Tristetraprolin Regulation of MyoD mRNA Stability Commits Quiescent Adult Muscle Stem Cells to Myogenesis

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Thesis Directed by Bradley B. Olwin

Abstract

In animals, tissue maintenance, plasticity and repair rely on adult stem cells which have been identified in nearly all tissues. Many adult stem cells are typically quiescent and only activate when required for maintenance and repair of adult tissues. Within hours of activation skeletal muscle stem cells called satellite cells begin to express MyoD, a muscle-specific transcription factor that functions as a master regulator, committing satellite cells to myogenesis. The earliest detectable event in satellite cells following muscle injury is phosphorylation of p38α/β MAPKs, which is required for MyoD induction and cell-cycle entry. Loss of Syndecan-4, a component of the satellite cell niche disrupts p38α/β MAPK activation and severely delays MyoD induction. We performed a microarray gene chip experiment to identify genes expressed during satellite cell activation. We identified differentially expressed genes by subtracting genes changing in *Sdc4*$^{-/-}$ satellite cells from those changing in WT satellite cells following 12h of muscle injury. Unexpectedly, we observed that 70% of RNA-binding proteins (RNA-BPs) decreased in activated satellite cells. Expression levels of the Tristetraprolin (TTP) family of RNA-BPs declined dramatically as satellite cells activated. The TTP family is known to direct mRNA decay and we identified the 3'UTR of MyoD as a direct TTP target. Furthermore, p38α/β MAPK signaling inhibits TTP-mediated mRNA decay in satellite cells. HuR, an RNA-BP that is induced during satellite cell activation is known to stabilize MyoD mRNA. The coordinate inhibition of TTP and induction of HuR may together function as a feed-forward loop to commit satellite cells to myogenesis by rapid induction of MyoD. A similar feed-forward circuit could operate in other

stem cell systems, implicating that post-transcriptional regulation of mRNA could play a major role in regulating adult stem cells to maintain and repair adult tissues.

Dedication

I would like to dedicate my dissertation to my husband, Lucas Velasquez. You have been there for me throughout graduate school and I am not sure I could have finished without your love and support. Thank you for always being able to make me smile.

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Chapter 1: Introduction

Nearly all tissues in vertebrates are thought to harbor adult stem cells. Populations of well characterized adult stem cells reside within bone marrow, skin, intestine and muscle [1,2]. Maintenance, homeostasis, plasticity, and repair of these tissues rely heavily on resident adult stem cells [3]. Although they reside within distinct tissues, adult stem cells have a number of important commonalities, 1) long-term maintenance of genomic stability 2) response to the micro-environment and 3) self-renewal of the stem cell population [3,4]. To maintain long-term genomic stability, most adult stem cells divide infrequently and can remain in a mitotically quiescent state for years [5]. When a tissue requires maintenance or repair, quiescent adult stem cells receive signals from their micro-environment or niche resulting in exit from quiescence and entry into the cell cycle [3]. Renewal of adult stem cell populations is not well understood. One hypothesis is that adult stem cells divide asymmetrically; where one daughter cell exits the cell cycle to renew the stem cell population while the other continues to proliferate generating enough cells appropriate for the response [6]. The mechanisms regulating adult stem cell quiescence are poorly understood; however, maintenance and exit from quiescence are absolutely critical aspects of adult stem cell function. Skeletal muscle regeneration provides an opportunity to study these important aspects of adult stem cells within the same tissue and often within the same individual over its lifetime [7]. Fully regenerated muscle contains a similar number of quiescent satellite cells compared to uninjured muscle and appears phenotypically normal illustrating the impressive ability of skeletal muscle to regenerate.

Skeletal Muscle

Skeletal muscles interconnect bones via tendons providing support and movement of the skeleton[8]. Each muscle contains fascicles, which are bundles of myofibers. Myofibers are

syncytial cells formed by the fusion of myoblasts during development. Myofibers contain the contractile subunits called myofibrils, comprising of actin and myosin filaments. Contraction of skeletal muscle is voluntary and each individual myofiber is innervated by a single branching axon of a motor neuron. Upon excitation of the nerve, actin and myosin filaments within myofibrils slide in opposing directions, functionally shortening the muscle resulting in movement of the bone [8].

Vertebrate survival depends on normal skeletal muscle function and skeletal muscle diseases are debilitating and cause mortality of the animal. Muscular dystrophies comprise a group of muscle diseases that cause progressive muscle weakness. Several genetic mutations cause muscular dystrophies but the most common is Duchenne's Muscular Dystrophy (DMD) [9]. DMD affects approximately 1:3,500 boys born in the United States [10]. Currently, there is no treatment for DMD and on average, people with this disease die in their thirties [10]. Treatment of muscular dystrophies like DMD may be made possible through our understanding of muscle development and adult muscle stem cells called satellite cells.

Skeletal Muscle Development

In amniotes, all skeletal muscle of the trunk and limbs originate from somites, segments of paraxial mesoderm that form on either side of the neural tube and notochord during embryogenesis [11]. Multi-potent progenitor cells located in the dermomyotome are the source of muscle precursor cells. From limb level somites, migration of muscle precursor cells into the limb buds requires c-met, the receptor for HGF. Once in the limb, muscle precursor cells commit to the myogenic lineage and become myoblasts, which are cycling muscle cells that express muscle specific transcription factors [11]. Upon induction of muscle differentiation, myoblasts exit the cell cycle to form myocytes, non-cycling mono-nucleated muscle cells. Differentiating myocytes align and fuse to form multi-nucleate myofibers. Myonuclei within myofibers are terminally differentiated and under normal physiological conditions do not re-enter into the cell-cycle [12].

Amniote limb muscle development is characterized by two waves of muscle differentiation, primary and secondary myogenesis [11]. Following a proliferation phase, embryonic myoblasts exit the cell cycle and fuse to form primary myotubes. Subsequently fetal myoblasts proliferate and execute myogenic differentiation. Secondary myotubes use primary myotubes as scaffolds and form the bulk of the limb musculature. During the late fetal stage, satellite cells are seen associated with myofibers sandwiched between the plasma membrane of the myofiber and the basal lamina [13]. Postnatal myogenesis is attributed to sustained satellite cell fusion with existing myofibers [14]. Insight into the mechanistic details of myogenesis began with the *in vitro* transcriptional characterization of myogenesis.

Muscle Transcription Factors

Myogenesis collectively refers to the process of forming multi-nucleated myofibers from non-committed mono-nucleated cells. A network of muscle regulatory transcription factors (MRFs) induce a suite of muscle specific genes sufficient to drive myogenesis [11]. The MRFs contain a basic helix-loop-helix domain required for DNA binding and heterodimerization [15]. Currently, four MRFs have been identified: MyoD, Myf5, MRF4, and Myogenin.

MyoD has been referred to as a master regulator of myogenesis [16]. All four MRFs are sufficient to convert cells into muscle *in vitro;* however, MRF regulation of embryonic and adult myogenesis *in vivo* is much more complicated.

The MRFs were systematically targeted for knockout or reporter knock-in in mice. The phenotypes of single, double and triple knock-out mice aided in defining the complex regulatory and compensatory relationships between the MRFs. In summary, Myf5 and MyoD commit multi-potent precursor cells to myoblasts and are overall functionally redundant during development [17-21]. In a subset of precursor cells in the myotome, MRF4 regulates commitment to the myogenic lineage and differentiation [21,22]. Myogenin is required for muscle differentiation; thus, Myogenin null neonates display only residual muscle formation [23-26]. However, Myf5 and

Myogenin expression alone is insufficient to support muscle differentiation in the absence of MyoD and MRF4 [27]. Further, Myf5 expression alone is not sufficient for muscle formation *in vitro* or *in vivo* [28], whereas cells isolated from all the other single and double MRF knockout mice are able to form muscle *in vitro* [17-21,23-26]. Embryonic myogenesis is one of the most understood processes of cell fate decisions and cellular differentiation because of the analysis of MRF knockout mice.

Adult Myogenesis - Maintenance and Repair of Adult Muscle Tissue

Adult myogenesis collectively refers to the process of satellite cell mediated muscle formation. In humans, satellite cell nuclei comprise 4-6% of all basal lamina incapsulated nuclei within muscle [29], and are able to remain quiescent for years [5]. Satellite cells based on their physiology during the adult myogenic process are grouped into four classes, 1) quiescent, 2) activated, 3) proliferating and 4) differentiating.

Quiescent Satellite Cells

The "satellite cell" was first described by Mauro in 1961 as cells "satellite" to the myofiber, anatomically defining this cell [30]. Satellite cells are sandwiched between the myofiber plasma membrane and the basement membrane [30]. The quiescent satellite cell is influenced by both the myofiber and the extracellular space and are anatomically polarized [31]. Satellite cell nuclei and the myonuclei of the myofiber are nearly indistinguishable because 1) myonuclei are located at the periphery of the myofiber and 2) satellite cells distort the sarcomere of myofibers [30]. Satellite cells were only distinguishable from myonuclei by electron microscopy until methods of immuno-detection by light microscopy were developed.

Early descriptions of satellite cell morphology by electron microscopy provided insights into satellite cell quiescence under normal physiological conditions. Comparison of satellite cells associated with muscle from young mice (1 -2 weeks old) to those associated with older muscle (5 - 50 weeks old) reveals several anatomical differences. Young mouse muscle contains satellite

cells characterized by more dispersed chromatin, many polysomes each containing 4-5 ribosomes, readily identifiable rough endoplasmic reticulum, Golgi cisternae, and mitochondria [32]. Human fetal satellite cells observed from 10 to 23 weeks gestation by electron microscopy displayed many common features as described in young murine muscle [33]. However, the morphological characteristics of satellite cells in young muscle dramatically change in adult muscle tissue implying that satellite cells enter into long-term quiescence in adult resting muscle.

In normal murine adult muscle, satellite cell nuclei are not radioactive after continuous perfusion of titrated thymidine over nine days, indicating that they are not entering into S-phase and are mitotically quiescent [34]. Satellite cell nuclei observed in adult mice have a lower ratio of dispersed to condensed chromatin compared to young satellite cells, indicating a shift towards more condensed chromatin in adult satellite cell nuclei [32]. Cytoplasmic anatomical changes in adult satellite cells include the absence of polysome structures and further, ribosomes are rarely found [32]. In addition, rough endoplasmic reticulum is considerably diminished and ordered Golgi cisternae are not identifiable [32]. Based on these early electron microscopy studies, quiescent adult satellite cells in resting muscle were thought to be both mitotically and metabolically inactive with low transcriptional and translational profiles.

Satellite cells appear metabolically inactive but express proteins involved in maintaining satellite cell quiescence such as Pax7, a paired-box transcription factor, expressed in quiescent satellite cells [35,36]. In Pax7 null mice, satellite cells are present at birth; however, they undergo apoptosis resulting in ablation of adult satellite cells [35,36]. The importance of Pax7 expression in satellite cells appears to be during early post-natal growth prior to post-natal day 21 (P21). During post-natal growth up until approximately P21, satellite cells are actively fusing to existing myofibers, and thus have not entered into long-term quiescence [37]. If Pax7 is conditionally deleted between P7 and P18, adult muscle repair is severely defective [37]. In contrast, normal adult muscle regeneration proceeds if Pax7 expression is conditionally knocked out after P21 [37]. These

data suggest that Pax7 may not required for satellite cell mediated adult muscle regeneration but for satellite cell entry into long-term quiescence after juvenile growth.

Quiescent satellite cells do not express detectable levels of the four MRFs when assayed by RT-PCR [38,39]. In disagreement, Cre-mediated lineage tracing suggests that progenitor cells contributing to adult satellite cells have expressed MyoD mRNA before entering into quiescence [40]. However, other alternative explanations are possible since entry of satellite cells into quiescence and maintenance of the quiescent state are poorly understood. Nevertheless, a fundamental cellular change occurs during the transition from a quiescent to activated satellite cell.

Activated Satellite Cells

Descriptive studies of satellite cells by electron microscopy implied that exit from quiescence results in a fundamental cellular change in satellite cells. In response to exercise, injury, disease or denervation of the muscle, satellite cells appear "activated" and display morphological characteristics divergent of satellite cells from uninjured muscle. As described by electron microscopy, activated satellite cells contain less condensed chromatin, increased cytoplasmic volume and ribosomal number, organization of ribosomes into polysomes, and increased rough ER and Golgi cisternae [41-46]. Pinpointing exactly when a satellite cell becomes "activated" is still under revision as the exit from quiescence continues to be molecularly defined. Perturbation of the muscle tissue inevitably activates satellite cells, thus "freshly isolated" satellite cells are activated. For the purpose of this thesis, I will define an "activated satellite cell" within the time frame of the initial signaling event occurring immediately after muscle damage up until cell-cycle entry. Currently, three major events have been described in activated satellite cells before cell cycle entry 1) extracellular receptor activation as identified by autophosphorylation of FGF receptor tyrosine kinases, 2) p38α/β MAPK activation and 3) induction of MyoD mRNA

leading to myogenic commitment. At the time of cell-cycle entry satellite cells are committed to the muscle lineage and I will refer to these cells as proliferating myoblasts.

Molecular changes occurring rapidly upon muscle damage that are mediated by receptors expressed by quiescent satellite cells. Proteins released by damaged muscle tissue bind to extracellular receptors on the surface of quiescent satellite cells which activates intracellular signaling [47]. Stretch-mediated activation of satellite cells has been shown to occur through HGF release which binds to the HGF receptor, c-met on the surface of satellite cells [48]. c-met mRNA is detected in 100% of freshly isolated satellite cells by single cell RT-PCR and c-met protein is detected in quiescent satellite cells in uninjured muscle sections [39]. In mice, knockout of c-met inhibits migration of muscle precursor cells into the limb and results in embryonic death [49]. An adult conditional c-met knockout has not been studied in the context of muscle regeneration.

Fibroblast Growth Factor Receptors (FGFRs) also play a role in satellite cell activation. Freshly isolated satellite cells express FGFR1 and FGFR4 at levels detectable by RT-PCR [50]. Conditional knockout of FGFR1 (Olwin lab, unpublished) and FGFR4 knockout results in muscle regeneration defects [51]. FGF receptors require Heparan Sulfate Proteoglycans (HSPGs) located on the cell surface for signaling [52]. Two HSPGs, Syndecan-3 and Syndecan-4 are expressed by satellite cells [53]. With respect to satellite cell activation, *Sdc4*$^{-/-}$ satellite cells delay satellite cell activation as defined by MyoD expression, and cell cycle entry [54]. While several FGFs have been shown to influence proliferation of cultured satellite cells [55], it appears that *in vivo* FGF-6 and FGF-2 are particularily important to satellite cell mediated muscle regeneration [56,57]. Likely a complex interplay between FGF receptors, FGFs and Heparan Sulfate Proteoglycans regulate satellite cell activation.

Another signaling molecule that has been demonstrated to play an important role in satellite cell activation is TNF-α. Intraperitoneal injection of TNF-α results in satellite cell activation in the absence of muscle injury [58]. TNF-α activates p38 MAPK and double knockout of

one subunit from each TNF-R1 and TNF-R2 (*p55*$^{-/-}$;*p75*$^{-/-}$) blocks p38 MAPK activation and results in muscle regeneration defects [59]. p38 MAPK activation is required for muscle regeneration and can be rescued by forced activation of p38 MAPK signaling [60]. We have shown that activation of p38α/β MAPK in satellite cells is required for satellite cell activation and entry into the cell cycle (discussed further below) [61]. The main source of TNF-α after acute muscle injury is from neutrophils and macrophages [11], which play a supportive role in the process of muscle regeneration [62]. However, increased systemic TNF-α due to dysregulation of TNF-α mRNA stability results in muscle cachexia [63]. Although TNF-α acts to initiate muscle repair through satellite cell activation, eventual inhibition of the inflammatory response is required for normal muscle repair [64]. HGF, FGF and TNF-α signaling all activate satellite cells; however, it is likely that the initial stimuli that results in satellite activation is context specific.

HGF, FGF, and TNF-α likely activate MAPK signaling in quiescent satellite cells. We have shown that activation of p38α/β acts as a critical molecular switch to activate quiescent satellite cells. The active dual-phosphorylated form of p38α/β is detected in 40% of satellite cells within 20 minutes following muscle injury [61]. Currently, phosphorylated p38α/β is the earliest molecular event identified during satellite cell activation [61]. Based on Cre-mediated genetic deletion of p38β, p38ɣ and p38δ, these isoforms are dispensible for normal adult muscle regeneration [65]. Cre-mediated genetic deletion of p38α results in increased Pax7 positive cells in neonates, but studies of adult muscle regeneration have not been published [66]. The downstream effectors of p38α MAPK signaling during satellite cell activation are not characterized. However, we have shown that inhibition of p38α signaling, blocks satellite cells from expressing MyoD and committing to the myogenic lineage [61].

Satellite cells express MyoD and commit to the myogenic lineage prior to entry into the cell-cycle. Following injury, MyoD mRNA is the first to be detected in rat and concurrent with Myf5 mRNA in mouse satellite cells by RT-PCR [38,39]. Within muscle cross-sections, ~28% of

satellite cells are positive for MyoD protein within 3 hours of muscle injury [67]. Further, MyoD protein is detected in ~40% of satellite cells associated with myofibers after 3h culture [61]. Prior to characterization of p38α/β phosphorylation, MyoD was the first known molecular event upon activation and still is often used as a marker of activated satellite cells [39]. Satellite cells from MyoD null mice are defective in proliferation and differentiation, reflecting an inability to progress through the normal regenerative process [50,68-70]. MyoD null mice with an mdx background, a mouse model for DMD, cannot repair muscle resulting in early death [68]. These data underscore the importance of MyoD during skeletal muscle repair. Once activated satellite cells express MyoD protein, they are committed to the myogenic lineage and are termed myoblasts that subsequently enter the cell-cycle.

Proliferating Myoblasts

Our understanding of the mechanisms regulating transition from G1 to S-phase has largely been from studies *in vitro.* Many studies have used the MM14 satellite cell line, which exhibits gene expression profiles similar to primary satellite cells[71]. FGF-2 strongly inhibits differentiation in MM14 cells and is required for entry into S-phase [72,73]. IGF-1 also induces proliferation of cultured myoblasts but it is also involved in induction of differentiation [74].

The decision of myoblasts to proliferate or differentiate is mutually exclusive; however, it appears that overlapping pathways regulate this decision. In MM14s, a decision point exists at the G1/S phase transition, where if the cells receive FGF, they enter into S-phase, if not they differentiate [55]. Activated-p38α/β signaling is required for MM14s to either enter S-phase or exit from the cell cycle for differentiation [61]. In primary satellite cells, p38α/β MAPK inhibition blocks MyoD expression and entry into the cell cycle [61]. Recent data shows that MyoD regulates entry into S-phase by transcriptional up-regulation of Cdc6 which is involved in licensing origins of DNA replication [75,76]. Thus, MyoD expression is required for entry into S-phase in satellite cells.

DNA replication in primary satellite cells begins approximately 12h after isolation, as incorporation of the Thymidine analog, BrdU is detected after 12h in culture but not after 6h [77]. Regulation of the proliferating myoblast pool has been shown to be regulated by Notch signaling [78]. Recently, we have shown that Syndecan-3 and Notch1 interact in a complex that regulates cell cycle progression and cell fate decisions in satellite cells [77]. As regeneration progresses, Notch signaling is inhibited by Numb and canonical Wnt signaling regulates myogenic differentiation [78,79].

Differentiating Myoblasts

The late stages of muscle differentiation are similar between embryogenesis and adult myogenesis. Myogenin and MRF4 mRNA are detected after 48h hours in culture as satellite cells begin to differentiate [38,39,80]. As myoblasts up-regulate Myogenin, p21, the cyclin dependent kinase inhibitor drives the myoblasts to exit the cell cycle [81]. Concomitantly, growth-factor receptors are down-regulated [72]. Myoblasts either fuse together to form muscle fibers *de novo* or fuse to damaged muscle fibers for reparation [82,83]. The decision to exit the cell cycle and differentiate requires activated p38α/β MAPK signaling [61,84].

The requirement of p38 MAPK signaling for skeletal muscle differentiation is well established [84,85]. Myogenesis is regulated by p38 MAPK phosphorylation of transcription factors and chromatin remodeling complexes which modulate the transcription of muscle specific gene targets [86]. Additionally, p38 MAPKs regulate the stability of myogenic mRNAs through phosphorylation of RNA-binding proteins [87].

Myogenic differentiation is largely regulated by the p38α MAPK isoform. Cre-mediated deletion of p38α inhibits myogenic fusion *in vitro* [66]. p38α phosphorylation of E-proteins [88], bHLH proteins required for MRF transcriptional activity [89], results in increased MRF/E-protein association and transcription [88]. Further, p38α directs Swi/Snf chromatin remodeling complexes to muscle differentiation genes [90] and phosphorylates MEF2, which in conjunction with MyoD

up-regulates muscle differentiation genes [86]. In contrast, p38ɣ blocks premature differentiation by phosphorylation of MyoD which promotes its association with a histone methyl-transferase that negatively regulates gene transcription [91]. Muscle differentiation is regulated by p38 MAPKs at the level of gene transcription but p38 MAPKs also post-transcriptionally regulate myogenic mRNA stability.

Regulation of Myogenic mRNA stability by p38 MAPKs

p38 MAPK signaling modulates mRNA stability though phosphorylation of several known RNA-binding proteins [87,92-94]. RNA-binding proteins regulate transcripts by binding to AU-rich elements within the target 3‘ untranslated region (UTR)[95]. RNA-binding proteins can either have a positive effect on mRNA stability or decrease the half-life of the target mRNA [95,96]. Changes as little as two-fold in mRNA half-life can significantly affect translated protein levels. For example, in mice, knockout of the protein, Tristetraprolin that regulates TNF-α mRNA stability, results in a 2-fold increase in TNF-α mRNA stability. This causes increased systemic levels of TNF-α which results in a severe inflammatory disorder [97,98] illustrating the importance of RNA-binding protein regulation.

Activated p38 MAPK mediated phosphorylation of Human Antigen R (HuR) and KH-type splicing regulatory protein (KSRP) plays a major role in muscle differentiation [87,99,100]. HuR, encoded by the *Elavl1* gene, is an RNA-binding protein that positively regulates the stability of target transcripts [96]. HuR binds to mRNAs in the nucleus and the cytoplasm but the ability of HuR to stabilize mRNA occurs in the cytoplasm [101,102]. p38 MAPK phosphorylation of HuR results in increased cytoplasmic localization and target stability [103]. KSRP binds 3‘UTR regions of myogenic transcripts and mediates their decay [87]. Activated-p38 phosphorylation of KSRP results in the dissociation of KSRP from the mRNA resulting in increased transcript stability [87]. Activated-p38 phosphorylation of both HuR and KSRP results in increased target stability. Both HuR and KSRP have been shown to directly bind Myogenin and p21 mRNA [87,100]. However, it

remains untested whether HuR and KSRP bind simultaneously to Myogenin and p21 mRNAs or compete for common binding sites. HuR also binds MyoD mRNA and increases its stability during myoblast differentiation [100]. Since HuR binds and regulates MyoD, Myogenin and p21 mRNAs, it may regulate myogenic differentiation on a global level. In agreement with this idea, siRNA-mediated knock-down of HuR in C2C12 myoblasts results in inhibition of myogenic differentiation [100]; whereas, over-expression of HuR results in accelerated differentiation of C2C12 myoblasts [99].

In addition to regulating myogenic differentiation, HuR positively influences C2C12 myoblast proliferation. Along with Pitx2, HuR binds and stabilizes CyclinD1 mRNA; but upon switch to differentiation conditions, this complex dissociates from the mRNA resulting in CyclinD1 mRNA decay and cell cycle exit (Gherzi, 2010). Thus, HuR stabilizes target mRNAs during proliferation and differentiation in C2C12s, two mutually exclusive states, indicating that regulation of HuR targets is either in trans or through competition of cis-binding sites.

Here, I present my thesis work characterizing the mechanism by which p38α/β MAPK signaling acts as a molecular switch to activate satellite cells. I present an in silico analysis of satellite cell activation, where it appears that post-transcriptional regulation of RNA switches quiescent satellite cells to committed myoblasts. I have found that TTP directly binds and regulates the half-life of the 3'UTR of MyoD mRNA. In satellite cells, MyoD protein induction is dependent upon activated-p38α/β inhibition of TTP function. I propose a model that MyoD mRNA in quiescent satellite cells is actively suppressed from being translated into protein. I also explore the possibility that TTP directs differential polyadenylation of HuR mRNA. TTP directed differential polyadenylation of HuR transcripts may result in inclusion of an AU-rich element in HuR mRNA. An AU-rich element within HuR mRNA may allow for TTP-mediated instability of HuR transcripts.

Chapter 2: In Silico Analysis of Satellite Cell Activation

Introduction

Skeletal muscle maintenance and regeneration rely on a resident adult stem cell population called the satellite cell. Satellite cells are a minor population in muscle, comprising only 4-6% of all basal lamina incapsulated nuclei within muscle [29]. Yet, this small population can rapidly regenerate muscle even after repeated severe injuries [104]. Satellite cells lie between the plasma membrane of the myofiber and the basal lamina surrounding the myofiber [30]. They remain in a mitotically quiescent state unless they receive signals from the muscle to activate in order to contribute to muscle maintenance and repair. The molecular mechanisms regulating satellite cells are still elusive despite fifty years of research.

Satellite cell morphology has been described by electron and light microscopy. As described by electron microscopy, the morphological characteristics of quiescent satellite cells implied that these cells were metabolically quiet [30]. Comparative analysis of activated satellite cells supported the idea of a cellular change to a more metabolically active state [32,105]. However, further understanding was not possible considering that at that time satellite cells were only distinguishable from myonuclei by electron microscopy. Identification of satellite cell specific expression of M(muscle)-Cadherin by immunocytochemistry (Bornemann, 1994) elicited a new era for the characterization of satellite cells by light microscopy. Soon other "markers" of satellite cells permitted identification of these cells with the light microscope and facilitated their isolation by FACS, aiding in understanding satellite cell gene expression changes occurring during the transition from quiescence to a proliferative state during muscle regeneration.

Several proteins have been identified that specifically mark quiescent, activated and proliferating satellite cells. Pax7, a paired-box transcription factor, is a marker of quiescent and proliferating satellite cells. Inducible lineage tracing of Pax7 expressing cells shows that cells marked during embryogenesis contribute to functional adult satellite cells that repair muscle [106].

However, it is currently uncharacterized whether all quiescent cells within the satellite cell position express Pax7. The receptor for HGF, c-met is another marker of satellite cells [50]. C-met is expressed by quiescent, activated, proliferating, and differentiating satellite cells [39]. The activation of satellite cells is thought to occur by HGF activation of c-met and/or FGF activation of FGFRs [107,108]. These receptor tyrosine kinases require Heparan Sulfate Proteoglycans (HSPGs) located on the cell surface for signaling [52]. Two HSPGs, Syndecan-3 and Syndecan-4 are expressed by satellite cells [53] and both Syndecan-3 and Syndecan-4 mark satellite cells in quiescence, proliferation, and differentiation [53].

Genetic deletion of *Sdc3* or *Sdc4* reveals their unique roles in muscle regeneration [54,77]. Whereas Syndecan-3 and Notch1 interact in a complex that regulates cell cycle progression and cell fate decisions in satellite cells [77], Syndecan-4 is required for muscle regeneration regeneration [54]. *Sdc4*$^{-/-}$ satellite cell defects include delayed satellite cell activation, MyoD expression, cell cycle entry and a failure to repair skeletal muscle upon an induced injury [54].

Gene Expression Profiles of Satellite Cells

Initial attempts to identify gene expression changes occurring during satellite cell activation utilized a candidate gene approach. An unbiased approach to identify genes regulated during satellite cell activation employed C2C12 myoblasts as a model for quiescent satellite cells[109]. When cultured in suspension, C2C12 myoblasts undergo a G0 cell-cycle arrest. G0-arrested C2C12s are not differentiated and re-enter the cell-cycle with similar kinetics as satellite cells upon activation. Importantly, G0-arrested C2C12s do not express detectable levels of MyoD or Myf5 [109,110]. Using differential display PCR, four transcripts were identified as preferentially expressed by synchronized C2C12s verses asynchronous or differentiated C2C12s [109]. Matrilin-2, Znf216, LPS-inducible CXC chemokine (LIX) and Tristetraprolin (TTP). These transcripts were expressed at low levels after synchronization in suspension but rapidly and transiently induced upon exit from G0. Both LIX and TTP transcripts rapidly decreased and contain AU-rich

elements within their 3'UTR regions which generally confer mRNA instability. Using focal freeze injury, where the boundaries of injury are distinguishable from uninjured muscle, both LIX and TTP transcripts are induced within the injured tissue [109]. Specifically, TTP mRNA is detected in cells underneath the basal lamina after injury by *in situ* hybridization.

We utilized microarray analysis to perform an unbiased global analysis of gene expression changes occurring during satellite cell activation and applied a similar subtraction strategy to reduce the numbers of genes for analysis. Here, I present my analysis of gene expression changes occurring in satellite cells during the initial 12 hours following an induced skeletal muscle injury.

Selection of Time Points Relevant to Satellite Cell Activation

The objective of our microarray analysis was to identify gene expression changes that occur when satellite cells transition from quiescence to an activated state. Isolation of quiescent satellite cells is currently not possible, as disruption of the muscle tissue invariably results in their activation [61]. Thus, purified satellite cells from uninjured muscle likely represent a mixed population of satellite cells at differing stages of early activation prior to the expression of MyoD [39]. To assist in identifying genes that were specific to satellite cell activation, we compared wild type satellite cells with activation defective satellite cells from uninjured muscle and 12h post-injury. Mutant Syndecan-4 null satellite cells delay expression of MyoD protein by 48h, are proliferation defective compared to wild type satellite cells and thus, activation-defective[54]. Thus, we hypothesized that changes occurring in mutant Syndecan-4 null satellite cells would not be relevant to satellite cell activation.

Results

Global Analysis of Gene Expression Changes Occurring Upon Satellite Cell Activation

Satellite cells are typically quiescent and can remain quiescent for years in humans [5]. To better understand the switch from a quiescent cell to an activated and proliferating myoblast, we examined global gene expression changes on Affymetrix gene chips. Wild type and *Sdc4*$^{-/-}$ satellite cells were purified using Fluorescence-Activated Cell Sorting (FACS) from uninjured Tibialis Anterior (TA) muscles and satellite cells from TA muscles 12h post injury. *Sdc4*$^{-/-}$ satellite cells are delayed in MyoD expression and cell cycle entry compared to wild type satellite cells. We identified gene expression changes occurring between wild type satellite cells from uninjured muscle and satellite cells 12h post injury. From this list of genes, we subtracted genes that also changed in *Sdc4*$^{-/-}$ satellite cells following 12h of muscle injury. The resulting genes will be referred to as the WT-S4 gene list (Appendix Table 1). I refined the WT-S4 gene list to genes of interest by identification of the following: 1) significantly over-represented groups of transcripts, defined by gene ontology annotation; 2) known targets of p38α/β MAPKs; and 3) genes known to participate in muscle development or regeneration.

Ontological Analysis

To visualize all gene expression changes within the activation dataset, I first generated a heat map based on a hierarchy defined by 1) the level of expression in uninjured satellite cells (UI-SCs) and 2) the directionality of change in transcript abundance between uninjured satellite cells and satellite cells 12h post injury. We observed about half of transcripts expressed in uninjured satellite cell decrease relative abundance 12h post-injury (Fig. 1; Total genes: 2850; Decreased: 1249 (44%) and, we postulated that transcripts decreasing in abundance may be required for maintenance of quiescence or to suppress satellite cell activation.

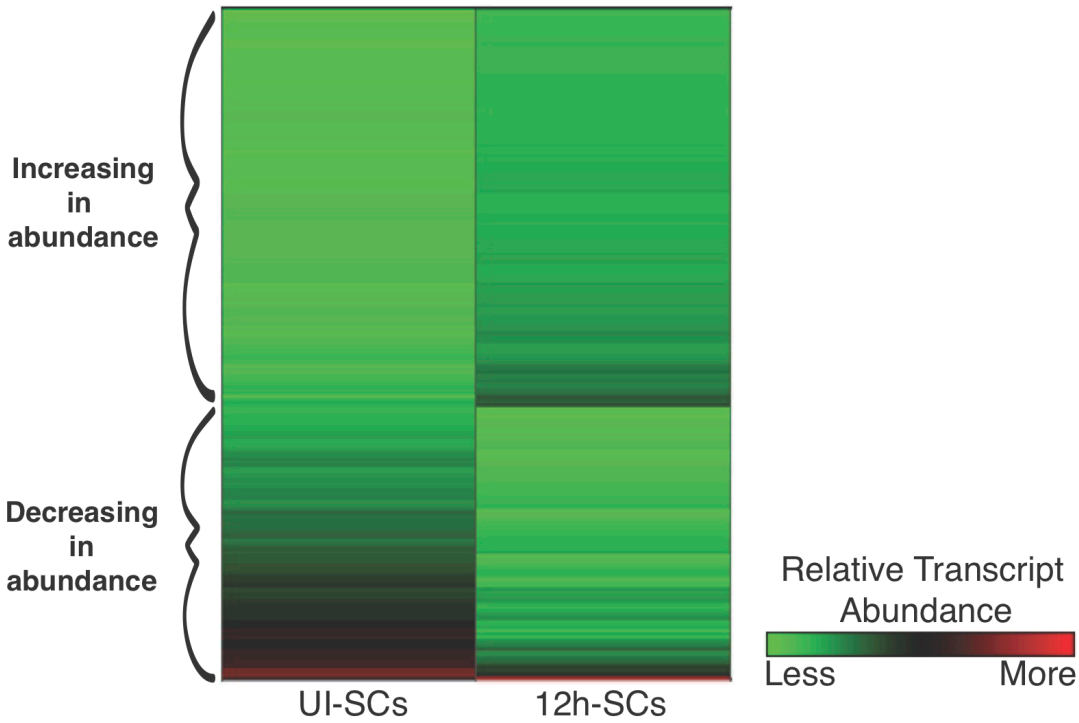

Figure 1: Heat map of WT-S4 gene list depicting gene expression changes occurring upon satellite cell activation.
Defined as WT-S4 gene list by 1) selecting genes significantly ($p<0.01$) changing more than 2-fold between UI and 12h post-injury in wild type satellite cells and 2) filtering out genes that also significantly change in *Sdc4*$^{-/-}$ satellite cells. Out of 2850 genes represented in the activation data set, 1249 genes decrease (44%). Hierarchical cluster arranged by 1) level of expression in wild type UI-SCs and 2) directionality of change after 12h post muscle injury. Green denotes lower level of relative expression while red denotes higher level of expression.

Gene ontology (GO) analysis identified several groups of genes to be enriched in the WT-S4 gene list compared to all annotated mouse transcripts. The gene ontology "Molecular Function" analysis, shows that the largest and most significantly over-represented category within the WT-S4 gene list was the GO term: Binding (Fig 2; data set: 49.6%; annotated mouse genes: 46.3%; p-value=9.81e-041). While the term "binding" is not informative, the significance of the p-value indicates that sub-categories within "binding" are highly over-represented.

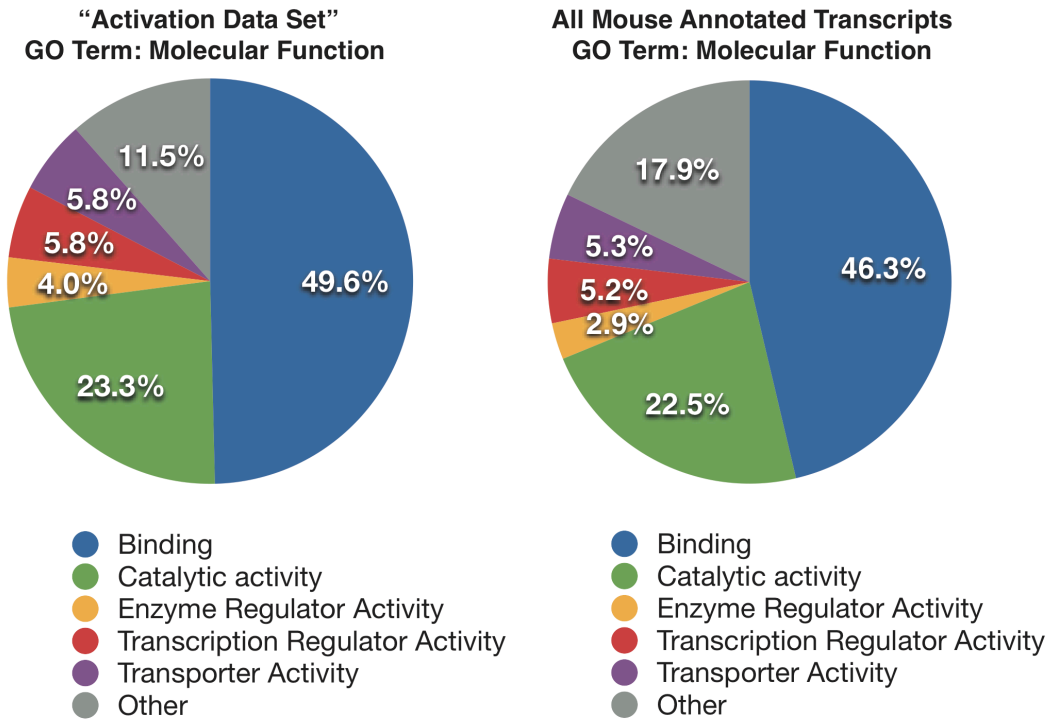

Figure 2: Molecular Function Gene Ontology Analysis Comparing All Mouse Annotated Transcripts Versus the WT-S4 gene list
Over-represented GO terms: Binding (p-value=9.81e-041), Catalytic Activity (p-value=5.71e-07), Enzyme Regulator Activity (p-value=1.52e-07), Transcription Regulator Activity (p-value=5.59e-04), Transporter Activity (p-value=8.33e-04). Categories in "other" are not significantly over-represented within the WT-S4 gene list.

Within the GO term: "binding" one of the over-represented groups is "nucleic acid binding." This group includes transcription factors, translation initiation factors, ribosomal protein subunits among others that are regulated during transition from quiescence to activation. Within "nucleic acid binding" the sub-category, "RNA binding" is significantly over-represented in the activation dataset. To visually represent these data, I produced a heat map defined by 1) the level of expression in uninjured satellite cells and 2) the directionality of change in transcript abundance between uninjured satellite cells and satellite cells 12h post-injury. Over half of "RNA binding" transcripts significantly decrease. Several decreasing transcripts encode proteins that target mRNA for decay. Thus, exclusion of stable mRNAs from polysomes or suppression of expressed mRNAs may be a mechanism where quiescent satellite cells are able to rapidly respond

to activating stimuli (Fig. 3; Total "RNA Binding" genes: 122; Decreased: 67 (55%) p-value=8.73e-05).

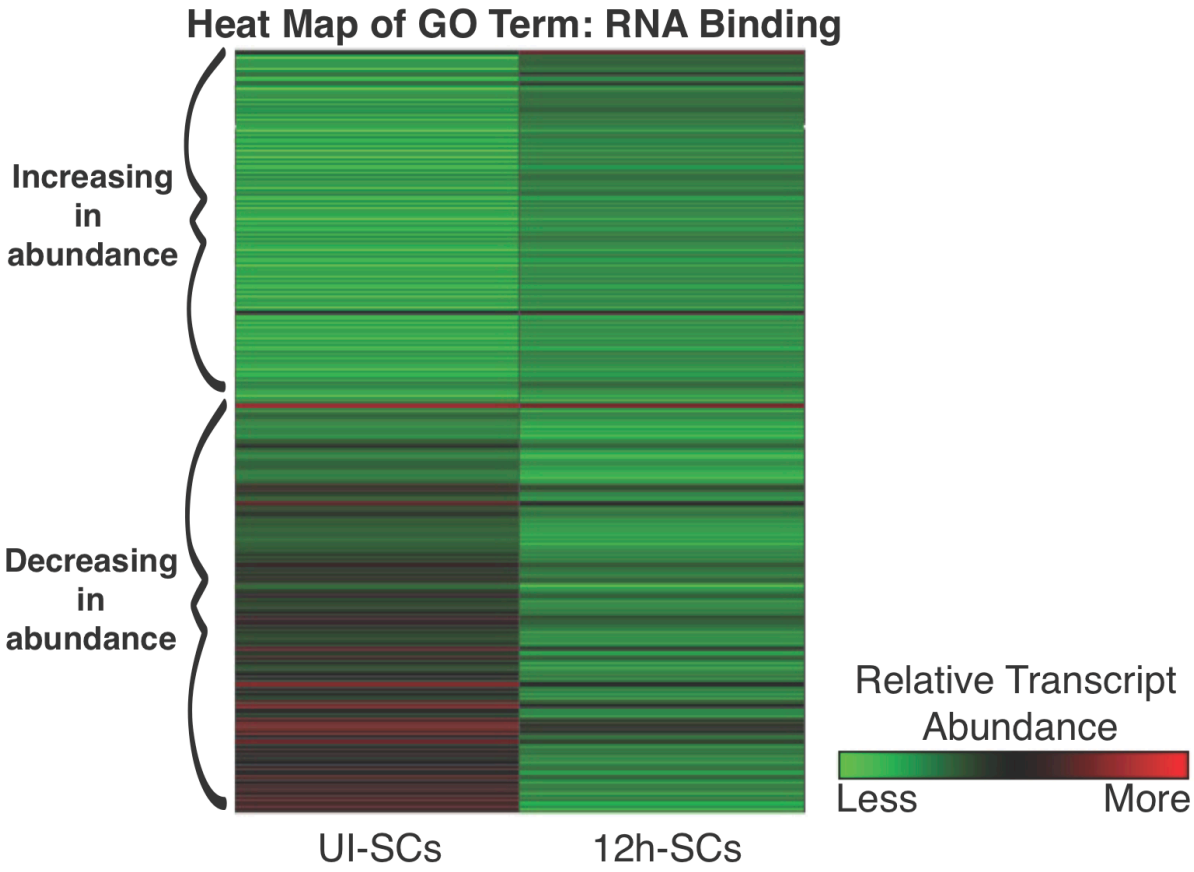

Figure 3: Heat map depicting transcripts filtered from the WT-S4 gene list with the Molecular Function GO term: RNA binding
Over half of transcripts with GO term: RNA binding decrease upon satellite cell activation but do not change in *Sdc4*$^{-/-}$ satellite cells. Total "RNA Binding" genes: 122; Decreased: 67 (55%) p-value=8.73e-05. Green denotes lower level of relative expression while red denotes higher relative level of expression.

Microarray Evidence that mRNA Turnover, Translation and Splicing Regulates Satellite Cell Activation

Gene expression is regulated by many different mechanisms; one such mechanism is through post-transcriptional regulation of mRNA. It is estimated that 5-8% of human mRNAs contain AU-rich elements (ARE) found within the 3'UTR of the transcript [111]. RNA binding proteins are known to interact with AREs and either stabilize or destabilize the transcript [112,113].

Splicing has also been shown to be important in switching from embryonic isoforms to adult splice variants of genes [114]. Therefore, I wanted to ask whether genes that are known post-transcriptional regulators of RNA, were differentially regulated as satellite cells activate.

To test whether splicing and/or ARE-BPs regulate satellite cell activation, I identified "RNA binding" transcripts that were ascribed "Biological Process" GO terms relating to translation, mRNA processing/cleavage/stabilization, and splicing. Based on the set of "Biological Process" GO terms, I assigned a category to each gene. The following categories were based on the protein's influence on mRNA turnover, translation, or splicing: negative regulator, positive regulator, splicing, or ambiguous/unknown. From the WT-S4 gene list: subset RNA binding, I identified 16 genes increasing and 43 decreasing in abundance that are known to regulate gene expression post-transcriptionally. I converted the signal intensity for each transcript from Log_2 to base 10 and calculated the difference between the expression in satellite cells 12h post-injury and in uninjured satellite cells. Positive values correspond to transcripts increasing in abundance (Table 1) where negative values denote decreasing transcripts (Table 2).

MGI symbol	Difference between UI-SCs vs 12h-SCs
Nudt21	15.86
Thoc1	19.30
Elavl1	12.63
Eif1a /// Gm8300	9.06
Nxf3	8.25
Lsm7	132.45
Eif2ak2	30.53
Piwil4	8.05
Ncbp2	31.71
Pum1	7.72
Lsm5	12.01
Cpsf3	8.82
Rbm9	12.21
Sf1	6.19
Rbmy1a1	8.17
Ptms	15.46
Lin28b	11.75

Table 1: Transcripts increasing in abundance between UI-SCs and 12h-SCs that were annotated as molecular function: RNA binding; Biological Process: RNA turnover, translation or splicing.
Blue: positive regulators; Red: negative regulators; Green: proteins involved in splicing; Black: ambiguous/unknown. False discovery rate (FDR) <0.05 and a p-value<0.01 was used to determine significance of change between uninjured satellite cells and 12 post-injury.

MGI Symbol	Difference between UI-SCs vs 12h-SCs		MGI Symbol	Difference between UI-SCs vs 12h-SCs
Eif4a2	-209.89		Snrpe	-968.20
Eif3g	-328.57		Zranb2	-98.03
Eif4h	-151.26		Hnrpll	-289.98
Pabpn1	-246.38		Snrpb	-420.55
Eif4e2	-247.48		Rbm39	-214.46
Eif1a	-126.37		Zcrb1	-180.64
Nxf1	-220.83		Sfrs3	-799.56
Eif2a	-86.80		Mbnl1	-1,154.03
Paip2	-613.81		Tra2b	-1,518.88
Calr	-453.17		Cwc15	-97.20
Zfp36l2	-218.64		Rbm39	-314.06
Cugbp1	-497.66		Syncrip	-62.83
Zfp36	-544.71		Hnrnpa2b1	-178.71
Nono	-347.61		Cherp	-131.05
Hnrnpk	-5,402.07		Sfrs2	-44.78
Cugbp2	-82.29		Sfrs7	-48.72
Rbm3	-428.55		Srrm1	-33.19
Ddx5	-622.74		Sf3b4	-23.15
Zfp36l1	-1,766.51		Hnrnpc	-1,110.43
Magoh	-52.92		Khdrbs1	-134.52
			Ddx19a	-24.63

Table 2: Transcripts decreasing in abundance between UI-SCs and 12h-SCs that were annotated as molecular function: RNA binding; Biological Process: RNA turnover, translation or splicing.
Blue: positive regulators; Red: negative regulators; Green: proteins involved in splicing; Black: ambiguous/unknown. False discovery rate (FDR) <0.05 and a p-value<0.01 was used to determine significance of change between uninjured satellite cells and 12 post-injury.

To visualize the overall trends of each category, I graphed the difference of each transcript, color coded to indicate the assigned category (Fig. 4). There are two major differences between increasing and decreasing post-translational regulators, 1) while I identified 42 different known post-transcriptional regulators decreasing in abundance, I only identified 16 that increased, and 2) the median of increasing transcripts is a relative expression value of 12.01 versus -219.7 for transcripts decreasing. The difference in magnitude of change between expression in uninjured satellite cells and satellite cells 12h post-injury underscores the importance of this switch in post-transcriptional regulators.

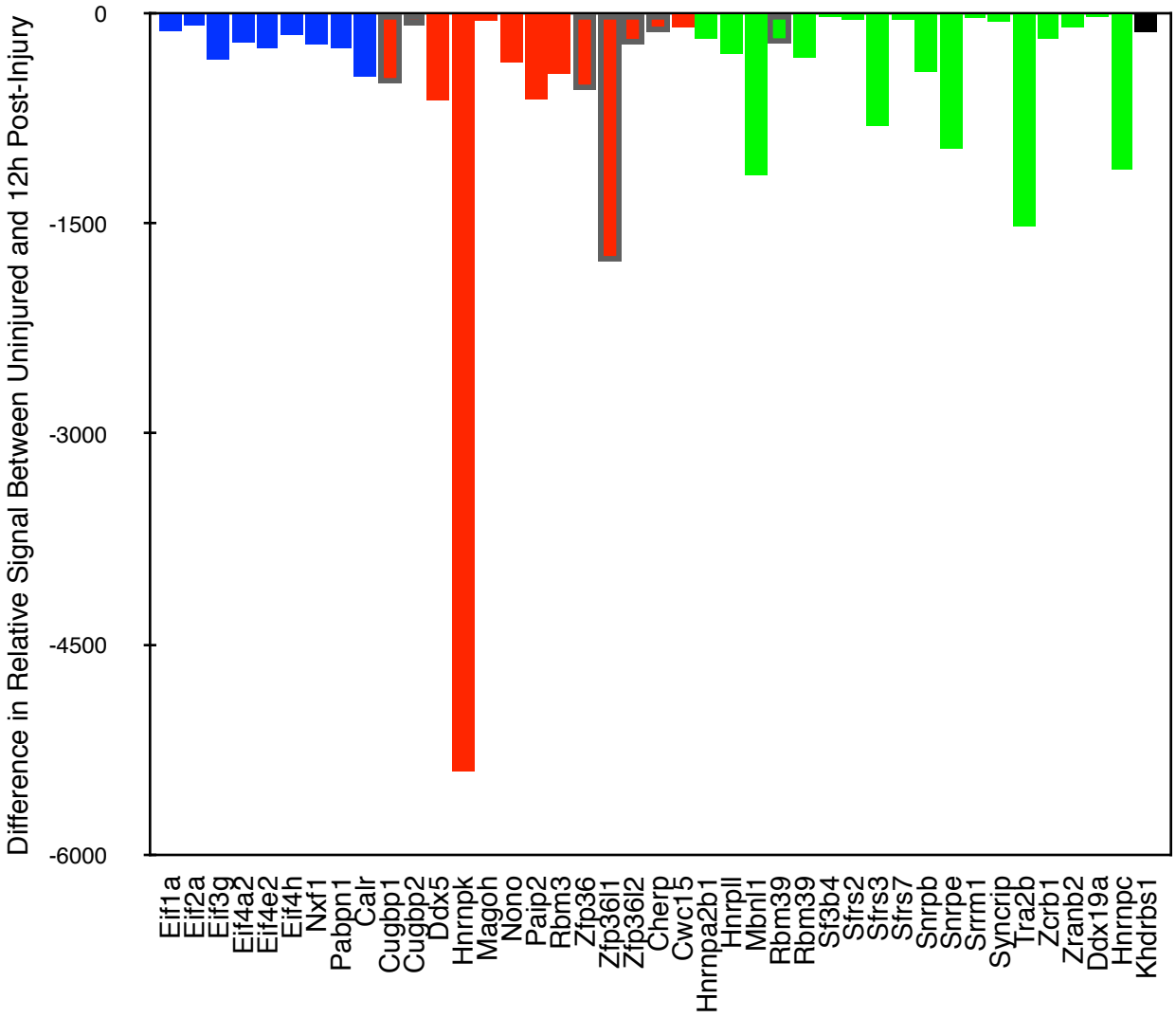

Figure 4: Post-transcriptional regulators decreasing in abundance.
Graph of post-transcriptional regulators decreasing in abundance upon satellite cell activation. Cugbp1, Cugbp2, Zfp36, Zfp36l1, Zfp36l2, and Mbnl1 (columns with grey outlines) are discussed further in the text.

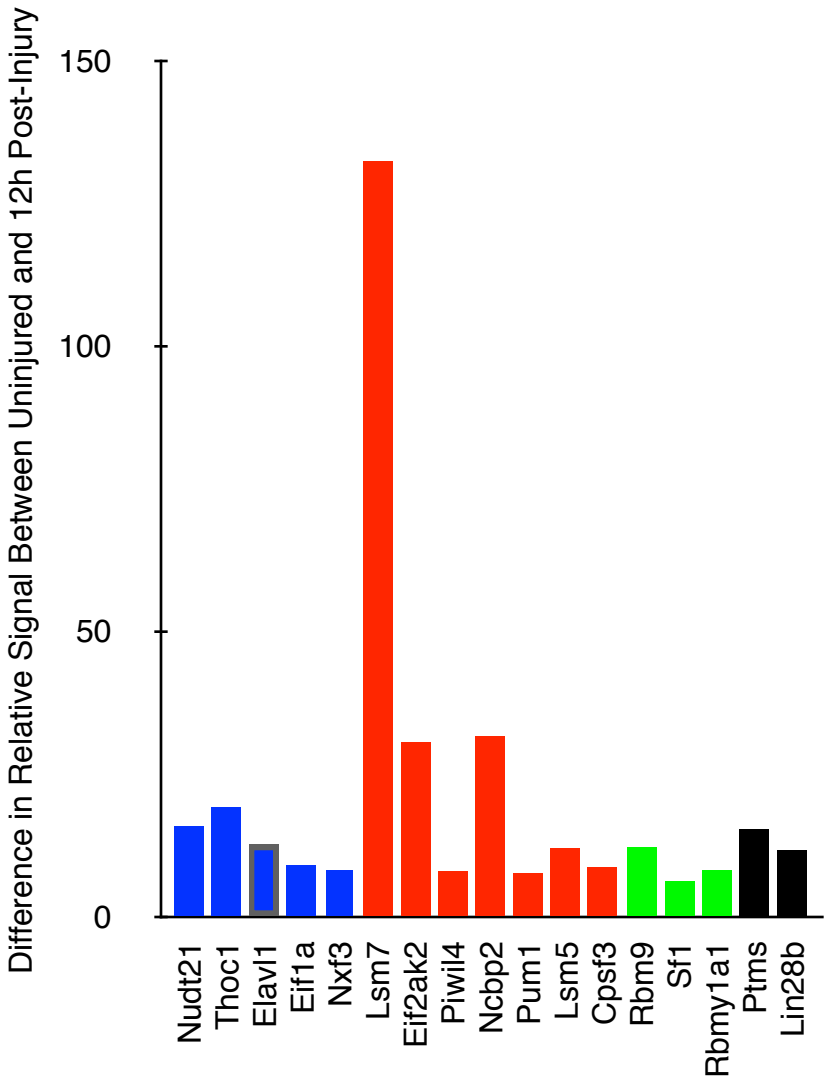

Figure 4 (continued): Post-transcriptional regulators increasing in abundance. Elavl1 is discussed further in the text.

My analysis shows that several known post-transcriptional regulators of myogenic transcripts are differentially regulated upon activation. For example, the AU-Rich element binding proteins, Cugbp1(-497.7), Cugbp2 (-82.3), and Elavl1 (protein known as HuR) (+12.6). Recently, knockdown of Cugbp1 in C2C12 myoblasts resulted in stabilization of MyoD mRNA and it appears that Cugbp1 binds to MyoD mRNA via a GU-Rich element (GRE) (Lee, 2010). HuR binds and stabilizes MyoD mRNA [99,100], thus it appears that these two proteins may antagonize each other during MyoD mRNA regulation. Several transcripts are regulated by HuR in conjunction with one or more proteins that influence mRNA turnover and/or negatively regulate translation (Pautz, 2010; Sureban, 2007; Mazan-Mamczarz K, 2007; Linker, 2005; Briata, 2003). Whether HuR and other RNA-BPs bind together or compete for binding to any given 3'UTR is less understood and likely sequence specific.

Three Tristetraprolin family members (TTP (*Zfp36),* Brf1 (*Zfp36l1),* and Brf2 *(Zfp356l2)*) significantly decrease between wild type uninjured satellite cells and satellite cells 12h post-injury but do not change in expression between uninjured *Sdc4*$^{-/-}$ satellite cells and *Sdc4*$^{-/-}$ satellite cells 12h post-injury (Fig. 5). Tristetraprolin (TTP) is currently the most well studied ARE-BP and has been shown to regulate the stability of several transcripts involved in innate immunity [115]. TTP binds to AU-rich elements within the 3'UTR of target transcripts and recruits mRNA decay enzymes to the transcript [116]. Activated-p38α/β signaling results in phosphorylation of TTP [117]. This results in TTP association with 14:3:3 proteins blocking its ability to recruit deadenylases which results in stabilization of the target transcripts [118,119].

These data support a model of post-transcriptional regulation of gene expression, including mRNA turnover and translation, as a mechanism of satellite cell maintenance of quiescence and/or suppression of activation.

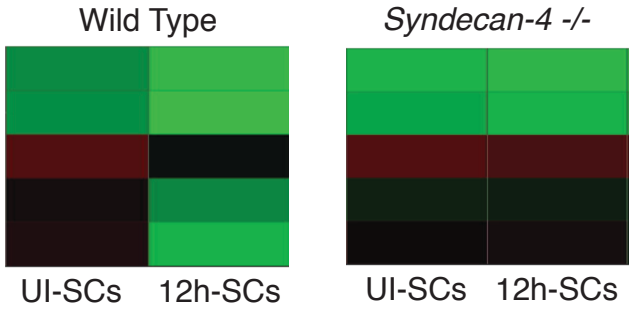

Figure 5: Transcripts encoding the TTP family (Zfp36) significantly decrease in wild type satellite cells 12h post injury while no change was observed in *Sdc4*$^{-/-}$ satellite cells after 12h of muscle injury.
Heat maps depicting gene expression change between uninjured satellite cells and satellite cells 12h post-injury in both wild type and Syndecan-4 null cells.

Identification of p38α/β Target Transcripts

Activated p38α/β MAPKs are detected within minutes of muscle injury [61]. Furthermore, p38α/β signaling is required for satellite cell activation, commitment to the myogenic lineage, and entry into the cell cycle, making p38α/β activation a critical molecular switch from quiescence to activation [61]. To identify p38α/β targets within the WT-S4 gene list: subset RNA binding, I entered these transcripts into Ingenuity Pathway Analysis (IPA) software, a bioinformatics program used to make connections between complex biological pathways. I queried the dataset for all known direct p38α/β targets. TTP was identified along with Brf1, which function is also inhibited by p38α/β MAPK signaling [94]. In addition, peroxisome proliferator-activated receptor gamma, coactivator 1 α (PPARGC1A or PCG-1α), ribosomal protein L22 (RPL22), and splicing factor, arginine/serine-rich 5 (SFRS5) were identified within the WT-S4 gene list: subset RNA binding. I decided to investigate whether the TTP family regulates satellite cell activation because 1) in human cells, TTP regulates HuR mRNA stability, a known regulator of myogenic transcripts, 2) HuR (Elavl1) and the TTP family (Zfp36, Zfp36l1 and Zfp36l2) of transcripts are differentially regulated in the WT-S4 gene list, and 4) p38α/β MAPK signaling inhibits TTP and Brf1 function. I speculated that in quiescent satellite cells, transcripts required for activation are

targeted by the TTP protein family for AU-rich mediated decay. Upon muscle injury, p38α/β MAPK signaling would inhibit TTP function and with a concurrent increase in HuR, "activation" transcripts may be rapidly stabilized.

Confirmation of Select Transcripts

I wanted to confirm the changes in transcript abundance between uninjured satellite cells and satellite cells 12h post injury. Consistent with the microarray data, expression of Zfp36, Zfp36l1, and Zfp36l2 all decreased, and Elavl1 increased in abundance between uninjured satellite cells and satellite cells 12 post-injury (Fig.6).

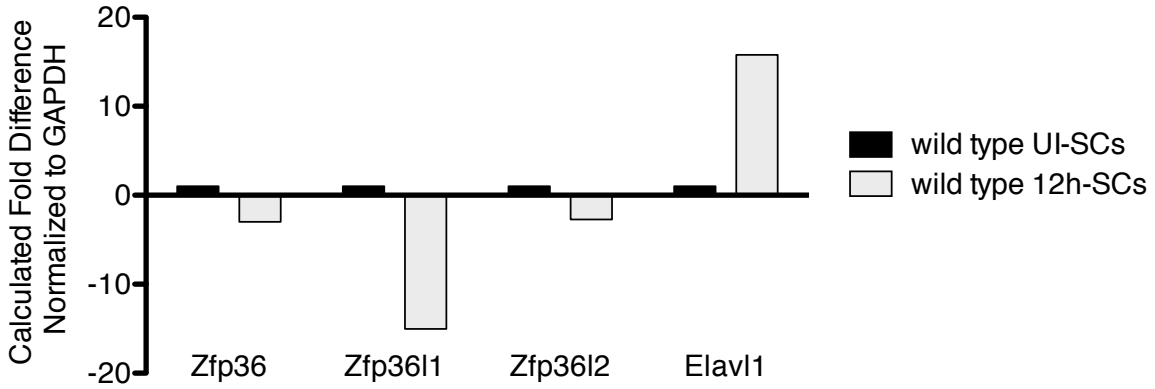

Figure 6: Expression of the *Zfp36* family and *Elavl1* are differentially regulated. Satellite cells were purified by FACS and expression of *Zfp36, Zfp36l1,* and *Zfp36l2* were detected by QT-PCR using primers directed to the Exon1/2 junction of each corresponding transcript. The transcript abundance was estimated using the delta-delta Ct method.

Microarray Data Mining with the ARE-Database

Knockout of TTP in mice results in early on-set arthritis, cachexia, and chronic inflammation [115]; thus, identifying targets of ARE-BPs may provide insights into these and other debilitating human diseases. TTP and other RNA-Binding proteins bind to AU-rich elements within the 3'UTR of target mRNA, and these sequences are thought to confer regulation of the stability of the transcript [120]. It is thought that between 5-8% of human mRNAs contain AU-rich sequences with the 3'UTR. The Human ARE-database (ARED) was developed as a bioinformatics search engine to identify novel genes which contain AU-rich elements (AREs) [111].

The ARED groups AU-rich sequences into five clusters. Clusters 1-4 contain $(AUUUA)_5$, $(AUUUA)_4$, $(AUUUA)_3$, and $(AUUUA)_2$ consecutive pentameric sequences, respectively. Cluster 5 contains one AUUUA within an AU-rich context [111]. To identify transcripts that could be post-transcriptionally regulated by RNA-binding proteins during satellite cell activation, we entered the WT-S4 gene list into the ARE Database. The ARE Database identified, TTP (Zfp36) and the TTP family members (Zfp36l1 and Zfp36l2) as containing AU-rich elements with their 3'UTRs. (Table 3). This is consistent with the fact that TTP has been shown to bind and regulate its own mRNA via an AU-rich element within its 3'UTR [93,121].

Select ARE containing genes			
MGI Symbol	**Gene Name**	**Difference: UI-SCs & 12h-SCs**	**AU-Rich Element Cluster**
Zfp36	**zinc finger protein 36**	**-544.71**	**Cluster 5**
Zfp36l1	**zinc finger protein 36, C3H type-like 1**	**-1,766.51**	**Cluster 4**
Zfp36l2	**zinc finger protein 36, C3H type-like 2**	**-218.64**	**Cluster 5**

Table 3: ARE-BP Genes Identified as containing AREs by the ARE database

<u>Myogenic/Satellite Cell Transcripts with AU-rich Elements</u>

Since p38α/β signaling antagonizes TTP-mediated mRNA decay [121] and we observe TTP mRNA decreasing by 12h post-injury, I expected putative TTP target transcripts to increase in abundance in satellite cells 12h post injury versus uninjured satellite cells. Several ARE-containing transcripts were identified for the WT-S4 gene list. Interestingly, many identified ARE-containing transcripts had previously been shown to be involved in muscle or myogenesis (Table 4).

Select ARE containing genes			
MGI Symbol	**Gene Name**	**Difference: UI-SCs & 12h-SCs**	**AU-Rich Element Cluster**
Elavl1 (HuR)*	**embryonic lethal abnormal vision-like 1**	**12.63**	**Cluster 2**
Mef2a	**myocyte enhancer factor 2A**	**14.77**	**Cluster 5**
Tiam1	**T-cell lymphoma invasion and metastasis 1**	**5.59**	**Cluster 5**
Id2	**inhibitor of DNA binding 2**	**-638.65**	**Cluster 5**

*Elavl1 - found using ARED 3.0, current ARED Organism does not identify Elavl1 as containing an AU-rich element.

Table 4: Myogenic genes or genes implicated in satellite cell biogenesis that contain AU-rich elements as determined by ARE Database.

Discussion

I sought to characterize the global transcriptional changes by microarray analysis that occur when satellite cells transition from quiescence to an activated, committed myoblast. Based on these data, it appears that regulation of mRNA turnover and translation suppresses activation in quiescent satellite cells. This conclusion is based on the following observations: 1) transcripts with GO term: RNA binding are over-represented within genes changing in wild type satellite cells and over half of these transcripts decrease in abundance; 2) the magnitude of change and number of negative regulators of mRNA turnover and translation that decrease compared to those that increase in abundance; 3) positive post-transcriptional regulators of myogenic transcripts increase while negative post-transcriptional regulators of myogenic transcripts decrease; 4) all known members of the TTP family of ARE-BPs are decreasing in abundance which are antagonized by p38α/β MAPK signaling, effectively "shutting off" mRNA decay mediated by these proteins. Post-transcriptional regulation of mRNA during satellite cell activation, may be a mechanism where satellite cells could rapidly switch from a quiescent state to an activated state.

Quiescence is generally regarded as a hypometabolic state [122] and quiescent satellite cells display morphological characteristics that are consistent with this idea [32]. However, we found that nearly half of all transcripts expressed by satellite cells from uninjured muscle significantly decrease 12h post-injury. This implies that uninjured satellite cells express several transcripts during quiescence that are no longer needed during muscle regeneration. I found positive regulators of myogenesis increasing whereas several negative post-transcriptional regulators of myogenic mRNAs significantly decrease after 12h of injury. Thus, it appears that myogenesis is actively suppressed in quiescent satellite cells.

Several molecular events occur upon satellite cell activation that are necessary for normal muscle regeneration. One of the earliest events is activation of p38α/β MAPK [61]; which is required for MyoD induction and entry into the cell cycle [61]. Considering the transcripts that are differentially regulated, it appears that there is a switch between suppressors of MyoD, (Cugbp1 [123], Id2, and Id3 [124]) to positive post-transcriptional regulators of MyoD mRNA (HuR [99,100]). Decreasing negative regulators of myogenesis represent a derepression of MyoD mRNA stability and MyoD transcriptional activity. Cugbp1 is a known splicing regulator [125] but has just been found to bind to the 3'UTR of MyoD mRNA and regulate its decay [123]. Inhibitor of DNA binding 2 (Id2) binds and negatively regulates MyoD transcriptional activity by forming a dominant negative heterodimer with MyoD [124]. Id2 decreases in abundance in satellite cells 12h post-injury, implying that quiescent satellite cells may produce Id2 protein in order to inhibit any MyoD protein if it were to be made. Another Id protein which negatively regulates MyoD transcriptional activity is Id3 [124]. Transcripts encoding Id3 decreased in as wild type satellite cells activated but did not change in *Sdc4*$^{-/-}$ satellite cells 12h post injury. Thus, MyoD appears to be suppressed in quiescent satellite cells by destabilzing MyoD mRNA and inhibiting MyoD transcriptional activity.

Increased positive post-transcriptional regulators, such as HuR, may stabilize target transcripts required for satellite cell activation and commitment to myogenesis. Regulation of myogenesis *in vitro* by HuR has been well established. HuR binds and stabilizes several myogenic transcripts, including MyoD, Myogenin, and p21 during C2C12 differentiation [99,100]. Knockdown of HuR inhibits C2C12 differentiation; whereas, over-expression of HuR accelerates C2C12 differentiation [99,100]. HuR positively influences C2C12 myoblast proliferation with Pitx2, by binding and stabilizing CyclinD1 mRNA. Upon switching to differentiation conditions, HuR and Pitx2 dissociate from the mRNA resulting in CyclinD1 mRNA decay and cell cycle exit (Gherzi, 2010). Thus, HuR stabilizes target mRNA during proliferation and differentiation in C2C12s, two

mutually exclusive states, indicating that regulation of HuR targets is either in trans or through competition of cis-binding sites. Currently, the regulation of HuR and its targets in satellite cells is poorly understood.

Transcripts that contain AU-rich elements and are represented in the WT-S4 gene list could represent additional targets of RNA-binding proteins which influence satellite cell activation and myogenic commitment. I have identified AU-rich containing transcripts using the ARE database and found several important genes known to regulate myogenesis (Table 4). Although not sufficient to drive myogenesis alone, myocyte enhancer factor 2A (Mef2a) transcriptionally regulates muscle-specific genes during development [126], adulthood [127] and potentially during regeneration [128]. p38 MAPKs regulate Mef2a by direct phosphorylation which increases its transcriptional activity [86]. Whether Mef2a mRNA turnover is post-transcriptionally regulated to ensure proper transcriptional induction of myogenic genes, remains uncharacterized. Another AU-rich containing transcript identified though the ARE Database was Tiam1 (Table 4). (T-cell lymphoma invasion and metastasis 1 (Tiam1) in conjunction with the Par3 polarity complex regulates epithelial cell polarity [59] and growth factor directed migration [129]. Recently, we have shown that Tiam1 forms a complex with ParD3, thus Tiam1 may regulate satellite cell migration and asymmetric cell division (Olwin Lab, unpublished data). Currently, post-transcriptional regulation of Tiam1 mRNA turnover remains uncharacterized.

Together these data support a previously unappreciated role for post-transcriptional regulation of gene expression during satellite cell activation.

Materials and Methods

Microarray Analysis

Satellite cells were isolated from Tibialis Anterior muscles that were either uninjured or 12h post injury with 50ul of 1.2% BaCl to induce myonecrosis. Satellite cells were purified by FACS based on Syndecan-3 expression from at least three age matched wild type or Syndecan-4 null mice as previously described [130]. Total RNA isolated using a PicoPure RNA Isolation Kit (Arcturus) was subjected to two rounds of linear T7-based amplification (RiboAmp HA Kit, Arcturus). Based on the number of cells collected, this resulted in an RNA equivalent of 5000 Syndecan-3 positive cells. Biotin-labeled cDNA was generated using an Affymetrix IVT Labeling Kit. Labeled cRNA was quantified and analyzed for quality using BioAnalyzer (Agilent). Labeled cRNA (5 μg) was fragmented and hybridized to Affymetrix 430 v.2 mouse microarrays at the University of Colorado Core facilities. Chips were scanned on a GeneChip Scanner 3000 (Affymetrix) and intensity data recovered in GCOS (Affymetrix). CEL files from three replicate genechips were imported directly into Spotfire (TIBCO) and normalized by GCRMA. Using a 99% confidence threshold (p-value ≤ 0.01), probe sets that changed in relative expression between Syndecan-4 uninjured satellite cells and Syndecan-4 satellite cells 12h post injury were subtracted from probe sets changing between wild type uninjured satellite cells and wild type satellite cells 12h post injury. This analysis resulted in the WT-S4 gene list. Heat map arranged by 1) level of expression in wild type satellite cells from uninjured muscle and 2) directionality of change after 12h post muscle injury. Gene ontology analysis was performed using Spotfire Ingenuity Pathway analysis.

Spotfire analysis

Analysis of the microarray data was performed using Spotfire Software. A Robust Multi-array Analysis (RMA) normalization across all of the microarray chips was performed. Spotfire performed a “scale” normalization between all of the arrays in order to equalize the median.

Statistical Analysis

Differences in gene expression over time and genotype were statistically analyzed by 2-way analysis of variance (Anova). The gene was considered expressed if the normalized $\log_2$ expression value was greater or equal to 2.0 and genes were considered for further analysis if a greater than 2 fold-change in relative expression between time points was calculated. Both of these assumptions were applied to wild type and *Sdc4*$^{-/-}$ data sets. Transcripts significantly changing were defined using a 99% confidence threshold (p-value ≤ 0.01) when comparing the difference between wild type uninjured satellite cells versus wild type satellite cell 12h post-injury. From this list, genes that significantly changed between *Sdc4*$^{-/-}$ uninjured satellite cells versus *Sdc4*$^{-/-}$ satellite cells 12h post-injury (p-value ≤ 0.01) were subtracted from the wild type gene list. The final list of genes is referred to as the WT-S4 gene list (Appendix Table 1).

Quantitative RT-PCR

Quantitative-PCR primers were designed against the first exon/exon junction for the following transcripts, Zfp36 (TTP), Zfp36l1 (Brf1), Zfp36l2 (Brf2), and Elavl1 (HuR). The fold difference was calculated as: 2*(-(deltaCt(12h)-deltaCt(UI)) normalized to GAPDH. Primer sequences: *Elavl1* Exon1/2; (FOR: 5' GCTTATTCGGGATAAAGTAGCAGGA; REV: 5' TTCACAAAACCGTAGCCCAAG). *Zfp36* Exon1/2; (FOR: 5' GCCATCTACGAGAGCCTCCA; REV: 5' CGTGGTCGGATGACAGGTC). *Zfp36l1* Exon1/2; (FOR: 5'CGAAGTTTTATGCAAGGGTAA; REV: 5' GCGCTGGGAGTGCTGTAGTT). *Zfp36l2* Exon1/2; (FOR 5'CGACCACACTTCTGTCACCCT; REV 5'GGATTTCTCCGTCTTGCACAA).

Chapter 3: Stabilization of MyoD mRNA is Required for Satellite Cell Activation

Introduction

Skeletal muscle is dynamic and able to respond rapidly to a multitude of different physical and chemical stresses [104]. Resident muscle stem cells called satellite cells are responsible for adult muscle growth and repair [7]. Satellite cells are typically quiescent and are able to remain mitotically quiescent for years [5,32]. Quiescent satellite cells have minimal cytoplasm, condensed chromatin, and few ribosomes [32,131]. When muscle requires repair, extracellular stimuli, such as HGF, FGF and/or TNF-α activate satellite cells to exit from G0 [56-58,132]. Activated satellite cells begin to express the muscle specific transcription factor, MyoD and form a proliferating myoblast population[61,75]. Upon differentiation, myoblasts begin to express Myogenin, a muscle specific transcription factor required for myogenic differentiation [133]. Fully regenerated muscle contains similar numbers of quiescent satellite cells as uninjured muscle and appears phenotypically normal. The mechanisms governing activation of satellite cells are poorly understood.

The earliest known molecular markers of activated satellite cells are activated p38α/β MAPKs which occurs within minutes of muscle injury [61]. Rapid activation of p38α/β MAPKs act as molecular switches to activate quiescent satellite cells [61]. If p38α/β MAPK signaling is blocked satellite cells fail to express MyoD and fail to enter the cell-cycle [61]. MyoD expression is critical for normal muscle regeneration [68]. MyoD expression commits satellite cells to myogenesis and facilitates S-phase entry by regulating the licensing of origins of replication [75]. Although MyoD expression is required upon satellite cell activation, aberrant MyoD activity in quiescent satellite cells may cause precocious differentiation and stem cell loss since forced MyoD expression is sufficient to induce the complete myogenic transcriptional program [134]. The mechanistic relationship between p38α/β MAPK signaling and MyoD induction during satellite cell activation has not been explored.

Syndecan-4 is a heparan sulfate proteoglycan expressed on the surface of satellite cells which facilitates p38α/β MAPK activation and MyoD induction in satellite cells [53,54]. Following muscle injury, *Sdc4-/-* satellite cells delay p38α/β MAPK activation and fail to commit to myogenesis or divide in the first 48h following isolation [54]. We compared gene expression profiles of wild type satellite cells to *Sdc4-/-* satellite cells FACS isolated from uninjured muscle and muscle 12h post injury . We subtracted gene expression changes occurring in *Sdc4-/-* satellite cells from gene expression changes occurring in wild type satellite cells over the initial 12h post muscle injury. Approximately half of transcripts expressed in satellite cells from uninjured muscle decreased 12h post injury. Many decreasing transcripts encode proteins that target mRNA for decay, suggesting a role for post-transcriptional gene regulation in satellite cell activation. We show that one of these RNA-binding proteins, Tristetraprolin (TTP) encoded by the *Zfp36* gene, can suppress myogenesis.

In macrophages, TTP binds and destabilizes pro-inflammatory cytokine mRNAs via AU-rich elements within the 3‘UTR of target transcripts targets [135]. TTP is rapidly inhibited upon activation of the p38α/β MAPK pathway resulting in the induction of cytokine expression. In macrophages, this mechanism quickly translates extracellular stimuli into robust changes in gene expression. In satellite cells, p38α/β MAPK inhibition of TTP may play a similar role in relaying muscle injury signals, rapidly changing gene expression through the regulation of mRNA stability. Here, we show that p38α/β MAPK regulation of MyoD mRNA stability plays a previously unappreciated key role in the activation of satellite cells. We show that the MyoD 3‘UTR is directly destabilized by TTP. Further, a mutant of TTP that constitutively decays target mRNAs is dominant over a known stabilizer of MyoD mRNA, the RNA-binding protein, HuR[99,100]. Upon activation of p38α/β MAPKs, TTP-mediated destabilization of MyoD mRNA is blocked in a manner dependent upon phosphorylation of TTP. Our data suggests that activated-p38α/β

MAPK inhibition of TTP increases MyoD mRNA stability rapidly switching quiescent satellite cells to activated myoblasts.

Results

Transcripts Encoding "RNA-Binding" Proteins Decrease Upon Satellite Cell Activation

Satellite cells are typically quiescent and can remain quiescent for years in humans [5]. Upon injury, satellite cells rapidly activate, commit to myogenesis, and repair the muscle tissue. We performed an Affymetrix gene chip experiment to better understand the global gene expression changes occurring as quiescent satellite cells switch to activated proliferating myoblasts. The gene expression profiles of satellite cells enriched by FACS from uninjured muscle were compared to satellite cells isolated from muscle 12h post-injury. Genes changing in wild type and mutant *Syndecan-4 (Sdc4$^{-/-}$)* null satellite cells over the first 12h post muscle injury were compared. *Sdc4$^{-/-}$* satellite cells are severely delayed in activation, MyoD expression, cell cycle entry, and are unable to repair muscle [54]. To identify genes regulating the switch to an activated satellite cell, we subtracted genes changing in wild type satellite cells that also changed in *Sdc4$^{-/-}$* satellite cells 12h post injury (Fig. 1A). The list of unique wild type genes will be referred to as the "WT-S4 gene list" (Appendix Table 1).

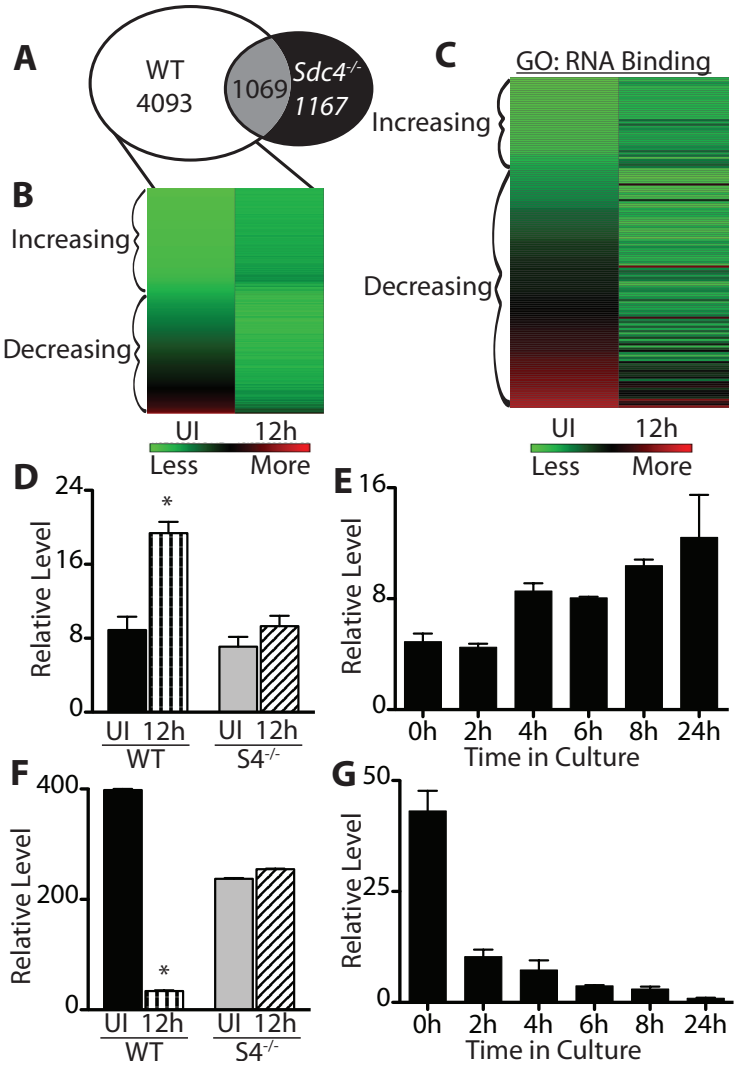

Figure 1: Transcripts Encoding RNA Binding Proteins are Differentially Regulated During Satellite Cell Activation.

A. Illustrative depiction of the WT-S4 gene list where transcripts changing from uninjured to 12h post injury in activation-deficient Syndecan-4 null were subtracted from genes changing in wild type satellite cells from uninjured to 12h post injury. **B.** Out of 4093 genes represented in the WT-S4 gene list, 1915 genes decrease (47%). Green denotes lower level of relative expression while red denotes higher level of expression. **C.** Heat map depicting transcripts filtered from the WT-S4 gene list with the Molecular Function GO term: RNA binding. Over half of transcripts with GO term: RNA binding decrease upon satellite cell activation but do not change in Sdc4 null satellite cells. Total "RNA Binding" genes: 152; Decreased: 107 (70%), p-value=8.73e-05. **D.** *Elavl1 p*robe sets encoding HuR significantly increase in wild type satellite cells but do not change in abundance in Sdc4 null satellite cells 12h post injury. **E.** HuR mRNA increases as satellite cells activate in culture. **F.** *Zfp36* probe sets encoding TTP significantly decrease in wild type satellite cells while no change was observed in Sdc4 null satellite cells 12h post injury. **G.** TTP mRNA expression decreases as wild type satellite activate *in vitro*. Graphs represent average +/- standard deviation. * p-value <0.01.

Satellite cells exit quiescence and undergo cell growth and organelle biogenesis [41-46]; thus, we expected mostly an increase in transcript abundance 12h following muscle injury. Unexpectedly, we observed that 47% of probe sets in the WT-S4 gene list decreased as satellite cells activated (Fig. 1B). To determine the types of genes represented within our gene list, we further examined the WT-S4 gene list for gene ontology (GO) terms with significant enrichment. Probe sets annotated as "nucleic acid binding: RNA binding," were significantly over-represented in the WT-S4 gene list (Fig. 1C). One of the transcripts encoding an "RNA binding"protein increasing in abundance 12h post-injury was *Elavl1,* which encodes HuR (Fig. 1D). HuR has been shown to positively regulate the stability of myogenic transcripts, including MyoD mRNA [99,100]. Since upon injury, MyoD is rapidly induced in satellite cells, HuR may stabilize MyoD mRNA during satellite cell activation. To verify the microarray data, quantitative PCR analysis of HuR mRNA in satellite cells indicated that HuR mRNA begins to increase after 4h in culture (Fig. 1E). After 12h in culture, we detect a 3-fold increase in HuR mRNA. These data are consistent with a role for HuR in the stabilization of MyoD transcripts upon satellite cell activation.

The gene ontology term "RNA binding" includes the genes encoding translational machinery. Since quiescent satellite cells drastically increase protein synthesis upon activation [42-45], we expected most transcripts encoding "RNA binding" proteins to increase upon satellite cell activation; however, we observed that 70% of genes encoding "RNA binding" proteins represented in the WT-S4 gene list significantly decreased 12h post-injury. We observed that some decreasing transcripts encoded proteins known to destabilize mRNA, thus we hypothesized that this may represent a derepression of genes required for satellite cell activation. One such decreasing "RNA binding" gene was *Zfp36*, which encodes Tristetraprolin (TTP) (Fig 1F.). Additionally, the two TTP family members, *Zfp36L1* and *Zfp36L2*, which encode Brf1 and Brf2, respectively, also decreased upon satellite cell activation (Fig. 1H and I). Previously, TTP was identified in a screen for genes that may regulate satellite cell activation [109]. TTP recruits decay

enzymes to mRNAs that contain AU-rich sequences in their 3'UTRs [116,119] and may repress mRNAs that are required for satellite cell activation. Quantitative PCR analysis of satellite cell mRNA showed that 2h after culture, TTP mRNA decreased 10-fold in abundance when compared to freshly isolated satellite cells (Fig. 1G). Quantitative PCR showed that Brf1 and Brf2 mRNAs also decreased as satellite cells activated (Fig 1J and K).

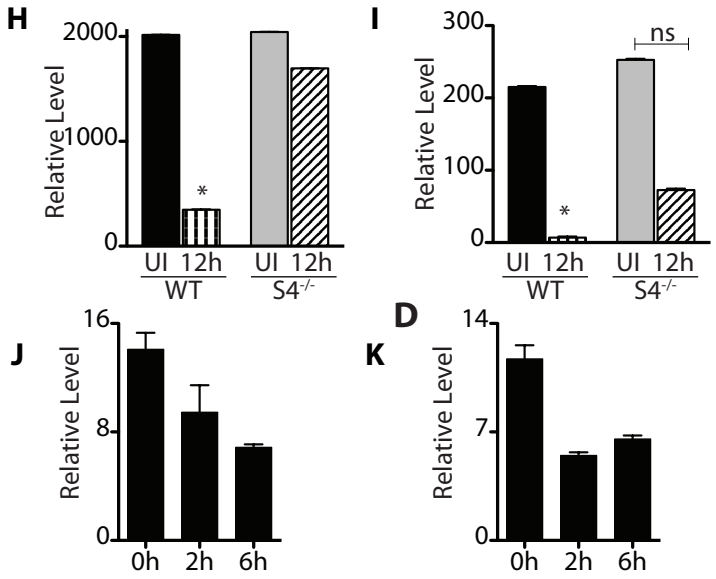

Figure 1 (cont.): Transcripts Encoding the RNA Binding Proteins Brf1 and Brf2 Decrease During Satellite Cell Activation.
H. and I. *Zfp36L1* and *Zfp36L2* probe sets encoding Brf1 and Brf2, respectively, significantly decrease in wild type satellite cells while no change was observed in Sdc4 null satellite cells 12h post injury. **J. and K.** Brf1 and Brf2 mRNA expression decreases as wild type satellite activate *in vitro*. Graphs represent average +/- standard deviation. * p-value <0.01.

In conjunction with decreased TTP mRNA abundance, TTP function may also be rapidly inhibited upon muscle injury. Previously, we have shown that p38α/β MAPK signaling is required for satellite cells to commitment to myogenesis and occurs within minutes of muscle injury [61] and TTP-mediated mRNA decay is inhibited by p38α/β MAPK signaling [136]. We postulated that TTP-mediated mRNA decay suppresses myogenesis in quiescent satellite cells and

that upon muscle injury p38α/β MAPK signaling rapidly inhibits TTP resulting in increased myogenic transcript stability.

siRNA Knockdown of TTP Induces Myogenesis

Following muscle injury, commitment of activated satellite cells to myogenesis may require p38α/β MAPK inhibition of TTP-mediated mRNA decay. To test whether TTP suppresses myogenesis, we knocked-down the *Zfp36* family members, TTP, Brf1 and Brf2 (denoted TTPmix) with siRNAs in C2C12 myoblasts. We targeted these three *Zfp36* members with siRNAs since they all possess the CCCH Zinc Finger RNA binding motif and may target common transcripts [115]. To test the efficacy of TTP knock-down, C2C12 myoblasts were co-transfected with myc-tagged TTP and either control siRNA or TTPmix siRNAs and were analyzed by western blotting for anti-myc. We observed approximately 50% knockdown of myc-tagged TTP when co-transfected with TTPmix siRNAs (Fig. 2A). The Brf1 and Brf2 siRNAs have been functionally tested using pulse-chase decay assays [137].

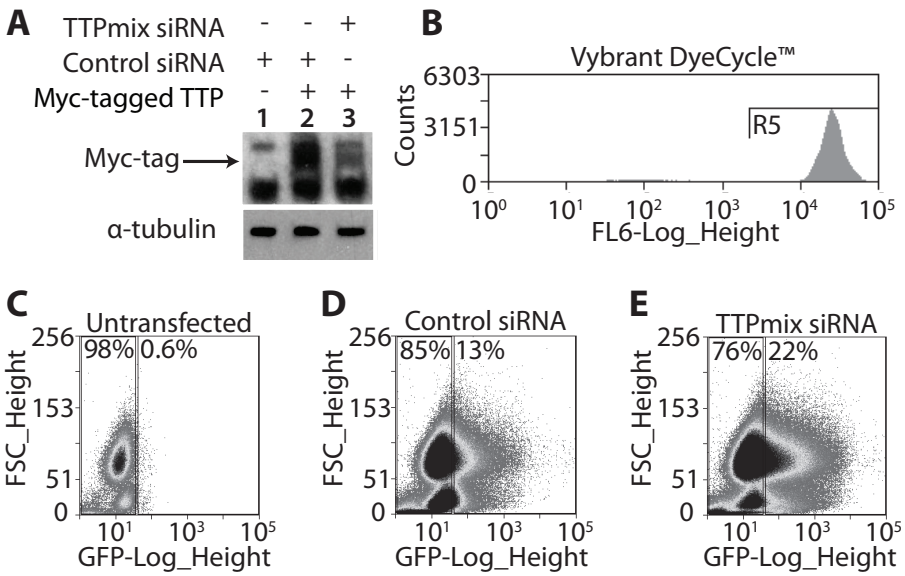

Figure 2: TTPmix siRNA knockdown
A. Proliferating C2C12 myoblasts were transfected with either empty vector or myc-tagged TTP (Lanes 2-5) and control siRNA (lanes 1,2) or TTPmix siRNA (lane 3) **B.-D.** FACS isolation of eGFP transfected cells either co-transfected with control siRNAs or 2.5ug TTPmix siRNAs. **B.** Cells were harvested by trypsin digestion and stained with Vybrant DyeCycle™ Vital Dye to detect viable cells. **C.** Untransfected control cells showing background fluorescence. **D.** Cells transfected with negative control siRNA and eGFP; 12.63% sorted as identified eGFP positive. **E.** Cells transfected with TTPmix siRNA and eGFP; 22.13% sorted as identified eGFP positive.

C2C12 myoblasts were co-transfected with TTPmix siRNA or negative control siRNA along with eGFP to serve as a transfection marker. Following FACS enrichment for live eGFP+ siRNA transfected C2C12s (Fig. 2B-E), the cells were analyzed by western blotting. TTPmix siRNA transfection resulted in an approximate 2.7-fold increase in MyoD protein when compared to control siRNA transfected cells (Fig. 3A). Typically MyoD induction in C2C12 myoblasts results in increased Myogenin expression which drives the cells to differentiate [138]. Thus, we tested whether the increase in MyoD observed in TTPmix siRNA transfected cells was sufficient to induce Myogenin in C2C12 myoblasts. Nearly 10-fold more C2C12 myoblasts expressed Myogenin while in proliferation conditions when transfected with TTPmix siRNA compared to control siRNA transfected cells (Fig. 3B and C). This result was recapitulated in the MM14 satellite cell line. TTPmix siRNA transfection resulted in a significant increase in the percentage

of Myogenin expressing MM14 cells under proliferation conditions (Fig. 3C). These data are consistent with the idea that TTP suppresses myogenesis in satellite cells.

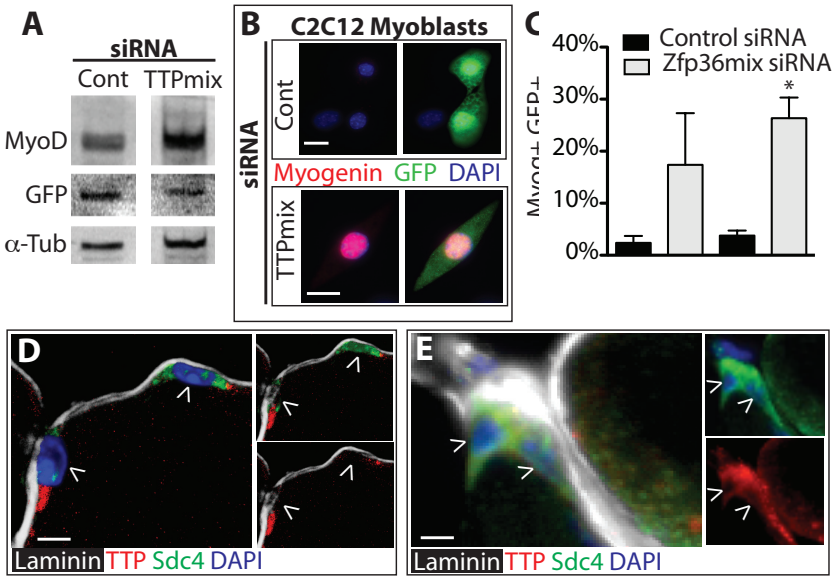

Figure 2: TTP Suppresses Myogenic Differentiation

A. Transfection of TTPmix siRNAs Increases MyoD Expression by ~3-Fold. Proliferating C2C12 myoblasts were transfected with either 2.5µg control siRNAs (Qiagen All-Star Negative control) or 2.5µg TTPmix which consisted of an equal mix of siRNAs against TTP, Brf1, and Brf2. Transfected cells were cultured for an additional 36h in proliferation conditions (15% horse serum). Transfected eGFP(+), DAPI(-) cells were enriched by FACS. MyoD signal intensities were normalized to α-Tubulin and eGFP as loading and transfection controls, respectively. Control siRNA normalized MyoD intensity was set to 100% and TTPmix siRNA normalized MyoD intensity fold-increase was calculated with respect to control siRNA. **B-C.** Transfection of TTPmix siRNA induces differentiation in proliferation conditions. **B and C.** Proliferating C2C12 and **C.** MM14 myoblasts were transfected with either 2.5µg control siRNA or 2.5µg TTPmix siRNA and cultured for an additional 36h in proliferation media. Cells were stained for myogenin (red) to detect differentiating cells, anti-GFP (green) to detect transfected cells and DAPI (blue). Average +/- Std Dev plotted for 3 independent experiments. *Student's 2-tailed t-test; p-value<0.01. **D.** TTP is very low or undetectable in Syndecan-4 positive satellite cells in perfused resting muscle. 4% paraformaldehyde was perfused throughout the mouse in order to preserve quiescent satellite cells and stained for TTP (red), Syndecan-4 (green) and Laminin (white) to identify sub-laminar satellite cells and DAPI to mark nuclei (blue). Carets denote sub-laminar Syndecan-4 positive satellite cells. **E.** The majority of TTP protein appears cytoplasmic in Syndecan-4 (S4) positive satellite cells in freshly isolated uninjured muscle. Fixed muscle tissue was stained as in D. Carets denote sub-laminar Syndecan-4 positive satellite cells. White scale bars = 25 µm.

TTP is Detected in Satellite Cells

Active TTP (unphosphorylated) is unstable making active TTP protein difficult to detect [97,139]. Conversely, p38α/β-mediated phosphorylation of TTP increases its protein stability resulting in a rapid increase in TTP [139]. To study quiescent satellite cells in resting muscle, we perfused a mouse with 4% PFA to fix the tissue *in situ*. Under these conditions, TTP was either undetectable or very low in satellite cells (Fig. 3D) and thus, quiescent satellite cells may have active TTP (unphosphorylated). Dissection of the muscle activates p38α/β MAPKs in satellite cells prior to fixation [61] and this may result in TTP phosphorylation and stabilization. We detected a greater intensity of TTP staining in most satellite cells from freshly isolated muscle when compared to perfused muscle (Fig. 3E). These data are consistent with the idea that TTP is stabilized by p38α/β MAPK signaling upon satellite cell activation.

p38α/β MAPKs phosphorylates TTP and regulates HuR expression in Satellite Cells

Muscle injury rapidly activates p38α/β MAPKs [61] but targets of p38α/β MAPKs in activated satellite cells have not been characterized. Both HuR and TTP are known targets of p38α/β MAPK signaling in other systems [103,117]. To test whether p38α/β MAPK signaling regulates TTP and HuR in satellite cells, we inhibited p38α/β MAPK signaling in freshly isolated satellite cells. Since muscle dissection activates p38α/β MAPKs [61]; we developed a method to inhibit p38α/β MAPK signaling prior to muscle dissection (Fig. 4A). By injecting mice intraperitoneal (i.p.) with a p38α/β MAPK inhibitor one hour prior to dissection, we significantly reduced p38α/β MAPK-mediated phosphorylation of TTP and HuR protein induction while the staining intensity of the satellite cell marker, Syndecan-4, did not differ in from the control condition (Fig 4 B-D). Additionally. we significantly reduced phosphorylated-MK2 staining, a direct downstream target of p38α/β MAPKS, in satellite cells (Fig. 4E). As a positive control, Lipopolysaccharide stimulation of RAW264.7 macrophages resulted in increased phospho-TTP intensity when compared to unstimulated controls (Fig. 4F).

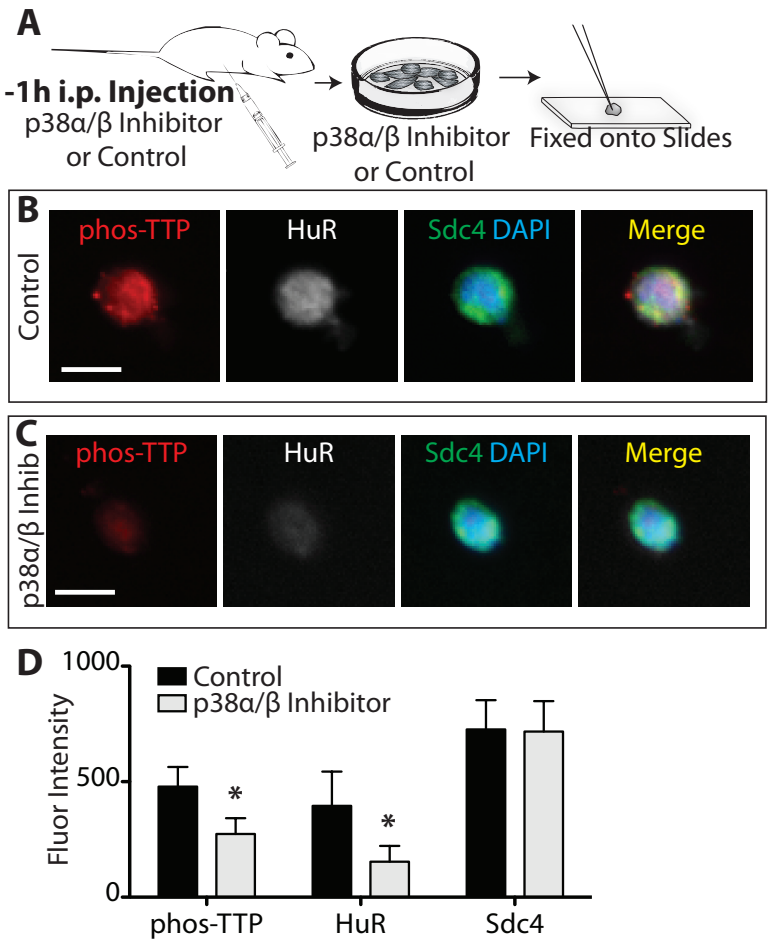

Figure 4: Inhibition of p38α/β MAPK reduces phosphorylation of TTP and HuR expression. **A.** Inhibition of p38α/β MAPK signaling in satellite cells prior and during isolation. Satellite cells were isolated 1h following either an intraperitoneal injection of 15mg/kg SB203580 or DMSO control. Dissected muscle tissue was placed immediately in media containing 25μM SB203580 or DMSO, and remained in inhibitor or control for the remainder of the procedure. Upon isolation of a single cell suspension, cells were dried down onto coverslips and immediately fixed with 4% paraformaldehyde. **B.** and **C.** Cells were stained with phospho-TTP (Red), HuR (white), Syndecan-4 (Green) and DAPI (Blue). **D.** Mean fluorescence intensity was measured using Slidebook software. Student's two-tailed t-test: phos-TTP and HuR; p-value<0.001. Average +/- SEM; N=4 independent experiments. White scale bars = 25 μm.

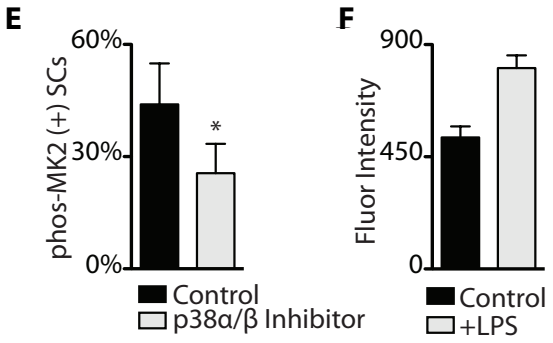

Figure 4 (cont.): Inhibition of p38α/β MAPK decreases phospho-MK2 positive satellite cells but LPS stimulation increases phospho-TTP intensity in macrophages.
E. Percentage of phosphorylated MK2 satellite cells. TA muscle was harvested 30min following $BaCl_2$ injury from either control of SB203580 injected mice. **F.** RAW 264.7 macrophages stimulated with LPS for 2h or unstimulated were stained with phosphorylated-TTP and DAPI. The average fluorescence intensity was calculated by drawing cell masks in Slidebook software as in Figure 3 B-D. Graphs represent average +/- SEM. * p-value <0.01.

Mutant TTP Blocks Satellite Cell Myogenic Commitment

p38α/β MAPK-mediated phosphorylation and inhibition of TTP may result in HuR induction which would stabilize MyoD mRNA committing the satellite cell to myogenesis. Activated-p38α/β acts through the downstream kinase, MAP kinase-activated protein kinase 2 (MK2) which directly phosphorylates TTP to inhibit its function [139-141]. We blocked p38α/β-mediated TTP inhibition during satellite cell activation by transfecting satellite cells with a constitutively active TTP mutant. Substitution of S52 and S178 residues with alanine results in a constitutively active TTP mutant [140]. $TTP_{S52AS178A}$ (TTP-AA-myc) binds TTP target transcripts and recruits mRNA decay factors resulting in target instability [119,140]. TTP-AA-myc is not inhibited by p38α/β-activated MK2 signaling [140]. Satellite cells on associated myofibers were transfected with either control (pcDNA3.1) or pcDNA3-TTP-AA-myc and cultured for an additional 24h. The majority of control transfected satellite cells express MyoD protein after 30h in culture (Fig. 5A); however, over-expression of TTP-AA-myc blocks MyoD expression in a significant subset of transfected satellite cells (Fig. 5B and C). The dotted line denotes the expected percentage of MyoD positive satellite cells at the time of transfection (20% MyoD(+)

after 6h culture) (Fig. 5C). The required time to isolate myofibers prior to transfection is a disadvantage of transfecting satellite cells associated with myofibers; however, *ex vivo* fiber culture retains satellite cell-fiber association resulting and increased retention of satellite cell stem cell characteristics [57,142,143]. The ability of TTP-AA-myc to block MyoD expression is consistent with the idea that TTP suppresses myogenesis in satellite cells.

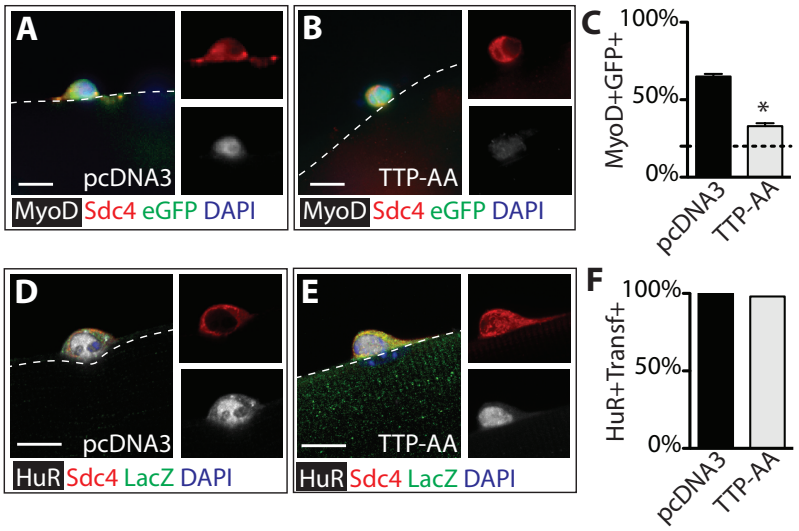

Figure 5: Mutant TTP is sufficient to block MyoD induction in satellite cells
Satellite cells associated with myofibers were transfected after harvest (6h post muscle dissection) with eGFP as a transfection marker and either **A.** control plasmid (pcDNA3) or **B.** a plasmid expressing TTP-AA-myc. Myofibers were cultured for an additional 24h for a total of 30h in culture. **A.** and **B.** Myofibers were stained with Syndecan-4 (Red) to mark satellite cells, MyoD (white) to detect activated satellite cells, and DAPI (blue) to mark nuclei. Transfected cells were identified by expression of eGFP. **C.** Average +/- SEM plotted for 3 independent experiments with all transfected satellite cells scored from at least 25 myofibers per condition. * Student's 2-tailed t-test; p-value<0.01. **D.** and **E.** TTP-AA-myc is insufficient to block HuR protein induction. Satellite cells associated with myofibers were transfected after harvest (6h post muscle dissection) with either **D.** pcDNA3 and CMV-LacZ or **E.** a plasmid expressing TTP-AA-myc. Myofibers were cultured for an additional 24h for a total of 30h in culture. **D.** and **E.** Myofibers were stained with Syndecan-4 (Red) to mark satellite cells, HuR (white), DAPI (Blue) and either β-Gal (Green) or Myc-tag (Green) to mark transfected cells. In two independent experiments, 100% of control and 98.4% of TTP-AA-myc transfected satellite cells stain positive for HuR after 30h in culture. White scale bars = 25 μm.

Mutant TTP is Not Sufficient to Block HuR Protein Induction

We observed that both phosphorylation of TTP and HuR protein induction were regulated by p38α/β MAPK signaling in primary satellite cells. The ability of the p38α/β MAPK phosphorylation mutant, TTP-AA-myc, to inhibit MyoD expression may be through constitutive decay of HuR mRNA since TTP has been shown to destabilize HuR mRNA [144]. Thus, we tested whether TTP-AA-myc over-expression was sufficient to block HuR protein induction. Satellite cells associated with myofibers were transfected with either pcDNA3-LacZ (Fig. 5D) or TTP-AA-myc (Fig. 5E) and stained for HuR after an additional 24h in culture. TTP-AA-myc transfection was not sufficient to block HuR protein expression (Fig. 5E). Thus, it appears that the ability of TTP-AA-myc to block MyoD expression in satellite cells is dominant over the presumed ability of HuR to stabilize MyoD mRNA during satellite cell activation.

TTP Binds and Regulates the MyoD 3'UTR

Activated satellite cells rapidly commit to myogenesis by inducing MyoD expression. The constitutively active TTP mutant, TTP-AA-myc is sufficient to block MyoD induction in primary satellite cells. To address whether TTP could directly bind and regulate MyoD mRNA, the MyoD 3'UTR was searched for TTP binding sites. The MyoD 3'UTR contains a TTP binding sequence, UAUUUAU, that is highly conserved among mammals and is downstream of HuR binding sites (U-rich regions) (Fig. 6A). The full length MyoD 3'UTR was cloned into a Tet-Off β-Globin reporter construct (referred to as β-MyoD) and utilized in co-immunoprecipitation and pulse-chase RNA decay assays to test whether TTP regulates MyoD mRNA. Wild type Flag-tagged-TTP efficiently co-immunoprecipitated β-MyoD when compared to a negative control β-globin reporter not bound by TTP (β-GAP) (Fig. 6B). As an internal positive control, a portion of the 3'UTR sequence of Granulocyte Macrophage Colony Stimulating factor (GM-CSF), which is directly regulated by TTP was efficiently pulled-down by wild type Flag-tagged-TTP (Fig. 6B). Conversely, the RNA binding defective TTP mutant (TTP_{F126N}) was ineffective at pelleting β-

MyoD mRNA or β-GM-CSF RNA (Fig. 6B). An unrelated non-RNA binding protein, the MS2 viral coat protein did not pull down β-GAP, β-MyoD nor β-GM-CSF (Fig. 6B). Based on these data, it appears that TTP directly binds the MyoD 3'UTR.

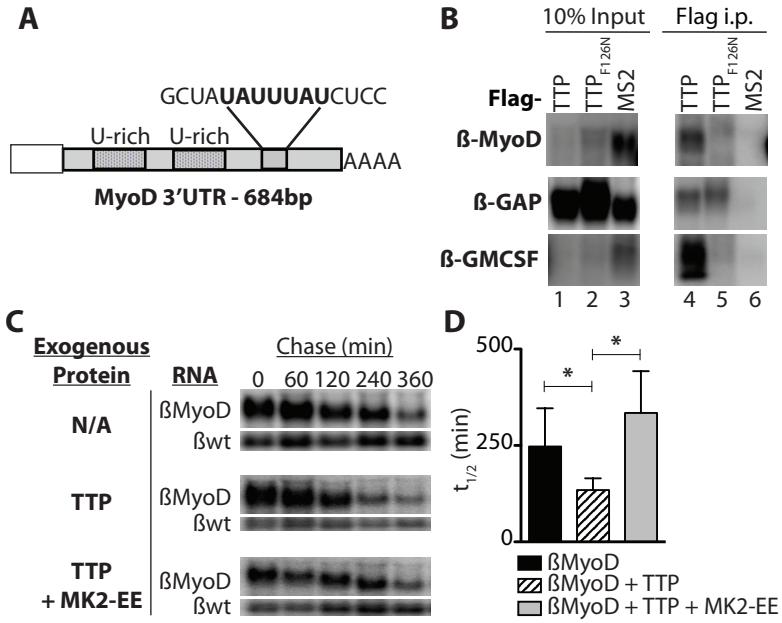

Figure 6: TTP binds and regulates the 3'UTR of MyoD
A. Illustration of the 684bp MyoD 3'UTR showing the putative TTP binding sequence. Upstream of the TTP binding sequence are U-rich HuR binding sites. **B.** TTP binds the MyoD 3'UTR. Northern blots showing co-immunoprecipitation assays of reporter transcripts from HEK293T extracts. Assays were performed using cells co-expressing FLAG-tagged wild type TTP (WT, lanes 1 and 4), an RNA binding mutant of TTP (F126N, lanes 2 and 5), or an unrelated non-RNA binding protein, (MS2, lanes 3 and 6) together with reporter β-globin mRNA containing the MyoD 3'UTR (β-MyoD) or the GM-CSF 3' UTR (β-GM-CSF). A β-globin reporter with no putative TTP binding sites served as an internal negative control (β-GAP). Pellet (lanes 4-6) and 10% input (lanes 1-3) fractions were loaded as indicated above the panels. **C.** and **D.** TTP regulates the MyoD 3'UTR. Tet-off Hela cells were transfected with pcTET2-β-MyoD and CMV-β-Globin, a tetracycline unresponsive loading and transfection control. **C.** Northern blots showing pulse-chase mRNA decay assays. Assays were performed with cells transfected with empty vector, TTP, or TTP and constitutively active MK2 (TTP+MK2-EE). **D.** Calculated half-life of β-MyoD. Average + SEM plotted of 7 independent experiments. Student's two-tailed t-test; * β-MyoD + TTP p-value<0.05; **β-MyoD + TTP + MK2EE p-value<0.01.

TTP binds to target transcripts and mediates their decay. Activated-p38α/β directly phosphorylates MAPKAP2 (MK2) which in turn phosphorylates TTP and inhibits its function [140]. To test whether TTP regulates the stability of the MyoD3'UTR, we performed pulse-chase RNA decay assays. β-MyoD contains a Tetracycline responsive element (TRE) upstream of the promoter which in the absence of tetracycline is bound by a Tet-trans-activator (tTA) that drives transcription of the reporter construct. Upon addition of tetracycline to the media, the tTA rapidly dissociates from the TRE causing the transcription to stop. β-MyoD transcription was pulsed for 6h and shut-off by the addition of tetracycline to the media. β-MyoD mRNA was chased for 6h, allowing for calculation of its half-life by northern blot probed for β-globin RNA (Fig. 6D). TTP co-transfection results in a significant decrease in β-MyoD mRNA stability (Fig. 6E). Whereas, inhibition of TTP function by co-transfection of a constitutively active mutant of MK2 (MK2-EE) results in a significant increase in β-MyoD mRNA stability (Fig.6E). These data are consistent with the hypothesis that TTP directly binds the 3'UTR of MyoD mRNA and regulates its decay.

Discussion

Activation of quiescent satellite cells and subsequent commitment to myogenesis are critical events for normal skeletal muscle regeneration [51,54,68,77]. Cellular quiescence is generally regarded as a low metabolic state [122] but surprisingly we observed a significant portion of transcripts expressed by satellite cells from uninjured muscle decrease in activated satellite cells. Transcripts encoding RNA-binding proteins were significantly over-represented and 70% of these transcripts decreased, consistent with a derepression of gene expression upon satellite cell activation. Here, we present evidence that TTP destabilizes MyoD mRNA and that satellite cell activation is dependent upon p38α/β MAPK inhibition of TTP-mediated mRNA decay.

Regulation of TTP mRNA

TTP mRNA increases in abundance and stability after cell isolation, stimulation by growth factors, or cellular stresses [145,146]. These data and our data are consistent with the idea that TTP function is high in quiescent satellite cells but the protein and mRNA levels are low.

Activated-p38α/β MAPK Signaling Rapidly Phosphorylates TTP in Satellite Cells

Characterization of satellite cell activation has been difficult considering that isolation of satellite cells inevitably results in their activation. We have shown that p38α/β MAPK activation occurs rapidly within the first minutes following an injury and is currently the earliest marker of activated satellite cells [61]. Downstream p38α/β signaling is critical to satellite cell activation since inhibiting p38α/β MAPK signaling blocks MyoD expression and cell-cycle entry in primary satellite cells [61]. The downstream targets of p38α/β MAPK were previously unknown, now we have established TTP as a downstream target of activated-p38α/β MAPK signaling in satellite cells. Since p38α/β is activated so rapidly in satellite cells, fixing the tissue *in situ* via whole mouse perfusion allows us to study quiescent satellite cells. When muscle is fixed *in situ,* detection of TTP by immunofluorescence in quiescent satellite cells is difficult, which is consistent with TTP

levels in serum starved fibroblasts and unstimulated macrophages, yet under these conditions it is well established that TTP is active and targeting transcripts for decay [93,147,148]. Due to the intrinsic complications of studying quiescent satellite cells, we developed a method to stall satellite cells early in the activation process by inhibiting p38α/β MAPK signaling prior to muscle dissection. Using this technique, we show that p38α/β MAPK signaling targets TTP for rapid phosphorylation in primary satellite cells. We now consider both activated-p38α/β MAPKs and phospho-TTP to be markers of activated satellite cells.

Distinct p38α/β MAPK Targets During Satellite Cell Activation vs. Myogenic Differentiation

Activated p38α/β MAPK signaling is required for both satellite cell activation and myogenic differentiation [61,84]. Here, we have established TTP as a downstream target of activated-p38α/β MAPK signaling during satellite cell activation. p38α/β has been shown to target another family member of RNA-binding proteins, KH-type Splicing Regulatory Protein (KSRP) during myogenic differentiation of C2C12 myoblasts [87]. Similarly to TTP, KSRP promotes decay of myogenic transcripts. Upon p38α/β activation, KSRP becomes phosphorylated and dissociates from myogenic transcripts [87]. This is distinct from TTP, since TTP remains bound to target transcripts when phosphorylated although its mRNA decay function is inhibited [119]. We hypothesize that this difference may be significant, as it is thought that phosphorylated-TTP which remains bound, protects target mRNAs from other RNA-binding proteins which mediate their decay [119]. In our array data using satellite cells, KSRP transcripts were not regulated in either wild type or Syndecan-4 null satellite cells 12h post injury. Thus, p38α/β MAPKs may target TTP during satellite cell activation and KSRP during myogenic differentiation.

TTP Regulation of MyoD is Dominant over HuR-mediated MyoD mRNA Stability

It is thought that HuR expression is ubiquitous [149-151], but it appears that freshly isolated satellite cells express low levels of HuR and inhibition of p38α/β appears to inhibit HuR protein

expression. Activated-p38α/β mediated induction of HuR may be due to a positive auto-regulatory loop since p38 MAPK phosphorylates HuR which increases its cytoplasmic localization, resulting in increased target mRNA stability, which includes its own mRNA [103,144,152]. Since HuR stabilizes MyoD and promotes cell-cycle entry in C2C12 myoblasts, *in vivo* it likely synergizes with phospho-TTP (inactive but stabilized) to promote MyoD mRNA stability. This may complement transcriptional induction of MyoD to rapidly and infallibly commit satellite cells to myogenesis. Nevertheless, TTP appears to be dominant over HuR-mediated MyoD mRNA stability, since constitutive TTP activity is able to block MyoD induction in the presence of HuR. In satellite cells, activated-p38α/β mediated inhibition of TTP function appears required for MyoD expression.

TTP Directly Regulates the 3‘UTR of MyoD

Constitutively active TTP blocks MyoD induction in a significant portion of transfected satellite cells; however, this does not prove that TTP is directly involved in blocking MyoD protein induction. However, we show that TTP directly binds and regulates the MyoD 3‘UTR; supporting a direct role for TTP in mediating MyoD protein induction. Direct TTP-mediated decay of MyoD mRNA would connect extracellular signals that activate p38α/β MAPK and cell-fate commitment in satellite cells. Also, this would allow for tight regulation of MyoD expression downstream of the MyoD locus since MyoD directly activates its own promoter [153]. This level of regulation must be necessary as increased levels of MyoD drives myoblasts out of the cell-cycle resulting in terminal differentiation; whereas lower levels of MyoD allows myoblasts to proliferate [154]. However, MyoD must be infallibly induced as quiescent satellite cells switch to proliferating myoblasts because MyoD expression is required for timely cell-cycle entry and induction of cdc6 which is essential in licensing origins of DNA replication at the G1/S transition [75].

Post-transcriptional regulation of MyoD mRNA stability in quiescent satellite cells may provide a mechanism for rapid commitment to the myogenic lineage upon activation. The idea

that TTP regulates MyoD mRNA in quiescent satellite cells requires that MyoD mRNA be present in quiescent satellite cells. We can envision two scenarios in which this may be achieved. Firstly, quiescent satellite cells may express very low levels of MyoD mRNA which is rapidly subjected to AU-rich mediated decay by TTP and/or its homologs Brf1 and Brf2. In the second scenario, MyoD mRNA is expressed by satellite cell progenitors, TTP binds the message but does not mediate decay and MyoD mRNA is stored and sequestered away from the translational machinery. In human cells, TTP has been shown to stably store AU-rich containing mRNAs and sequester them away from the translational machinery when mRNA decay factors are limiting [137]. Either of these scenarios are not mutually exclusive. The second scenario requires that the MyoD locus be active in satellite cell progenitors. By using Cre-mediated lineage tracing of the MyoD locus, satellite cell progenitors were shown to have activated the MyoD locus prior to entering quiescence [40]. If the MyoD locus was still active in quiescent satellite cells, Cre may be detected as it would not be subjected to AU-rich mediated decay. Cre protein was not detected by immunofluorescence in 90% of freshly isolated satellite cells. However, we would expect that if the MyoD locus was active in quiescent satellite cells, it would be expressed at a very low level, possibly too low for Cre protein detection by immunofluorescence. Either mechanism would ensure that quiescent satellite cells rapidly activate and commit to the myogenic lineage upon receiving activation signals from the muscle. Alternatively, if MyoD mRNA is not actively expressed or stored in quiescent satellite cells, once MyoD transcription was activated, phosphorylated-TTP may synergize with HuR resulting in stabilized MyoD mRNA.

Here, we provide the first *in vivo* evidence that post-transcriptional regulation of MyoD mRNA, a master regulatory transcription factor in muscle, is essential for satellite cell commitment to myogenesis. This may be a general mechanism for stringent control of other transcription factors with AU-rich elements involved in cell fate decisions.

Materials and Methods

Mice

Mice were bred and housed according to National Institutes of Health (NIH) guidelines for the ethical treatment of animals in a pathogen-free facility at the University of Colorado. Wild-type mice were C57Bl/6xDBA2 (B6D2F1; Jackson Labs); Syndecan-4 null mice are previously described [54]. Cells or myofibers were harvested from female mice 3–6 months old.

Microarray Analysis

Satellite cells were isolated from Tibialis Anterior muscles that were either uninjured or 12h post injury with 50ul of 1.2% BaCl to induce myonecrosis. Satellite cells were purified by FACS based on Syndecan-3 expression from at least three age matched wild type or Syndecan-4 null mice as previously described [130]. Total RNA isolated using a PicoPure RNA Isolation Kit (Arcturus) was subjected to two rounds of linear T7-based amplification (RiboAmp HA Kit, Arcturus). Based on the number of cells collected, this resulted in an RNA equivalent of 5000 Syndecan-3 positive cells. Biotin-labeled cDNA was generated using an Affymetrix IVT Labeling Kit. Labeled cRNA was quantified and analyzed for quality using BioAnalyzer (Agilent). Labeled cRNA (5 mg) was fragmented and hybridized to Affymetrix 430 v.2 mouse microarrays at the University of Colorado Core facilities. Chips were scanned on a GeneChip Scanner 3000 (Affymetrix) and intensity data recovered in GCOS (Affymetrix). CEL files from three replicate genechips were imported directly into Spotfire (TIBCO) and normalized by GCRMA. Using a 99% confidence threshold (p-value ≤ 0.01), probe sets that changed in relative expression between Syndecan-4 uninjured satellite cells and Syndecan-4 satellite cells 12h post injury were subtracted from probe sets changing between wild type uninjured satellite cells and wild type satellite cells 12h post injury. This analysis resulted in the WT-S4 gene list (available upon request). Heat map arranged by 1) level of expression in wild type satellite cells from uninjured muscle and 2)

directionality of change after 12h post muscle injury. Gene ontology analysis was performed using Spotfire Ingenuity Pathway analysis.

QT-PCR Analysis

For *in vitro* activation, satellite cells were isolated from 5 wild type mice, pooled, and cultured for 0h (freshly isolated), 2h, 4h, 8h and 12h; 2 independent experiments. Superscript III RT was used for reverse transcription of RNA into cDNA. Fast SYBR Green™ master mix was used according to manufacture's instructions to amplify target transcripts using primers spanning exon/exon junctions for Elavl1 and Zfp36. 18S rRNA was used as a reference gene and samples were analyzed in triplicate. Primer sequences: *Elavl1* Exon1/2; (FOR: 5' GCTTATTCGGGATAAAGTAGCAGGA; REV: 5' TTCACAAAACCGTAGCCCAAG). *Zfp36* Exon1/2; (FOR: 5' GCCATCTACGAGAGCCTCCA; REV: 5' CGTGGTCGGATGACAGGTC)

Cryosection Immunofluorescence

Whole Tibialis Anterior muscles were either perfused or fixed upon dissection from the limb with 4% Paraformaldehyde for 2h on ice. Muscles were sunk in 30% sucrose and mounted in OCT. Cryosections were post-fixed onto slides, permeablized for 5 min with 0.5% TritonX-100 in 1X PBS, blocked for 1h at room temperature with 10% normal goat serum. Primary antibodies were used at the following dilutions: 1:300 Rat anti-Laminin (4HB-2 Sigma), 1 μg/ml Rabbit anti-TTP (ab33058 Abcam), 1:1000 Chicken anti-Syndecan-4. DNA was stained with DAPI and sections were mounted with Vectashield (Vector Labs).

Immunofluorescence of cell lines and primary satellite cells

C2C12 myoblasts were grown on sterilized uncoated coverslips from Corning in DMEM with 10% Fetal Bovine Serum. MM14 myoblasts were grown on gelatin-coated coverslips in F12-C with 15% Horse serum and 2nM FGF-2. Primary satellite cells were dried down on gelatin coated-coverslips as described in Figure 3. All cells were fixed with 4% Paraformadehyde for 10min at room temperature. Syndecan-4 staining for the primary satellite cells was done as on

fibers. Primary antibodies: 1:2000 chicken anti-GFP (Abcam ab13970); Neat F5D mouse anti-myogenin supernatant; 1:500 mouse anti-HuR (Steitz Lab) and 1:200 Rabbit anti-phospho-TTP (Stoecklin Lab). For fluorescence intensity: blinded to the condition, masks overlapping Syndecan-4 staining were made plus a mask corresponding to background staining and Slidebook calculated mean intensity for all fluorescence channels.

Transfection and Enrichment for siRNA transfected C2C12 myoblasts by FACS

C2C12 myoblasts were plated at $2.5x10^4$ cells/well and MM14 cells were plated at $1.5x10^4$ cells/well 24h prior to transfection. C2C12 cells were transfected with Dharmafect Duo and MM14 cells were transfected with Qiagen Transmessenger reagent according to manufacture's instructions. AllStars Negative siRNA Cat# 1027292 or an equal amount of *Zfp36, Zfp36l1* and *Zfp36l2* totaling 2.0ug of siRNA per well. siRNA sequences: *Zfp36* 5' UUAUGUUCCAAAGUCCUCCGA; *Zfp36l1* 5' UUAGAUGAAGUUUAAACCCAG; *Zfp36l2* 5' UUCCGCAUCACAACCGCCCTG.

Transfected C2C12s were washed with PBS and briefly incubated 0.1% trypsin-EDTA. Cell suspensions were washed with DMEM with 10% FBS to remove the trypsin. Viable cells were detected by staining the cell suspensions with DyeCycle Vital Dye Violet according to manufacture's instructions. Sorting gates were determined using non-transfected cells to detect autofluorescence that had also been stained with Vital dye. Only live cells were sorted and the sorting conditions were set for enrichment. Sorted cells were washed twice with cold 1X PBS and lysed immediately in 2X protein sample buffer. Proteins were separated by 10% SDS-PAGE and transferred onto PDVF membrane. Antibodies: 1:500 mouse anti-MyoD (5.8A Novus Cat #NB100-56511), 1:5000 chicken anti-GFP (Abcam ab13970) and 1:1000 mouse α-Tubulin (Sigma Cat #T-6199) were detected by antibody staining and secondary HRP antibodies from Millipore and detected using ECL Plus western blotting detection kit (GE Healthcare Cat #RPN2132) HRP

substrate. Blot was scanned using a Storm phosphoimager and the bands quantified with ImageQuant software.

Preparation, Transfection and Immunofluorescence of Myofibers

Muscle was dissected from hind limbs and digested for 1.5 h at 37deg C in 400U/ml Type I Collagenase (Worthington). Muscle slurry was placed into tissue culture dishes containing 15% horse serum in F12-C media. Fibers were teased apart from the muscle using pulled glass pipets and placed into fresh media. Fifty fibers were transferred to 6-well plates containing 2ml 15%HS F12-C + 2nM FGF-2. Fibers were transfected with 2.75ug TTP-AA-myc + 0.25ug eGFP-N1 with Lipofectamine 2000 according to manufactures instructions for 4 hours. Fibers were then washed with fresh media and incubated for an additional 20h for a total of 30h in culture. Fibers were washed with PBS and fixed with 4% paraformaldehyde for 10 minutes. After incubation of the fibers with 10% goat serum for 1h at room temperature, fibers were incubated overnight with 1:1000 chicken anti-Syndecan-4 antibody. Secondary staining was performed with anti-chicken 1:1000 AlexaFluor 555, then fibers were post-fixed and permeabilized to detect internal epitopes. Following a 1h block with 10% goat serum, 1:50 mouse anti-MyoD (Vector Labs) or 1:500 mouse anti-HuR (Steitz lab) were incubated overnight at 4 deg C. 1:500 Alexa Fluor 647 was incubated with the fibers for 1h at room temperature and mounted on slides with Vectashield with DAPI.

Intraperitoneal Injection and inhibition of p38α/β with SB203580

Dosage is 15mg/kg of body weight. SB203580 was diluted with 1X saline to a final concentration of 1.5mg/ml. Mice were weighed and injected with 10ul/gram with the diluted drug. Control mice were diluted with a corresponding amount of DMSO drug carrier. Injections were performed 1hr prior to harvest. Upon harvest, muscle tissue was immediately placed in 25μM SB 203580. Muscle was digested with 400U/ml Type I Collagenase (Worthington) for 1h with brief vortexing every 10 minutes. During isolation, satellite cells were maintained in either SB203580 or DMSO control and fixed immediately upon isolation of a single cell suspension.

RNA Decay Assays with the β-Globin-MyoD 3'UTR Reporter

The entire 3'UTR of MyoD was amplified by PCR from C2C12 myoblast cDNA using the following primers: (FOR: 5' GCATCCATGCGGCCGCGGATGGTGTCCCTGGTTCTT; REV 5' GCAATCATGCGGCCGCGCGTCTTTATTTCCAACACCT). The PCR product was cloned into NotI sites of the Tetracycline responsive β-Globin reporter construct as previously described [155]. Tet-off Hela cells were transfected with 2.25ug pcTET2-β-MyoD and 0.05ug CMV-β-Globin, a tetracycline unresponsive loading and transfection control with or without 0.05ug CMV-wtTTP and 0.5ug Flag-MK2EE. Transcription was pulsed for 6h by removal of tetracycline from the media. Tetracycline was added for 20min prior to cell harvest to fully shut off transcription. RNA was chased for at least 6h, purified with Trizol according to the manufacture's instructions and separated on a 1.2% Agarose Formaldehyde gel. RNA was transferred to Nylon membrane, probed for β-globin, and the 1/2 life was calculated as previously described [156].

Flag-tagged Immunoprecipitations of TTP bound to the MyoD 3'UTR

HEK293T were plated onto 15cm plates 24 hours prior to transfection with FLAG-tagged wild type TTP, an RNA binding mutant of TTP (F126N), or an unrelated non-RNA binding protein, (MS2) together with reporter β-globin mRNA containing the MyoD 3'UTR (β-MyoD) or the GM-CSF 3' UTR (β-GM-CSF). A β-globin reporter with no putative TTP binding sites served as an internal negative control (β-GAP). Cells were transfected with Lipofectamine 2000 according to manufacture's directions. Pellet and 10% input fractions were separated on a 1.2% agarose formaldehyde gel, transferred to nylon, and probed for β-Globin as previously described [156].

Chapter 4: Evidence of Differential Polyadenylation of HuR mRNA in Quiescent Versus Activated Satellite Cells

Introduction

One mechanism cells use to rapidly change gene expression profiles is through post-transcriptional regulation of mRNA stability. Upon satellite cell activation, we observe a dynamic switch in proteins which are known negative post-transcriptional regulators of mRNA stability with proteins that positively regulate myogenic transcript stability. Tristetraprolin (TTP), a known negative regulator of mRNA stability plays a significant role in satellite cell activation. TTP binds to AU-rich elements within the 3'UTR of target mRNAs and recruits mRNA decay enzymes to destabilize the transcript [113,116]. Activated-p38α/β signaling results in phosphorylation of TTP [117]. This results in TTP association with 14:3:3 adapter proteins which block its ability to recruit deadenylases resulting in stabilization of the target transcript [118,119]. I have shown that p38α/β mediated inhibition of TTP is required for satellite cells to express the muscle transcription factor MyoD. MyoD expression is required for satellite cells to commit to myogenesis and for normal muscle regeneration [68]. TTP binds and directly regulates the MyoD 3'UTR. My hypothesis is that upon muscle injury, TTP is inhibited by activated-p38α/β MAPK signaling resulting in rapid stabilization of MyoD mRNA. However, MyoD mRNA has been shown to be regulated by other AU-rich RNA binding proteins such as HuR. HuR binds and stabilizes MyoD mRNA in C2C12 myoblasts [99,100]. We observe an increase in HuR mRNA as satellite cells activate; however, the mechanism of HuR mRNA regulation in satellite cells during muscle repair is unknown.

In humans, the HuR mRNA 3'UTR has been shown to be differentially polyadenylated, resulting in three transcripts of differing lengths [144]. The longest form of the human HuR transcript contains an AU-rich element that is regulated by TTP [144]. The yeast homolog of TTP, Cth2 was recently shown to direct differential polyadenylation of several yeast genes resulting in extended transcripts containing AU-rich elements [157]. Cth2 directed differential polyadenylation

was specific for genes containing AU-rich elements that were downstream of the standard polyA site, thus genes without 3' AU-rich elements were not extended [157]. Cth2 and TTP share the highly conserved tandem zinc finger domains required for RNA binding, but it is unknown whether TTP is able to direct differential polyadenylation resulting in transcripts containing AU-rich elements. If TTP were to direct differential polyadenylation, it would need to be localized to the nucleus. In fact, TTP is located in the nucleus in unstimulated macrophages and it is actively directing mRNA decay [158]. Upon p38α/β MAPK activation, TTP accumulates in the cytoplasm, concurrent with inhibition of AU-rich mediated decay [158]. If TTP does regulate HuR transcript length and stability, this may be a mechanism where HuR mRNA is rapidly stabilized as satellite cells activate, similar to TTP regulation of MyoD mRNA. I have found that proliferating C2C12 myoblasts express a long form of HuR mRNA which possibly contains an AU-rich element. While TTP did not regulate the stability of a short form of the HuR 3'UTR expressed from a reporter plasmid, a long form of the HuR 3'UTR reporter appeared more unstable in the presence of TTP. Finally, I present evidence supporting a possible ARE-containing polyadenylation variant of HuR mRNA expressed in uninjured satellite cells, which appeared to decrease 12h following muscle injury.

Results

Human cells contain three differentially polyadenylated species of HuR mRNA, the longest transcript contains an AU-rich element regulated by TTP [144]. To look for evidence of differential polyadenylation of the HuR 3'UTR, I investigated the gene that encodes HuR, *Elavl1*, using the University of California, Santa Cruz (UCSC) genome browser. Based on 1) mouse mRNAs from GenBank, 2) mouse ESTs including unspliced, 3) locations of the conical polyadenylation sequence, AATAAA, and 4) regions of high mammalian conservation, there was evidence for two or three alternative HuR transcripts (Fig. 1).

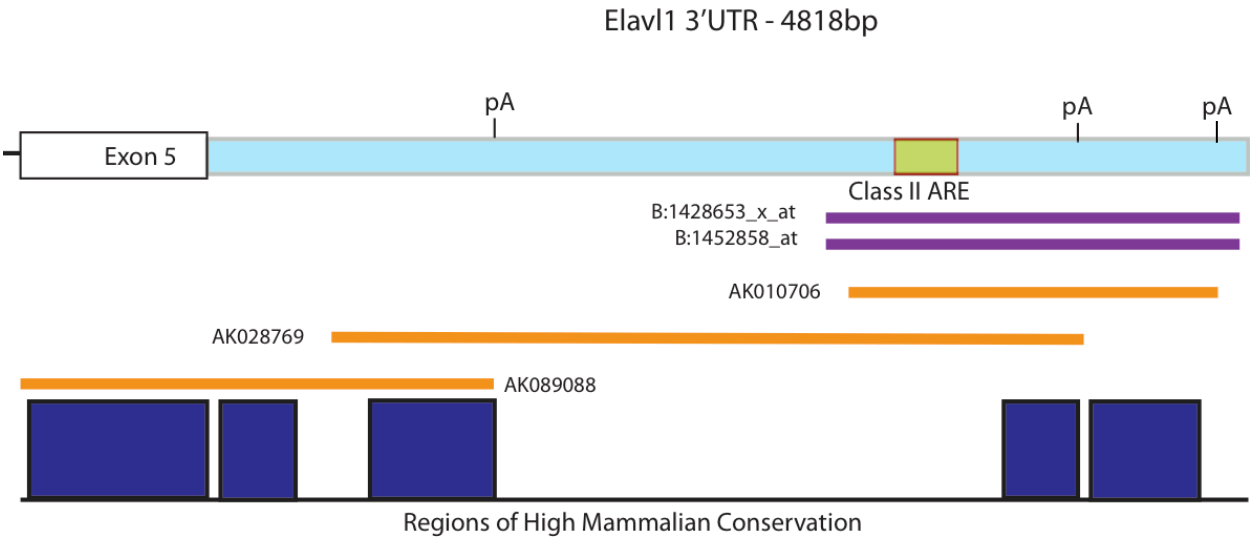

Figure 1: Schematic of the 3' end of *Elavl1*.
Within the 3'UTR of *Elavl1* (light blue box) three putative polyadenylation sites are shown as pA. These predictions are based on 1) the presence of a conical polyA sequence (AATAAA), 2) mouse mRNAs from GenBank (shown in orange) 3) mouse ESTs including unspliced (not shown), and 4) regions of high mammalian conservancy (shown in dark blue boxes, height of the boxes indicates amount conserved). Depicted by the red and yellow box is the TTP preferred class II AU-rich element. The purple lines represent the probe sets identified as regulated in wild type satellite cells but not in activation-deficient Syndecan-4 null satellite cells 12h post-injury.

To determine whether C2C12 myoblasts produced a long form of HuR, I performed QT-PCR analysis of proliferating C2C12 myoblasts. Primers were designed against a proximal region and a distal region of putative HuR transcripts (Fig. 2A). Proliferating C2C12 cDNA was

amplified by QT-PCR using primers against the junction of exon 1 and 2, proximal, and distal regions of HuR mRNA. Preliminary data suggested that approximately 50% of HuR mRNA expressed by proliferating C2C12 myoblasts contained the distal region of the 3'UTR (Fig 2B).

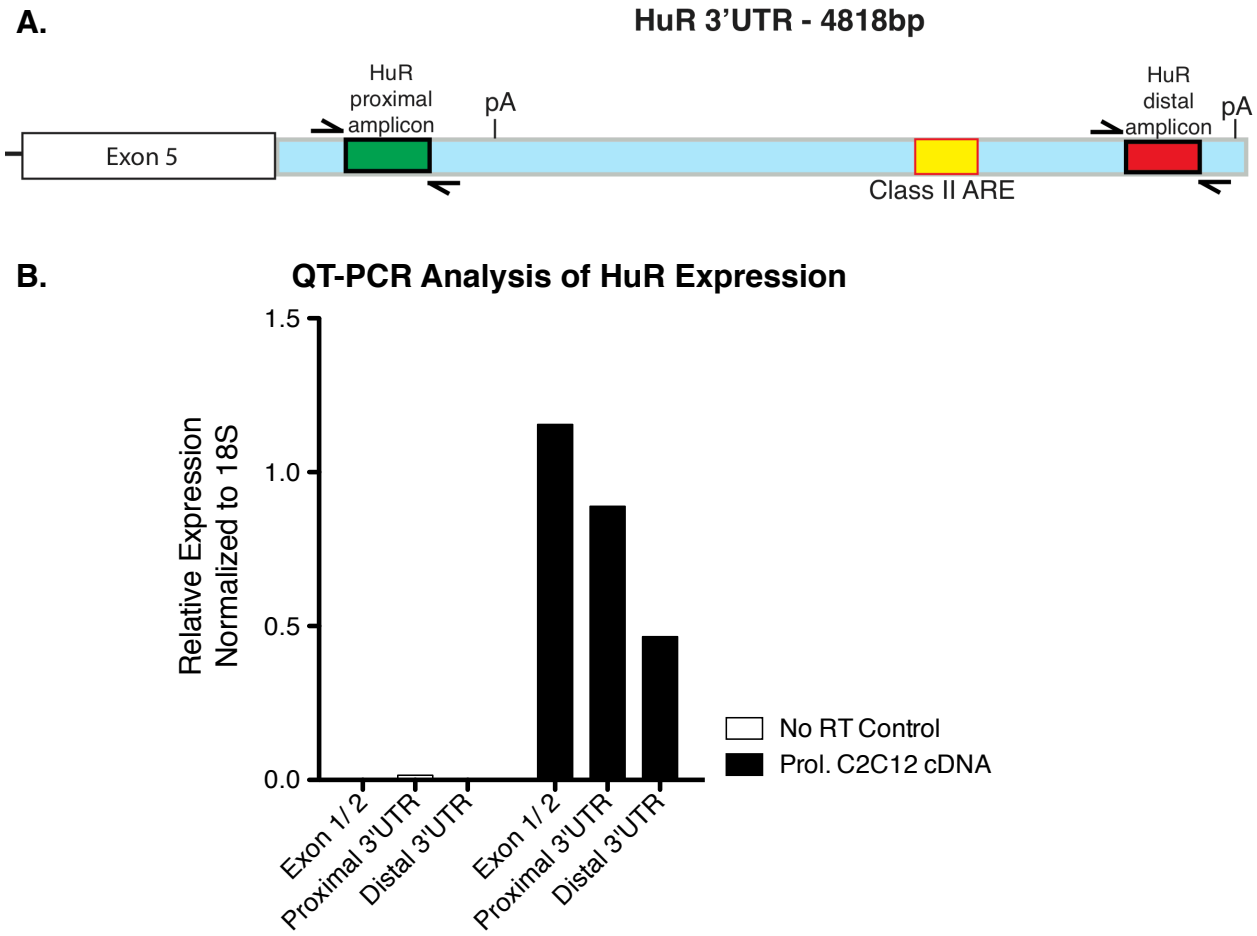

Figure 2: Approximately 50% of HuR mRNA expressed by C2C12 myoblasts is the distal form. RNA purified from C2C12 myoblasts was subjected to reverse transcription reactions with or without Superscript III RT. QT-PCR amplification was run in triplicate.

If HuR mRNA contains a class II AU-rich element, it is likely to be regulated by TTP. To test whether TTP regulates HuR mRNA stability, I cloned the full length HuR 3'UTR into a Tet-Off β-Globin reporter construct (β-HuR). In Hela cells and C2C12 myoblasts, the major β-HuR band by Northern blot was 1.85 kb (Fig 3 Major band). By performing pulse-chase assays, I found that the half-life of the 1.85 kb β-HuR band was not responsive to TTP (Data not shown).

This band was considerably shorter than the expected full length 3'UTR of HuR, which would have produced an approximately 4.4kb band. Upon close inspection of Northern Blots of β-HuR transfected C2C12s, I observed a 4.4 kb band that could represent a long form of β-HuR (Fig. 3, Minor band). Upon transfection with TTP, this band was no longer detectable (Fig 3; star); however, I have no direct evidence that its stability was being regulated by TTP.

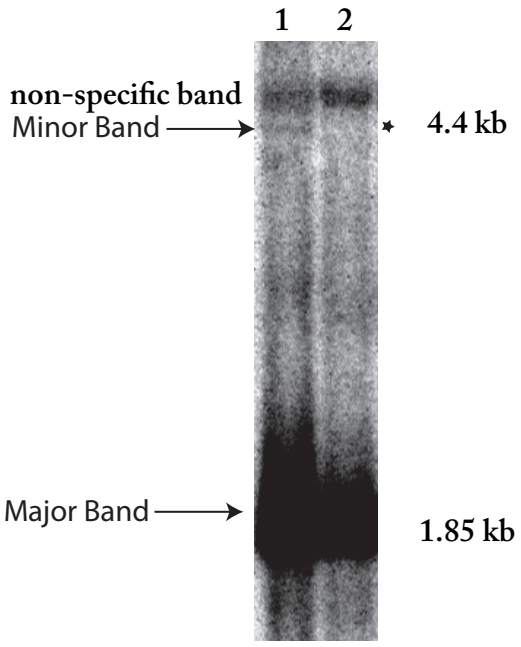

Figure 3: Northern Blot Analysis of Bands produced by β-HuR reporter.
Transfection of β-HuR reporter into C2C12 myoblasts resulted in one major and one minor band produced. Lane 1: β-HuR; Lane 2: β-HuR + 0.1ug wild type TTP. Star denotes band that decreases in the presence of TTP. nsb=non-specific band.

If TTP regulates HuR mRNA stability in satellite cells, I would expect satellite cells to express an AU-rich containing form of HuR mRNA. To determine whether satellite cells express a long form of HuR that contains an ARE, QT-PCR primers were designed to flank the ARE in the 3'UTR of HuR. Expression of three regions of HuR mRNA were compared between satellite cells isolated from uninjured muscle to satellite cells isolated 12h post-injury. Preliminary data

suggest that satellite cells from uninjured muscle (UI) express 5-fold more ARE-containing HuR mRNA than satellite cells 12h post-injury (UI-SC (Distal ARE Avg Ct=33.2, Avg GAPDH Ct=18.7); 12h-SC (Distal ARE Avg Ct=37.3, GAPDH Avg Ct=20.1) (Fig. 4). Based on the Raw Ct value of the Distal ARE 3'UTR amplicon, satellite cells 12h post muscle injury express very little if any HuR mRNA that contains an ARE.

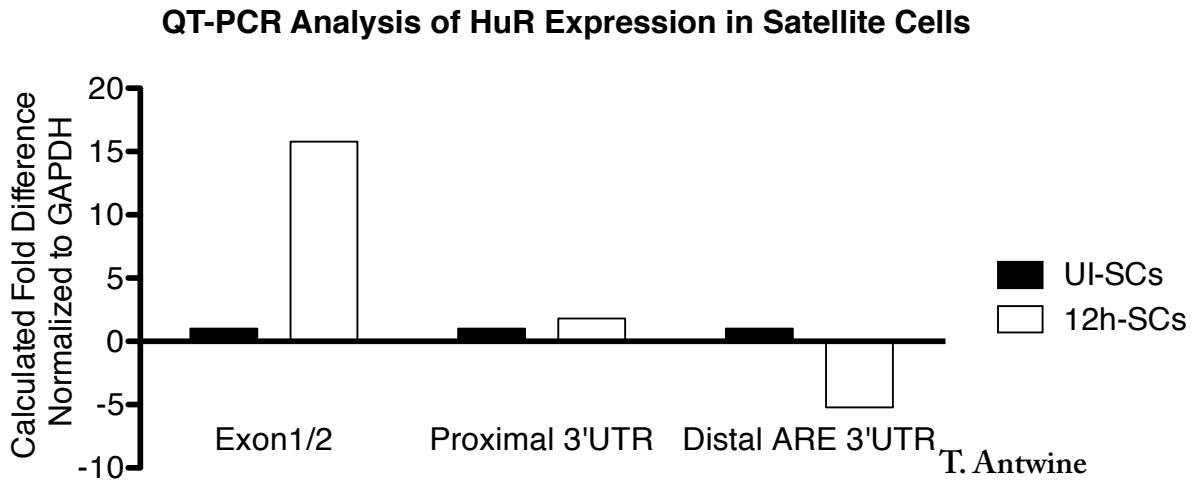

Figure 4: Satellite cells from uninjured muscle (UI-SCs) express ~5-fold more ARE containing HuR mRNA than satellite cells after 12h of muscle injury (12h-SCs).
$Delta_{(Ct)}$-$Delta_{(Ct)}$ fold differences were calculated to estimate the difference in expression between UI-SCs and 12h-SCs.

Discussion

In chapter 3, I presented data showing that 1) HuR is differentially regulated with respect to TTP, 2) inhibition of p38α/β MAPK signaling blocks early HuR protein induction and 3) a constitutively active mutant TTP when over-expressed is insufficient to block HuR protein induction in satellite cells. Here, I have shown that an ARE containing HuR transcript is expressed in uninjured satellite cells but is no longer present 12h following muscle injury. This implies that upon satellite cell activation, a switch occurs between a form of HuR mRNA that may be regulated by TTP to a form that is not regulated by TTP. These data are consistent with data showing that early HuR protein induction was regulated by p38α/β MAPK signaling and may be dependent upon inhibition of TTP by activated-p38α/β MAPK signaling. Data showing that the constitutively active TTP mutant (TTP-AA) was unable to block HuR protein induction in satellite cells, 24h after transfection is consistent with the idea that the HuR transcript switches to a form which TTP no longer regulates. This is in contrast to the ability of the TTP-AA mutant to block MyoD protein induction in satellite cells 24h after transfection. Clearly, MyoD protein induction is dependent upon activated-p38α/β MAPK inhibition of TTP-mediated MyoD mRNA decay. Alternatively, p38α/β MAPK signaling may regulate HuR protein induction completely independent of its regulation of TTP and this is why I observed an inhibition of HuR protein induction early in satellite cell activation. The data presented here supports the idea that a long form of HuR mRNA containing an ARE is being made in uninjured satellite cells. However, I have no data as to whether TTP directly influences the production of this form of HuR mRNA.

To test whether TTP would be able to mediate differential polyadenylation, I would attempt to force C2C12 myoblasts to make the HuR mRNA containing an ARE by transfecting them with wild type TTP. Since the yeast homolog of TTP regulates differential polyadenylation not through its RNA binding domain but through a region within the N-terminus, I would also

transfect mutant TTP proteins which either had a truncated N-terminus or C-terminus. I would then perform QT-PCR to address whether I could detect any increase in an ARE containing HuR mRNA under any of these conditions. This experiment may provide insight into whether TTP was able to direct read through of the normal polyadenylation site resulting in the production of an HuR mRNA containing an AU-rich element within its 3'UTR. If TTP could direct extension of transcripts and differential polyadenylation in mammalian cells, it may provide a mechanism to force AU-rich mediated decay on several transcripts not normally containing AU-rich elements. This may result in post-transcriptional regulation of many transcripts that would now be subjected to AU-rich mediated decay. In quiescent satellite cells, if TTP is directing the production of an HuR mRNA containing an AU-rich element and mediating its decay, this would be consistent with TTP suppression of myogenesis since HuR is known to stabilize myogenic transcripts [99,100].

Materials and Methods

QT-PCR Analysis

Proliferating C2C12 RNA was purified using a GE Illustra RNAspin Mini kit, including on-column DNase treatment. cDNA was made using Superscript III RT and amplification of cDNA and no RT controls was performed using Fast SYBR Green PCR master mix from Applied Biosystems according to manufactures instructions. Primary satellite cells were purified by FACS analysis as previously described (Tanaka, 2009). Tissue used for sorted satellite cells was the Tibialis anterior muscle, either uninjured or injured with 50ul $BaCl_2$ for 12h to produce myonecrosis. RNA was purified using Arcturus PicoPure RNA isolation kit, quantified using a nanospec and equal amounts of RNA were amplified using Nugen's WT-Ovation FFPE System v1.0. Input RNA for GAPDH, Exon1/Exon2 and Proximal was 2ng while for distal 3'ARE HuR was 31.25ng. Primers sequences: Exon1/Exon2 junction (FOR

5’GCTTATTCGGGATAAAGTAGCAGGA; REV 5'TTCACAAAACCGTAGCCCAAG). Proximal 3‘UTR (FOR 5’GGACCAAAGAGTTTCAGGGC; REV 5’CAGACGCTCAGGATGTCAGAGG). Distal 3‘UTR (FOR 5’ AGGCTGGGCAGAAATACAGA; REV 5‘GGGTTGTGACTTTTCCTCCA). Distal ARE 3‘UTR (FOR 5’CCTTTTGCTGATGTGGTTCA; REV GCAAATACTTGGCAGCTGGT). GAPDH (FOR 5’CACCACCATGGAGAAGGCC; REV 5’GATGACCCTTTTGGCTCCAC. 18S rRNA (FOR 5‘GCCGCTAGAGGTGAAATTCTTG; REV 5‘CTTTCGCTCTGGTCCGTCTT).

Northern Blot Analysis

The β-HuR reporter construct: the full length HuR 3‘UTR was cloned into the NotI site of pcTET2-β-globin, a tet-off construct previously described (Lykke-Andersen, 2000). Primers for 3‘UTR HuR (FOR 5’ C2C12 myoblasts were transfected with 1ug Tet-trans repressor, 2ug β-HuR reporter construct and either with or without 0.1ug of pcDNA3-wtTTP. Twenty-four hours following transfection, tetracycline was added to the media for 20min to turn off transcription from the β-HuR plasmid. Total RNA was purified using Trizol according to the manufactures instructions. Samples were boiled in Formamide/Formaldehyde loading buffer and were run on a 1.2% agarose formaldehyde gel at 80V overnight at room temperature. RNA was blotted onto nylon membrane using upward capillary transfer overnight. Blots were cross-linked using the auto settings on a Stratalinker 2000 and subsequently blocked and probed with anti-sense β-globin P^{32} labelled riboprobes overnight at 60deg C. Blots were washed and exposed to a phophor screen overnight and scanned using a Storm Phosphoimager.

Chapter 5: Discussion

Maintenance of Long-term Stem Cell Quiescence

Human satellite cells maintain a quiescent state for years without losing the capacity to regenerate muscle [5,11]. Furthermore, the quiescent satellite cell population is renewed even after many rounds of skeletal muscle injury [104]. Thus, skeletal muscle regeneration mediated by satellite cells is a relevant model for studying adult stem cell quiescence. Other adult stem cell populations are also able to maintain quiescence for extended periods of time, for example a dormant population within the hematopoietic stem cell (HSC) population divides only five times over the lifetime of the mouse [4].

Little is known about the molecular mechanisms regulating long-term quiescence of vertebrate stem cell populations. Nevertheless there appears to be a correlation between the timing of entry into long-term quiescence between HSCs and satellite cells. Four weeks after birth, mouse HSCs undergo a dramatic switch from a highly proliferative and self-renewing state to a quiescent state with less self-renewing capabilities [159]. Approximately three weeks after birth, satellite cells undergo a similar switch characterized by reduced fusion with existing muscle fibers and entry into quiescence [37]. The relatively similar timing of these two stem cell populations entering into quiescence, corresponds to onset of puberty in mice [160]. Since puberty is characterized by hormonal regulation of gamete maturation, there may exist a systemic mechanism to switch from post-natal growth characterized by ongoing stem cell proliferation to a state of stem cell quiescence and tissue maintenance. The timing of entry into quiescence of these two stem cell populations has just been characterized, thus it is unknown whether the mechanisms regulating this switch into quiescence are similar.

The switch to quiescence observed in HSCs and satellite cells is the inverse of what is observed in both of these two populations in response to either bone marrow injury or muscle

injury, respectively. Both HSCs and satellite cells exit G0, enter the cell cycle within 24h, and continue to proliferate in response to injury [4,77]. Whether satellite cells can reversibly switch from proliferation back to quiescence is unknown. However, long-term dormant HSCs were shown to be able to re-enter into quiescence following a proliferative state in response to bone marrow injury [4]. There are several important differences between the dormant HSC population and quiescent satellite cells. First, satellite cells remain quiescent for much longer periods of time in normal resting muscle. Second, activated satellite cells rapidly commit to the myogenic lineage; whereas dormant HSCs give rise to multi-potent blood lineage stem cells [4,61,75]. The ability of the dormant HSC population to activate upon injury, proliferate, and re-enter quiescence is a mechanism of self-renewal that has not yet been characterized in satellite cells.

Post-transcriptional Suppression of Satellite Cell Activation

Quiescence is generally regarded as low metabolic state [122] and satellite cells display characteristics of a metabolically quiet cells [32]. These characteristics include: condensed chromatin, no identifiable polysome structures, no rough endoplasmic reticulum (ER), or Golgi cisternae, and very few ribosomes [32]. Once a satellite cell is activated, it grows in size concurrent with the appearance of polysomes, rough ER, Golgi cisternae and less condensed chromatin [41-46]. By physical differences alone, it is obvious that a quiescent satellite cell undergoes a fundamental cellular change upon activation in response to muscle injury. Thus, it seems reasonable to assume that a quiescent satellite cell is metabolically inactive. Further, I would expect that activation of a quiescent satellite cell would require an induction in gene expression.

Microarray gene chip experiments allow for a global view of gene expression in cells. To better understand the gene expression changes that occur upon satellite cell activation, we performed Affymetrix microarray analysis on FACS isolated satellite cells from uninjured muscle and satellite cells isolated after 12h post muscle injury. In order to isolate genes that were more likely to be involved in satellite cell activation, we identified gene expression changes occurring in

wild type satellite cells that did not occur in mutant *Sdc4*$^{-/-}$ satellite cells. Upon muscle injury, *Sdc4*$^{-/-}$ satellite cells fail to activate and commit to the myogenic lineage [54]. Further, they do not divide within the first 48h following isolation [54]. We subtracted gene expression changes occurring in *Sdc4*$^{-/-}$ satellite cells from gene expression changes occurring in wild type satellite cells during the initial 12h post muscle injury. Approximately half of transcripts expressed in satellite cells from uninjured muscle decrease 12h post injury. Moreover, RNA binding proteins were over-represented within the WT-S4 gene list compared to the proportion of known RNA binding proteins in the mouse transcriptome. RNA binding proteins that regulate mRNA stability and splicing were differentially expressed implying that post-transcriptional mechanisms could be playing a role in satellite cell activation. Within this subset of RNA-Binding proteins, known negative regulators of myogenesis decreased whereas known positive regulators of myogenesis increased in abundance 12h post-injury. Thus, I hypothesized that myogenesis is actively suppressed in quiescent satellite cells. In support of this hypothesis, I have shown that p38α/β MAPK-dependent inhibition of TTP is required for MyoD induction in satellite cells. TTP binds to the MyoD 3‘UTR and mediates the decay of the MyoD transcript. Thus, it appears that TTP and/or its homologs Brf1 and Brf2 suppress myogenesis in quiescent satellite cells by directly regulating MyoD mRNA (Fig. 1)

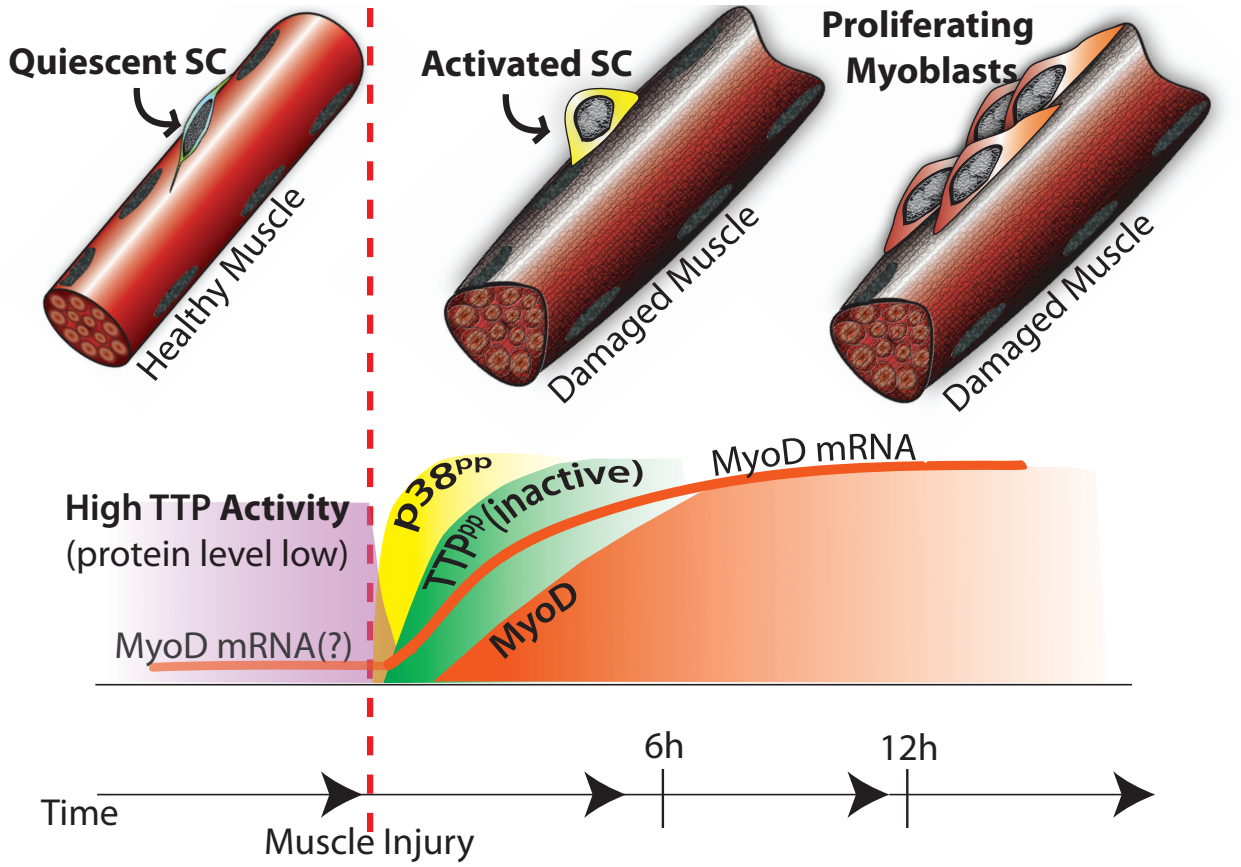

Figure 1: Activated-p38α/β Inhibition of TTP Stabilizes MyoD to Commit Satellite Cells to the Myogenic Lineage.
Quiescent satellite cells must activate and commit to myogenesis to repair muscle. We propose that in quiescent satellite cells very low levels of MyoD mRNA are present; however, it is either actively destabilized by TTP or sequestered away from translational machinery by TTP. Upon muscle injury, p38α/β MAPKs are rapidly activated resulting in phosphorylation of TTP. Phosphorylated-TTP no longer suppresses MyoD mRNA resulting in rapid induction of MyoD likely accompanied by transcriptional up-regulation of the MyoD gene locus and increased MyoD mRNA stability mediated by HuR.

Post-transcriptional regulation of MyoD mRNA in quiescent satellite cells may provide a mechanism for rapid commitment of satellite cells to the myogenic lineage upon activation. The idea that TTP regulates MyoD mRNA in quiescent satellite cells requires that MyoD mRNA is present. Quiescent satellite cells may express very low levels of MyoD mRNA which is rapidly subjected to AU-rich mediated decay by TTP and/or its homologs Brf1 and Brf2. Alternatively, MyoD mRNA is expressed by satellite cell progenitors and TTP binds the message and sequesters MyoD mRNA away from the translational machinery. In human cells, TTP has been shown to stably store AU-rich containing mRNAs and sequester them away from the translational machinery when mRNA decay factors are limiting [137]. However, this hypothesis requires that the MyoD locus be active in satellite cell progenitors. By using Cre-mediated lineage tracing of the MyoD locus, satellite cell progenitors were shown to have activated the MyoD locus prior to entering quiescence [40]. The MyoD locus may be active at a very low levels in quiescent satellite cells; however, this has not been directly tested.

Storage and sequestration of MyoD message or active MyoD mRNA decay in quiescent satellite cells would provide a pool of available MyoD mRNA for translation. Upon receiving activation signals, a quiescent satellite cell could mobilize this available pool of MyoD mRNA to be rapidly translated into MyoD protein (Fig 1). Alternatively, if MyoD mRNA is not actively expressed or stored in quiescent satellite cells, upon satellite cell activation MyoD transcription would be up-regulated. Phosphorylated-TTP and HuR may bind nascent MyoD mRNA and synergistically stabilize MyoD transcripts.

TTP regulation of MyoD mRNA may be involved in driving satellite cells to re-enter quiescence. MyoD is required for satellite cells to enter the cell cycle [75], and during *ex-vivo* myofiber culture, all satellite cells enter into the first round of cell division following isolation (Olwin Lab, unpublished). Thus, satellite cells are MyoD positive prior to entering the first cell division. A sub-population of satellite cells exit the cell cycle after the first cell division following

isolation (Olwin Lab, unpublished). MyoD protein is undetectable in the majority of this non-dividing sub-population of satellite cells (Olwin Lab, unpublished). Thus, MyoD expression may have been down-regulated in this non-dividing satellite cell population. Down-regulation of MyoD expression may be achieved by transcriptional, post-transcriptional and post-translational mechanisms. TTP may mediate decay of MyoD mRNA at the post-transcriptional level to assist in down-regulation of MyoD in this sub-population of non-dividing satellite cells. This sub-population of non-dividing satellite cells express Pax 7, a paired box transcription factor expressed in quiescent satellite cells [35] (Olwin lab, unpublished). Pax7 appears to play a central role in down-regulation of MyoD at the post-translational level in proliferating satellite cells. Pax7 mediates instability of MyoD protein [161] and directly up-regulates Id3, an inhibitor of MyoD transcriptional activity [162]. The combination of TTP directed MyoD mRNA decay and Pax7 post-translational regulation of MyoD may be able to effectively switch satellite cells to a MyoD negative status upon exit from the cell cycle.

Concluding Remarks

Collectively, my data support the hypothesis that post-transcriptional regulation of mRNA plays an important role in the switch from a quiescent satellite cell to an activated proliferating myoblast. In particular, activated-p38α/β MAPK inhibition of the Tristetraprolin family of RNA binding proteins is essential for satellite cells to induce MyoD and commit to the myogenic lineage upon satellite cell activation.

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Appendix

Appendix Table 1: WT-S4 gene list. Sorted by Fold Change.

Increasing Probe Set ID	Gene Symbol	Fold Change	p value
1447751_x_at	Dus2l	37	4.41E-03
1419439_at	Stk22s1	30	5.75E-05
1457014_x_at	Slc16a8	28	1.71E-09
1442183_at	LOC236069	25	1.33E-03
1438643_at	Camk1d	18	2.60E-03
1440797_at	Dlx6os2	17	3.84E-04
1419166_at	Slc5a2	16	3.60E-08
1454353_at	4833420D23Rik	16	6.05E-03
1436740_at	LOC100041567	14	5.20E-05
1439087_a_at	Pik3ip1	13	4.94E-07
1438873_at	OTTMUSG00000018077	12	2.93E-03
1452396_at	Sfrs15	12	1.10E-06
1443772_at	Dzip1	12	9.64E-03
1437717_x_at	LOC100041567	12	2.52E-05
1428993_at	1110017I16Rik	11	9.39E-07
1433383_at	1500002K03Rik	11	6.24E-05
1446380_at	9430076C15Rik	11	5.59E-07
1417896_at	Tjp3	10	9.63E-09
1453962_at	Pfn3	10	2.61E-05
1441958_s_at	Ager	10	7.81E-06
1428870_at	Nolc1	10	5.30E-10
1445445_s_at	Ptger1	9	1.16E-05
1435219_x_at	Becn1	9	9.15E-05
1432896_at	9030409K20Rik	9	7.31E-03
1447517_at	Skiv2l2	9	1.89E-03
1457228_x_at	Gle1	9	1.61E-04
1422173_at	Pdx1	9	6.30E-08
1427278_at	Clip4	9	9.99E-04
1426929_at	Brunol4	9	1.88E-07
1439434_x_at	Sh2d5	9	2.39E-04
1446851_at	Col22a1	9	2.55E-09
1426007_a_at	Ubxd3	9	1.71E-05
1437183_at	Lrrc4b	8	2.02E-05
1439759_x_at	Sult6b1	8	8.67E-08
1437407_at	9930039A11Rik	8	1.05E-07
1459878_a_at	A430107O13Rik	8	1.88E-03
1422515_at	Svs7	8	2.65E-03
1434542_at	Gpt2	8	2.71E-06
1456171_at	March10	8	4.15E-07
1428358_at	1810010M01Rik	8	6.99E-06
1441837_at	Chrnb2	8	1.13E-05
1450683_at	Tagln3	8	1.90E-06
1460418_x_at	H2-T18	8	6.72E-05
1438632_x_at	Tnp1	8	6.07E-10
1431227_at	4930421J07Rik	8	1.30E-05
1453438_x_at	Gsdma2	7	3.03E-04
1452416_at	Il6ra	7	4.62E-04
1427930_at	Pdxk	7	3.26E-04
1453484_at	1700081D17Rik	7	1.47E-04
1425195_a_at	Acat2	7	1.84E-07
1417238_at	Ewsr1	7	3.00E-07
1429130_at	Ttc25	7	3.86E-10
1427457_a_at	Bmp1	7	1.52E-08
1445942_at	AU015858	7	4.70E-04
1429926_at	Apool	7	6.99E-03
1431117_x_at	1810029B16Rik	7	1.81E-04
1455632_at	Gnb5	7	3.05E-06
1430257_at	Card11	7	7.61E-03
1451578_at	Ccdc65	7	3.39E-07
1421630_at	Zfy1	7	5.31E-05
1422106_a_at	Spsb2	7	4.80E-06
1447861_x_at	Mrg1	7	5.78E-05
1451203_at	Mb	7	4.62E-03
1437754_at	AW146299	7	1.12E-05
1421184_a_at	Higd1c	7	1.54E-04
1437453_s_at	Pcsk9	6	7.94E-06
1450582_at	H2-Q5	6	3.71E-04
1431213_a_at	LOC100041156	6	1.68E-06
1452272_a_at	Gfer	6	5.94E-03
1439346_at	Gpr135	6	8.73E-06
1437952_at	AU040096	6	6.54E-05
1419095_a_at	Apom	6	3.68E-06
1441234_at	Serhl	6	1.05E-04
1453217_at	4930527E24Rik	6	6.56E-06
1455853_x_at	Tspan31	6	1.19E-04
1439617_s_at	Pck1	6	1.61E-05
1454870_x_at	Gpr172b	6	7.53E-04
1450318_a_at	P2ry2	6	4.33E-06
1421356_at	Tex9	6	1.39E-03
1420807_a_at	Dlk2	6	1.99E-06
1443573_at	Parp1	6	4.91E-03
1453799_at	9430038I01Rik	6	3.08E-04
1438608_at	Tnni2	6	1.47E-04
1451371_at	Mrap	6	8.93E-08
1427514_at	LOC624295	6	2.15E-03
1451022_at	Lrp6	6	1.03E-04
1422870_at	Hoxc4	6	2.39E-06
1421451_at	Crb1	6	9.43E-05
1430836_at	4933437G19Rik	6	2.23E-06
1445511_at	Cetn4	6	6.63E-03
1451511_at	Hibch	6	7.78E-07
1427859_at	Igk-V19-14	6	2.54E-05
1422674_s_at	Crygb	6	4.29E-04

1427768_s_at	Myl3	6	2.05E-07
1460386_a_at	Slc1a1	6	2.24E-05
1451955_a_at	Cacna2d2	6	9.03E-04
1423436_at	Gsta3	6	1.90E-05
1439232_at	1500016L03Rik	6	4.16E-07
1442922_at	Chfr	6	7.20E-07
1430442_at	Nos1ap	6	4.30E-05
1452987_at	Josd3	5	1.36E-04
1449901_a_at	Map3k6	5	4.94E-04
1418913_at	Bhmt2	5	2.03E-05
1454357_at	3110067C02Rik	5	3.22E-06
1439144_at	Cwf19l1	5	6.38E-04
1421063_s_at	Snrpn	5	1.81E-07
1430230_at	Rcsd1	5	1.75E-05
1416023_at	Fabp3	5	1.47E-03
1422224_at	Tcp10a	5	8.02E-08
1438896_at	Dnajc6	5	6.97E-03
1437386_at	Lingo1	5	1.38E-03
1454046_x_at	Pgs1	5	1.33E-03
1426372_a_at	Bet1l	5	1.49E-03
1459586_at	C78452	5	1.93E-03
1451191_at	Crabp2	5	1.50E-05
1460258_at	Lect1	5	1.76E-05
1432335_at	4930551O13Rik	5	1.39E-04
1433342_at	5730416F02Rik	5	2.73E-05
1419450_at	Ormdl3	5	8.24E-05
1459046_at	4930473A06Rik	5	4.92E-04
1427220_a_at	Svs5	5	2.05E-05
1449682_s_at	Tubb2b	5	3.51E-06
1428196_a_at	1200015F23Rik	5	9.47E-03
1453989_at	Stxbp4	5	9.78E-07
1450196_s_at	Gys1	5	1.01E-05
1444786_at	Nol3	5	3.37E-05
1435627_x_at	Marcksl1	5	3.48E-04
1459977_x_at	Cox10	5	5.55E-04
1425395_at	Adam26a	5	1.38E-04
1436383_at	Cplx2	5	1.50E-03
1438378_at	1700013G23Rik	5	1.29E-08
1425201_a_at	Hyi	5	2.88E-06
1457640_x_at	Pigs	5	1.11E-03
1440178_x_at	Zap70	5	1.32E-05
1460715_x_at	Tcfcp2l1	5	4.67E-06
1454585_at	1110065P19Rik	5	5.36E-06
1429035_at	Dpep3	5	3.20E-05
1417313_at	Lsm7	5	3.81E-04
1427781_at	Usmg2	5	7.44E-05
1416965_at	Pcsk1n	5	2.81E-05
1442156_at	E030030I06Rik	5	1.98E-04
1437880_at	Lbxcor1	5	2.09E-05
1433294_at	4930449I04Rik	5	1.88E-04
1447007_at	1700008I05Rik	5	3.08E-04
1451278_a_at	2610205E22Rik	5	4.03E-06
1430844_at	1700018M17Rik	5	2.76E-04
1421780_a_at	Cabp5	5	6.30E-07
1426702_at	4632419K20Rik	5	1.00E-06
1440517_x_at	Cmah	5	5.19E-06
1436814_at	1810010D01Rik	5	4.65E-06
1442788_at	Afap1	5	1.10E-06
1450838_x_at	Rpl37	5	1.64E-05
1453447_at	1700109H08Rik	5	4.94E-06
1447673_x_at	1700015C15Rik	5	5.62E-07
1432590_at	4930573O21Rik	5	2.62E-03
1459054_at	Casz1	5	3.62E-05
1439330_at	D230040J21Rik	5	2.56E-04
1436264_at	BC025920	5	7.48E-06
1429496_x_at	2300002M23Rik	5	7.24E-04
1432519_at	1810059H22Rik	5	6.68E-08
1432883_at	4932431P20Rik	5	2.86E-04
1451727_at	Slu7	5	2.12E-04
1430240_a_at	Clgn	5	7.91E-07
1453718_at	Bcl2l12	5	6.73E-04
1444330_at	D2Ertd173e	5	2.83E-03
1431663_a_at	Cntfr	5	3.14E-04
1427527_a_at	Pthlh	5	2.83E-07
1430659_at	4930548H24Rik	5	7.24E-05
1436798_at	Rpl9	4	7.13E-05
1451862_a_at	Prf1	4	2.10E-07
1447066_at	LOC100042125	4	4.47E-06
1460546_at	Lgi3	4	8.94E-04
1442281_at	D4Ertd796e	4	3.32E-04
1453233_s_at	Calr3	4	5.59E-04
1429542_at	1700007B14Rik	4	8.98E-04
1437920_at	Epha5	4	3.00E-07
1442712_at	LOC100039191	4	1.85E-08
1459101_at	C78760	4	1.83E-03
1449218_at	Cox8b	4	9.47E-03
1419474_a_at	Ehf	4	3.73E-06
1427567_a_at	Tpm3	4	3.75E-08
1445852_at	D19Ertd200e	4	1.35E-04
1439071_at	5430416N02Rik	4	2.82E-03
1452831_s_at	Ppat	4	1.36E-03
1425797_a_at	Syk	4	4.41E-03
1421667_at	Nmur1	4	4.19E-05
1435980_x_at	Wnt6	4	7.72E-07
1438654_x_at	Mmd2	4	1.01E-04
1430297_a_at	2010301N04Rik	4	5.08E-05

1434322_at	Micall2	4	2.16E-03
1438979_s_at	1700029I15Rik	4	3.59E-05
1458635_at	4832428D23Rik	4	6.94E-05
1449400_at	Csl	4	2.52E-04
1426106_a_at	Syt6	4	1.16E-03
1439966_x_at	Sfxn2	4	3.61E-06
1448432_at	Plcd1	4	3.11E-04
1419959_s_at	Cphx	4	1.97E-05
1431024_a_at	Arid4b	4	1.01E-06
1455527_at	Cd163l1	4	3.41E-03
1431494_at	A930008B05Rik	4	3.17E-05
1417359_at	Mfap2	4	1.94E-04
1419877_x_at	2810449G22Rik	4	2.62E-05
1437019_at	2200001I15Rik	4	6.36E-04
1456420_at	Arid4a	4	5.78E-05
1454028_at	4931402H11Rik	4	2.06E-04
1443473_at	C79562	4	4.24E-05
1427871_at	Ptafr	4	4.64E-05
1448271_a_at	Ddx21	4	5.13E-03
1450712_at	Kcnj9	4	6.93E-03
1442959_at	Birc6	4	2.42E-03
1430408_at	Cacna1a	4	3.23E-04
1444228_s_at	Herc2	4	2.22E-05
1419576_at	Hoxb13	4	2.59E-04
1427687_at	Pcdha10	4	6.85E-06
1456242_at	EG653016	4	2.08E-06
1438722_at	2610014I16Rik	4	9.20E-04
1422934_x_at	Defcr-rs7	4	7.07E-05
1430572_at	Psmg3	4	9.19E-03
1426936_at	LOC629242	4	9.40E-03
1457150_at	AI428301	4	3.00E-04
1427986_a_at	Col16a1	4	3.60E-03
1422068_at	Pou3f1	4	1.55E-09
1439250_at	Slitrk3	4	3.57E-05
1460473_at	6230400D17Rik	4	2.79E-04
1421245_at	Sost	4	7.57E-04
1453822_at	Dnalc1	4	1.43E-07
1423454_a_at	Sema6c	4	1.84E-03
1432725_at	4930445G23Rik	4	2.70E-07
1423460_at	Perq1	4	2.78E-04
1419193_a_at	Gmfg	4	7.71E-04
1416492_at	Ccne1	4	8.02E-05
1448669_at	Dkk3	4	1.25E-04
1457777_at	Gsdma1	4	7.09E-09
1458510_at	AU019823	4	1.28E-05
1436895_at	Centd1	4	1.33E-04
1430864_at	Ttll9	4	5.01E-05
1436775_a_at	Ankrd17	4	3.93E-03
1432289_a_at	Jsrp1	4	7.48E-04
1421466_at	Asb10	4	3.74E-05
1424796_at	1700054N08Rik	4	3.81E-03
1431854_a_at	4930452B06Rik	4	4.42E-08
1436808_x_at	Mcm5	4	5.57E-03
1433280_at	4933417G07Rik	4	2.78E-04
1449390_at	Gpatch4	4	3.31E-04
1425249_a_at	Tyro3	4	1.87E-03
1428988_at	Abcc3	4	3.42E-03
1436863_at	1700010I14Rik	4	7.65E-05
1451192_a_at	Ttc4	4	1.52E-04
1457754_at	4930430F08Rik	4	7.22E-03
1446168_at	LOC100041495	4	9.16E-03
1452827_at	1500009C09Rik	4	6.34E-03
1427386_at	Arhgef16	4	1.11E-04
1434502_x_at	Slc4a1	4	7.75E-03
1447785_x_at	D11Wsu99e	4	2.95E-03
1441956_s_at	Cutl1	4	6.51E-09
1429989_at	1700008A04Rik	4	1.12E-06
1449088_at	Fbp2	4	9.19E-05
1429338_a_at	Nol9	4	4.58E-04
1422006_at	Eif2ak2	4	1.15E-04
1447495_at	Fank1	4	3.02E-04
1446991_at	Gcn1l1	4	8.19E-03
1442031_at	Ccdc109a	4	9.00E-10
1439947_at	Cyp11a1	4	7.58E-06
1460658_at	Ap1g1	4	1.00E-03
1455920_x_at	Lyzl6	4	2.27E-05
1425558_at	Klc3	4	1.13E-04
1419134_at	Rhbg	4	4.95E-04
1453041_at	Tmem16j	4	1.03E-07
1449411_at	Dscam	4	3.17E-04
1441302_at	LOC100043375	4	1.03E-04
1435533_s_at	4933426K21Rik	4	2.24E-03
1441295_at	Lman2l	4	1.68E-05
1436369_at	2900076A07Rik	4	2.13E-04
1431533_at	4921530D09Rik	4	5.17E-05
1456525_at	AA881470	4	2.03E-03
1447222_at	Hspa12a	4	2.36E-04
1443695_at	Habp2	4	5.59E-04
1446291_at	9330175H22Rik	4	1.49E-04
1448764_a_at	Fabp1	4	3.53E-10
1430168_at	Cstad	4	2.59E-06
1454212_x_at	Gsdmdc2	4	2.26E-03
1422984_at	Clip2	4	3.51E-03
1451164_a_at	Mrps18b	4	6.97E-05
1437387_at	Susd5	4	6.65E-04
1418391_at	Phf21a	4	7.47E-04

1443648_at	9530003O04Rik	4	9.56E-06
1453562_a_at	Nmral1	4	1.68E-05
1427903_at	Phpt1	4	3.32E-04
1421675_at	1700123K08Rik	4	1.60E-03
1444649_at	ENSMUSG00000071036	4	1.49E-06
1434652_at	Cdc42bpb	4	1.12E-03
1454759_at	Git1	4	2.74E-05
1459678_at	LOC497255	4	3.45E-03
1448169_at	Krt18	4	7.82E-04
1440726_at	A230062I15Rik	4	3.31E-07
1426563_at	Zfp553	4	6.43E-05
1440187_at	Taf3	4	1.70E-06
1442363_at	1110012J17Rik	4	7.59E-03
1438308_at	4931433A01Rik	4	6.66E-05
1428692_at	Hddc3	4	1.56E-03
1428972_at	Tctex1d2	4	7.40E-04
1440180_x_at	Zbtb3	4	7.84E-04
1458449_at	Fbxl11	4	4.71E-05
1423015_at	Kirrel	4	1.45E-05
1442599_at	Slc12a9	4	2.33E-04
1444725_at	Mastl	4	3.07E-05
1416076_at	Ccnb1	4	6.85E-04
1447484_x_at	Snhg7	4	4.57E-04
1420176_x_at	Igll1	4	3.59E-03
1450451_at	Spock2	4	1.30E-04
1418197_at	Ucp1	4	3.82E-06
1436789_at	Ccnjl	4	2.30E-03
1435015_at	Zfp787	4	9.07E-10
1445930_at	Fndc7	4	7.97E-06
1440472_at	LOC100048815	4	6.44E-07
1434505_a_at	6430548M08Rik	4	3.08E-05
1452684_at	Akt1s1	4	7.52E-05
1421673_s_at	Stx1b1	4	3.75E-07
1432586_at	5730596P11Rik	4	2.96E-07
1428860_at	4930572J05Rik	4	5.46E-04
1439451_x_at	Gpr172b	4	4.70E-03
1436720_s_at	Oog3	4	4.78E-05
1444981_at	Punc	4	1.34E-04
1457010_at	3010001F23Rik	4	1.25E-04
1438479_at	Zfp213	4	1.25E-03
1419621_at	Ankrd2	4	1.33E-03
1425341_at	Kcnk3	4	2.88E-05
1455552_at	Snapc4	4	3.79E-03
1451128_s_at	Kif22	4	1.19E-04
1450246_at	Fut2	4	1.54E-05
1442064_at	AW556556	4	4.02E-03
1420214_at	1810012K16Rik	4	8.43E-05

1458976_at	C230035I16Rik	4	3.32E-04
1417447_at	Tcf21	4	5.77E-04
1430132_at	Krt28	4	2.65E-04
1425426_a_at	Mef2a	4	1.22E-05
1430952_at	3110039C02Rik	4	2.25E-08
1445649_x_at	Zfp142	4	6.49E-05
1432566_at	1700129I15Rik	4	1.89E-03
1453957_a_at	Igf2bp3	4	3.53E-05
1437595_at	E030010A14Rik	4	2.97E-04
1433788_at	Nrxn3	4	4.67E-06
1449512_a_at	Zfx	4	2.68E-08
1422405_at	H2-D4	4	8.65E-04
1447954_at	Lrrc49	4	1.49E-04
1457258_at	1700017L05Rik	4	4.40E-06
1451966_at	Mrap	4	7.08E-05
1440499_at	D9Ertd26e	4	1.60E-08
1443412_s_at	Mmp16	4	1.33E-05
1449284_at	1700008P20Rik	4	1.78E-05
1431532_at	4931400O07Rik	4	1.75E-07
1433207_at	5033430J17Rik	4	1.95E-03
1446214_at	D430018E03Rik	4	7.90E-05
1421362_a_at	Frk	4	3.20E-05
1454913_at	9930104L06Rik	4	3.21E-06
1449104_at	Upk3a	4	2.99E-04
1439593_s_at	C030010B13Rik	4	1.75E-03
1432481_a_at	Lyzl6	4	3.51E-07
1457574_at	LOC635668	4	7.80E-03
1431463_at	1700041C02Rik	4	2.20E-06
1445717_at	E130108L08Rik	4	2.14E-06
1451056_at	Psmd7	4	4.08E-03
1427791_a_at	Adam1a	4	1.53E-03
1450292_a_at	Hormad1	4	3.32E-07
1457044_at	4732474O15Rik	4	1.91E-07
1456704_at	9530010C24Rik	4	1.92E-05
1417643_at	Rsph1	4	6.21E-03
1427538_at	Zfp369	4	1.77E-03
1416450_at	Taf8	4	1.31E-03
1445510_at	C79601	4	2.01E-03
1448750_at	Hand1	3	1.94E-03
1449660_s_at	Coro1c	3	2.54E-04
1437381_x_at	Gpr172b	3	8.41E-05
1443508_at	Dlgap1	3	5.22E-04
1415978_at	Tubb3	3	4.03E-04
1425443_at	Tcfap2d	3	9.07E-07
1424909_at	Lrrc46	3	6.20E-04
1456091_at	Sec22c	3	2.64E-03
1448065_at	Ppox	3	8.22E-05
1441420_at	Igsf9	3	4.75E-03

1427960_at	Ugt2b34	3	6.47E-03
1425836_a_at	Limk1	3	4.28E-04
1457149_at	Ttc22	3	3.34E-03
1444567_at	1700066J03Rik	3	8.82E-05
1453427_at	Csnk2a1	3	1.55E-06
1457029_at	C030010B13Rik	3	7.03E-05
1430450_at	Atp5sl	3	5.89E-06
1425309_at	Catsper2	3	1.64E-03
1453879_at	1700016H13Rik	3	2.71E-06
1451181_at	Tmem121	3	1.63E-03
1454433_at	6330526H18Rik	3	4.74E-06
1430037_at	Snx27	3	3.97E-03
1418165_at	Itln1	3	6.70E-04
1429704_at	Lrp2bp	3	8.63E-06
1450194_a_at	Myb	3	1.05E-06
1420712_a_at	Hpn	3	5.64E-03
1435496_at	5730469M10Rik	3	6.22E-04
1449369_at	Tmprss2	3	2.91E-04
1453821_at	N6amt1	3	2.48E-04
1422420_at	Mb	3	1.67E-03
1429432_at	Bat2d	3	2.97E-06
1449683_x_at	Tubb2a-ps2	3	3.09E-08
1443961_at	LOC100043292	3	1.85E-03
1452219_at	Tmem63b	3	4.97E-03
1432376_at	3830403N18Rik	3	4.19E-07
1454202_a_at	1700061J05Rik	3	4.61E-03
1437340_x_at	Gkn1	3	2.92E-05
1441622_at	EG433023	3	9.27E-05
1432371_a_at	1700109K24Rik	3	2.23E-04
1429368_at	Lrig3	3	6.59E-03
1431189_a_at	Fahd2a	3	1.26E-03
1456994_at	Rassf1	3	2.25E-09
1437936_at	6330534C20Rik	3	3.40E-04
1449499_at	Hoxa7	3	8.31E-04
1435840_x_at	LOC625360	3	2.90E-07
1431253_s_at	Tbc1d9	3	2.78E-03
1430403_at	Usp32	3	3.97E-03
1449766_at	Syt6	3	4.99E-06
1430012_at	1110050K14Rik	3	1.74E-03
1425812_a_at	Cacna1b	3	7.73E-07
1440469_at	ENSMUSG00000056509	3	3.06E-05
1427632_x_at	Daf2	3	1.31E-08
1421005_at	Cep110	3	1.75E-03
1421761_a_at	Barx2	3	1.25E-03
1456184_at	Tmem63c	3	3.22E-04
1427282_a_at	Fxn	3	1.16E-05
1423582_at	Dmrt1	3	4.81E-05
1443569_at	4930430E16Rik	3	1.17E-03
1424178_at	Tmem38a	3	3.54E-05
1437075_at	Frmd3	3	2.14E-05
1426134_at	Trdn	3	2.54E-08
1431436_a_at	Katnal2	3	9.30E-03
1437293_x_at	Ust	3	4.95E-07
1424459_at	Lpcat1	3	1.06E-03
1432822_at	4930557B21Rik	3	7.26E-04
1440144_x_at	C330046E03	3	2.59E-03
1442308_at	Smyd4	3	1.95E-04
1429780_at	Ccdc39	3	5.94E-07
1453210_at	5730507C01Rik	3	8.88E-04
1447483_s_at	Snhg7	3	1.45E-03
1420860_at	Itga9	3	9.27E-06
1417473_a_at	Ppcs	3	1.45E-07
1417956_at	Cidea	3	2.08E-03
1435737_a_at	Nde1	3	7.94E-03
1449943_at	Lfng	3	2.86E-04
1416196_at	Rpsa	3	3.81E-07
1448093_s_at	C77405	3	1.18E-05
1439190_at	Fhad1	3	3.33E-06
1440376_at	Fbxo41	3	3.91E-05
1415750_at	Tbl3	3	2.18E-04
1430181_at	H1fnt	3	2.47E-03
1442923_at	Ptk6	3	1.64E-07
1449248_at	Clcn2	3	1.25E-03
1421754_at	AY036118	3	1.35E-03
1425998_at	Sytl4	3	5.10E-06
1449767_x_at	Syt6	3	7.19E-08
1436658_at	B130024G19Rik	3	3.15E-05
1457703_at	Cacna2d4	3	4.61E-03
1456010_x_at	Hes5	3	4.24E-07
1423979_a_at	Slc25a29	3	5.31E-03
1433168_x_at	5830456J23Rik	3	1.77E-08
1456977_at	Samd11	3	3.19E-04
1451822_a_at	Scrn2	3	2.00E-04
1423171_at	Gpr88	3	2.89E-04
1457396_at	LOC100045013	3	1.04E-04
1457604_x_at	Cyp11a1	3	2.38E-08
1420043_s_at	Thoc1	3	8.60E-04
1452098_at	Chtf18	3	1.12E-04
1431565_at	4930511J24Rik	3	2.23E-03
1439007_at	Alg6	3	3.94E-06
1433855_at	Abat	3	8.34E-07
1452481_at	Plcb2	3	2.70E-04
1426770_at	Pex5	3	5.84E-03
1422723_at	Stra6	3	1.69E-04
1426151_a_at	Stx3	3	7.30E-05

1433083_at	4930448K20Rik	3	4.00E-05
1432560_at	1700127D06Rik	3	3.69E-05
1435628_x_at	LOC629242	3	4.94E-04
1429677_at	1700056E22Rik	3	4.61E-06
1449487_at	Ccdc70	3	1.79E-04
1429181_at	1700009P17Rik	3	5.32E-03
1458621_at	Wdr78	3	3.11E-04
1432539_a_at	Nup54	3	1.25E-03
1418306_at	Crybb1	3	2.41E-03
1445266_at	Ercc1	3	9.88E-06
1430498_at	9130009I01Rik	3	2.33E-04
1419822_at	Eif3e	3	2.43E-03
1422695_at	Ttyh1	3	1.90E-03
1423379_at	Nfatc4	3	2.69E-03
1422409_at	Hes3	3	2.98E-05
1443525_at	Dbx2	3	7.23E-08
1444692_at	AI316844	3	4.46E-06
1421682_a_at	Tcte3	3	7.51E-07
1419240_at	Tex14	3	4.64E-03
1458745_at	D18Ertd201e	3	2.40E-03
1432283_at	4930417G10Rik	3	4.30E-11
1440798_x_at	Lrrc6	3	3.89E-04
1434100_x_at	Ppargc1a	3	3.64E-04
1445120_at	AU021977	3	7.60E-07
1437890_at	1500005I02Rik	3	3.33E-04
1430872_at	4930412O13Rik	3	7.10E-04
1439370_x_at	Sf3b5	3	1.02E-05
1419408_at	Six6	3	3.37E-12
1429992_at	Speer4b	3	5.79E-06
1453604_a_at	Hbs1l	3	3.26E-05
1426809_at	C430004E15Rik	3	6.82E-04
1442040_at	Tmem125	3	4.14E-06
1429675_at	1700023A16Rik	3	1.01E-03
1423506_a_at	Nnat	3	1.69E-03
1433255_at	8430437B07Rik	3	3.59E-03
1434803_a_at	Sycn	3	4.37E-04
1439793_at	Gja3	3	1.11E-05
1427851_x_at	Igh-VJ558	3	5.57E-05
1441563_at	2410017P07Rik	3	3.52E-03
1444251_x_at	D4Ertd111e	3	1.31E-05
1430374_at	Slc25a37	3	7.11E-09
1450368_a_at	Ppp3r1	3	1.24E-05
1433877_at	4732473B16Rik	3	6.24E-07
1438327_at	Zfp533	3	2.74E-03
1457541_at	Akap14	3	3.42E-04
1454124_at	1700067K01Rik	3	7.03E-04
1455802_x_at	Agr2	3	2.21E-08
1429306_at	Lzic	3	1.12E-03
1446120_at	Uhmk1	3	3.27E-03
1433673_at	E130309D14Rik	3	6.85E-04
1443506_at	Kctd2	3	4.51E-04
1459935_at	AA517562	3	2.34E-05
1458310_at	A230056J06Rik	3	1.74E-05
1416898_a_at	Irf3	3	7.26E-05
1457606_x_at	AU015228	3	8.31E-04
1451454_at	Pcdh20	3	2.84E-06
1447570_s_at	A430106A12Rik	3	1.63E-03
1428679_s_at	0610010K14Rik	3	1.23E-04
1440911_at	Col23a1	3	4.99E-05
1447536_at	Lysmd2	3	2.24E-04
1439112_at	2810442I21Rik	3	1.65E-03
1438189_s_at	Epb4.9	3	3.89E-06
1445871_at	AI315376	3	2.08E-04
1453277_at	3021401N23Rik	3	2.19E-04
1427217_at	Zfp455	3	4.03E-07
1437702_at	Tgm6	3	1.30E-09
1430714_at	4930451C15Rik	3	7.13E-05
1447821_at	1700051K22Rik	3	3.22E-04
1436815_x_at	1810010D01Rik	3	5.10E-04
1456332_at	Tmem17	3	4.83E-07
1439376_x_at	Dmtf1	3	1.05E-04
1456428_at	Cxcl15	3	6.24E-03
1426811_at	Ppp2r5b	3	1.92E-03
1435495_at	Adora1	3	1.15E-04
1428266_at	Myl3	3	5.88E-05
1429981_a_at	4933426K21Rik	3	2.00E-04
1430073_at	2900016B01Rik	3	7.52E-05
1437860_at	Prkce	3	2.08E-07
1443656_at	Fut8	3	7.43E-03
1437693_at	D1Pas1	3	1.15E-03
1437232_at	Bpil2	3	1.47E-04
1441909_s_at	9530066K23Rik	3	5.88E-07
1453921_at	4930429F11Rik	3	1.38E-05
1451580_a_at	Ttr	3	2.05E-03
1437644_at	B3galt2	3	2.72E-07
1452631_at	Rufy2	3	9.10E-07
1459790_x_at	Alx3	3	1.15E-04
1460238_at	Msln	3	4.55E-04
1433469_at	Lrrn2	3	8.72E-05
1458439_a_at	Dzip3	3	4.77E-04
1437367_at	Bat1a	3	3.74E-03
1450782_at	Wnt4	3	2.31E-04
1441618_at	Arhgap29	3	6.62E-05
1425963_at	Cabp7	3	5.37E-03
1431083_a_at	1810014B01Rik	3	4.91E-04
1440074_at	EG432988	3	1.35E-03

1440767_at	Defb41	3	5.81E-04
1427612_at	Defb9	3	3.50E-06
1452386_at	Sall3	3	2.94E-06
1424177_at	Tmem38a	3	7.55E-03
1433029_at	Kcnj9	3	2.78E-03
1420269_at	2610201A13Rik	3	3.04E-03
1452600_at	Taf6l	3	7.24E-04
1424878_at	Lrch4	3	1.23E-03
1455865_at	Insm1	3	1.96E-07
1421543_at	Fbxo4	3	8.18E-05
1448766_at	Gjb1	3	2.24E-03
1453073_at	5830403F22Rik	3	2.28E-04
1440735_at	Polr3k	3	2.61E-04
1454045_a_at	Pgs1	3	3.08E-04
1417215_at	Rab27b	3	2.37E-03
1448768_at	Mog	3	3.20E-05
1419746_at	4933428G20Rik	3	1.54E-03
1432512_at	4931433A01Rik	3	1.85E-07
1423045_at	Ncbp2	3	1.88E-03
1430545_at	Dbf4	3	1.40E-06
1432851_at	Phactr1	3	1.14E-03
1454768_at	Kcnf1	3	1.73E-04
1440921_at	Nlrp12	3	1.29E-03
1421418_a_at	Psg19	3	4.46E-07
1447272_s_at	Atp10a	3	3.38E-06
1442353_at	Itpa	3	3.39E-03
1422008_a_at	Aqp3	3	4.39E-09
1422986_at	Esrrb	3	2.72E-03
1446901_at	AU022077	3	2.53E-06
1422504_at	Glrb	3	1.02E-07
1422273_at	Mmp1b	3	2.14E-04
1426699_at	AU040320	3	2.86E-03
1439296_at	Prickle3	3	6.19E-04
1447292_at	Actr1b	3	4.94E-04
1437140_at	4930412F15Rik	3	1.89E-04
1447603_x_at	1700027J05Rik	3	3.68E-04
1419831_at	AA416453	3	9.27E-03
1459809_x_at	1700063D05Rik	3	2.39E-04
1460415_a_at	Cd40	3	9.05E-04
1447273_x_at	Atp10a	3	3.21E-03
1451899_a_at	Gtf2ird1	3	1.56E-03
1449488_at	Pitx1	3	2.51E-04
1424719_a_at	Mapt	3	7.42E-05
1431181_a_at	Luc7l	3	2.12E-03
1432564_at	1700066C05Rik	3	9.96E-05
1451553_at	Art5	3	1.29E-04
1425870_a_at	Kcnip2	3	1.73E-06
1429280_at	Col22a1	3	1.82E-04
1415864_at	Bpgm	3	4.24E-03
1450354_a_at	Ptdss2	3	6.07E-03
1422383_at	V1rb6	3	1.41E-08
1446685_at	EG665033	3	3.43E-04
1422260_x_at	Ccr5	3	3.60E-04
1443839_at	1700010H22Rik	3	3.82E-07
1417658_at	Tbrg4	3	2.06E-03
1416055_at	Amy2	3	2.69E-04
1460437_at	Pscd4	3	1.48E-03
1454653_at	Cpne9	3	2.59E-04
1450476_at	Cnr2	3	4.28E-04
1430658_a_at	Gsdma2	3	2.53E-07
1460127_at	Hnf4g	3	7.68E-09
1455748_at	Tmem181	3	6.02E-04
1433373_at	Supt7l	3	1.62E-07
1434214_at	0910001L09Rik	3	5.31E-04
1428575_at	Fcho1	3	7.97E-04
1423856_at	Popdc3	3	7.93E-04
1425803_a_at	Mbd2	3	6.81E-03
1432459_a_at	Zbtb32	3	1.36E-04
1455198_a_at	Ppp2r3a	3	8.42E-06
1423438_at	Kptn	3	2.05E-03
1449033_at	Tnfrsf11b	3	9.83E-05
1445229_at	Dgat1	3	2.94E-03
1443713_at	Chl1	3	3.76E-08
1432398_at	1700084J12Rik	3	4.10E-08
1451940_x_at	Trdn	3	5.01E-08
1432218_a_at	Nol9	3	1.23E-03
1438464_at	Arid4a	3	4.30E-04
1451991_at	Epha7	3	1.17E-03
1447747_x_at	Adal	3	3.51E-03
1433272_at	A430110A21Rik	3	9.35E-03
1427864_at	Hist1h3b	3	6.63E-05
1429873_at	1700125H20Rik	3	3.82E-08
1420733_at	Cab39l	3	9.72E-03
1425427_at	AF067061	3	2.98E-04
1431953_at	Atp8a2	3	9.32E-05
1421348_a_at	Cend1	3	4.70E-05
1437623_x_at	Xrcc3	3	8.17E-07
1450631_x_at	Defcr24	3	1.56E-05
1445271_at	9230105E10Rik	3	6.05E-06
1430569_at	Ttc9c	3	2.64E-03
1439984_at	Ptdss2	3	4.41E-03
1453227_at	Rhobtb3	3	9.47E-04
1437794_at	Cabin1	3	9.15E-04
1438337_x_at	9930032O22Rik	3	3.03E-08
1451103_at	D14Ertd500e	3	5.98E-03
1430764_at	1700023F06Rik	3	1.18E-05

1441913_at	Luzp2	3	1.84E-07
1422252_a_at	Cdc25c	3	5.81E-05
1450912_at	Ms4a1	3	2.88E-05
1444860_at	Lama3	3	9.75E-04
1430462_at	2310002L09Rik	3	6.80E-03
1449539_at	Ms4a6d	3	1.31E-07
1422422_at	Defcr4	3	1.89E-07
1426714_at	Slc46a1	3	3.47E-03
1451062_a_at	Pex5l	3	6.43E-03
1441590_at	Kcnj5	3	2.83E-04
1457645_at	C130079G13Rik	3	6.09E-07
1432499_a_at	Ube4b	3	1.40E-04
1435996_at	Card11	3	4.19E-03
1429756_at	4931428F04Rik	3	3.91E-05
1454035_at	3110009E22Rik	3	2.66E-04
1425075_at	Gatad2b	3	5.90E-04
1430002_at	Iqcf1	3	1.78E-05
1426650_at	Myh8	3	2.96E-07
1439263_at	LOC14210	3	2.33E-04
1445674_at	Atg9b	3	4.76E-09
1436831_at	Iqub	3	8.02E-07
1457002_at	Zfp408	3	2.30E-04
1442960_at	Muc20	3	2.24E-03
1431768_a_at	Prmt3	3	1.08E-07
1422392_at	V1rc6	3	2.87E-04
1454323_at	5830433D23Rik	3	1.95E-03
1435544_at	Exosc6	3	7.09E-03
1439446_at	BC048507	3	4.96E-03
1438829_at	Rnf165	3	4.12E-03
1437104_at	Arfgef1	3	3.60E-06
1453889_at	4930461C15Rik	3	3.29E-04
1453382_at	Fbxo42	3	9.89E-03
1434905_at	Ndufa4l2	3	6.08E-03
1422987_at	Ntn1	3	6.59E-03
1436314_at	Scyl2	3	5.48E-04
1429978_at	5830467E07Rik	3	2.65E-08
1453389_a_at	Sh2b2	3	9.55E-03
1460383_at	Gnao1	3	9.77E-04
1458100_at	C87482	3	7.30E-04
1436903_at	Ubqln3	3	8.99E-03
1426389_at	Camk1d	3	1.12E-04
1442612_at	C730036E19Rik	3	8.75E-09
1460549_a_at	Cdc23	3	2.01E-04
1432121_a_at	Lrrc44	3	1.20E-05
1423504_at	Jam3	3	5.28E-04
1419966_at	Tubb2a-ps2	3	1.46E-07
1435336_at	Celsr2	3	9.41E-04
1452017_at	Sox15	3	1.15E-04

1426224_x_at	Cmtm2a	3	1.06E-06
1441087_at	2810011L19Rik	3	3.14E-03
1453710_at	Tmem116	3	3.09E-03
1443229_at	Atad2	3	1.46E-04
1443154_at	6030438J01	3	9.23E-04
1417939_at	Rad51ap1	3	5.13E-08
1440166_x_at	Htr1d	3	6.94E-04
1425450_at	Chi3l4	3	1.75E-03
1456560_at	Gm93	3	7.98E-04
1429387_at	Grap	3	2.24E-03
1433300_at	2900005I04Rik	3	1.94E-07
1450832_at	Hoxc5	3	1.27E-03
1455968_x_at	Tmed2	3	7.09E-03
1459346_at	Tsen2	3	6.17E-04
1431352_s_at	Pvt1	3	1.15E-06
1419892_at	1110021J02Rik	3	1.47E-04
1459231_at	Pkn1	3	2.40E-06
1456595_x_at	Gh	3	7.42E-06
1455691_at	Cyp21a1	3	8.75E-04
1438617_at	Serpina7	3	5.03E-04
1451269_at	Pdzd11	3	4.73E-03
1453533_at	4933403O08Rik	3	1.67E-06
1419002_s_at	Baat	3	3.73E-04
1431675_a_at	Gtf2i	3	5.75E-06
1450327_at	P2rxl1	3	3.50E-03
1450240_a_at	Sytl1	3	2.42E-03
1455234_at	B3galt1	3	1.50E-07
1420301_at	AA414903	3	1.14E-03
1421951_at	Lhx1	3	1.19E-04
1418245_a_at	Rbm9	3	8.19E-03
1440491_at	Slc1a3	3	1.44E-06
1449872_at	Hspb3	3	3.21E-04
1445582_at	LOC100045340	3	1.98E-04
1449120_a_at	Pcm1	3	3.81E-09
1421591_at	Cylc1	3	4.48E-07
1453114_at	Nol9	3	1.81E-05
1444058_at	Dzip3	3	3.50E-03
1429741_at	Kcnv1	3	6.28E-06
1438270_at	AI846148	3	1.96E-03
1451633_a_at	Gngt1	3	5.08E-05
1433423_at	2210008N01Rik	3	1.29E-03
1445700_at	2310047M15Rik	3	6.97E-06
1450049_a_at	Hira	3	1.66E-05
1439753_x_at	Six4	3	4.82E-05
1431560_at	Dcakd	3	4.98E-03
1427826_a_at	Slco1b2	3	7.72E-08
1447617_at	Cdk2	3	7.28E-07
1454903_at	Ngfr	3	1.65E-03

1444127_at	Asb1	3	7.78E-04
1443657_at	6330505N24Rik	3	4.17E-03
1422872_at	Bmpr1b	3	8.30E-03
1459940_at	Acn9	3	1.38E-05
1438356_x_at	4933432K03Rik	3	1.84E-06
1434099_at	Ppargc1a	3	3.58E-07
1458229_at	Robo2	3	4.35E-06
1416006_at	Mdk	3	3.92E-05
1437653_at	Irgq	3	7.84E-05
1431183_at	1700066M21Rik	3	6.04E-05
1431387_at	ENSMUSG00000052323	3	9.82E-07
1458662_at	Daam1	3	4.98E-04
1438125_at	C230085N15Rik	3	1.02E-03
1419294_at	1700011H14Rik	3	1.15E-03
1435657_at	AI425999	3	4.10E-04
1421437_x_at	Pcdhb14	3	2.66E-08
1417797_a_at	1810019J16Rik	3	1.22E-07
1453621_at	LOC100044696	3	3.84E-07
1419512_at	Prpf40b	3	2.98E-03
1445537_at	2310039F13Rik	3	2.26E-03
1422773_at	Myt1	3	1.25E-05
1419237_at	Usp29	3	5.36E-04
1443840_x_at	1700010H22Rik	3	1.65E-04
1449253_at	Smc1b	3	4.19E-04
1457933_at	Gm1964	3	2.52E-04
1454464_at	2700078F05Rik	3	1.59E-03
1422284_at	Nkx2-9	3	6.34E-03
1438874_at	Nme7	3	2.28E-05
1425090_s_at	Kcnc4	3	2.33E-05
1453711_at	Rspo4	3	1.22E-03
1450763_x_at	Wnt3	3	9.11E-07
1426897_at	Rcc2	3	4.23E-04
1421032_a_at	Dnajb12	3	2.74E-03
1457869_at	ENSMUSG00000073000	3	6.65E-03
1419792_at	Mphosph1	3	3.19E-09
1437464_at	Spata7	3	4.19E-03
1453153_at	Lins2	3	2.41E-03
1439353_x_at	Tmem56	3	1.94E-06
1439654_at	EG319225	3	3.51E-03
1439953_at	Pmm2	3	1.01E-03
1449742_at	AA522020	3	7.09E-07
1449374_at	Pipox	3	5.31E-03
1459849_x_at	Vcpip1	3	9.67E-06
1438286_at	Otud7a	3	3.73E-04
1424901_at	Gcnt3	3	4.55E-06
1432975_at	2310038E17Rik	3	1.44E-03
1425117_at	0610012D14Rik	3	1.24E-04
1443640_at	Zfp617	3	7.91E-06
1443457_at	A230055J12Rik	3	3.59E-04
1440017_at	Plekhg3	3	8.47E-06
1440775_at	1700054K19Rik	3	2.17E-04
1446633_at	Atg7	3	8.17E-04
1439236_at	D15Ertd509e	3	1.16E-03
1432173_at	Serpinb12	3	8.57E-05
1437578_at	Clca2	3	9.23E-07
1421422_at	5033411D12Rik	3	5.57E-04
1430749_at	2810040C05Rik	3	4.51E-08
1432179_x_at	2810433K01Rik	3	7.82E-04
1427122_at	Copg2as2	3	1.62E-07
1450460_at	Aqp3	3	5.35E-04
1431620_at	4930442J19Rik	3	1.23E-04
1444593_at	Phlppl	3	4.40E-03
1432630_at	Tnks	3	2.61E-04
1460015_at	Sohlh1	3	1.91E-04
1421395_at	Zik1	3	6.09E-08
1422083_at	Tlr9	3	1.99E-03
1434464_at	Aqp12	3	8.13E-03
1454118_at	LOC100043319	3	7.22E-04
1437931_at	Tlr12	3	9.46E-03
1447217_at	Uhrf2	3	5.98E-03
1444534_at	F830021D11Rik	3	5.46E-03
1429369_at	Tnpo3	3	4.27E-03
1458354_x_at	Krt28	3	1.85E-03
1453340_at	1700057D03Rik	3	1.68E-04
1420567_at	Prkcn	3	7.94E-05
1430619_a_at	Mvk	3	2.82E-04
1426731_at	Des	3	3.85E-04
1422617_at	Xmr	3	7.47E-05
1437575_at	Mcm9	3	9.74E-07
1447682_x_at	Traf5	3	2.23E-06
1416960_at	B3gat3	3	9.09E-03
1426711_at	Tmco3	3	2.55E-03
1437569_at	Tmem132e	3	1.18E-05
1424870_at	Osbpl10	3	4.13E-03
1435853_at	Cyp2d12	3	1.16E-04
1436392_s_at	Tcfap2c	3	1.87E-04
1434759_at	Lrrtm3	3	6.93E-06
1451438_s_at	Clec2h	3	7.24E-05
1438332_at	Slc22a6	3	7.23E-04
1447937_a_at	4933409K07Rik	3	1.44E-03
1457227_at	AI843755	3	1.31E-05
1435412_at	1700007E06Rik	3	3.51E-04
1438007_at	AI851790	3	2.73E-05
1436628_at	Ulk4	3	8.82E-04

1457245_at	Dirc2	3	2.84E-04
1445557_at	0610040B10Rik	3	5.05E-05
1437567_at	BC023179	3	6.73E-06
1443502_at	Birc7	3	1.13E-03
1453086_at	6330408A02Rik	3	5.57E-04
1440191_s_at	Leng9	3	9.19E-04
1458944_at	LOC100043132	3	8.82E-05
1442938_at	D12Ertd247e	3	2.21E-05
1442860_at	Dgkb	3	2.50E-04
1445089_at	D16Ertd778e	3	1.69E-06
1436718_at	Nxph1	3	1.01E-04
1427663_a_at	Clk4	3	1.83E-03
1438791_at	1700016P04Rik	3	1.34E-03
1437018_at	Pnma2	3	9.52E-03
1453305_at	Iqcd	3	4.82E-04
1430074_x_at	8430426H19Rik	3	1.11E-03
1449128_at	Ccdc43	3	9.30E-06
1456862_at	Six4	3	8.71E-08
1454121_x_at	Ccdc18	3	2.33E-07
1418278_at	Apoc3	3	3.02E-04
1447567_at	D130007H15Rik	3	3.54E-04
1456643_at	9230114K14Rik	3	1.33E-03
1456869_at	Zfp787	3	4.87E-04
1429540_at	Cnfn	3	1.41E-05
1431425_a_at	4930535B03Rik	3	1.23E-07
1428653_x_at	Elavl1	3	9.80E-07
1427767_a_at	Cftr	3	2.17E-05
1418555_x_at	Spic	3	5.18E-03
1437415_at	4933427D06Rik	3	9.08E-06
1439379_x_at	Prm1	3	3.26E-05
1438324_at	9330182L06Rik	3	1.53E-06
1423084_at	B3galt2	3	3.06E-07
1444790_at	1810005K13Rik	3	1.53E-05
1449913_at	Zfp2	3	2.62E-05
1424977_at	4930418G15Rik	3	3.22E-05
1451147_x_at	Csdc2	3	8.80E-03
1453865_a_at	Otud5	3	2.46E-04
1417729_at	Myh6	3	3.71E-06
1443851_at	8430415E04Rik	3	1.31E-03
1452577_at	Igh	3	1.73E-03
1433419_at	4930405A07Rik	3	1.40E-06
1432113_at	Ccdc18	3	3.84E-07
1456718_at	Tmem56	3	1.41E-06
1456969_at	Adamts5	3	4.23E-07
1448326_a_at	Crabp1	3	1.15E-05
1427170_at	Psma8	3	4.44E-03
1453046_at	LOC100042000	3	5.37E-03
1431115_at	Tgif2	3	1.37E-03

1417604_at	Camk1	3	6.60E-04
1443000_at	D3Ertd300e	3	2.86E-03
1443055_at	B230369F24Rik	3	9.03E-05
1419972_at	Slc35a5	3	1.51E-03
1422203_at	Slc18a3	3	9.25E-03
1445243_at	D10Ertd533e	3	1.23E-04
1445849_at	BC061212	3	6.17E-06
1450812_at	Bcl2a1a	3	1.91E-05
1452029_a_at	Purg	3	1.80E-04
1457009_at	Rhobtb3	3	2.43E-05
1430331_at	1110005A03Rik	3	2.08E-06
1455973_at	OTTMUSG00000005148	3	3.64E-06
1436725_at	E130306D19Rik	3	2.57E-04
1418600_at	Klf1	3	1.24E-05
1453715_at	Sv2c	3	2.52E-04
1427783_at	Erbb4	3	2.44E-04
1424917_a_at	Wipi1	3	3.13E-03
1457634_at	LOC100044317	3	8.09E-08
1425711_a_at	Akt1	3	1.99E-06
1438709_at	Wipi1	3	7.82E-04
1426281_at	Catsper1	3	2.47E-04
1443749_x_at	Slc1a3	3	6.72E-04
1442060_at	Prepl	3	5.74E-06
1429768_at	Dtna	3	2.37E-04
1437258_at	Sprr2a	3	3.20E-04
1437092_at	LOC100048376	3	5.30E-03
1438574_at	Gpr152	3	4.85E-05
1449834_at	Magix	3	3.61E-04
1445743_at	E330024J20Rik	3	1.06E-07
1433283_s_at	Orly	3	2.81E-03
1430787_at	2310050B05Rik	3	1.21E-04
1425466_at	Senp2	3	3.69E-03
1427009_at	Lama5	3	9.78E-03
1431407_at	2310024H09Rik	3	2.21E-08
1443987_at	Klhl18	3	9.19E-03
1456723_at	B130055M24Rik	3	4.08E-05
1458956_at	Pitpnm3	3	1.59E-03
1437983_at	Sall1	3	4.49E-04
1444573_at	Lmtk3	3	3.00E-04
1447794_x_at	Plac8l1	3	5.20E-08
1441204_at	A130019P10Rik	3	2.74E-03
1449240_at	Gsbs	3	4.50E-04
1415883_a_at	Ela3	3	1.14E-03
1450614_x_at	Ifna5	3	5.64E-03
1454527_at	8430437B07Rik	3	9.80E-07
1453476_at	1700060J05Rik	3	4.16E-03
1436612_at	2410004I01Rik	3	8.85E-05

1458318_at	3110047M12Rik	3	3.65E-07
1426185_at	Cacna2d2	3	8.45E-05
1453428_at	2700045P11Rik	3	1.32E-03
1430086_at	Chrna9	3	8.03E-07
1427462_at	E2f3	3	3.25E-04
1419632_at	Tecta	3	2.83E-03
1421738_at	Gabra2	3	9.38E-05
1456246_x_at	Tpbpb	3	2.13E-05
1418866_at	Cyp24a1	3	1.95E-04
1454750_a_at	BC057552	3	5.25E-03
1447738_s_at	Ankrd13d	3	5.39E-03
1459006_a_at	LOC100040529	3	6.94E-05
1458373_at	Gen1	3	1.33E-05
1424913_at	2310044G17Rik	3	6.01E-06
1418903_at	Aqp2	3	7.14E-05
1437555_at	Barhl2	3	2.35E-05
1455431_at	Slc5a1	3	5.66E-03
1456368_at	EG214321	3	1.76E-03
1439157_at	Btnl9	3	4.52E-06
1431946_a_at	Necab3	3	4.44E-03
1438190_x_at	Tpbpa	3	4.65E-07
1456068_at	Nfasc	3	2.41E-03
1440177_at	9630027E17Rik	3	1.18E-06
1433137_at	5031415H12Rik	3	4.55E-03
1429934_at	4930502E18Rik	3	9.94E-04
1416711_at	Tbr1	3	4.80E-05
1431693_a_at	Il17b	3	4.74E-03
1450989_at	Tdgf1	3	2.93E-04
1435200_at	6330419J24Rik	3	1.50E-03
1441379_at	AU045094	3	5.70E-04
1434249_s_at	Trim9	3	9.15E-08
1457121_at	Obsl1	3	1.22E-03
1440821_x_at	Odf1	3	9.21E-09
1451583_a_at	BC025076	3	4.01E-03
1427360_at	4930507D05Rik	3	2.96E-03
1437719_x_at	A230046K03Rik	3	7.32E-05
1426919_at	Itgb1	3	1.25E-06
1456995_at	2700045P11Rik	3	2.12E-06
1440002_at	Rnmt	3	9.69E-04
1437659_at	Als2cr11	3	7.81E-07
1442809_at	Scn9a	3	5.04E-05
1460728_s_at	Ing4	3	5.32E-04
1433944_at	Hectd2	3	5.38E-05
1437824_at	Grid2	3	2.24E-08
1429203_at	2410076I21Rik	3	7.04E-04
1425212_a_at	Tnfrsf19	3	5.22E-03
1456224_x_at	Cage1	3	1.58E-06
1417556_at	Fabp1	3	1.01E-03

1445140_at	AU022804	3	1.23E-03
1447308_at	Lass5	3	1.54E-06
1441777_at	Emx1	3	2.89E-04
1438080_at	Mrpl11	3	2.23E-04
1455100_at	Akr1d1	3	8.81E-07
1430897_at	4931428L18Rik	3	2.09E-03
1438193_at	Nrxn3	3	3.27E-03
1458119_at	Slc25a27	3	4.82E-03
1453452_at	4930517J16Rik	3	6.07E-03
1457352_x_at	Svopl	3	7.03E-08
1417765_a_at	Amy1	3	6.17E-03
1457550_at	9530059O14Rik	3	1.82E-04
1429901_at	Nkain2	3	2.86E-06
1456511_x_at	Eras	3	6.74E-04
1454138_a_at	Stk31	3	1.35E-07
1457456_at	Map3k10	3	3.53E-03
1441387_at	BC030343	3	1.62E-03
1452938_at	Anks1b	3	2.95E-07
1456882_at	Sox12	3	7.42E-03
1454570_at	5830432F11Rik	3	1.81E-05
1425959_x_at	Klra1	3	3.33E-06
1420748_a_at	Adat1	3	3.12E-07
1427863_at	Hist1h3b	3	1.70E-03
1455415_at	A730056A06Rik	3	8.73E-07
1427391_a_at	Col12a1	3	1.32E-03
1436476_at	Dand5	3	2.47E-03
1456266_at	Rpl30	3	1.04E-07
1430106_at	1700126L10Rik	3	7.09E-07
1451800_at	Gcc2	3	8.97E-07
1427936_at	Thnsl1	3	4.91E-04
1440077_at	6330549D23Rik	3	2.80E-05
1429643_a_at	Pde1c	3	8.59E-03
1456671_at	Tbrg3	3	7.91E-04
1454225_s_at	D3Ertd751e	3	1.36E-05
1454392_at	9230112J17Rik	3	6.03E-05
1430219_at	Aktip	3	4.06E-06
1439834_at	2400009B08Rik	3	1.84E-03
1454472_at	2900092N22Rik	3	4.72E-04
1423550_at	Slc1a4	3	8.38E-03
1453319_at	Ccar1	3	4.32E-08
1430803_at	Lin28b	3	4.10E-05
1453647_at	E130112N10Rik	3	1.78E-03
1457545_at	9530036O11Rik	3	3.97E-04
1443927_at	Uba6	3	5.35E-08
1442158_at	Mast4	3	5.61E-05
1445257_at	AU022531	3	1.18E-06
1423832_at	Prkag2	3	7.12E-07
1439738_at	5630401D24Rik	3	3.65E-04

1429952_at	Mospd4	3	3.69E-04
1427764_a_at	Tcfe2a	3	3.41E-03
1418735_at	Krt4	3	6.92E-03
1446629_at	C85938	3	5.58E-08
1445348_at	Cdc40	3	7.67E-06
1442579_at	9330111N05Rik	3	3.76E-05
1443135_at	Cog4	3	4.72E-06
1456001_at	Lce3a	3	7.82E-05
1453669_at	4930578C19Rik	3	1.06E-04
1431587_at	Ccdc7	3	6.52E-04
1455519_at	Dsg1b	3	7.86E-08
1432150_at	Tmem59	3	6.45E-08
1454308_at	1700030C10Rik	3	1.33E-06
1458966_at	C80278	3	1.86E-07
1447276_at	D13Ertd37e	3	1.09E-04
1458151_at	4833444G19Rik	3	6.35E-03
1433229_at	9430031J08Rik	3	5.84E-03
1426303_at	B4galt7	3	1.79E-06
1449833_at	Sprr2f	3	1.18E-06
1425487_at	Slu7	3	3.01E-03
1417050_at	C1qtnf4	3	3.13E-03
1457838_at	Cdc45l	3	4.30E-04
1435365_at	4732415M23Rik	3	2.36E-07
1456631_at	LOC100040766	3	1.47E-07
1455695_at	St8sia1	3	1.62E-04
1443984_at	Lin9	3	7.45E-05
1418855_at	Lce1l	3	4.25E-08
1459990_at	Ddr1	3	2.90E-03
1455280_at	Frem1	3	4.28E-04
1432537_at	4930465A12Rik	3	9.16E-03
1438113_at	Zmat4	3	1.24E-08
1424100_s_at	Cend1	3	1.51E-04
1457627_x_at	Ropn1l	3	1.17E-04
1451976_s_at	Cmtm2a	3	8.78E-04
1422336_at	Hoxa13	3	6.54E-03
1428399_a_at	Armc9	3	1.44E-04
1451838_a_at	Tc2n	3	7.39E-07
1447498_at	Edar	3	6.93E-06
1427249_x_at	Mup3	3	3.68E-08
1426479_a_at	Cnpy3	3	9.65E-03
1439427_at	Cldn9	3	3.94E-03
1450310_at	Grid2ip	3	3.55E-03
1417629_at	Prodh	3	1.26E-03
1445711_at	BB163080	3	3.52E-04
1452024_a_at	Ldb1	3	4.39E-03
1431839_a_at	Ccdc81	3	2.44E-05
1437195_x_at	Mapk10	3	7.26E-06
1439075_at	Polr3f	3	1.21E-03

1444240_at	Shank1	3	2.86E-03
1444529_at	EG666806	3	3.78E-05
1426729_at	2900046G09Rik	3	7.59E-03
1441939_x_at	2410003I16Rik	2	1.56E-05
1438449_at	Cdc42bpa	2	1.90E-07
1425995_s_at	Wt1	2	1.87E-03
1444358_at	Fbxl11	2	1.11E-04
1433417_at	8030497O21Rik	2	5.11E-05
1439003_s_at	1700008F21Rik	2	8.18E-05
1431722_a_at	Afmid	2	5.93E-03
1448514_at	Cox5b	2	7.86E-03
1456282_at	6720457D02Rik	2	2.16E-05
1429522_at	Ankrd42	2	1.44E-10
1444512_at	Arhgap29	2	6.99E-03
1442763_s_at	Ttll10	2	7.56E-04
1433787_at	Nell1	2	1.21E-03
1447786_at	Pscd1	2	1.09E-04
1440382_at	BC051628	2	6.78E-05
1459216_at	Tdrd7	2	7.77E-03
1460427_a_at	Adam28	2	6.40E-03
1457881_at	Osbpl6	2	1.28E-04
1435147_x_at	Cadm2	2	1.01E-04
1427137_at	Ces5	2	1.08E-04
1430745_at	5930409G06Rik	2	1.88E-04
1451389_at	Dph4	2	3.36E-04
1451787_at	Cyp2b10	2	1.97E-03
1430828_at	Trmu	2	5.34E-03
1420345_at	Cldn14	2	8.69E-04
1438375_at	Fbln2	2	2.47E-05
1420215_x_at	1810012K16Rik	2	9.34E-04
1420468_at	Asb17	2	7.03E-03
1432018_at	Ascl2	2	4.73E-04
1436484_at	C030019I05Rik	2	6.85E-05
1450999_a_at	1700029H14Rik	2	1.96E-04
1454188_at	4921508D12Rik	2	6.66E-03
1418311_at	Fn3k	2	3.26E-06
1457119_at	1110003F02Rik	2	3.33E-05
1450481_at	Mybl1	2	5.49E-04
1452853_at	Carkl	2	7.31E-05
1440549_at	B230334L07Rik	2	2.97E-04
1431410_at	D16Ertd472e	2	6.66E-07
1419416_a_at	Rarg	2	4.94E-04
1443442_at	AU022084	2	6.19E-05
1460693_a_at	Col9a3	2	6.99E-05
1436483_at	Myt1l	2	1.56E-04
1452407_at	Spag4	2	1.34E-03
1455363_at	Bai1	2	8.07E-03
1445667_at	Tbc1d10a	2	1.12E-03

1441743_at	Pax3	2	1.13E-05
1419712_at	Il3ra	2	3.83E-03
1457319_at	A130038J17Rik	2	1.46E-03
1427631_x_at	Mup3	2	7.47E-06
1457182_at	Map2k7	2	3.20E-05
1454265_a_at	Abcb10	2	9.17E-03
1451701_x_at	Cldn3	2	2.65E-04
1422270_a_at	Il6ra	2	9.79E-03
1443225_at	Acvr1c	2	1.70E-07
1420784_at	Scn11a	2	2.29E-04
1458934_at	D5Ertd505e	2	6.05E-05
1422830_s_at	Drd4	2	1.83E-03
1446597_at	ENSMUSG00000073100	2	4.04E-03
1424494_s_at	Flywch2	2	3.33E-04
1456198_at	1810007D17Rik	2	2.92E-09
1457984_at	Crh	2	1.16E-07
1434429_at	Syt16	2	2.27E-10
1458977_at	A530021J07Rik	2	6.45E-07
1449245_at	Grin2c	2	1.79E-03
1452136_at	Slc5a9	2	1.32E-03
1441603_at	Sstr3	2	7.53E-05
1456035_at	Nxf3	2	1.22E-07
1445021_at	Spg11	2	1.57E-04
1425031_at	Fktn	2	6.21E-03
1430255_at	Klf5	2	2.81E-03
1455907_x_at	Phox2b	2	3.32E-07
1420335_at	Dmc1	2	1.79E-06
1448098_at	AA517545	2	1.03E-05
1432970_at	4933423K11Rik	2	5.91E-04
1418867_at	Cyp24a1	2	1.96E-05
1437935_at	4930486G11Rik	2	6.80E-08
1429602_at	Cd164l2	2	1.76E-04
1432977_at	9030607L02Rik	2	3.83E-06
1419434_at	Slc2a10	2	1.50E-03
1442325_at	Tbc1d24	2	9.55E-05
1439425_x_at	BC024814	2	1.67E-07
1422618_x_at	Xmr	2	1.04E-07
1433703_s_at	Bahd1	2	2.42E-03
1458679_a_at	Tatdn1	2	7.53E-03
1444216_at	Emx1	2	1.94E-05
1456127_at	Cnpy1	2	1.17E-03
1429924_at	1700019O17Rik	2	1.76E-03
1422255_at	Kcna4	2	9.24E-03
1447799_x_at	1700001P01Rik	2	2.20E-04
1431964_at	4921518J05Rik	2	2.67E-03
1419937_at	OTTMUSG00000005802	2	1.13E-03
1442604_at	Ercc6	2	6.28E-05
1447847_x_at	Stoml3	2	7.37E-03
1420633_a_at	Csn1s2a	2	5.69E-07
1442806_at	9430030N17Rik	2	1.47E-03
1419404_s_at	Siah1a	2	1.46E-06
1451664_x_at	Klra1	2	9.73E-05
1434583_at	Tmem26	2	2.02E-05
1456938_at	Smarcb1	2	8.68E-04
1447326_s_at	Zmym3	2	3.70E-03
1433977_at	Hs3st3b1	2	4.30E-06
1419052_at	Ovol1	2	5.87E-03
1424282_at	Pet112l	2	1.32E-03
1451410_a_at	Crip3	2	9.82E-03
1419133_at	Evpl	2	8.68E-05
1442566_at	C78878	2	4.73E-04
1446501_at	A830053O21Rik	2	9.67E-03
1426229_s_at	Kras	2	1.74E-07
1457807_at	Gnpnat1	2	9.74E-04
1419349_a_at	Cyp2d9	2	2.10E-03
1434490_at	Scarf1	2	7.68E-07
1426512_at	Olfm3	2	8.56E-05
1424422_s_at	Flad1	2	3.79E-03
1435288_at	Coro1a	2	2.96E-05
1440945_at	Glcci1	2	6.55E-05
1423344_at	Epor	2	4.40E-03
1452486_a_at	Cryaa	2	4.37E-04
1433387_at	2900022M07Rik	2	3.37E-04
1456512_at	Pdzrn4	2	1.98E-03
1450709_at	Defcr5	2	1.01E-03
1420676_at	Lce1a1	2	1.06E-06
1438697_at	Tmem132c	2	7.53E-05
1437184_at	Guf1	2	7.33E-06
1457120_at	Itk	2	1.98E-06
1439139_at	D2Ertd640e	2	1.62E-04
1458652_at	2410014A08Rik	2	8.58E-05
1448717_at	Gcdh	2	4.36E-08
1420605_at	Mtag2	2	4.05E-04
1459580_at	G630055G22Rik	2	8.44E-04
1460154_at	AI194348	2	1.48E-06
1442155_at	4632427E13Rik	2	7.35E-04
1443131_at	Lrp1b	2	1.51E-05
1448826_at	Myh6	2	7.36E-04
1438804_at	Sept10	2	8.29E-06
1440927_x_at	Apol11b	2	4.99E-04
1454106_a_at	Cxxc1	2	6.32E-06
1431966_at	Agbl3	2	1.37E-07
1431631_at	2900057B20Rik	2	6.67E-03
1458323_at	LOC73980	2	1.26E-05

1452704_at	1200015F23Rik	2	9.46E-06
1449241_at	Klhl1	2	1.13E-06
1430008_x_at	Speer5-ps1	2	1.18E-05
1442872_at	Kri1	2	6.03E-03
1427215_at	Acsm2	2	1.92E-03
1447611_at	1700073E17Rik	2	2.10E-05
1432122_at	Lrrc44	2	1.79E-06
1429664_at	Cdkl1	2	1.66E-04
1444784_at	4930564K09Rik	2	6.70E-03
1437876_at	Il20rb	2	2.20E-04
1420054_s_at	Slc35c2	2	7.66E-06
1456384_at	Nlgn3	2	1.84E-03
1436592_at	6030490I01Rik	2	2.42E-04
1427752_a_at	Tcrb-V8.2	2	2.59E-06
1460183_at	Adprh	2	3.21E-05
1429969_at	4833403J16Rik	2	2.28E-03
1448168_a_at	Spt1	2	1.12E-03
1431016_at	Cwf19l1	2	1.89E-03
1434810_a_at	Cage1	2	2.42E-05
1452954_at	Ube2c	2	3.06E-03
1427963_s_at	Rdh9	2	2.29E-03
1447744_s_at	1700110K17Rik	2	2.20E-03
1447574_s_at	Slc32a1	2	6.96E-04
1424627_at	Cst12	2	4.99E-03
1423203_a_at	Cetn1	2	1.65E-03
1432640_at	4633401L03Rik	2	7.89E-08
1419198_at	Cbx8	2	3.33E-05
1425861_x_at	Cacna2d1	2	2.99E-05
1437190_at	Styk1	2	1.16E-03
1427380_at	Klk1b3	2	4.06E-05
1424753_at	Nudt14	2	2.27E-03
1424518_at	2310016F22Rik	2	9.51E-04
1429875_at	1700034J05Rik	2	5.71E-07
1433326_at	4930488N24Rik	2	8.57E-03
1438596_at	LOC668215	2	1.39E-06
1419742_at	1700037H04Rik	2	2.38E-03
1457995_at	AA617406	2	8.76E-04
1430200_at	LOC100044513	2	5.34E-03
1418267_at	Mst1	2	4.20E-03
1446267_at	D17Ertd657e	2	6.23E-06
1421806_at	Defb3	2	2.09E-05
1425892_a_at	Pnoc	2	1.51E-04
1431198_x_at	9430038I01Rik	2	2.44E-03
1429099_at	LOC100039227	2	5.84E-04
1441432_at	C820005J03Rik	2	6.22E-04
1450993_at	Pask	2	9.30E-03
1420685_at	Grap2	2	4.22E-03
1417370_at	Tff3	2	7.66E-03

1453232_at	Calr3	2	2.71E-03
1438309_at	Acvr1c	2	4.32E-03
1424699_at	Ccdc136	2	9.06E-03
1431732_at	Spag16	2	4.14E-06
1430701_a_at	5730528L13Rik	2	7.01E-05
1446316_at	Lpin2	2	2.08E-06
1430723_at	Pdss2	2	1.03E-03
1456565_s_at	Map3k12	2	4.38E-03
1454869_at	Wdr40b	2	6.38E-04
1439297_at	Pif1	2	5.15E-03
1434858_x_at	Zfp511	2	7.96E-03
1430134_a_at	Yars2	2	1.12E-05
1441936_x_at	4930447M23Rik	2	2.19E-04
1441451_at	Brwd3	2	2.75E-07
1439378_at	BC048671	2	1.72E-06
1443176_at	Sfmbt2	2	6.72E-04
1436634_at	Robo3	2	3.39E-09
1429341_at	Oaz3	2	1.43E-05
1438733_at	Zfp689	2	3.77E-04
1422225_s_at	Tcp10a	2	3.25E-03
1438394_x_at	Krt4	2	1.04E-03
1444350_at	Slfn10	2	1.36E-05
1431538_at	4931415C17Rik	2	3.48E-05
1453127_at	Ppm1j	2	1.77E-03
1445192_at	D8Ertd575e	2	2.12E-07
1439785_at	9630013A20Rik	2	3.38E-08
1452027_a_at	Trp63	2	5.40E-04
1441824_at	Mboat1	2	7.92E-03
1443063_at	Rlbp1l2	2	1.41E-06
1448105_at	Prm2	2	7.02E-03
1428338_at	Spata2L	2	5.71E-04
1453595_at	2900064B18Rik	2	8.02E-03
1430218_at	4933424M12Rik	2	3.00E-03
1454253_at	2810452K22Rik	2	3.56E-04
1430831_at	Lyrm1	2	1.65E-03
1454372_at	Cd80	2	3.85E-03
1445044_at	Ptgis	2	2.84E-04
1426251_at	Cpz	2	3.53E-04
1442518_at	C030044O21Rik	2	6.30E-05
1452263_at	Slc35f4	2	6.97E-03
1447362_at	Bub1b	2	1.95E-03
1436694_s_at	Neurod4	2	3.32E-06
1457827_at	Arsj	2	9.95E-08
1419106_at	2210409E12Rik	2	6.87E-04
1422689_at	4930547C10Rik	2	2.77E-03
1427598_at	Snord116	2	4.16E-03
1441717_at	D9Ertd596e	2	6.71E-05
1458189_at	Emid2	2	1.81E-04

1433191_at	A430105P17Rik	2	2.06E-06
1456766_at	C330001K17Rik	2	6.36E-03
1458198_at	C81508	2	5.88E-04
1421948_a_at	Ccdc123	2	3.31E-04
1431643_at	Speer6-ps1	2	5.16E-03
1439924_x_at	Tubgcp5	2	2.74E-08
1450737_at	Polr3k	2	9.87E-08
1456937_at	Cdh26	2	2.27E-05
1457582_at	Uty	2	5.45E-07
1457899_at	Kalrn	2	2.15E-07
1419338_at	BC051019	2	2.64E-07
1450555_at	Tex13	2	2.16E-08
1437433_at	B3galt2	2	3.94E-08
1446381_at	LOC100042648	2	6.29E-07
1431273_at	2810417H13Rik	2	3.69E-04
1433258_at	A330102K18Rik	2	1.39E-06
1417787_at	Dkkl1	2	1.75E-04
1456275_at	Mrpl21	2	2.96E-03
1426204_a_at	Oprl1	2	4.11E-06
1447597_at	Rpo1-4	2	1.25E-07
1420790_x_at	Klra16	2	3.82E-06
1440509_at	Sox30	2	2.26E-04
1455374_at	Kcnj3	2	1.00E-07
1440738_at	B020011L13Rik	2	8.03E-09
1456495_s_at	Osbpl6	2	8.61E-04
1443106_at	4930562C15Rik	2	3.26E-04
1460457_at	2810405F17Rik	2	2.21E-04
1429330_at	Gabra4	2	1.08E-05
1445193_x_at	D8Ertd575e	2	1.30E-06
1422774_at	1700088E04Rik	2	3.29E-03
1433071_at	6430605C03Rik	2	1.04E-05
1436675_at	Wdr63	2	4.48E-05
1440828_x_at	Phf7	2	5.33E-04
1418490_at	Sdsl	2	4.70E-03
1424867_a_at	Glyat	2	1.58E-05
1451876_a_at	Trp63	2	7.11E-05
1430006_x_at	1700024B05Rik	2	7.05E-07
1426576_at	Sgms1	2	6.01E-03
1450529_at	H2-M9	2	1.17E-09
1420042_at	Thoc1	2	4.87E-03
1455526_at	Diras1	2	9.14E-03
1438380_at	Ddx47	2	9.71E-06
1426520_at	Btg4	2	7.68E-03
1447564_x_at	Piwil4	2	2.70E-07
1440186_s_at	Psapl1	2	1.20E-06
1444647_at	Plaa	2	1.31E-07
1450991_at	Dnajb7	2	3.24E-04
1431733_at	Alpk1	2	1.79E-03
1428802_at	Mgat3	2	8.28E-03
1453661_at	9130403I23Rik	2	6.68E-04
1458940_at	5730507A11Rik	2	2.13E-08
1456548_at	Mtdh	2	9.74E-06
1421718_at	Strm	2	7.09E-06
1433365_at	4930563N14Rik	2	2.58E-05
1448675_at	Ankzf1	2	5.00E-03
1432587_at	5730596P11Rik	2	2.71E-03
1442930_at	AW061147	2	4.55E-04
1450771_at	Fut9	2	2.76E-07
1456528_x_at	Ncl	2	5.77E-03
1438333_at	Prtg	2	2.47E-06
1426282_at	Hnt	2	3.63E-04
1418959_at	Tmprss5	2	7.09E-04
1430234_at	Arl14	2	1.49E-03
1433109_at	Mif	2	4.99E-03
1439653_at	Adam6	2	1.95E-04
1421253_at	Nrap	2	1.36E-03
1444640_at	Pigg	2	4.54E-06
1437292_at	Rlbp1l2	2	6.07E-03
1421411_at	Pstpip2	2	1.97E-03
1420743_a_at	Ppp3cc	2	1.49E-06
1431648_at	4930528F23Rik	2	1.90E-03
1425613_at	Pcdha11	2	5.29E-03
1435983_at	1700019P01Rik	2	3.92E-04
1455683_a_at	Tbc1d8	2	5.85E-07
1447346_s_at	5530400B01Rik	2	3.38E-03
1431757_s_at	5033417F24Rik	2	5.93E-03
1423463_a_at	D2Ertd750e	2	1.27E-03
1453717_s_at	Ttll10	2	3.26E-03
1453628_s_at	Lrrc2	2	8.83E-03
1420031_at	Chek1	2	6.05E-04
1448910_at	Pecr	2	4.48E-03
1430684_s_at	Lrp2bp	2	6.24E-04
1422315_x_at	LOC100047682	2	5.83E-03
1439217_at	Nlrp9c	2	7.11E-06
1422386_at	LOC100046375	2	3.75E-03
1432807_at	5830426K05Rik	2	1.77E-03
1424583_at	Farp2	2	3.90E-04
1453801_at	Them5	2	2.70E-06
1429894_a_at	Mtap7	2	5.66E-03
1430173_x_at	Cyp4f16	2	7.35E-03
1440019_at	Cog5	2	2.56E-05
1432690_at	9030407C09Rik	2	3.76E-03
1432149_at	Dph1	2	3.99E-03
1441881_x_at	3110032G18Rik	2	6.07E-05
1451681_at	BC089597	2	3.32E-03
1421804_at	Fabp9	2	1.50E-04

1452539_a_at	Cd247	2	8.56E-06
1449879_at	1700008F21Rik	2	1.98E-06
1453156_s_at	Zadh1	2	1.46E-03
1447598_x_at	Rpo1-4	2	2.35E-04
1422634_a_at	Vsig2	2	7.19E-03
1455810_a_at	E130112L23Rik	2	9.60E-05
1447645_x_at	Kcnk13	2	1.87E-06
1453440_at	4921539E11Rik	2	2.62E-03
1458487_at	Klf3	2	6.47E-04
1415811_at	Uhrf1	2	7.91E-03
1429944_at	Tchhl1	2	4.41E-04
1433619_at	AI894139	2	1.43E-03
1421980_at	Kcnc3	2	3.33E-03
1452212_at	Lmna	2	2.54E-04
1443432_at	AU022680	2	5.00E-04
1431685_at	4930549O18Rik	2	7.65E-09
1445726_at	Rsl1	2	3.55E-05
1431357_a_at	Rpgrip1	2	9.77E-06
1455830_s_at	C87414	2	4.04E-06
1439162_at	1700011J10Rik	2	7.48E-06
1430881_at	7630403G23Rik	2	2.87E-03
1443200_at	OTTMUSG00000007392	2	5.12E-05
1457789_at	Cln3	2	5.46E-03
1427577_x_at	Igk-V8	2	1.89E-03
1415844_at	Syt4	2	5.29E-04
1447889_x_at	Gm50	2	1.18E-04
1454120_a_at	Pcgf6	2	7.42E-04
1440639_at	Dlgap1	2	7.33E-03
1459929_at	Zfp568	2	5.31E-03
1432701_at	2810403G07Rik	2	4.99E-04
1422321_a_at	Sf1	2	4.24E-05
1460468_s_at	2810451A06Rik	2	1.13E-03
1418559_at	Tesp1	2	5.53E-03
1438613_at	Kcna4	2	1.34E-04
1426150_at	Gipc3	2	5.70E-03
1442812_at	EG433844	2	2.16E-03
1450286_at	Npr3	2	6.65E-05
1426031_a_at	Nfatc2	2	3.56E-03
1422936_at	LOC100048871	2	7.65E-04
1448235_s_at	Hmg1l1	2	1.56E-04
1427799_x_at	Igk-V8	2	2.22E-05
1426129_at	Brms1	2	8.10E-03
1437678_at	Gm1564	2	1.48E-06
1442833_at	D15Ertd30e	2	6.24E-03
1429904_at	4930507A01Rik	2	3.13E-03
1458770_at	D11Ertd4e	2	2.56E-03
1425191_at	Ocel1	2	1.96E-03
1458676_at	Nktr	2	1.90E-04
1431512_at	4933437F24Rik	2	2.27E-06
1447798_at	1700123O21Rik	2	3.13E-08
1431332_a_at	Terf1	2	1.23E-07
1457663_at	1700006F04Rik	2	1.51E-07
1450979_at	Ceacam14	2	5.83E-09
1443498_at	Mmab	2	3.82E-05
1418956_at	Tssk6	2	5.87E-04
1425666_at	Zic5	2	6.59E-05
1443262_at	Mrps14	2	9.65E-03
1432516_at	4930447F04Rik	2	3.45E-08
1453443_at	1110015O18Rik	2	1.14E-07
1441551_at	Mypn	2	1.93E-03
1422297_at	Pfdn5	2	3.67E-05
1432063_at	4833427F10Rik	2	9.10E-03
1458368_at	Myh4	2	1.01E-05
1457647_x_at	1600023N17Rik	2	9.78E-08
1446468_at	Csmd1	2	1.46E-03
1419698_at	Cxcl11	2	3.31E-03
1457327_at	Shprh	2	6.43E-05
1443294_at	Crkrs	2	8.51E-03
1430874_at	9430085M18Rik	2	5.07E-03
1433361_at	4930527F18Rik	2	6.61E-04
1428983_at	Scx	2	1.28E-03
1423498_at	Aldoart2	2	7.45E-03
1453354_at	Ndufs1	2	4.33E-04
1422274_at	Gja8	2	1.38E-03
1429263_at	4933425D22Rik	2	1.63E-04
1440075_at	Pias4	2	1.24E-03
1434308_at	Slc43a2	2	3.25E-03
1458626_at	Nos1	2	1.45E-03
1433714_at	Sult4a1	2	1.80E-03
1444156_at	9230112E08Rik	2	2.68E-04
1437285_at	1110020G09Rik	2	7.78E-03
1417678_at	Mmp24	2	2.26E-05
1437787_at	Lrrtm2	2	1.87E-07
1428305_at	Pcsk2	2	4.19E-05
1447513_at	Kcnd3	2	1.87E-07
1450673_at	Col9a2	2	8.16E-04
1426439_at	Ddx3y	2	2.26E-04
1436615_a_at	Otc	2	4.47E-03
1435073_a_at	Armc9	2	7.30E-03
1443210_at	ENSMUSG00000058736	2	1.89E-06
1440124_at	B230334C09Rik	2	1.02E-03
1448073_at	LOC541456	2	2.27E-07
1433409_at	C030014O09Rik	2	8.09E-03
1421617_at	Trpm8	2	1.25E-05

1425034_at	Slc17a2	2	1.65E-04
1460608_at	Cacna1b	2	8.33E-09
1445450_x_at	A530021J07Rik	2	1.28E-06
1429211_at	Cadm2	2	1.48E-03
1431439_at	5830487J09Rik	2	3.21E-07
1429946_at	2610301F02Rik	2	2.11E-04
1434030_at	Gtpbp10	2	9.22E-03
1447966_a_at	Tmem69	2	1.67E-04
1430017_at	1600016N20Rik	2	6.25E-03
1422761_at	Tbl1xr1	2	7.28E-04
1437656_at	Arhgef4	2	4.16E-03
1431144_at	Srrd	2	2.63E-03
1441941_x_at	Serpinb5	2	1.39E-04
1436769_at	Psma1	2	6.10E-07
1460494_at	Ttll10	2	4.97E-04
1439056_at	EG636791	2	5.87E-09
1430627_at	5330420P17Rik	2	4.51E-03
1440794_x_at	1700029M03Rik	2	2.17E-06
1452275_at	LOC100048107	2	4.72E-03
1422077_at	Acot4	2	3.16E-03
1449979_a_at	Spock3	2	1.88E-06
1458342_at	Tmem90a	2	5.88E-03
1431624_a_at	2610206B13Rik	2	3.26E-03
1433459_x_at	Prss2	2	3.42E-07
1422722_at	1700001K19Rik	2	5.59E-03
1449060_at	Kif2c	2	9.07E-04
1459012_at	A730041O05Rik	2	1.34E-04
1448083_at	Nalcn	2	2.18E-04
1429697_at	1700023D19Rik	2	2.69E-03
1438885_at	BB182387	2	3.05E-08
1459500_at	C85351	2	2.78E-03
1419160_at	Golga3	2	8.34E-03
1418614_at	Kcnj1	2	2.86E-04
1447997_s_at	Timm8a2	2	3.40E-03
1427376_a_at	Map4k5	2	2.13E-03
1437522_x_at	Gh	2	2.20E-03
1457668_x_at	LOC100041290	2	5.69E-08
1445798_at	Dlg1	2	6.83E-06
1419001_at	Baat	2	3.99E-07
1418617_x_at	Clgn	2	4.28E-04
1457173_at	BB217526	2	2.13E-03
1429492_x_at	Ptdss2	2	1.27E-03
1434636_at	Homez	2	2.97E-05
1449612_x_at	Mphosph1	2	9.18E-09
1425667_at	Acot11	2	7.30E-03
1451948_at	Gm1409	2	4.96E-03
1452609_at	1190005I06Rik	2	4.31E-04
1458003_at	Zfp398	2	8.30E-04
1429824_at	4930550C14Rik	2	3.19E-08
1454737_at	Dusp9	2	2.71E-05
1422421_at	Defcr-rs12	2	5.83E-03
1455621_at	BC066107	2	2.39E-04
1457680_a_at	Tmem69	2	2.33E-03
1452655_at	Zdhhc2	2	1.07E-04
1455909_at	9530002K18Rik	2	1.59E-03
1419586_at	Rp2h	2	4.50E-03
1442795_x_at	1700016G05Rik	2	3.55E-04
1431184_a_at	4930503B20Rik	2	2.88E-05
1447550_at	EG666892	2	6.70E-04
1453960_a_at	Capzb	2	7.36E-04
1451487_at	Rabepk	2	4.10E-03
1457783_at	Rab12	2	3.19E-04
1450337_a_at	Nek8	2	6.37E-03
1422309_a_at	Lenep	2	1.71E-04
1427669_a_at	Cit	2	4.64E-04
1441458_at	Rasa4	2	3.49E-04
1437818_at	9430016H08Rik	2	2.98E-03
1453727_at	Esf1	2	1.46E-08
1442878_at	Prdx6	2	7.84E-05
1416626_at	Pla2g1b	2	3.62E-07
1441187_at	E330037M01Rik	2	1.19E-04
1429138_at	Npas3	2	8.92E-03
1440782_at	Skap1	2	4.93E-07
1433823_at	Ptpdc1	2	5.85E-07
1450404_at	Slc23a1	2	1.03E-05
1417605_s_at	Camk1	2	1.76E-03
1440762_at	Syn2	2	7.42E-03
1433404_at	4930423O20Rik	2	6.15E-03
1446186_at	Usp15	2	2.60E-04
1429834_a_at	1110014N23Rik	2	1.70E-03
1455421_x_at	6330503C03Rik	2	2.45E-08
1426142_a_at	Trdn	2	6.77E-03
1449381_a_at	Pacsin1	2	2.67E-03
1452528_a_at	Nkx2-3	2	5.70E-03
1453341_a_at	Tmem202	2	8.38E-04
1422415_at	Ang2	2	3.62E-04
1445296_at	D7Ertd715e	2	3.23E-08
1425775_at	LOC100044276	2	1.34E-06
1447857_at	Enox1	2	1.83E-03
1447551_x_at	Lphn3	2	9.56E-03
1428034_a_at	Tnfrsf9	2	6.65E-03
1425754_a_at	Btn1a1	2	1.66E-06
1446399_at	Cdh10	2	3.25E-03
1455948_x_at	Matn3	2	8.96E-05
1450956_at	Scd3	2	8.07E-03
1435747_at	Fgf14	2	6.59E-08

1452411_at	Lrrc1	2	1.63E-05
1438440_at	Rnasen	2	9.62E-04
1427517_at	Boc	2	2.11E-03
1460627_at	Thsd7b	2	6.48E-04
1457365_at	EG628262	2	1.23E-04
1445195_at	C77631	2	3.16E-03
1448044_a_at	ENSMUSG00000074284	2	3.82E-05
1441394_at	C76554	2	2.91E-06
1432253_at	4921523P09Rik	2	7.05E-04
1455408_at	Pla2g4f	2	7.32E-06
1430524_at	1700020N15Rik	2	9.81E-08
1451451_at	Gca	2	9.12E-04
1449006_at	Gla	2	4.22E-03
1436670_x_at	1700019G17Rik	2	1.08E-04
1441550_at	9330184L24Rik	2	1.05E-07
1454911_at	EG382106	2	2.52E-03
1425981_a_at	Rbl2	2	8.26E-04
1458488_at	Dclk2	2	7.46E-06
1453418_at	Col24a1	2	1.98E-08
1429143_at	Tekt3	2	4.17E-04
1415774_at	Elp2	2	8.13E-04
1457981_x_at	Gins1	2	3.95E-04
1424943_at	LOC100044218	2	3.29E-03
1457361_at	Zfp804a	2	5.41E-05
1457046_s_at	C77370	2	8.05E-05
1450384_at	Bace1	2	7.07E-03
1440247_at	Phf14	2	1.23E-05
1433371_at	5430427N15Rik	2	2.17E-04
1428111_at	Slc38a4	2	3.27E-04
1430894_at	5530401N12Rik	2	2.94E-03
1429547_at	4930578I06Rik	2	1.65E-06
1450175_a_at	Ctsm	2	2.65E-03
1436872_at	Tacc3	2	3.48E-03
1453614_a_at	Nfe2l3	2	2.25E-03
1443723_at	Trpm3	2	1.62E-07
1429316_at	Rasgef1a	2	5.01E-05
1420786_a_at	Rbmy1a1	2	5.69E-04
1443523_at	1700010C24Rik	2	4.27E-03
1432365_a_at	4930556L07Rik	2	3.22E-03
1422247_a_at	Uty	2	1.07E-03
1459738_x_at	Gla	2	1.43E-04
1430855_at	Col20a1	2	2.38E-03
1441961_at	Mtap9	2	6.20E-08
1428595_at	Slc6a19	2	6.05E-07
1429312_s_at	Ror1	2	1.38E-03
1440504_at	Ccdc39	2	2.77E-05
1418138_at	Sult1d1	2	6.03E-03
1443968_at	Adarb1	2	4.01E-03
1443844_at	1700123J19Rik	2	3.51E-06
1457418_at	LOC100042819	2	9.08E-04
1430364_at	Atf7ip2	2	4.39E-06
1453397_at	9130016M20Rik	2	2.10E-07
1425313_at	Carf	2	5.82E-05
1425167_a_at	Gngt1	2	9.97E-04
1456811_at	Cxxc4	2	3.70E-04
1445046_at	D8Ertd317e	2	3.40E-03
1451518_at	Zfp709	2	1.26E-05
1440112_at	Lrrtm3	2	1.87E-04
1443365_at	Htr4	2	2.44E-04
1436998_at	Ankrd43	2	1.36E-06
1457990_at	Anks1b	2	2.36E-04
1437054_x_at	Prm1	2	1.64E-06
1445950_at	C87926	2	3.18E-03
1443272_at	Nope	2	4.02E-04
1445921_at	D2Ertd397e	2	3.32E-08
1444684_at	8030475D13Rik	2	7.62E-07
1420504_at	Slc6a14	2	2.34E-07
1445660_at	2700094F01Rik	2	5.00E-05
1437263_at	A730089K16Rik	2	7.79E-03
1435307_at	Ankrd34b	2	9.83E-07
1427987_at	Safb2	2	1.28E-03
1425564_at	Rest	2	9.61E-05
1442528_at	Xpo4	2	1.96E-06
1421774_at	Vax1	2	1.09E-03
1417728_at	Mbd3	2	5.85E-04
1444023_at	Ank2	2	2.02E-05
1422395_at	V1rc22	2	1.11E-06
1425314_at	Gpr98	2	3.27E-03
1437204_a_at	Tcf25	2	1.29E-04
1416449_x_at	Stxbp2	2	1.26E-03
1438083_at	Hhip	2	3.91E-09
1453478_at	Pou3f2	2	2.69E-04
1457066_at	Abcc8	2	1.41E-03
1449123_at	Itih3	2	5.43E-03
1417485_at	Ibsp	2	3.03E-03
1428990_at	2310047K21Rik	2	4.86E-05
1450287_at	Npas3	2	7.25E-04
1423950_at	Kcnab3	2	7.63E-06
1418656_at	Lsm5	2	6.37E-03
1432491_at	Pcdh8	2	1.92E-03
1436653_at	Tctex1d4	2	4.26E-04
1453751_at	Dhx38	2	2.34E-05
1430471_at	LOC100041960	2	6.78E-03
1455813_at	OTTMUSG00000010009	2	1.28E-03

1455635_at	4732460I02Rik	2	4.54E-05
1456090_at	Pdhx	2	1.25E-03
1435426_s_at	Pisd	2	8.67E-05
1440924_at	Mphosph1	2	4.74E-10
1453699_at	4930448D08Rik	2	2.38E-06
1430281_at	Glipr1l1	2	4.70E-07
1459480_at	D6Ertd90e	2	4.39E-03
1444254_at	Tns4	2	9.08E-03
1437168_at	Srrp	2	6.78E-08
1432156_a_at	Rnf32	2	1.60E-03
1436738_at	Pif1	2	7.12E-03
1432511_s_at	Cep27	2	2.31E-03
1459945_at	ENSMUSG00000056023	2	1.49E-08
1431873_a_at	Tube1	2	3.61E-04
1437652_at	Sema6c	2	3.61E-04
1429592_at	Lhfpl3	2	9.32E-06
1453613_at	A130006I12Rik	2	1.99E-04
1438311_at	2010002M12Rik	2	3.50E-07
1454339_at	4930551I15Rik	2	6.09E-05
1437499_at	Ankrd39	2	8.51E-03
1423029_at	Hes2	2	3.14E-05
1421886_at	Sos1	2	3.84E-05
1427281_at	Scn2a1	2	3.86E-06
1431265_at	Zfp28	2	5.79E-05
1444694_at	LOC100042793	2	1.97E-03
1428303_at	1500005I02Rik	2	5.66E-06
1459755_x_at	1700082C02Rik	2	9.76E-05
1438523_x_at	1500001A10Rik	2	1.38E-04
1430278_a_at	Dqx1	2	7.02E-03
1453058_at	Wdr5b	2	5.21E-04
1429858_at	1700011E24Rik	2	5.98E-05
1447817_at	Hif1an	2	1.33E-03
1435724_at	4933400N17Rik	2	1.16E-04
1451235_at	Cend1	2	2.47E-03
1459882_at	Mcm9	2	4.70E-03
1430564_at	Mobkl1a	2	4.07E-03
1431211_s_at	Them5	2	4.21E-05
1457773_at	Slamf6	2	4.61E-06
1437996_s_at	1500012D20Rik	2	5.14E-06
1435944_s_at	Cenpb	2	4.22E-05
1448983_at	Cdrt4	2	1.09E-04
1430879_at	C030008P14Rik	2	2.84E-03
1423124_x_at	Rad54l	2	5.21E-03
1447496_s_at	Fank1	2	4.88E-04
1450121_at	Scn1a	2	1.70E-07
1458493_a_at	2410089E03Rik	2	1.61E-03
1440109_at	D7Ertd413e	2	9.47E-08

1423415_at	Gpr83	2	1.01E-03
1435760_at	Csta	2	1.44E-06
1443821_at	Lect2	2	6.69E-06
1432671_at	4933407A17Rik	2	1.37E-04
1453739_at	Tmem126b	2	5.88E-06
1426619_at	Aim2	2	5.83E-04
1421838_at	Rps18	2	2.00E-06
1457494_at	LOC100039282	2	3.07E-08
1429405_at	2010317E24Rik	2	5.53E-04
1451548_at	Upp2	2	8.15E-08
1457344_at	Neto2	2	8.36E-03
1433650_at	Haghl	2	3.83E-03
1432452_at	1700054O19Rik	2	5.92E-03
1427141_at	2700099C18Rik	2	1.40E-06
1419837_at	Treml2	2	1.18E-04
1452142_at	Slc6a1	2	2.53E-05
1438512_at	BC048679	2	3.06E-03
1454504_at	Kcnip1	2	8.72E-04
1422434_a_at	2210010C04Rik	2	4.71E-04
1443584_at	1110028C15Rik	2	9.34E-07
1440786_x_at	Sfxn2	2	4.10E-06
1430959_at	4930546H06Rik	2	3.41E-03
1453225_at	A930038C07Rik	2	4.32E-07
1440598_at	Sntg1	2	3.83E-08
1422080_at	Il7	2	1.59E-09
1457702_at	Gpr12	2	1.23E-03
1435048_at	AI854703	2	5.23E-09
1447243_at	BC040756	2	6.11E-04
1454359_at	9530023I19Rik	2	2.40E-06
1427042_at	Mal2	2	5.61E-07
1448359_a_at	Higd1a	2	1.61E-04
1458932_at	Pex5l	2	4.64E-03
1438875_at	OTTMUSG00000006163	2	4.13E-09
1432405_a_at	Plcz1	2	7.01E-08
1421548_at	Pcdhb2	2	9.09E-05
1441587_at	Plch2	2	6.53E-03
1440507_at	LOC100126795	2	1.51E-03
1420529_at	Neud4	2	4.19E-04
1431559_at	6430710C18Rik	2	3.63E-04
1436794_at	Nlrp4f	2	1.64E-04
1457403_at	9130409I23Rik	2	1.50E-07
1419970_at	Slc35a5	2	7.87E-03
1430188_at	1700037C18Rik	2	4.69E-03
1439431_x_at	Bicd1	2	4.83E-05
1455338_at	A4galt	2	4.56E-07
1431454_at	4930523O13Rik	2	1.91E-06
1446857_at	C87115	2	2.05E-05

1419940_at	C030018P15Rik	2	5.72E-05
1431867_a_at	1700007B13Rik	2	5.61E-04
1436710_at	Zswim4	2	1.94E-04
1439923_at	Tubgcp5	2	5.42E-06
1454951_at	Zfp606	2	2.41E-03
1435408_at	BC037393	2	3.72E-07
1432362_at	Cenpp	2	1.05E-03
1451929_a_at	Vrk2	2	1.17E-03
1456987_at	4932418E24Rik	2	6.56E-03
1450748_at	Smpd3	2	1.30E-03
1432346_a_at	Cdh23	2	2.16E-03
1431640_at	4933431J24Rik	2	6.71E-08
1456096_at	6430573F11Rik	2	2.07E-03
1425317_x_at	Stk31	2	8.65E-05
1429867_at	4933424C08Rik	2	1.86E-03
1434760_at	Lrrtm3	2	7.75E-03
1443766_x_at	Rab11fip4	2	2.22E-04
1430192_at	Casp3	2	6.58E-04
1440617_at	Cpa6	2	1.50E-04
1456137_at	Nrxn3	2	4.63E-05
1420680_at	Cts8	2	4.70E-08
1451811_at	Cacng6	2	2.23E-03
1420259_at	Pkp2	2	9.66E-05
1453887_a_at	Tiam1	2	1.26E-03
1417859_at	Gas7	2	5.17E-03
1422979_at	Suv39h2	2	3.00E-09
1453012_at	Tsc22d2	2	5.23E-03
1424363_at	Mycbpap	2	4.03E-04
1447591_x_at	A830082N09Rik	2	1.10E-04
1440806_x_at	5730526G10Rik	2	6.72E-09
1417802_at	1110032A04Rik	2	9.03E-04
1436501_at	Mtus1	2	4.66E-03
1443867_at	Ankrd12	2	1.19E-03
1453693_at	Wdr20b	2	3.20E-04
1423410_at	Meig1	2	2.07E-06
1435012_x_at	Ela3	2	2.37E-03
1453901_at	Aldoart1	2	1.08E-06
1438887_a_at	Gmcl1	2	2.32E-04
1455132_at	A430107D22Rik	2	1.89E-04
1431103_at	1700003P14Rik	2	1.32E-05
1420553_x_at	Serpina1a	2	7.32E-08
1449963_at	2310040M23Rik	2	2.56E-08
1441009_at	4732491K20Rik	2	1.64E-05
1417337_at	Epb4.2	2	4.65E-05
1450338_x_at	V2r9	2	1.63E-05
1454144_a_at	Ccnc	2	4.08E-03
1420761_at	Chrnd	2	5.34E-03
1458414_at	D2Ertd93e	2	2.06E-04

1439712_at	Ints10	2	1.67E-05
1433282_at	Orly	2	2.55E-08
1447702_x_at	Igsf1	2	1.03E-05
1437328_x_at	Cpsf3	2	3.79E-04
1455075_at	Pigv	2	7.14E-04
1428023_at	3110009E18Rik	2	3.47E-03
1431947_at	Ldlr	2	4.84E-03
1450676_at	Tceb3	2	2.36E-03
1456619_at	Liph	2	3.79E-05
1458909_at	1810010D01Rik	2	1.19E-03
1420536_at	Crybb2	2	1.37E-09
1445387_at	Senp6	2	6.19E-05
1424386_at	Reep2	2	9.35E-07
1441800_at	Rabgap1	2	1.74E-04
1428728_at	Ddx51	2	3.49E-03
1423437_at	Gsta3	2	1.88E-03
1444691_at	Prkcn	2	4.99E-06
1440875_a_at	Rsad1	2	4.02E-06
1432161_a_at	Ptar1	2	2.47E-05
1415992_at	Pigo	2	8.84E-03
1430236_s_at	Gsdma2	2	1.02E-06
1428469_a_at	Dzip1	2	2.17E-03
1421010_at	Mobp	2	7.36E-04
1430000_at	B230117O15Rik	2	2.66E-03
1432039_a_at	Lrp2bp	2	1.17E-05
1423439_at	Pck1	2	2.13E-03
1427624_s_at	Il22	2	7.88E-05
1459804_at	Crebbp	2	5.41E-03
1443395_at	D6Ertd490e	2	2.04E-04
1451817_at	Suv420h1	2	7.99E-03
1437116_at	Letmd1	2	1.03E-04
1460360_at	Asrgl1	2	8.26E-03
1442571_at	ENSMUSG00000074303	2	1.77E-03
1423640_at	Synpr	2	4.33E-06
1420122_at	AA517858	2	5.72E-06
1448424_at	Frzb	2	8.36E-03
1442920_at	Klf3	2	3.44E-04
1426119_at	Tyms-ps	2	3.34E-04
1448795_a_at	Tbrg4	2	2.45E-03
1436065_at	A130091K22Rik	2	3.46E-03
1440705_at	AU021720	2	3.84E-06
1429855_at	1700023I07Rik	2	5.47E-05
1420134_at	OTTMUSG00000001246	2	1.43E-03
1454180_at	Armc2	2	8.29E-07
1426191_a_at	Bcl2l1	2	6.43E-03
1439818_at	AI931714	2	1.27E-06

1450317_at	Clec2g	2	1.94E-04
1422625_at	Ly6h	2	7.95E-03
1456409_at	Klhdc7a	2	2.00E-04
1457160_at	Fjx1	2	2.87E-04
1457307_at	Apol11b	2	9.38E-04
1420777_a_at	4933400A11Rik	2	1.36E-05
1441369_at	C030017B01Rik	2	7.29E-04
1440282_at	Tulp4	2	1.24E-03
1451054_at	Orm1	2	1.01E-05
1441533_at	LOC100043515	2	1.20E-08
1458533_at	9330169L03Rik	2	4.27E-08
1424855_at	Olah	2	8.33E-03
1455557_at	LOC553095	2	1.02E-05
1441300_at	Kcnf1	2	2.93E-07
1447820_x_at	Cpt2	2	8.17E-05
1433615_at	Tmem117	2	3.41E-03
1432813_at	2900064F13Rik	2	1.84E-05
1427900_at	Pip5kl1	2	2.87E-04
1454147_at	2810429I04Rik	2	8.07E-08
1445274_at	BC062127	2	7.74E-06
1421349_x_at	Cend1	2	6.20E-05
1421039_at	Mip	2	5.71E-03
1436973_at	Cct8	2	7.84E-06
1435521_at	Msi2	2	2.88E-07
1421084_at	Rs1	2	2.68E-04
1453242_x_at	2810047C21Rik	2	4.55E-04
1423412_at	Rbm47	2	7.80E-04
1426042_at	Fgd4	2	2.03E-05
1440796_at	A330021E22Rik	2	2.48E-05
1421803_at	Apbh	2	6.68E-03
1451809_s_at	Rwdd3	2	7.84E-03
1451597_at	Tmprss11d	2	2.40E-04
1456954_at	Kcna6	2	5.28E-03
1425611_a_at	Cux1	2	1.07E-03
1454259_s_at	4931433A01Rik	2	9.68E-03
1426712_at	Slc6a15	2	1.25E-04
1434136_at	6332401O19Rik	2	7.08E-05
1433183_at	6720477C19Rik	2	8.87E-06
1443001_at	C78344	2	2.35E-07
1439720_at	Ralgps1	2	5.75E-03
1457153_at	LOC552882	2	4.03E-03
1440518_at	1700029I01Rik	2	9.54E-05
1426606_at	Crtac1	2	1.44E-03
1415885_at	Chgb	2	3.99E-03
1456076_at	Defb19	2	1.53E-04
1445053_at	AU022537	2	1.47E-07
1430501_at	C030047K22Rik	2	1.37E-04
1459508_at	C85600	2	7.70E-07

1443334_at	D430042O09Rik	2	4.12E-03
1430812_at	4930511A02Rik	2	1.15E-03
1457105_at	Pkd2l1	2	1.52E-05
1458986_at	4930534H18Rik	2	5.82E-04
1429374_at	Cypt12	2	1.29E-06
1430007_a_at	Cabyr	2	2.94E-04
1423851_a_at	Tmem46	2	2.60E-04
1432334_at	Cylc2	2	4.71E-03
1440699_at	Mtap2	2	9.81E-04
1427454_at	Hoxc6	2	7.36E-03
1422042_at	Gje1	2	5.35E-03
1454115_at	4930572J10Rik	2	6.66E-09
1430466_at	2310005G13Rik	2	4.72E-03
1417278_a_at	Nkd1	2	1.01E-03
1428292_at	Ndor1	2	5.25E-03
1453245_at	9130024F11Rik	2	2.57E-07
1436901_at	Notch4	2	3.53E-05
1447394_at	Clca6	2	3.26E-05
1439119_a_at	BC010304	2	3.72E-04
1439916_at	ENSMUSG00000051848	2	6.79E-04
1436403_at	BC025575	2	3.11E-03
1419058_at	Polr1e	2	1.74E-05
1429729_at	1500004A13Rik	2	1.08E-07
1444689_at	Wdr67	2	1.50E-03
1458110_at	D430030G11Rik	2	4.65E-05
1439717_at	Gabrg3	2	6.12E-04
1427175_at	AI428936	2	1.68E-03
1416900_s_at	Gdf1	2	4.47E-04
1428642_at	Slc35d3	2	1.54E-05
1437147_at	Gabrg2	2	7.33E-08
1427834_at	Spi16	2	8.97E-03
1436744_x_at	Fbxw14	2	2.05E-05
1437427_at	4933405O20Rik	2	7.74E-05
1444623_at	E530011L22Rik	2	1.67E-03
1434539_at	Lrrn3	2	9.92E-05
1435227_at	Bcl11b	2	7.08E-03
1449065_at	Acot1	2	2.17E-03
1438020_at	Hapln1	2	6.46E-03
1433526_at	Klhl8	2	2.85E-03
1454485_at	4930456G14Rik	2	4.02E-05
1437705_at	Zfp551	2	4.91E-03
1452298_a_at	Myo5b	2	4.85E-03
1427654_a_at	Htr4	2	5.92E-04
1441579_at	Dmrta1	2	7.73E-06
1419729_at	Tex11	2	9.41E-04
1455060_at	G3bp1	2	3.37E-03
1416265_at	Capn10	2	1.46E-03

1440202_at	EG622175	2	6.46E-05
1438344_at	4833424O15Rik	2	6.54E-04
1442868_at	C130026L21Rik	2	6.73E-03
1439033_at	Zcchc7	2	1.31E-04
1444668_at	Astx	2	3.80E-03
1459716_at	AI835735	2	2.15E-04
1446710_at	C76669	2	2.58E-06
1444087_at	Prpf38a	2	3.85E-09
1429984_at	5730455O13Rik	2	5.43E-05
1446747_at	Spef2	2	1.50E-03
1430931_at	4933403O03Rik	2	1.58E-05
1429324_at	1700012A16Rik	2	3.24E-05
1422152_at	Hmx1	2	8.87E-03
1432796_at	3110067C02Rik	2	2.20E-03
1426064_at	Cyp3a44	2	1.36E-03
1454176_at	Ercc8	2	6.75E-04
1433947_at	Rab37	2	2.15E-03
1418734_at	BE136769	2	3.00E-05
1427118_at	5430421N21Rik	2	2.55E-03
1421476_a_at	Cant1	2	2.72E-03
1444163_at	Nek5	2	6.44E-05
1430329_at	Cgn	2	1.79E-03
1432169_at	4930523O13Rik	2	3.63E-06
1418033_s_at	Zkscan6	2	4.92E-04
1424824_at	Slain1	2	1.51E-05
1418220_at	Foxf2	2	5.46E-06
1426638_at	Six3	2	6.55E-03
1424847_at	Nefh	2	1.29E-03
1445705_x_at	Dpp8	2	2.25E-05
1424225_at	Asb8	2	2.94E-04
1434146_at	Gria2	2	6.31E-07
1454566_at	4933439C20Rik	2	3.70E-03
1439494_at	Slc5a9	2	9.87E-08
1458329_x_at	LOC100039227	2	6.40E-08
1457314_at	L1td1	2	4.47E-04
1457495_at	2900052N01Rik	2	9.34E-03
1439948_at	BC046401	2	8.06E-03
1444804_at	D17Ertd96e	2	1.91E-04
1443143_at	Flrt1	2	1.04E-04
1443323_at	Ccdc76	2	5.83E-05
1456095_at	Tyr	2	7.42E-07
1419626_at	Adam25	2	9.07E-07
1437605_at	Nphs2	2	8.31E-05
1429659_at	Smc2	2	2.99E-05
1428042_at	ENSMUSG00000058934	2	2.50E-05
1421874_a_at	Mrps23	2	3.90E-03
1447289_at	AA763521	2	4.91E-05
1453935_a_at	Ccdc7	2	3.43E-06
1436282_at	4732440D04Rik	2	6.72E-04
1449518_at	Qpctl	2	5.34E-03

Decreasing Probe Set ID	Gene Symbol	Fold change	p value
1438629_x_at	Grn	374	2.25E-11
1437708_x_at	Vamp3	273	5.28E-06
1455997_a_at	Uqcrb	203	1.47E-04
1434897_a_at	Slc25a4	182	2.71E-06
1452222_at	Utrn	179	9.02E-07
1437526_x_at	Hnrnpr	168	3.24E-06
1438658_a_at	Edg3	164	4.93E-05
1438554_x_at	Eif4h	157	1.56E-09
1427442_a_at	App	152	1.57E-09
1415933_a_at	Cox5a	151	7.25E-09
1455875_x_at	Tm9sf2	146	6.75E-05
1416058_s_at	Atp5c1	145	3.14E-08
1449686_s_at	Scp2	143	6.35E-04
1420558_at	Selp	143	1.18E-03
1443762_s_at	Sbf2	141	6.15E-04
1437211_x_at	Elovl5	140	9.75E-04
1456245_x_at	Vamp3	132	7.10E-06
1437143_a_at	Txndc1	125	1.15E-05
1426593_a_at	Fbxo22	124	1.47E-04
1433488_x_at	Gns	122	1.93E-09
1450297_at	Il6	111	2.65E-04
1451989_a_at	Mapre2	110	4.82E-03
1437165_a_at	Pcolce	110	8.27E-07
1416941_s_at	Eif4h	106	3.71E-07
1436568_at	Jam2	105	1.94E-05
1437478_s_at	Efhd2	100	6.58E-09
1437309_a_at	Rpa1	100	1.79E-03
1423110_at	Col1a2	96	3.87E-07
1433723_s_at	Serf2	96	1.73E-05
1437993_x_at	Qdpr	95	3.45E-04
1456056_a_at	D6Wsu116e	95	4.36E-04
1448102_a_at	Wdr61	94	6.15E-04
1450884_at	Cd36	93	1.71E-03
1448909_a_at	Mrpl39	93	5.45E-06
1448178_a_at	Cct3	92	7.10E-05
1438169_a_at	Frmd4b	91	8.94E-04
1424463_at	2210010L05Rik	91	3.34E-03
1456567_x_at	Grn	89	4.31E-09
1456739_x_at	Armcx2	88	3.79E-04
1438318_x_at	Ngdn	87	1.14E-06
1419252_at	Eps15	86	2.04E-04
1445897_s_at	Ifi35	84	6.51E-04
1438091_a_at	H2afz	83	1.98E-04
1426682_at	LOC100046343	81	1.30E-03
1428608_at	Mylc2b	81	2.81E-06
1452757_s_at	Hba-a1	80	6.22E-04
1415821_at	Nptn	80	1.10E-07
1456736_x_at	5230400G24Rik	79	3.46E-04
1437073_x_at	AV025504	76	3.95E-04
1439267_x_at	Cox5a	76	4.09E-10
1435386_at	Vwf	76	1.08E-04
1416021_a_at	Fabp5	75	4.60E-04
1439766_x_at	Vegfc	75	3.01E-04
1424017_a_at	Hint1	74	3.19E-05
1417327_at	Cav2	74	2.34E-04
1460240_a_at	Hnrnpc	74	9.54E-05
1427040_at	Mdfic	72	7.90E-05
1450881_s_at	Gpr137b	72	6.07E-03
1448493_at	Paip2	72	4.20E-08
1450783_at	Ifit1	71	1.45E-03
1416454_s_at	Acta2	70	4.86E-04
1429085_at	Vezf1	69	1.71E-04
1433475_a_at	C78339	68	2.09E-03
1420928_at	St6gal1	68	4.35E-05
1456012_x_at	Rnaset2a	67	3.79E-07
1420829_a_at	Ywhaq	66	3.62E-04
1434056_a_at	Ndufb6	65	1.50E-06
1436152_a_at	Hbxip	64	1.41E-03
1433786_x_at	Serf2	64	6.68E-07
1452692_a_at	Ndufv2	64	1.35E-03
1439184_s_at	Txndc17	63	7.92E-06
1423057_at	Capza2	63	1.18E-04
1434339_at	Fnbp1l	63	1.38E-06
1416295_a_at	Il2rg	63	1.85E-06
1436292_a_at	Oaz1	62	7.80E-09
1437735_at	Ppp1r12a	62	2.08E-03
1437456_x_at	Ythdf1	62	7.14E-04
1422490_at	Bnip2	62	3.82E-07
1437687_x_at	Fkbp9	62	2.30E-03
1437223_s_at	Xbp1	61	9.55E-05
1422241_a_at	Ndufa1	61	5.04E-11
1455816_a_at	Kctd3	61	1.98E-03
1436944_x_at	4933439C20Rik	61	6.48E-05
1440173_x_at	Selp	60	1.78E-03
1416727_a_at	Cyb5	60	1.43E-04
1427965_at	Ssbp1	60	1.99E-04
1448123_s_at	Tgfbi	59	1.47E-07
1455792_x_at	Ndn	59	9.12E-03
1423043_s_at	Ddx3x	58	1.36E-03
1418436_at	Stx7	57	7.31E-06
1450883_a_at	Cd36	57	8.00E-06
1439271_x_at	Ik	57	2.93E-08
1455908_a_at	Scpep1	57	6.31E-06
1436997_x_at	Sh3bgrl	57	2.71E-06

1437458_x_at	Clu	55	2.80E-04
1438941_x_at	Ampd2	55	4.86E-03
1416185_a_at	Adh5	55	1.13E-06
1422824_s_at	Eps8	55	2.41E-05
1448995_at	Cxcl4	54	6.44E-06
1455815_a_at	Ywhab	54	7.13E-04
1420830_x_at	Ywhaq	54	8.35E-04
1436708_x_at	Mcm4	54	7.42E-03
1424131_at	Col6a3	53	7.15E-08
1451313_a_at	1110067D22Rik	53	2.08E-06
1459986_a_at	Rps17	52	1.23E-07
1417749_a_at	Tjp1	52	8.35E-04
1434011_a_at	Ints5	52	1.25E-03
1450857_a_at	Col1a2	52	4.50E-04
1436759_x_at	Cnn3	51	9.90E-05
1416175_a_at	Vdac3	50	1.00E-04
1416815_s_at	Bub3	50	1.45E-05
1456057_x_at	Tmem109	50	2.17E-05
1437009_a_at	Zfp364	49	5.43E-04
1434202_a_at	BC055107	49	3.52E-03
1416970_a_at	Cox7a2	49	2.82E-03
1417292_at	Ifi47	48	2.04E-04
1441870_s_at	Pkd2	48	1.58E-03
1418273_a_at	Rpl30	47	4.71E-08
1416082_at	Rab1	47	6.13E-05
1437008_x_at	Tmem109	47	2.11E-04
1454615_x_at	Srp14	47	1.93E-04
1425336_x_at	H2-K1	47	2.67E-04
1419738_a_at	Tpm2	47	2.31E-03
1435652_a_at	Gnai2	46	2.62E-06
1426900_at	Jmjd1c	46	3.67E-05
1436959_x_at	Nelf	46	8.61E-04
1437688_x_at	Atp6ap2	46	3.06E-04
1451172_at	Tprgl	46	3.50E-04
1459835_s_at	Dnaja1	46	3.60E-05
1438171_x_at	Mettl9	46	3.88E-05
1448005_at	Sash1	46	6.91E-06
1416417_a_at	Ndufb7	45	1.75E-06
1452734_at	Rnaset2a	45	3.03E-04
1439462_x_at	Tmed10	45	1.18E-04
1418142_at	Kcnj8	45	2.56E-06
1417222_a_at	Tmem123	45	1.24E-07
1417606_a_at	Calr	45	4.50E-07
1447923_at	1810026B05Rik	45	8.12E-05
1429184_at	Gvin1	44	1.23E-03
1432270_a_at	Chmp5	43	1.37E-06
1454666_at	LOC100046855	43	8.91E-06
1452683_at	Dnajc8	42	2.26E-03

1425231_a_at	Zfp46	42	8.00E-06
1416179_a_at	Rdx	42	3.57E-03
1460621_x_at	Ywhaq	42	3.29E-03
1454688_x_at	Tmed10	42	1.23E-06
1454747_a_at	Klhdc3	42	3.38E-03
1417872_at	Fhl1	42	3.45E-03
1456728_x_at	Aco1	41	3.08E-03
1433984_a_at	Mdh2	41	8.49E-04
1454942_at	Niban	41	4.05E-04
1438868_at	D14Ertd668e	41	5.66E-04
1430288_x_at	Rps21	41	6.22E-05
1421571_a_at	Ly6c1	41	2.68E-05
1456086_x_at	Pqbp1	41	5.02E-04
1416415_a_at	H2afz	40	4.48E-05
1422045_a_at	Ptpn12	40	1.63E-06
1456279_a_at	Bcap31	40	1.07E-03
1428289_at	Klf9	40	5.08E-04
1439389_s_at	Myadm	40	3.50E-05
1451177_at	Dnajb4	40	1.09E-04
1436173_at	Dlc1	40	3.93E-06
1415796_at	Dazap2	39	6.47E-07
1422487_at	Smad4	39	3.56E-05
1449256_a_at	Rab11a	39	2.13E-04
1420000_s_at	Igbp1	39	2.72E-04
1416742_at	Cfdp1	39	1.70E-03
1448694_at	Jun	39	3.11E-06
1440167_s_at	Lpp	39	3.61E-04
1423166_at	Cd36	38	4.84E-04
1417810_a_at	Kcnb1	38	3.19E-04
1449363_at	Atf3	38	2.32E-06
1421849_at	Stag2	38	1.07E-03
1449929_at	Dynlt3	38	2.93E-04
1460197_a_at	Steap4	38	8.80E-05
1416589_at	Sparc	38	2.35E-05
1436180_at	Dnajc5	37	1.05E-03
1420642_a_at	2010100O12Rik	37	2.41E-06
1437837_x_at	Poldip3	37	5.73E-06
1438652_x_at	Pigq	37	9.04E-03
1459861_s_at	Fbxl10	37	1.88E-03
1424800_at	Enah	37	2.12E-03
1449368_at	Dcn	36	1.39E-03
1455032_at	Ccnyl1	36	4.73E-05
1448775_at	Ifi203	36	5.02E-05
1449622_s_at	Atp6ap1	36	1.04E-04
1455662_x_at	Rps17	36	4.94E-06
1455939_x_at	Srp14	36	8.47E-04
1448623_at	Tmem123	36	1.11E-06
1426906_at	Ifi203	35	8.25E-03

1428107_at	Sh3bgrl	35	4.55E-05
1455927_x_at	Nsmce1	35	3.34E-03
1455854_a_at	Ssh1	35	4.61E-04
1437689_x_at	Clu	35	5.74E-04
1428615_at	P2ry5	35	3.23E-04
1460716_a_at	Cbfb	35	5.00E-04
1416943_at	Ube2e1	35	4.19E-07
1455824_x_at	Stt3a	35	9.32E-07
1417409_at	Jun	35	2.70E-04
1435103_x_at	Farsb	35	1.20E-03
1423607_at	Lum	35	6.25E-07
1428236_at	Acbd5	35	1.83E-04
1456580_s_at	Atp5d	34	2.46E-06
1436994_a_at	Hist1h1c	34	4.25E-05
1427918_a_at	Rhoq	34	3.87E-04
1426642_at	Fn1	34	3.12E-08
1426708_at	Antxr2	34	3.22E-03
1447624_s_at	Stox2	34	2.00E-06
1418674_at	Osmr	34	1.12E-03
1452544_x_at	LOC100045864	34	3.83E-11
1433951_at	Arl5a	34	3.91E-04
1418885_a_at	Idh3b	34	1.50E-03
1435112_a_at	Atp5h	33	2.62E-04
1415840_at	Elovl5	33	1.24E-03
1437999_x_at	Pigq	33	6.17E-03
1437626_at	Zfp36l2	33	9.79E-05
1423763_x_at	Rps28	33	5.02E-04
1418072_at	Hist1h2bc	33	7.16E-04
1456205_x_at	Tbca	33	1.62E-04
1448788_at	Cd200	33	2.03E-04
1449556_at	H2-T23	33	5.73E-03
1433833_at	Fndc3b	33	8.66E-05
1418101_a_at	Rtn3	33	1.82E-05
1454760_at	Htatsf1	33	1.86E-03
1423662_at	Atp6ap2	33	3.49E-04
1455696_a_at	Prpf4b	32	6.14E-04
1426645_at	Hsp90aa1	32	1.66E-03
1420376_a_at	H3f3b	32	3.57E-05
1451188_at	Wdr26	32	1.34E-03
1439466_s_at	Bud31	32	7.03E-04
1427651_x_at	LOC100045864	32	2.56E-11
1416143_at	Atp5j	32	1.28E-05
1420249_s_at	Ccl6	32	4.93E-05
1455105_at	Ptpn12	32	2.22E-06
1437172_x_at	Hadhb	32	7.33E-04
1415991_a_at	Klhdc3	32	8.91E-04
1448591_at	Ctss	32	1.43E-05
1418090_at	Plvap	32	1.67E-03

1417907_at	Ube2l3	31	2.54E-03
1460208_at	Fbn1	31	6.71E-04
1424139_at	Rap1a	31	9.86E-04
1448238_at	2700060E02Rik	31	3.54E-03
1456530_x_at	Elovl1	31	2.20E-04
1416926_at	Trp53inp1	31	2.10E-03
1437465_a_at	P4hb	31	1.74E-05
1456293_s_at	Ccnh	31	9.81E-03
1438723_a_at	Rps10	31	3.43E-05
1450430_at	Mrc1	31	3.59E-03
1416472_at	Syap1	31	3.87E-05
1422881_s_at	Sypl	31	7.19E-06
1426407_at	Cugbp1	31	2.06E-03
1460179_at	Dnaja1	30	1.22E-04
1451195_a_at	Txndc1	30	1.27E-03
1423956_at	Smap1	30	8.13E-06
1434285_at	Frmd4a	30	2.46E-03
1448400_a_at	Smarcd2	30	1.63E-03
1449507_a_at	Cd47	30	1.20E-04
1454778_x_at	LOC100043527	30	6.86E-04
1416951_a_at	Atp6v1d	30	1.98E-03
1429028_at	Dock11	30	2.65E-04
1415672_at	Golga7	30	3.10E-04
1438092_x_at	H2afz	30	3.45E-05
1418886_s_at	Idh3b	30	3.22E-04
1427886_at	Pom121	30	6.90E-05
1423217_a_at	2510049I19Rik	30	5.27E-04
1423256_a_at	Atp6v1g1	29	1.25E-03
1436848_x_at	Impa1	29	5.82E-03
1416440_at	Cd164	29	2.65E-04
1423188_a_at	6720456B07Rik	29	7.38E-04
1428286_at	2900097C17Rik	29	3.34E-05
1440739_at	Vegfc	29	2.97E-09
1415691_at	Dlg1	29	2.22E-03
1435906_x_at	Gbp2	29	4.92E-04
1417321_at	D4Wsu132e	29	1.39E-03
1416498_at	Ppic	29	3.19E-04
1435315_s_at	2900034E22Rik	29	7.08E-03
1437907_a_at	Tbca	29	2.24E-04
1432176_a_at	Eng	29	2.51E-03
1424309_a_at	Mocs2	29	2.37E-04
1429151_at	Wdr68	29	1.49E-05
1452231_x_at	Ifi203	28	3.68E-03
1451074_at	Rnf13	28	9.52E-06
1416508_at	Med28	28	2.59E-03
1455546_s_at	Sf3a2	28	2.01E-03
1452767_at	Rrbp1	28	4.29E-04
1416187_s_at	Pnrc2	28	2.65E-05

1442434_at	D8Ertd82e	28	2.42E-03
1455164_at	Cdgap	28	1.93E-04
1436783_x_at	Ywhab	28	1.25E-03
1416153_at	Srp54a	28	2.10E-04
1450985_a_at	Tjp2	28	2.48E-03
1438922_x_at	Slc25a5	28	9.15E-08
1427347_s_at	Tubb2a	28	6.73E-03
1437838_x_at	Grsf1	27	3.11E-03
1434801_x_at	Slc25a5	27	1.75E-05
1435429_x_at	Rps27l	27	2.10E-05
1437849_x_at	Armcx2	27	1.82E-05
1423263_at	H3f3a	27	1.85E-04
1452123_s_at	Frmd4b	27	4.93E-03
1433897_at	AI597468	27	1.11E-03
1451652_a_at	Tmem188	27	3.28E-04
1451564_at	Parp14	27	9.87E-03
1450021_at	Ubqln2	27	1.03E-03
1459854_s_at	Dynlt3	27	4.08E-03
1450138_a_at	Serpinb6a	27	7.66E-04
1426819_at	LOC100048439	27	5.34E-05
1448504_a_at	Cbx3	27	5.40E-04
1419186_a_at	St8sia4	27	4.84E-04
1438024_at	Ccdc90a	27	8.97E-04
1433746_at	Wdr3	27	2.14E-04
1417733_at	Rnf146	27	5.02E-03
1415822_at	Scd2	27	9.10E-05
1451294_s_at	Snrpe	27	4.90E-05
1419170_at	Tmem157	26	9.29E-04
1416499_a_at	Dctn6	26	2.10E-03
1415724_a_at	Cdc42	26	2.15E-05
1434935_at	Aak1	26	2.29E-03
1423939_a_at	Yif1a	26	3.95E-03
1416699_at	1110008F13Rik	26	5.04E-04
1416083_at	Zfand5	26	1.00E-04
1422437_at	Col5a2	26	9.98E-03
1428624_at	2810482I07Rik	26	1.06E-04
1454813_at	Ccdc72	26	1.68E-03
1433751_at	Slc39a10	26	4.25E-03
1418189_s_at	Malat1	26	1.86E-04
1437016_x_at	Rap2c	26	6.53E-04
1435416_x_at	Pigq	26	5.75E-03
1429251_at	Prdm2	26	3.74E-03
1433776_at	Lhfp	26	1.71E-06
1452176_at	Nup153	26	2.57E-03
1440831_at	Bach1	26	1.59E-04
1433537_at	Atrx	26	1.67E-04
1415962_at	Eif3h	25	5.62E-03
1416326_at	Crip1	25	5.56E-04

1419945_s_at	Rab2	25	1.07E-03
1433476_at	C78339	25	1.76E-03
1427923_at	Zmpste24	25	4.09E-03
1439078_at	Klhl4	25	1.40E-06
1420880_a_at	Ywhab	25	5.54E-05
1418505_at	Nudt4	25	5.02E-06
1423692_at	Ndufa8	25	2.96E-04
1455009_at	Cpd	25	9.07E-05
1417646_a_at	Snx5	25	1.36E-04
1416233_at	Eif3i	25	3.23E-03
1434232_a_at	2610030H06Rik	25	5.28E-03
1438503_x_at	Edf1	25	3.55E-07
1424545_at	BC003965	25	9.87E-04
1425742_a_at	Tsc22d1	25	9.63E-04
1451086_s_at	Rac1	25	2.91E-05
1460707_at	Ptp4a2	25	1.34E-04
1439444_x_at	Tmed10	25	5.55E-05
1417367_at	Ppp2ca	25	3.69E-03
1448688_at	Podxl	25	1.95E-04
1416101_a_at	Hist1h1c	25	2.84E-03
1420815_at	Gdi2	25	7.89E-06
1425568_a_at	Tmem33	25	5.91E-06
1452737_at	2810008M24Rik	25	1.29E-03
1416749_at	Htra1	25	3.41E-04
1452867_at	Col4a3bp	25	1.13E-03
1448903_at	Sepp1	25	1.02E-03
1417647_at	Snx5	25	7.17E-04
1428314_at	Pcnp	24	1.45E-03
1415783_at	Vps35	24	1.49E-06
1416756_at	Dnajb1	24	2.77E-04
1424318_at	1110067D22Rik	24	1.43E-04
1428288_at	2310051E17Rik	24	5.36E-03
1417962_s_at	Ghr	24	7.91E-04
1448100_at	4833439L19Rik	24	1.26E-03
1420952_at	Son	24	4.43E-05
1428178_s_at	Trappc6b	24	4.65E-03
1448322_a_at	Cox4i1	24	6.18E-05
1434356_a_at	Psma5	24	6.90E-06
1448791_at	Snx5	24	1.44E-03
1415688_at	Ube2g1	24	1.39E-04
1451005_at	Sumo1	24	1.79E-03
1456061_at	Gimap8	24	4.06E-03
1426476_at	Rasa1	24	3.61E-03
1438360_x_at	Slc25a5	24	7.88E-08
1436951_x_at	Txndc9	24	5.11E-04
1459866_x_at	Cyfip1	24	9.47E-03
1433704_s_at	Tloc1	24	6.66E-04
1418392_a_at	Gbp3	24	1.82E-04

1427407_s_at	Trip11	24	4.57E-03
1417586_at	Timeless	24	9.43E-04
1415942_at	Rpl10	24	4.57E-04
1447100_s_at	5730508B09Rik	24	4.00E-03
1456032_x_at	H2afz	24	1.63E-07
1422892_s_at	H2-Ea	23	5.80E-09
1421751_a_at	Psmd14	23	1.58E-03
1435547_at	ENSMUSG00000075401	23	2.81E-03
1433562_s_at	Atp5f1	23	1.20E-03
1438631_x_at	Ttc13	23	6.08E-03
1423792_a_at	Cmtm6	23	3.54E-04
1416329_at	Cyfip1	23	1.54E-06
1447518_at	Tpx2	23	1.79E-03
1422480_at	Snx3	23	8.37E-05
1433676_at	Wnk1	23	7.64E-05
1456873_at	Clic5	23	9.00E-05
1417763_at	Ssr1	23	1.11E-03
1428301_at	ENSMUSG00000057445	23	1.49E-06
1418511_at	Dpt	23	1.88E-04
1450011_at	Hsd17b12	23	2.04E-03
1437144_x_at	Psma6	23	2.78E-05
1450714_at	Azin1	23	1.84E-04
1420486_at	Nol7	23	4.36E-04
1423106_at	Ube2b	23	3.02E-04
1421840_at	Abca1	23	2.03E-06
1422671_s_at	Naalad2	23	3.58E-07
1448770_a_at	Atpif1	23	5.03E-04
1438312_s_at	Ltbp3	23	3.83E-03
1439441_x_at	Lats2	23	1.50E-04
1433546_at	Gns	22	1.91E-04
1433754_at	Mbnl2	22	1.07E-03
1415829_at	Lbr	22	3.91E-05
1451756_at	Flt1	22	3.68E-03
1429044_at	Camsap1l1	22	3.21E-04
1436902_x_at	Tmsb10	22	2.18E-04
1422608_at	Arpp19	22	1.44E-05
1426342_at	Stt3b	22	1.92E-03
1447919_x_at	Ndufab1	22	2.09E-04
1436569_at	C030045D06Rik	22	1.34E-05
1418483_a_at	Ggta1	22	3.24E-03
1438656_x_at	Timm17b	22	6.29E-03
1451446_at	Antxr1	22	5.94E-07
1460698_a_at	Sec11c	22	8.23E-05
1437714_x_at	Usp14	22	3.94E-07
1448313_at	Tpp1	22	1.74E-04

1437874_s_at	Hexb	22	6.48E-04
1428334_at	Ostm1	22	3.02E-03
1448259_at	Fstl1	22	1.03E-03
1454874_at	Btbd7	22	1.24E-03
1447898_s_at	Sfrs6	22	6.45E-05
1422895_at	Vamp4	22	5.05E-03
1435616_at	Cyp20a1	21	5.30E-03
1420886_a_at	Xbp1	21	1.94E-03
1452192_at	BC053440	21	4.47E-03
1456726_x_at	Qars	21	5.65E-05
1416600_a_at	Rcan1	21	3.40E-03
1448148_at	Grn	21	1.13E-03
1416446_at	Tmem30a	21	3.64E-04
1452285_a_at	Eif3f	21	5.24E-05
1451495_at	Wac	21	1.34E-05
1427475_a_at	Pdlim5	21	2.48E-04
1416911_a_at	6330407G11Rik	21	8.48E-07
1421923_at	Sh3bp5	21	1.51E-03
1428554_a_at	1810035L17Rik	21	6.96E-03
1438505_s_at	Rnasen	21	5.15E-03
1434888_a_at	Matr3	21	1.54E-03
1452700_s_at	Kbtbd7	21	6.93E-05
1454652_at	Zranb2	21	4.44E-05
1427233_at	Tshz1	21	6.80E-04
1438971_x_at	Ube2h	21	1.64E-03
1425020_at	Ubxd4	21	2.00E-03
1429265_a_at	Rnf130	21	3.76E-04
1437908_a_at	Ergic1	21	2.05E-04
1437402_x_at	Tmem41b	21	9.84E-05
1429177_x_at	Sox17	21	6.33E-04
1434434_s_at	Tcerg1	20	2.97E-04
1417184_s_at	Hbb-b1	20	8.21E-03
1434835_at	Wapal	20	2.46E-03
1454650_at	Trim35	20	3.82E-04
1426854_a_at	Set	20	3.27E-06
1421907_at	Med1	20	1.16E-03
1455236_x_at	Serf2	20	1.21E-05
1423641_s_at	Cnot7	20	6.45E-05
1421750_a_at	Vbp1	20	1.25E-03
1433749_at	Gna13	20	8.60E-08
1438292_x_at	Adk	20	2.04E-03
1416194_at	Cyp4b1	20	6.73E-06
1453118_s_at	Rpl22	20	5.35E-04
1448284_a_at	Ndufc1	20	1.47E-03
1424283_at	Jtb	20	6.87E-03
1448527_at	Pdcd10	20	1.43E-03
1422032_a_at	Zfand6	20	5.30E-03
1419360_a_at	Ss18	20	3.65E-03

1448129_at	Arpc5	20	1.19E-03
1417351_a_at	Snrpa1	20	4.58E-04
1455570_x_at	Cnn3	20	2.70E-03
1452225_at	2010106G01Rik	20	4.59E-04
1416144_a_at	Dhx15	20	6.82E-06
1448436_a_at	Irf1	20	1.98E-05
1435630_s_at	Acat2	20	1.68E-03
1431008_at	H2-Q6	20	4.09E-05
1448236_at	Rdx	20	2.20E-03
1455056_at	Lmo7	20	2.17E-04
1419925_s_at	Txndc10	20	4.90E-03
1456600_a_at	Rnf7	20	6.44E-03
1416024_x_at	Cct3	19	3.63E-03
1433835_at	Ppp3cb	19	2.65E-04
1417936_at	Ccl9	19	5.52E-04
1452952_at	9030418K01Rik	19	1.00E-03
1434219_at	Stim2	19	1.06E-03
1433834_at	March6	19	1.46E-03
1448343_a_at	Nbr1	19	9.21E-04
1449396_at	Aoc3	19	4.33E-05
1435106_at	Limch1	19	7.14E-04
1448210_at	Rab1	19	1.16E-04
1417111_at	Man1a	19	1.51E-04
1450186_s_at	Gnas	19	1.06E-04
1415841_at	Dync1i2	19	1.43E-06
1416908_s_at	Tsn	19	3.04E-03
1416731_at	Top2b	19	1.06E-05
1452843_at	Il6st	19	1.32E-04
1415687_a_at	Psap	19	3.69E-06
1426382_at	Ppm1b	19	7.40E-04
1450706_a_at	Arl3	19	1.86E-03
1455197_at	Rnd1	19	6.95E-06
1454626_at	Cltc	19	2.63E-07
1426964_at	3110003A17Rik	19	5.58E-04
1417674_s_at	Golga4	19	7.14E-06
1447676_x_at	S100a16	19	2.52E-04
1439153_at	Rnf144b	19	6.86E-07
1436809_a_at	Spin1	19	6.41E-03
1449078_at	St3gal6	19	5.20E-05
1453174_at	2310076G13Rik	19	5.60E-04
1434310_at	Bmpr2	18	4.62E-03
1450784_at	Reck	18	3.35E-09
1416799_at	Trpm7	18	2.08E-03
1437327_x_at	Enoph1	18	5.09E-03
1428219_at	Rybp	18	8.90E-06
1452169_a_at	Dgkz	18	2.84E-04
1417366_s_at	Calm1	18	4.85E-04
1453467_s_at	Rps15a	18	7.93E-06

1452156_a_at	Nisch	18	1.97E-04
1424781_at	Reep3	18	3.34E-03
1452773_at	5730494N06Rik	18	4.52E-04
1450934_at	Eif4a2	18	2.31E-03
1451216_at	Zfp330	18	2.56E-04
1449630_s_at	Mark1	18	1.37E-05
1427054_s_at	Abi3bp	18	1.55E-03
1437382_at	Acvr2a	18	6.96E-03
1448736_a_at	Hprt1	18	2.05E-03
1439459_x_at	Acly	18	9.47E-04
1451449_at	4933407N01Rik	18	4.46E-04
1435164_s_at	Ube1c	18	6.31E-04
1436650_at	Filip1	18	5.74E-08
1423262_a_at	H3f3a	18	1.98E-04
1452047_at	Cacybp	18	5.13E-04
1455994_x_at	Elovl1	18	1.14E-03
1450031_at	Aff4	18	1.60E-03
1436298_x_at	Paics	18	1.13E-04
1455265_a_at	Rgs16	18	6.39E-05
1426269_at	Vamp7	18	7.09E-03
1448204_at	Sav1	18	1.77E-03
1423486_at	Cript	18	3.11E-03
1424632_a_at	Rev3l	18	9.90E-03
1452038_at	Capza1	18	3.43E-06
1424873_at	Rnf2	18	3.50E-03
1435749_at	Gda	18	1.36E-04
1415723_at	Eif5	18	2.29E-03
1434111_at	Lphn2	18	6.69E-04
1454758_a_at	Tsc22d1	18	3.52E-04
1441866_s_at	Ptdss1	18	1.99E-03
1417612_at	Ier5	18	3.83E-04
1420879_a_at	Ywhab	18	2.69E-04
1419470_at	Gnb4	18	2.12E-05
1452051_at	Actr3	18	2.47E-05
1417762_a_at	Rpl8	18	8.57E-04
1417258_at	Cct5	18	3.93E-05
1431057_a_at	Prss23	18	7.53E-04
1423564_a_at	Paics	17	1.22E-03
1448647_at	Man2a1	17	2.72E-06
1449360_at	Csf2rb2	17	1.08E-04
1416000_a_at	Prdx1	17	4.40E-04
1447720_x_at	Prkaca	17	6.89E-03
1424000_a_at	Rps11	17	2.91E-04
1451089_a_at	Arcn1	17	3.48E-07
1423489_at	Mmd	17	2.57E-03
1418025_at	Bhlhb2	17	1.66E-04
1427126_at	Hspa1b	17	1.87E-03
1419300_at	Flt1	17	1.47E-05

1448548_at	Tulp4	17	9.60E-04
1448682_at	Dynll1	17	1.28E-04
1455938_x_at	Rad21	17	4.77E-06
1435967_s_at	Hibadh	17	4.00E-03
1433654_at	Mgea5	17	2.13E-03
1418240_at	Gbp2	17	1.10E-03
1452670_at	Myl9	17	1.85E-06
1420478_at	Nap1l1	17	9.64E-03
1456083_x_at	Eif3c	17	9.92E-04
1434303_at	Raph1	17	1.69E-04
1440009_at	Olfr78	17	2.22E-10
1429599_a_at	1110019K23Rik	17	3.08E-03
1435988_x_at	Ik	17	1.52E-04
1416060_at	Tbc1d15	17	2.39E-03
1448279_at	Arpc3	17	2.80E-06
1423785_at	Egln1	17	1.62E-03
1416176_at	Hmgb1	17	7.16E-05
1416668_at	Ttc35	17	1.07E-03
1452519_a_at	Zfp36	17	1.23E-06
1455251_at	Itga1	17	1.26E-03
1419292_at	Htra3	17	1.47E-06
1450394_at	Golph3	17	4.25E-04
1433645_at	Slc44a1	17	1.30E-04
1452997_at	6820431F20Rik	17	4.29E-04
1427250_at	Atp2a2	17	5.31E-04
1437035_x_at	Rnf14	17	7.38E-08
1424347_at	Ppp6c	17	5.59E-03
1460602_at	Dlc1	17	1.02E-06
1424373_at	Armcx3	17	2.59E-03
1452659_at	Dek	16	6.49E-03
1423535_at	LOC100047794	16	8.34E-06
1416039_x_at	Cyr61	16	1.35E-04
1428167_a_at	Mpzl1	16	4.34E-05
1426236_a_at	Glul	16	2.26E-04
1415949_at	Cpe	16	9.17E-03
1435745_at	5031439G07Rik	16	7.05E-03
1415683_at	Nmt1	16	1.07E-04
1448103_s_at	Nono	16	3.75E-03
1427129_a_at	Hnrnpr	16	8.68E-03
1429005_at	Mfhas1	16	7.97E-03
1436523_s_at	1810022K09Rik	16	1.38E-03
1428776_at	Slc10a6	16	8.81E-04
1433634_at	Irf2bp2	16	5.41E-03
1434860_at	Narg3	16	2.24E-03
1450690_at	Ranbp2	16	6.64E-04
1428082_at	Acsl5	16	3.14E-03
1448570_at	Gmfb	16	5.08E-04
1427875_a_at	Rpl34	16	9.87E-05

1423898_a_at	Trip12	16	1.40E-03
1433439_at	Cpne1	16	8.44E-04
1434540_a_at	Clta	16	1.93E-03
1415749_a_at	Rragc	16	3.35E-03
1417625_s_at	Cxcr7	16	1.71E-03
1429002_at	Snw1	16	6.51E-04
1422475_a_at	Rps3a	16	7.28E-04
1418970_a_at	Bcl10	16	8.73E-03
1434875_a_at	Hmgn3	16	1.27E-03
1438610_a_at	Cryz	16	8.44E-03
1451462_a_at	Ifnar2	16	9.79E-05
1450925_a_at	Rps27l	16	1.22E-04
1419879_s_at	Trim25	16	8.59E-03
1451080_at	Usp1	16	3.79E-03
1454966_at	Itga8	16	2.33E-04
1448162_at	Vcam1	16	5.18E-03
1426776_at	Wasl	16	5.09E-05
1416877_a_at	Mrpl51	16	3.44E-04
1451101_a_at	Rps28	16	4.25E-04
1454774_at	Zfp445	16	7.08E-03
1435526_at	Tor1aip2	16	5.13E-04
1455978_a_at	Matn2	16	1.09E-08
1449445_x_at	Mfap1a	16	3.30E-04
1449167_at	Epb4.1l4a	16	5.64E-05
1416090_at	Pdhb	15	7.20E-04
1452163_at	Ets1	15	9.62E-04
1433916_at	Vamp3	15	1.34E-05
1437608_x_at	Ywhaq	15	2.78E-03
1452281_at	Sos2	15	2.54E-04
1447519_x_at	Tpx2	15	1.64E-03
1438176_x_at	1110031B06Rik	15	7.10E-03
1453095_at	Rab10	15	3.13E-04
1420459_at	Ripply3	15	8.55E-04
1435888_at	Egfr	15	2.40E-05
1433920_at	Sema4c	15	1.40E-08
1455825_s_at	Lnx1	15	9.06E-04
1425614_x_at	LOC100045864	15	2.44E-07
1433781_a_at	Cldn12	15	2.11E-03
1453321_at	Fndc1	15	1.55E-05
1420116_s_at	Golph3	15	4.58E-03
1452877_at	2700029M09Rik	15	1.81E-03
1433616_a_at	2310028O11Rik	15	2.29E-04
1452349_x_at	Ifi205	15	8.39E-04
1460709_a_at	Bat5	15	2.20E-04
1418223_at	Sec11a	15	3.06E-03
1417071_s_at	Cyp4v3	15	9.05E-03
1416479_a_at	Tmem14c	15	4.25E-04
1455039_a_at	Sin3b	15	5.49E-03

1455928_x_at	Lztr1	15	6.46E-04
1417141_at	Igtp	15	2.60E-04
1428094_at	Lamp2	15	1.94E-03
1434624_x_at	Rps9	15	1.04E-06
1429328_at	Nsfl1c	15	4.91E-03
1424782_at	Tmem77	15	1.81E-03
1417054_a_at	0610009D07Rik	15	4.50E-03
1435122_x_at	Dnmt1	15	3.91E-04
1425528_at	Prrx1	15	4.21E-04
1419545_a_at	Atp6v1c1	15	3.90E-03
1434423_at	Gulp1	15	1.88E-06
1426355_a_at	6330578E17Rik	15	3.85E-03
1451385_at	2310056P07Rik	15	1.24E-03
1453029_s_at	Zfp650	15	6.69E-03
1450919_at	Mpp1	15	3.58E-04
1422823_at	Eps8	15	9.01E-03
1423772_x_at	Slc25a5	15	1.82E-04
1449906_at	Selp	15	4.28E-07
1440816_x_at	Ddx1	15	3.05E-04
1423346_at	Degs1	15	6.14E-03
1426808_at	Lgals3	15	7.19E-04
1433866_x_at	Prdx1	15	4.13E-08
1458659_at	Plac9	15	1.73E-07
1434796_at	Vamp4	15	1.32E-03
1460660_x_at	Rer1	15	4.03E-03
1452016_at	Alox5ap	15	9.36E-04
1422906_at	Abcg2	15	1.46E-03
1448416_at	Mgp	15	4.93E-04
1423754_at	Ifitm3	15	3.25E-03
1427564_at	Diap2	15	5.86E-03
1434648_a_at	Ccm2	15	9.04E-03
1448484_at	Amd1	15	3.68E-03
1452207_at	Cited2	14	4.05E-04
1433806_x_at	Calr	14	1.40E-04
1434892_x_at	Rbbp4	14	4.18E-03
1418699_s_at	Fech	14	1.03E-04
1417124_at	Dstn	14	1.43E-03
1450642_at	3110001I20Rik	14	1.10E-04
1448206_at	Psma2	14	2.52E-03
1450724_at	Drctnnb1a	14	3.47E-03
1460547_a_at	Hnrpk	14	5.91E-03
1428083_at	2310043N10Rik	14	1.01E-03
1456730_x_at	Actl6a	14	9.43E-06
1418591_at	Dnaja4	14	3.76E-06
1450907_at	Spcs2	14	5.49E-03
1424106_at	1200003C05Rik	14	7.06E-03
1416054_at	Rps5	14	2.20E-03
1436431_at	1700025G04Rik	14	3.72E-05

1434141_at	Gucy1a3	14	2.17E-05
1416509_at	Tm9sf3	14	1.95E-05
1423176_at	Tob1	14	2.46E-05
1426789_s_at	Ssrp1	14	4.91E-05
1450896_at	Arhgap5	14	6.64E-07
1455206_at	C130006E23	14	4.45E-03
1417842_at	Caml	14	4.17E-04
1450941_at	Sdcbp	14	4.89E-08
1424594_at	Lgals7	14	2.25E-04
1429476_s_at	Dnaja2	14	5.12E-03
1419595_a_at	Ggh	14	5.91E-03
1416488_at	Ccng2	14	1.06E-04
1434580_at	Enpp4	14	5.59E-04
1426999_at	Zc3h14	14	2.83E-04
1425486_s_at	Mtmr6	14	2.78E-04
1428847_a_at	Macf1	14	6.79E-06
1423332_at	Sdcbp	14	2.05E-04
1428369_s_at	Arhgap21	14	7.67E-04
1448363_at	Yap1	14	2.32E-04
1425028_a_at	Tpm2	14	2.48E-03
1424008_a_at	Rbpms2	14	6.09E-07
1451567_a_at	Ifi203	14	5.54E-03
1455788_x_at	Poldip3	14	5.31E-05
1433741_at	Cd38	14	1.37E-03
1454961_at	Synj1	14	2.81E-03
1418134_at	Slc25a46	14	4.41E-03
1445684_s_at	Hdac2	14	4.70E-03
1417157_at	Actr10	14	3.50E-03
1425436_x_at	Klra3	14	4.91E-03
1438487_s_at	Zzz3	14	9.08E-05
1426219_at	Scp2	14	6.14E-03
1448461_a_at	Thoc7	14	2.70E-04
1416636_at	Rheb	14	5.79E-03
1423782_at	Mobkl1b	14	1.61E-07
1417573_at	2010311D03Rik	14	3.63E-03
1454074_a_at	Rsrc2	14	3.71E-03
1437193_s_at	Snrpb	14	1.70E-04
1428829_at	6820401H01Rik	14	3.94E-03
1419835_s_at	Plec1	14	1.47E-05
1434823_x_at	Myeov2	14	4.35E-03
1415897_a_at	Mgst1	14	9.25E-03
1434301_at	D330050I23Rik	14	2.15E-05
1436874_x_at	Slc25a5	14	9.56E-04
1437450_x_at	2700060E02Rik	14	8.57E-03
1424628_a_at	1500032D16Rik	14	2.29E-03
1441906_x_at	Syap1	14	5.54E-06
1451310_a_at	Ctsl	14	2.12E-03
1415741_at	Tmem165	14	5.82E-03

1457404_at	Nfkbiz	14	9.43E-04
1449505_at	Kpna1	14	8.19E-04
1455534_s_at	Osbpl11	13	7.68E-03
1454849_x_at	Clu	13	1.08E-03
1448993_at	Atg3	13	7.53E-04
1434132_at	E430025E21Rik	13	6.24E-03
1416478_a_at	Mdh2	13	1.55E-03
1422529_s_at	Casq2	13	1.84E-07
1452833_at	Rapgef2	13	7.85E-03
1419554_at	Cd47	13	2.46E-05
1451049_at	Bcap31	13	3.85E-03
1415751_at	Hp1bp3	13	6.99E-04
1435811_a_at	Unc50	13	1.50E-03
1417540_at	Elf1	13	1.34E-03
1454916_s_at	Arfip1	13	5.18E-03
1416971_at	Cox7a2	13	2.56E-04
1417818_at	Wwtr1	13	1.78E-04
1425616_a_at	Ccdc23	13	3.46E-04
1448822_at	Psmb6	13	1.56E-03
1422568_at	Ndel1	13	1.63E-03
1434637_x_at	Sin3b	13	1.99E-03
1417718_at	Eif3g	13	2.48E-03
1425458_a_at	Grb10	13	4.74E-04
1447234_s_at	Snx6	13	2.62E-03
1448697_s_at	Rpl36al	13	8.50E-03
1420514_at	Tmem47	13	3.18E-03
1416666_at	Serpine2	13	3.81E-03
1439401_x_at	Ppp2r5e	13	3.45E-03
1434283_at	LOC100044968	13	9.94E-03
1434896_at	Zfp422-rs1	13	9.40E-05
1434403_at	Spred2	13	6.22E-05
1415906_at	Tmsb4x	13	3.68E-06
1417684_at	Thumpd3	13	2.92E-03
1451075_s_at	Ctdsp2	13	6.22E-04
1415700_a_at	Ssr3	13	3.22E-05
1448590_at	Col6a1	13	6.43E-05
1448733_at	Bmi1	13	2.00E-03
1452731_x_at	ENSMUSG00000057445	13	5.51E-06
1428259_at	Pxdn	13	5.09E-04
1438420_at	Rbm39	13	3.21E-03
1428179_at	Ndufv2	13	3.74E-04
1436390_a_at	Clcc1	13	2.46E-03
1448967_at	Nipsnap3a	13	4.16E-03
1456170_x_at	Calr	13	1.34E-04
1433561_at	Centb2	13	9.20E-04
1451254_at	Ikbkap	13	9.33E-03

1438133_a_at	Cyr61	13	8.82E-09
1455317_at	Epc2	13	9.37E-03
1439421_x_at	Cbx3	13	1.32E-03
1417010_at	Zfp238	13	4.23E-03
1417490_at	Ctsb	13	5.32E-04
1419047_at	Pcnx	13	6.81E-03
1448213_at	Anxa1	13	3.92E-04
1422452_at	Bag3	13	8.21E-05
1433913_at	C80913	13	5.69E-04
1423804_a_at	Idi1	13	6.98E-03
1416719_a_at	Rps10	13	4.12E-03
1423759_a_at	Tmco1	13	1.52E-03
1421858_at	Adam17	13	3.16E-04
1434541_x_at	Khdrbs1	13	2.68E-04
1416679_at	Abcd3	13	1.57E-03
1425718_a_at	Ivns1abp	13	4.33E-03
1449003_a_at	Vti1b	13	1.95E-03
1424015_at	Rab6ip1	13	1.70E-03
1436980_x_at	Cnot2	13	4.98E-04
1423149_at	Skp1a	13	2.76E-03
1427889_at	Spna2	13	7.87E-04
1460552_at	Ascc3l1	12	1.39E-03
1424443_at	Hdgfrp3	12	1.50E-03
1424324_at	Esco1	12	4.73E-03
1428662_a_at	Hopx	12	7.14E-04
1447522_s_at	Tnks2	12	3.20E-05
1423197_a_at	Smek2	12	7.03E-03
1458345_s_at	Colec11	12	4.73E-04
1447819_x_at	Col8a1	12	1.87E-04
1415889_a_at	Hsp90b1	12	2.29E-04
1435595_at	1810011O10Rik	12	5.02E-03
1428489_at	Zcrb1	12	7.25E-03
1418990_at	Ms4a4d	12	1.52E-03
1428868_a_at	Oaz1	12	1.97E-03
1449322_at	Ptp4a1	12	4.00E-06
1417850_at	Rb1	12	2.53E-03
1418536_at	H2-Q5	12	3.99E-04
1435884_at	Itsn1	12	8.69E-03
1423781_at	Nae1	12	3.28E-03
1417349_at	Pldn	12	3.38E-04
1435805_at	Lin7a	12	1.47E-04
1419639_at	Efnb2	12	1.68E-03
1455688_at	Ddr2	12	8.88E-05
1460367_at	Hbp1	12	8.18E-03
1450664_at	Gabpa	12	5.35E-04
1426799_at	Rab8b	12	2.22E-03
1415758_at	Fryl	12	1.25E-03
1447584_s_at	Myct1	12	1.58E-03

1421594_a_at	Sytl2	12	1.87E-07
1423985_at	Gng5	12	7.06E-04
1444232_at	Prkg1	12	1.14E-05
1417368_s_at	Ndufa2	12	1.74E-03
1416150_a_at	Sfrs3	12	3.10E-05
1457682_at	9030420J04Rik	12	1.76E-09
1416344_at	Lamp2	12	7.35E-03
1454959_s_at	Gnai1	12	2.68E-03
1416164_at	Fbln5	12	6.27E-04
1416156_at	Vcl	12	2.60E-03
1429648_at	Slc35a3	12	6.74E-03
1424365_at	1810037I17Rik	12	4.72E-03
1455827_at	Mbnl2	12	1.74E-03
1448929_at	F13a1	12	6.17E-03
1422495_a_at	Hmgn1	12	7.08E-03
1428374_at	Glce	12	1.17E-04
1434705_at	Ctbp2	12	4.48E-04
1428187_at	Cd47	12	4.17E-05
1423206_s_at	2310003F16Rik	12	2.77E-03
1435580_at	C230081A13Rik	12	3.09E-03
1416405_at	Bgn	12	2.83E-04
1417768_at	Pnpla8	12	9.98E-03
1424104_at	Syf2	12	9.87E-04
1434968_a_at	Actr3	12	2.48E-04
1437615_s_at	Vps37c	12	4.28E-03
1454851_at	Nr2c2	12	3.13E-05
1433507_a_at	Hmgn2	12	4.49E-03
1456609_at	Camk2n1	12	1.72E-05
1422619_at	Ppap2a	12	5.32E-03
1421375_a_at	S100a6	12	1.25E-05
1426285_at	Lama2	12	5.30E-03
1451214_at	Kbtbd2	12	4.28E-04
1450911_at	Ppib	12	1.53E-03
1423747_a_at	Pdk1	12	4.94E-03
1456250_x_at	Tgfbi	12	1.98E-04
1425545_x_at	H2-D1	12	6.80E-04
1437511_x_at	Clcc1	12	3.23E-03
1460332_at	Pln	12	6.22E-11
1420618_at	Cpeb4	12	5.00E-04
1449007_at	Btg3	12	1.49E-03
1423566_a_at	Hsp110	12	1.38E-03
1429637_at	2210419I08Rik	12	5.63E-04
1455627_at	Col8a1	12	3.26E-03
1437360_at	Pcdh19	12	6.80E-03
1435738_x_at	Serf2	12	9.32E-05
1435484_at	Slc5a3	12	4.09E-03
1447933_at	Kif26a	11	2.15E-03
1435413_x_at	2700060E02Rik	11	6.48E-03
1425780_a_at	Tmem167	11	8.88E-03
1416328_a_at	Atp6v0e	11	1.02E-03
1452214_at	Skil	11	7.59E-04
1416072_at	Cd34	11	1.39E-06
1457823_at	Cyr61	11	2.20E-03
1455126_x_at	2310028O11Rik	11	8.42E-03
1427131_s_at	Lrrc58	11	1.85E-04
1441081_a_at	1110038B12Rik	11	5.87E-03
1448305_at	Rab6	11	2.29E-04
1428604_at	2610305D13Rik	11	1.97E-03
1423732_at	Tram1	11	1.13E-03
1434180_at	Fermt2	11	4.61E-03
1450897_at	Arhgap5	11	9.60E-04
1442340_x_at	Cyr61	11	1.54E-03
1437044_a_at	Gba	11	5.63E-03
1460192_at	Osbpl1a	11	9.81E-03
1449335_at	Timp3	11	2.89E-04
1423729_a_at	Rnf181	11	8.96E-04
1437238_x_at	Nmd3	11	3.81E-03
1439452_x_at	Dnpep	11	6.12E-03
1436739_at	Agtr1a	11	1.85E-05
1452866_at	Nars	11	1.93E-03
1431177_a_at	Rpl10a	11	4.02E-03
1433655_at	Rnf141	11	1.19E-03
1434933_at	Rc3h1	11	1.75E-03
1433534_a_at	Cct2	11	2.95E-03
1416282_at	Psmc3	11	6.91E-04
1454997_at	Msrb3	11	2.07E-04
1416904_at	Mbnl1	11	5.28E-04
1433443_a_at	Hmgcs1	11	1.38E-03
1437773_x_at	Ddx17	11	4.76E-03
1439455_x_at	Capza1	11	1.79E-03
1418664_at	Mpdz	11	9.36E-05
1448673_at	Pvrl3	11	5.89E-07
1423651_at	Isca1	11	1.18E-03
1427157_at	Ccdc85a	11	1.51E-07
1438407_at	Dsel	11	2.44E-03
1433914_at	AI747699	11	9.30E-03
1433868_at	Btbd3	11	1.96E-04
1460694_s_at	Svil	11	8.18E-03
1456042_s_at	Cramp1l	11	2.96E-04
1418152_at	Nsbp1	11	5.43E-03
1432158_a_at	Trappc2	11	1.09E-05
1455801_x_at	Tbcd	11	8.42E-03
1447885_x_at	Nedd9	11	9.26E-06
1434976_x_at	Eif4ebp1	11	3.83E-04
1433668_at	Pnrc1	11	5.09E-03

1433718_a_at	LOC100047028	11	3.01E-04
1416912_at	6330407G11Rik	11	4.08E-04
1415759_a_at	Hbxip	11	3.88E-03
1424039_at	Tmem66	11	2.44E-06
1448670_at	Ube2e3	11	1.72E-04
1433935_at	AU020206	11	4.18E-05
1456135_s_at	Pxn	11	5.28E-04
1423126_at	Atp1b3	11	4.95E-04
1456603_at	1500005K14Rik	11	1.35E-03
1421062_s_at	Clta	11	6.81E-05
1415734_at	Rab7	11	6.96E-04
1439830_at	LOC675366	11	9.85E-04
1427884_at	Col3a1	11	1.61E-05
1455522_at	Arhgef15	11	1.72E-06
1434084_at	5730601F06Rik	11	3.08E-05
1447349_s_at	Ep400	11	2.04E-03
1419486_at	Foxc1	11	5.16E-05
1435874_at	Prkab2	11	6.71E-03
1420495_a_at	Vps26a	11	7.05E-03
1448665_at	Dmd	11	3.69E-06
1451508_at	Larp2	11	1.41E-03
1433721_x_at	Rps21	11	6.33E-04
1426829_at	Uimc1	11	3.75E-04
1428471_at	Sorbs1	11	8.23E-03
1460680_a_at	Rpl23	11	1.13E-04
1459987_s_at	Cct3	11	5.32E-03
1423044_at	Prosc	11	6.09E-03
1453586_at	Entpd1	11	6.72E-03
1417460_at	Ifitm2	11	2.11E-04
1415752_at	BC031181	11	1.43E-03
1443787_x_at	Casp14	11	1.24E-03
1452092_at	4631426J05Rik	10	1.89E-05
1460671_at	Gpx1	10	6.31E-04
1424988_at	Mylip	10	3.09E-03
1436586_x_at	Rps14	10	5.92E-04
1460656_a_at	Sft2d1	10	6.70E-03
1422660_at	LOC100043257	10	5.99E-04
1433549_x_at	Rps21	10	6.95E-04
1447862_x_at	Thbs2	10	1.06E-09
1451988_s_at	Chmp4b	10	2.05E-04
1423113_a_at	Ube2d3	10	1.56E-03
1418300_a_at	Mknk2	10	2.03E-04
1451068_s_at	Rps25	10	2.43E-05
1421023_at	Pik3c2a	10	8.90E-03
1416937_at	Gabarap	10	6.43E-05
1427061_at	Rbbp8	10	2.01E-05
1423839_a_at	Btf3	10	6.67E-05
1433976_at	Reep3	10	1.21E-04

1426840_at	Ythdf3	10	1.08E-03
1428982_at	Atad2b	10	4.86E-03
1434358_x_at	Rps21	10	1.06E-04
1426124_a_at	Clk1	10	1.93E-03
1424574_at	Tmed5	10	1.81E-03
1460430_at	Rap2c	10	5.48E-03
1423838_s_at	2400003C14Rik	10	2.64E-04
1437336_x_at	Prickle4	10	3.92E-05
1423031_at	Maea	10	1.10E-05
1417185_at	Ly6a	10	5.71E-03
1425241_a_at	Wsb1	10	4.01E-03
1416766_at	Mosc2	10	1.45E-03
1426486_at	Ubxd2	10	1.37E-03
1416145_at	Dhx15	10	1.30E-04
1428875_at	Golim4	10	7.06E-06
1427991_s_at	Usp45	10	7.28E-03
1451521_x_at	Eif4h	10	3.71E-05
1436883_at	Mbtps2	10	3.74E-04
1419089_at	Timp3	10	1.24E-03
1456587_x_at	2010005J08Rik	10	5.12E-03
1455976_x_at	Dbi	10	1.58E-04
1423195_at	Hiat1	10	1.48E-03
1455072_at	Cep350	10	1.43E-03
1453055_at	Sema6d	10	5.04E-03
1433670_at	Emp2	10	3.29E-05
1452918_at	D19Ertd737e	10	6.48E-03
1452985_at	Uaca	10	2.42E-04
1417451_a_at	Ppia	10	6.19E-03
1436181_at	Ddef2	10	1.98E-05
1417964_at	Ap3d1	10	1.13E-03
1428252_at	Chmp2b	10	1.26E-03
1449679_s_at	Stx5a	10	2.26E-03
1433991_x_at	Dbi	10	7.24E-03
1423958_a_at	Ttc33	10	2.16E-03
1416505_at	Nr4a1	10	5.84E-03
1416442_at	Ier2	10	4.97E-04
1436028_at	Tmem33	10	1.37E-03
1426615_s_at	Ndrg4	10	1.96E-04
1455019_x_at	Ckap4	10	1.57E-03
1428998_at	Phf3	10	9.13E-04
1454963_at	E430028B21Rik	10	1.33E-03
1433702_at	Ermp1	10	7.82E-03
1447877_x_at	Dnmt1	10	1.27E-04
1449889_a_at	Ociad1	10	2.27E-03
1434597_at	Larp5	10	9.65E-03
1418249_at	Crcp	10	4.20E-03
1451206_s_at	Pscdbp	10	4.77E-03

1423133_at	Cwc15	10	4.14E-04
1418817_at	Chmp1b	10	8.90E-03
1456244_x_at	Glrx3	10	1.36E-03
1449408_at	Jam2	10	4.19E-03
1426392_a_at	Actr3	10	1.44E-03
1434895_s_at	Ppp1r13b	10	1.07E-03
1448808_a_at	Nme2	10	4.38E-03
1423349_at	Socs5	10	1.56E-04
1435377_at	2410002O22Rik	10	7.38E-03
1434731_x_at	Prdx1	10	1.65E-05
1449181_at	Fech	10	3.02E-04
1451622_at	Lmbrd1	10	1.38E-03
1448882_at	Tmem93	10	4.07E-03
1415794_a_at	Spin1	10	9.55E-04
1434196_at	Dnaja4	10	8.74E-05
1460545_at	Thrap3	10	6.91E-05
1429579_at	6330407I18Rik	10	1.58E-07
1416543_at	Nfe2l2	10	1.73E-03
1418825_at	Irgm	10	4.92E-06
1419067_a_at	Rabgef1	10	5.66E-04
1450484_a_at	Tyki	10	2.13E-03
1452052_s_at	Eif3j	10	2.14E-03
1416952_at	Atp6v1d	10	9.83E-03
1435349_at	Nrp2	10	6.31E-05
1435777_at	E030018N11Rik	10	1.58E-03
1434383_at	Pja2	10	5.09E-05
1437850_a_at	Cnbp	10	3.90E-06
1423449_a_at	Actn4	10	5.98E-03
1454724_x_at	5730446C15Rik	10	2.06E-03
1433968_a_at	Megf9	10	1.40E-03
1451703_s_at	Aprt	10	7.76E-03
1428423_at	Pcgf3	10	1.36E-03
1424311_at	0710008K08Rik	10	1.37E-03
1426522_at	Hadhb	10	3.52E-03
1434037_s_at	Pcaf	10	5.30E-03
1419914_s_at	LOC100047601	10	8.28E-04
1454887_at	Pak2	10	4.07E-03
1436079_s_at	Vapb	10	1.43E-04
1450372_a_at	Rpl18	10	1.57E-03
1452371_at	Sfrs11	10	1.31E-03
1418067_at	Cfl2	10	4.83E-03
1459749_s_at	Fat4	10	6.10E-05
1451146_at	Zfp386	10	2.83E-04
1434120_a_at	Metap2	9	2.15E-03
1426852_x_at	Nov	9	5.42E-06
1448166_a_at	Psmb1	9	2.06E-03
1423511_at	Asf1a	9	8.28E-03
1441947_x_at	BC033915	9	1.62E-03
1426364_at	Mrrf	9	9.51E-03
1416630_at	Id3	9	5.35E-06
1427269_at	Sfrs11	9	2.71E-04
1418872_at	Abcb1b	9	5.69E-03
1452398_at	Plce1	9	5.75E-06
1417394_at	Klf4	9	6.25E-03
1437628_s_at	Rhoa	9	4.38E-03
1452330_a_at	Mxra8	9	6.01E-07
1423088_at	Tmod3	9	2.37E-04
1448758_at	Nrbf2	9	1.17E-03
1426671_a_at	Rbm39	9	3.15E-03
1420326_s_at	Cramp1l	9	6.08E-03
1426705_s_at	Iars	9	2.14E-05
1453122_at	4921533L14Rik	9	2.11E-03
1423645_a_at	Ddx5	9	2.34E-05
1439456_x_at	Atp6ap2	9	2.59E-04
1456079_x_at	Apex1	9	6.63E-03
1428844_a_at	Bclaf1	9	2.41E-03
1456019_at	Cwf19l2	9	4.17E-03
1426827_at	Ythdc1	9	8.01E-03
1448153_at	Cox5a	9	1.01E-03
1426820_at	2610507B11Rik	9	9.11E-04
1417508_at	Rnf19a	9	9.10E-03
1440151_s_at	Edf1	9	1.85E-04
1426483_at	Prkrir	9	6.52E-03
1426877_a_at	Pbrm1	9	3.84E-03
1452984_at	LOC100044842	9	6.59E-05
1455965_at	Adamts4	9	1.07E-03
1435879_at	Akt3	9	5.20E-04
1433444_at	Hmgcs1	9	3.02E-04
1447776_x_at	Rab6	9	3.05E-03
1428922_at	1200009O22Rik	9	2.50E-09
1428103_at	Adam10	9	4.49E-03
1449283_a_at	Mapk12	9	2.29E-03
1420859_at	Pkia	9	3.21E-06
1436226_at	Tceb1	9	8.99E-05
1424255_at	Supt5h	9	9.27E-04
1416004_at	Ywhah	9	1.89E-03
1417162_at	Tmbim1	9	3.79E-03
1439824_at	Chm	9	7.67E-03
1423567_a_at	Psma7	9	3.39E-03
1448108_at	Serinc1	9	1.84E-03
1433613_at	Pank3	9	3.72E-03
1424918_at	Tbc1d19	9	5.43E-03
1437197_at	Sorbs2	9	3.66E-06
1424902_at	Plxdc1	9	6.87E-06
1434022_at	Zbtb33	9	3.54E-03

1426440_at	Dhrs7	9	1.93E-04
1422457_s_at	Sumo3	9	7.96E-03
1422731_at	Limd1	9	2.63E-04
1415863_at	Eif4g2	9	1.23E-03
1455101_at	AV158170	9	4.33E-07
1434468_at	Otud4	9	5.33E-03
1455145_at	Pcdh19	9	2.91E-04
1453015_at	4933407C03Rik	9	3.34E-03
1424269_a_at	Myl6	9	9.32E-03
1436747_at	1110014K08Rik	9	1.32E-05
1418232_s_at	Lims1	9	1.63E-05
1422561_at	Adamts5	9	9.34E-05
1460346_at	Arsa	9	8.20E-04
1434042_s_at	Mtmr3	9	7.60E-03
1415692_s_at	Canx	9	9.28E-07
1436299_at	Gls	9	5.34E-04
1422620_s_at	Ppap2a	9	9.81E-04
1415908_at	Tspyl1	9	4.89E-04
1421841_at	Fgfr3	9	6.58E-09
1433910_at	Zcchc6	9	9.06E-03
1416506_at	Psma6	9	3.59E-03
1457252_x_at	Pld2	9	2.21E-03
1457094_at	She	9	8.61E-04
1422506_a_at	Cstb	9	3.17E-04
1422848_a_at	Pabpn1	9	2.58E-04
1416468_at	Aldh1a1	9	7.59E-08
1451065_a_at	Ddx39	9	3.39E-03
1425815_a_at	Hmmr	9	1.24E-03
1451247_at	Mfsd1	9	6.86E-03
1456390_at	Ppp2ca	9	3.97E-03
1425183_a_at	Rpl4	9	8.37E-07
1416244_a_at	Cnbp	9	6.03E-04
1418229_s_at	Nfu1	9	4.80E-03
1454890_at	Amot	9	2.38E-03
1416740_at	Col5a1	9	6.02E-04
1451415_at	1810011O10Rik	9	4.80E-04
1437339_s_at	Pcsk5	9	2.42E-03
1455975_x_at	Zfp313	9	3.61E-04
1418652_at	Cxcl9	9	6.07E-04
1434248_at	Prkch	9	3.36E-04
1437437_x_at	Dnpep	9	8.36E-03
1448399_at	Tax1bp1	9	2.41E-03
1448317_at	Tmem128	9	7.03E-03
1448240_at	Mbtps1	9	4.38E-05
1425492_at	Bmpr1a	9	1.65E-04
1448939_at	Usp25	9	1.53E-03
1415778_at	Morf4l2	9	8.03E-06
1426774_at	Parp12	9	7.22E-04

1428546_at	Syncrip	9	6.32E-03
1416808_at	Nid1	9	7.82E-03
1455626_at	Hoxa9	9	1.88E-03
1424071_s_at	BC018507	9	5.95E-03
1448174_at	Cul1	9	1.39E-03
1417251_at	Palmd	9	1.14E-09
1448234_at	Dnajb6	9	7.23E-03
1458308_at	Sbno2	9	5.55E-05
1428861_at	4631422O05Rik	9	8.63E-04
1430133_at	Tbc1d8b	9	8.00E-04
1438790_x_at	Tmem41b	9	2.09E-03
1422593_at	Ap3s1	9	1.91E-04
1421982_a_at	Unc50	9	6.60E-03
1426646_at	9130011J15Rik	9	5.64E-03
1450874_at	Matr3	9	6.38E-04
1435414_s_at	Dctn1	9	4.91E-03
1448152_at	Igf2	9	1.20E-06
1435028_at	Wdr7	8	1.69E-03
1460203_at	Itpr1	8	4.47E-04
1459980_x_at	Rab3a	8	1.29E-04
1434005_at	Rbms1	8	3.02E-03
1452197_at	Smc4	8	8.23E-03
1435253_at	Rab11b	8	4.15E-03
1433784_at	9030612M13Rik	8	9.62E-03
1417644_at	Sspn	8	2.04E-06
1448304_a_at	Rab6	8	3.92E-04
1418016_at	Pum2	8	1.00E-03
1428237_at	2700059D21Rik	8	7.21E-03
1460682_s_at	Ceacam1	8	1.35E-04
1433722_at	Akap13	8	9.23E-07
1418282_x_at	Serpina1b	8	5.37E-10
1450084_s_at	Ivns1abp	8	1.89E-03
1424041_s_at	C1s	8	5.27E-06
1433993_at	4931406P16Rik	8	3.24E-04
1415981_at	Herpud2	8	1.32E-03
1455166_at	Arl5b	8	3.68E-03
1415961_at	Itm2c	8	1.64E-04
1447936_at	2410006H16Rik	8	1.44E-03
1434281_at	Dda1	8	3.20E-03
1452032_at	Prkar1a	8	1.38E-03
1422508_at	Atp6v1a	8	6.55E-03
1451204_at	Scara5	8	1.13E-03
1416979_at	Pomp	8	9.03E-03
1422601_at	Serpinb9	8	5.04E-06
1424573_at	Tmed5	8	2.83E-03
1435058_x_at	Stxbp3a	8	1.54E-03
1418560_at	Pdha1	8	7.13E-03
1415963_at	Hnrph2	8	5.48E-04

1428408_a_at	D12Ertd551e	8	8.84E-04
1443869_at	E430028B21Rik	8	6.67E-04
1422541_at	Ptprm	8	9.17E-04
1429236_at	Galntl2	8	1.03E-05
1455912_x_at	Unc45a	8	5.00E-03
1426977_at	Usp47	8	3.11E-03
1416656_at	Clic1	8	4.98E-04
1435732_x_at	Atp6v0c	8	1.70E-05
1428871_at	LOC100047441	8	2.11E-03
1415879_a_at	Rplp2	8	1.80E-03
1448392_at	LOC100046740	8	2.74E-03
1416161_at	Rad21	8	2.11E-04
1451025_at	Arl1	8	3.37E-03
1423079_a_at	Tomm20	8	5.60E-03
1436999_at	5033414K04Rik	8	4.27E-03
1416973_at	Nhp2l1	8	3.86E-03
1422714_at	Ube2i	8	6.19E-03
1434625_at	4930432O21Rik	8	3.21E-03
1433999_at	Slk	8	5.82E-04
1458550_at	Myo1d	8	3.83E-04
1433605_at	Inpp5a	8	1.06E-03
1456898_at	LOC100045958	8	5.60E-05
1419917_s_at	Tmed7	8	2.81E-03
1424156_at	Rbl1	8	7.36E-03
1428335_a_at	Scfd1	8	2.24E-03
1417751_at	Stk10	8	3.47E-05
1454973_at	Atf7ip	8	6.79E-04
1419493_a_at	Tpd52	8	5.91E-04
1438969_x_at	Dhx30	8	5.45E-03
1419181_at	Zfp326	8	4.86E-03
1423374_at	Ncoa6	8	6.57E-03
1423347_at	Sec23a	8	2.33E-03
1423997_at	Csde1	8	4.71E-03
1435081_at	Sypl	8	1.86E-05
1443721_x_at	Sbno2	8	7.59E-06
1427943_at	Acyp2	8	3.50E-05
1433624_at	5830434P21Rik	8	4.89E-04
1415702_a_at	Ctbp1	8	6.86E-03
1447806_s_at	Srpk3	8	2.93E-08
1424024_at	Mcfd2	8	2.46E-05
1436954_at	Wipf1	8	7.64E-04
1426775_s_at	Scamp1	8	5.49E-03
1431390_a_at	Grinl1a	8	5.11E-04
1452288_at	Mtmr10	8	1.93E-03
1433771_at	5730446C15Rik	8	2.56E-03
1421344_a_at	Jub	8	3.01E-06
1430542_a_at	Slc25a5	8	3.31E-03
1418578_at	Dgka	8	4.38E-07
1423883_at	Acsl1	8	2.41E-03
1452152_at	Clint1	8	4.49E-03
1418063_at	Kera	8	4.75E-04
1424681_a_at	Psma5	8	8.05E-04
1460039_at	Clec1a	8	6.00E-05
1427971_at	Cdc73	8	9.21E-03
1428409_at	Nat13	8	3.42E-03
1453572_a_at	Plp2	8	5.67E-04
1420688_a_at	Sgce	8	1.35E-04
1452795_at	Fcf1	8	8.64E-03
1452587_at	Actr2	8	2.40E-03
1424455_at	Gprasp1	8	3.47E-05
1419922_s_at	Atrnl1	8	8.10E-03
1438560_x_at	Cct4	8	1.56E-03
1427053_at	Abi3bp	8	2.46E-04
1426972_at	Sec24d	8	2.06E-03
1422442_at	Smu1	8	5.34E-03
1416733_at	Mkln1	8	5.31E-03
1452960_at	Scyl3	8	1.30E-04
1455633_at	Zfp647	8	8.00E-04
1452125_at	Thrap3	8	9.61E-03
1423505_at	Tagln	8	1.98E-04
1454701_at	4930503L19Rik	8	2.38E-03
1436113_a_at	St13	8	3.24E-03
1421812_at	Tapbp	8	1.06E-03
1419984_s_at	Zfp644	8	5.10E-04
1452717_at	Slc25a24	7	5.57E-03
1422467_at	Ppt1	7	3.89E-04
1454899_at	Lpp	7	5.18E-04
1454740_at	Mib1	7	4.98E-03
1443486_at	Cog7	7	1.62E-03
1454809_at	Ncoa7	7	1.21E-05
1426778_at	Dag1	7	3.78E-03
1434866_x_at	Cpt1a	7	2.71E-03
1452648_at	Tbrg1	7	2.94E-03
1454641_at	Cggbp1	7	7.86E-03
1423684_at	Hnrpk	7	3.89E-03
1459713_s_at	Tmem16a	7	5.50E-03
1441462_at	Dock4	7	1.27E-03
1454136_a_at	4921524J17Rik	7	5.41E-03
1456480_at	Fry	7	1.00E-06
1455069_x_at	Slc25a4	7	1.65E-03
1437390_x_at	Stx1a	7	3.12E-04
1438081_at	Mcc	7	2.85E-05
1434551_at	Hnrpul2	7	3.44E-05
1454643_at	Ubap2l	7	7.49E-03
1452584_at	1500032L24Rik	7	6.73E-03

1416547_at	Ndufb3	7	1.35E-04
1419468_at	Clec14a	7	2.47E-06
1440339_at	Enpp1	7	7.34E-04
1423677_at	Fkbp9	7	1.13E-07
1428561_at	2610002J23Rik	7	3.69E-03
1452251_at	Nbea	7	3.76E-03
1426994_at	Phlpp	7	9.19E-04
1434478_at	LOC100045753	7	1.97E-03
1424355_a_at	Sin3b	7	6.66E-03
1454736_at	Ankrd57	7	3.17E-04
1425814_a_at	Calcrl	7	2.64E-04
1449109_at	Socs2	7	6.35E-05
1431299_a_at	2310014H01Rik	7	4.15E-04
1423721_at	Tpm1	7	2.49E-03
1450968_at	Uqcrfs1	7	7.70E-03
1426558_x_at	0610010B08Rik	7	1.71E-04
1453651_a_at	Brp44l	7	7.84E-04
1424147_at	Ahsa1	7	2.48E-03
1416452_at	Oat	7	2.86E-03
1433567_at	Gmps	7	1.97E-03
1448340_at	Tmem30a	7	7.91E-05
1428782_a_at	Uqcrc1	7	2.63E-03
1437200_at	Fcho2	7	1.39E-06
1452155_a_at	Ddx17	7	5.79E-03
1435551_at	Fhod3	7	5.36E-05
1460337_at	Sh3kbp1	7	6.60E-03
1428251_at	Smchd1	7	3.11E-03
1423058_at	Capza2	7	7.99E-03
1423350_at	Socs5	7	1.28E-03
1416807_at	Rpl36a	7	8.27E-05
1428853_at	Ptch1	7	7.89E-03
1452898_at	Vps36	7	5.44E-03
1424452_at	Sltm	7	2.12E-03
1452083_a_at	Pja1	7	1.79E-03
1425328_at	BC008163	7	5.88E-05
1450638_at	Pdcd5	7	9.96E-04
1448272_at	Btg2	7	5.15E-05
1451931_x_at	H2-L	7	3.31E-03
1455494_at	Col1a1	7	5.70E-05
1417296_at	Atf1	7	9.84E-03
1426904_s_at	Dnajc10	7	8.56E-04
1417530_a_at	Srp9	7	6.45E-03
1419536_a_at	Rela	7	4.11E-03
1423177_a_at	Abi1	7	6.01E-03
1448769_at	Slc35b1	7	5.63E-03
1428210_s_at	Chuk	7	5.94E-04
1426459_s_at	AW549877	7	9.63E-03
1416939_at	Ppa1	7	7.69E-03
1448258_a_at	Spcs1	7	6.15E-03
1420534_at	Gucy1a3	7	4.87E-11
1454805_at	Wtap	7	2.48E-03
1423694_at	Kctd10	7	4.09E-03
1434972_x_at	Sfrs1	7	5.24E-04
1419041_at	Itfg1	7	9.90E-05
1416404_s_at	Rps16	7	1.45E-04
1426524_at	Gnpda2	7	5.87E-03
1424343_a_at	Eif1a	7	1.56E-03
1418892_at	Rhoj	7	4.57E-04
1436762_x_at	Elp3	7	7.45E-03
1436175_at	Atxn7	7	1.72E-03
1425332_at	Zfp106	7	1.60E-03
1433689_s_at	Rps9	7	7.73E-03
1423976_at	4930453N24Rik	7	4.21E-03
1435220_s_at	Cdc42se2	7	1.56E-03
1436885_a_at	Cherp	7	5.47E-03
1436220_at	Zfp287	7	1.49E-03
1453299_a_at	Pnp	7	3.58E-03
1455159_at	Appl1	7	2.71E-03
1437715_x_at	Apex1	7	4.46E-03
1448664_a_at	Speg	7	1.61E-04
1428808_at	Prickle2	7	8.48E-06
1428502_at	Actr6	7	6.74E-03
1460688_s_at	Unc119b	7	1.51E-03
1418156_at	Kcne4	7	4.64E-04
1433445_x_at	Hmgcs1	7	3.10E-04
1434510_at	Papss2	7	3.57E-03
1451076_s_at	Eif3m	7	7.99E-03
1423321_at	Myadm	7	1.61E-04
1416855_at	Gas1	7	5.44E-05
1427127_x_at	Hspa1b	7	4.14E-03
1416385_a_at	M6pr	7	7.05E-05
1425267_a_at	Pear1	7	7.01E-04
1417791_a_at	Zfml	7	4.50E-03
1428224_at	Hnrpdl	7	3.99E-05
1418066_at	Cfl2	7	8.29E-06
1456213_x_at	Qars	7	1.86E-05
1449196_a_at	Rps27a	7	5.59E-03
1432144_a_at	Rchy1	7	2.06E-03
1439557_s_at	Ldb2	7	1.83E-03
1435440_at	Pdzd8	7	2.25E-04
1438984_x_at	Psmb4	7	2.78E-03
1448505_at	C1d	7	1.78E-03
1419703_at	Col5a3	7	1.10E-03
1435079_at	Sfrs18	7	6.86E-03
1415676_a_at	Psmb5	7	1.79E-03
1426424_at	Sugt1	7	2.46E-04

1423709_s_at	Farsb	7	6.44E-03
1456540_s_at	Mtmr6	7	1.73E-03
1445669_at	Spry4	7	3.25E-03
1448526_at	Kpnb1	7	1.04E-03
1419469_at	Gnb4	7	3.34E-05
1425476_at	Col4a5	7	9.11E-07
1437503_a_at	Scotin	7	1.70E-04
1418507_s_at	Socs2	7	1.20E-03
1422449_s_at	Rcn2	7	3.28E-04
1417766_at	Cyb5b	7	8.40E-04
1426709_a_at	Usp33	7	1.55E-03
1423104_at	Irs1	7	5.52E-09
1449090_a_at	Yes1	7	2.39E-03
1435519_at	Rap1b	7	1.95E-03
1428473_at	Ppp3cb	7	3.00E-03
1454696_at	Gnb1	7	2.82E-03
1435662_at	Nkap	7	9.85E-03
1448762_at	Rad17	7	1.15E-03
1426205_at	Ppp1cb	7	1.41E-03
1422716_a_at	Acp1	7	6.43E-03
1424684_at	Rab5c	7	3.32E-04
1416564_at	Sox7	7	4.64E-05
1424165_a_at	Sharpin	7	3.30E-03
1449885_at	Tmem47	7	6.61E-03
1420809_a_at	1500003O03Rik	7	1.66E-03
1427086_at	Slit3	7	4.56E-04
1459679_s_at	Myo1b	7	1.71E-04
1438117_x_at	Tmem41b	7	3.75E-03
1436908_at	LOC100044052	7	1.38E-03
1428125_at	4921506J03Rik	7	7.75E-03
1428506_at	Atic	7	4.08E-04
1451572_a_at	5230400G24Rik	7	5.82E-04
1426725_s_at	Ets1	7	3.68E-03
1420875_at	Twf1	7	3.97E-04
1415874_at	Spry1	7	5.12E-05
1439398_x_at	Nelf	7	6.49E-04
1415990_at	Vdac2	7	7.68E-04
1434392_at	Usp34	7	7.55E-03
1451109_a_at	Nedd4	7	9.59E-03
1424468_s_at	Phldb1	7	9.71E-03
1417454_at	Cul4b	7	2.65E-03
1434038_at	Dnajc13	7	1.85E-03
1426851_a_at	Nov	7	8.37E-06
1452749_at	Papd1	6	2.16E-03
1434336_s_at	Rcor1	6	2.94E-04
1437338_x_at	Elp3	6	1.56E-03
1449516_a_at	Rgs3	6	1.13E-04
1427878_at	0610010O12Rik	6	5.06E-05

1439549_at	Prrg3	6	4.04E-04
1449142_a_at	Yipf5	6	5.61E-03
1415999_at	Hey1	6	8.18E-05
1439424_x_at	Herpud2	6	2.51E-06
1428657_at	Rreb1	6	7.71E-03
1418071_s_at	Cdyl	6	1.65E-03
1435740_at	ENSMUSG00000072684	6	3.59E-03
1436953_at	Wipf1	6	8.84E-03
1429691_at	Ptprg	6	6.73E-04
1434853_x_at	Mkrn1	6	3.64E-03
1454706_at	Uvrag	6	8.32E-03
1437706_x_at	Rps14	6	4.91E-04
1450637_a_at	Aebp1	6	1.30E-03
1428300_at	Specc1l	6	4.95E-04
1428772_at	Xpot	6	9.93E-03
1436302_at	Slc10a7	6	2.42E-04
1423686_a_at	Prr13	6	6.41E-03
1435148_at	Atp1b2	6	5.05E-05
1418486_at	Vnn1	6	1.92E-06
1416924_at	Bri3	6	1.41E-03
1433611_s_at	Bud31	6	6.87E-03
1453752_at	Rpl17	6	7.80E-03
1449628_s_at	Stard7	6	1.12E-04
1421998_at	Tor3a	6	4.26E-03
1425099_a_at	Arntl	6	2.94E-06
1447931_at	Whsc1l1	6	1.68E-03
1417166_at	Psip1	6	2.88E-04
1417435_at	Large	6	2.87E-03
1416027_at	Pdcd6	6	4.12E-03
1439774_at	Prrx1	6	9.73E-06
1424591_at	5830433M19Rik	6	5.75E-03
1419417_at	Vegfc	6	5.98E-07
1416791_a_at	Nxf1	6	4.90E-04
1417789_at	Ccl11	6	3.52E-03
1433698_a_at	Txnl4a	6	8.93E-03
1415706_at	Copa	6	2.87E-03
1456288_at	Slfn5	6	2.96E-06
1451783_a_at	Kifap3	6	8.86E-04
1428619_at	2310005N03Rik	6	3.11E-03
1426832_at	Ddx26b	6	1.42E-03
1434452_x_at	Eif2a	6	1.10E-03
1426583_at	Atf2	6	1.05E-03
1415712_at	Zranb1	6	1.81E-04
1426248_at	Stk24	6	1.69E-03
1420091_s_at	Morc3	6	7.10E-03
1452953_at	Fam18b	6	7.98E-03
1452850_s_at	Brms1l	6	1.00E-03

1416897_at	Parp9	6	1.14E-04
1426788_a_at	Ssrp1	6	1.05E-03
1455915_at	Galnt4	6	8.47E-03
1428600_at	Nin	6	6.84E-03
1426234_s_at	BC002199	6	7.81E-03
1456175_a_at	Copb2	6	2.97E-03
1428168_at	Mpzl1	6	1.07E-06
1453139_at	Nudt12	6	7.27E-05
1429063_s_at	Kif16b	6	1.05E-03
1451096_at	Ndufs2	6	4.03E-03
1460565_at	Slc41a1	6	2.27E-05
1417793_at	Iigp2	6	1.97E-05
1452791_at	Coq2	6	5.36E-03
1440338_at	E430028B21Rik	6	7.04E-07
1447824_x_at	Hspa5	6	4.93E-04
1429429_s_at	Pcmtd1	6	1.58E-03
1415880_a_at	Lamp1	6	5.06E-05
1418424_at	Tnfaip6	6	9.64E-03
1416018_at	Dr1	6	8.70E-03
1447320_x_at	Rpo1-3	6	2.41E-03
1422697_s_at	Jarid2	6	8.83E-04
1419370_a_at	Mfap1a	6	4.97E-03
1437871_at	Pgm5	6	3.42E-06
1450644_at	Zfp36l1	6	1.07E-04
1441835_x_at	Mtmr11	6	1.27E-04
1454795_at	Cobll1	6	5.04E-03
1416755_at	Dnajb1	6	1.37E-03
1426419_at	Rbm26	6	6.68E-03
1448708_at	Med1	6	6.26E-03
1426830_a_at	Ahcyl1	6	1.97E-03
1455308_at	Tmem16f	6	5.37E-03
1460201_a_at	Rpl24	6	7.47E-03
1429273_at	Bmper	6	4.71E-03
1454705_at	D15Ertd621e	6	6.38E-04
1436871_at	Sfrs7	6	4.71E-03
1455680_at	9630025H16Rik	6	6.36E-04
1428824_at	2310003C23Rik	6	9.38E-03
1452973_at	Ppm1k	6	9.58E-05
1452882_at	Pgrmc2	6	6.29E-03
1455103_at	LOC100046698	6	7.36E-03
1460735_at	Svil	6	3.80E-06
1427874_at	Zfp313	6	2.75E-04
1454872_at	B230308N11Rik	6	2.87E-03
1448176_a_at	Hnrpk	6	4.17E-03
1428197_at	Tspan9	6	4.10E-03
1436859_at	2700007P21Rik	6	3.34E-03
1456070_at	Ptprg	6	3.26E-03
1420011_s_at	Xbp1	6	3.48E-03
1423811_at	Sf3a3	6	7.58E-03
1449465_at	Reln	6	1.68E-09
1428889_at	Alkbh3	6	1.67E-03
1433803_at	Jak1	6	5.67E-03
1450798_at	Tnxb	6	2.59E-04
1415935_at	Smoc2	6	1.09E-04
1448118_a_at	Ctsd	6	4.27E-03
1419834_x_at	Mark1	6	1.59E-04
1416617_at	Acss1	6	6.69E-04
1425582_a_at	Emcn	6	2.82E-05
1435228_at	BC023829	6	5.85E-04
1434108_at	Fbxo11	6	6.94E-03
1434115_at	Cdh13	6	3.10E-04
1426677_at	Flna	6	1.36E-05
1424442_a_at	Pja2	6	2.44E-04
1452232_at	Galnt7	6	2.23E-03
1423986_a_at	Scotin	6	2.58E-03
1452366_at	4732435N03Rik	6	4.57E-03
1416327_at	Ufc1	6	9.36E-04
1417753_at	Pkd2	6	1.07E-03
1420502_at	Sat1	6	6.33E-04
1423919_at	BC023882	6	9.83E-03
1422429_at	Rnf14	6	6.34E-05
1455564_at	Bcr	6	2.37E-06
1424621_at	Krcc1	6	4.13E-03
1426985_s_at	2810485I05Rik	6	6.78E-03
1448578_at	Pafah1b1	6	5.93E-04
1437423_a_at	Sra1	6	8.08E-03
1416841_at	1110059E24Rik	6	8.85E-06
1457256_x_at	Ptch2	6	6.75E-04
1418979_at	Akr1c14	6	7.81E-05
1440609_at	Map4k4	6	1.04E-03
1416119_at	Txn1	6	2.18E-03
1439432_x_at	Morf4l2	6	5.82E-04
1451179_a_at	Qk	6	3.16E-03
1436067_at	Zbtb10	6	8.95E-04
1451220_at	Wdr20a	6	7.36E-03
1426487_a_at	Rbbp6	6	9.36E-03
1454060_a_at	Nras	6	8.61E-03
1429893_at	Il17rd	6	5.78E-10
1454689_at	Srrm1	6	3.64E-05
1429302_at	LOC100046483	6	2.99E-03
1435524_at	2010109N14Rik	6	7.01E-03
1416884_at	Cbx3	6	5.57E-03
1417927_at	Ddx19a	6	3.24E-04
1455003_at	Thap1	6	1.20E-03
1450388_s_at	Twsg1	5	2.63E-06

1424801_at	Enah	5	9.81E-05
1418014_a_at	B4galt1	5	4.90E-03
1418758_a_at	Pscd3	5	2.24E-03
1451201_s_at	Rnh1	5	9.95E-04
1448268_at	Tmed9	5	6.99E-03
1438532_at	Hmcn1	5	1.55E-06
1449125_at	Tnfaip8l1	5	1.49E-03
1426245_s_at	Mapre2	5	2.91E-03
1417418_s_at	Cox6a1	5	7.79E-03
1427912_at	Cbr3	5	4.19E-03
1417126_a_at	Rpl22l1	5	4.66E-04
1434063_at	Zfp664	5	6.89E-05
1437974_a_at	Hk1	5	5.49E-03
1436216_s_at	2610204M08Rik	5	2.21E-03
1447816_x_at	Oxnad1	5	3.40E-03
1435862_at	Son	5	6.58E-03
1434756_at	5430421B17	5	3.07E-05
1423855_x_at	Rpl17	5	7.79E-04
1434671_at	B230337E12Rik	5	1.43E-03
1427113_s_at	Ttl	5	8.89E-03
1417771_a_at	Psmc6	5	8.00E-04
1423739_x_at	Aplp2	5	7.24E-05
1428785_at	Amotl1	5	6.50E-04
1436033_at	BC031353	5	1.05E-03
1428490_at	C1galt1	5	1.12E-03
1442982_at	Ccdc66	5	6.47E-03
1437260_at	Mmrn1	5	7.52E-06
1425979_a_at	Fbf1	5	1.17E-03
1448990_a_at	Myo1b	5	7.25E-03
1417235_at	Ehd3	5	5.02E-08
1448184_at	Fkbp1a	5	5.84E-03
1416288_at	Dnaja1	5	7.77E-03
1452694_at	Ihpk1	5	3.18E-03
1428594_at	Garnl1	5	8.95E-03
1455180_at	AA407270	5	8.22E-03
1451644_a_at	H2-Q6	5	3.72E-05
1417311_at	Crip2	5	9.28E-05
1420142_s_at	Pa2g4	5	8.92E-03
1428696_at	Rftn1	5	7.05E-04
1416369_at	Hiatl1	5	1.47E-03
1456735_x_at	Acpl2	5	3.40E-05
1428368_at	Arhgap21	5	3.26E-03
1416001_a_at	Cotl1	5	4.59E-04
1450102_a_at	Amfr	5	1.68E-05
1422669_at	Ebag9	5	1.98E-03
1438972_x_at	2810410L24Rik	5	4.25E-06
1460708_s_at	Cdc42	5	2.98E-04
1454923_at	AW214353	5	7.05E-03

1416178_a_at	Plekhb1	5	7.45E-05
1437982_x_at	Cox15	5	9.21E-03
1448447_at	Vps28	5	4.49E-03
1422272_at	Phxr4	5	1.32E-03
1456156_at	Lepr	5	5.48E-07
1422742_at	Hivep1	5	1.98E-03
1418843_at	Slc30a4	5	3.85E-03
1449389_at	Tal1	5	3.63E-04
1435522_a_at	2310016E02Rik	5	4.07E-03
1434687_at	C730026J16	5	2.07E-05
1423911_at	Ppp2r5a	5	1.32E-04
1415780_a_at	Armcx2	5	8.21E-06
1417985_at	Nrarp	5	9.24E-03
1439787_at	P2rx7	5	1.26E-03
1436319_at	Sulf1	5	4.84E-06
1439827_at	Adamts12	5	2.45E-06
1460175_at	Rps23	5	9.71E-05
1435032_at	Golgb1	5	8.21E-03
1453032_at	Mobkl3	5	4.07E-03
1435157_at	5830454D03Rik	5	1.09E-03
1425896_a_at	Fbn1	5	1.26E-03
1424042_at	Tmem5	5	5.29E-04
1460510_a_at	Coq10b	5	1.35E-03
1449860_at	Higd1b	5	3.46E-04
1433455_at	LOC100047863	5	7.67E-03
1454838_s_at	AW548124	5	3.70E-05
1418854_at	Birc2	5	3.76E-04
1433748_at	Zdhhc18	5	4.64E-03
1452384_at	Enpp3	5	1.11E-06
1451513_x_at	Serpina1a	5	1.62E-07
1419499_at	Gpam	5	9.21E-03
1425914_a_at	Armcx1	5	1.41E-04
1451114_at	Cmtm6	5	4.40E-03
1436993_x_at	Pfn2	5	6.74E-03
1429856_at	Tspan18	5	3.22E-07
1419498_at	Tmigd1	5	5.58E-05
1455357_x_at	Tomm20	5	6.08E-03
1451728_at	Wdr13	5	1.99E-04
1427174_at	RP23-376N23.4	5	9.21E-04
1440355_at	Kctd12b	5	8.68E-04
1423254_x_at	Rps27l	5	1.25E-05
1439161_at	Saps3	5	7.06E-03
1426670_at	Agrn	5	8.31E-04
1415858_at	Eif3c	5	7.79E-03
1415895_at	Snrpn	5	1.53E-03
1447845_s_at	Vnn1	5	6.17E-07
1438832_x_at	Dhx30	5	6.02E-03

1456482_at	Pik3r3	5	6.74E-03
1449415_at	Chd1l	5	9.52E-03
1424029_at	Tspyl4	5	1.65E-07
1428806_at	Csnk1g1	5	3.09E-03
1452113_a_at	Rab23	5	4.26E-04
1434150_a_at	Mettl7a	5	3.30E-03
1416290_a_at	Psmc4	5	2.10E-05
1417432_a_at	Gnb1	5	9.07E-03
1437489_x_at	Sdhd	5	3.51E-04
1434002_at	Foxn3	5	1.59E-03
1434557_at	Hip1	5	9.56E-03
1437763_at	Dcun1d3	5	7.77E-04
1435485_at	C230096C10Rik	5	2.39E-04
1421870_at	Trim44	5	5.82E-03
1417407_at	Fbxl14	5	2.37E-03
1417492_at	Ctsb	5	8.71E-03
1444596_at	Pax7	5	4.84E-05
1434769_at	Btbd9	5	8.52E-03
1450641_at	Vim	5	4.05E-03
1451168_a_at	Arhgdia	5	3.68E-03
1460681_at	Ceacam1	5	3.36E-05
1433558_at	Dab2ip	5	3.75E-05
1424650_at	Pdia5	5	2.04E-05
1445539_at	Pde7b	5	2.98E-03
1426448_at	Pja1	5	9.13E-03
1450954_at	Yme1l1	5	7.34E-05
1434483_at	Usp12	5	7.82E-03
1457687_at	Bcl2	5	2.54E-03
1448347_a_at	Caprin1	5	5.58E-03
1453771_at	Gulp1	5	7.52E-06
1434188_at	Slc16a12	5	3.03E-04
1424559_at	Rpap2	5	2.42E-08
1452193_a_at	Wasl	5	2.20E-03
1448196_at	Mat2b	5	1.49E-03
1452590_a_at	Plac9	5	9.23E-03
1443524_x_at	Bcl10	5	3.98E-04
1436562_at	Ddx58	5	8.76E-06
1435769_at	Akap9	5	5.48E-03
1453851_a_at	Gadd45g	5	1.26E-03
1419286_s_at	Ift81	5	7.29E-04
1436359_at	Ret	5	7.44E-04
1417901_a_at	Ica1	5	1.06E-04
1456130_at	LOC553091	5	6.68E-06
1424595_at	F11r	5	5.88E-05
1448437_a_at	Gtpbp2	5	7.98E-04
1417271_a_at	Eng	5	1.07E-04
1428549_at	Ccdc3	5	3.38E-08

1422788_at	Slc43a3	5	4.94E-03
1447728_x_at	Hspa9	5	2.72E-03
1434694_at	Lrrc8a	5	4.68E-03
1422912_at	Bmp4	5	2.21E-10
1416308_at	Ugdh	5	6.52E-03
1416771_at	Trappc3	5	4.60E-03
1444139_at	Ddit4l	5	2.14E-05
1448962_at	Myh11	5	1.03E-04
1415679_at	Psenen	5	6.60E-03
1454877_at	Sertad4	5	1.76E-04
1448715_x_at	Ccrn4l	5	3.03E-03
1435880_at	Ankrd50	5	1.23E-03
1439089_at	Zbtb41	5	1.01E-04
1423385_at	Actr8	5	1.64E-03
1454613_at	Dpysl3	5	2.00E-03
1455080_at	Ppp1r16b	5	1.56E-05
1415995_at	Casp6	5	6.60E-04
1460207_s_at	E2f5	5	1.35E-03
1424568_at	Tspan2	5	2.56E-05
1424002_at	Pdcl3	5	1.12E-03
1416121_at	Lox	5	6.90E-03
1460701_a_at	Mrpl52	5	2.84E-03
1427060_at	Mapk3	5	8.33E-05
1450891_at	Srp19	5	1.81E-04
1435195_at	Vash1	5	7.87E-08
1451238_at	1200003C05Rik	5	6.18E-03
1454797_at	Tmem55b	5	1.36E-03
1443906_at	Cd55	5	8.92E-07
1423990_at	Rab28	5	5.93E-03
1417065_at	Egr1	5	8.80E-03
1426390_a_at	Arf1	5	8.67E-04
1450639_at	Slc28a2	5	2.11E-03
1428282_at	Tbce	5	6.37E-03
1426242_at	Polr2a	5	6.32E-04
1424033_at	Sfrs7	5	7.72E-03
1433743_at	Dach1	5	7.97E-04
1437235_x_at	Lpp	5	2.72E-04
1436870_s_at	Afap1l2	5	6.77E-07
1430345_at	5530402H23Rik	5	3.12E-03
1415887_at	Tfg	5	9.46E-03
1425562_s_at	Trnt1	5	7.31E-03
1434609_at	Vprbp	5	6.60E-05
1454990_at	Arid2	5	2.00E-03
1423771_at	Prkcdbp	5	8.36E-07
1450866_a_at	Mrpl17	5	4.25E-03
1452790_x_at	Ndufa3	5	3.33E-03
1417101_at	Hspa2	5	9.77E-03
1454934_at	Ppm1f	5	3.23E-04

1434026_at	Atp8b2	5	4.35E-04
1417202_s_at	Ube1c	5	1.86E-03
1455090_at	Angptl2	5	1.35E-04
1452908_at	Dip2a	5	3.88E-04
1457632_s_at	Meis2	5	2.60E-06
1460350_at	Osbp	5	6.64E-03
1435387_at	Slc2a13	5	1.08E-05
1424231_s_at	Exoc6	5	5.95E-04
1451601_a_at	Spns2	4	7.44E-03
1416337_at	Uqcrb	4	4.92E-03
1450012_x_at	Ywhag	4	2.10E-03
1421733_a_at	Tpst1	4	3.99E-05
1424615_at	Frag1	4	2.84E-03
1438756_at	Ankrd29	4	4.62E-05
1449818_at	Abcb4	4	2.83E-03
1418510_s_at	Fbxo8	4	9.27E-06
1439196_at	Hook3	4	3.92E-06
1457566_at	Zfp677	4	8.10E-03
1441952_x_at	Lynx1	4	1.21E-04
1423080_at	Tomm20	4	9.34E-03
1416420_a_at	Rpl9	4	1.71E-03
1448875_at	Zhx1	4	3.48E-03
1424291_at	Nup93	4	6.74E-04
1416307_at	Ap1m1	4	1.79E-04
1419918_at	Tmed7	4	6.26E-03
1454727_at	Afap1l1	4	4.18E-03
1452813_a_at	Tmem188	4	3.32E-03
1434057_at	Ndufb6	4	1.71E-03
1452148_at	Lrpap1	4	2.99E-03
1416528_at	Sh3bgrl3	4	9.40E-03
1455547_at	Zc3h7b	4	4.52E-05
1427447_a_at	Triobp	4	3.88E-08
1431375_s_at	Parva	4	9.22E-04
1448931_at	F2rl1	4	1.67E-08
1453181_x_at	Plscr1	4	2.17E-03
1427785_x_at	Solh	4	6.98E-03
1417480_at	Fbxo9	4	1.41E-03
1424639_a_at	Hmgcl	4	8.15E-04
1448354_at	G6pdx	4	7.80E-03
1430558_at	Zfp318	4	5.52E-03
1449709_s_at	Ate1	4	2.33E-03
1447364_x_at	Myo1b	4	7.04E-03
1440859_at	Akap6	4	8.45E-06
1433592_at	Calm1	4	2.39E-03
1451896_a_at	Cherp	4	4.39E-05
1428412_at	Tm9sf3	4	2.28E-03
1425560_a_at	S100a16	4	4.61E-05
1429615_at	Zfp91	4	1.67E-03
1426209_at	Strn4	4	1.09E-03
1451330_a_at	Inpp5b	4	1.40E-04
1415671_at	Atp6v0d1	4	6.67E-03
1429430_at	Pcmtd1	4	3.63E-06
1450852_s_at	F2r	4	2.92E-03
1425567_a_at	Anxa5	4	2.31E-03
1441994_at	Pcdhb16	4	6.25E-03
1451069_at	Pim3	4	5.51E-03
1420814_at	Gdi2	4	1.90E-03
1434628_a_at	Rhpn2	4	1.99E-07
1448243_at	Napa	4	1.02E-05
1433480_at	2900010J23Rik	4	9.69E-04
1452276_at	Smarcad1	4	9.32E-04
1425627_x_at	Gstm1	4	3.06E-09
1415869_a_at	Trim28	4	9.37E-03
1417615_a_at	Rpl11	4	3.43E-03
1442062_at	7120426M23Rik	4	8.71E-04
1424346_at	Ppp6c	4	5.92E-03
1452703_at	4631427C17Rik	4	1.12E-03
1423753_at	Bambi	4	2.12E-03
1435612_at	Opcml	4	4.47E-07
1429027_at	0610007N19Rik	4	5.62E-07
1439249_at	LOC100044766	4	7.97E-04
1433530_at	2210411K19Rik	4	7.24E-03
1419435_at	Aox1	4	4.80E-07
1436030_at	LOC100047857	4	8.82E-04
1434124_x_at	2400001E08Rik	4	5.20E-03
1425462_at	Fbxw11	4	1.87E-03
1427120_at	Zfp26	4	7.10E-03
1423135_at	Thy1	4	1.92E-03
1448626_at	Cdk5rap1	4	6.84E-03
1438684_at	Nuak1	4	1.78E-04
1434957_at	Cdon	4	2.55E-08
1428272_at	Eif1b	4	1.23E-03
1433729_x_at	Pmpcb	4	1.51E-03
1456437_x_at	C1r	4	1.60E-03
1433768_at	Palld	4	8.04E-04
1434703_at	Extl3	4	9.46E-03
1443858_at	EG667823	4	1.57E-03
1457776_at	D9Ertd720e	4	3.23E-04
1429058_at	Tmem107	4	1.98E-03
1417714_x_at	Hba-a1	4	7.54E-03
1418338_at	Wdr33	4	9.10E-03
1449729_at	Fgf4	4	4.80E-05
1436405_at	Dock4	4	9.43E-03
1459363_at	Atxn2	4	2.07E-04
1436659_at	Dclk1	4	5.32E-03
1438666_at	Ldlrad3	4	3.10E-04

1438120_x_at	Irak1	4	9.25E-03
1452368_at	Bcr	4	5.70E-03
1460356_at	Esam1	4	2.54E-03
1436899_at	2700019D07Rik	4	6.46E-03
1434071_a_at	Pelo	4	7.29E-04
1456857_at	1500011B03Rik	4	5.53E-04
1418626_a_at	Clu	4	2.59E-07
1452718_at	Ubr5	4	7.37E-04
1451037_at	Ptpn9	4	3.42E-05
1415816_at	Cct7	4	7.59E-03
1443771_x_at	Smad7	4	7.54E-04
1428883_at	Tmem57	4	7.18E-03
1418195_at	Galnt10	4	8.18E-03
1420944_at	Zfp185	4	1.62E-04
1449714_at	5730472N09Rik	4	7.48E-03
1433680_x_at	Siva1	4	5.93E-03
1433942_at	Myo6	4	1.01E-06
1435930_at	Scaper	4	2.07E-05
1416891_at	Numb	4	3.94E-03
1422571_at	Thbs2	4	2.93E-03
1438546_x_at	Slc25a5	4	3.38E-03
1451569_at	Nr2c2	4	7.67E-03
1433588_at	D6Wsu116e	4	1.38E-03
1422567_at	Niban	4	7.49E-03
1436266_x_at	LOC100047028	4	3.17E-04
1437479_x_at	Tbx3	4	1.69E-04
1460234_at	Wdr81	4	2.86E-03
1418616_at	Mafk	4	1.45E-05
1415944_at	Sdc1	4	5.17E-03
1438397_a_at	Rbm39	4	2.49E-03
1415705_at	9130011J15Rik	4	5.48E-03
1428756_at	Aasdhppt	4	1.75E-03
1415806_at	Plat	4	2.51E-04
1425660_at	Btbd3	4	4.31E-04
1452446_a_at	Tmub2	4	9.55E-04
1419659_s_at	Chic2	4	5.76E-03
1453212_at	Zfp383	4	3.00E-08
1422818_at	Nedd9	4	4.02E-03
1425539_a_at	Rtn3	4	3.94E-03
1450691_at	Caskin2	4	1.93E-04
1423352_at	Crispld1	4	1.07E-06
1436946_s_at	Gng5	4	3.12E-03
1418494_at	Ebf2	4	2.67E-03
1435016_at	Trak2	4	2.77E-05
1438114_x_at	Efs	4	2.51E-05
1435793_at	Aph1b	4	3.61E-03
1436795_at	9630058J23Rik	4	3.71E-04
1417937_at	Dact1	4	8.59E-03

1417565_at	Abhd5	4	3.50E-03
1453023_at	Ankhd1	4	6.87E-03
1430500_s_at	Mtx2	4	9.27E-04
1423107_at	Ube2b	4	8.02E-03
1424450_at	Gprc5c	4	6.60E-10
1415754_at	Polr2f	4	1.75E-03
1455254_at	4833420G11Rik	4	6.51E-03
1419403_at	BC017612	4	3.86E-05
1419730_at	4631427C17Rik	4	4.05E-03
1449297_at	Casp12	4	7.36E-06
1416720_at	Sfrs6	4	1.74E-04
1418547_at	Tfpi2	4	7.20E-04
1417408_at	F3	4	4.59E-03
1422889_at	Pcdh18	4	8.88E-05
1447725_at	C030034E14Rik	4	1.27E-05
1424619_at	Sf3b4	4	5.39E-03
1423408_a_at	2500003M10Rik	4	4.21E-03
1438999_a_at	Nfat5	4	1.96E-03
1426940_at	Sidt2	4	5.65E-04
1423395_at	Tsnax	4	7.57E-05
1422640_at	Pcdhb9	4	1.06E-07
1425495_at	Zfp62	4	8.62E-03
1429896_at	5830408B19Rik	4	1.67E-03
1447947_at	Zfyve16	4	8.34E-03
1421022_x_at	Acyp1	4	7.32E-03
1416824_at	B230118H07Rik	4	3.21E-03
1417001_a_at	D4Wsu53e	4	3.94E-03
1452689_at	Zfp512	4	1.07E-03
1456466_x_at	Atxn10	4	5.77E-03
1419272_at	Myd88	4	5.73E-04
1434451_at	ENSMUSG00000074917	4	1.14E-03
1450625_at	Col5a2	4	8.08E-03
1460574_at	Fat4	4	2.12E-07
1427404_x_at	Eno1	4	7.46E-03
1426912_at	Rfwd2	4	2.42E-03
1450950_at	Smc3	4	9.83E-04
1451536_at	Mtfr1	4	3.07E-03
1451971_at	Cul4a	4	1.94E-03
1439505_at	Clic5	4	5.47E-04
1458274_at	Zfp69	4	6.66E-04
1431110_at	Plxdc2	4	1.42E-03
1417107_at	Tpd52l2	4	4.41E-03
1448648_at	9130005N14Rik	4	1.09E-04
1419070_at	Cys1	4	9.00E-06
1447841_x_at	St3gal6	4	2.44E-03
1419457_at	Rgnef	4	1.86E-08

1417535_at	Fbxo25	4	3.98E-03
1427151_at	Qser1	4	8.77E-03
1455278_at	Wdr37	4	7.25E-03
1437594_x_at	Pigt	4	3.82E-06
1417056_at	Psme1	4	6.60E-04
1435693_at	Mall	4	3.18E-03
1435767_at	Scn3b	4	1.14E-04
1424770_at	Cald1	4	3.55E-03
1450418_a_at	Yipf4	4	1.12E-03
1438354_x_at	Cnn3	4	8.72E-04
1424247_at	Erc1	4	9.46E-03
1452632_at	Aak1	4	3.14E-07
1451311_a_at	Adipor1	4	4.48E-03
1419380_at	Zfp423	4	1.96E-08
1452847_at	2410008K03Rik	4	3.97E-05
1452856_at	Crebzf	4	2.16E-03
1452993_at	5430416O09Rik	4	8.89E-07
1455617_at	Lmbrd1	4	9.79E-03
1448989_a_at	Myo1b	4	4.54E-03
1433857_at	Fat1	4	4.46E-03
1460344_at	2310033F14Rik	4	1.49E-03
1415876_a_at	Rps26	4	5.56E-03
1440156_s_at	AI851523	4	1.77E-04
1419376_at	1110018M03Rik	4	7.12E-05
1452072_at	Myct1	4	5.78E-06
1433782_at	Cldn12	4	2.81E-04
1456629_at	Ankrd47	4	9.03E-06
1424602_s_at	Xrcc4	4	2.17E-03
1433708_at	Srp68	4	2.66E-03
1436514_at	Gpc4	4	6.97E-04
1451440_at	Chodl	4	8.70E-06
1451747_a_at	Atg12	4	9.71E-03
1418092_s_at	Trip10	4	9.72E-04
1424567_at	Tspan2	4	1.20E-05
1434477_at	Heca	4	1.52E-03
1433755_at	Mier1	4	2.50E-03
1423399_a_at	Yaf2	4	4.11E-03
1448933_at	Pcdhb17	4	6.51E-03
1415769_at	Itch	3	3.48E-03
1425340_a_at	Ptpra	3	2.36E-03
1437262_x_at	Bcas2	3	8.71E-03
1434959_at	Dhh	3	8.28E-04
1416458_at	Arf2	3	3.75E-03
1424236_at	Tbc1d10b	3	4.19E-03
1418219_at	Il15	3	7.58E-03
1427928_s_at	Pigu	3	1.76E-07
1454965_at	LOC634842	3	8.61E-04
1456018_at	Brd9	3	1.31E-03

1455776_x_at	Bola2	3	6.53E-04
1435878_at	Stk38l	3	4.00E-03
1448302_at	Kctd20	3	9.46E-03
1424154_a_at	Isca2	3	4.30E-03
1452922_at	Ppp1r3d	3	4.23E-04
1426212_s_at	Tmem161a	3	6.43E-03
1432417_a_at	Tspan2	3	7.49E-04
1448029_at	Tbx3	3	2.08E-04
1427235_at	Utx	3	1.50E-03
1433752_s_at	D030016E14Rik	3	5.53E-03
1441902_x_at	Slc29a4	3	7.01E-09
1418007_at	1810007M14Rik	3	4.95E-03
1416982_at	Foxo1	3	1.87E-03
1448325_at	Myd116	3	4.53E-03
1416469_at	Luzp1	3	2.57E-03
1437152_at	Mex3b	3	9.47E-05
1417616_at	St6galnac2	3	3.92E-05
1428681_at	Gm608	3	5.28E-04
1423532_at	Rnf44	3	3.44E-03
1431079_at	C1qtnf2	3	5.60E-04
1447160_at	Nono	3	4.62E-04
1426825_at	Fmnl3	3	1.54E-04
1439680_at	Tnfsf10	3	2.33E-04
1452332_at	Ccdc85a	3	2.55E-03
1422629_s_at	Shroom3	3	3.36E-03
1423362_at	Sort1	3	1.28E-03
1439187_at	Vps13d	3	9.89E-03
1416534_at	Dpf2	3	9.58E-03
1451634_at	2810051F02Rik	3	2.93E-11
1452304_a_at	Arhgef5	3	1.59E-03
1451821_a_at	Sp100	3	4.02E-04
1451683_x_at	H2-D1	3	3.98E-04
1416084_at	Zfand5	3	2.02E-03
1435370_a_at	Ces3	3	3.13E-03
1440237_at	Ercc4	3	9.90E-05
1434233_at	2610030H06Rik	3	2.12E-03
1416983_s_at	Foxo1	3	2.99E-04
1433623_at	Zfp367	3	5.13E-03
1428401_at	Zcchc3	3	1.88E-03
1460248_at	Cpxm2	3	3.21E-05
1448655_at	Lrp1	3	1.04E-03
1455215_at	C530028O21Rik	3	3.44E-06
1436315_at	Myst3	3	2.78E-04
1438545_at	Slc25a5	3	3.74E-03
1435545_at	BC032203	3	7.55E-03
1439964_at	Tmem170	3	4.98E-04

1426388_s_at	Ryk	3	7.08E-04
1438648_x_at	1190003M12Rik	3	1.30E-05
1456041_at	Snx16	3	8.30E-03
1436062_at	Arcn1	3	8.52E-03
1430030_at	5330426P16Rik	3	1.50E-03
1425626_at	Gstm1	3	1.39E-11
1421507_at	Olfr78	3	2.20E-07
1425029_a_at	Mboat2	3	1.17E-03
1423259_at	Id4	3	8.17E-04
1448902_at	Ttc23	3	1.15E-03
1435344_at	1110029I05Rik	3	1.34E-04
1419078_at	Nin	3	2.61E-03
1459911_at	Cdr2l	3	5.14E-03
1448190_at	Mrpl33	3	4.70E-03
1455188_at	Ephb1	3	1.11E-04
1448787_at	Moap1	3	5.22E-03
1435463_s_at	Myo1d	3	3.46E-03
1429166_s_at	Clmn	3	2.91E-03
1452242_at	Cep55	3	9.47E-04
1424239_at	2310066E14Rik	3	3.57E-03
1436029_at	Bicc1	3	7.34E-03
1439500_at	Scrn1	3	3.07E-05
1428342_at	Rcor3	3	7.38E-04
1451593_at	H2-D1	3	8.49E-10
1440226_at	Zfp760	3	1.53E-04
1448398_s_at	Rpl22	3	9.06E-06
1448487_at	Lrrfip1	3	3.97E-04
1436386_x_at	OTTMUSG00000010671	3	4.53E-04
1444076_at	Zfp81	3	1.47E-04
1455018_at	Lmtk2	3	3.04E-03
1428620_at	Ensa	3	2.70E-05
1429240_at	Stard4	3	1.33E-04
1437196_x_at	Rps16	3	5.53E-03
1416705_at	Rpe	3	3.44E-03
1449959_x_at	Lce1h	3	3.09E-04
1454731_at	Myo10	3	3.54E-03
1426997_at	Thra	3	1.68E-05
1422850_at	Pabpn1	3	9.19E-03
1460249_at	Lnx2	3	1.65E-05
1416387_at	Pip4k2c	3	7.02E-04
1449188_at	Midn	3	5.14E-04
1429943_at	Ctbs	3	5.77E-06
1435196_at	Ntrk2	3	7.08E-06
1454611_a_at	Calm1	3	3.60E-03
1434305_at	U2af1l4	3	1.25E-04
1423865_at	Slc44a1	3	1.87E-04
1418205_at	Thsd1	3	2.72E-03

1448589_at	Ndufb5	3	6.33E-03
1424596_s_at	Lmcd1	3	4.32E-05
1419467_at	Clec14a	3	2.10E-03
1428337_at	1810034K20Rik	3	2.28E-04
1423151_at	Dnajb11	3	7.94E-03
1426937_at	6330406I15Rik	3	5.37E-03
1435348_at	D930009K15Rik	3	7.15E-03
1418228_at	Nfu1	3	6.53E-04
1459601_at	Snf1lk	3	3.29E-03
1420752_at	Dtx3	3	2.11E-06
1419062_at	Epb4.1l3	3	1.89E-04
1428134_at	Coq9	3	2.17E-05
1416968_a_at	Hsd3b7	3	1.17E-03
1436498_at	Arih1	3	8.11E-03
1418515_at	Mtf2	3	2.01E-03
1416398_at	Mesdc1	3	4.65E-03
1433712_at	AW555464	3	7.42E-05
1417013_at	Hspb8	3	1.33E-03
1439461_x_at	Nsmce4a	3	2.14E-04
1419371_s_at	Gosr2	3	6.45E-03
1455142_at	Socs4	3	4.03E-04
1456470_x_at	Tubb2c	3	3.86E-08
1417272_at	9130005N14Rik	3	9.46E-04
1431777_a_at	Hmgn3	3	1.27E-04
1433639_at	5730593F17Rik	3	2.20E-07
1423103_at	Rfx5	3	7.48E-03
1453009_at	Cpm	3	8.14E-03
1438442_at	AI450236	3	9.56E-04
1452733_at	Pank2	3	2.54E-03
1426803_at	Rbm26	3	5.77E-07
1449226_at	Hic1	3	6.60E-05
1454815_at	Sertad2	3	9.76E-03
1415738_at	Txndc12	3	5.87E-04
1460399_at	Ccdc117	3	1.51E-04
1428367_at	Ndst1	3	4.24E-03
1453129_a_at	Rgs12	3	1.27E-05
1454856_x_at	Rpl35	3	6.51E-03
1435568_at	AK129128	3	7.04E-03
1417562_at	Eif4ebp1	3	8.77E-03
1435339_at	Kctd15	3	4.52E-03
1434081_at	LOC100047920	3	2.57E-03
1448155_at	Pdcd6ip	3	3.54E-03
1439068_at	Erap1	3	8.47E-03
1418651_at	Spata6	3	1.02E-03
1421088_at	Gpc4	3	2.29E-03
1424099_at	2310016C16Rik	3	6.29E-04
1460580_at	Pcnx	3	2.39E-04

1455967_at	Sorbs1	3	4.10E-03
1438078_at	Dgke	3	8.88E-15
1439272_at	Lcorl	3	6.74E-03
1431745_a_at	Zc3h14	3	4.82E-05
1423155_at	Sri	3	9.85E-03
1433583_at	Zfp365	3	1.92E-03
1438925_x_at	Atp6v0c	3	1.79E-04
1434840_at	Hrb	3	1.13E-04
1435603_at	Sned1	3	6.39E-06
1428896_at	Pdgfrl	3	2.69E-03
1449008_at	Tulp3	3	8.54E-03
1444409_at	Rph3al	3	8.25E-08
1451003_at	Map3k7ip2	3	3.47E-03
1426982_at	Flywch1	3	5.76E-06
1450618_a_at	Sprr2a	3	8.13E-07
1435910_at	Fads3	3	3.61E-04
1416598_at	Glis2	3	1.37E-06
1448960_at	Cxxc5	3	3.11E-05
1440860_at	Nbea	3	1.50E-03
1437710_x_at	1700021P22Rik	3	4.29E-03
1437563_at	Phf20l1	3	1.65E-04
1440021_at	Gpr20	3	2.81E-03
1449371_at	Hars2	3	9.44E-04
1437512_x_at	Ebna1bp2	3	3.48E-03
1429131_at	Ube2v2	3	1.76E-04
1451261_s_at	Stap2	3	7.96E-03
1431340_a_at	2310002J21Rik	3	3.87E-03
1435243_at	Zfp746	3	2.98E-03
1449988_at	Gimap1	3	4.61E-03
1418399_at	Kctd9	3	3.91E-03
1449343_s_at	Sin3a	3	1.60E-09
1456789_at	Zfp462	3	3.24E-03
1434267_at	Nek1	3	2.05E-04
1434765_at	Ep300	3	4.68E-03
1455247_at	Amotl1	3	2.78E-05
1433936_at	0610010E21Rik	3	8.02E-03
1436426_at	Cc2d2a	3	3.02E-03
1425809_at	Fabp4	3	2.29E-03
1460196_at	Cbr1	3	3.95E-03
1419045_at	Slc25a23	3	1.10E-04
1435255_at	Plxnb1	3	4.42E-05
1434058_at	Mtmr12	3	8.76E-03
1424133_at	Tmem98	3	1.70E-04
1426766_at	6330403K07Rik	3	1.76E-12
1451041_at	Rock2	3	1.46E-03
1428719_at	2010309G21Rik	3	3.31E-04
1417455_at	Tgfb3	3	6.90E-05
1455538_at	6330403M23Rik	3	4.02E-03

1448839_at	Ankrd47	3	8.06E-03
1434021_at	C230096C10Rik	3	8.11E-03
1417438_at	Rdh14	3	1.82E-04
1438421_at	Pvrl1	3	7.70E-04
1451985_at	Lrrk1	3	9.79E-03
1435559_at	Myo6	3	4.66E-03
1420416_at	Sema3a	3	8.72E-03
1434786_at	Ppp1r12b	3	5.78E-03
1435567_at	Phka1	3	6.14E-03
1439273_at	Ripk1	3	4.60E-03
1450431_a_at	Nedd4	3	7.89E-03
1439016_x_at	Sprr2a	3	4.88E-04
1434269_at	AA536717	3	7.37E-03
1426782_at	Gpr125	3	1.18E-04
1424635_at	Eef1a1	3	1.82E-03
1434105_at	Epm2aip1	3	3.00E-04
1419302_at	Heyl	3	4.51E-06
1455817_x_at	Zxdb	3	1.01E-04
1426733_at	Itpk1	3	3.95E-03
1437426_at	Wac	3	1.50E-03
1435998_at	Ccnb1ip1	3	5.12E-03
1417848_at	Zfp704	3	5.99E-05
1435470_at	LOC547150	3	3.81E-03
1452387_a_at	Amotl2	3	1.00E-04
1449550_at	Myo1c	3	6.84E-03
1451490_at	Lyplal1	3	5.16E-04
1448433_a_at	Pcolce	3	2.75E-04
1436011_at	Elmo2	3	7.94E-03
1449070_x_at	Apcdd1	3	1.00E-05
1448116_at	Uba1	3	5.88E-04
1429018_at	3830408D24Rik	3	7.76E-03
1455055_at	4930562D19Rik	3	8.23E-03
1420855_at	Eln	3	1.59E-05
1437576_at	2810427A07Rik	3	7.94E-03
1454604_s_at	Tspan12	3	2.68E-03
1428121_at	2610528K11Rik	3	8.45E-03
1424400_a_at	Aldh1l1	3	6.56E-03
1416289_at	Plod1	3	2.34E-03
1422216_at	Mid2	3	2.49E-03
1433736_at	Hcfc1	3	2.19E-03
1456146_at	LOC100047530	3	1.25E-06
1456521_at	Nr5a2	3	3.14E-03
1426801_at	Sept8	3	4.52E-03
1455901_at	Chpt1	3	1.27E-05
1424762_at	C1qtnf5	3	1.76E-08
1429764_at	1500005K14Rik	3	8.04E-03
1448222_x_at	Cox8a	3	6.05E-03

1448949_at	Car4	3	1.50E-03
1435882_at	Ubap2l	3	1.93E-03
1433525_at	Ednra	3	5.82E-03
1455666_at	Zfp595	3	9.38E-03
1426981_at	Pcsk6	3	4.23E-04
1440736_at	AI131651	3	8.90E-05
1454717_at	Ankrd27	3	3.32E-03
1440838_at	AI852064	3	1.90E-04
1458353_at	Nwd1	3	2.74E-04
1423389_at	Smad7	3	7.60E-03
1424671_at	Plekhf1	3	4.05E-03
1418714_at	Dusp8	3	3.21E-03
1428867_at	Exoc3l2	3	7.91E-04
1427902_at	Srrm2	3	2.81E-04
1442800_x_at	A830059I20Rik	3	1.22E-03
1460615_at	Nt5dc1	3	7.58E-03
1417568_at	Ncald	3	3.14E-03
1434139_at	Parp11	3	2.54E-04
1437424_at	Syde2	3	1.66E-04
1424119_at	Prkab1	3	9.85E-03
1453025_at	Macrod2	3	5.68E-05
1422465_a_at	Nxn	3	1.16E-03
1425977_a_at	Slk	3	4.41E-03
1434956_at	Rnf170	3	3.85E-03
1436068_at	Zbtb10	3	8.16E-03
1435682_at	Lars2	3	1.86E-04
1428527_at	Snx7	3	8.77E-03
1435492_at	Socs6	3	2.47E-03
1429359_s_at	Rbpms	3	1.48E-04
1435781_at	Cand1	3	6.85E-03
1428357_at	2610019F03Rik	3	6.38E-03
1425482_s_at	Ankmy2	3	2.65E-03
1434691_at	Sfrs2ip	3	1.48E-03
1415968_a_at	Kap	3	9.24E-03
1436924_x_at	Ero1l	3	6.54E-03
1427356_at	2310031A18Rik	3	6.21E-05
1425095_at	BC002059	3	5.52E-03
1456027_at	Rbm41	3	5.73E-03
1424968_at	2210023G05Rik	3	2.70E-04
1449023_a_at	Ezh1	3	8.25E-04
1416354_at	Rbmx	3	5.05E-03
1423472_at	Sept2	3	3.32E-03
1419207_at	Zfp37	3	5.48E-05
1437930_at	Glt25d2	3	5.82E-07
1427568_a_at	Ift80	3	5.31E-03
1427349_x_at	2810021G02Rik	2	9.46E-03
1449154_at	Col11a1	2	8.71E-03
1438685_at	Zmym6	2	3.66E-03
1436547_at	Dgke	2	1.96E-06
1418485_at	Slc4a3	2	1.50E-04
1443377_at	Adam1a	2	9.79E-03
1448755_at	Col15a1	2	3.20E-03
1416411_at	Gstm2	2	3.37E-03
1439447_x_at	Rpl37a	2	8.62E-05
1417273_at	Pdk4	2	2.40E-04
1416220_at	Spcs1	2	3.01E-03
1417567_at	Ctnnbip1	2	8.06E-03
1433626_at	Plscr4	2	1.58E-04
1455189_at	Trim33	2	2.50E-03
1417581_at	Dhodh	2	7.77E-03
1423701_at	Coasy	2	4.97E-03
1420429_at	Pcdhb3	2	6.09E-04
1443785_x_at	Pdlim7	2	5.59E-03
1419743_s_at	Carm1	2	3.83E-03
1450535_at	Krtap12-1	2	2.57E-04
1437834_s_at	Pacsin3	2	4.75E-03
1438760_x_at	Adam15	2	1.67E-03
1424415_s_at	Spon1	2	5.60E-03
1429022_at	Adcyap1r1	2	5.18E-05
1428573_at	Chn2	2	3.37E-03
1438349_at	BC043476	2	8.82E-05
1448693_at	Gltpd1	2	7.70E-03
1429841_at	Megf10	2	4.85E-04
1452223_s_at	Gcap14	2	6.45E-03
1438766_at	Pnrc2	2	1.71E-03
1450144_at	Pla2r1	2	4.27E-03
1424240_at	Arfip2	2	9.75E-03
1449362_a_at	Mink1	2	5.38E-03
1416513_at	Lamb2	2	8.24E-03
1458930_at	A4gnt	2	7.69E-03
1451046_at	Zfpm1	2	4.12E-04
1420903_at	St6galnac3	2	7.20E-04
1438708_x_at	Ywhab	2	3.07E-03
1451187_at	0610037P05Rik	2	5.14E-03
1452440_at	Tnfsf12	2	6.31E-05
1426063_a_at	Gem	2	4.50E-07
1449213_at	Lage3	2	2.01E-03
1439618_at	Pde10a	2	4.41E-04
1424525_at	Grp	2	3.59E-03
1450066_at	Ubr1	2	1.86E-03
1417199_at	Tmem183a	2	7.91E-03
1432235_at	Epsti1	2	8.53E-03
1443790_x_at	4930414L22Rik	2	1.63E-07
1450920_at	Ccnb2	2	8.89E-03
1460008_x_at	Ero1l	2	4.64E-03
1435991_at	Nr3c2	2	7.41E-03

1449435_at	B4galt3	2	4.74E-03
1457671_at	9330120H11Rik	2	7.31E-05
1451550_at	Ephb3	2	9.42E-04
1455369_at	Apba1	2	1.52E-03
1449804_at	Pnmt	2	9.82E-05
1416621_at	Llgl1	2	1.12E-03
1437161_x_at	Rbpms	2	8.40E-03
1455040_s_at	1110062M06Rik	2	9.05E-04
1433760_a_at	Rhbdd3	2	2.58E-03
1435823_x_at	Egfl7	2	1.05E-03
1460584_at	Hisppd2a	2	9.59E-03
1450935_at	Ercc5	2	6.28E-03
1438667_at	5730410E15Rik	2	1.99E-03
1448154_at	Ndrg2	2	2.47E-06
1429469_at	A930013F10Rik	2	8.65E-03
1433777_at	L3mbtl2	2	1.00E-02
1455420_at	Rad23b	2	5.26E-03
1429281_at	2610008E11Rik	2	2.08E-03
1438843_x_at	Mtch2	2	1.23E-03
1434126_at	4930402H24Rik	2	6.01E-05
1456050_at	C80998	2	1.74E-04
1441911_x_at	Gart	2	1.11E-03
1428693_at	2610044O15Rik	2	6.32E-05
1439849_at	OTTMUSG00000008561	2	9.54E-03
1423353_at	Crispld1	2	2.81E-04
1458358_at	Pank2	2	3.91E-03
1440381_at	2410085M17Rik	2	6.33E-04
1416255_at	Gja4	2	6.49E-04
1420930_s_at	Ctnnal1	2	8.07E-04
1429581_at	Acad9	2	2.77E-03
1459807_x_at	4933406E20Rik	2	2.57E-03
1417952_at	Cyp2j6	2	2.09E-03
1418791_at	Sh3gl2	2	4.93E-06
1448106_at	Necap1	2	5.75E-04
1429869_at	1110020C03Rik	2	3.26E-12
1435561_at	Erf	2	6.77E-03
1447540_at	Tigd3	2	6.79E-03
1439665_at	Gpr23	2	3.72E-03
1433433_at	Myst2	2	5.58E-05
1441114_at	9330156P08Rik	2	5.20E-03
1440452_at	Drp2	2	2.83E-03
1418428_at	Kif5b	2	2.90E-03
1457342_at	Ikzf4	2	1.08E-03
1429106_at	4921509J17Rik	2	4.24E-03
1451070_at	Gdi1	2	1.47E-03
1423611_at	Alpl	2	3.31E-03
1450424_a_at	Il18bp	2	1.54E-03

1460601_at	Myrip	2	5.83E-04
1440803_x_at	Tacr3	2	3.44E-05
1449583_at	Pcdhb20	2	6.65E-03
1432517_a_at	Nnmt	2	8.49E-04
1429235_at	Galntl2	2	6.93E-04
1460292_a_at	Smarca1	2	2.48E-04
1448778_at	Sfrs4	2	9.50E-03
1426481_at	Klhl22	2	5.51E-03
1433529_at	E430002G05Rik	2	5.45E-03
1427290_at	Krt81	2	8.38E-09
1434507_at	Npepl1	2	3.39E-03
1449334_at	Timp3	2	9.45E-03
1448032_at	Azi2	2	2.03E-03
1429147_at	Gas2	2	1.49E-09
1449531_at	Leprel2	2	8.25E-04
1432104_a_at	Allc	2	2.14E-05
1417180_at	Pcsk7	2	3.96E-03
1435844_at	A330009N23Rik	2	5.56E-05
1434153_at	Shb	2	3.20E-03
1436425_at	Ankrd38	2	1.72E-04
1456422_at	D030011O10Rik	2	2.47E-03
1456373_x_at	Rps20	2	5.55E-03
1425388_a_at	Tpk1	2	1.21E-04
1431561_a_at	Dhx34	2	1.13E-03
1417009_at	C1r	2	4.89E-05
1451396_at	Pomt2	2	2.20E-04
1436071_at	Ankrd26	2	2.54E-03
1453330_at	Ccdc88c	2	1.88E-03
1436906_at	Rnf166	2	8.48E-04
1449131_s_at	Cd1d1	2	7.54E-03
1428384_at	D4Bwg0951e	2	3.22E-04
1438142_s_at	1700021K14Rik	2	1.11E-03
1445914_at	Nrf1	2	1.02E-05
1426933_at	Oxsr1	2	8.99E-03
1452062_at	Prpsap2	2	6.87E-03
1434361_at	Sh3px3	2	4.03E-03
1423800_at	Dars	2	2.37E-03
1442371_at	Lmbr1	2	7.18E-03
1420780_at	Ascl3	2	3.84E-11
1438291_x_at	Rpl37	2	7.55E-05
1442063_at	Adamtsl1	2	1.24E-05
1460228_at	LOC100047980	2	9.67E-04
1424850_at	Map3k1	2	9.04E-03
1424986_s_at	Fbxw7	2	4.01E-03
1444343_at	A130064L14Rik	2	1.62E-03
1438861_at	Bnc2	2	6.99E-06

1434385_at	Tom1l2	2	9.49E-03
1423672_at	Ttc30b	2	1.02E-04
1452284_at	Ptprz1	2	7.48E-04
1460106_at	Hydin	2	1.11E-08
1451115_at	Pias3	2	3.52E-03
1424123_at	Flvcr2	2	5.46E-03
1460620_at	Zfp592	2	1.66E-03
1421528_a_at	Med22	2	7.43E-03
1419054_a_at	Ptpn21	2	8.15E-03
1452669_at	2810012G03Rik	2	9.01E-03
1419552_at	Echdc1	2	9.70E-03
1434337_at	ENSMUSG00000051554	2	7.55E-03
1428072_a_at	Dolpp1	2	7.48E-03
1418446_at	Slc16a2	2	1.88E-03
1427428_at	Clec4g	2	4.12E-03
1438008_at	Gga3	2	5.12E-03
1424634_at	Tceal1	2	6.44E-03
1458197_x_at	Adam1a	2	4.45E-04
1434791_at	Atp6v0a2	2	9.01E-03
1452961_at	1200009O22Rik	2	5.07E-04
1429284_at	Mobkl2b	2	7.16E-04
1453734_at	Atrx	2	1.03E-03
1420556_at	Oxt	2	8.65E-06