365	down	Gatad2a	Mus musc	NM_145596
A_55_P19	0.01162	5.323214	down	0.015958	3.122111	down	Atg4c	Mus musc	NM_175029
A_55_P21	0.045811	21.6475	down	0.042404	2.571367	down	LOC10004	PREDICT	XM_001474135
A_55_P21	0.011469	3.988355	down	0.007126	5.47725	down	0610042G0	PREDICT	XM_001472222
A_30_P01	0.02381	4.78086	down	0.037359	4.711155	down		lincRNA:chr3:79069438-79073704 reverse strand	
A_30_P01	0.036101	2.905475	down	0.039649	3.538238	down		lincRNA:chr8:122712014-122732520 reverse strand	
A_30_P01	0.007731	2.06799	down	0.003834	1.793287	down		lincRNA:chr13:62734450-62785325 reverse strand	
A_55_P20	0.03899	1.544178	down	0.023481	3.709742	down	E430029J2	Mus musc	NM_001162938
A_51_P47	0.003435	1.620497	down	0.031655	2.271173	down		T-cell rec	U07661
A_51_P16	0.024667	8.465845	down	0.0101	4.513149	down	3110082D0	Mus musc	NM_028474
A_55_P20	0.040681	1.65501	down	9.58E-04	2.335628	down	Fcho1	Mus musc	NM_028715

A_55_P20	0.010623	4.826582	down	0.028502	8.149054	down	LOC10004	PREDICT	XM_001472253
A_52_P28	0.017742	9.384303	down	0.0107	11.21525	down	Ankrd33b	Mus musc	NM_026153
A_51_P29	0.043189	3.58531	down	0.031685	1.529207	down	Clnk	Mus musc	NM_013748
A_52_P51	0.027171	3.720786	down	0.013344	1.999019	down	Wdfy1	Mus musc	NM_027057
A_55_P20	0.017056	20.13611	down	0.021981	2.352448	down	Sly	Mus musc	NM_201530
A_55_P20	0.047639	2.455867	down	0.004744	3.778955	down	Gm9296	PREDICT	XM_001478977
A_55_P20	0.03031	3.200131	down	0.002275	2.4238	down	Meox1	Mus musc	NM_010791
A_55_P20	0.024809	2.160979	down	0.036334	1.829008	down	Gzma	Mus musc	NM_010370
A_51_P14	0.036617	2.397697	down	0.013344	2.083553	down	Gabrd	Mus musc	NM_008072
A_30_P01	0.014368	2.586654	down	0.048932	1.860279	down		lincRNA:chr5:23195569-23218551 reverse strand	
A_55_P21	0.029731	11.51629	down	0.047924	17.08078	down		Ig lambda	AF290571
A_66_P11	0.024048	2.106461	down	0.006687	1.661957	down	Ccnd1	Mus musc	NM_007631
A_30_P01	0.027862	5.300273	down	1.14E-05	6.805373	down		lincRNA:chr17:22420025-22457650 reverse strand	
A_55_P20	0.020234	18.29459	down	0.037515	3.230222	down	Sly	Mus musc	NM_201530
A_30_P01	0.00263	7.577049	down	0.001815	6.850274	down		lincRNA:chr14:103751075-103769725 forward strand	
A_51_P33	0.013527	9.957335	down	0.009053	11.28684	down	Prim2	Mus musc	NM_008922
A_30_P01	0.029023	2.946623	down	8.36E-04	2.345588	down		lincRNA:chr12:73860757-73862034 reverse strand	
A_52_P61	0.022736	3.437111	down	0.028846	3.577397	down		V kappa li	M61952
A_55_P19	0.001871	3.885832	down	0.002318	3.755014	down	Hjrp	Mus musc	NM_198652
A_30_P01	0.012332	2.334927	down	0.020187	2.61659	down		lincRNA:chr13:62734450-62785325 reverse strand	
A_55_P20	0.025277	11.59193	down	0.038917	16.33192	down		immunogl	AY170502
A_55_P20	0.04085	2.605319	down	0.046172	3.346037	down	Cib3	Mus musc	NM_001080812
A_55_P20	0.043013	7.001909	down	0.012151	6.072753	down	Gm11223	PREDICT	XM_001474074
A_55_P21	0.018691	10.386	down	0.027727	12.24049	down	Camk2b	Mus musc	NM_001174053
A_55_P19	0.001786	4.484832	down	0.045465	3.944906	down	6330416L0	Mus musc	NM_176962
A_30_P01	0.01252	3.214065	down	0.020772	2.702309	down		lincRNA:chr11:95644899-95658549 forward strand	
A_55_P19	0.029512	2.984355	down	0.003485	4.262222	down	Cyp4f18	Mus musc	AF233647
A_52_P32	0.006434	3.771619	down	0.027846	3.137321	down	Trim16	Mus musc	NM_053169
A_30_P01	0.014601	10.80351	down	0.020723	4.095983	down		lincRNA:chr3:127037711-127111912 reverse strand	
A_55_P21	0.010634	16.24299	down	0.005363	24.08433	down	Slfn8	Mus musc	NM_181545
A_55_P20	0.024952	16.67972	down	0.011468	2.898945	down		LOC3809	XM_979799
A_55_P21	0.018833	2.29709	down	0.009975	2.42495	down	Gm1667	PREDICT	XM_358618
A_51_P14	0.038584	1.539592	down	0.001502	1.75466	down	Vps13b	Mus musc	NM_177151

A_55_P20	0.032138	1.78735	down	0.025082	1.802377	up	Gm10621	Putative u	XM_001476249
A_55_P19	0.039213	1.823112	down	0.024352	1.61185	down	Hdac1	Mus musc	NM_008228
A_55_P21	0.003135	5.161512	down	0.005768	4.395121	down	Cmpk2	Mus musc	NM_020557
A_66_P12	0.022115	2.067096	down	0.049442	1.786302	down	Kit	Mus musc	NM_001122733
A_30_P01	0.005779	6.267376	down	0.044553	3.031704	down		lincRNA:chr17:36136010-36136696 forward strand	
A_52_P58	0.011091	1.687325	down	0.033623	1.712149	down	Entpd4	Mus musc	NM_026174
A_30_P01	0.001882	2.085378	down	0.046747	2.227439	down		lincRNA:chr5:23195569-23218551 reverse strand	
A_55_P21	0.027398	2.073539	down	0.020638	2.008719	down	Cd164l2	Mus musc	NM_027152
A_52_P51	0.013593	11.40098	down	7.62E-04	24.98324	down	Col4a6	Mus musc	NM_053185
A_55_P19	0.031527	3.487929	down	0.04122	2.097781	down	Gm10406	Mus musc	NM_001164727
A_55_P20	0.016083	4.032634	down	0.001249	5.071094	down	Cyp4f18	Mus musc	NM_024444
A_30_P01	0.001284	6.840605	down	0.006457	5.85713	down		lincRNA:chr14:103751075-103769725 forward strar	
A_55_P19	0.006056	2.666708	down	0.015071	2.32029	down	Gm4864	PREDICT	XR_032827
A_52_P49	0.03211	1.665965	down	0.033072	1.933862	down	Hist1h2ak	Mus musc	NM_178183
A_52_P69	0.020457	2.20313	down	0.010735	2.645035	down	Rimkla	Mus musc	NM_177572
A_30_P01	0.009343	3.690205	down	0.015592	5.031628	down		lincRNA:chr3:79069438-79073704 reverse strand	
A_30_P01	0.010128	29.73755	down	8.10E-04	9.630994	down		lincRNA:chr3:127037711-127111912 reverse strand	
A_55_P20	0.011149	4.260608	down	0.028552	2.684605	down	Gm3642	PREDICT	XM_001477672
A_52_P11	0.001494	8.333726	down	0.004879	6.451733	down	Gm7146	PREDICT	XM_909745
A_55_P19	0.005146	13.19314	down	0.04206	29.52719	down		immunogl	AY679096
A_51_P46	0.012659	2.060597	down	0.026235	2.275076	down	Ccl8	Mus musc	NM_021443
A_55_P19	0.044127	2.493168	down	0.035532	2.532605	down	Trim16	Mus musc	NM_053169
A_55_P21	0.010443	9.45655	down	0.013781	21.47969	down		Ig heavy c	XM_919047
A_55_P21	0.022795	25.87889	down	0.00824	51.4732	down		Mouse m	X53355
A_55_P21	0.021624	2.588942	down	0.014662	3.508281	down	Dock7	Mus musc	NM_026082
A_55_P20	0.010698	5.910721	down	0.008688	3.208023	down	Myom3	Mus musc	NM_001085509
A_30_P01	0.025095	5.795648	down	0.0072	9.129706	down		lincRNA:chr17:32044823-32045974 reverse strand	
A_55_P19	0.038917	3.395154	down	0.014109	2.099565	down	Pmepa1	Mus musc	NM_022995
A_55_P19	0.0202	7.870457	down	0.006329	17.14978	down	Speer4d	Mus musc	NM_025759
ERCC-00	0.040912	2.422092	down	0.04176	2.215312	down		Unknown	
A_30_P01	0.016339	2.890886	down	0.030575	2.37086	down		lincRNA:chr17:36131460-36136694 forward strand	
A_55_P21	0.002795	15.66037	down	0.027376	23.04683	down		Mus musc	U19317
A_51_P48	0.043219	15.13555	down	0.039678	19.68088	down		Ig lambda	AF138742

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p-value (T)	FCAbsolute	regulation	GeneSymbol	Description	GenbankAccession
0.007947	2.27525	up	Asap3	Mus musc	NM_001008232
0.010974	2.70849	up		PREDICT	XM_484811
0.021228	4.77809	up	Baiap2l2	Mus musc	NM_177580
0.030765	2.76432	up		lincRNA:chr4:101010948-101032148 forward strand	
0.019447	2.10083	up	Wbp2	Mus musc	NM_016852
0.020599	1.75794	up	Ppp1r2	Mus musc	NM_025800
0.004739	4.08894	up		Ets2 repressor factor Gene [Source:MGI (curated);Acc:MGI:109637] [ENSMUST000001163]	
0.023052	4.33543	up	Med16	Mus musc	NM_198107
0.049704	2.58544	up	Gm6343	PREDICT	XR_031357
0.022162	1.74257	up	Snx33	Mus musc	NM_175483
0.039535	1.72305	up	Rce1	Mus musc	NM_023131
0.046001	3.02648	up	A430017K	Mus musc	AK079696
0.007434	4.59868	up		lincRNA:chr18:35974770-35975091 forward strand	
0.039907	4.71424	up	LOC10004	PREDICT	XM_001473610
0.022029	2.94014	up		lincRNA:chr6:90745692-90777977 reverse strand	
0.023715	2.53244	up	Upk3b	Mus musc	NM_175309
0.019042	2.31591	up	LOC10004	PREDICT	XM_001472633
0.021199	1.55775	up	D330038C	Mus musc	NM_177899
0.013215	1.79598	up	LOC10004	PREDICT	XR_031900
0.031006	1.71159	up		lincRNA:chr12:110944403-110988678 forward strand	
0.010614	2.57813	up		lincRNA:chr4:88563206-88563835 reverse strand	
0.015487	2.75741	up	Nova1	Mus musc	NM_021361
0.042854	3.58725	up	LOC63029	PREDICT	XM_903418
0.020163	1.5154	up	Kdm3b	Mus musc	NM_001081256
0.034672	2.78677	up	Gsn	Mus musc	NM_146120
0.028952	3.69921	up	170006111	RIKEN cl	XM_485306
0.007239	1.63868	up	5430410E	PREDICT	XM_001475205
0.008006	1.61846	up	2610018G	Mus musc	NM_133729
0.002003	5.96024	up	Sox14	Mus musc	NM_011440
0.004627	1.81425	up	Pisd-ps3	Mus musc	NR_003518
0.039076	3.63463	up	Prss33	Mus musc	NM_001081399
0.011369	2.41386	up		Mus musc	AK145039

0.019261	3.11189	up		lincRNA:chr2:117781720-117937595 forward strand
0.00502	4.49104	up		lincRNA:chr13:64044376-64045368 reverse strand
0.017107	4.45233	up	Gm4125	PREDICT XM_001472807
0.019878	2.55743	up		Putative u XM_980696
0.003743	1.76561	up		lincRNA:chr4:129497990-129515290 forward strand
0.034616	3.53174	up		RIKEN cl XM_001473797
0.045681	3.91125	up		lincRNA:chr8:122712014-122732520 forward strand
0.036094	2.83982	up	LOC43346	Mus musc AK051942
0.043603	3.96701	up	Rap1a	Mus musc NM_145541
0.035239	3.6576	up	2010320M	60209170 BF531481
0.028845	3.23371	up		lincRNA:chr7:16584852-16657252 reverse strand
0.009305	3.1586	up	Gm3142	PREDICT XM_001475080
0.015208	4.03482	up		lincRNA:chr3:96289850-96301078 forward strand
0.049798	2.46802	up	LOC10004	PREDICT XR_031783
0.013675	2.51154	up		lincRNA:chr1:134237581-134248506 reverse strand
0.035093	3.70792	up		lincRNA:chr6:5311375-5328075 forward strand
0.019477	1.96516	up	Mpp7	Mus musc NM_001081287
0.044885	1.96313	up		myosin, h BC116417
0.012584	6.12915	up	Tcl1b2	Mus musc NM_013775
0.038541	3.60046	up		lincRNA:chr2:132079092-132087069 reverse strand
0.023311	2.88876	up	Gpr25	Mus musc NM_001101516
0.016547	2.49356	up		lincRNA:chr15:102947390-102971082 reverse strand
0.043472	1.83583	up	Adcy3	Mus musc NM_138305
0.00387	1.56819	up		lincRNA:chr8:42462791-42466106 reverse strand
0.009563	2.11664	up		lincRNA:chr19:57426515-57435165 reverse strand
0.017917	2.03988	up		lincRNA:chr18:35976163-35976530 forward strand
0.035524	1.75789	up	Gm3001	PREDICT XM_001475388
0.046262	6.27704	up		lincRNA:chr11:97505439-97522274 forward strand
0.02509	2.63578	up		lincRNA:chr10:94900849-94928059 reverse strand
0.039772	3.96416	up		lincRNA:chr12:76771424-76772158 forward strand
0.037088	2.2909	up	Raver1	Mus musc NM_027911
0.010807	4.92401	up		lincRNA:chr18:78190463-78235438 forward strand
0.016622	9.71198	up		lincRNA:chr13:97700327-97700876 forward strand

5.94E-04	3.16724	up	A530083I2	Mus musc	AK136855
0.007323	2.27834	up		lincRNA:chr13:24833082-24838462	forward strand
0.047175	4.25834	up	1300002K	Mus musc	NM_028788
0.006533	1.80539	up		transmem	AK051974
0.029735	4.22981	up	AI852580	UI-M-BH	AI852580
0.020001	1.93523	up		lincRNA:chr3:35831966-35841638	forward strand
0.030835	1.90662	up		lincRNA:chr4:3169583-3180017	forward strand
0.036909	3.88465	up	Tpsb2	Mus musc	NM_010781
0.023923	3.69924	up	Ms4a4a	PREDICT	XM_889011
0.027346	1.84402	up	Kcna7	Mus musc	NM_010596
0.044974	1.90842	up	Sgsm2	Mus musc	NM_197943
0.027712	2.73056	up	LOC67035	PREDICT	XM_001476496
0.018163	2.37504	up		lincRNA:chr19:61226425-61270975	reverse strand
0.048212	2.17846	up		lincRNA:chr17:88469443-88470068	forward strand
0.046481	1.71678	up	Egfr	Mus musc	NM_007912
0.011297	2.09993	up		protein ty	AK047640
0.039375	1.62211	up		lincRNA:chr8:41934312-41945487	reverse strand
0.003585	1.90269	up	Susd5	Mus musc	NM_001101510
0.047118	4.63727	up		lincRNA:chr6:126445920-126446242	reverse strand
0.043954	2.30602	up	Neurog3	Mus musc	NM_009719
0.027729	3.19242	up	Gdf1	Mus musc	NM_008107
0.047728	2.62416	up	Ccr3	Mus musc	NM_009914
0.025285	1.94249	up	Olfr791	Mus musc	NM_146930
0.007313	1.98237	up		Putative u	AK135819
0.038593	2.71051	up	Epn2	Mus musc	NM_010148
0.003885	3.47895	up		lincRNA:chr17:8088950-8106700	reverse strand
0.013041	2.85099	up		lincRNA:chr13:67802775-67829550	forward strand
0.021104	3.60433	up		lincRNA:chr10:84005221-84022896	reverse strand
0.045853	1.68935	up		predicted	XM_001472868
0.020199	2.52115	up	E230006M	Mus musc	AK053951
0.04429	1.82362	up		lincRNA:chr4:124206166-124334412	reverse strand
0.024815	1.81841	up	Rwdd1	Mus musc	NM_025614
0.025522	1.76647	up	Tmem154	Mus musc	NM_177260

0.007922	2.21744	up		lincRNA:chr11:6748267-6818192 forward strand
0.044004	1.93588	up	Efcab4a	Mus musc AK140493
0.028307	3.28522	up	Olfr314	Mus musc NM_001011760
0.009858	2.04216	up		lincRNA:chr6:31017987-31174287 reverse strand
0.039918	2.27903	up		lincRNA:chr7:71093563-71095094 forward strand
0.003639	1.5601	up	Slc4a1ap	Mus musc NM_009206
0.03613	3.34146	up	Ssbp2	Mus musc NM_024272
0.044889	2.43667	up		lincRNA:chr15:102100964-102104552 forward strand
0.020034	1.66851	up		lincRNA:chr9:20784567-20799942 reverse strand
0.003574	5.77901	up	LOC62709	Mus musc AK147870
0.036848	2.75863	up		lincRNA:chr14:21437920-21464655 reverse strand
0.035158	1.60258	up		lincRNA:chr17:21785442-21801542 reverse strand
0.028363	1.96029	up	P4ha2	Mus musc NM_011031
0.046617	2.80151	up		lincRNA:chr14:65433420-65434061 reverse strand
0.035597	1.62594	up	Sos1	Mus musc NM_009231
0.033328	2.608	up	Defa-rs2	Mus musc NM_007847
0.023841	1.76938	up	Syt7	Mus musc NM_173068
0.003591	1.60008	up		lincRNA:chr11:79549532-79575807 forward strand
0.026124	2.92389	up	Myoz1	Mus musc NM_021508
0.010369	6.29626	up	Fbxw13	Mus musc NM_177598
0.00639	3.26766	up	Olfr128	Mus musc NM_206816
0.031644	5.12464	up		lincRNA:chr9:34192364-34192810 reverse strand
0.029613	1.58296	up	Guk1	Mus musc NM_008193
0.005013	8.55266	up		lincRNA:chr4:116790373-116797823 forward strand
0.003667	1.96803	up	Mylk3	Mus musc NM_175441
0.036586	1.93414	up		anthrax to AK013005
0.032602	2.2855	up		lincRNA:chr9:66981366-67061725 forward strand
0.014068	2.14972	up		lincRNA:chr6:126766225-126771309 reverse strand
0.017941	3.55436	up		lincRNA:chr7:114369337-114407862 reverse strand
0.03397	1.50002	up		TATA bo BC033926
0.011616	1.79866	up	Gm7302	PREDICT XM_917569
0.031811	2.25778	up	Cyp2d13	Mus musc NR_003552
0.00853	4.21803	up		lincRNA:chr9:118060025-118085050 forward strand

0.013521	2.9218	up		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:O88605] [ENSMUST000
0.046448	3.09194	up	Gm1123	Mus musc NM_001080776
0.041239	4.08835	up		lincRNA:chr7:88131123-88136898 reverse strand
0.024209	1.70748	up	Crybb3	Mus musc NM_021352
0.049334	1.88586	up		lincRNA:chr8:128933150-128943375 forward strand
0.047845	1.8778	up		lincRNA:chr1:81632600-81644175 forward strand
0.034635	2.11322	up	Prss29	Mus musc NM_053260
0.013571	2.39196	up		lincRNA:chr12:74883691-74893323 reverse strand
0.022062	2.27511	up	Tars2	Mus musc NM_027931
0.004155	2.13417	up	Ncam1	Mus musc NM_010875
0.008272	1.9492	up	Ppyr1	Mus musc NM_008919
0.038603	5.70756	up	LOC10004	PREDICT XM_001478120
0.033564	2.48267	up	Zfp352	Mus musc NM_153102
9.40E-04	6.74153	up		lincRNA:chr4:124202159-124202824 forward strand
0.046063	2.31416	up	Bnip2	Mus musc NM_001008238
0.041255	2.08617	up	LOC10004	PREDICT XM_001472211
0.012605	1.88823	up		lincRNA:chr10:83364590-83364873 forward strand
0.006401	2.00266	up		PREDICT XM_001473591
0.001374	2.6687	up		lincRNA:chr1:137482591-137625604 forward strand
0.005088	3.49613	up		lincRNA:chr3:108763862-108772151 forward strand
0.036649	1.83324	up		lincRNA:chr7:134779841-134840591 forward strand
0.00767	3.92428	up		lincRNA:chr8:131178212-131180657 forward strand
0.038115	1.67359	up		enhancer AK052020
0.012666	1.94063	up		lincRNA:chr2:108456668-108532418 reverse strand
0.043608	5.65567	up		lincRNA:chr13:19618491-19618836 reverse strand
0.030461	1.5308	up	Tsc2	Mus musc NM_011647
0.030763	1.84615	up	Gm2115	Mus musc AK137174
0.007192	1.62715	up	Srprb	Mus musc NM_009275
9.57E-04	1.59731	up	2900057C	Mus musc BC125023
0.029329	4.74199	up	Olfr870	Mus musc NM_146904
0.001501	4.90419	up		lincRNA:chr10:24269165-24276690 reverse strand
0.021457	3.62522	up		lincRNA:chr4:35106125-35127700 forward strand
0.044989	1.86721	up		lincRNA:chr11:33414450-33450750 reverse strand

0.013543	1.58262	up		lincRNA:chr2:132722530-132726802 forward strand
0.013323	2.35848	up	Gm2976	PREDICT XR_032174
2.34E-04	2.23794	up	Map3k7	Mus musc NM_009316
0.03572	1.95213	up	Scn1b	Mus musc NM_011322
0.01381	5.04308	up		lincRNA:chr9:106170918-106177894 reverse strand
0.010714	2.63681	up	Apoc3	apolipoprotein C-III Gene [Source:MGI (curated);Acc:MGI:88055] [ENSMUST00000118649]
0.024321	1.51414	up		lincRNA:chr8:26343277-26352902 reverse strand
0.038847	2.47426	up		lincRNA:chr1:196843592-196865102 forward strand
0.005846	3.72078	up	Il12rb1	Mus musc NM_008353
0.041414	1.95579	up		lincRNA:chr4:129479254-129480362 reverse strand
0.006527	3.20103	up	Ttpa	Mus musc NM_015767
0.02677	2.89321	up	Gm7372	PREDICT XR_031550
0.017202	2.07236	up		lincRNA:chr1:36012298-36020311 reverse strand
0.040852	1.85065	up		lincRNA:chr11:3538125-3554450 forward strand
0.030097	1.69018	up	Ctsw	Mus musc NM_009985
0.026379	3.12051	up		lincRNA:chr3:85571525-85645700 reverse strand
0.01741	3.44023	up	Ugt3a1	Mus musc NM_207216
0.030048	4.68913	up	H2-T18	PREDICT XM_912024
0.022476	2.0778	up		lincRNA:chr4:98943050-98959998 reverse strand
0.043996	2.13093	up		lincRNA:chr5:112205091-112240992 forward strand
0.02818	2.0185	up		lincRNA:chr11:3538125-3554450 reverse strand
0.044839	1.86547	up	Xpnpep3	Mus musc NM_177310
0.029826	1.513	up	Gm6553	PREDICT XR_032598
3.32E-04	2.29156	up		lincRNA:chr6:128389484-128403407 reverse strand
0.0289	2.47195	up		lincRNA:chr12:53669892-53710742 reverse strand
0.049767	1.5552	up	Pwwp2a	Mus musc NM_027557
0.009921	1.87236	up		lincRNA:chr16:4867322-4874772 reverse strand
0.00799	4.48277	up		tribbles homolog AK041212
0.033338	2.53966	up	Bai2	Mus musc NM_173071
0.015161	3.53224	up	Bcl11a	B-cell CLL/lymphoma 11A (zinc finger protein) Gene [Source:MGI (curated);Acc:MGI:1061]
0.025777	2.56937	up		lincRNA:chr17:88466300-88495175 forward strand
0.04687	2.49532	up	Cdhr2	Mus musc NM_001033364
0.036797	2.24482	up		lincRNA:chr15:77575125-77585575 forward strand

0.044823	2.8383	up		lincRNA:chr14:79724027-79729152 forward strand
0.009861	2.92937	up		lincRNA:chr14:55317199-55317670 reverse strand
0.044904	1.82781	up	Gm11543	PREDICT XM_975056
0.040852	2.02385	up	Dbx1	Mus musc NM_001005232
0.025478	2.14223	up	Zbtb5	Mus musc NM_001163284
0.020037	2.44522	up	Drp2	Mus musc NM_010078
2.80E-04	5.47855	up		lincRNA:chr17:15226181-15250333 reverse strand
0.043192	1.68888	up	Ssbp2	Mus musc NM_024272
0.029536	2.7045	up		lincRNA:chr18:57124435-57134910 reverse strand
0.011436	2.88162	up		lincRNA:chr11:50994911-51050704 forward strand
0.001177	3.65282	up	Lypd6	Mus musc NM_177139
0.014099	1.99709	up	Stk32a	Mus musc NM_178749
0.003615	1.94322	up	LOC10004	PREDICT XM_001478470
0.030765	3.1966	up		lincRNA:chr14:101834175-102005450 forward strand
0.034007	1.90788	up		lincRNA:chr6:39205913-39248468 forward strand
0.015087	1.78117	up	5430417L	Mus musc NR_030716
0.009395	2.29698	up		phosphod AK031275
0.005096	1.98847	up	Snapc3	Mus musc NM_029949
0.016567	2.65937	up		lincRNA:chr9:118060025-118085050 forward strand
0.007554	2.99974	up		lincRNA:chr8:124355710-124401160 forward strand
0.003386	1.98899	up		lincRNA:chr2:165780133-165800663 reverse strand
0.009737	3.25451	up	Klk10	Mus musc NM_133712
0.042715	1.94646	up		lincRNA:chr13:67806242-67830110 reverse strand
0.046714	1.86713	up		
0.003395	3.15306	up		lincRNA:chr7:129294998-129295498 forward strand
0.035102	4.35695	up		Brain cDN AB041806
0.032047	1.8052	up		lincRNA:chr9:43738583-43757007 forward strand
0.025101	1.55387	up		lincRNA:chr3:35782698-35789932 forward strand
0.040375	2.46545	up		lincRNA:chr6:90937606-90938335 reverse strand
0.028241	3.62393	up	A930005H	Mus musc NR_015487
0.024752	2.35214	up	Slamf6	Mus musc NM_030710
0.046728	5.76097	up		lincRNA:chr1:71939741-71947891 forward strand
0.004972	2.2983	up		lincRNA:chr17:46972160-46997919 reverse strand

0.006934	3.909	up	Zfp112	Mus musc	NM_021307
0.042066	2.86119	up		lincRNA:chr2:36112429-36112792 forward strand	
0.033541	4.19365	up	Pabpc5	Mus musc	NM_053114
0.013009	1.91549	up	Gm2982	PREDICT	XM_001475326
0.02192	3.25787	up		lincRNA:chr18:35204950-35216650 forward strand	
0.025975	4.04172	up	LOC10004	PREDICT	XM_001473489
0.012102	3.79353	up		lincRNA:chr5:33174092-33200792 forward strand	
2.51E-05	5.9975	up	9130214F1	Mus musc	AK020279
0.011298	2.39796	up	LOC10004	PREDICT	XM_001475860
0.011768	2.45545	up	2900073C	PREDICT	XM_001473664
0.031791	2.67207	up		lincRNA:chr19:14911511-14911831 reverse strand	
4.53E-04	14.492	up		lincRNA:chr2:170029045-170034220 forward strand	
0.008616	1.65631	up	Padi2	Mus musc	NM_008812
0.014271	2.87388	up		lincRNA:chr8:90000619-90061169 forward strand	
0.029322	1.82881	up	Gm8164	PREDICT	XR_001891
0.01092	1.66242	up		lincRNA:chr10:24269317-24270145 reverse strand	
0.009159	1.83929	up		lincRNA:chr6:91928958-91936887 reverse strand	
0.037409	2.36995	up	2410024N	Mus musc	AK035593
0.022562	2.94214	up		lincRNA:chr18:46954653-46955671 forward strand	
0.013381	3.02896	up		lincRNA:chr13:28918991-28919231 forward strand	
0.028486	2.95987	up	Npw	Mus musc	NM_001099664
0.006083	4.8372	up		lincRNA:chr1:71730139-71730720 forward strand	
0.045891	2.86427	up		lincRNA:chr9:96664617-96683617 forward strand	
0.01208	2.38237	up	LOC10004	PREDICT	XM_001473785
0.020915	1.62309	up		lincRNA:chr3:41143423-41359623 forward strand	
0.039352	2.73203	up	Itga9	Mus musc	NM_133721
0.014709	1.50689	up	Nanos3	Mus musc	NM_194059
0.011548	2.13867	up		lincRNA:chr8:126396600-126407275 forward strand	
0.035758	2.58316	up	Gm826	Mus musc	NM_001033411
0.028105	2.02078	up	2810433D	Mus musc	NR_033474
0.006425	2.38328	up	LOC10004	PREDICT	XM_001473504
0.012952	1.70963	up	Lancl1	Mus musc	NM_021295
0.049095	1.78834	up	Gm5968	PREDICT	XR_030900

0.046738	1.85207	up	Cecr2	Mus musc	NM_001128151
0.024983	1.88526	up	Reg3d	Mus musc	NM_013893
0.028921	3.30262	up			lincRNA:chr1:85300475-85331475 reverse strand
0.019929	3.59423	up			lincRNA:chr1:167797581-167803031 forward strand
0.034991	2.14076	up	Gpbar1	Mus musc	NM_174985
0.003802	1.65711	up			lincRNA:chr7:66562376-66579519 forward strand
0.038985	1.99349	up			lincRNA:chr4:82156098-82196298 forward strand
0.039915	2.30249	up			lincRNA:chr4:3406175-3443875 forward strand
0.011421	2.7603	up			lincRNA:chr12:74135916-74142780 forward strand
0.019067	3.53971	up	Sstr4	Mus musc	NM_009219
0.044405	1.5185	up			lincRNA:chr16:11024315-11055740 forward strand
0.003707	3.34306	up			lincRNA:chr12:116850878-116855932 reverse strand
0.039436	2.56502	up			lincRNA:chr4:155560050-155570900 reverse strand
0.029276	2.40151	up			paired iml AK041413
0.004984	1.61399	up			lincRNA:chr9:111214181-111260465 forward strand
0.007865	4.05145	up	GlrX	Mus musc	NM_053108
0.008161	2.55623	up			lincRNA:chr8:18895366-18925423 forward strand
0.027121	1.78703	up	Dffa	Mus musc	NM_001025296
0.047271	1.59367	up	Renbp	Mus musc	NM_023132
0.021958	6.56902	up	Thbs2	Mus musc	NM_011581
0.037721	2.00691	up	Pltp	Mus musc	NM_011125
0.015831	4.08037	up			lincRNA:chr9:41488229-41545481 reverse strand
0.027761	5.42707	up	Pycr1	Mus musc	NM_144795
0.039215	3.09092	up			lincRNA:chr5:92548501-92566401 reverse strand
0.011077	4.87943	up			lincRNA:chr17:33368400-33393525 forward strand
0.003011	4.44217	up			lincRNA:chr5:33773842-33942967 reverse strand
0.029502	1.56613	up	Faf1	Mus musc	NM_007983
0.047096	1.65433	up	B230216G	PREDICT	XM_620381
0.01801	4.99635	up			lincRNA:chr13:34186976-34210579 forward strand
0.021572	3.58077	up	Shoc2	Mus musc	NM_019658
0.001216	3.05888	up			lincRNA:chr6:127588224-127609749 reverse strand
0.006056	1.97407	up	H1foo	Mus musc	NM_138311
0.001475	1.52675	up			lincRNA:chr15:82036791-82037660 reverse strand

0.035089	1.94052	up		tyrosyl-D	AK033868
0.031218	2.00664	up		lincRNA:chr5:54053882-54054174	forward strand
0.002101	6.34545	up		lincRNA:chr3:21964899-21974885	forward strand
0.010753	4.03905	up	LOC10004	PREDICT	XM_001478469
0.038774	2.30803	up	Gm4121	PREDICT	XM_001472111
0.035168	3.60205	up		lincRNA:chr6:82608223-82669023	forward strand
0.042422	1.85911	up	AU015791	Mus musc	AK139027
0.028388	3.01158	up		lincRNA:chr3:37797734-37891650	forward strand
0.034035	1.75155	up		lincRNA:chr1:94077196-94077860	forward strand
0.041176	3.23992	up	H2-M10.3	Mus musc	NM_201608
0.006702	2.76128	up		lincRNA:chr2:117024098-117025009	reverse strand
0.049359	5.08216	up	LOC10004	PREDICT	XM_001478711
0.013855	2.34724	up	Magix	Mus musc	NM_018832
0.042485	1.76019	up	Rexo1	Mus musc	NM_025852
0.01408	2.41644	up	Fam160b2	Mus musc	NM_194345
0.039224	1.50134	up	D330012F	Mus musc	NM_178752
0.003156	2.00638	up		lincRNA:chr15:97495641-97503721	forward strand
0.027864	2.27138	up	Pglyrp2	Mus musc	NM_021319
0.007543	1.61046	up	Aph1a	Mus musc	NM_146104
0.040644	1.67383	up		lincRNA:chr11:69184157-69201732	reverse strand
0.018277	3.33064	up	Hcctr1	Mus musc	NM_198959
0.029566	2.87869	up		lincRNA:chr9:14480441-14483362	forward strand
2.51E-04	8.05917	up	Tas2r118	Mus musc	NM_207022
0.009496	1.94502	up		lincRNA:chr11:117768049-117807949	reverse strand
0.024156	1.88636	up		lincRNA:chr4:136856064-136875614	reverse strand
0.034813	3.79045	up		lincRNA:chr12:3173375-3203075	reverse strand
0.005422	3.67286	up		lincRNA:chr10:117021051-117038683	reverse strand
0.023949	5.94236	up	LOC10004	PREDICT	XM_001477532
0.015138	1.6	up	Nudc	Mus musc	NM_010948
0.043609	2.72824	up		lincRNA:chr8:18587198-18592948	forward strand
0.030746	1.94623	up		lincRNA:chr18:4415233-4415995	forward strand
0.029305	4.82059	up	Car14	Mus musc	NM_011797
0.013	3.05961	up		lincRNA:chr7:129294166-129301366	forward strand

0.022995	3.4845	up	49305970	RIKEN cl	XM_989547
0.045137	1.9124	up	Rhbdl2	Mus musc	NM_183163
0.010438	3.69472	up	Tas2r117	Mus musc	NM_207021
9.41E-04	2.63477	up		lincRNA:chr1:139713316-139913366 reverse strand	
0.032658	2.4531	up	Hist2h2bb	Mus musc	NM_175666
0.026677	2.29351	up	D830039M	PREDICT	XR_035204
0.024302	3.10197	up	Cdkn1a	Mus musc	NM_001111099
0.043196	4.61154	up	LOC10004	PREDICT	XM_001477926
0.02629	1.61551	up	Gm6466	PREDICT	XM_888549
0.032855	1.96508	up		lincRNA:chr5:52581905-52637135 forward strand	
0.028696	1.95771	up		lincRNA:chr3:63673371-63703295 reverse strand	
0.043903	1.5295	up		lincRNA:chr3:88009045-88036270 reverse strand	
0.017866	2.44336	up		lincRNA:chr2:156654675-156665430 reverse strand	
0.048621	2.25516	up		lincRNA:chr9:56379670-56429822 reverse strand	
0.033747	1.52598	up	Sox10	Mus musc	NM_011437
0.034534	1.9895	up		lincRNA:chr16:29711373-29712035 reverse strand	
0.021686	5.54842	up		lincRNA:chr8:108153471-108159672 reverse strand	
0.014873	1.74625	up		lincRNA:chr5:30550467-30559008 reverse strand	
0.035381	2.73564	up	4932412D	Mus musc	AK016521
0.016398	2.27726	up		lincRNA:chr8:122963590-122964126 forward strand	
1.36E-05	3.74116	up		lincRNA:chr16:13752215-13764390 reverse strand	
0.022309	1.66171	up	LOC10004	PREDICT	XM_001472591
0.026417	2.35561	up		lincRNA:chrX:98680220-98718445 reverse strand	
0.017637	3.37374	up		lincRNA:chr6:47915489-47916089 forward strand	
0.007824	1.57811	up	Gm6686	PREDICT	XM_891173
0.034438	2.28997	up		lincRNA:chr19:4207767-4208004 forward strand	
0.01	1.7672	up	Zfhx4	Mus musc	NM_030708
0.0244	3.07124	up		lincRNA:chr11:19960515-19961093 reverse strand	
0.015185	3.79898	up		lincRNA:chr5:30550467-30559008 reverse strand	
0.027342	1.54258	up	Rfxank	Mus musc	NM_011266
0.040282	1.60386	up	Btbd3	Mus musc	NM_145534
0.009002	2.90288	up	Olfr1410	Mus musc	NM_146491
0.004444	1.65069	up	Uhrf1bp1l	Mus musc	NM_029166

0.027999	3.43252	up		lincRNA:chr3:27837825-27880925 forward strand
0.023517	2.01041	up	Ccr8	Mus musc NM_007720
0.013301	1.58217	up	4930557J0	Mus musc AK016164
0.02202	3.59658	up	Cd300c	Mus musc NM_199225
0.030955	2.97832	up		lincRNA:chr5:121759042-121789992 reverse strand
0.031921	2.5076	up		peroxired AK165551
0.0012	6.3016	up	2900052N	Mus musc NR_015605
0.005817	2.0569	up	Prkrir	Mus musc NM_028410
0.006926	1.6517	up	Gm5491	PREDICT XR_032837
0.001081	1.75242	up	Gm2285	PREDICT XM_001473039
0.0317	2.12792	up	Mmp24	Mus musc NM_010808
0.043941	2.70535	up		lincRNA:chr2:77807600-77836075 forward strand
0.006975	5.18263	up		lincRNA:chr2:22753100-22780375 reverse strand
5.05E-04	3.17185	up	Agrn	Mus musc NM_021604
0.027049	2.39	up	LOC54734	Mus musc NM_001025208
0.01197	1.71399	up		lincRNA:chr11:87872568-87880978 reverse strand
0.003325	4.07085	up	Olfr531	Mus musc NM_146953
0.043555	1.78306	up		lincRNA:chrX:90997595-91009570 reverse strand
0.006037	3.38026	up		lincRNA:chr10:39607282-39619520 forward strand
0.03121	1.6726	up	Cdk4	Mus musc NM_009870
0.011495	1.93662	up	Acss3	Mus musc NM_198636
0.032998	1.67153	up	Gm5459	PREDICT XM_484358
0.014466	1.73245	up	Mapk8ip3	Mus musc AF178637
0.004571	2.14026	up		Putative u AK170322
0.004877	3.65377	up		lincRNA:chr17:5795893-5835243 reverse strand
0.016459	2.66326	up		lincRNA:chr16:11024315-11055740 forward strand
0.038353	3.11159	up		lincRNA:chr6:93029101-93031007 forward strand
0.024312	3.97853	up		lincRNA:chr11:82588507-82594501 forward strand
0.007392	3.45639	up	Olfr656	Mus musc NM_147075
0.036094	2.27791	up		PREDICT XM_001477525
0.014444	1.61693	up	Gm7464	PREDICT XR_031091
0.043717	2.31941	up		lincRNA:chr5:74487385-74497428 forward strand
0.049888	2.68648	up		lincRNA:chr16:8738782-8830148 reverse strand

0.046063	4.19651	up		lincRNA:chr18:75513062-75523889 forward strand
0.011208	2.11137	up	Muc5ac	Mus musc NM_010844
0.013506	2.40986	up		RIKEN cl AK018312
0.00734	2.00629	up		lincRNA:chr13:48620882-48643532 reverse strand
0.005827	3.23964	up		lincRNA:chr17:95150800-95180650 reverse strand
0.04129	1.8489	up		lincRNA:chr17:6602100-6615425 forward strand
0.008648	1.51897	up	Camp	Mus musc NM_009921
0.032862	1.85518	up	Cwf19l2	Mus musc NM_027545
0.013905	1.98084	up		lincRNA:chr7:26054813-26063725 forward strand
0.012704	1.56085	up		lincRNA:chr16:43623581-43642715 forward strand
0.030092	1.58309	up	Olfr1348	Mus musc NM_146913
0.003692	2.28444	up		lincRNA:chr5:123582742-123588202 forward strand
0.005153	2.10803	up	Gm3985	Mus musc NM_001177589
0.001748	2.80147	up		lincRNA:chr8:37582187-37621987 forward strand
0.035818	1.96004	up	Trim65	Mus musc NM_178802
0.028564	3.29661	up		lincRNA:chr7:3309825-3331151 reverse strand
0.03467	2.36661	up	Aqp5	Mus musc NM_009701
0.008553	5.66071	up		lincRNA:chr13:108825897-108833335 reverse strand
0.043362	2.92357	up		lincRNA:chr4:140609589-140614789 forward strand
0.021	1.78395	up		lincRNA:chr1:94611439-94613779 reverse strand
0.019022	2.57006	up	Capn12	Mus musc NM_001110807
0.022894	3.12427	up		lincRNA:chr17:15111725-15139800 reverse strand
0.040119	1.91509	up		lincRNA:chr3:145269449-145298239 forward strand
0.024683	4.78586	up		lincRNA:chr1:82892851-82943201 reverse strand
0.022778	1.53504	up	Cdk9	Mus musc NM_130860
0.021291	1.65405	up		lincRNA:chr4:155585650-155608700 forward strand
0.030511	1.93604	up	Kcnk13	Mus musc NM_146037
0.036218	1.96259	up	Gm3902	PREDICT XM_001478420
0.004138	2.10019	up	Gm6404	PREDICT XM_887605
0.025139	1.91867	up	Tmem200l	PREDICT XM_001475812
0.005984	1.61136	up	Adora1	Mus musc NM_001008533
0.030502	1.84182	up		lincRNA:chr5:143676800-143704125 reverse strand
0.01329	2.86564	up	Paqr6	Mus musc NM_198410

0.005828	1.51708	up		rabaptin, I	BC003921
0.019914	3.60008	up		lincRNA:chr19:4994325-4994537 reverse strand	
0.012278	3.36842	up		lincRNA:chr15:79764481-79809909 forward strand	
0.030022	1.63993	up	Hint3	Mus musc	NM_025798
0.015521	1.54112	up	Pik3ap1	Mus musc	NM_031376
0.048631	1.56211	up	LOC67454	PREDICT	XR_033362
0.00314	2.36073	up	Bcat1	Mus musc	NM_007532
0.013128	5.36931	up		lincRNA:chr8:110196655-110390197 forward strand	
0.027105	2.40195	up	Pcdh11x	PREDICT	XM_001472925
0.032498	1.88323	up	MacroD1	Mus musc	NM_134147
0.035129	1.81013	up		PREDICT	XM_001474827
0.007455	1.81618	up	Ing5	Mus musc	NM_025454
0.001436	2.43457	up	LOC10004	PREDICT	XR_032019
0.001021	2.50169	up		lincRNA:chr10:21688115-21710890 reverse strand	
0.009368	1.85511	up		cyclic nuc	XM_001476198
0.011891	2.59778	up		lincRNA:chr17:21785442-21801542 forward strand	
0.043285	1.50617	up	Yeats2	Mus musc	NM_001033237
0.016326	2.62293	up		lincRNA:chr17:6455677-6476228 forward strand	
0.018621	3.75587	up	Plekhg6	Mus musc	NM_198604
0.03259	2.27785	up		lincRNA:chr17:13806767-13824342 reverse strand	
0.026031	3.00083	up		lincRNA:chr6:50361567-50406200 reverse strand	
9.75E-04	1.60638	up	Foxi2	Mus musc	NM_183193
0.021739	4.71702	up		lincRNA:chr15:96091428-96115684 forward strand	
0.023791	3.23095	up		lincRNA:chr9:121207045-121269020 forward strand	
0.008804	1.70709	up		Rho-relate	AK081381
0.023325	1.52116	up	Sars2	Mus musc	NM_023637
0.0021	1.81365	up	Dhrsx	Mus musc	NM_001033326
0.031152	2.97837	up		lincRNA:chr7:80763588-80764230 forward strand	
0.009302	2.36482	up		lincRNA:chr15:85476512-85498105 forward strand	
0.04978	1.62289	up		lincRNA:chr5:113609906-113622032 reverse strand	
0.037501	1.56138	up	LOC10004	PREDICT	XM_001478127
0.008897	1.75477	up		lincRNA:chr14:67585234-67596823 reverse strand	
0.041181	1.80994	up		lincRNA:chr3:27837825-27880925 forward strand	

0.032154	2.0954	up		lincRNA:chr8:114477602-114488627 reverse strand
0.017146	3.1622	up	Gm10389	Mus musc NR_033541
0.022577	3.20644	up		lincRNA:chr13:51248372-51259297 forward strand
0.034479	2.2543	up		lincRNA:chr11:87841800-87858725 reverse strand
0.030401	3.28584	up		lincRNA:chr11:95483973-95490751 forward strand
0.020829	2.11399	up		lincRNA:chr11:97457180-97487074 reverse strand
0.007949	1.70225	up		lincRNA:chr6:86425510-86450160 forward strand
0.018692	2.21603	up		lincRNA:chrX:45814752-45816313 reverse strand
0.013763	2.26164	up		lincRNA:chr14:77258025-77278750 forward strand
0.022566	1.78744	up		lincRNA:chr5:110158475-110223700 forward strand
0.017587	3.64358	up	Gm6284	PREDICT XR_030892
7.88E-04	6.07284	up		lincRNA:chr2:155269145-155303251 forward strand
0.027447	2.18503	up		lincRNA:chr17:15111725-15139800 reverse strand
7.10E-05	1.50869	up	Ptges3	Mus musc NM_019766
0.012473	1.63525	up	1700102J0	Mus musc AK007112
0.02537	3.10577	up	H2-T24	Mus musc NM_008207
0.024393	1.87335	up		lincRNA:chr10:126818382-126856582 forward strand
0.002068	3.87136	up	Gm13032	Mus musc AK049241
0.022308	2.15346	up		lincRNA:chr7:16584852-16657252 forward strand
0.025087	1.80075	up		lincRNA:chr5:136371885-136372424 reverse strand
0.009101	1.55082	up		lincRNA:chr19:4994325-4994537 reverse strand
0.0308	1.58221	up		midline 2 AK039479
0.027731	1.71669	up		lincRNA:chr2:22782700-22801900 forward strand
0.043207	1.9123	up		lincRNA:chr7:4827340-4863315 reverse strand
0.03488	3.50487	up	Olfr332	Mus musc NM_001011770
0.046758	1.68099	up	N4bp1	Mus musc NM_030563
0.047014	3.95991	up	Nap115	Mus musc NM_021432
0.040762	2.68045	up	Pik3cg	Mus musc NM_020272
1.72E-04	3.04849	up		Putative u AK052046
0.008727	1.73752	up	Olfr460	Mus musc NM_146383
0.041566	1.65388	up		lincRNA:chrX:75813213-75829323 forward strand
0.011038	1.70929	up		lincRNA:chr4:88604248-88645948 forward strand
0.006248	3.16494	up	BC049349	Mus musc NM_001164581

0.00919	1.90116	up		lincRNA:chr17:15111725-15139800 forward strand
0.00117	3.77095	up		fetal and a BC115805
0.021047	1.71537	up	Fam181b	Mus musc NM_021427
0.019867	1.84927	up		lincRNA:chr8:57977383-57985712 forward strand
0.045002	1.57642	up	Loxhd1	Mus musc NM_172834
0.002181	1.87528	up	Rnf112	Mus musc NM_009548
0.041467	3.03492	up		lincRNA:chr4:114585803-114588898 forward strand
0.005717	2.284	up		lincRNA:chrX:120134722-120138152 reverse strand
0.013117	1.6651	up		lincRNA:chr14:33901152-33976129 reverse strand
8.85E-04	2.15881	up		lincRNA:chr3:27760757-27761151 forward strand
0.026349	1.51674	up	Olfr139	Mus musc NM_147003
0.040349	2.59122	up		lincRNA:chr8:108153471-108159672 forward strand
0.026469	1.88534	up	Gm4475	PREDICT XM_001480026
0.001307	1.64559	up	Rnmt	Mus musc NM_026440
0.04677	9.67454	up	Gpnmb	Mus musc NM_053110
0.009034	2.96863	up		lincRNA:chr2:25774411-25783757 reverse strand
0.019014	2.51879	up	Fam129c	Mus musc NM_001166213
0.003538	1.58887	up		lincRNA:chr4:35106125-35127700 forward strand
0.022477	1.73346	up		Putative u AK160609
0.047779	1.58871	up	LOC10004	PREDICT XR_034330
0.042657	2.21119	up		lincRNA:chr6:133054025-133069850 reverse strand
0.035498	3.91841	up		lincRNA:chr12:103151385-103157735 forward strand
3.60E-04	3.69748	up	Olfr353	Mus musc NM_146941
0.037831	1.85647	up		Putative u AK036729
0.049291	2.61471	up	Gfer	Mus musc NM_023040
0.005161	1.88142	up	Bcat1	Mus musc NM_007532
0.040556	2.51672	up	Mtus2	Mus musc NM_029920
0.003053	2.14294	up	Cited2	Mus musc NM_010828
0.045867	1.52094	up		lincRNA:chr11:53592946-53637922 forward strand
0.00343	1.64201	up		CDC23 (d AK044478
0.024535	1.59922	up		
0.045797	1.51674	up	Cnst	Mus musc NM_146105
0.012303	1.71134	up	Ccbe1	Mus musc NM_178793

0.024996	1.6861	up	4933424M	PREDICT	XM_001474219
0.014994	2.41339	up	Synpo2	Mus musc	NM_080451
0.018407	1.93874	up	2900079G	Mus musc	NR_033431
0.039612	1.82073	up		lincRNA:chr17:45524689-45525320 reverse strand	
0.041312	1.88107	up		lincRNA:chrX:47893703-47996700 forward strand	
0.022993	2.39651	up	Slc39a8	Mus musc	NM_001135150
0.033751	1.84138	up		lincRNA:chr4:8865575-8899400 reverse strand	
0.016795	1.56077	up	Icmt	Mus musc	NM_133788
0.043135	1.76148	up		integrator	AK047093
0.011208	3.17228	up	Prnt3	Mus musc	NM_172487
0.023819	2.16289	up	Rasgef1b	Mus musc	NM_145839
0.033465	2.17255	up		lincRNA:chr4:88582120-88582754 forward strand	
0.010922	1.57666	up		lincRNA:chr15:66685663-66686113 reverse strand	
0.037086	1.9196	up		lincRNA:chr13:74712775-74728450 reverse strand	
0.034928	4.14309	up		lincRNA:chr12:82500406-82501102 forward strand	
0.03575	1.85872	up		lincRNA:chr8:13200727-13207714 forward strand	
0.046193	1.62561	up		lincRNA:chr15:79709500-79714700 forward strand	
0.001282	1.71792	up		lincRNA:chr6:12062275-12075800 reverse strand	
0.031025	2.14959	up	Foxi3	Mus musc	NM_001101464
0.048664	1.56594	up	Tmem29	PREDICT	XM_001474106
0.039635	1.57889	up		lincRNA:chr8:74431707-74442440 forward strand	
0.012693	2.65539	up		lincRNA:chr7:134620707-134626739 forward strand	
0.012174	3.54307	up		lincRNA:chr17:15111725-15139800 reverse strand	
0.028893	1.59812	up		lincRNA:chr15:73455424-73477275 reverse strand	
0.017309	2.27184	up	LOC10004	PREDICT	XM_001474483
0.011614	2.56745	up		lincRNA:chr3:145269449-145298239 forward strand	
0.030219	1.57973	up		fibroblast	AK158492
0.008101	1.67347	up		lincRNA:chr9:41408354-41420812 forward strand	
0.049094	4.92553	up	Clec4d	Mus musc	NM_010819
0.004634	2.05768	up		lincRNA:chr2:75489436-75490163 reverse strand	
0.004643	1.89454	up	Gm8667	PREDICT	XR_032610
0.038937	1.69257	up	Med1	Mus musc	NM_013634
0.008635	3.9572	up	Adcy1	Mus musc	NM_009622

0.04112	1.53688	up		lincRNA:chr15:96032592-96116907 forward strand
0.030136	1.66485	up		lincRNA:chr12:82500406-82501102 forward strand
0.035887	1.58571	up	Cask	Mus musc NM_009806
0.032158	1.92603	up		lincRNA:chr1:95871175-95886625 forward strand
0.003692	3.31785	up	Gm7684	PREDICT XM_001476311
0.035433	2.85208	up		staufen (R AK028390
0.015756	1.55778	up	C920025E	PREDICT XM_001473226
0.034765	3.14272	up	C530028O	Mus musc NM_175696
0.007493	3.48338	up		lincRNA:chr11:120041124-120052299 forward strand
0.013123	1.64655	up	Gm7575	PREDICT XR_031580
0.003679	4.55203	up		lincRNA:chrX:73008593-73009966 reverse strand
0.039283	1.50093	up	Rapgef6	Mus musc NM_175258
0.033353	1.86911	up	Gjc2	Mus musc NM_175452
0.024795	2.19171	up	AW987390	AGENCC BQ938751
0.049459	2.95185	up		Putative u AK050906
0.027211	1.56836	up	Cecr5	Mus musc NM_144815
0.043099	2.0008	up		lincRNA:chr2:67834535-67834914 forward strand
0.049787	7.75557	up	Lypd1	Mus musc NM_145100
0.028753	1.52467	up	Birc2	Mus musc NM_007465
0.016494	1.57698	up		lincRNA:chr4:129497990-129515290 forward strand
0.027689	1.80707	up		lincRNA:chr9:13224147-13424397 reverse strand
0.024824	1.51957	up		lincRNA:chr11:112898724-113062945 forward strand
0.024787	1.5807	up	Tjp2	Mus musc NM_011597
0.015984	1.8593	up		lincRNA:chr8:122945743-122946192 forward strand
0.029242	1.93785	up	Gm7928	PREDICT XR_033855
0.014541	1.82156	up	2500002B	Mus musc AK141659
0.001402	67.9035	up	Hal	Mus musc NM_010401
0.002501	4.49292	up		lincRNA:chrX:146945573-146950036 reverse strand
0.039786	1.80215	up		lincRNA:chr19:61226425-61270975 reverse strand
0.032716	5.63651	up	Atp6v0d2	Mus musc NM_175406
0.012253	19.5859	up	Gm2922	PREDICT XM_001475122
0.023972	1.54392	up	Id1	Mus musc NM_010495
0.024549	1.62458	up		lincRNA:chr8:114477602-114488627 reverse strand

0.049478	1.95588	up		lincRNA:chr8:72663625-72673010 reverse strand
0.0446	2.85285	up		Putative u AK139474
0.019476	1.71777	up		Putative u AK140482
0.007643	1.62482	up		lincRNA:chr19:9060613-9060851 forward strand
0.034653	2.03215	up		RNA bind AK014289
0.002117	1.78207	up		lincRNA:chr12:88235624-88264465 reverse strand
0.015154	2.12754	up	Gm14231	PREDICT XM_485172
0.034526	1.58536	up	Shq1	Mus musc NM_181590
0.03353	1.78502	up	Sms	Mus musc NM_009214
0.049134	1.69205	up	Muc2	Mus musc NM_023566
0.021921	2.08946	up	Mttr15	myotubula AK173087
0.047985	1.82426	up	Gm8618	PREDICT XM_001479170
0.046932	2.42135	up	Dock8	Mus musc NM_028785
0.027822	2.18909	up		lincRNA:chr12:76771424-76772158 forward strand
0.037623	1.7625	up		lincRNA:chr4:131734714-131742542 reverse strand
0.022824	2.89904	up	Tnfaip8l3	tumor nec AK154109
0.036502	1.53455	up		lincRNA:chr5:34696192-34722842 reverse strand
0.03586	1.54651	up		lincRNA:chr17:6455677-6476228 forward strand
0.028777	2.26722	up		lincRNA:chr4:11102287-11118421 reverse strand
0.049451	1.55919	up	Ang2	Mus musc NM_007449
0.037109	2.00781	up		lincRNA:chr11:3538125-3554450 reverse strand
0.02539	1.51576	up		lincRNA:chr2:52241435-52245307 forward strand
0.043639	3.17598	up	Ccl3	Mus musc NM_011337
0.007159	4.32685	up		lincRNA:chr15:101084597-101095097 forward strand
0.019856	1.66918	up	Olfr690	Mus musc NM_020290
0.025316	1.82779	up		lincRNA:chr12:73838608-73862621 reverse strand
0.040808	2.10431	up	Gm8826	PREDICT XR_030888
0.017077	1.79138	up	Padi2	Mus musc NM_008812
0.025317	1.85055	up		lincRNA:chr5:92563184-92566678 reverse strand
0.02668	1.98402	up		lincRNA:chr4:101075685-101080461 reverse strand
0.026587	2.01847	up		lincRNA:chr12:12876192-12918398 forward strand
0.008821	1.53513	up		lincRNA:chr17:26911397-26917047 reverse strand
0.003695	3.6512	up	Klra5	Mus musc NM_008463

0.049926	2.60024	up		lincRNA:chr10:81816994-81863610 forward strand
0.046261	1.97152	up		lincRNA:chrX:146832315-146875680 reverse strand
0.03985	2.53167	up	Nnt	Mus musc NM_008710
0.013467	1.58228	up	Gm9634	PREDICT XR_004753
0.039029	1.50956	up	Eif4ebp3	Mus musc NM_201256
0.040344	1.72342	up		lincRNA:chr1:183783306-183834531 reverse strand
0.012427	4.29983	up	Slc6a4	Mus musc NM_010484
0.040142	1.67344	up	Ankrd34a	Mus musc NM_001024851
0.040455	2.27552	up	Gm8230	PREDICT XR_030655
0.019507	1.87325	up	Heca	Mus musc NM_001033432
0.01472	1.76753	up	Ntrk3	Mus musc NM_008746
0.004161	1.94801	up	2410018L	Mus musc NR_015504
0.03904	1.61708	up	Kctd18	Mus musc NM_001159864
0.019825	1.7177	up	Ascl1	Mus musc NM_008553
0.011915	1.64564	up	Stxbp4	Mus musc NM_011505
0.034375	2.53911	up	Scyl2	Mus musc NM_198021
0.029762	1.50611	up		lincRNA:chrX:20555593-20591971 forward strand
0.027537	2.58298	up		lincRNA:chr6:133054025-133069850 reverse strand
0.041605	1.58016	up	Hif3a	Mus musc NM_016868
0.00919	1.66942	up	Inpp5k	Mus musc NM_008916
0.045426	3.28118	up		lincRNA:chr11:58136882-58143829 reverse strand
0.037272	2.75074	up	Sox7	Mus musc NM_011446
0.026541	1.58223	up	Cyb5r4	Mus musc NM_024195
0.04501	1.50353	up	Pitpna	Mus musc NM_008850
0.045406	1.73072	up		lincRNA:chrX:90997595-91009570 forward strand
0.009831	2.03651	up	Gm8840	PREDICT XR_032645
0.026247	5.10206	up	Kank4	Mus musc NM_172872
0.030002	2.34641	up	Agtr1b	Mus musc NM_175086
0.030461	2.09521	up	Depdc5	Mus musc NM_177786
0.028267	1.67789	up		lincRNA:chr11:87872568-87880978 reverse strand
0.046723	1.66132	up	20101110	RIKEN cl AK167772
0.011787	2.35019	up	Ntrk3	Mus musc NM_008746
0.039516	1.75072	up		lincRNA:chr18:32389816-32394927 forward strand

0.021887	1.81931	up	Rbm41	Mus musc	NM_001172147
0.039242	6.44349	up	Atp6v0d2	Mus musc	NM_175406
0.037178	1.58875	up	Gm5509	PREDICT	XM_001475540
0.022485	1.85835	up		a disinteg	AK086734
0.005141	3.13939	up	Zfp868	Mus musc	NM_172754
0.002189	3.18238	up		lincRNA:chr17:6265275-6362150 reverse strand	
0.021741	1.57975	up	Narg2	Mus musc	NM_145618
0.046936	1.61444	up	Rnf144b	Mus musc	NM_146042
0.035058	1.67234	up		Ssu72 RN	BC016544
0.020276	1.9578	up	Neb	Mus musc	NM_010889
0.011739	1.8882	up	Rgs2	Mus musc	NM_009061
0.010851	1.50076	up	2610019E	VP01_04	DV070132
0.008866	1.50553	up	Zfp397	Mus musc	NM_027007
0.017485	1.71839	up	9130019O	Mus musc	NM_030226
0.033172	1.62527	up	Nfx1	Mus musc	NM_023739
0.045292	2.19755	up		lincRNA:chr3:90425270-90435820 forward strand	
0.005027	1.57043	up	Vwce	Mus musc	NM_027913
0.048023	2.07228	up	Mt1	Mus musc	NM_013602
0.04607	1.55088	up	Acvr2a	Mus musc	NM_007396
0.034556	1.72345	up	Txndc11	Mus musc	NM_029582
0.020183	1.50099	up		lincRNA:chr17:79042382-79051807 reverse strand	
0.037923	1.62427	up	Ppp4r2	Mus musc	NM_182939
0.032761	1.57253	up	Arhgap42	Mus musc	NM_027823
0.014303	2.56076	up		transmem	BC096660
0.046545	1.93688	up	2810021J2	Mus musc	NM_172403
0.031862	2.20828	up	AI314976	Mus musc	NM_207219
0.03203	3.28418	up		lincRNA:chr8:74820025-74833350 forward strand	
0.020238	1.8515	up		poly (AD	AK037903
0.022239	2.98728	up	Ubiad1	Mus musc	NM_027873
0.037671	22.6598	up	Syt10	Mus musc	NM_018803
0.012875	1.74284	up	LOC22657	PREDICT	XR_034285
0.032122	2.36442	up	Mtus2	Mus musc	NM_029920
0.04614	1.72726	up		lincRNA:chr6:121035524-121061074 forward strand	

0.017689	2.16366	up		lincRNA:chr17:26911397-26917047 forward strand
0.016198	1.65198	up		Putative uAK161240
0.012626	1.78858	up		lincRNA:chr10:3227840-3233588 forward strand
0.018007	1.58898	up	Tmem68	Mus musc NM_028097
0.040141	1.70165	up	Gm7606	PREDICT XR_031541
3.15E-05	1.72272	up	Lcorl	ligand dep XM_001475371
0.03217	1.91783	up	Wdr76	Mus musc NM_030234
0.032891	1.54765	up	Aars	Mus musc NM_146217
0.023471	1.99177	up		lincRNA:chr16:7947710-7948066 reverse strand
0.002264	2.16677	up		lincRNA:chrX:90997595-91009570 reverse strand
0.025353	1.71702	up	Gm8225	PREDICT XM_985281
0.043171	1.59319	up	Med6	Mus musc NM_027213
0.008326	1.79373	up	Ttc15	Mus musc NM_178811
0.023232	1.50679	up	Wwox	Mus musc NM_019573
0.0335	1.57778	up	Lhpp	Mus musc NM_029609
0.030395	1.59613	up	Mphosph1	Mus musc NM_026483
0.001056	1.67567	up	Mgat2	Mus musc NM_146035
0.017819	1.60677	up		Unknown
0.010768	2.01759	up	LOC10004	PREDICT XM_001479479
0.001175	1.63532	up	Pnpla6	Mus musc NM_001122818
0.048613	3.19735	up	Chdh	Mus musc NM_175343
0.027015	2.43077	up	2810474O	Mus musc NM_026054
0.002907	1.63698	up		lincRNA:chr12:81719382-81731865 forward strand
0.017131	1.78022	up		lincRNA:chrX:47890565-47915775 forward strand
0.006879	1.68438	up	2310010J1	PREDICT XM_896611
0.02397	1.81266	up	Nop56	Mus musc NM_024193
0.023938	1.90946	up		lincRNA:chr6:13801450-13853450 forward strand
0.007231	1.58906	up		nuclear fa EU887629
0.029296	1.80247	up	D3Ert751	Mus musc NM_027271
0.047153	1.57627	up	4933406C	PREDICT XM_001480777
0.040086	3.42569	up	Klra16	Mus musc NM_013794
0.029883	1.57148	up	E2f4	Mus musc NM_148952
0.008201	1.50959	up	Zfp259	Mus musc NM_011752

0.008711	1.57008	up	Zfp58	Mus musc	NM_001007575
0.009057	2.19043	up	4933407K	Mus musc	AK163097
0.018965	3.71525	up	LOC64096	killer cell	XM_918210
0.019009	3.19539	up	Rnf39	Mus musc	NM_001099632
0.00962	2.51454	up	Egr2	Mus musc	NM_010118
0.024381	2.39626	up		lincRNA:chr15:100888823-100889131 forward strand	
0.011272	2.05422	up	Ogdh	Mus musc	NM_010956
0.022848	1.59276	up	Gm6211	PREDICT	XR_002190
0.017333	1.5568	up	Vegfb	Mus musc	NM_011697
0.031312	2.08947	up		lincRNA:chr17:79042382-79051807 reverse strand	
0.039103	2.42731	up	Clcc1	Mus musc	NM_001177770
0.006329	1.50152	up		lincRNA:chr10:6497224-6497863 reverse strand	
0.032395	1.90928	up	Sfi1	Mus musc	NM_030207
0.002932	1.68631	up	Wdr75	Mus musc	NM_028599
0.029957	1.68171	up		Unknown	
0.010216	2.1216	up	Klra5	Mus musc	NM_008463
0.018005	3.07515	up		lincRNA:chr1:196843592-196865102 forward strand	
0.026892	1.50148	up	Soat1	Mus musc	NM_009230
0.029769	2.37176	up		lincRNA:chr14:115423660-115463160 reverse strand	
0.022679	1.59219	up	Rbm8a	Mus musc	NM_025875
0.025264	1.53266	up	2310051F0	Mus musc	AK075904
0.016408	1.527	up		lincRNA:chr5:92563184-92566678 reverse strand	
0.02572	1.66602	up		lincRNA:chr2:118408095-118415745 forward strand	
0.022603	2.06939	up		lincRNA:chr17:17492400-17507525 reverse strand	
0.01829	1.88038	up	Gorasp1	Mus musc	NM_028976
0.005445	2.31798	up		lincRNA:chr17:6265275-6362150 reverse strand	
0.034205	4.48486	up	Klra22	Mus musc	NM_053152
0.008673	1.54069	up	Hipk1	Mus musc	NM_010432
0.002154	2.50201	up		lincRNA:chr9:113648970-113715170 reverse strand	
0.03279	5.20109	down	C130079G	Mus musc	NM_177661
0.039483	1.8604	down		lincRNA:chr5:106121842-106127192 reverse strand	
0.040813	10.3706	down	9030625G	Mus musc	AK018576
0.005164	5.98222	down	LOC43533	PREDICT	XM_917510

0.039045	2.17372	down	9430011C	Mus musc	AK034586
0.013764	2.45504	down		lincRNA:chr17:21177225-21187525 reverse strand	
0.018745	1.69378	down	Ephb1	Mus musc	NM_173447
0.001302	1.72716	down	Trib2	Mus musc	NM_144551
0.045522	9.32942	down	Igfals	Mus musc	NM_008340
0.038342	5.55881	down	Gm13241	PREDICT	XM_485486
0.004433	2.13735	down	Cdkn2b	Mus musc	NM_007670
0.004445	17.4067	down		Mus musc	AF045501
0.041233	1.62197	down	Atrnl1	Mus musc	NM_181415
0.017933	3.90837	down		B-cell CL	AK165756
0.021452	1.59819	down		lincRNA:chr6:120670699-120677449 forward strand	
0.025952	4.01964	down		lincRNA:chr1:71718767-71719614 forward strand	
0.025897	2.39374	down	Pfkfb4	Mus musc	NM_173019
0.017496	5.05554	down	Gas2l2	Mus musc	NM_001013759
0.036773	1.54265	down	Arhgap11a	Mus musc	NM_181416
0.018332	1.5947	down		lincRNA:chr5:15033568-15033987 forward strand	
0.023435	2.21873	down	Gm10394	Mus musc	NM_001177538
0.025028	4.38552	down	Gm3002	Mus musc	NR_033388
0.002141	2.19573	down	Ccdc99	Mus musc	NM_027411
0.040228	1.6683	down	Sema3c	Mus musc	NM_013657
5.05E-05	1.72641	down	Gpn2	Mus musc	NM_133884
0.004597	1.7492	down	2010002M	Mus musc	NM_053217
0.00918	1.56472	down	Plagl1	Mus musc	NM_009538
0.033154	1.97542	down		RIKEN cl	XR_035219
0.002249	2.32491	down		lincRNA:chr19:54011403-54019143 reverse strand	
0.029503	1.91063	down	AA060545	mj69c10.y	AI595487
0.044572	1.65143	down	Gm7677	PREDICT	XM_977642
0.025566	2.82322	down	Nrarp	Mus musc	NM_025980
0.042308	2.32137	down		lincRNA:chr11:112898724-113062945 reverse strand	
5.27E-04	2.48265	down		lincRNA:chr10:18036490-18059965 reverse strand	
0.007923	4.47851	down	LOC64097	PREDICT	XM_918237
0.044843	3.25959	down	Gm16525	PREDICT	XM_001477897
0.044138	3.06425	down	C6	Mus musc	NM_016704

0.009368	2.86287	down	Nrxn1	Mus musc	NM_020252
0.045306	1.73817	down	C130009A	Mus musc	AK142864
0.014956	1.70832	down	C230098O	Mus musc	AK082735
0.024872	10.5747	down		Mus musc	U18580
0.019924	1.6201	down		lincRNA:chr3:60292527-60292880 reverse strand	
0.011414	2.12261	down	Bcl2l14	Mus musc	NM_025778
0.024664	1.68851	down	Fam101a	Mus musc	NM_028443
0.009215	3.99376	down	Apln	Mus musc	NM_013912
0.019923	1.56345	down	Pdia2	Mus musc	NM_001081070
0.046232	3.63699	down	Gm3705	PREDICT	XM_001475676
0.042881	4.38423	down		lincRNA:chr5:22887983-22939658 reverse strand	
0.011121	3.24846	down		lincRNA:chr5:22801058-22939737 reverse strand	
0.010747	1.87209	down	Oxt	Mus musc	NM_011025
0.018874	1.90616	down	Ltb	Mus musc	NM_008518
0.043523	4.35445	down		lincRNA:chr5:22887983-22939658 reverse strand	
0.005892	2.42019	down	Pacsin1	Mus musc	NM_011861
0.00329	1.54644	down		lincRNA:chr11:112905201-113062945 reverse strand	
0.027049	1.81485	down	Cd3g	Mus musc	NM_009850
0.009694	3.43948	down	LOC10003	PREDICT	XM_001472072
0.044383	1.58805	down	Gm8659	PREDICT	XR_002032
0.044182	1.60723	down		lincRNA:chr14:62263564-62307496 forward strand	
0.038813	1.63871	down	LOC10004	PREDICT	XM_001476392
0.014098	2.22077	down	Sfrs13b	Mus musc	NM_177774
0.019015	1.51596	down		lincRNA:chr5:31856417-31916414 forward strand	
0.047214	1.81637	down		lincRNA:chr14:61321789-61325711 forward strand	
0.009038	3.67293	down		Mus musc	DQ372800
0.03224	1.55594	down		lincRNA:chr4:146507925-146532650 forward strand	
0.044446	2.08836	down	Prima1	Mus musc	NM_133364
0.035479	25.2365	down	LOC66493	PREDICT	XR_031164
0.0274	1.93661	down	Dchs1	Mus musc	NM_001162943
0.046457	2.10559	down	Sell	Mus musc	NM_001164059
0.043808	2.404	down	Klhl31	Mus musc	NM_172925
0.039055	2.9823	down	5830419E	Mus musc	AK134048

0.044799	2.65684	down	Hrasls	Mus musc	NM_013751
2.47E-04	1.50515	down		lincRNA:chr12:117623500-117643575 reverse strand	
0.014641	1.96518	down	Bcl6b	Mus musc	NM_007528
0.042467	5.22065	down	Iqcf4	Mus musc	NM_026090
0.019489	2.17154	down	Cd19	Mus musc	NM_009844
0.007742	1.90965	down		NLR fami	AY360472
0.024614	4.01927	down	Gm2897	Mus musc	NM_001177715
0.014005	6.98069	down	1700084K	PREDICT	XM_001001317
0.003811	7.69039	down		Ig kappa c	X67625
0.011281	8.9054	down			XM_001473125
0.045473	2.95353	down	Tdrd5	Mus musc	AK138828
0.017234	1.64719	down	Itgal	Mus musc	NM_008400
0.042315	2.56673	down		lincRNA:chr11:112905201-113062945 reverse strand	
0.005626	9.06962	down	LOC67748	PREDICT	XM_001003989
0.031684	2.11601	down	Dlk1	Mus musc	NM_010052
0.001018	14.5685	down	4933438K	Mus musc	AK017111
0.001805	3.60839	down		lincRNA:chr11:69196530-69197001 forward strand	
0.032251	1.94367	down	Pou2f2	Mus musc	NM_001163554
0.031626	1.85147	down	Cbfa2t3	Mus musc	NM_001109873
0.006189	1.8589	down	C430049B	PREDICT	XM_980571
0.032456	4.08518	down	ENSMUSC	Mus musc	NM_001029930
0.033554	1.8745	down		lincRNA:chr4:146156575-146175425 reverse strand	
0.033067	2.83721	down	Sez6l2	Mus musc	NM_144926
0.007119	9.31328	down		lincRNA:chr5:22801058-22939737 reverse strand	
0.007335	1.64593	down		lincRNA:chr1:87374975-87412500 reverse strand	
0.02514	10.222	down		RIKEN cl	XM_001473370
0.031195	1.50234	down	Gm13948	PREDICT	XM_283255
0.018713	2.79094	down	Gm5556	PREDICT	XM_001478331
8.56E-04	6.9007	down	Btg4	Mus musc	NM_019493
0.010293	7.36867	down	Tnfrsf13c	Mus musc	NM_028075
0.008136	1.56651	down	Trmt1	Mus musc	NM_198020
0.010329	1.99313	down		lin-7 hom	AK077191
0.049119	1.89694	down	Vmn1r183	Mus musc	NM_203489

0.021435	14.6049	down	LOC63644	PREDICT	XM_911832
0.011445	2.57924	down		S100P bir	AK139097
0.036577	2.33577	down	Trav3n-3	Mus musc	AK037357
0.014204	5.0256	down	Troap	Mus musc	NM_030159
0.049227	5.53604	down	Olfr39	Mus musc	NM_146825
0.037078	4.19229	down		lincRNA:chr5:22890322-22939119 reverse strand	
0.044517	7.2495	down	Gm2715	PREDICT	XM_001474506
0.036937	2.9351	down	F2rl3	Mus musc	NM_007975
0.024304	12.474	down		lincRNA:chrX:120590872-120598071 reverse strand	
0.044601	5.94936	down	Gml	GPI anch	BC171937
0.006786	1.50211	down	2610035D	Mus musc	NR_015556
0.009575	1.61631	down		lincRNA:chr12:21548850-21568550 reverse strand	
0.042003	2.49293	down		lincRNA:chr6:40693617-40720167 forward strand	
0.044516	2.05313	down	Xaf1	Mus musc	NM_001037713
0.042265	1.71789	down	Scn11a	Mus musc	NM_011887
0.03822	1.50487	down	Pappa2	Mus musc	NM_001085376
0.041069	6.78282	down	LOC10004	Mus musc	NM_001160142
0.021092	1.95648	down	Cd6	Mus musc	NM_009852
0.002904	5.40774	down		lincRNA:chr10:60473030-60535340 forward strand	
0.046625	2.4115	down		lincRNA:chr8:91569369-91594119 forward strand	
0.021566	2.72849	down	Zfp672	Mus musc	NR_028331
0.024516	5.489	down		Mus musc	U18577
0.02512	2.60825	down	LOC10004	PREDICT	XM_001476052
0.031651	1.59998	down	Gm2598	PREDICT	XM_001474084
0.026671	1.60058	down	Nr1d1	Mus musc	NM_145434
0.042717	2.10197	down		lincRNA:chr11:16838587-16850933 reverse strand	
0.037177	1.61067	down	Cmya5	Mus musc	NM_023821
0.004971	1.50131	down		lincRNA:chr5:113594167-113645342 forward strand	
0.007859	3.28448	down	Cenpm	Mus musc	NM_178269
0.042506	5.59216	down	LOC54490	VDJ com	XM_914633
0.049283	5.51438	down	Ms4a1	Mus musc	NM_007641
0.036402	2.20539	down	Syt1	Mus musc	NM_009306
0.040329	3.69395	down		Putative u	AK084071

0.020038	1.98918	down	5330426L	PREDICT	XR_035439
0.041459	1.68357	down	Gpr68	Mus musc	NM_175493
0.036727	1.54501	down		protein ki	AK076352
0.032283	5.60959	down		lincRNA:chr7:30645026-30667034	reverse strand
0.027845	3.50433	down		Novel pro	XM_001473318
0.01105	3.71732	down		lincRNA:chr5:31856417-31916414	forward strand
0.046657	3.4363	down	Cc2d2b	PREDICT	XM_001000795
0.019149	2.70765	down		lincRNA:chr18:47327300-47333819	forward strand
0.017798	2.43276	down	Hist1h2al	PREDICT	XR_035232
0.010288	1.81808	down	Sct	Mus musc	NM_011328
0.003713	2.18349	down	Dact2	Mus musc	NM_172826
0.007532	1.7699	down		lincRNA:chr8:122920901-123008463	reverse strand
0.009608	2.43039	down		lincRNA:chr12:111824094-111838478	forward strand
0.031789	1.90718	down		lincRNA:chr3:34793853-34800591	forward strand
0.036546	3.59039	down		lincRNA:chr5:149751979-149808240	reverse strand
0.031755	1.76756	down	Kif24	Mus musc	NM_024241
0.026127	2.45836	down		lincRNA:chr17:86219507-86220112	forward strand
0.047107	2.1336	down		lincRNA:chr17:15226181-15250333	reverse strand
0.04987	2.26531	down	4930429B	Mus musc	NR_027966
0.021073	2.5371	down	Oprl1	Mus musc	NM_011012
0.043168	1.58132	down	Gm4072	PREDICT	XM_001479342
0.023356	2.13164	down		lincRNA:chr1:139814266-139817889	reverse strand
0.04585	1.97181	down		lincRNA:chr9:67414463-67483185	reverse strand
0.00206	12.2244	down		immunog	AF296422
0.03702	1.8086	down		lincRNA:chr17:88466300-88495175	reverse strand
0.013741	3.35493	down	Col25a1	Mus musc	NM_029838
0.032134	1.97367	down	Gm7716	PREDICT	XM_978208
0.002034	11.3614	down	Gm5957	PREDICT	XM_001476729
0.013651	6.71895	down		Igk protei	S60874
0.024669	1.83803	down		lincRNA:chr12:73789535-73799787	forward strand
0.04499	2.77022	down	4930529I2	Mus musc	AK015936
0.031447	2.01014	down	Dmbx1	Mus musc	NM_130865
0.027685	4.10857	down		olfactory	BC108946

0.011464	13.1235	down		Mus musc	U18569
0.04897	1.62325	down	Ldlrad2	Mus musc	NM_001033979
0.041116	2.18691	down		lincRNA:chr13:112717680-112733330 forward strand	
0.04937	2.08274	down	Dact1	Mus musc	NM_021532
0.009947	3.18709	down	Gm3002	Mus musc	NR_033388
0.031211	2.24274	down	LOC10004	PREDICT	XM_001473112
0.028325	9.05648	down	4921515L2	Mus musc	AK014901
0.048657	2.00462	down	Gm7303	PREDICT	XM_925112
0.018006	2.94937	down	4930414F1	Mus musc	AK019576
0.025555	3.22165	down		lincRNA:chr6:31001656-31002219 reverse strand	
0.040922	5.15955	down	Fmr1nb	Mus musc	NM_174993
0.031572	1.60042	down		lincRNA:chr7:126872550-126886125 reverse strand	
0.015181	3.02573	down	Gm16462	PREDICT	XM_001476250
0.03743	2.00961	down	Folr1	Mus musc	NM_008034
0.001285	1.62184	down		lincRNA:chr1:13058312-13099826 forward strand	
0.035131	2.51002	down	Gm5606	PREDICT	XM_489223
0.038801	3.0965	down	Gm7990	PREDICT	XR_030829
0.038748	4.36895	down		lincRNA:chr5:22890322-22939119 reverse strand	
0.040948	5.52496	down	Hjurp	Mus musc	NM_198652
0.006087	4.77965	down	LOC64061	PREDICT	XM_917662
0.013558	1.53602	down	E030046B	Mus musc	AK053225
0.00563	2.67616	down		lincRNA:chr18:73870981-73877247 forward strand	
0.011627	2.2623	down	LOC10004	PREDICT	XM_001479348
0.035035	1.65642	down	Fbxo34	Mus musc	NM_001146085
0.043783	1.82119	down	Il19	Mus musc	NM_001009940
0.02472	2.38426	down		lincRNA:chr15:85534202-85537090 forward strand	
0.005708	2.97359	down		lincRNA:chr15:85412264-85549139 reverse strand	
0.002369	3.39094	down		lincRNA:chr5:31856417-31916317 forward strand	
0.022266	2.5017	down		lincRNA:chr3:41325168-41332366 reverse strand	
0.015779	2.45712	down	Mapk1ip1	Mus musc	NM_178684
0.003464	1.52459	down	Gm13710	PREDICT	XM_001475504
0.02578	1.66957	down		lincRNA:chr10:6081900-6105500 forward strand	
0.035441	1.76551	down		T-cell rec	GU599645

0.014759	2.77592	down	Gm7544	PREDICT	XM_975463
0.026015	1.96167	down		Putative u	AK015696
0.004706	2.18151	down	2900001G	Mus musc	AK013461
0.03129	1.81346	down	Mybl2	Mus musc	NM_008652
0.032049	2.36506	down	Zkscan2	Mus musc	NM_001081329
0.04773	3.91361	down	Cacna1s	Mus musc	NM_001081023
0.005996	2.18248	down		lincRNA:chr18:60812427-60819775 reverse strand	
0.020279	2.59865	down	LOC43295	Mus musc	AK041852
0.010581	1.61705	down		lincRNA:chr13:108577843-108679708 reverse strand	
0.037149	2.46224	down		lincRNA:chr10:118385588-118439338 forward strand	
0.01995	2.3775	down	5033425G	PREDICT	XM_001475910
0.009925	2.93494	down	Rims1	Mus musc	NM_053270
0.048921	3.65389	down	Gm8028	PREDICT	XM_977531
0.02883	1.54391	down	Emilin3	Mus musc	NM_182840
0.030555	2.45394	down	Nwd1	NACHT a	BC144786
0.026936	2.28044	down	Arhgdig	Mus musc	NM_008113
0.012579	16.6386	down		PREDICT	XM_001004859
0.003853	3.09809	down	Olfr1415	Mus musc	NM_001011525
0.00956	1.6625	down	LOC10004	PREDICT	XM_001474431
0.016824	5.45064	down		immunog	AY170578
0.035912	2.2141	down	C87490	H3058B0	BG080844
0.004539	2.94356	down		lincRNA:chr10:39659425-39674200 forward strand	
0.037628	3.12572	down		lincRNA:chr11:102878974-102888924 forward strand	
0.012185	2.391	down		lincRNA:chr2:155298877-155303251 forward strand	
0.007648	2.07777	down		Mouse Ig	E10834
0.019377	1.90454	down		lincRNA:chr4:3406175-3443875 forward strand	
0.021141	2.28079	down		lincRNA:chr5:52584616-52595441 reverse strand	
0.012481	8.33231	down	4930445G	Mus musc	AK015390
0.024627	1.61534	down		lincRNA:chr11:31647436-31647791 reverse strand	
0.027569	2.97117	down	Gm16525	PREDICT	XM_001477897
0.04439	2.0542	down		Ig heavy c	FM179587
0.032811	2.06382	down		lincRNA:chr6:90848183-90861277 reverse strand	
0.004981	1.68632	down		lincRNA:chrX:50407969-50410370 reverse strand	

0.046052	1.86542	down		lincRNA:chr10:41368681-41393645 reverse strand	
0.013421	2.01644	down		lincRNA:chr1:95871175-95886625 reverse strand	
0.019561	22.3999	down		Igk protein X75105	
0.020397	5.03657	down	Gm3099		XM_001475922
0.049529	3.89281	down	LOC10004	PREDICT	XM_001477170
0.043441	2.5299	down	Gm6810	PREDICT	XM_892615
0.0058	2.13112	down	B930007M	Mus musc	NM_198659
0.035666	3.04312	down	2010012P1	Mus musc	AK008218
0.00114	2.27051	down		lincRNA:chr1:137482591-137625604 reverse strand	
0.017669	2.78902	down	Tmem200	PREDICT	XM_001480132
0.013616	3.36424	down	LOC10004	PREDICT	XM_001479909
0.027595	2.37162	down		lincRNA:chr13:103101941-103102362 forward strand	
0.029469	2.74272	down	Lzts1	Mus musc	NM_199364
0.01661	1.54925	down		lincRNA:chrX:11671167-11700242 reverse strand	
0.007068	3.28489	down	Magea1	Mus musc	NM_020015
0.033381	2.63652	down		Putative u	AK149623
0.031591	2.28233	down	Nfe2	Mus musc	NM_008685
0.004801	2.61215	down	H2-DMb2	Mus musc	NM_010388
0.01152	7.77915	down		PREDICT	XM_911832
0.025648	3.69788	down	4930547M	PREDICT	XM_001476789
0.006222	3.0161	down	LOC10003	Mus musc	AK016549
0.029911	1.8738	down	G630055G	Mus musc	AK090337
0.00963	1.52088	down		lincRNA:chr9:88575075-88611650 forward strand	
0.026822	1.83054	down		lincRNA:chr6:50339188-50409363 forward strand	
0.029852	1.66236	down		peroxisomal biogenesis factor 5-like Gene [Source:MGI (curated);Acc:MGI:1916672] [ENSEM	
0.042299	1.8268	down	A730028G	Mus musc	AK042831
0.015076	1.95659	down		lincRNA:chr13:114111261-114117957 forward strand	
0.019109	14.5148	down	LOC10003	PREDICT	XM_001473640
0.009587	2.0337	down	Olfm1	Mus musc	NM_001038612
0.044145	1.52023	down	LOC10004	PREDICT	XM_001472387
0.02477	3.92546	down		lincRNA:chr2:35828611-35838083 forward strand	
0.014525	5.83614	down	Mlf1ip	Mus musc	NM_027973
0.012335	3.66063	down	4933437N	AGENCC	CN842534

0.018461	2.32312	down	A430093F	Mus musc	NR_027805
0.046221	2.2018	down		lincRNA:chr10:95144321-95202671 reverse strand	
0.018306	2.89384	down	Gm3411	PREDICT	XM_001476596
0.02435	3.01028	down		phospholi	AK039149
1.99E-04	3.95578	down	Gm7144	PREDICT	XM_090565
0.022874	2.36366	down	H1fx	Mus musc	NM_198622
0.00355	2.06967	down	LOC10004	nudix (nu	XM_001478680
0.004701	9.80314	down		lincRNA:chr13:66381200-66410200 reverse strand	
0.017151	2.20143	down	Gm5222	Mus musc	U76382
0.044366	1.89111	down	Sep-01	Mus musc	NM_017461
0.013892	2.31522	down		lincRNA:chr8:86705694-86711244 forward strand	
0.044586	2.25134	down	Gm8008	PREDICT	XM_001477516
0.026133	1.8697	down		lincRNA:chr8:129336539-129400338 reverse strand	
0.019872	2.81433	down		lincRNA:chr5:123440192-123451767 reverse strand	
0.021213	1.96961	down	Sass6	Mus musc	NM_028349
0.01593	2.12804	down	Slco1a4	Mus musc	NM_030687
0.016609	2.84323	down	2700068H	Mus musc	AK012503
0.032252	5.80816	down			
0.03648	3.5531	down	Smcr8	Mus musc	NM_175491
0.048594	3.26826	down		lincRNA:chr10:126151060-126156450 reverse strand	
0.007866	2.20657	down	F2rl3	Mus musc	NM_007975
0.005487	10.8191	down		lincRNA:chrX:120812236-121038407 reverse strand	
0.015446	2.22302	down		Putative u	AK036529
0.041436	3.18119	down		lincRNA:chr6:86477309-86537554 reverse strand	
0.01527	1.87592	down	LOC10004	PREDICT	XR_033326
0.043811	1.91488	down	Gm4703	PREDICT	XM_001481156
0.021787	1.74029	down	Rnf213	PREDICT	XM_001476651
0.034128	2.62059	down		lincRNA:chr8:110197171-110206546 reverse strand	
0.036685	4.81303	down	Slc25a37	Mus musc	NM_026331
0.012646	1.97123	down	Ggt6	Mus musc	NM_027819
0.028887	1.69742	down		lincRNA:chrX:35825525-35877700 reverse strand	
0.014227	1.96765	down	A830035A	PREDICT	XM_986896
0.046064	2.50197	down		lincRNA:chr18:36470130-36489110 forward strand	

0.001006	2.31237	down		topoisome	AK164443
0.004459	2.12421	down		lincRNA:chr9:61881173-61881351	reverse strand
0.004342	3.67217	down	Ltb4r2	Mus musc	NM_020490
0.029618	1.56905	down	Pde11a	Mus musc	NM_001081033
0.002725	2.46728	down	B230104I2	Mus musc	AK140029
0.04589	2.64936	down	Kcne1l	Mus musc	NM_021487
0.045003	3.37215	down	Gm6745	PREDICT	XR_033591
0.011124	3.36244	down		lincRNA:chr12:77544397-77564122	reverse strand
0.032221	2.07763	down		Eph recep	AK134673
0.007897	2.1243	down	Slc10a7	Mus musc	NM_029736
0.04677	1.74909	down	6530401N	Mus musc	NM_029545
0.026175	2.4825	down	AI451458	UI-M-FY	CA328248
0.042205	5.63706	down	D3Bwg05	Mus musc	NM_177664
7.26E-04	2.69383	down	Gm12128	PREDICT	XM_001472488
0.039828	3.74767	down		predicted	XM_915944
0.02781	2.43357	down		lincRNA:chr3:35236023-35241498	reverse strand
0.013857	1.74689	down		lincRNA:chr3:126989696-127112471	reverse strand
0.001151	2.97063	down	Fam19a3	Mus musc	NM_183224
0.00229	2.55199	down		MDIGGVBC immunoglobulin variable region {Mus musculus domesticus}	(exp=-1; wgp=0;
0.005931	1.78448	down	LOC62995	PREDICT	XM_905767
0.018701	2.09009	down		lincRNA:chr12:110973190-110987668	forward strand
0.022393	1.76864	down	Ssxb9	Mus musc	NM_199066
0.036296	4.67599	down		lincRNA:chr8:126396600-126407275	forward strand
0.034377	2.18372	down		lincRNA:chr11:112898724-113062945	reverse strand
0.03932	2.359	down	Gm14124	Mus musc	NM_001142410
0.019123	2.56886	down		Putative u	AK030541
0.039985	4.0063	down		lincRNA:chr8:10886200-10905925	reverse strand
0.022844	4.06767	down		lincRNA:chr9:65089730-65091897	reverse strand
0.026842	1.90255	down	Krtap16-8	Mus musc	NM_130856
0.020578	3.08254	down		lincRNA:chr16:9249688-9275013	reverse strand
0.032267	2.26867	down		lincRNA:chr19:4209657-4210475	reverse strand
0.039637	1.57472	down	B3gat2	Mus musc	NM_172124
0.029951	2.8277	down		lincRNA:chr13:31736054-31781679	reverse strand

0.030463	1.95988	down		lincRNA:chr11:6421951-6429173 forward strand
0.006295	2.45792	down		lincRNA:chr2:172343878-172344212 reverse strand
0.041052	3.41947	down	Il12rb2	Mus musc NM_008354
0.04053	2.93095	down		lincRNA:chr17:87483814-87493039 forward strand
0.017632	1.79863	down	Gm3230	Mus musc NR_033642
0.034696	1.66007	down		lincRNA:chr4:128060015-128075590 forward strand
0.012815	3.17516	down		lincRNA:chr4:131737612-131738100 reverse strand
0.042559	2.98734	down	LOC64006	PREDICT XM_916809
0.013781	1.84813	down	Blm	Mus musc NM_007550
0.042605	1.837	down		Novel member of the keratin associated protein 3 (Krtap3) family [Source:UniProtKB/TrEMBL]
0.028702	2.836	down	Gm3225	PREDICT XM_001476062
0.041625	4.28553	down	4933430A	Mus musc AK016987
0.012803	2.39479	down	Prl3c1	Mus musc NM_001163218
0.027564	2.75188	down	Olfir1441	Mus musc NM_146683
9.56E-04	1.6869	down		lincRNA:chr14:43408099-43415349 forward strand
0.020236	2.33288	down	LOC10004	PREDICT XM_001473350
0.012155	2.98154	down	Gm2571	PREDICT XM_001473997
0.03039	4.20276	down	St8sia2	Mus musc NM_009181
0.045748	1.81445	down		RIKEN cl AK032721
0.003869	3.68763	down		lincRNA:chrX:148732853-148761972 reverse strand
0.016378	1.64376	down		lincRNA:chr12:53700970-53703612 reverse strand
0.02355	1.885	down	C330011M	PREDICT XR_035219
0.041048	3.08209	down	P4ha3	Mus musc NM_177161
0.032719	2.03783	down	Spef2	Mus musc NM_177123
0.025212	1.85497	down	Vash1	Mus musc NM_177354
0.044735	2.86997	down	Gm6811	PREDICT XM_892630
0.001264	6.06868	down	Gm6445	PREDICT XM_001474206
0.044739	2.22304	down		lincRNA:chr12:33808493-33829143 forward strand
0.027458	2.33586	down	Olfir122	Mus musc NM_146288
0.035608	2.05354	down		lincRNA:chr9:96664617-96683617 forward strand
0.040382	2.10778	down	Bzrap1	Mus musc NM_172449
0.027461	2.59406	down		lincRNA:chr12:21548850-21568550 reverse strand
0.021859	1.68904	down		lincRNA:chr7:6296401-6311486 forward strand

0.013885	3.78743	down	Gm2942	PREDICT	XM_001475175
0.026438	2.19287	down			lincRNA:chr1:73437958-73451628 reverse strand
0.044034	2.06387	down			lincRNA:chr3:37547973-37548436 reverse strand
0.041083	2.85389	down			MMU231226 immunoglobulin light chain variable region {Mus musculus} (exp=-1; wgp=0; c
0.008775	2.58019	down			lincRNA:chr2:143963320-143984245 forward strand
0.030797	2.32382	down			lincRNA:chr8:41941084-41947630 reverse strand
0.002248	2.05525	down	1700003G	Mus musc	AK012020
0.00544	2.67531	down			lincRNA:chr7:149108190-149123890 forward strand
0.045336	1.59039	down			lincRNA:chr3:60292527-60292880 reverse strand
0.033123	1.79242	down	Gm6225	Mus musc	NR_033457
0.025551	3.52407	down	4930555G	Mus musc	NM_175393
0.015693	2.06057	down	Gm7694	PREDICT	XM_001001448
0.027296	2.23805	down			lincRNA:chr13:104591573-104599048 reverse strand
0.047301	2.79719	down			lincRNA:chr17:13020750-13033750 forward strand
0.047669	2.04294	down			lincRNA:chr4:135896689-135918414 reverse strand
0.032666	3.52988	down			lincRNA:chr2:84344350-84370075 reverse strand
0.038571	1.9159	down			glutathione S-transferase, mu 6 Gene [Source:MGI (curated);Acc:MGI:1309467] [ENSMUST
0.006062	3.08957	down			lincRNA:chr7:132218864-132329172 forward strand
0.036316	4.94603	down			lincRNA:chr5:22890322-22939119 reverse strand
0.008173	2.97669	down	Fpr-rs3	Mus musc	NM_008040
0.03183	2.28609	down			lincRNA:chr10:81165750-81236400 forward strand
0.023049	1.72157	down			lincRNA:chr13:62734450-62785325 reverse strand
0.02109	2.10739	down			lincRNA:chr9:37071677-37072244 reverse strand
0.040456	3.27683	down			lincRNA:chr5:124667541-124700029 forward strand
0.029061	2.61855	down	Olfr476	Mus musc	NM_146924
0.012523	2.38788	down	9430008C	Mus musc	NR_015463
0.029432	2.25772	down	LOC63533	PREDICT	XM_910366
0.022216	1.68395	down			lincRNA:chr1:94077221-94091396 reverse strand
0.045128	1.56125	down	Clip4	Mus musc	NM_030179
0.041285	3.39944	down			lincRNA:chr5:125078875-125098525 reverse strand
0.020348	3.89693	down			lincRNA:chr8:49853937-49874087 reverse strand
0.038863	1.71827	down	9.13E+15	Mus musc	AK018644
0.025728	4.68415	down	Clec4a2	Mus musc	NM_001170333

0.031578	1.93918	down	Gm4123	PREDICT	XM_001479696
0.041977	1.71604	down	Xrcc2	Mus musc	NM_020570
0.033487	1.56782	down	Gm9077	PREDICT	XR_031680
0.022672	2.63585	down	Otog	Mus musc	NM_013624
0.034459	1.81282	down	LOC10004	PREDICT	XM_001473884
0.023212	3.38556	down	Kndc1	Mus musc	NM_177261
0.037385	2.54788	down		lincRNA:chr4:54851872-54866706	reverse strand
0.019746	1.5316	down	Slc1a6	Mus musc	NM_009200
0.033467	4.4276	down		lincRNA:chr8:13507348-13543773	reverse strand
0.038768	3.10557	down		keratin as	XM_001474426
0.044231	2.4103	down	1700092C	AGENCC	CD772809
0.027977	3.24147	down		Putative u	AK019581
0.011021	1.95955	down		lincRNA:chr3:30032959-30079659	forward strand
0.002973	1.95436	down		lincRNA:chr5:122047900-122065325	forward strand
0.003834	1.58847	down		lincRNA:chr18:60906766-60920702	forward strand
0.017633	3.62551	down	BB217526	Mus musc	AK083592
0.030007	2.09345	down		plastin 1 (I-isoform)	Gene [Source:MGI (curated);Acc:MGI:104809] [ENSMUST0000011976]
0.006016	3.4485	down	BB557941	Mus musc	AK163349
0.011887	2.87821	down		lincRNA:chr7:140011140-140018815	reverse strand
0.001563	5	down	Olfr312	Mus musc	NM_001011819
0.032431	2.87269	down	1700066J0	AGENCC	CN840722
0.047917	7.6678	down	4930455J1	Mus musc	AK030052
0.011408	1.70609	down	Lta	Mus musc	NM_010735
0.020758	2.97194	down	Gm4434	PREDICT	XM_001476831
0.044572	2.34266	down	Gm831	PREDICT	XM_001477145
0.023539	2.19281	down	E030025P	Mus musc	NM_001085512
0.022823	1.55713	down	Lmnbl	Mus musc	NM_010721
0.039511	5.1114	down	LOC63774	PREDICT	XM_913514
0.041447	1.55154	down		lincRNA:chr13:94193230-94193710	forward strand
0.024284	2.5314	down	Wfikkn2	Mus musc	NM_181819
0.003769	5.53779	down		lincRNA:chr13:56286339-56298089	forward strand
0.008264	2.82315	down		lincRNA:chr14:115423660-115463160	reverse strand
0.010895	2.04651	down	Rrad	Mus musc	NM_019662

0.025117	7.84824	down		lincRNA:chr16:50715231-50841124 reverse strand
0.043274	3.08232	down	Olfr18	Mus musc NM_146563
0.033196	2.63704	down		
0.006876	4.71367	down	AI450886	vv70h06.x AI604347
0.006863	1.87006	down		lincRNA:chr18:38836368-38935650 forward strand
0.024986	1.71705	down		lincRNA:chr16:64758224-64765700 forward strand
0.001518	1.69139	down	Gm9444	PREDICT XM_001479912
0.023004	1.59629	down	Cdh15	Mus musc NM_007662
0.012335	2.97627	down	3110009E	Mus musc NM_001172074
0.027705	2.10811	down		lincRNA:chr6:148162552-148176577 forward strand
0.036567	1.77116	down		lincRNA:chr10:60473030-60535340 forward strand
0.007235	3.33978	down		PREDICT XM_001472731
0.04587	2.21901	down	Gm8350	PREDICT XM_986833
0.017969	3.40328	down	Foxp3	Mus musc NM_054039
0.005581	2.55547	down		lincRNA:chr13:104591573-104599048 reverse strand
0.017819	2.05735	down	LOC10004	PREDICT XM_001480694
0.021478	1.99108	down		lincRNA:chr3:95443575-95462543 reverse strand
0.020202	5.20514	down		lincRNA:chr6:126766225-126771309 forward strand
0.029721	4.59154	down		lincRNA:chr13:19618491-19618836 reverse strand
0.013628	4.44334	down	Gm7356	PREDICT XM_972876
0.029878	3.12089	down	Gsdma2	Mus musc NM_029727
0.008169	2.73695	down		lincRNA:chrX:20389063-20389702 forward strand
0.022625	3.20222	down		lincRNA:chr7:3338500-3360725 reverse strand
0.024043	2.91394	down		lincRNA:chr17:38132217-38157667 reverse strand
0.014694	2.32706	down	Gm2453	PREDICT XM_001473654
0.003236	4.76382	down		lincRNA:chr3:145390505-145398253 forward strand
0.048065	2.10299	down	4921534A	PREDICT XM_001474893
0.008013	2.69448	down		lincRNA:chr7:71093563-71095094 forward strand
0.002049	4.06113	down		lincRNA:chr13:104591573-104599048 forward strand
0.030824	2.80019	down	Fam165b	family with sequence similarity 165, member B Gene [Source:MGI (curated);Acc:MGI:19161
0.048639	8.76633	down	Gm8090	PREDICT XM_001472293
0.028316	18.5421	down	LOC10004	PREDICT XR_031612
0.047205	8.14149	down	Hs3st6	Mus musc NM_001012402

0.048079	1.99477	down	Krtap20-2	Mus musc	NM_001163615
0.009409	1.638	down	Rgs16	Mus musc	NM_011267
0.044438	2.69666	down	Gm4590	PREDICT	XM_001478833
0.033079	4.42494	down		PREDICT	XM_898698
0.004335	7.00833	down		RIKEN cl	AK015114
0.042409	4.87909	down		PREDICT	XM_001477132
0.009441	9.69828	down	LOC10004	PREDICT	XM_001477334
0.004087	1.97848	down	Ogdhl	Mus musc	NM_001081130
0.031649	3.10906	down		Ig heavy c	XM_001477926
0.036074	1.66098	down	Rap1gap	Mus musc	NM_001081155
0.040695	2.24727	down		lincRNA:chr15:77575125-77585575 forward strand	
0.028882	3.23054	down	Olfr700	Mus musc	NM_146600
0.02795	2.17633	down	Mageb1	Mus musc	NM_010759
0.036891	1.61523	down	Hbb-y	Mus musc	NM_008221
0.04585	3.07505	down		lincRNA:chrX:121970356-121970881 reverse strand	
0.031803	1.72252	down	G2e3	Mus musc	NM_001167963
0.003344	2.26796	down	LOC10004	PREDICT	XM_001479936
0.039679	2.28155	down	Vangl2	Mus musc	NM_033509
0.038806	2.21461	down	Atp12a	Mus musc	NM_138652
0.039927	4.13203	down		lincRNA:chr13:53100475-53113850 reverse strand	
0.006002	3.27634	down	2010001M	Mus musc	NM_027222

00062071]

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90] [ENSMUST000000109516

1UST00000108219

cg=0), complete [TC1725107

BL;Acc:A2A592] [ENSMUST00000104931

g=0), complete [TC170642

00000106680]

ProbeName	p-value (T)	FCAbsolute	regulation	p-value (T)	FCAbsolute	regulation	GeneSym	Description	GenbankAccession
A_52_P22	0.020352	6.997649	up	0.006445	2.837351	up	Synpo2	Mus musc	NM_080451
A_55_P20	0.018867	30.17038	up	0.002392	6.861074	up	Sfrp5	Mus musc	NM_018780
A_55_P20	0.039601	9.651007	up	0.009316	6.103708	up	Mest	Mus musc	NM_008590
A_55_P21	0.026741	2.378243	up	4.24E-04	1.580225	up	Fbxo27	Mus musc	NM_001163702
A_51_P18	0.032049	14.63608	up	0.015378	5.512877	up	F12	Mus musc	NM_021489
A_55_P20	0.046299	2.680934	up	0.045161	2.260174	up	Insc	Mus musc	NM_173767
A_51_P47	0.026272	34.22065	up	0.024605	3.481148	up	1110059M	Mus musc	NM_026841
A_51_P34	0.030235	25.35479	up	0.018639	10.61975	up	Apoh	Mus musc	NM_013475
A_51_P48	0.042738	3.85918	up	0.037255	2.393296	up	Pramef12	Mus musc	NM_029948
A_30_P01	0.040558	2.580427	up	0.01153	5.20555	up		lincRNA:chr17:38132217-38157667 forward strand	
A_30_P01	0.043236	4.398212	up	0.023703	1.81637	up		lincRNA:chr4:149445201-149445902 forward strand	
A_51_P36	0.027106	11.56796	up	0.006545	5.274117	up	Klf14	Mus musc	NM_001135093
A_30_P01	0.02813	1.940611	up	0.003062	2.691802	up		lincRNA:chr3:131153358-131154061 forward strand	
A_55_P22	0.002059	2.77254	up	0.003518	21.84637	up	4933438K	Mus musc	AK017111
A_55_P20	0.01053	42.8246	up	0.007065	76.21433	up	Slc5a7	Mus musc	NM_022025
A_66_P13	0.031165	2.274826	up	0.049103	2.4745	up	Olfm1	Mus musc	NM_019498
A_55_P22	0.027109	2.217311	up	0.012597	2.430355	up	Tsc22d2	Mus musc	NM_001081229
A_55_P20	0.016533	21.42756	up	0.001464	8.011006	up	Gm5627	Mus musc	NR_033301
A_66_P11	0.020705	1.66222	up	0.027487	3.298353	up	Optn	Mus musc	NM_181848
A_51_P12	0.047564	9.542769	up	0.016945	7.042808	up	Mest	Mus musc	NM_008590
A_55_P20	0.049641	2.583586	up	0.00471	1.671665	up	Unc79	Mus musc	NM_001081017
A_55_P20	0.026789	11.26092	up	0.001418	5.993639	up	Duoxa1	Mus musc	NM_145395
A_55_P19	0.017389	10.56868	up	0.008841	4.64745	up	Lctl	Mus musc	NM_145835
A_30_P01	0.022495	4.182756	up	0.048521	1.808037	up		lincRNA:chr4:149445201-149445902 forward strand	
A_52_P87	0.031349	2.996408	up	0.008502	3.609168	down	Mfsd4	Mus musc	NM_001114662
A_52_P49	0.011389	2.191009	up	0.039177	1.887489	up	Hist1h2ak	Mus musc	NM_178183
A_66_P11	0.011367	3.2116	up	0.019483	1.737327	up	Tmem91	Mus musc	NM_177102
A_51_P47	0.029774	3.409516	up	0.035746	1.814362	up	Duox1	Mus musc	NM_001099297
A_51_P15	0.04445	2.015776	down	0.019271	2.978861	down	2010002N	Mus musc	NM_134133
A_55_P20	0.005751	2.462439	down	0.008958	2.787504	down		cathepsin	AK152524
A_30_P01	0.029467	1.805069	down	0.019803	1.932499	down		lincRNA:chr2:126501651-126510026 forward strand	
A_55_P21	0.046504	1.5518	down	0.036925	1.578272	down	Gem	Mus musc	NM_010276

A_30_P01	0.022435	2.127077	down	8.21E-04	1.733717	down		lincRNA:chr19:5771425-5848475 reverse strand
A_52_P29	0.004641	1.502998	down	0.026818	1.816779	down	Tshz2	Mus musc NM_080455
A_52_P49	0.045582	2.272059	down	0.021387	2.056476	down	Efnb3	Mus musc NM_007911
A_55_P20	0.046868	1.740295	down	0.021494	1.534934	down	importin 1	AK164311
A_55_P20	0.039543	1.734446	down	0.020871	1.984448	down	Gm5736	Mus musc NM_001127686
A_30_P01	0.029485	2.327699	down	0.008448	1.64366	down		lincRNA:chr15:83281223-83284791 reverse strand
A_55_P20	0.013074	1.522112	down	0.015507	1.606307	down		kinesin lig BC005746
A_55_P20	0.008224	2.389522	down	0.00342	3.014663	down	Zfhx4	Mus musc NM_030708
A_55_P21	0.009938	1.70741	down	0.009584	2.329048	down	Palm3	Mus musc NM_028877
A_66_P13	0.02715	1.744258	down	0.039641	1.729682	down	Rbm4b	Mus musc NM_025717
A_51_P43	0.048647	5.457607	down	0.020512	4.032059	down	Tst	Mus musc NM_009437
A_55_P20	0.00796	2.340081	down	0.005159	1.672594	down	Malat1	Mus musc NR_002847
A_55_P19	0.017938	1.66279	down	0.049103	2.155626	down	Pkdcc	Mus musc NM_134117
A_51_P29	0.018908	1.844106	down	0.049655	1.696548	down	Col4a3	Mus musc NM_007734
A_55_P19	0.00988	2.213296	down	0.022451	2.977324	down	Pappa2	Mus musc NM_001085376
A_55_P21	0.00103	1.583343	down	0.038143	1.659291	down	2610027L	Mus musc NM_026403
A_55_P21	0.00198	2.880586	down	0.040999	3.633428	down	Prrt1	proline-ric AK137892
A_30_P01	0.034603	2.341814	down	0.010076	1.888873	down		lincRNA:chr19:5795689-5802671 reverse strand
A_52_P48	0.035443	1.996649	down	0.007866	1.51332	down	Col27a1	Mus musc NM_025685
A_55_P20	0.001688	1.519339	down	0.014171	1.634846	down	Zfp879	Mus musc NM_173387
A_55_P24	0.011477	2.368812	down	0.036711	1.840407	down	2210416C	Mus musc AK008958
A_55_P20	0.033639	1.671655	down	7.63E-05	2.303089	down	Egflam	Mus musc NM_178748
A_55_P22	0.002865	2.602618	down	0.04331	3.861574	down	A530020C	Mus musc AK040960
A_55_P19	0.002609	1.5718	down	0.034813	1.633375	down		POGZ_MOUSE (Q8BZH4) Pogo transposable elem
A_55_P22	0.043158	1.627047	down	0.023638	2.030979	up	LOC4329	Mus musc AK041852
A_52_P17	0.036702	2.282385	down	0.048283	2.098507	down	Lrp3	Mus musc NM_001024707
A_55_P20	0.009917	1.57443	down	0.028396	1.568824	down	LOC6742	PREDICT XM_972872
A_30_P01	0.003557	1.898964	down	0.013273	2.390628	down		lincRNA:chr7:77555482-77634858 forward strand
A_52_P55	9.68E-04	2.284548	down	0.024515	3.442781	down	Tspan11	Mus musc NM_026743
A_55_P20	0.025246	2.119523	down	0.025397	4.117753	down		XM_356827
A_51_P23	0.029623	1.957595	down	0.012082	2.268032	down	Pla2g2d	Mus musc NM_011109
A_55_P20	0.047199	1.861423	down	0.002747	1.730653	up	Gm10621	Putative u XM_001476249
A_52_P73	0.010012	3.483243	down	0.021004	2.186735	down		WD repea AK077037

A_52_P62	0.041167	2.344954	down	0.046408	2.72684	down	Tgm1	Mus musc	NM_019984
A_30_P01	0.009982	2.047901	down	0.006463	1.762302	down		lincRNA:chr19:5795689-5802671 reverse strand	
A_52_P49	0.033122	1.660584	down	0.0378	1.614381	down	Peo1	Mus musc	NM_153796
A_30_P01	0.034932	1.765889	down	0.0286	1.616208	down		lincRNA:chr8:47813487-47824869 forward strand	
A_55_P21	0.035308	2.056955	down	0.003902	2.367988	down	Pla2g2d	Mus musc	NM_011109
A_55_P21	0.029857	9.214009	down	0.026686	7.422753	down	Hpca	Mus musc	NM_001130419
A_51_P49	0.022413	3.43587	down	0.039718	3.145469	down	Plekhb1	Mus musc	NM_013746
A_30_P01	0.007461	2.131582	down	0.005871	1.701044	down		lincRNA:chr19:5795689-5802671 reverse strand	

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ent with ZNF domain, partial (4%) [TC1612650]

ProbeName	p-value (T)	FCAbsolute	regulation	GeneSymbol	Description	GenbankAccession
A_52_P20	0.0076	1.60623	up	Nova1	Mus musc	NM_021361
A_52_P64	0.04168	2.04223	up	Sox14	Mus musc	NM_011440
A_55_P20	0.04113	1.6563	up	Gm2382	Mus musc	NM_001128601
A_55_P19	0.03495	1.85377	up	Lym5	Mus musc	NM_001163628
A_30_P01	0.04833	2.62406	up		lincRNA:chr12:111617728-111665403 forward strand	
A_55_P19	0.04845	1.50794	up		PREDICT	XM_001476868
A_55_P19	0.00395	2.45085	up	BC05511	Mus musc	NM_183182
A_52_P51	0.04395	2.05661	up	Cdc42ep1	Mus musc	NM_027219
A_51_P13	0.04686	2.43967	up	Oas1f	Mus musc	NM_145153
A_30_P01	0.01581	1.50417	up		lincRNA:chr6:99472981-99484210 reverse strand	
A_52_P22	0.03129	1.55911	up	Flnb	Mus musc	NM_134080
A_55_P19	0.00423	5.99776	up	LOC1000	PREDICT	XM_001474758
A_55_P19	0.0158	2.60157	up	Klra23	Mus musc	NM_024470
A_55_P19	0.0264	45.2871	up	Rdh7	Mus musc	NM_001150749
A_30_P01	0.0215	2.97733	up		lincRNA:chr4:21683562-21694344 reverse strand	
A_55_P21	0.00676	1.97533	up		Mus musc	AK046125
A_55_P20	0.02333	2.89674	up	Ctbs	Mus musc	NM_028836
A_30_P01	0.01754	1.92007	up		lincRNA:chr19:5001448-5001810 reverse strand	
A_52_P67	0.03315	1.54547	up		RIKEN cl	AK086343
A_30_P01	0.03325	1.80801	up		lincRNA:chr1:163508244-163586072 forward strand	
A_55_P19	0.00686	2.48355	up	Gm5168	Mus musc	NM_001025607
A_52_P31	0.01732	3.90975	up	Saa1	Mus musc	NM_009117
A_30_P01	0.04397	6.4228	up		lincRNA:chr1:85304494-85305390 reverse strand	
A_55_P19	0.0072	2.988	up	Arhgap11	Mus musc	NM_181416
A_55_P19	0.03682	1.693	up	Pla2g4a	Mus musc	NM_008869
A_55_P19	0.04616	2.39182	up		Putative uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:Q6R5E0] [ENSMUST00	
A_55_P19	0.01261	2.28561	up	Robo1	Mus musc	NM_019413
A_66_P11	0.04682	5.08983	up	Gm9054	PREDICT	XM_001001089
A_55_P21	0.04907	1.91238	up	Foxo4	Mus musc	NM_018789
A_55_P20	0.02765	2.22235	up	Oas2	Mus musc	NM_145227
A_51_P47	0.03044	1.79043	up	St8sia6	Mus musc	NM_145838

A_55_P20	0.02023	26.5728	up	Kng1	Mus musc	NM_023125
A_55_P20	0.00677	2.63845	up	Scd3	Mus musc	NM_024450
A_55_P19	0.02076	1.88954	up	Arhgap11	Mus musc	NM_181416
A_55_P20	0.01397	85.3956	up	Mup4	Mus musc	NM_008648
A_55_P20	0.01305	2.25468	up	1700030C	Mus musc	NR_015521
A_30_P01	0.02069	1.53747	up		lincRNA:chrX:98658045-98677545 forward strand	
A_55_P20	0.0054	1.6972	up		cell divisi	AK161246
A_55_P20	0.03428	2.27822	up	Cd97	Mus musc	NM_011925
A_30_P01	0.017	1.98841	up		lincRNA:chr17:38132217-38157667 forward strand	
A_55_P19	0.00191	2.75705	up	Masp2	Mus musc	NM_001003893
A_66_P13	0.04919	2.10953	up		AHNAK	XM_001477593
A_55_P19	0.02427	1.71169	up	D1Ert62	Mus musc	NM_133825
A_66_P10	0.00601	9.23154	up	AW82225	PREDICT	XM_001474711
A_55_P20	0.01583	2.78518	up	Gm9733	Mus musc	NM_001076679
A_55_P19	0.04079	19.4	up	Saa2	Mus musc	NM_011314
A_51_P48	0.0403	1.69673	up	Ifi44	Mus musc	NM_133871
A_55_P19	0.01411	1.90164	up	Me3	Mus musc	NM_181407
A_55_P19	0.03583	1.60882	up		Putative u	AK149124
A_55_P21	0.01497	66.6139	up	Mup-ps3	PREDICT	XR_035681
A_55_P20	0.03497	2.16766	up	Gm3293	PREDICT	XM_001476247
A_55_P20	0.00186	8.26856	up	Klra23	Mus musc	NM_024470
A_55_P20	0.00194	1.6068	up	Fgd3	FYVE, RL	AK157835
A_51_P27	0.00117	2.68677	up	Chst8	Mus musc	NM_175140
A_51_P41	0.02214	1.53422	up	Tmem106	Mus musc	NM_027992
A_55_P20	0.02597	16.1959	up	Mup21	Mus musc	NM_001009550
A_55_P20	0.0285	1.59475	up	LOC1000	PREDICT	XM_001480037
A_55_P20	0.04292	1.72648	up	Gm4452	PREDICT	XM_001480050
A_55_P20	0.00442	1.8631	up	2810433D	Mus musc	NR_033474
A_30_P01	0.03133	1.79967	up		lincRNA:chr1:175705225-175717250 forward strand	
A_30_P01	0.00934	1.73457	up		lincRNA:chr18:46646048-46659873 reverse strand	
A_52_P58	0.01689	2.00261	up	Adcy7	Mus musc	NM_001037724
A_55_P21	0.00339	1.96276	up	Arhgap11	Mus musc	NM_181416

A_51_P43	0.011	1.58395	up	Mapre2	Mus musc	NM_153058
A_51_P27	0.03743	2.96228	up	Gltpd2	Mus musc	NM_146020
A_51_P43	0.03704	2.39763	up	Slc6a13	Mus musc	NM_144512
A_30_P01	0.03237	1.8715	up		lincRNA:chr2:143988645-143993945 reverse strand	
A_51_P50	0.03308	1.96092	up	Pcyox1	Mus musc	NM_025823
A_55_P20	0.00453	1.99969	up	Prrg1	Mus musc	NM_027322
A_51_P23	0.04091	1.95342	up	Phf8	Mus musc	NM_001113354
A_66_P13	0.04285	1.61184	up		demethyl-	AK158380
A_51_P50	0.03562	1.80539	up	Nek2	Mus musc	NM_010892
A_55_P20	0.02924	1.76357	up	Pde7a	Mus musc	NM_001122759
A_51_P49	0.04619	2.39702	up	Dnmt3l	Mus musc	NM_019448
A_30_P01	0.02922	1.97938	up		lincRNA:chr11:69184157-69201732 reverse strand	
A_30_P01	0.0496	1.61384	up		lincRNA:chr14:65785477-65815777 reverse strand	
A_55_P20	0.0474	1.79338	up	Gstm1	Mus musc	NM_010358
A_55_P20	0.04611	3.2554	up	Itih5	Mus musc	NM_172471
A_30_P01	0.04003	1.58085	up		lincRNA:chr8:35652473-35703370 reverse strand	
A_51_P21	0.03622	1.5069	up	Hbp1	Mus musc	NM_177993
A_30_P01	0.03193	1.6102	up		lincRNA:chr2:77146893-77155643 reverse strand	
A_30_P01	0.02173	1.91623	up		lincRNA:chr2:156654675-156665430 reverse strand	
A_51_P30	0.02126	2.22376	up	Atp8a2	Mus musc	NM_015803
A_52_P41	0.03275	61.3259	up	Mup5	Mus musc	NM_008649
A_55_P20	0.00649	5.15801	up	Klra4	Mus musc	NM_010649
A_55_P19	0.02359	2.06469	up	1700057K	Mus musc	NM_028540
A_51_P38	0.03227	1.55615	up	Olfr187	Mus musc	NM_146322
A_66_P11	0.00536	1.83459	up	Adora2b	Mus musc	NM_007413
A_55_P21	0.02737	2.43191	up		cDNA seq	AK137204
A_55_P21	0.00817	1.94839	up	Fam174a	Mus musc	NM_026321
A_30_P01	0.02505	1.81117	up		lincRNA:chr13:74712775-74728450 forward strand	
A_55_P20	0.03223	2.02037	up	LOC1000	PREDICT	XM_001473814
A_51_P18	0.01168	2.14285	up	Olfr531	Mus musc	NM_146953
A_30_P01	0.01132	1.56076	up		lincRNA:chrX:90997595-91009570 reverse strand	
A_30_P01	0.00955	2.05919	up		lincRNA:chr16:11024315-11055740 forward strand	

A_30_P0	0.02123	2.06331	up		lincRNA:chr8:37582187-37621987 reverse strand
A_30_P0	0.01117	2.84213	up		lincRNA:chr10:95729303-95755173 forward strand
A_55_P2	0.03289	1.69705	up	EG64014	PREDICT XM_001479924
A_55_P2	0.03333	1.7926	up		PREDICT XM_001477525
A_30_P0	0.00918	2.38989	up		lincRNA:chr9:14460976-14488051 forward strand
A_55_P2	0.02004	1.89936	up		RIKEN cl AK085283
A_30_P0	0.04528	2.23719	up		lincRNA:chr5:79860066-79860625 forward strand
A_55_P2	0.04789	2.32665	up	Gm9435	PREDICT XR_031978
A_30_P0	0.04262	1.96571	up		lincRNA:chr19:23068397-23190256 reverse strand
A_30_P0	0.04221	1.70175	up		lincRNA:chr10:117021051-117038683 forward strand
A_30_P0	0.02529	2.31221	up		lincRNA:chr9:58301467-58323783 reverse strand
A_51_P5	0.04661	1.70312	up	Sdr42e1	Mus musc NM_028725
A_51_P2	0.02399	1.97099	up	4933427C	RIKEN cl XM_133717
A_51_P2	0.02707	2.40972	up	Gnb3	Mus musc NM_013530
A_30_P0	0.00222	2.29516	up		lincRNA:chr3:96074625-96086375 reverse strand
A_51_P4	0.00818	1.91464	up	Cib4	Mus musc NM_028483
A_52_P1	0.00144	1.65512	up	Aph1b	Mus musc NM_177583
A_55_P1	0.04895	3.76893	up	Gm8954	PREDICT XM_001473041
A_52_P2	0.04613	1.5826	up		RIKEN cl XM_354798
A_30_P0	0.01632	1.98165	up		lincRNA:chr8:59966759-59989065 reverse strand
A_51_P1	0.01782	53.9355	up	Akr1c6	Mus musc NM_030611
A_30_P0	0.0122	1.81839	up		lincRNA:chr4:155560050-155570900 reverse strand
A_55_P1	0.04034	1.89321	up	Me3	Mus musc NM_181407
A_55_P2	0.0434	1.51128	up	Slc25a44	Mus musc NM_001145877
A_55_P1	0.01992	1.72567	up	Casz1	Mus musc NM_027195
A_30_P0	0.01347	2.17984	up		lincRNA:chr13:24833082-24838462 reverse strand
A_30_P0	0.02912	1.63673	up		lincRNA:chr9:118291593-118324230 reverse strand
A_55_P2	0.04727	3.43064	up		Putative u AK146072
A_52_P1	0.03209	1.50127	up	Tbc1d8b	Mus musc NM_001081499
A_51_P4	0.01752	54.5041	up	Ahsg	Mus musc NM_013465
A_51_P1	0.0341	1.94095	up	Kcnk13	Mus musc NM_146037
A_55_P1	0.04727	2.08945	up	Gm7660	PREDICT XR_031289

A_30_P0	0.01814	2.60954	up		lincRNA:chr9:14460976-14488051 forward strand
A_55_P2	0.04986	1.53624	up	Gas2l1	Mus musc NM_144560
A_55_P2	0.01547	1.99818	up	Paqr6	Mus musc NM_198410
A_55_P2	0.03155	1.71999	up	E130304f	Mus musc NM_175538
A_55_P2	0.01644	1.64895	up	Pcdh11x	PREDICT XM_001472925
A_51_P2	0.00353	5.02784	up	Plekkg6	Mus musc NM_198604
A_30_P0	0.0485	1.98863	up		lincRNA:chr8:86705694-86711244 forward strand
A_55_P1	0.03307	2.40165	up	Slx	Mus musc NM_001136476
A_55_P2	0.0249	1.95988	up	Sema3e	Mus musc NM_011348
A_52_P2	0.03619	1.54529	up	Ccnh	Mus musc NM_023243
A_51_P3	0.01652	68.8174	up	Fgg	Mus musc NM_133862
A_30_P0	0.03247	1.94186	up		lincRNA:chr12:77544397-77564122 forward strand
A_51_P5	0.0449	1.8157	up	Calm1	Mus musc NM_009790
A_55_P2	0.04663	1.59558	up	1500004A	Mus musc AK075724
A_55_P2	0.03563	39.3078	up		PREDICT XR_030567
A_55_P2	0.04271	2.07934	up	Lgr4	Mus musc NM_172671
A_55_P2	0.03983	294.218	up	LOC1000	Mus musc NM_001134644
A_30_P0	0.01338	1.59843	up		lincRNA:chr14:77258025-77278750 forward strand
A_55_P2	0.04002	1.55775	up	Gjc1	Mus musc NM_008122
A_65_P1	0.02127	72.939	up	Ttr	Mus musc NM_013697
A_52_P1	0.02122	13.0302	up	Ptgfr	Mus musc NM_008966
A_51_P2	0.03738	1.82064	up	Gm4922	Mus musc NM_177706
A_55_P2	0.01991	32.9494	up	Mup2	Mus musc NM_001045550
A_55_P2	0.02325	1.82361	up	Enho	Mus musc NM_027147
A_55_P2	0.04794	1.59842	up	Gpr180	Mus musc NM_021434
A_30_P0	0.04998	2.39686	up		lincRNA:chr5:15033568-15033987 forward strand
A_51_P3	0.02368	1.90986	up	Glb1	Mus musc NM_009752
A_30_P0	0.03	2.19393	up		lincRNA:chrX:120324027-120326909 reverse strand
A_51_P1	0.02285	38.0032	up	Ambp	Mus musc NM_007443
A_55_P2	0.0054	1.52154	up	Hk1	Mus musc NM_001146100
A_55_P1	0.02851	2.25246	up	Vmn1r18	Mus musc NM_203489
A_30_P0	0.04782	1.69365	up		lincRNA:chr9:100977450-100989325 reverse strand

A_30_P01	0.03145	1.90931	up		lincRNA:chr15:97856041-97867907 reverse strand
A_30_P01	0.03958	2.01304	up		lincRNA:chr6:112552041-112560067 forward strand
A_30_P01	0.02329	1.99493	up		lincRNA:chr14:26834450-26847000 reverse strand
A_55_P15	0.03926	243.091	up	LOC1001	Mus musc NM_001135127
A_55_P15	0.03891	254.396	up	Mup9	Mus musc NM_001126319
A_52_P64	0.00214	1.61815	up	Agtr1a	Mus musc NM_177322
A_51_P45	0.01602	2.11197	up	9530008L	Mus musc NM_175417
A_55_P21	0.02166	1.54194	up	Ccdc72	Mus musc NM_183250
A_30_P01	0.01873	1.62877	up		lincRNA:chr2:36112819-36114110 forward strand
A_55_P22	0.00897	2.29174	up	B930018F	Mus musc AK047086
A_51_P46	0.00972	1.63968	up	Prkcd	Mus musc NM_011103
A_55_P15	0.00448	2.71512	up	Hist2h2aa	Mus musc NM_013549
A_30_P01	0.00443	1.55956	up		lincRNA:chr4:35106125-35127700 forward strand
A_55_P20	0.03905	84.661	up	Mup-ps13	PREDICT XR_030662
A_55_P20	0.00982	1.72542	up	E430029J	Mus musc NM_001162938
A_55_P15	0.00996	2.21319	up	Ctcf1	Mus musc NM_001081387
A_66_P11	0.02013	1.62852	up	LOC1000	PREDICT XR_034330
A_55_P15	0.03857	2.72753	up	6430411K	Mus musc NR_002848
A_55_P21	0.0397	3.34654	up	Creb3l3	Mus musc NM_145365
A_51_P46	0.01981	1.84233	up	Ostm1	Mus musc NM_172416
A_55_P20	0.01676	1.9805	up	Hpse	Mus musc NM_152803
A_55_P20	0.03028	1.83109	up	Oasl1	Mus musc NM_145209
A_51_P46	0.04233	15.9475	up	Agxt	Mus musc NM_016702
A_52_P35	0.00792	1.67572	up	Ccp1	Mus musc NM_028181
A_30_P01	0.01968	2.36052	up		lincRNA:chr9:14460976-14488051 forward strand
A_55_P15	0.03919	2.08587	up	Cyp2s1	Mus musc NM_028775
A_51_P13	0.0264	2.61417	up	Fcna	Mus musc NM_007995
A_30_P01	0.01025	1.62004	up		lincRNA:chr6:129151512-129208737 forward strand
A_30_P01	0.04837	1.90765	up		lincRNA:chr2:92582386-92599365 forward strand
A_55_P15	0.01103	1.65549	up	Hsd12	Mus musc NM_024255
A_55_P20	0.00939	2.49099	up	Gm15452	PREDICT XM_001472867
A_30_P01	0.0425	1.56637	up		lincRNA:chr11:6796679-6797670 forward strand

A_55_P2	0.0387	1.54937	up	LOC1000	PREDICT	XM_001479988
A_55_P2	0.00711	1.85798	up	Nans	Mus musc	NM_053179
A_55_P2	0.03989	2.1497	up	Hpgd	Mus musc	NM_008278
A_30_P0	0.00809	1.54981	up			lincRNA:chr10:62347876-62374346 reverse strand
A_30_P0	0.0331	2.22142	up			lincRNA:chr6:120670699-120677449 reverse strand
A_55_P2	0.02956	1.91713	up	Gfpt2	Mus musc	NM_013529
A_55_P2	0.00569	1.67934	up		RIKEN cl	XM_001472312
A_51_P2	0.04478	9.52385	up	Ugt2a3	Mus musc	NM_028094
A_52_P6	0.02861	1.85365	up	Herc5	Mus musc	NM_025992
A_55_P1	0.04127	1.80939	up	Ifih1	Mus musc	NM_027835
A_30_P0	0.01428	1.55177	up			lincRNA:chr18:35970772-35971449 forward strand
A_30_P0	0.00401	1.81487	up			lincRNA:chr13:94180737-94182912 forward strand
A_30_P0	0.03227	1.51074	up			lincRNA:chr8:35652473-35703370 reverse strand
A_30_P0	0.03513	2.06166	up			lincRNA:chr2:127988295-128194920 reverse strand
A_55_P1	0.01632	19.9363	up	Apob	Mus musc	NM_009693
A_55_P2	0.02883	46.4274	up	Pzp	Mus musc	NM_007376
A_52_P1	0.02494	4.35148	up	AI182371	Mus musc	NM_178885
A_52_P1	0.0129	2.02023	up	Tsga14	Mus musc	NM_031998
A_51_P3	0.02713	3.60381	up	Clec4d	Mus musc	NM_010819
A_52_P5	0.00698	6.36076	up	Klra15	Mus musc	NM_013793
A_55_P1	0.04932	1.65947	up	Gm13089	PREDICT	XR_030771
A_55_P2	0.0194	62.9483	up	Cpamd8	Mus musc	NM_008646
A_55_P1	8.11E-04	7.29133	up	Ranbp3l	Mus musc	NM_198024
A_51_P5	0.00525	4.71349	up	Krt14	Mus musc	NM_016958
A_30_P0	0.04996	2.28973	up			lincRNA:chr9:14460976-14488051 forward strand
A_55_P2	0.00532	2.53092	up	Gm9296	PREDICT	XM_001478977
A_51_P4	0.03779	1.60108	up	Hexb	Mus musc	NM_010422
A_30_P0	0.04969	2.46489	up			lincRNA:chr15:83181291-83197750 reverse strand
A_55_P2	0.00148	1.50219	up	Tsr2	Mus musc	NM_001164578
A_30_P0	0.03663	2.29756	up			lincRNA:chr11:120041124-120052299 forward strand
A_52_P5	0.04334	1.70715	up	Fzd1	Mus musc	NM_021457
A_51_P1	0.01982	2.44384	up	Ccl17	Mus musc	NM_011332

A_51_P2	0.02214	2.58433	up	Dclk1	Mus musc	NM_019978
A_51_P1	0.03319	2.18155	up	Smpdl3a	Mus musc	NM_020561
A_55_P2	0.00501	1.73987	up	Tbrg1	Mus musc	NM_025289
A_55_P2	0.04585	10.6418	up	Slc27a5	Mus musc	NM_009512
A_52_P2	0.03084	1.98702	up	Gm4862	PREDICT	XM_143595
A_52_P6	0.01569	1.94035	up	Tmem5	Mus musc	NM_153059
A_30_P0	0.03221	1.95592	up		lincRNA:chr3:86827945-86886695 forward strand	
A_55_P2	0.01703	1.95797	up		Putative u	AK156988
A_55_P2	0.0062	1.64705	up	Tagln2	Mus musc	NM_178598
A_55_P2	0.00733	1.99337	up	Sgsm1	Mus musc	NM_001162965
A_55_P2	0.0327	146.14	up		major urin	XR_030536
A_55_P2	0.03669	5.65724	up	Ankrd29	Mus musc	NM_001190371
A_55_P2	0.01851	1.82612	up		PREDICT	XM_985370
A_51_P5	0.03791	1.95935	up	Stx11	Mus musc	NM_029075
A_51_P1	0.04192	1.76868	up	4921507P	Mus musc	NM_027564
A_51_P1	0.02337	2.46535	up	Ang3	Mus musc	NM_001123394
A_51_P4	0.01236	1.55508	up	Ly96	Mus musc	NM_016923
A_52_P4	0.04129	1.67951	up	5330426P	Mus musc	NR_028300
A_30_P0	0.01489	2.10091	up		lincRNA:chr10:24269165-24276690 reverse strand	
A_55_P2	0.02266	1.97741	up	A930018N	Mus musc	AK034241
A_30_P0	0.02012	1.78903	up		lincRNA:chr6:99472981-99484210 reverse strand	
A_55_P2	0.04886	2.86543	up	Gm5460	Mus musc	NM_001034880
A_55_P2	0.00503	1.77479	up	LOC6405	PREDICT	XM_917484
A_52_P3	0.00515	2.04416	up	Gm3819	PREDICT	XM_001477163
A_30_P0	0.00278	1.60091	up		lincRNA:chrX:91000651-91005855 reverse strand	
A_55_P2	0.04293	2.40921	up	1300014I	Mus musc	NM_025831
A_55_P1	0.04324	2.53132	up	Ube1y1	Mus musc	NM_011667
A_30_P0	0.0406	1.74458	up		lincRNA:chr1:85117750-85129200 forward strand	
A_55_P2	0.01496	1.72184	up	Gm6936	PREDICT	XM_001480183
A_51_P4	0.00504	5.58326	up	Dock8	Mus musc	NM_028785
A_55_P2	0.03904	1.65664	up	Lifr	Mus musc	NM_001113386
A_66_P1	0.02964	1.58123	up	Ang3	Mus musc	NM_001123394

A_55_P2	0.02713	1.55053	up	Aim1	Mus musc	NM_172393
A_55_P2	0.02943	2.21917	up	LOC1000	PREDICT	XM_001477710
A_55_P1	0.0034	1.99572	up	Stard6	Mus musc	NM_029019
A_55_P2	0.00288	2.18232	up	C79777	H3045B0	BG066537
A_65_P0	0.04916	1.57061	up	Wtap	Mus musc	NM_175394
A_30_P0	0.02048	1.63379	up			lincRNA:chr10:3227840-3233588 reverse strand
A_51_P3	0.04865	2.23668	up	Ang2	Mus musc	NM_007449
A_52_P4	0.02357	2.18014	up	3830403N	Mus musc	NM_027510
A_55_P1	0.01128	2.08692	up	Gm16430	Mus musc	NM_001166601
A_51_P2	0.02305	1.81369	up	Plcg2	Mus musc	NM_172285
A_55_P2	5.95E-04	1.9646	up	Ulk2	Mus musc	NM_013881
A_30_P0	0.00686	1.79905	up			lincRNA:chrX:50087925-50101700 forward strand
A_55_P2	0.02903	2.39448	up	Klra7	Mus musc	NM_001110323
A_52_P1	0.0205	1.59622	up	Txn14a	Mus musc	NM_025299
A_51_P1	0.03993	2.0272	up	Oca2	Mus musc	NM_021879
A_55_P2	0.01873	69.91	up	Mup-ps10	PREDICT	XR_001996
A_52_P3	0.0272	3.89186	up	Fam83a	Mus musc	NM_173862
A_55_P1	0.02637	39.5202	up	Apoa2	Mus musc	NM_013474
A_51_P4	0.00682	1.66449	up	Adap2	Mus musc	NM_172133
A_55_P2	0.03253	2.04677	up	Gml	Mus musc	NM_001177524
A_55_P1	0.03059	84.279	up	Mup3	Mus musc	NM_001039544
A_30_P0	0.0364	1.62638	up			lincRNA:chr13:48576557-48581632 forward strand
A_66_P1	0.02153	1.63525	up	Ikzf1	Mus musc	NM_001025597
A_30_P0	0.008	1.5796	up			lincRNA:chr1:183783306-183834531 reverse strand
A_55_P2	0.00733	1.60458	up	Ssty2	Mus musc	NM_023546
A_55_P2	0.02198	1.54878	up	Dnajc14	Mus musc	NM_028873
A_55_P2	0.03517	2.51036	up	Hist1h2an	Mus musc	NM_178184
A_51_P2	0.03368	28.5902	up	Slc27a5	Mus musc	NM_009512
A_65_P0	0.01243	1.63602	up	Serf2	Mus musc	NM_011354
A_55_P2	0.00942	1.94664	up	Ggn	Mus musc	NM_182696
A_51_P3	8.58E-06	1.71262	up	Zpbp	Mus musc	NM_015785
A_55_P2	0.03546	1.50161	up	Kdm1b	Mus musc	NM_172262

A_51_P3	0.04109	14.8427	up	Gc	Mus musc	NM_008096
A_55_P2	0.0129	2.33343	up	Fgf9	Mus musc	NM_013518
A_55_P2	0.0124	162.685	up	Mup20	Mus musc	NM_001012323
A_55_P2	0.00275	2.02001	up	Dnm1	Mus musc	NM_010065
A_55_P2	0.03581	1.52588	up	Prkcd	Mus musc	NM_011103
A_51_P1	0.01954	1.56546	up	Zdhhc12	Mus musc	NM_025428
A_55_P2	0.00566	2.59308	up	Sntg2	Mus musc	NM_172951
A_30_P0	0.0071	1.70732	up		lincRNA:chr1:85117750-85129200 forward strand	
A_66_P1	0.02757	2.20425	up	Hn1l	Mus musc	NM_198937
A_51_P3	0.03458	9.79721	up	Arg1	Mus musc	NM_007482
A_66_P1	0.03473	16.0488	up	Ugt2b38	Mus musc	NM_133894
A_30_P0	0.01405	1.7596	up		lincRNA:chr4:16144314-16144967 forward strand	
A_52_P3	0.02797	2.15604	up	Gm5077	Mus musc	NM_173864
A_55_P2	0.03534	3.05377	up	Asb16	ankyrin re	AK038411
A_30_P0	0.03719	1.70847	up		lincRNA:chr6:112552041-112560067 forward strand	
A_30_P0	0.02083	2.82846	up		lincRNA:chr18:3003075-3016150 reverse strand	
A_55_P1	0.00478	1.69078	up		PREDICT	XM_001475751
A_51_P1	5.63E-04	9.54706	up	Adh4	Mus musc	NM_011996
A_55_P2	0.04144	431.571	up	Mup20	Mus musc	NM_001012323
A_55_P2	0.03288	1.73577	up	Irak2	Mus musc	NM_172161
A_51_P3	8.10E-04	1.61548	up	Ifit1	Mus musc	NM_008331
A_51_P1	0.03656	2.29859	up	Vsig2	Mus musc	NM_020518
A_66_P1	0.01313	1.64364	up	Cyb5r4	Mus musc	NM_024195
A_51_P3	0.03786	3.09115	up	Nudcd1	Mus musc	NM_026149
A_55_P1	0.02378	2.18521	up	Nkd1	Mus musc	NM_027280
A_55_P1	0.02798	6.03671	up	Ankrd29	Mus musc	NM_001190371
A_55_P1	0.04397	2.16338	up	Lamb3	Mus musc	NM_008484
A_55_P2	0.01319	2.63586	up		coiled-coi	AK170295
A_52_P5	0.03385	1.69573	up	Acsl5	Mus musc	NM_027976
A_30_P0	0.01778	2.03251	up		lincRNA:chr18:3003075-3016150 reverse strand	
A_55_P2	0.04196	1.55112	up	Yipf6	Mus musc	NM_207633
A_30_P0	0.04306	1.90101	up		lincRNA:chr18:36481237-36481819 forward strand	

A_51_P4	0.04524	2.94237	up	Itga11	Mus musc	NM_176922
A_30_P0	0.0072	1.8664	up			lincRNA:chr1:85117750-85129200 forward strand
A_55_P2	0.0167	1.55549	up	Gm15442	PREDICT	XR_032938
A_30_P0	0.0354	2.00681	up			lincRNA:chr13:48576557-48581836 forward strand
A_51_P1	0.00633	1.56488	up	Parvb	Mus musc	NM_133167
A_55_P2	0.04347	1.76017	up	Synpo2	Mus musc	NM_080451
A_51_P5	0.02784	1.85885	up	1700001L	Mus musc	NR_027980
A_30_P0	0.04157	1.5069	up			lincRNA:chr6:100518251-100519726 reverse strand
A_55_P2	0.04603	2.2189	up	AI661453	Mus musc	NM_145489
A_51_P4	0.01195	1.85515	up	Hpgd	Mus musc	NM_008278
A_55_P1	0.00578	1.74431	up	LOC6304	PREDICT	XM_903593
A_30_P0	0.04758	2.47421	up			lincRNA:chr1:167219841-167220505 forward strand
A_55_P2	0.00958	1.5368	up	St6galnac	Mus musc	NM_016973
A_55_P2	0.01781	2.20697	up	LOC1000	PREDICT	XM_001477951
A_66_P1	0.01756	2.24327	up	Akr1c13	Mus musc	NM_013778
A_55_P2	0.00145	1.544	up	LOC1000	PREDICT	XM_001475183
A_55_P1	0.01634	1.5633	up	Gm8212	PREDICT	XM_985174
A_30_P0	0.02791	1.62403	up			lincRNA:chr14:44284425-44300475 reverse strand
A_30_P0	0.04371	1.62419	up			lincRNA:chrX:90997595-91009570 forward strand
A_55_P2	0.04364	1.61136	up	Yipf6	Mus musc	NM_207633
A_55_P1	0.03632	214.653	up	LOC1001	Mus musc	NM_001135127
A_30_P0	0.03561	1.53751	up			lincRNA:chr7:140081171-140123058 reverse strand
A_30_P0	0.03722	1.90765	up			lincRNA:chr2:128217275-128217972 reverse strand
A_55_P1	0.03283	1.66054	up	LOC1000	PREDICT	XM_001473001
A_55_P2	0.02479	2.39887	up	Fmo5	Mus musc	NM_001161765
A_55_P2	0.00255	1.97634	up	Gm9629	PREDICT	XM_001478781
A_55_P1	0.03069	1.51647	up	Chrdl1	Mus musc	NM_001114385
A_51_P1	0.03237	1.77234	up	Rnase6	Mus musc	NM_030098
A_30_P0	0.0281	1.59885	up			lincRNA:chr14:77511189-77522852 forward strand
A_51_P3	0.02801	2.22345	up	Slc2a10	Mus musc	NM_130451
A_55_P1	0.03097	3.05035	up	Cxx1c	Mus musc	NM_028375
A_51_P4	0.02904	1.52234	up	Reep4	Mus musc	NM_180588

A_52_P5	0.04203	2.33664	up	Epdr1	Mus musc	NM_134065
A_55_P20	0.02129	2.32475	up	Tmsb15b2	Mus musc	NM_001080967
A_52_P65	0.04327	2.83168	up	Gm8221	Mus musc	NR_033577
A_55_P20	0.04406	5.06944	up	Csprs	Mus musc	NM_033616
A_30_P0	0.02318	1.57597	up			lincRNA:chr2:172343878-172344212 reverse strand
A_30_P0	0.0125	1.67618	up			lincRNA:chrX:90997595-91009570 reverse strand
A_51_P35	0.04417	1.75226	up	Ntrk2	Mus musc	NM_001025074
A_55_P2	0.0289	1.97559	up	4930427A	Mus musc	NM_134041
A_55_P15	0.04406	1.73218	up	Fmo5	Mus musc	NM_001161765
A_30_P0	0.00712	1.76821	up			lincRNA:chr15:12119755-12127230 forward strand
A_51_P32	0.02754	28.5704	up	Hpx	Mus musc	NM_017371
A_30_P0	0.04947	1.66687	up			lincRNA:chr1:87343550-87362900 forward strand
A_51_P45	0.01403	1.98903	up	Crot	Mus musc	NM_023733
A_30_P0	0.04974	1.80667	up			lincRNA:chr13:48576557-48581632 reverse strand
A_55_P2	0.01258	1.53945	up	Usp18	Mus musc	NM_011909
A_51_P37	0.04594	1.83911	up	Sts	Mus musc	NM_009293
A_52_P30	0.01368	3.1122	up	Cyp4v3	Mus musc	NM_133969
A_55_P15	0.01862	1.62053	up	Trim16	Mus musc	NM_053169
A_55_P2	0.00576	5.27876	up	Klra12	Mus musc	NM_010646
A_55_P15	0.02865	1.54136	up	Entpd4	Mus musc	NM_026174
A_30_P0	0.02772	1.84349	up			lincRNA:chr2:143963320-143984245 forward strand
A_55_P20	0.04272	1.52862	up	LOC1000	PREDICT	XM_001472583
A_51_P45	0.04974	1.52894	up	Dstn	Mus musc	NM_019771
A_55_P15	0.04092	3.25702	up	Gamt	Mus musc	NM_010255
A_30_P0	0.01033	1.66349	up			lincRNA:chr4:44181997-44249172 forward strand
A_55_P15	0.03166	104.677	up	Mup-ps12	PREDICT	XR_030567
A_30_P0	0.04757	1.87838	up			lincRNA:chr6:47595238-47601893 reverse strand
A_30_P0	0.01154	1.83152	up			lincRNA:chr5:107504871-107507830 forward strand
A_55_P20	0.03316	2.9005	up	Tmsb15b1	Mus musc	NM_001081983
A_52_P1	6.28E-05	1.55393	up	Ptpn6	Mus musc	NM_001077705
A_51_P30	0.04439	4.65862	up	Ehd3	Mus musc	NM_020578
A_55_P22	0.04799	1.82263	up	1300015D	Mus musc	AK005014

A_30_P0	0.0441	2.47498	up		lincRNA:chr1:135956616-135957485 reverse strand
A_55_P2	0.00122	1.80131	up	Sqstm1	Mus muscNM_011018
A_30_P0	0.02245	2.11552	up		lincRNA:chr6:13801450-13853450 forward strand
A_55_P2	0.01342	3.06359	up	MacroD2	MACRO BC076574
A_52_P6	0.00873	3.82441	up	Zdhhc2	Mus muscNM_178395
A_30_P0	0.02166	1.55769	up		lincRNA:chr10:83399729-83399790 forward strand
A_55_P2	0.01161	5.00061	up	LOC6409	killer cell XM_918210
A_30_P0	0.03888	4.69687	up		lincRNA:chr4:149445201-149445902 forward strand
A_55_P2	0.04571	1.56022	up		Putative u AK045810
A_52_P2	0.02806	4.17834	up	Bmp3	Mus muscNM_173404
A_30_P0	0.01227	2.20539	up		lincRNA:chr18:5119300-5181600 reverse strand
A_51_P5	0.00978	7.98983	up	Afp	Mus muscNM_007423
A_52_P3	0.02477	3.2546	up	Ric3	Mus muscNM_001038624
A_55_P1	0.0174	2.96187	up	Speer4d	Mus muscNM_025759
A_55_P2	0.00723	1.93101	up	LOC1000	Mus muscNR_004442
A_51_P1	0.0062	2.00626	up	Klra5	Mus muscNM_008463
A_52_P5	0.02714	1.56484	up	Cadm3	Mus muscNM_053199
A_55_P2	0.01502	1.83675	up	Ormdl2	Mus muscNM_024180
A_52_P1	0.03014	13.7357	up	Defb20	Mus muscNM_176950
A_55_P2	0.01705	2.42958	up	Kiss1r	Mus muscNM_053244
A_52_P8	0.02977	2.59397	up	Stard6	Mus muscNM_029019
A_55_P2	0.00307	1.92511	up	Olfr720	Mus muscNM_146392
A_66_P1	0.0242	1.54445	up	Wnt16	Mus muscNM_053116
A_55_P2	0.01323	2.51885	up	Apol9a	Mus muscNM_173786
A_55_P2	0.01353	2.27692	up	Ms4a6b	Mus muscNM_027209
A_55_P2	0.02615	5.84014	up	Ccr11	Mus muscAY072938
A_51_P3	0.03173	1.58605	up	D17Wsu9	Mus muscNM_001033279
A_51_P1	0.00542	3.71768	up	Zdhhc2	zinc finge AK046533
A_55_P1	0.03211	6.36768	up	Cd300ld	Mus muscNM_145437
A_55_P2	0.04922	4.6286	up	Rpl19-ps5	PREDICT XR_031444
A_55_P2	0.0266	1.92483	up	Egln2	Mus muscNM_053208
A_55_P1	0.01277	4.60329	up	AI987944	Mus muscNM_183167

A_51_P14	0.00317	3.08025	up	Zfp429	Mus musc	NM_001080941
A_55_P20	0.03607	1.60515	up	Slc39a11	Mus musc	NM_001166503
A_51_P20	0.00374	1.79903	up	Galnt1	Mus musc	NM_013814
A_55_P2	0.02601	3.68144	up	BB01443	Mus musc	NM_001007591
A_52_P38	7.26E-04	2.76564	up	Cpne8	Mus musc	NM_001033851
A_51_P10	0.03472	7.37896	up	Apon	Mus musc	NM_133996
A_55_P20	0.00876	1.62051	up		mitochondrial ribosomal protein S14 Gene [Source:MGI (curated);Acc:MGI:1928141] [ENSEMBL]	
A_55_P2	0.0457	1.91488	up	Ssty1	Mus musc	NM_009220
A_52_P64	0.01799	2.00648	up	Sec24a	Mus musc	NM_175255
A_30_P0	0.01792	3.05508	up		lincRNA:chr12:110909258-110913909 forward strand	
A_55_P20	0.02494	1.61434	up	Bnip3l	Mus musc	NM_009761
A_55_P20	0.02082	1.8328	up	Gm4619	PREDICT	XM_001476246
A_55_P20	0.01243	1.75552	down	Ncrna000	Mus musc	NM_001162909
A_30_P0	0.02944	1.52548	down		lincRNA:chr15:68161768-68193518 reverse strand	
A_30_P0	0.00149	1.66739	down		lincRNA:chr1:6199946-6200603 reverse strand	
A_55_P20	0.03708	2.01545	down	2810416C	PREDICT	XM_001474539
A_30_P0	0.04619	2.17344	down		lincRNA:chr14:65431652-65437902 reverse strand	
A_55_P2	0.03291	2.89253	down	Angpt1	Mus musc	NM_009640
A_52_P58	0.0437	1.50016	down	Arap2	Mus musc	NM_178407
A_55_P20	0.0171	1.74471	down	Mettl6	Mus musc	NM_025907
A_55_P2	0.04739	1.57455	down	Gm5937	PREDICT	XR_032803
A_30_P0	0.01623	1.75315	down		lincRNA:chr2:67836003-67836461 forward strand	
A_52_P62	0.03829	1.63031	down	Usp36	Mus musc	NM_001033528
A_66_P13	0.02848	2.20653	down	Stfa2	Mus musc	NM_001082545
A_30_P0	0.0057	2.2101	down		lincRNA:chr7:134779841-134840591 forward strand	
A_55_P20	0.03964	2.63187	down	Tomm40l	Mus musc	NM_001037170
A_55_P2	0.03796	1.77727	down	D930016I	Mus musc	NR_030673
A_55_P20	0.01478	3.83349	down	Gm2154	PREDICT	XM_001472648
A_30_P0	0.03937	1.78154	down		lincRNA:chrX:54636915-54638388 reverse strand	
A_52_P62	0.00618	1.80223	down	Accs	Mus musc	NM_183220
A_55_P19	0.02831	1.79683	down	Osbp	Mus musc	NM_001033174
A_55_P20	0.01653	1.90586	down	Pi4kb	Mus musc	NM_175356

A_55_P1	0.04558	2.57629	down	9430078C	PREDICT	XR_035208
A_55_P2	0.02551	1.71535	down	Hps4	Mus musc	NM_138646
A_55_P1	0.01986	1.63272	down	C030010C	PREDICT	XM_001472491
A_30_P0	0.03811	1.52135	down		lincRNA:chr6:122741562-122743423 reverse strand	
A_55_P2	0.00217	7.00077	down	Olfr224	Mus musc	NM_207695
A_66_P1	0.0128	1.90068	down	Stk38l	Mus musc	NM_172734
A_52_P2	0.00976	1.72282	down	Agpat6	Mus musc	NM_018743
A_52_P5	0.03707	1.51433	down	Hmbox1	Mus musc	NM_177338
A_30_P0	0.00306	1.92661	down		lincRNA:chr5:35975265-35982561 reverse strand	
A_55_P2	0.03512	1.56128	down	Chd9	Mus musc	NM_177224
A_55_P2	0.04563	2.43412	down	Ccdc158	coiled-coi	XR_031282
A_30_P0	0.0424	1.5547	down		lincRNA:chr15:68161768-68193518 reverse strand	
A_52_P6	0.00835	1.55719	down	Tcte2	Mus musc	NM_022311
A_30_P0	0.01144	2.56652	down		lincRNA:chr12:115365529-115379374 reverse strand	
A_51_P3	0.00167	2.36211	down	Tmem114	Mus musc	NM_029070
A_51_P2	0.03736	2.24046	down	Ntm	Mus musc	NM_172290
A_55_P2	0.00479	2.60185	down	4930458D	Mus musc	AK036594
A_55_P2	0.0062	1.61695	down	3110057C	Mus musc	NM_026622
A_30_P0	0.03257	1.80517	down		lincRNA:chr18:54115625-54123729 forward strand	
A_55_P2	0.03388	1.705	down	Smcr8	Mus musc	NM_001085440
A_30_P0	0.04772	1.51021	down		lincRNA:chr1:63168439-63172297 forward strand	
A_52_P2	0.03404	1.60116	down	BC032203	Mus musc	NM_001100452
A_55_P2	0.03284	1.5305	down	Nmb	Mus musc	NM_026523
A_55_P1	0.04131	1.63095	down	Slc17a5	Mus musc	NM_172773
A_30_P0	0.00774	1.50474	down		lincRNA:chrX:54627918-54638568 reverse strand	
A_30_P0	0.0405	1.5359	down		lincRNA:chr1:6199946-6200603 reverse strand	
A_30_P0	0.03081	1.57524	down		lincRNA:chr17:39960567-39992817 reverse strand	
A_30_P0	0.04085	1.59044	down		lincRNA:chr4:88604248-88645948 forward strand	
A_55_P2	0.01315	1.77952	down	Phf20l1	Mus musc	NM_001081409
A_30_P0	0.03037	2.12787	down		lincRNA:chr9:41184479-41240162 forward strand	
A_30_P0	0.0045	1.53857	down		lincRNA:chr3:95457337-95458070 reverse strand	
A_51_P4	0.04869	1.96266	down	Dhdpsl	Mus musc	NM_026152

A_30_P0	0.02853	3.22204	down		lincRNA:chr11:79531768-79532127 forward strand
A_30_P0	0.01744	1.76552	down		lincRNA:chrX:54636915-54638388 reverse strand
A_55_P2	0.00304	1.60337	down	LOC1000	PREDICT_XM_001477810
A_30_P0	0.03734	1.64817	down		lincRNA:chr15:102026122-102033725 reverse strand
A_30_P0	0.02548	1.79599	down		lincRNA:chr2:67836003-67836461 forward strand
A_52_P5	0.0464	1.67874	down	Arhgap32	Mus muscNM_177379
A_55_P2	0.04681	1.7812	down	Gm11686	PREDICT_XM_001480374
A_30_P0	0.03351	1.63832	down		lincRNA:chr18:46954653-46955671 forward strand
A_55_P2	0.04833	2.11782	down		glucan (1,AK013167
A_30_P0	0.04313	2.12755	down		lincRNA:chr11:116562925-116574575 reverse strand
A_55_P1	0.04561	1.71919	down	Col8a2	Mus muscNM_199473
A_55_P2	0.04806	1.78051	down	Pgc	Mus muscNM_025973
A_55_P2	0.00723	1.89134	down	Mgll	Mus muscNM_001166250
A_30_P0	0.01595	1.52413	down		lincRNA:chr6:86776350-86799379 reverse strand
A_51_P3	0.02197	8.93065	down	Myh4	Mus muscNM_010855
A_30_P0	0.03486	1.5122	down		lincRNA:chr5:22928221-22939127 reverse strand
A_55_P2	0.00345	1.50431	down	Pisd-ps2	Mus muscNR_003519
A_55_P2	0.03045	1.63518	down	Gm2262	PREDICT_XM_001472967
A_30_P0	0.02076	2.08799	down		lincRNA:chr6:47595238-47601893 forward strand
A_51_P4	0.03702	1.55937	down	Sobp	Mus muscNM_175407
A_30_P0	0.03805	1.76347	down		lincRNA:chr4:59306575-59317850 reverse strand
A_55_P1	0.04423	1.94988	down	Kctd18	Mus muscNM_030211
A_52_P1	0.04815	1.98759	down	Nrxn1	Mus muscNM_020252
A_66_P1	0.00548	1.77619	down	Zbtb44	Mus muscNM_001115130
A_30_P0	0.04537	1.57757	down		lincRNA:chr10:39383665-39442690 forward strand
A_55_P2	0.00115	1.69194	down		Putative uAK136654
A_55_P2	0.04173	2.15312	down	Ddo	Mus muscNM_027442
A_30_P0	0.03886	2.43465	down		lincRNA:chr3:60292527-60292880 reverse strand
A_30_P0	0.01104	1.80521	down		lincRNA:chr11:117835849-117842574 forward strand
A_52_P2	0.031	2.70713	down	Rwdd3	Mus muscNM_028456
A_30_P0	0.01909	2.41993	down		lincRNA:chr8:91569369-91594119 forward strand
A_51_P3	0.0247	1.8417	down	Bcl2l14	Mus muscNM_025778

A_55_P15	0.00205	1.74939	down	2900006K	Mus musc	NM_028377
A_30_P01	7.71E-04	2.18042	down			lincRNA:chr5:35975265-35982561 reverse strand
A_55_P15	0.03437	2.93481	down	Ccdc67	Mus musc	NM_181816
A_30_P01	0.04467	2.57009	down			lincRNA:chr6:134838675-134847075 forward strand
A_55_P15	0.01725	1.5921	down	Ptma	Mus musc	NM_008972
A_55_P20	0.01825	1.72896	down	Vps13a	Mus musc	NM_173028
A_30_P01	0.01035	1.8392	down			lincRNA:chr18:84760623-84761084 forward strand
A_55_P20	0.03111	1.55939	down	Mrpl47	mitochond	XM_001476597
A_55_P22	0.00571	1.84131	down	9330175E	Mus musc	AK034303
A_55_P22	0.00457	1.56539	down	E230012F	Mus musc	AK054025
A_30_P01	0.01758	1.96306	down			lincRNA:chr2:80338640-80339980 reverse strand
A_55_P15	0.02644	1.76165	down	Hist2h4	Mus musc	NM_033596
A_55_P22	0.04609	2.1036	down	4933417C	Mus musc	AK016840
A_30_P01	0.01181	1.63807	down			lincRNA:chr18:84735774-84760824 forward strand
A_55_P22	0.03091	1.56244	down	Zfp467	Mus musc	NM_001085417
A_55_P15	0.03978	1.63523	down	Rad18	Mus musc	NM_001167730
A_55_P20	0.00836	1.57583	down	LOC1000	PREDICT	XM_001478625
A_55_P15	0.04401	1.65897	down	A930033F	PREDICT	XR_002305
A_66_P12	0.02774	1.51019	down	Mrpl47	Mus musc	NM_029017
A_30_P01	0.04958	1.72001	down			lincRNA:chr19:16078625-16110246 reverse strand
A_30_P01	0.02224	1.61627	down			lincRNA:chr15:102032892-102033838 reverse strand
A_30_P01	0.01032	2.77001	down			lincRNA:chr5:92548501-92566401 forward strand
A_30_P01	0.02106	2.32984	down			lincRNA:chr6:86476240-86513483 forward strand
A_55_P22	0.03416	1.92573	down	4933416A	Mus musc	AK016828
A_55_P22	0.02021	1.63286	down	2610019N	Mus musc	AK138804
A_30_P01	0.00421	1.74544	down			lincRNA:chr12:117623500-117643575 reverse strand
A_55_P20	0.03944	2.30436	down	Sep-06	Mus musc	NM_001177324
A_52_P70	0.04842	2.11457	down	Tob2	Mus musc	NM_020507
A_52_P32	0.02868	1.69955	down		Putative u	AK047780
A_55_P22	0.02853	1.60712	down	Prpf40b	Mus musc	NM_018786
A_51_P30	0.03631	7.45092	down	Asb14	Mus musc	NM_001170748
A_55_P20	0.02404	1.94859	down	Hrk	Mus musc	NM_007545

A_30_P0	0.04295	1.55708	down		lincRNA:chr15:68161768-68193518 reverse strand
A_30_P0	0.04616	1.7032	down		lincRNA:chr8:26869173-26869823 reverse strand
A_55_P2	0.00459	1.88989	down	Sorcs2	Mus musc NM_030889
A_51_P2	0.00934	1.55037	down	1500011H	Mus musc NM_026883
A_30_P0	0.00337	1.76357	down		lincRNA:chr7:137669440-137672712 forward strand
A_55_P2	0.03186	1.68	down	Mll2	Mus musc NM_001033276
A_52_P4	0.00706	1.57804	down	Fgd1	Mus musc NM_008001
A_55_P2	0.04423	2.0541	down	5830419E	Mus musc AK134048
A_55_P2	0.03686	1.53076	down	Ankrd5	Mus musc NM_175667
A_30_P0	0.02041	1.66202	down		lincRNA:chr15:96091428-96115684 reverse strand
A_55_P2	0.03695	1.90817	down	Gm8273	PREDICT XM_001004569
A_55_P2	0.0103	2.43265	down		Ral GTPa AK157932
A_55_P2	0.03439	1.7641	down	BC035044	Mus musc AK088258
A_51_P4	0.01938	2.45218	down	Bcl6b	Mus musc NM_007528
A_30_P0	0.02914	3.05274	down		lincRNA:chr3:127037711-127111912 reverse strand
A_55_P2	0.00135	3.54536	down	Rgs2	Mus musc NM_009061
A_30_P0	0.0205	1.62553	down		lincRNA:chr14:73757550-73758159 reverse strand
A_30_P0	0.00115	1.51487	down		lincRNA:chrX:54627918-54638568 reverse strand
A_55_P1	0.03219	1.54205	down	Slc25a42	Mus musc NM_001007570
A_55_P1	0.03281	1.6538	down	Atf4	Mus musc NM_009716
A_55_P2	0.01589	2.03342	down	Fam40a	Mus musc NM_153563
A_51_P2	0.03333	1.62271	down	Socs1	Mus musc NM_009896
A_55_P2	0.00783	1.67584	down	C430048I	Mus musc NM_198957
A_30_P0	0.04311	1.65197	down		lincRNA:chr17:88993214-89025839 forward strand
A_51_P2	0.03054	1.82137	down	Cxxc5	Mus musc NM_133687
A_55_P2	0.04811	1.64071	down	4931408A	Mus musc NM_027627
A_55_P2	0.03062	1.8989	down	Gm13271	Mus musc NM_001085528
A_52_P2	0.04762	1.65721	down	Atxn3	Mus musc NM_029705
A_51_P2	0.03144	2.24889	down	Ier3	Mus musc NM_133662
A_30_P0	0.02192	2.30863	down		lincRNA:chr10:59385064-59385436 forward strand
A_52_P3	0.03371	1.88892	down		Ig kappa c X67625
A_55_P2	0.03431	3.60727	down	Camp	Mus musc NM_009921

A_52_P4	0.01524	1.79653	down	D3300380	Mus musc	NM_177899
A_30_P0	0.00149	1.56142	down			lincRNA:chr2:176583825-176714400 forward strand
A_52_P5	0.01449	1.57803	down	Flywch1	Mus musc	NM_153791
A_30_P0	0.0112	2.1697	down			lincRNA:chr4:82156098-82196298 reverse strand
A_55_P2	0.04851	1.84698	down	BC062258	Mus musc	AK144577
A_55_P2	0.01729	1.64383	down			RAR-related orphan receptor alpha Gene [Source:MGI (curated);Acc:MGI:104661] [ENSMU
A_55_P1	0.01976	1.55823	down	Brd2	Mus musc	NM_001025387
A_55_P1	0.0254	2.20882	down	Gm13017	PREDICT	XM_001475143
A_52_P4	0.0258	1.75049	down	Svil	supervilli	AK041925
A_52_P1	0.00273	1.60262	down	Zfp317	Mus musc	NM_172918
A_30_P0	0.04831	1.55267	down			lincRNA:chr7:134595900-134610975 forward strand
A_52_P3	0.0442	3.13835	down	Unc93a	Mus musc	NM_199252
A_55_P2	0.035	1.69208	down	Hexim2	Mus musc	NM_027658
A_30_P0	0.01351	1.54459	down			lincRNA:chr17:15357376-15385701 forward strand
A_52_P2	0.0257	2.17462	down	CK13795	Mus musc	NM_001134733
A_55_P2	0.02751	2.23468	down	Dlk1	Mus musc	NM_010052
A_52_P6	0.02197	1.7164	down	Capn12	Mus musc	NM_001110807
A_30_P0	0.04266	2.00859	down			lincRNA:chr7:99879368-99889978 reverse strand
A_55_P1	0.04819	1.81668	down	Rbm47	Mus musc	NM_178446
A_30_P0	0.03282	1.773	down			lincRNA:chr7:118248833-118267766 reverse strand
A_30_P0	0.00487	1.96425	down			lincRNA:chr1:173254292-173257445 reverse strand
A_30_P0	0.02401	1.73743	down			lincRNA:chr12:25852471-25852681 forward strand
A_52_P3	0.03184	1.56532	down			B-cell CLAK038789
A_55_P2	0.04194	1.68602	down	Nos2	Mus musc	NM_010927
A_55_P2	0.02314	1.57792	down	ATP8	mitochond	AK131577
A_30_P0	0.00884	1.73973	down			lincRNA:chr1:94077196-94077860 forward strand
A_55_P1	0.02741	1.8719	down	1810014F	Mus musc	NM_026928
A_55_P1	0.03775	1.6663	down	Adora3	Mus musc	NM_009631
A_30_P0	0.00243	2.50632	down			lincRNA:chr2:168136389-168136560 reverse strand
A_51_P2	0.01631	2.91846	down	Dennd2d	Mus musc	NM_028110
A_30_P0	0.01823	1.67033	down			lincRNA:chr18:84757475-84757969 reverse strand
A_55_P2	0.01355	1.5791	down	LOC1000	PREDICT	XR_033752

A_51_P4	0.01625	2.04805	down	2410004A	Mus musc	NM_025890
A_30_P0	0.02507	1.61551	down			lincRNA:chr1:58443698-58449898 reverse strand
A_30_P0	0.01859	1.56194	down			lincRNA:chr17:17462450-17488725 forward strand
A_66_P1	0.047	1.88522	down	Dnahc10	Mus musc	NM_019536
A_55_P2	0.01304	1.93181	down	Erdr1	Mus musc	NM_133362
A_55_P2	0.00569	3.37193	down	Bhlhe41	Mus musc	NM_024469
A_55_P2	0.04163	1.62187	down	Ube4b	Mus musc	NM_022022
A_55_P1	0.00488	1.89313	down	Atg4c	Mus musc	NM_175029
A_51_P2	0.02663	1.73293	down	Zfp768	Mus musc	NM_146202
A_30_P0	0.01318	2.22212	down			lincRNA:chr2:60531602-60543635 reverse strand
A_55_P2	0.02914	1.67812	down	4930506C	Mus musc	AK015714
A_55_P2	0.00948	1.99286	down		RIKEN cl	AK006468
A_55_P2	0.00487	2.12352	down	BC018473	Mus musc	NR_003364
A_55_P1	0.03224	2.38939	down	Gm9992	Mus musc	NM_001142539
A_55_P2	0.00128	1.85617	down	Wdr67	Mus musc	NM_001081396
A_55_P1	0.00211	1.82338	down	5830433I	PREDICT	XM_974092
A_66_P1	5.83E-04	1.56592	down	Zfp703	Mus musc	NM_001110508
A_55_P2	0.02266	2.44801	down		cytokine r	AK078569
A_30_P0	0.02891	2.37197	down			lincRNA:chr10:118385588-118439338 reverse strand
A_55_P2	0.03045	2.57633	down	Nol4	Mus musc	NM_199024
A_51_P1	0.01141	1.54545	down	Ptar1	Mus musc	NM_028208
A_55_P2	0.02588	1.74989	down	Dsg1c	Mus musc	NM_181680
A_51_P3	0.00747	2.78215	down		lin-7 hom	AK077191
A_51_P2	0.01048	1.52757	down	A2ld1	Mus musc	NM_145466
A_55_P2	0.00358	1.64522	down	A430071A	Mus musc	AK137878
A_55_P2	0.00531	4.19431	down		Immunog	XM_001001076
A_30_P0	0.01905	1.90698	down			lincRNA:chr1:92546371-92551596 forward strand
A_30_P0	0.00625	1.58212	down			lincRNA:chr18:84760623-84761084 forward strand
A_55_P2	0.03485	1.51229	down	Gm3622	PREDICT	XM_001477370
A_30_P0	0.02619	2.27475	down			lincRNA:chr16:64758224-64765700 forward strand
A_52_P5	0.02425	2.74173	down	Foxo6	Mus musc	NM_194060
A_51_P2	0.02097	2.09573	down	Sprr4	Mus musc	NM_173070

A_55_P13	0.04513	1.6591	down	Sohlh1	Mus musc	NM_001001714
A_55_P22	0.01424	1.54959	down	4930474N	Mus musc	AK015577
A_30_P01	0.01323	1.64396	down			lincRNA:chr2:72818943-72826893 reverse strand
A_55_P23	0.01306	1.74233	down	8030453C	Mus musc	AK141726
A_55_P20	0.03206	2.25687	down	Gm4092	PREDICT	XM_001479101
A_55_P20	0.02108	1.70637	down	Snap25	Mus musc	NM_011428
A_30_P01	0.0074	1.72037	down			lincRNA:chr1:167797581-167803031 reverse strand
A_55_P20	0.01916	1.65613	down	Fam131a	Mus musc	NM_133778
A_30_P01	0.0283	1.8919	down			lincRNA:chr2:35829956-35830757 reverse strand
A_55_P23	0.02981	1.76216	down	A530064I	Mus musc	AK080119
A_55_P19	0.02056	1.6121	down	LOC1000	PREDICT	XM_001472353
A_55_P20	0.00524	1.66809	down	Grm4	Mus musc	NM_001013385
A_30_P01	0.04751	1.87779	down			lincRNA:chr3:151746091-151753763 reverse strand
A_55_P23	0.0011	1.56671	down	3300002A	Mus musc	AK012244
A_55_P23	0.02376	3.77481	down	1810059H	PREDICT	XR_035221
A_65_P13	0.01362	1.57628	down	Pum1	Mus musc	NM_030722
A_51_P21	0.02295	2.06808	down	Prodh	Mus musc	NM_011172
A_55_P19	0.00854	1.53976	down	Osbp2	Mus musc	NM_152818
A_55_P20	0.03701	1.52007	down	C130039C	Mus musc	NM_001163502
A_66_P13	0.04942	1.5932	down	Safb	Mus musc	NM_001163300
A_30_P01	0.03741	1.51706	down			lincRNA:chr15:68170864-68171544 reverse strand
A_30_P01	0.01741	2.00343	down			lincRNA:chr14:73729977-73751877 forward strand
A_55_P23	0.04261	1.69659	down	1200014J	Mus musc	NM_025818
A_30_P01	0.01773	2.81322	down			lincRNA:chrX:50400250-50410825 reverse strand
A_52_P47	0.04194	2.40617	down		RIKEN cl	AK053142
A_55_P23	0.03487	2.81872	down	6820445E	Mus musc	AK135532
A_30_P01	0.02097	5.70296	down			lincRNA:chr9:40268246-40268441 reverse strand
A_30_P01	0.0254	1.77667	down			lincRNA:chr3:21973306-21974266 reverse strand
A_52_P24	0.03066	1.7123	down		Ellis van C	AK039759
A_51_P20	0.01381	1.63397	down	Nat6	Mus musc	NM_019750
A_30_P01	0.046	1.7192	down			lincRNA:chr9:75316023-75344401 forward strand
A_51_P38	0.02352	1.82181	down	Ebf2	Mus musc	NM_010095

A_55_P2	0.01407	1.85384	down	Ddhd2	Mus musc	NM_028102
A_55_P1	0.04407	1.85752	down	Npnt	Mus musc	NM_033525
A_30_P0	0.0348	2.02373	down			lincRNA:chr15:100905367-100905654 reverse strand
A_52_P3	0.03956	2.00202	down	B330016I	Mus musc	NR_030695
A_55_P2	0.04414	2.45779	down	Cdkn2c	Mus musc	NM_007671
A_55_P2	0.01454	1.56104	down	L2hgdh	Mus musc	NM_145443
A_30_P0	0.03748	1.52975	down			lincRNA:chrX:11671249-11671715 reverse strand
A_30_P0	0.00718	2.38732	down			lincRNA:chr9:41300137-41301556 forward strand
A_30_P0	0.01956	2.0941	down			lincRNA:chr15:100909469-100910253 forward strand
A_30_P0	4.31E-04	1.82877	down			lincRNA:chr8:125031410-125075960 reverse strand
A_30_P0	0.01076	1.64061	down			lincRNA:chr12:21548850-21568550 reverse strand
A_30_P0	0.00945	1.82555	down			lincRNA:chr2:94008913-94019798 reverse strand
A_55_P1	0.00859	1.57387	down	Zbtb11	Mus musc	NM_173026
A_55_P2	0.0054	1.6856	down		RIKEN cl	BC038884
A_30_P0	0.01377	2.34914	down			lincRNA:chr12:3173375-3203075 reverse strand
A_51_P4	0.00173	2.01974	down	Erv3	Mus musc	NM_001166206
A_55_P2	0.02064	1.60812	down	Nr2f1	Mus musc	NM_010151
A_30_P0	0.00425	1.7838	down			lincRNA:chr15:83281223-83284791 reverse strand
A_55_P2	0.04673	1.66763	down	Hmcn2	PREDICT	XM_001473893
A_55_P2	0.03011	1.75562	down	Terf2ip	Mus musc	NM_020584
A_55_P2	0.02595	2.10908	down	LOC6399	PREDICT	XM_916664
A_51_P2	0.04643	1.8596	down	Angptl7	Mus musc	NM_001039554
A_30_P0	0.02895	2.17556	down			lincRNA:chr12:72103832-72116875 reverse strand
A_55_P2	0.04449	2.16719	down	Rffl	Mus musc	NM_001164569
A_30_P0	0.04578	1.6689	down			lincRNA:chr4:40720362-40729687 forward strand
A_30_P0	9.55E-04	1.66934	down			lincRNA:chr10:110980223-110980667 reverse strand
A_30_P0	0.04809	1.51889	down			lincRNA:chr15:59059450-59070576 reverse strand
A_52_P3	0.00276	1.5003	down		mitochond	BC012020
A_51_P2	0.04167	1.65634	down	Clnk	Mus musc	NM_013748
A_55_P1	0.0202	5.8827	down	Ppargc1b	Mus musc	NM_133249
A_55_P2	0.01688	1.68834	down	Tmem53	Mus musc	NM_026837
A_51_P2	0.0217	3.09681	down	Cyr61	Mus musc	NM_010516

A_55_P1	0.01604	2.33178	down	Bcat2	Mus musc	NM_009737
A_30_P0	0.03774	1.57611	down			lincRNA:chr10:66559716-66647841 reverse strand
A_55_P2	0.00723	1.6886	down	Rnf144b	Mus musc	NM_146042
A_30_P0	0.01754	1.96485	down			lincRNA:chr11:18367482-18393258 reverse strand
A_51_P2	0.02493	1.95021	down	Epyc	Mus musc	NM_007884
A_55_P2	0.02094	1.89977	down	Oscp1	Mus musc	NM_172701
A_55_P2	0.00312	1.92992	down	Tcl1b4	Mus musc	NM_013774
A_30_P0	0.01801	1.67903	down			lincRNA:chr1:87343550-87362900 reverse strand
A_30_P0	0.0442	1.50296	down			lincRNA:chr12:85252300-85253597 reverse strand
A_55_P2	0.02816	1.80536	down	Chd7	Mus musc	NM_001081417
A_51_P2	0.04321	1.83882	down	Kctd6	Mus musc	NM_027782
A_30_P0	0.03944	2.21134	down			lincRNA:chr5:113594167-113645342 forward strand
A_55_P2	0.02557	1.63543	down			PREDICT XM_001473956
A_51_P2	0.02177	1.77634	down			Putative u AK155400
A_55_P2	0.03034	1.76514	down	LOC1000	PREDICT XM_001473825	
A_30_P0	0.00518	1.67587	down			lincRNA:chr1:63163023-63180223 forward strand
A_51_P4	9.44E-04	1.62653	down	Mepe	Mus musc	NM_053172
A_55_P1	0.00472	2.06894	down	LOC1000	PREDICT XR_030659	
A_51_P3	0.02472	1.70164	down	Doc2g	Mus musc	NM_021791
A_52_P6	0.00812	1.97937	down	Fam71f1	Mus musc	NM_207258
A_55_P1	0.01669	1.94851	down	E330009J	Mus musc	NM_175528
A_55_P2	1.85E-04	1.97749	down	D9Wsu90	Mus musc	AK038263
A_30_P0	0.0193	2.04977	down			lincRNA:chr12:110842149-110845695 forward strand
A_55_P2	0.03294	1.65611	down	Ttl4	Mus musc	NM_001014974
A_30_P0	0.0271	1.51318	down			lincRNA:chr1:63163023-63180223 forward strand
A_55_P2	0.01552	1.7382	down	LOC1000	PREDICT XR_032320	
A_30_P0	0.02314	1.56891	down			lincRNA:chr17:21787577-21828406 forward strand
A_66_P1	0.0414	1.53941	down	Ppip5k1	Mus musc	NM_178795
A_66_P1	0.0356	2.91637	down	Gm6328	PREDICT XM_897144	
A_52_P6	0.04536	2.10421	down	Palm2	Mus musc	NM_172868
A_55_P2	0.02721	2.07467	down	4930528A	Mus musc	NR_028384
A_30_P0	0.017	1.79982	down			lincRNA:chr10:16603950-16794075 forward strand

A_30_P0	0.03804	2.02243	down		lincRNA:chrX:100688896-100701764 forward strand
A_55_P2	0.00192	2.2084	down	Ublcp1	Mus muscNM_024475
A_30_P0	0.02765	4.94379	down		lincRNA:chr9:40268246-40268441 reverse strand
A_51_P4	0.00888	3.56614	down	Lypd1	Mus muscNM_145100
A_55_P2	0.00797	1.91417	down	Trp53tg5	PREDICTXR_033202
A_55_P2	0.0132	1.57748	down	Tbx6	Mus muscNM_011538
A_51_P1	0.01088	1.66612	down	3110021A	Mus muscNR_030776
A_55_P2	0.00403	3.04695	down	Camp	Mus muscNM_009921
A_51_P2	0.00881	1.75406	down	1190005I	Mus muscNM_197988
A_30_P0	0.03495	2.6705	down		lincRNA:chr13:70745306-70837331 reverse strand
A_52_P4	0.04018	1.60316	down		PHD fingAK045780
A_30_P0	0.02718	1.75998	down		lincRNA:chr17:9943615-9967953 reverse strand
A_55_P2	0.04979	1.51278	down	Gon4l	Mus muscNM_027389
A_30_P0	0.00257	2.0422	down		lincRNA:chr9:121256738-121257487 forward strand
A_30_P0	0.00431	2.09979	down		lincRNA:chr5:35975265-35982561 reverse strand
A_30_P0	0.00848	1.69247	down		lincRNA:chr9:56910620-56919667 reverse strand
A_51_P3	0.01418	1.58336	down	Fbxo31	Mus muscNM_133765
A_55_P2	0.02992	5.59427	down	Zcchc12	Mus muscNM_028325
A_55_P2	0.02555	2.00314	down	BC023969	Mus muscAK144629
A_55_P2	0.02043	1.60151	down	Gm5488	PREDICTXM_001480385
A_30_P0	0.03779	2.44767	down		lincRNA:chr9:41368823-41369514 forward strand
A_55_P2	0.00101	1.58844	down	Nol9	Mus muscNM_028727
A_55_P2	0.03882	1.55517	down	Snap23	Mus muscNM_001177792
A_55_P2	0.04144	1.76056	down	Gm5294	PREDICTXM_001000706
A_55_P2	0.00163	1.94324	down	Gm6603	PREDICTXM_898851
A_55_P2	0.00735	1.54975	down	Gm2559	PREDICTXM_001474103
A_55_P2	0.03567	1.59873	down	Pnpla1	Mus muscNM_001034885
A_66_P1	0.01202	1.78428	down	Glis3	Mus muscNM_175459
A_55_P2	0.02708	1.60013	down		sacsin GeAK046501
A_51_P2	0.00816	1.55076	down	Nrbp2	Mus muscNM_144847
A_51_P1	0.0411	1.68377	down	Arid2	Mus muscNM_175251
A_30_P0	0.01273	5.22572	down		lincRNA:chr9:40266027-40266460 reverse strand

A_55_P1	0.02201	1.81002	down	Cpped1	Mus musc	NM_146067
A_30_P0	0.04516	1.50184	down			lincRNA:chr4:138657728-138687028 reverse strand
A_55_P2	0.0049	1.57033	down	Zfp568	Mus musc	NM_001167872
A_52_P6	0.02286	2.11492	down	Cabp4	Mus musc	NM_144532
A_30_P0	0.04794	2.6547	down			lincRNA:chr5:149751979-149808240 reverse strand
A_30_P0	0.04507	1.85328	down			lincRNA:chr19:59001589-59006474 reverse strand
A_66_P1	0.02629	1.64453	down	Nfyc	Mus musc	NM_008692
A_55_P2	0.03302	1.51454	down	Pex5	Mus musc	NM_008995
A_55_P2	0.02869	2.04175	down		PREDICT	XM_990953
A_30_P0	0.04069	1.87966	down			lincRNA:chr4:136856064-136877219 forward strand
A_55_P2	0.00346	1.79805	down	AU01583	Mus musc	NR_028320
A_55_P2	0.01405	2.04861	down	Fbxo44	Mus musc	NM_173401
A_30_P0	0.02921	1.75999	down			lincRNA:chr18:84735774-84760824 reverse strand
A_52_P5	0.04831	1.56534	down	Sh2d5	Mus musc	NM_001099631
A_55_P2	0.01059	1.78415	down	LOC1000	PREDICT	XM_001475613
A_55_P2	0.02857	1.59353	down	D130095	Mus musc	AK084110
A_30_P0	0.03174	1.61558	down			lincRNA:chr15:96091428-96115684 reverse strand
A_30_P0	0.02109	1.83437	down			lincRNA:chr17:35080914-35090009 forward strand
A_55_P2	0.01443	2.19251	down		Mus musc	AK142897
A_30_P0	0.00538	1.94685	down			lincRNA:chr19:12079745-12088620 reverse strand
A_55_P2	0.00671	1.58812	down	Col11a2	Mus musc	NM_009926
A_55_P2	0.00113	2.03457	down	Gm7716	PREDICT	XM_978208
A_55_P2	0.03363	2.76368	down	Jun	Mus musc	NM_010591
A_30_P0	0.03275	1.87344	down			lincRNA:chr2:60038543-60046318 reverse strand
A_55_P2	0.04186	1.79463	down	Gm10638	Mus musc	AK133595
A_55_P2	0.02125	2.02049	down	Rfx3	Mus musc	NM_011265
A_55_P2	0.04351	1.81804	down	9430063H	Mus musc	AK020472
A_30_P0	0.01671	1.85896	down			lincRNA:chr3:93564825-93576725 forward strand
A_51_P3	0.04566	1.72361	down	Crip3	Mus musc	NM_053250
A_30_P0	0.03646	1.50367	down			lincRNA:chr8:4325209-4348788 forward strand
A_55_P2	0.01479	2.02286	down	Gm13271	Mus musc	NM_001085528
A_55_P2	0.008	2.90857	down	Arc	Mus musc	NM_018790

A_52_P3	0.00669	3.37141	down		olfactory	BC108946
A_66_P1	0.00672	2.99262	down		RIKEN cl	AK088235
A_55_P2	0.03499	1.69071	down	Dand5	Mus musc	NM_201227
A_55_P2	0.02977	1.6193	down		MAP kin	AK177092
A_30_P0	0.04482	4.56992	down		lincRNA:chr9:40266027-40266460 reverse strand	
A_30_P0	0.04803	1.66002	down		lincRNA:chr2:32950586-32984936 reverse strand	
A_55_P2	0.02444	1.82088	down	Papln	Mus musc	NM_130887
A_55_P2	0.01377	2.05266	down		PREDICT	XM_001479428
A_66_P1	0.00327	2.52723	down	6030408E	Mus musc	NR_033803
A_55_P2	0.01426	1.85811	down	5730522E	Mus musc	NR_027973
A_30_P0	0.02843	1.85207	down		lincRNA:chr7:6108350-6119600 reverse strand	
A_52_P3	0.02369	1.71139	down	Zbtb11	Mus musc	NM_173026
A_30_P0	0.01971	1.86219	down		lincRNA:chr17:3103174-3114885 reverse strand	
A_55_P1	0.02347	1.53688	down	Unc5b	Mus musc	NM_029770
A_55_P2	0.0269	1.83755	down	H2afb3-ps	PREDICT	XM_889501
A_30_P0	0.04811	1.61931	down		lincRNA:chr2:174088550-174109425 forward strand	
A_51_P1	0.03386	1.64005	down	Zadh2	Mus musc	NM_146090
A_30_P0	0.00327	1.94802	down		lincRNA:chr12:103151385-103157735 forward strand	
A_55_P2	0.01508	2.80682	down		RIKEN cl	AK003851
A_51_P4	0.01285	7.04733	down		immunog	X87228
A_30_P0	0.04508	1.87118	down		lincRNA:chr5:149751979-149808240 reverse strand	
A_30_P0	0.038	1.56393	down		lincRNA:chr11:19778600-19815950 forward strand	
A_55_P1	0.03203	1.50292	down	Pogz	Mus musc	NM_172683
A_51_P2	0.03192	1.52898	down	2610306M	Mus musc	NR_028298
A_55_P2	0.01983	3.04671	down	Plekhhb1	Mus musc	NM_013746
A_55_P2	0.00727	1.56709	down		SET dom	AK141316
A_30_P0	0.01268	2.12601	down		lincRNA:chr5:149751979-149808240 reverse strand	
A_30_P0	0.00934	1.92726	down		lincRNA:chr10:5950116-5958250 reverse strand	
A_51_P3	0.0371	1.82386	down	Rfx2	Mus musc	NM_009056
A_55_P2	0.0121	2.78659	down	Gm1971	PREDICT	XM_001472879
A_55_P1	0.00878	1.74209	down	Lca5l	Mus musc	NM_001001492
A_55_P2	0.02155	1.50022	down	Mc5r	Mus musc	NM_013596

A_30_P0	0.04929	1.70086	down		lincRNA:chr1:36012298-36020311 reverse strand
A_30_P0	0.02609	1.50843	down		lincRNA:chr11:60728207-60745369 forward strand
A_30_P0	0.02573	2.45887	down		lincRNA:chr8:67213300-67271700 forward strand
A_30_P0	0.02294	1.65596	down		lincRNA:chr5:74487385-74497428 reverse strand
A_55_P2	0.02632	1.54245	down		Putative uAK149319
A_55_P2	0.04524	1.61031	down		AU RNA AK019978
A_55_P1	0.04604	2.77616	down	LOC1000	PREDICT XR_033948
A_55_P2	0.0244	1.59999	down	LOC1000	PREDICT XR_034828
A_66_P1	0.00837	1.63064	down	Skint5	Mus musc NM_001167878
A_52_P5	0.02669	3.7714	down	A8300181	Mus musc NM_177173
A_30_P0	0.04091	1.90936	down		lincRNA:chr18:60812427-60819775 reverse strand
A_55_P2	0.03067	1.82938	down	4933428C	Mus musc AK016962
A_30_P0	0.0388	1.56651	down		lincRNA:chr1:58443698-58449898 reverse strand
A_30_P0	0.01662	2.24218	down		lincRNA:chr5:125713450-125735500 reverse strand
A_55_P2	0.00195	1.66416	down	Pde4dip	Mus musc NM_001039376
A_51_P2	0.04304	2.32575	down	Gm9767	Mus musc NR_028030
A_55_P2	0.02014	1.60948	down	5230400M	Mus musc AK030345
A_30_P0	0.00706	1.62076	down		lincRNA:chr2:25182970-25188091 reverse strand
A_30_P0	0.04814	1.73787	down		lincRNA:chr5:149947200-149979950 forward strand
A_55_P1	0.00429	1.61364	down	LOC1000	PREDICT XM_001473588
A_30_P0	0.00131	2.01136	down		lincRNA:chr2:22782700-22801900 reverse strand
A_30_P0	0.02827	1.52134	down		lincRNA:chr14:118774481-118873242 reverse strand
A_55_P2	0.0373	1.53485	down	Emilin3	Mus musc NM_182840
A_52_P2	0.02592	1.81126	down	Slc26a9	Mus musc NM_177243
A_66_P1	0.02242	2.41711	down		Mouse T-M11859
A_30_P0	0.02855	2.23754	down		lincRNA:chr7:99879368-99889978 reverse strand
A_30_P0	0.0481	2.34016	down		lincRNA:chr2:173121033-173124485 forward strand
A_55_P2	0.01113	1.56494	down	Zfp691	Mus musc NM_183140
A_66_P1	0.01419	3.13006	down	Axin2	Mus musc NM_015732
A_55_P1	0.02126	1.87787	down	LOC1000	PREDICT XM_001471788
A_55_P1	0.04804	1.88369	down	Mamdc4	Mus musc NM_001081199
A_55_P2	0.04613	1.6097	down	Syngap1	PREDICT XM_915205

A_52_P4	0.03961	1.54593	down		RIKEN cl	AK044654
A_55_P2	0.02083	2.34886	down	1700012I	PREDICT	XM_001474730
A_55_P2	0.03783	1.63748	down	Papln	Mus musc	NM_130887
A_30_P0	0.01512	1.548	down			lincRNA:chr12:52950465-52950990 reverse strand
A_30_P0	0.01166	1.73991	down			lincRNA:chr5:35492530-35492959 reverse strand
A_55_P2	0.01042	1.71943	down			acidic (leu BC093506
A_30_P0	0.03389	1.94419	down			lincRNA:chr12:72103832-72116875 reverse strand
A_55_P1	0.00143	1.78643	down		ribosomal	AK041476
A_55_P1	0.00175	2.15144	down	Gm4385	PREDICT	XM_001480022
A_51_P3	0.00226	7.37652	down	Lrtm1	Mus musc	NM_176920
A_55_P2	0.03444	1.55443	down	Grm5	Mus musc	NM_001143834
A_30_P0	0.01983	4.82782	down			lincRNA:chr11:102878974-102888924 forward strand
A_55_P2	0.02149	1.70358	down	LOC6363	PREDICT	XM_922121
A_55_P2	0.006	2.30298	down	Dmc1	Mus musc	NM_010059
A_30_P0	0.03894	1.76347	down			lincRNA:chr2:155269145-155303251 reverse strand
A_30_P0	0.00357	2.45022	down			lincRNA:chr9:41300137-41301556 forward strand
A_55_P1	0.02623	2.12256	down	Gm8639	PREDICT	XM_990610
A_55_P1	0.01218	1.57554	down		PREDICT	XM_001476348
A_30_P0	0.03928	1.64126	down			lincRNA:chr18:84760623-84761084 forward strand
A_55_P2	0.02582	1.50851	down	Zfp316	Mus musc	NM_017467
A_55_P2	0.03574	1.64972	down	Krtap11-1	Mus musc	NM_001113406
A_52_P2	0.00785	1.95738	down		RIKEN cl	AK040674
A_30_P0	0.01851	1.74945	down			lincRNA:chr9:65376063-65390480 reverse strand
A_30_P0	0.01038	1.65125	down			lincRNA:chr14:21461716-21462270 forward strand
A_51_P4	0.04175	4.46178	down	C2cd4b	Mus musc	NM_001081314
A_55_P2	0.01462	1.8765	down	Tom1	Mus musc	NM_001136259
A_55_P1	0.00306	1.62405	down	Pde4dip	Mus musc	NM_001039376
A_55_P2	0.01721	1.76514	down	Tmem121	Mus musc	NM_153776
A_55_P2	0.03273	1.67148	down	Psg18	Mus musc	NM_011963
A_55_P2	0.04927	6.79273	down	Clec18a	Mus musc	NM_181549
A_30_P0	0.0228	2.16579	down			lincRNA:chr11:120097758-120098581 forward strand
A_55_P2	0.01065	1.80588	down	Ppp1r15a	Mus musc	NM_008654

A_30_P0	0.04183	1.68858	down		lincRNA:chr8:48476637-48492537 reverse strand
A_30_P0	0.04465	2.38859	down		lincRNA:chr1:95871175-95886625 reverse strand
A_55_P1	0.02054	1.67328	down	Cdkl3	Mus musc NM_153785
A_30_P0	0.02712	1.76759	down		lincRNA:chr2:94017095-94019092 reverse strand
A_55_P2	0.01626	2.99172	down	Olfr220	Mus musc NM_207694
A_55_P2	0.02564	1.50596	down	C530014F	Mus musc AK049648
A_30_P0	0.00387	1.72745	down		lincRNA:chr3:84609788-84618062 reverse strand
A_30_P0	0.04542	1.90663	down		lincRNA:chr7:6210340-6229115 forward strand
A_55_P2	0.04394	1.72818	down	Gm3099	XM_001475922
A_55_P2	0.0029	2.16921	down		Novel pro AK083112
A_55_P2	0.02524	1.69151	down	Gm2204	PREDICT XM_001472809
A_30_P0	0.04559	1.80474	down		lincRNA:chr14:33115110-33131171 forward strand
A_55_P2	0.01426	1.83781	down		Putative u XM_001472329
A_30_P0	0.02313	1.5985	down		lincRNA:chr19:56820850-56837925 forward strand
A_52_P4	0.03958	1.90015	down	1810014F	Mus musc NM_026928
A_51_P2	0.02624	1.83117	down	Cdkl1	Mus musc NM_183294
A_55_P2	0.02776	1.58062	down	AU01558	AU01558 AU015584
A_55_P2	0.02142	8.05861	down	Pou1f1	Mus musc NM_008849
A_30_P0	0.01341	1.69814	down		lincRNA:chr10:60473030-60535340 forward strand
A_30_P0	0.04901	1.53858	down		lincRNA:chrX:54627918-54638568 reverse strand
A_30_P0	0.00908	2.40651	down		lincRNA:chr3:88323145-88335770 reverse strand
A_55_P2	0.04826	1.84101	down		RIKEN cl AK019527
A_30_P0	0.04274	1.52537	down		lincRNA:chr8:18895366-18925423 reverse strand
A_55_P1	0.00443	1.63547	down	4933408B	Mus musc NM_177773
A_55_P2	0.02827	2.18274	down	Tmem200	PREDICT XM_001480132
A_51_P4	0.02923	1.52089	down	Olfr1358	olfactory XM_981298
A_30_P0	0.00102	1.51395	down		lincRNA:chr1:58443698-58449898 reverse strand
A_55_P2	3.35E-04	2.69144	down	Magea1	Mus musc NM_020015
A_52_P6	0.03561	2.14484	down	LOC6411	PREDICT XM_918536
A_30_P0	0.04432	1.79667	down		lincRNA:chr15:5975553-5994636 reverse strand
A_66_P1	0.03328	1.69658	down	Mamdc4	Mus musc NM_001081199
A_55_P2	0.04342	1.8599	down	LOC1000	Mus musc AK016549

A_30_P0	0.04851	1.84531	down		lincRNA:chr2:71575871-71583454 reverse strand
A_30_P0	0.01173	1.97492	down		lincRNA:chrX:75813213-75829323 forward strand
A_30_P0	0.02895	4.65467	down		lincRNA:chr17:32229024-32229663 forward strand
A_30_P0	0.02133	1.79466	down		lincRNA:chr1:34735032-34781146 forward strand
A_55_P2	0.04469	1.68632	down	Pip5kl1	Mus muscNM_198191
A_30_P0	0.00362	1.92024	down		lincRNA:chr16:90116006-90119297 reverse strand
A_30_P0	9.48E-05	1.6168	down		lincRNA:chr13:112207480-112213280 reverse strand
A_55_P2	0.01133	1.63957	down	Whsc1	Mus muscNM_001081102
A_30_P0	0.02293	2.1634	down		lincRNA:chr6:86476240-86513483 forward strand
A_55_P2	0.03144	2.43304	down	Gm9992	Mus muscNM_001142539
A_55_P2	0.02096	3.29989	down	Ccdc30	Mus muscNM_029286
A_55_P2	0.02376	1.63942	down		
A_30_P0	0.02604	4.1909	down		lincRNA:chr2:35828611-35838083 forward strand
A_52_P1	0.02121	1.67119	down	AI428936	Mus muscNM_153577
A_30_P0	0.0434	1.67532	down		lincRNA:chr1:63264155-63345773 forward strand
A_55_P2	0.00693	1.90496	down	Oc90	Mus muscNM_010953
A_55_P1	0.02667	2.19716	down	Cachd1	Mus muscNM_198037
A_51_P4	0.00128	2.04873	down	Has1	Mus muscNM_008215
A_30_P0	0.04617	1.61016	down		lincRNA:chr1:196802568-196847687 forward strand
A_55_P2	0.0248	1.58485	down	Pard6g	Mus muscNM_053117
A_30_P0	0.00122	1.76422	down		lincRNA:chr2:67836003-67836461 forward strand
A_55_P2	0.02206	2.26644	down		Putative uXM_001478824
A_30_P0	0.00358	2.3133	down		lincRNA:chr7:77323753-77482708 reverse strand
A_30_P0	0.01539	2.34136	down		lincRNA:chr1:45800000-45834825 reverse strand
A_55_P2	0.02485	2.05596	down	C7	PREDICTXM_356827
A_51_P4	0.00938	1.6461	down	Cpne6	Mus muscNM_009947
A_55_P2	0.02223	3.44986	down		phospholiAK039149
A_55_P1	0.00309	1.93228	down	BC050254	PREDICTXR_035237
A_51_P4	0.02503	2.25209	down	Grifin	Mus muscNM_030022
A_55_P2	0.01526	1.61393	down	Homer1	Mus muscNM_011982
A_55_P2	0.03556	1.61758	down	Gm7957	PREDICTXR_001840
A_55_P2	0.00967	1.6255	down	Hhat	Mus muscNM_144881

A_30_P0	0.03738	1.87831	down		lincRNA:chr7:88126007-88138301 reverse strand
A_30_P0	0.0293	1.54035	down		lincRNA:chrX:148819227-148844227 forward strand
A_55_P2	0.0074	1.96321	down	C81189	Mus musc AK158814
A_30_P0	0.03992	1.57409	down		lincRNA:chr3:96205368-96217943 forward strand
A_30_P0	6.29E-05	2.06887	down		lincRNA:chr2:77146893-77155643 forward strand
A_55_P2	0.01308	2.73383	down		
A_30_P0	0.01185	3.69983	down		lincRNA:chr17:32035750-32056000 forward strand
A_55_P1	0.00188	2.06942	down	Il9r	Mus musc NM_001134458
A_51_P4	2.04E-04	1.86759	down	Elf4	Mus musc NM_019680
A_30_P0	0.01312	1.52982	down		lincRNA:chr7:134643558-134644056 forward strand
A_52_P5	0.03049	2.53477	down	Cdc14a	Mus musc NM_001173553
A_55_P2	0.00155	1.51922	down	Ppp1r8	Mus musc NM_146154
A_30_P0	0.03722	1.53009	down		lincRNA:chr2:157838320-157853495 reverse strand
A_30_P0	0.00891	2.19616	down		lincRNA:chr8:119732348-119749198 reverse strand
A_55_P2	0.01197	1.92803	down	Olfr469	Mus musc NM_146426
A_55_P2	0.0186	1.50695	down	Cmpk2	Mus musc NM_020557
A_30_P0	0.00128	1.66039	down		lincRNA:chr9:89167172-89168980 forward strand
A_52_P5	0.0133	2.32592	down		caveolin 2 AB049605
A_30_P0	0.03162	2.11733	down		lincRNA:chr17:36136010-36136696 forward strand
A_55_P2	0.01714	1.60342	down	Gm3939	PREDICT XM_001478549
A_65_P1	0.0192	1.59527	down	Ldb3	Mus musc NM_011918
A_52_P3	4.39E-04	3.26901	down	Rgs2	Mus musc NM_009061
A_52_P5	0.0129	1.53315	down	Chd1l	Mus musc NM_026539
A_55_P2	0.03462	2.99706	down	Agbl4	Mus musc NM_030231
A_30_P0	0.02461	3.64939	down		lincRNA:chr9:61881173-61881351 reverse strand
A_51_P2	0.03905	1.61599	down	Ltb4r2	Mus musc NM_020490
A_30_P0	0.02714	1.6855	down		lincRNA:chr8:44232164-44267061 reverse strand
A_55_P1	0.01508	3.07802	down	Pde11a	Mus musc NM_001081033
A_66_P1	0.00414	1.94274	down	Nfia	Mus musc NM_001122953
A_55_P2	0.00563	2.09781	down		RIKEN cl XM_001474539
A_66_P1	0.04069	2.92492	down	Gm454	PREDICT XR_032409
A_55_P1	0.03494	1.64992	down	Its1n1	Mus musc NM_010587

A_30_P0	0.00269	1.56858	down		lincRNA:chr18:84735774-84760824 reverse strand
A_30_P0	0.01308	2.15754	down		lincRNA:chr9:41300137-41301556 forward strand
A_55_P2	0.02339	2.41495	down	AI451458	UI-M-FY CA328248
A_30_P0	0.02817	2.85045	down		lincRNA:chr16:30936314-30954449 reverse strand
A_55_P2	0.03012	1.734	down	Fgf23	Mus musc NM_022657
A_55_P2	0.03552	1.86814	down	Gm12128	PREDICT XM_001472488
A_66_P1	0.02104	1.97002	down	Gm9908	PREDICT XM_001473828
A_30_P0	0.02191	1.65224	down		lincRNA:chr9:81536195-81538236 forward strand
A_52_P2	0.0476	1.6459	down	Acot4	Mus musc NM_134247
A_55_P2	0.04523	1.63026	down	Zfp142	Mus musc NM_029888
A_55_P2	0.03063	1.60497	down	6230400D	Mus musc AK018074
A_55_P1	0.03951	1.52842	down		Putative u AK145331
A_55_P2	0.04351	1.58886	down	1700081L	Mus musc NM_001081045
A_52_P4	0.02429	1.88846	down	1110028C	Mus musc NM_177645
A_55_P1	0.0121	1.61737	down	Vmn2r11	Mus musc NM_001102584
A_55_P2	0.03429	1.53814	down	Srpx	Mus musc NM_016911
A_30_P0	0.03216	1.96785	down		lincRNA:chr13:112210279-112212150 reverse strand
A_55_P2	0.03984	2.49031	down	Gm2485	PREDICT XM_001474163
A_51_P4	0.02046	2.28455	down	Nup214	Mus musc NM_172268
A_30_P0	0.04565	1.5479	down		lincRNA:chr6:86776350-86799379 reverse strand
A_55_P1	0.01249	4.86793	down	Megf10	Mus musc NM_001001979
A_55_P2	0.00243	1.52917	down	Rbm12	copine I C AK020481
A_30_P0	0.00228	1.90418	down		lincRNA:chr9:121256738-121257487 forward strand
A_51_P3	9.35E-04	1.62612	down	Wipf3	Mus musc NM_001167860
A_55_P2	6.52E-04	1.91593	down	Gm3230	Mus musc NR_033642
A_51_P3	0.01153	2.48531	down	Mfi2	Mus musc NM_013900
A_51_P3	8.61E-04	1.98832	down	2810459M	Mus musc NM_001144992
A_55_P2	0.00503	1.72429	down	Gm6420	predicted XM_887803
A_30_P0	0.02678	1.83295	down		lincRNA:chr10:119960546-119979696 reverse strand
A_55_P1	0.03134	2.14386	down	Lca5l	Mus musc NM_001001492
A_55_P2	0.01351	1.52513	down	Pdxk	Mus musc NM_172134
A_55_P1	0.03413	1.61606	down	Adck4	Mus musc NM_133770

A_30_P0	0.02317	3.13435	down		lincRNA:chr3:127037711-127111912 reverse strand
A_55_P1	0.02859	1.71748	down	Gm3268	PREDICT_XM_001476140
A_30_P0	0.00875	1.64851	down		lincRNA:chr14:43408099-43415349 forward strand
A_55_P2	0.01847	2.06298	down	Trim43b	Mus musc NM_001170884
A_55_P2	6.53E-04	1.53873	down	L2hgdh	Mus musc NM_145443
A_55_P1	0.0176	2.63763	down	Olfr1262	Mus musc NM_146974
A_55_P2	0.01483	1.87953	down	Spata22	Mus musc NM_001045531
A_51_P2	0.02534	2.52292	down	St8sia2	Mus musc NM_009181
A_55_P2	0.03174	1.55751	down		RIKEN cl AK032721
A_52_P1	0.01614	1.81335	down	Irs1	Mus musc NM_010570
A_30_P0	0.0401	1.85821	down		lincRNA:chr5:33174092-33200792 reverse strand
A_55_P2	0.04193	1.65707	down	D230040J	Mus musc AK084413
A_51_P2	0.01513	1.56018	down	Tbc1d20	Mus musc NM_024196
A_55_P2	0.02077	1.79505	down	C330011N	PREDICT_XR_035219
A_30_P0	0.00513	3.47698	down		lincRNA:chr10:98718526-98719169 reverse strand
A_51_P1	0.00229	1.5242	down	Socs2	Mus musc NM_007706
A_30_P0	0.00328	3.62977	down		lincRNA:chr12:12768528-12849976 forward strand
A_55_P2	0.01305	1.76251	down	Lrig1	Mus musc NM_008377
A_51_P3	0.01695	2.68836	down	4921517D	Mus musc NM_026338
A_52_P5	0.02821	1.70207	down	Zfp558-ps	Mus musc NM_028935
A_30_P0	0.04031	1.70607	down		lincRNA:chr8:26345571-26346095 reverse strand
A_55_P2	0.00529	1.65539	down	Ncrna000	Mus musc AK048874
A_30_P0	0.04629	2.40296	down		lincRNA:chr11:119794849-119803349 forward strand
A_55_P2	0.01599	2.47372	down	Tceanc	Mus musc NM_001007577
A_55_P2	0.01924	2.38323	down	Palm2	Mus musc NM_172868
A_30_P0	0.02227	1.88177	down		lincRNA:chr15:100906946-100907748 reverse strand
A_52_P6	0.01172	2.26366	down	Acer1	Mus musc NM_175731
A_66_P1	0.0229	2.76374	down	Ffar3	Mus musc NM_001033316
A_55_P2	0.00464	1.83431	down	Ddi2	Mus musc NM_001017966
A_30_P0	0.02516	1.73906	down		lincRNA:chr9:41184479-41240162 forward strand
A_55_P2	0.0428	1.62517	down	A430033F	Mus musc NM_183025
A_55_P2	0.01515	1.62268	down	Srrm3	Mus musc NM_021403

A_51_P2	0.02298	4.00816	down	Nr4a1	Mus musc	NM_010444
A_55_P2	0.02209	5.39536	down	BC051070	Mus musc	NM_178412
A_55_P2	0.00465	2.41154	down	D4Ert68	Mus musc	AK078562
A_30_P0	0.02657	3.86182	down			lincRNA:chr5:124667541-124700029 forward strand
A_30_P0	0.03835	1.68108	down			lincRNA:chr8:106592650-106603525 reverse strand
A_55_P1	0.0061	1.50698	down	Gm5050	PREDICT	XR_032332
A_30_P0	0.00677	1.88627	down			lincRNA:chr1:94077221-94091396 reverse strand
A_55_P2	0.00935	1.61688	down		Putative u	AK158028
A_30_P0	0.02775	3.92066	down			lincRNA:chrX:45814752-45816313 reverse strand
A_52_P5	0.04499	2.3119	down	Rbpjl	Mus musc	NM_009036
A_30_P0	0.01892	1.77517	down			lincRNA:chr13:74642700-74701900 forward strand
A_51_P1	0.04384	2.105	down	Adrbk2	Mus musc	NM_177078
A_30_P0	0.04144	3.34434	down			lincRNA:chrX:11671167-11700242 forward strand
A_55_P1	0.04592	1.84236	down	Atad3a	Mus musc	NM_179203
A_52_P3	0.02885	1.72217	down	Kndc1	Mus musc	NM_177261
A_55_P1	0.01721	1.98426	down	Pcgf2	Mus musc	NM_009545
A_55_P2	0.00429	1.96802	down	9530003C	Mus musc	AK020539
A_55_P2	0.01727	1.75338	down	Ms4a10	Mus musc	NM_023529
A_52_P8	0.01245	1.51502	down	Thrb	Mus musc	NM_009380
A_51_P4	0.03061	3.03657	down	Rtp1	Mus musc	NM_001004151
A_30_P0	0.03497	1.59774	down			lincRNA:chr9:65651848-65652920 reverse strand
A_55_P2	0.00547	3.14861	down	1700092C	AGENCC	CD772809
A_30_P0	0.01061	2.39165	down			lincRNA:chr7:99879368-99889978 reverse strand
A_55_P2	0.01633	2.21346	down	Gm10419	Mus musc	AK165889
A_30_P0	0.01767	1.62617	down			lincRNA:chr15:84737071-84753513 reverse strand
A_55_P1	0.03464	2.62506	down	Tmem121	Mus musc	NM_153776
A_55_P2	0.00423	1.76048	down	Pcdhb10	Mus musc	NM_053135
A_55_P1	0.01677	2.50957	down	Gm4925	Mus musc	NM_001037166
A_30_P0	0.04524	2.001	down			lincRNA:chr15:59059450-59070576 reverse strand
A_55_P2	7.82E-05	2.36361	down	Madcam1	Mus musc	NM_013591
A_55_P2	0.04711	2.05515	down	4930488N	Mus musc	AK015648
A_30_P0	0.03688	2.08276	down			lincRNA:chr9:65376063-65390480 forward strand

A_55_P2	0.03841	2.07445	down			
A_55_P20	0.02916	2.52691	down	Gm101	Mus musc	NM_001115074
A_52_P34	0.04509	1.51455	down	1190005F	Mus musc	NM_026876
A_51_P1	0.00293	1.57712	down	Zbtb43	Mus musc	NM_027947
A_55_P20	0.02348	1.96282	down	Zmym4	Mus musc	NM_001114399
A_55_P20	0.03724	1.77613	down	Gm6578	Mus musc	NR_003631
A_55_P2	0.02475	4.37698	down	1700066J	AGENC	CN840722
A_30_P0	0.00462	1.58194	down		lincRNA:chr13:98062189-98066613 forward strand	
A_30_P0	0.04897	2.18822	down		lincRNA:chr13:28760289-28977218 reverse strand	
A_55_P2	0.04815	1.60076	down	4933415J	Mus musc	AK016822
A_55_P20	0.04588	2.87914	down	Pde3a	Mus musc	NM_018779
A_30_P0	0.01781	2.19354	down		lincRNA:chr15:73227424-73257474 forward strand	
A_55_P20	0.04191	1.91415	down	Gm3718	PREDICT	XM_001477716
A_51_P3	0.00825	1.84341	down	Hells	Mus musc	NM_008234
A_55_P2	0.00273	2.82324	down	E230024E	Mus musc	AK054157
A_51_P5	0.00867	1.96941	down	Nr5a2	Mus musc	NM_030676
A_51_P2	0.03929	6.20552	down	Mmd2	Mus musc	NM_175217
A_51_P3	0.01579	1.65297	down		RIKEN cl	AK015429
A_52_P50	0.03573	2.28509	down	Mmp9	Mus musc	NM_013599
A_55_P20	0.03739	1.52645	down	Errfi1	Mus musc	NM_133753
A_52_P40	0.03271	1.6581	down	Tmem33	Mus musc	NM_028975
A_30_P0	6.86E-04	2.2305	down		lincRNA:chr16:64758224-64765700 forward strand	
A_51_P4	0.04741	1.55054	down	Cdh15	Mus musc	NM_007662
A_51_P3	0.01717	3.08498	down	3110009E	Mus musc	NM_001172074
A_30_P0	0.04799	2.1276	down		lincRNA:chr15:86035939-86042539 forward strand	
A_51_P4	0.02511	1.82579	down	Socs3	Mus musc	NM_007707
A_52_P6	0.03953	2.7572	down	Gm129	Mus musc	NM_001033302
ERCC-00	0.04977	1.55061	down		Unknown	
A_30_P0	0.00843	1.58165	down		lincRNA:chr4:138657728-138687028 reverse strand	
A_55_P20	0.01268	1.62251	down	Rab4a	Mus musc	NM_009003
A_30_P0	0.04565	3.60107	down		lincRNA:chr16:23992037-24001037 forward strand	
A_30_P0	0.02312	1.62572	down		lincRNA:chr15:76193801-76194225 forward strand	

A_51_P3	0.00611	2.46197	down	Hydin	Mus musc	NM_172916
A_66_P1	0.04605	1.57508	down	Ddo	Mus musc	NM_027442
A_30_P0	0.02266	1.82653	down		lincRNA:chr8:108153471-108159346 reverse strand	
A_30_P0	0.04211	2.59081	down		lincRNA:chrX:34360500-34388500 reverse strand	
A_30_P0	0.00477	1.59965	down		lincRNA:chr7:134620707-134626739 reverse strand	
A_30_P0	0.01063	3.17012	down		lincRNA:chr11:58659807-58676282 reverse strand	
A_55_P2	0.00792	1.93457	down	Gm2453	PREDICT	XM_001473654
A_30_P0	0.00505	1.81359	down		lincRNA:chr17:15226181-15250333 reverse strand	
A_55_P2	0.01454	2.04402	down	5930430L	Mus musc	AK148051
A_30_P0	0.00302	2.30188	down		lincRNA:chr14:76237150-76237464 reverse strand	
A_55_P1	0.02529	1.5051	down	Purb	Mus musc	NM_011221
A_30_P0	0.03743	4.07421	down		lincRNA:chr7:71093563-71095094 forward strand	
A_55_P2	0.04581	1.54041	down	6330416L	Mus musc	NM_176962
A_55_P1	0.04108	1.57371	down	Fam40b	Mus musc	NM_001037740
A_55_P1	0.00864	2.98945	down	Fam165b	family with sequence similarity 165, member B Gene [Source:MGI (curated);Acc:MGI:1916]	
A_55_P2	0.0042	2.67376	down	Gm4590	PREDICT	XM_001478833
A_55_P1	0.02831	1.70521	down	Zfp606	Mus musc	NM_001039951
A_30_P0	0.03153	1.52132	down		lincRNA:chr1:63163019-63164281 forward strand	
A_30_P0	0.00534	2.16345	down		lincRNA:chr19:54011403-54018978 forward strand	
A_30_P0	0.01237	2.5249	down		lincRNA:chr3:93564825-93576725 reverse strand	
A_55_P2	0.00119	1.64691	down	1600014K	Mus musc	NM_028046
A_51_P1	0.02252	2.51132	down	Ogdhl	Mus musc	NM_001081130
A_30_P0	0.01771	1.71281	down		lincRNA:chr9:118291593-118324230 forward strand	
A_30_P0	0.01828	1.55103	down		lincRNA:chr7:118248833-118267766 reverse strand	
A_55_P2	0.00438	2.05465	down	Ccr10	Mus musc	NM_007721
A_66_P1	0.01391	1.57201	down	Gm4428	PREDICT	XM_001479159
A_55_P2	0.00307	3.12693	down	Rbmy1a1	Mus musc	NM_011253
A_52_P2	0.00514	1.93984	down	Mobkl2b	Mus musc	NM_178061
A_55_P2	0.04743	1.63466	down	1600027N	Mus musc	NM_028479
A_52_P1	0.0289	1.50735	down	Tmem49	Mus musc	NM_029478
A_55_P2	0.03271	1.53605	down	D7Ert59	AU02304	AU023048
A_30_P0	0.04961	1.94709	down		lincRNA:chr15:82769917-82770296 reverse strand	

A_30_P0	0.04427	1.92066	down		lincRNA:chr2:35828611-35838083 forward strand

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MUST0000009719E

JST00000064920

186] [ENSMUST0000011806.

ProbeName	p-value (T)	FCAbsolute	regulation	GeneSymbol	Description	GenbankAccession
A_55_P19	0.009805	6.799838	up	C130079C	Mus musc	NM_177661
A_55_P20	0.00208	1.548496	up	Slc36a1	Mus musc	NM_153139
A_55_P21	0.037903	2.266519	up	Wnt8b	Mus musc	NM_011720
A_30_P01	0.03735	1.514682	up		lincRNA:chr15:79764481-79809909 forward strand	
A_66_P10	0.036745	3.279265	up	Gm2650	PREDICT	XM_001474283
A_55_P20	0.027311	1.569606	up	Nqo2	Mus musc	NM_020282
A_30_P01	0.031961	1.791535	up		lincRNA:chr17:21177225-21187525 reverse strand	
A_55_P20	0.028938	1.837247	up	Gm7969	PREDICT	XM_001473218
A_55_P21	0.03554	1.617143	up		WD repeat domain 67 Gene [Source:MGI Symbol;Acc:MGI:2684931] [ENSMUSTO	
A_51_P49	0.018947	1.530801	up	Cyp4f14	Mus musc	NM_022434
A_30_P01	0.038292	3.04376	up		lincRNA:chr11:117835849-117842574 reverse strand	
A_55_P19	0.037021	10.86369	up	LOC3809	Mus musc	NM_001037748
A_55_P19	0.049555	1.583836	up	Ncaph	Mus musc	NM_144818
A_30_P01	0.010819	6.588181	up		lincRNA:chr9:96670035-96682896 forward strand	
A_51_P27	0.028538	2.263291	up	Igfals	Mus musc	NM_008340
A_66_P13	0.022558	1.508461	up	Olfir532	Mus musc	NM_147026
A_55_P19	0.032277	3.054115	up	LOC1000	PREDICT	XM_001474157
A_30_P01	0.008003	2.102996	up		lincRNA:chr3:34497447-34501170 reverse strand	
A_51_P29	7.15E-04	2.092281	up	Pde7a	Mus musc	NM_008802
A_51_P31	0.026182	1.554278	up	Tubb4	Mus musc	NM_009451
A_51_P47	0.010887	1.918763	up	2010317E	Mus musc	NM_001081085
A_52_P49	0.007467	6.706902	up	Paqr9	Mus musc	NM_198414
A_55_P21	0.015027	2.612485	up	Gm13138	Mus musc	NM_001177767
A_55_P22	0.015288	6.208603	up	E330011C	Mus musc	AK087725
A_30_P01	0.02195	2.819619	up		lincRNA:chr17:88890039-88905680 forward strand	
A_55_P21	0.017833	2.734763	up	Neurog3	Mus musc	NM_009719
A_55_P19	0.016993	2.140015	up	Pfkfb4	Mus musc	NM_173019
A_55_P21	0.044969	1.866095	up	LOC6759	PREDICT	XR_004857
A_52_P75	0.039757	2.161005	up	Ccdc99	Mus musc	NM_027411
A_30_P01	0.011742	2.191377	up		lincRNA:chr5:92548501-92566401 forward strand	
A_52_P87	0.029288	1.819761	up	Sema3c	Mus musc	NM_013657
A_30_P01	0.049796	1.894643	up		lincRNA:chr1:138570107-138632310 forward strand	

A_51_P33	0.020698	1.570124	up	Ints7	Mus musc	NM_178632
A_55_P21	0.027727	4.527254	up	Pla2g2e	Mus musc	NM_012044
A_51_P50	0.015338	2.487842	up	Nrarp	Mus musc	NM_025980
A_55_P20	0.020065	1.777555	up		predicted	XM_001479512
A_51_P42	0.033564	1.517725	up	Senp5	Mus musc	NM_177103
A_55_P19	0.037707	2.148233	up			
A_30_P01	0.03477	1.603932	up		lincRNA:chr4:124127144-124334840 reverse strand	
A_55_P19	0.038227	1.800418	up	LOC1000	PREDICT	XM_001480399
A_55_P22	0.002996	1.715869	up	C230098C	Mus musc	AK082735
A_51_P43	0.002865	1.651234	up	Paqr7	Mus musc	NM_027995
A_51_P25	0.014311	4.733183	up	S100a8	Mus musc	NM_013650
A_51_P20	0.008652	2.247297	up	Apln	Mus musc	NM_013912
A_55_P20	0.031831	3.192969	up	Otop1	Mus musc	NM_172709
A_51_P25	0.020785	6.431943	up	Kcnj14	Mus musc	NM_145963
A_55_P20	0.008293	1.909125	up	2810032G	Mus musc	AK029678
A_52_P65	0.038182	2.304325	up	6720463M	Mus musc	NM_175265
A_51_P20	0.027738	1.659969	up	Metrn	Mus musc	NM_133719
A_30_P01	0.030224	1.811043	up		lincRNA:chr6:117329899-117516899 forward strand	
A_55_P19	0.046836	1.831294	up	Hn1l	Mus musc	NM_198937
A_66_P12	0.004441	1.853483	up	1700113I2	Mus musc	NM_026865
A_55_P19	0.008862	1.838453	up	LOC1000	PREDICT	XM_001474652
A_51_P27	0.001536	4.625752	up	Fam83d	Mus musc	NM_027975
A_55_P22	0.039839	2.863076	up	2700081L	BX51587	BX515870
A_55_P21	0.007348	4.466902	up	LOC1000	PREDICT	XM_001472072
A_66_P12	0.01994	2.350119	up	Gm7969	PREDICT	XM_001473218
A_55_P20	0.035026	1.890313	up	Unc5a	Mus musc	NM_153131
A_55_P20	0.04027	2.391578	up	Sdsl	Mus musc	NM_133902
A_55_P19	0.013442	1.619735	up		strawberry	BC064113
A_55_P21	0.03649	1.826282	up	Rrm2	Mus musc	NM_009104
A_30_P01	0.005362	1.513904	up		lincRNA:chr4:146507925-146532650 forward strand	
A_30_P01	0.005149	1.771258	up		lincRNA:chr2:127988295-128194920 reverse strand	
A_52_P63	0.04936	2.006216	up	Kcnk3	Mus musc	NM_010608
A_51_P19	0.032556	6.108851	up	Gtse1	Mus musc	NM_013882

A_52_P33	0.026583	2.519645	up	Fanca	Mus musc	NM_016925
A_55_P20	0.036642	3.218771	up	Adamts17	Mus musc	NM_001033877
A_55_P21	0.011087	6.853046	up	Mest	Mus musc	NM_008590
A_55_P20	0.03543	1.607685	up	Golga3	Mus musc	NM_008146
A_55_P20	0.02134	2.163577	up	Tk1	Mus musc	NM_009387
A_51_P41	0.015455	1.880684	up	Polr3g	Mus musc	NM_001081176
A_55_P21	0.035818	1.677734	up	Pdlim7	Mus musc	NM_026131
A_55_P21	0.041067	9.152267	up	Bhmt	Mus musc	NM_016668
A_52_P11	0.018642	2.732186	up	Tg	Mus musc	NM_009375
A_55_P22	0.007662	5.918094	up	C730029A	Mus musc	AK083183
A_55_P20	0.013061	2.222634	up	Kcnh2	Mus musc	NM_013569
A_30_P01	0.022219	1.795134	up		lincRNA:chr5:14923900-15062725 forward strand	
A_30_P01	0.047746	1.865746	up		lincRNA:chr12:25866632-25874507 forward strand	
A_55_P20	0.012797	3.149867	up	Poln	Mus musc	NM_181857
A_51_P17	0.036059	1.72264	up	LOC1000	Mus musc	NM_001173459
A_30_P01	0.015176	2.033655	up		lincRNA:chr4:146156575-146175425 reverse strand	
A_55_P20	0.046491	1.971278	up	Gm7337	Mus musc	NR_003652
A_52_P68	9.58E-04	11.7975	up	Defb14	Mus musc	NM_183026
A_51_P42	0.049441	6.707296	up		RIKEN cl	XM_001473370
A_55_P20	0.00625	4.72959	up	Gm2305	PREDICT	XM_001473102
A_51_P20	0.040362	1.655261	up	Rtn2	Mus musc	NM_013648
A_55_P24	0.024763	2.893086	up	Gm11520	UI-M-BH	BE647330
A_55_P21	0.023463	3.493671	up	Spag11b	Mus musc	NM_001039563
A_55_P20	0.007613	2.285459	up	Gm5556	PREDICT	XM_001478331
A_51_P25	0.006054	2.841335	up	Traip	Mus musc	NM_011634
A_52_P27	0.043458	1.522505	up	Osbp17	Mus musc	NM_001081434
A_55_P20	0.023598	3.56529	up	Poln	Mus musc	NM_181857
A_55_P20	0.003214	2.371539	up	Melk	Mus musc	NM_010790
A_55_P19	0.015643	1.727674	up	Cyp2r1	Mus musc	NM_177382
A_55_P24	0.038983	6.364416	up	Ncan	Mus musc	NM_007789
A_55_P19	0.030422	2.253677	up	Ryr3	Mus musc	NM_177652
A_55_P20	0.034741	1.517444	up	Fam89a	Mus musc	NM_001081120
A_52_P63	0.01745	2.273833	up	Troap	Mus musc	NM_030159

A_51_P44	0.035199	1.664706	up	Ptgr1	Mus musc	NM_025968
A_52_P57	0.01822	1.554152	up	Tmem144	Mus musc	NM_027495
A_55_P21	0.049163	1.761751	up	Gm2379	PREDICT	XM_001473765
A_55_P20	0.048758	1.771568	up	Hist1h2ag	Mus musc	NM_178186
A_55_P20	0.016793	1.52865	up	Dusp5	Mus musc	NM_001085390
A_55_P20	0.035834	1.792731	up	Tnfrsf9	Mus musc	NM_011612
A_30_P01	0.049569	1.821073	up		lincRNA:chr13:112337405-112356455 reverse strand	
A_51_P13	0.049464	1.773776	up	Lrrc66	Mus musc	NM_153568
A_55_P20	0.012784	1.90977	up	F2rl3	Mus musc	NM_007975
A_51_P16	0.008967	4.821676	up	3110082D	Mus musc	NM_028474
A_55_P19	0.031867	1.539833	up		Putative u	XM_897445
A_30_P01	0.04471	1.668003	up		lincRNA:chr12:111617728-111665403 reverse strand	
A_55_P20	0.016936	12.22237	up	Gm3586	PREDICT	XM_001477872
A_51_P39	0.043141	9.030991	up	Dapl1	Mus musc	NM_029723
A_55_P21	6.71E-04	5.028315	up	Acox1	Mus musc	NM_028765
A_52_P23	0.010905	6.094574	up	Fgf21	Mus musc	NM_020013
A_52_P57	8.49E-04	3.605612	up	Cela1	Mus musc	NM_033612
A_55_P21	0.033861	1.522246	up		RIKEN cl	XM_001475271
A_66_P12	0.016045	1.594271	up	Ulbp1	Mus musc	NM_029975
A_55_P21	0.03616	2.044242	up	Gm7000	PREDICT	XM_901778
A_51_P49	0.033396	3.662586	up	Fam64a	Mus musc	NM_144526
A_55_P19	0.003976	2.798372	up	LOC1000	PREDICT	XM_001474051
A_55_P20	0.021808	9.390637	up	Sly	Mus musc	NM_201530
A_55_P24	0.048328	2.352582	up	D7Ertd66	H3085D1	BG070263
A_30_P01	0.009553	2.438366	up		lincRNA:chr7:6302922-6306477 forward strand	
A_55_P20	0.048382	1.794226	up	Adap1	Mus musc	NM_172723
A_55_P20	0.006576	1.624355	up	Tnip3	Mus musc	NM_001001495
A_52_P47	0.003371	4.838473	up	Crtac1	Mus musc	NM_145123
A_51_P46	0.020097	2.385722	up	Cenpm	Mus musc	NM_178269
A_30_P01	0.043134	1.510184	up		lincRNA:chr4:15233302-15233632 reverse strand	
A_51_P32	0.02614	3.181123	up	Kif23	Mus musc	NM_024245
A_55_P21	0.025462	1.765503	up	Gm3711	PREDICT	XR_033357
A_55_P19	0.027516	1.61954	up	Sep-09	Mus musc	NM_001113487

A_55_P20	0.024464	2.141183	up	Nup210	Mus musc	NM_018815
A_55_P20	0.00815	6.137976	up	Mosc1	Mus musc	NM_001081361
A_51_P36	0.044793	1.514565	up	Tle6	Mus musc	NM_053254
A_66_P11	0.035736	5.067561	up	Pla2g2e	Mus musc	NM_012044
A_55_P19	0.034653	1.747913	up	Csprs	Mus musc	NM_033616
A_55_P20	0.029679	1.518003	up	Malt1	Mus musc	NM_172833
A_51_P41	4.44E-04	9.470829	up	Mogat2	Mus musc	NM_177448
A_30_P01	0.037415	2.23931	up			lincRNA:chr1:85036677-85038530 reverse strand
A_55_P21	0.014856	2.315969	up			Putative u
A_30_P01	0.010157	1.648379	up			lincRNA:chr8:82836971-82849309 reverse strand
A_30_P01	0.04723	2.174298	up			lincRNA:chr7:48794017-48815817 reverse strand
A_30_P01	0.017351	2.472386	up			lincRNA:chr1:139814266-139817889 reverse strand
A_55_P21	0.019642	2.993972	up	Gm5957	PREDICT	XM_001476729
A_52_P33	0.041066	1.806418	up	Lin9	Mus musc	NM_001103182
A_30_P01	0.035317	1.938832	up			lincRNA:chr15:99765243-99783300 forward strand
A_55_P19	5.78E-05	2.835842	up	Krt79	Mus musc	NM_146063
A_51_P32	0.01048	1.737159	up	Snrnp25	Mus musc	NM_030093
A_55_P22	0.03544	1.613842	up	Fzd3	Mus musc	NM_021458
A_55_P20	0.030991	10.41347	up	Sly	Mus musc	NM_201530
A_30_P01	0.012055	1.753838	up			lincRNA:chr14:103751075-103769725 forward strand
A_55_P21	0.007798	1.542982	up	Tmem128	transmem	AK076679
A_30_P01	0.037802	1.552033	up			lincRNA:chr17:95150800-95180650 reverse strand
A_55_P20	0.008216	5.918116	up	Mosc1	Mus musc	NM_001081361
A_55_P20	0.031289	1.751542	up	Gm7303	PREDICT	XM_925112
A_55_P19	0.038273	2.058856	up	Shc3	Mus musc	NM_009167
A_55_P21	0.011372	2.299864	up	Myl4	Mus musc	NM_010858
A_55_P20	0.012816	2.825975	up	LOC1000	PREDICT	XM_001479348
A_30_P01	0.019299	3.330504	up			lincRNA:chr18:77968421-77972209 reverse strand
A_55_P20	0.033368	2.364119	up	Gm7609	Mus musc	NM_001081746
A_55_P21	3.81E-04	3.105826	up	Mapk1ip1	Mus musc	NM_178684
A_30_P01	0.037923	1.571175	up			lincRNA:chr13:62734450-62785325 reverse strand
A_30_P01	0.00383	2.154209	up			lincRNA:chr10:118385588-118439338 reverse strand
A_55_P20	0.016786	3.72358	up	Car12	Mus musc	NM_178396

A_55_P20	0.019324	5.010589	up	Gm8028	PREDICT	XM_977531
A_66_P12	0.012423	3.100709	up	Duoxa1	Mus musc	NM_145395
A_55_P20	0.003263	2.949701	up	Zfyve28	Mus musc	NM_001015039
A_55_P22	0.039626	1.746647	up	4930572J	Mus musc	AK016280
A_51_P25	6.65E-04	2.05997	up	Mki67	Mus musc	NM_001081117
A_55_P21	0.022829	1.876473	up		RIKEN cl	XM_001476159
A_52_P32	0.005645	6.446623	up	Cpa2	Mus musc	NM_001024698
A_55_P19	0.016404	1.530508	up	Tdrd7	Mus musc	NM_146142
A_55_P22	0.009752	2.49714	up	9430041J	Mus musc	AK051461
A_55_P21	0.029869	2.744017	up	Fam20c	Mus musc	NM_030565
A_51_P28	0.040571	1.8455	up	Hrh3	Mus musc	NM_133849
A_51_P43	0.021235	2.685268	up	2310016C	Mus musc	NM_023516
A_51_P49	0.029995	2.597481	up	Ube2c	Mus musc	NM_026785
A_55_P22	0.015414	5.057642	up	4930445G	Mus musc	AK015390
A_55_P21	0.009002	1.764204	up	Snrnp25	Mus musc	NM_030093
A_30_P01	0.016236	2.292756	up		lincRNA:chr6:145647711-145756861 reverse strand	
A_55_P20	0.020472	2.687314	up	2310016C	Mus musc	NM_023516
A_51_P20	0.001394	10.76796	up	Lipf	Mus musc	NM_026334
A_55_P19	0.044561	3.568705	up	Gm3983	PREDICT	XM_001478663
A_30_P01	0.016771	1.874296	up		lincRNA:chr1:90149027-90152254 forward strand	
A_66_P13	0.016427	1.831479	up	Capn9	Mus musc	NM_023709
A_55_P21	0.036252	2.065433	up		Putative u	AK159059
A_51_P40	0.003815	2.349189	up	Ccne1	Mus musc	NM_007633
A_55_P19	0.01379	2.545543	up	Ghrh	Mus musc	NM_010285
A_55_P19	0.017984	2.20927	up	Fam55c	Mus musc	NM_001134494
A_52_P32	0.012199	1.539025	up	Trim16	Mus musc	NM_053169
A_51_P29	0.015378	2.37263	up	Insig1	Mus musc	NM_153526
A_55_P20	0.017247	2.613207	up	Gm8956	PREDICT	XR_030853
A_52_P53	0.004172	2.04439	up	Chrna1	Mus musc	NM_007389
A_51_P48	0.021287	1.652844	up	Dhcr24	Mus musc	NM_053272
A_55_P20	0.038173	3.145877	up	LOC1000	PREDICT	XM_001478751
A_55_P21	0.040939	1.659181	up	LOC5462	PREDICT	XM_001479766
A_51_P21	0.049591	1.956056	up	Slc41a2	Mus musc	NM_177388

A_55_P20	0.028537	10.29024	up		LOC3809	XM_979799
A_55_P20	0.035138	3.60273	up	Gm6611	PREDICT	XM_894394
A_55_P20	0.010732	1.517803	up	Gm9643	PREDICT	XR_032212
A_51_P20	0.002082	2.47115	up	Dio2	Mus musc	NM_010050
A_55_P20	0.04768	10.19083	up	LOC1000	PREDICT	XM_001473640
A_66_P10	0.032381	3.646278	up	Gm3367	PREDICT	XM_001476471
A_55_P21	0.032512	2.514855	up	Olfm1	Mus musc	NM_001038612
A_55_P19	0.02487	1.662629	up	Palld	Mus musc	NM_001081390
A_51_P24	0.026677	4.525498	up	Mlf1ip	Mus musc	NM_027973
A_55_P20	0.020811	1.52531	up	Plekha8	Mus musc	NM_001164361
A_30_P01	0.039417	1.658789	up		lincRNA:chr5:125190100-125209625 reverse strand	
A_55_P20	0.006882	1.780982	up	Rgp1	Mus musc	NM_172866
A_30_P01	0.003146	2.181279	up		lincRNA:chr5:14923900-15062725 forward strand	
A_55_P21	0.021528	1.586053	up		centrosom	BC060146
A_55_P21	0.002102	1.58916	up	LOC1000	nudix (nu	XM_001478680
A_55_P19	0.03575	3.469088	up	Gm8126	PREDICT	XR_033489
A_55_P20	0.042506	1.514992	up	Larp1b	Mus musc	NM_001040399
A_30_P01	0.013905	1.822386	up		lincRNA:chr8:129336539-129400338 reverse strand	
A_51_P33	0.03142	1.502282	up	Slco1a4	Mus musc	NM_030687
A_55_P22	0.036132	2.779695	up	2700068H	Mus musc	AK012503
A_51_P19	0.028408	10.85424	up	Spinlw1	Mus musc	NM_029325
A_51_P40	0.008694	5.494044	up	Bpil3	Mus musc	NM_199303
A_55_P21	0.004792	2.404371	up	BC030307	Mus musc	NM_153595
A_55_P21	0.03653	2.037117	up	Gm4703	PREDICT	XM_001481156
A_55_P19	0.040082	2.383016	up	Gm12813	PREDICT	XR_032022
A_30_P01	0.008396	1.900516	up		lincRNA:chr8:110197171-110206546 reverse strand	
A_30_P01	0.026768	1.700359	up		lincRNA:chrX:35825525-35877700 reverse strand	
A_55_P23	0.039102	2.021983	up	C430049E	Mus musc	AK141396
A_66_P13	0.030784	1.56479	up	A830035A	PREDICT	XM_986896
A_55_P21	0.019342	2.049881	up	LOC6205	PREDICT	XM_884904
A_55_P21	0.040136	2.037772	up		topoisome	AK164443
A_55_P20	0.03654	1.687212	up	Gm13011	Mus musc	NM_001126318
A_52_P37	0.019949	3.033988	up	Lep	Mus musc	NM_008493

A_55_P20	0.00884	2.547273	up	Hist2h3c1	Mus musc	NM_178216
A_55_P21	0.030022	1.971546	up	Slc10a7	Mus musc	NM_029736
A_52_P47	0.010634	6.263956	up	D3Bwg05	Mus musc	NM_177664
A_51_P49	0.035086	3.787621	up	Dfna5	Mus musc	NM_018769
A_52_P57	0.012965	2.541978	up	Fam19a3	Mus musc	NM_183224
A_55_P20	0.027171	3.285339	up	Acox1	Mus musc	NM_028765
A_30_P01	0.03654	1.520273	up			lincRNA:chr12:110973190-110987668 forward strand
A_55_P21	0.014211	6.257006	up	Fgf13	Mus musc	NM_010200
A_51_P12	9.33E-04	2.330294	up	2410076I2	Mus musc	NM_028598
A_55_P20	0.00728	1.684801	up	Ssxb9	Mus musc	NM_199066
A_55_P20	0.00543	3.333646	up	Cenpi	Mus musc	NM_145924
A_55_P19	0.012386	1.579245	up	Gm2312	PREDICT	XM_001473116
A_55_P19	0.033842	3.281829	up	Spc25	Mus musc	NM_025565
A_55_P20	0.001009	2.234069	up	Mki67	Mus musc	NM_001081117
A_55_P21	0.004823	1.730687	up	Als2cr12	Mus musc	NM_175370
A_30_P01	0.038463	1.666232	up			lincRNA:chr14:103751075-103769725 forward strand
A_66_P13	0.028688	1.57069	up	Cdc6	Mus musc	NM_011799
A_66_P11	0.046164	2.953303	up	Dgki	Mus musc	NM_001081206
A_55_P22	0.009144	2.410566	up	4930588A	Mus musc	AK046275
A_55_P21	0.037431	2.389072	up	LOC1000	PREDICT	XM_001476561
A_55_P20	0.048569	1.529307	up	Hipk2	Mus musc	NM_001136065
A_55_P20	0.004762	2.151959	up	Arhgap40	Mus musc	NM_001145015
A_55_P19	0.011019	2.465342	up	Prl3c1	Mus musc	NM_001163218
A_51_P33	0.037811	4.173244	up	Orm1	Mus musc	NM_008768
A_30_P01	0.013731	1.695722	up			lincRNA:chr6:127111250-127142925 forward strand
A_55_P19	0.009091	2.171642	up	Gm2366	PREDICT	XM_001473124
A_55_P19	7.50E-04	2.089685	up	Gm3014	PREDICT	XM_001475360
A_55_P21	0.023849	3.057016	up	Hist2h3c2	Mus musc	NM_054045
A_30_P01	0.007938	2.249169	up			lincRNA:chrX:148732853-148761972 reverse strand
A_55_P20	0.020256	2.362771	up		sideroflex	BC089588
A_30_P01	3.44E-04	2.211071	up			lincRNA:chr10:60473030-60535340 forward strand
A_55_P24	0.010147	1.776353	up	Gprin3	GPRIN fa	BC040234
A_66_P13	0.038074	3.748035	up	Gm14635	PREDICT	XM_001475018

A_55_P21	0.009791	1.799733	up		Putative u	AK137609
A_30_P01	0.012276	1.68921	up		lincRNA:chr9:96664617-96683617 forward strand	
A_55_P20	0.03064	1.557753	up	Ubp2	Mus musc	NM_026872
A_30_P01	9.86E-04	1.651045	up		lincRNA:chr7:6296401-6311486 forward strand	
A_55_P20	0.011465	2.177195	up	Gm2942	PREDICT	XM_001475175
A_30_P01	0.014354	2.664386	up		lincRNA:chr15:60656586-60685333 reverse strand	
A_30_P01	0.019191	2.396038	up		lincRNA:chr8:87504644-87513694 forward strand	
A_55_P20	0.014038	1.622069	up	Dhcr7	Mus musc	NM_007856
A_55_P21	0.044794	2.315615	up	Defa23	Mus musc	NM_001012307
A_55_P23	0.008745	1.54458	up	1700003G	Mus musc	AK012020
A_66_P12	0.041894	1.580599	up	Gm6225	Mus musc	NR_033457
A_55_P21	0.02571	1.961252	up	Tuba1b	Mus musc	NM_011654
A_30_P01	0.022329	2.546243	up		lincRNA:chr7:132218864-132329172 forward strand	
A_55_P21	0.008875	1.508257	up	Fstl3	Mus musc	NM_031380
A_55_P19	0.025629	3.875592	up	Acss2	Mus musc	NM_019811
A_30_P01	0.030061	2.638075	up		lincRNA:chr10:81165750-81236400 forward strand	
A_30_P01	0.046147	1.583137	up		lincRNA:chr13:62734450-62785325 reverse strand	
A_55_P20	0.005324	1.588046	up	9430008C	Mus musc	NR_015463
A_30_P01	0.005989	2.132399	up		lincRNA:chr11:69106907-69112857 forward strand	
A_55_P20	0.011319	2.149066	up	Htr3a	Mus musc	NM_013561
A_55_P20	0.042243	6.400979	up	Mum11	Mus musc	NM_001164630
A_55_P20	0.030126	2.246507	up	Ankle1	Mus musc	NM_172756
A_55_P20	0.041783	1.808734	up	Prune2	Mus musc	NM_181348
A_55_P20	0.008897	6.387668	up	Golga7b	Mus musc	NM_001141983
A_51_P51	0.041243	2.622571	up	Sag	Mus musc	NM_009118
A_30_P01	0.048746	2.31395	up		lincRNA:chr2:157361470-157379813 forward strand	
A_52_P42	0.04471	1.554584	up	Hist1h2ab	Mus musc	NM_175660
A_55_P21	0.018678	2.086644	up	Ppih	Mus musc	NM_001110130
A_55_P21	0.042603	8.802448	up	Bhmt	Mus musc	NM_016668
A_30_P01	0.013916	8.732582	up		lincRNA:chr14:43418592-43428090 forward strand	
A_55_P20	0.002677	3.070075	up	Olf312	Mus musc	NM_001011819
A_66_P10	0.007129	1.770902	up	Mutyh	Mus musc	AY007717
A_55_P19	0.043891	1.508761	up	Mutyh	Mus musc	NM_001159581

A_51_P51	0.035372	1.919187	up	Qpctl	Mus musc	NM_026111
A_55_P21	0.03646	3.266761	up	Ndufb2	Mus musc	NM_026612
A_55_P20	0.009337	1.575127	up	Mcoln2	Mus musc	NM_026656
A_30_P01	0.035221	1.776602	up			lincRNA:chrX:146827709-146913398 reverse strand
A_66_P12	0.023292	1.989525	up	Gm6567	PREDICT	XM_001479033
A_30_P01	0.024495	2.239595	up			lincRNA:chr14:115423660-115463160 reverse strand
A_51_P37	0.034563	1.65178	up	Coq3	Mus musc	NM_172687
A_55_P20	0.009798	2.796777	up	Gsdma2	Mus musc	NM_029727
A_55_P20	0.041781	4.703969	up	Mapk4	Mus musc	NM_172632
A_30_P01	0.025732	1.988885	up			lincRNA:chr17:38132217-38157667 reverse strand
A_55_P22	0.03953	2.118888	up	C230029N	Mus musc	AK082258
A_30_P01	0.019934	1.908682	up			lincRNA:chr2:128211990-128215223 reverse strand
A_55_P19	0.029845	4.661127	up	Gm14316	Mus musc	NM_001040055
A_55_P20	0.047709	3.092166	up	Gm4641	PREDICT	XM_001480938
A_55_P19	0.041323	10.29057	up	LOC1000	PREDICT	XR_031612
A_55_P20	0.00544	1.533225	up	Krtap20-2	Mus musc	NM_001163615
A_52_P51	0.024466	1.546248	up	Pcdh12	Mus musc	NM_017378
A_65_P17	0.027453	1.645901	up	Gse1	Mus musc	NM_198671
A_30_P01	0.019181	1.870487	up			lincRNA:chr6:67155508-67216941 forward strand
A_30_P01	0.022062	2.160457	up			lincRNA:chr2:128217275-128217972 reverse strand
A_30_P01	0.002023	2.017395	up			lincRNA:chr15:12126433-12126745 reverse strand
A_55_P20	0.038864	1.628007	down	Asap3	Mus musc	NM_001008232
A_55_P20	0.034779	1.507708	down	4930480K	PREDICT	XM_001477965
A_51_P31	0.016071	1.968073	down	Cxcr3	Mus musc	NM_009910
A_51_P22	0.008988	1.736577	down	Snx33	Mus musc	NM_175483
A_55_P20	2.68E-04	3.408511	down	Igsf1	Mus musc	NM_177591
A_30_P01	0.037392	1.682442	down			lincRNA:chr8:19682258-19700836 forward strand
A_55_P20	0.019973	1.779859	down	Trem1	Mus musc	NM_021406
A_30_P01	0.040779	2.109335	down			lincRNA:chr4:3745750-3756200 forward strand
A_66_P13	0.041526	2.859577	down	Sfrp1	Mus musc	NM_013834
A_55_P19	0.020157	2.715675	down	Gdpd2	Mus musc	NM_023608
A_55_P20	0.037985	2.088082	down	Gm4125	PREDICT	XM_001472807
A_55_P22	0.02734	1.86296	down	LOC4334	Mus musc	AK051942

A_55_P23	0.025505	2.09066	down	2010320M	60209170	BF531481
A_51_P21	0.040423	2.301149	down	Scn2b	Mus musc	NM_001014761
A_52_P24	0.009433	2.397221	down		Mus musc	AK038006
A_30_P01	0.033859	2.394105	down		lincRNA:chr7:16584852-16657252 reverse strand	
A_30_P01	0.043158	2.288997	down		lincRNA:chr3:96289850-96301078 forward strand	
A_51_P22	0.026805	1.79458	down	Lrfn2	Mus musc	NM_027452
A_55_P19	0.009697	1.891855	down	Krtap20-2	Mus musc	NM_001163615
A_30_P01	0.014758	1.550299	down		lincRNA:chr15:83266264-83294664 reverse strand	
A_30_P01	0.032116	2.924586	down		lincRNA:chr6:5311375-5328075 forward strand	
A_55_P23	0.036682	1.832875	down	A130033F	Mus musc	AK037654
A_55_P21	0.013995	1.55854	down	Gm14288	Mus musc	NM_001033123
A_30_P01	4.62E-05	1.942755	down		lincRNA:chr5:29779847-29784383 forward strand	
A_30_P01	0.021968	2.19142	down		lincRNA:chr19:57426515-57435165 reverse strand	
A_30_P01	0.011379	2.240481	down		lincRNA:chr18:35976163-35976530 forward strand	
A_55_P22	0.049185	2.455213	down	9630028H	Mus musc	AK049057
A_52_P48	0.016067	1.554746	down	Cpsf4	Mus musc	NM_178576
A_51_P51	0.032716	3.460959	down	Mkx	Mus musc	NM_177595
A_52_P51	0.025592	1.654536	down	Bcl2l1	Mus musc	NM_009743
A_55_P19	0.048333	2.009745	down		MTERF domain containing 2 Gene [Source:MGI (curated);Acc:MGI:1918355] [EN]	
A_55_P19	0.038248	1.924236	down	Slc16a14	solute car	AK049846
A_30_P01	0.040945	3.645142	down		lincRNA:chr12:76771424-76772158 forward strand	
A_30_P01	0.007323	1.511881	down		lincRNA:chr18:84735774-84760824 reverse strand	
A_30_P01	0.01658	8.744689	down		lincRNA:chr13:97700327-97700876 forward strand	
A_55_P24	0.016125	3.550395	down	A530083I	Mus musc	AK136855
A_55_P20	0.016577	3.95525	down	Stac	Mus musc	NM_016853
A_55_P20	8.44E-04	1.815195	down	Lamc3	Mus musc	NM_011836
A_30_P01	0.005216	2.298697	down		lincRNA:chr13:67211950-67217199 reverse strand	
A_55_P19	0.011182	1.646076	down		transmem	AK051974
A_55_P22	0.035566	3.682073	down	AI852580	UI-M-BH	AI852580
A_55_P20	0.025209	1.855637	down	Rtkn	Mus musc	NM_133641
A_30_P01	0.03647	2.578522	down		lincRNA:chr2:60038543-60046318 forward strand	
A_30_P01	0.011498	2.027127	down		lincRNA:chr12:81217572-81233910 reverse strand	
A_55_P20	0.027468	2.589887	down	Dusp14	Mus musc	NM_019819

A_55_P21	0.049586	2.017835	down	Pm20d2	Mus musc	NM_001034867
A_55_P19	0.026826	2.977549	down	Sgsm1	Mus musc	NM_172718
A_55_P20	0.039113	2.89742	down	B930041F	Mus musc	NM_178699
A_52_P15	0.029668	5.238837	down	Scgb1c1	Mus musc	NM_001099742
A_51_P46	0.032025	2.916178	down	Gdf1	Mus musc	NM_008107
A_51_P28	0.018774	2.450836	down	Pdcd1	Mus musc	NM_008798
A_51_P31	0.034222	1.638858	down	Olf791	Mus musc	NM_146930
A_30_P01	0.01604	2.245765	down			lincRNA:chr17:8088950-8106700 reverse strand
A_52_P31	0.043343	3.095799	down	Tpm2	Mus musc	NM_009416
A_55_P20	0.020772	2.127825	down	Adam23	Mus musc	NM_011780
A_55_P23	0.04719	1.717469	down	D330022F	Mus musc	AK021285
A_55_P23	0.042324	1.562452	down	E230006N	Mus musc	AK053951
A_55_P20	0.042194	2.560346	down	Gm4368	PREDICT	XM_001479985
A_55_P21	0.031852	2.287199	down	Grhl1	Mus musc	NM_145890
A_30_P01	0.021086	1.875707	down			lincRNA:chr11:6748267-6818192 forward strand
A_51_P20	0.034899	1.954907	down	Fam198a	Mus musc	NM_177743
A_30_P01	0.037059	1.936011	down			lincRNA:chr6:31017987-31174287 reverse strand
A_51_P22	0.032076	2.966478	down	Wisp1	Mus musc	NM_018865
A_55_P20	0.046879	1.520826	down	9630025I2	Mus musc	NM_001076791
A_30_P01	0.043671	1.924145	down			lincRNA:chr15:102100964-102104552 forward strand
A_30_P01	0.01193	1.620038	down			lincRNA:chr9:20784567-20799942 reverse strand
A_55_P22	0.003099	4.328038	down	LOC62705	Mus musc	AK147870
A_30_P01	0.028461	1.641805	down			lincRNA:chr11:59206727-59207172 reverse strand
A_51_P17	0.024109	4.275963	down	Pklr	Mus musc	NM_013631
A_55_P20	0.01316	1.552986	down	Cmtm5	Mus musc	NM_026066
A_55_P21	0.046131	1.684534	down	Gm11826	PREDICT	XR_031506
A_30_P01	2.90E-04	2.731792	down			lincRNA:chr13:70745306-70837331 forward strand
A_55_P21	0.0335	1.711866	down	Crtc1	Mus musc	NM_001004062
A_52_P35	0.011161	4.320117	down	Fbxw13	Mus musc	NM_177598
A_66_P13	0.007121	1.833027	down	Gm5607	Mus musc	NR_027975
A_51_P20	0.015822	3.702308	down	Gpr88	Mus musc	NM_022427
A_30_P01	0.002574	6.30055	down			lincRNA:chr4:116790373-116797823 forward strand
A_30_P01	0.010096	1.788541	down			lincRNA:chr4:129376440-129391690 reverse strand

A_55_P19	0.033897	1.938432	down		thymocyte	XM_001473004
A_30_P01	0.034779	1.882507	down			lincRNA:chr5:122047900-122065325 forward strand
A_51_P40	0.008665	1.506033	down	Ankrd35	Mus musc	NM_001081139
A_30_P01	0.032576	1.704519	down			lincRNA:chr9:66981366-67061725 forward strand
A_30_P01	0.030272	2.160981	down			lincRNA:chrX:20539200-20563428 forward strand
A_55_P20	0.002319	1.741328	down	Gm7302	PREDICT	XM_917569
A_55_P19	0.036393	2.162247	down	Cyp2d13	Mus musc	NR_003552
A_55_P23	0.044869	1.537773	down	AI956758	UI-M-GV	CV883746
A_30_P01	0.017811	1.565051	down			lincRNA:chr3:51890691-51891781 reverse strand
A_55_P19	0.007574	2.09126	down	Mtap1b	Mus musc	NM_008634
A_55_P20	0.033197	1.808972	down	Gm12776	Mus musc	NM_001099330
A_55_P19	0.043605	1.711575	down	Crybb3	Mus musc	NM_021352
A_30_P01	0.021515	1.717732	down			lincRNA:chr10:39383665-39442690 reverse strand
A_55_P19	0.026487	2.797331	down	Prss29	Mus musc	NM_053260
A_55_P20	0.025178	2.478242	down	Gm7693	PREDICT	XR_033989
A_30_P01	0.01609	1.882522	down			lincRNA:chr12:74883691-74893323 reverse strand
A_30_P01	0.036596	1.857507	down			lincRNA:chr16:43623581-43642715 reverse strand
A_52_P17	0.020984	2.229063	down	Gria3	Mus musc	NM_016886
A_51_P40	0.030193	1.654333	down	Mett11d1	Mus musc	NM_001029990
A_55_P20	0.014661	3.251851	down	Ncam1	Mus musc	NM_010875
A_55_P20	0.043527	4.782315	down	LOC1000	PREDICT	XM_001478120
A_55_P19	0.024395	3.541428	down	H19	Mus musc	NR_001592
A_30_P01	0.022244	1.510256	down			lincRNA:chr10:83364590-83364873 forward strand
A_55_P19	0.018933	1.519167	down			PREDICT XM_001473591
A_30_P01	0.013795	2.934334	down			lincRNA:chr1:137482591-137625604 forward strand
A_30_P01	0.002094	2.638345	down			lincRNA:chr3:108763862-108772151 forward strand
A_51_P20	0.012518	4.87447	down	Prtn3	Mus musc	NM_011178
A_55_P19	0.011509	1.862394	down	Icos	Mus musc	NM_017480
A_52_P56	0.034747	1.958189	down	Chia	Mus musc	NM_023186
A_55_P21	0.03622	1.587403	down	Zfp444	Mus musc	NM_001146024
A_55_P23	0.032352	1.880124	down	F830034J0	Mus musc	AK156640
A_55_P21	0.027144	2.94845	down	Cited2	Mus musc	NM_010828
A_30_P01	0.0126	1.68147	down			lincRNA:chr11:6421951-6429173 forward strand

A_55_P20	0.043699	1.567537	down	Tsc2	Mus musc	NM_011647
A_51_P37	0.018769	2.989389	down	Myo15b	myosin X	AK087906
A_30_P01	0.030451	2.670553	down		lincRNA:chr10:24269165-24276690 reverse strand	
A_51_P21	0.032989	3.428466	down	Alpk3	Mus musc	NM_054085
A_52_P36	0.048751	2.247345	down	Mtap1b	Mus musc	NM_008634
A_52_P46	0.008019	3.025027	down	Alox12	Mus musc	NM_007440
A_30_P01	0.02665	3.324996	down		lincRNA:chr9:106170918-106177894 reverse strand	
A_30_P01	0.037294	1.547649	down		lincRNA:chr8:26343277-26352902 reverse strand	
A_52_P64	0.003941	1.796988	down	Camk2n1	Mus musc	NM_025451
A_51_P35	0.03102	1.964565	down	Lgi3	Mus musc	NM_145219
A_55_P20	0.040679	1.630913	down	Il12rb1	Mus musc	NM_008353
A_66_P11	0.027516	2.11568	down	Bend5	Mus musc	NM_026279
A_55_P20	0.01099	1.875922	down	Cpe	Mus musc	NM_013494
A_66_P12	0.023873	3.188011	down	Ttpa	Mus musc	NM_015767
A_30_P01	0.024447	1.627899	down		lincRNA:chr1:36012298-36020311 reverse strand	
A_55_P20	0.014631	1.81394	down	Ctsw	Mus musc	NM_009985
A_52_P57	0.007035	2.120379	down	Vat1l	Mus musc	NM_173016
A_30_P01	0.030293	1.696673	down		lincRNA:chr9:43738583-43757007 reverse strand	
A_55_P20	0.021577	3.300457	down	Cryba4	crystallin,	AK161601
A_55_P20	0.04092	2.857501	down	H2-T18	PREDICT	XM_912024
A_30_P01	0.043262	1.615494	down		lincRNA:chr1:59773381-59775888 forward strand	
A_30_P01	0.037928	2.236138	down		lincRNA:chr11:112898724-113062945 reverse strand	
A_30_P01	3.93E-04	3.367629	down		lincRNA:chr2:108456668-108532418 reverse strand	
A_52_P16	0.026063	1.82291	down	Ivns1abp	Mus musc	NM_001039511
A_55_P21	0.024268	3.101178	down	Ikzf4	Mus musc	NM_011772
A_51_P13	0.04001	2.739271	down	Card14	Mus musc	NM_130886
A_30_P01	0.012781	3.122801	down		lincRNA:chrX:47890565-47915775 forward strand	
A_30_P01	0.019348	2.507838	down		lincRNA:chr17:88466300-88495175 forward strand	
A_51_P24	0.044367	2.167485	down	Mt2	Mus musc	NM_008630
A_30_P01	0.03183	3.528053	down		lincRNA:chr14:79724027-79729152 forward strand	
A_30_P01	0.023543	2.526496	down		lincRNA:chr14:55317199-55317670 reverse strand	
A_51_P15	0.016438	2.65551	down	Dbx1	Mus musc	NM_001005232
A_55_P20	0.049	1.875834	down	Gm10653	Mus musc	NR_003965

A_30_P01	0.028089	3.416024	down		lincRNA:chr18:57124435-57134910 reverse strand
A_55_P22	0.045947	1.962727	down	9530048J2	Mus musc AK033136
A_51_P10	0.031627	2.380354	down	Slc39a4	Mus musc NM_028064
A_51_P22	0.03748	2.231506	down	Ppp2r2b	Mus musc NM_028392
A_51_P17	0.021705	2.060155	down	Bcl11b	Mus musc NM_021399
A_55_P20	0.009153	3.221499	down	Lypd6	Mus musc NM_177139
A_30_P01	0.043027	1.886171	down		lincRNA:chr11:120041124-120052299 reverse strand
A_30_P01	0.004118	2.183118	down		lincRNA:chr1:183783306-183834531 reverse strand
A_30_P01	0.013985	2.182281	down		lincRNA:chr9:118060025-118085050 forward strand
A_30_P01	0.02046	2.067207	down		lincRNA:chr8:124355710-124401160 forward strand
A_55_P20	0.004606	1.71269	down	LOC1000	PREDICT XM_001481225
A_52_P50	0.02578	2.005038	down	Slamf6	Mus musc NM_030710
A_30_P01	0.033202	1.59826	down		lincRNA:chr5:124694137-124695689 reverse strand
A_30_P01	0.007301	1.980349	down		lincRNA:chr17:46972160-46997919 reverse strand
A_55_P21	0.011422	2.460212	down	Zfp112	Mus musc NM_021307
A_55_P20	0.047677	3.311868	down	Pabpc5	Mus musc NM_053114
A_55_P19	0.008556	2.020452	down	LOC1000	PREDICT XM_001475860
A_51_P40	0.012341	3.213934	down	Tmem213	Mus musc NM_029921
A_30_P01	0.009084	2.595735	down		lincRNA:chr2:170029045-170034220 forward strand
A_55_P20	0.005404	2.217043	down	Padi2	Mus musc NM_008812
A_30_P01	0.019379	2.22256	down		lincRNA:chr11:112898724-113062945 reverse strand
A_55_P21	0.041814	1.659429	down	Cebpe	Mus musc NM_207131
A_55_P23	0.035046	2.811633	down	2410024N	Mus musc AK035593
A_30_P01	0.015067	2.000408	down		lincRNA:chr5:137392195-137426421 reverse strand
A_52_P76	0.044651	1.51966	down	Sp2	Mus musc NM_030220
A_55_P20	0.00668	2.295563	down	Pacsin1	Mus musc NM_011861
A_30_P01	0.019148	1.641354	down		lincRNA:chr8:126396600-126407275 forward strand
A_55_P21	0.049453	2.248896	down	Gm826	Mus musc NM_001033411
A_51_P19	0.008025	2.564792	down	Wfdc1	Mus musc NM_023395
A_30_P01	0.007209	2.078954	down		lincRNA:chr11:112905201-113062945 reverse strand
A_66_P10	0.035518	1.70317	down	COX1	mitochond AK165865
A_51_P35	0.036735	3.774874	down	Krt19	Mus musc NM_008471
A_55_P19	0.034492	2.294848	down	Slc16a3	Mus musc NM_030696

A_51_P17	0.035773	2.541787	down	Cd14	Mus musc	NM_009841
A_55_P20	0.021819	2.002637	down	Reg3d	Mus musc	NM_013893
A_30_P01	0.040567	2.624866	down			lincRNA:chr1:85300475-85331475 reverse strand
A_30_P01	0.022476	2.780754	down			lincRNA:chr1:167797581-167803031 forward strand
A_30_P01	0.04496	1.784253	down			lincRNA:chr12:72103832-72116875 reverse strand
A_55_P19	0.028388	1.750738	down	Dnajc5	DnaJ (Hsp40) homolog, subfamily C, member 5 Gene [Source:MGI (curated);Acc:V	
A_30_P01	0.019162	2.607377	down			lincRNA:chr12:74135916-74142780 forward strand
A_51_P12	0.022173	3.022378	down	Sstr4	Mus musc	NM_009219
A_66_P10	0.040122	2.107623	down	Clec9a	Mus musc	NM_172732
A_55_P19	0.047261	2.658778	down	Dio3os	Mus musc	NR_002866
A_30_P01	0.045141	2.798047	down			lincRNA:chr4:155560050-155570900 reverse strand
A_52_P40	0.003368	1.850826	down	Rab11fip4	RAB11 fa	AK147344
A_55_P20	0.035573	1.595184	down		paired imr	AK041413
A_51_P47	0.028992	1.700775	down	Gpr171	Mus musc	NM_173398
A_55_P20	0.00968	1.798882	down		M.muscul	X79554
A_30_P01	0.021213	2.987991	down			lincRNA:chr9:41488229-41545481 reverse strand
A_55_P21	0.032189	1.853766	down	Sectm1a	Mus musc	NM_145373
A_55_P21	0.015938	7.538637	down	Pycr1	Mus musc	NM_144795
A_30_P01	0.03811	2.800318	down			lincRNA:chr5:92548501-92566401 reverse strand
A_30_P01	0.016154	3.558616	down			lincRNA:chr17:33368400-33393525 forward strand
A_51_P48	0.003662	2.709764	down	Steap1	Mus musc	NM_027399
A_30_P01	0.003661	2.973541	down			lincRNA:chr6:127588224-127609749 reverse strand
A_30_P01	0.044046	2.069157	down			lincRNA:chr11:112898724-113062945 reverse strand
A_55_P20	0.030205	2.035862	down		tyrosyl-D	AK033868
A_51_P19	0.043026	2.255066	down	Spon1	Mus musc	NM_145584
A_30_P01	0.037746	2.872511	down			lincRNA:chr3:37797734-37891650 forward strand
A_55_P19	0.034013	1.546169	down	Wnt5b	Mus musc	NM_009525
A_30_P01	0.012921	1.528912	down			lincRNA:chr17:27703181-27716306 forward strand
A_51_P37	0.032957	2.398632	down	5830405N	Mus musc	NM_183264
A_51_P40	0.005565	1.519471	down	Aph1a	Mus musc	NM_146104
A_52_P49	0.009116	1.525085	down	AI467606	Mus musc	NM_178901
A_55_P21	0.035076	2.896157	down	Hcrtr1	Mus musc	NM_198959
A_66_P11	0.04086	1.724238	down		Mus musc	DQ372793

A_30_P01	0.003771	3.244651	down		lincRNA:chr10:117021051-117038683 reverse strand
A_30_P01	0.040475	1.679215	down		lincRNA:chr7:140016236-140016772 reverse strand
A_55_P21	0.021987	1.521705	down	Gm9735	PREDICT XR_035629
A_30_P01	2.75E-04	2.761854	down		lincRNA:chr7:129294166-129301366 forward strand
A_66_P11	0.029833	3.360076	down	49305970	RIKEN cd XM_989547
A_55_P21	0.042625	2.21308	down	Tas2r117	Mus musc NM_207021
A_55_P22	0.034519	1.677538	down	LOC1000	Mus musc AK081449
A_30_P01	0.032748	1.639517	down		lincRNA:chr4:11102287-11118421 reverse strand
A_55_P19	0.03175	2.64621	down	Cdkn1a	Mus musc NM_001111099
A_30_P01	0.012197	1.525155	down		lincRNA:chr12:117623500-117643575 reverse strand
A_55_P20	0.042388	4.646663	down	Ppp1r1b	Mus musc NM_144828
A_51_P44	0.049606	3.467727	down	Celsr1	Mus musc NM_009886
A_55_P20	0.016206	1.801895	down	LOC1000	PREDICT XM_001472591
A_55_P20	0.023354	2.48965	down	C3	Mus musc NM_009778
A_55_P21	0.048003	1.951361	down	Slc38a1	Mus musc NM_134086
A_30_P01	0.018988	3.126013	down		lincRNA:chr6:47915489-47916089 forward strand
A_30_P01	0.003783	2.47335	down		lincRNA:chr11:19960515-19961093 reverse strand
A_30_P01	0.020081	3.456855	down		lincRNA:chr5:30550467-30559008 reverse strand
A_52_P67	0.023681	1.944707	down	Btbd3	Mus musc NM_145534
A_52_P71	0.001984	3.08345	down	Olf1r1410	Mus musc NM_146491
A_66_P11	0.021173	1.992505	down	Zfp354c	Mus musc NM_013922
A_55_P20	0.022078	2.432477	down	Cd300c	Mus musc NM_199225
A_30_P01	0.02186	1.908395	down		lincRNA:chr4:135896689-135918414 reverse strand
A_30_P01	0.029417	2.564677	down		lincRNA:chr5:121759042-121789992 reverse strand
A_51_P47	0.018954	1.582663	down	Vangl2	vang-like AK082938
A_52_P43	0.012651	1.859443	down	Prkrir	Mus musc NM_028410
A_55_P20	0.025481	1.921695	down	Gm2285	PREDICT XM_001473039
A_30_P01	0.028432	1.755474	down		lincRNA:chr13:61703445-62094670 forward strand
A_55_P20	0.021919	1.534332	down	S100a5	Mus musc NM_011312
A_30_P01	0.001128	3.980805	down		lincRNA:chr2:22753100-22780375 reverse strand
A_55_P20	0.01142	3.315911	down	Agrn	Mus musc NM_021604
A_55_P19	0.006178	2.123145	down	LOC5473	Mus musc NM_001025208
A_55_P21	0.038591	1.659729	down	Cdk4	Mus musc NM_009870

A_30_P01	0.009357	1.573287	down		lincRNA:chr15:102100397-102105872 reverse strand
A_30_P01	0.023179	1.736353	down		lincRNA:chr14:76912477-76931702 forward strand
A_52_P57	0.0083	2.439796	down	Acss3	Mus musc NM_198636
A_55_P20	0.004817	2.818547	down		Putative u AK170322
A_30_P01	0.024609	4.045437	down		lincRNA:chr6:93029101-93031007 forward strand
A_55_P20	0.023598	2.804121	down	Kcnj10	Mus musc NM_001039484
A_30_P01	7.01E-04	2.299147	down		lincRNA:chr5:74487385-74497428 forward strand
A_55_P20	0.023367	1.632543	down	Gmfg	Mus musc NM_022024
A_55_P19	0.028871	2.370197	down		RIKEN cl AK018312
A_51_P13	0.018035	2.090025	down	Cpxm1	Mus musc NM_019696
A_52_P66	0.049817	1.718784	down	Inadl	Mus musc NM_001005784
A_30_P01	0.019468	1.966066	down		lincRNA:chr13:48620882-48643532 reverse strand
A_30_P01	0.046516	2.127085	down		lincRNA:chr2:175432867-175469471 reverse strand
A_51_P24	0.007481	1.663471	down		RIKEN cl AK076700
A_51_P33	0.033188	1.597678	down	Cwf19l2	Mus musc NM_027545
A_51_P37	0.037439	1.64289	down	Srebf2	Mus musc NM_033218
A_55_P20	0.043563	2.383442	down	Arhgef19	Mus musc NM_172520
A_55_P21	0.001593	1.790238	down	Igf2	Mus musc NM_010514
A_55_P21	0.020732	2.393904	down	Il17rb	Mus musc NM_019583
A_52_P46	0.037379	3.422005	down	Cda	Mus musc NM_028176
A_30_P01	0.037447	1.959804	down		lincRNA:chr10:21855725-21867925 reverse strand
A_30_P01	0.004013	1.752224	down		lincRNA:chr5:123582742-123588202 forward strand
A_55_P19	0.048866	3.526403	down	Txndc6	Mus musc NM_001165957
A_55_P19	0.009092	1.786878	down	Gm3985	Mus musc NM_001177589
A_30_P01	0.033851	2.531993	down		lincRNA:chr8:37582187-37621987 forward strand
A_30_P01	0.01466	1.787961	down		lincRNA:chr11:112905201-113062945 reverse strand
A_55_P20	0.043336	1.776489	down	Trim65	Mus musc NM_178802
A_55_P20	0.047014	1.666098	down	Myo6	Mus musc NM_001039546
A_55_P20	0.013508	3.791651	down	Aqp5	Mus musc NM_009701
A_30_P01	0.009384	4.924017	down		lincRNA:chr13:108825897-108833335 reverse strand
A_52_P27	0.032013	2.367903	down	LOC1000	PREDICT XM_001479478
A_30_P01	0.038764	2.913531	down		lincRNA:chr8:122997422-122998001 forward strand
A_30_P01	0.018874	1.591333	down		lincRNA:chr3:19211659-19213735 forward strand

A_52_P24	0.042563	2.669483	down	Tcf7	Mus musc	NM_009331
A_55_P21	0.040956	1.66462	down	LOC1000	PREDICT	XM_001478504
A_55_P20	0.031653	1.590802	down	Zfhx2as	Mus musc	NR_004444
A_30_P01	0.033979	3.659186	down			lincRNA:chr1:82892851-82943201 reverse strand
A_55_P19	0.00248	2.412559	down	LOC1000	PREDICT	XM_001474498
A_30_P01	0.010715	1.964104	down			lincRNA:chr2:75444518-75497268 reverse strand
A_55_P20	0.028605	1.816521	down	Gm6404	PREDICT	XM_887605
A_65_P17	0.038726	2.770244	down	Pgm5	Mus musc	NM_175013
A_55_P20	0.040877	1.627538	down	Plp1	Mus musc	NM_011123
A_30_P01	0.003605	1.543845	down			lincRNA:chr12:86415200-86415483 forward strand
A_55_P21	0.025708	1.528832	down	Gm9465	PREDICT	XM_001474101
A_30_P01	0.037715	2.499265	down			lincRNA:chr3:96289850-96301078 forward strand
A_30_P01	0.018213	4.173795	down			lincRNA:chr8:110196655-110390197 forward strand
A_30_P01	0.048686	2.418713	down			lincRNA:chr19:46422690-46423478 reverse strand
A_51_P21	0.01313	1.797067	down	Macrodl	Mus musc	NM_134147
A_52_P41	0.042827	1.74364	down			PREDICT XM_001474827
A_52_P18	0.019608	2.743064	down	Crabp1	Mus musc	NM_013496
A_66_P14	0.040997	2.664896	down	LOC1000	predicted	XM_001476590
A_51_P38	0.029615	4.461882	down	Glod5	Mus musc	NM_027227
A_52_P26	0.004055	1.566149	down	Ing5	Mus musc	NM_025454
A_51_P21	0.045424	1.747313	down	Vcam1	Mus musc	NM_011693
A_30_P01	0.025548	2.366483	down			lincRNA:chr10:21688115-21710890 reverse strand
A_55_P21	0.014004	1.756253	down			cyclic nuc XM_001476198
A_30_P01	0.012216	1.810002	down			lincRNA:chr17:21785442-21801542 forward strand
A_52_P28	0.011077	1.553411	down	Yeats2	Mus musc	NM_001033237
A_30_P01	0.031147	1.698226	down			lincRNA:chr12:117623500-117643575 reverse strand
A_55_P21	0.003291	1.807478	down	Gm4662	PREDICT	XM_001479134
A_30_P01	0.021314	1.601777	down			lincRNA:chr15:61870759-61938796 forward strand
A_30_P01	0.031943	2.276821	down			lincRNA:chr17:13806767-13824342 reverse strand
A_30_P01	0.03755	2.480786	down			lincRNA:chr6:50361567-50406200 reverse strand
A_30_P01	0.008924	2.164792	down			lincRNA:chr1:160888257-160910594 reverse strand
A_30_P01	0.005894	3.880017	down			lincRNA:chr15:96091428-96115684 forward strand
A_55_P21	0.022874	1.676659	down	E230025N	Mus musc	NM_172831

A_30_P01	0.04258	2.778828	down		lincRNA:chrX:47890565-47915775 forward strand
A_30_P01	0.049866	4.49961	down		lincRNA:chr13:94198298-94198965 reverse strand
A_30_P01	0.013686	2.675963	down		lincRNA:chr8:93337794-93348869 reverse strand
A_52_P25	0.009462	2.190703	down	Syt13	Mus muscNM_030725
A_30_P01	0.048832	1.730275	down		lincRNA:chr16:43623581-43642715 reverse strand
A_55_P20	0.025162	2.010748	down	Rgs11	Mus muscNM_001081069
A_51_P10	0.030605	1.641058	down	Flrt2	Mus muscNM_201518
A_55_P20	9.41E-04	1.588478	down	Trpc2	Mus muscNM_011644
A_55_P20	0.040011	2.861988	down	Aldoc	Mus muscNM_009657
A_55_P19	0.023107	2.923127	down	Ikzf4	Mus muscNM_011772
A_55_P19	0.016046	2.516265	down	Tceal3	Mus muscNM_001029978
A_55_P19	0.027062	2.760769	down	Aqp5	Mus muscNM_009701
A_55_P21	0.034003	1.772281	down		aryl hydrocarbon receptor nuclear translocator Gene [Source:MGI (curated);Acc:MC
A_55_P20	0.015119	1.608207	down	Zfp605	Mus muscNM_001163996
A_30_P01	0.016286	2.550999	down		lincRNA:chr15:85476512-85498105 forward strand
A_30_P01	1.03E-04	1.612117	down		lincRNA:chr14:67585234-67596823 reverse strand
A_55_P20	0.042652	2.895483	down	Igfbp2	Mus muscNM_008342
A_51_P35	0.027921	1.787243	down	Itgb7	Mus muscNM_013566
A_30_P01	0.039903	1.821329	down		lincRNA:chr8:114477602-114488627 reverse strand
A_55_P20	0.042056	1.997479	down	Ngb	Mus muscNM_022414
A_30_P01	0.021796	3.284842	down		lincRNA:chr13:51248372-51259297 forward strand
A_30_P01	0.040302	1.964685	down		lincRNA:chr11:87841800-87858725 reverse strand
A_30_P01	0.030346	3.412056	down		lincRNA:chr11:95483973-95490751 forward strand
A_55_P21	0.049225	1.967618	down	Gli1	Mus muscNM_010296
A_30_P01	0.042351	1.729755	down		lincRNA:chr11:97457180-97487074 reverse strand
A_55_P20	0.020916	3.126454	down	AU021034	Mus muscNM_177629
A_66_P14	0.020721	1.755973	down	Itga4	Mus muscNM_010576
A_30_P01	0.013401	1.888932	down		lincRNA:chr8:96983590-96994419 forward strand
A_51_P50	0.01982	1.914997	down	Il18r1	Mus muscNM_008365
A_30_P01	0.006401	2.602022	down		lincRNA:chrX:45814752-45816313 reverse strand
A_30_P01	0.020535	2.639549	down		lincRNA:chr5:110158475-110223700 forward strand
A_30_P01	0.016142	1.60036	down		lincRNA:chr4:56480568-56658018 forward strand
A_52_P48	0.024211	1.869	down	Plek2	Mus muscNM_013738

A_66_P12	0.021777	3.251566	down	Cldn2	Mus musc	NM_016675
A_30_P01	0.021977	2.033983	down			lincRNA:chr5:113594167-113645342 reverse strand
A_55_P20	0.021178	1.64547	down	Gjc2	Mus musc	NM_175452
A_51_P29	0.041953	2.159537	down	Vit	Mus musc	NM_028813
A_30_P01	0.010794	1.936047	down			lincRNA:chr2:155269145-155303251 forward strand
A_55_P20	0.033701	1.849573	down	Mtmt15	Mus musc	NM_177893
A_55_P20	0.010515	1.587071	down	H2-T24	Mus musc	NM_008207
A_55_P21	0.026817	3.25839	down	Gm606	Mus musc	NM_001013761
A_30_P01	0.005595	1.549217	down			lincRNA:chr10:126818382-126856582 forward strand
A_55_P22	0.004131	2.478853	down	Gm13032	Mus musc	AK049241
A_30_P01	0.043779	1.614467	down			lincRNA:chr16:13752215-13764390 forward strand
A_51_P16	0.033982	1.974042	down	Lbx2	Mus musc	NM_010692
A_52_P67	0.013482	5.361019	down	Dner	Mus musc	NM_152915
A_55_P20	0.013725	2.121431	down	Hao	Mus musc	NM_025325
A_30_P01	0.012729	2.496671	down			lincRNA:chr7:16584852-16657252 forward strand
A_30_P01	0.030335	1.588993	down			lincRNA:chr6:31017987-31174287 reverse strand
A_55_P23	0.021457	1.509762	down	AI853106	60335611	BI734998
A_30_P01	0.032709	1.506556	down			lincRNA:chr15:77575125-77585575 forward strand
A_55_P19	0.03165	1.759197	down		Mouse T d	M97158
A_51_P37	0.011052	1.650838	down	P2ry13	Mus musc	NM_028808
A_55_P21	0.048405	2.782612	down	Slc45a3	Mus musc	NM_145977
A_55_P20	0.03314	2.522374	down	LOC6319	PREDICT	XM_905950
A_30_P01	0.013242	1.94996	down			lincRNA:chr5:125078875-125098525 reverse strand
A_30_P01	0.019634	1.600209	down			lincRNA:chr2:116796887-116797441 forward strand
A_51_P48	0.007219	2.897485	down		Putative u	AK052046
A_55_P20	0.014276	2.172717	down	Srcin1	Mus musc	NM_018873
A_51_P32	0.032943	1.589598	down	1700025G	Mus musc	NM_197990
A_51_P18	0.016859	1.542552	down	Olf460	Mus musc	NM_146383
A_30_P01	0.017301	1.759648	down			lincRNA:chr4:88604248-88645948 forward strand
A_55_P20	0.012632	2.782285	down	Gas1	Mus musc	NM_008086
A_66_P13	0.040199	3.377468	down	Igfbp2	Mus musc	NM_008342
A_30_P01	0.011535	1.605402	down			lincRNA:chr8:74439200-74441363 forward strand
A_55_P20	0.0303	3.280358	down	BC005764	Mus musc	NM_181681

A_55_P21	0.010194	2.883807	down		fetal and a	BC115805
A_55_P22	0.006275	1.587893	down	AU020147	H3078F05	BG069650
A_30_P01	0.030876	1.583879	down		lincRNA:chr5:106126051-106128392 reverse strand	
A_55_P19	0.042874	1.555161	down	Bcl2a1d	Mus musc	NM_007536
A_30_P01	0.00919	1.890922	down		lincRNA:chr8:57977383-57985712 forward strand	
A_55_P21	5.18E-04	1.725626	down	Thsd7a	Mus musc	NM_001164805
A_51_P10	0.017339	1.88308	down	Gh	Mus musc	NM_008117
A_30_P01	0.042381	1.777988	down		lincRNA:chr9:100977450-100989325 forward strand	
A_55_P23	0.002649	2.492748	down	Rnf112	Mus musc	NM_009548
A_55_P19	0.047742	4.348163	down	Rorc	Mus musc	NM_011281
A_30_P01	0.010044	2.324496	down		lincRNA:chrX:120134722-120138152 reverse strand	
A_55_P21	0.026033	2.045001	down	Gprasp1	Mus musc	NM_026081
A_30_P01	0.004519	1.887457	down		lincRNA:chr16:4585697-4594022 reverse strand	
A_52_P55	0.026404	2.110337	down	Sned1	sushi, nidd	AJ584850
A_51_P44	0.040862	2.078208	down	1110028C	Mus musc	NM_177645
A_30_P01	0.006614	1.698894	down		lincRNA:chr2:92582386-92599365 forward strand	
A_52_P67	0.001695	1.677528	down		RIKEN cl	AK087115
A_51_P42	0.012279	2.159344	down	Mgp	Mus musc	NM_008597
A_51_P31	0.017228	4.203298	down	D11Bwg0	Mus musc	NM_001024931
A_30_P01	0.046607	1.556732	down		lincRNA:chr12:81217572-81233910 reverse strand	
A_30_P01	0.024829	1.839561	down		lincRNA:chr4:135896689-135918414 forward strand	
A_51_P40	0.0397	3.738045	down	1500015C	Mus musc	NM_024283
A_30_P01	0.00731	1.843124	down		lincRNA:chr11:112905201-113062945 reverse strand	
A_30_P01	0.047793	2.800284	down		lincRNA:chr3:27837825-27880925 reverse strand	
A_55_P21	0.007276	1.598249	down		non-metastatic cells 1, protein (NM23A) expressed in Gene [Source:MGI (curated);/	
A_51_P27	0.046804	3.209419	down	2310007B	Mus musc	NM_172411
A_30_P01	0.025855	2.531042	down		lincRNA:chr2:155298877-155303251 forward strand	
A_55_P19	0.033387	2.328392	down	B230319C	Mus musc	NR_028382
A_55_P21	0.040159	3.250844	down	Dok7	Mus musc	NM_172708
A_55_P20	0.037509	1.665125	down	Gapt	Mus musc	NM_177713
A_51_P42	0.006614	2.57601	down	Mtus2	Mus musc	NM_029920
A_51_P35	0.038282	1.733399	down	Rab39	Mus musc	NM_175562
A_55_P19	0.020414	1.694139	down	Hccs	Mus musc	NM_008222

A_55_P21	0.003259	2.72793	down	Cited2	Mus musc	NM_010828
A_30_P01	0.001429	1.583037	down			lincRNA:chr11:53592946-53637922 forward strand
A_30_P01	0.047026	1.779803	down			lincRNA:chr12:81217572-81233910 reverse strand
A_55_P20	0.016034	1.674645	down			CDC23 (c
A_55_P20	0.023623	1.522107	down	Zfp553	Mus musc	AK044478
A_30_P01	0.00873	2.105049	down			NM_146201
A_55_P20	0.048397	1.792376	down	Pdpn	Mus musc	lincRNA:chr11:120041124-120052299 reverse strand
A_30_P01	0.008039	3.414424	down			NM_010329
A_55_P23	0.034976	1.67747	down	A330062J	Mus musc	lincRNA:chr7:149761435-149764019 reverse strand
A_30_P01	0.018397	1.726345	down			AK039561
A_52_P39	0.031377	2.085832	down	Ccbe1	Mus musc	lincRNA:chr15:96111929-96114921 reverse strand
A_51_P47	0.01372	1.658606	down	Zcchc3	Mus musc	NM_178793
A_55_P20	0.036694	2.215107	down	Ccl19	Mus musc	NM_175126
A_55_P22	0.031548	2.248955	down	AI790276	Mus musc	NM_011888
A_52_P23	0.022751	1.552979	down	2610035D	Mus musc	BC028446
A_52_P45	0.002691	1.525011	down	2900079G	Mus musc	NR_015556
A_51_P45	0.009269	3.028971	down	Foxj1	Mus musc	NR_033431
A_52_P56	0.010698	2.1322	down	BC034090	Mus musc	NM_008240
A_66_P11	0.028108	1.616166	down	Sart1	Mus musc	XM_148974
A_65_P16	0.037428	2.897507	down	Bex1	Mus musc	NM_016882
A_30_P01	0.035968	1.581383	down			NM_009052
A_55_P20	0.019852	1.603626	down	Klra2	Mus musc	lincRNA:chr10:93774693-93893616 forward strand
A_55_P19	0.027377	3.244534	down	Ahsa2	Mus musc	NM_001170851
A_51_P28	0.006127	2.515938	down	Il2rb	Mus musc	NM_172391
A_30_P01	2.43E-04	1.765843	down			NM_008368
A_66_P11	3.45E-04	2.414085	down			lincRNA:chr13:74712775-74728450 reverse strand
A_52_P66	0.035419	2.065429	down	Pak1	Mus musc	RIKEN cl
A_52_P31	0.013157	3.376176	down	Ddit4l	Mus musc	AK021325
A_30_P01	0.033048	2.262774	down			NM_011035
A_52_P42	0.044178	1.506248	down	Nfe2l3	Mus musc	NM_030143
A_30_P01	0.02487	1.652076	down			lincRNA:chr8:13200727-13207714 forward strand
A_30_P01	0.002191	1.547741	down			NM_010903
A_52_P11	0.031562	1.631636	down			lincRNA:chr6:12062275-12075800 reverse strand
						lincRNA:chr7:77481448-77495548 forward strand
						anaphase
						BC057201

A_55_P21	0.018319	4.090777	down	Dao	Mus musc	NM_010018
A_55_P20	0.00972	2.072768	down	Il20rb	Mus musc	NM_001033543
A_55_P19	0.001249	1.828502	down		BY201561	BY201563
A_51_P47	0.018632	1.639746	down	Paqr6	Mus musc	NM_198410
A_55_P20	0.046427	2.372262	down	Lcn2	Mus musc	NM_008491
A_30_P01	0.018569	2.760071	down		lincRNA:chr7:134620707-134626739 forward strand	
A_30_P01	0.035678	1.533047	down		lincRNA:chr3:65729664-65731697 reverse strand	
A_55_P19	0.024602	2.242502	down	Pdzd4	Mus musc	NM_001029868
A_30_P01	0.004223	4.194848	down		lincRNA:chr2:32950586-32984936 forward strand	
A_52_P62	0.037354	3.02013	down	Wfikkn2	Mus musc	NM_181819
A_55_P21	0.001136	2.220166	down	Zkscan3	Mus musc	NM_001145778
A_30_P01	0.030036	1.783317	down		lincRNA:chr11:120046656-120050065 forward strand	
A_52_P20	0.020014	1.659748	down	Adam11	Mus musc	NM_001110778
A_30_P01	0.018983	1.734433	down		lincRNA:chr3:145269449-145298239 forward strand	
A_51_P38	0.041411	2.784613	down	Rab17	Mus musc	NM_008998
A_30_P01	0.049117	1.852805	down		lincRNA:chr9:41408354-41420812 forward strand	
A_30_P01	0.043703	1.768125	down		lincRNA:chr2:75489436-75490163 reverse strand	
A_55_P21	0.012468	1.760258	down	Hist2h2be	Mus musc	NM_178214
A_55_P20	0.018031	1.604514	down	2610203C	Mus musc	NR_015483
A_52_P99	0.041258	1.610356	down	Cxcl16	Mus musc	NM_023158
A_30_P01	0.016708	3.381375	down		lincRNA:chr2:115900355-115900904 forward strand	
A_51_P19	0.020686	2.306833	down	Adcy1	Mus musc	NM_009622
A_30_P01	0.002043	1.617057	down		lincRNA:chr15:96032592-96116907 forward strand	
A_52_P10	0.046803	2.30194	down	Glis2	Mus musc	NM_031184
A_55_P20	0.026906	1.793131	down	Cask	Mus musc	NM_009806
A_51_P15	0.029621	3.279358	down		docking p	AK170454
A_30_P01	0.042666	1.758238	down		lincRNA:chr1:95871175-95886625 forward strand	
A_52_P81	0.040464	2.101715	down	Slc17a6	Mus musc	NM_080853
A_55_P21	0.040091	1.646079	down	Gm7684	PREDICT	XM_001476311
A_55_P21	0.023509	1.653948	down	Sytl1	Mus musc	NM_031393
A_30_P01	0.004577	2.603515	down		lincRNA:chrX:148803114-148851243 forward strand	
A_55_P19	0.004721	3.243962	down	Ccl21b	Mus musc	NM_011335
A_51_P32	0.025145	1.559807	down	Igsf3	Mus musc	NM_207205

A_30_P01	0.011808	1.559637	down		lincRNA:chr11:3538125-3554450 forward strand
A_30_P01	0.046445	1.846452	down		lincRNA:chr5:122982442-123000053 reverse strand
A_52_P63	0.018554	3.57383	down	Cytl1	Mus musc NM_001081106
A_51_P25	0.030603	2.581304	down	Hdc	Mus musc NM_008230
A_52_P56	0.027358	2.112118	down	Vwa1	Mus musc NM_147776
A_52_P35	0.042507	2.051846	down	Scn7a	Mus musc NM_009135
A_55_P20	0.048512	1.945288	down	Slc25a34	Mus musc NM_001013780
A_30_P01	0.030795	1.53548	down		lincRNA:chr7:118248833-118267766 reverse strand
A_52_P27	0.013729	2.696038	down	Bmp7	Mus musc NM_007557
A_55_P19	0.027425	1.723822	down	Vmn1r168	Mus musc NM_001166842
A_55_P19	0.022757	2.379541	down	Cbx7	Mus musc NM_144811
A_30_P01	0.022903	1.802865	down		lincRNA:chr2:67834535-67834914 forward strand
A_55_P20	0.04472	1.65144	down	Hopx	Mus musc NM_175606
A_30_P01	0.022972	3.392102	down		lincRNA:chr2:115900355-115900904 forward strand
A_55_P20	0.038365	1.943531	down	Sgsm1	Mus musc NM_001162965
A_55_P20	0.037768	2.039437	down	Wfikkn2	Mus musc NM_181819
A_55_P20	0.046222	2.384751	down	Slc16a3	Mus musc NM_030696
A_55_P20	0.009841	4.565578	down	Ccl21a	Mus musc NM_011124
A_30_P01	0.046523	1.740609	down		lincRNA:chr16:4592919-4594230 reverse strand
A_55_P20	0.02492	1.788323	down	Gimap3	Mus musc NM_031247
A_30_P01	0.015998	1.757628	down		lincRNA:chr11:112898724-113062945 forward strand
A_55_P20	0.035478	2.22935	down		predicted AK144847
A_30_P01	0.049992	1.894974	down		lincRNA:chr10:62267317-62269871 reverse strand
A_30_P01	0.007699	1.555562	down		lincRNA:chr10:39383665-39442690 reverse strand
A_51_P25	0.032388	1.583125	down	Per3	Mus musc NM_011067
A_55_P20	0.040752	1.579584	down	Gm1998	PREDICT XM_001472042
A_55_P20	0.017304	1.56361	down	BC019943	Mus musc NM_001112729
A_55_P21	0.003674	2.416647	down	LOC1000	PREDICT XM_001474011
A_55_P22	0.039108	2.178294	down	Bnc2	Mus musc NM_172870
A_30_P01	5.18E-04	2.044285	down		lincRNA:chr7:111530578-111539097 reverse strand
A_30_P01	0.006935	1.605728	down		lincRNA:chr15:100905367-100905654 reverse strand
A_51_P46	0.034326	2.690419	down	Fbxl22	Mus musc NM_175206
A_55_P20	0.014869	1.620776	down	Id1	Mus musc NM_010495

A_30_P01	0.047837	3.488819	down		lincRNA:chr6:93029101-93031007 forward strand
A_55_P20	0.028884	2.416509	down	F8	Mus musc NM_001161374
A_55_P21	0.032038	1.696728	down	Rasd2	Mus musc NM_029182
A_30_P01	0.014303	2.3305	down		lincRNA:chr3:127170996-127201096 forward strand
A_51_P25	0.034892	2.625102	down	Dnajc22	Mus musc NM_176835
A_30_P01	0.044995	2.213157	down		lincRNA:chrX:133315875-133338600 forward strand
A_51_P17	0.021588	2.40871	down	B3gnt8	Mus musc NM_146184
A_30_P01	0.004808	1.579122	down		lincRNA:chr1:88524037-88540731 reverse strand
A_55_P20	0.037417	2.154633	down	LOC1000	PREDICT XM_001472845
A_55_P20	0.01844	1.737234	down	Gm5595	Mus musc NM_001008427
A_55_P21	0.044528	1.747516	down	Rarg	Mus musc NM_011244
A_52_P46	0.016523	1.524374	down	Fam178a	Mus musc NM_001081225
A_30_P01	0.042315	1.572399	down		lincRNA:chr5:100845342-100869667 reverse strand
A_30_P01	0.023424	1.951728	down		lincRNA:chr4:40194362-40202712 reverse strand
A_51_P33	0.0316	2.086131	down	Crybb1	Mus musc NM_023695
A_30_P01	0.019318	1.715067	down		lincRNA:chr1:63163023-63180223 forward strand
A_55_P20	0.043562	2.657017	down	Mtmr15	myotubula AK173087
A_55_P19	0.035032	1.666587	down	Syt6	Mus musc NM_018800
A_55_P21	0.033889	1.673551	down		zinc finger AK170207
A_51_P37	0.006142	2.246549	down	Gstt3	Mus musc NM_133994
A_55_P19	0.041072	1.668024	down	Cradd	Mus musc NM_009950
A_55_P20	0.020651	1.744321	down	Gm11517	Mus musc NR_033523
A_55_P21	0.015799	2.516531	down	Tnfaip8l3	tumor nec AK154109
A_30_P01	0.011881	2.677303	down		lincRNA:chr18:36449530-36456800 reverse strand
A_30_P01	0.020181	1.819337	down		lincRNA:chr4:8566129-8568514 reverse strand
A_30_P01	0.04657	1.719347	down		lincRNA:chr17:21177225-21187525 reverse strand
A_55_P20	0.015929	2.456266	down	LOC1000	PREDICT XM_001476512
A_30_P01	0.003622	2.603863	down		lincRNA:chr4:11102287-11118421 reverse strand
A_52_P30	0.024419	1.509393	down	Gm4815	PREDICT XR_031538
A_55_P24	0.02593	1.988079	down	1300014J	Mus musc AK005005
A_30_P01	0.020554	1.796955	down		lincRNA:chr8:87504644-87513694 reverse strand
A_51_P41	0.012649	2.659994	down	Scnn1b	Mus musc NM_011325
A_30_P01	0.003967	2.49032	down		lincRNA:chr9:118059348-118079494 forward strand

A_30_P01	0.033349	2.288165	down		lincRNA:chr1:183783306-183834531 reverse strand
A_30_P01	0.016706	1.702259	down		lincRNA:chr12:86415200-86415483 forward strand
A_30_P01	0.04897	2.285283	down		lincRNA:chr15:101084597-101095097 forward strand
A_55_P20	0.004085	2.232659	down	Padi2	Mus musc NM_008812
A_66_P12	0.046102	1.66668	down	Gm4804	PREDICT XR_032386
A_51_P35	0.040909	2.634651	down	Lancl3	Mus musc NM_173414
A_55_P21	0.046235	1.596841	down	18100320	Mus musc NR_027821
A_55_P21	0.034956	2.276413	down	Inpp5j	Mus musc NM_172439
A_55_P22	0.023266	4.126779	down	E030046B	Mus musc AK053225
A_51_P31	0.033452	2.070384	down	Usp11	Mus musc NM_145628
A_55_P19	0.028581	4.088622	down	D11Bwg0	Mus musc NM_001039167
A_55_P21	0.023104	1.914598	down	Enah	Mus musc NM_010135
A_51_P17	0.023467	2.677138	down	Arhgdig	Mus musc NM_008113
A_52_P25	0.0439	3.108648	down	Eps8l2	Mus musc NM_133191
A_30_P01	0.029479	1.580817	down		lincRNA:chr17:26911397-26917047 reverse strand
A_55_P20	0.013422	1.672889	down	Siva1	Mus musc NM_013929
A_55_P19	0.019063	1.528139	down	Sepr1	Mus musc NM_029100
A_52_P15	0.039519	1.666532	down	LOC6740	PREDICT XM_972673
A_30_P01	0.010283	1.537099	down		lincRNA:chr10:81816994-81863610 forward strand
A_55_P21	0.025169	1.528671	down	28104220	Mus musc NM_027279
A_52_P26	0.049732	3.354777	down	Vil1	Mus musc NM_009509
A_51_P25	0.032344	3.646738	down	Paqr5	Mus musc NM_028748
A_30_P01	0.033749	1.857361	down		lincRNA:chr3:85784436-85784624 reverse strand
A_51_P33	0.01257	2.681604	down	Galnt14	Mus musc NM_027864
A_52_P30	0.019125	2.582737	down	Plxnb1	Mus musc NM_172775
A_55_P19	0.010153	1.673333	down	Gm9634	PREDICT XR_004753
A_51_P23	0.046114	4.072977	down	Inhba	Mus musc NM_008380
A_55_P20	0.010869	1.556865	down	Gm11787	PREDICT XM_984338
A_52_P27	0.023764	1.596993	down	Eif4ebp3	Mus musc NM_201256
A_30_P01	0.040278	1.758135	down		lincRNA:chr8:41941084-41947630 reverse strand
A_30_P01	0.012254	2.303147	down		lincRNA:chr10:41368681-41393645 reverse strand
A_55_P19	0.034382	1.597029	down	Cyba	Mus musc NM_007806
A_55_P20	0.038526	1.904287	down	Has2as	Mus musc NR_002874

A_66_P12	0.020103	1.976008	down	Kcnd3	Mus musc	NM_001039347
A_55_P20	0.03845	1.689071	down		Putative u	AK143696
A_55_P21	0.047171	1.839778	down	Ankrd34a	Mus musc	NM_001024851
A_55_P21	0.042809	2.677302	down	Tmem25	Mus musc	NM_027865
A_55_P20	0.011037	1.509841	down	Anapc7	Mus musc	NM_019805
A_55_P20	0.019242	2.654591	down	Arhgdig	Mus musc	NM_008113
A_55_P24	0.003899	1.524318	down	LOC6750	PREDICT	XM_979388
A_52_P39	0.016341	2.121924	down	Chst3	Mus musc	NM_016803
A_51_P49	0.034499	12.17948	down	Cyp2f2	Mus musc	NM_007817
A_51_P13	0.013368	2.4988	down	Cst7	Mus musc	NM_009977
A_51_P43	0.021354	1.691148	down	Ascl1	Mus musc	NM_008553
A_30_P01	0.032803	1.732863	down		lincRNA:chr5:122982442-123000053 reverse strand	
A_55_P20	0.010966	2.268081	down	Crocc	Mus musc	NM_172122
A_30_P01	0.018591	2.862615	down		lincRNA:chr8:93337794-93348869 reverse strand	
A_51_P21	0.040278	2.170434	down	Abp1	Mus musc	NM_029638
A_55_P20	0.041497	2.288892	down	Neurl1a	Mus musc	NM_021360
A_52_P57	0.028899	2.044384	down	Igsf11	Mus musc	NM_170599
A_55_P21	0.024528	2.256301	down	Gbp8	Mus musc	NM_029509
A_55_P19	0.04505	1.514953	down	Ensa	Mus musc	NM_019561
A_55_P19	0.043052	2.05423	down	6330549D	Mus musc	NR_003619
A_51_P37	0.010227	1.613719	down	Glpr1	Mus musc	NM_028608
A_30_P01	0.010299	1.90434	down		lincRNA:chr2:158169020-158191295 forward strand	
A_30_P01	0.025578	2.799318	down		lincRNA:chr8:93337794-93348869 reverse strand	
A_55_P20	0.04995	3.006063	down	BC068157	Mus musc	NM_207203
A_55_P21	0.024019	2.59285	down	A330049N	Mus musc	NM_001168500
A_52_P36	0.003268	2.140437	down	Celsr2	Mus musc	NM_017392
A_55_P20	0.049437	1.518523	down	Usp21	Mus musc	NM_013919
A_52_P20	0.030964	3.363708	down	Plcxd3	Mus musc	NM_177355
A_65_P19	0.036017	1.850112	down	Zdhhc23	zinc finger	AK137472
A_30_P01	0.017203	1.695722	down		lincRNA:chr11:87872568-87880978 reverse strand	
A_55_P19	0.02287	1.963876	down	Dnm3os	Mus musc	NR_002870
A_51_P28	0.017881	1.788183	down	Wdr38	WD repea	AK077027
A_52_P13	0.013861	1.947874	down	H2-DMb2	Mus musc	NM_010388

A_55_P20	0.030756	2.457336	down	Nrg2	Mus musc	NM_001167891
A_66_P11	0.00188	1.878544	down	Mtmr7	Mus musc	NM_001040699
A_55_P19	0.013239	1.529343	down	28104220	Mus musc	NM_027279
A_55_P20	0.034921	1.672218	down	Ddb2	Mus musc	NM_028119
A_55_P20	0.036763	2.063132	down	Ano1	Mus musc	NM_178642
A_30_P01	0.037867	3.610891	down		lincRNA:chr3:95502970-95503399 reverse strand	
A_66_P12	0.024365	2.496198	down	Tceal6	Mus musc	NM_025355
A_66_P12	0.031069	1.537691	down	Phldb3	Mus musc	NM_001102613
A_55_P20	0.009619	2.878608	down	Fam159a	Mus musc	NM_001099303
A_55_P20	0.047176	1.88073	down	Tmem132	Mus musc	NM_001190352
A_51_P49	0.00896	1.716792	down	Nkg7	Mus musc	NM_024253
A_30_P01	0.032083	1.696458	down		lincRNA:chr4:33375464-33377138 reverse strand	
A_30_P01	0.005578	1.701971	down		lincRNA:chr13:94182877-94203935 forward strand	
A_55_P20	0.017341	1.746271	down	Fmn2	Mus musc	NM_019445
A_55_P19	0.026705	2.631507	down	Mdk	Mus musc	NM_010784
A_30_P01	0.005109	1.608632	down		lincRNA:chr10:96098058-96098623 forward strand	
A_55_P20	0.002882	2.510179	down	Gm7078	PREDICT	XR_031221
A_30_P01	0.047819	1.979119	down		lincRNA:chr8:13200727-13207714 forward strand	
A_55_P20	0.041101	1.939328	down		a disintegr	AK086734
A_51_P35	0.020135	1.628389	down	Gstt2	Mus musc	NM_010361
A_51_P32	0.0336	1.796667	down	Sftpc	Mus musc	NM_011359
A_52_P23	0.022247	1.546388	down	Gm5595	Mus musc	NM_001008427
A_51_P46	0.023096	1.55956	down	Narg2	Mus musc	NM_145618
A_55_P21	0.048053	1.594615	down		Ssu72 RN	BC016544
A_30_P01	0.002545	3.09299	down		lincRNA:chr3:35236023-35241498 reverse strand	
A_51_P22	0.030484	1.590747	down	Cd27	Mus musc	NM_001033126
A_55_P22	0.028102	4.884096	down	Gm7455	Mus musc	NM_001167923
A_52_P50	0.016839	3.882349	down	1600029D	Mus musc	NM_029639
A_30_P01	0.032159	1.852413	down		lincRNA:chr9:41422319-41425855 forward strand	
A_55_P20	0.033933	1.711429	down	Nrtn	Mus musc	NM_008738
A_55_P20	4.20E-04	1.984201	down	Cpe	Mus musc	NM_013494
A_55_P22	0.022455	2.770443	down	9130219A	Mus musc	AK162333
A_52_P62	0.023203	1.859735	down	Asph	Mus musc	NM_133723

A_30_P01	0.018039	1.731656	down		lincRNA:chr4:126710640-126721240 reverse strand
A_30_P01	0.043961	1.824808	down		lincRNA:chr7:88131123-88136898 forward strand
A_66_P11	0.037921	2.506223	down	Gm9647	PREDICT_XM_001481199
A_30_P01	0.027933	2.346195	down		lincRNA:chr11:112898724-113062945 reverse strand
A_52_P30	0.0289	2.208696	down	Gnaz	Mus musc NM_010311
A_51_P12	0.007536	1.750324	down	Vwce	Mus musc NM_027913
A_55_P21	0.045531	2.20596	down	LOC1000	PREDICT_XM_001474741
A_55_P19	0.049932	2.528171	down	Ckb	Mus musc NM_021273
A_55_P19	0.004299	1.600676	down	Usp27x	ubiquitin s AK028249
A_55_P20	0.021027	1.584217	down	4930434E	Mus musc NM_029440
A_55_P20	0.043707	1.980453	down	Gm2054	PREDICT_XM_001472317
A_30_P01	0.004185	2.785966	down		lincRNA:chr2:75484041-75484815 reverse strand
A_66_P11	0.037976	1.930841	down	Mt1	Mus musc NM_013602
A_55_P21	0.031759	2.259509	down	Btg1	Mus musc NM_007569
A_52_P19	0.006695	1.625898	down	Txndc11	Mus musc NM_029582
A_51_P48	0.048984	1.617695	down	H2afy3	Mus musc NR_003523
A_55_P19	0.025119	1.684475	down		CDK5 regulatory subunit associated protein 1-like 1 Gene [Source:MGI (curated);A
A_30_P01	0.042702	1.843833	down		lincRNA:chr17:79042382-79051807 reverse strand
A_30_P01	0.034969	1.732867	down		lincRNA:chr11:87872568-87880978 reverse strand
A_55_P20	0.027227	3.985921	down	Tst	Mus musc NM_009437
A_30_P01	0.0328	1.601196	down		lincRNA:chr4:133212951-133214017 reverse strand
A_30_P01	0.030487	2.122615	down		lincRNA:chr1:183783306-183834531 reverse strand
A_55_P23	0.04037	2.040805	down	9530009M	Mus musc AK035285
A_55_P24	0.026612	2.540011	down	AW05000	UI-M-BH AW050000
A_52_P79	0.038218	2.075381	down	Tmem171	Mus musc NM_001025606
A_55_P19	0.028374	1.834534	down	Bzrap1	Mus musc NM_172449
A_55_P20	0.015799	2.049677	down	Mtus2	Mus musc NM_029920
A_30_P01	0.042493	2.020239	down		lincRNA:chr6:121035524-121061074 forward strand
A_30_P01	0.036951	1.760154	down		lincRNA:chr17:26911397-26917047 forward strand
A_51_P32	0.034691	2.035603	down		Putative u AK161240
A_55_P21	0.004252	2.769785	down		dynein, ax AK082443
A_51_P33	0.036999	1.555034	down	Zfpm2	Mus musc NM_011766
A_51_P44	0.04146	1.804433	down	2310047K	PREDICT_XM_001479258

A_55_P20	0.029984	1.62627	down	Apol10b	Mus musc	NM_177820
A_30_P01	0.019188	1.802082	down			lincRNA:chr16:7947710-7948066 reverse strand
A_55_P20	0.038425	2.394988	down	Neurl1a	Mus musc	NM_021360
A_55_P23	0.026732	1.574861	down	A330106F	Mus musc	AK039774
A_51_P21	0.009699	3.028739	down	Slc6a17	Mus musc	NM_172271
A_51_P39	0.005374	1.709163	down	Hyal3	Mus musc	NM_178020
A_55_P20	0.010999	1.566744	down	Gm6483	PREDICT	XR_032846
A_55_P19	0.048983	1.638302	down	Gm8225	PREDICT	XM_985281
A_66_P10	0.027588	1.681979	down	Acp1	Mus musc	NM_001110239
A_55_P20	0.017281	2.635645	down	Penk	Mus musc	NM_001002927
A_51_P39	0.03341	2.104409	down	Fgf2	Mus musc	NM_008006
A_55_P20	0.034585	3.412245	down	Krt42	Mus musc	NM_212483
A_51_P23	0.030127	2.788347	down	Sorcs2	Mus musc	NM_030889
A_55_P20	0.014772	1.931935	down	Gm3218	PREDICT	XM_001476005
A_30_P01	0.01706	2.848392	down			lincRNA:chr17:46972160-46997919 reverse strand
A_52_P85	0.026043	1.810815	down	Gadd45gi	Mus musc	NM_183358
A_51_P40	0.02848	2.472521	down	Rarres1	Mus musc	NM_001164763
A_55_P22	0.044744	3.444184	down	Scube1	Mus musc	NM_022723
A_55_P20	0.002783	2.613324	down	Ush1c	Mus musc	NM_001163733
A_55_P21	0.020688	1.903212	down	Sema4d	Mus musc	NM_013660
A_55_P22	0.015013	1.642225	down	LOC5414	BB161756	BB161756
A_51_P24	0.021237	1.778048	down	Traf3ip3	Mus musc	NM_153137
A_52_P65	0.014464	1.703708	down	Ccnjl	Mus musc	NM_001045530
A_51_P51	0.039435	3.37709	down	Itm2a	Mus musc	NM_008409
A_55_P20	0.014282	1.775031	down	Crebzf	Mus musc	NM_145151
A_55_P19	0.003006	1.632776	down	Pnpla6	Mus musc	NM_001122818
A_30_P01	0.003886	1.764225	down			lincRNA:chr17:15357376-15385701 forward strand
A_55_P20	0.002676	1.663937	down	Tgtp2	Mus musc	NM_001145164
A_30_P01	0.006232	2.30316	down			lincRNA:chrX:47890565-47915775 forward strand
A_30_P01	0.032162	1.697021	down			lincRNA:chr2:174088550-174109425 forward strand
A_55_P20	0.039436	1.677574	down		ankyrin re	AK051017
A_30_P01	0.041416	1.841353	down			lincRNA:chr3:85806420-85889300 reverse strand
A_51_P13	0.012222	1.981455	down	2310010J	PREDICT	XM_896611

A_55_P20	0.015843	1.709839	down	Agrp	Mus musc	NM_007427
A_30_P01	0.028202	1.897868	down			lincRNA:chr11:116936834-116948799 reverse strand
A_30_P01	0.028198	1.982984	down			lincRNA:chr7:144563845-144603732 forward strand
A_55_P20	0.031064	1.836516	down			RNA binding motif protein 39 Gene [Source:MGI (curated);Acc:MGI:2157953] [EN
A_55_P20	0.036337	2.102905	down	Tspan33	Mus musc	NM_146173
A_55_P19	0.034204	2.022489	down			spondin 1 AK134774
A_55_P19	0.047301	2.244124	down	Slc23a3	Mus musc	NM_194333
A_55_P21	0.014176	1.742258	down	LOC1000	PREDICT	XM_001475526
A_55_P20	0.03391	1.734273	down	Rpl3	Mus musc	NM_013762
A_30_P01	0.041306	2.183864	down			lincRNA:chr15:83091086-83093818 reverse strand
A_55_P20	0.032541	2.67849	down	Fam179a	Mus musc	NM_177087
A_55_P20	0.022147	2.020182	down	Rapgef1	Mus musc	NM_001080925
A_51_P37	0.004821	7.105575	down	Angpt4	Mus musc	NM_009641
A_55_P21	0.033147	2.234026	down	Lrrc4	Mus musc	NM_138682
A_55_P21	0.030669	2.618528	down	B930041F	Mus musc	NM_178699
A_55_P20	0.010338	2.174951	down	Lhx3	Mus musc	NM_001039653
A_66_P10	0.041999	4.520897	down	A530001N	PREDICT	XM_001477625
A_30_P01	0.023503	2.301335	down			lincRNA:chr6:117827499-117851478 reverse strand
A_51_P11	0.02077	1.570208	down	Ncs1	Mus musc	NM_019681
A_30_P01	0.042275	1.561695	down			lincRNA:chr2:153163620-153170845 reverse strand
A_55_P19	0.02243	2.923148	down	AI854703	Mus musc	NR_027236
A_51_P37	0.035008	1.958292	down	Fxyd7	Mus musc	NM_022007
A_30_P01	0.039902	1.522006	down			lincRNA:chr13:34872696-34906407 reverse strand
A_52_P60	0.00548	1.823159	down	Greb1l	Mus musc	NM_001083628
A_30_P01	0.036771	2.098988	down			lincRNA:chr1:196843592-196865102 forward strand
A_55_P20	0.005016	1.754827	down	Aifm3	Mus musc	NM_175178
A_51_P36	0.031889	1.933544	down	Ankrd43	Mus musc	NM_183173
A_55_P20	0.049897	2.693699	down	Rap1gap	Mus musc	NM_001081155
A_52_P13	0.042905	2.006892	down	Kcna6	Mus musc	NM_013568
A_30_P01	0.009799	1.745182	down			lincRNA:chr13:70762342-70776512 reverse strand
A_52_P21	0.008061	2.996747	down	Sox9	Mus musc	NM_011448
A_55_P20	0.005881	2.972379	down	Rap1gap	Mus musc	NM_001081155
A_55_P21	0.034605	3.540821	down	Gria1	Mus musc	NM_001113325

A_30_P01	0.021394	2.532401	down		lincRNA:chr1:160888257-160910594 reverse strand	
A_55_P20	0.013208	2.294375	down	Lrrc10b	Mus musc	NM_001111140
A_55_P20	0.042723	3.867931	down	Gm1574	Mus musc	NM_001005422
A_55_P19	0.012712	1.603351	down	Bbs10	Mus musc	NM_027914
A_51_P11	0.037331	1.644718	down	Igtp	Mus musc	NM_018738
A_52_P60	0.017979	2.00132	down	Fbxl2	F-box and	AK089994

0000110178]

SMUST00000112942]

1GI:892995] [ENSMUST00000108796]

И:88071] [ENSMUST00000107160]

Acc:MGI:97355] [ENSMUST00000107844]

cc:MGI:1921765] [ENSMUST00000110323]

√SMUST000000109584]

Annotator Enrichment Score: 2.5916051096518933

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR002971	6	0.828729	1.41E-05	NM_00104	521	12	17763	17.04702	0.012501	0.012501	0.021933
PIR_SUPER	PIRSF00021	4	0.552486	8.18E-05	NM_00104	226	4	8136	36	0.019601	0.019601	0.105667
SP_PIR_KE	pheromone	4	0.552486	4.47E-04	NM_00104	516	6	17854	23.06718	0.14949	0.077769	0.612928
INTERPRO	IPR002345	7	0.966851	0.00212	NM_00744	521	46	17763	5.188225	0.849685	0.37734	3.25045
INTERPRO	IPR000566	7	0.966851	0.00294	NM_00744	521	49	17763	4.870579	0.927863	0.408939	4.481147
INTERPRO	IPR012674	7	0.966851	0.003977	NM_00744	521	52	17763	4.589584	0.971508	0.447346	6.015958
PIR_SUPER	PIRSF00251	4	0.552486	0.012528	NM_00104	226	18	8136	8	0.952681	0.533599	15.03541
GOTERM	GO:000555	6	0.828729	0.153912	NM_00104	385	98	13288	2.11312	1	0.93434	91.29661
GOTERM	GO:000554	6	0.828729	0.192414	NM_00104	385	106	13288	1.953639	1	0.936284	95.59226

Annotator Enrichment Score: 2.078903222892897

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM	GO:001087	12	1.657459	0.00105	NM_00969	387	128	13588	3.291667	0.84009	0.600113	1.761696
GOTERM	GO:000686	11	1.519337	0.002073	NM_00969	387	119	13588	3.245565	0.973262	0.700974	3.450597
GOTERM	GO:000531	5	0.690608	0.037604	NM_00969	385	44	13288	3.922078	1	0.854908	42.87383
SP_PIR_KE	lipid transp	5	0.690608	0.059064	NM_00969	516	51	17854	3.392233	1	0.816449	56.69102

Annotator Enrichment Score: 1.5930312245409755

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR013600	6	0.828729	9.75E-05	NM_01064	521	17	17763	12.03319	0.083357	0.042585	0.151657
PIR_SUPER	PIRSF03831	5	0.690608	2.37E-04	NM_01064	226	12	8136	15	0.055681	0.028239	0.30551
GOTERM	GO:000552	13	1.79558	0.006375	NM_02692	385	181	13288	2.478927	0.971081	0.829945	8.919773
GOTERM	GO:003024	17	2.348066	0.021957	NM_02692	385	317	13288	1.850924	0.999995	0.871257	27.69802
SP_PIR_KE	Lectin	11	1.519337	0.023212	NM_00111	516	167	17854	2.279093	0.999797	0.654488	27.58946
INTERPRO	IPR001304	8	1.104972	0.058387	NM_01064	521	118	17763	2.311461	1	0.93186	60.81247
UP_SEQ	Fl domain:C-t	7	0.966851	0.058986	NM_00111	494	90	16021	2.522425	1	0.999909	63.20177
INTERPRO	IPR016186	8	1.104972	0.079637	NM_01064	521	127	17763	2.147657	1	0.942171	72.53469
INTERPRO	IPR018378	7	0.966851	0.084851	NM_00111	521	104	17763	2.294792	1	0.946742	74.86009
SMART	SM00034:C	8	1.104972	0.102355	NM_01064	308	118	9131	2.009905	1	0.981263	74.72941
SP_PIR_KE	Signal-anch	16	2.209945	0.197001	NM_13366	516	405	17854	1.366944	1	0.855887	95.09908
KEGG_PAT	mmu05332	4	0.552486	0.219133	NM_00111	161	58	5738	2.457914	1	0.895343	94.71319

KEGG_PATH mmu04650 6 0.828729 0.253293 NM_00111 161 122 5738 1.752775 1 0.894012 96.8934

Annotator Enrichment Score: 1.5674308028181563

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORD	cell adhesion	21	2.900552	0.007614	NM_17229	516	380	17854	1.912148	0.937144	0.424998	9.973041
GOTERM	GO:0007154	24	3.314917	0.050579	NM_17229	387	561	13588	1.50208	1	0.983705	58.4457
GOTERM	GO:002261	24	3.314917	0.051535	NM_17229	387	562	13588	1.499407	1	0.978658	59.14808

Annotator Enrichment Score: 1.3909586225136688

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR001849	15	2.071823	0.02181	NM_15281	521	261	17763	1.959428	1	0.806207	29.06263
INTERPRO	IPR011993	16	2.209945	0.023353	NM_15281	521	289	17763	1.88756	1	0.778479	30.78518
SMART	SM00233:FLN	15	2.071823	0.056806	NM_15281	308	261	9131	1.703799	0.999998	0.998439	52.52688
UP_SEQ_DOMAIN	FLN domain:PH	11	1.519337	0.094359	NM_15281	494	202	16021	1.766054	1	0.999888	80.40183

Annotator Enrichment Score: 1.3832074586700498

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR006117	3	0.414365	0.021305	NM_14522	521	8	17763	12.78527	1	0.825919	28.4901
INTERPRO	IPR018952	3	0.414365	0.053904	NM_14522	521	13	17763	7.867858	1	0.926049	57.80451
INTERPRO	IPR006116	3	0.414365	0.061699	NM_14522	521	14	17763	7.305868	1	0.924605	62.90477

Annotator Enrichment Score: 1.364937792459442

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR014716	4	0.552486	0.022414	NM_13386	521	21	17763	6.494105	1	0.789267	29.74162
INTERPRO	IPR002181	4	0.552486	0.04754	NM_13386	521	28	17763	4.870579	1	0.922585	53.16133
UP_SEQ_DOMAIN	FLN domain:Fil	4	0.552486	0.04904	NM_13386	494	27	16021	4.804618	1	0.999826	56.25646
SMART	SM00186:FLN	4	0.552486	0.066393	NM_13386	308	28	9131	4.235158	1	0.99366	58.31989

Annotator Enrichment Score: 1.357261127071822

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM	GO:004316	136	18.78453	0.006292	NM_18302	385	3885	13288	1.208222	0.969711	0.969711	8.808534
GOTERM	GO:004316	136	18.78453	0.009867	NM_18302	385	3934	13288	1.193173	0.995886	0.839763	13.48463
GOTERM	GO:004687	131	18.09392	0.019716	NM_18302	385	3850	13288	1.174382	0.999984	0.889904	25.2405

GOTERM_!GO:000827	73	10.08287	0.067532	NM_17525	385	2105	13288	1.196932	1	0.869808	63.99098
SP_PIR_KE' zinc	66	9.116022	0.073789	NM_18302	516	1886	17854	1.210844	1	0.804513	65.13269
SP_PIR_KE' metal-bind	89	12.29282	0.103531	NM_00748	516	2682	17854	1.148199	1	0.820963	77.73721
GOTERM_!GO:004691	85	11.74033	0.144748	NM_00748	385	2608	13288	1.12489	1	0.933261	89.81334
SP_PIR_KE' zinc-finger	42	5.801105	0.151674	NM_13368	516	1204	17854	1.207004	1	0.862598	89.57502

Annotator Enrichment Score: 1.349278858163124

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:004662		4	0.552486	7.31E-04	NM_00989	387	7	13588	20.06349	0.720957	0.720957	1.229946
GOTERM_!GO:004662		4	0.552486	0.002352	NM_00989	387	10	13588	14.04444	0.983586	0.560414	3.90629
KEGG_PAT mmu04930		6	0.828729	0.011229	NM_00989	161	49	5738	4.364051	0.807695	0.807695	12.56004
GOTERM_!GO:004858		5	0.690608	0.113044	NM_00989	387	65	13588	2.700855	1	0.979276	86.86165
GOTERM_!GO:000996		9	1.243094	0.114537	NM_00989	387	171	13588	1.847953	1	0.978921	87.231
GOTERM_!GO:000193		7	0.966851	0.130381	NM_00989	387	121	13588	2.031221	1	0.97783	90.59212
GOTERM_!GO:001064		9	1.243094	0.160359	NM_00989	387	186	13588	1.698925	1	0.974641	94.80344
GOTERM_!GO:003135		7	0.966851	0.32817	NM_00989	387	165	13588	1.489562	1	0.989913	99.88051
KEGG_PAT mmu04630		6	0.828729	0.41883	NM_00989	161	152	5738	1.406832	1	0.922385	99.84204

Annotator Enrichment Score: 1.3429706004819135

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:003027		6	0.828729	0.016939	NM_05317	387	53	13588	3.974843	1	0.949268	25.10281
GOTERM_!GO:007016		3	0.414365	0.074319	NM_05317	387	16	13588	6.583333	1	0.983153	72.92612
GOTERM_!GO:003050		3	0.414365	0.074319	NM_05317	387	16	13588	6.583333	1	0.983153	72.92612

Annotator Enrichment Score: 1.3084464005098033

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000075		6	0.828729	0.013368	NM_00102	349	51	12504	4.215068	0.982824	0.741986	16.47444
GOTERM_!GO:000572		3	0.414365	0.014785	NM_00102	349	7	12504	15.35489	0.988872	0.675212	18.06514
GOTERM_!GO:000077		4	0.552486	0.600891	NM_00102	349	111	12504	1.291102	1	0.976448	99.99954

Annotator Enrichment Score: 1.3038938580378359

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:004257		8	1.104972	0.025945	NM_13424	349	104	12504	2.756006	0.999643	0.733706	29.64675

GOTERM_(GO:000577	8	1.104972	0.025945	NM_13424	349	104	12504	2.756006	0.999643	0.733706	29.64675
SP_PIR_KE'peroxisom	7	0.966851	0.059167	NM_13424	516	96	17854	2.522973	1	0.793408	56.75627
UP_SEQ_Flshort sequi	4	0.552486	0.152837	NM_13424	494	44	16021	2.948289	1	0.999981	93.46065

Annotator Enrichment Score: 1.1732186147712482

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
PIR_SUPER	PIRSF00631	3	0.414365	0.004404	NM_00989	226	4	8136	27	0.656314	0.299534	5.544375
KEGG_PAT	mmu04930	6	0.828729	0.011229	NM_00989	161	49	5738	4.364051	0.807695	0.807695	12.56004
INTERPRO	IPR001496	5	0.690608	0.020393	NM_00989	521	36	17763	4.735285	1	0.841175	27.44629
UP_SEQ_Fl	domain:SO	5	0.690608	0.02397	NM_00989	494	36	16021	4.50433	1	0.999764	32.89741
SMART	SM00253:5	5	0.690608	0.031687	NM_00989	308	36	9131	4.117514	0.999188	0.999188	33.64753
SP_PIR_KE	Signal tran	4	0.552486	0.068784	NM_00989	516	33	17854	4.194033	1	0.820906	62.45198
SP_PIR_KE	SH2 domai	7	0.966851	0.077504	NM_00989	516	103	17854	2.351509	1	0.784978	67.00658
KEGG_PAT	mmu04910	8	1.104972	0.089986	NM_00989	161	138	5738	2.066073	0.999999	0.899189	67.39718
INTERPRO	IPR000980	7	0.966851	0.107409	NM_00989	521	111	17763	2.150075	1	0.949429	82.95595
GOTERM_(GO:004858		5	0.690608	0.113044	NM_00989	387	65	13588	2.700855	1	0.979276	86.86165
GOTERM_(GO:001074		3	0.414365	0.157747	NM_00989	387	25	13588	4.213333	1	0.975238	94.52308
SP_PIR_KE	growth reg	4	0.552486	0.16742	NM_02847	516	49	17854	2.824553	1	0.882299	91.94201
SMART	SM00252:5	7	0.966851	0.170183	NM_00989	308	111	9131	1.869574	1	0.9838	90.71158
UP_SEQ_Fl	domain:SH	5	0.690608	0.30029	NM_00989	494	90	16021	1.801732	1	0.999994	99.71821
KEGG_PAT	mmu04630	6	0.828729	0.41883	NM_00989	161	152	5738	1.406832	1	0.922385	99.84204

Annotator Enrichment Score: 1.1728322792573809

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_(GO:000079		6	0.828729	0.013368	NM_00102	349	51	12504	4.215068	0.982824	0.741986	16.47444
GOTERM_(GO:000078		11	1.519337	0.017083	NM_03359	349	165	12504	2.388539	0.994504	0.646803	20.58529
GOTERM_(GO:000022		8	1.104972	0.052094	NM_00954	349	121	12504	2.368799	1	0.867293	51.11214
GOTERM_(GO:004442		15	2.071823	0.061474	NM_01944	349	318	12504	1.690004	1	0.881034	57.20164
GOTERM_(GO:000569		17	2.348066	0.062913	NM_01089	349	378	12504	1.611316	1	0.832029	58.07102
GOTERM_(GO:000632		15	2.071823	0.06743	AK141316,	387	315	13588	1.671958	1	0.987103	69.30761
GOTERM_(GO:000572		4	0.552486	0.072715	NM_00954	349	35	12504	4.094638	1	0.826882	63.5726
GOTERM_(GO:001656		12	1.657459	0.074022	NM_02847	387	236	13588	1.785311	1	0.98491	72.779
GOTERM_(GO:000633		7	0.966851	0.090169	NM_03359	387	109	13588	2.254842	1	0.978394	79.78644

GOTERM_!GO:004445	6	0.828729	0.159482	NM_00954	349	103	12504	2.087073	1	0.917792	90.2119
GOTERM_!GO:005127	16	2.209945	0.178367	AK141316,	387	404	13588	1.390539	1	0.97592	96.39911
GOTERM_!GO:000075	4	0.552486	0.196908	NM_00954	349	55	12504	2.605679	1	0.898083	94.67781

Annotator Enrichment Score: 1.159672083150719

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:003250		21	2.900552	0.012785	NM_00973	387	409	13588	1.802771	1	0.917493	19.56414
GOTERM_!GO:004860		21	2.900552	0.012785	NM_00973	387	409	13588	1.802771	1	0.917493	19.56414
GOTERM_!GO:000727		17	2.348066	0.027285	NM_02187	387	331	13588	1.80329	1	0.968194	37.37798
GOTERM_!GO:001995		19	2.624309	0.027447	NM_02187	387	386	13588	1.728267	1	0.960744	37.5546
GOTERM_!GO:004823		10	1.381215	0.299827	NM_00969	387	255	13588	1.376906	1	0.987858	99.75958
GOTERM_!GO:000728		10	1.381215	0.299827	NM_00969	387	255	13588	1.376906	1	0.987858	99.75958
SP_PIR_KEY'spermatog		4	0.552486	0.692993	NM_00116	516	123	17854	1.125228	1	0.978745	99.99999

Annotator Enrichment Score: 1.154538977882701

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000804		15	2.071823	0.013428	NM_19860	385	249	13288	2.079174	0.999441	0.846245	17.92086
GOTERM_!GO:000509		12	1.657459	0.023846	NM_00116	385	192	13288	2.157143	0.999998	0.851931	29.71108
GOTERM_!GO:003069		18	2.486188	0.032742	NM_19860	385	361	13288	1.720934	1	0.871164	38.51066
GOTERM_!GO:000509		5	0.690608	0.034953	NM_00116	385	43	13288	4.013289	1	0.860692	40.5322
GOTERM_!GO:006058		18	2.486188	0.037612	NM_19860	385	367	13288	1.692799	1	0.82965	42.88069
GOTERM_!GO:000508		12	1.657459	0.058672	NM_00116	385	223	13288	1.857271	1	0.892805	58.65603
GOTERM_!GO:005105		12	1.657459	0.061029	NM_00116	387	228	13588	1.847953	1	0.985394	65.54177
GOTERM_!GO:004657		10	1.381215	0.073477	NM_00116	387	181	13588	1.93984	1	0.986375	72.50649
UP_SEQ_F!domain:PH		4	0.552486	0.074414	AK157835,	494	32	16021	4.053897	1	0.999976	71.95997
GOTERM_!GO:003231		6	0.828729	0.077132	NM_00116	387	80	13588	2.633333	1	0.979571	74.28499
UP_SEQ_F!domain:PH		4	0.552486	0.080066	AK157835,	494	33	16021	3.931051	1	0.999971	74.64671
UP_SEQ_F!domain:Ra		4	0.552486	0.080066	NM_00116	494	33	16021	3.931051	1	0.999971	74.64671
GOTERM_!GO:003231		4	0.552486	0.09827	NM_00116	387	39	13588	3.60114	1	0.978517	82.62509
GOTERM_!GO:003248		4	0.552486	0.09827	NM_00116	387	39	13588	3.60114	1	0.978517	82.62509
SP_PIR_KEY'GTPase act		8	1.104972	0.098944	NM_17737	516	136	17854	2.03534	1	0.819921	76.11911
INTERPRO IPR000195		4	0.552486	0.09918	NM_00116	521	38	17763	3.588847	1	0.945785	80.33768
GOTERM_!GO:000509		5	0.690608	0.118344	NM_00116	385	65	13288	2.654945	1	0.924557	84.11709

GOTERM_!GO:004308	6	0.828729	0.125026	NM_00116	387	93	13588	2.265233	1	0.97944	89.56244
SMART SM00164:1	4	0.552486	0.134544	NM_00116	308	38	9131	3.120643	1	0.989559	84.12969
GOTERM_!GO:005135	8	1.104972	0.322332	NM_00116	387	196	13588	1.433107	1	0.989823	99.86167

Annotator Enrichment Score: 1.0947465036901873

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:001604		11	1.519337	0.004892	NM_00886	387	134	13588	2.882255	0.999808	0.75982	7.962986
GOTERM_!GO:000939		3	0.414365	0.082694	NM_00886	387	17	13588	6.196078	1	0.976843	76.78527
INTERPRO IPR018029		7	0.966851	0.091004	NM_00886	521	106	17763	2.251494	1	0.941584	77.36706
GOTERM_!GO:000664		9	1.243094	0.093428	NM_00886	387	163	13588	1.93865	1	0.977707	80.97697
GOTERM_!GO:001629		6	0.828729	0.095737	NM_00886	385	84	13288	2.465306	1	0.90202	77.00919
GOTERM_!GO:000462		5	0.690608	0.108729	NM_00886	385	63	13288	2.739229	1	0.921979	81.39016
GOTERM_!GO:001963		9	1.243094	0.128934	NM_00886	387	176	13588	1.795455	1	0.978147	90.3238
UP_SEQ_Fl domain:C2		5	0.690608	0.156855	NM_00886	494	68	16021	2.384645	1	0.999977	93.95245
SP_PIR_KE lipid degra		5	0.690608	0.193846	NM_00886	516	79	17854	2.189922	1	0.857739	94.82764

Annotator Enrichment Score: 1.0782685637636251

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO IPR017447		3	0.414365	0.078325	NM_02818	521	16	17763	6.392634	1	0.951917	71.91894
UP_SEQ_Fl domain:CS		3	0.414365	0.085361	NM_02818	494	16	16021	6.080845	1	0.999921	76.9424
INTERPRO IPR007052		3	0.414365	0.087103	NM_02818	521	17	17763	6.016597	1	0.945331	75.80652

Annotator Enrichment Score: 1.0769660586226895

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:004424		7	0.966851	0.004953	NM_00886	387	56	13588	4.388889	0.999827	0.709983	8.05798
GOTERM_!GO:003014		3	0.414365	0.051059	NM_17573	387	13	13588	8.102564	1	0.981244	58.79983
GOTERM_!GO:004646		3	0.414365	0.051059	NM_17573	387	13	13588	8.102564	1	0.981244	58.79983
GOTERM_!GO:000664		5	0.690608	0.108371	NM_01697	387	64	13588	2.743056	1	0.981743	85.6402
GOTERM_!GO:000666		4	0.552486	0.257919	NM_01697	387	62	13588	2.265233	1	0.986934	99.35713
GOTERM_!GO:000667		3	0.414365	0.272672	NM_01697	387	36	13588	2.925926	1	0.985607	99.54231
GOTERM_!GO:004651		3	0.414365	0.293877	NM_01697	387	38	13588	2.77193	1	0.987328	99.72257

Annotator Enrichment Score: 1.0172391144982789

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KEY	amyloid	3	0.414365	0.045267	NM_00911	516	12	17854	8.650194	1	0.782266	47.0985
GOTERM_	GO:003436	3	0.414365	0.071701	NM_00911	349	16	12504	6.717765	1	0.846252	63.03645
SP_PIR_KEY	hdl	3	0.414365	0.084923	NM_00911	516	17	17854	6.106019	1	0.799376	70.47276
GOTERM_	GO:003435	3	0.414365	0.172478	NM_00911	349	27	12504	3.980898	1	0.916745	92.05353
GOTERM_	GO:003295	3	0.414365	0.172478	NM_00911	349	27	12504	3.980898	1	0.916745	92.05353

Annotator Enrichment Score: 0.9475585123087121

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR013781	5	0.690608	0.016804	AK013167,	521	34	17763	5.013831	1	0.849183	23.19428
GOTERM_	GO:000602	4	0.552486	0.183271	NM_17247	387	52	13588	2.700855	1	0.976674	96.74596
GOTERM_	GO:001605	5	0.690608	0.19833	NM_00108	387	81	13588	2.167353	1	0.978879	97.62496
GOTERM_	GO:000597	5	0.690608	0.265382	AK013167,	387	92	13588	1.908213	1	0.986034	99.45819

Annotator Enrichment Score: 0.9438912467269355

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:001676	4	0.552486	0.064069	NM_00973	385	32	13288	4.314286	1	0.869699	61.98714
SP_PIR_KEY	Aminotran	3	0.414365	0.15144	NM_00973	516	24	17854	4.325097	1	0.871246	89.53548
GOTERM_	GO:000848	3	0.414365	0.151858	NM_00973	385	24	13288	4.314286	1	0.937029	90.98279

Annotator Enrichment Score: 0.9236386945357603

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_FL	domain:VV	5	0.690608	0.084152	NM_19803	494	54	16021	3.002886	1	0.999958	76.4359
INTERPRO	IPR002035	6	0.828729	0.115745	NM_19803	521	88	17763	2.324594	1	0.952704	85.27293
SMART	SM00327:\	6	0.828729	0.173987	NM_19803	308	88	9131	2.021325	1	0.978512	91.2397

Annotator Enrichment Score: 0.8848809302488807

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_FL	metal ion-t	4	0.552486	0.040325	NM_14606	494	25	16021	5.188988	1	0.999921	49.17697
UP_SEQ_FL	metal ion-t	4	0.552486	0.040325	NM_14606	494	25	16021	5.188988	1	0.999921	49.17697
GOTERM_	GO:000808	6	0.828729	0.056975	NM_00108	385	72	13288	2.87619	1	0.901861	57.55419
INTERPRO	IPR002073	3	0.414365	0.124747	NM_00108	521	21	17763	4.870579	1	0.959878	87.44212
GOTERM_	GO:000411	3	0.414365	0.151858	NM_00108	385	24	13288	4.314286	1	0.937029	90.98279

INTERPRO IPR003607	3	0.414365	0.15504	NM_00108	521	24	17763	4.261756	1	0.969761	92.74382
GOTERM_!GO:000411	3	0.414365	0.162072	NM_00108	385	25	13288	4.141714	1	0.934198	92.44549
UP_SEQ_Flregion of ir	4	0.552486	0.175409	NM_00114	494	47	16021	2.7601	1	0.999963	95.80554
SMART SM00471:f	3	0.414365	0.192346	NM_00108	308	24	9131	3.705763	1	0.965685	93.42079
SP_PIR_KE'camp	3	0.414365	0.192848	NM_00108	516	28	17854	3.707226	1	0.870095	94.73897
KEGG_PAT mmu00230	5	0.690608	0.643429	NM_02617	161	157	5738	1.135024	1	0.974578	99.99952

Annotator Enrichment Score: 0.8671218149958797

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
KEGG_PAT mmu04930		6	0.828729	0.011229	NM_00989	161	49	5738	4.364051	0.807695	0.807695	12.56004
GOTERM_!GO:005073		3	0.414365	0.020121	NM_00989	387	8	13588	13.16667	1	0.947963	29.1006
GOTERM_!GO:000193		4	0.552486	0.026432	NM_00989	387	23	13588	6.10628	1	0.972561	36.44318
GOTERM_!GO:004232		4	0.552486	0.040188	NM_00989	387	27	13588	5.201646	1	0.97209	50.04208
GOTERM_!GO:004593		4	0.552486	0.048178	NM_00989	387	29	13588	4.842912	1	0.983477	56.63103
GOTERM_!GO:001056		4	0.552486	0.048178	NM_00989	387	29	13588	4.842912	1	0.983477	56.63103
BIOCARTA m_il2rbPat		4	0.552486	0.061305	NM_00989	31	36	1171	4.197133	0.996633	0.996633	49.75427
GOTERM_!GO:003140		4	0.552486	0.092565	NM_00989	387	38	13588	3.695906	1	0.978768	80.66851
GOTERM_!GO:004858		5	0.690608	0.113044	NM_00989	387	65	13588	2.700855	1	0.979276	86.86165
GOTERM_!GO:000193		7	0.966851	0.130381	NM_00989	387	121	13588	2.031221	1	0.97783	90.59212
BIOCARTA m_ghPathv		3	0.414365	0.132354	NM_00989	31	25	1171	4.532903	0.999997	0.985866	78.65759
GOTERM_!GO:003226		5	0.690608	0.148096	NM_00989	387	72	13588	2.438272	1	0.974781	93.35866
GOTERM_!GO:005124		5	0.690608	0.181026	NM_00989	387	78	13588	2.250712	1	0.976414	96.59131
GOTERM_!GO:005073		4	0.552486	0.190472	NM_00989	387	53	13588	2.649895	1	0.977658	97.19879
GOTERM_!GO:003226		11	1.519337	0.273648	NM_00989	387	280	13588	1.379365	1	0.984927	99.55259
GOTERM_!GO:003139		7	0.966851	0.32817	NM_00989	387	165	13588	1.489562	1	0.989913	99.88051
GOTERM_!GO:004232		9	1.243094	0.583965	NM_00989	387	290	13588	1.089655	1	0.998711	99.99996
GOTERM_!GO:001922		9	1.243094	0.626017	NM_00989	387	301	13588	1.049834	1	0.998956	99.99999
GOTERM_!GO:005117		9	1.243094	0.626017	NM_00989	387	301	13588	1.049834	1	0.998956	99.99999
GOTERM_!GO:004354		3	0.414365	0.974562	NM_17216	387	192	13588	0.548611	1	1	100
GOTERM_!GO:005133		3	0.414365	0.978618	NM_17216	387	199	13588	0.529313	1	1	100

Annotator Enrichment Score: 0.8650309235170337

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR

INTERPRO IPR002890	3	0.414365	0.032942	NM_00737	521	10	17763	10.22821	1	0.863874	40.64312
GOTERM_!GO:000486	9	1.243094	0.095324	NM_00744	385	161	13288	1.92937	1	0.910453	76.85528
GOTERM_!GO:003041	9	1.243094	0.138067	NM_00744	385	176	13288	1.764935	1	0.935671	88.58703
INTERPRO IPR000010	3	0.414365	0.197232	NM_00108	521	28	17763	3.652934	1	0.97865	96.73182
SMART SM00043(C	3	0.414365	0.242237	NM_00108	308	28	9131	3.176368	1	0.966815	97.07978
GOTERM_!GO:000486	3	0.414365	0.311571	NM_00108	385	39	13288	2.654945	1	0.978295	99.57199

Annotator Enrichment Score: 0.8514454898634436

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000252		8	1.104972	0.008106	NM_00963	387	81	13588	3.467764	0.999999	0.830585	12.86511
GOTERM_!GO:005160		7	0.966851	0.055592	NM_00744	387	96	13588	2.560185	1	0.981543	62.00546
GOTERM_!GO:000225		8	1.104972	0.067825	NM_00963	387	126	13588	2.229277	1	0.985392	69.52669
GOTERM_!GO:000254		4	0.552486	0.081589	NM_00100	387	36	13588	3.901235	1	0.981939	76.30733
GOTERM_!GO:000695		4	0.552486	0.081589	NM_00100	387	36	13588	3.901235	1	0.981939	76.30733
GOTERM_!GO:004858		10	1.381215	0.08378	NM_01737	387	186	13588	1.887694	1	0.975864	77.2459
GOTERM_!GO:000225		6	0.828729	0.097787	NM_00100	387	86	13588	2.449612	1	0.979832	82.46675
GOTERM_!GO:000695		11	1.519337	0.108343	NM_00963	387	225	13588	1.716543	1	0.983156	85.63242
GOTERM_!GO:000244		6	0.828729	0.109061	NM_00963	387	89	13588	2.367041	1	0.980768	85.82693
GOTERM_!GO:001648		6	0.828729	0.112954	NM_00100	387	90	13588	2.340741	1	0.980673	86.8391
GOTERM_!GO:005160		5	0.690608	0.113044	NM_00100	387	65	13588	2.700855	1	0.979276	86.86165
GOTERM_!GO:000961		15	2.071823	0.119122	NM_00748	387	347	13588	1.517771	1	0.977985	88.30479
GOTERM_!GO:000268		10	1.381215	0.134299	NM_01737	387	206	13588	1.704423	1	0.977917	91.28416
GOTERM_!GO:000270		5	0.690608	0.137683	NM_01737	387	70	13588	2.507937	1	0.977659	91.84298
GOTERM_!GO:000695		18	2.486188	0.14529	NM_01133	387	448	13588	1.410714	1	0.975328	92.97868
GOTERM_!GO:000244		5	0.690608	0.169786	NM_00100	387	76	13588	2.309942	1	0.977075	95.70708
GOTERM_!GO:000695		18	2.486188	0.186928	NM_01133	387	471	13588	1.341826	1	0.977653	96.98391
GOTERM_!GO:005077		7	0.966851	0.190519	NM_01737	387	136	13588	1.80719	1	0.976798	97.20152
GOTERM_!GO:000695		4	0.552486	0.197744	NM_00100	387	54	13588	2.600823	1	0.979422	97.59542
GOTERM_!GO:000695		3	0.414365	0.209209	NM_00100	387	30	13588	3.511111	1	0.98052	98.11516
GOTERM_!GO:000269		5	0.690608	0.240451	NM_01737	387	88	13588	1.994949	1	0.984599	99.04702
GOTERM_!GO:000245		3	0.414365	0.262056	NM_00100	387	35	13588	3.009524	1	0.986583	99.41516
GOTERM_!GO:001606		4	0.552486	0.265625	NM_00100	387	63	13588	2.229277	1	0.985622	99.46121
GOTERM_!GO:001972		4	0.552486	0.281116	NM_00100	387	65	13588	2.160684	1	0.985966	99.62437

GOTERM_!GO:000225	4	0.552486	0.428434	NM_00100	387	84	13588	1.671958	1	0.995033	99.99224
GOTERM_!GO:000246	4	0.552486	0.428434	NM_00100	387	84	13588	1.671958	1	0.995033	99.99224
GOTERM_!GO:004508	4	0.552486	0.589832	NM_00100	387	107	13588	1.312565	1	0.998773	99.99997

Annotator Enrichment Score: 0.8463013909655118

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:004001		4	0.552486	0.040188	NM_00884	387	27	13588	5.201646	1	0.97209	50.04208
GOTERM_!GO:005124		9	1.243094	0.093428	NM_00102	387	163	13588	1.93865	1	0.977707	80.97697
GOTERM_!GO:004592		4	0.552486	0.212482	NM_00884	387	56	13588	2.507937	1	0.980402	98.24288
GOTERM_!GO:003090		6	0.828729	0.516304	NM_00884	387	167	13588	1.261477	1	0.997807	99.99954

Annotator Enrichment Score: 0.833497832158071

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_Fl domain:Ch		3	0.414365	0.023398	NM_17722	494	8	16021	12.16169	1	0.999981	32.24737
GOTERM_!GO:000633		7	0.966851	0.090169	NM_03359	387	109	13588	2.254842	1	0.978394	79.78644
SP_PIR_KE' chromatin		9	1.243094	0.191555	NM_02847	516	192	17854	1.621911	1	0.875126	94.62196
INTERPRO IPR000953		3	0.414365	0.207996	NM_17722	521	29	17763	3.526971	1	0.980337	97.35144
SMART SM00298(C		3	0.414365	0.254826	NM_17722	308	29	9131	3.066838	1	0.961234	97.64098
GOTERM_!GO:000368		6	0.828729	0.465793	NM_00884	385	155	13288	1.336037	1	0.991418	99.98947

Annotator Enrichment Score: 0.833121365050507

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000300		7	0.966851	0.032168	NM_00102	387	84	13588	2.925926	1	0.957988	42.48995
GOTERM_!GO:001081		8	1.104972	0.072471	NM_00116	387	128	13588	2.194444	1	0.987424	71.99692
GOTERM_!GO:003294		9	1.243094	0.160359	NM_17732	387	186	13588	1.698925	1	0.974641	94.80344
GOTERM_!GO:004690		10	1.381215	0.177372	NM_01670	387	221	13588	1.588738	1	0.977307	96.32466
GOTERM_!GO:000726		12	1.657459	0.203109	NM_00102	387	290	13588	1.452874	1	0.98021	97.8535
GOTERM_!GO:004687		3	0.414365	0.325503	NM_00963	387	41	13588	2.569106	1	0.990066	99.87222
GOTERM_!GO:000991		3	0.414365	0.335968	NM_00963	387	42	13588	2.507937	1	0.989439	99.90192

Annotator Enrichment Score: 0.8261754127898726

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:004698		17	2.348066	0.037915	NM_01059	385	340	13288	1.725714	1	0.807412	43.14345

GOTERM_IGO:004286	9	1.243094	0.193323	NM_00744	385	193	13288	1.609474	1	0.933125	95.66417
GOTERM_IGO:004286	10	1.381215	0.453289	NM_00744	385	290	13288	1.190148	1	0.99101	99.98524

Annotator Enrichment Score: 0.7881638792108506

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_IGO:000486		9	1.243094	0.095324	NM_00744	385	161	13288	1.92937	1	0.910453	76.85528
SP_PIR_KEY	protease inhibitor	7	0.966851	0.095496	NM_00744	516	109	17854	2.222068	1	0.822745	74.83206
GOTERM_IGO:003041		9	1.243094	0.138067	NM_00744	385	176	13288	1.764935	1	0.935671	88.58703
GOTERM_IGO:000486		11	1.519337	0.164556	NM_00744	385	243	13288	1.562375	1	0.927283	92.76613
SP_PIR_KEY	Serine protease	5	0.690608	0.211178	NM_00744	516	82	17854	2.109803	1	0.858847	96.20348
GOTERM_IGO:000486		5	0.690608	0.426127	NM_00744	385	115	13288	1.500621	1	0.99243	99.97002

Annotator Enrichment Score: 0.7672970199468121

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_IGO:000486		5	0.690608	0.078088	NM_01044	385	56	13288	3.081633	1	0.894829	69.50814
INTERPRO	IPR001628	4	0.552486	0.158242	NM_01044	521	47	17763	2.901621	1	0.967237	93.16036
INTERPRO	IPR001723	4	0.552486	0.165367	NM_01044	521	48	17763	2.841171	1	0.970078	94.00831
UP_SEQ_FL	zinc finger	4	0.552486	0.167782	NM_01044	494	46	16021	2.820102	1	0.99996	95.11994
UP_SEQ_FL	DNA-binding	4	0.552486	0.167782	NM_01044	494	46	16021	2.820102	1	0.99996	95.11994
GOTERM_IGO:000370		4	0.552486	0.167987	NM_01044	385	49	13288	2.817493	1	0.926643	93.18811
INTERPRO	IPR000536	4	0.552486	0.172584	NM_01044	521	49	17763	2.783188	1	0.970534	94.76623
INTERPRO	IPR008946	4	0.552486	0.172584	NM_01044	521	49	17763	2.783188	1	0.970534	94.76623
INTERPRO	IPR013088	4	0.552486	0.202278	NM_01044	521	53	17763	2.573136	1	0.97937	97.03747
SMART	SM00399:Zn	4	0.552486	0.209345	NM_01044	308	47	9131	2.523073	1	0.961011	94.98249
UP_SEQ_FL	region of interest	3	0.414365	0.224035	NM_01044	494	29	16021	3.354949	1	0.999991	98.45605
SMART	SM00430:R	4	0.552486	0.227082	NM_01044	308	49	9131	2.42009	1	0.964865	96.2419

Annotator Enrichment Score: 0.74802542917305

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_IGO:003101		14	1.933702	0.091762	NM_01359	349	309	12504	1.623279	1	0.874596	72.40331
GOTERM_IGO:004442		6	0.828729	0.113465	NM_03352	349	92	12504	2.336614	1	0.897018	80.03123
GOTERM_IGO:000557		13	1.79558	0.12633	NM_01359	349	297	12504	1.568232	1	0.909207	83.57786
GOTERM_IGO:000560		5	0.690608	0.145565	NM_03352	349	73	12504	2.453978	1	0.917955	87.80735

KEGG_PATH mmu04512	4	0.552486	0.409503	NM_03352	161	83	5738	1.717578	1	0.929498	99.80913
SP_PIR_KEYWORD extracellular	8	1.104972	0.414479	NM_01359	516	213	17854	1.29956	1	0.937214	99.9362

Annotator Enrichment Score: 0.7165656442308159

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:005509	3	0.414365	0.167854	NM_00969	387	26	13588	4.051282	1	0.976999	95.5349
GOTERM_	GO:004263	3	0.414365	0.167854	NM_00969	387	26	13588	4.051282	1	0.976999	95.5349
GOTERM_	GO:005508	3	0.414365	0.251443	NM_00969	387	34	13588	3.098039	1	0.986692	99.25533

Annotator Enrichment Score: 0.696083722188282

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:003001	4	0.552486	0.135694	NM_13408	349	46	12504	3.115485	1	0.91342	85.78238
GOTERM_	GO:003167	4	0.552486	0.182743	NM_13408	349	53	12504	2.704006	1	0.912644	93.2755
GOTERM_	GO:003001	5	0.690608	0.183168	NM_13408	349	80	12504	2.239255	1	0.895964	93.32218
GOTERM_	GO:004444	5	0.690608	0.217637	NM_13408	349	86	12504	2.083028	1	0.915476	96.24878
GOTERM_	GO:003001	5	0.690608	0.247581	NM_13408	349	91	12504	1.968576	1	0.908032	97.77434
GOTERM_	GO:004329	5	0.690608	0.272142	NM_13408	349	95	12504	1.885688	1	0.925183	98.57223

Annotator Enrichment Score: 0.6940991572194516

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000557	68	9.392265	0.001304	NM_00748	349	1680	12504	1.450184	0.325738	0.325738	1.730608
SP_PIR_KEYWORD	Secreted	57	7.872928	0.010537	NM_00104	516	1420	17854	1.388904	0.978388	0.472225	13.54952
SP_PIR_KEYWORD	signal	101	13.95028	0.051742	NM_00104	516	2970	17854	1.176659	1	0.798651	51.82216
SP_PIR_KEYWORD	glycoprote	116	16.0221	0.117363	NM_00964	516	3600	17854	1.114914	1	0.812467	82.02134
SP_PIR_KEYWORD	disulfide br	81	11.18785	0.142213	NM_00104	516	2469	17854	1.135141	1	0.862377	87.85831
UP_SEQ_KEYWORD	signal pept	101	13.95028	0.166739	NM_00104	494	2963	16021	1.105484	1	0.999972	95.01837
UP_SEQ_KEYWORD	disulfide br	80	11.04972	0.245545	NM_00104	494	2379	16021	1.090582	1	0.999992	99.02753
UP_SEQ_KEYWORD	glycosylati	112	15.46961	0.307013	NM_00964	494	3444	16021	1.054672	1	0.999994	99.75957
SP_PIR_KEYWORD	membrane	160	22.09945	0.511184	NR_00284	516	5507	17854	1.005289	1	0.954253	99.99466
UP_SEQ_KEYWORD	topological	63	8.701657	0.762324	NM_13366	494	2174	16021	0.939818	1	1	100
UP_SEQ_KEYWORD	topological	81	11.18785	0.765658	NM_13366	494	2780	16021	0.944937	1	1	100
UP_SEQ_KEYWORD	transmem	117	16.16022	0.87735	NR_00284	494	4113	16021	0.92255	1	1	100
SP_PIR_KEYWORD	transmem	125	17.26519	0.997041	NR_00284	516	5237	17854	0.825873	1	0.999999	100

GOTERM_(GO:001602	135	18.64641	0.997327	NR_00284	349	5709	12504	0.847222	1	1	100
GOTERM_(GO:003122	139	19.1989	0.998476	NR_00284	349	5914	12504	0.842087	1	1	100

Annotator Enrichment Score: 0.6801786185924595

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR001715	5	0.690608	0.13811	NM_13408	521	68	17763	2.506915	1	0.969583	90.11737
SMART	SM00033:(	5	0.690608	0.194782	NM_13408	308	68	9131	2.179861	1	0.958904	93.66911
UP_SEQ_Fl	domain:CH	3	0.414365	0.338603	NM_15305	494	39	16021	2.494706	1	0.999993	99.88837

Annotator Enrichment Score: 0.6786147491667618

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_(GO:001062		10	1.381215	0.032885	NM_00985	387	155	13588	2.265233	1	0.953623	43.20593
GOTERM_(GO:001074		5	0.690608	0.240451	NM_01737	387	88	13588	1.994949	1	0.984599	99.04702
GOTERM_(GO:001064		7	0.966851	0.449839	NM_00102	387	189	13588	1.300412	1	0.995864	99.99593
GOTERM_(GO:000996		6	0.828729	0.542581	NM_01737	387	172	13588	1.224806	1	0.99809	99.99982

Annotator Enrichment Score: 0.6694205579321544

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_(GO:000022		8	1.104972	0.052094	NM_00954	349	121	12504	2.368799	1	0.867293	51.11214
GOTERM_(GO:000075		3	0.414365	0.327045	NM_01005	349	42	12504	2.559149	1	0.953442	99.49991
GOTERM_(GO:000075		4	0.552486	0.575899	NM_01005	349	107	12504	1.339367	1	0.971236	99.99896

Annotator Enrichment Score: 0.6690976609279796

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_(GO:001571		3	0.414365	0.100238	NM_17277	387	19	13588	5.54386	1	0.978505	83.25565
GOTERM_(GO:004694		5	0.690608	0.310005	NM_01670	387	99	13588	1.773288	1	0.988503	99.81234
GOTERM_(GO:001584		5	0.690608	0.316449	NM_01670	387	100	13588	1.755556	1	0.989403	99.83988

Annotator Enrichment Score: 0.6690206200860679

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_(GO:000508		12	1.657459	0.058672	NM_00116	385	223	13288	1.857271	1	0.892805	58.65603
GOTERM_(GO:005105		12	1.657459	0.061029	NM_00116	387	228	13588	1.847953	1	0.985394	65.54177
GOTERM_(GO:004657		10	1.381215	0.073477	NM_00116	387	181	13588	1.93984	1	0.986375	72.50649

GOTERM_IGO:000508	5	0.690608	0.218684	NM_17726	385	83	13288	2.079174	1	0.948801	97.28093
UP_SEQ_Fldomain:DF	4	0.552486	0.247598	AK157835,	494	56	16021	2.316512	1	0.99999	99.07014
GOTERM_IGO:000508	7	0.966851	0.252169	NM_17726	385	147	13288	1.643537	1	0.962571	98.56608
INTERPRO IPR000219	4	0.552486	0.296567	AK157835,	521	65	17763	2.098095	1	0.992616	99.58217
GOTERM_IGO:000508	4	0.552486	0.337539	AK157835,	385	71	13288	1.944467	1	0.982988	99.75593
SP_PIR_KE' guanine-nu	5	0.690608	0.339556	NM_17726	516	102	17854	1.696116	1	0.921551	99.66612
SMART SM00325:F	4	0.552486	0.374354	AK157835,	308	65	9131	1.824376	1	0.981431	99.74561
GOTERM_IGO:003502	4	0.552486	0.443492	AK157835,	387	86	13588	1.633075	1	0.995784	99.99506
INTERPRO IPR001331	3	0.414365	0.462227	NM_1986C	521	53	17763	1.929852	1	0.998929	99.99362

Annotator Enrichment Score: 0.6676139250333292

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR003616	3	0.414365	0.069849	AK141316,	521	15	17763	6.81881	1	0.939874	67.61635
SMART	SM00508:F	3	0.414365	0.088728	AK141316,	308	15	9131	5.929221	1	0.983539	69.38242
SP_PIR_KE'	methyItran	6	0.828729	0.390226	AK141316,	516	142	17854	1.462005	1	0.930933	99.88855
INTERPRO	IPR001214	3	0.414365	0.401913	AK141316,	521	47	17763	2.176216	1	0.997802	99.96659
SMART	SM00317:S	3	0.414365	0.472351	AK141316,	308	47	9131	1.892305	1	0.98791	99.97096

Annotator Enrichment Score: 0.6669026836747282

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE'	FAD	8	1.104972	0.038412	NM_02582	516	109	17854	2.539506	0.999999	0.757783	41.63137
UP_SEQ_FI	nucleotide	5	0.690608	0.102868	NM_02744	494	58	16021	2.795791	1	0.999848	83.21973
SP_PIR_KE'	Flavoprote	6	0.828729	0.176847	NM_01117	516	103	17854	2.015579	1	0.874074	93.10945
GOTERM_IGO:004803		8	1.104972	0.471704	NM_00827	385	226	13288	1.221745	1	0.990452	99.99105
GOTERM_IGO:005066		6	0.828729	0.4936	NM_00827	385	160	13288	1.294286	1	0.992036	99.99518
GOTERM_IGO:005066		3	0.414365	0.612625	NM_00116	385	71	13288	1.45835	1	0.997616	99.9999

Annotator Enrichment Score: 0.6650584031107444

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_IGO:000906		4	0.552486	0.197744	NM_00973	387	54	13588	2.600823	1	0.979422	97.59542
GOTERM_IGO:004639		5	0.690608	0.19833	NM_00973	387	81	13588	2.167353	1	0.978879	97.62496
GOTERM_IGO:001605		5	0.690608	0.19833	NM_00973	387	81	13588	2.167353	1	0.978879	97.62496
GOTERM_IGO:000931		4	0.552486	0.281116	NM_00973	387	65	13588	2.160684	1	0.985966	99.62437

Annotator Enrichment Score: 0.6598756447301835

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM	GO:000635	61	8.425414	0.082115	NM_18302	387	1772	13588	1.208678	1	0.980448	76.53611
GOTERM	GO:000367	62	8.563536	0.087225	NM_17525	385	1781	13288	1.201508	1	0.899566	73.63717
SP_PIR_KE	Transcripti	61	8.425414	0.105814	NM_18302	516	1769	17854	1.19313	1	0.814914	78.50371
GOTERM	GO:004544	73	10.08287	0.126132	NM_17525	387	2227	13588	1.150926	1	0.978866	89.7834
GOTERM	GO:000635	48	6.629834	0.209062	NM_00869	387	1465	13588	1.150398	1	0.981192	98.10924
SP_PIR_KE	transcripti	51	7.044199	0.212309	NM_14615	516	1546	17854	1.141423	1	0.853364	96.23836
GOTERM	GO:005125	48	6.629834	0.238272	NM_00869	387	1488	13588	1.132616	1	0.985048	98.9997
SP_PIR_KE	dna-bindin	46	6.353591	0.247604	NM_00869	516	1404	17854	1.133644	1	0.882996	97.99684
SP_PIR_KE	nucleus	114	15.74586	0.37882	NM_18302	516	3808	17854	1.035843	1	0.929469	99.85622
GOTERM	GO:003052	33	4.558011	0.722134	NM_00869	385	1206	13288	0.944421	1	0.999228	100
GOTERM	GO:000370	20	2.762431	0.805022	NM_00869	385	776	13288	0.889543	1	0.999821	100

Annotator Enrichment Score: 0.647477435916525

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR007087	29	4.005525	0.04336	NM_17525	521	681	17763	1.451876	1	0.915761	49.85613
INTERPRO	IPR013087	22	3.038674	0.079379	NM_17302	521	514	17763	1.459278	1	0.947885	72.41488
INTERPRO	IPR015880	27	3.729282	0.094895	NM_17525	521	676	17763	1.361745	1	0.943421	78.82962
UP_SEQ_Fl	zinc finger	10	1.381215	0.123874	NM_14620	494	187	16021	1.734287	1	0.99996	88.63414
INTERPRO	IPR001909	13	1.79558	0.146998	NM_18302	521	291	17763	1.523102	1	0.968663	91.59042
UP_SEQ_Fl	zinc finger	10	1.381215	0.184986	NM_14620	494	206	16021	1.574329	1	0.999971	96.53857
UP_SEQ_Fl	zinc finger	7	0.966851	0.20212	NM_14620	494	128	16021	1.77358	1	0.999985	97.55928
SMART	SM003552	27	3.729282	0.262482	NM_17525	308	676	9131	1.18409	1	0.959406	97.93177
SMART	SM003491	13	1.79558	0.272437	NM_18302	308	291	9131	1.324396	1	0.959034	98.26056
UP_SEQ_Fl	zinc finger	11	1.519337	0.276566	NM_14620	494	259	16021	1.377386	1	0.999994	99.51243
COG_ONT	Transcripti	5	0.690608	0.284483	NM_14620	61	92	2040	1.817534	0.998763	0.964828	92.17425
UP_SEQ_Fl	zinc finger	6	0.828729	0.2981	NM_14620	494	118	16021	1.649043	1	0.999995	99.70335
UP_SEQ_Fl	zinc finger	7	0.966851	0.320993	NM_14620	494	151	16021	1.503432	1	0.999995	99.82803
UP_SEQ_Fl	zinc finger	5	0.690608	0.370348	NM_14620	494	100	16021	1.621559	1	0.999998	99.95028
UP_SEQ_Fl	zinc finger	10	1.381215	0.380208	NM_14620	494	252	16021	1.286951	1	0.999997	99.96165
UP_SEQ_Fl	zinc finger	10	1.381215	0.381256	NM_14620	494	254	16021	1.276818	1	0.999996	99.9627

UP_SEQ_FIzinc finger	4	0.552486	0.526644	NM_14620	494	90	16021	1.441386	1	0.999999	99.99954
UP_SEQ_FIzinc finger	3	0.414365	0.654456	NM_00108	494	72	16021	1.351299	1	1	100

Annotator Enrichment Score: 0.6313323961830231

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000985	22	3.038674	0.112105	NM_00869	387	557	13588	1.386794	1	0.981502	86.62448
GOTERM_	GO:001656	12	1.657459	0.129073	NM_00112	385	259	13288	1.599117	1	0.928641	86.71814
GOTERM_	GO:004594	19	2.624309	0.131803	NM_00869	387	475	13588	1.404444	1	0.977502	90.84907
GOTERM_	GO:004589	17	2.348066	0.134743	NM_00869	387	416	13588	1.434829	1	0.976935	91.3595
GOTERM_	GO:004593	20	2.762431	0.14204	NM_00869	387	510	13588	1.376906	1	0.975594	92.51301
GOTERM_	GO:005125	17	2.348066	0.142145	NM_00869	387	419	13588	1.424556	1	0.974395	92.52849
GOTERM_	GO:001062	19	2.624309	0.156074	NM_00869	387	488	13588	1.367031	1	0.976441	94.33608
GOTERM_	GO:003132	21	2.900552	0.158597	NM_00869	387	552	13588	1.335749	1	0.974646	94.61586
GOTERM_	GO:005117	20	2.762431	0.170492	NM_00869	387	526	13588	1.335023	1	0.976463	95.76845
GOTERM_	GO:001055	20	2.762431	0.177853	NM_00869	387	530	13588	1.324948	1	0.976607	96.36086
GOTERM_	GO:000635	48	6.629834	0.209062	NM_00869	387	1465	13588	1.150398	1	0.981192	98.10924
GOTERM_	GO:004594	14	1.933702	0.219498	NM_17525	387	358	13588	1.37306	1	0.981759	98.48976
GOTERM_	GO:005125	48	6.629834	0.238272	NM_00869	387	1488	13588	1.132616	1	0.985048	98.9997
GOTERM_	GO:001060	22	3.038674	0.262754	NM_00869	387	633	13588	1.220291	1	0.986292	99.42443
GOTERM_	GO:000635	20	2.762431	0.393293	NM_17525	387	616	13588	1.139971	1	0.993716	99.97871
SP_PIR_KE	activator	16	2.209945	0.437436	NM_00869	516	484	17854	1.143827	1	0.944548	99.96318
GOTERM_	GO:004356	18	2.486188	0.441774	NM_00869	385	556	13288	1.117369	1	0.992506	99.97998
GOTERM_	GO:000566	8	1.104972	0.477905	NM_00869	349	234	12504	1.224892	1	0.959948	99.98323
GOTERM_	GO:003052	33	4.558011	0.722134	NM_00869	385	1206	13288	0.944421	1	0.999228	100
GOTERM_	GO:000370	20	2.762431	0.805022	NM_00869	385	776	13288	0.889543	1	0.999821	100

Annotator Enrichment Score: 0.6145872061059704

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_FI	cross-link:(	9	1.243094	0.147386	NM_02582	494	168	16021	1.737384	1	0.999983	92.73326
SP_PIR_KE	isopeptide	12	1.657459	0.176969	NM_03359	516	277	17854	1.498951	1	0.866599	93.12353
SP_PIR_KE	ubl conjug	16	2.209945	0.549396	XM_00147	516	524	17854	1.056512	1	0.953576	99.99826

Annotator Enrichment Score: 0.6028323623700216

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR000910	4	0.552486	0.187277	NM_01144	521	51	17763	2.674043	1	0.975364	96.04041
SMART	SM00398:f	4	0.552486	0.245091	NM_01144	308	51	9131	2.325185	1	0.962006	97.21686
UP_SEQ_FI	DNA-bindir	3	0.414365	0.338603	NM_01144	494	39	16021	2.494706	1	0.999993	99.88837

Annotator Enrichment Score: 0.5933401943901669

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR000008	8	1.104972	0.087598	NM_00886	521	130	17763	2.098095	1	0.940569	76.00988
INTERPRO	IPR018029	7	0.966851	0.091004	NM_00886	521	106	17763	2.251494	1	0.941584	77.36706
SMART	SM00239:C	8	1.104972	0.147858	NM_00886	308	130	9131	1.824376	1	0.980336	86.97396
UP_SEQ_FI	domain:C2	5	0.690608	0.156855	NM_00886	494	68	16021	2.384645	1	0.999977	93.95245
KEGG_PAT	mmu04666	4	0.552486	0.518356	NM_00886	161	98	5738	1.454684	1	0.95252	99.98306
UP_SEQ_FI	domain:C2	3	0.414365	0.527316	NM_00103	494	57	16021	1.706904	1	0.999999	99.99955
UP_SEQ_FI	domain:C2	3	0.414365	0.527316	NM_00103	494	57	16021	1.706904	1	0.999999	99.99955
KEGG_PAT	mmu04664	3	0.414365	0.672375	NM_00886	161	82	5738	1.303893	1	0.971037	99.99983

Annotator Enrichment Score: 0.5932661536632986

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_I	GO:000377	13	1.79558	0.12907	NM_00108	385	288	13288	1.557937	1	0.935057	86.71747
SP_PIR_KE	actin-bindi	10	1.381215	0.207132	NM_13408	516	226	17854	1.531008	1	0.858287	95.88394
GOTERM_I	GO:000809	15	2.071823	0.31122	NM_00108	385	414	13288	1.250518	1	0.979701	99.56879
GOTERM_I	GO:001562	7	0.966851	0.509092	NM_13408	349	205	12504	1.223398	1	0.965174	99.99264

Annotator Enrichment Score: 0.5896183151572557

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_I	GO:000205	3	0.414365	0.12822	NM_01057	387	22	13588	4.787879	1	0.978975	90.18879
GOTERM_I	GO:001046	3	0.414365	0.137914	NM_01057	387	23	13588	4.57971	1	0.976553	91.87999
GOTERM_I	GO:000828	5	0.690608	0.962895	NM_00884	387	284	13588	0.618153	1	1	100

Annotator Enrichment Score: 0.5881940198899169

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_FI	domain:RG	3	0.414365	0.224035	NM_01573	494	29	16021	3.354949	1	0.999991	98.45605
INTERPRO	IPR000342	3	0.414365	0.251518	NM_01573	521	33	17763	3.099459	1	0.988444	98.90154

SMART	SM00315:F	3	0.414365	0.305163	NM_01573	308	33	9131	2.6951	1	0.959983	99.03218

Annotation Enrichment Score: 0.5795751843817571

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
PIR_SUPER	PIRSF0010:	3	0.414365	0.07888	NM_03009	226	17	8136	6.352941	1	0.963629	65.42144
UP_SEQ_Fl	region of ir	8	1.104972	0.091246	NM_00748	494	125	16021	2.075595	1	0.999918	79.26443
GOTERM_I	GO:000452	3	0.414365	0.112529	NM_03009	385	20	13288	5.177143	1	0.921425	82.5162
INTERPRO	IPR001427	3	0.414365	0.115001	NM_03009	521	20	17763	5.114107	1	0.955713	85.07878
GOTERM_I	GO:001689	3	0.414365	0.141779	NM_03009	385	23	13288	4.501863	1	0.934934	89.28436
SMART	SM00092:F	3	0.414365	0.144156	NM_03009	308	20	9131	4.446916	1	0.986435	86.23428
GOTERM_I	GO:001689	3	0.414365	0.172405	NM_03009	385	26	13288	3.982418	1	0.92726	93.69792
GOTERM_I	GO:000452	3	0.414365	0.445859	NM_03009	385	52	13288	1.991209	1	0.991848	99.98202
SP_PIR_KE	Endonuclea	3	0.414365	0.563218	NM_03009	516	65	17854	1.596959	1	0.954555	99.99886
GOTERM_I	GO:000454	3	0.414365	0.589029	NM_03009	385	68	13288	1.522689	1	0.997356	99.99977
SP_PIR_KE	nuclease	3	0.414365	0.797296	NM_03009	516	102	17854	1.01767	1	0.990167	100
GOTERM_I	GO:000451	3	0.414365	0.802847	NM_03009	385	103	13288	1.00527	1	0.999825	100
GOTERM_I	GO:000451	3	0.414365	0.939976	NM_03009	385	154	13288	0.672356	1	0.999996	100

Annotation Enrichment Score: 0.5788151972262701

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR000330	4	0.552486	0.061214	NM_02653	521	31	17763	4.399232	1	0.931856	62.6049
UP_SEQ_Fl	short sequ	4	0.552486	0.080066	NM_02653	494	33	16021	3.931051	1	0.999971	74.64671
GOTERM_I	GO:000633	7	0.966851	0.090169	NM_03359	387	109	13588	2.254842	1	0.978394	79.78644
UP_SEQ_Fl	domain:He	5	0.690608	0.272658	NM_02653	494	86	16021	1.885533	1	0.999995	99.46726
UP_SEQ_Fl	domain:He	5	0.690608	0.293347	NM_02653	494	89	16021	1.821976	1	0.999995	99.66854
INTERPRO	IPR014021	5	0.690608	0.329523	NM_02653	521	99	17763	1.721922	1	0.995147	99.80208
INTERPRO	IPR001650	5	0.690608	0.336189	NM_02653	521	100	17763	1.704702	1	0.995397	99.8306
INTERPRO	IPR014001	5	0.690608	0.356211	NM_02653	521	103	17763	1.655051	1	0.996368	99.89485
SMART	SM00490:F	5	0.690608	0.427549	NM_02653	308	99	9131	1.497278	1	0.98575	99.91798
SP_PIR_KE	helicase	5	0.690608	0.4568	NM_02653	516	120	17854	1.441699	1	0.941123	99.97725
SMART	SM00487:I	5	0.690608	0.457621	NM_02653	308	103	9131	1.439131	1	0.98724	99.95875
GOTERM_I	GO:000368	6	0.828729	0.465793	NM_00884	385	155	13288	1.336037	1	0.991418	99.98947
GOTERM_I	GO:000438	5	0.690608	0.514585	NM_02653	385	129	13288	1.337763	1	0.993708	99.9974

Annotator Enrichment Score: 0.5747633474587276

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:001060	21	2.900552	0.086171	NM_01059	387	506	13588	1.457181	1	0.976339	78.22998
GOTERM_	GO:001656	10	1.381215	0.156126	NM_00884	385	211	13288	1.635748	1	0.93191	91.62341
GOTERM_	GO:004593	15	2.071823	0.236435	NM_01015	387	397	13588	1.326616	1	0.985048	98.95807
GOTERM_	GO:005117	15	2.071823	0.252736	NM_01015	387	401	13588	1.313383	1	0.986544	99.27679
GOTERM_	GO:004589	12	1.657459	0.258747	NM_00884	387	308	13588	1.367965	1	0.986673	99.36915
GOTERM_	GO:001648	14	1.933702	0.26038	NM_01015	387	372	13588	1.321386	1	0.986622	99.39227
GOTERM_	GO:005125	12	1.657459	0.266971	NM_00884	387	310	13588	1.35914	1	0.985505	99.47767
GOTERM_	GO:001062	15	2.071823	0.276652	NM_01015	387	410	13588	1.284553	1	0.985264	99.58289
GOTERM_	GO:001055	15	2.071823	0.29919	NM_01015	387	418	13588	1.259968	1	0.988101	99.75585
GOTERM_	GO:000012	9	1.243094	0.3339	NM_00884	387	231	13588	1.367965	1	0.989989	99.89663
GOTERM_	GO:003132	15	2.071823	0.335936	NM_01015	387	430	13588	1.224806	1	0.989737	99.90184
GOTERM_	GO:000989	15	2.071823	0.358913	NM_01015	387	434	13588	1.213518	1	0.991679	99.9459
GOTERM_	GO:000635	20	2.762431	0.393293	NM_17525	387	616	13588	1.139971	1	0.993716	99.97871
SP_PIR_KE	repressor	13	1.79558	0.473906	NM_02765	516	391	17854	1.150409	1	0.941306	99.98535

Annotator Enrichment Score: 0.5699256871403441

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:001406	4	0.552486	0.168869	NM_00102	349	51	12504	2.810046	1	0.921063	91.57729
GOTERM_	GO:003042	6	0.828729	0.192125	NM_00102	349	110	12504	1.954259	1	0.899852	94.23782
GOTERM_	GO:004295	20	2.762431	0.245801	AK041925,	349	575	12504	1.246194	1	0.912324	97.70288
GOTERM_	GO:004446	7	0.966851	0.335966	NM_00102	349	170	12504	1.475274	1	0.95455	99.58167
GOTERM_	GO:004300	8	1.104972	0.527667	NM_00102	349	245	12504	1.169896	1	0.965984	99.99561

Annotator Enrichment Score: 0.5638341301567927

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR000152	8	1.104972	0.02036	NM_00100	521	94	17763	2.901621	1	0.870096	27.40721
INTERPRO	IPR001881	7	0.966851	0.050723	NM_00100	521	91	17763	2.622619	1	0.924414	55.54
SMART	SM00179:E	7	0.966851	0.085529	NM_00100	308	91	9131	2.28047	1	0.992845	67.98498
INTERPRO	IPR018097	6	0.828729	0.141521	NM_00100	521	94	17763	2.176216	1	0.969621	90.70914
SP_PIR_KE	egf-like doi	10	1.381215	0.193392	NM_00100	516	222	17854	1.558593	1	0.86397	94.78753

UP_SEQ_Fl domain:EG	6	0.828729	0.227899	NM_0010C	494	106	16021	1.835727	1	0.99999	98.57774
UP_SEQ_Fl domain:CU	3	0.414365	0.281495	NM_0010C	494	34	16021	2.861574	1	0.999994	99.56427
UP_SEQ_Fl domain:CU	3	0.414365	0.281495	NM_0010C	494	34	16021	2.861574	1	0.999994	99.56427
INTERPRO IPR013032	12	1.657459	0.297162	NM_17386	521	310	17763	1.31977	1	0.992129	99.58765
INTERPRO IPR013091	4	0.552486	0.328773	NM_03352	521	69	17763	1.976467	1	0.995455	99.7986
UP_SEQ_Fl domain:EG	4	0.552486	0.331813	NM_0010C	494	66	16021	1.965526	1	0.999996	99.86795
UP_SEQ_Fl domain:EG	3	0.414365	0.338603	NM_0010C	494	39	16021	2.494706	1	0.999993	99.88837
INTERPRO IPR000742	8	1.104972	0.361073	NM_0010C	521	199	17763	1.370615	1	0.996136	99.90656
UP_SEQ_Fl domain:EG	4	0.552486	0.440375	NM_0010C	494	79	16021	1.642085	1	0.999998	99.99285
UP_SEQ_Fl domain:EG	3	0.414365	0.458056	NM_0010C	494	50	16021	1.94587	1	0.999998	99.99578
INTERPRO IPR000859	3	0.414365	0.462227	NM_0010C	521	53	17763	1.929852	1	0.998929	99.99362
SMART SM00042:C	3	0.414365	0.536449	NM_0010C	308	53	9131	1.678081	1	0.993245	99.99442
INTERPRO IPR006210	7	0.966851	0.541436	NM_0010C	521	203	17763	1.175657	1	0.9996	99.99947
INTERPRO IPR013111	3	0.414365	0.619539	NM_0010C	521	71	17763	1.440594	1	0.999821	99.99997
SMART SM00181:F	7	0.966851	0.683341	NM_0010C	308	203	9131	1.022279	1	0.997967	99.99996
INTERPRO IPR006209	4	0.552486	0.727784	NM_17386	521	128	17763	1.065439	1	0.999986	100

Annotator Enrichment Score: 0.5576115033221996

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_IGO:00027C		5	0.690608	0.137683	NM_01737	387	70	13588	2.507937	1	0.977659	91.84298
GOTERM_IGO:005077		7	0.966851	0.190519	NM_01737	387	136	13588	1.80719	1	0.976798	97.20152
GOTERM_IGO:000271		3	0.414365	0.209209	NM_01737	387	30	13588	3.511111	1	0.98052	98.11516
GOTERM_IGO:00028E		3	0.414365	0.209209	NM_01737	387	30	13588	3.511111	1	0.98052	98.11516
GOTERM_IGO:00026C		5	0.690608	0.240451	NM_01737	387	88	13588	1.994949	1	0.984599	99.04702
GOTERM_IGO:000282		3	0.414365	0.475238	NM_01737	387	56	13588	1.880952	1	0.996881	99.99817
GOTERM_IGO:000281		3	0.414365	0.475238	NM_01737	387	56	13588	1.880952	1	0.996881	99.99817
GOTERM_IGO:00027C		3	0.414365	0.554985	NM_01737	387	65	13588	1.620513	1	0.998327	99.99989

Annotator Enrichment Score: 0.5567200344797232

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_IGO:00028E		3	0.414365	0.066238	NM_00963	387	15	13588	7.022222	1	0.988077	68.63711
GOTERM_IGO:00321C		4	0.552486	0.09827	NM_00963	387	39	13588	3.60114	1	0.978517	82.62509
GOTERM_IGO:00027C		5	0.690608	0.137683	NM_01737	387	70	13588	2.507937	1	0.977659	91.84298

GOTERM_!GO:000269	4	0.552486	0.141812	NM_01737	387	46	13588	3.05314	1	0.977905	92.47932
GOTERM_!GO:005072	3	0.414365	0.147762	NM_00963	387	24	13588	4.388889	1	0.975768	93.31447
GOTERM_!GO:006062	5	0.690608	0.210134	NM_00963	387	83	13588	2.115127	1	0.980165	98.15214
GOTERM_!GO:005072	4	0.552486	0.219938	NM_00963	387	57	13588	2.463938	1	0.980556	98.50411
GOTERM_!GO:000269	5	0.690608	0.240451	NM_01737	387	88	13588	1.994949	1	0.984599	99.04702
GOTERM_!GO:005105	6	0.828729	0.321422	NM_01198	387	132	13588	1.59596	1	0.989978	99.85849
GOTERM_!GO:003210	5	0.690608	0.33584	NM_00963	387	103	13588	1.704423	1	0.99002	99.9016
GOTERM_!GO:003134	3	0.414365	0.484522	NM_00963	387	57	13588	1.847953	1	0.997091	99.99865
GOTERM_!GO:000269	4	0.552486	0.536955	NM_00963	387	99	13588	1.418631	1	0.998011	99.99978
GOTERM_!GO:005086	4	0.552486	0.550536	NM_00963	387	101	13588	1.390539	1	0.998241	99.99987
GOTERM_!GO:000269	5	0.690608	0.640982	NM_00963	387	154	13588	1.139971	1	0.999072	100
GOTERM_!GO:005086	5	0.690608	0.651003	NM_00963	387	156	13588	1.125356	1	0.999213	100
GOTERM_!GO:005124	3	0.414365	0.918956	NM_00102	387	144	13588	0.731481	1	0.999994	100

Annotator Enrichment Score: 0.5509136876762678

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000562		20	2.762431	0.152752	NM_00116	349	528	12504	1.357124	1	0.918161	89.10994
GOTERM_!GO:000562		19	2.624309	0.179439	NM_01057	349	510	12504	1.334772	1	0.916971	92.90259
GOTERM_!GO:000026		21	2.900552	0.225183	NM_00116	349	596	12504	1.262399	1	0.909985	96.70495
GOTERM_!GO:000579		7	0.966851	0.365764	NM_00969	349	176	12504	1.42498	1	0.956074	99.77364
GOTERM_!GO:004259		7	0.966851	0.395686	NM_00969	349	182	12504	1.378003	1	0.955139	99.88141
SP_PIR_KE' microsome		4	0.552486	0.554023	NM_00115	516	100	17854	1.384031	1	0.9539	99.99849

Annotator Enrichment Score: 0.5436872638151544

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000156		11	1.519337	0.157673	NM_00969	387	244	13588	1.582878	1	0.976311	94.51486
GOTERM_!GO:000194		11	1.519337	0.174679	NM_00969	387	250	13588	1.544889	1	0.977784	96.11567
GOTERM_!GO:004851		8	1.104972	0.331176	NM_00969	387	198	13588	1.418631	1	0.989823	99.88924
GOTERM_!GO:000152		4	0.552486	0.733154	NM_01051	387	133	13588	1.055973	1	0.999666	100

Annotator Enrichment Score: 0.5329699279432876

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000664		9	1.243094	0.093428	NM_00886	387	163	13588	1.93865	1	0.977707	80.97697

GOTERM_!GO:001963	9	1.243094	0.128934	NM_00886	387	176	13588	1.795455	1	0.978147	90.3238
GOTERM_!GO:004648	6	0.828729	0.304656	NM_00969	387	129	13588	1.633075	1	0.98776	99.78614
KEGG_PAT mmu00562	3	0.414365	0.447251	NM_17535	161	54	5738	1.979986	1	0.933122	99.91296
GOTERM_!GO:003038	3	0.414365	0.538021	NM_19819	387	63	13588	1.671958	1	0.997991	99.99979
GOTERM_!GO:000665	3	0.414365	0.718089	NM_19819	387	88	13588	1.19697	1	0.999615	100

Annotator Enrichment Score: 0.5305824537813422

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000729		5	0.690608	0.074359	NM_01005	387	56	13588	3.134921	1	0.981045	72.94595
GOTERM_!GO:004513		7	0.966851	0.075733	NM_01005	387	104	13588	2.363248	1	0.980287	73.61772
GOTERM_!GO:000754		7	0.966851	0.165278	NM_01005	387	130	13588	1.890598	1	0.976551	95.2952
GOTERM_!GO:004654		4	0.552486	0.219938	NM_01005	387	57	13588	2.463938	1	0.980556	98.50411
GOTERM_!GO:000840		5	0.690608	0.240451	NM_01005	387	88	13588	1.994949	1	0.984599	99.04702
GOTERM_!GO:004666		4	0.552486	0.273359	NM_01005	387	64	13588	2.194444	1	0.985321	99.54957
GOTERM_!GO:002260		3	0.414365	0.387456	NM_01005	387	47	13588	2.241135	1	0.993273	99.97497
GOTERM_!GO:004269		3	0.414365	0.397551	NM_01005	387	48	13588	2.194444	1	0.993973	99.9811
GOTERM_!GO:000858		3	0.414365	0.446793	NM_01005	387	53	13588	1.987421	1	0.995772	99.99553
GOTERM_!GO:004654		3	0.414365	0.446793	NM_01346	387	53	13588	1.987421	1	0.995772	99.99553
GOTERM_!GO:000300		9	1.243094	0.475601	NM_01005	387	264	13588	1.19697	1	0.996807	99.99819
GOTERM_!GO:004666		3	0.414365	0.484522	NM_01346	387	57	13588	1.847953	1	0.997091	99.99865
GOTERM_!GO:004860		5	0.690608	0.507143	NM_01005	387	130	13588	1.350427	1	0.997647	99.99937
GOTERM_!GO:004851		3	0.414365	0.771677	NM_01005	387	98	13588	1.07483	1	0.999774	100

Annotator Enrichment Score: 0.5299790979301972

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000300		7	0.966851	0.032168	NM_00102	387	84	13588	2.925926	1	0.957988	42.48995
GOTERM_!GO:000726		3	0.414365	0.272672	NM_01142	387	36	13588	2.925926	1	0.985607	99.54231
GOTERM_!GO:000683		4	0.552486	0.397911	NM_01142	387	80	13588	1.755556	1	0.99383	99.98129
GOTERM_!GO:000150		3	0.414365	0.529373	NM_01142	387	62	13588	1.698925	1	0.997918	99.99971
GOTERM_!GO:000726		6	0.828729	0.573206	NM_00812	387	178	13588	1.183521	1	0.998521	99.99994
GOTERM_!GO:001922		7	0.966851	0.624021	NM_00812	387	226	13588	1.087512	1	0.998975	99.99999

Annotator Enrichment Score: 0.5206356881221597

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
KEGG_PAT	mmu00531	3	0.414365	0.133668	NM_15280	161	23	5738	4.648663	1	0.902479	81.8312
GOTERM_	GO:000576	8	1.104972	0.227819	NM_13406	349	178	12504	1.610251	1	0.906145	96.85178
GOTERM_	GO:000032	8	1.104972	0.231923	NM_13406	349	179	12504	1.601255	1	0.904033	97.06838
GOTERM_	GO:000577	8	1.104972	0.340973	NM_13406	349	204	12504	1.405023	1	0.953648	99.62195
SP_PIR_KE	glycosidase	4	0.552486	0.360262	NM_02883	516	74	17854	1.870312	1	0.926328	99.7845
SP_PIR_KE	lysosome	6	0.828729	0.401687	NM_17277	516	144	17854	1.441699	1	0.935066	99.91414
KEGG_PAT	mmu04142	4	0.552486	0.650669	NM_02617	161	119	5738	1.197975	1	0.971872	99.99963

Annotator Enrichment Score: 0.5203676175531491

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_Fl	domain:UE	4	0.552486	0.160256	NM_00101	494	45	16021	2.882771	1	0.999971	94.34129
INTERPRO	IPR015940	3	0.414365	0.381095	NM_00101	521	45	17763	2.272937	1	0.997175	99.94309
SMART	SM00165:U	3	0.414365	0.449831	NM_00101	308	45	9131	1.976407	1	0.987745	99.95054

Annotator Enrichment Score: 0.4914382734899072

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:004246	3	0.414365	0.118697	NM_00102	387	21	13588	5.015873	1	0.979104	88.20891
GOTERM_	GO:000175	3	0.414365	0.137914	NM_00102	387	23	13588	4.57971	1	0.976553	91.87999
GOTERM_	GO:004246	3	0.414365	0.167854	NM_00102	387	26	13588	4.051282	1	0.976999	95.5349
GOTERM_	GO:004653	3	0.414365	0.188373	NM_00102	387	28	13588	3.761905	1	0.977491	97.07333
GOTERM_	GO:000165	7	0.966851	0.288329	NM_00102	387	157	13588	1.565464	1	0.986864	99.68328
GOTERM_	GO:004859	4	0.552486	0.343579	NM_00102	387	73	13588	1.923896	1	0.99043	99.9193
GOTERM_	GO:000742	9	1.243094	0.44424	NM_17540	387	257	13588	1.229572	1	0.995714	99.99517
GOTERM_	GO:004301	4	0.552486	0.718883	NM_00102	387	130	13588	1.080342	1	0.9996	100
GOTERM_	GO:004866	7	0.966851	0.841075	NM_00102	387	292	13588	0.841705	1	0.999929	100
GOTERM_	GO:003018	9	1.243094	0.884285	NM_00102	387	399	13588	0.79198	1	0.999978	100

Annotator Enrichment Score: 0.46869148845136854

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000664	3	0.414365	0.272672	NM_00969	387	36	13588	2.925926	1	0.985607	99.54231
GOTERM_	GO:004648	6	0.828729	0.304656	NM_00969	387	129	13588	1.633075	1	0.98776	99.78614
GOTERM_	GO:000663	3	0.414365	0.346384	NM_00969	387	43	13588	2.449612	1	0.990599	99.92494

GOTERM_!GO:000666	3	0.414365	0.367049	NM_00969	387	45	13588	2.340741	1	0.992069	99.95642
GOTERM_!GO:000663	3	0.414365	0.367049	NM_00969	387	45	13588	2.340741	1	0.992069	99.95642
GOTERM_!GO:001890	3	0.414365	0.397551	NM_00969	387	48	13588	2.194444	1	0.993973	99.9811

Annotator Enrichment Score: 0.4638768107455616

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000837		3	0.414365	0.112529	NM_01697	385	20	13288	5.177143	1	0.921425	82.5162
INTERPRO	IPR001675	3	0.414365	0.115001	NM_01697	521	20	17763	5.114107	1	0.955713	85.07878
GOTERM_!GO:000013		7	0.966851	0.182836	NM_17737	349	137	12504	1.830632	1	0.904184	93.28572
GOTERM_!GO:003122		3	0.414365	0.223417	NM_01697	349	32	12504	3.358883	1	0.914844	96.60303
GOTERM_!GO:003017		3	0.414365	0.223417	NM_01697	349	32	12504	3.358883	1	0.914844	96.60303
GOTERM_!GO:003130		5	0.690608	0.379427	NM_01697	349	112	12504	1.599468	1	0.956385	99.83085
GOTERM_!GO:000910		5	0.690608	0.426191	NM_01697	387	117	13588	1.500475	1	0.995276	99.99171
GOTERM_!GO:004443		8	1.104972	0.448642	NM_17737	349	227	12504	1.262664	1	0.959674	99.96522
GOTERM_!GO:003130		4	0.552486	0.452416	NM_01697	349	89	12504	1.610251	1	0.958862	99.96828
GOTERM_!GO:004341		4	0.552486	0.480418	NM_01697	387	91	13588	1.543346	1	0.996971	99.99845
GOTERM_!GO:007008		4	0.552486	0.480418	NM_01697	387	91	13588	1.543346	1	0.996971	99.99845
GOTERM_!GO:000648		4	0.552486	0.480418	NM_01697	387	91	13588	1.543346	1	0.996971	99.99845
SP_PIR_KEY	glycosyltra	7	0.966851	0.514397	AK013167,	516	199	17854	1.217113	1	0.953876	99.99513
GOTERM_!GO:000910		5	0.690608	0.60446	NM_01697	387	147	13588	1.194255	1	0.998887	99.99998
UP_SEQ_FL	topological	11	1.519337	0.823929	NM_02617	494	414	16021	0.861698	1	1	100

Annotator Enrichment Score: 0.45241866221072163

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR016040	8	1.104972	0.155083	NM_00827	521	151	17763	1.806307	1	0.967292	92.74955
SP_PIR_KEY	nad	7	0.966851	0.361618	NM_00827	516	169	17854	1.433168	1	0.924144	99.7907
INTERPRO	IPR002347	3	0.414365	0.491024	NM_00827	521	56	17763	1.826467	1	0.999238	99.99729
INTERPRO	IPR002198	3	0.414365	0.56287	NM_00827	521	64	17763	1.598159	1	0.999728	99.99975

Annotator Enrichment Score: 0.44961250510477363

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000150		11	1.519337	0.291438	NM_05317	387	285	13588	1.355166	1	0.987176	99.7059
GOTERM_!GO:000150		5	0.690608	0.355279	NM_17340	387	106	13588	1.656184	1	0.991664	99.94047

GOTERM_!GO:006034	5	0.690608	0.432561	NM_17340	387	118	13588	1.487759	1	0.995226	99.99314

Annotator Enrichment Score: 0.44171153359227283

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000630		3	0.414365	0.137914	NM_00823	387	23	13588	4.57971	1	0.976553	91.87999
GOTERM_!GO:000630		3	0.414365	0.137914	NM_00823	387	23	13588	4.57971	1	0.976553	91.87999
GOTERM_!GO:000630		3	0.414365	0.147762	NM_00823	387	24	13588	4.388889	1	0.975768	93.31447
GOTERM_!GO:001656		4	0.552486	0.516155	NM_00954	387	96	13588	1.462963	1	0.997866	99.99954
GOTERM_!GO:004002		3	0.414365	0.59544	NM_00823	387	70	13588	1.504762	1	0.998827	99.99998
GOTERM_!GO:004341		3	0.414365	0.603194	NM_00823	387	71	13588	1.483568	1	0.998892	99.99998
GOTERM_!GO:003225		3	0.414365	0.661187	NM_00823	387	79	13588	1.333333	1	0.99926	100
GOTERM_!GO:000673		3	0.414365	0.849427	NM_00823	387	117	13588	0.900285	1	0.99994	100

Annotator Enrichment Score: 0.42885823343085067

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000225		8	1.104972	0.067825	NM_00963	387	126	13588	2.229277	1	0.985392	69.52669
GOTERM_!GO:000244		6	0.828729	0.109061	NM_00963	387	89	13588	2.367041	1	0.980768	85.82693
GOTERM_!GO:000244		5	0.690608	0.169786	NM_00100	387	76	13588	2.309942	1	0.977075	95.70708
GOTERM_!GO:001250		5	0.690608	0.702744	NM_01044	387	167	13588	1.051231	1	0.999533	100
GOTERM_!GO:000691		5	0.690608	0.702744	NM_01044	387	167	13588	1.051231	1	0.999533	100
GOTERM_!GO:004306		6	0.828729	0.83747	NM_01359	387	248	13588	0.849462	1	0.999925	100
GOTERM_!GO:004306		6	0.828729	0.842469	NM_01359	387	250	13588	0.842667	1	0.99993	100
GOTERM_!GO:001094		6	0.828729	0.847342	NM_01359	387	252	13588	0.835979	1	0.999937	100

Annotator Enrichment Score: 0.42878136485504903

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:002260		6	0.828729	0.142	NM_17726	387	97	13588	2.171821	1	0.976811	92.50715
GOTERM_!GO:001097		4	0.552486	0.14849	NM_00102	387	47	13588	2.98818	1	0.973822	93.41036
GOTERM_!GO:003042		6	0.828729	0.192125	NM_00102	349	110	12504	1.954259	1	0.899852	94.23782
GOTERM_!GO:003134		4	0.552486	0.219938	NM_00102	387	57	13588	2.463938	1	0.980556	98.50411
GOTERM_!GO:004566		5	0.690608	0.329369	NM_00102	387	102	13588	1.721133	1	0.989814	99.88406
GOTERM_!GO:001076		3	0.414365	0.417505	NM_17726	387	50	13588	2.106667	1	0.994849	99.98931
GOTERM_!GO:005076		5	0.690608	0.519161	NM_00102	387	132	13588	1.329966	1	0.997851	99.99958

GOTERM_	GO:005196	5	0.690608	0.609813	NM_00102	387	148	13588	1.186186	1	0.998933	99.99999
GOTERM_	GO:006028	5	0.690608	0.665684	NM_00102	387	159	13588	1.104123	1	0.999284	100
GOTERM_	GO:004866	7	0.966851	0.841075	NM_00102	387	292	13588	0.841705	1	0.999929	100
GOTERM_	GO:003018	9	1.243094	0.884285	NM_00102	387	399	13588	0.79198	1	0.999978	100

Annotator Enrichment Score: 0.4258097338750229

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR004827	4	0.552486	0.209881	NM_01059	521	54	17763	2.525485	1	0.97967	97.44791
INTERPRO	IPR011616	3	0.414365	0.218819	NM_01059	521	30	17763	3.409405	1	0.981858	97.86225
SMART	SM00338:F	4	0.552486	0.272493	NM_01059	308	54	9131	2.196008	1	0.952964	98.26226
UP_SEQ_Fl	DNA-bindir	5	0.690608	0.701908	NM_01059	494	154	16021	1.05296	1	1	100
UP_SEQ_Fl	domain:Lei	3	0.414365	0.84578	NM_01059	494	107	16021	0.909285	1	1	100

Annotator Enrichment Score: 0.42273482212333424

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	GTPase act	8	1.104972	0.098944	NM_17737	516	136	17854	2.03534	1	0.819921	76.11911
UP_SEQ_Fl	domain:Rh	3	0.414365	0.527316	NM_17737	494	57	16021	1.706904	1	0.999999	99.99955
INTERPRO	IPR000198	3	0.414365	0.587874	NM_17737	521	67	17763	1.526599	1	0.999738	99.9999
SMART	SM00324:F	3	0.414365	0.664227	NM_17737	308	67	9131	1.327437	1	0.998248	99.99991

Annotator Enrichment Score: 0.4140277636084719

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_Fl	domain:Su	3	0.414365	0.26999	NM_00100	494	33	16021	2.948289	1	0.999996	99.4342
UP_SEQ_Fl	domain:Su	3	0.414365	0.26999	NM_00100	494	33	16021	2.948289	1	0.999996	99.4342
SP_PIR_KE	'sushi	3	0.414365	0.384481	NM_00100	516	46	17854	2.256572	1	0.930173	99.87322
INTERPRO	IPR000436	3	0.414365	0.462227	NM_00100	521	53	17763	1.929852	1	0.998929	99.99362
INTERPRO	IPR016060	3	0.414365	0.471933	NM_00100	521	54	17763	1.894114	1	0.998962	99.99519
SMART	SM00032:C	3	0.414365	0.536449	NM_00100	308	53	9131	1.678081	1	0.993245	99.99442

Annotator Enrichment Score: 0.4109941876879539

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:001659	3	0.414365	0.246879	NM_01670	385	33	13288	3.137662	1	0.962085	98.41056
GOTERM_	GO:003140	4	0.552486	0.44703	NM_01670	385	85	13288	1.624202	1	0.991407	99.98257

GOTERM_!GO:004317	3	0.414365	0.529904	NM_01670	385	61	13288	1.697424	1	0.994273	99.99837

Annotator Enrichment Score: 0.39668254648745066

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000759		3	0.414365	0.219714	NM_00973	387	31	13588	3.397849	1	0.98116	98.49684
GOTERM_!GO:003087		4	0.552486	0.443492	NM_00973	387	86	13588	1.633075	1	0.995784	99.99506
GOTERM_!GO:004873		6	0.828729	0.662534	NM_00973	387	197	13588	1.069374	1	0.999259	100

Annotator Enrichment Score: 0.38969130913359895

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:004665		4	0.552486	0.116197	NM_05325	387	42	13588	3.343915	1	0.978699	87.62995
GOTERM_!GO:007066		4	0.552486	0.122427	NM_05325	387	43	13588	3.26615	1	0.978985	89.02533
GOTERM_!GO:003294		4	0.552486	0.122427	NM_05325	387	43	13588	3.26615	1	0.978985	89.02533
GOTERM_!GO:000828		10	1.381215	0.270856	NM_05325	387	247	13588	1.421502	1	0.98606	99.52259
GOTERM_!GO:003018		3	0.414365	0.377287	NM_00884	387	46	13588	2.289855	1	0.992485	99.96693
GOTERM_!GO:004211		4	0.552486	0.382482	NM_00884	387	78	13588	1.80057	1	0.992903	99.9713
GOTERM_!GO:000177		9	1.243094	0.398248	NM_05325	387	246	13588	1.284553	1	0.993684	99.98147
GOTERM_!GO:004532		8	1.104972	0.427901	NM_05325	387	219	13588	1.282598	1	0.995132	99.99212
GOTERM_!GO:004664		7	0.966851	0.459886	NM_05325	387	191	13588	1.286795	1	0.996296	99.99702
GOTERM_!GO:000252		5	0.690608	0.577043	NM_17241	387	142	13588	1.236307	1	0.99858	99.99995
GOTERM_!GO:003009		4	0.552486	0.632797	NM_00884	387	114	13588	1.231969	1	0.999002	100
GOTERM_!GO:004211		3	0.414365	0.846022	NM_05325	387	116	13588	0.908046	1	0.999936	100
GOTERM_!GO:003009		5	0.690608	0.929435	NM_17241	387	251	13588	0.699425	1	0.999996	100
GOTERM_!GO:004853		5	0.690608	0.960606	NM_17241	387	281	13588	0.624753	1	0.999999	100
GOTERM_!GO:000252		5	0.690608	0.970274	NM_17241	387	295	13588	0.595104	1	1	100

Annotator Enrichment Score: 0.38573674185817214

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
KEGG_PAT	mmu05322	7	0.966851	0.067033	NM_03359	161	103	5738	2.422119	0.99996	0.920546	56.16357
SP_PIR_KE	citruillinitic	3	0.414365	0.076344	NM_03359	516	16	17854	6.487645	1	0.797525	66.43196
GOTERM_!GO:000633		7	0.966851	0.090169	NM_03359	387	109	13588	2.254842	1	0.978394	79.78644
INTERPRO	IPR009072	4	0.552486	0.264569	NM_00869	521	61	17763	2.235675	1	0.990449	99.16473
GOTERM_!GO:003299		4	0.552486	0.347314	NM_03359	349	75	12504	1.910831	1	0.95348	99.66781

INTERPRO IPR007125	3	0.414365	0.349315	NM_03359	521	42	17763	2.435289	1	0.996157	99.87587
GOTERM_!GO:003149	4	0.552486	0.359183	NM_03359	387	75	13588	1.872593	1	0.991469	99.94629
SP_PIR_KE' nucleosom	3	0.414365	0.363723	NM_03359	516	44	17854	2.359144	1	0.922487	99.79999
GOTERM_!GO:006500	4	0.552486	0.366966	NM_03359	387	76	13588	1.847953	1	0.992289	99.95632
GOTERM_!GO:000078	3	0.414365	0.518329	NM_03359	349	62	12504	1.733617	1	0.966425	99.99429
GOTERM_!GO:000632	4	0.552486	0.550536	NM_03359	387	101	13588	1.390539	1	0.998241	99.99987
SP_PIR_KE' chromosom	5	0.690608	0.554712	NM_03359	516	136	17854	1.272087	1	0.952676	99.99852
GOTERM_!GO:000633	3	0.414365	0.618363	NM_03359	387	73	13588	1.442922	1	0.998952	99.99999
GOTERM_!GO:003472	3	0.414365	0.640275	NM_03359	387	76	13588	1.385965	1	0.999085	100
GOTERM_!GO:003462	6	0.828729	0.742485	NM_03359	387	217	13588	0.970814	1	0.999699	100
GOTERM_!GO:003462	6	0.828729	0.829728	NM_03359	387	245	13588	0.859864	1	0.999912	100
GOTERM_!GO:006500	8	1.104972	0.849781	NM_03359	387	338	13588	0.831032	1	0.999939	100
GOTERM_!GO:004393	8	1.104972	0.900974	NM_03359	387	367	13588	0.765365	1	0.999988	100
GOTERM_!GO:007027	4	0.552486	0.958561	AB049605,	387	227	13588	0.618698	1	0.999999	100
GOTERM_!GO:000646	4	0.552486	0.958561	AB049605,	387	227	13588	0.618698	1	0.999999	100

Annotator Enrichment Score: 0.3846834411533381

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO IPR003598		10	1.381215	0.099196	NM_17229	521	187	17763	1.823211	1	0.940807	80.34295
INTERPRO IPR013098		7	0.966851	0.169022	NM_17229	521	127	17763	1.8792	1	0.970338	94.40416
SMART SM00408:I		10	1.381215	0.178412	NM_17229	308	187	9131	1.585353	1	0.973195	91.819
INTERPRO IPR013151		8	1.104972	0.26681	NM_17229	521	178	17763	1.532317	1	0.990138	99.20349
UP_SEQ_Fl domain:Ig-		6	0.828729	0.371196	NM_17229	494	130	16021	1.496823	1	0.999997	99.95137
UP_SEQ_Fl domain:Ig-		6	0.828729	0.377327	NM_17229	494	131	16021	1.485397	1	0.999997	99.95861
INTERPRO IPR013783		21	2.900552	0.419698	NM_17229	521	644	17763	1.111762	1	0.998329	99.97912
UP_SEQ_Fl domain:Ig-		4	0.552486	0.503816	NM_17229	494	87	16021	1.491088	1	1	99.99901
INTERPRO IPR003599		10	1.381215	0.569165	NM_17229	521	313	17763	1.089267	1	0.999742	99.9998
INTERPRO IPR003596		6	0.828729	0.589686	XM_90359	521	176	17763	1.162297	1	0.999726	99.99991
SP_PIR_KE' Immunoglob		13	1.79558	0.629044	NM_17229	516	443	17854	1.015373	1	0.967252	99.99988
SMART SM00406:I		6	0.828729	0.710801	XM_90359	308	176	9131	1.010663	1	0.998299	99.99999
SMART SM00409:I		10	1.381215	0.731704	NM_17229	308	313	9131	0.94716	1	0.998437	99.99999
INTERPRO IPR007110		16	2.209945	0.778637	NM_17229	521	604	17763	0.903154	1	0.999996	100
INTERPRO IPR013106		9	1.243094	0.839843	XM_90359	521	364	17763	0.842985	1	1	100

Annotator Enrichment Score: 0.38213589554320165

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:001602	14	1.933702	0.368231	NM_01042	349	414	12504	1.211578	1	0.95413	99.78514
GOTERM_	GO:003198	14	1.933702	0.387125	NM_01042	349	420	12504	1.194269	1	0.954057	99.85686
GOTERM_	GO:003141	16	2.209945	0.445303	NM_02617	349	508	12504	1.128443	1	0.960678	99.9623
GOTERM_	GO:003198	16	2.209945	0.466476	NM_02617	349	519	12504	1.104527	1	0.957667	99.9776

Annotator Enrichment Score: 0.37769684399280573

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR002290	12	1.657459	0.153598	NM_17273	521	265	17763	1.543882	1	0.97115	92.54844
GOTERM_	GO:000467	17	2.348066	0.16359	AK006468,	385	421	13288	1.393688	1	0.931073	92.64294
SP_PIR_KE	kinase	26	3.59116	0.170264	AK006468,	516	707	17854	1.272447	1	0.878938	92.31221
INTERPRO	IPR008271	14	1.933702	0.250789	AK006468,	521	360	17763	1.32588	1	0.989149	98.88475
SMART	SM00220:S	12	1.657459	0.276252	NM_17273	308	265	9131	1.342465	1	0.949063	98.37322
INTERPRO	IPR017442	14	1.933702	0.291834	AK006468,	521	374	17763	1.276248	1	0.992489	99.53619
SP_PIR_KE	serine/thre	14	1.933702	0.324781	AK006468,	516	384	17854	1.261487	1	0.921026	99.54745
UP_SEQ_Fl	active site:	23	3.176796	0.381943	NM_00827	494	662	16021	1.126763	1	0.999995	99.96337
UP_SEQ_Fl	domain:Pro	17	2.348066	0.394997	AK006468,	494	476	16021	1.158256	1	0.999995	99.97422
GOTERM_	GO:000467	19	2.624309	0.419188	AK006468,	385	583	13288	1.124822	1	0.99221	99.96427
SP_PIR_KE	atp-binding	39	5.38674	0.460364	AK006468,	516	1287	17854	1.048508	1	0.940788	99.97922
INTERPRO	IPR017441	15	2.071823	0.504047	AK006468,	521	467	17763	1.095098	1	0.999252	99.99819
INTERPRO	IPR000719	15	2.071823	0.578649	AK006468,	521	491	17763	1.04157	1	0.999704	99.99986
UP_SEQ_Fl	nucleotide	27	3.729282	0.675636	AK006468,	494	907	16021	0.965426	1	1	100
UP_SEQ_Fl	binding site	16	2.209945	0.708078	AK006468,	494	545	16021	0.952108	1	1	100
GOTERM_	GO:000646	16	2.209945	0.813609	AK006468,	387	640	13588	0.877778	1	0.999882	100
GOTERM_	GO:001631	18	2.486188	0.814335	AK006468,	387	718	13588	0.880223	1	0.999882	100
GOTERM_	GO:000675	19	2.624309	0.93881	AK006468,	387	866	13588	0.770336	1	0.999998	100
GOTERM_	GO:000675	19	2.624309	0.93881	AK006468,	387	866	13588	0.770336	1	0.999998	100

Annotator Enrichment Score: 0.37327649529143436

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:003033	3	0.414365	0.283282	NM_00963	387	37	13588	2.846847	1	0.986069	99.64306

GOTERM_!GO:005127	3	0.414365	0.325503	NM_00963	387	41	13588	2.569106	1	0.990066	99.87222
GOTERM_!GO:004001	3	0.414365	0.356747	NM_00963	387	44	13588	2.393939	1	0.991622	99.94273
GOTERM_!GO:003033	4	0.552486	0.487667	NM_00963	387	92	13588	1.52657	1	0.997161	99.99878
GOTERM_!GO:005127	4	0.552486	0.589832	NM_00963	387	107	13588	1.312565	1	0.998773	99.99997
GOTERM_!GO:004001	4	0.552486	0.608634	NM_00963	387	110	13588	1.276768	1	0.99894	99.99999

Annotator Enrichment Score: 0.3722648050389094

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000852		5	0.690608	0.393473	NM_17732	385	110	13288	1.568831	1	0.99157	99.93272
GOTERM_!GO:000165		5	0.690608	0.393473	NM_17732	385	110	13288	1.568831	1	0.99157	99.93272
GOTERM_!GO:004227		6	0.828729	0.4936	NM_17732	385	160	13288	1.294286	1	0.992036	99.99518

Annotator Enrichment Score: 0.37013242115454215

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
PIR_SUPER	PIRSF03781	3	0.414365	0.0191	NM_02794	226	8	8136	13.5	0.990598	0.606772	22.06079
UP_SEQ_Fl	domain:BT	4	0.552486	0.680203	NM_02778	494	113	16021	1.148006	1	1	100
INTERPRO	IPR000210	5	0.690608	0.776435	NM_02778	521	180	17763	0.947057	1	0.999996	100
INTERPRO	IPR011333	5	0.690608	0.776435	NM_02778	521	180	17763	0.947057	1	0.999996	100
SMART	SM00225:F	5	0.690608	0.860473	NM_02778	308	180	9131	0.823503	1	0.999885	100
INTERPRO	IPR013069	3	0.414365	0.89247	NM_02794	521	128	17763	0.799079	1	1	100

Annotator Enrichment Score: 0.3620742199542745

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_Fl	domain:PD	5	0.690608	0.335239	NM_01191	494	95	16021	1.706904	1	0.999994	99.87865
INTERPRO	IPR001478	6	0.828729	0.43705	NM_01191	521	148	17763	1.382191	1	0.998361	99.98699
SMART	SM00228:F	6	0.828729	0.559618	NM_01191	308	148	9131	1.201869	1	0.994363	99.9971

Annotator Enrichment Score: 0.36187278185875826

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR000626	3	0.414365	0.401913	NM_00101	521	47	17763	2.176216	1	0.997802	99.96659
INTERPRO	IPR019955	3	0.414365	0.432498	NM_00101	521	50	17763	2.045643	1	0.998345	99.98525
SMART	SM00213:L	3	0.414365	0.472351	NM_00101	308	47	9131	1.892305	1	0.98791	99.97096

Annotator Enrichment Score: 0.3557227565209062

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_FI	domain:EF-	4	0.552486	0.098082	NM_02057	494	36	16021	3.603464	1	0.999861	81.68561
INTERPRO	IPR018249	9	1.243094	0.250665	NM_02057	521	205	17763	1.496812	1	0.989965	98.88189
INTERPRO	IPR018247	9	1.243094	0.275265	NM_02057	521	211	17763	1.454249	1	0.991023	99.33511
UP_SEQ_FI	calcium-bir	5	0.690608	0.439929	NM_14453	494	110	16021	1.474144	1	0.999998	99.99275
UP_SEQ_FI	domain:EF-	4	0.552486	0.464566	NM_14453	494	82	16021	1.582008	1	0.999999	99.99654
INTERPRO	IPR011992	8	1.104972	0.491951	NM_02057	521	227	17763	1.201552	1	0.999187	99.99737
UP_SEQ_FI	calcium-bir	5	0.690608	0.507104	NM_14453	494	120	16021	1.351299	1	0.999999	99.99911
INTERPRO	IPR002048	5	0.690608	0.572275	NM_14453	521	137	17763	1.244308	1	0.999737	99.99982
SMART	SM00054:EF	5	0.690608	0.681732	NM_14453	308	137	9131	1.081975	1	0.99821	99.99995
UP_SEQ_FI	domain:EF-	5	0.690608	0.72981	NM_14453	494	160	16021	1.013474	1	1	100
UP_SEQ_FI	domain:EF-	5	0.690608	0.734265	NM_14453	494	161	16021	1.007179	1	1	100
INTERPRO	IPR018248	4	0.552486	0.746728	NM_14453	521	132	17763	1.033153	1	0.999992	100

Annotator Enrichment Score: 0.35345031544455396

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_FI	GO:000762	10	1.381215	0.239792	NM_17540	387	239	13588	1.469084	1	0.984954	99.03293
GOTERM_FI	GO:004233	4	0.552486	0.602431	NM_01133	387	109	13588	1.288481	1	0.998908	99.99998
GOTERM_FI	GO:000693	4	0.552486	0.602431	NM_01133	387	109	13588	1.288481	1	0.998908	99.99998

Annotator Enrichment Score: 0.3325801156840574

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	Synaptosoi	3	0.414365	0.246234	NM_01142	516	33	17854	3.145525	1	0.88664	97.9461
GOTERM_FI	GO:001971	3	0.414365	0.552131	NM_01142	349	66	12504	1.628549	1	0.968742	99.99784
SP_PIR_KE	synapse	6	0.828729	0.739384	NM_01198	516	213	17854	0.97467	1	0.984951	100

Annotator Enrichment Score: 0.31364646048747047

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	mitochond	4	0.552486	0.320622	NM_02797	516	69	17854	2.005842	1	0.921479	99.5076
GOTERM_FI	GO:000574	4	0.552486	0.385397	NM_02797	349	80	12504	1.791404	1	0.956187	99.85136
GOTERM_FI	GO:003196	4	0.552486	0.437754	NM_02797	349	87	12504	1.647268	1	0.962412	99.95483
GOTERM_FI	GO:001986	4	0.552486	0.459688	NM_02797	349	90	12504	1.592359	1	0.959458	99.97347

GOTERM_!GO:000574	11	1.519337	0.652805	NM_01117	349	391	12504	1.007951	1	0.985059	99.99993
GOTERM_!GO:003196	9	1.243094	0.808618	NM_01117	349	368	12504	0.87623	1	0.995069	100

Annotator Enrichment Score: 0.3064289384686562

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR019787	4	0.552486	0.424404	AK045780,	521	81	17763	1.683657	1	0.998207	99.98161
INTERPRO	IPR019786	4	0.552486	0.470541	AK045780,	521	87	17763	1.567543	1	0.999017	99.99499
INTERPRO	IPR001965	4	0.552486	0.500355	AK045780,	521	91	17763	1.49864	1	0.999257	99.99797
SMART	SM00249:F	4	0.552486	0.595153	AK045780,	308	91	9131	1.303125	1	0.995488	99.99901

Annotator Enrichment Score: 0.30559271420232376

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR000961	3	0.414365	0.462227	NM_17273	521	53	17763	1.929852	1	0.998929	99.99362
UP_SEQ_Fl	domain:AC	3	0.414365	0.48847	NM_17273	494	53	16021	1.835727	1	0.999999	99.99837
SMART	SM00133:S	3	0.414365	0.536449	NM_17273	308	53	9131	1.678081	1	0.993245	99.99442

Annotator Enrichment Score: 0.3041886917761314

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:001060		6	0.828729	0.411761	NM_00865	387	148	13588	1.423423	1	0.994494	99.98738
GOTERM_!GO:000641		4	0.552486	0.543775	NM_00865	387	100	13588	1.404444	1	0.998075	99.99983
SP_PIR_KE	'translation	3	0.414365	0.546223	NM_00865	516	63	17854	1.647656	1	0.956857	99.99808

Annotator Enrichment Score: 0.30205531029018956

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	wnt signali	5	0.690608	0.444017	NM_01573	516	118	17854	1.466135	1	0.93895	99.96868
KEGG_PAT	mmu05217	3	0.414365	0.456682	NM_01573	161	55	5738	1.943986	1	0.932731	99.92906
GOTERM_!GO:001605		5	0.690608	0.507143	NM_01573	387	130	13588	1.350427	1	0.997647	99.99937
KEGG_PAT	mmu04310	5	0.690608	0.602053	NM_01059	161	149	5738	1.195965	1	0.968238	99.99825

Annotator Enrichment Score: 0.2925020414386366

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000809		3	0.414365	0.300831	NM_01005	385	38	13288	2.724812	1	0.97791	99.46338
GOTERM_!GO:001688		9	1.243094	0.567607	NM_01580	385	281	13288	1.10544	1	0.996533	99.99952

GOTERM_	GO:004262	6	0.828729	0.776469	NM_01580	385	223	13288	0.928635	1	0.999708	100

Annotator Enrichment Score: 0.27646686886324984

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	(GO:000578	6	0.828729	0.41693	NM_17737	349	152	12504	1.414266	1	0.956411	99.92652
GOTERM_	(GO:004217	6	0.828729	0.460693	NM_17737	349	160	12504	1.343553	1	0.9576	99.97412
GOTERM_	(GO:001250	16	2.209945	0.526586	NM_00116	349	535	12504	1.071494	1	0.967343	99.99547
GOTERM_	(GO:004442	6	0.828729	0.774796	NM_17737	349	231	12504	0.930599	1	0.994	100

Annotator Enrichment Score: 0.2689038939475838

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	(GO:001406	4	0.552486	0.168869	NM_00102	349	51	12504	2.810046	1	0.921063	91.57729
GOTERM_	(GO:004520	10	1.381215	0.53204	NM_00102	349	319	12504	1.123137	1	0.965696	99.99612
GOTERM_	(GO:004445	7	0.966851	0.542099	NM_00102	349	212	12504	1.183003	1	0.967246	99.9971
SP_PIR_KE	'postsynapt	4	0.552486	0.618801	NM_01198	516	110	17854	1.25821	1	0.966277	99.99983
GOTERM_	(GO:003005	13	1.79558	0.661915	NM_05319	349	470	12504	0.990989	1	0.985783	99.99995
GOTERM_	(GO:004521	4	0.552486	0.68571	NM_01198	349	126	12504	1.137399	1	0.988682	99.99998
SP_PIR_KE	'cell junctio	11	1.519337	0.697962	NM_01198	516	392	17854	0.97094	1	0.979132	99.99999
SP_PIR_KE	'synapse	6	0.828729	0.739384	NM_01198	516	213	17854	0.97467	1	0.984951	100

Annotator Enrichment Score: 0.2635254289960897

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR003959	3	0.414365	0.391544	XR_034330	521	46	17763	2.223525	1	0.99751	99.95634
GOTERM_	(GO:001688	9	1.243094	0.567607	NM_01580	385	281	13288	1.10544	1	0.996533	99.99952
INTERPRO	IPR003593	5	0.690608	0.578043	NM_01005	521	138	17763	1.235292	1	0.999725	99.99985
SMART	SM003827	5	0.690608	0.687242	NM_01005	308	138	9131	1.074134	1	0.997793	99.99996

Annotator Enrichment Score: 0.2599732465776168

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	'immune re	7	0.966851	0.43886	NM_00100	516	184	17854	1.316334	1	0.940778	99.96445
GOTERM_	(GO:004508	4	0.552486	0.589832	NM_00100	387	107	13588	1.312565	1	0.998773	99.99997
SP_PIR_KE	'innate imm	3	0.414365	0.641247	NM_00100	516	75	17854	1.384031	1	0.968826	99.99992

Annotator Enrichment Score: 0.25625284076510174

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:002003	6	0.828729	0.403244	NM_00744	385	144	13288	1.438095	1	0.992152	99.94693
GOTERM_	GO:004690	6	0.828729	0.443226	NM_00744	385	151	13288	1.371429	1	0.992109	99.98073
GOTERM_	GO:000550	11	1.519337	0.528596	NM_00744	385	343	13288	1.106872	1	0.994527	99.99831
SP_PIR_KE	iron	10	1.381215	0.581788	NM_01737	516	321	17854	1.077906	1	0.960053	99.99937
SP_PIR_KE	heme	5	0.690608	0.588941	NM_01737	516	142	17854	1.218337	1	0.961255	99.99951
UP_SEQ_Fl	metal ion-t	4	0.552486	0.591448	NM_13396	494	99	16021	1.31035	1	1	99.99996
GOTERM_	GO:000905	5	0.690608	0.839771	NM_13396	385	202	13288	0.854314	1	0.999909	100

Annotator Enrichment Score: 0.25476394044522654

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	kinase	26	3.59116	0.170264	AK006468,	516	707	17854	1.272447	1	0.878938	92.31221
GOTERM_	GO:003055	47	6.491713	0.413083	AK006468,	385	1535	13288	1.056789	1	0.992089	99.95837
GOTERM_	GO:000552	44	6.077348	0.438692	AK006468,	385	1443	13288	1.052411	1	0.992715	99.97831
GOTERM_	GO:000188	47	6.491713	0.44813	AK006468,	385	1548	13288	1.047914	1	0.990946	99.98307
SP_PIR_KE	atp-binding	39	5.38674	0.460364	AK006468,	516	1287	17854	1.048508	1	0.940788	99.97922
GOTERM_	GO:003255	44	6.077348	0.47097	AK006468,	385	1460	13288	1.040157	1	0.990933	99.99087
GOTERM_	GO:000188	47	6.491713	0.473076	AK006468,	385	1558	13288	1.041188	1	0.990045	99.99138
UP_SEQ_Fl	nucleotide	27	3.729282	0.675636	AK006468,	494	907	16021	0.965426	1	1	100
GOTERM_	GO:000016	61	8.425414	0.687868	AK006468,	385	2183	13288	0.96444	1	0.998792	100
UP_SEQ_Fl	binding site	16	2.209945	0.708078	AK006468,	494	545	16021	0.952108	1	1	100
GOTERM_	GO:001707	51	7.044199	0.748913	AK006468,	385	1871	13288	0.940796	1	0.999527	100
GOTERM_	GO:003255	48	6.629834	0.791726	AK006468,	385	1796	13288	0.922431	1	0.999784	100
GOTERM_	GO:003255	48	6.629834	0.791726	AK006468,	385	1796	13288	0.922431	1	0.999784	100
GOTERM_	GO:001631	18	2.486188	0.814335	AK006468,	387	718	13588	0.880223	1	0.999882	100
SP_PIR_KE	nucleotide	42	5.801105	0.845491	AK006468,	516	1631	17854	0.891007	1	0.994485	100

Annotator Enrichment Score: 0.24809852654349546

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:004323	55	7.596685	0.487881	NM_01092	349	1919	12504	1.02686	1	0.961598	99.98705
GOTERM_	GO:004322	55	7.596685	0.487881	NM_01092	349	1919	12504	1.02686	1	0.961598	99.98705
GOTERM_	GO:000585	29	4.005525	0.756966	NM_00108	349	1122	12504	0.926038	1	0.99263	100

Annotator Enrichment Score: 0.23667494259979951

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:0008203	4	0.552486	0.431742	NM_010513	385	83	13288	1.663339	1	0.992496	99.97403
SP_PIR_KEYWORD	heparin-binding	3	0.414365	0.454577	NM_010513	516	53	17854	1.958534	1	0.94215	99.97594
GOTERM_	GO:0005524	4	0.552486	0.644381	NM_010513	385	114	13288	1.211028	1	0.998022	99.99997
GOTERM_	GO:0001874	4	0.552486	0.719988	NM_010513	385	128	13288	1.078571	1	0.99925	100
GOTERM_	GO:003024	4	0.552486	0.719988	NM_010513	385	128	13288	1.078571	1	0.99925	100

Annotator Enrichment Score: 0.22129927239526428

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000865	3	0.414365	0.356747	NM_00973	387	44	13588	2.393939	1	0.991622	99.94273
GOTERM_	GO:000930	3	0.414365	0.618363	NM_00973	387	73	13588	1.442922	1	0.998952	99.99999
GOTERM_	GO:004635	4	0.552486	0.768422	NM_00973	387	141	13588	0.99606	1	0.999781	100
GOTERM_	GO:001605	4	0.552486	0.768422	NM_00973	387	141	13588	0.99606	1	0.999781	100

Annotator Enrichment Score: 0.2189307004956926

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000715	5	0.690608	0.426191	NM_18168	387	117	13588	1.500475	1	0.995276	99.99171
INTERPRO	IPR002126	4	0.552486	0.577591	NM_18168	521	102	17763	1.337022	1	0.999745	99.99985
SMART	SM001120	4	0.552486	0.672073	NM_18168	308	102	9131	1.162592	1	0.998197	99.99993
GOTERM_	GO:001633	6	0.828729	0.804704	NM_18168	387	236	13588	0.892655	1	0.999868	100

Annotator Enrichment Score: 0.211298610772139

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:003286	3	0.414365	0.346384	NM_01346	387	43	13588	2.449612	1	0.990599	99.92494
GOTERM_	GO:003287	3	0.414365	0.493703	NM_01346	387	58	13588	1.816092	1	0.997285	99.999
GOTERM_	GO:003286	3	0.414365	0.50278	NM_01346	387	59	13588	1.785311	1	0.997537	99.99927
GOTERM_	GO:000972	5	0.690608	0.693765	NM_01670	387	165	13588	1.063973	1	0.999509	100
GOTERM_	GO:004343	3	0.414365	0.756608	NM_01346	387	95	13588	1.108772	1	0.999766	100
GOTERM_	GO:000971	5	0.690608	0.771421	NM_01670	387	184	13588	0.954106	1	0.999779	100
GOTERM_	GO:001003	10	1.381215	0.953087	NM_01670	387	505	13588	0.69527	1	0.999999	100

Annotator Enrichment Score: 0.20857253884112942

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000905	20	2.762431	0.489958	NM_17340	387	654	13588	1.073734	1	0.997189	99.99887
SP_PIR_KE	'ubli conjug	15	2.071823	0.534297	NM_17340	516	484	17854	1.072338	1	0.958406	99.99726
GOTERM_	GO:004426	18	2.486188	0.565458	NM_17340	387	609	13588	1.037767	1	0.998529	99.99992
GOTERM_	GO:001994	15	2.071823	0.585336	NM_17340	387	508	13588	1.036745	1	0.998706	99.99997
GOTERM_	GO:004363	15	2.071823	0.585336	NM_17340	387	508	13588	1.036745	1	0.998706	99.99997
GOTERM_	GO:005160	15	2.071823	0.659807	NM_17340	387	534	13588	0.986267	1	0.99926	100
GOTERM_	GO:004425	15	2.071823	0.667927	NM_17340	387	537	13588	0.980757	1	0.999296	100
GOTERM_	GO:003016	15	2.071823	0.716797	NM_17340	387	556	13588	0.947242	1	0.999615	100
GOTERM_	GO:000650	26	3.59116	0.828233	NM_01359	387	1034	13588	0.882871	1	0.99991	100

Annotator Enrichment Score: 0.20407404604696708

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_Fl	domain:RR	3	0.414365	0.394259	AK020481,	494	44	16021	2.211216	1	0.999996	99.97369
UP_SEQ_Fl	domain:RR	4	0.552486	0.511489	AK020481,	494	88	16021	1.474144	1	0.999999	99.99923
UP_SEQ_Fl	domain:RR	4	0.552486	0.511489	AK020481,	494	88	16021	1.474144	1	0.999999	99.99923
INTERPRO	IPR000504	7	0.966851	0.590729	NM_01125	521	212	17763	1.125747	1	0.999709	99.99991
INTERPRO	IPR012677	7	0.966851	0.595324	NM_01125	521	213	17763	1.120462	1	0.999714	99.99992
SMART	SM00360:F	7	0.966851	0.722856	NM_01125	308	212	9131	0.978881	1	0.998412	99.99999
UP_SEQ_Fl	domain:RR	3	0.414365	0.813194	NM_01125	494	99	16021	0.982763	1	1	100
GOTERM_	GO:000372	17	2.348066	0.821899	AK141316,	385	672	13288	0.873129	1	0.999857	100
SP_PIR_KE	'rna-binding	12	1.657459	0.831141	NM_01125	516	485	17854	0.856102	1	0.993204	100

Annotator Enrichment Score: 0.20033999351120985

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	'palmitate	7	0.966851	0.548864	NM_17732	516	206	17854	1.175754	1	0.954877	99.99823
UP_SEQ_Fl	lipid moiety	6	0.828729	0.628998	NM_17732	494	175	16021	1.111926	1	1	99.99999
SP_PIR_KE	'lipoprotein	16	2.209945	0.725881	NM_17229	516	589	17854	0.939919	1	0.983586	100

Annotator Enrichment Score: 0.19378446359434182

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:001064	7	0.966851	0.449839	NM_00102	387	189	13588	1.300412	1	0.995864	99.99593

GOTERM_!GO:005104	4	0.552486	0.693798	NM_00102	387	125	13588	1.123556	1	0.999496	100
GOTERM_!GO:006034	4	0.552486	0.840149	NM_00102	387	161	13588	0.872326	1	0.999929	100

Annotator Enrichment Score: 0.19314341037860475

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000660		5	0.690608	0.525118	NM_17226	387	133	13588	1.319967	1	0.997946	99.99966
GOTERM_!GO:000688		9	1.243094	0.525809	NM_17226	387	276	13588	1.144928	1	0.997849	99.99967
GOTERM_!GO:004690		13	1.79558	0.570198	NM_02907	387	431	13588	1.059036	1	0.998568	99.99994
GOTERM_!GO:003461		9	1.243094	0.618541	NM_17226	387	299	13588	1.056856	1	0.998926	99.99999
GOTERM_!GO:007072		9	1.243094	0.626017	NM_17226	387	301	13588	1.049834	1	0.998956	99.99999
GOTERM_!GO:000810		21	2.900552	0.655564	NM_00108	387	753	13588	0.979194	1	0.999239	100
GOTERM_!GO:001503		17	2.348066	0.760288	NM_02907	387	651	13588	0.91688	1	0.999767	100
GOTERM_!GO:004518		17	2.348066	0.77054	NM_02907	387	656	13588	0.909892	1	0.999786	100
SP_PIR_KE`protein tra		12	1.657459	0.780289	NM_17226	516	461	17854	0.900671	1	0.988854	100

Annotator Enrichment Score: 0.1892471769139025

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000751		6	0.828729	0.563114	NM_13408	387	176	13588	1.19697	1	0.99851	99.99992
GOTERM_!GO:000751		3	0.414365	0.610835	NM_13408	387	72	13588	1.462963	1	0.998892	99.99999
GOTERM_!GO:006053		3	0.414365	0.625779	NM_13408	387	74	13588	1.423423	1	0.99898	99.99999
GOTERM_!GO:001470		4	0.552486	0.704028	NM_13408	387	127	13588	1.105862	1	0.999533	100
GOTERM_!GO:006053		4	0.552486	0.746849	NM_13408	387	136	13588	1.03268	1	0.999712	100

Annotator Enrichment Score: 0.1892228506401325

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_(GO:004445		17	2.348066	0.348981	NM_00869	349	513	12504	1.187285	1	0.950929	99.67898
GOTERM_(GO:000565		19	2.624309	0.405291	NM_00869	349	599	12504	1.13645	1	0.953918	99.90429
GOTERM_(GO:003198		23	3.176796	0.737556	NM_00869	349	883	12504	0.933234	1	0.992306	100
GOTERM_(GO:007001		27	3.729282	0.875289	NM_00869	349	1133	12504	0.853802	1	0.99802	100
GOTERM_(GO:004323		27	3.729282	0.878411	NM_00869	349	1136	12504	0.851548	1	0.998048	100
GOTERM_(GO:003197		27	3.729282	0.912956	NM_00869	349	1174	12504	0.823985	1	0.998916	100

Annotator Enrichment Score: 0.18848973643667616

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	'cell cycle	17	2.348066	0.227218	XM_00147	516	447	17854	1.315913	1	0.868461	97.10728
GOTERM_	GO:000704	20	2.762431	0.373163	BC093506,	387	611	13588	1.1493	1	0.992406	99.96302
GOTERM_	GO:005132	3	0.414365	0.407569	BC093506,	387	49	13588	2.14966	1	0.994266	99.98577
GOTERM_	GO:005132	3	0.414365	0.427357	BC093506,	387	51	13588	2.065359	1	0.995229	99.99199
GOTERM_	GO:002240	11	1.519337	0.68366	NM_02529	387	393	13588	0.982754	1	0.999444	100
GOTERM_	GO:005130	8	1.104972	0.690525	NM_02529	387	281	13588	0.999605	1	0.99949	100
GOTERM_	GO:000027	7	0.966851	0.696343	NM_02529	387	244	13588	1.007286	1	0.999509	100
GOTERM_	GO:002240	9	1.243094	0.718674	NM_02529	387	328	13588	0.963415	1	0.999609	100
SP_PIR_KE	'cell division	7	0.966851	0.751578	NM_02529	516	256	17854	0.946115	1	0.98605	100
SP_PIR_KE	'mitosis	4	0.552486	0.893137	NM_02529	516	179	17854	0.773202	1	0.997512	100
GOTERM_	GO:000027	6	0.828729	0.908167	NM_02529	387	283	13588	0.744405	1	0.999991	100
GOTERM_	GO:000028	4	0.552486	0.909812	NM_02529	387	190	13588	0.739181	1	0.999991	100
GOTERM_	GO:000706	4	0.552486	0.909812	NM_02529	387	190	13588	0.739181	1	0.999991	100
GOTERM_	GO:000008	4	0.552486	0.91689	NM_02529	387	194	13588	0.72394	1	0.999993	100
GOTERM_	GO:004828	4	0.552486	0.921862	NM_02529	387	197	13588	0.712916	1	0.999994	100

Annotator Enrichment Score: 0.18235869034881522

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:001990	3	0.414365	0.612625	NM_01101	385	71	13288	1.45835	1	0.997616	99.9999
GOTERM_	GO:001989	7	0.966851	0.653171	NM_01101	385	229	13288	1.055022	1	0.998178	99.99998
GOTERM_	GO:001990	3	0.414365	0.709091	NM_01101	385	85	13288	1.218151	1	0.999134	100

Annotator Enrichment Score: 0.17804627372380374

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:005081	3	0.414365	0.59544	NM_02312	387	70	13588	1.504762	1	0.998827	99.99998
GOTERM_	GO:000759	3	0.414365	0.59544	NM_02312	387	70	13588	1.504762	1	0.998827	99.99998
GOTERM_	GO:000759	3	0.414365	0.603194	NM_02312	387	71	13588	1.483568	1	0.998892	99.99998
GOTERM_	GO:005087	3	0.414365	0.723889	NM_02312	387	89	13588	1.183521	1	0.999622	100
GOTERM_	GO:004206	3	0.414365	0.831693	NM_02312	387	112	13588	0.940476	1	0.999914	100

Annotator Enrichment Score: 0.16772160600716376

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR

UP_SEQ_Fl domain:F-l	3	0.414365	0.607161	NM_17340	494	66	16021	1.474144	1	1	99.99998
INTERPRO IPR001810	3	0.414365	0.683862	NM_17340	521	80	17763	1.278527	1	0.999962	100
SMART SM00256:F	3	0.414365	0.756072	NM_17340	308	80	9131	1.111729	1	0.998862	100

Annotator Enrichment Score: 0.15438918871567453

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:004306	17	2.348066	0.525494	NM_01359	387	560	13588	1.065873	1	0.997899	99.99967
GOTERM_	GO:001094	17	2.348066	0.536084	NM_01359	387	563	13588	1.060193	1	0.998038	99.99977
GOTERM_	GO:004298	16	2.209945	0.610756	NM_01359	387	553	13588	1.015873	1	0.998921	99.99999
GOTERM_	GO:004306	7	0.966851	0.696343	NM_17732	387	244	13588	1.007286	1	0.999509	100
GOTERM_	GO:006054	7	0.966851	0.700076	NM_17732	387	245	13588	1.003175	1	0.999533	100
GOTERM_	GO:004306	6	0.828729	0.813351	NM_17732	387	239	13588	0.88145	1	0.999885	100
GOTERM_	GO:004306	6	0.828729	0.83747	NM_01359	387	248	13588	0.849462	1	0.999925	100
GOTERM_	GO:004306	6	0.828729	0.842469	NM_01359	387	250	13588	0.842667	1	0.99993	100
GOTERM_	GO:001094	6	0.828729	0.847342	NM_01359	387	252	13588	0.835979	1	0.999937	100

Annotator Enrichment Score: 0.15213366661237368

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000742	9	1.243094	0.44424	NM_17540	387	257	13588	1.229572	1	0.995714	99.99517
GOTERM_	GO:004247	3	0.414365	0.571504	NM_17540	387	67	13588	1.572139	1	0.998519	99.99994
GOTERM_	GO:004247	3	0.414365	0.640275	NM_17540	387	76	13588	1.385965	1	0.999085	100
GOTERM_	GO:004883	3	0.414365	0.718089	NM_17540	387	88	13588	1.19697	1	0.999615	100
GOTERM_	GO:004358	3	0.414365	0.799392	NM_17540	387	104	13588	1.012821	1	0.999852	100
GOTERM_	GO:004856	6	0.828729	0.818945	NM_17540	387	241	13588	0.874136	1	0.999891	100
GOTERM_	GO:004856	4	0.552486	0.840149	NM_17540	387	161	13588	0.872326	1	0.999929	100
GOTERM_	GO:004859	7	0.966851	0.944882	NM_17540	387	359	13588	0.684618	1	0.999998	100

Annotator Enrichment Score: 0.14315066702753912

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000176	3	0.414365	0.59544	NM_00899	387	70	13588	1.504762	1	0.998827	99.99998
GOTERM_	GO:004887	8	1.104972	0.701021	NM_00969	387	284	13588	0.989045	1	0.999529	100
GOTERM_	GO:005167	8	1.104972	0.701021	NM_00969	387	284	13588	0.989045	1	0.999529	100
GOTERM_	GO:000692	10	1.381215	0.720004	NM_00969	387	367	13588	0.956706	1	0.999599	100

GOTERM_!GO:001647	5	0.690608	0.913296	NM_02049	387	240	13588	0.731481	1	0.999992	100

Annotator Enrichment Score: 0.142628394404058

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	thiol prote	5	0.690608	0.463154	NM_02970	516	121	17854	1.429784	1	0.94008	99.98065
GOTERM_!GO:001679		4	0.552486	0.607873	NM_13424	385	108	13288	1.278307	1	0.997596	99.99988
GOTERM_!GO:000422		3	0.414365	0.612625	NM_02970	385	71	13288	1.45835	1	0.997616	99.9999
GOTERM_!GO:000823		5	0.690608	0.612656	NM_02970	385	146	13288	1.181996	1	0.997448	99.9999
GOTERM_!GO:000417		10	1.381215	0.863424	NM_01359	385	421	13288	0.819817	1	0.999952	100
GOTERM_!GO:007001		14	1.933702	0.894053	NM_01359	385	603	13288	0.801327	1	0.999978	100
GOTERM_!GO:000823		14	1.933702	0.922785	NM_01359	385	629	13288	0.768203	1	0.99999	100
SP_PIR_KE	Protease	10	1.381215	0.960141	NM_01359	516	509	17854	0.679779	1	0.999622	100

Annotator Enrichment Score: 0.14105282673957883

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000689		6	0.828729	0.621759	NM_00100	387	188	13588	1.120567	1	0.99896	99.99999
GOTERM_!GO:001032		6	0.828729	0.621759	NM_00100	387	188	13588	1.120567	1	0.99896	99.99999
SP_PIR_KE	Endocytosi	3	0.414365	0.753465	NM_01006	516	93	17854	1.116154	1	0.985872	100
GOTERM_!GO:001604		7	0.966851	0.78918	NM_00100	387	272	13588	0.903595	1	0.999815	100
GOTERM_!GO:001619		11	1.519337	0.857535	NM_02907	387	466	13588	0.828803	1	0.999949	100

Annotator Enrichment Score: 0.13206819583086948

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000941		4	0.552486	0.530078	NM_14453	387	98	13588	1.433107	1	0.997883	99.99972
GOTERM_!GO:000931		4	0.552486	0.776623	NM_14453	387	143	13588	0.982129	1	0.999783	100
GOTERM_!GO:000962		4	0.552486	0.975542	NM_14453	387	251	13588	0.55954	1	1	100

Annotator Enrichment Score: 0.12839139766649685

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000838		7	0.966851	0.507772	NM_01125	387	201	13588	1.222775	1	0.997603	99.99938
SP_PIR_KE	mrna splici	6	0.828729	0.648638	NM_01125	516	191	17854	1.086935	1	0.969978	99.99994
GOTERM_!GO:000639		7	0.966851	0.7588	NM_01125	387	262	13588	0.938083	1	0.999771	100
GOTERM_!GO:001607		8	1.104972	0.759021	NM_01125	387	302	13588	0.930096	1	0.999766	100

SP_PIR_KE mrna proc	6	0.828729	0.825715	NM_01125	516	240	17854	0.865019	1	0.992852	100
GOTERM_ GO:000568	3	0.414365	0.863922	NM_02529	349	124	12504	0.866808	1	0.997579	100
GOTERM_ GO:000635	9	1.243094	0.933047	NM_01125	387	437	13588	0.723112	1	0.999997	100

Annotator Enrichment Score: 0.12548490874084625

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_FI	repeat:TPR	3	0.414365	0.508143	NM_00833	494	55	16021	1.768973	1	0.999999	99.99914
UP_SEQ_FI	repeat:TPR	3	0.414365	0.564118	NM_00833	494	61	16021	1.594976	1	1	99.99988
UP_SEQ_FI	repeat:TPR	4	0.552486	0.708215	NM_00833	494	118	16021	1.099362	1	1	100
UP_SEQ_FI	repeat:TPR	3	0.414365	0.723042	NM_00833	494	82	16021	1.186506	1	1	100
UP_SEQ_FI	repeat:TPR	4	0.552486	0.767703	NM_00833	494	130	16021	0.997882	1	1	100
UP_SEQ_FI	repeat:TPR	4	0.552486	0.767703	NM_00833	494	130	16021	0.997882	1	1	100
INTERPRO	IPR001440	3	0.414365	0.771036	NM_00833	521	95	17763	1.076654	1	0.999995	100
SP_PIR_KE	tpr repeat	4	0.552486	0.776997	NM_00833	516	141	17854	0.981582	1	0.988772	100
INTERPRO	IPR019734	3	0.414365	0.843826	NM_00833	521	112	17763	0.913233	1	1	100
INTERPRO	IPR013026	3	0.414365	0.850849	NM_00833	521	114	17763	0.897212	1	1	100
SMART	SM00028:1	3	0.414365	0.895193	NM_00833	308	112	9131	0.794092	1	0.999953	100
INTERPRO	IPR011990	3	0.414365	0.936686	NM_00833	521	150	17763	0.681881	1	1	100

Annotator Enrichment Score: 0.12197349421421755

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_ GO:005132		3	0.414365	0.718089	NM_01005	387	88	13588	1.19697	1	0.999615	100
GOTERM_ GO:000712		3	0.414365	0.718089	NM_01005	387	88	13588	1.19697	1	0.999615	100
GOTERM_ GO:002240		9	1.243094	0.718674	NM_02529	387	328	13588	0.963415	1	0.999609	100
GOTERM_ GO:005132		3	0.414365	0.729589	NM_01005	387	90	13588	1.17037	1	0.999648	100
GOTERM_ GO:000027		6	0.828729	0.908167	NM_02529	387	283	13588	0.744405	1	0.999991	100

Annotator Enrichment Score: 0.12041210536911837

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_ GO:000591		5	0.690608	0.713764	NM_00812	349	173	12504	1.035494	1	0.990571	99.99999
GOTERM_ GO:004329		3	0.414365	0.776313	NM_18168	349	101	12504	1.0642	1	0.993789	100
GOTERM_ GO:001632		3	0.414365	0.785547	NM_18168	349	103	12504	1.043536	1	0.994295	100

Annotator Enrichment Score: 0.11084408016396212

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:004405	6	0.828729	0.679717	NM_00102	387	201	13588	1.048093	1	0.999413	100
GOTERM_	GO:005080	3	0.414365	0.781267	NM_00102	387	100	13588	1.053333	1	0.999797	100
GOTERM_	GO:005196	3	0.414365	0.812101	NM_00102	387	107	13588	0.984424	1	0.999884	100
GOTERM_	GO:003164	3	0.414365	0.835384	NM_00102	387	113	13588	0.932153	1	0.999922	100

Annotator Enrichment Score: 0.10704556814479865

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR000372	5	0.690608	0.28976	NM_17692	521	93	17763	1.833013	1	0.99276	99.51458
SMART	SM00013:L	5	0.690608	0.381731	NM_17692	308	93	9131	1.593877	1	0.980468	99.78129
INTERPRO	IPR000483	3	0.414365	0.70323	NM_17692	521	83	17763	1.232315	1	0.999973	100
SMART	SM00082:L	3	0.414365	0.773924	NM_17692	308	83	9131	1.071546	1	0.99908	100
INTERPRO	IPR001611	5	0.690608	0.846445	NM_17692	521	202	17763	0.843912	1	1	100
INTERPRO	IPR003591	3	0.414365	0.894987	NM_17692	521	129	17763	0.792885	1	1	100
SP_PIR_KE	leucine-ricl	6	0.828729	0.901582	NM_17692	516	275	17854	0.754926	1	0.997716	100
UP_SEQ_Fl	repeat:LRR	5	0.690608	0.912166	NM_17692	494	221	16021	0.733737	1	1	100
UP_SEQ_Fl	repeat:LRR	6	0.828729	0.915657	NM_17692	494	266	16021	0.73153	1	1	100
UP_SEQ_Fl	repeat:LRR	6	0.828729	0.915657	NM_17692	494	266	16021	0.73153	1	1	100
SMART	SM00369:L	3	0.414365	0.934716	NM_17692	308	129	9131	0.689444	1	0.999993	100
UP_SEQ_Fl	repeat:LRR	5	0.690608	0.946298	NM_17692	494	245	16021	0.661861	1	1	100
UP_SEQ_Fl	repeat:LRR	4	0.552486	0.951632	NM_17692	494	203	16021	0.639038	1	1	100
UP_SEQ_Fl	repeat:LRR	3	0.414365	0.956454	NM_00788	494	157	16021	0.619704	1	1	100
UP_SEQ_Fl	repeat:LRR	3	0.414365	0.979316	NM_00788	494	185	16021	0.525911	1	1	100

Annotator Enrichment Score: 0.10639158695308314

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	Apoptosis	9	1.243094	0.759982	NM_00865	516	337	17854	0.924056	1	0.986498	100
GOTERM_	GO:000691	12	1.657459	0.774201	NM_00865	387	465	13588	0.906093	1	0.999782	100
GOTERM_	GO:000821	13	1.79558	0.781196	NM_02977	387	507	13588	0.900285	1	0.999802	100
GOTERM_	GO:001250	12	1.657459	0.792428	NM_00865	387	473	13588	0.890768	1	0.999826	100
GOTERM_	GO:001626	13	1.79558	0.806613	NM_02977	387	519	13588	0.879469	1	0.999872	100

Annotator Enrichment Score: 0.09457928035445619

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_FI	repeat:ANI	3	0.414365	0.48847	NM_17566	494	53	16021	1.835727	1	0.999999	99.99837
UP_SEQ_FI	repeat:ANI	4	0.552486	0.644022	NM_17566	494	107	16021	1.21238	1	1	100
UP_SEQ_FI	repeat:ANI	3	0.414365	0.6971	NM_17566	494	78	16021	1.247353	1	1	100
UP_SEQ_FI	repeat:ANI	4	0.552486	0.74906	NM_17566	494	126	16021	1.029561	1	1	100
UP_SEQ_FI	repeat:ANI	4	0.552486	0.871323	NM_17566	494	159	16021	0.815879	1	1	100
UP_SEQ_FI	repeat:ANI	4	0.552486	0.93632	NM_17566	494	191	16021	0.679187	1	1	100
UP_SEQ_FI	repeat:ANI	4	0.552486	0.93632	NM_17566	494	191	16021	0.679187	1	1	100
SP_PIR_KE	'ank repeat	4	0.552486	0.956853	NM_17566	516	222	17854	0.623437	1	0.999588	100
INTERPRO	IPR002110	4	0.552486	0.960767	NM_17566	521	223	17763	0.611552	1	1	100
SMART	SM00248:/	4	0.552486	0.982121	NM_17566	308	223	9131	0.531769	1	1	100

Annotator Enrichment Score: 0.08843872767305289

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_(GO:000574		11	1.519337	0.652805	NM_01117	349	391	12504	1.007951	1	0.985059	99.99993
GOTERM_(GO:004442		14	1.933702	0.704699	NM_01670	349	524	12504	0.957239	1	0.989994	99.99999
GOTERM_(GO:003105		21	2.900552	0.741945	NM_01117	349	809	12504	0.930024	1	0.992327	100
GOTERM_(GO:003196		14	1.933702	0.743804	NM_01117	349	540	12504	0.928876	1	0.992081	100
GOTERM_(GO:003197		14	1.933702	0.748445	NM_01117	349	542	12504	0.925449	1	0.992143	100
GOTERM_(GO:003196		9	1.243094	0.808618	NM_01117	349	368	12504	0.87623	1	0.995069	100
SP_PIR_KE	'mitochond	4	0.552486	0.901493	NM_00114	516	183	17854	0.756301	1	0.99781	100
GOTERM_(GO:000574		6	0.828729	0.918723	NM_01117	349	296	12504	0.726245	1	0.999045	100
SP_PIR_KE	'mitochond	18	2.486188	0.919266	NM_00973	516	790	17854	0.788372	1	0.998507	100
GOTERM_(GO:001986		6	0.828729	0.938284	NM_01117	349	312	12504	0.689002	1	0.999415	100
GOTERM_(GO:000573		28	3.867403	0.969912	NM_01117	349	1322	12504	0.75884	1	0.999899	100

Annotator Enrichment Score: 0.07559058938415683

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_I	GO:000484	3	0.414365	0.807173	NM_00954	385	104	13288	0.995604	1	0.999816	100
GOTERM_I	GO:001687	5	0.690608	0.813076	NM_00954	385	193	13288	0.894152	1	0.999831	100
GOTERM_I	GO:001688	4	0.552486	0.862701	NM_00954	385	166	13288	0.83167	1	0.999955	100
GOTERM_I	GO:001978	3	0.414365	0.880399	NM_00954	385	125	13288	0.828343	1	0.999973	100

Annotator Enrichment Score: 0.07193308685974868

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:0001706	7	0.966851	0.774371	NM_009695	387	267	13588	0.920516	1	0.999777	100
GOTERM_	GO:0048561	6	0.828729	0.818945	NM_175406	387	241	13588	0.874136	1	0.999891	100
GOTERM_	GO:0043005	10	1.381215	0.850167	NM_009695	387	421	13588	0.833993	1	0.999938	100
GOTERM_	GO:0009758	10	1.381215	0.857529	NM_009695	387	425	13588	0.826144	1	0.99995	100
GOTERM_	GO:0048561	7	0.966851	0.944882	NM_175406	387	359	13588	0.684618	1	0.999998	100

Annotator Enrichment Score: 0.07175136633301872

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:0044272	9	1.243094	0.629726	NM_009731	387	302	13588	1.046358	1	0.998999	99.99999
GOTERM_	GO:0009166	4	0.552486	0.87575	NM_015806	387	174	13588	0.807152	1	0.99997	100
GOTERM_	GO:0034655	4	0.552486	0.887457	NM_015806	387	179	13588	0.784606	1	0.99998	100
GOTERM_	GO:0034406	4	0.552486	0.887457	NM_015806	387	179	13588	0.784606	1	0.99998	100
GOTERM_	GO:0006166	3	0.414365	0.904583	NM_015806	387	137	13588	0.768856	1	0.99999	100
GOTERM_	GO:0006166	3	0.414365	0.944534	NM_015806	387	160	13588	0.658333	1	0.999998	100

Annotator Enrichment Score: 0.07066150687493293

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:0048872	10	1.381215	0.71404	NM_009695	387	365	13588	0.961948	1	0.999602	100
GOTERM_	GO:0030003	4	0.552486	0.737782	NM_028041	387	134	13588	1.048093	1	0.999682	100
GOTERM_	GO:0055088	5	0.690608	0.771421	NM_028041	387	184	13588	0.954106	1	0.999779	100
GOTERM_	GO:0055066	4	0.552486	0.788476	NM_028041	387	146	13588	0.961948	1	0.999817	100
GOTERM_	GO:0030003	4	0.552486	0.81062	NM_028041	387	152	13588	0.923977	1	0.999882	100
GOTERM_	GO:0050806	6	0.828729	0.922667	NM_028041	387	293	13588	0.718999	1	0.999994	100
GOTERM_	GO:0006872	5	0.690608	0.941703	NM_028041	387	261	13588	0.672627	1	0.999998	100
GOTERM_	GO:0042595	12	1.657459	0.946921	NM_009695	387	584	13588	0.721461	1	0.999999	100
GOTERM_	GO:0055088	5	0.690608	0.949102	NM_028041	387	268	13588	0.655058	1	0.999999	100
GOTERM_	GO:0019722	6	0.828729	0.96884	NM_028041	387	343	13588	0.614189	1	1	100

Annotator Enrichment Score: 0.05847071758130346

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR

KEGG_PATH mmu04080	10	1.381215	0.300073	NM_17732	161	260	5738	1.37076	1	0.885869	98.56013
SP_PIR_KEYWORD receptor	54	7.458564	0.993666	NM_01192	516	2465	17854	0.757989	1	0.999993	100
GOTERM_000716	50	6.906077	0.999062	NM_00964	387	2495	13588	0.703629	1	1	100
SP_PIR_KEYWORD transducer	25	3.453039	0.999503	NM_01359	516	1467	17854	0.589652	1	1	100
PIR_SUPERPIRSF80001	17	2.348066	0.99988	NM_00103	226	1200	8136	0.51	1	1	100
GOTERM_000718	30	4.143646	0.999968	NM_01359	387	1877	13588	0.561179	1	1	100
SP_PIR_KEYWORD g-protein c	20	2.762431	0.999975	NM_00103	516	1411	17854	0.490443	1	1	100
INTERPRO IPR000276	20	2.762431	0.999993	NM_00103	521	1458	17763	0.467682	1	1	100
INTERPRO IPR017452	21	2.900552	0.999998	NM_00103	521	1575	17763	0.454587	1	1	100

Annotator Enrichment Score: 0.05738231732121542

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_000600		4	0.552486	0.764231	NM_00108	387	140	13588	1.003175	1	0.999763	100
GOTERM_000193		4	0.552486	0.862978	NM_00108	387	169	13588	0.831032	1	0.999956	100
GOTERM_000595		4	0.552486	0.911631	NM_00108	387	191	13588	0.735311	1	0.999992	100
GOTERM_000605		4	0.552486	0.980454	NM_00108	387	261	13588	0.538101	1	1	100

Annotator Enrichment Score: 0.045338275205585955

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_000575		4	0.552486	0.836221	NM_01670	349	163	12504	0.879217	1	0.996422	100
GOTERM_000319		4	0.552486	0.836221	NM_01670	349	163	12504	0.879217	1	0.996422	100
SP_PIR_KEYWORD transit pep		10	1.381215	0.914283	NM_00973	516	457	17854	0.757129	1	0.998335	100
SP_PIR_KEYWORD mitochond		18	2.486188	0.919266	NM_00973	516	790	17854	0.788372	1	0.998507	100
UP_SEQ_FLtransit pep		10	1.381215	0.937723	NM_00973	494	449	16021	0.722298	1	1	100
GOTERM_000573		28	3.867403	0.969912	NM_01117	349	1322	12504	0.75884	1	0.999899	100

Annotator Enrichment Score: 0.043029826405814715

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORD gpi-anchor		3	0.414365	0.876633	NM_17229	516	124	17854	0.837116	1	0.996781	100
UP_SEQ_FLpropeptide		5	0.690608	0.910394	NM_17229	494	220	16021	0.737072	1	1	100
GOTERM_000312		4	0.552486	0.930815	NM_17229	349	207	12504	0.69233	1	0.999302	100

Annotator Enrichment Score: 0.04049080687506125

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000682	3	0.414365	0.887859	NM_02187	387	130	13588	0.810256	1	0.99998	100
GOTERM_	GO:000850	3	0.414365	0.893567	NM_02187	385	130	13288	0.796484	1	0.999979	100
GOTERM_	GO:005508	9	1.243094	0.95292	NM_17226	387	460	13588	0.686957	1	0.999999	100

Annotator Enrichment Score: 0.03809916670439874

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
KEGG_PAT	mmu03010	3	0.414365	0.715644	XR_032332	161	89	5738	1.20134	1	0.978181	99.99997
SP_PIR_KE	ribosomal	4	0.552486	0.888726	XR_032332	516	177	17854	0.781938	1	0.997346	100
GOTERM_	GO:000584	4	0.552486	0.906377	XR_032332	349	192	12504	0.746418	1	0.99875	100
GOTERM_	GO:000373	3	0.414365	0.935452	XM_00147	385	151	13288	0.685714	1	0.999995	100
SP_PIR_KE	ribonucleo	5	0.690608	0.950784	XR_032332	516	266	17854	0.650391	1	0.999457	100
GOTERM_	GO:000519	8	1.104972	0.977407	NM_01695	385	450	13288	0.613587	1	1	100
GOTERM_	GO:003052	7	0.966851	0.990084	XR_032332	349	462	12504	0.54285	1	0.999991	100
GOTERM_	GO:000641	3	0.414365	0.999039	XM_00147	387	319	13588	0.330199	1	1	100

Annotator Enrichment Score: 0.03651424437424678

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
KEGG_PAT	mmu04144	6	0.828729	0.670612	NM_02057	161	202	5738	1.058606	1	0.972758	99.99981
GOTERM_	GO:000552	5	0.690608	0.992509	NM_02057	385	354	13288	0.48749	1	1	100
GOTERM_	GO:003256	5	0.690608	0.993875	NM_02057	385	363	13288	0.475403	1	1	100
GOTERM_	GO:001900	5	0.690608	0.993875	NM_02057	385	363	13288	0.475403	1	1	100
SP_PIR_KE	gtp-binding	3	0.414365	0.998987	NM_14488	516	313	17854	0.331637	1	1	100

Annotator Enrichment Score: 0.02998038105459525

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000697	6	0.828729	0.91423	NM_02653	387	287	13588	0.73403	1	0.999993	100
SP_PIR_KE	DNA dama	4	0.552486	0.921516	NM_02653	516	194	17854	0.713418	1	0.998546	100
GOTERM_	GO:003355	8	1.104972	0.94415	NM_00865	387	404	13588	0.69527	1	0.999998	100
GOTERM_	GO:000628	4	0.552486	0.953847	NM_02653	387	222	13588	0.632633	1	0.999999	100

Annotator Enrichment Score: 0.025652881792733177

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR

GOTERM_!GO:000738	6	0.828729	0.909717	NM_01126	387	284	13588	0.741784	1	0.999992	100
GOTERM_!GO:000995	3	0.414365	0.93446	NM_00954	387	153	13588	0.688453	1	0.999997	100
GOTERM_!GO:000300	3	0.414365	0.985313	NM_00954	387	214	13588	0.492212	1	1	100

Annotator Enrichment Score: 0.024945229392543664

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000004		3	0.414365	0.59544	NM_02804	387	70	13588	1.504762	1	0.998827	99.99998
GOTERM_!GO:000526		3	0.414365	0.891046	NM_14603	385	129	13288	0.802658	1	0.999979	100
GOTERM_!GO:000524		4	0.552486	0.894265	NM_14603	385	179	13288	0.771269	1	0.999976	100
GOTERM_!GO:002283		4	0.552486	0.894265	NM_14603	385	179	13288	0.771269	1	0.999976	100
GOTERM_!GO:000681		3	0.414365	0.944534	NM_14603	387	160	13588	0.658333	1	0.999998	100
GOTERM_!GO:001567		3	0.414365	0.945847	NM_19803	387	161	13588	0.654244	1	0.999998	100
GOTERM_!GO:003000		7	0.966851	0.987729	NM_14603	387	442	13588	0.556058	1	1	100
GOTERM_!GO:002283		4	0.552486	0.988936	NM_14603	385	281	13288	0.491307	1	1	100
GOTERM_!GO:004687		4	0.552486	0.991054	NM_14603	385	290	13288	0.476059	1	1	100
GOTERM_!GO:000681		8	1.104972	0.992003	NM_14603	387	515	13588	0.545415	1	1	100
GOTERM_!GO:001567		4	0.552486	0.992566	NM_14603	387	303	13588	0.463513	1	1	100
GOTERM_!GO:000526		3	0.414365	0.994478	NM_14603	385	248	13288	0.417512	1	1	100
GOTERM_!GO:000681		11	1.519337	0.996692	NM_14603	387	712	13588	0.542447	1	1	100
GOTERM_!GO:000521		4	0.552486	0.997863	NM_14603	385	349	13288	0.395579	1	1	100
GOTERM_!GO:002283		4	0.552486	0.998374	NM_14603	385	360	13288	0.383492	1	1	100
GOTERM_!GO:001526		4	0.552486	0.998565	NM_14603	385	365	13288	0.378239	1	1	100
GOTERM_!GO:002280		4	0.552486	0.998565	NM_14603	385	365	13288	0.378239	1	1	100
SP_PIR_KE ion transp		6	0.828729	0.999606	NM_14603	516	543	17854	0.382329	1	1	100

Annotator Enrichment Score: 0.024343499069138956

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:004866		7	0.966851	0.841075	NM_00102	387	292	13588	0.841705	1	0.999929	100
GOTERM_!GO:003018		9	1.243094	0.884285	NM_00102	387	399	13588	0.79198	1	0.999978	100
GOTERM_!GO:004866		4	0.552486	0.894	NM_14453	387	182	13588	0.771673	1	0.999984	100
GOTERM_!GO:000090		4	0.552486	0.942883	NM_14453	387	212	13588	0.662474	1	0.999998	100
GOTERM_!GO:000740		3	0.414365	0.948385	NM_01388	387	163	13588	0.646217	1	0.999999	100
GOTERM_!GO:003117		4	0.552486	0.94972	NM_01388	387	218	13588	0.644241	1	0.999999	100

GOTERM_!GO:004881	3	0.414365	0.962317	NM_01388	387	176	13588	0.598485	1	1	100
GOTERM_!GO:004885	3	0.414365	0.980158	NM_01388	387	202	13588	0.521452	1	1	100
GOTERM_!GO:003003	5	0.690608	0.981887	AK157835,	387	319	13588	0.550331	1	1	100
GOTERM_!GO:003295	3	0.414365	0.984555	NM_01388	387	212	13588	0.496855	1	1	100
GOTERM_!GO:000090	4	0.552486	0.993544	NM_14453	387	309	13588	0.454513	1	1	100
GOTERM_!GO:003298	4	0.552486	0.997638	NM_14453	387	351	13588	0.400127	1	1	100

Annotator Enrichment Score: 0.018205448068836557

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR001841	6	0.828729	0.924475	NM_00954	521	286	17763	0.71526	1	1	100
INTERPRO	IPR017907	5	0.690608	0.942183	NM_00954	521	254	17763	0.671143	1	1	100
SMART	SM00184:F	6	0.828729	0.96682	NM_00954	308	286	9131	0.621946	1	0.999999	100
UP_SEQ_Fl	zinc finger	3	0.414365	0.973665	NM_00954	494	176	16021	0.552804	1	1	100
INTERPRO	IPR018957	3	0.414365	0.988978	NM_00954	521	219	17763	0.467042	1	1	100

Annotator Enrichment Score: 0.01782383055536635

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR008957	4	0.552486	0.91436	NM_00113	521	187	17763	0.729284	1	1	100
INTERPRO	IPR003961	3	0.414365	0.977301	NM_00111	521	191	17763	0.535509	1	1	100
SMART	SM00060:F	3	0.414365	0.989425	NM_00111	308	191	9131	0.465646	1	1	100

Annotator Enrichment Score: 0.005378879357105174

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	sh3 domain	3	0.414365	0.982424	NM_17737	516	204	17854	0.508835	1	0.999934	100
INTERPRO	IPR001452	3	0.414365	0.986431	NM_17737	521	211	17763	0.48475	1	1	100
SMART	SM00326:S	3	0.414365	0.994256	NM_17737	308	211	9131	0.421509	1	1	100

Annotator Enrichment Score: 0.0038447574015537255

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR015943	5	0.690608	0.979796	NM_17226	521	305	17763	0.558919	1	1	100
INTERPRO	IPR001680	4	0.552486	0.982735	NM_17226	521	259	17763	0.526549	1	1	100
UP_SEQ_Fl	repeat:WD	3	0.414365	0.986959	NM_01353	494	202	16021	0.481651	1	1	100
INTERPRO	IPR017986	3	0.414365	0.991289	NM_01353	521	228	17763	0.448606	1	1	100

UP_SEQ_Flrepeat:WD	3	0.414365	0.991597	NM_01353	494	218	16021	0.446301	1	1	100
INTERPRO IPR019781	3	0.414365	0.992752	NM_01353	521	235	17763	0.435243	1	1	100
SMART SM00320:\	4	0.552486	0.993371	NM_17226	308	259	9131	0.457855	1	1	100
UP_SEQ_Flrepeat:WD	3	0.414365	0.994141	NM_01353	494	231	16021	0.421184	1	1	100
UP_SEQ_Flrepeat:WD	3	0.414365	0.994759	NM_01353	494	235	16021	0.414015	1	1	100
UP_SEQ_Flrepeat:WD	3	0.414365	0.994759	NM_01353	494	235	16021	0.414015	1	1	100
INTERPRO IPR019775	3	0.414365	0.99606	NM_01353	521	258	17763	0.396442	1	1	100
SP_PIR_KEY wd repeat	3	0.414365	0.996175	NM_01353	516	263	17854	0.394686	1	0.999998	100

Annotator Enrichment Score: 2.718552935577551E-7

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM	!GO:005087	23	3.176796	0.999997	NM_14642	387	1681	13588	0.480402	1	1	100
KEGG_PAT	mmu04740	9	1.243094	0.999999	NM_00104	161	960	5738	0.334123	1	1	100
GOTERM	!GO:005089	18	2.486188	0.999999	NM_14642	387	1480	13588	0.427027	1	1	100
GOTERM	!GO:000760	15	2.071823		1 NM_14642	387	1402	13588	0.375654	1	1	100
PIR_SUPER	PIRSF00311	6	0.828729		1 NM_00104	226	901	8136	0.239734	1	1	100
GOTERM	!GO:000760	8	1.104972		1 NM_00104	387	1117	13588	0.251467	1	1	100
GOTERM	!GO:000498	8	1.104972		1 NM_00104	385	1135	13288	0.243272	1	1	100
INTERPRO	IPR000725	8	1.104972		1 NM_00104	521	1134	17763	0.240522	1	1	100
GOTERM	!GO:000760	8	1.104972		1 NM_00104	387	1192	13588	0.235645	1	1	100

Annotation Enrichment Score: 3.297639545046697

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE'	signal	137	20.08798	3.14E-08	NM_00100	526	2970	17854	1.565719	1.23E-05	1.23E-05	4.36E-05
GOTERM_ (GO:000557		86	12.60997	1.02E-07	NM_01969	363	1680	12504	1.763322	2.76E-05	2.76E-05	1.34E-04
SP_PIR_KE'	Secreted	76	11.1437	4.66E-07	NM_01969	526	1420	17854	1.816666	1.83E-04	9.15E-05	6.48E-04
UP_SEQ_Fl	signal pept	137	20.08798	5.46E-07	NM_00100	498	2963	16021	1.487473	7.43E-04	7.43E-04	8.97E-04
SP_PIR_KE'	disulfide bc	111	16.27566	3.73E-06	NM_00100	526	2469	17854	1.52599	0.001467	4.89E-04	0.005195
UP_SEQ_Fl	disulfide bc	110	16.12903	1.18E-05	NM_00100	498	2379	16021	1.487505	0.015869	0.007966	0.019309
SP_PIR_KE'	glycoprotei	138	20.2346	4.93E-04	NM_00116	526	3600	17854	1.301147	0.176198	0.047301	0.683791
GOTERM_ (GO:004442		39	5.718475	9.68E-04	NM_01969	363	774	12504	1.735665	0.230865	0.122997	1.266167
UP_SEQ_Fl	glycosylatic	134	19.64809	0.002701	NM_00116	498	3444	16021	1.251705	0.974743	0.706601	4.343849
UP_SEQ_Fl	topological	86	12.60997	0.013377	NM_01688	498	2174	16021	1.272621	1	0.989732	19.83661
UP_SEQ_Fl	topological	103	15.10264	0.035296	NM_02745	498	2780	16021	1.191935	1	0.997777	44.56618
UP_SEQ_Fl	transmemk	146	21.40762	0.04021	XM_00147	498	4113	16021	1.141969	1	0.997974	49.02403
SP_PIR_KE'	membrane	177	25.95308	0.097236	XM_00147	526	5507	17854	1.090958	1	0.786947	75.90428
SP_PIR_KE'	transmemk	158	23.16716	0.401431	NM_20151	526	5237	17854	1.024057	1	0.924664	99.92072
GOTERM_ (GO:001602		162	23.75367	0.695199	NM_20151	363	5709	12504	0.977456	1	0.988574	99.99998
GOTERM_ (GO:003122		167	24.4868	0.729016	NM_20151	363	5914	12504	0.972697	1	0.988656	100

Annotation Enrichment Score: 1.610927169071029

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_ (GO:006054		11	1.612903	0.003492	NM_00859	399	124	13588	3.02102	0.997875	0.953901	5.752779
GOTERM_ (GO:003032		8	1.173021	0.044522	NM_00859	399	111	13588	2.454424	1	0.942796	53.75893
GOTERM_ (GO:003529		14	2.052786	0.048005	NM_01176	399	264	13588	1.805954	1	0.938667	56.53173
GOTERM_ (GO:003032		8	1.173021	0.048229	NM_00859	399	113	13588	2.410983	1	0.928266	56.70452

Annotation Enrichment Score: 1.5572577576906517

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_ (GO:004856		18	2.639296	7.54E-04	NM_01176	399	241	13588	2.543537	0.734647	0.734647	1.269198
GOTERM_ (GO:004856		11	1.612903	0.020186	NM_00988	399	161	13588	2.326749	1	0.988709	29.20298
GOTERM_ (GO:004247		7	1.026393	0.023803	NM_00988	399	76	13588	3.136657	1	0.97877	33.50141
GOTERM_ (GO:004358		8	1.173021	0.033018	NM_00988	399	104	13588	2.619626	1	0.947816	43.36925
GOTERM_ (GO:004883		7	1.026393	0.044267	NM_00988	399	88	13588	2.708931	1	0.953258	53.54892
GOTERM_ (GO:004247		6	0.879765	0.046274	NM_00988	399	67	13588	3.049714	1	0.937836	55.17385
GOTERM_ (GO:004859		16	2.346041	0.105361	NM_01164	399	359	13588	1.517778	1	0.934124	84.8247

GOTERM_	GO:000742	12	1.759531	0.134917	NM_00988	399	257	13588	1.590123	1	0.95192	91.40885

Annotation Enrichment Score: 1.5472067026881227

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	Immunogl	26	3.812317	0.001504	NM_03071	526	443	17854	1.992138	0.446497	0.093878	2.072102
INTERPRO	IPR007110	31	4.545455	0.002499	NM_03071	509	604	17763	1.791114	0.896343	0.678042	3.827899
INTERPRO	IPR013783	32	4.692082	0.003396	NM_00836	509	644	17763	1.734054	0.954145	0.537249	5.169109
INTERPRO	IPR003598	11	1.612903	0.04292	NM_01087	509	187	17763	2.052814	1	0.96356	49.56015
INTERPRO	IPR003599	15	2.199413	0.066886	NM_03071	509	313	17763	1.67242	1	0.975014	66.04088
INTERPRO	IPR013098	8	1.173021	0.072335	NM_01087	509	127	17763	2.198289	1	0.977161	69.00644
SMART	SM00408:1	11	1.612903	0.075748	NM_01087	292	187	9131	1.839444	1	0.981275	62.80179
SMART	SM00409:1	15	2.199413	0.125912	NM_03071	292	313	9131	1.498589	1	0.97942	81.53881
INTERPRO	IPR013106	12	1.759531	0.470336	NM_03071	509	364	17763	1.150478	1	0.999876	99.99506

Annotation Enrichment Score: 1.4365711155782108

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	growth fac	12	1.759531	0.00132	NM_01078	526	127	17854	3.207209	0.404894	0.098597	1.820544
GOTERM_	GO:000808	12	1.759531	0.001874	NM_01078	369	141	13288	3.064752	0.626475	0.388833	2.683039
INTERPRO	IPR017948	4	0.58651	0.088419	NM_00755	509	37	17763	3.772739	1	0.977905	76.4076
INTERPRO	IPR001839	4	0.58651	0.088419	NM_00755	509	37	17763	3.772739	1	0.977905	76.4076
SMART	SM00204:1	4	0.58651	0.112769	NM_00755	292	37	9131	3.3806	1	0.982194	77.73461
PIR_SUPER	PIRSF8000	3	0.439883	0.173355	NM_00755	237	26	8136	3.961052	1	0.999997	91.76963
INTERPRO	IPR015615	3	0.439883	0.232549	NM_00755	509	32	17763	3.271672	1	0.998468	98.3905

Annotation Enrichment Score: 1.3355159975709827

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	cell divisor	17	2.492669	0.003859	XR_030853	526	256	17854	2.254025	0.7812	0.155359	5.23725
GOTERM_	GO:005130	17	2.492669	0.008799	XR_030853	399	281	13588	2.060275	1	0.979484	13.90137
SP_PIR_KE	cell cycle	23	3.372434	0.013243	XR_030853	526	447	17854	1.746506	0.994695	0.312179	16.9284
SP_PIR_KE	mitosis	11	1.612903	0.039169	NM_01980	526	179	17854	2.085881	1	0.602958	42.64392
GOTERM_	GO:000028	11	1.612903	0.053205	NM_01980	399	190	13588	1.971613	1	0.920401	60.3823
GOTERM_	GO:000706	11	1.612903	0.053205	NM_01980	399	190	13588	1.971613	1	0.920401	60.3823
GOTERM_	GO:000704	26	3.812317	0.057567	NM_00111	399	611	13588	1.449155	1	0.916519	63.36279
GOTERM_	GO:000008	11	1.612903	0.059596	NM_01980	399	194	13588	1.930961	1	0.91902	64.67583
GOTERM_	GO:004828	11	1.612903	0.064693	NM_01980	399	197	13588	1.901556	1	0.909362	67.78221

GOTERM_↓GO:000027	14	2.052786	0.073628	XR_030853	399	283	13588	1.684706	1	0.905592	72.61596
GOTERM_↓GO:002240	14	2.052786	0.169156	XR_030853	399	328	13588	1.453573	1	0.969954	95.66458
GOTERM_↓GO:002240	16	2.346041	0.175261	XR_030853	399	393	13588	1.386469	1	0.969627	96.17361
GOTERM_↓GO:000027	11	1.612903	0.179997	NM_01980	399	244	13588	1.535273	1	0.965141	96.52919

Annotation Enrichment Score: 1.238430304863903

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR006210	15	2.199413	0.002174	AK018312,	509	203	17763	2.578658	0.860845	0.860845	3.338959
INTERPRO	IPR013032	19	2.785924	0.003742	AK018312,	509	310	17763	2.1389	0.966522	0.493065	5.68144
INTERPRO	IPR000742	14	2.052786	0.004861	AK018312,	509	199	17763	2.455124	0.9879	0.520858	7.319885
SMART	SM00181:E	15	2.199413	0.005406	AK018312,	292	203	9131	2.310632	0.665467	0.665467	6.579184
SP_PIR_KE	egf-like doi	15	2.199413	0.006151	NM_17802	526	222	17854	2.293444	0.91152	0.215335	8.226297
INTERPRO	IPR000152	8	1.173021	0.018169	AJ584850,	509	94	17763	2.970029	1	0.906821	24.87836
INTERPRO	IPR006209	9	1.319648	0.030762	AJ584850,	509	128	17763	2.453754	1	0.970945	38.58142
INTERPRO	IPR001881	7	1.026393	0.04622	AJ584850,	509	91	17763	2.684449	1	0.963042	52.20555
INTERPRO	IPR018097	7	1.026393	0.05265	AJ584850,	509	94	17763	2.598775	1	0.961874	56.99279
SMART	SM00179:E	7	1.026393	0.069997	AJ584850,	292	91	9131	2.405427	1	0.99245	59.78938
UP_SEQ_FI	domain:EG	4	0.58651	0.075841	AJ584850,	498	32	16021	4.021335	1	0.999216	72.60857
UP_SEQ_FI	domain:EG	5	0.733138	0.077248	NM_00988	498	52	16021	3.093335	1	0.998923	73.28539
UP_SEQ_FI	domain:EG	4	0.58651	0.093621	NM_00988	498	35	16021	3.676649	1	0.99875	80.08878
UP_SEQ_FI	domain:EG	3	0.439883	0.126534	NM_00988	498	20	16021	4.825602	1	0.999155	89.15195
UP_SEQ_FI	domain:EG	3	0.439883	0.181062	NM_00988	498	25	16021	3.860482	1	0.999844	96.23537
INTERPRO	IPR013091	4	0.58651	0.315947	NM_14512	509	69	17763	2.023063	1	0.999338	99.73254
UP_SEQ_FI	domain:EG	3	0.439883	0.31931	AJ584850,	498	37	16021	2.608434	1	0.999995	99.81916
UP_SEQ_FI	domain:EG	3	0.439883	0.342187	AJ584850,	498	39	16021	2.474668	1	0.999997	99.89683
UP_SEQ_FI	domain:EG	5	0.733138	0.418265	AJ584850,	498	106	16021	1.517485	1	0.999999	99.98629
UP_SEQ_FI	domain:EG	3	0.439883	0.611605	AJ584850,	498	66	16021	1.462304	1	1	99.99998
UP_SEQ_FI	domain:EG	3	0.439883	0.708011	AJ584850,	498	79	16021	1.221671	1	1	100

Annotation Enrichment Score: 1.2304287516499264

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_↑GO:001526		22	3.225806	0.001299	NM_01032	369	365	13288	2.170516	0.494533	0.494533	1.866624
GOTERM_↑GO:002280		22	3.225806	0.001299	NM_01032	369	365	13288	2.170516	0.494533	0.494533	1.866624
GOTERM_↑GO:002283		21	3.079179	0.002531	NM_01032	369	360	13288	2.100632	0.73563	0.358194	3.607567
GOTERM_↑GO:001527		10	1.466276	0.002689	NM_17765	369	106	13288	3.397249	0.756764	0.297726	3.829115

GOTERM_↑GO:002283	10	1.466276	0.002689	NM_17765	369	106	13288	3.397249	0.756764	0.297726	3.829115
SP_PIR_KE' ionic chanr	18	2.639296	0.007975	NM_01688	526	301	17854	2.029812	0.957002	0.248779	10.54104
GOTERM_↑GO:000521	19	2.785924	0.008608	NM_01688	369	349	13288	1.960476	0.989314	0.53068	11.78126
SP_PIR_KE' ion transpc	27	3.958944	0.01044	NM_01688	526	543	17854	1.687772	0.983828	0.271863	13.58473
GOTERM_↑GO:002283	16	2.346041	0.011804	NM_01688	369	281	13288	2.050439	0.998038	0.58958	15.81621
GOTERM_↑GO:003142	12	1.759531	0.028615	NM_00103	369	206	13288	2.097719	1	0.782208	34.35772
INTERPRO IPR005821	8	1.173021	0.04015	NM_17765	509	111	17763	2.51516	1	0.975587	47.23357
GOTERM_↑GO:000526	13	1.906158	0.043767	NM_00913	369	248	13288	1.887665	1	0.835912	47.73743
GOTERM_↑GO:000681	30	4.398827	0.045246	NM_01688	399	712	13588	1.434907	1	0.9397	54.34852
GOTERM_↑GO:004687	14	2.052786	0.060724	NM_00913	369	290	13288	1.738454	1	0.871981	59.67977
GOTERM_↑GO:000524	3	0.439883	0.071092	NM_00103	369	16	13288	6.752033	1	0.883623	65.67353
UP_SEQ_Fl short sequ	5	0.733138	0.08161	NM_00103	498	53	16021	3.03497	1	0.998391	75.28476
SP_PIR_KE' voltage-gat	8	1.173021	0.103622	NM_00103	526	135	17854	2.011435	1	0.784631	78.1702
GOTERM_↑GO:003095	7	1.026393	0.109478	NM_00103	369	118	13288	2.136236	1	0.920845	81.38381
SP_PIR_KE' potassium	7	1.026393	0.134745	NM_00103	526	118	17854	2.013566	1	0.803113	86.64836
GOTERM_↑GO:002284	7	1.026393	0.144628	NM_00103	369	128	13288	1.969343	1	0.935029	89.61738
GOTERM_↑GO:001567	13	1.906158	0.179807	NM_15313	399	303	13588	1.461112	1	0.96723	96.51552
SP_PIR_KE' potassium	6	0.879765	0.20716	NM_00103	526	107	17854	1.903344	1	0.850521	96.04227
GOTERM_↑GO:002283	8	1.173021	0.228381	NM_00103	369	179	13288	1.609423	1	0.95143	97.66956
GOTERM_↑GO:000524	8	1.173021	0.228381	NM_00103	369	179	13288	1.609423	1	0.95143	97.66956
GOTERM_↑GO:000526	6	0.879765	0.286723	NM_00103	369	129	13288	1.674923	1	0.960255	99.25464
GOTERM_↑GO:000524	5	0.733138	0.294061	NM_00103	369	99	13288	1.818729	1	0.961788	99.35842
SP_PIR_KE' potassium	4	0.58651	0.339349	NM_00103	526	70	17854	1.939598	1	0.90244	99.6871
GOTERM_↑GO:00300C	15	2.199413	0.413078	NM_00913	399	442	13588	1.155717	1	0.991416	99.98795
SP_PIR_KE' transport	49	7.184751	0.41353	NM_17517	526	1571	17854	1.058692	1	0.922504	99.94033
GOTERM_↑GO:000681	17	2.492669	0.443191	NM_00913	399	515	13588	1.12415	1	0.991691	99.99506
GOTERM_↑GO:00347C	6	0.879765	0.484171	NM_00103	363	158	12504	1.308087	1	0.972344	99.98349
GOTERM_↑GO:000681	6	0.879765	0.505514	NM_00103	399	160	13588	1.277068	1	0.994389	99.99934
GOTERM_↑GO:00347C	4	0.58651	0.521961	NM_00103	363	95	12504	1.45037	1	0.978645	99.99393

Annotation Enrichment Score: 1.2120467804452135

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_Fl	topological	86	12.60997	0.013377	NM_01688	498	2174	16021	1.272621	1	0.989732	19.83661
GOTERM_↑GO:000588		96	14.07625	0.096373	NM_00117	363	2906	12504	1.137936	1	0.917636	73.63607
SP_PIR_KE'	cell membr	58	8.504399	0.179293	NM_01688	526	1713	17854	1.149266	1	0.821936	93.60019

Annotation Enrichment Score: 1.1767197239914462

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000173	3	0.439883	0.00807	NM_00988	399	5	13588	20.43308	0.999999	0.991358	12.82288
GOTERM_	GO:000716	3	0.439883	0.016301	NM_00988	399	7	13588	14.59506	1	0.983916	24.29584
GOTERM_	GO:000184	5	0.733138	0.0266	NM_00988	399	39	13588	4.366043	1	0.973955	36.65546
GOTERM_	GO:006060	5	0.733138	0.0266	NM_00988	399	39	13588	4.366043	1	0.973955	36.65546
GOTERM_	GO:001402	5	0.733138	0.033825	NM_00988	399	42	13588	4.054183	1	0.936154	44.16423
GOTERM_	GO:002191	7	1.026393	0.034742	NM_00988	399	83	13588	2.87212	1	0.933082	45.05504
GOTERM_	GO:000173	3	0.439883	0.03952	NM_00988	399	11	13588	9.287765	1	0.941402	49.48336
GOTERM_	GO:003529	14	2.052786	0.048005	NM_01176	399	264	13588	1.805954	1	0.938667	56.53173
GOTERM_	GO:000184	5	0.733138	0.06171	NM_00988	399	51	13588	3.338739	1	0.917076	65.99717
GOTERM_	GO:000183	5	0.733138	0.073048	NM_00988	399	54	13588	3.153254	1	0.907691	72.32405
GOTERM_	GO:003514	5	0.733138	0.094102	NM_00988	399	59	13588	2.886029	1	0.939423	81.24464
GOTERM_	GO:006042	13	1.906158	0.1017	NM_01049	399	271	13588	1.633641	1	0.940139	83.7379
GOTERM_	GO:000200	9	1.319648	0.136043	NM_01144	399	173	13588	1.771655	1	0.951497	91.59624
GOTERM_	GO:001633	5	0.733138	0.194919	NM_00988	399	78	13588	2.183022	1	0.965781	97.45693
GOTERM_	GO:004872	10	1.466276	0.263959	NM_01144	399	238	13588	1.430888	1	0.978144	99.4429
GOTERM_	GO:003523	7	1.026393	0.385547	NM_01032	399	171	13588	1.39407	1	0.990252	99.97382
GOTERM_	GO:006056	5	0.733138	0.409894	NM_00988	399	111	13588	1.534015	1	0.991416	99.9868

Annotation Enrichment Score: 1.1672227807894908

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_F	region of ir	3	0.439883	0.018186	AK161601,	498	7	16021	13.78744	1	0.993209	26.01713
UP_SEQ_F	site:Suscep	3	0.439883	0.051606	AK161601,	498	12	16021	8.042671	1	0.998571	58.10224
SP_PIR_KE	'oxidation	3	0.439883	0.054336	AK161601,	526	13	17854	7.832992	1	0.648496	54.03326
UP_SEQ_F	region of ir	4	0.58651	0.054782	XM_91202	498	28	16021	4.595812	1	0.998314	60.34692
PIR_SUPER	PIRSF00228	3	0.439883	0.060627	AK161601,	237	14	8136	7.356239	1	1	55.97531
UP_SEQ_F	domain:Be	3	0.439883	0.077272	AK161601,	498	15	16021	6.434137	1	0.998393	73.29667
UP_SEQ_F	domain:Be	3	0.439883	0.077272	AK161601,	498	15	16021	6.434137	1	0.998393	73.29667
UP_SEQ_F	domain:Be	3	0.439883	0.077272	AK161601,	498	15	16021	6.434137	1	0.998393	73.29667
UP_SEQ_F	domain:Be	3	0.439883	0.077272	AK161601,	498	15	16021	6.434137	1	0.998393	73.29667
INTERPRO	IPR001064	3	0.439883	0.08368	AK161601,	509	17	17763	6.158442	1	0.980913	74.41968
SMART	SM00247:K	3	0.439883	0.100578	AK161601,	292	17	9131	5.518332	1	0.986192	73.5735
GOTERM_	GO:000521	3	0.439883	0.113798	AK161601,	369	21	13288	5.144406	1	0.920899	82.65141

SP_PIR_KE' eye lens pr 3 0.439883 0.115856 AK161601, 526 20 17854 5.091445 1 0.779586 81.96902

Annotation Enrichment Score: 1.1185560247831734

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
KEGG_PAT	mmu04115	7	1.026393	0.010102	NM_00763	155	69	5738	3.755587	0.735532	0.358115	11.1657
BIOCARTA	m_RacCycI	4	0.58651	0.021365	NM_00763	31	24	1171	6.295699	0.764715	0.764715	19.86834
GOTERM_	(GO:000030	3	0.439883	0.0263	NM_00763	363	9	12504	11.48209	0.99927	0.764146	29.57535
BIOCARTA	m_p53PatI	3	0.439883	0.060955	NM_00763	31	16	1171	7.082661	0.985209	0.878383	47.53575
BIOCARTA	m_cellcycle	3	0.439883	0.115149	NM_00763	31	23	1171	4.927069	0.999724	0.871153	71.48431
KEGG_PAT	mmu04110	7	1.026393	0.128895	NM_00763	155	128	5738	2.024496	1	0.83597	79.99496
BIOCARTA	m_g1Pathw	3	0.439883	0.132354	NM_00763	31	25	1171	4.532903	0.999926	0.850793	76.68574
SP_PIR_KE'	cyclin	4	0.58651	0.1669	NM_00104	526	48	17854	2.82858	1	0.833716	92.11642
GOTERM_	(GO:005172	6	0.879765	0.755528	NM_00763	399	214	13588	0.954817	1	0.999373	100

Annotation Enrichment Score: 1.1107064340160735

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	(GO:004856	18	2.639296	7.54E-04	NM_01176	399	241	13588	2.543537	0.734647	0.734647	1.269198
GOTERM_	(GO:000189	6	0.879765	0.032784	NM_01082	399	61	13588	3.349686	1	0.954316	43.13663
GOTERM_	(GO:004859	16	2.346041	0.105361	NM_01164	399	359	13588	1.517778	1	0.934124	84.8247
GOTERM_	(GO:000189	6	0.879765	0.111725	NM_01082	399	87	13588	2.34863	1	0.940165	86.55282
GOTERM_	(GO:004300	17	2.492669	0.173886	NM_01176	399	421	13588	1.375148	1	0.970897	96.06412
GOTERM_	(GO:000979	17	2.492669	0.179117	NM_01176	399	425	13588	1.362206	1	0.96894	96.46559
GOTERM_	(GO:006071	3	0.439883	0.273609	NM_01169	399	35	13588	2.919012	1	0.977613	99.55448
GOTERM_	(GO:000170	9	1.319648	0.52478	NM_01082	399	267	13588	1.147926	1	0.994671	99.99966

Annotation Enrichment Score: 1.0457856051344383

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	(GO:000187	9	1.319648	0.025931	NM_02963	369	128	13288	2.532012	0.999999	0.784028	31.67813
GOTERM_	(GO:003024	9	1.319648	0.025931	NM_02963	369	128	13288	2.532012	0.999999	0.784028	31.67813
GOTERM_	(GO:000553	7	1.026393	0.096801	NM_02963	369	114	13288	2.211192	1	0.911929	77.14952
UP_SEQ_FI	region of ir	3	0.439883	0.106028	NM_02963	498	18	16021	5.36178	1	0.997751	84.12137
GOTERM_	(GO:003024	13	1.906158	0.171555	NM_02963	369	317	13288	1.476785	1	0.935729	93.47029
GOTERM_	(GO:000820	5	0.733138	0.197871	NM_02963	369	83	13288	2.169328	1	0.94059	95.91099
SP_PIR_KE'	heparin-bir	4	0.58651	0.204067	NM_02963	526	53	17854	2.561733	1	0.851693	95.82193

Annotation Enrichment Score: 1.003778589511261

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000823	26	3.812317	0.044603	NM_01969	369	629	13288	1.488524	1	0.81933	48.39649
GOTERM_	GO:000823	9	1.319648	0.05023	AK028249,	369	146	13288	2.219846	1	0.835316	52.63165
GOTERM_	GO:007001	24	3.519062	0.075266	NM_01969	369	603	13288	1.433267	1	0.884923	67.84342
GOTERM_	GO:00065C	38	5.571848	0.118354	NM_01969	399	1034	13588	1.251543	1	0.941614	88.155
SP_PIR_KE	Protease	20	2.932551	0.167729	NM_01969	526	509	17854	1.333712	1	0.827929	92.22494
GOTERM_	GO:000417	15	2.199413	0.283535	NM_01117	369	421	13288	1.283047	1	0.96322	99.20485

Annotation Enrichment Score: 0.9272126313063458

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	laminin egf	5	0.733138	0.009797	NM_00988	526	29	17854	5.852235	0.979128	0.275624	12.80076
INTERPRO	IPR006209	9	1.319648	0.030762	AJ584850,	509	128	17763	2.453754	1	0.970945	38.58142
INTERPRO	IPR002049	5	0.733138	0.033894	NM_00988	509	43	17763	4.057888	1	0.968919	41.60536
SMART	SM00180:E	5	0.733138	0.047147	NM_00988	292	43	9131	3.63611	0.999942	0.992386	45.46428
UP_SEQ_FI	domain:Lar	3	0.439883	0.181062	AK018312,	498	25	16021	3.860482	1	0.999844	96.23537
UP_SEQ_FI	domain:Lar	3	0.439883	0.19236	NM_00988	498	26	16021	3.712002	1	0.999886	97.00317
UP_SEQ_FI	domain:Lar	3	0.439883	0.19236	AK018312,	498	26	16021	3.712002	1	0.999886	97.00317
UP_SEQ_FI	domain:Lar	3	0.439883	0.19236	NM_00988	498	26	16021	3.712002	1	0.999886	97.00317
INTERPRO	IPR001791	3	0.439883	0.370132	NM_00988	509	45	17763	2.326523	1	0.999729	99.92619
SMART	SM00282:L	3	0.439883	0.422633	NM_00988	292	45	9131	2.084703	1	0.985983	99.8988
INTERPRO	IPR013320	3	0.439883	0.650815	NM_00988	509	77	17763	1.359656	1	0.999994	99.99999

Annotation Enrichment Score: 0.9208304181872129

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:004874	5	0.733138	0.013635	AK170454,	399	32	13588	5.321115	1	0.992013	20.74588
GOTERM_	GO:004874	5	0.733138	0.024419	AK170454,	399	38	13588	4.480939	1	0.973319	34.20817
GOTERM_	GO:000752	4	0.58651	0.028603	AK170454,	399	23	13588	5.922633	1	0.966731	38.82746
GOTERM_	GO:004311	4	0.58651	0.039388	AK170454,	399	26	13588	5.239252	1	0.947408	49.36575
GOTERM_	GO:004311	3	0.439883	0.053939	AK170454,	399	13	13588	7.858878	1	0.917987	60.89982
GOTERM_	GO:00508C	5	0.733138	0.054712	AK170454,	399	49	13588	3.475014	1	0.915775	61.43681
GOTERM_	GO:000717	3	0.439883	0.069895	AK170454,	399	15	13588	6.811028	1	0.905603	70.68584
GOTERM_	GO:00550C	5	0.733138	0.073048	AK170454,	399	54	13588	3.153254	1	0.907691	72.32405
GOTERM_	GO:00550C	5	0.733138	0.103243	AK170454,	399	61	13588	2.791405	1	0.937834	84.20454
GOTERM_	GO:000751	5	0.733138	0.160033	AK170454,	399	72	13588	2.36494	1	0.965643	94.78381

GOTERM_	GO:006053	5	0.733138	0.171397	AK170454,	399	74	13588	2.301023	1	0.970349	95.8584
GOTERM_	GO:005114	5	0.733138	0.263884	AK170454,	399	89	13588	1.91321	1	0.978705	99.44193
GOTERM_	GO:004306	7	1.026393	0.271841	AK170454,	399	149	13588	1.599906	1	0.978686	99.53575
GOTERM_	GO:001470	6	0.879765	0.315512	NM_01176	399	127	13588	1.608904	1	0.983692	99.83713
GOTERM_	GO:000716	8	1.173021	0.332138	AK170454,	399	192	13588	1.418964	1	0.985397	99.8926
GOTERM_	GO:006053	6	0.879765	0.367832	NM_01176	399	136	13588	1.502433	1	0.988964	99.95763
GOTERM_	GO:004362	5	0.733138	0.38997	NM_00945	399	108	13588	1.576627	1	0.990666	99.97683
GOTERM_	GO:000751	7	1.026393	0.411777	NM_01176	399	176	13588	1.354466	1	0.991454	99.98749
GOTERM_	GO:004269	5	0.733138	0.449293	AK170454,	399	117	13588	1.455348	1	0.992234	99.9959

Annotation Enrichment Score: 0.915001324203212

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:005196	10	1.466276	0.030133	NM_01366	399	148	13588	2.301023	1	0.965393	40.43861
GOTERM_	GO:005076	5	0.733138	0.031303	NM_01366	399	41	13588	4.153066	1	0.955303	41.64318
GOTERM_	GO:004559	11	1.612903	0.03338	NM_01366	399	175	13588	2.140609	1	0.941789	43.72672
GOTERM_	GO:006028	10	1.466276	0.044421	NM_01366	399	159	13588	2.141833	1	0.94819	53.67555
GOTERM_	GO:001072	5	0.733138	0.048168	NM_01366	399	47	13588	3.622887	1	0.933705	56.65801
SP_PIR_KE'	neurogene	9	1.319648	0.062659	NM_01366	526	144	17854	2.121435	1	0.685234	59.35264
GOTERM_	GO:005077	3	0.439883	0.069895	NM_01366	399	15	13588	6.811028	1	0.905603	70.68584
GOTERM_	GO:005109	11	1.612903	0.098784	NM_01366	399	214	13588	1.750498	1	0.945197	82.82035
GOTERM_	GO:003134	3	0.439883	0.14489	NM_01366	399	23	13588	4.441975	1	0.957773	92.94063
GOTERM_	GO:001097	4	0.58651	0.158361	NM_01366	399	47	13588	2.89831	1	0.966873	94.60519
GOTERM_	GO:004566	6	0.879765	0.179453	NM_01366	399	102	13588	2.003243	1	0.968082	96.48998
GOTERM_	GO:005076	7	1.026393	0.190914	NM_01366	399	132	13588	1.805954	1	0.965166	97.23398
GOTERM_	GO:003134	4	0.58651	0.233241	NM_01366	399	57	13588	2.389834	1	0.974001	98.88658
GOTERM_	GO:005077	3	0.439883	0.31725	NM_01366	399	39	13588	2.619626	1	0.983728	99.84399
GOTERM_	GO:001076	3	0.439883	0.432843	NM_01366	399	50	13588	2.043308	1	0.991545	99.99326
GOTERM_	GO:002260	4	0.58651	0.543948	NM_01366	399	97	13588	1.404336	1	0.995364	99.99983
GOTERM_	GO:005113	4	0.58651	0.697973	NM_01366	399	122	13588	1.116562	1	0.998642	100

Annotation Enrichment Score: 0.9036489453574675

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:001062	22	3.225806	0.050866	NM_01176	399	488	13588	1.535273	1	0.927464	58.69187
GOTERM_	GO:003132	24	3.519062	0.056822	NM_01176	399	552	13588	1.480658	1	0.918716	62.86934
GOTERM_	GO:000989	24	3.519062	0.061059	NM_01176	399	557	13588	1.467367	1	0.919432	65.59488

GOTERM_	GO:004594	17	2.492669	0.06183	NM_01176	399	358	13588	1.617143	1	0.91289	66.07056
GOTERM_	GO:001055	23	3.372434	0.064333	NM_01176	399	530	13588	1.477864	1	0.916978	67.57164
GOTERM_	GO:004594	21	3.079179	0.066621	NM_01176	399	475	13588	1.505596	1	0.902913	68.88819
GOTERM_	GO:005117	22	3.225806	0.09328	NM_01176	399	526	13588	1.424359	1	0.940612	80.95441
GOTERM_	GO:004589	18	2.639296	0.103795	NM_01176	399	416	13588	1.47354	1	0.936311	84.36848
GOTERM_	GO:005125	18	2.639296	0.110215	NM_01176	399	419	13588	1.462989	1	0.940024	86.16042
GOTERM_	GO:004593	21	3.079179	0.11739	NM_01176	399	510	13588	1.40227	1	0.944431	87.93378
GOTERM_	GO:001060	25	3.665689	0.117817	NM_01176	399	633	13588	1.34499	1	0.942939	88.03204
GOTERM_	GO:000635	22	3.225806	0.266114	NM_01176	399	616	13588	1.216255	1	0.97776	99.46988
GOTERM_	GO:000635	46	6.744868	0.397144	NM_01176	399	1465	13588	1.069308	1	0.990995	99.98104
GOTERM_	GO:005125	46	6.744868	0.431219	NM_01176	399	1488	13588	1.05278	1	0.991535	99.99292
GOTERM_	GO:004544	58	8.504399	0.886284	NM_01176	399	2227	13588	0.886932	1	0.999965	100

Annotation Enrichment Score: 0.8687205880673915

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_FI	domain:lg-	5	0.733138	0.061024	NM_01087	498	48	16021	3.351113	1	0.997794	64.4345
UP_SEQ_FI	domain:lg-	3	0.439883	0.086554	NM_01169	498	16	16021	6.032003	1	0.998466	77.38102
UP_SEQ_FI	domain:lg-	5	0.733138	0.095401	NM_01087	498	56	16021	2.872382	1	0.998486	80.7213
UP_SEQ_FI	domain:lg-	6	0.879765	0.133308	NM_00836	498	87	16021	2.218668	1	0.999258	90.4537
INTERPRO	IPR013151	9	1.319648	0.13893	NM_01366	509	178	17763	1.764497	1	0.995576	90.30514
UP_SEQ_FI	domain:lg-	7	1.026393	0.216941	NM_00836	498	130	16021	1.732268	1	0.999944	98.19583
UP_SEQ_FI	domain:lg-	7	1.026393	0.221917	NM_00836	498	131	16021	1.719044	1	0.999942	98.37512
UP_SEQ_FI	domain:lg-	3	0.439883	0.249865	NM_01169	498	31	16021	3.113292	1	0.999974	99.10878

Annotation Enrichment Score: 0.8497483237490924

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000562	21	3.079179	0.104221	NM_01031	363	510	12504	1.418376	1	0.91672	76.49434
GOTERM_	GO:000562	21	3.079179	0.1329	NM_01031	363	528	12504	1.370023	1	0.93673	84.6801
GOTERM_	GO:000026	22	3.225806	0.203834	NM_01031	363	596	12504	1.271507	1	0.947219	95.01534

Annotation Enrichment Score: 0.8292594635346336

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	chemotaxis	6	0.879765	0.035424	NM_01133	526	62	17854	3.284803	0.999999	0.587651	39.45397
GOTERM_	GO:000761	19	2.785924	0.052258	NM_00742	399	405	13588	1.597648	1	0.922045	59.70588
SP_PIR_KE	inflammato	6	0.879765	0.079592	NM_01133	526	78	17854	2.610997	1	0.742856	68.45832

GOTERM_↑GO:00080C	4	0.58651	0.087312	NM_01133	369	38	13288	3.790615	1	0.909121	73.41063
GOTERM_↑GO:004237	4	0.58651	0.092738	NM_01133	369	39	13288	3.693419	1	0.912236	75.61307
GOTERM_↑GO:004233	7	1.026393	0.100676	NM_01133	399	109	13588	2.187027	1	0.940871	83.4211
GOTERM_↑GO:000693	7	1.026393	0.100676	NM_01133	399	109	13588	2.187027	1	0.940871	83.4211
KEGG_PAT mmu04062	9	1.319648	0.11529	NM_00916	155	182	5738	1.830627	1	0.898978	76.03243
INTERPRO IPR000827	3	0.439883	0.120046	NM_01133	509	21	17763	4.985406	1	0.991995	86.40036
PIR_SUPER PIRSF00195	3	0.439883	0.122783	NM_01133	237	21	8136	4.904159	1	1	82.0651
GOTERM_↑GO:000762	11	1.612903	0.163323	NM_00988	399	239	13588	1.567391	1	0.966937	95.11924
GOTERM_↑GO:000695	17	2.492669	0.247182	NM_00836	399	448	13588	1.292271	1	0.97726	99.18399
SP_PIR_KE cytokine	8	1.173021	0.265864	NM_01133	526	177	17854	1.534145	1	0.876826	98.64278
INTERPRO IPR001811	3	0.439883	0.285922	NM_01133	509	37	17763	2.829555	1	0.999171	99.47724
SMART SM00199:5	3	0.439883	0.330975	NM_01133	292	37	9131	2.53545	1	0.982743	99.35652
GOTERM_↑GO:000695	9	1.319648	0.339152	NM_00116	399	225	13588	1.362206	1	0.98518	99.91018
GOTERM_↑GO:000512	7	1.026393	0.381295	NM_01133	369	180	13288	1.400422	1	0.971282	99.90523
GOTERM_↑GO:000961	12	1.759531	0.438662	NM_01078	399	347	13588	1.177699	1	0.991696	99.99434

Annotation Enrichment Score: 0.8276279579766234

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
KEGG_PAT mmu05217		5	0.733138	0.059236	NM_02145	155	55	5738	3.365396	0.999664	0.798074	50.93771
GOTERM_↑GO:001605		8	1.173021	0.087559	NM_02145	399	130	13588	2.095701	1	0.934903	78.81378
SP_PIR_KE wnt signali		7	1.026393	0.134745	NM_02145	526	118	17854	2.013566	1	0.803113	86.64836
KEGG_PAT mmu04916		5	0.733138	0.280705	NM_02145	155	100	5738	1.850968	1	0.909092	97.85544
KEGG_PAT mmu04310		6	0.879765	0.37086	NM_02145	155	149	5738	1.490712	1	0.936667	99.5501

Annotation Enrichment Score: 0.7863654199368936

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_F domain:W/		3	0.439883	0.029923	NM_18181	498	9	16021	10.72356	1	0.998978	39.2735
GOTERM_↑GO:000485		13	1.906158	0.038329	NM_18181	369	243	13288	1.926506	1	0.845151	43.25851
INTERPRO IPR018069		3	0.439883	0.075215	NM_18181	509	16	17763	6.543345	1	0.975974	70.47371
INTERPRO IPR002223		3	0.439883	0.110621	NM_00104	509	20	17763	5.234676	1	0.990127	83.94132
INTERPRO IPR008197		3	0.439883	0.120046	NM_18181	509	21	17763	4.985406	1	0.991995	86.40036
SMART SM00131:k		3	0.439883	0.132172	NM_00104	292	20	9131	4.690582	1	0.97211	83.13176
SMART SM00217:v		3	0.439883	0.143153	NM_18181	292	21	9131	4.467221	1	0.968807	85.62383
GOTERM_↑GO:000486		8	1.173021	0.159732	NM_00997	369	161	13288	1.789359	1	0.937258	91.98097
GOTERM_↑GO:003041		8	1.173021	0.216277	NM_00997	369	176	13288	1.636856	1	0.948973	97.07958

GOTERM_↑GO:000486	3	0.439883	0.294089	NM_00997	369	39	13288	2.770065	1	0.959551	99.35879
GOTERM_↑GO:000486	4	0.58651	0.621485	NM_00104	369	115	13288	1.252551	1	0.99359	99.99992
SP_PIR_KE' protease in	4	0.58651	0.625682	NM_00997	526	109	17854	1.245613	1	0.97897	99.99988
SP_PIR_KE' Serine prot	3	0.439883	0.699238	NM_18181	526	82	17854	1.241816	1	0.987373	99.99999

Annotation Enrichment Score: 0.7757458256077417

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE'	osteogene	5	0.733138	0.003548	NM_00859	526	22	17854	7.71431	0.752585	0.160195	4.824039
GOTERM_↑GO:	006034	7	1.026393	0.132775	NM_00859	399	118	13588	2.02022	1	0.954661	91.04141
GOTERM_↑GO:	006034	3	0.439883	0.176063	NM_01144	399	26	13588	3.929439	1	0.96907	96.23613
GOTERM_↑GO:	00015C	9	1.319648	0.598999	NM_00859	399	285	13588	1.075425	1	0.996917	99.99998
GOTERM_↑GO:	00015C	4	0.58651	0.604349	NM_00859	399	106	13588	1.2851	1	0.996923	99.99998
GOTERM_↑GO:	00487C	4	0.58651	0.738061	NM_01144	399	130	13588	1.04785	1	0.999191	100

Annotation Enrichment Score: 0.7696003856813287

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE'	synapse	12	1.759531	0.050553	NM_01880	526	213	17854	1.91228	1	0.658019	51.40745
GOTERM_↑GO:	00452C	15	2.199413	0.080993	NM_01880	363	319	12504	1.619731	1	0.921388	67.082
SP_PIR_KE'	postsynapt	7	1.026393	0.105668	NM_02545	526	110	17854	2.160007	1	0.768455	78.8533
SP_PIR_KE'	cell junctio	17	2.492669	0.116983	NM_01880	526	392	17854	1.472016	1	0.772729	82.28615
GOTERM_↑GO:	001406	4	0.58651	0.183039	NM_02545	363	51	12504	2.701669	1	0.952341	93.00238
GOTERM_↑GO:	004445	9	1.319648	0.274877	NM_01880	363	212	12504	1.462342	1	0.945166	98.54246
GOTERM_↑GO:	000523	4	0.58651	0.276029	NM_01688	369	66	13288	2.182475	1	0.966343	99.07514
GOTERM_↑GO:	003005	17	2.492669	0.288319	NM_01880	363	470	12504	1.245929	1	0.938772	98.86051
GOTERM_↑GO:	004521	6	0.879765	0.301329	NM_02545	363	126	12504	1.640299	1	0.937737	99.10607
SP_PIR_KE'	neurotrans	3	0.439883	0.329755	NM_00111	526	40	17854	2.545722	1	0.904337	99.6176

Annotation Enrichment Score: 0.7602867597408864

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_↑GO:	000715	23	3.372434	0.102526	NM_01667	399	561	13588	1.3962	1	0.939076	83.98941
GOTERM_↑GO:	002261	23	3.372434	0.104	NM_01667	399	562	13588	1.393716	1	0.934166	84.42881
GOTERM_↑GO:	001633	10	1.466276	0.256192	NM_01667	399	236	13588	1.443014	1	0.977632	99.33451
SP_PIR_KE'	cell adhesio	14	2.052786	0.332983	AK134774,	526	380	17854	1.25053	1	0.903702	99.64243

Annotation Enrichment Score: 0.7184722341669352

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:004358	8	1.173021	0.033018	NM_00988	399	104	13588	2.619626	1	0.947816	43.36925
GOTERM_	GO:004883	7	1.026393	0.044267	NM_00988	399	88	13588	2.708931	1	0.953258	53.54892
GOTERM_	GO:006011	3	0.439883	0.218984	NM_00116	399	30	13588	3.405514	1	0.974097	98.47892
GOTERM_	GO:004249	3	0.439883	0.284552	NM_00116	399	36	13588	2.837928	1	0.98029	99.65547
GOTERM_	GO:000760	3	0.439883	0.709975	NM_00116	399	84	13588	1.216255	1	0.998843	100
GOTERM_	GO:005095	3	0.439883	0.755991	NM_00116	399	92	13588	1.110494	1	0.999365	100

Annotation Enrichment Score: 0.717687865050905

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR002209	3	0.439883	0.08368	NM_02001	509	17	17763	6.158442	1	0.980913	74.41968
KEGG_PAT	mmu05218	5	0.733138	0.122468	NM_00987	155	71	5738	2.606997	1	0.882258	78.20448
INTERPRO	IPR002348	3	0.439883	0.139444	NM_02001	509	23	17763	4.551892	1	0.994663	90.39503
SMART	SM00442:F	3	0.439883	0.165641	NM_02001	292	23	9131	4.078767	1	0.974217	89.70475
KEGG_PAT	mmu04810	8	1.173021	0.364392	NM_01013	155	217	5738	1.364769	1	0.940806	99.49311
KEGG_PAT	mmu04010	8	1.173021	0.572919	NM_00108	155	265	5738	1.117565	1	0.946761	99.99509

Annotation Enrichment Score: 0.7011071460146985

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
KEGG_PAT	mmu04514	11	1.612903	0.00812	NM_01667	155	154	5738	2.64424	0.656309	0.413748	9.06929
INTERPRO	IPR003006	7	1.026393	0.062031	XM_91202	509	98	17763	2.492703	1	0.973382	63.17729
KEGG_PAT	mmu04940	5	0.733138	0.088071	XM_91202	155	63	5738	2.938044	0.999994	0.866398	65.87375
KEGG_PAT	mmu05320	5	0.733138	0.127124	XM_91202	155	72	5738	2.570789	1	0.861792	79.51547
PIR_SUPER	PIRSF00195	3	0.439883	0.152701	XM_91202	237	24	8136	4.291139	1	1	88.62355
INTERPRO	IPR011161	4	0.58651	0.164477	XM_91202	509	49	17763	2.848803	1	0.997016	93.93989
GOTERM_	GO:004261	4	0.58651	0.190379	XM_91202	363	52	12504	2.649714	1	0.950818	93.78581
KEGG_PAT	mmu05330	4	0.58651	0.203309	XM_91202	155	58	5738	2.553059	1	0.880778	92.9384
KEGG_PAT	mmu05332	4	0.58651	0.203309	XM_91202	155	58	5738	2.553059	1	0.880778	92.9384
GOTERM_	GO:001988	5	0.733138	0.250976	XM_91202	399	87	13588	1.957192	1	0.976841	99.2509
GOTERM_	GO:004800	3	0.439883	0.273609	XM_91202	399	35	13588	2.919012	1	0.977613	99.55448
INTERPRO	IPR001039	3	0.439883	0.328384	XM_91202	509	41	17763	2.5535	1	0.999454	99.79912
GOTERM_	GO:004261	3	0.439883	0.344368	XM_91202	363	42	12504	2.460449	1	0.954589	99.61271
INTERPRO	IPR003597	4	0.58651	0.425036	XM_91202	509	83	17763	1.681824	1	0.999849	99.98221
KEGG_PAT	mmu04612	4	0.58651	0.443736	XM_91202	155	91	5738	1.627224	1	0.922781	99.89294
KEGG_PAT	mmu05416	4	0.58651	0.464904	XM_91202	155	94	5738	1.575292	1	0.922684	99.9319

SMART	SM00407:1	4	0.58651	0.496151	XM_91202	292	83	9131	1.507014	1	0.990103	99.9817
KEGG_PAT	mmu04144	6	0.879765	0.637217	XM_91202	155	202	5738	1.099585	1	0.957683	99.99927

Annotation Enrichment Score: 0.6844513246537749

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:00508C	5	0.733138	0.054712	AK170454,	399	49	13588	3.475014	1	0.915775	61.43681
GOTERM_	GO:000726	14	2.052786	0.085189	NM_00738	399	290	13588	1.644041	1	0.932815	77.86228
GOTERM_	GO:000726	6	0.879765	0.600529	NM_00916	399	178	13588	1.147926	1	0.996927	99.99998
GOTERM_	GO:001922	7	1.026393	0.653429	NM_00916	399	226	13588	1.054805	1	0.997782	100

Annotation Enrichment Score: 0.6569027379304958

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:003142	12	1.759531	0.028615	NM_00103	369	206	13288	2.097719	1	0.782208	34.35772
GOTERM_	GO:001567	13	1.906158	0.179807	NM_15313	399	303	13588	1.461112	1	0.96723	96.51552
GOTERM_	GO:000527	3	0.439883	0.181146	NM_00913	369	28	13288	3.858304	1	0.932138	94.48475
SP_PIR_KE	sodium cha	3	0.439883	0.198571	NM_00913	526	28	17854	3.636746	1	0.849105	95.40219
SP_PIR_KE	Sodium tra	6	0.879765	0.228417	NM_00913	526	111	17854	1.834755	1	0.864423	97.28827
GOTERM_	GO:000681	6	0.879765	0.304	NM_00913	399	125	13588	1.634647	1	0.982308	99.78396
GOTERM_	GO:00314C	5	0.733138	0.319126	NM_00101	369	103	13288	1.748099	1	0.963417	99.62016
SP_PIR_KE	Sodium	5	0.733138	0.359284	NM_00101	526	103	17854	1.647717	1	0.908973	99.79569
GOTERM_	GO:00300C	15	2.199413	0.413078	NM_00913	399	442	13588	1.155717	1	0.991416	99.98795
GOTERM_	GO:000681	17	2.492669	0.443191	NM_00913	399	515	13588	1.12415	1	0.991691	99.99506

Annotation Enrichment Score: 0.6537141434896033

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000701	13	1.906158	0.021712	NM_00945	399	211	13588	2.098184	1	0.978958	31.04751
GOTERM_	GO:000701	6	0.879765	0.174525	NM_00945	399	101	13588	2.023077	1	0.97023	96.11536
SP_PIR_KE	microtubul	8	1.173021	0.473038	NM_00945	526	221	17854	1.228705	1	0.944638	99.98653
GOTERM_	GO:001563	14	2.052786	0.543655	NM_00945	363	450	12504	1.071662	1	0.979047	99.99671
GOTERM_	GO:000587	8	1.173021	0.552906	NM_00945	363	240	12504	1.148209	1	0.97823	99.99748

Annotation Enrichment Score: 0.6490716568731006

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:004873	12	1.759531	0.030625	NM_01144	399	197	13588	2.074425	1	0.959977	40.94784
GOTERM_	GO:006034	7	1.026393	0.132775	NM_00859	399	118	13588	2.02022	1	0.954661	91.04141

GOTERM_	GO:00020C	9	1.319648	0.136043	NM_01144	399	173	13588	1.771655	1	0.951497	91.59624
GOTERM_	GO:006074	3	0.439883	0.176063	NM_01144	399	26	13588	3.929439	1	0.96907	96.23613
GOTERM_	GO:006051	3	0.439883	0.186678	NM_01144	399	27	13588	3.783904	1	0.96652	96.9782
GOTERM_	GO:005121	5	0.733138	0.194919	NM_00859	399	78	13588	2.183022	1	0.965781	97.45693
GOTERM_	GO:002261	5	0.733138	0.231884	NM_01144	399	84	13588	2.027092	1	0.974851	98.85275
GOTERM_	GO:004872	10	1.466276	0.263959	NM_01144	399	238	13588	1.430888	1	0.978144	99.4429
GOTERM_	GO:003085	3	0.439883	0.31725	NM_01144	399	39	13588	2.619626	1	0.983728	99.84399
GOTERM_	GO:00486C	5	0.733138	0.531335	NM_01144	399	130	13588	1.309813	1	0.994744	99.99973
GOTERM_	GO:000165	5	0.733138	0.623268	NM_01144	399	146	13588	1.166272	1	0.997151	99.99999
GOTERM_	GO:000176	4	0.58651	0.713524	NM_01144	399	125	13588	1.089764	1	0.998895	100

Annotation Enrichment Score: 0.6481639124927263

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR013111	6	0.879765	0.052429	AJ584850,	509	71	17763	2.949113	1	0.969349	56.83572
UP_SEQ_FI	domain:EG	6	0.879765	0.059686	NM_00111	498	68	16021	2.83859	1	0.998401	63.5928
GOTERM_	GO:000722	6	0.879765	0.071875	NM_01112	399	76	13588	2.688564	1	0.907957	71.72514
SP_PIR_KE	' integrin	5	0.733138	0.104456	NM_00111	526	61	17854	2.78221	1	0.775769	78.45122
INTERPRO	IPR002870	4	0.58651	0.178635	NM_00111	509	51	17763	2.737085	1	0.997376	95.35814
INTERPRO	IPR001590	4	0.58651	0.19311	NM_00111	509	53	17763	2.633799	1	0.9977	96.48256
INTERPRO	IPR006586	3	0.439883	0.253878	NM_00111	509	34	17763	3.079221	1	0.998196	98.96314
SP_PIR_KE	' metallopro	7	1.026393	0.259913	NM_01969	526	146	17854	1.627402	1	0.879039	98.48144
GOTERM_	GO:000823	8	1.173021	0.261715	NM_01969	369	187	13288	1.540571	1	0.961264	98.77155
INTERPRO	IPR001762	3	0.439883	0.285922	NM_00111	509	37	17763	2.829555	1	0.999171	99.47724
SMART	SM00608:A	3	0.439883	0.295454	NM_00111	292	34	9131	2.759166	1	0.975843	98.76803
UP_SEQ_FI	domain:Dis	3	0.439883	0.330776	NM_00111	498	38	16021	2.539791	1	0.999996	99.86318
SMART	SM00050:U	3	0.439883	0.330975	NM_00111	292	37	9131	2.53545	1	0.982743	99.35652
UP_SEQ_FI	domain:Pe	3	0.439883	0.342187	NM_00111	498	39	16021	2.474668	1	0.999997	99.89683
INTERPRO	IPR018358	3	0.439883	0.380414	NM_00111	509	46	17763	2.275946	1	0.999761	99.9429
GOTERM_	GO:000422	4	0.58651	0.615572	NM_00111	369	114	13288	1.263538	1	0.994032	99.9999
UP_SEQ_FI	compositio	3	0.439883	0.923301	NM_00111	498	134	16021	0.720239	1	1	100

Annotation Enrichment Score: 0.6400028045095678

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR018488	3	0.439883	0.190339	XM_00147	509	28	17763	3.739054	1	0.99791	96.28934
INTERPRO	IPR000595	3	0.439883	0.232549	XM_00147	509	32	17763	3.271672	1	0.998468	98.3905

SMART	SM00100:c	3	0.439883	0.271612	XM_00147	292	32	9131	2.931614	1	0.985989	98.12911

Annotation Enrichment Score: 0.6368608276844274

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR003659	4	0.58651	0.143922	NM_01366	509	46	17763	3.034595	1	0.994562	91.14585
SMART	SM00423:F	4	0.58651	0.180118	NM_01366	292	46	9131	2.719178	1	0.973929	91.73577
UP_SEQ_FI	domain:Sei	3	0.439883	0.215206	NM_01366	498	28	16021	3.446859	1	0.999954	98.12908
INTERPRO	IPR001627	3	0.439883	0.221924	NM_01366	509	31	17763	3.37721	1	0.99849	98.00541
SMART	SM00630:S	3	0.439883	0.259676	NM_01366	292	31	9131	3.026182	1	0.98694	97.7056
KEGG_PAT	mmu0436C	5	0.733138	0.469526	NM_01366	155	131	5738	1.412952	1	0.919277	99.93845

Annotation Enrichment Score: 0.6347575422017956

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	extracellular	10	1.466276	0.176394	NM_14558	526	213	17854	1.593566	1	0.823306	93.2784
GOTERM_	GO:000557	12	1.759531	0.245953	AK134774,	363	297	12504	1.391769	1	0.947263	97.56166
GOTERM_	GO:003101	12	1.759531	0.287338	AK134774,	363	309	12504	1.33772	1	0.943231	98.83966

Annotation Enrichment Score: 0.6345605569287548

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	Symport	7	1.026393	0.102285	AK049846,	526	109	17854	2.179823	1	0.792077	77.71308
GOTERM_	GO:001529	7	1.026393	0.159976	AK049846,	369	132	13288	1.909666	1	0.93224	92.01471
GOTERM_	GO:001517	4	0.58651	0.160417	NM_01032	369	50	13288	2.880867	1	0.927396	92.07519
GOTERM_	GO:001517	3	0.439883	0.191213	NM_15313	369	29	13288	3.725259	1	0.938295	95.39032
GOTERM_	GO:000527	4	0.58651	0.253468	NM_01032	369	63	13288	2.286403	1	0.959124	98.55685
INTERPRO	IPR011701	4	0.58651	0.470094	AK049846,	509	89	17763	1.568442	1	0.999892	99.99502
GOTERM_	GO:001529	3	0.439883	0.604413	NM_15313	369	73	13288	1.479898	1	0.993728	99.99986

Annotation Enrichment Score: 0.6239827608427387

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_FI	nucleotide	5	0.733138	0.105163	NM_01001	498	58	16021	2.773335	1	0.998157	83.86725
UP_SEQ_FI	binding site	3	0.439883	0.147874	NM_01001	498	22	16021	4.386911	1	0.999449	92.77251
GOTERM_	GO:004803	10	1.466276	0.176813	NM_02963	369	226	13288	1.5934	1	0.931994	94.04611
SP_PIR_KE	FAD	6	0.879765	0.217707	NM_01001	526	109	17854	1.86842	1	0.860434	96.71503
GOTERM_	GO:005066	4	0.58651	0.314006	NM_17517	369	71	13288	2.02878	1	0.965043	99.57657
GOTERM_	GO:000905	8	1.173021	0.330585	NM_17517	369	202	13288	1.426172	1	0.960902	99.70302

SP_PIR_KE\Flavoprote	5	0.733138	0.359284	NM_01001	526	103	17854	1.647717	1	0.908973	99.79569
GOTERM_↑GO:005066	6	0.879765	0.456391	NM_17517	369	160	13288	1.350407	1	0.980757	99.98548

Annotation Enrichment Score: 0.6004015314178583

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_↑GO:000418		3	0.439883	0.122983	NM_01969	369	22	13288	4.910569	1	0.929335	85.08353
INTERPRO	IPR000834	3	0.439883	0.169649	NM_01969	509	26	17763	4.026674	1	0.996997	94.4994
SMART	SM00631:2	3	0.439883	0.200368	NM_01969	292	26	9131	3.60814	1	0.976809	93.96264
GOTERM_↑GO:000823		3	0.439883	0.232085	NM_01969	369	33	13288	3.273713	1	0.950901	97.82662
SP_PIR_KE\carboxypep		3	0.439883	0.242152	NM_01969	526	32	17854	3.182153	1	0.872035	97.88787
GOTERM_↑GO:000418		3	0.439883	0.252734	NM_01969	369	35	13288	3.086643	1	0.961391	98.53615
SP_PIR_KE\metallopro		7	1.026393	0.259913	NM_01969	526	146	17854	1.627402	1	0.879039	98.48144
GOTERM_↑GO:000823		8	1.173021	0.261715	NM_01969	369	187	13288	1.540571	1	0.961264	98.77155
UP_SEQ_F\active site:		7	1.026393	0.421866	NM_01969	498	168	16021	1.340445	1	0.999999	99.98762
GOTERM_↑GO:000823		3	0.439883	0.581476	NM_01969	369	70	13288	1.543322	1	0.99306	99.99967

Annotation Enrichment Score: 0.5598589065299753

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_↑GO:000181		7	1.026393	0.223108	NM_00103	399	139	13588	1.715007	1	0.974523	98.60937
GOTERM_↑GO:000181		4	0.58651	0.272777	NM_00108	399	62	13588	2.197106	1	0.978453	99.54575
GOTERM_↑GO:005124		7	1.026393	0.343637	NM_00811	399	163	13588	1.462491	1	0.985827	99.91997

Annotation Enrichment Score: 0.5555949910550761

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_F\lipid moiety		9	1.319648	0.177718	NM_00921	498	175	16021	1.654492	1	0.99986	95.97486
SP_PIR_KE\palmitate		9	1.319648	0.260376	NM_00921	526	206	17854	1.482945	1	0.875012	98.49459
SP_PIR_KE\lipoprotein		19	2.785924	0.465462	NM_00114	526	589	17854	1.094934	1	0.942862	99.98357

Annotation Enrichment Score: 0.5463681745339464

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_↑GO:004306		24	3.519062	0.064631	NM_17517	399	560	13588	1.459506	1	0.913574	67.74592
GOTERM_↑GO:001094		24	3.519062	0.068247	NM_17517	399	563	13588	1.451729	1	0.90425	69.79346
GOTERM_↑GO:004298		23	3.372434	0.090067	NM_17517	399	553	13588	1.416398	1	0.937151	79.77857
GOTERM_↑GO:000691		6	0.879765	0.115789	NM_01082	399	88	13588	2.321941	1	0.94421	87.55755
GOTERM_↑GO:004306		10	1.466276	0.265409	NM_01082	399	239	13588	1.424901	1	0.978089	99.46119

GOTERM_	GO:004306	10	1.466276	0.287521	NM_01082	399	244	13588	1.395702	1	0.980727	99.6789
GOTERM_	GO:006054	10	1.466276	0.291199	NM_01082	399	245	13588	1.390006	1	0.980381	99.70585
GOTERM_	GO:004306	9	1.319648	0.45053	NM_17517	399	250	13588	1.225985	1	0.992202	99.99606
GOTERM_	GO:001094	9	1.319648	0.459324	NM_17517	399	252	13588	1.216255	1	0.992512	99.997
GOTERM_	GO:004306	8	1.173021	0.593189	NM_17517	399	248	13588	1.098553	1	0.99676	99.99998
GOTERM_	GO:004352	3	0.439883	0.684366	NM_00855	399	80	13588	1.277068	1	0.99837	100
GOTERM_	GO:00125C	3	0.439883	0.958696	NM_17517	399	167	13588	0.611769	1	0.999999	100
GOTERM_	GO:000691	3	0.439883	0.958696	NM_17517	399	167	13588	0.611769	1	0.999999	100

Annotation Enrichment Score: 0.5459935561111189

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR000884	4	0.58651	0.238058	NM_14558	509	59	17763	2.365955	1	0.99847	98.56161
SMART	SM00209:T	4	0.58651	0.290276	NM_14558	292	59	9131	2.120037	1	0.978675	98.64942
UP_SEQ_FI	domain:TSI	3	0.439883	0.307798	NM_14558	498	36	16021	2.68089	1	0.999995	99.76183
UP_SEQ_FI	domain:TSI	3	0.439883	0.307798	NM_14558	498	36	16021	2.68089	1	0.999995	99.76183

Annotation Enrichment Score: 0.543852566554085

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000669	3	0.439883	0.14489	NM_05327	399	23	13588	4.441975	1	0.957773	92.94063
GOTERM_	GO:00082C	5	0.733138	0.14896	NM_03321	399	70	13588	2.43251	1	0.960208	93.48857
GOTERM_	GO:001612	5	0.733138	0.188946	NM_03321	399	77	13588	2.211373	1	0.965937	97.11777
GOTERM_	GO:001612	3	0.439883	0.218984	NM_05327	399	30	13588	3.405514	1	0.974097	98.47892
GOTERM_	GO:00082C	7	1.026393	0.333219	NM_03321	399	161	13588	1.480658	1	0.985278	99.89551
GOTERM_	GO:000669	3	0.439883	0.620014	NM_05327	399	71	13588	1.438949	1	0.997175	99.99999
GOTERM_	GO:000861	7	1.026393	0.845362	NM_05327	399	285	13588	0.836442	1	0.999901	100

Annotation Enrichment Score: 0.5407566034284631

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:005125	5	0.733138	0.160033	NM_02817	399	72	13588	2.36494	1	0.965643	94.78381
GOTERM_	GO:000646	10	1.466276	0.222521	NM_02817	399	227	13588	1.500226	1	0.975015	98.59144
GOTERM_	GO:007027	10	1.466276	0.222521	NM_02817	399	227	13588	1.500226	1	0.975015	98.59144
GOTERM_	GO:004393	14	2.052786	0.273287	NM_00945	399	367	13588	1.299106	1	0.978068	99.55112
GOTERM_	GO:00650C	13	1.906158	0.289054	NM_00945	399	338	13588	1.309813	1	0.980203	99.6904
GOTERM_	GO:004362	5	0.733138	0.38997	NM_00945	399	108	13588	1.576627	1	0.990666	99.97683
GOTERM_	GO:003462	9	1.319648	0.427716	NM_00945	399	245	13588	1.251005	1	0.991483	99.99215

GOTERM_	GO:003462	8	1.173021	0.452078	NM_00945	399	217	13588	1.255489	1	0.992206	99.99624

Annotation Enrichment Score: 0.5347649741914914

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:001648	5	0.733138	0.270384	NM_05327	399	90	13588	1.891952	1	0.978735	99.51977
GOTERM_	GO:00516C	4	0.58651	0.296836	NM_05327	399	65	13588	2.095701	1	0.98162	99.74305
GOTERM_	GO:00516C	5	0.733138	0.30989	NM_05327	399	96	13588	1.773705	1	0.983052	99.81292

Annotation Enrichment Score: 0.5301177075174888

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	'mitogen	3	0.439883	0.275109	NM_01078	526	35	17854	2.909397	1	0.878442	98.86216
GOTERM_	GO:005178	3	0.439883	0.284552	NM_01078	399	36	13588	2.837928	1	0.98029	99.65547
GOTERM_	GO:00513C	3	0.439883	0.32808	NM_01078	399	40	13588	2.554135	1	0.985202	99.881

Annotation Enrichment Score: 0.520424931067439

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000077	4	0.58651	0.197792	NM_17826	363	53	12504	2.599719	1	0.949524	94.49413
GOTERM_	GO:000077	6	0.879765	0.21905	NM_14592	363	111	12504	1.861961	1	0.938689	96.13291
GOTERM_	GO:000077	4	0.58651	0.251341	NM_17826	363	60	12504	2.296419	1	0.939292	97.7812
SP_PIR_KE	'kinetochor	4	0.58651	0.266735	NM_17826	526	61	17854	2.225768	1	0.87338	98.665
GOTERM_	GO:000077	4	0.58651	0.267034	NM_17826	363	62	12504	2.222341	1	0.945143	98.32086
GOTERM_	GO:000079	5	0.733138	0.375026	NM_17826	363	107	12504	1.609639	1	0.961849	99.79374
GOTERM_	GO:004442	11	1.612903	0.439678	NM_14592	363	318	12504	1.191538	1	0.964559	99.95096
GOTERM_	GO:000569	12	1.759531	0.536713	NM_14592	363	378	12504	1.093533	1	0.980438	99.99598

Annotation Enrichment Score: 0.5127421153589568

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:003527	5	0.733138	0.160033	NM_01082	399	72	13588	2.36494	1	0.965643	94.78381
GOTERM_	GO:002198	3	0.439883	0.208152	NM_00103	399	29	13588	3.522945	1	0.970958	98.0793
GOTERM_	GO:002153	3	0.439883	0.306381	NM_00103	399	38	13588	2.688564	1	0.982528	99.79614
GOTERM_	GO:00309C	4	0.58651	0.871324	NM_00103	399	167	13588	0.815692	1	0.999947	100

Annotation Enrichment Score: 0.5088569212519516

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000701	6	0.879765	0.174525	NM_00945	399	101	13588	2.023077	1	0.97023	96.11536

GOTERM_↑GO:000377	4	0.58651	0.32925	AK052046,	369	73	13288	1.973197	1	0.962221	99.69432
GOTERM_↑GO:000377	6	0.879765	0.335677	AK052046,	369	138	13288	1.565689	1	0.961354	99.73414
INTERPRO IPR001752	3	0.439883	0.359783	AK052046,	509	44	17763	2.379398	1	0.999691	99.90482
SMART SM00129:k	3	0.439883	0.411501	AK052046,	292	44	9131	2.132083	1	0.988465	99.87138

Annotation Enrichment Score: 0.5064659028812163

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_↑GO:004308		6	0.879765	0.137129	NM_00116	399	93	13588	2.197106	1	0.951037	91.77348
GOTERM_↑GO:000804		11	1.612903	0.154787	NM_17517	369	249	13288	1.59084	1	0.942038	91.26883
GOTERM_↑GO:003231		5	0.733138	0.207037	NM_00116	399	80	13588	2.128446	1	0.971225	98.03296
GOTERM_↑GO:005133		9	1.319648	0.217723	NM_17517	399	196	13588	1.563756	1	0.974275	98.43677
GOTERM_↑GO:000509		8	1.173021	0.284836	NM_00811	369	192	13288	1.500452	1	0.961585	99.22554
GOTERM_↑GO:006058		13	1.906158	0.322969	NM_00100	369	367	13288	1.275588	1	0.961238	99.65008
GOTERM_↑GO:003069		12	1.759531	0.419138	NM_00100	369	361	13288	1.197036	1	0.976545	99.96205
GOTERM_↑GO:005105		8	1.173021	0.510221	NM_00116	399	228	13588	1.194917	1	0.994538	99.99944
GOTERM_↑GO:004657		6	0.879765	0.615341	NM_00116	399	181	13588	1.1289	1	0.997077	99.99999
GOTERM_↑GO:000508		6	0.879765	0.743942	NM_00811	369	223	13288	0.968902	1	0.9985	100

Annotation Enrichment Score: 0.5045145670585109

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
KEGG_PAT mmu04110		7	1.026393	0.128895	NM_00763	155	128	5738	2.024496	1	0.83597	79.99496
KEGG_PAT mmu04114		5	0.733138	0.372509	NM_00763	155	115	5738	1.609537	1	0.929653	99.56366
KEGG_PAT mmu04914		4	0.58651	0.400511	NM_01980	155	85	5738	1.742087	1	0.916473	99.74377
KEGG_PAT mmu04120		5	0.733138	0.498833	NM_01980	155	136	5738	1.361006	1	0.91904	99.96828

Annotation Enrichment Score: 0.5020428162618962

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_↑GO:000701		15	2.199413	0.099094	NM_01165	399	326	13588	1.566954	1	0.943195	82.9204
GOTERM_↑GO:003003		6	0.879765	0.532867	NM_00116	399	165	13588	1.238369	1	0.994754	99.99975
GOTERM_↑GO:003002		6	0.879765	0.590478	NM_00116	399	176	13588	1.160971	1	0.996824	99.99997

Annotation Enrichment Score: 0.49345503497822363

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_↑GO:004316		120	17.59531	0.10319	NM_17517	369	3885	13288	1.112304	1	0.91676	79.38448
GOTERM_↑GO:004687		118	17.30205	0.125315	NM_17517	369	3850	13288	1.103709	1	0.925982	85.64854

GOTERM_↑GO:004316	120	17.59531	0.134673	NM_17517	369	3934	13288	1.09845	1	0.933607	87.72103
GOTERM_↑GO:004691	78	11.43695	0.281844	NM_01969	369	2608	13288	1.077011	1	0.964652	99.17721
GOTERM_↑GO:000827	59	8.651026	0.539757	NM_01969	369	2105	13288	1.00933	1	0.990747	99.9987
SP_PIR_KE' metal-bind	77	11.29032	0.657562	NM_01880	526	2682	17854	0.9745	1	0.983244	99.99997
SP_PIR_KE' zinc	52	7.624633	0.759852	NM_01969	526	1886	17854	0.935861	1	0.992684	100
SP_PIR_KE' zinc-finger	31	4.545455	0.85224	NM_17512	526	1204	17854	0.873947	1	0.996913	100

Annotation Enrichment Score: 0.47888274700492856

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE'	acute phas	3	0.439883	0.156142	NM_00116	526	24	17854	4.242871	1	0.827229	90.57583
GOTERM_↑GO:	000695	9	1.319648	0.339152	NM_00116	399	225	13588	1.362206	1	0.98518	99.91018
GOTERM_↑GO:	000252	3	0.439883	0.690936	NM_00116	399	81	13588	1.261301	1	0.99852	100

Annotation Enrichment Score: 0.4673832581187551

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_↑GO:	000688	3	0.439883	0.016301	NM_02806	399	7	13588	14.59506	1	0.983916	24.29584
GOTERM_↑GO:	005506	3	0.439883	0.021317	NM_02806	399	8	13588	12.77068	1	0.985175	30.57488
GOTERM_↑GO:	000687	11	1.612903	0.237992	NM_17517	399	261	13588	1.435274	1	0.975428	98.99783
GOTERM_↑GO:	005508	11	1.612903	0.261369	NM_17517	399	268	13588	1.397786	1	0.978966	99.40875
GOTERM_↑GO:	00300C	6	0.879765	0.356163	NM_17765	399	134	13588	1.524857	1	0.98773	99.94225
GOTERM_↑GO:	00508C	11	1.612903	0.35814	NM_17517	399	293	13588	1.278521	1	0.9878	99.94518
GOTERM_↑GO:	001972	12	1.759531	0.422651	NM_17517	399	343	13588	1.191433	1	0.991632	99.99088
GOTERM_↑GO:	005506	6	0.879765	0.42605	NM_17765	399	146	13588	1.399526	1	0.991469	99.99175
GOTERM_↑GO:	00300C	6	0.879765	0.460532	NM_17765	399	152	13588	1.344282	1	0.992479	99.99711
GOTERM_↑GO:	000687	4	0.58651	0.564671	NM_17765	399	100	13588	1.362206	1	0.995995	99.99992
GOTERM_↑GO:	005506	4	0.58651	0.604349	NM_17765	399	106	13588	1.2851	1	0.996923	99.99998
GOTERM_↑GO:	005508	6	0.879765	0.629828	NM_17765	399	184	13588	1.110494	1	0.997276	100
GOTERM_↑GO:	004887	11	1.612903	0.630554	NM_17517	399	365	13588	1.026319	1	0.997253	100
GOTERM_↑GO:	00423C	4	0.58651	0.681791	NM_17517	399	119	13588	1.144711	1	0.998329	100
GOTERM_↑GO:	000687	3	0.439883	0.750604	NM_17765	399	91	13588	1.122697	1	0.999319	100
GOTERM_↑GO:	005507	3	0.439883	0.771554	NM_17765	399	95	13588	1.075425	1	0.999529	100
GOTERM_↑GO:	00425C	13	1.906158	0.926535	NM_02127	399	584	13588	0.758077	1	0.999993	100

Annotation Enrichment Score: 0.46626461162141475

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR

GOTERM_	GO:001403	3	0.439883	0.251711	NM_01144	399	33	13588	3.095922	1	0.976491	99.26326
GOTERM_	GO:001403	3	0.439883	0.251711	NM_01144	399	33	13588	3.095922	1	0.976491	99.26326
GOTERM_	GO:001403	3	0.439883	0.402233	NM_01144	399	47	13588	2.173732	1	0.991032	99.98358
GOTERM_	GO:004876	3	0.439883	0.422731	NM_01144	399	49	13588	2.085008	1	0.991443	99.9909
GOTERM_	GO:006048	3	0.439883	0.432843	NM_01144	399	50	13588	2.043308	1	0.991545	99.99326

Annotation Enrichment Score: 0.4531202689163125

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	extracellular	10	1.466276	0.176394	NM_14558	526	213	17854	1.593566	1	0.823306	93.2784
INTERPRO	IPR002035	4	0.58651	0.46269	NM_14777	509	88	17763	1.586265	1	0.999886	99.99382
SMART	SM00327:\	4	0.58651	0.535631	NM_14777	292	88	9131	1.421389	1	0.99211	99.99343

Annotation Enrichment Score: 0.4490657602458108

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000392	7	1.026393	0.144628	NM_00945	369	128	13288	1.969343	1	0.935029	89.61738
GOTERM_	GO:000552	13	1.906158	0.278084	NM_00945	369	354	13288	1.322432	1	0.965066	99.11249
GOTERM_	GO:001900	13	1.906158	0.308169	NM_00945	369	363	13288	1.289644	1	0.964378	99.52123
GOTERM_	GO:003256	13	1.906158	0.308169	NM_00945	369	363	13288	1.289644	1	0.964378	99.52123
SP_PIR_KE	gtp-binding	9	1.319648	0.705279	NM_13364	526	313	17854	0.975996	1	0.987783	100
UP_SEQ_FI	nucleotide	8	1.173021	0.750306	NM_00945	498	274	16021	0.93929	1	1	100

Annotation Enrichment Score: 0.447810809476957

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR011511	5	0.733138	0.088132	NM_17244	509	59	17763	2.957444	1	0.981321	76.29152
INTERPRO	IPR001452	8	1.173021	0.399928	NM_17244	509	211	17763	1.323141	1	0.999838	99.96534
SMART	SM00326:S	8	1.173021	0.512101	NM_17244	292	211	9131	1.185613	1	0.990686	99.98778
SP_PIR_KE	sh3 domain	7	1.026393	0.557412	NM_17244	526	204	17854	1.16471	1	0.970407	99.99881
UP_SEQ_FI	domain:SH	6	0.879765	0.573189	NM_01186	498	163	16021	1.184197	1	1	99.99992

Annotation Enrichment Score: 0.4437311943286627

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR004827	4	0.58651	0.200454	NM_01090	509	54	17763	2.585025	1	0.997849	96.95018
SMART	SM00338:E	4	0.58651	0.246835	NM_01090	292	54	9131	2.316337	1	0.98778	97.1527
UP_SEQ_FI	DNA-binding	6	0.879765	0.522521	NM_03321	498	154	16021	1.253403	1	1	99.99946
UP_SEQ_FI	domain:Lei	4	0.58651	0.649457	NM_03321	498	107	16021	1.202642	1	1	100

Annotation Enrichment Score: 0.4415735564445817

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR001478	7	1.026393	0.249791	XM_14897	509	148	17763	1.650573	1	0.998511	98.87088
SMART	SM00228:F	7	1.026393	0.333181	XM_14897	292	148	9131	1.479012	1	0.979717	99.38265
UP_SEQ_FI	domain:PD	4	0.58651	0.568883	NM_00102	498	95	16021	1.354555	1	1	99.9999

Annotation Enrichment Score: 0.4400171213153229

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:001605	5	0.733138	0.213176	XR_032386	399	81	13588	2.102169	1	0.972798	98.27556
GOTERM_	GO:001931	8	1.173021	0.227282	NM_17301	399	169	13588	1.612078	1	0.974961	98.7306
GOTERM_	GO:000600	7	1.026393	0.227849	XR_032386	399	140	13588	1.702757	1	0.974473	98.7463
KEGG_PAT	mmu00010	4	0.58651	0.275097	XR_032386	155	68	5738	2.177609	1	0.916182	97.65213
GOTERM_	GO:000595	8	1.173021	0.327398	NM_17301	399	191	13588	1.426393	1	0.985419	99.87894
SP_PIR_KE	glycolysis	3	0.439883	0.351326	XR_032386	526	42	17854	2.424498	1	0.905815	99.75741
GOTERM_	GO:000605	3	0.439883	0.370864	XR_032386	399	44	13588	2.321941	1	0.98893	99.96095
GOTERM_	GO:001932	3	0.439883	0.452779	XR_032386	399	52	13588	1.964719	1	0.992113	99.99632
GOTERM_	GO:000600	3	0.439883	0.452779	XR_032386	399	52	13588	1.964719	1	0.992113	99.99632
GOTERM_	GO:004636	3	0.439883	0.472309	XR_032386	399	54	13588	1.891952	1	0.992941	99.99801
GOTERM_	GO:000605	9	1.319648	0.502633	NM_17517	399	261	13588	1.174315	1	0.994269	99.99927
GOTERM_	GO:004427	3	0.439883	0.528289	XR_032386	399	60	13588	1.702757	1	0.994725	99.9997
GOTERM_	GO:004616	3	0.439883	0.57177	XR_032386	399	65	13588	1.571776	1	0.996096	99.99994

Annotation Enrichment Score: 0.43918375022804285

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000275	3	0.439883	0.176063	NM_00849	399	26	13588	3.929439	1	0.96907	96.23613
GOTERM_	GO:004688	3	0.439883	0.284552	NM_00849	399	36	13588	2.837928	1	0.98029	99.65547
GOTERM_	GO:005104	5	0.733138	0.500434	NM_00988	399	125	13588	1.362206	1	0.994455	99.99921
GOTERM_	GO:006034	5	0.733138	0.698374	NM_00988	399	161	13588	1.057613	1	0.998624	100

Annotation Enrichment Score: 0.4357922373142862

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:005133	9	1.319648	0.217723	NM_17517	399	196	13588	1.563756	1	0.974275	98.43677
GOTERM_	GO:004328	3	0.439883	0.432843	NM_17517	399	50	13588	2.043308	1	0.991545	99.99326
GOTERM_	GO:005254	3	0.439883	0.432843	NM_17517	399	50	13588	2.043308	1	0.991545	99.99326

GOTERM_	GO:005254	3	0.439883	0.44286	NM_17517	399	51	13588	2.003243	1	0.991836	99.99501

Annotation Enrichment Score: 0.43196313731226754

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:003003	16	2.346041	0.048953	NM_00945	399	319	13588	1.708095	1	0.925479	57.25903
GOTERM_	GO:003117	10	1.466276	0.190423	NM_02139	399	218	13588	1.562162	1	0.965884	97.20543
GOTERM_	GO:004866	12	1.759531	0.233191	NM_02139	399	292	13588	1.399526	1	0.974714	98.88535
GOTERM_	GO:003018	15	2.199413	0.280177	NM_00100	399	399	13588	1.280268	1	0.97937	99.618
GOTERM_	GO:000090	12	1.759531	0.297092	NM_01144	399	309	13588	1.32253	1	0.981221	99.74463
GOTERM_	GO:003298	13	1.906158	0.330459	NM_01032	399	351	13588	1.261301	1	0.985381	99.88793
GOTERM_	GO:004885	8	1.173021	0.379506	NM_02139	399	202	13588	1.348718	1	0.989819	99.9691
GOTERM_	GO:000090	8	1.173021	0.428148	NM_01144	399	212	13588	1.2851	1	0.99134	99.99225
GOTERM_	GO:003299	8	1.173021	0.428148	NM_02139	399	212	13588	1.2851	1	0.99134	99.99225
GOTERM_	GO:000740	6	0.879765	0.522005	NM_02139	399	163	13588	1.253563	1	0.994788	99.99963
GOTERM_	GO:000741	4	0.58651	0.550919	NM_00103	399	98	13588	1.390006	1	0.995555	99.99987
GOTERM_	GO:004881	6	0.879765	0.590478	NM_02139	399	176	13588	1.160971	1	0.996824	99.99997
GOTERM_	GO:004866	6	0.879765	0.620207	NM_02139	399	182	13588	1.122697	1	0.997126	99.99999
GOTERM_	GO:000165	4	0.58651	0.842889	NM_02139	399	157	13588	0.867647	1	0.999901	100
GOTERM_	GO:004301	3	0.439883	0.89789	NM_02139	399	130	13588	0.785888	1	0.999977	100

Annotation Enrichment Score: 0.4171630037459058

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:004654	4	0.58651	0.202442	NM_01144	399	53	13588	2.570199	1	0.969507	97.83077
GOTERM_	GO:004666	4	0.58651	0.233241	NM_01144	399	57	13588	2.389834	1	0.974001	98.88658
GOTERM_	GO:000300	11	1.612903	0.250601	NM_14614	399	264	13588	1.418964	1	0.977334	99.24453
GOTERM_	GO:000858	3	0.439883	0.31725	NM_01144	399	39	13588	2.619626	1	0.983728	99.84399
GOTERM_	GO:000754	5	0.733138	0.531335	NM_01144	399	130	13588	1.309813	1	0.994744	99.99973
GOTERM_	GO:004860	5	0.733138	0.531335	NM_01144	399	130	13588	1.309813	1	0.994744	99.99973
GOTERM_	GO:004513	4	0.58651	0.591392	NM_01144	399	104	13588	1.309813	1	0.996803	99.99997
GOTERM_	GO:000840	3	0.439883	0.733827	NM_01144	399	88	13588	1.160971	1	0.999155	100

Annotation Enrichment Score: 0.4090631008984598

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000823	9	1.319648	0.05023	AK028249,	369	146	13288	2.219846	1	0.835316	52.63165
SP_PIR_KE	thiol protei	6	0.879765	0.283964	AK028249,	526	121	17854	1.683122	1	0.879643	99.041

INTERPRO	IPR018200	3	0.439883	0.450162	AK028249,	509	53	17763	1.975349	1	0.999861	99.99114
INTERPRO	IPR001394	3	0.439883	0.48798	AK028249,	509	57	17763	1.836728	1	0.999911	99.99709
GOTERM_	GO:000422	3	0.439883	0.589229	AK028249,	369	71	13288	1.521585	1	0.993413	99.99975
GOTERM_	GO:001679	3	0.439883	0.804888	AK028249,	369	108	13288	1.000301	1	0.999425	100
GOTERM_	GO:000651	3	0.439883	0.921604	AK028249,	399	141	13588	0.724577	1	0.999991	100

Annotation Enrichment Score: 0.4079921405207906

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:004443	28	4.105572	0.180963	NM_01688	363	774	12504	1.246119	1	0.958509	92.76487
GOTERM_	GO:000585	36	5.278592	0.342162	NM_01688	363	1122	12504	1.105228	1	0.95726	99.59521
GOTERM_	GO:004322	55	8.064516	0.61391	NM_01688	363	1919	12504	0.987257	1	0.984389	99.99963
GOTERM_	GO:004323	55	8.064516	0.61391	NM_01688	363	1919	12504	0.987257	1	0.984389	99.99963

Annotation Enrichment Score: 0.38837482905278176

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:001064	9	1.319648	0.190916	NM_01082	399	189	13588	1.621673	1	0.964107	97.23409
GOTERM_	GO:000996	8	1.173021	0.240313	NM_01082	399	172	13588	1.58396	1	0.97574	99.0483
GOTERM_	GO:004341	3	0.439883	0.402233	NM_00103	399	47	13588	2.173732	1	0.991032	99.98358
GOTERM_	GO:004340	4	0.58651	0.515452	NM_01049	399	93	13588	1.464737	1	0.994725	99.99953
GOTERM_	GO:001062	5	0.733138	0.669687	NM_01049	399	155	13588	1.098553	1	0.998099	100
GOTERM_	GO:001074	3	0.439883	0.733827	NM_00103	399	88	13588	1.160971	1	0.999155	100

Annotation Enrichment Score: 0.38145147497676324

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:004338	3	0.439883	0.349591	NM_17283	399	42	13588	2.43251	1	0.986749	99.93141
GOTERM_	GO:005110	4	0.58651	0.369318	NM_17283	399	74	13588	1.840818	1	0.988941	99.95929
GOTERM_	GO:005109	3	0.439883	0.381398	NM_17283	399	45	13588	2.270343	1	0.989862	99.97066
GOTERM_	GO:004409	11	1.612903	0.407683	NM_17517	399	306	13588	1.224204	1	0.991335	99.98594
GOTERM_	GO:005109	4	0.58651	0.493471	NM_17283	399	90	13588	1.513562	1	0.994112	99.99901
GOTERM_	GO:005109	3	0.439883	0.519241	NM_17283	399	59	13588	1.731617	1	0.994796	99.99959

Annotation Enrichment Score: 0.3813556161265222

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_FI	DNA-bindir	3	0.439883	0.342187	NM_01144	498	39	16021	2.474668	1	0.999997	99.89683
INTERPRO	IPR000910	3	0.439883	0.430669	NM_01144	509	51	17763	2.052814	1	0.999849	99.98474

SMART SM00398:1 3 0.439883 0.486997 NM_01144 292 51 9131 1.839444 1 0.990432 99.97705

Annotation Enrichment Score: 0.38076237851497985

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	oxidoreduc	23	3.372434	0.121007	NM_02963	526	572	17854	1.36484	1	0.774817	83.37695
SP_PIR_KE	iron	14	2.052786	0.152809	NM_17517	526	321	17854	1.480379	1	0.828192	90.04458
GOTERM_	GO:00055C	14	2.052786	0.158975	NM_17517	369	343	13288	1.46983	1	0.941602	91.8756
GOTERM_	GO:005511	25	3.665689	0.180856	NM_17517	399	672	13588	1.266932	1	0.964635	96.59026
SP_PIR_KE	heme	7	1.026393	0.240282	NM_00781	526	142	17854	1.673245	1	0.874683	97.81419
GOTERM_	GO:000905	8	1.173021	0.330585	NM_17517	369	202	13288	1.426172	1	0.960902	99.70302
GOTERM_	GO:002003	6	0.879765	0.36872	NM_00781	369	144	13288	1.500452	1	0.968256	99.87312
UP_SEQ_F	metal ion-k	5	0.733138	0.368968	NM_00781	498	99	16021	1.624782	1	0.999998	99.94786
SP_PIR_KE	nadp	6	0.879765	0.406028	NM_02596	526	142	17854	1.43421	1	0.922621	99.92878
GOTERM_	GO:00469C	6	0.879765	0.407297	NM_00781	369	151	13288	1.430894	1	0.975545	99.94915
INTERPRO	IPR002401	3	0.439883	0.59897	NM_00781	509	70	17763	1.495622	1	0.999988	99.99994
INTERPRO	IPR017973	3	0.439883	0.677972	NM_00781	509	81	17763	1.292513	1	0.999995	100
INTERPRO	IPR001128	3	0.439883	0.715451	NM_00781	509	87	17763	1.203374	1	0.999997	100
INTERPRO	IPR017972	3	0.439883	0.727105	NM_00781	509	89	17763	1.176332	1	0.999998	100
COG_ONTC	Secondary	3	0.439883	0.748224	NM_00781	50	109	2040	1.122936	1	0.990807	99.9954
GOTERM_	GO:000579	5	0.733138	0.754245	NM_00781	363	176	12504	0.978588	1	0.989194	100
GOTERM_	GO:004259	5	0.733138	0.776977	NM_00781	363	182	12504	0.946326	1	0.990664	100
SP_PIR_KE	microsome	3	0.439883	0.797106	NM_00781	526	100	17854	1.018289	1	0.995289	100
SP_PIR_KE	Monooxyg	3	0.439883	0.830755	NM_00781	526	108	17854	0.94286	1	0.996412	100

Annotation Enrichment Score: 0.36209241941014797

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:003294	9	1.319648	0.179978	NM_01880	399	186	13588	1.647829	1	0.966245	96.52785
GOTERM_	GO:00469C	9	1.319648	0.321657	NM_01880	399	221	13588	1.386861	1	0.984433	99.86019
GOTERM_	GO:000688	5	0.733138	0.403265	NM_01880	399	110	13588	1.547961	1	0.990954	99.98405
SP_PIR_KE	exocytosis	3	0.439883	0.434752	NM_01887	526	50	17854	2.036578	1	0.930684	99.96426
GOTERM_	GO:00030C	3	0.439883	0.709975	NM_00849	399	84	13588	1.216255	1	0.998843	100
GOTERM_	GO:001619	10	1.466276	0.932733	NM_01880	399	466	13588	0.730797	1	0.999995	100

Annotation Enrichment Score: 0.3613085246257001

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR

UP_SEQ_Fl domain:Ca	3	0.439883	0.096149	NM_00988	498	17	16021	5.677179	1	0.998068	80.98139
UP_SEQ_Fl domain:Ca	3	0.439883	0.31931	NM_00988	498	37	16021	2.608434	1	0.999995	99.81916
UP_SEQ_Fl domain:Ca	3	0.439883	0.39817	NM_00988	498	44	16021	2.193456	1	0.999999	99.97605
UP_SEQ_Fl domain:Ca	3	0.439883	0.409109	NM_00988	498	45	16021	2.144712	1	0.999999	99.98228
UP_SEQ_Fl domain:Ca	3	0.439883	0.441321	NM_00988	498	48	16021	2.010668	1	0.999999	99.99294
UP_SEQ_Fl domain:Ca	3	0.439883	0.441321	NM_00988	498	48	16021	2.010668	1	0.999999	99.99294
INTERPRO IPR002126	3	0.439883	0.79335	NM_00988	509	102	17763	1.026407	1	1	100
SMART SM00112:C	3	0.439883	0.841423	NM_00988	292	102	9131	0.919722	1	0.999909	100
GOTERM_!GO:000715	3	0.439883	0.861328	NM_00988	399	117	13588	0.873209	1	0.999934	100

Annotation Enrichment Score: 0.35692708921964716

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:001984		5	0.733138	0.432306	NM_00823	369	121	13288	1.488051	1	0.978938	99.97278
GOTERM_!GO:007027		3	0.439883	0.443316	NM_00823	369	54	13288	2.000602	1	0.97961	99.97951
GOTERM_!GO:003017		3	0.439883	0.443316	NM_00823	369	54	13288	2.000602	1	0.97961	99.97951

Annotation Enrichment Score: 0.346109843405604

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:003258		5	0.733138	0.132939	NM_01082	399	67	13588	2.541428	1	0.953109	91.07009
GOTERM_!GO:001055		4	0.58651	0.187426	NM_01082	399	51	13588	2.670991	1	0.965964	97.02492
GOTERM_!GO:000635		22	3.225806	0.266114	NM_01176	399	616	13588	1.216255	1	0.97776	99.46988
GOTERM_!GO:004589		11	1.612903	0.418621	NM_01144	399	308	13588	1.216255	1	0.991316	99.98974
GOTERM_!GO:005125		11	1.612903	0.423407	NM_01144	399	310	13588	1.208408	1	0.991329	99.99108
GOTERM_!GO:003132		14	2.052786	0.491082	NM_01176	399	430	13588	1.108772	1	0.994163	99.99892
GOTERM_!GO:004593		13	1.906158	0.502262	NM_01176	399	397	13588	1.115156	1	0.994362	99.99926
GOTERM_!GO:005117		13	1.906158	0.51384	NM_01176	399	401	13588	1.104032	1	0.994712	99.9995
GOTERM_!GO:001648		12	1.759531	0.526487	NM_01144	399	372	13588	1.098553	1	0.994694	99.99968
GOTERM_!GO:000989		14	2.052786	0.53035	NM_01176	399	434	13588	1.098553	1	0.994776	99.99972
GOTERM_!GO:001055		13	1.906158	0.570175	NM_01176	399	418	13588	1.059131	1	0.996162	99.99994
GOTERM_!GO:001062		12	1.759531	0.660083	NM_01144	399	410	13588	0.996736	1	0.997935	100
GOTERM_!GO:000012		7	1.026393	0.674062	NM_01176	399	231	13588	1.031974	1	0.998127	100
GOTERM_!GO:001060		14	2.052786	0.725496	NM_01176	399	506	13588	0.942237	1	0.999085	100
GOTERM_!GO:001656		5	0.733138	0.840272	NM_01176	369	211	13288	0.853337	1	0.999752	100

Annotation Enrichment Score: 0.338625527256511

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR000483	5	0.733138	0.213559	NM_20151	509	83	17763	2.102279	1	0.998341	97.6433
INTERPRO	IPR001611	9	1.319648	0.222923	AK089994,	509	202	17763	1.554854	1	0.998249	98.04499
SMART	SM00082:L	5	0.733138	0.272173	NM_20151	292	83	9131	1.883768	1	0.981882	98.14712
INTERPRO	IPR003591	6	0.879765	0.309571	NM_20151	509	129	17763	1.623155	1	0.999322	99.69088
SMART	SM00369:L	6	0.879765	0.393316	NM_20151	292	129	9131	1.454444	1	0.989833	99.81153
SP_PIR_KE	leucine-ric	10	1.466276	0.418316	AK089994,	526	275	17854	1.23429	1	0.923121	99.94676
UP_SEQ_FI	repeat:LRR	8	1.173021	0.443597	AK089994,	498	203	16021	1.26781	1	0.999999	99.9934
INTERPRO	IPR000372	4	0.58651	0.499234	NM_20151	509	93	17763	1.500982	1	0.999913	99.99794
UP_SEQ_FI	repeat:LRR	7	1.026393	0.51419	AK089994,	498	185	16021	1.217269	1	1	99.99929
UP_SEQ_FI	repeat:LRR	4	0.58651	0.516948	AK089994,	498	88	16021	1.462304	1	1	99.99935
UP_SEQ_FI	repeat:LRR	5	0.733138	0.526512	AK089994,	498	122	16021	1.318471	1	1	99.99953
UP_SEQ_FI	repeat:LRR	8	1.173021	0.533381	AK089994,	498	221	16021	1.16455	1	1	99.99963
SMART	SM00013:L	4	0.58651	0.573306	NM_20151	292	93	9131	1.34497	1	0.994557	99.99773
UP_SEQ_FI	repeat:LRR	9	1.319648	0.585666	AK089994,	498	266	16021	1.088482	1	1	99.99995
UP_SEQ_FI	repeat:LRR	9	1.319648	0.585666	AK089994,	498	266	16021	1.088482	1	1	99.99995
UP_SEQ_FI	repeat:LRR	5	0.733138	0.594966	AK089994,	498	133	16021	1.209424	1	1	99.99996
UP_SEQ_FI	repeat:LRR	4	0.58651	0.623839	AK089994,	498	103	16021	1.249347	1	1	99.99999
UP_SEQ_FI	repeat:LRR	8	1.173021	0.640452	AK089994,	498	245	16021	1.050471	1	1	99.99999
UP_SEQ_FI	repeat:LRR	5	0.733138	0.722013	AK089994,	498	157	16021	1.024544	1	1	100

Annotation Enrichment Score: 0.3358731201088658

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000809	14	2.052786	0.363146	NM_00108	369	414	13288	1.217758	1	0.967715	99.85588
GOTERM_	GO:001562	8	1.173021	0.387311	NM_00941	363	205	12504	1.344245	1	0.960762	99.84115
GOTERM_	GO:000377	10	1.466276	0.403943	NM_00941	369	288	13288	1.250376	1	0.975794	99.94481
SP_PIR_KE	actin-bindin	6	0.879765	0.79808	NM_00941	526	226	17854	0.901141	1	0.995148	100

Annotation Enrichment Score: 0.3323197497624226

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	Antimicrob	4	0.58651	0.323164	NM_00103	526	68	17854	1.996645	1	0.908996	99.56183
SP_PIR_KE	defensin	3	0.439883	0.444784	NM_00103	526	51	17854	1.996645	1	0.934157	99.97215
GOTERM_	GO:000961	6	0.879765	0.488804	NM_00103	399	157	13588	1.30147	1	0.994094	99.99884
SP_PIR_KE	antibiotic	3	0.439883	0.502788	NM_00103	526	57	17854	1.786472	1	0.95429	99.994
GOTERM_	GO:004274	4	0.58651	0.617033	NM_00103	399	108	13588	1.261301	1	0.997097	99.99999

Annotation Enrichment Score: 0.3269967125605258

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000181	7	1.026393	0.223108	NM_00103	399	139	13588	1.715007	1	0.974523	98.60937
GOTERM_	GO:003264	3	0.439883	0.240776	NM_00103	399	32	13588	3.192669	1	0.975244	99.05806
GOTERM_	GO:000270	4	0.58651	0.296836	NM_00824	399	65	13588	2.095701	1	0.98162	99.74305
GOTERM_	GO:004858	8	1.173021	0.303877	NM_17283	399	186	13588	1.464737	1	0.982722	99.78332
GOTERM_	GO:000270	4	0.58651	0.337145	NM_00824	399	70	13588	1.946008	1	0.985445	99.90545
GOTERM_	GO:000268	8	1.173021	0.40159	NM_17283	399	206	13588	1.32253	1	0.991163	99.98327
GOTERM_	GO:005124	6	0.879765	0.414457	NM_17283	399	144	13588	1.418964	1	0.991389	99.98842
GOTERM_	GO:000269	6	0.879765	0.471899	NM_17283	399	154	13588	1.326824	1	0.993052	99.99799
GOTERM_	GO:000269	4	0.58651	0.478546	NM_00824	399	88	13588	1.547961	1	0.993418	99.99837
GOTERM_	GO:005086	6	0.879765	0.48319	NM_17283	399	156	13588	1.309813	1	0.993719	99.9986
GOTERM_	GO:000282	3	0.439883	0.491414	NM_00824	399	56	13588	1.824382	1	0.994061	99.99894
GOTERM_	GO:000281	3	0.439883	0.491414	NM_00824	399	56	13588	1.824382	1	0.994061	99.99894
GOTERM_	GO:003134	3	0.439883	0.500802	NM_00108	399	57	13588	1.792376	1	0.994362	99.99922
GOTERM_	GO:005125	4	0.58651	0.522666	NM_17283	399	94	13588	1.449155	1	0.994728	99.99964
GOTERM_	GO:000269	4	0.58651	0.557827	NM_17283	399	99	13588	1.375965	1	0.995826	99.9999
GOTERM_	GO:005077	5	0.733138	0.56713	NM_17283	399	136	13588	1.252027	1	0.996062	99.99993
GOTERM_	GO:005086	4	0.58651	0.571451	NM_17283	399	101	13588	1.348718	1	0.996157	99.99994
GOTERM_	GO:004508	4	0.58651	0.610725	NM_00836	399	107	13588	1.273089	1	0.997041	99.99999
GOTERM_	GO:005086	4	0.58651	0.617033	NM_17283	399	108	13588	1.261301	1	0.997097	99.99999
GOTERM_	GO:003294	3	0.439883	0.684366	NM_00824	399	80	13588	1.277068	1	0.99837	100
GOTERM_	GO:005067	3	0.439883	0.684366	NM_00824	399	80	13588	1.277068	1	0.99837	100
GOTERM_	GO:007066	3	0.439883	0.697394	NM_00824	399	82	13588	1.24592	1	0.998656	100
GOTERM_	GO:000225	3	0.439883	0.722116	NM_17283	399	86	13588	1.18797	1	0.999043	100

Annotation Enrichment Score: 0.323080975733843

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	Apoptosis	12	1.759531	0.403762	NM_13364	526	337	17854	1.208652	1	0.923654	99.92491
GOTERM_	GO:001250	16	2.346041	0.41572	NM_17517	399	473	13588	1.151971	1	0.991348	99.98884
GOTERM_	GO:000691	15	2.199413	0.496492	NM_17517	399	465	13588	1.098553	1	0.994246	99.9991
GOTERM_	GO:000821	16	2.346041	0.520385	NM_17517	399	507	13588	1.074718	1	0.994773	99.99961
GOTERM_	GO:001626	16	2.346041	0.559026	NM_17517	399	519	13588	1.049869	1	0.995814	99.9999

Annotation Enrichment Score: 0.3201796718828312

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:001517	4	0.58651	0.160417	NM_01032	369	50	13288	2.880867	1	0.927396	92.07519
GOTERM_	GO:000527	4	0.58651	0.253468	NM_01032	369	63	13288	2.286403	1	0.959124	98.55685
GOTERM_	GO:000686	3	0.439883	0.620014	NM_01032	399	71	13588	1.438949	1	0.997175	99.99999
GOTERM_	GO:001583	3	0.439883	0.755991	NM_01032	399	92	13588	1.110494	1	0.999365	100
GOTERM_	GO:004694	3	0.439883	0.790956	NM_01032	399	99	13588	1.031974	1	0.99965	100
GOTERM_	GO:001584	3	0.439883	0.795574	NM_01032	399	100	13588	1.021654	1	0.99968	100

Annotation Enrichment Score: 0.31188193115242746

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR001810	4	0.58651	0.402009	AK089994,	509	80	17763	1.744892	1	0.99979	99.96717
SMART	SM00256:F	4	0.58651	0.47168	AK089994,	292	80	9131	1.563527	1	0.989979	99.9668
UP_SEQ_FI	domain:F-b	3	0.439883	0.611605	AK089994,	498	66	16021	1.462304	1	1	99.99998

Annotation Enrichment Score: 0.30894225528132424

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR003961	8	1.173021	0.306331	AJ584850,	509	191	17763	1.46169	1	0.999464	99.66747
SMART	SM00060:F	8	1.173021	0.408351	AJ584850,	292	191	9131	1.309761	1	0.990043	99.86247
UP_SEQ_FI	domain:Fib	5	0.733138	0.513473	AJ584850,	498	120	16021	1.340445	1	1	99.99927
UP_SEQ_FI	domain:Fib	5	0.733138	0.520013	AJ584850,	498	121	16021	1.329367	1	1	99.99942
INTERPRO	IPR008957	6	0.879765	0.622632	AJ584850,	509	187	17763	1.119717	1	0.99999	99.99998
UP_SEQ_FI	domain:Fib	3	0.439883	0.673532	AJ584850,	498	74	16021	1.304217	1	1	100

Annotation Enrichment Score: 0.3036184498656572

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR002110	9	1.319648	0.30728	NM_20125	509	223	17763	1.408433	1	0.999384	99.67449
SP_PIR_KE	ank repeat	9	1.319648	0.328573	NM_20125	526	222	17854	1.376066	1	0.906705	99.60811
SMART	SM00248:A	9	1.319648	0.417939	NM_20125	292	223	9131	1.26204	1	0.987383	99.88797
UP_SEQ_FI	repeat:ANK	5	0.733138	0.847841	AK051017,	498	191	16021	0.842164	1	1	100
UP_SEQ_FI	repeat:ANK	5	0.733138	0.847841	AK051017,	498	191	16021	0.842164	1	1	100

Annotation Enrichment Score: 0.2870670693867654

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000170	4	0.58651	0.248945	NM_01144	399	59	13588	2.308823	1	0.977317	99.21574

GOTERM_£GO:004516	5	0.733138	0.628623	NM_01144	399	147	13588	1.158338	1	0.997278	99.99999
SP_PIR_KE'DNA bindir	6	0.879765	0.879642	NM_01144	526	258	17854	0.789371	1	0.998082	100

Annotation Enrichment Score: 0.28009947809624686

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE'	lipid degrad	4	0.58651	0.411494	NM_17735	526	79	17854	1.718631	1	0.92364	99.93738
GOTERM_£	GO:001629	4	0.58651	0.412383	NM_17735	369	84	13288	1.714802	1	0.975809	99.95512
GOTERM_£	GO:000462	3	0.439883	0.524233	NM_17735	369	63	13288	1.714802	1	0.989827	99.9979
GOTERM_£	GO:001604	5	0.733138	0.555364	NM_17735	399	134	13588	1.270714	1	0.995756	99.99989
GOTERM_£	GO:000409	3	0.439883	0.804888	NM_01204	369	108	13288	1.000301	1	0.999425	100

Annotation Enrichment Score: 0.27530805292950394

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_£	GO:00065C	38	5.571848	0.118354	NM_01969	399	1034	13588	1.251543	1	0.941614	88.155
SP_PIR_KE'	ubl conjug	15	2.199413	0.563604	AK089994,	526	484	17854	1.051951	1	0.969925	99.99902
GOTERM_£	GO:00516C	16	2.346041	0.603937	AK089994,	399	534	13588	1.020379	1	0.996965	99.99998
GOTERM_£	GO:004425	16	2.346041	0.61268	AK089994,	399	537	13588	1.014678	1	0.997012	99.99999
GOTERM_£	GO:001994	15	2.199413	0.631384	AK089994,	399	508	13588	1.005565	1	0.997235	100
GOTERM_£	GO:004363	15	2.199413	0.631384	AK089994,	399	508	13588	1.005565	1	0.997235	100
GOTERM_£	GO:000905	19	2.785924	0.642259	AK089994,	399	654	13588	0.989369	1	0.997539	100
GOTERM_£	GO:003016	16	2.346041	0.665887	AK089994,	399	556	13588	0.980004	1	0.998012	100
GOTERM_£	GO:004426	16	2.346041	0.790944	AK089994,	399	609	13588	0.894716	1	0.999658	100

Annotation Enrichment Score: 0.2683784998212667

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_£	GO:000574	4	0.58651	0.409683	XM_00147	363	80	12504	1.722314	1	0.955188	99.90262
GOTERM_£	GO:003196	4	0.58651	0.463367	XM_00147	363	87	12504	1.583737	1	0.970228	99.97222
GOTERM_£	GO:001986	4	0.58651	0.485727	XM_00147	363	90	12504	1.530946	1	0.970801	99.98413
SP_PIR_KE'	mitochond	3	0.439883	0.606395	XM_00147	526	69	17854	1.475781	1	0.976226	99.99977
GOTERM_£	GO:003196	11	1.612903	0.626417	NM_17517	363	368	12504	1.029644	1	0.985526	99.99976
GOTERM_£	GO:000574	11	1.612903	0.700399	NM_17517	363	391	12504	0.969077	1	0.988604	99.99999

Annotation Enrichment Score: 0.2674613624249689

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_£	GO:000194	10	1.466276	0.311658	NM_01082	399	250	13588	1.362206	1	0.983098	99.82087

GOTERM_	GO:004851	7	1.026393	0.524186	NM_01082	399	198	13588	1.20397	1	0.994736	99.99966
GOTERM_	GO:000156	8	1.173021	0.575927	NM_01082	399	244	13588	1.116562	1	0.99626	99.99995
GOTERM_	GO:000152	3	0.439883	0.904947	NM_00112	399	133	13588	0.768161	1	0.999982	100

Annotation Enrichment Score: 0.2604094859010449

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:001701	3	0.439883	0.471154	NM_13364	369	57	13288	1.895307	1	0.983071	99.99026
GOTERM_	GO:003126	3	0.439883	0.489243	NM_13364	369	59	13288	1.83106	1	0.985732	99.99412
GOTERM_	GO:005102	3	0.439883	0.515638	NM_13364	369	62	13288	1.74246	1	0.989228	99.99728
GOTERM_	GO:001989	6	0.879765	0.764416	NM_13364	369	229	13288	0.943515	1	0.998789	100

Annotation Enrichment Score: 0.2580413977342818

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000614	4	0.58651	0.377324	NM_02817	399	75	13588	1.816274	1	0.98973	99.96721
GOTERM_	GO:004576	3	0.439883	0.528289	NM_13384	399	60	13588	1.702757	1	0.994725	99.9997
GOTERM_	GO:005133	3	0.439883	0.546035	NM_13384	399	62	13588	1.647829	1	0.995412	99.99984
GOTERM_	GO:003127	3	0.439883	0.546035	NM_13384	399	62	13588	1.647829	1	0.995412	99.99984
GOTERM_	GO:003081	3	0.439883	0.57177	NM_13384	399	65	13588	1.571776	1	0.996096	99.99994
GOTERM_	GO:003081	3	0.439883	0.588331	NM_13384	399	67	13588	1.524857	1	0.996784	99.99997
GOTERM_	GO:003080	3	0.439883	0.612273	NM_13384	399	70	13588	1.459506	1	0.997054	99.99999
GOTERM_	GO:003080	3	0.439883	0.612273	NM_13384	399	70	13588	1.459506	1	0.997054	99.99999
GOTERM_	GO:003079	3	0.439883	0.635138	NM_13384	399	73	13588	1.399526	1	0.997345	100

Annotation Enrichment Score: 0.2438083693630212

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR009072	4	0.58651	0.253428	XR_032212	509	61	17763	2.288383	1	0.998433	98.95333
KEGG_PAT	mmu05322	5	0.733138	0.298875	NM_17566	155	103	5738	1.797056	1	0.913543	98.40865
SP_PIR_KE	methylation	9	1.319648	0.324263	XR_032386	526	221	17854	1.382293	1	0.9065	99.57162
INTERPRO	IPR007125	3	0.439883	0.338903	NM_17566	509	42	17763	2.492703	1	0.999525	99.84297
SP_PIR_KE	chromosome	6	0.879765	0.370947	NM_14592	526	136	17854	1.497484	1	0.91187	99.84177
SP_PIR_KE	nucleosome	3	0.439883	0.372652	NM_17566	526	44	17854	2.314293	1	0.910276	99.84763
GOTERM_	GO:003462	9	1.319648	0.427716	NM_00945	399	245	13588	1.251005	1	0.991483	99.99215
GOTERM_	GO:003462	8	1.173021	0.452078	NM_00945	399	217	13588	1.255489	1	0.992206	99.99624
GOTERM_	GO:000078	3	0.439883	0.539718	NM_17566	363	62	12504	1.666756	1	0.979635	99.99631
GOTERM_	GO:000632	4	0.58651	0.571451	NM_17566	399	101	13588	1.348718	1	0.996157	99.99994

SP_PIR_KE\ ubl conjug	16	2.346041	0.579702	XR_030853	526	524	17854	1.036426	1	0.97123	99.99942
UP_SEQ_Fl cross-link:C	6	0.879765	0.600094	NM_01165	498	168	16021	1.148953	1	1	99.99997
GOTERM_ E GO:000633	4	0.58651	0.623271	NM_14481	399	109	13588	1.24973	1	0.997093	99.99999
GOTERM_ E GO:000633	3	0.439883	0.635138	NM_17566	399	73	13588	1.399526	1	0.997345	100
GOTERM_ C GO:003299	3	0.439883	0.6435	NM_17566	363	75	12504	1.377851	1	0.984577	99.99987
GOTERM_ E GO:003149	3	0.439883	0.649788	NM_17566	399	75	13588	1.362206	1	0.997737	100
GOTERM_ E GO:006500	3	0.439883	0.656936	NM_17566	399	76	13588	1.344282	1	0.997866	100
GOTERM_ E GO:003472	3	0.439883	0.656936	NM_17566	399	76	13588	1.344282	1	0.997866	100
GOTERM_ C GO:000078	5	0.733138	0.708034	NM_01082	363	165	12504	1.043827	1	0.987598	99.99999
GOTERM_ E GO:001657	3	0.439883	0.755991	NM_01391	399	92	13588	1.110494	1	0.999365	100
GOTERM_ E GO:001656	3	0.439883	0.776546	NM_01391	399	96	13588	1.064223	1	0.99957	100
SP_PIR_KE\ isopeptide	7	1.026393	0.827875	NM_01165	526	277	17854	0.857764	1	0.996382	100
GOTERM_ E GO:000632	7	1.026393	0.903463	NM_01391	399	315	13588	0.756781	1	0.999982	100
GOTERM_ E GO:005127	9	1.319648	0.909624	NM_01391	399	404	13588	0.758654	1	0.999985	100
GOTERM_ E GO:001656	4	0.58651	0.971027	NM_01391	399	236	13588	0.577206	1	1	100
SP_PIR_KE\ chromatin	3	0.439883	0.978354	NM_01391	526	192	17854	0.530359	1	0.999944	100

Annotation Enrichment Score: 0.24376774295510464

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_Fl	zinc finger	11	1.612903	0.2694	NM_01176	498	254	16021	1.393219	1	0.999982	99.42212
UP_SEQ_Fl	zinc finger	9	1.319648	0.309971	XM_00147	498	206	16021	1.405515	1	0.999994	99.77382
UP_SEQ_Fl	zinc finger	8	1.173021	0.361039	XM_00147	498	187	16021	1.376286	1	0.999998	99.936
UP_SEQ_Fl	zinc finger	10	1.466276	0.381832	NM_01176	498	252	16021	1.276614	1	0.999999	99.96282
UP_SEQ_Fl	zinc finger	10	1.466276	0.413537	NM_01176	498	259	16021	1.242111	1	0.999999	99.98434
INTERPRO	IPR013087	16	2.346041	0.499976	NM_00114	509	514	17763	1.086314	1	0.999902	99.99799
UP_SEQ_Fl	zinc finger	6	0.879765	0.505064	XM_00147	498	151	16021	1.278305	1	1	99.99903
UP_SEQ_Fl	zinc finger	3	0.439883	0.658843	NM_14620	498	72	16021	1.340445	1	1	100
INTERPRO	IPR007087	19	2.785924	0.668541	NM_00114	509	681	17763	0.973655	1	0.999995	100
UP_SEQ_Fl	zinc finger	4	0.58651	0.713386	XM_00147	498	118	16021	1.090532	1	1	100
INTERPRO	IPR001909	8	1.173021	0.730306	NM_19906	509	291	17763	0.959391	1	0.999998	100
INTERPRO	IPR015880	18	2.639296	0.741262	NM_00114	509	676	17763	0.929232	1	0.999998	100
UP_SEQ_Fl	zinc finger	4	0.58651	0.763356	XM_00147	498	128	16021	1.005334	1	1	100
UP_SEQ_Fl	zinc finger	3	0.439883	0.773217	NM_14620	498	90	16021	1.072356	1	1	100
UP_SEQ_Fl	zinc finger	3	0.439883	0.8211	NM_14620	498	100	16021	0.96512	1	1	100
SMART	SM00349:k	8	1.173021	0.825785	NM_19906	292	291	9131	0.859671	1	0.999883	100

SMART	SM00355:2	18	2.639296	0.876981	NM_00114	292	676	9131	0.832648	1	0.999958	100

Annotation Enrichment Score: 0.23971477442423822

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_C	GO:003122	8	1.173021	0.396434	NM_00114	363	207	12504	1.331257	1	0.955387	99.8696
SP_PIR_KE	gpi-anchor	5	0.733138	0.497063	NM_01087	526	124	17854	1.368668	1	0.95355	99.99296
UP_SEQ_FI	propeptide	4	0.58651	0.968886	AK018312,	498	220	16021	0.584922	1	1	100

Annotation Enrichment Score: 0.23168415918424926

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_I	GO:00167C	3	0.439883	0.56565	NM_13372	369	68	13288	1.588714	1	0.992694	99.99944
GOTERM_I	GO:00167C	3	0.439883	0.573616	NM_13372	369	69	13288	1.565689	1	0.993074	99.99957
SP_PIR_KE	dioxygenas	3	0.439883	0.621983	NM_13372	526	71	17854	1.43421	1	0.97897	99.99987

Annotation Enrichment Score: 0.22844247518006733

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_E	GO:000692	14	2.052786	0.273287	NM_01032	399	367	13588	1.299106	1	0.978068	99.55112
GOTERM_E	GO:005167	8	1.173021	0.730574	NM_00824	399	284	13588	0.9593	1	0.999137	100
GOTERM_E	GO:004887	8	1.173021	0.730574	NM_00824	399	284	13588	0.9593	1	0.999137	100
GOTERM_E	GO:001647	6	0.879765	0.836148	NM_00824	399	240	13588	0.851378	1	0.999884	100

Annotation Enrichment Score: 0.22734906871062074

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_I	GO:00167C	10	1.466276	0.216158	NM_17301	369	238	13288	1.513061	1	0.952373	97.07316
GOTERM_I	GO:000472	4	0.58651	0.53324	NM_00108	369	101	13288	1.426172	1	0.990452	99.99841
GOTERM_I	GO:000472	5	0.733138	0.610768	NM_00108	369	152	13288	1.184567	1	0.993946	99.99989
INTERPRO	IPR000387	3	0.439883	0.65777	NM_00108	509	78	17763	1.342225	1	0.999995	99.99999
INTERPRO	IPR000387	3	0.439883	0.684486	NM_00108	509	82	17763	1.27675	1	0.999995	100
INTERPRO	IPR016130	3	0.439883	0.715451	NM_00108	509	87	17763	1.203374	1	0.999997	100
GOTERM_E	GO:001631	4	0.58651	0.786167	NM_00108	399	141	13588	0.966103	1	0.999633	100
GOTERM_E	GO:000647	3	0.439883	0.851339	NM_00108	399	114	13588	0.896188	1	0.999914	100

Annotation Enrichment Score: 0.21653417502092864

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR013089	4	0.58651	0.432645	XR_004857	509	84	17763	1.661802	1	0.999834	99.98555

INTERPRO	IPR000210	6	0.879765	0.588863	XM_00147	509	180	17763	1.163261	1	0.999986	99.9999
INTERPRO	IPR011333	6	0.879765	0.588863	XM_00147	509	180	17763	1.163261	1	0.999986	99.9999
SMART	SM00225:E	6	0.879765	0.684727	XM_00147	292	180	9131	1.042352	1	0.998949	99.99995
UP_SEQ_Fl	domain:BT	4	0.58651	0.685512	XM_00147	498	113	16021	1.138785	1	1	100
INTERPRO	IPR013069	4	0.58651	0.71302	XM_00147	509	128	17763	1.090557	1	0.999997	100

Annotation Enrichment Score: 0.21428808019672585

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000165	4	0.58651	0.591305	NM_00921	369	110	13288	1.309485	1	0.993245	99.99977
GOTERM_	GO:000852	4	0.58651	0.591305	NM_00921	369	110	13288	1.309485	1	0.993245	99.99977
GOTERM_	GO:004227	5	0.733138	0.650896	NM_00921	369	160	13288	1.125339	1	0.995558	99.99998

Annotation Enrichment Score: 0.2067931136881773

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:004308	6	0.879765	0.174525	NM_05327	399	101	13588	2.023077	1	0.97023	96.11536
GOTERM_	GO:004409	7	1.026393	0.190914	NM_05327	399	132	13588	1.805954	1	0.965166	97.23398
GOTERM_	GO:003367	3	0.439883	0.44286	NM_01164	399	51	13588	2.003243	1	0.991836	99.99501
GOTERM_	GO:000646	3	0.439883	0.44286	NM_01164	399	51	13588	2.003243	1	0.991836	99.99501
GOTERM_	GO:005134	3	0.439883	0.462596	NM_01164	399	53	13588	1.927649	1	0.992377	99.99729
GOTERM_	GO:004232	7	1.026393	0.856673	AK170454,	399	290	13588	0.822021	1	0.999925	100
GOTERM_	GO:000193	3	0.439883	0.873692	AK170454,	399	121	13588	0.844342	1	0.999949	100
GOTERM_	GO:001922	7	1.026393	0.879177	AK170454,	399	301	13588	0.79198	1	0.999957	100
GOTERM_	GO:005117	7	1.026393	0.879177	AK170454,	399	301	13588	0.79198	1	0.999957	100
GOTERM_	GO:004585	4	0.58651	0.913082	NM_01164	399	186	13588	0.732369	1	0.999987	100
GOTERM_	GO:004354	4	0.58651	0.923456	NM_01164	399	192	13588	0.709482	1	0.999992	100
GOTERM_	GO:005133	4	0.58651	0.934122	NM_01164	399	199	13588	0.684525	1	0.999995	100
GOTERM_	GO:003139	3	0.439883	0.956578	AK170454,	399	165	13588	0.619184	1	0.999999	100
GOTERM_	GO:003226	5	0.733138	0.966253	NM_20125	399	280	13588	0.608127	1	1	100

Annotation Enrichment Score: 0.19639040736452298

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_Fl	DNA-bindir	6	0.879765	0.522521	NM_03321	498	154	16021	1.253403	1	1	99.99946
INTERPRO	IPR001092	4	0.58651	0.619101	NM_03321	509	111	17763	1.25758	1	0.999991	99.99997
UP_SEQ_Fl	domain:He	4	0.58651	0.661793	NM_03321	498	109	16021	1.180576	1	1	100
SMART	SM00353:f	4	0.58651	0.69226	NM_03321	292	111	9131	1.126867	1	0.998888	99.99996

INTERPRO	IPR011598	3	0.439883	0.703383	NM_03321	509	85	17763	1.231688	1	0.999997	100

Annotation Enrichment Score: 0.1954318270758192

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
PIR_SUPER	PIRSF00228	3	0.439883	0.457771	NM_14606	237	53	8136	1.943157	1	1	99.96741
UP_SEQ_FI	region of ir	3	0.439883	0.550395	NM_14606	498	59	16021	1.635797	1	1	99.9998
UP_SEQ_FI	region of ir	3	0.439883	0.550395	NM_14606	498	59	16021	1.635797	1	1	99.9998
INTERPRO	IPR016044	3	0.439883	0.59897	NM_14606	509	70	17763	1.495622	1	0.999988	99.99994
UP_SEQ_FI	region of ir	3	0.439883	0.603264	NM_14606	498	65	16021	1.484801	1	1	99.99997
UP_SEQ_FI	region of ir	3	0.439883	0.603264	NM_14606	498	65	16021	1.484801	1	1	99.99997
UP_SEQ_FI	region of ir	3	0.439883	0.603264	NM_14606	498	65	16021	1.484801	1	1	99.99997
UP_SEQ_FI	region of ir	3	0.439883	0.611605	NM_14606	498	66	16021	1.462304	1	1	99.99998
INTERPRO	IPR018039	3	0.439883	0.61435	NM_14606	509	72	17763	1.454077	1	0.999991	99.99996
INTERPRO	IPR001664	3	0.439883	0.61435	NM_14606	509	72	17763	1.454077	1	0.999991	99.99996
UP_SEQ_FI	region of ir	3	0.439883	0.619812	NM_14606	498	67	16021	1.440478	1	1	99.99999
SP_PIR_KE	Intermedia	3	0.439883	0.644464	NM_14606	526	74	17854	1.376066	1	0.981397	99.99994
SP_PIR_KE	keratin	3	0.439883	0.834588	NM_14606	526	109	17854	0.93421	1	0.996347	100
GOTERM_	(GO:000588	3	0.439883	0.910357	NM_14606	363	137	12504	0.754298	1	0.997647	100
GOTERM_	(GO:004511	3	0.439883	0.916539	NM_14606	363	140	12504	0.738135	1	0.997797	100

Annotation Enrichment Score: 0.19000450282090492

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	(GO:003250	13	1.906158	0.539459	NM_14614	399	409	13588	1.082437	1	0.995144	99.9998
GOTERM_	(GO:004860	13	1.906158	0.539459	NM_14614	399	409	13588	1.082437	1	0.995144	99.9998
GOTERM_	(GO:000728	4	0.58651	0.571451	NM_14614	399	101	13588	1.348718	1	0.996157	99.99994
GOTERM_	(GO:001995	12	1.759531	0.580526	NM_14614	399	386	13588	1.058709	1	0.996443	99.99996
GOTERM_	(GO:000727	10	1.466276	0.637332	NM_14614	399	331	13588	1.028856	1	0.997386	100
GOTERM_	(GO:000728	6	0.879765	0.871852	NM_02839	399	255	13588	0.801297	1	0.999947	100
GOTERM_	(GO:004823	6	0.879765	0.871852	NM_02839	399	255	13588	0.801297	1	0.999947	100

Annotation Enrichment Score: 0.18973685295232462

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	Lectin	6	0.879765	0.546874	NM_17273	526	167	17854	1.219508	1	0.968463	99.99835
GOTERM_	(GO:000552	6	0.879765	0.565414	NM_17273	369	181	13288	1.19373	1	0.993069	99.99943
INTERPRO	IPR018378	4	0.58651	0.574854	NM_17273	509	104	17763	1.342225	1	0.999984	99.99984

INTERPRO	IPR001304	4	0.58651	0.660118	NM_17273	509	118	17763	1.182978	1	0.999994	100
INTERPRO	IPR016186	4	0.58651	0.70803	NM_17273	509	127	17763	1.099145	1	0.999997	100
SMART	SM00034:C	4	0.58651	0.731232	NM_17273	292	118	9131	1.060019	1	0.999372	99.99999
UP_SEQ_FI	domain:C-t	3	0.439883	0.773217	NM_17273	498	90	16021	1.072356	1	1	100

Annotation Enrichment Score: 0.17402754325421585

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:00091C	3	0.439883	0.563311	NM_17268	399	64	13588	1.596335	1	0.995996	99.99992
GOTERM_	GO:000673	5	0.733138	0.606915	NM_01036	399	143	13588	1.190739	1	0.996921	99.99999
GOTERM_	GO:005118	3	0.439883	0.750604	NM_17268	399	91	13588	1.122697	1	0.999319	100
GOTERM_	GO:005118	5	0.733138	0.784519	NM_01036	399	182	13588	0.935581	1	0.999627	100

Annotation Enrichment Score: 0.16968996590974278

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_FI	repeat:TPR	4	0.58651	0.293651	NM_01980	498	61	16021	2.109553	1	0.999993	99.668
UP_SEQ_FI	repeat:TPR	4	0.58651	0.469884	NM_01980	498	82	16021	1.569302	1	0.999999	99.99702
UP_SEQ_FI	repeat:TPR	3	0.439883	0.51249	NM_01980	498	55	16021	1.754765	1	1	99.99925
UP_SEQ_FI	repeat:TPR	4	0.58651	0.713386	NM_01980	498	118	16021	1.090532	1	1	100
UP_SEQ_FI	repeat:TPR	4	0.58651	0.772455	NM_01980	498	130	16021	0.989867	1	1	100
UP_SEQ_FI	repeat:TPR	4	0.58651	0.772455	NM_01980	498	130	16021	0.989867	1	1	100
SP_PIR_KE'	tpr repeat	4	0.58651	0.788025	NM_01980	526	141	17854	0.962921	1	0.994782	100
INTERPRO	IPR019734	3	0.439883	0.834229	NM_01980	509	112	17763	0.934764	1	1	100
INTERPRO	IPR013026	3	0.439883	0.841474	NM_01980	509	114	17763	0.918364	1	1	100
SMART	SM00028:T	3	0.439883	0.876975	NM_01980	292	112	9131	0.837604	1	0.999967	100
INTERPRO	IPR011990	3	0.439883	0.93106	NM_01980	509	150	17763	0.697957	1	1	100

Annotation Enrichment Score: 0.16450839681223503

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000635	22	3.225806	0.266114	NM_01176	399	616	13588	1.216255	1	0.97776	99.46988
GOTERM_	GO:000635	46	6.744868	0.397144	NM_01176	399	1465	13588	1.069308	1	0.990995	99.98104
GOTERM_	GO:005125	46	6.744868	0.431219	NM_01176	399	1488	13588	1.05278	1	0.991535	99.99292
GOTERM_	GO:00037C	22	3.225806	0.57656	NM_14589	369	776	13288	1.020926	1	0.992971	99.99961
GOTERM_	GO:004356	15	2.199413	0.681469	NM_17759	369	556	13288	0.971515	1	0.996896	99.99999
GOTERM_	GO:003052	31	4.545455	0.759903	NM_01176	369	1206	13288	0.925652	1	0.998754	100
SP_PIR_KE'	transcriptic	41	6.01173	0.82559	NM_01176	526	1546	17854	0.900169	1	0.996559	100

GOTERM_	GO:004544	58	8.504399	0.886284	NM_01176	399	2227	13588	0.886932	1	0.999965	100
GOTERM_	GO:000367	43	6.304985	0.889468	NM_01176	369	1781	13288	0.869436	1	0.99994	100
SP_PIR_KE	Transcripti	44	6.451613	0.923949	NM_01176	526	1769	17854	0.844257	1	0.999239	100
GOTERM_	GO:000635	44	6.451613	0.925165	NM_01176	399	1772	13588	0.845613	1	0.999992	100
SP_PIR_KE	dna-bindin	32	4.692082	0.966326	NM_01176	526	1404	17854	0.773629	1	0.999853	100
SP_PIR_KE	nucleus	91	13.34311	0.993505	NM_00103	526	3808	17854	0.811137	1	0.999996	100

Annotation Enrichment Score: 0.1576501191903425

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR011993	9	1.319648	0.587244	NM_00916	509	289	17763	1.086784	1	0.999988	99.9999
INTERPRO	IPR001849	8	1.173021	0.621359	NM_13364	509	261	17763	1.069666	1	0.999991	99.99997
SMART	SM00233:F	8	1.173021	0.731875	NM_13364	292	261	9131	0.958484	1	0.999243	99.99999
UP_SEQ_FI	domain:PH	5	0.733138	0.876599	NM_13364	498	202	16021	0.796304	1	1	100

Annotation Enrichment Score: 0.15469496653703776

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:003005	3	0.439883	0.573751	NM_01013	363	66	12504	1.56574	1	0.980095	99.99866
GOTERM_	GO:001632	5	0.733138	0.586597	NM_01013	363	141	12504	1.221499	1	0.981495	99.9991
GOTERM_	GO:000591	3	0.439883	0.816444	NM_01013	363	106	12504	0.974895	1	0.992458	100
GOTERM_	GO:007016	3	0.439883	0.875448	NM_01013	363	123	12504	0.840153	1	0.996262	100

Annotation Enrichment Score: 0.15461535912835453

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:003166	5	0.733138	0.436241	NM_00859	399	115	13588	1.480658	1	0.991775	99.99391
GOTERM_	GO:000995	5	0.733138	0.549418	NM_00859	399	133	13588	1.280268	1	0.995547	99.99986
GOTERM_	GO:004001	3	0.439883	0.649788	NM_00811	399	75	13588	1.362206	1	0.997737	100
GOTERM_	GO:000972	4	0.58651	0.866028	NM_00859	399	165	13588	0.825579	1	0.999941	100
GOTERM_	GO:000971	4	0.58651	0.90935	NM_00859	399	184	13588	0.740329	1	0.999985	100
GOTERM_	GO:001003	10	1.466276	0.96304	NM_00859	399	505	13588	0.674359	1	0.999999	100

Annotation Enrichment Score: 0.14895040806856027

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000425	6	0.879765	0.603952	NM_00112	369	189	13288	1.143201	1	0.994015	99.99985
INTERPRO	IPR018114	5	0.733138	0.630569	NM_00112	509	151	17763	1.155558	1	0.999991	99.99998
INTERPRO	IPR001254	5	0.733138	0.670482	NM_00112	509	159	17763	1.097416	1	0.999995	100

GOTERM_!GO:000823	6	0.879765	0.703088	NM_00112	369	212	13288	1.019175	1	0.997556	100
GOTERM_!GO:001717	6	0.879765	0.706981	NM_00112	369	213	13288	1.01439	1	0.997577	100
SMART SM00020:T	5	0.733138	0.751316	NM_00112	292	159	9131	0.983351	1	0.999387	100
INTERPRO IPR001314	4	0.58651	0.780143	NM_00112	509	143	17763	0.976163	1	1	100
SP_PIR_KE' Serine prot	4	0.58651	0.86469	NM_00112	526	164	17854	0.827877	1	0.997523	100

Annotation Enrichment Score: 0.14637516123855412

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE'	electron tra	5	0.733138	0.33917	NM_17517	526	100	17854	1.697148	1	0.90553	99.68591
GOTERM_!GO:00229C		5	0.733138	0.416507	NM_17517	399	112	13588	1.520319	1	0.991244	99.98909
GOTERM_!GO:003196		11	1.612903	0.626417	NM_17517	363	368	12504	1.029644	1	0.985526	99.99976
GOTERM_!GO:000574		11	1.612903	0.700399	NM_17517	363	391	12504	0.969077	1	0.988604	99.99999
GOTERM_!GO:003196		15	2.199413	0.70307	NM_17517	363	540	12504	0.956841	1	0.987569	99.99999
GOTERM_!GO:003197		15	2.199413	0.708195	NM_17517	363	542	12504	0.95331	1	0.986896	99.99999
GOTERM_!GO:003109		22	3.225806	0.730827	NM_17517	363	809	12504	0.936734	1	0.988272	100
GOTERM_!GO:004442		13	1.906158	0.83574	NM_14614	363	524	12504	0.854583	1	0.993568	100
GOTERM_!GO:000574		7	1.026393	0.862445	NM_17517	363	296	12504	0.814608	1	0.995373	100
GOTERM_!GO:001986		7	1.026393	0.892785	NM_17517	363	312	12504	0.772833	1	0.997028	100
SP_PIR_KE'	mitochond	4	0.58651	0.908458	AK165865,	526	183	17854	0.741923	1	0.998896	100
SP_PIR_KE'	mitochond	17	2.492669	0.958373	NM_17517	526	790	17854	0.730418	1	0.999772	100
GOTERM_!GO:000573		27	3.958944	0.989736	NM_17517	363	1322	12504	0.703517	1	0.999968	100

Annotation Enrichment Score: 0.14505152183510633

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_F!	domain:C2	3	0.439883	0.531704	NM_01880	498	57	16021	1.693194	1	1	99.99961
UP_SEQ_F!	domain:C2	3	0.439883	0.531704	NM_01880	498	57	16021	1.693194	1	1	99.99961
INTERPRO	IPR018029	3	0.439883	0.810671	NM_01880	509	106	17763	0.987675	1	1	100
INTERPRO	IPR000008	3	0.439883	0.889834	NM_01880	509	130	17763	0.805335	1	1	100
SMART	SM00239:C	3	0.439883	0.923101	NM_01880	292	130	9131	0.721628	1	0.999992	100

Annotation Enrichment Score: 0.1441017642365608

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_!GO:000252		5	0.733138	0.601369	NM_17283	399	142	13588	1.199125	1	0.996904	99.99998
GOTERM_!GO:004532		7	1.026393	0.623242	NM_17283	399	219	13588	1.08852	1	0.997206	99.99999
GOTERM_!GO:003009		4	0.58651	0.653412	NM_17283	399	114	13588	1.194917	1	0.997826	100

GOTERM_	GO:003021	3	0.439883	0.656936	NM_02139	399	76	13588	1.344282	1	0.997866	100
GOTERM_	GO:004664	6	0.879765	0.662319	NM_17283	399	191	13588	1.069795	1	0.997971	100
GOTERM_	GO:004211	4	0.58651	0.664975	NM_17283	399	116	13588	1.174315	1	0.998021	100
GOTERM_	GO:004211	3	0.439883	0.670882	NM_17283	399	78	13588	1.309813	1	0.998099	100
GOTERM_	GO:000177	7	1.026393	0.731113	NM_17283	399	246	13588	0.969049	1	0.999127	100
GOTERM_	GO:000252	7	1.026393	0.867297	NM_17283	399	295	13588	0.808088	1	0.999942	100
GOTERM_	GO:004853	6	0.879765	0.918198	NM_17283	399	281	13588	0.727156	1	0.99999	100
GOTERM_	GO:003009	5	0.733138	0.939216	NM_17283	399	251	13588	0.678389	1	0.999996	100

Annotation Enrichment Score: 0.1421711552549909

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000625	14	2.052786	0.462392	NM_00910	399	421	13588	1.132475	1	0.992519	99.99728
GOTERM_	GO:000697	8	1.173021	0.740429	AY007717,	399	287	13588	0.949272	1	0.999195	100
SP_PIR_KE	dna repair	5	0.733138	0.75257	AY007717,	526	173	17854	0.981011	1	0.992229	100
GOTERM_	GO:000628	6	0.879765	0.783043	AY007717,	399	222	13588	0.920409	1	0.999623	100
SP_PIR_KE	DNA dama	5	0.733138	0.826076	AY007717,	526	194	17854	0.874819	1	0.996428	100
GOTERM_	GO:003355	10	1.466276	0.841642	AY007717,	399	404	13588	0.842949	1	0.9999	100

Annotation Enrichment Score: 0.13933501195761297

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:003001	3	0.439883	0.678199	NM_00941	363	80	12504	1.291736	1	0.987593	99.99997
GOTERM_	GO:004444	3	0.439883	0.716156	NM_00941	363	86	12504	1.201614	1	0.987416	99.99999
GOTERM_	GO:003001	3	0.439883	0.744854	NM_00941	363	91	12504	1.135592	1	0.989048	100
GOTERM_	GO:004329	3	0.439883	0.765992	NM_00941	363	95	12504	1.087777	1	0.989712	100

Annotation Enrichment Score: 0.1321966089577534

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000712	3	0.439883	0.733827	NM_01944	399	88	13588	1.160971	1	0.999155	100
GOTERM_	GO:005132	3	0.439883	0.733827	NM_01944	399	88	13588	1.160971	1	0.999155	100
GOTERM_	GO:005132	3	0.439883	0.745115	NM_01944	399	90	13588	1.135171	1	0.999253	100

Annotation Enrichment Score: 0.13058047835814576

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:000802	3	0.439883	0.590069	NM_01880	363	68	12504	1.519689	1	0.980971	99.9992
SP_PIR_KE	cytoplasmic	7	1.026393	0.681227	NM_01880	526	232	17854	1.024141	1	0.986145	99.99999

GOTERM_(GO:003013	4	0.58651	0.701008	NM_01880	363	124	12504	1.11117	1	0.987983	99.99999
GOTERM_(GO:001602	11	1.612903	0.764589	NM_01880	363	414	12504	0.915239	1	0.990064	100
GOTERM_(GO:003198	11	1.612903	0.779651	NM_01880	363	420	12504	0.902165	1	0.990514	100
GOTERM_(GO:003141	13	1.906158	0.80442	NM_01880	363	508	12504	0.881499	1	0.991825	100
GOTERM_(GO:003013	3	0.439883	0.80806	NM_01880	363	104	12504	0.993643	1	0.99185	100
GOTERM_(GO:003198	13	1.906158	0.826386	NM_01880	363	519	12504	0.862816	1	0.992865	100

Annotation Enrichment Score: 0.12241011667632293

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_(GO:000578		5	0.733138	0.645711	NM_17765	363	152	12504	1.133101	1	0.984002	99.99988
GOTERM_(GO:004217		5	0.733138	0.685053	NM_17765	363	160	12504	1.076446	1	0.987843	99.99997
GOTERM_(GO:004443		6	0.879765	0.80323	NM_17765	363	231	12504	0.894709	1	0.992104	100
GOTERM_(GO:001250		12	1.759531	0.911502	NM_17765	363	535	12504	0.772627	1	0.997591	100

Annotation Enrichment Score: 0.11126129305051527

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR018249	6	0.879765	0.701442	NM_01365	509	205	17763	1.0214	1	0.999997	100
UP_SEQ_FI	domain:EF-	3	0.439883	0.727204	NM_02370	498	82	16021	1.176976	1	1	100
UP_SEQ_FI	domain:EF-	5	0.733138	0.735608	NM_01365	498	160	16021	1.005334	1	1	100
UP_SEQ_FI	domain:EF-	5	0.733138	0.740026	NM_01365	498	161	16021	0.99909	1	1	100
INTERPRO	IPR011992	6	0.879765	0.781257	NM_01365	509	227	17763	0.92241	1	0.999999	100
INTERPRO	IPR018247	5	0.733138	0.857243	NM_01365	509	211	17763	0.826963	1	1	100
INTERPRO	IPR018248	3	0.439883	0.894811	NM_01365	509	132	17763	0.793133	1	1	100

Annotation Enrichment Score: 0.1068670908079491

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_(GO:001656		7	1.026393	0.727103	NM_01144	369	259	13288	0.973266	1	0.998187	100
GOTERM_(GO:000371		5	0.733138	0.738688	NM_01082	369	180	13288	1.000301	1	0.998441	100
GOTERM_(GO:000371		3	0.439883	0.769112	NM_01082	369	100	13288	1.080325	1	0.99883	100
GOTERM_(GO:000813		6	0.879765	0.904659	NM_01082	369	288	13288	0.750226	1	0.999966	100

Annotation Enrichment Score: 0.09946632187557614

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_FI	repeat:6	3	0.439883	0.651302	NM_01013	498	71	16021	1.359325	1	1	100
UP_SEQ_FI	repeat:5	3	0.439883	0.739398	NM_01013	498	84	16021	1.148953	1	1	100

UP_SEQ_FI repeat:4	3	0.439883	0.825354	NM_01013	498	101	16021	0.955565	1	1	100
UP_SEQ_FI repeat:1	4	0.58651	0.842032	AK164443,	498	148	16021	0.869478	1	1	100
UP_SEQ_FI repeat:2	4	0.58651	0.851644	AK164443,	498	151	16021	0.852204	1	1	100
UP_SEQ_FI repeat:3	3	0.439883	0.887799	NM_01013	498	119	16021	0.811026	1	1	100

Annotation Enrichment Score: 0.083680400366396

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
KEGG_PAT	mmu03010	4	0.58651	0.429448	NM_01376	155	89	5738	1.663791	1	0.920727	99.8561
SP_PIR_KE	ribonucleo	6	0.879765	0.894997	XR_004753	526	266	17854	0.765631	1	0.998516	100
SP_PIR_KE	ribosomal	4	0.58651	0.896254	NM_01376	526	177	17854	0.767073	1	0.998496	100
GOTERM_	GO:000584	4	0.58651	0.919853	NM_01376	363	192	12504	0.717631	1	0.997892	100
GOTERM_	GO:003052	10	1.466276	0.923161	NM_14614	363	462	12504	0.74559	1	0.997875	100
GOTERM_	GO:000373	3	0.439883	0.924823	NM_01376	369	151	13288	0.715447	1	0.999985	100
GOTERM_	GO:000641	6	0.879765	0.959444	NM_01376	399	319	13588	0.640536	1	0.999999	100

Annotation Enrichment Score: 0.08192659452271484

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:005080	3	0.439883	0.795574	NM_00988	399	100	13588	1.021654	1	0.99968	100
GOTERM_	GO:005196	3	0.439883	0.825445	NM_00988	399	107	13588	0.954817	1	0.999849	100
GOTERM_	GO:004405	5	0.733138	0.844496	NM_00988	399	201	13588	0.847143	1	0.999901	100
GOTERM_	GO:003164	3	0.439883	0.847867	NM_00988	399	113	13588	0.904119	1	0.999907	100

Annotation Enrichment Score: 0.07578082106051622

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	gtp-binding	9	1.319648	0.705279	NM_13364	526	313	17854	0.975996	1	0.987783	100
UP_SEQ_FI	nucleotide	8	1.173021	0.750306	NM_00945	498	274	16021	0.93929	1	1	100
UP_SEQ_FI	short sequ	3	0.439883	0.78361	NM_02918	498	92	16021	1.049044	1	1	100
INTERPRO	IPR013753	3	0.439883	0.864624	NM_02918	509	121	17763	0.865236	1	1	100
GOTERM_	GO:000726	6	0.879765	0.878146	NM_13364	399	258	13588	0.79198	1	0.999956	100
INTERPRO	IPR001806	3	0.439883	0.889834	NM_02918	509	130	17763	0.805335	1	1	100
SP_PIR_KE	prenylator	3	0.439883	0.929604	NM_02918	526	145	17854	0.702268	1	0.99932	100
INTERPRO	IPR005225	3	0.439883	0.950722	NM_02918	509	164	17763	0.638375	1	1	100

Annotation Enrichment Score: 0.06491286295679688

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR

GOTERM_	GO:00351C	3	0.439883	0.854739	NM_13372	399	115	13588	0.888395	1	0.999922	100
GOTERM_	GO:00351C	3	0.439883	0.854739	NM_13372	399	115	13588	0.888395	1	0.999922	100
GOTERM_	GO:004873	3	0.439883	0.867642	NM_13372	399	119	13588	0.858533	1	0.999941	100
GOTERM_	GO:006017	3	0.439883	0.867642	NM_13372	399	119	13588	0.858533	1	0.999941	100

Annotation Enrichment Score: 0.06448799673302014

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:003227	3	0.439883	0.795574	NM_00987	399	100	13588	1.021654	1	0.99968	100
GOTERM_	GO:005124	3	0.439883	0.83323	NM_00987	399	109	13588	0.937297	1	0.999877	100
GOTERM_	GO:003226	5	0.733138	0.966253	NM_20125	399	280	13588	0.608127	1	1	100

Annotation Enrichment Score: 0.058623640470786775

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR015943	10	1.466276	0.510286	NM_17759	509	305	17763	1.144191	1	0.999915	99.99855
INTERPRO	IPR019775	6	0.879765	0.864463	NM_02944	509	258	17763	0.811578	1	1	100
INTERPRO	IPR019782	5	0.733138	0.864544	NM_02944	509	214	17763	0.81537	1	1	100
INTERPRO	IPR001680	6	0.879765	0.866634	NM_02944	509	259	17763	0.808444	1	1	100
UP_SEQ_FI	repeat:WD	5	0.733138	0.876599	NM_02839	498	202	16021	0.796304	1	1	100
SP_PIR_KE	'wd repeat	6	0.879765	0.889448	NM_02944	526	263	17854	0.774364	1	0.998357	100
INTERPRO	IPR017986	5	0.733138	0.894522	NM_02944	509	228	17763	0.765303	1	1	100
UP_SEQ_FI	repeat:WD	3	0.439883	0.901056	NM_02839	498	124	16021	0.778323	1	1	100
UP_SEQ_FI	repeat:WD	5	0.733138	0.909995	NM_02839	498	218	16021	0.73786	1	1	100
SMART	SM00320:\	6	0.879765	0.920441	NM_02944	292	259	9131	0.724414	1	0.999993	100
UP_SEQ_FI	repeat:WD	5	0.733138	0.930952	NM_02839	498	231	16021	0.696335	1	1	100
UP_SEQ_FI	repeat:WD	5	0.733138	0.936452	NM_02839	498	235	16021	0.684483	1	1	100
UP_SEQ_FI	repeat:WD	5	0.733138	0.936452	NM_02839	498	235	16021	0.684483	1	1	100
UP_SEQ_FI	repeat:WD	3	0.439883	0.962133	NM_02839	498	161	16021	0.599454	1	1	100
INTERPRO	IPR019781	4	0.58651	0.966116	NM_02944	509	235	17763	0.594006	1	1	100

Annotation Enrichment Score: 0.044969961515243885

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	'mrna proc	6	0.879765	0.838032	NM_00103	526	240	17854	0.848574	1	0.996422	100
SP_PIR_KE	'Spliceosom	3	0.439883	0.84202	NM_00111	526	111	17854	0.917377	1	0.996381	100
GOTERM_	GO:000568	3	0.439883	0.878307	NM_00111	363	124	12504	0.833378	1	0.996287	100
GOTERM_	GO:000639	6	0.879765	0.886128	NM_00103	399	262	13588	0.779889	1	0.999965	100

SP_PIR_KE'mrna splici	4	0.58651	0.922706	NM_00103	526	191	17854	0.710847	1	0.999243	100
GOTERM_£GO:000838	4	0.58651	0.936908	NM_00103	399	201	13588	0.677714	1	0.999996	100
GOTERM_£GO:001607	6	0.879765	0.944146	NM_00103	399	302	13588	0.676592	1	0.999997	100
GOTERM_£GO:000639	8	1.173021	0.974348	NM_00103	399	437	13588	0.623435	1	1	100

Annotation Enrichment Score: 0.04173270696080376

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_£GO:000576		4	0.58651	0.892901	NM_15313	363	178	12504	0.774074	1	0.996867	100
GOTERM_£GO:000032		4	0.58651	0.895067	NM_15313	363	179	12504	0.769749	1	0.996861	100
GOTERM_£GO:000577		4	0.58651	0.937871	NM_15313	363	204	12504	0.675417	1	0.998397	100

Annotation Enrichment Score: 0.03739305790510258

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_£GO:001604		6	0.879765	0.90415	NM_00111	399	272	13588	0.751216	1	0.999982	100
GOTERM_£GO:001032		4	0.58651	0.916674	NM_00111	399	188	13588	0.724577	1	0.999989	100
GOTERM_£GO:000689		4	0.58651	0.916674	NM_00111	399	188	13588	0.724577	1	0.999989	100
GOTERM_£GO:001619		10	1.466276	0.932733	NM_01880	399	466	13588	0.730797	1	0.999995	100

Annotation Enrichment Score: 0.031087109586997095

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR017970	5	0.733138	0.882466	NM_17759	509	222	17763	0.785987	1	1	100
SP_PIR_KE'	Homeobox	6	0.879765	0.889448	NM_17759	526	263	17854	0.774364	1	0.998357	100
INTERPRO	IPR001356	5	0.733138	0.935074	NM_17759	509	254	17763	0.686965	1	1	100
INTERPRO	IPR012287	5	0.733138	0.941024	NM_17759	509	259	17763	0.673703	1	1	100
SMART	SM00389:†	5	0.733138	0.964281	NM_17759	292	254	9131	0.615562	1	1	100
UP_SEQ_FI	DNA-bindir	3	0.439883	0.977257	NM_01069	498	180	16021	0.536178	1	1	100

Annotation Enrichment Score: 0.027867844199876163

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_FI	metal ion-k	3	0.439883	0.833589	XM_00147	498	103	16021	0.93701	1	1	100
SP_PIR_KE'	magnesiurr	6	0.879765	0.992712	AK165865,	526	403	17854	0.505354	1	0.999996	100
GOTERM_£GO:000028		5	0.733138	0.996831	NM_00962	369	409	13288	0.44023	1	1	100

Annotation Enrichment Score: 0.024308405054309503

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR

GOTERM_	GO:004427	7	1.026393	0.881068	NM_00910	399	302	13588	0.789357	1	0.999959	100
GOTERM_	GO:000916	3	0.439883	0.965357	NM_00910	399	174	13588	0.587158	1	1	100
GOTERM_	GO:003440	3	0.439883	0.96947	NM_00910	399	179	13588	0.570757	1	1	100
GOTERM_	GO:003465	3	0.439883	0.96947	NM_00910	399	179	13588	0.570757	1	1	100

Annotation Enrichment Score: 0.011472567742558048

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
INTERPRO	IPR002290	6	0.879765	0.879055	NM_00987	509	265	17763	0.79014	1	1	100
SMART	SM00220:S	6	0.879765	0.929307	NM_00987	292	265	9131	0.708012	1	0.999993	100
SP_PIR_KEY	serine/thre	8	1.173021	0.937405	NM_00987	526	384	17854	0.707145	1	0.999424	100
INTERPRO	IPR008271	7	1.026393	0.947475	NM_00987	509	360	17763	0.678569	1	1	100
GOTERM_	GO:000467	8	1.173021	0.949721	NM_00987	369	421	13288	0.684291	1	0.999996	100
INTERPRO	IPR017442	7	1.026393	0.958757	NM_00987	509	374	17763	0.653168	1	1	100
SP_PIR_KEY	kinase	14	2.052786	0.976632	NM_02127	526	707	17854	0.672138	1	0.999935	100
GOTERM_	GO:000646	12	1.759531	0.982546	NM_00763	399	640	13588	0.638534	1	1	100
GOTERM_	GO:000679	16	2.346041	0.992084	NM_00108	399	866	13588	0.629194	1	1	100
GOTERM_	GO:000679	16	2.346041	0.992084	NM_00108	399	866	13588	0.629194	1	1	100
GOTERM_	GO:000467	9	1.319648	0.992546	NM_00987	369	583	13288	0.555913	1	1	100
INTERPRO	IPR017441	7	1.026393	0.992729	NM_00987	509	467	17763	0.523094	1	1	100
GOTERM_	GO:001631	12	1.759531	0.995293	NM_00763	399	718	13588	0.569167	1	1	100
INTERPRO	IPR000719	7	1.026393	0.995497	NM_00987	509	491	17763	0.497525	1	1	100
UP_SEQ_FI	domain:Pro	7	1.026393	0.997345	NM_00987	498	476	16021	0.473098	1	1	100
UP_SEQ_FI	binding site	8	1.173021	0.998286	NM_00987	498	545	16021	0.47223	1	1	100
SP_PIR_KEY	transferase	25	3.665689	0.998856	NM_01103	526	1385	17854	0.612689	1	1	100
UP_SEQ_FI	active site:	9	1.319648	0.999618	NM_02963	498	662	16021	0.437366	1	1	100
UP_SEQ_FI	nucleotide	14	2.052786	0.999667	NM_02127	498	907	16021	0.496571	1	1	100

Annotation Enrichment Score: 0.006856733328159702

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:001660	3	0.439883	0.920436	NM_00111	363	142	12504	0.727738	1	0.997812	100
GOTERM_	GO:000566	4	0.58651	0.967834	NM_00987	363	234	12504	0.588825	1	0.999601	100
GOTERM_	GO:004445	8	1.173021	0.993164	NM_00987	363	513	12504	0.537174	1	0.999986	100
GOTERM_	GO:000565	9	1.319648	0.99662	NM_00987	363	599	12504	0.517557	1	0.999997	100
GOTERM_	GO:003198	12	1.759531	0.999755	NM_00987	363	883	12504	0.468126	1	1	100
GOTERM_	GO:007001	16	2.346041	0.999911	NM_14614	363	1133	12504	0.486444	1	1	100

GOTERM_C GO:004323	16	2.346041	0.999916	NM_14614	363	1136	12504	0.485159	1	1	100
GOTERM_C GO:003197	16	2.346041	0.99996	NM_14614	363	1174	12504	0.469455	1	1	100

Annotation Enrichment Score: 0.006700327633797727

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE'	mitochond	17	2.492669	0.958373	NM_17517	526	790	17854	0.730418	1	0.999772	100
SP_PIR_KE'	transit pep	6	0.879765	0.997759	NM_17268	526	457	17854	0.445641	1	1	100
UP_SEQ_FI	transit pep	6	0.879765	0.998479	NM_17268	498	449	16021	0.429898	1	1	100

Annotation Enrichment Score: 0.006230457523112262

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_E GO:003461		5	0.733138	0.977375	NM_01164	399	299	13588	0.569484	1	1	100
GOTERM_E GO:007072		5	0.733138	0.978321	NM_01164	399	301	13588	0.5657	1	1	100
GOTERM_E GO:000688		4	0.58651	0.988595	NM_01164	399	276	13588	0.493553	1	1	100
GOTERM_E GO:004690		5	0.733138	0.998888	NM_01013	399	431	13588	0.395071	1	1	100

Annotation Enrichment Score: 0.005856946182306301

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_I GO:001707		43	6.304985	0.944785	NM_17517	369	1871	13288	0.827614	1	0.999995	100
GOTERM_I GO:003255		39	5.718475	0.974121	NM_01031	369	1796	13288	0.781973	1	1	100
GOTERM_I GO:003255		39	5.718475	0.974121	NM_01031	369	1796	13288	0.781973	1	1	100
SP_PIR_KE'	kinase	14	2.052786	0.976632	NM_02127	526	707	17854	0.672138	1	0.999935	100
GOTERM_I GO:000188		31	4.545455	0.990295	NM_17517	369	1558	13288	0.716519	1	1	100
GOTERM_I GO:000016		46	6.744868	0.990602	NM_00103	369	2183	13288	0.758818	1	1	100
GOTERM_I GO:003055		30	4.398827	0.992282	NM_17517	369	1535	13288	0.703795	1	1	100
GOTERM_I GO:000188		30	4.398827	0.993398	NM_17517	369	1548	13288	0.697884	1	1	100
GOTERM_I GO:000552		26	3.812317	0.997283	NM_00962	369	1443	13288	0.648844	1	1	100
SP_PIR_KE'	nucleotide-	32	4.692082	0.997697	NM_01031	526	1631	17854	0.665956	1	1	100
GOTERM_I GO:003255		26	3.812317	0.997846	NM_00962	369	1460	13288	0.641289	1	1	100
SP_PIR_KE'	atp-binding	23	3.372434	0.998645	NM_02127	526	1287	17854	0.606595	1	1	100
UP_SEQ_FI	nucleotide	14	2.052786	0.999667	NM_02127	498	907	16021	0.496571	1	1	100

Annotation Enrichment Score: 0.0050250582186932525

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
UP_SEQ_FI	zinc finger	3	0.439883	0.97466	NM_17880	498	176	16021	0.548364	1	1	100

INTERPRO	IPR001841	4	0.58651	0.989305	NM_17880	509	286	17763	0.488082	1	1	100
INTERPRO	IPR017907	3	0.439883	0.994873	NM_17880	509	254	17763	0.412179	1	1	100
SMART	SM00184:F	4	0.58651	0.995288	NM_17880	292	286	9131	0.43735	1	1	100

Annotation Enrichment Score: 0.004106751445089308

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
GOTERM_	GO:00081C	15	2.199413	0.977492	NM_00116	399	753	13588	0.678389	1	1	100
GOTERM_	GO:001503	11	1.612903	0.99323	NM_00116	399	651	13588	0.575432	1	1	100
GOTERM_	GO:004518	11	1.612903	0.993804	NM_00116	399	656	13588	0.571047	1	1	100
SP_PIR_KE	protein tra	6	0.879765	0.997951	NM_00116	526	461	17854	0.441774	1	1	100

Annotation Enrichment Score: 9.334799375937827E-8

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrich	Bonferroni	Benjamini	FDR
SP_PIR_KE	transducer	19	2.785924	0.999998	NM_14649	526	1467	17854	0.439616	1	1	100
SP_PIR_KE	g-protein c	17	2.492669	0.999999	NM_14649	526	1411	17854	0.408951	1	1	100
GOTERM_	GO:005087	21	3.079179		1 NM_14649	399	1681	13588	0.425436	1	1	100
GOTERM_	GO:000718	25	3.665689		1 NM_01031	399	1877	13588	0.453585	1	1	100
PIR_SUPER	PIRSF8000C	12	1.759531		1 NM_00921	237	1200	8136	0.343291	1	1	100
GOTERM_	GO:005089	16	2.346041		1 NM_14649	399	1480	13588	0.368164	1	1	100
INTERPRO	IPR017452	16	2.346041		1 NM_14649	509	1575	17763	0.354518	1	1	100
GOTERM_	GO:00076C	13	1.906158		1 NM_14649	399	1402	13588	0.315775	1	1	100
INTERPRO	IPR000276	13	1.906158		1 NM_14649	509	1458	17763	0.31116	1	1	100
PIR_SUPER	PIRSF0031C	5	0.733138		1 NM_14693	237	901	8136	0.190506	1	1	100
KEGG_PAT	mmu0474C	4	0.58651		1 NM_14693	155	960	5738	0.154247	1	1	100
GOTERM_	GO:00076C	7	1.026393		1 NM_14693	399	1192	13588	0.199988	1	1	100
GOTERM_	GO:000498	5	0.733138		1 NM_14693	369	1135	13288	0.158638	1	1	100
INTERPRO	IPR000725	5	0.733138		1 NM_14693	509	1134	17763	0.153871	1	1	100
GOTERM_	GO:00076C	5	0.733138		1 NM_14693	399	1117	13588	0.15244	1	1	100