Identification of Genomic Targets of Krüppel-like Factor 9 in Mouse Hippocampal Neurons: Evidence for a role in modulating peripheral circadian clocks

by

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To my parents, who never once questioned my decision to become the other kind of doctor,

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ABSTRACT

Krüppel-like factor 9 (Klf9) is a transcription factor that has diverse roles in development and physiology. Earlier work showed that Klf9 functions in neuronal differentiation, but nothing was known of its target genes in neurons. I used the mouse hippocampus-derived cell line HT22 to identify Klf9 genomic targets. I engineered HT22 cells to express Klf9 under the control of the tet repressor, and used RNA sequencing to identify genes modulated by Klf9. I identified 567 genes repressed, and 201 induced by Klf9. I also engineered HT22 cells to co-express biotin ligase and a Klf9 fusion protein containing an N-terminal polypeptide that can be biotinylated. Using chromatin-streptavidin precipitation (ChSP) sequencing I identified 3,516 genomic regions where Klf9 associated. Seventy five percent were <1 kilobase from transcription start sites, and Klf9 associated in chromatin with 60% of repressed genes. Computer analysis revealed GC-rich consensus motifs at 98% of regions where Klf9 associated. Transient transfection assays showed that Klf9 repressed promoter activity, which was abrogated after mutation of GC-rich motifs. Expression analysis of a subset of Klf9 target genes in hippocampus of wild type and *Klf9*-null mice showed that all were dysregulated in the mutants. Gene ontology analysis revealed that Klf9 regulates genes involved in neuronal morphogenesis, neurotrophin signaling, apoptosis and cell division.

Analysis of my ChSP-seq data showed that Klf9 associated in chromatin with genes involved in the cellular circadian clock. *Klf9* mRNA showed circadian oscillation in synchronized HT22 cells, and in mouse liver and hippocampus *in vivo*. Klf9 showed rhythmic association with several clock-output genes in mouse liver, supporting a role in regulating circadian gene expression. Forced expression of Klf9 repressed transcription of the clock-output gene *Dbp* and inhibited activation of the *Dbp* promoter by CLOCK/Bmal1, supporting that Klf9 antagonizes the CLOCK/Bmal1 complex that forms the positive limb of the circadian oscillator. My dissertation work represents the first analysis of Klf9 genomic targets in neurons, and supports a predominant repressor role for Klf9 in gene transcription. My findings also support that Klf9 acts as a novel component of the negative limb of the circadian clock.

CHAPTER 1
INTRODUCTION

1. Introduction

Spatiotemporal specificity in gene expression in eukaryotes is achieved in part by DNA-binding transcription factors (TFs) acting to induce or repress gene transcription through their interactions with chromatin, chromatin-modifying enzymes and other TFs. For my dissertation research I characterized the cistrome (set of cis-acting genomic targets of a trans-acting transcription factor) of the TF Krüppel-like factor 9 (Klf9) in mouse hippocampal neurons, and investigated its role in the regulation of peripheral circadian clocks and circadian clock output. In the Introduction to this dissertation I first describe the Krüppel-like factor family of transcription factors, with an emphasis on Klf9. I then provide a brief review of the cellular circadian oscillator, its modulation by adrenal steroids, and the known roles of Krüppel-like factors in circadian gene regulation. Portions of Section 2 have been previously published as part of the review paper "Krüppel-like factors are effectors of nuclear receptor signaling" (Knoedler and Denver 2014).

2. Krüppel-like factors

Krüppel-like factors (Klf) comprise a family of transcription factors characterized by a highly conserved C-terminal DNA binding region (DBD) consisting of three cys2-his2 (C2H2) zinc fingers (McConnell and Yang 2010). The Klf DBD is shared with the Specificity Protein

(Sp) family of proteins and binds to GC/GT rich sites in the genome (Sogawa et al. 1993). There are seventeen Klfs in mammals designated Klf1-17 (McConnell and Yang 2010). While C2H2 domain-containing proteins are present in all eukaryotes, the Klf family is restricted to opisthokonts (animals, fungi and related protists such as choanoflagellates). In metazoans the family has diversified extensively; only Klf15 is shared between metazoans and nonmetazoans. Vertebrates whose genomes have been sequenced have as few as 8 or as many as 45 Klf genes (Pei and Grishin 2015; Presnell et al. 2015).

2.1 Krüppel-like factors divide into subfamilies based on shared N-terminal domains

While the DBDs are nearly identical among Klfs, both within and across species (Hoopfer et al. 2002), the N-terminal regions are highly variable. The 17 Klf family members in mammals group into three major subfamilies based on similarities in their N-terminal domains (Moore et al. 2011). A molecular phylogenetic tree of mammalian Klfs is shown in Figure 1.1. Krüppel-like factors 3, 8, and 12 (Group 1) typically repress gene transcription by binding to the C-terminal binding proteins (CtBPs), a family of transcriptional repressors that recruit chromatin-modifying enzymes that add repressive marks to histones (Turner and Crossley 1998). Krüppel-like factors 1, 2, 4, 6 and 7 (Group 2) share acidic activation domains and thus typically act as transcriptional activators. Krüppel-like factors 9, 10, 11, 13, 14 and 16 (Group 3) share a Sin3a-interacting domain (SID), an α-helical motif that interacts with the repressor protein Sin3a (Zhang et al. 2001). These factors can repress transcription of target genes, but they are also capable of acting as transcriptional activators (Imataka et al. 1992). Whether a Group 3 KLF functions in transrepression or transactivation may depend on the stage of cellular differentiation when it is expressed. For example, KLF9 activates the *Fgfr1* promoter in myoblasts but represses it in differentiated myotubes via the same DNA binding site, although the mechanism behind this developmental switch is unknown (Mitchell and DiMario 2010). Krüppel-like factors 5, 15 and 17 do not group into any of the other families based on their amino acid sequence (McConnell and Yang 2010; Moore et al. 2011). In some cases, KLFs of the same subfamily have overlapping or redundant functions and can compensate for each other if one is lost or deleted (Veldman et al. 2007; Heard et al. 2012).

3. Krüppel-like factor 9 is an effector of nuclear receptor action

Since its discovery in 1992, the transcription factor Krüppel-like factor 9 (Klf9) has been implicated in a growing number of developmental and physiological processes, including cellular morphogenesis, differentiation, proliferation and apoptosis. However, fundamental questions remain about its mechanism of action. In particular, there are limited data regarding its genomic targets, and very little is known about how it functions in chromatin. In this section of the Introduction I will provide a review of the structure and biochemical function of Klf9 and its known roles as a mediator of nuclear receptor action in neuronal morphogenesis and uterine homeostasis.

3.1 Structure and biochemical function of Klf9

Krüppel-like factor 9 was originally identified in a screen of a rat liver cDNA library for proteins that bind the Basic Transcription Element (BTE), a GC-rich motif in the promoter of the *Cyp1a1* gene (Imataka et al. 1992). Early studies reported that it could activate or repress transcription based on the number of BTE sequences present in the promoter (Imataka et al. 1992). Similar to other members of the Klf Group 3 subfamily, Klf9 has a Sin3a interacting motif in its N-terminal region (Zhang et al. 2001). It also has two separable transactivation domains that are required for full transactivation (Kobayashi et al. 1995). Apart from Sin3a, data on the protein-protein interaction partners of Klf9 is limited; although it has been reported to co-immunoprecipitate with the progesterone receptor (PR), GATA2 and C/EBPα, there is little understanding of the mechanisms of how Klf9 binds to/associates with these proteins or the consequences of this association for chromatin structure and gene regulation (Zhang et al. 2002; Ohguchi et al. 2008; Pei et al. 2011).

3.2 Klf9 mediates some actions of thyroid hormone in neural development

Thyroid hormone (TH) is critical for proper neurological development. Lack of TH during late fetal and early neonatal development leads to irreversible growth and neurological impairment (Bernal 2005). Thyroid hormone acts in part by binding to its cognate nuclear receptors (TH receptors - TRα and TRβ). The TRs are typically constitutively bound to TH response elements (TREs) in DNA. In the absence of TH they repress, and upon ligand binding they activate transcription of target genes (Cheng et al. 2010). Krüppel-like factor 9 is a major target of TH and mediates some actions of the hormone on development and physiology, especially in the central nervous system (CNS).

3.2.1 Klf9 is a thyroid hormone-regulated gene in amphibians and mammals

A subtractive hybridization screen for TH-regulated genes in the frog *Xenopus laevis* found that Klf9 was among the most rapidly and strongly TH-induced genes in the tadpole brain, and that its expression increased across development (Denver et al. 1997). Further studies showed that *Klf9* was also induced by TH in rodent brain (Denver et al. 1999). Its transactivation in frog and mammal brain is mediated by TH response elements (TREs) located in the 5’ flanking regions (Furlow and Kanamori 2002; Denver and Williamson 2009). Thus, Klf9 is a phylogenetically ancient target of TH signaling.

3.2.2 Klf9 mediates actions of thyroid hormone on neuronal morphology during development

Several lines of evidence support that KLF9 mediates the actions of TH on neuronal differentiation. For example, in the mouse neuroblastoma cell line Neuro2a forced expression of Klf9 induced neurite outgrowth, similar to the action of TH on these cells (Denver et al. 1999). Knockdown of Klf9 blocked TH-induced neurite branching in cultured rat fetal cortical neurons, supporting that Klf9 functions as an intermediary for TH action on branching morphogenesis in immature cortical neurons (Cayrou et al. 2002). In mature neurons, Klf9 acts to maintain a differentiated state. Moore and colleagues (2009) showed that Klf9 overexpression inhibited neurite outgrowth in cultured retinal ganglion cells. As Klf9 expression is low at birth and rises postnatally, this suggests that it acts to maintain a differentiated state and therefore inhibits regeneration (Moore et al. 2009). In further support of this model, Klf9 mediated the inhibitory actions of TH on axon regeneration in cultured cerebellar Purkinje cells (Avci et al. 2012). In addition to its inhibition of axon regeneration, KLF9 also mediates TH-dependent survival of Purkinje neurons in cerebellar culture (Lebrun et al. 2013). Klf9 therefore mediates some actions of TH on neurons during development, but its functions may vary by cell type and developmental stage.

3.2.3 Klf9 promotes myelination in the mammalian central nervous system (CNS)

Krüppel-like factor 9 also mediates some of the actions of TH on the development of myelinating cells in the CNS. A hallmark of developmental hypothyroidism is delayed or absent myelination (Walters and Morell 1981). Thyroid hormone induces expression of myelin-associated genes and promotes differentiation of oligodendrocytes, the primary myelinating cells in the CNS (Tosic et al. 1992; Barres et al. 1994). Forced expression of KLF9 in oligodendrocyte precursors initiated oligodendrocyte differentiation and induced expression of myelination-associated genes (Dugas et al. 2012). Conversely, siRNA knockdown of KLF9 prevented TH-induced oligodendrocyte differentiation. Myelination during development is not affected in *Klf9*-null mice, but they show poor recovery after demyelinating lesions (Dugas et al. 2012). Taken together, the data support that KLF9 mediates the actions of TH on neuron and oligodendrocyte differentiation.

3.2.4 Klf9 enhances *Trb* autoinduction in tadpoles of the frog *Xenopus laevis*

In amphibians, KLF9 influences TH signaling by regulating the expression of TRβ. In *X. laevis* tadpoles the TRβ gene (*Trb*) is directly regulated by liganded TR via one or more TREs located in the promoter (i.e., the gene is autoinduced) (Kanamori and Brown 1992; Machuca and Tata 1992; Machuca et al. 1995). Machuca and Tata (Machuca and Tata 1992) found that *Trb* autoinduction is partially sensitive to protein synthesis inhibition, suggesting that upregulation of other proteins is required for *Trb* autoinduction. The rapid kinetics of *Klf9* induction by TH (Furlow and Kanamori 2002) and the presence of seven GC-boxes in the *X. laevis Trb* 5' flanking region led Bagamasbad and colleagues (2008) to hypothesize that Klf9 participates in *TRβ* autoinduction. In support of this hypothesis they found that Klf9 associated with the *Trb* promoter *in vivo* in tadpole brain and tail, and in *Xenopus* tissue culture cells (XTC-2) by chromatin-immunoprecipitation (ChIP) assay. Forced expression of Klf9 in XTC-2 cells accelerated and enhanced TH-dependent induction of *Trb* mRNA and promoter activity (Bagamasbad et al. 2008). The action of KLF9 on *Trb* depended on the N-terminal transactivation domains, but not on the DNA binding capacity of KLF9, as determined by deletion analysis and site-directed mutagenesis. Similar results were obtained in tadpole brain *in vivo* using electroporation-mediated gene transfer (Hu et al. 2016b). These findings support that the rapid induction of KLF9 supports *Trb* autoinduction through KLF9 acting as an accessory transcription factor for TR action.

3.3 Role of Klf9 in uterine physiology

While Klf9 is strongly expressed in the brain, especially the hippocampus and cerebellum, it is also expressed in many other tissues, including liver, epidermis and uterine endometrium (Wang et al. 1997; Ohguchi et al. 2008; Sporl et al. 2012). In this section I review evidence that Klf9 plays a vital role in progesterone receptor (PR) signaling in the uterus and is essential for optimal fertility in female rodents. This is another of several examples that illustrate the capacity of Klf9 to act as an integrator of nuclear receptor signaling.

3.3.1 Klf9 is an accessory transcription factor for the progesterone receptor that promotes progesterone responsiveness in the uterus

Krüppel-like factor 9 functions in PR signaling in the uterus by acting as an accessory TF for the PR. Wang and colleagues (1997) showed that Klf9 is expressed in epithelial and stromal cells of porcine pregnancy endometrium. Female mice null for *Klf9* have smaller litters than wild-type mice due to failed embryo implantation (Simmen et al. 2004). Progesterone receptor levels in uterine stromal cells of *Klf9*-null mice are reduced during pregnancy compared to wild type animals (Velarde et al. 2005). Consistent with this finding, many PR-responsive genes that are important for normal pregnancy, including *SLP1* and *Hoxa10*, display an aberrant response to progesterone (P4) in the absence of Klf9. Many progesterone-responsive genes are also regulated by Klf9. In porcine endometrial epithelial cells and cultured human endometrial carcinoma cells, Klf9 overexpression was sufficient to activate the *uteroferrin* (*UF*) promoter. Cotransfection of PR with Klf9 further increased promoter activity in a P4-dependent manner, suggesting that Klf9 and liganded PR cooperatively activated this promoter (Simmen et al. 1999). In tissue culture cells Klf9 enhanced P4-dependent transactivation of the PR isoform B but not A, and Klf9 was found to exist in a protein complex with PRB in the mouse uterus by co-immunoprecipitation (Co-IP). (Zhang et al. 2003)

The Wnt pathway inhibitor *Dickkopf* (*DKK1*) is cooperatively regulated by Klf9 and PR in cultured human endometrial stromal cells (HESCs). Expression of *DKK1* is increased by P4 treatment. Knockdown of Klf9 enhanced *DKK1* mRNA and protein expression in HESCs after P4 treatment, while knockdown of PR reduced expression of both. Combined knockdown of both PR and Klf9 did not significantly reduce *DKK1* mRNA but led to an almost total loss of DKK protein; one possible explanation would be altered expression of a PR/KLF9 target regulating translation of *DKK1* mRNA. Both Klf9 and PR associated with the *DKK1* promoter by ChIP assay, suggesting cooperative regulation wherein Klf9 may modulate the response of *DKK1* to P4/PR. DNA microarray analysis of HESCs subjected to PR or combined PR/Klf9 siRNA knockdown showed that PR and KLF9 coregulated many genes related to endometrial function, further supporting a role for KLF9 as an accessory TF for the PR (Pabona et al. 2012). Taken together, these results suggest that Klf9 acts as an accessory transcription factor for the PR and is necessary for optimal PR regulation of uterine receptivity and pregnancy. However, little is presently known about how Klf9 and PR interact at a mechanistic level.

3.3.2 A role for Klf9 in estrogen receptor autorepression

Krüppel-like factor 9 regulates estrogen (E2) receptor (ER) signaling by influencing ER expression, and thus cellular sensitivity to E2. It accomplishes this by promoting ERα autorepression. Autorepression, or the downregulation of the NR by its cognate ligand, is a common phenomenon that may serve to maintain homeostasis by dampening the response to a hormonal signal (Bagamasbad and Denver 2011). Estrogen receptor α autorepression is observed in both breast cancer cell lines and in the mouse mammary gland *in vivo* (Berkenstam et al. 1989; Hatsumi and Yamamuro 2006). Velarde et al. (2007) reported a role for KLF9 in ER autorepression in the human endometrial adenocarcinoma cell line Ishikawa. In these cells, treatment with E2 resulted in ERα recruitment to the *ERα* promoter and a ~50% decrease in *ERα* mRNA. Knockdown of Klf9, but not the closely related Klf13, by siRNA completely eliminated the E2-dependent decrease in *ERα* mRNA and protein. While ChIP assay did not support Klf9 association with the *ERα* proximal promoter, siRNA knockdown of Klf9 eliminated the E2-dependent increase in ERα recruitment to the promoter. Forced expression of Klf9 also reduced E2-dependent ER transactivation of an E2-responsive promoter in a transfection-reporter assay. Taken together, these results identify Klf9 as a cooperative transcriptional repressor of ERα at negatively regulated promoters and as an inhibitor of ERα transactivity at positively regulated promoters (Velarde et al. 2007). However, Klf9 was not found to interact with ERα by Co-IP. It may therefore promote ERα recruitment to the *ERα* promoter by indirect mechanisms.

3.3.3 Klf9 participates in transcriptional networks with Klf13 during pregnancy

Krüppel-like factors 9 and 13 participate in a transcriptional network with bone morphogenic protein 2 (BMP2) to maintain uterine receptivity to pregnancy. Bone morphogenic protein 2 is a critical regulator of uterine receptivity. Mice with targeted *Bmp2* deletion in the uterus fail to decidualize (respond to P4 to prepare for embryo implantation), leading to pregnancy failure (Lee et al. 2007). Bone morphogenic protein 2 is not expressed in predecidual uterine stromal cells but increases during decidualization. Expression of Klf9 in uterine stromal cells peaks prior to decidualization, when BMP2 is undetectable (Simmen et al. 2004; Velarde et al. 2005; Pabona et al. 2010). Krüppel-like factor 9 negatively regulates *BMP2* expression; *Klf9*-null mice have higher *Bmp2* levels in the uterus 3.5 days post-conception, and siRNA knockdown of *Klf9* in HESCs increases *BMP2* expression. In turn, application of BMP2 to HESCs represses *Klf9* expression, suggesting feedback to control expression of these genes at different stages of the uterine cycle/pregnancy.

In contrast to Klf9, Klf13 expression is low in predecidual stroma and increases as decidualization proceeds. Krüppel-like factor 13 represses *Klf9* expression but activates *BMP2* expression, as inferred from siRNA knockdown of *Klf13* in HESCs. Increased expression of Klf13 as decidualization proceeds therefore leads to reduced Klf9 expression, in turn leading to increased BMP2 levels, and expression of BMP2-regulated genes that promote uterine receptivity. Finally, although Klf9 and Kfl13 have antagonistic effects on each other and BMP2 expression, both are necessary for maximal expression of *PRB* as demonstrated by reduced *PRB* expression after siRNA knockdown in HESCs, although their effects are restricted to particular stages of decidualization. Krüppel-like factor 9 promotes *PRB* expression only in predecidual stroma, while Klf13 does so only in decidualizing stroma. The net result is sustained uterine sensitivity to P4 even as many other molecular events are taking place (Pabona et al. 2010). Thus, two Klfs and one extracellular signaling molecule regulate each other to allow decidualization to proceed.

Despite the high degree of sequence similarity between Klf9 and Klf13 (Suske et al. 2005) and the expression of both KLFs in uterine tissues, *Klf9*-null mice are subfertile while *Klf13*-null mice do not show any fertility defects (Heard et al. 2012). In *Klf13*-null mice, Klf9 protein levels are higher in the nuclear fraction of whole-uterus protein extracts at 3.5 days post-conception. This supports compensatory upregulation of Klf9 in the absence of Klf13. Unlike protein expression, *Klf9* mRNA levels did not differ between the two genotypes, which suggests that the compensatory response occurs at the level of translation of *Klf9* mRNA. Translation of Klf9 is inhibited by the uterine-expressed miRNA miR-200C, which is dysregulated in endometrial carcinoma and weakly induced by ovarian steroids (Panda et al. 2012). Altered expression of this transcript may explain the compensatory upregulation of KLF9 protein in the *Klf13*-null mouse. Expression of Klf13 protein is higher in early pregnant uteri of *Klf9*-null mice compared to WT (Simmen et al. 2004), but apparently it is unable to compensate to the same extent as Klf9. Taken together, these data show that Klf9 and Klf13 have both complementary and overlapping functions in the uterus, forming a robust transcriptional network to mediate the actions of P4/PR on uterine receptivity to implantation and the maintenance of pregnancy.

3.5 Summary of the role of Klf9 in nuclear receptor signaling

There is abundant evidence that Klf9 serves as a mediator and integrator of nuclear receptor signaling. In the CNS it mediates some actions of TH on neural development and function, while in the uterus it acts as an accessory transcription factor to promote progesterone responsiveness. It is also induced by adrenal steroids (Bonett et al. 2009; Bagamasbad et al. 2012), but its role in the stress response is unknown. Identifying genomic targets of Klf9 is necessary to understand how it mediates these developmental and physiological processes. Furthermore, Klf9 participates in transcriptional networks with closely related Klf proteins with similar DNA-binding properties; a complete understanding of its role in the cell will ultimately need to incorporate the activity of these proteins as well.

4. Evidence for a role of Klf9 in circadian regulation of gene expression

In the process of identifying genomic targets of Klf9 I found that many were genes that regulated circadian rhythms. All organisms must adapt to the 24-hour rotation of the earth that leads to predictable changes from night to day. This has led to the evolution of circadian rhythms (entrainable self-sustained oscillations with a period of ~24 hours). In this section of the Introduction I review the transcriptional mechanisms that function in cellular circadian timekeeping, their interactions with the hypothalamo-pituitary-adrenal (HPA) axis, and the known roles of Klfs in circadian regulation of physiology.

4.1 A transcription-translation feedback loop marks time in mammalian cells

In mammals the ‘master clock’ is thought to reside in the suprachiasmatic nucleus of the hypothalamus (SCN); lesions of this region, but not other hypothalamic nuclei, abolish circadian rhythmicity in locomotor activity in rats (Stephan and Zucker 1972). An intricate transcription-translation feedback loop (TTFL) functions in nearly every cell in the body to maintain circadian rhythmicity (Figure 1.2). At the core of this TTFL are the proteins CLOCK (Circadian locomotor output cycles kaput), Bmal1 (Brain and muscle Arnt-like protein 1), Per1, 2 and 3 (Period homologue 1, 2 and 3), and Cry1 and 2 (Cryptochrome1 and 2) (Dardente and Cermakian 2007). The CLOCK and Bmal1 proteins form a heterodimer and bind to E-box (CACGTG) motifs in the promoters of *Per* and *Cry* (Gekakis et al. 1998; Kondratov et al. 2006). The protein products of these genes accumulate in the cytoplasm, where they heterodimerize and translocate to the nucleus and disrupt the CLOCK/Bmal1 heterodimer. This shuts off their own transcription, ultimately reducing their ability to disrupt CLOCK/Bmal1. This in turn enhances the activity of the CLOCK/Bmal1 complex and leads to increased *Per* and *Cry* transcription, starting the cycle over again. This 'core loop' is stabilized by an accessory loop wherein CLOCK/Bmal1 activate transcription of the orphan nuclear receptors *Nr1d1* (Rev-erbα) and *Nr1f2* (RORα) (Sato et al. 2004; Ripperger 2006). The protein products of these genes activate (ROR) or repress (Rev-erb) transcription of the *Bmal1* by binding to retinoid response elements (RREs) in the *Bmal1* genomic region. This leads to daily oscillations in *Bmal1* mRNA level.

Another loop involves CLOCK/Bmal1 upregulation of the basic helix-loop-helix-containing transcription factors *Bhlhe40* and *Bhlhe41* (coding for Dec1 and Dec2), which can inhibit transcriptional activation by CLOCK/Bmal1 through competitive binding to E-box motifs (Honma et al. 2002; Kawamoto et al. 2004; Nakashima et al. 2008). These interacting loops orchestrate the clock output, genes whose transcription is modulated in 24 hour cycles by the activity of the CLOCK/Bmal1, Per/Cry and Rev-erb and ROR proteins. These genes frequently contain E-boxes and are transcriptional targets of CLOCK/BMal1; hence, the same feedback mechanisms that maintain cyclicity of the clock also maintain oscillating expression of clock-output genes. This leads to 24-hour oscillations in gene expression that mediate circadian rhythms in metabolism, behavior and physiology. For example, the clock-output transcription factors *Dbp*, *Tef* and *Hlf* are required for circadian coordination of xenobiotic detoxification in the liver (Gachon et al. 2006)

4.2 Modulation of peripheral clocks by glucocorticoids

The genes of the TTFL show strong circadian oscillations in the SCN (Shearman et al. 1997; Honma et al. 1998). However, they also oscillate in nearly every other organ in the body, although rhythms in these clocks can be dampened or abolished by lesions of the SCN (Sakamoto et al. 1998). These ‘peripheral’ or ‘slave’ oscillators orchestrate circadian rhythms in physiology and metabolism in nearly all organs. They can be synchronized or entrained by many external stimuli, including body temperature and food availability (Stokkan et al. 2001; Buhr et al. 2010). One important mechanism for synchronizing peripheral clocks is the diurnal secretion of glucocorticoids (CORT) from the adrenal glands. In the next section I discuss how the SCN and the cellular oscillator orchestrate diurnal variations in CORT secretion and how CORT in turn may affect the cellular pacemaker.

4.2.1 Regulation of adrenal steroid secretion and production by the cellular circadian clock

Secretion of CORT by the adrenal glands follows both circadian rhythms (rising a few hours before the active phase of the sleep-wake cycle) and ultradian rhythms (pulsatile release every ~90 minutes) (Dickmeis et al. 2013). These cycles are regulated at multiple levels of the hypothalamo-pituitary-adrenal (HPA) axis. At the level of the hypothalamus, electrophysiological and fiber-tracing studies support the existence of connections between the SCN and the neurosecretory neurons in the paraventricular nucleus of the hypothalamus (Hermes and Renaud 1993; Vrang et al. 1995). Lesions of the SCN result in greater CORT secretion in response to stress, supporting an inhibitory effect of the SCN on the HPA (Buijs et al. 1993).

Adrenocorticotropic hormone (ACTH), which stimulates secretion of CORT from the adrenal gland, shows a circadian rhythm in serum concentration that is abolished following lesioning of the SCN; however, circadian variation in CORT concentration persisted in some animals despite lack of variation in ACTH (Szafarczyk et al. 1979). This suggests alternative mechanisms by which adrenal steroid release can be controlled. Later studies found evidence of sympathetic inputs to the adrenal gland that could drive rapid decreases in CORT secretion independently of ACTH concentration (Jasper and Engeland 1994; Buijs et al. 1999). Finally, local clocks in the adrenal gland modulate CORT synthesis and release. Mice null for the clock genes *Per2* and *Cry1* show defective circadian gene expression in the adrenal gland and defective circadian rhythms of CORT secretion; furthermore, explanted WT but not *Per2/Cry1*$^{-/-}$ adrenal glands showed time-of-day-dependent sensitivity to ACTH (Oster et al. 2006). This suggests the existence of a gating mechanism that regulates diurnal variations in sensitivity to ACTH.

4.2.2 Influence of glucocorticoids on the cellular circadian oscillator

The daily rise in CORT has been proposed to function as an entraining signal for peripheral clocks. In tissue culture cells a one-hour pulse of the synthetic glucocorticoid dexamethasone (DEX) was sufficient to synchronize circadian rhythms; furthermore, DEX injection into mice led to a phase shift in gene expression in peripheral organs at every time of day, while the SCN (which does not express GR) was unaffected (Balsalobre et al. 2000). This supports that GCs act as potent entrainment signals for peripheral (non-SCN) organs. Further studies refined this hypothesis by defining the molecular mechanisms by which CORT upregulates the *Per1* gene. The GR associates with a GRE present upstream of the *Per1* gene and mediates rapid upregulation of *Per1* mRNA in response to restraint stress or DEX treatment

(Yamamoto et al. 2005; Reddy et al. 2012). In the brain this is associated with accumulation of Per1 protein, supporting that stress has the potential to disrupt clock function (Al-Safadi et al. 2015). There is also evidence that liganded GR represses the accessory loop gene *Nr1d1* at the transcriptional level (Torra et al. 2000), adding an additional mechanism by which CORT can reset the clock.

4.3 Known roles of Klfs in circadian physiology

A recent ChIP-seq study of CLOCK association in chromatin in mouse liver found that many members of the Klf family are clock-output genes with circadian expression in the liver (Yoshitane et al. 2014). Krüppel-like factors 9, 10, 11, 13, 15 and 16 all showed CLOCK/Bmal1 association in chromatin within their genomic regions and circadian expression in the liver; forced expression of CLOCK and Bmal1 activated transcription from reporter constructs containing CLOCK-associated genomic fragments from *Klf11* and *Klf13*. An emerging literature implicates Krüppel-like factors as important circadian clock-output genes that mediate daily fluctuations in multiple metabolic and physiological processes.

4.3.1 Klf15 is a clock-output gene that orchestrates circadian variation in metabolism and physiology in the heart and liver

The CLOCK/Bmal1 complex associates with an E-box-containing region located in the first intron of *Klf15* in a rhythmic manner in both the mouse heart and liver (Jeyaraj et al. 2012a; Jeyaraj et al. 2012b). This E-box supports circadian oscillation of Klf15 mRNA and protein. Circadian regulation of Klf15 results in rhythmic regulation of genes involved in nitrogen metabolism and bile acid synthesis in the liver and supports a biphasic gene expression program in the heart (Jeyaraj et al. 2012b; Han et al. 2015; Zhang et al. 2015). In the liver, *Klf15*$^{-/-}$ null mice showed reduced mRNA levels of the amino acid catabolic enzymes *Bcat2* and *Alt* and lacked the circadian oscillation in the mRNA level of these genes that was seen in WT mice. In WT mice Klf15 showed rhythmic recruitment to the *Alt* promoter, suggesting a mechanism for oscillating expression of this gene (Jeyaraj et al. 2012b). The mRNA levels of the enzymes *Cyp7a1* and *Cyp7b*, which are rate-limiting for bile acid synthesis, show circadian oscillations in WT mice, but in *Klf15*$^{-/-}$ overall expression of these enzymes is lower and rhythmicity is lost; the mice consequently show deficits and lack circadian variation in bile acid production (Han et al. 2015). In the heart, Klf15 also shows circadian oscillations in expression and regulates the expression of ion channels that modulate cardiac repolarization; knockout of *Klf15* consequently reduces diurnal variations in cardiac physiology (Jeyaraj et al. 2012a). Transcriptomic studies showed that cardiac *Klf15* deficiency led to derangement of the cardiac circadian transcriptome, with 1,003 genes losing rhythmicity that was seen in WT animals and 473 previously arrhythmic genes gaining circadian rhythmicity (Zhang et al. 2015). Taken together, these results show that Klf15 mediates circadian rhythmicity of multiple metabolic and physiological processes in multiple tissues.

4.3.2 Klf9 mediates circadian variations in cell proliferation in human keratinocytes

Several genome-wide studies using both microarrays and RNA-seq have found that *Klf9* mRNA shows circadian oscillation in many tissues, including mouse liver (Ueda et al. 2002; Yoshitane et al. 2014), implantation-stage rat uterine endometrial stromal cells (Tasaki et al. 2013), mouse pituitary (Guillaumond et al. 2012), and human keratinocytes (Sporl et al. 2012). In human keratinocytes Klf9 fluctuates in parallel with diurnal plasma CORT concentration and mediates the antiproliferative effects of CORT (Sporl et al. 2012). No other studies have investigated the functional significance of circadian *Klf9* regulation.

4.3.3 Klf10 is a clock-output gene that contributes to circadian regulation of lipid homeostasis

Krüppel-like factor 10 (Klf10; formerly TGFβ-inducible early gene, Tieg) was originally identified as a gene that is rapidly induced in many tissues by TGFβ and plays a role in cardiac development and bone differentiation (Rajamannan et al. 2007). Genome-wide studies found that its expression is circadian in liver (Ueda et al. 2002). In transient transfection assays the *Klf10* promoter was activated by CLOCK/Bmal1, while the Bmal1 protein associated with the promoter in ChIP assays on mouse liver tissue. Microarray analysis on the livers of *Klf10*$^{-/-}$ mice showed that many genes involved in lipid homeostasis were dysregulated. These mice showed increased *Pepck* expression, increased glucose production at activity onset and dysregulated circadian expression of lipogenesis-related genes in liver, supporting that circadian regulation of *Klf10* is important for energy homeostasis (Guillaumond et al. 2010).

5. Summary of the dissertation

Previous work from the Denver lab found that *Klf9* was strongly induced by TH in the tadpole brain, that this regulation is conserved in mammals, and that Klf9 plays a role in the morphological maturation of neurons (Denver et al. 1997; Denver et al. 1999; Cayrou et al. 2002). In the frog brain Klf9 cooperates with TR to promote *Trb* autoinduction (Bagamasbad et al. 2008; Hu et al. 2016a). It is also strongly upregulated by CORT in both amphibians and mammals (Bonett et al. 2009; Bagamasbad et al. 2012; Al-Safadi et al. 2015). The gene is synergistically regulated by TH and GCs via an ultraconserved nuclear receptor enhancer module located 5-6 kb upstream of the transcription start site of tetrapod *Klf9* genes (Bagamasbad et al. 2015). However, its genomic targets in neurons are unknown, and the mechanisms by which it functions in chromatin are poorly understood. The goal of my dissertation research was to identify Klf9 genomic targets in the mouse CNS to better understand the mechanism by which it regulates neural development and physiology, and to provide a basis for understanding the functional significance of its induction by nuclear hormone receptors.

In Chapter 2, I present the results of two genome-wide analyses to identify genomic targets of Klf9 in the mouse hippocampus. I used the cell line HT22 as a model for mature hippocampal neurons. I first engineered HT22 cells to express *Klf9* under control of the Tet operator (TO), which allowed controlled expression of *Klf9*. This enabled me to compare the transcriptome of cells with or without forced *Klf9* expression by RNA sequencing (RNA-seq). Next, I engineered HT22 cells to co-express the biotin ligase BirA and a variant of Klf9 with an N-terminal FLAG tag and biotin ligase recognition peptide (FLBIO-Klf9). This allowed high affinity purification of Klf9 in chromatin by streptavidin precipitation. I then used deep sequencing to identify genomic regions where FLBIO-Klf9 associated. I found that Klf9 acted primarily as a transcriptional repressor, that it was associated most often with GC-box-containing regions near transcription start sites, and that its genomic targets included many genes involved in cytoskeletal remodeling, cell morphology, and apoptotic cell death.

In Chapter 3, I present evidence that Klf9 plays a role in the cellular circadian oscillator. When I analyzed my ChSP-seq data set I found that many Klf9 genomic targets were genes that participated in circadian timekeeping, including the clock genes *Per1*, *Per3, Nr1d1*, *Nr1d2*, *Bhlhe40* and *Bhlhe41*, and the clock-output genes *Dbp*, *Tef* and *Wee1*. Because previous studies have found that *Klf9* may be a clock-output gene that shows circadian oscillations in expression (Sporl et al. 2012; Yoshitane et al. 2014), I tested the hypothesis that Klf9 acts as a negative regulator of the clock by repressing expression of clock- and clock-output genes. I found that *Klf9* mRNA level is circadian both in synchronized HT22 cells and in the mouse hippocampus and liver *in vivo*. Forced expression of Klf9 repressed the clock-output gene *Dbp* in HT22 cells; forced Klf9 expression also inhibited CLOCK/Bmal1-dependent activation of a reporter construct containing the *Dbp* genomic region. These data support that Klf9 may be a negative regulator of the clock output.

The clock gene *Per1* is strongly induced by CORT, which may be a mechanism for resetting of circadian rhythms by adrenal steroids (Yamamoto et al. 2005; Reddy et al. 2012). Because Klf9 is also induced by CORT (Bagamasbad et al. 2012) and associates with the *Per1* promoter, I hypothesized that it exerts a repressive effect on *Per1* expression to fine-tune phase resetting in peripheral tissues. To test this hypothesis I examined the effect of forced Klf9 expression on *Per1* induction by CORT in HT22 cells, and the effect of loss of *Klf9* on *Per1* induction after forced restraint in wild-type and *Klf9*$^{-/-}$ mice. Forced expression of Klf9 slowed *Per1* induction in HT22 cells, but mice null for *Klf9* appeared to show inhibited *Per1* induction after one hour of forced restraint, suggesting a complex role for Klf9 in modulating the transcriptional response to CORT signaling.

There is mounting evidence that Klf9 plays stage-dependent roles in the development and maintenance of neuronal morphology (Denver et al. 1999; Cayrou et al. 2002; Scobie et al. 2009; Avci et al. 2012; Lebrun et al. 2013), acts as an accessory transcription factor to modulate liganded nuclear receptor action (Zhang et al. 2002; Zhang et al. 2003; Velarde et al. 2007; Bagamasbad et al. 2008; Hu et al. 2016a) and regulates apoptosis under conditions of oxidative and xenobiotic stress (Mannava et al. 2012; Zucker et al. 2014). However, a detailed understanding of how Klf9 functions is lacking, and new functions for Klf9 remain to be discovered. The work presented in this dissertation is the first to identify Klf9 genomic targets in mammalian neurons and to provide support for a key role in the cellular circadian oscillator.

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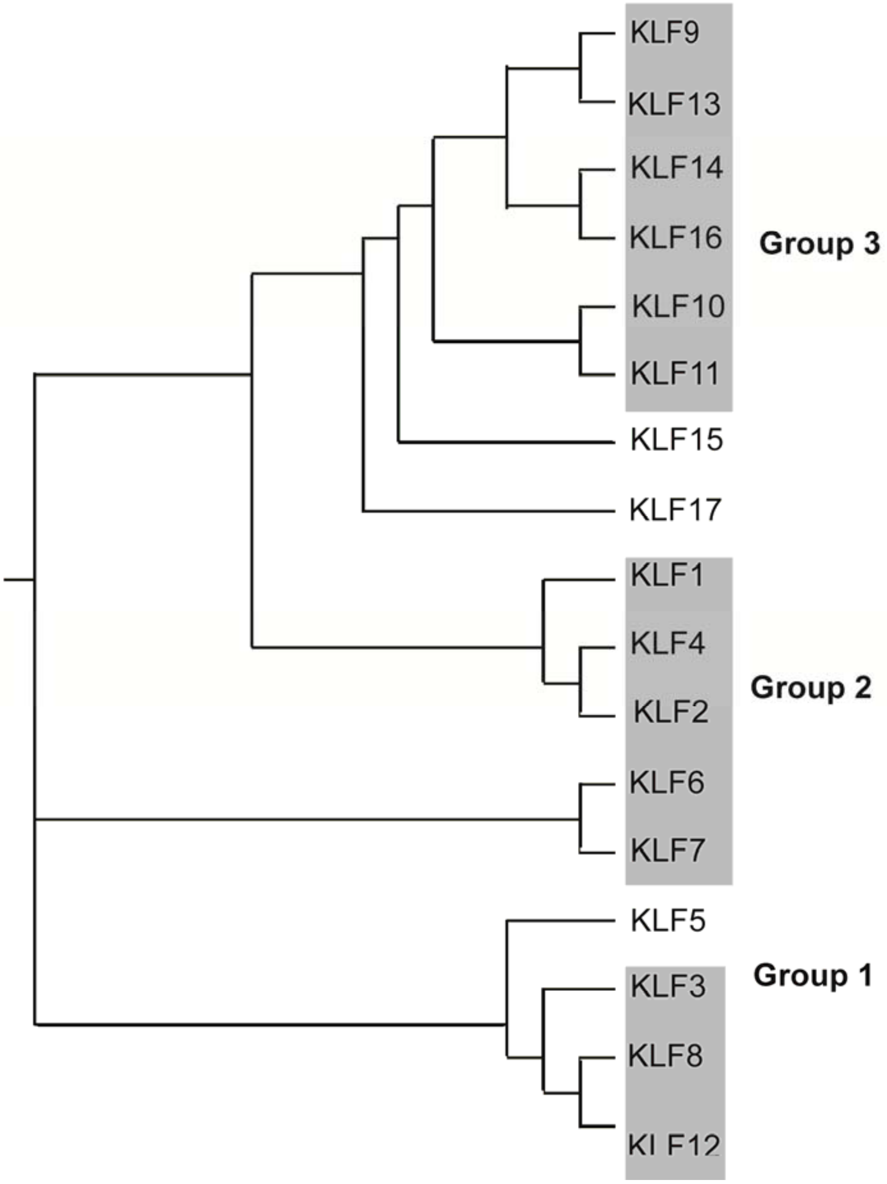

Figure 1.1. A molecular phyologram of mammalian Krüppel-like factors. Group 1 Klfs contain CtBP-interacting domains and typically act as repressors. Group 2 Klfs contain acidic activation domains and typically act as transcriptional activators. Group 3 Klfs (including Klf9) share a Sin3a-interacting domain and act predominantly as transcriptional repressors.

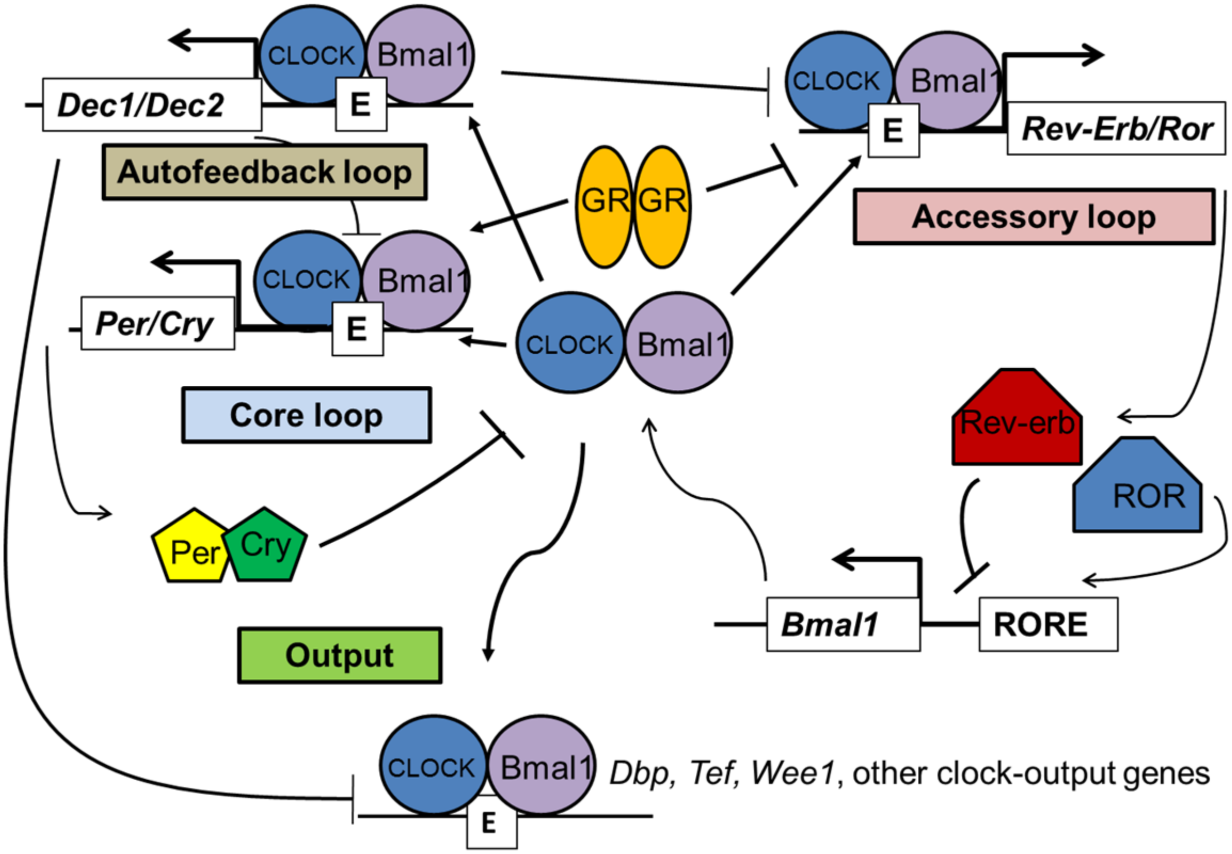

Figure 1.2. Diagram of the mammalian cellular circadian oscillator. The proteins CLOCK and Bmal1 heterodimerize and activate transcription from E-box containing promoters (E). Among their targets are the genes *Per* and *Cry,* whose protein products inhibit transactivation by the CLOCK/Bmal1 heterodimer, which closes the 'core loop'. In the accessory loop CLOCK and Bmal1 activate transcription of *Rev-Erb* and *ROR* (*Nr1d1* and *Nr1f1*), which repress (Rev-Erb) or activated (ROR) transcription of *Bmal1* via a retinoid response element (RORE). The autofeedback loop genes *Dec1* and *Dec2* are upregulated by CLOCK/Bmal1; their protein products repress transcription from E-box-containing promoters. The glucocorticoid receptor (GR) can upregulate *Per1* expression and repress *Nr1d1* expression upon binding to glucocorticoids. Finally, clock-output genes (*Dbp*, *Tef*, *Hlf*, etc.) mediate daily variations in physiology, metabolism and behavior (Figure adapted from Dickmeis et al. 2013).

CHAPTER 2

KRÜPPEL-LIKE FACTOR 9 FUNCTIONS PREDOMINANTLY AS A TRANSCRIPTIONAL REPRESSOR IN MOUSE HIPPOCAMPAL NEURONS

Abstract

Krüppel-like factor 9 (Klf9) is a transcription factor that functions in neuronal differentiation and physiology, but little is known about its target genes or mechanism of action in neurons. I used the mouse hippocampal-derived neuronal cell line HT22 to identify Klf9-regulated genes. I engineered HT22 cells to express a Klf9 transgene under control of the tet repressor, and used RNA sequencing to identify genes modulated by Klf9. I found 567 genes repressed and 201 induced by Klf9. I also engineered HT22 cells to co-express biotin ligase and a Klf9 fusion protein containing an N-terminal biotin ligase recognition peptide. Using chromatin-streptavidin precipitation (ChSP) sequencing I identified 3,516 genomic regions where Klf9 associated. Seventy-five percent of these were within 1 kb of transcription start sites, and Klf9 associated in chromatin with 60% of genes repressed by forced Klf9 expression. Computer analysis revealed GC-rich consensus motifs at 98% of Klf9 ChSP peaks. I analyzed the promoters of several repressed genes containing Klf9 ChSP peaks by transient transfection, and found that Klf9

repressed promoter activity, which was abrogated after mutation of GC-boxes. Expression analysis of a subset of Klf9 target genes in hippocampus of *Klf9*-null mice showed that all were dysregulated, and chromatin immunoprecipitation showed that Klf9 associated in chromatin with these genes in the brain of wild type mice. Gene ontology analysis revealed that Klf9 regulates genes involved in neuronal morphogenesis, apoptosis and cell division. My results provide a basis for understanding Klf9 functions in hippocampal neurons.

Introduction

Krüppel-like factors (Klfs) comprise a family of zinc-finger transcription factors (TFs) that function in metabolism, development and oncogenesis (McConnell and Yang 2010). They have a highly conserved DNA binding domain, comprised of three zinc fingers, that binds to GC/GT rich regions in the genome. Members of this family are distinguished by their N-terminal domains which are highly divergent, and therefore recruit different chromatin modifying factors that in part govern whether the Klf functions as a transcriptional activator or repressor (McConnell and Yang 2010).

Krüppel-like factor 9 (Klf9; formerly basic transcription element binding protein 1 – BTEB1) was identified in a screen of a rat liver cDNA library for proteins that bound the basic transcription element (BTE), a GC-rich motif in the promoter of the *Cyp1a1* (Cytochrome P450) gene (Imataka et al. 1992). The zinc fingers of Klf9 have high sequence identity with those of Sp1, which binds to similar motifs and typically activates transcription (Imataka et al. 1992). Transient transfection assays showed that Klf9 repressed transcription from a reporter construct containing the BTE sequence. However, Klf9 activated transcription from a promoter containing six tandem repeats of the BTE, suggesting that its activity may be governed by the number of binding sites at a locus (Imataka et al. 1992). The N-terminal region of Klf9 contains two separable transactivation domains required for full activation of the six-repeat BTE promoter, and an α-helical motif that interacts with the repressor protein Swi-independent 3a (Sin3a) (Kobayashi et al. 1995; Zhang et al. 2001).

In the mouse central nervous system (CNS) Klf9 is most prominently expressed in the hippocampus and cerebellum (Morita et al. 2003). Expression of Klf9 is low at birth, but rises postnatally, reaching a peak at approximately postnatal day 30 (Denver and Williamson 2009). In immature and developing neurons, Klf9 mediates the actions of thyroid hormone (TH) on neurite extension (Cayrou et al. 2002). However, in mature neurons Klf9 inhibits neurite regeneration and remodeling (Moore et al. 2009). It is also required for survival of adult-born dentate granule neurons and Purkinje neurons of the cerebellum (Scobie et al. 2009; Lebrun et al. 2013). Its roles in the brain are not limited to neurons; Klf9 also promotes expression of myelinating genes in oligodendrocytes (Dugas et al. 2012). Consistent with the findings described above, Klf9-null mice show neurological defects, including deficits in fear conditioning and late-stage neurogenesis (Morita et al. 2003; Scobie et al. 2009).

One notable feature of the *Klf9* gene is its rapid and robust upregulation by multiple extracellular stimuli, including glucocorticoids (Bagamasbad et al. 2012), thyroid hormone (TH) (Denver and Williamson 2009), electrical activity (Scobie et al. 2009) and oxidative stress (Zucker et al. 2014). The induction of *Klf9* by TH plus CORT is synergistic, and is mediated by an ultraconserved enhancer module that contains response elements for nuclear receptors and other TFs (Bagamasbad et al. 2015). Thus, Klf9 can mediate the actions of diverse extracellular stimuli.

Despite evidence for a diversity of developmental and physiological roles for Klf9, very little is known about Klf9 genomic targets in any cell type, and nothing is known about the genes that Klf9 regulates in neurons. In the current study, I identified direct genomic targets of Klf9 in the mouse hippocampus. I used the mouse hippocampal-derived neuronal cell line HT22 as a model for mature hippocampal neurons. This cell line expresses neuronal markers such as enolase and neurofilament proteins, but does not express the glial marker glial fibrillary acidic protein (Morimoto and Koshland 1990a; Morimoto and Koshland Jr 1990; Maher and Davis 1996; Sagara et al. 1998). I engineered several HT22 cell lines to allow for the control of *Klf9* expression to study Klf9-dependent transcriptional responses by RNA sequencing (RNA-seq), to identify genomic regions where Klf9 associates in chromatin, and to investigate the consequences of *Klf9* deletion for gene transcription. I validated my findings from HT22 cells using a Klf9 mouse knockout line. I show that Klf9 acts primarily as a transcriptional repressor in hippocampal-derived neurons, that it associates in chromatin near transcription start sites, and that it regulates transcription of genes involved in cystokeletal remodeling, neurotrophin signaling and apoptosis.

Materials and Methods

Plasmids

I used the pRSV-BTEB plasmid (gift of Dr. Fuji-Kuriyama) as template for PCR to amplify the full-length Klf9 cDNA, which I then directionally cloned into the pCS2 (gift of Dr. David Turner), pCDNA4:TO (Invitrogen) and pEF1α-FLBIO (gift of Jianlong Wang; Kim et al., 2009) expression vectors at the XhoI/XbaI (pCDNA4:TO) or BamHI/XbaI (pEF1α-FLBIO) sites. I constructed a BirA expression vector by amplifying by PCR the entire promoter, coding and polyadenylation sequence of BirA using the pEF1α-BirA vector (gift of Jianlong Wang; Kim et al., 2009) as template, and subcloned the resulting DNA fragment into the pSV40 zeocin plasmid (gift of Dr. Michael Uhler) at the NotI and NheI sites; note that HT22 cells are resistant to G418 and the pEF1α-BirA plasmid contains a neomycin resistance cassette.

I constructed the pGL4.23-3xBTE reporter plasmid by synthesizing oligonucleotides with three tandem repeats of the Basic Transcription Element (BTE;(Imataka et al. 1992)) and ligating the duplex oligonucleotide DNA into pGL4.23 (Invitrogen) at the HindIII and NheI sites. I isolated the 5' flanking regions of *Klf13* (439 bp), *Limk1* (800 bp), *Klf16* (2200 bp), and *Mapk11* (887 bp) by PCR using HT22 cell genomic DNA as template (isolated using the DNEasy DNA extraction kit; Qiagen) and subcloned the DNA into pGL4.23 at the SacI/HindII, NheI/ KpnI, NheI/HindIII, or SacI/ XhoI sites to create pGL4.23[*Klf13*]promoter, pGL4.23[*Limk1*]promoter, pGL4.23[*Klf16*]promoter and pGL4.23[*Mapk11*]promoter respectively.

Using the pGL4.23[*Klf13*]promoter plasmid as template, I did site-directed mutagenesis targeting putative Klf9 binding sites using the Quikchange kit (Agilent). I converted seven nucleotides within each Klf9 consensus sequence (described below) to adenines. The Klf13 5' flanking region contains six predicted Klf9 binding sites (GC boxes 1-6); we first generated two vectors with mutations in individual GC boxes #1 or 2 (Supplemental Figure 6); to create pGL4.23[*Klf13*]promoter1mut and pGL4.23[*Klf13*]promoter2mut), and one double mutant (Box #1+2; pGL4.23[*Klf13*]promoter1+2mut). To generate a Klf13 promoter fragment with mutations in all six predicted Klf9 binding sites I synthesized the entire 439 bp fragment corresponding to that in the pGL4.23[*Klf13*]promoter with mutations in all six GC boxes (Invitrogen) and subcloned this into pGL4.23 to create pGL4.23[*Klf13*]promoter6mut. All oligonucleotides used for subcloning and site-directed mutagenesis are given in Supplemental Table 2.1.

Generation and characterization of stable, doxycycline-inducible HT22 cell lines

I cultured HT22 cells (gift of Dr. David Schubert) in high-glucose DMEM (Invitrogen) supplemented with 10% fetal bovine serum (Hyclone or Sigma), penicillin G (100 U/ml) and streptomycin sulfate (100 μg/ml) under a humidified atmosphere of 5% CO_2 at 37°C. This cell line was originally derived from mouse hippocampus using the Simian Virus 40 T antigen (Morimoto and Koshland 1990c; Morimoto and Koshland 1990b). To generate stably transfected HT22[TR/TO-*Klf9*] cell lines I seeded 5 x 10^6 cells in 100 mm plates and transfected with 5 μg each of pCDNA4:TO-Klf9 and pCDNA6:TR (Invitrogen) using Fugene6 (Invitrogen). Twenty four hr after transfection I replaced the medium with medium containing 100 μg/ml zeocin plus 5 μg/ml blasticidin (Research Products International). After the majority of cells had been killed, I isolated and subcultured drug-resistant cells by affixing cloning cylinders dipped in autoclaved silicone grease to the plate, washing cells with Dulbecco's Phosphate Buffered Saline (DPBS; Sigma) and passaging with 0.25% trypsin (Gibco). I then seeded trypsinized cells in 6-well plates and expanded the clonal lines. I tested seven clonal HT22[TR/TO-*Klf9*] lines for dox-inducible *Klf9* mRNA by culturing them in 6-well plates and treating with 1 μg/ml dox (Sigma) or vehicle (0.1% DMSO) for 8 hr, then cells were harvested, RNA isolated and analyzed for Klf9 mRNA levels by RT-qPCR (described below). To test if the stable cell lines expressed functional Klf9 I seeded cells at 5 x 10^4 per well in 24 well plates and co-transfected cells with pGL4.23-3xBTE (200 μg) plus pRenilla (10 μg)(Promega). I treated transfected cells with vehicle or dox for 8 hr and harvested for dual luciferase assay (Promega). As a control, I co-transfected parent HT22 cells with pGL4.23-3xBTE plus a Klf9 expression vector (pCS2-Klf9) to independently determine the action of Klf9 on this reporter.

For RNA extraction from cell culture I plated HT22 cells in either 6- or 12-well plates at densities of either 2.5 x 10^5 or 1.25 x 10^5 respectively. All dox treatments were begun 24 hours after plating. For luciferase assays, cells were cultured in 24-well plates at a density of 5 x 10^4 cells/well. 24 hours after plating they were transfected with 200 ng/well of the luciferase vector and 10 ng/well pRenilla plasmid to monitor transfection efficiency. 24 hours after transfection they were treated with or without 1 μg/ml dox for either 8 (pGL4.23-3xBTE vector) or 24 hours (all other luciferase vectors). Cells were harvested for luciferase assay using the Dual Luciferase Reporter Assay System (Promega) according to manufacturer's instructions. Firefly luciferase activity was quantified using a luminometer (Femtometer FB 12; Zylux Corp) and normalized to

Renilla luciferase activity. All reporter assays were repeated at least two times with 5-6 replicates/treatment.

RNA extraction, reverse transcription and quantitative PCR

I extracted total RNA from HT22 cells or mouse brain (hippocampal region; see Bagamasbad et al., 2012 for method) using the TRIzol reagent (Invitrogen) following the manufacturer's instructions. I treated total RNA with DNase 1 (20U; Roche) to remove contaminating genomic DNA and conducted reverse transcription with 1 μg RNA using the High Capacity Reverse Transcription kit with ribonuclease inhibitor (Applied Biosystems, Life Technologies Corp). For real-time quantitative PCR (RTqPCR) I conducted Taqman assays for *Gapdh* and *Klf9* (described by (Bagamasbad et al. 2015)) and SYBR green assays for all other genes. All oligonucleotide primer sequences are given in Supplemental Table 2.5. I conducted RTqPCR using an ABI 7500 fast real-time PCR machine with Absolute qPCR low ROX mix (for Taqman assays) or Absolute qPCR SYBR low ROX mix (ABgene). I designed SYBR green assays using Integrated DNA Technology's RealTime qPCR Assay tool; where possible I designed assays to span exon-exon boundaries. I used a relative quantitation method using cDNA pools to generate standard curves. I normalized all genes to the reference gene *Gapdh*, whose mRNA level was unaffected by treatments (data not shown.)

Generation of stable HT22 cell lines that express biotinylated Klf9

I produced stable cell lines that express biotinylated Klf9 by culturing HT22 cells in 100 mm plates and transfecting them with 5 μg each of pEF1α-BirA and pEF1α-FLBIO-Klf9 (HT22[BirA/FLBIO-Klf9]). To produce stable control cell lines expressing only the biotin ligase BirA (HT22[BirA]) I transfected with 5 μg pEF1α-BirA. Twenty four hr after transfection I changed to medium containing 100 μg/ml zeocin plus 1 μg/ml puromycin (only zeocin was used for the control BirA only cell line). Following antibiotic selection for 5 days individual cells were isolated with cloning cylinders, trypsinized and subcultured as described above.

Expression of BirA and the FLBIO-Klf9 fusion protein was assayed by Western blotting of nuclear extracts. For nuclear extraction I cultured HT22[BirA] and HT22[BirA/FLBIO-Klf9] in 100-mm plates until they reached 95% confluency. I then collected cells with a cell scraper into hypotonic buffer (10 mM HEPES pH 7.9, 10 mM KCl, 1 mM DTT), allowed them to swell for 30 minutes, then lysed them with a motorized homogenizer and added 0.1 volume of sucrose restore buffer (50 mM HEPES pH7.9, 10 mM KCl, 1mM DTT, 6.75% sucrose). Nuclei were centrifuged at 4000 X g for 15 minutes and the supernatant (cytoplasmic fraction) was removed. I then suspended the nuclei in nuclear extraction buffer (50 mM HEPES pH 7.9, 0.5 M KCl, 1 mM DTT), incubated on ice for 40 minutes with vortexing every 10 minutes, then centrifuged for 1 hr at 100,000 x *g*. I quantified the protein concentration of the extracts using the Pierce assay (Thermoscientific), fractionated 40 μg of nuclear protein per lane on a 10% SDS-PAGE gel and transferred proteins to nitrocellulose membrane. To detect BirA I blocked the membrane with SuperBlock (Thermo) and incubated with V5 antibody (Millipore) diluted 1:5000 overnight at 4°C before washing and incubation with HRP-conjugated goat anti-rabbit secondary antibody diluted 1:30,000. To detect FLBIO-Klf9 I first blocked the membrane with PBS containing 5% bovine serum albumin, 10% normal goat serum, 0.5% Triton-X, incubated with Streptavidin-HRP (Thermo) diluted 1:1000 for 1 hr. Immune or streptavidin-HRP complexes were revealed by incubation with peroxide (Pierce) followed by chemiluminescence detection using either film or Phosporimager (BioRad).

RNA Sequencing

For RNA-seq analysis I first extracted total RNA using TRIzol reagent, then purified it using the QIAgen RNEasy kit. Library construction and next generation sequencing were done at the University of Michigan DNA Sequencing Core on twelve RNA samples (1 μg/ sample) representing four treatments (HT22 parent line +/- 1 μg/ml dox for 8 hr, HT22[TR/TO-*Klf9*] line 2-1 +/- 1 μg/ml dox for 8 hr, n=3/treatment). The twelve samples were analyzed on two lanes of an Illumina 2000 HI-seq machine, which generated 23,555,652-50,630,253 million reads per sample. The sequencing reads were de-multiplexed by the University of Michigan DNA Sequencing Core, evaluated and filtered using FastQC software (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/) and aligned to the mouse genome (build mm8) using the program Bowtie (Langmead et al. 2009b). Gene expression was quantified using DESeq (Anders and Huber 2010).

Chromatin extraction and precipitation

Chromatin extraction and chromatin immunoprecipitation (ChIP) were done as described previously (Denver and Williamson 2009; Bagamasbad et al. 2012; Bagamasbad et al. 2015). HT22 cells were grown in 100 mm plates, and for some experiments (i.e. preparation of samples for ChSP-seq libraries) two plates were pooled to increase the total starting quantity of chromatin. For hormone treatment experiments cells were cultured in DMEM with TH-stripped FBS (Samuels et al. 1979) and treated with vehicle (0.1% DMSO) or 30 nM T_3 for 24 hr. After washing with DPBS, I fixed and crosslinked cells by incubation in 1% formaldehyde and 200 nM dithiobis(succinimidyl propionate)(DSP; Thermo) for 10 minutes each, then extracted chromatin. I sonicated the chromatin using a Covaris M220 Focused-Ultrasonicator for 20 minutes using a 2% duty factor, and checked that the DNA had been sheared to 500-600 bp by electrophoresis in a 1% TAE agarose gel. I then flash froze the chromatin with liquid nitrogen and stored it at -80°C until analysis. For each ChIP reaction I used 5 μg purified IgG from goat anti-mBTEB-C17, goat anti-mSin3a-K20, or normal goat IgG (all from Santa Cruz Biosciences).

Chromatin-streptavidin precipitation was done following the method of (Ramadoss et al. 2014). I first washed MyOne T1 streptavidin-conjugated Dynabeads (Invitrogen; 50 ul/reaction) three times with phosphate buffered saline (PBS; pH 7.4), then mixed the beads with 50 μg of chromatin (5 μg of chromatin was reserved for input) and the total volume was brought to 1 ml with ChIP dilution buffer (.01% SDS, 1.1% Triton X-100, 1.2 mM EDTA, 16.7 mM Tris-HCl pH 8.1, 150 mM NaCl). The chromatin and beads were rocked overnight at 4°C. The beads were then collected by magnet and the supernatant removed, then washed three times with 1 ml of 0.5X RIPA buffer (5 mM Tris-Cl pH 8.0, 0.5 mM EDTA, 0.25 mM EGTA, 70 mM NaCl, 0.5% Triton X-100, 0.05% sodium deoxycholate, 0.05% SDS). After the final wash, I resuspended the beads in decrosslinking buffer (50 mM Tris-Cl pH 8.0, 1 mM EDTA, 100 mM NaCl, 0.5% SDS) and removed crosslinks by incubation at 65°C overnight (after this step the input samples were processed simultaneously with the ChSP samples). The DNA was then extracted with phenol:choloroform:isoamyl alcohol (Invitrogen) and precipitated with 0.3 M sodium acetate and 100% ethanol. I added 20 μg (1 μl) molecular biology-grade glycogen (Roche) before precipitation to visualize DNA pellets. After precipitation I resuspended the DNA in 25 μl nuclease-free water and analyzed by qPCR for the *Klf13* promoter and intronic regions. Samples were quantified as percentage of corresponding input sample.

Chromatin streptavidin precipitation (ChSP) sequencing

For ChSP sequencing (ChSP-seq) I prepared DNA from 150 µg of chromatin/sample as described above and submitted ten samples to the University of Michigan DNA Sequencing Core for next generation sequencing: one pooled input DNA sample (pooled from four input samples) from each of the two cell lines HT22[BirA] and HT22[BirA/FLBIO-Klf9], and four ChSP DNA samples from each cell line. I ran 5 samples per lane which generated 18,818,940-27,816,127 million reads per sample. I filtered the sequenced reads using FastQC and aligned them to the mouse mm8 genome using Bowtie (Langmead et al. 2009a). Peaks were identified using MACS (REF) and PePr software (Zhang et al. 2008; Zhang et al. 2014), and assigned to genes using ChIP-enrich (Welch et al. 2014). Additional analysis of the locations of peaks and mapping of regions of highest peak density was conducted using Cis-regulatory Element Annotation System software (Shin et al. 2009). I clustered peaks by shape using the program SIC-ChIP (Cremona et al. 2015). Motif enrichment was analyzed using HOMER (Heinz et al. 2010), and gene ontology analysis was done using GeneCoDis (Carmona-Saez et al. 2007; Nogales-Cadenas et al. 2009; Tabas-Madrid et al. 2012).

Generation of HT22 Klf9-knockout cells using CRISPR/Cas9 genome editing

I constructed a guide RNA (gRNA)/Cas9 expression plasmid (OriGene) containing the gRNA sequence 5’ ggggcgctccggaagccgag 3’ (this gRNA targets a sequence in the 5’ region of the *Klf9* gene). I transfected the parent HT22 cell line with this vector which expresses enhanced green fluorescent protein, and conducted fluorescence-assisted-cell sorting (FACS) at the University of Michigan Flow Cytometry core to isolate EGFP positive cells. I isolated clonal lines of the FACS sorted cells as described above, extracted genomic DNA and screened for mutations by direct DNA sequencing of PCR-amplified DNA subcloned into pGEM T-easy vector (Promega) corresponding to *Klf9* exon 1. I selected Klf9-null clones (defined by the absence of a wild-type *Klf9* allele and the presence of mutations predicted to create nonsense or prematurely truncated proteins) cultured them simultaneously with the parent HT22 line, harvested cells, extracted RNA and analyzed gene expression by RTqPCR.

Animals

I purchased C57BL/6 mice from Jackson Labs and maintained them on a 12L:12D photoperiod with food and water provided *ad libitum.* Animals were killed by rapid decapitation and a section of the brain that included the hippocampus was dissected and flash-frozen for subsequent chromatin or RNA extraction. Mice null for Klf9 were bred from animals provided by Dr. Yoshiaki Fuji-Kuriyama and Dr. Frank Simmen (Morita et al. 2003). All procedures involving animals were approved by the University of Michigan University Committee on the Care and Use of Animals.

Statistical analysis

Derived (normalized) values from RTqPCR, ChIP/ChSP and dual luciferase assay were $\log_{10}$ transformed before analysis by one-way ANOVA followed by the Holm-Sidak multiple comparison test, or by unpaired Student's *t*-test using SYSTAT (version 13; SPSS Inc., Chicago, IL). Data are reported as mean ± standard error of the mean (SEM).

Results

Validation of stable HT-22 cell lines for the identification of Klf9 genomic targets

I analyzed seven HT-22 pCDNA4:TO-Klf9::pCDNA6:TR clonal lines for baseline and dox-inducible *Klf9* mRNA, and selected one line (2-1) for further analysis. The mean baseline *Klf9* mRNA level of clonal line 2-1 (hereafter referred to as HT22[TR/TO-Klf9]) was slightly higher than the parent line, but was not significantly different (*p*=.063, Holm-Sidak post-hoc test). After dox treatment for 8 hr *Klf9* mRNA increased approximately 10-fold (Figure 2.1A), which is within the physiological range seen in HT22 cells and neonatal mouse brain following hormone treatment (Bagamasbad et al. 2015), and in mouse brain during development (Denver and Williamson 2009). To determine if the elevated *Klf9* mRNA following dox treatment resulted in increased production of functional Klf9 protein I conducted a transient transfection reporter assay in HT22[TR/TO-Klf9] cells with a luciferase vector containing three tandem repeats of the BTE sequence (pGL4.23-3xBTE), which supports Klf9-dependent transactivation or transrepression depending on the cell type (Imataka et al. 1992; Hoopfer et al. 2002). Dox treatment for 8 hr decreased luciferase activity from the pGL4.23-3xBTE vector by 20%; no change was seen in activity from pGL4.23-empty (Figure 2.1B). I also co-transfected parent HT22 cells with the reporter pGL4.23-3xBTE and the pCS2-Klf9 expression vector, and observed significant reduction in luciferase activity compared with cells transfected with the pCS2 empty vector (Figure 2.1C). Taken together, my results show that *Klf9* can be induced within the physiological range by dox in HT22[TR/TO-Klf9] cells, and this leads to the production of functional Klf9 protein.

I next engineered HT22 cells to express the *E. coli* biotin ligase BirA (HT22[BirA]) or BirA plus a Klf9 fusion protein with an N-terminal FLAG tag and biotin ligase recognition peptide

(HT22[BirA/FLBIO-Klf9]) (Kim et al. 2009). This allows for high-affinity purification of Klf9 in chromatin by streptavidin precipitation (ChSP). The biotinylated fusion protein was readily detected in nuclear extracts of HT22 cells by Western blotting with streptavidin-HRP (Fig. 1D). Klf9 associates in chromatin with the *Klf13* 5' upstream region in NIH 3T3 cells (M. Nikiforov, unpublished results). I therefore looked at whether Klf9 associated with this region in HT22 cells by both chromatin immunoprecipitation (ChIP; for Klf9) in parent HT22 cells, and by ChSP in HT22[BirA] and HT22[BirA/FLBIO-Klf9] cells. The ChIP for Klf9 showed ~5 fold enrichment above background (mock ChIP with normal goat IgG) at the *Klf13* 5' upstream region in HT22 parent cells; however, this enrichment was only evident after Klf9 expression was induced by 24 hr treatment with 30 nM TH (Figure 2.1E). In contrast, ChSP resulted in ~25 fold enrichment above background (HT22[BirA/FLBIO-Klf9] versus HT22[BirA]; Figure 2.1F). Neither technique showed enrichment at a *Klf13* intronic region lacking candidate Klf9 binding sites (Figure 2.1E and F). These results show that both native Klf9 and FLBIO-Klf9 associate in chromatin at the candidate locus *Klf13*, and the ChSP technique results in a much higher signal/noise ratio than ChIP.

Identification of Klf9-regulated genes in dox-inducible cells by RNA sequencing

I conducted RNA sequencing (RNA-seq) on parent HT22 cells and the HT22[TR/TO-Klf9] cell line treated with or without 1 μg/ml dox for 8 hours (n=3 replicates/treatment for parent +/- dox, 3 replicates for HT22[TR/TO-Klf9]-dox and 2 replicates for HT22[TR/TO-Klf9]+dox; a third replicate had to be discarded due to technical errors). Sequencing reads were aligned to the mm8 build of the mouse genome using Bowtie (Langmead et al. 2009a), and differences in transcript abundance were quantified using DESeq (Langmead et al. 2009a; Anders and Huber

2010). Comparing the parent HT22 line treated with or without dox we found no annotated transcripts that showed statistically significant expression differences and so we pooled these data for further comparison with the HT22[TR/TO-Klf9] cells. Comparing the parent line with vehicle-treated and with dox-treated HT22[TR/TO-Klf9] cells found 5,378 and 5,523 differentially expressed genes, respectively (FDR-adjusted $p<.05$). Most (3,472) of these genes were common to both comparisons, but did not differ between dox-treated and untreated HT22[TR/TO-Klf9] cells, suggesting that they represent a common response to stable transfection and antibiotic selection. Comparing the vehicle and dox-treated HT22[TR/TO-Klf9] cells found 768 differentially expressed genes; because dox treatment did not have any effect on the parent line transcriptome I interpret these as Klf9-regulated genes. In support of this interpretation, most of these genes (623) were also differentially expressed between the parent line and dox-treated HT22[TR/TO-Klf9] cells. I found 567 downregulated and 201 upregulated by Klf9, suggesting that it functions primarily as a transcriptional repressor in these cells. The changes in expression level after 8 hr dox treatment ranged from from -1.2 to 1.52 ($\log_2$ fold change). Because the fold-changes were small, I did not apply a fold-change cutoff; all genes are identified based on FDR-adjusted p value alone. In practice, the minimum mRNA $\log_2$ fold change required to identify a gene as significantly changes was -.23 or .23. The top 10 up- and top 10 down-regulated genes are given in Table 2.1, and a list of all differentially regulated genes is given in Supplemental Table 2.1. I validated gene repression by Klf9 using RT-qPCR on RNA isolated from parent and HT22[TO/TR-Klf9] cells treated with or without dox for 8 hr (Fig. 2.2A).

To further validate the RNA-seq data set and better understand the kinetics of Klf9-dependent repression, I performed RT-qPCR on HT22[TO/TR-Klf9] cells treated with dox for 0, 2, 4, 8, 12 or 24 hr. *Klf9* mRNA was significantly elevated by 2 hr of dox treatment, peaked at 4 hr and remained elevated through 24 hr. Time course analysis of ten genes confirmed repression by Klf9, although with different kinetics and magnitude. Nine of the ten genes analyzed that were found to be repressed by Klf9 in the RNA-seq experiment were confirmed by RT-qPCR (Fig. 2.2B). One gene (*Hhipl*) was not significantly repressed when examined by RT-qPCR (data not shown). In contrast, only two upregulated genes (*Rnf34* and *Rpp38*) of five tested (*Mitd*, *Cryl1* and *B3galt*) showed increased expression after dox treatment, and neither was upregulated during the time course induction experiment (not shown).

Identification of sites of Klf9 association in chromatin across the genome of HT22 cells

I conducted ChSP sequencing (ChSP-seq) on DNA isolated from HT22[BirA] and HT22[BirA/FLBIO-Klf9] cells to identify sites of Klf9 association in chromatin. I used two independent peak calling programs (MACS and PePr) to identify genomic regions with higher densities of mapped reads (Zhang et al. 2008; Zhang et al. 2014). MACS analysis identified 8,841 while PePr analysis identified 3,382 peaks that were present in HT22[BirA/FLBIO-Klf9] but not in HT22[BirA] cells. All but four of the peaks called by PePr were also called by MACS; the peaks called by both programs were more enriched (higher fold-change in the number of mapped reads in HT22[BirA/FLBIO-Klf9] cells compared to HT22[BirA]) than those called only by MACS. To focus on the highest-confidence Klf9 peaks I restricted further analysis to only those peaks called by both programs (total = 3,378). I then used the program PeakSplitter to identify and subdivide regions with multiple closely spaced peaks (Salmon-Divon et al. 2010). Peaksplitter is only compatible with MACS; I therefore analyzed the MACS dataset with Peaksplitter, then used the program BedTools to extract the overlap of these split peaks with the peaks called by PePr (Quinlan and Hall 2010). Examples of the results of this approach are shown in Figure 2.3. This approach gave a final count of 3,516 Klf9 peaks, which ranged from 8 to 2,429 bp in length (average 881 bp). All peak coordinates, nearest gene and average sequencing read density across the peak (based on build mm8 of the mouse genome) are given in Supplemental Table 2.3. Sequencing and analysis of ChSP DNA from HT22[BirA] cells showed very few regions (20 by MACS, 52 by PePr) with higher mapped sequencing read density compared with HT22[BirA/FLBIO-Klf9] cells. This demonstrates that the BirA-FLBIO platform allowed for identification of Klf9-associated genomic regions with very low background.

Klf9 associates in chromatin in HT22 cells primarily with proximal promoter regions

I used the ChIP-enrich web tool (Welch et al. 2014) to assign Klf9 peaks to genes based on the nearest transcription start site, and to identify where the peaks were distributed with respect to the transcription start sites (TSS) annotated genes. Based on this analysis, 88.6% of the peaks fell within 10 kb of a TSS, and of these, 86% (or 76.2% of total peaks) were centered at 1 kb or less from a TSS (Figure 2.4A). The ChIP-enrich software pairs peaks with genes based on the closest TSS, which results in some genes having multiple peaks associated with them. After accounting for such double-counted targets, this left 2,847 unique genes with at least one associated Klf9 peak; 2,749 had at least one peak within 10 kb of a transcription start site. Of 567 genes that were repressed by Klf9 in the RNA-seq experiment, 307 (54%) have a Klf9 peak within 10 kb of their TSS. In contrast, of the 201 upregulated genes only 10 (5%) had a peak within 10 kb of their TSS (Figure 2.4B).

I next used the HOMER peak annotation program to analyze the distribution of Klf9 peaks relative to the TSS. The majority of Klf9 peaks were within 1 kb of a TSS; 32.7% were centered upstream, 21.7% were centered within the 5' UTR, and 27.1% were centered either in the first exon or the first intron (Figure 2.4C). I then used the Cis-regulatory element annotation system (CEAS) to map how sequencing reads were distributed with respect to genomic features (Shin et al. 2009). Analysis of the distribution of mapped sequencing reads around TSS regions showed a slight bias towards the region immediately upstream of the TSS (Figure 2.3D). Therefore, the larger peaks tend to be centered in 5' flanking regions, but as many or more of the peaks occur downstream of the TSS.

Validation of Klf9 peaks identified by ChSP in HT22 cells

To validate the ChSP-seq dataset I analyzed 8 Klf9 peaks representing a range of peak heights (20-220 overlapping reads) using targeted ChSP- and ChIP-qPCR assays. The aligned sequencing read densities from the 8 genomic regions are shown in Fig. 2.5A, with peaks arranged from highest (200 reads; upper left panel) to lowest (20 reads; lower right panel). The small peak at the *Mapk11* 5' upstream region was detected by MACS but not by PePr (see also Figure 2.3). *Mapk11* was repressed by forced Klf9 expression (Figure 2.2B and C), so I analyzed this region to investigate the lower limit of detection of the ChSP-seq data set. All genomic regions tested showed significant ChIP signals in chromatin from HT22[BirA/FLBIO-Klf9] cells compared with HT22[BirA] cells (Fig. 2.5B). This was confirmed at all 8 regions by targeted ChIP assay for Klf9 on chromatin from HT22[TR/TO-Klf9] cells treated with or without dox for 8 hr (Fig. 2.5C). I also conducted ChIP assay on chromatin extracted from the parent HT22 cell line treated with or without T_3 for 24 hr. This showed significant Klf9 ChIP signal at four genes which was unaffected by T_3 (Figure 2.6). I detected no significant enrichment of Klf9 ChSP signal at intronic regions located 10 kb or more downstream from the identified Klf9 peaks in the *Klf16*, *Limk1* and *Nr3c1* genes (Supplemental Figure 2.7A).

Klf9 associates in chromatin from mouse hippocampus with genomic regions identified by ChSP-seq in HT22 cells

To determine if Klf9 associates in chromatin in mouse hippocampus at genomic sites identified in HT22[BirA/FLBIO-Klf9] cells, I conducted targeted ChIP assays using chromatin isolated from the hippocampal region of brains of adult C57BL/6 mice (five male and five female). I targeted the same 8 genomic regions described above, and found significant Klf9 ChIP signal at 7 of the 8 regions (Fig. 2.5D). All 7 regions showed signal above ChIP with NGS IgG in both sexes (not shown); therefore I pooled data from both. The failure to detect Klf9 ChIP signal at the 5' upstream region of *Mapk11* is consistent with this region having the lowest ChSP and ChIP signal in HT22 cells. I detected no significant enrichment of Klf9 ChIP signal in mouse hippocampal chromatin at intronic regions located 10 kb or more downstream from the identified Klf9 peaks in the *Klf13*, *Klf16*, *Limk1* and *Nr3c1* genes (Supplemental Fig. 2.7B).

Forced expression of Klf9 promotes recruitment of Sin3a to Klf9 peaks at Klf9-repressed genes

My RNA-seq experiment showed that Klf9 is predominantly a transcriptional repressor in HT22 cells. The scaffolding repressor protein Sin3a interacts with histone deacetylases (HDACs), which generate a compact chromatin structure, and Klf9 possesses an N-terminal Sin3a-interacting motif (Zhang et al. 2001). I therefore investigated whether Sin3a was recruited to genomic regions of Klf9 association in chromatin by conducting ChIP assay for Sin3a on chromatin isolated from HT22[TR/TO-Klf9] cells treated with or without dox for 12 hr. This treatment led to a significant increase in the Klf9 ChIP signal at the *Klf13*, *Klf16*, *Limk1* and *Mapk11* promoters (Fig. 2.8A), and Sin3a signal was increased at the *Klf16* and *Limk1* promoters, but was unchanged at the *Klf13* promoter and was reduced at the *Mapk11* promoter (Fig. 2.8B).

Identification of consensus Klf9 binding sites at Klf9 ChSP-seq peaks

I used the program HOMER to identify enriched DNA sequence motifs in Klf9 ChSP-seq peaks (Heinz et al. 2010). The most highly enriched sequence was a GC-rich Sp/Krüppel-like motif (GCCACGCCCMCY) that was present in 75.6% of all peaks; hereafter I refer to this sequence as the 'Klf9 consensus motif' (Table 2.2). I identified 18 additional GC-rich motifs that are enriched at Klf9 peaks that have sequence similarity with the Klf9 consensus motif (Supplemental Table 2.4). The Klf9 consensus motif and the 18 additional GC-rich motifs are hereafter collectively referred to as "GC box". At least one GC box was present in 98% of all Klf9 peaks, supporting that the presence of GC boxes is important for targeting Klf9 in the genome. In addition, HOMER identified 18 significantly enriched motifs in Klf9 peaks other than the Klf9 consensus motif, the most significantly enriched of which ($p<1*10^{-20}$) matched previously reported binding sites for Egr2, Elk4, E2f1, Fosl2, bHLH/E-box binding factors and Rfxdc2 (Table 2.2A). A complete list of enriched motifs is shown in Table 2.

The Klf9 consensus motif tended to occur at or near the center of peaks, and the average density of mapped sequencing reads across the peaks closely matched the frequency of motif occurrence (Fig. 2.9A). The peaks contained between 0 and 19 GC boxes (one outlier contained 48), with an average of 4.47/peak. There was a weak but statistically significant correlation between the number of non-redundant GC boxes and average peak height (Spearman Rank Order correlation, R=.245, *p*=.0000002) (Fig. 2.9B).

I also used HOMER to analyze the promoters of genes that were induced by Klf9. Sequences of 1000 bp in length located upstream of the TSSs of the upregulated genes were downloaded from the UCSC genome browser. *De novo* motif discovery using HOMER found much lower frequency of Sp/Klf motifs at these peaks compared with the downregulated genes (40.43% vs 75%).

Peak shape clustering revealed different categories of Klf9 peaks that correlate with repression by Klf9

I analyzed Klf9 peaks using the program SIC-ChIP (Cremona et al. 2015), which clusters peaks based on five shape parameters (peak height, peak width at half-maximum height, peak area, number of local peaks, and overall complexity normalized to height). Boxplots of the distribution of each parameter in each cluster and a scatterplot of how shape parameters correlate with each other and group peaks by cluster are shown in Fig. 2.10. By these criteria we divided the peaks into three categories, examples of which are shown in Fig. 2.11A. Peaks in Cluster 1 (2115 peaks) are of low average height and low complexity; peaks in Cluster 2 (812 peaks) are of low height but greater complexity; peaks in Cluster 3 (549 peaks) are large and of low complexity.

The Klf9 consensus motif was highly enriched in peaks from all three categories. In peaks of Clusters 1 and 3, the motifs tended to be located near the center of the peak, while in peaks of Cluster 2, their distribution was spread almost evenly across the peak (Fig. 2.11B, upper panel). The density of mapped reads (reflective of peak height) closely matched the distribution of Klf9 consensus motifs in all three clusters (Fig. 2.11B, lower panel). Sequencing read density (peak height) therefore correlates with the presence of Klf9 consensus motifs even in complex peaks with multiple local maxima. Peaks from clusters 1, 2 and 3 had an average of 3.5, 5.87 and 5.62 GC boxes, respectively (Fig. 2.11C, upper panel). There was no significant difference between Clusters 2 and 3 in overall number of GC boxes, but peaks from Cluster 3 contained more copies of the Klf9 consensus motif (1.9/peak in Cluster 3 versus 1.1 and 1.3/peak in Clusters 1 and 2; Fig. 2.11C, lower panel).

The proportion of peaks associated with Klf9-repressed genes varied by cluster; 8.1, 12.3 and 18.36% of peaks from cluster 1, 2 and 3 respectively were associated with Klf9-repressed genes (Fig. 2.11D). Peaks from Cluster 3 accounted for 15% of total peaks, but 31.3% of Klf9-repressed genes with at least one peak associated had a peak from Cluster 3 in their genomic region. Peaks of Cluster 1 accounted for 60% of all peaks, but only 52.9% of peak-associated repressed genes had a peak from Cluster 1 in their genomic region (after excluding genes that also had peaks from Clusters 2 or 3 this proportion drops to 40%). Peaks from Cluster 2 were also disproportionately likely to be associated with repressed genes; peaks from Cluster 2 accounted for 23% of all peaks but 32% of peak-associated repressed genes had at least one peak from Cluster 2 (Fig. 2.11E). Peaks from Clusters 2 and 3 are therefore more likely to be associated with repression by forced Klf9 expression, although the presence of such peaks is neither necessary nor sufficient for repression.

Repression by Klf9 requires intact GC boxes within regulated promoters

To determine if the Klf9 consensus and GC-box motifs that I identified are important for transcriptional repression of Klf9 target genes we transfected HT22[TR/TO-Klf9] cells with pGL4.23 reporter vectors containing DNA fragments (500-2000 bp) corresponding to the 5' upstream regions of *Klf13*, *Klf16*, *Limk1* and *Mapk11.* Treatment with dox for 24 hr reduced luciferase activity from pGL4.23-Klf13 by 33%, from pGL4.23-Klf16 by 45%, and from pGL4.23-Limk1 by 19.5% (Fig. 2.12A); luciferase activity from the pGL4.23-Mapk11 vector was unaffected by dox treatment. The 439-bp fragment of the *Klf13* 5' upstream region contains 6 GC box motifs (Fig. 2.12B). We used site-directed mutagenesis to convert each of these motifs to a series of 7 T-nucleotides; the complete sequence of the *Klf13* promoter fragment and the location of the mutated nucleotides are shown in Fig. 2.13. Mutation of two of the 6 sites (Box 1 and Box 2) did not significantly influence repression by Klf9, either individually or in combination (Fig. 2.12C). However, mutation of all six sites abolished Klf9-dependent repression of this promoter (Fig. 2.12C).

Klf9 knockout leads to dysregulation of Klf9 regulated genes in HT22 cells and in mouse brain *in vivo*

To determine if loss of Klf9 influences expression of Klf9 target genes I generated Klf9 knockout HT22 cell lines using CRISPR/Cas9 genome editing. I derived two lines (designated CRISPR Line 1 and CRISPR Line 2) that had deletions that led to either frame-shift mutations or premature stop codons in the *Klf9* gene. This led to increased expression of *Slc1a2*, *Klf13, Klf16, Limk1* and *Klf11* in CRISPR Line 1 and increased expression of *Klf13, Limk1* and *Klf11* in CRISPR Line 2 (with a trend towards increased expression of *Klf16*)(Fig. 2.14A). Expression of *Mapk11* was not significantly altered in either line. This shows that deletion of Klf9 in HT22 cells leads to de-repression of Klf9 target genes and subsequent increased expression.

I analyzed the mRNA levels of Klf9-regulated genes using RNA isolated from the hippocampus of wild-type and Klf9-null mice and found dysregulation of all 5 genes analyzed. The Klf9-repressed genes *Klf13*, *Limk1* and *Mapk11* showed differential expression between WT and Klf9-null mice, although the direction of dysregulation varied. Expression of *Limk1* was higher in Klf9-null mouse brain, consistent with repression of this gene by Klf9 in HT22 cells. However, *Klf13* and *Mapk11* showed decreased expression (Fig. 2.14B). The Klf9-repressed genes *Apc2* and *Nlgn2* showed higher and lower expression respectively in Klf9-null mouse brains (Fig. 2.15).

Klf9-regulated genes are associated with cystokeleton, cell growth and cell survival

I conducted pathway analysis using GeneCoDis on Klf9 regulated genes (Table 2.3) (Carmona-Saez et al. 2007; Nogales-Cadenas et al. 2009; Tabas-Madrid et al. 2012). The most enriched PANTHER pathway among Klf9-repressed genes was “P00047:PDGF signaling pathway”. The second-most enriched pathway was “P00016:Cytoskeletal regulation by Rho GTPase”. Among the Klf9-regulated genes in this category are *Limk1*, which has been shown to promote neurite extension through inhibition of actin depolymerization (Endo et al. 2003), and *Mapk7* (ERK5), which positively regulates neurite extension and arborization in hippocampal neurons (Wang et al. 2014). This is consistent with previous reports that showed that forced *Klf9* expression can repress neurite outgrowth and regeneration in mature neurons (Moore et al. 2009; Avci et al. 2012).

I then conducted pathway analysis on genes that Klf9 was found to associate with in chromatin. The most enriched PANTHER pathways among this set of genes were “Apoptosis”, “Integrin signaling pathway”, “Inflammation mediated by chemokine and cytokine signaling pathway" and "Cytoskeletal regulation by Rho-GTPase" (Table 2.4 and Supplemental Table 2.5). Pathway analysis on the subsets of genes associated with different classes of peaks revealed a partitioning of functions (Table 2.5). The top PANTHER pathways enriched in genes associated with Cluster 1 peaks were "Apoptosis", "Wnt signaling pathway" and "Egf receptor signaling pathway". In contrast, the top pathways enriched in the set of genes associated with Cluster 2 peaks were "Cytoskeletal regulation by Rho GTPase" and "Metabotropic glutamate receptor group II pathway", while Cluster 3 peaks were associated with genes in the pathways "PDGF signaling", "Fas signaling pathway" and "Cytoskeletal regulation by Rho GTPase".

Discussion

Here I report the first genome-wide analysis of Klf9 genomic targets in neurons. Klf9 has been implicated in several aspects of neural development and regeneration, and is an evolutionarily conserved immediate early target of several signaling pathways, including CORT (Bagamasbad et al. 2012), TH (Denver and Williamson 2009), NFκB (Bagamasbad et al. 2015), oxidative stress (Zucker et al. 2014), and electrical activity (Scobie et al. 2009). I therefore set out to identify its genomic targets in neurons to understand how it may mediate the transcriptional responses to these stimuli, and regulate neuronal differentiation, survival and plasticity. We identified Klf9-regulated genes and regions of association in chromatin in the mouse hippocampal-derived neuronal cell line HT22, and verified that many of these genes were *bona fide* targets in mouse brain *in vivo*.

Klf9 is predominantly a repressor of gene transcription in HT22 cells, and associates in chromatin in close proximity to transcription start sites

Our RNA-seq experiment conducted on HT22 cells showed that Klf9 acts predominately as a transcriptional repressor. This is consistent with a recent study that suggests that Klf9 functions primarily as a repressor in glioblastoma cells (Ying et al. 2014). The genes *Rnf34* and *Rpp38* were upregulated after 6 or 8 hours in separate experiments (not shown), but I was unable to validate either these or the genes *Mitd1*, *B3galt* and *Cryl1* in the time course experiment shown in Figure 2.2B. The Klf9-upregulated genes in my study may therefore be mostly false positives or indirect targets. Early studies on Klf9 function showed that it could act as a transcriptional activator or repressor depending on the number of GC boxes present in the regulator element (Imataka et al. 1992; Kobayashi et al. 1995). In CV-1 cells, Klf9 activated transcription from promoters containing multiple GC boxes, but repressed transcription from promoters containing a single GC box. My ChSP experiment found that Klf9 associates predominantly with genomic regions within 1 kb of TSSs, and that repressed genes were much more likely than induced genes to have Klf9 associated. These findings support that Klf9 represses gene transcription by interacting in chromatin at, or in close proximity to, proximal promoters. Only 5% (10) of Klf9-induced genes had associated Klf9 peaks.

Integrated analysis by multiple peak calling programs assists in identification of genomic regions where Klf9 associates in chromatin

I used two peak-calling programs (MACS and PePr) to identify genomic regions where Klf9 associates in chromatin in HT22 cells. Both programs identified 3,378 peaks (which was extended to 3,516 with PeakSplitter); MACS identified an additional 5,463 peaks that were uniformly only slightly above the HT22[BirA] background Some of these small peaks were associated with genes repressed by Klf9, including *Mapk11*. Forced expression of Klf9 reduced *Mapk11* mRNA and Klf9 protein was detectable at *Mapk11* HT22[TR/TO-Klf9] cells (Fig. 2.2B and 2.5C), but Klf9 did not associate with *Mapk11 in vivo* (Fig. 2.5D), the *Mapk11* promoter did not support repression in a transient transfection assay (Fig. 2.12A) and Klf9 knockout did not change *Mapk11* expression in HT22 cells (Fig. 2.14A). However, *Mapk11* was dysregulated in Klf9-null mice, and I have evidence that *Mapk11* expression is reduced after combined TH and CORT treatment, which robustly increases *Klf9* expression (P. Bagamasbad, unpublished data). This suggests that *Mapk11* is only regulated by Klf9 under conditions of overexpression. Many ChIP-seq data sets rely on over-expressed tagged proteins; my data suggests that such results should be interpreted with care to ensure downstream analyses focus on only the most high-confidence peaks.

Klf9 association in chromatin is strongly associated with the presence of GC boxes

I identified a Klf9 consensus motif and a large array of GC-rich motifs that were highly enriched at Klf9 peaks. Nearly all peaks (98%) had at least one GC box, and 75% had at least one copy of the highest-confidence consensus motif (GCCACGCCCMCY). The consensus motif tended to occur near the center of peaks and its position correlated with the density of mapped reads, supporting that Klf9 binds directly to these DNA sequences. Early studies showed that Klf9 acted as a transcriptional activator at promoters with multiple GC boxes. Most Klf9 peaks (88%) had more than one GC box, but Klf9 acted almost exclusively as a repressor, so its regulatory activity is not necessarily related to the number of GC boxes present. Other studies have shown that Klf9 can activate or repress the same promoter in the same cell type depending on developmental stage (Mitchell and DiMario 2010). The chromatin environment and the complement of interacting proteins may be more important than the promoter sequence for determining whether Klf9 acts as an activator or repressor. Many other TF-responsive motifs were found to be highly overrepresented in Klf9 peaks (Table 2.2), including motifs for TFs for immediate early genes involved in neural activity-dependent transcription such as Egr and Fos (Benito and Barco 2015); this provides a basis for predicting which signaling pathways may be influenced by Klf9 in neurons.

Clustering analysis provides a basis for differentiating peaks associated with repressed genes

Different types of chromatin-associated proteins tend to have different characteristic association profiles (e.g. broad regions for histones, discrete regions for TFs) and different genomic regions associated with the same factor may have different ‘shapes’ (Cremona et al. 2015). I used a novel clustering algorithm (SIC-ChIP) to group peaks based on shape to determine if different binding profiles were associated with distinct sets of genes or sequence environments. I found that peaks segregated into three categories. Large, sharp peaks (Cluster 3) or broad, complex peaks (Cluster 2) were more likely to be associated with genes repressed by forced Klf9 expression than smaller, less complex peaks (Cluster 1). The different binding signatures could reflect at least three different types of differences between peaks: different numbers of Klf9 molecules recruited, differences in chromatin environment (nucleosome density and histone modifications) or differences in protein-protein interactions. Peaks from Clusters 2 and 3 had more GC boxes present than peaks from Cluster 1 (Fig. 2.11C), which is consistent with recruitment of a greater number of Klf9 molecules and their greater enrichment as measured by height and area under the curve (Fig. 2.10C and D). Cluster 3 peaks had the same average number of GC-boxes as Cluster 2 peaks, but they contained more copies of the Klf9 consensus motif (Fig. 2.10C); the high, sharp signal at these loci may reflect a greater likelihood of Klf9 association, or greater likelihood of occurrence of protein-protein interaction partners that lead to increased crosslinking efficiency. These same cofactors may also promote dynamic repression by changes in Klf9 level, as a greater proportion of Cluster 3 peaks were associated with Klf9-repressed genes (Fig. 2.610 and E). Future genome-wide analyses on histone modifications, DNA accessibility and RNA polymerase association in either HT22 cells or mouse hippocampus will help correlate these binding signatures with the chromatin environment, shedding light on how Klf9 functions in chromatin.

Repression by Klf9 requires intact GC boxes that may function redundantly

To investigate the mechanisms of Klf9-dependent repression, I isolated and subcloned DNA fragments corresponding to the 5' upstream regions of four Klf9-responsive genes corresponding to peaks identified by ChSP-seq. I showed via site-directed mutagenesis of the *Klf13* promoter that it is possible for many GC-rich motifs to act redundantly; deletion of two of six consensus sites in a 500 bp fragment of the *Klf13* promoter had no effect on repression by Klf9. Deletion of all six resulted in a loss of repression. The presence of multiple GC boxes at most Klf9 peaks implies that such redundancy may be a feature of many, if not most, Klf9 genomic targets. These sites could also potentially act as binding sites for other Sp or Klf-like proteins, which suggests a potential for combinatorial regulation by a network of Klfs (Jiang et al. 2008). Previous work has shown that Klf9 can enhance *Trb* autoinduction in the absence of an intact DNA binding domain in the frog *Xenopus laevis* (Bagamasbad et al. 2008; Hu et al.

2016). At present I do not know if Klf9 can function in the absence of normal DNA binding capacity in the mammalian brain.

The Klf9 cistrome in HT22 cells is enriched in cystoskeleton- and apoptosis-related genes

Several genes involved in actin polymerization, such as *Limk1*, were direct genomic targets of Klf9. The repression of positive regulators of actin polymerization such as *Limk1* is consistent with existing work showing that Klf9 represses dendritic and axonal remodeling and outgrowth in mature neurons (Moore et al. 2009; Avci et al. 2012). However, this does not explain how Klf9 promotes neurite elaboration and outgrowth in immature neurons (Denver et al. 1999; Cayrou et al. 2002). It may regulate a different set of genes, perhaps repressing repressors of growth, or it may upregulate rather than repress the same loci identified in this study at earlier developmental stages (Mitchell and DiMario 2010).

Genes with Klf9 associated in their genomic regions, but not those whose expression was repressed by Klf9, were associated with pro-apoptotic signaling. Of the 31 Klf9-associated genes in the "Apoptosis" category, at least 12 have the associated GO term "Positive regulation of apoptosis" as indicated by the DAVID gene ontology web tool (Huang da et al. 2009a; Huang da et al. 2009b). Previous work has shown that Klf9 can promote xenobiotic and oxidative stress-induced cell death (Mannava et al. 2012; Zucker et al. 2014). When I conducted pathway analysis on subsets of genes associated with different peak clusters, we found that only Cluster 1 peaks were associated with apoptotic signaling, while peaks from Clusters 2 and 3 were enriched in cytoskeletal and morphology-related pathways. This supports a model where rapid Klf9 upregulation under normal physiological conditions suppresses morphological remodeling by rapid regulation of a set of 'strong' targets (highly enriched peaks), while prolonged upregulation of Klf9 or upregulation under toxic or stressful conditions may promote regulation of apoptotic genes (‘weak’ targets), ultimately leading to cell death.

Klf9 associates with the promoters of several Klfs and directly represses *Klf13* and *Klf16*

I found that *Klf10*, *11*, *13*, and *16* all showed Klf9 binding to their proximal promoters. Klf9 directly repressed expression of *Klf13* and *Klf16,* and knockout of Klf9 increased *Klf11* expression in HT22 cells. Klf9 and Klf13 have previously been shown to interact in the regulation of decidualization in the mammalian uterus, but to my knowledge this is the first evidence of direct cross-regulation between these proteins by association with promoter regions (Pabona et al. 2010; Heard et al. 2011; Heard et al. 2012). Krüppel-like factors 9, 10, 11 and 13 and 16 all belong to the Sin3a binding subfamily and share significant sequence homology in their N-terminal regions (Zhang et al. 2001; Knoedler and Denver 2014). Cross-regulation by Sin3a-binding Klfs may be a mechanism for adjusting where Sin3a is targeted in the genome. The *Sin3a* genomic region contained a Klf9 peak (Fig. 2. 5) but the gene was not repressed or upregulated by forced Klf9 expression. Klf9 may regulate its expression under other conditions, adding another mechanism to regulate global gene repression.

In addition, the *Klf9* gene itself showed evidence of Klf9 association to both its proximal promoter and an upstream nuclear receptor enhancer region, although since we have previously shown that this region can interact with the proximal promoter by chromosomal looping it is unclear where the protein is actually associating (Bagamasbad et al. 2015). This raises the possibility that Klf9 may regulate its own transcription, which may be a feedback mechanism for controlling its expression after upregulation by hormones and other stimuli.

Summary and Future Directions

The data presented in this chapter provide a basis for further exploration of Klf9's mechanisms of action in neurons. Because Klf9 associates with many more genes than were regulated by forced Klf9 expression, future transcriptomic studies should be conducted to determine if loss of Klf9 results in higher or lower mRNA levels of these genomic targets. Since Klf9 associated with many genes involved in pro-apoptotic signaling it will be important to determine if *Klf9*$^{-/-}$ mice show greater or lesser vulnerability to neuronal cell death in response to neurological insults. Finally proteomic studies should be conducted to elucidate the mechanisms by which Klf9 regulates target genes and functions in chromatin.

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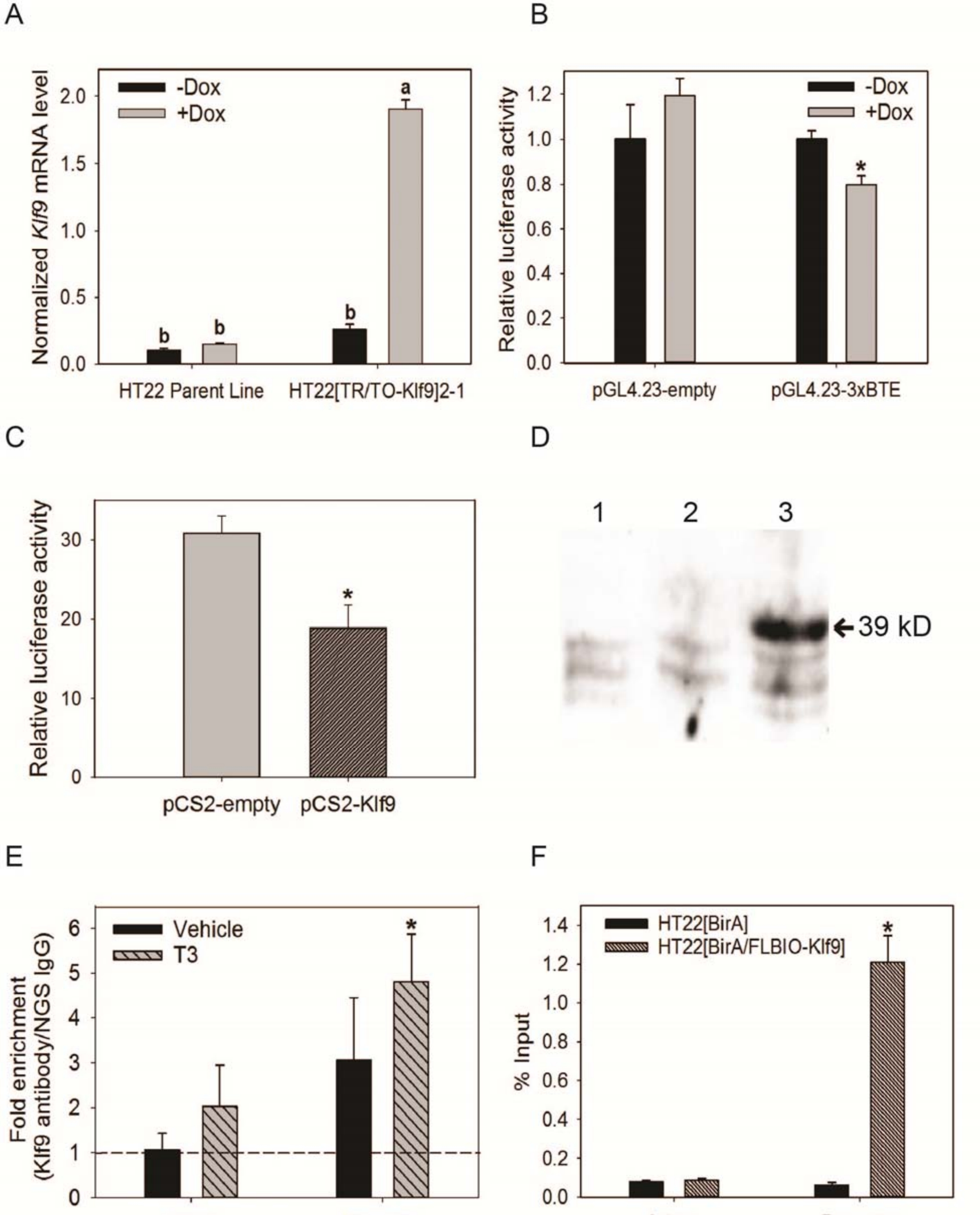

A
B
Normalized *Klf9* mRNA level
-Dox
+Dox
a
b
b
b
2.0
1.5
1.0
0.5
0.0
HT22 Parent Line
HT22[TR/TO-Klf9]2-1
Relative luciferase activity
1.2
1.0
0.8
0.6
0.4
0.2
0.0
*
pGL4.23-empty
pGL4.23-3xBTE
C
D
Relative luciferase activity
30
20
10
0
*
pCS2-empty
pCS2-Klf9
1
2
3
39 kD
E
F
Fold enrichment (Klf9 antibody/NGS IgG)
Vehicle
T3
6
5
4
3
2
1
0
*
Intron
Promoter
% Input
HT22[BirA]
HT22[BirA/FLBIO-Klf9]
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
*
Intron
Promoter

Figure 2.1 Stably transfected HT22 cell lines expression functional Klf9 protein that associates in chromatin. . A) Eight hours of doxycycline treatment does not affect *Klf9* mRNA in the parent HT22 cell line but increases expression by ~10 fold in HT22[TR/TO-Klf9] cells. Baseline *Klf9* expression did not differ between parent and [TR/TO-Klf9] line as tested by one-way ANOVA ($F_{(3,8)}$=480.974, *p*<.001). **B)** Forced expression of Klf9 by dox addition represses transcription from the pGL4.23-3xBTE plasmid but not from the pGL4.23-empty vector. *Significantly different from control by two-sample t-test. t(5)=3.752, *p*<.05. **C)** Forced expression of Klf9 by transient transfection of the pCS2-Klf9 expression vector represses luciferase activation by 20% from the pGL4.23-3xBTE vector.*Significantly different from empty vector-transfected cells by two-sample t-test (t(6)=3.292, *p*<.05). **D)** Blotting with streptavidin-HRP demonstrates expression of biotinylated Klf9 protein in HT22[BirA/FLBIO-Klf9] cells (lane 3) but not in HT22[BirA] (lane 2) or HT22 parent cells (lane 1). **E)** ChIP for endogenous Klf9 protein shows association at *Klf13* promoter in parent HT22 cells treated with T_3; no association is evident at a *Klf13* intronic region or from non-hormone-treated cells. *Significantly different than NGS IgG pulldown by two-sample t-test on log-transformed data. Intronic region: t(6)=.850, *p*=4.28; Promoter region: t(6)=3.607, *p*<.05. **F)** Chromatin-streptavidin precipitation shows ~25-fold enrichment at *Klf13* promoter in cells expressing BirA+FLBIO-Klf9 versus cells expressing BirA alone; no difference between lines is evident at the *Klf13* intron. *Significant difference between BirA and BirA/FLBIO-Klf9 line by two-sample t-test. Promoter region: t(6)=-8.315, *p*<.0005.

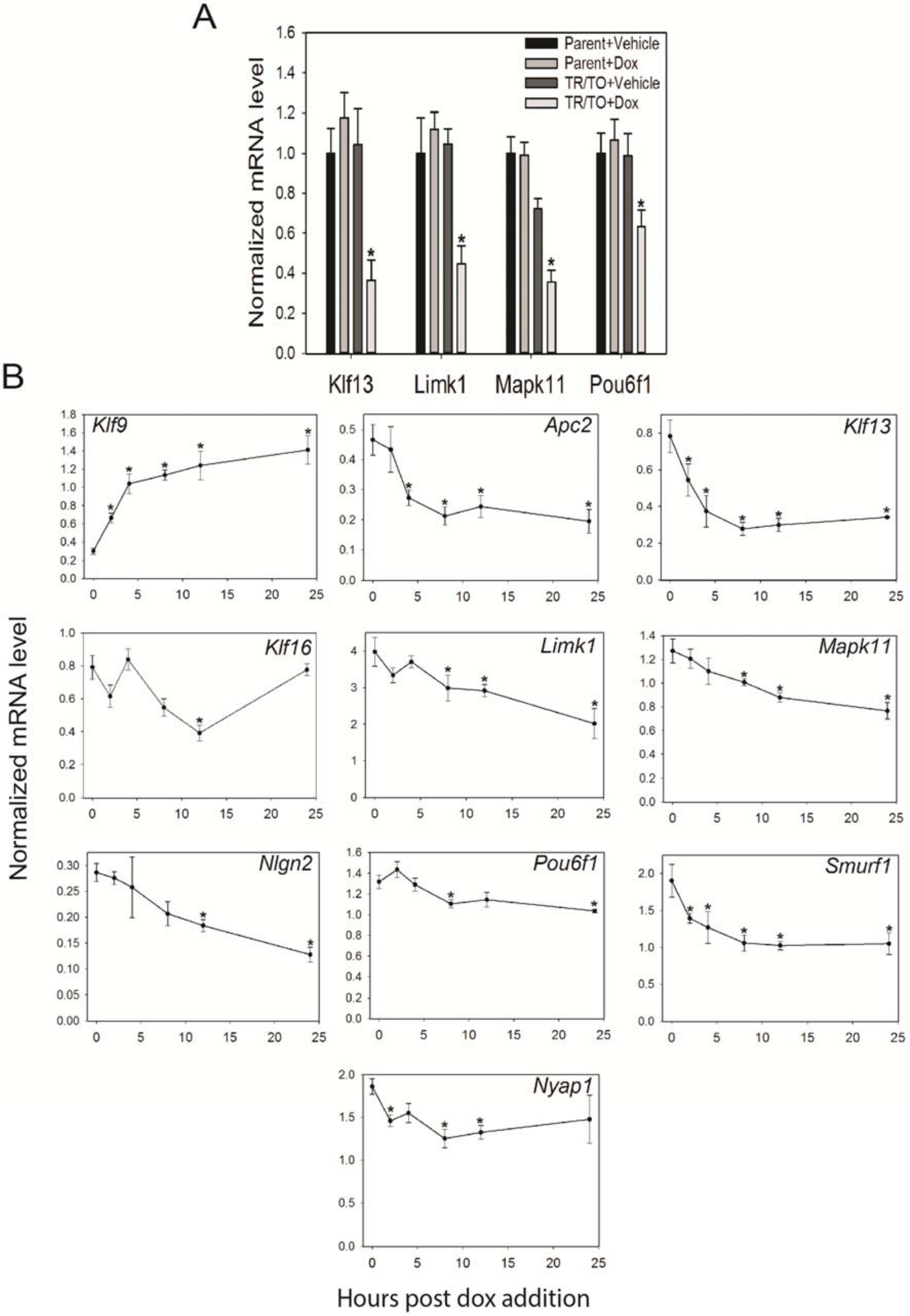

A
Normalized mRNA level
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
1.6
Parent+Vehicle
Parent+Dox
TR/TO+Vehicle
TR/TO+Dox
*
Klf13
Limk1
Mapk11
Pou6f1
B
Normalized mRNA level
Klf9
Apc2
Klf13
Klf16
Limk1
Mapk11
Nlgn2
Pou6f1
Smurf1
Nyap1
0
5
10
15
20
25
Hours post dox addition

Figure 2.2 Klf9 functions predominantly as a transcriptional repressor A) RT-qPCR validation of several repressed genes from samples used for RNA-seq. Dox treatment did not change expression in the parent line but led to repression the HT22[TR/TO-Klf9]. *Significantly different from parent line and from stable line –Dox by one-way ANOVA. *Klf13*: $F_{(3,19)}$=7.708, *p*<.005; *Limk1*: $F_{(3,17)}$=6.417, *p*<.005; *Mapk11*: $\mathrm{F}_{(3,19)}$=22.107, *p*<.001; *Pou6f1*: $F_{(3,19)}$=4.286, *p*<.05. **B)** Time-course data showing upregulation of *Klf9* and repression of Klf9 target genes after treatment with dox for indicated durations (hrs). Differences between time points were tested by one-way ANOVA; * indicates significantly different from 0 time point (*p*<.05 by Tukey's post-hoc test). *Klf9*: $F_{(5,16)}$=14.97, *p*<.001; *Apc2*: $F_{(5,16)}$=5.548, *p*<.005; *Klf13*: $F_{(5,16)}$=6.642, *p*<.001; *Klf16*: $F_{(5,14)}$=6.914; *Limk1*: $F_{(5,15)}$=4.048; *Mapk11*: $F_{(5,16)}$=4.787, *p*<.01; *Nlgn2*: $F_{(5,16)}$=3.185, *p*<.05; *Pou6f1*: $F_{(5,15)}$=4.527, *p*<.05; *p*<.05; *Smurf1*: $F_{(5,16)}$=4.689, *p*<.01;, *p*<.005; *Nyap1*: $F_{(5,16)}$=3.474, *p*<.05).

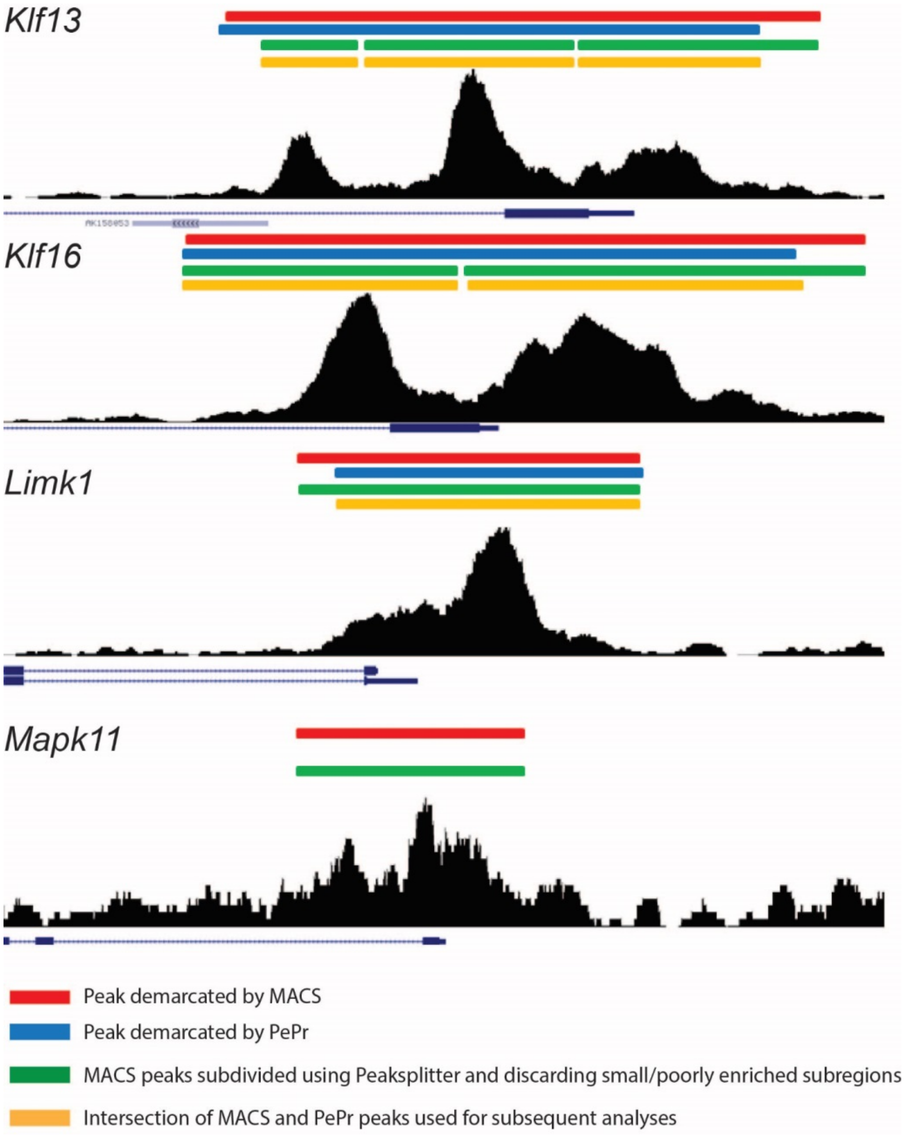


Figure 2.3. Peak calling and classification paradigm. Schematic of aligned read density aligned to genomic loci and how different peak callers were used to refine how peaks were demarcated.

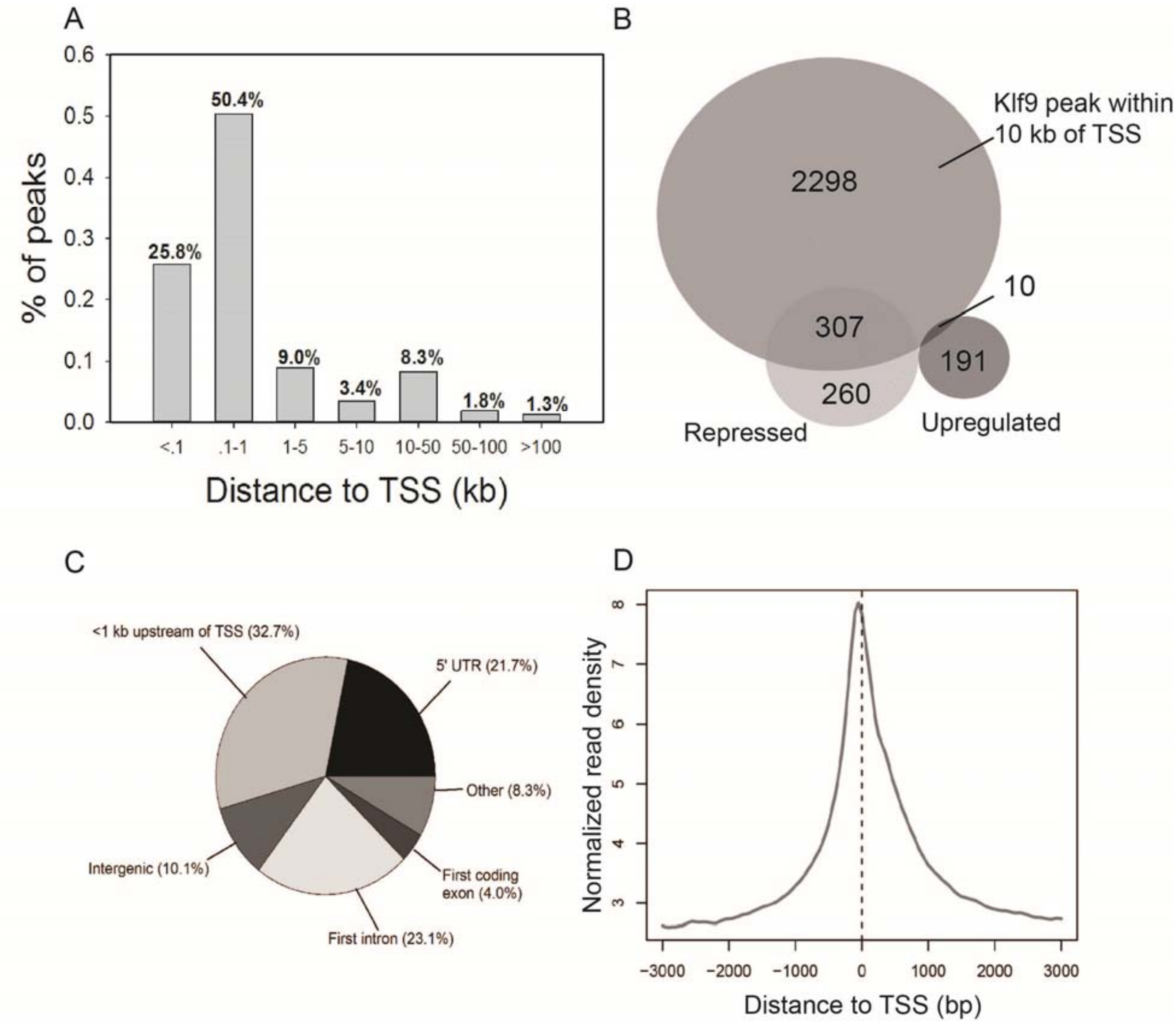


Figure 2.4 FLBIO-Klf9 associates near transcription sites and is more likely to be associated with repressed than upregulated genes. A) Distribution of peaks with respect to transcription start sites (TSS). **B)** Overlap of Klf9-regulated genes with genes with Klf9 associated with 10 kb of their TSS. **C)** Distribution of peaks with respect to features of genes. **D)** Average signal enrichment within 3kb of transcription start sites (TSS).

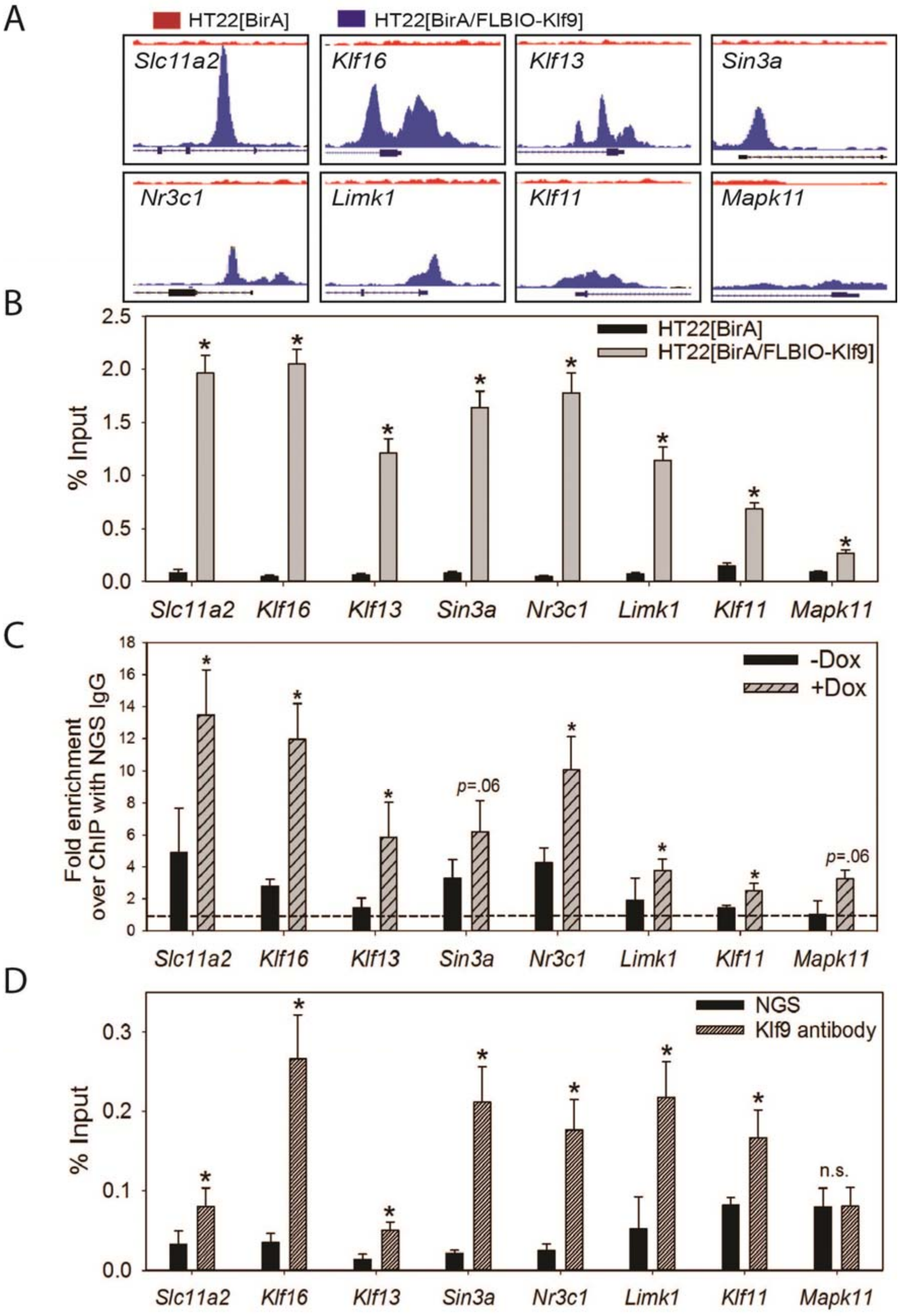

A
HT22[BirA]
HT22[BirA/FLBIO-Klf9]
Slc11a2
Klf16
Klf13
Sin3a
Nr3c1
Limk1
Klf11
Mapk11
B
% Input
2.5
2.0
1.5
1.0
0.5
0.0
HT22[BirA]
HT22[BirA/FLBIO-Klf9]
*
Slc11a2
Klf16
Klf13
Sin3a
Nr3c1
Limk1
Klf11
Mapk11
C
Fold enrichment over ChIP with NGS IgG
18
16
14
12
10
8
6
4
2
0
-Dox
+Dox
p=.06
p=.06
*
Slc11a2
Klf16
Klf13
Sin3a
Nr3c1
Limk1
Klf11
Mapk11
D
% Input
0.3
0.2
0.1
0.0
NGS
Klf9 antibody
n.s.
*
Slc11a2
Klf16
Klf13
Sin3a
Nr3c1
Limk1
Klf11
Mapk11

Figure 2.5. Klf9 protein associates with peaks identified by ChSP-seq *in vitro* and *in vivo*. **A)** Genome browser views showing location of Klf9 peaks. Blue track=reads from cells expressing BirA alone; red track=cells expressing BirA+FLBIO-Klf9. Full gene locus is shown; bars represent exons while lines represent introns. **B)** Chromatin-streptavidin precipitation followed by quantitative PCR showing enrichment in FLBIO-Klf9 expressing cells relative to BirA expressing cells.*Significantly different by two-sample *t*-test. *Slc1a2*: t(6)=-10.981, *p*<.001; *Klf16*: *t*(6)=-14.417, *p*<.001; *Klf13*: *t*(6)=-10.981, *p*<.001; *Sin3a*: t(6)=-10.135, *p*<.001; *Nr3c1*: t(6)=-9.402, *p*<.001; *Limk1*: *t*(6)=-8.561, *p*<.001; *Klf11*: t(6)=-8.653, *p*<.001; *Mapk11*: *t*(6)=-5.448, *p*<.005. **C)** ChIP-qPCR against Klf9 protein on dox-treated HT22[TR/TO-Klf9] cells. *Significantly increase in fold enrichment in dox-treated cells compared with vehicle-treated cells by two-sample t-test on log-transformed values. *Slc1a2*: t(7)=-4.628, *p*<.005; *Klf16*: *t*(8)=-4.628, *p*<.005; *Klf13*: *t*(10)=-2.829 *p*<.05; *Sin3a*: t(9)=-2.138, *p*=.06; *Nr3c1*: t(10)=-2.684, *p*<.05; *Limk1*: *t*(8)=-2.334, *p*<.05; *Klf11*: t(7)=-2.371, *p*<.05; *Mapk11*: *t*(6)=-2.299, *p*=.06. **D)** ChIP-qPCR against Klf9 using chromatin extracted from adult mouse hippocampus shows that Klf9 associates with these loci *in vivo*. *Significantly different from NGS IgG by two-sample t-test on log-transformed values. *Slc1a2*: t(13)=2.260, *p*<.05; *Klf16*: *t*(12)=.4.458, *p*<.001; *Klf13*: *t*(13)=3.752, *p*<.005; *Sin3a*: t(12)=5.659, *p*<.0005; *Nr3c1*: t(10)=-2.684, *p*<.05; *Limk1*: *t*(11)=3.887, *p*<.005; *Klf11*: t(16)=2.246, *p*<.05; *Mapk11*: *t*(16)=-.0265, *p*=.979.

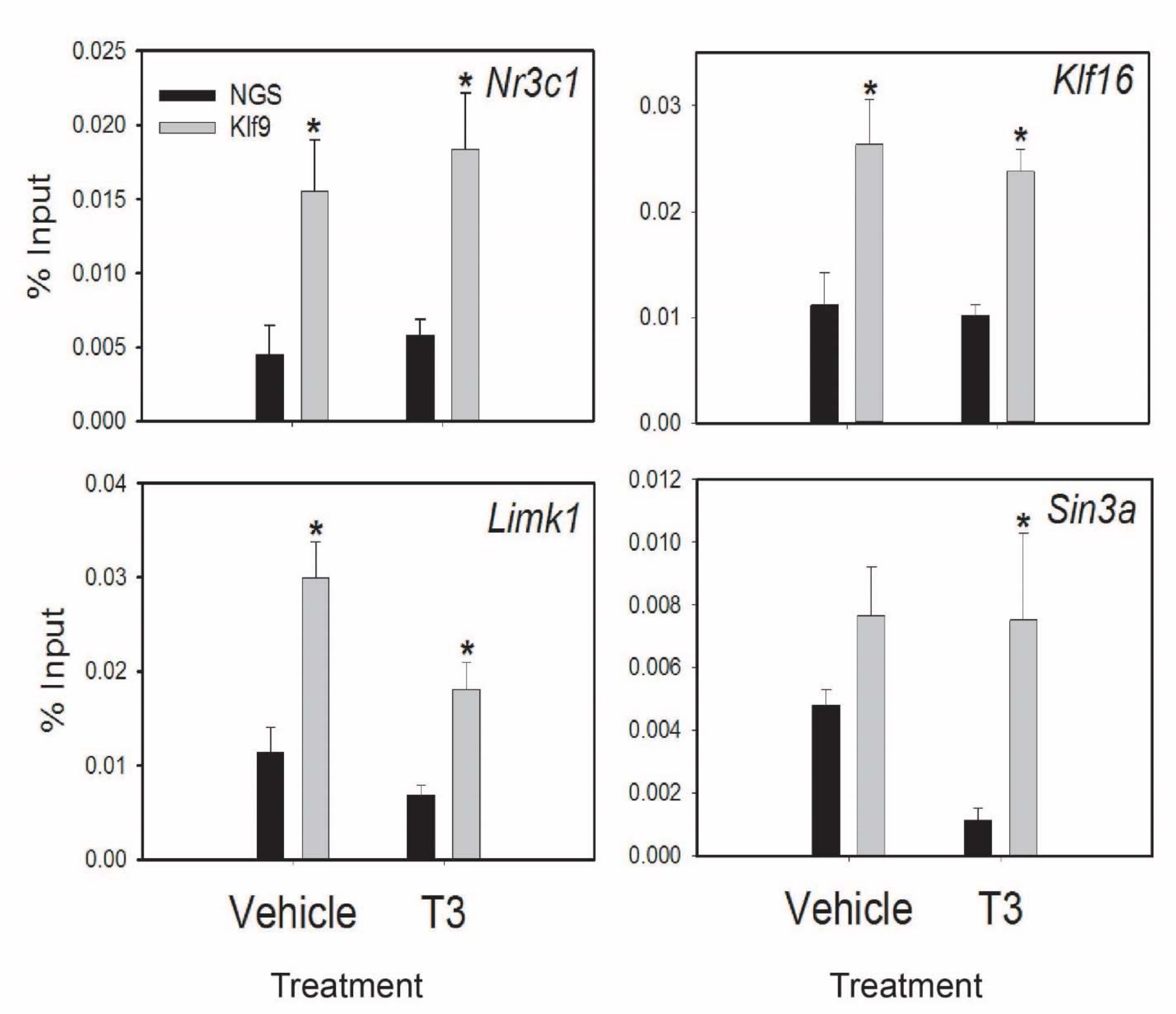


Figure 2.6. Endogenous Klf9 protein associates with peaks in parent HT22 cells. ChIP on parent HT22 cells treated with or without T3 found endogenous Klf9 associated with peaks discovered by chromatin-streptavidin precipitation.. *Significantly different from NGS IgG pulldown by two-sample t-test on log-transformed data. *Nr3c1* (vehicle): t(6)=2.757, *p*<.05; *Nr3c1*(T3): t(4)=3.778, *p*<.05; *Klf16* (vehicle): t(5)=2.590, *p*<.05; *Klf16* (T3): t(4)=6.285, *p*<.005; *Limk1*(vehicle): t(6)=4.460, *p*<.005; *Limk1* (T3): t(4)=4.093, *p*<.05; *Sin3a* (vehicle): t(6)=1.939, *p*=.101; *Sin3a* (T3): t(5)=3.159, *p*<.05.

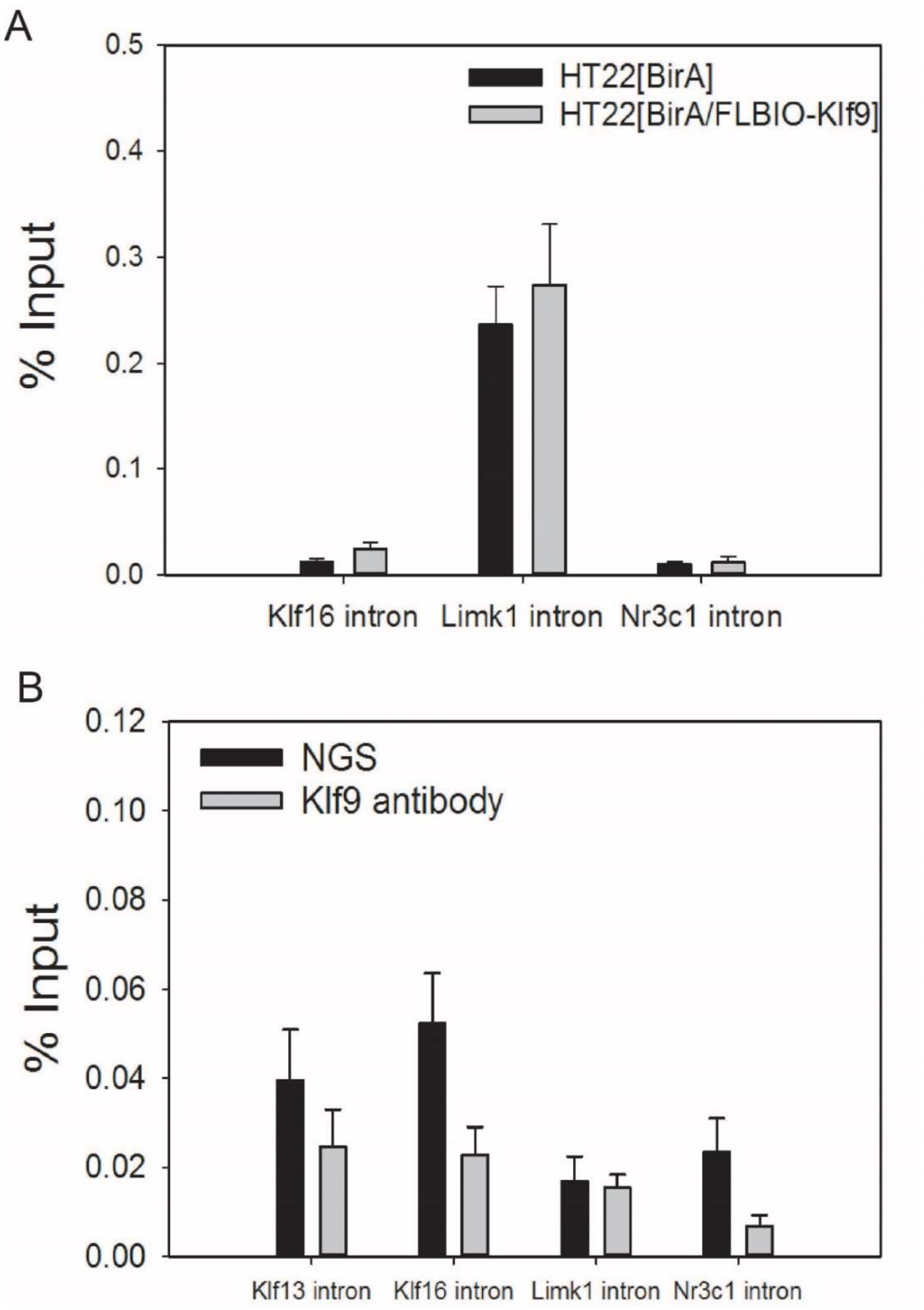


Figure 2.7. ChSP and ChIP at negative control regions A) No difference between HT22[BirA] and HT22[BirA+FLBIO-Klf9] cells was evident at intronic regions distant from peaks after chromatin-streptavidin precipitation. **B)** No association of Klf9 protein was evident at intronic regions after Klf9 ChIP on chromatin from the mouse hippocampus.

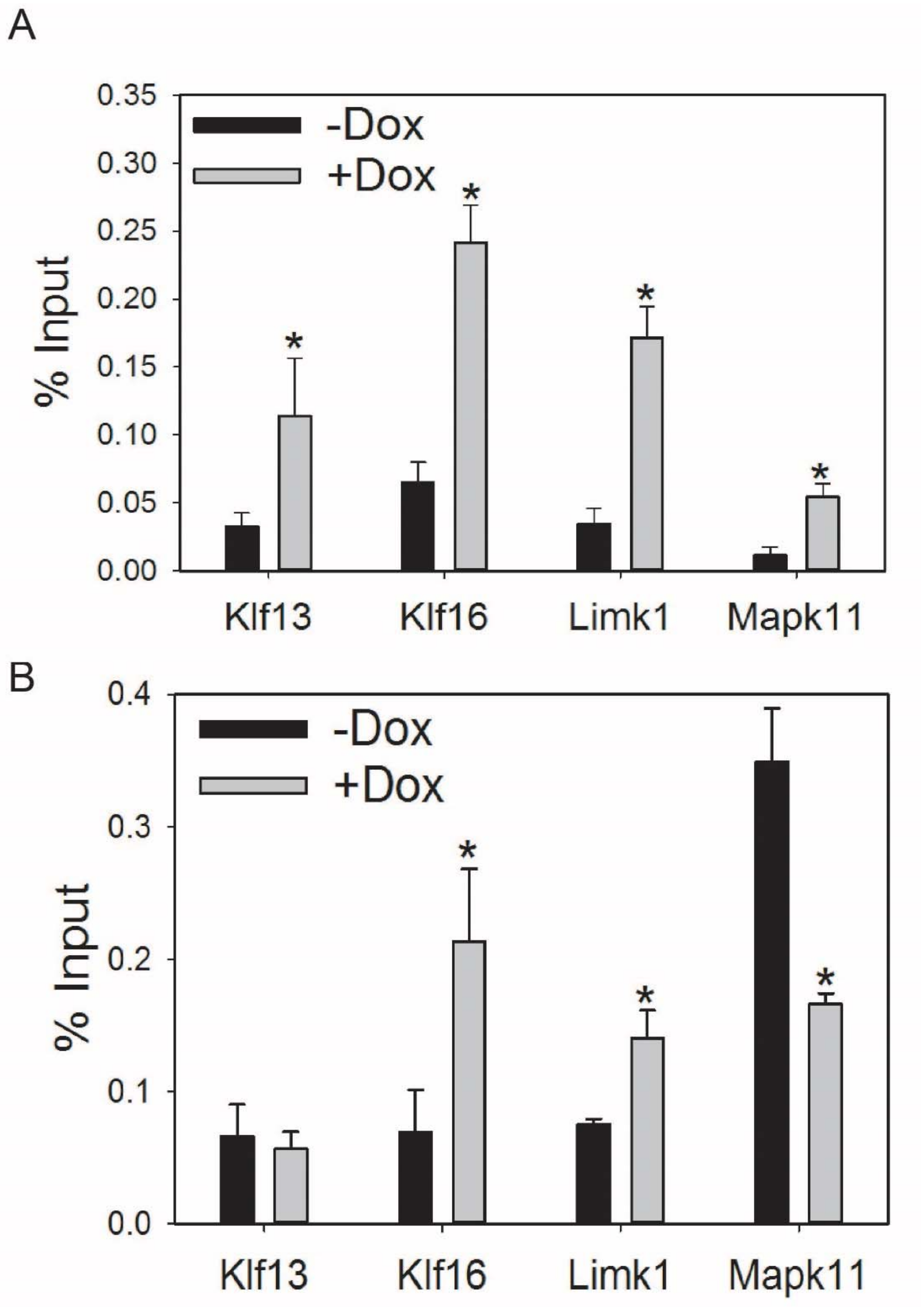


Figure 2.8. Recruitment of Sin3a to Klf9 peaks A) ChIP-qPCR against Klf9 protein showing increased recruitment to target promoters upon forced expression of Klf9 in HT22 cells. *Significantly different from control by two-sample t-test on log-transformed values. *Klf13*: t(10)=-2.758, *p*<.05; *Klf16*: t(10)=-4.797, *p*<.001; *Limk1*: t(10)=-4.099, *p*<.005; *Mapk11*: t(7)=-2.359, *p*=.05. **B)** Forced expression of Klf9 leads to increased *Sin3a* recruitment at *Klf16* and *Limk1* promoters, reduced association at *Mapk11*, and no change in association at *Klf13*. *Klf16*: t(8)=-2.736, *p*<.05; *Limk1*: t(6)=-2.922, *p*<.05; *Mapk11*: t(6)=6.617, *p*<.001.

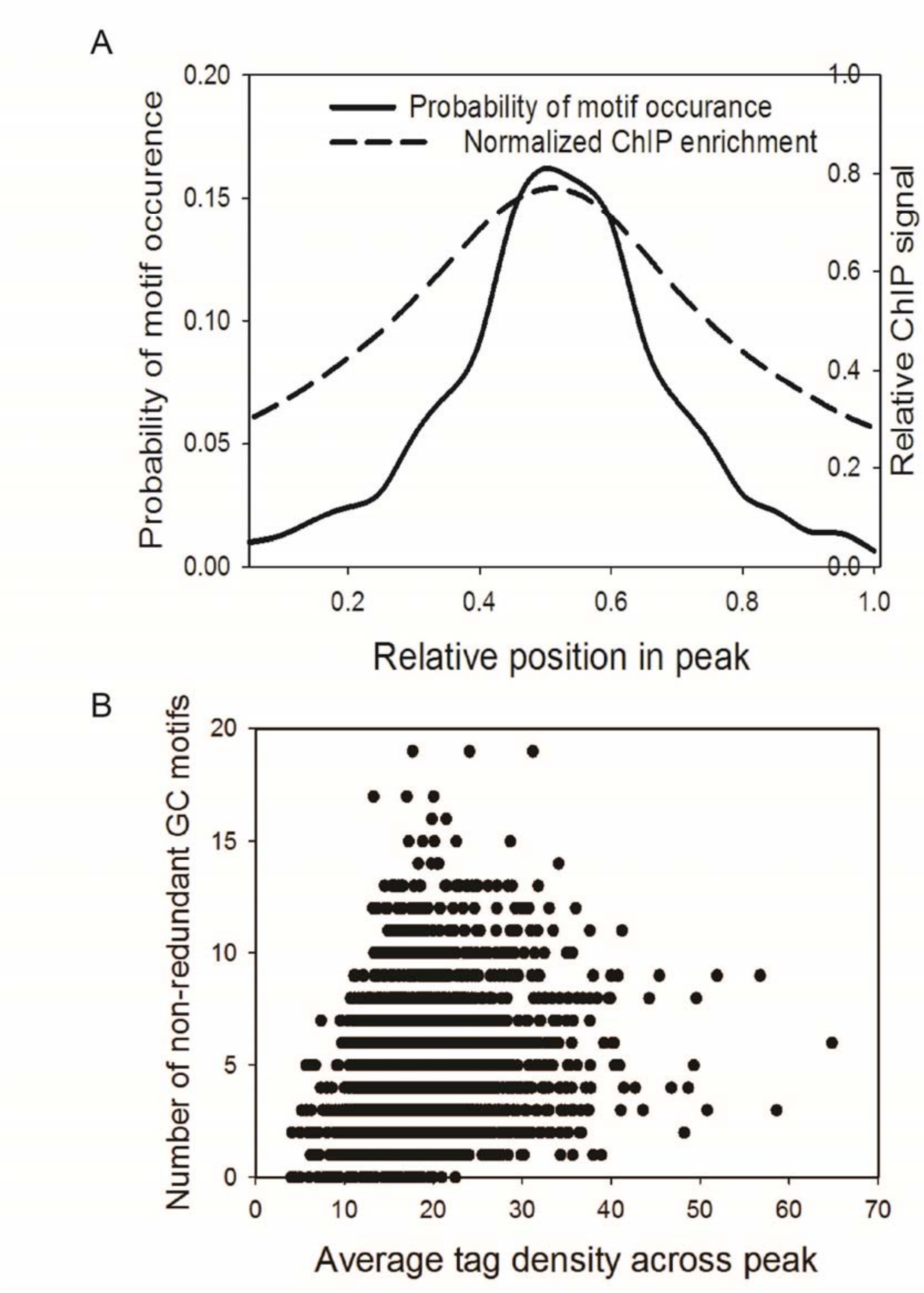


Figure 2.9. GC-rich motifs correlate with sequencing tag density within peaks and with overall peak height. A) Histogram showing the probability of consensus motif occurrence (solid) and average enrichment (number of mapped reads; dashed) across all Klf9 peaks. **B)** Number of non-redundant GC motifs shows moderate correlation with overall ChIP enrichment across peak (R=.245, *p*=.0000002).

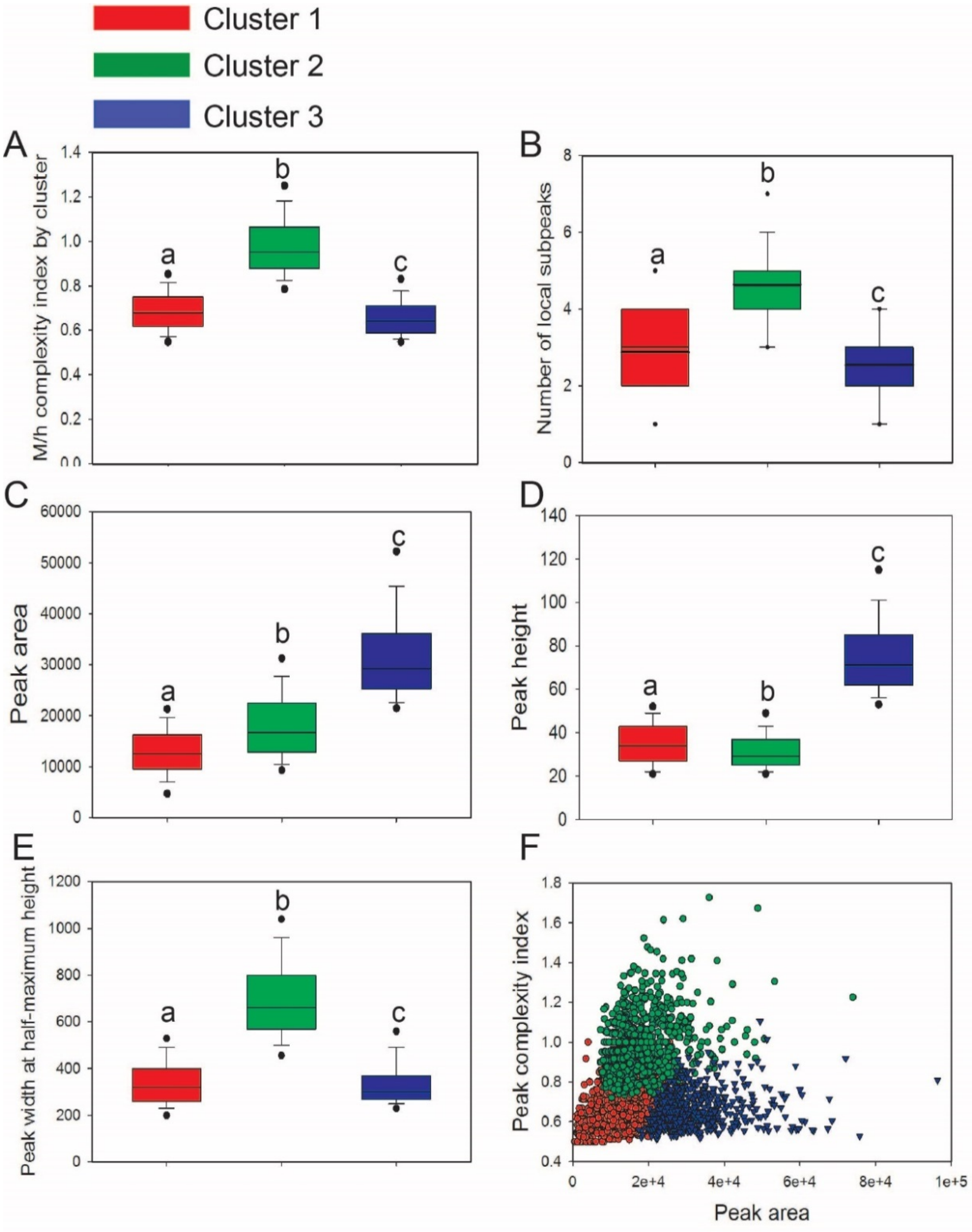


Figure 2.10. Peak clustering parameters A)-E) Parameters from each cluster. Cluster parameters were analyzed by Kruskal-Wallis non-parametric ANOVA; boxplots with the same letter are not significantly different from one another. Boxplot whiskers indicate 75% and 25% quantiles; dots indicate 95% and 5% quantiles. Peak height: H(2)=1421.09, *p*<.001; Peak area: H(2)=1496.965, *p*<.001; Peak width at half-maximum: H(2)=1655.065, *p*<.001; Peak complexity index/height: H(2)=1714.902, *p*<.001; Number of local subpeaks: H(2)=1044.368, *p*<.001. **F)** Scatterplot showing peak area versus complexity index. Peaks group based on cluster they were assigned to.

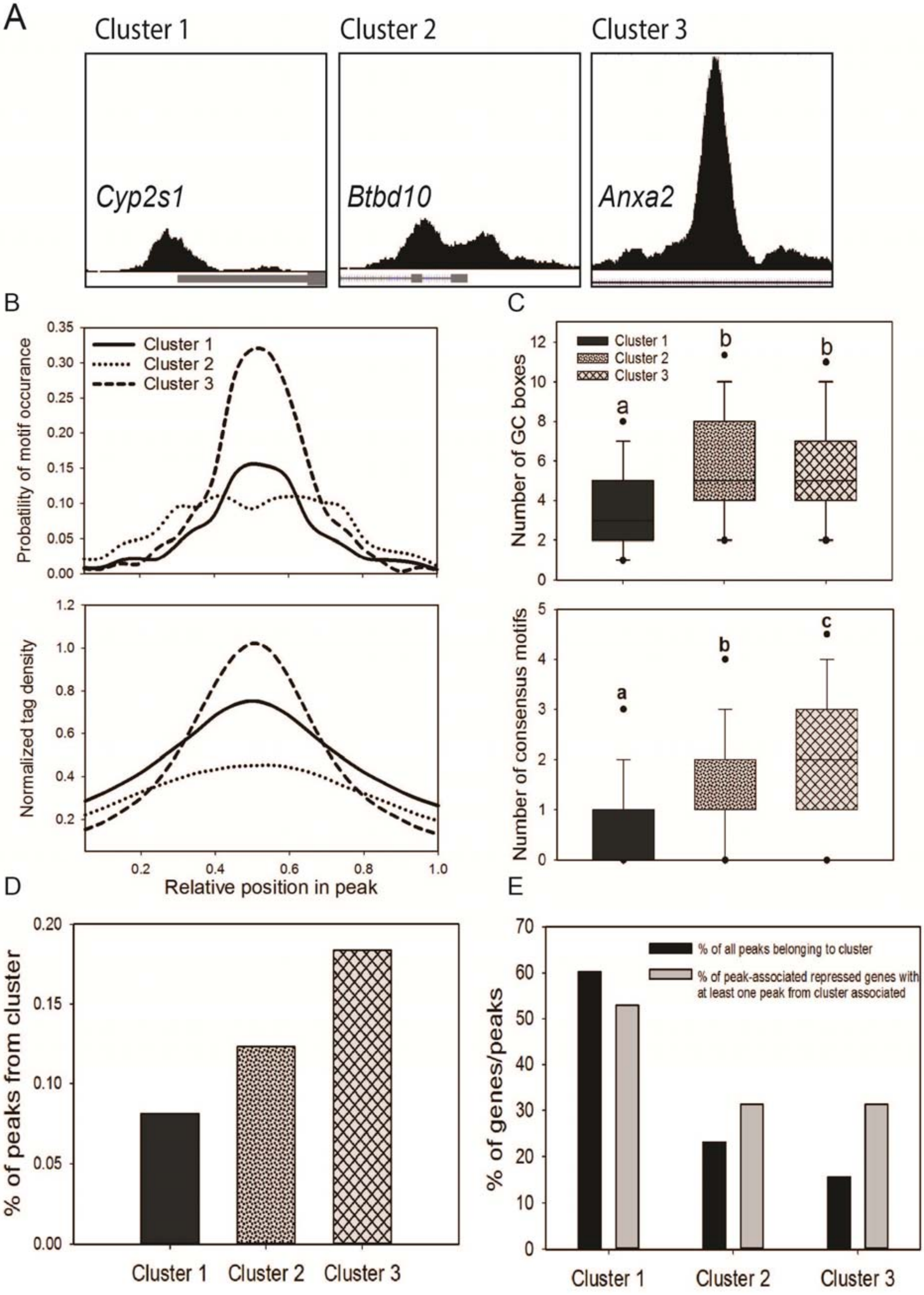
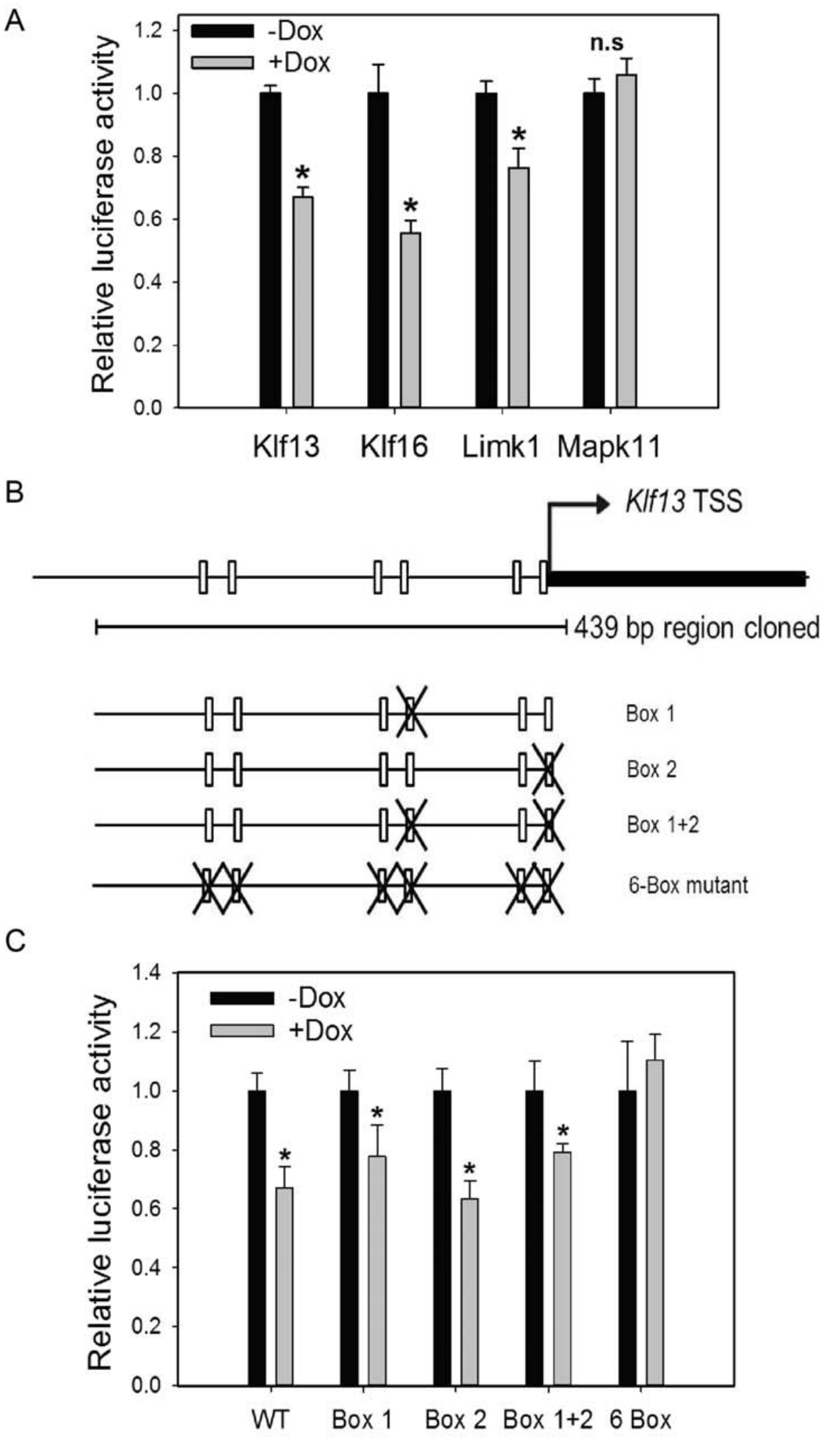

A
Cluster 1
Cluster 2
Cluster 3
Cyp2s1
Btbd10
Anxa2
B
Cluster 1
Cluster 2
Cluster 3
Probability of motif occurance
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35
Normalized tag density
0.2
0.4
0.6
0.8
1.0
1.2
0.2
0.4
0.6
0.8
1.0
Relative position in peak
C
Cluster 1
Cluster 2
Cluster 3
Number of GC boxes
0
2
4
6
8
10
12
a
b
b
Number of consensus motifs
0
1
2
3
4
5
a
b
c
D
% of peaks from cluster
0.00
0.05
0.10
0.15
0.20
Cluster 1
Cluster 2
Cluster 3
E
% of genes/peaks
0
10
20
30
40
50
60
70
% of all peaks belonging to cluster
% of peak-associated repressed genes with at least one peak from cluster associated
Cluster 1
Cluster 2
Cluster 3

Figure 2.11. Klf9 peaks group into shape clusters that show different likelihood of association with repressed genes. A) Examples of Klf9 peaks from each cluster; graph height and viewing window size are constant. **B)** Distribution of the Klf9 consensus motif (top) and tag enrichment (bottom) across each cluster of peaks. **C)** Number of GC boxes and number of Klf9 consensus motifs present in peaks belonging to each cluster. Boxplots indicate 75% and 25% quantiles; dots indicate 5% and 95% quantiles. Quantities with the same letter are not significantly different from each other by Kruskal-Wallis non-parametric ANOVA. Ttop; $H(2)=528.802$, $p<.001$); peaks of cluster 3 have more Klf9 consensus motifs (bottom; $H(2)=245.055$, $p<.001$). **D)** Proportion of peaks of each class associated with repressed genes. **E)** Percentage of peak-associated repressed genes with each class of peak associated graphed against proportion of peaks falling into each cluster.



A
Relative luciferase activity
0.0
0.2
0.4
0.6
0.8
1.0
1.2
-Dox
+Dox
n.s
*
*
*
Klf13
Klf16
Limk1
Mapk11
B
Klf13 TSS
439 bp region cloned
Box 1
Box 2
Box 1+2
6-Box mutant
C
Relative luciferase activity
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
-Dox
+Dox
*
*
*
*
WT
Box 1
Box 2
Box 1+2
6 Box

Figure 2.12. Forced expression of Klf9 represses transcription from sequences corresponding to Klf9 peaks in a GC box-dependent manner. A) HT22 TR/TO-Klf9 cells were transfected with reporter constructs containing Klf9-bound regions associated with the indicated genes. Forced expression of Klf9 repressed transcriptional activity from these constructs. *Significantly different from control by two-sample t-test. *Klf13*: t(10)=8.512, $p<10^{-5}$; *Klf16*: t(10)=4.430, $p<.005$; *Limk1*: t(10)=3.275, $p<.01$; *Mapk11*: t(9)=1.509, $p=.166$. **B)** Diagram of Klf13 promoter region clones for luciferase assays. Open rectangles indicate relative positions of predicted Klf9 binding sites with 500 bp of the TSS. Diagrams below indicate which boxes were mutated (changed to TTTTTTT; see Supplemental Fig. 6). **C)** Deletion of all six sites eliminated Klf9-dependent repression but deletion of one or two sites did not have any effect (WT reproduced from Fig. 7A). *Significantly different from control by two-sample t-test. Wild-type promoter: t(10)=8.512, $p<10^{-5}$, $p<.05$; Box 1 mutant: t(10)=4.283, $p<.005$; Box 2 mutant: t(9)=8.872, $p<10^{-5}$; Box 1+2 mutant: t(8)=3.912, $p<.005$; 6-box mutant: $t(10)=-.1.331$, $p=.213$..

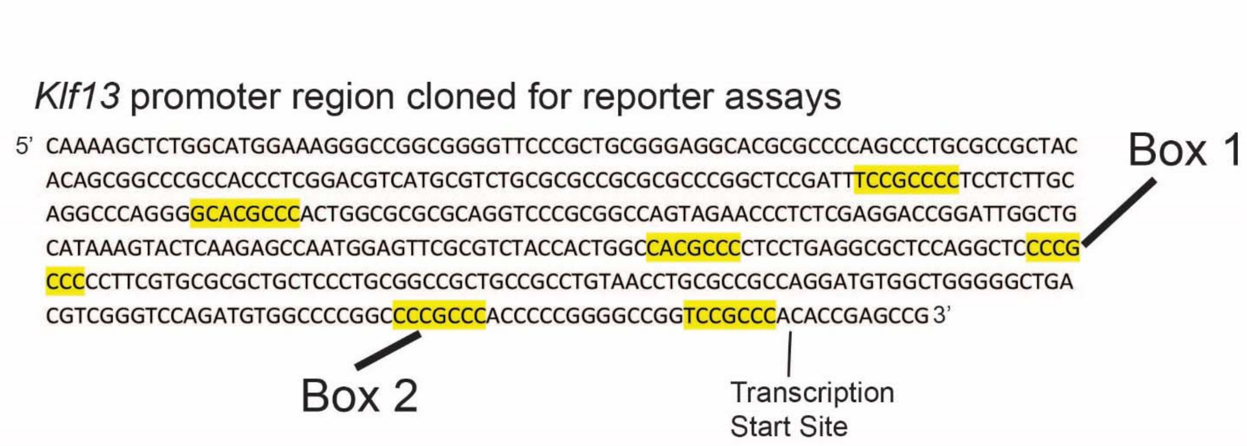


Figure 2.13. *Klf13* 5' upstream region cloned for functional analysis. Region of *Klf13* promoter cloned for promoter analyses with GC motifs matching the consensus motif or redundant motifs highlighted. Indicated regions were mutated to 7 Ts as described in the main text.

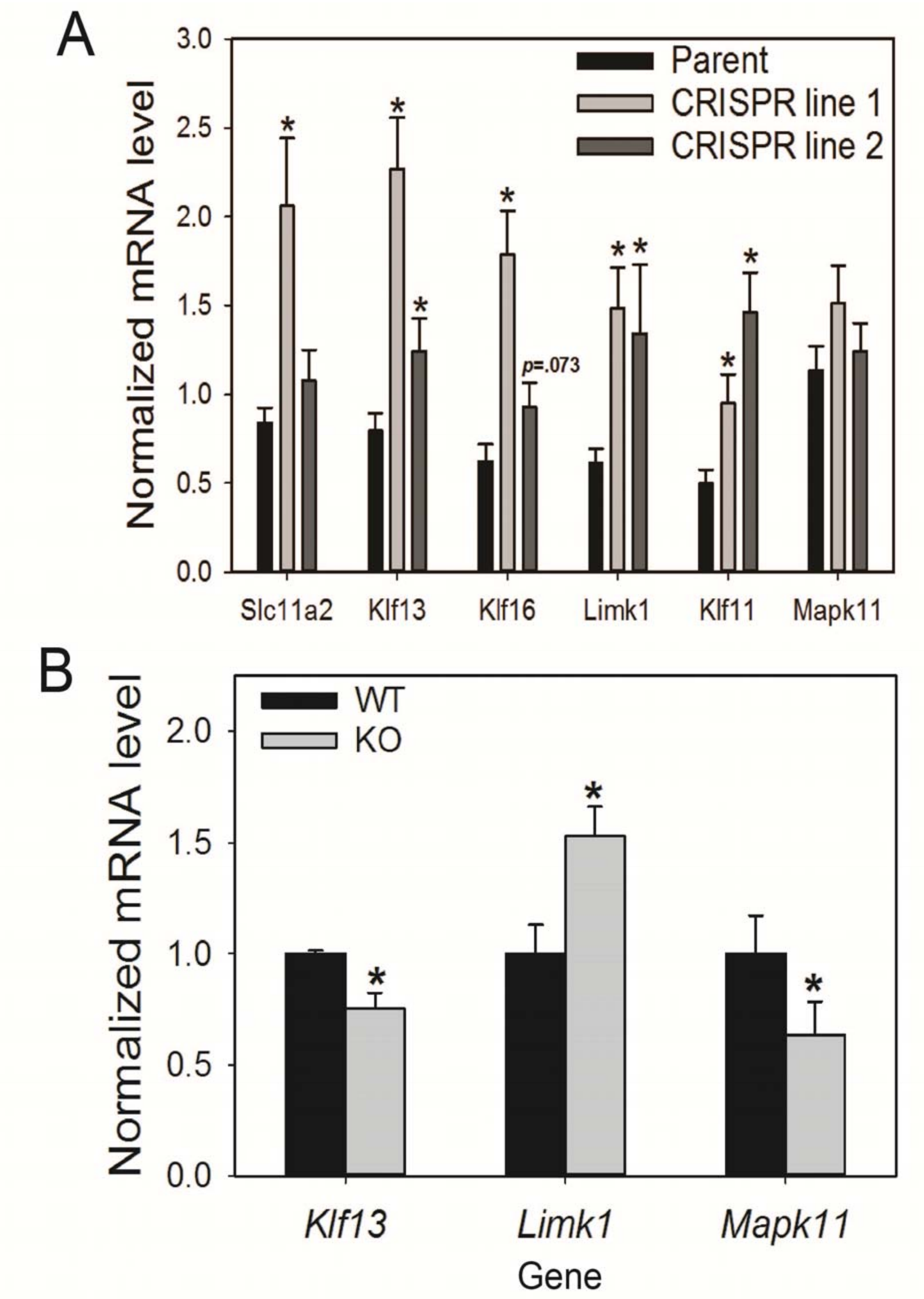

A
Normalized mRNA level
3.0
2.5
2.0
1.5
1.0
0.5
0.0
Parent
CRISPR line 1
CRISPR line 2
*
p=.073
Slc11a2
Klf13
Klf16
Limk1
Klf11
Mapk11
B
Normalized mRNA level
2.0
1.5
1.0
0.5
0.0
WT
KO
*
Klf13
Limk1
Mapk11
Gene

Figure 2.14. Klf9 target genes are dysregulated in *Klf9* HT22 knockout cells and in *Klf9* knockout mice. A) Klf9 target genes are dysregulated in HT22 cells with Klf9 knocked down by CRISPR/Cas9 genome editing. *Significantly different from parent HT22 line by one-way ANOVA and Holm-Sidak post-hoc test on log-transformed values; exact *p*-values are given in instances in which a trend was clear. *Slc1a2*: $F_{(2,12)}$=9.091, $p<.005$; *Klf13*: $F_{(2,12)}$=14.267, $p<.001$; *Klf16*: $F_{(2,13)}$=14.135, $p<.001$; *Limk1*: $F_{(2,13)}$=5.875, $p<.05$; *Klf11*: $F_{(2,11)}$=9.1, $p<.01$; *Mapk11*: $F_{(2,13)}$=.922, $p=.422$. **B)** Dysregulation of Klf9 genomic targets in the hippocampus of *Klf9*-null mice. *Different from WT by two-sample t-test. *Klf13*: t(5)=-3.785, $p<.01$; *Limk1*, t(5)=-2.763, $p<.05$; *Mapk11*: t(4)=2.777, $p=.05$.

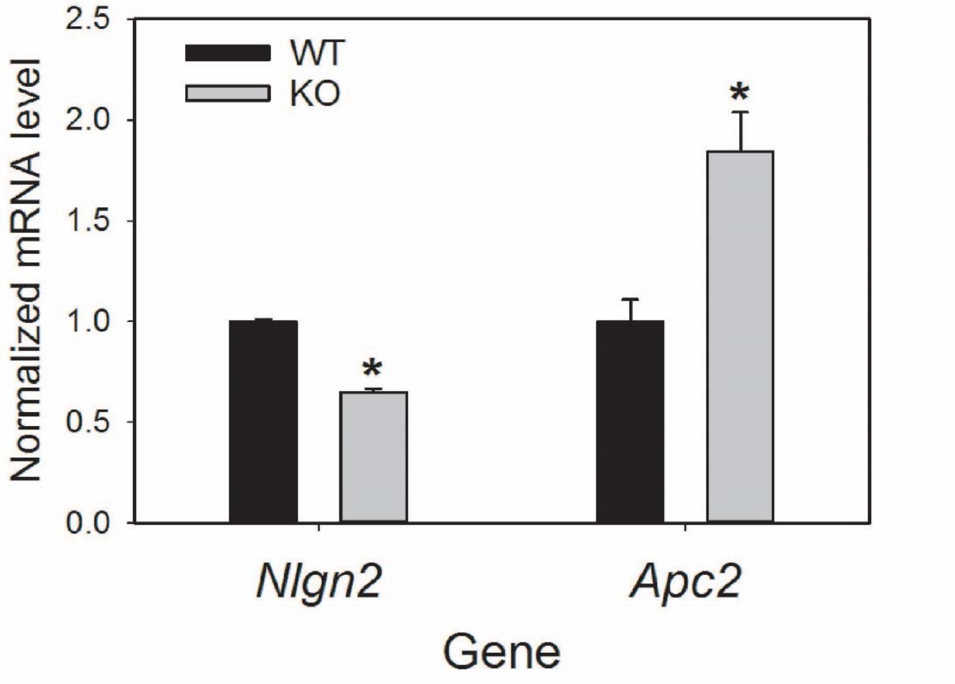


Figure 2.15. Dysregulation of Klf9-regulated genes (with no associated peaks) in *Klf9*-null mouse hippocampus. *Significantly different from wild type. *Nlgn2*: t(4)=17.847, *p*<.001; *Apc2*:t(6)=-3.785, *p*<.01.

Table 2.1: Top 10 up- and down-regulated genes in HT22[TR/TO-Klf9] cells +/- 8 hours of dox treatment

Gene Symbol	Gene name	Log2 fold change
Cd93	Cluster of differentiation 93	-1.21
Klf13	Krüppel-like factor 13	-1.12
Chad	Chondroadherin	-1.11
Rptoros	Regulatory associated protein of MTOR, complex 1, opposite strand	-1.04
Celf3	CUGBP, Elav-like Family Member 3	-1.02
Zfp964	Zinc finger protein 964	-0.96
Gpr161	G Protein-coupled receptor 161	-0.95
Apc2	Adenomatosis polyposis coli 2	-0.92
Zfp704	Zinc finger protein 704	-0.89
Arhgap39	Rho GTPase Activating Protein 39	-0.88
Rilpl2	Rab Interacting Lysosomal Protein-Like 2	0.51
Mitd1	Microtubule Interacting and Transport Domain Containing 1	0.51
Zfp930	Zinc finger protein 930	0.52
Ccnb1ip1	Cyclin B1 Interacting Protein 1, E3 Ubiquitin Protein Ligase	0.53
Cdkn3	Cyclin-Dependent Kinase Inhibitor 3	0.56
Hoxa2	Homeobox A3	0.60
6720489N17Rik	Riken cDNA 6720489N17	0.60
Arxes1	Adipocyte-related X-chromosome expressed sequence 1	0.67
Enpp3	Ectonucleotide pyrophosphatase/phosphodiesterase family member 3	0.77
Tfpi	Tissue factor pathway inhibitor	1.52

Table 2.2: Motifs enriched in Klf9 peaks

HOMER motif	*p* value	% of peaks with motif	% of background sequences with motif	Closest match identified by HOMER
 *	$1*10^{-702}$	75.6	29.2	Klf5
	$1*10^{-61}$	28.55	17.19	Egr2
	$1*10^{-43}$	31.28	21.21	Elk4
	$1*10^{-34}$	14.84	8.56	POL003.1_GC-box
	$1*10^{-31}$	28.15	19.83	E2F1
	$1*10^{-28}$	21.21	14.18	Fosl1
	$1*10^{-28}$	24.31	16.94	Basic helix-loop-helix
	$1*10^{-22}$	46.43	38.26	Rfxdc2
	$1*10^{-20}$	47	39.26	Zbtb33
	$1*10^{-18}$	25.05	19.03	P0031.1_IRC900814_1
	$1*10^{-17}$	6.43	3.49	GFY
	$1*10^{-15}$	14.09	9.76	NFATC2
	$1*10^{-15}$	27.36	21.61	Pitx1
	$1*10^{-14}$	40.88	34.45	CHR
	$1*10^{-14}$	16.91	12.41	NRF1

	1*10^{-13}	30.83	25.24	Irf4
	1*10^{-12}	18.76	14.26	TRP(MYB)
	1*10^{-12}	1.31	0.35	Sp1
	1*10^{-12}	2.45	1.03	MEF2a

*Klf9 consensus motif

Table 2.3: All GO:PANTHER pathways enriched in set of genes repressed by Klf9

Id	Items	Items_Details	Support	List size	Reference Support	Reference size	Hyp_c
11	Panther:P00047	PDGF signaling pathway	11	479	103	37681	5.141E-06
13	Panther:P00016	Cytoskeletal regulation by Rho GTPase	7	479	62	37681	0.0002716
36	Panther:P00020	FAS signaling pathway	5	479	24	37681	0.0003339
12	Panther:P00005	Angiogenesis	9	479	120	37681	0.0003567
17	Panther:P00034	Integrin signalling pathway	9	479	131	37681	0.0005706
29	Panther:P00029	Huntington disease	8	479	106	37681	0.0006425
23	Panther:P00006	Apoptosis signaling pathway	7	479	93	37681	0.0015997
9	Panther:P00036	Interleukin signaling pathway	6	479	73	37681	0.0025004
10	Panther:P00056	VEGF signaling pathway	5	479	50	37681	0.0028192
15	Panther:P00003	Alzheimer disease-amyloid secretase pathway	5	479	54	37681	0.0036329
0	Panther:P00031	Inflammation mediated by chemokine and cytokine signaling pathway	9	479	197	37681	0.0049452
24	Panther:P00059	p53 pathway	5	479	60	37681	0.0053593
35	Panther:P00048	PI3 kinase pathway	4	479	39	37681	0.006769
5	Panther:P00049	Parkinson disease	5	479	75	37681	0.011395
3	Panther:P00021	FGF signaling pathway	5	479	90	37681	0.0217582
27	Panther:P00053	T cell activation	4	479	56	37681	0.0221192
43	Panther:P04396	Vitamin D metabolism and pathway	2	479	10	37681	0.02354

Table 2.4: Top ten GO:PANTHER pathways enriched in genes with Klf9 associated in their genomic region

Id	Items	Items_Details	Support	List size	Reference Support	Reference size	Adjusted *p* value
32	Panther:P00006	Apoptosis signaling pathway	31	2870	93	37681	8.67E-11
23	Panther:P00034	Integrin signalling pathway	36	2870	131	37681	2.79E-10
0	Panther:P00031	Inflammation mediated by chemokine and cytokine signaling pathway	46	2870	197	37681	3.16E-10
19	Panther:P00016	Cytoskeletal regulation by Rho GTPase	23	2870	62	37681	1.28E-09
18	Panther:P00005	Angiogenesis	33	2870	120	37681	1.51E-09
1	Panther:P00057	Wnt signaling pathway	42	2870	197	37681	1.75E-08
16	Panther:P00056	VEGF signaling pathway	19	2870	50	37681	2.64E-08
17	Panther:P00047	PDGF signaling pathway	28	2870	103	37681	2.82E-08
13	Panther:P04393	Ras Pathway	20	2870	59	37681	7.85E-08
5	Panther:P00021	FGF signaling pathway	24	2870	90	37681	4.71E-07

Table 2.5: Top GO: Panther pathways associated with genes associated with Klf9 peaks of different clusters

Cluster 1

Id	Items	Items_Details	Support	List size	Reference Support	Reference size	Adjusted *p* value
31	Panther:P00006	Apoptosis signaling pathway	19	1575	93	37681	8.48E-07
1	Panther:P00057	Wnt signaling pathway	26	1575	197	37681	1.17E-05
6	Panther:P00018	EGF receptor signaling pathway	14	1575	93	37681	0.001042
23	Panther:P00034	Integrin signalling pathway	17	1575	131	37681	0.00085
66	Panther:P04391	Oxytocin receptor mediated signaling pathway	10	1575	50	37681	0.000698
62	Panther:P04394	Thyrotropin-releasing hormone receptor signaling pathway	10	1575	53	37681	0.000985
7	Panther:P00049	Parkinson disease	12	1575	75	37681	0.000878
5	Panther:P00021	FGF signaling pathway	13	1575	90	37681	0.001149
34	Panther:P00009	Axon guidance mediated by netrin	6	1575	20	37681	0.001358
63	Panther:P04385	Histamine H1 receptor mediated signaling pathway	8	1575	39	37681	0.00175

Cluster 2

Id	Items	Items_Details	Support	List size	Reference Support	Reference size	Hyp_c
18	Panther:P00016	Cytoskeletal regulation by Rho GTPase	10	706	62	37681	1.86E-05

50	Panther:P00040	Metabotropic glutamate receptor group II pathway	7	706	41	37681	4.22E-04
63	Panther:P04396	Vitamin D metabolism and pathway	4	706	10	37681	0.000649
54	Panther:P04378	Beta2 adrenergic receptor signaling pathway	6	706	36	37681	0.000848
61	Panther:P04377	Beta1 adrenergic receptor signaling pathway	6	706	36	37681	0.000848
9	Panther:P04373	5HT1 type receptor mediated signaling pathway	6	706	39	37681	0.001129
3	Panther:P00039	Metabotropic glutamate receptor group III pathway	7	706	57	37681	0.001094
0	Panther:P00031	Inflammation mediated by chemokine and cytokine signaling pathway	13	706	197	37681	0.00101
42	Panther:P05731	GABA-B receptor II signaling	5	706	31	37681	0.002382
19	Panther:P00043	Muscarinic acetylcholine receptor 2 and 4 signaling pathway	6	706	50	37681	0.002771

Cluster 3

Id	Items	Items_Details	Support	List size	Reference Support	Reference size	Hyp_c
11	Panther:P00047	PDGF signaling pathway	11	479	103	37681	5.14E-06
36	Panther:P00020	FAS signaling pathway	5	479	24	37681	3.34E-04

13	Panther:P00016	Cytoskeletal regulation by Rho GTPase	7	479	62	37681	0.000272
12	Panther:P00005	Angiogenesis	9	479	120	37681	0.000357
17	Panther:P00034	Integrin signalling pathway	9	479	131	37681	0.000571
29	Panther:P00029	Huntington disease	8	479	106	37681	0.000643
23	Panther:P00006	Apoptosis signaling pathway	7	479	93	37681	0.0016
9	Panther:P00036	Interleukin signaling pathway	6	479	73	37681	0.0025
10	Panther:P00056	VEGF signaling pathway	5	479	50	37681	0.002819
15	Panther:P00003	Alzheimer disease-amyloid secretase pathway	5	479	54	37681	0.003633

CHAPTER 3

KRÜPPEL-LIKE FACTOR 9 IS A NOVEL NEGATIVE REGULATOR OF THE CLOCK OUTPUT THAT PLAYS A ROLE IN MODULATION OF PERIPHERAL CLOCKS BY ADRENAL STEROIDS

Abstract

An intricate transcription-translation feedback loop (TTFL) governs cellular circadian rhythms in mammals. Here I report evidence that the transcription factor Krüppel-like factor 9 (Klf9) is a direct output gene of this TTFL that feeds back on clock gene expression and modulates the clock output. Chromatin-streptavidin precipitation followed by deep sequencing (ChSP-seq) on a mouse hippocampal-derived cell line (HT22) showed that Klf9 associated with the genomic regions of many genes coding for clock- or clock-output proteins, including *Per1*, *Per3*, *Dbp*, *Tef*, *Bhlhe40*, *Bhlhe41*, *Nr1d1*, and *Nr1d2*. The *Klf9* gene showed circadian oscillation in mRNA level in synchronized HT22 cells, and in mouse hippocampus and liver *in vivo*. I showed by chromatin immunoprecipitation (ChIP) that Klf9 showed diurnal variation in association with *Tef, Nr1d1* and *Klf16* in the mouse liver *in vivo*, suggesting a role for Klf9 in regulating the rhythmic expression of these genes. In HT22 cells forced expression of Klf9 repressed transcription of the clock-output gene *Dbp*. Transient transfection experiments showed that Klf9 repressed activity from a construct containing the *Dbp* genomic region and inhibited transcriptional activation of this construct by CLOCK/Bmal1, supporting that Klf9 can act

antagonistically to the CLOCK/Bmal1 complex that forms the positive limb of the TTFL loop. The TTFL can be reset by glucocorticoids (CORT) acting through the GR. Forced expression of Klf9 inhibited upregulation of the clock gene *Per1* by CORT in mouse tissue culture cells, but mice null for *Klf9* showed impaired *Per1* induction in response to an acute restraint stress, supporting a complex role for Klf9 in regulating the transcriptional response to stress and adrenal steroids. I propose that Klf9 acts as a novel regulator of the circadian oscillator by regulating diurnal variations in mRNA levels of circadian genes, repressing transcription of certain clock-output genes, and modulating the transcriptional response to CORT and the GR.

Introduction

Cellular circadian rhythms in mammals are maintained in part by a cell-autonomous clock consisting of an intricate transcription-translation feedback loop (TTFL). At the core of the TTFL are the transcription factors CLOCK and Bmal1. CLOCK and Bmal1 heterodimerize and bind to E-box motifs (CACGTG) in the genome, where they activate the transcription of hundreds of genes, including *Period* (*Per*) and *Cryptochrome* (*Cry*) (Dardente and Cermakian 2007). Per and Cry accumulate in the cytoplasm, form Per/Cry heterodimers and translocate to the nucleus, where they disrupt the CLOCK/Bmal1 heterodimer and inhibit transcription of their own genes (Griffin et al. 1999). This leads to a reduction in *Per* and *Cry* mRNA and protein levels, which in turn leads to a reduction in their ability to disrupt Clock/Bmal1. This results in a reciprocal oscillation in the activity of these two complexes that takes about 24 hours.

The Clock/Bmal1 heterodimer also binds to E-boxes in the promoters of the orphan nuclear receptors *Nr1d1/2* (Rev-erbα/β) and *Nr1f1* (RORα) and regulates daily oscillations in transcription of these genes. Their protein products then regulate the *Bmal1* gene through competitive binding to a retinoid orphan response element (RORE) in its promoter (Preitner et al. 2002; Ueda et al. 2002; Sato et al. 2004; Liu et al. 2008). This 'accessory loop' both regulates the period length of the TTFL and plays a role in circadian gene regulation. For example, in the liver Rev-erbα/β regulated circadian oscillation of lipid and bile acid-related gene expression (Cho et al. 2012). An additional feedback mechanism involves CLOCK/Bmal upregulation of *Bhlhe40* and *Bhlhe41* (Dec1 and Dec2). These transcription factors repress transcription from E-box containing promoters and can inhibit Clock/Bmal1 from upregulating clock- and clock-output genes (Honma et al. 2002; Kawamoto et al. 2004). This 'autofeedback loop' adds an additional layer of control and robustness to the clock; forced expression of Dec1 can phase-delay expression of circadian genes with E-box containing promoters, while removal of Dec1 phase-advances expression of these genes (Nakashima et al. 2008). The kinases Csnk1δ/ε can also regulate the pace of the clock by phosphorylating Per1, which inhibits its nuclear translocation (Vielhaber et al. 2000; Etchegaray et al. 2009). Finally, the oscillating activity of the various components of this loop leads to circadian variation in the expression of clock-output genes such as the transcription factors *Dbp*, *Tef* and *Hlf*, which in turn mediate circadian variations in physiology, metabolism and other biological processes. Many thousands of genes are direct clock targets. The activity of the cellular TTFL therefore orchestrates circadian variation in many metabolic and physiological processes (Yoshitane et al. 2014).

Glucocorticoid (CORT) secretion by the adrenal gland follows a circadian rhythm, with peak secretion occurring near the onset of the activity phase (early morning in diurnal mammals, early evening in nocturnal mammals (Dickmeis et al. 2013)). This circadian oscillation is regulated by hypothalamic corticotrophin releasing hormone (CRH) and pituitary adrenocorticotropic hormone (ACTH), autonomic innervation of the adrenal glands, and local clocks modulating synthesis and release of CORT (reviewed in (Leliavski et al. 2015)). CORT in turn can act as an entraining signal for the TTFL. Treatment with the synthetic glucocorticoid dexamethasone (dex) synchronized circadian rhythms in tissue culture cells and temporarily phase-shifted circadian gene expression rhythms *in vivo* (Balsalobre et al. 2000). Acute stress and corticosteroid treatment rapidly upregulates *Per1* via a glucocorticoid response element (GRE) located in its 5' upstream region, which may be a mechanism by which adrenal steroids synchronize circadian gene expression (Yamamoto et al. 2005; Reddy et al. 2012). Adrenalectomy and glucocorticoid replacement can alter and phase-shift circadian rhythms in peripheral organs, suggesting that normal diurnal oscillations in CORT secretion are important to maintain circadian synchronicity throughout the body (Pezuk et al. 2012; Woodruff et al. 2016)

My ChSP-seq study (Chapter 2) showed that Klf9 associated with many genes involved in the TTFL, including the core-loop genes *Per1* and *Per3*, the accessory loop genes *Nr1d1* and *Nr1d2*, the autofeedback loop genes *Bhlhe40*, *Bhlhe41*, and the clock-output genes *Dbp*, *Tef* and *Wee1*. Previous studies have shown that *Klf9* is a clock-output gene in human keratinocytes and mouse liver (Sporl et al. 2012; Yoshitane et al. 2014). However, no studies have reported interactions of Klf9 with the circadian TTFL. For this section of my dissertation I tested two related hypotheses. First, I examined whether Klf9 acts as a negative regulator of the circadian oscillator and/or the clock output through repression of clock- and clock-output genes. Because *Klf9* is rapidly and strongly upregulated by CORT I also examined whether Klf9 acts as a feed-forward inhibitor of CORT/GR transactivation of the *Per1* gene (Bagamasbad et al. 2012; Sasse et al. 2013). Transient transfection, ChIP and RT-qPCR assays showed that Klf9 can repress transcription from several clock-output loci and that it inhibits transactivation of these loci by CLOCK/Bmal1. I also present evidence that Klf9 inhibits induction of *Per1* by CORT *in vitro*, but that it may be required for CORT induction of this gene by acute stress in the mouse liver *in vivo*. Taken together, these data suggest that Klf9 acts at the interface between the clock and the clock-output by interfering with transcription of clock-output genes and modulating resetting of the clock by CORT.

Materials and methods

Bioinformatic analysis

I identified enriched E-box motifs in Klf9 ChSP-seq peaks (Chapter 2), scanned peaks for occurrences of E-box motifs and mapped their proximity to Klf9 consensus motifs using the HOMER program (Heinz et al. 2010). I conducted gene ontology analysis on genes with Klf9 peaks associated using GeneCoDis (Carmona-Saez et al. 2007; Nogales-Cadenas et al. 2009; Tabas-Madrid et al. 2012). Locations of CLOCK binding sites (Yoshitane et al. 2014) were visualized using the UCSC genome browser (Raney et al. 2014). Sequences of the *Dbp* intron were downloaded using the UCSC genome browser's sequence conservation track (Kent et al. 2002).

Plasmids

The pSFV-Dbp-luc plasmid (Stratmann et al. 2012) was a generous gift of Dr. Ueli Schibler (University of Geneva). The pShuttle-Bmal1, pShuttle-Clock and pShuttle-Per1 expression vectors were generously provided by Dr. Lei Yin (University of Michigan). I isolated 5' upstream fragments of *Tef* (1 kb; -997 bp to +3 from TSS) and *Wee1* (1300 bp; -1022 to +278 from TSS) by PCR using genomic DNA from HT22 cells (extracted using the DNEasy kit

(Qiagen)). I then subcloned these fragments into the pGL4.23 vector (Promega) using the SacI and NheI restriction sites (*Tef*) or the XhoI and HindIII sites (*Wee1*) to create the pGL4.23-mTef and pGL4.23-mWee1 vectors. The pCS2-Klf9 vector was constructed by using PCR to amplify the full-length Klf9 cDNA coding sequence from the pRSV-BTEB plasmid (Imataka et al. 1994) and directionally cloning the sequence into the pCS2 expression vector. All oligonucleotide sequences used for cloning, ChIP-qPCR and RT-qPCR are given in Supplemental Table 3.1.

Cell culture and transfection assays

I cultured HT22 cells (gift of Dr. David Schubert at the Salk Institute) and HEK293 cells in high-glucose DMEM (Invitrogen) supplemented with 10% fetal bovine serum (FBS; Hyclone or Sigma), penicillin G (100 U/ml) and streptomycin sulfate (100 µg/ml). They were kept in a humidified atmosphere of 5% CO_2 at 37° C. Plasmid transfection was conducted using Fugene6 at a mass:volume ratio of 3:1 following manufacturer's instructions.

To synchronize circadian rhythms and analyze gene expression in HT22 cells I cultured the cells in 6-well plates in DMEM containing 1% FBS stripped of steroid hormones (Yao et al. 2008). At six hour-intervals I replaced the media on a new plate of cells with serum-free DMEM (SFM) containing either 1 µM corticosterone (CORT) or .01% ethanol (EtOH). After one hour I washed the cells once with SFM, then kept them in DMEM with 1% steroid-stripped FBS (Bagamasbad et al. 2012). I continued this protocol for 48 hours (N=3 wells/treatment/time point), after which I harvested all cells for RNA extraction and RT-qPCR. For the 'zero' time point I harvested cells immediately after 1 hour CORT or EtOH treatment to verify that the cells responded to CORT as determined by *Klf9*, *Per1*, and *Per2* induction. To analyze circadian variations in Klf9 association in chromatin, I cultured HT22 cells in 100 mm plates in DMEM with 1% steroid-stripped FBS and subjected the cells to 1-hour pulses of CORT followed by washout as described above every four hours for 24 hours (4 plates/time point). At the end of the time course I harvested the cells for chromatin extraction. For this experiment I also cultured and treated HT22 cells the same way in parallel for RNA extraction and RT-qPCR (12-well plates, n=4 wells/time point). One RNA time point was treated 6.5 hr after the previous and 1.5 hr before the following time point due to experimenter error; this is still included in the data set as it provides temporal information on mRNA level changes.

RNA extraction, reverse transcription and qPCR

I extracted total RNA from mouse brain, liver and cultured cells using the TRIzol reagent (Invitrogen) according to the manufacturer's instructions. Reverse transcription reactions were programmed with 1 μg of RNA using the High Capacity Reverse Transcription kit with ribonuclease inhibitor from Applied Biosystems (Life Technologies Corp). I treated the RNA with DNase 1 (20U; Roche) prior to RT to ensure that no contaminating genomic DNA was present. For real-time quantitative PCR (RTqPCR) I used Taqman assays for *Gapdh* and *Klf9* (described in (Bagamasbad et al. 2015b)) and SYBR green primers for all other assays. All oligonucleotide primer sequences are given in Supplemental Table 3.1. Real-time quantitative PCR was conducted using an API 7500 fast real-time PCR machine with Absolute qPCR low ROX mix or Absolute qPCR SYBR low ROX mix (ABgene). I designed SYBR assays using Integrated DNA Technology's RealTime qPCR Assay tool; whenever possible assays were designed to span an exon-exon boundary. Standard curves were constructed by pooling cDNA from all samples and making serial 1:10 dilutions. For cell culture and hippocampal gene expression experiments all mRNA levels were normalized to *Gapdh*. For liver gene expression experiments all mRNA levels were normalized to *Ppia.*

Chromatin extraction and immunoprecipitation

Chromatin extraction and chromatin immunoprecipitation (ChIP) were done as described previously (Denver and Williamson 2009; Bagamasbad et al. 2012; Bagamasbad et al. 2015a). HT22 cells were grown in 100 mm plates, and for some experiments two plates were pooled to increase the total starting quantity of chromatin. After washing with DPBS, we exposed cells to 1% formaldehyde and 200 nM dithiobis(succinimidyl propionate)(DSP; Thermo) for 10 minutes each, then extracted chromatin. We sonicated the chromatin using a Covaris M220 Focused-Ultrasonicator for 20 minutes using a 2% duty factor, and checked that the DNA had been sheared to 500-600 bp by electrophoresis in a 1% TAE agarose gel. We then flash froze the chromatin with liquid nitrogen and stored it at -80°C until analysis. For each ChIP reaction we used 5 μg purified IgG from goat anti-mBTEB-C17, or normal goat IgG (all from Santa Cruz Biosciences). ChIP DNA was quantified by SYBR Green real-time quantitative PCR using a standard curve with serial 1:10 dilutions of one input chromatin sample. ChIP data was normalized one of two ways. For circadian ChIP samples from the liver (Figure 3.4) Klf9 ChIP signal was calculated by taking the ratio of the quantity measured from Klf9 ChIP samples to that measured from normal goat IgG ChIP from the same animal. This value is reported as 'fold enrichment'. For circadian HT22 and hippocampal ChIP samples (Figure 3.6) Klf9 ChIP and normal goat IgG values at each time point were transformed to set the average value of the normal goat IgG amplified quantity to 1. This is reported as "Klf9 ChIP enrichment".

Luciferase Assay

For luciferase assays on HT22[TR/TO-Klf9] cells, cells were cultured in 24-well plates at a density of $5*10^4$ cells/well. 24 hours after plating they were transfected with 200 ng/well of the luciferase vector and 10 ng/well pRenilla plasmid to monitor transfection efficiency. 24 hours after transfection they were treated with or without 1 μg/ml dox for either 8 (pGL4.23-3xBTE vector) or 24 hours (all others). Cells were harvested for luciferase assay using the Dual Luciferase Reporter Assay System (Promega) according to manufacturer's instructions. Firefly luciferase activity was quantified using a luminometer (Femtometer FB 12; Zylux Corp) and normalized to Renilla luciferase activity. All reporter assays were repeated at least two times with 5-6 replicates/treatment.

For luciferase assays on HEK293 cells, cells were cultured in 24-well plates at a density of $5*10^4$ cells/well. 24 hours after plating each well was transfected with 100 ng of luciferase reporter vector (pGL3-7.5 kb mKlf9, pSFV-Dbp-Luc, pGL4.23-Tef, or pGL4.23-Wee1), 10 ng of pRenilla (Invitrogen), and pCS2-Klf9 (.1, 1 or 10 ng), pShuttle-CLOCK and pShuttle-Bmal1 (0, 1, 3, 10, 30, 100 ng each for dose-response experiment, 15 ng each for all others), and/or pShuttle-Per1 vectors (0, 1, 3, 10, 30, or 60 ng for dose-response, 30 ng for all others). The pCS2-empty vector was added as needed to keep total plasmid quantity consistent.

Animals

We purchased C57BL/6 mice from Jackson Labs and maintained them on a 12L:12D photoperiod with food and water provided *ad libitum.* I generated *Klf9* null mice (*Klf9*$^{-/-}$) by breeding male homozygous *Klf9*$^{-/-}$ mice provided by Frank Simmen with wild type female C57BL/6 mice (the original *Klf9*$^{-/-}$ line was made in a C57BL6/J background) (Morita et al.

2003). To analyze diurnal variation in gene expression and Klf9 recruitment to chromatin I housed 6-8 month-old male mice in a four-chamber lightproof cabinet with separate light timers to minimize disturbance prior to tissue collection. I then sacrificed mice by rapid decapitation every four hours beginning at zeitgeber time 2 (ZT02; two hours after lights on) for 20 hours (final collection point was at ZT22; n=4 animals/time point). To induce stress I restrained animals in 50 ml conical tubes (Falcon) with ~1 inch sections of 15 ml conical tubing slid over their tails to inhibit further movement. I drilled two air holes into each tube and drilled a hole in the cap of the tube to fit the mouse's tail through after the cap was screwed on (Zimprich et al. 2014). I restrained mice for 1 hour, after which I either allowed them to recover for two hours in their home cage or sacrificed them immediately (diagrammed in Fig. 3.8A). I sacrificed control animals immediately after removal from their home cage. I timed these experiments such that all animals were sacrificed between ZT0530 and ZT0700 regardless of treatment to minimize diurnal variation in gene expression. For both circadian and restraint stress experiments I collected trunk blood in heparinized tubes, dissected out forebrain, hippocampal and cerebellar brain regions and small pieces of liver and snap-froze all tissue in liquid nitrogen. All procedures involving animals were approved by the University of Michigan University Committee on the Care and Use of Animals.

Data analysis and statistics

All Student's unpaired t-test and one-way ANOVA analyses with Holm-Sidak post-hoc tests were conducted using Sigmaplot (Systat Software). All ChIP data was $\log_{10}$-transformed prior to analysis. Cosine fitting to analyze circadian oscillation was conducted using CircWave software (Oster et al. 2006a).

Results

Klf9 associates in chromatin at circadian clock gene loci in HT22 cells

My ChSP-seq study on HT22 cells (Chapter 2) found that Klf9 associated in chromatin with seven genes that function in the circadian oscillator: the core loop genes *Per1* and *Per3*, the accessory loop genes *Nr1d1* and *Nr1d2*, the autofeedback loop genes *Bhelhe40* and *Bhlhe41*, and the loop-modulating kinase *Csnk1d*. I also found that Klf9 associated with the well-characterized clock-output genes *Dbp, Tef* and *Wee1* (Figure 3.1A). There were thirteen separate Klf9 peaks between all ten loci. Twelve of thirteen contained E-boxes, and nine overlapped with CLOCK/Bmal1 peaks identified in mouse liver by ChIP-seq (Yoshitane et al. 2014). Gene ontology and pathway analysis using GeneCoDis (Carmona-Saez et al. 2007; Nogales-Cadenas et al. 2009; Tabas-Madrid et al. 2012) identified mammalian circadian rhythms as an enriched GO:PANTHER pathway in genes with Klf9 associated in their genomic regions, further supporting that Klf9 association with these regions may be functionally important. I conducted ChIP for Klf9 on chromatin isolated from mouse hippocampus and confirmed that Klf9 associates with the genomic regions of *Dbp*, *Tef* and *Wee1* (Figure 3.2). No Klf9 ChIP signal was evident at *Csnk1d* (not shown).

Klf9 peaks contain Klf9 consensus motifs in close proximity to E-boxes

I analyzed the DNA sequences at Klf9 peaks from my ChSP-seq analysis (Chapter 2) using the *de novo* motif discovery program HOMER (Heinz et al. 2010). The most highly enriched motif was a GC-rich motif similar to previously identified Klf/Sp binding sites (Daftary et al. 2012);the seventh-most enriched motif was an E-box-like motif similar to the previously identified CLOCK/Bmal1 consensus motif (Figure 3.1B). This motif, along with two similar E-Box-like enriched motifs, is shown in Table 3.1. Of 3,516 Klf9 peaks identified in my previous ChSP-seq study, 1,028 contained at least one of these three E-box-like motifs. I then used HOMER to map the distribution of predicted E-boxes and Klf9 consensus motifs in the 1,028 E-box containing Klf9 peaks. In these peaks, the Klf9 consensus motif tended to occur in the center of the peak. The E-box motif was more spread out but still showed a bias towards occurring in the center, supporting that it occurred in close proximity to the Klf9 consensus motif (Figure 3.1C).

Klf9* is a CLOCK/Bmal1-regulated gene that shows circadian oscillations in HT22 cells and in mouse tissues *in vivo

To determine if *Klf9* mRNA undergoes circadian oscillation in tissue culture cells I synchronized HT22 cells by treatment with 1 μM corticosterone (CORT) for 1 hr (Balsalobre et al. 2000) and analyzed clock gene and *Klf9* mRNA levels by RT-qPCR. The 1 hr exposure to CORT was sufficient to synchronize circadian gene expression rhythms in the cells as demonstrated by analysis of *Per2* and *Dbp* mRNA (Figure 3.3A and B). Cosine fitting with CircWave (Oster et al. 2006b) showed that *Per1* and *Dbp* displayed circadian oscillation in CORT-treated cells but not in vehicle (EtOH) treated cells (p<.05). The *Klf9* mRNA also oscillated in CORT-treated but not vehicle-treated cells (p<.01 for CORT-treated cells; p=.42) (Figure 3.3C). Both *Per2* and *Dbp* mRNA level peaked between 24 and 30 hours post-treatment, while *Klf9* peaked 30 hours post-treatment, showing that in HT22 cells its phase is slightly behind that of these two clock genes. I also measured *Klf9* mRNA level in the hippocampus of male C57/BL6 mice killed every four hours over the course of one 20-hour period. One-way ANOVA showed that *Klf9* mRNA level varied significantly over the course of the day (p<.05). These data support that *Klf9* mRNA oscillates in CORT-synchronized mouse hippocampal tissue culture cells and in the mouse hippocampus.

Previous work has shown that *Klf9* mRNA undergoes circadian oscillations in human keratinocytes and in mouse liver (Sporl et al. 2012; Yoshitane et al. 2014). These studies showed association of CLOCK near E-boxes in the *Klf9* 5' upstream region. In mouse liver the maximum CLOCK ChIP signal occurred at a conserved canonical E-box located at 5.36 kb upstream of the *Klf9* transcription start site (TSS), which is just upstream of a nuclear receptor enhancer (Klf9 synergy module) centered at +5.3 kb relative to the TSS (Yoshitane et al. 2014; Bagamasbad et al. 2015a). Circadian variation in the *Klf9* mRNA level was absent in *Bmal1*-deficient mice, supporting that *Klf9* oscillations are driven by the cellular circadian oscillator (Yoshitane et al. 2014). To determine if the mouse *Klf9* promoter can be activated by CLOCK/Bmal1 I co-transfected CLOCK- and Bmal1-expression vectors with a luciferase reporter construct containing 7.5 kb of the mouse *Klf9* 5' flanking region into HEK293 cells. Forced expression of CLOCK and Bmal1 increased luciferase activity by 36%. This increase was eliminated by co-transfection of a Per1 expression vector (Figure 3.3E). This supports that CLOCK/Bmal1 can activate transcription from the *Klf9* 5' flanking region.

***Klf9* mRNA shows diurnal variation in the mouse liver and is phase-advanced relative to putative target genes**

I sacrificed 8-week old male C57/BL6 mice every four hours for 20 hours and harvested liver and hippocampal tissue to examine gene expression and Klf9 recruitment to chromatin. In the liver *Klf9* mRNA level showed two peaks, at ZT2 6 and 22 (corresponding to late in the dark phase of the cycle and early in the light phase), which is consistent with previous genome-wide studies (Ueda et al. 2002). The mRNA levels of the clock-output genes *Dbp*, *Tef* and *Wee1* all peaked at ZT10, as did the Klf9 target genes *Klf13* and *Klf16* (Figure 3.4A-F).

I then conducted ChIP for Klf9 at each time point to examine Klf9 recruitment to several of these loci. To control for variability both within and between treatment groups all values are expressed as ratio of Klf9 ChIP signal to NGS IgG signal from the same animal (fold ChIP enrichment over background). The Klf9 ChIP signal at the *Tef* and *Klf16* 5' upstream regions was highest at ZT6, which paralleled peak *Klf9* mRNA levels, and preceded the peak mRNA levels of these target genes by 4 hours (Figure 3.5A and B). In contrast, Klf9 association at *Nr1d1* reached its highest level at ZT14 (Figure 3.5C). There was also an apparent increase in Klf9 association at the *Wee1* promoter at ZT14, but there was no difference in Klf9 ChIP enrichment between any of the time points, most likely due to high variability between samples (Figure 3.45). There was no evidence for association with *Dbp* at any time point (Figure 3.5E). As a negative control, I examined ChIP signal at an intronic region in the *Klf16* gene that was not associated with Klf9 in HT22 cells or in the hippocampus (Chapter 2). No Klf9 ChIP signal was evident at this locus at any time point (Figure 3.5F).

The *Dbp* locus contains an evolutionarily conserved GC-box motif in close proximity to a conserved E-box

The *Dbp* gene is a direct clock-output gene whose expression can oscillate by as much as 160-fold over the course of the day (Fonjallaz et al. 1996). Because Klf9 associated with this locus in HT22 cells and in the mouse brain (Figure 3.1 3.2), I hypothesized that Klf9 repressed *Dbp* transcription. I first examined the Klf9 peak located in the first intron of the *Dbp* gene (Fig. 3.56). An evolutionarily conserved GC-box closely matching the Klf9 consensus motif (Table 2.2) is located near the center of the peak. This GC-box is 10 bp upstream from a conserved E-box motif. Previous work showed that CLOCK and Bmal1 associate in chromatin at the location of the E-box motif in a time-of-day dependent manner, and that this motif is required for circadian oscillation in *Dbp* transcription (Ripperger et al. 2000; Ripperger and Schibler 2006). I used the tet-inducible HT22[TR/TO-Klf9] cell line (Figure 2.1) to determine if forced expression of Klf9 could modulate *Dbp* mRNA level. Six hours of dox treatment reduced *Dbp* mRNA level by 44% (Fig. 3.6B). I then synchronized circadian gene expression in parent HT22 cells by 1 hr CORT treatment and harvested chromatin from cells treated at 4-hour intervals to analyze Klf9 association in chromatin by ChIP assay. I also harvested RNA from identically treated cells cultured in parallel to determine if changes in mRNA correlate with changes in Klf9 association in chromatin. Peak Klf9 association with the *Dbp* intron occurred at 34 hours post-CORT. This time point coincided with minimum *Dbp* mRNA level, consistent with rhythmic repression of this locus by Klf9 (Fig. 3.6C).

Forced expression of Klf9 represses *Dbp* transcription and antagonizes CLOCK/Bmal1 activation of the *Dbp* locus

To investigate the mechanism by which Klf9 represses *Dbp* I used a reporter vector containing a 9.6 kb genomic fragment encompassing all the *Dbp* exons and introns plus 0.5 and 0.6 kb of 5' and 3' flanking regions respectively, with an IRES:Luciferase cassette inserted into the fourth exon (pSFV-Dbp-luc; Fig. 3.7A)(Stratmann et al. 2012). When transfected into NIH 3T3 cells this construct exhibits circadian oscillations in luciferase expression after the cells are synchronized by serum shock or dexamethasone treatment (Stratmann et al. 2012). I transfected HT22[TR/TO-Klf9] cells with this reporter and treated them with dox for 12 or 24 hr. Forced expression of Klf9 reduced luciferase activity ~25 % at both time points analyzed (Supplemental Figure 3.2A).

Because the predicted Klf9-responsive motif and the E-box were so close together, I hypothesized that Klf9 and CLOCK/Bmal1 may interfere with each other in co-regulation of this gene. I first tested whether CLOCK/Bmal1 could upregulate luciferase activity from the pSFV-Dbp-luc vector. Co-transfection of CLOCK/Bmal1 with this pSFV-Dbp-luc led to a dose-dependent increase in luciferase activity in HEK293 cells and parent HT22 cells, with maximal activation of ~7-fold (HEK293 cells, Fig. 3.7 B) and ~1.6 fold (HT22 cells, data not shown). Since HEK293 cells showed a much more robust response to CLOCK/Bmal1, I used them to examine how Klf9 and CLOCK/Bmal1 interact in regulation of the pSFV-Dbp-luc vector.

Transfection of the pCS2-Klf9 expression vector into HEK293 cells led to a dose-dependent decrease in transcription from the Dbp-luc vector, with the highest dose of pCS2-Klf9 repressing luciferase activity by 65% (Fig. 3.7C). Transfection of CLOCK/Bmal1 alone increased luciferase activity by 3.2 fold. Co-transfecting pCS2-Klf9 with CLOCK/Bmal1 led to a dose-dependent inhibition of transcription; 10 ng of pCS2-Klf9 was sufficient to reduce luciferase activity to the level of cells transfected only with pCS2-empty (Fig. 3.7C). This shows that Klf9 can both repress activity from this locus and inhibit CLOCK/Bmal1-dependent transactivation.

I next tested whether Klf9 can act synergistically with Per1 to inhibit CLOCK/Bmal1 transactivation. I first verified that co-transfection of the pShuttle-Per1 expression vector caused a dose-dependent decrease in transcriptional activity from the pSFV-Dbp-luc vector in HEK293 cells transfected with CLOCK/Bmal1 (Fig. 3.7D). I then tested the effect of co-transfection of Per1 and Klf9 expression vectors. Co-transfection of Per1 with CLOCK/Bmal1 reduced transcription from pSFV-Dbp luc by 26% compared with CLOCK/Bmal1 alone. However, adding increasing doses of pCS2-Klf9 repressed transcription to the same extent whether or not Per1 was co-expressed; there was no additive or synergistic effect evident (Fig. 3.7E). Klf9 and Per1 may therefore act via distinct and non-overlapping mechanisms to abrogate CLOCK/Bmal1 transactivation of *Dbp*.

Because Klf9 potently repressed transcription from the *Dbp* locus, I cloned the 5' upstream regions of the clock-output genes *Tef* and *Wee1* into pGL4.23 and tested the effect of CLOCK/Bmal1 and Klf9 on luciferase activity. Both *Tef* and *Wee1* are direct clock-output targets (Fonjallaz et al. 1996; Matsuo et al. 2003) and have Klf9 peaks associated with their genomic regions (Fig. 1). They therefore offer a route to determine whether the antagonism seen between Klf9 and CLOCK/Bmal1 at the *Dbp* locus is specific to *Dbp,* or if it may be generalizable to other clock-output genes. Forced expression of Klf9 repressed activity from both pGL4.23-Tef and pGL4.23-Wee1 (Figure 3.8B and C). Co-transfection of CLOCK/Bmal1 activated transcription from pGL4.23-Tef in HEK293 cells, but forced Klf9 expression did not inhibit this transactivation (Figure 3.9A). CLOCK/Bmal1 co-transfection repressed luciferase activity from pGL4.23-Wee1, in contrast with previous results showing activation in NIH3T3 cells (Matsuo et al. 2003). Forced expression of Klf9 also repressed activity from pGL4.23-Wee1 (Supplemental Figure 3.9).

Forced expression of Klf9 inhibits CORT induction of *Per1*, *Wee1* and *Klf9* mRNAs

The Klf9 peak located in the 5' region of the *Per1* gene overlaps with a GRE that mediates rapid induction of *Per1* by CORT acting via the GR (Yamamoto et al. 2005; Reddy et al. 2009; Reddy et al. 2012). The *Per2* gene is also upregulated by CORT and contains a putative GRE (Reddy et al. 2009), but Klf9 did not associate with *Per2* in HT22 cells. Because Klf9 is a CORT-induced transcriptional repressor ((Bagamasbad et al. 2012) and Chapter 2) I used the HT22[TR/TO-Klf9] cell line to test the hypothesis that Klf9 acts as a feed-forward modulator of clock genes that counteracts induction of *Per1* by CORT. I treated the cells with or without dox for 4 hr, after which I treated them with 100 nM CORT for 1 or 2 hr (dox treatment continued throughout this time period). Compared with the parent cell line, HT22[TR/TO-Klf9] cells had slower kinetics of induction of *Per1* mRNA, with mRNA levels 20-30% below that of the parent line after one hour of CORT treatment with or without dox. However, there was no difference in *Per1* mRNA level by 2 hours between any group (Figure 3.10A). The clock-output gene *Wee1*, which was upregulated by CORT in HT22 cells (P. Bagamasbad, unpublished data) also showed slower induction by CORT after forced expression of Klf9, with reduced mRNA level in dox-treated HT22[TR/TO-Klf9] cells compared to parent HT22 cells after one hour of CORT treatment but no difference after two hours (Figure 3.10B). My ChSP-seq study found Klf9 associated with the endogenous *Klf9* promoter. Because *Klf9* is a CORT target gene (Bagamasbad et al. 2012) I tested the hypothesis that Klf9 could inhibit is own induction by

CORT. I conducted RT-qPCR for the endogenous *Klf9* mRNA using a SYBR green assay targeting the 3' UTR of the *Klf9* transcript (the TO-Klf9 transgene does not contain either the 5' or 3' UTR). Dox-treated cells showed lower induction by CORT of the endogenous *Klf9* transcript at 1 and 2 hours than vehicle-treated cells (Figure 3.10C).

The clock genes *Per1* and *Per2* are both targets of CORT acting through the GR (Reddy et al. 2009), but only *Per1* has Klf9 associated with its promoter in HT22 cells. To test whether inhibition of protein synthesis differentially affected these two genes I performed RT-qPCR on RNA extracted from HT22 cells treated with or without CORT and with or without cycloheximide (CHX) for four hours. After CHX treatment, *Per1* showed both 7-fold higher baseline and 3.7 higher CORT-induced mRNA level in CHX-treated cells than in vehicle-treated cells. In contrast, baseline *Per2* was 3.2 higher in CHX-treated cells, but CORT-induced Per2 was almost unaffected (1.13-fold higher)(Figure 3.11A and B).

The liver *Per1* mRNA response to restraint stress is impaired in *Klf9*-null mice

To determine if the absence of *Klf9* led to a dysregulated response to acute restraint stress I subjected wild-type (WT) and Klf9-null ($Klf9^{-/-}$) mice to 1 hour of forced restraint and examined *Per1* expression in the liver by RTqPCR). In male and female WT mice *Per1* was induced approximately 2-fold following one hour of forced restraint and returned to baseline after two hours of recovery (Figure 3.12A). Neither male nor female $Klf9^{-/-}$ mice displayed any evidence of *Per1* induction (to date I have not generated enough $Klf9^{-/-}$ animals to test their recovery from stress). To determine whether this reflected a failure to mount a normal transcriptional response to stress I examined mRNA level of the GRE-containing gene *Fkbp5*

(Hubler and Scammell 2004). Both male and female *Klf9*$^{-/-}$ mice showed induction of *Fkbp5* after one hour of restraint (2-fold for males, 2.5-fold for females), while WT mice did not show significant induction of this gene after one hour, but did show elevated mRNA levels after the two-hour recovery period (Figure 3.12B).

Discussion

Klf9 associates with clock- and clock-output genes in mouse hippocampal neurons

My ChSP-seq study found that Klf9 associated with components of the circadian clock. Klf9 was present near the genomic regions of *Per1*, *Per3*, *Nr1d1*, *Nr1d2*, *Bhlhe40*, *Bhlhe41*, *Dbp*, *Tef*, *Wee1* and *Csnk1d*. Only *Per3* was identified as repressed by Klf9 in the RNA-seq experiment (Chapter 2), but Klf9 peaks at most of these genes overlapped with CLOCK binding sites identified by ChIP-seq for CLOCK in the liver. This raised the possibility that Klf9 augments or inhibits transactivation of these genes by the CLOCK/Bmal1 heterodimer. *De novo* motif discovery using HOMER found that E-box motifs were enriched in Klf9 peaks, and they tended to occur in close proximity to the Klf9 consensus motif. Taken together, these results suggest that Klf9 has the potential to interact with the core circadian loop to regulate expression of clock and clock-output genes.

Klf9 is a clock-output gene

Up to 10% of the transcriptome may show circadian oscillations in expression in any given tissue (Dardente and Cermakian 2007). In order to understand how Klf9 interacts with the cellular circadian pacemaker and modulates the clock output it is important to understand whether *Klf9* is itself a clock-output gene that shows circadian variations in protein and/or mRNA level. A consensus E-box motif conserved in mammals is present approximately 5.3 kb upstream of the *Klf9* TSS in mouse.In mouse liver CLOCK protein associated with this region, and the *Klf9* transcript showed diurnal variation in expression (Yoshitane et al. 2014). In HEK293 cells the *Klf9* promoter was activated by forced expression of CLOCK/Bmal1; this activation was prevented by co-expression of Per1. The *Klf9* transcript showed circadian oscillation in CORT-synchronized HT22 cells and in the mouse liver and hippocampus *in vivo*. This, together with evidence from existing genome-wide studies (Ueda et al. 2002; Sporl et al. 2012; Yoshitane et al. 2014), supports that *Klf9* is a CLOCK/Bmal1 target gene whose circadian oscillation in mRNA level is under control of the cellular circadian pacemaker. It is noteworthy that the conserved E-box motif to which CLOCK most likely bind is very close to a conserved NR enhancer element important for GR-mediated CORT induction of *Klf9* (Bagamasbad et al. 2015a). The CLOCK protein can inhibit GR transactivation by acetylating its hinge region, inhibiting DNA binding (Nader et al. 2009); the close proximity of these response elements raises the possibility of crosstalk between the circadian oscillator and GR signaling at the level of *Klf9* upregulation. Many extracellular and intracellular stimuli, including glucocorticoids and oxidative stress, are potent inducers of *Klf9* (Zucker et al. 2014; Bagamasbad et al. 2015a). Both glucocorticoids and oxidative signaling show circadian variation and are connected with the circadian clock (Dickmeis et al. 2013; Patel et al. 2014). Diurnal variation in *Klf9* may help to integrate these systems.

The Klf9 peak at the first *Dbp* intron contains a conserved GC-box adjacent to a conserved E-box

The CLOCK/Bmal1 heterodimer shows rhythmic association with intronic E-box-containing enhancers at the *Dbp* locus (Ripperger and Schibler 2006). Binding of CLOCK/Bmal1 to these regions is correlated with rhythmic changes in chromatin environment, with positive histone marks becoming prominent during the 'active' phase of transcription and negative marks appearing when the gene is repressed (Ripperger and Schibler 2006). My ChSP-seq experiment found that Klf9 associated with this intronic enhancer; furthermore, at the center of the peak was a conserved GC-box motif in close proximity to the E-box known to be important for rhythmic *Dbp* expression. ChIP on HT22 cells synchronized with pulses of CORT showed that Klf9 protein is only recruited to the *Dbp* intron at one point in the 24-hour cycle, consistent with rhythmic association of Klf9 with this locus (Figure 3.3C). Future studies should investigate corresponding changes in chromatin environment associated with Klf9 association with this locus.

Forced Klf9 expression antagonizes CLOCK/Bmal1 transactivation of the *Dbp* locus

Using promoter-reporter assays I found that forced expression of Klf9 repressed *Dbp* transcription, and completely blocked CLOCK/Bmal1 transactivation of the *Dbp* locus (Figure 3.C). This is, to my knowledge, the first evidence of a GC-box-binding factor interfering with CLOCK/Bmal1-dependent transcription. This has potentially far-reaching implications for the transcriptional regulation of CLOCK-output genes.Future studies should examine the role of individual sequence motifs to determine that these response elements are important for Klf9's repression of the *Dbp* locus and its antagonism of CLOCK/Bmal1-dependent transcription. While the Klf9 peak in the first *Dbp* intron is an attractive candidate given its proximity to the well-characterized CLOCK binding site (Ripperger and Schibler 2006), another Klf9 peak is present near the 3' end of exon 2 (Figure 3.1A). The center of this peak corresponds very closely to a DNAse-hypersensitive region mapped in a previous study (Ripperger et al. 2000); this region does not contain E-boxes and did not show obvious circadian variations in DNAse-sensitivity, but it is possible that Klf9 or other Klf/Sp proteins associate at this region and contribute to circadian regulation of *Dbp* mRNA transcription. It will also be important to investigate whether Klf9 modifies chromatin structure at this locus to contribute to its inhibition of CLOCK/Bmal1-dependent transactivation.

Klf9$^{-/-}$ mice fail to induce *Per1* in response to acute restraint stress

Because Klf9 functions primarily as a transcriptional repressor I tested the possibility that acute stress would cause an amplified or lengthened induction of the *Per1* gene in mice lacking *Klf9*. However, preliminary data suggests the opposite – the *Klf9* knockout mice failed to show any transcriptional induction of *Per1* in the liver after one hour of forced restraint stress. In contrast, *Per1* was induced approximately 2-fold in both male and female WT mice (Figure 3.8A). Two hours of recovery was sufficient for *Per1* to return to baseline in male and female WT mice. As of this writing I have not generated enough *Klf9*$^{-/-}$ mice to determine if they show any differences at this time point, although a single *Klf9*$^{-/-}$ female subjected to restraint+recovery showed *Per1* expression close to the mean values for the control and restraint groups (data not shown). I examined expression of *Fkbp5*, a well-known stress/CORT-responsive gene, and found that *Klf9*$^{-/-}$ mice upregulate this gene in response to a one-hour restraint stress to an even greater degree than WT mice, showing that their overall stress responsivity is not impaired at least at this locus.

There are a number of possible explanations for this result. One is that despite its role as a repressor in cell-based assays, *in vivo* in the liver Klf9 acts as an accessory factor that is required for GR induction of *Per1*, similar to what has been seem for Klf15 in the GR-mediated transcriptional response in airway cells (Sasse et al. 2013). This would lead to an impaired response in *Klf9*$^{-/-}$ mice. On the other hand, the *Per1* gene is extremely fast-responding and fast-recovering (Fig. 3.8A); it is possible that in the absence of Klf9 *Per1* mRNA is induced extremely rapidly and then drops back to baseline within one hour. Future studies should look at earlier time points (e.g. after 30 min restaint). It is also possible that there are differences in the kinetics of CORT release after the stressor that delay *Per1* induction, but the rapid rise in *Fkbp5* mRNA argues against this possibility. *Fkbp5* was upregulated somewhat faster in *Klf9*$^{-/-}$ mice; it was significantly higher than baseline after one hour of restraint in both male and female KO mice but not in WT mice. Future studies should address other CORT/GR target genes that are also Klf9 targets, GR recruitment (or lack thereof) to *Per1* and other loci, and what consequences this may have for circadian rhythms and how they are perturbed (or not perturbed) by stress.

Summary and future directions

Previous published work suggests that *Klf9* is a clock-output gene that mediates circadian variation in some physiological processes (Sporl et al. 2012). Here I present evidence that Klf9 may act at the interface between the clock and clock output and may therefore be a novel component of the negative limb of the cellular circadian pacemaker. I also present the first evidence that *Klf9*$^{-/-}$ mice show a dyregulated transcriptional response to acute stress. Antagonism between CLOCK/Bmal1 and GC-box-binding factors such as Klf9 may be widespread mechanism for fine-tuning circadian oscillation of gene expression.

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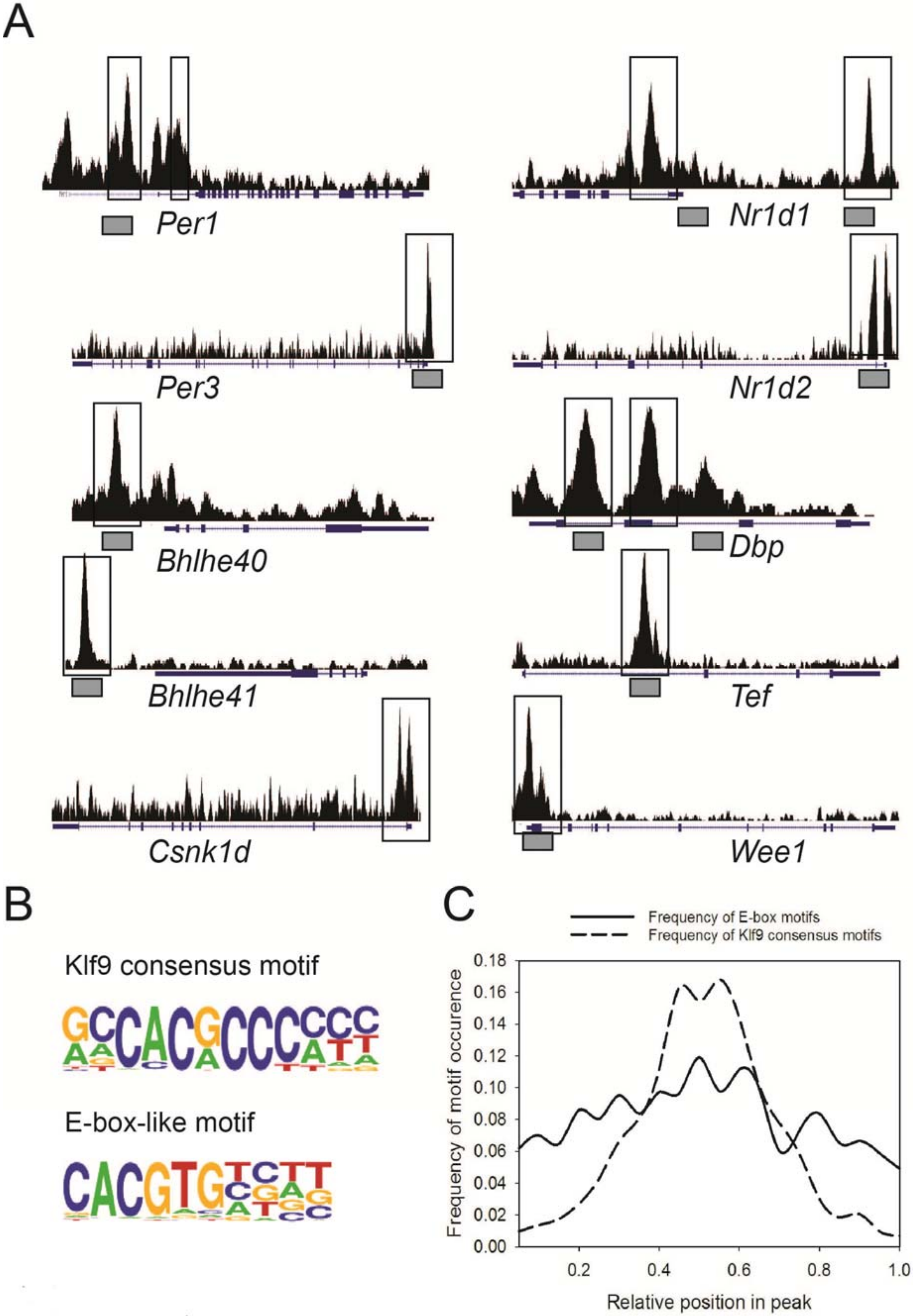

A
Per1
Nr1d1
Per3
Nr1d2
Bhlhe40
Dbp
Bhlhe41
Tef
Csnk1d
Wee1
B
Klf9 consensus motif
E-box-like motif
C
Frequency of E-box motifs
Frequency of Klf9 consensus motifs
Frequency of motif occurence
0.00
0.02
0.04
0.06
0.08
0.10
0.12
0.14
0.16
0.18
0.2
0.4
0.6
0.8
1.0
Relative position in peak

Figure 3.1: Klf9 associates in chromatin in close proximity to E-box motifs at several clock-output genes. A) Mapped sequencing reads from Klf9 ChSP-seq in HT22 cells aligned to the genome at clock- and clock-output regions. Open boxed regions indicate Klf9 peaks identified by MACS and PePr (see Chapter 2). Gray boxes indicate approximate locations of CLOCK binding sites (E-boxes) identified by ChIP-seq in mouse liver (Yoshitane et al. 2014). **B)** Klf9 consensus motif (present in 75% of all peaks) and E-box/CLOCK-like motif (present in 24% of all peaks) identified by *de novo* analysis of Klf9 ChSP-seq peaks using HOMER. **C)** Frequency of occurrence of Klf9 consensus and E-box motifs across peaks in the subset of Klf9 peaks that contained E-boxes.

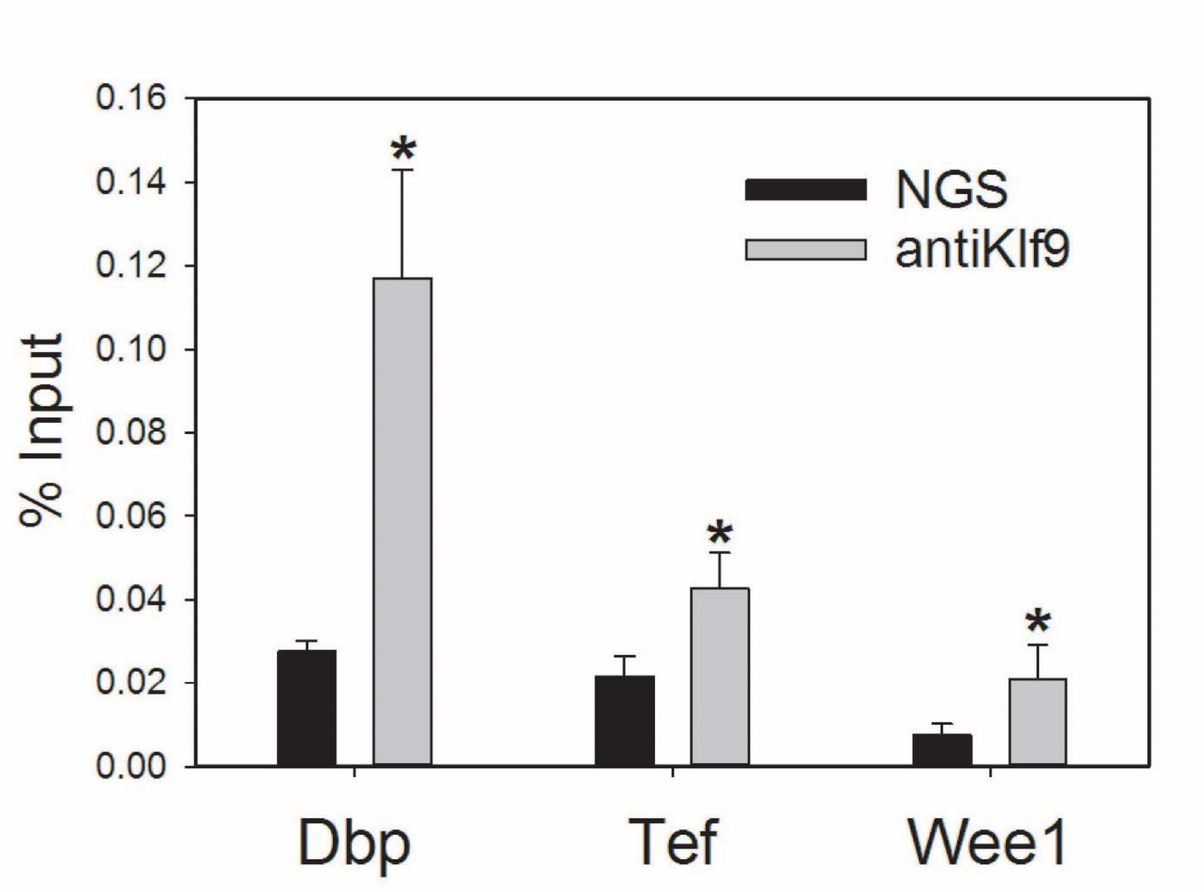


Figure 3.2: Klf9 associates with clock-output genes in mouse hippocampus. Male and female C57/BL6 mice were sacrificed and hippocampal tissue harvested for chromatin extraction (n=9 animals). ChIP for Klf9 shows enrichment at *Dbp*, *Tef* and *Wee1*peaks discovered in HT22[BirA/FLBIO-Klf9] cells. *Indicates significant difference from NGS IgG by t-test on log-transformed data. *Dbp*: t(13)=2.695, *p*<.05. *Tef*: t(12)=2.327, *p*<.05; *Wee1*: t(11)=2.287, *p*<.05.

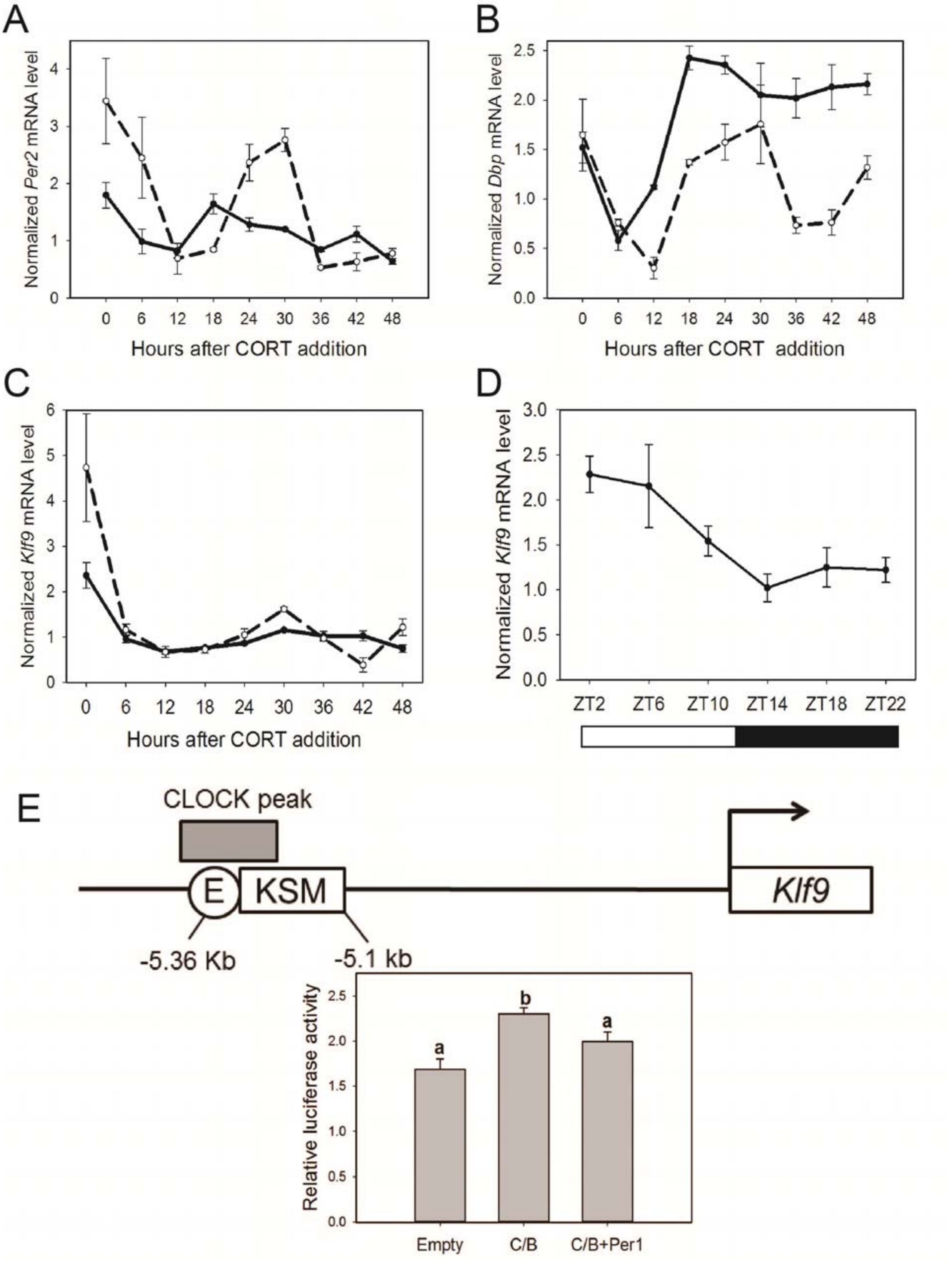

A
Normalized Per2 mRNA level
0
1
2
3
4
0 6 12 18 24 30 36 42 48
Hours after CORT addition
B
Normalized Dbp mRNA level
0.0
0.5
1.0
1.5
2.0
2.5
0 6 12 18 24 30 36 42 48
Hours after CORT addition
C
Normalized Klf9 mRNA level
0
1
2
3
4
5
6
0 6 12 18 24 30 36 42 48
Hours after CORT addition
D
Normalized Klf9 mRNA level
0.0
0.5
1.0
1.5
2.0
2.5
3.0
ZT2 ZT6 ZT10 ZT14 ZT18 ZT22
E
CLOCK peak
E
KSM
Klf9
-5.36 Kb
-5.1 kb
Relative luciferase activity
0.0
0.5
1.0
1.5
2.0
2.5
a
b
a
Empty
C/B
C/B+Per1

Figure 3.3: *Klf9* is a Clock/Bmal1-regulated gene whose mRNA level oscillates in CORT-synchronized HT22 cells. A) and **B)** The mRNA levels of the clock gene *Per2* and the clock-output gene *Dbp* oscillate in HT22 cells synchronized by one-hour pulses of 1 μM CORT (dashed lines) but not in cells treated with pulses of EtOH (solid lines). Cosine fits to verify circadian oscillation were conducted using CircWave software (Oster et al. 2006a). CORT treated: *Per2*: $p<.05$, period=26 hr; *Dbp*: $p<.05$, period=26 hr. Vehicle: *Per2*: $p=.16$; *Dbp*: $p=.2$. **C)** *Klf9* mRNA level oscillates in CORT-synchronized HT22 cells but not in EtOH-treated cells. CORT: $p<.05$, period=26 hours; EtOH**:** $p=.42$. Klf9 mRNA level peaks slightly later than *Dbp* and *Per1*. **D)** *Klf9* shows diurnal variation in mouse hippocampus. $F_{(5,15)}=4.279$, $p<.05$. **E)** Schematic of the *Klf9* 5' upstream region. 'KSM' indicates nuclear receptor synergy module that supports CORT/T_3-regulation of *Klf9* (Bagamasbad et al. 2015b). Gray box indicates location of CLOCK ChIP-seq peak identified in the liver (Yoshitane et al. 2014). 'E' indicates conserved E-box motif. Numbers indicate distance upstream of the transcription start site (TSS; indicated by arrow). Graph: Forced expression of CLOCK and Bmal1 activates transcription from the pGL3-7.5kb-mKlf9 construct in HEK293 cells; co-expression of Per1 abrogates the transcriptional response. C/B: co-transfected with pShuttle-CLOCK and pShuttle-Bmal1. Per1: co-transfected with pShuttle-Per1. Bars with the same letter are not significantly different by one-way ANOVA and Holm-Sidak post-hoc test (n=6 wells/treatment; $F_{(2,15)}=9.858$, $p<.005$).

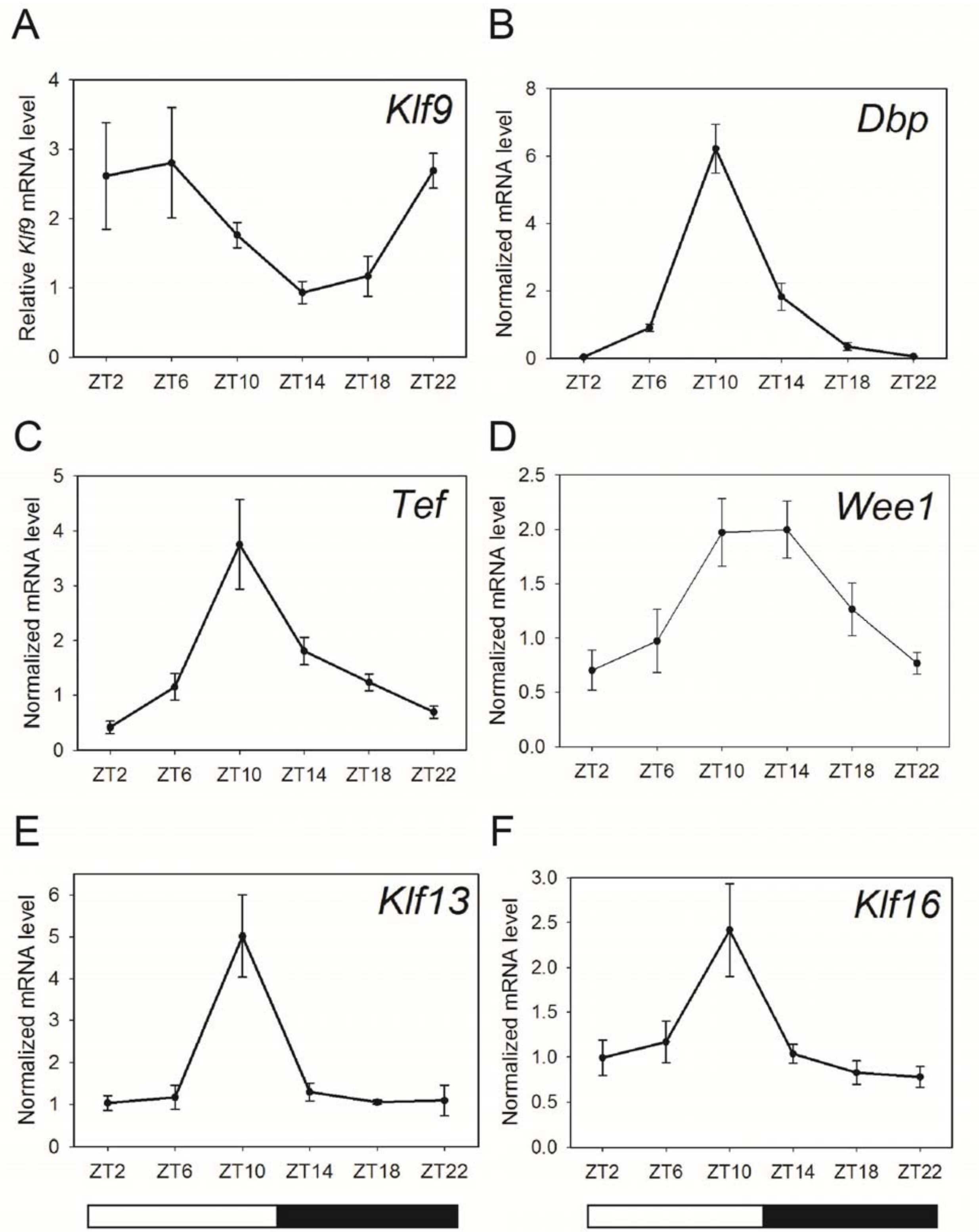

A
B
C
D
E
F
Klf9
Relative Klf9 mRNA level
0
1
2
3
4
Dbp
Normalized mRNA level
0
2
4
6
8
Tef
Normalized mRNA level
0
1
2
3
4
5
Wee1
Normalized mRNA level
0.0
0.5
1.0
1.5
2.0
2.5
Klf13
Normalized mRNA level
0
1
2
3
4
5
6
Klf16
Normalized mRNA level
0.0
0.5
1.0
1.5
2.0
2.5
3.0
ZT2
ZT6
ZT10
ZT14
ZT18
ZT22

Figure 3.4: Klf9 mRNA is circadian in liver and is phase-advanced compared with Klf9 target genes. Male C57/BL6 mice were sacrificed every 4 hours for 20 hours beginning two hours after lights on (ZT2) and RNA was extracted from liver (n=3-4 animals/time point). Bars under panels E and F indicate lights on (open) and lights off (filled) periods. **A)** *Klf9* mRNA level peaks at ZT2-Z6. **B)-F)** The Klf9 target genes *Dbp, Tef*, *Wee1*, *Klf13*, and *Klf16* (see Fig. 3.1 and Chapter 2) peak in expression at ZT10 after *Klf9* mRNA level has decreased. Rhythmicity was confirmed by one-way ANOVA on log-transformed values. *Klf9*: $F_{(5,13)}$=4.811, p<.05; *Dbp*: $F_{(5,16)}$=66.881, p<.001; *Tef*: $F_{(5,17)}$=14.658, p<.001; *Wee1*: $F_{(5,17)}$=4.846, p<.01; *Klf13*: $F_{(5,16)}$=7.208, p<.001; *Klf16*: $F_{(5,17)}$=4.325, p<.05.

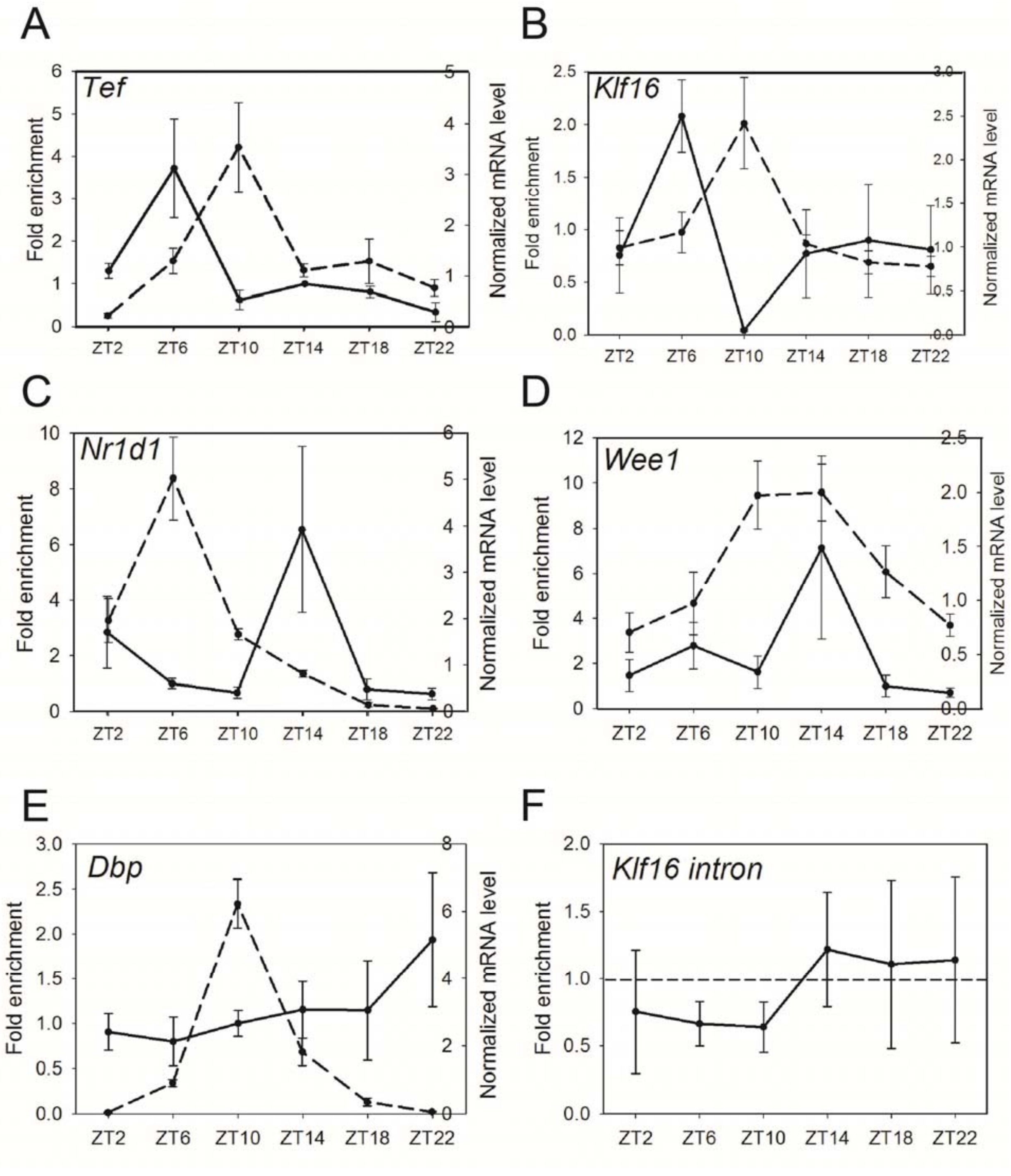

A
Tef
Fold enrichment
Normalized mRNA level
0
1
2
3
4
5
6
0
1
2
3
4
5
ZT2
ZT6
ZT10
ZT14
ZT18
ZT22
B
Klf16
Fold enrichment
Normalized mRNA level
0.0
0.5
1.0
1.5
2.0
2.5
0.0
0.5
1.0
1.5
2.0
2.5
3.0
ZT2
ZT6
ZT10
ZT14
ZT18
ZT22
C
Nr1d1
Fold enrichment
Normalized mRNA level
0
2
4
6
8
10
0
1
2
3
4
5
6
ZT2
ZT6
ZT10
ZT14
ZT18
ZT22
D
Wee1
Fold enrichment
Normalized mRNA level
0
2
4
6
8
10
12
0.0
0.5
1.0
1.5
2.0
2.5
ZT2
ZT6
ZT10
ZT14
ZT18
ZT22
E
Dbp
Fold enrichment
Normalized mRNA level
0.0
0.5
1.0
1.5
2.0
2.5
3.0
0
2
4
6
8
ZT2
ZT6
ZT10
ZT14
ZT18
ZT22
F
Klf16 intron
Fold enrichment
0.0
0.5
1.0
1.5
2.0
ZT2
ZT6
ZT10
ZT14
ZT18
ZT22

Figure 3.5: Klf9 shows circadian recruitment to CLOCK-output genes in mouse liver. A) and **B)** Klf9 shows peak association with the *Tef* and *Klf16* 5' upstream regions at ZT6. Klf9 ChIP enrichment is ratio of Klf9 antibody ChIP to mock ChIP with NGS IgG from same sample. Circadian oscillation in Klf9 fold enrichment over NGS IgG was evaluated by one-way ANOVA on log-transformed enrichment values. *Tef*: $F_{(5,15)}$=4.795, p<.01; *Klf16*: $F_{(5,15)}$=3.048, *p*<.05. **C)** Klf9 associates with the *Nr1d1* locus at ZT14 when *Nr1d1* expression is low. *Nr1d1* Klf9 ChIP enrichment: $F_{(5,16)}$=3.115, *p*<.05; *Nr1d1* mRNA: $F_{(5,16)}$=67.372, *p*<.001. **D)** Klf9 shows higher ChIP enrichment at the *Wee1* locus at ZT14 but does not differ across the day ($F_{(5,17)}$=1.647, *p*=.201). **E)** Klf9 is not associated with the *Dbp* locus in the liver at any time point ($F_{(5,17)}$=.571, *p*=.722. **F)** Klf9 does not associate with the *Klf16* intron (negative control) in the mouse liver at any time point ($F_{(5,14)}$=.650, *p*=.666. In all panels dashed lines indicate mRNA level, while solid lines indicate ChIP enrichment.

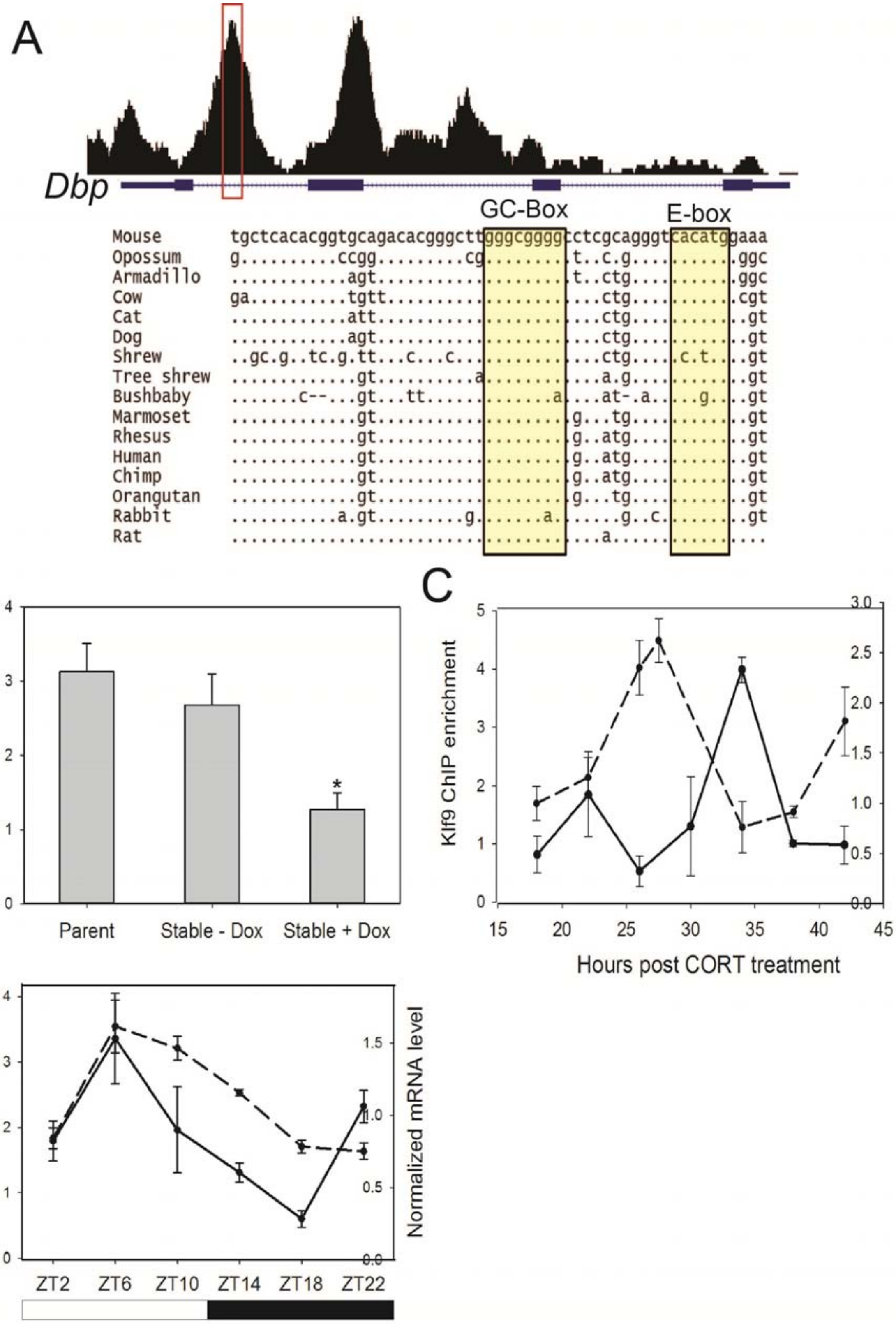
A
Dbp
GC-Box
E-box
Mouse tgctcacacggtgcagacacgggcttgggcggggctcgcagggtcacatggaaa
Opossum g.........ccgg..........cg........t..c.g...........ggc
Armadillo ....agt....................t..ctg...........ggc
Cow ga.........tgtt......................ctg...........cgt
Cat ....att.......................ctg............gt
Dog ....agt.......................ctg............gt
Shrew ..gc.g..tc.g.tt...c...c..............ctg.....c.t....gt
Tree shrew ....gt...........a...........a.g............gt
Bushbaby ....c--..gt...tt..............a...at-.a.....g....gt
Marmoset ....gt....................g...tg............gt
Rhesus ....gt....................g..atg............gt
Human ....gt....................g..atg............gt
Chimp ....gt....................g..atg............gt
Orangutan ....gt....................g...tg............gt
Rabbit ....a.gt..........g.......a......g..c.........gt
Rat ....a................
B
Relative Dbp mRNA
4
3
2
1
0
*
Parent
Stable - Dox
Stable + Dox
C
Klf9 ChIP enrichment
5
4
3
2
1
0
Normalized mRNA level
3.0
2.5
2.0
1.5
1.0
0.5
0.0
15
20
25
30
35
40
45
Hours post CORT treatment
D
Klf9 ChIP enrichment
4
3
2
1
0
Normalized mRNA level
1.5
1.0
0.5
0.0
ZT2
ZT6
ZT10
ZT14
ZT18
ZT22

Figure 3.6: Klf9 represses *Dbp* mRNA level and shows circadian recruitment to an evolutionarily conserved E-box motif that is required for circadian *Dbp* expression. A) Schematic of *Dbp* locus showing Klf9 peaks. Location of DNA sequence aligned below is boxes. The DNA sequence at the indicated region in the first intron contains an evolutionarily conserved putative Klf9 binding site in close proximity to an E-box motif that is required for CLOCK/Bmal1 association and rhythmic *Dbp* expression (Ripperger and Schibler 2006). **B)** Forced *Klf9* expression represses *Dbp* mRNA level in HT22[TR/TO-Klf9] cells (see Chapter 2). Cells were treated with or without 1 μg/ml dox for 6 hours (n=3-4/treatment; HT22 parent cells were treated with dox). *Significantly different from parent line by one-way ANOVA ($F_{(2,6)}$=7.415, p<.05). **C)** Klf9 shows rhythmic association with the *Dbp* intronic peak indicated in panel A in CORT-synchronized HT22 cells. HT22 cells were synchronized by 1 hr pulses with 1 μM CORT every four hours and harvested 18-42 hours after treatment for chromatin extraction or RT-qPCR (n=3-4 plates/wells per time point for ChIP and RNA respectively). Peak Klf9 association (solid line) coincides with low *Dbp* mRNA level (dashed line). Rhythmicity was evaluated by one-way ANOVA. *Dbp* mRNA level: $F_{(6,19)}$=9.240, p<.001; Klf9 ChIP normalized enrichment over NGS: $F_{(6,16)}$=6.348, p<.001. **D)** *Dbp* shows diurnal variation in mRNA level and Klf9 shows rhythmic recruitment to the *Dbp* intron in the mouse hippocampus. *Dbp* mRNA level (dashed): $F_{(5,17)}$=12.829, p<.001. Normalized Klf9 ChIP enrichment(solid): $F_{(5,14)}$=6.881, p<.005.

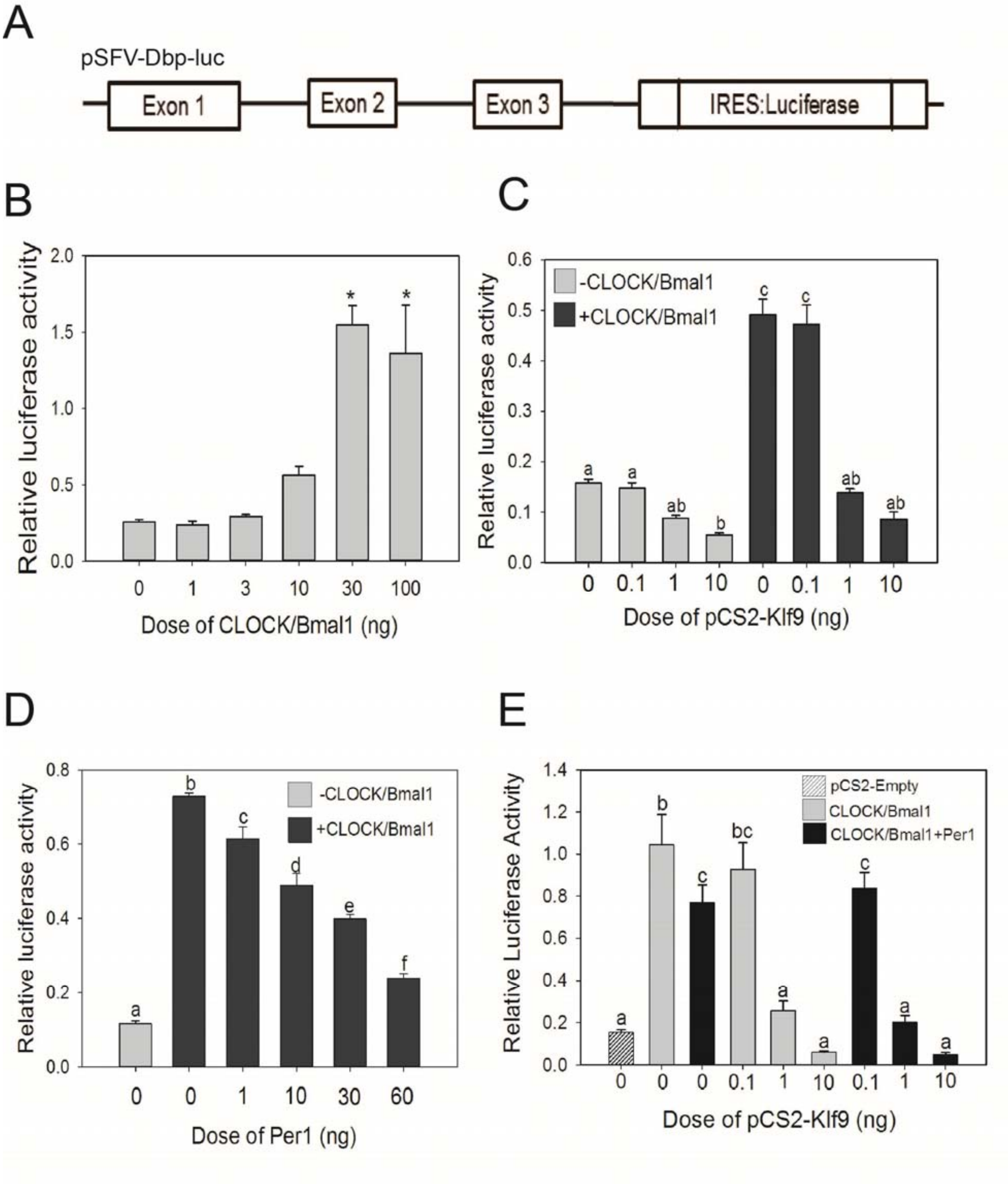

A
pSFV-Dbp-luc
Exon 1
Exon 2
Exon 3
IRES:Luciferase
B
Relative luciferase activity
0.0
0.5
1.0
1.5
2.0
*
*
0
1
3
10
30
100
Dose of CLOCK/Bmal1 (ng)
C
Relative luciferase activity
0.0
0.1
0.2
0.3
0.4
0.5
0.6
-CLOCK/Bmal1
+CLOCK/Bmal1
a
a
ab
b
c
c
ab
ab
0
0.1
1
10
0
0.1
1
10
Dose of pCS2-Klf9 (ng)
D
Relative luciferase activity
0.0
0.2
0.4
0.6
0.8
-CLOCK/Bmal1
+CLOCK/Bmal1
a
b
c
d
e
f
0
0
1
10
30
60
Dose of Per1 (ng)
E
Relative Luciferase Activity
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
pCS2-Empty
CLOCK/Bmal1
CLOCK/Bmal1+Per1
a
b
c
bc
a
a
c
a
a
0
0
0
0.1
1
10
0.1
1
10
Dose of pCS2-Klf9 (ng)

Figure 3.7: Klf9 represses transcription of the *Dbp* promoter and antagonizes CLOCK/Bmal1 transactivation of *Dbp* in HEK293 cells. A) Schematic of pSFV-Dbp-luc vector (Stratmann et al. 2012). This vector contains the complete *Dbp* coding sequence with an IRES: luciferase cassette inserted into the fourth exon. **B)** Co-transfection of CLOCK/Bmal1 expression vectors causes a dose-dependent increase in luciferase activity from the pSFV-Dbp-luc vector in HEK293 cells (n=4 wells/treatment). *Significantly different from control (0 ng CLOCK/Bmal1) by one-way ANOVA and Holm-Sidak post-hoc test ($F_{(5,18)}$=17.505, p<.001). **C)** Co-transfection of the pCS2-Klf9 expression vector causes dose-dependent repression of luciferase activity from the pSFV-Dbp-luc vector in the absence of CLOCK/Bmal1 expression (gray) and a dose-dependent inhibition of CLOCK/Bmal1 transactivation (black). Quantities that share at least one letter in common are not significantly different by one-way ANOVA and Holm-Sidak post-hoc test (n=6 wells/treatment; $F_{(7,39)}$=79.969, p<.001). **D)** Co-transfection of Per1 expression vector leads to dose-dependent abrogation of transcriptional activation of pSFV-Dbp-luc by CLOCK/Bmal1. Quantities with different letters are significantly different by one-way ANOVA and Holm-Sidak post-hoc test (n=5-6 wells/treatment, $F_{(5,29)}$=122.693, p<.001). **E)** Co-transfection of Per1 does not increase Klf9 abrogation of CLOCK/Bmal1 transactivation of pSFV-Dbp-luc. Quantities that share at least one letter in common are not significantly different by one-way ANOVA and Holm-Sidak post-hoc test (n=6 wells/treatment, $F_{(8,45)}$=173.737, p<.001.

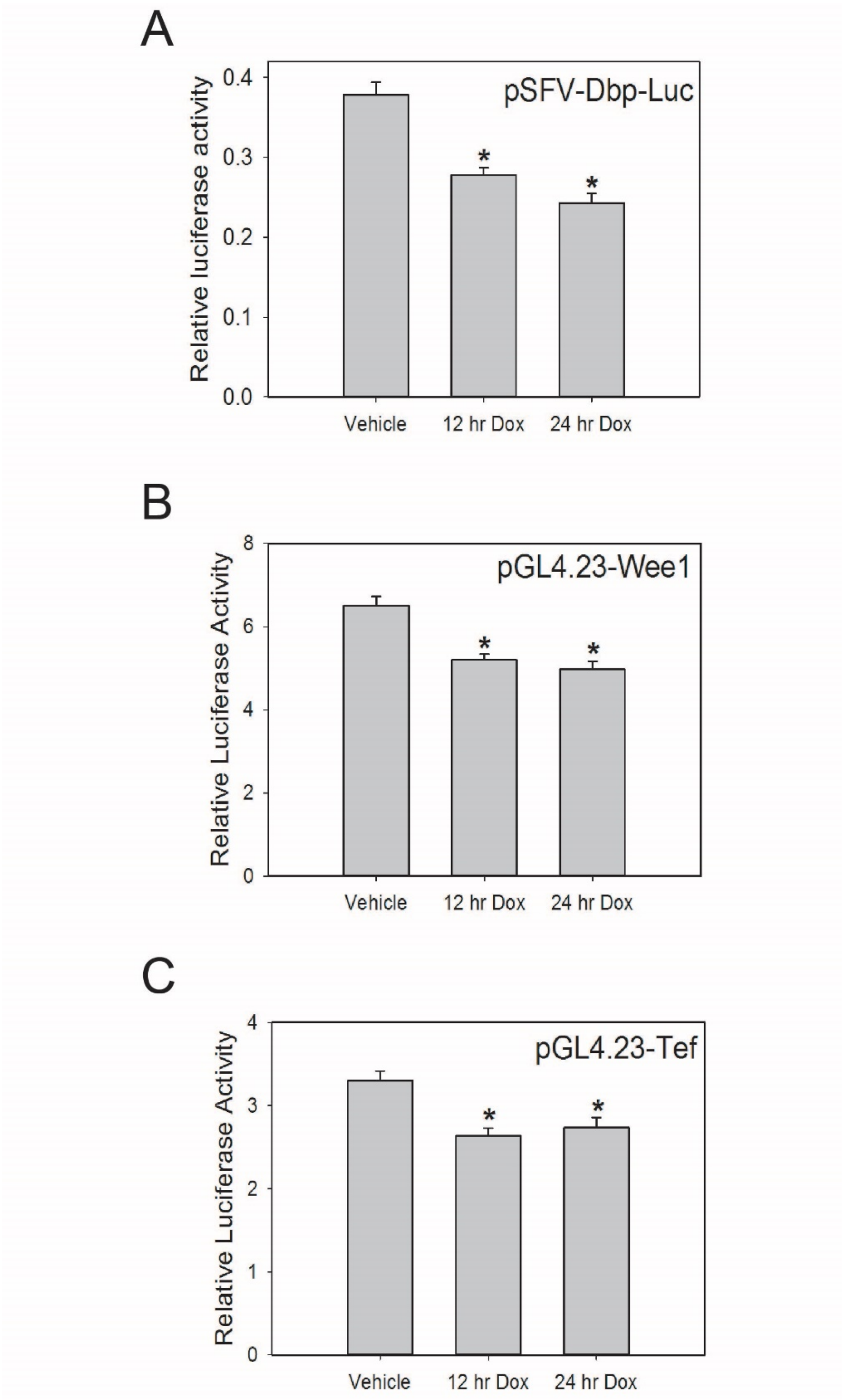


Figure 3.8: Forced expression of Klf9 represses transcription for *Dbp*, *Tef,* and *Wee1* promoters. HT22[TR/TO-Klf9] cells were transfected with pSFV-Dbp-luc, pGL4.23-Wee1, or pGL4.23-Tef vectors and treated with 1 µg/ml dox for 12 or 24 hours. *Indicates significant difference from control by one-way ANOVA. pSFV-Dbp-luc: $F_{(2,21)}=22.798$, $p<.001$; pGL4.23-Wee1: $F_{(2,15)}=18.831$, $p<.001$; pGL4.23-Tef: $F_{(2,10)}=10.341$, $p<.005$.

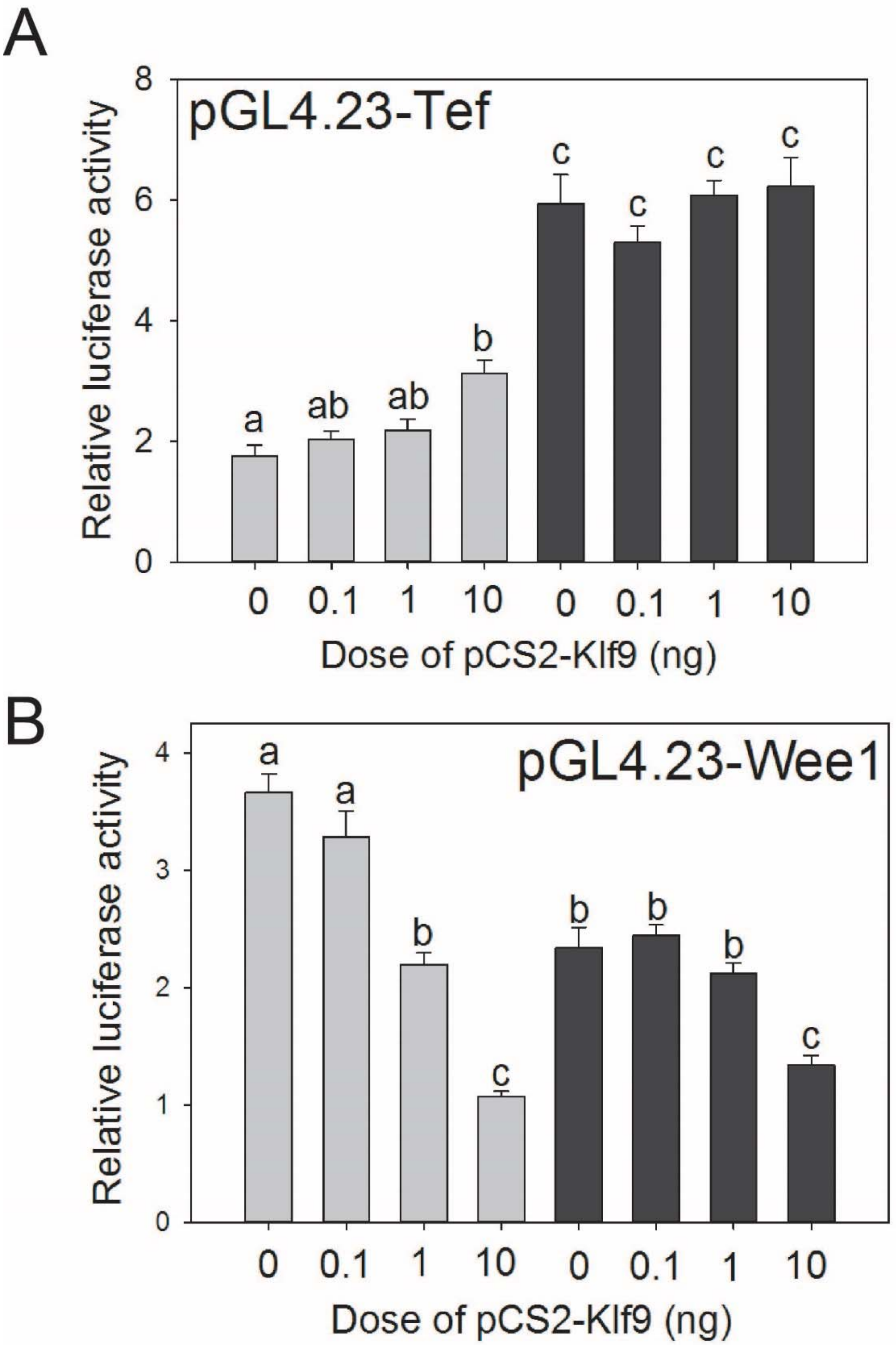
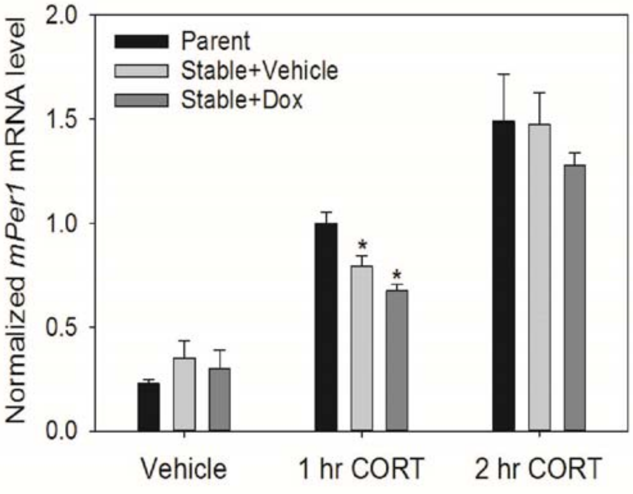
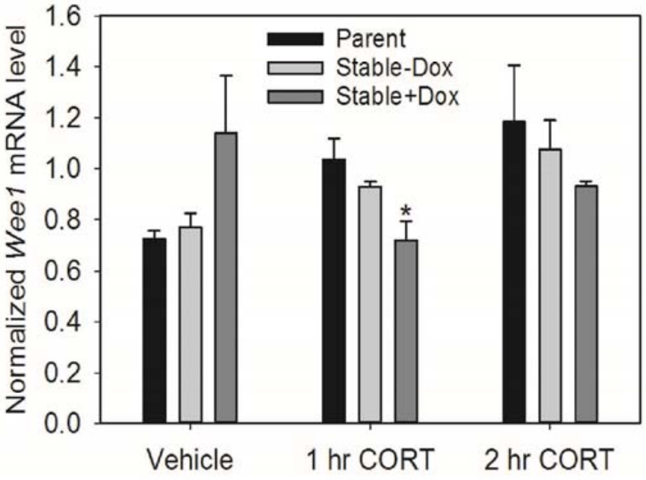


Figure 3.9: Klf9 does not inhibit CLOCK/Bmal1 transactivation of *Tef* and *Wee1* promoters. HEK293 cells were transfected with pGL4.23-Tef (**A**) or pGL4.23-Wee1 (**B**) vectors with increasing doses of pCS2-Klf9 with (black bars) or without (gray bars) CLOCK/Bmal1. Quantities with the same letter are not significantly different from each other by one-way ANOVA with Holm-Sidak post-hoc test. pGL4.23-Tef: $F_{(7,40)}$=42.658, p<.001. pGL4.23-Wee1: $F_{(7,34)}$=47.231, p<.001.

A


Normalized mPer1 mRNA level
0.0
0.5
1.0
1.5
2.0
Parent
Stable+Vehicle
Stable+Dox
*
*
Vehicle
1 hr CORT
2 hr CORT

B


Normalized Wee1 mRNA level
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
1.6
Parent
Stable-Dox
Stable+Dox
*
Vehicle
1 hr CORT
2 hr CORT

C

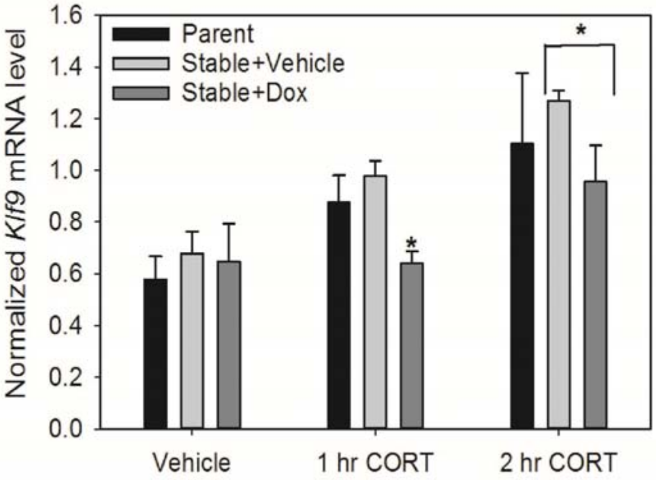

Normalized Klf9 mRNA level
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
1.6
Parent
Stable+Vehicle
Stable+Dox
*
*
Vehicle
1 hr CORT
2 hr CORT

Figure 3.10: Klf9 interferes with CORT induction of *Per1* and *Klf9*. A) *Per1*shows slower induction in HT22[TR/TO-Klf9] cells in response to 100 nM CORT compared to response in parent line. *Indicates significant difference from parent line within treatment by one-way ANOVA with Holm-Sidak post-hoc test. Vehicle: $F_{(2,9)}$=.746, *p*=.502; 1 hr CORT: $F_{(2,9)}$=12.445, *p*<.005; 2 hr CORT: $F_{(2,8)}$=.402, *p*=.682. **B)** *Wee1* mRNA shows reduced induction by 1 hour of CORT treatment in dox-treated HT22[TR/TO-Klf] cells. Quantities that share a letter are not significantly different by one-way ANOVA with Holm-Sidak post-hoc test; Vehicle: $F_{(2,6)}$=2.767, *p*=.141; 1 hr CORT: $F_{(2,9)}$=6.155, *p*<.05; 2 hr CORT: $F_{(2,8)}$=.584, *p*=.580. **C)** The endogenous *Klf9* gene (measured by RTqPCR against the *Klf9* 3'UTR) shows slower CORT induction after forced expression of Klf9 by dox pretreatment. * indicates significantly different from parent (1 hr CORT) or from Stable+Vehicle (2 hr CORT) ANOVA and Holm-Sidak post-hoc test (Vehicle and 1 hr CORT). Vehicle: $F_{(2,9)}$=.886, *p*=.446; 1 hr CORT: $F_{(2,9)}$=21.472, *p*<.001; 2 hr (Stable+Vehicle vs. Stable+Dox): t(5)=4.302, *p*<.01.

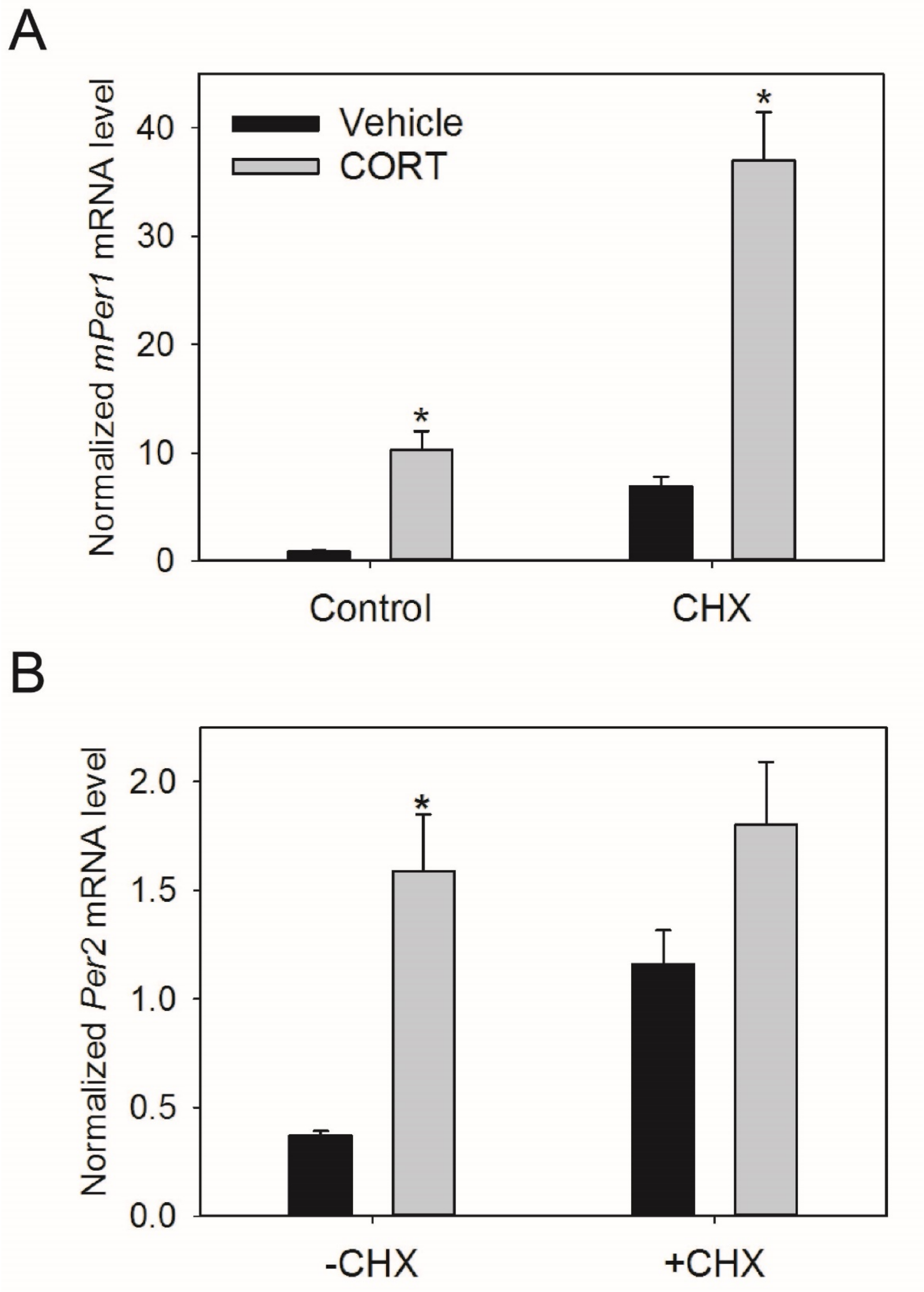


Figure 3.11: Inhibition of protein synthesis enhances upregulation of *Per1,* but not *Per2,* in response to CORT. Treatment with cyclohexamide (CHX) increases baseline and CORT-induced *Per1* mRNA level but does not increase baseline or CORT-induced *Per2* mRNA level. *Significantly different from vehicle-treated cells by two-sample t-test. *Per1*-CHX: t(6)=-5.402, *p*<.005; *Per1*+CHX: t(5)=-5.638, *p*<.005. *Per2*-CHX: t(6)=-4.648, *p*<.005; *Per2*+CHX: t(5)=-1.750, *p*=.140.

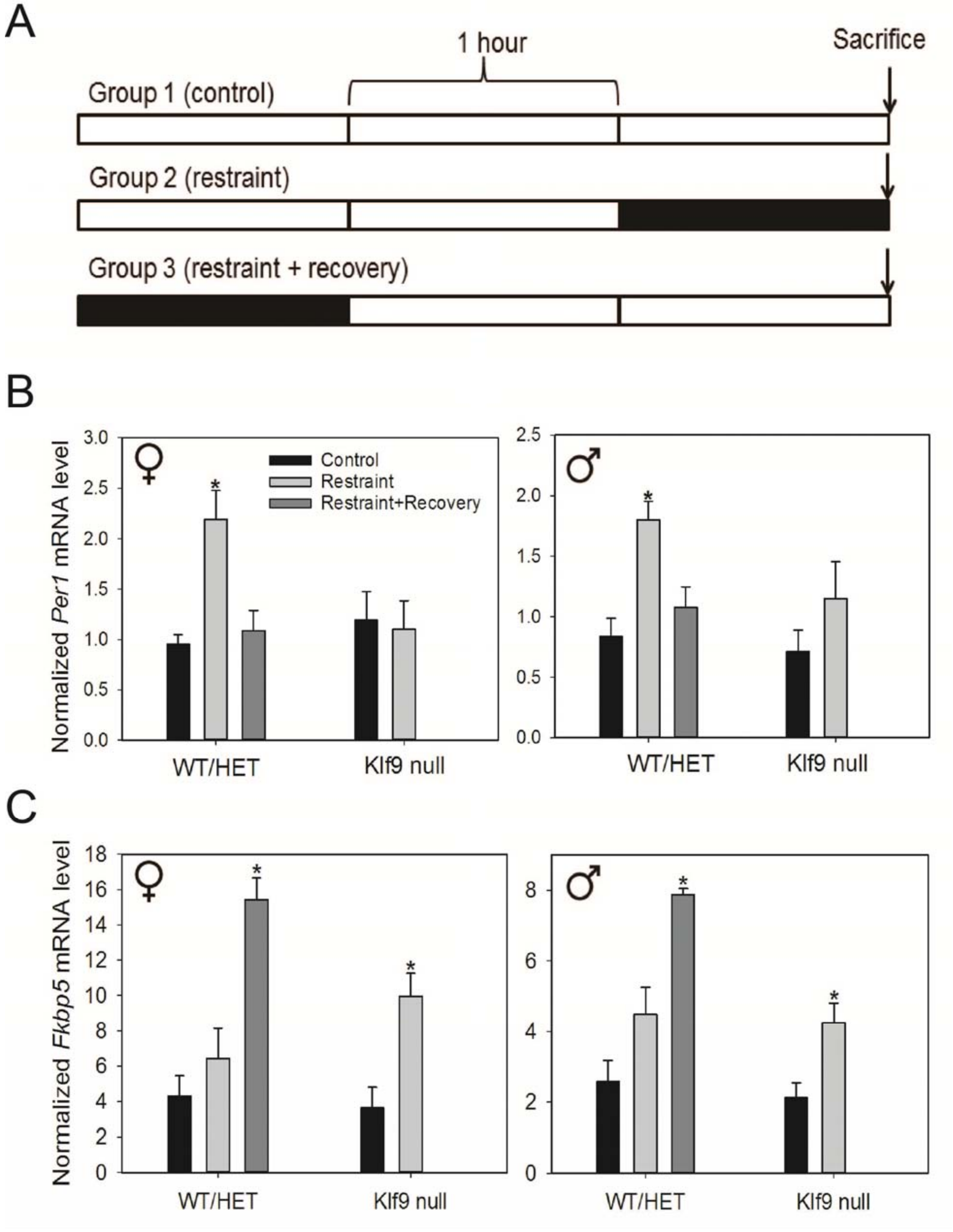

A
1 hour
Sacrifice
Group 1 (control)
Group 2 (restraint)
Group 3 (restraint + recovery)
B
Normalized *Per1* mRNA level
3.0
2.5
2.0
1.5
1.0
0.5
0.0
♀
Control
Restraint
Restraint+Recovery
*
WT/HET
Klf9 null
2.5
2.0
1.5
1.0
0.5
0.0
♂
*
WT/HET
Klf9 null
C
Normalized *Fkbp5* mRNA level
18
16
14
12
10
8
6
4
2
0
♀
*
*
WT/HET
Klf9 null
8
6
4
2
0
♂
*
*
WT/HET
Klf9 null

Figure 3.12: Klf9-null mice show impaired *Per1* induction in response to acute restraint stress. A) Outline of experimental protocol for forced restraint and recovery. Mice were either left unhandled (group 1), restrained for one hour and immediately sacrificed (group 2), or restrained for one hour, allowed to recover in their home cage for two hours, and then sacrificed (group 3). Open bars indicate one-hour periods in home cage; filled bars indicate one-hour periods of restraint. **B)** Male and female wild-type (WT) mice upregulate *Per1* ~2 fold after one hour restraint; $Klf9^{-/-}$ mice fail to upregulated *Per1* under these conditions. *Different from control by one-way ANOVA with Holm-Sidak post-hoc test. Female WT/HET: $F_{(2,22)}$=9.09, p<.001; Female KO: t(6)=.229, t=.827; Male WT/HET: $F_{(2,10)}$=10.124, p<.005; Male KO: t(6)=-1.258, p=.255. **C)** Both WT and $Klf9^{-/-}$ mice upregulate *FKBP5* after restraint stress, although WT animals do not show significantly elevated *FKBP5* until three hours after stress. *Different from control by one-way ANOVA with Holm-Sidak post-hoc test or two-sample t-test. Female WT/HET: $F_{(2,11)}$=6.491, p<.05; Female KO: t(5)=-3.618, p<.05; Male WT/HET: $F_{(2,10)}$=15.364, p<.001; Male KO: t(5)=-3.080, p<.05.

Table 3.1. E-box motifs discovered in Klf9 peaks by HOMER. Average number of occurrences/peak only includes the 1,028 peaks with at least one E-box.

De novo motif discovered by HOMER	*p* value	% of peaks with motif	% of background sequences with motif	Average number of occurrences/peak
	$1*10^{-28}$	24.31%	16.94%	1.7
	$1*10^{-23}$	24.28%	17.53%	1.5
	$1*10^{-13}$	11.56%	7.87%	0.7

CHAPTER 4

CONCLUSIONS AND FUTURE DIRECTIONS

Krüppel-like factor 9 has been shown to function in neuronal development and is an evolutionarily conserved target of thyroid hormone and glucocorticoid receptors, but its genomic targets in the central nervous system are largely unknown. In this dissertation I presented two genome-wide studies to characterize the Klf9 cistrome in the mouse cell line HT22, a model for mature hippocampal neurons. These data provide insight into Klf9's genomic targets and the signaling pathways affected by Klf9. I also showed that many of the genomic targets identified in HT22 cells are targets of Klf9 in the mouse brain. Among the genomic targets of Klf9 discovered in these studies were many genes involved in the cellular circadian oscillator. I found that *Klf9* is a clock-output gene that can modulate other direct clock-output genes and mediate crosstalk between the hypothalamo-pituitary-adrenal (HPA) axis and the circadian clock. Together these data have uncovered a new role for Klf9 in circadian regulation of gene expression, and provide a basis for future studies on how Klf9 functions in chromatin and impacts cellular physiology.

Klf9 acts as a repressor of gene transcription in hippocampal neurons

Early studies on Klf9 suggested that it could act as an activator or repressor depending on the number of basic transcription element (BTE) sequences in the promoter (Imataka et al. 1992). More recent studies have shown that Klf9 transactivates the *Pparg* and *Dio1* genes in adipocytes and liver, respectively (Ohguchi et al. 2008; Pei et al. 2011). Our work in the frog

Xenopus laevis also supports a transactivation function for Klf9, as it enhances *Trb* autoinduction (Bagamasbad et al. 2008; Hu et al. 2016). However, a recent combined ChIP-seq and RNA-seq study in glioblastoma cells found that Klf9 acted primarily as a transcriptional repressor in these cells (Ying et al. 2014). My data are consistent with Klf9 primarily functioning as a transcriptional repressor; in HT22 cells 567 genes were repressed by forced expression of Klf9, compared to 201 induced. Furthermore, repressed genes were much more likely than upregulated genes to have Klf9 peaks associated with their genomic regions. This suggests that, at least in this neuronal cell line, Klf9's primary effect on transcription is repressive.

De novo motif analysis found that the most highly enriched motif within Klf9 peaks was a GC-rich sequence that was similar to previously reported consensus motifs for Klfs. This motif was present in 75% of all peaks; when considering similar GC-rich motifs identified by computer analysis, 98% of all Klf9 peaks had at least one GC-box sequence, and 88% had two or more. I used transient transfection assays to examine whether these sequences were important for repression by Klf9. At a 439-bp fragment of the *Klf13* promoter, mutation of 2 of 6 GC-boxes did not affect Klf9-dependent transcriptional repression, but mutation of all six abrogated it completely. This supports that multiple GC boxes may function redundantly in supporting repression by Klf9

It should be noted that these results do not directly test whether DNA binding to GC boxes is required for Klf9 association in chromatin and effects on transcription in neuronal cells. Our studies in *Xenopus laevis* showed that a mutant Klf9 protein that does not bind DNA is capable of enhancing transcription at the *Trb* locus (Bagamasbad et al. 2008; Hu et al. 2016). Similar findings have been reported for other members of the Klf family. ChIP-seq studies using mutant, truncated and chimeric proteins have shown that the N-terminal region of the Klf3 protein influences where it is targeted in the genome of mouse embryonic fibroblasts independent of the DNA-binding preference of its C-terminus (Burdach et al. 2014; Lim et al. 2015). Targeting of Klfs to specific genomic regions may therefore involve protein-protein interactions in addition to binding to GC-box regions; this may be a mechanism to impart functional specificity to different Klfs despite their nearly identical DNA-binding domains. Whether similar mechanisms dictate where Klfs besides Klf3 are targeted in the genome is not known.

To understand how Klf9 represses target genes it will be necessary to define the protein-interaction partners of Klf9. Studies on the closely related Klf16 showed that it acted predominantly as a repressor, but could couple to both positive (the histone acetyltransferase CREB binding protein) and negative (the histone deacetylase-binding Sin3a and Sin3b) chromatin-modifying enzymes (Daftary et al. 2012). The BirA-FLBIO-Klf9 platform could be used for proteomic studies to identify Klf9 binding partners by mass spectrometry. This will clarify many unanswered questions about Klf9. For example, it could provide a basis for developing mechanistic models for understanding how it represses or activates target genes. It will also allow dissection of the function of Klf9's N-terminal protein interacting domains; at present only the Sin3a binding domain has been investigated in any detail (Zhang et al. 2001).

Evidence for a role for Klf9 in the cellular circadian oscillator

Several genome-wide studies have found that *Klf9* shows circadian oscillation in expression in different tissues including liver, uterine endometrial stromal cells, mouse pituitary and human keratinocytes (Ueda et al. 2002; Guillaumond et al. 2012; Sporl et al. 2012; Tasaki et al. 2013; Yoshitane et al. 2014). The only published study on the role of Klf9 in the circadian oscillator concluded that Klf9 functioned as a clock-output gene rather than as a component of the core clock oscillator loop. However, this was based on one finding: knockdown of Klf9 protein by ~50% did not affect the circadian luciferase rhythm in a luciferase reporter line (Sporl et al. 2012). My ChSP-seq data showed that Klf9 associated with the genomic regions of ten different clock- and clock-output genes, suggesting that it may play a more prominent role in the regulation of the cellular circadian clock in addition to acting as a clock-output transcription factor. All of the Klf9 peaks associated with clock genes contained E-boxes, and at 9/10 genes at least one Klf9 peak overlapped with a previously identified CLOCK ChIP-seq peak (Yoshitane et al. 2014). In addition, the Klf9 peak in the 5' upstream region of the *Per1* gene overlapped with a well-characterized glucocorticoid response element (GRE) (Yamamoto et al. 2005). Because Klf9 acts primarily as a repressor of transcription, I tested two related hypotheses. First, I examined the hypothesis that Klf9 is a novel component of the negative limb of the cellular circadian oscillator. Second, because Klf9 is potently induced by corticosteroids (CORT) and CORT can reset circadian rhythms, I tested the hypothesis that Klf9 acts as a feed-forward repressor that fine-tunes CORT-dependent modulation of the circadian oscillator (Balsalobre et al. 2000; Bagamasbad et al. 2012).

Klf9 is a novel modulator of the clock-output

I found that Klf9 expression was rhythmic in CORT-synchronized HT22 cells, in the mouse liver and hippocampus *in vivo*. Forced expression of Klf9 repressed transcription of the clock-output gene *Dbp* and strongly inhibited CLOCK/Bmal1 transactivation of this gene. There are several possible mechanisms by which this may occur. Klf9 may physically prevent CLOCK/Bmal1 from binding to the E-box in the *Dbp* intron, preventing it from activating transcription. It may recruit chromatin-modifying enzymes or other proteins that repress transcription, counteracting the positive effects exerted by CLOCK/Bmal1. It may also physically interact with CLOCK/Bmal1 and prevent either its association with chromatin or its ability to activate transcription. Because Klf9 can repress *Dbp* transcription on its own, it is unlikely that it acts soley by inhibiting CLOCK/Bmal1 from binding with E-boxes. Future experiments should first examine how mutating the E-box and GC-box motifs in the *Dbp* intron singly or in combination affects regulation by Klf9 and Clock/Bma11. If Klf9 acts primarily by competing with CLOCK/Bmal1 for occupancy then mutating its predicted binding site should inhibit its ability to inhibit CLOCK/Bmal1 activation. Because Klf9 binds Sin3a one obvious mechanism by which it represses *Dbp* and inhibits CLOCK/Bmal1 would be by recurimenet of histone deacetylases (HDAC), which would lead to a repressive chromatin state. If this is the case, treatment with HDAC inhibitors or knockdown of Sin3a should reduce Klf9-depndent repression. Co-immuoprecipitation could be used to determine if Klf9 exists in a complex with CLOCK and/or Bmal1, or with Per or Cry proteins. It should be noted that both Klf9 and CLOCK/Bmal1 associate with multiple sites within the *Dbp* locus, not all of which overlap; see Figure 3.1. More than one mechanism may be at work; it will be important to study the contribution of each region to regulation and co-regulation of the *Dbp* gene. Because E-box and GC-box motifs are present in close proximity at many other clock- and clock-output genes, careful examination of how these factors interact at the *Dbp* locus will help predict the effects of Klf9's interactions with CLOCK/Bmal1 at other loci.

I also showed that Klf9 recruitment to chromatin is circadian in liver and brain, supporting a role for Klf9 in regulating daily oscillations in gene expression. However, the function of rhythmic Klf9 association with target genes is at present unclear. If Klf9 functions primarily as a transcriptional repressor *in vivo*, its rhythmic association in chromatin could either repress transcription after the circadian peak (‘deactivation’), prevent transcriptional activation during the circadian nadir (‘maintenance repression’), or delay upregulation by associating during a time period when CLOCK/Bmal1 activity is increasing (‘phase delaying’). In the liver, peak Klf9 association with the genes *Klf16* and *Tef* occurred prior to peak mRNA level of these genes, which is consistent with either ‘maintenance repression’ or ‘phase delaying’. Association with *Nr1d1* in the liver peaked when *Nr1d1* mRNA was low, consistent with a ‘maintenance repression’ model. In synchronized HT22 cells, Klf9 associated with the *Dbp* locus after the peak *Dbp* mRNA level was reached, consistent with ‘deactivation’ and ‘maintenance repression’. In the hippocampus its association with the *Dbp* locus peaked roughly in parallel with peak *Dbp* mRNA level, which could represent a ‘phase delay’ function. In order to distinguish between these mechanisms, we will have to look at circadian expression of these genes in *Klf9*-null mice to see if and how it is dysregulated in the absence of Klf9.

Despite Klf9’s association with the *Dbp* locus in the hippocampus and its repression of transcription from the *Dbp* genomic region, in the liver there was no evidence for Klf9 association with the *Dbp* locus at any time point. The *Dbp* mRNA level oscillates with significantly greater amplitude than *Tef* in the liver (in my data set, 150-fold versus 9-fold difference between maximum and minimum mRNA level for *Dbp* and *Tef*, respectively) and *Dbp* mRNA in the liver shows a much higher-amplitude oscillation than it does in the hippocampus (based on my data, 150-fold in liver versus 1.9-fold in hippocampus) (Fonjallaz et al. 1996; Gachon et al. 2004). It is therefore possible that Klf9 association with target promoters has the effect of dampening the maximum amplitude of oscillation. One would therefore predict that in *Klf9*$^{-/-}$ mice, *Dbp* and *Tef* would show greater amplitude oscillation in the brain, while only *Tef* would show greater-amplitude oscillation in the liver. This would also be consistent with Klf9's ability to inhibit CLOCK/Bmal1 activation of the *Dbp* promoter. I hypothesize that modulation of transcription by Klf9, and perhaps other GC-box binding factors is a novel mechanism to set the amplitude of clock gene oscillation in different tissues.

Predicting the consequences of *Klf9* disruption on the core circadian clock

In HT22 cells Klf9 associated with genes that block transcriptional activation by the E-box binding factors CLOCK and Bmal. These genes include *Per1* and *Per3,* whose protein product directly disrupt the CLOCK/Bmal1 heterodimer, *Bhlhe40* and *41*, which antagonize transactivation of CLOCK/Bmal1 target genes by competitive binding to E-boxes, and *Nr1d1* and *Nr1d2*, which repress *Bmal1* transcription. Because Klf9 typically acts as a repressor of transcription, one would predict that forced expression of Klf9 would repress transcription of these negative limb components, while Klf9 depletion would lead to increased transcription of these genes. There is evidence that dysregulation negative-limb genes can affect the period length of circadian gene expression and activity rhythms. Mice null for *Per1* show normal activity rhythms under a light:dark cycle, but in constant darkness (free-running) they have a shorter circadian period (Bae et al. 2001; Cermakian et al. 2001). Rats with constitutive overexpression of *Per1* in the SCN had free-running rhythms 0.6-1 hour longer than wild-type animals (Numano et al. 2006). However, mice with both of the E-box binding repressive factors *Bhlhe40* (Dec1) and *Bhlhe41* (Dec2) deleted showed an increased period length (Rossner et al. 2008). These data suggest that removal of negative clock regulators can strongly impact circadian output, although with different outcomes.

Predicting the effect of Klf9 dysregulation on the clock output is also complicated by the fact that Klf9 itself can repress transcription from many clock-related loci and inhibit

CLOCK/Bmal1 transcriptional actions, at least from the *Dbp* locus. If deletion of Klf9 leads to increased protein levels of Per1, Dec1, and Dec2, there are at least three possibilities for the outcome of Klf9 deletion on the clock:

1. Increased expression of negative regulators leads to a net repressive effect on CLOCK/Bmal1 and transcription mediated by E-boxes, leading to a lengthening of the circadian period.
2. Increased expression of negative regulators is balanced by a lack of Klf9-dependent repressive transcription, leading to no net effect on the circadian period.
3. Loss of Klf9-dependent repression overbalances the increased expression of negative regulators and leads to reduced circadian period.

Future studies using *Klf9*$^{-/-}$ mice and HT22 cells with *Klf9* deleted by CRISPR/Cas9 will be necessary to address these questions. Mice null for *Klf9*$^{-/-}$ can be used to determine if loss of Klf9 results in changes in the free-running activity rhtythm or affects how quickly the rhythm can be reset by a light, temperature or timed feeding stimulus (Stokkan et al. 2001; Buhr et al. 2010; Sujino et al. 2012). Deletion of Klf9 in HT22 or other cell lines should be paired with continuous bioluminescent monitoring of circadian promoters driving luciferase to examine subtle changes in period, phase or amplitude of gene expression. Genome editing could also be used to mutate GC-boxes at circadian gene loci to dermine if this disrupts Klf9 association in chromatin, and if so, how this affects the clock output. This would support the hypothesis that Klf9's presence in chromatin is important for its effects on the circadian oscillator. In addition to its potential effects on the core clock loop, loss of Klf9 could result in changes in circadian regulation of many clock-output genes, as was seen for *Klf10* and *Klf15* (Han et al. 2015; Zhang et al. 2015). If *Klf9*$^{-/-}$ mice show changes in circadian behavior, physiology or clock gene expression, transcriptomic studies can be performed to examine how loss of Klf9 affects daily oscillations in gene expression.

A Klf network for fine-tuning gene expression

Among the most strongly Klf9-repressed genes were *Klf13* and *Klf16.* Both of these genes had large Klf9 peaks in their proximal promoters, and ChIP on chromatin from mouse hippocampus supported that the endogenous Klf9 protein associates with the promoters of these genes *in vivo*. Both of these Klfs are members of the Sin3a-binding subfamily of Klfs and have high sequence similarity to Klf9 (Zhang et al. 2001; Suske et al. 2005). At present there are no studies on the roles of either of these proteins in the brain. However, because they have similar DNA binding specificities it is possible that they associate with some of the same regions as Klf9. Future ChIP-seq and RNA-seq studies on Klf13 and Klf16 could provide important insight into how these closely related factors might cooperate to regulate gene transcription. Another hypothesis is that the relative levels of Klfs 9, 10 and 16 in neurons is a mechanism to control where Sin3a is targeted in the genome. It would be instructive to conduct ChIP-seq for Sin3a in cell lines or animals in which one or more Klfs have been deleted, and compare its association profile with that of wild-type cells.

In addition, *Klf10*, *11*, *13* and *16* are CLOCK/Bmal1 targets that show circadian oscillation in the liver (Yoshitane et al. 2014). All of these are also targets of Klf9, creating a potential for a "Clock/Klf loop" that exerts time-of-day-dependent control of genes with GC-boxes in their promoters. Examining the circadian transcriptomes of animals with these Klfs deleted will yield further insight into how this family of transcription factors influences circadian variations in gene expression and hence in metabolism, physiology and behavior.

Concluding remarks

The results presented in this dissertation are the first to define the Klf9 cistrome in neurons, which represents an important step in understanding how it functions in neural development and plasticity. I also provide evidence that Klf9 is a circadian gene that acts at the interface between the clock and the clock-output by regulating expression of clock genes and antagonizing CLOCK/Bmal1-dependent transactivation of major clock-output genes. These data provide a basis for understanding the mechanism behind Klf9's many roles in the brain and other tissues. The experimental platforms I developed will also be useful for future studies of other Klfs and transcription factors in neurons.

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APPENDIX

Supplemental Table 2.1: Oligonucleotide sequences

<u>For RTqPCR</u>

<u>Taqman assays</u>

Klf9 mRNA
Taqman probe: 5' 6FAM-AAAGTCTATGGAAAATCC 3'
Forward: 5’ GCACAAGTGCCCCTACAGT 3’
Reverse: 5' TGTATGCACTCTGTAATGGGCTTT 3'

Gapdh mRNA
Taqman probe: 5’ 6FAM-AAG GTC GGT GTG AAC G 3’
Forward: 5’ TCG TCC CGT AGA CAA AAT GGT 3’
Reverse: 5’ CGC CCA ATA CGG CCA AA 3’

<u>Sybr green assays</u>

<u>For RT-qPCR</u>

Gene	Forward	Reverse
Klf13 mRNA	CTACAGCCGCTCCGATG	CTGTTTTGCTGTGGACTTCTC
Apc2 mRNA	CTGCGTAATCTGTCATGGAGG	AGCACTGAGCACACTCTTTAG
Smurf1 mRNA	TCACAGTTCCGTTCTACAAGC	CTCCACGCAGAAGGTATGATC
Nlgn2 mRNA	TCTCCAAGAACGATGTCATGC	TCCACACTACCTCTTCAAAGC
Nyap1 mRNA	CTGAACCCCGCAAGTCTG	TCAAGCCTCAAGGAGACCTAG
Limk1 mRNA	ATCACAGAGTACATCAAGGC	GTTCATCGAATGGAGGTAGGC
Mapk11 mRNA	CCCATGAAATTGAGCAGTGAG	GGTCCCAGGTTAAGTGTCAG
Pou6f1 mRNA	GTGAGGGTCTGGTTCTGTAAT	AGTGACTTCGGCTGGTTG
Klf16 mRNA	CTGTCCCTTCCATGGCTG	ATCAGAACTGGCGAACTTC
Slc11a2 mRNA	GGGTTGGCAGTGTTTGATTG	CTGGGCTGTTAGTCATCTGG
Klf11 mRNA	CAGGTAGACTTTTCCCGAAGG	TTCTTGTCACAGCCGTCC

<u>For ChIP-qPCR</u>

Locus	Forward	Reverse
Slc11a2 peak	GACATCCTCTGTGCCATC	GGGCTGTCCAGTTCTCTTGT
Klf16 peak	GTACGCACTACCCTCACCAG	GGTGGGCGTAACTCTCAAAG
Sin3a peak	CGCCTCCTTAGCAGTGAAG	ACCGTTCCCAGTCTACAAGG
Nr3c1 peak	CGAGGTGAAGGGAGAAATGT	CGGCCTTATCTGCTAGAAGTG
Limk1 peak	CAGAATTGTCCCTGCTTGG	AGGGCGTGGCTGTTATTAAG

Mapk11 peak	GGGTGGAGGTTGAGGGTT	TGCAGAAGATGAAGGTGGAG
Klf11 peak	GCGTGCTTGGAGGAGATATT	CCCACAGTCCTACCAGAGGT
Klf13 peak	TCAGAGTCGGCCTGTCTTAG	GAACTGCGACCACAACTTG
Klf13 intron	GTGCCTTATTCTTATTTGCTATCCC	GATTCTGACTCCACCCTGAAC
Klf16 intron	ACTAAACTCCACCCCACAAC	TCTTTCAAACACTCCCTCGC
Nr3c1 intron	AAATACCACTCACCGAAGCC	GCTTTTGGGTATGCTGTTGAC
Limk1 intron	GAGGACAAAGGGAACACAGG	GGTTACAGAGAAAGATCCCAGC

Primers for amplification of genomic regions for cloning into pGL4.23 vector

Mapk11 promoter	ATAGAGCTCTCCTCACCCTGGCCACAAG	ATACTCGAGCCTGCCAGCGAGTGGAATCT
Limk1 Promoter	ATAGCTAGCGCGTTGCCGCTGCCTGAGAA	ATAGGTACCTCTGCATGGCTCCACCCGTCA
Klf16 promoter	ATAGCTAGCCCTGTCCCAGTCTCAAAG	ATTAAGCTTAACCCTGCGCGAGAGTCTTC
Klf13 promoter	AAGAGCTCCAAAAGCTCTGGCATGGAAAGGG	ATAAGCTTCGGCTCGGTGTGGGCGGACCGGCC

Primers for cloning *Klf9* cDNA into pCDNA4:TO and pEF1α-FLBIO vectors

FLBIO
Forward: 5' AAATGATCATCTCCGCGGCCGCCTAC 3'
Reverse: 5' GCTCTAGATCACAAGGGGCTGGCAA 3'

TO
Forward: 5' AACTCGAGATGTCCGCGGCCGCCTA 3'
Reverse: 5' GCTCTAGATCACAAGGGGCTGGCAA 3'

Primers for amplifying pEF1α-BirAV5-pABGH cassette

Forward: 5' ATAGCGGCCGCGCTCCGGTGCCCGTC 3'
Reverse: 5' ATAGCTAGCGAGCCCACCGCATCCCC 3'

Oligonucleotides used to make pGL4.23-3xBTE vector

5' CTAGAGAAGGAGGCGTGGCCAGAAGGAGGCGTGGCCAGAAGGAGGCGTGGCC 3'
5' AGCTGGCCACGCCTCCTTCTGGCCACGCCTCCTTCTGGCCACGCCTCCTTCT 3'

Oligonucleotides for site-directed mutagenesis of *Klf13* promoter

GC-box 1
5' CTCCTGAGGCGCTCCAGGCTCTTTTTTTCCTTCGTGCGCGCTGCTCCCT 3'
5' AGGGAGCACGCGCACGAAGGAAAAAAAGAGCCTGGAGCGCCTCAGGAG 3'
GC-box 2
5' GATGTGGCCCCGGCTTTTTTTACCCCCGGGGCCGGTCCGCCCATATC 3'
5' TGGGCGGACCGGCCCCGGGGGTAAAAAAAGCCGGGGCCACATC 3'

Primers to verify mutation in Klf9-CRISPR knockout cells

5' GACACGTTTGCAGTCGAATAAAC 3'
5' GGGCTTTAAGATGGGAGGATTT 3'

gRNA sequences for CRISPR-Cas9 genome editing

Round 1: 5’ GGGGCGCTCCGGAAGCCGAG 3’
5’ GCCGGAGCACGGGGGCGCTC 3’

Supplemental Table 2.2. All Klf9-regulated genes

Gene name	Read Counts (-Dox)	Read Counts (+Dox)	Fold change	$\log_2$ FC	*p*-value	FDR-adjusted *p* value
Cd93	34.46	14.92	0.43	-1.21	0.000489477	0.018974957
Klf13	582.35	268.62	0.46	-1.12	8.08756E-24	1.09105E-19
Chad	39.17	18.10	0.46	-1.11	0.001501054	0.040059289
Rptoros	89.31	43.32	0.48	-1.04	3.37965E-06	0.000500315
Celf3	80.44	39.78	0.49	-1.02	0.000238495	0.011450896
Zfp964	50.28	25.80	0.51	-0.96	0.002055547	0.048821042
Gpr161	229.15	118.76	0.52	-0.95	9.09563E-07	0.000171615
Apc2	560.05	295.13	0.53	-0.92	1.29596E-16	6.99328E-13
Zfp704	229.90	123.87	0.54	-0.89	3.8697E-09	2.17517E-06
Arhgap39	256.48	139.04	0.54	-0.88	1.05729E-10	1.13868E-07
Armc7	321.41	175.72	0.55	-0.87	9.69896E-11	1.13777E-07
Mex3a	816.98	452.47	0.55	-0.85	2.404E-18	2.16207E-14
Wdfy2	252.68	140.48	0.56	-0.85	1.23044E-06	0.000214184
Fam212a	92.03	51.92	0.56	-0.83	0.001645281	0.042037247
Nlgn2	1179.72	672.25	0.57	-0.81	5.92466E-18	3.99633E-14
1700109K24Rik	511.67	295.81	0.58	-0.79	4.97975E-05	0.003860882
Btbd9	169.23	99.39	0.59	-0.77	5.09917E-06	0.000684481
Sft2d1	421.90	247.85	0.59	-0.77	9.38727E-09	4.61773E-06
Arap1	209.16	123.07	0.59	-0.77	7.89504E-07	0.000152154
Kcnh2	236.83	139.63	0.59	-0.76	9.57267E-07	0.000178124
Plxna3	964.79	570.55	0.59	-0.76	2.79572E-16	1.25719E-12
Vav2	542.08	322.05	0.59	-0.75	1.68189E-12	3.24135E-09
Nadk2	323.48	192.45	0.59	-0.75	6.17814E-09	3.33385E-06
Lzts3	553.16	334.05	0.60	-0.73	5.16E-11	6.62961E-08
Plxnd1	501.53	305.30	0.61	-0.72	6.54734E-09	3.4638E-06
Evi5l	142.91	87.13	0.61	-0.71	0.000196045	0.010270879
Lonrf1	398.49	243.00	0.61	-0.71	3.49059E-07	8.18953E-05
Clip2	1243.77	758.98	0.61	-0.71	5.24297E-16	1.76826E-12
Nynrin	103.15	63.24	0.61	-0.71	0.000160393	0.008778017
5330426P16Rik	154.79	94.91	0.61	-0.71	8.44879E-05	0.005579686
Zfp382	284.69	175.59	0.62	-0.70	1.89109E-07	5.0023E-05
Arhgap33	289.80	179.34	0.62	-0.69	4.43623E-05	0.003551747
Cul7	963.06	597.06	0.62	-0.69	2.61489E-08	1.06897E-05
Fchsd1	228.15	141.73	0.62	-0.69	4.84398E-06	0.000676589
Pram1	113.30	70.67	0.62	-0.68	0.000633704	0.022090381
Gpsm1	529.14	330.54	0.62	-0.68	9.58426E-09	4.61773E-06
Ttc28	784.61	490.42	0.63	-0.68	5.37778E-12	9.06861E-09
Klf16	743.47	465.70	0.63	-0.67	7.78912E-12	1.16755E-08
Brsk1	154.28	96.76	0.63	-0.67	0.000333224	0.014501659
2410018M08Rik	124.54	78.13	0.63	-0.67	0.001082625	0.031854192
Slc22a4	177.77	111.72	0.63	-0.67	1.85544E-05	0.001918074
Rufy3	551.43	346.72	0.63	-0.67	4.48427E-10	3.52776E-07
Armcx2	1453.15	915.63	0.63	-0.67	2.30019E-15	5.64196E-12
Sgsm2	858.39	543.25	0.63	-0.66	6.72986E-12	1.06811E-08
Prune2	1318.10	835.09	0.63	-0.66	9.96141E-10	6.55533E-07
4933428G20Rik	166.66	105.67	0.63	-0.66	6.14265E-05	0.004479319
Gm10532	92.89	59.27	0.64	-0.65	0.001878387	0.045782072
Nyap1	255.38	163.19	0.64	-0.65	6.09532E-06	0.000786879
Prmt2	697.81	446.88	0.64	-0.64	2.16058E-10	1.88047E-07
Ctdspl	733.62	470.93	0.64	-0.64	8.74224E-11	1.07216E-07
Zbtb12	440.94	283.46	0.64	-0.64	2.28313E-08	9.47712E-06
Mblac2	203.71	131.06	0.64	-0.64	0.000140013	0.007986525
Usp27x	118.24	76.22	0.64	-0.63	0.00097709	0.029856017
Radil	272.53	175.94	0.65	-0.63	0.000290261	0.013128734
D930005D10Rik	272.53	175.94	0.65	-0.63	0.000290261	0.013128734
C030037D09Rik	176.80	114.55	0.65	-0.63	9.67317E-05	0.006126571
Limk1	869.59	564.76	0.65	-0.62	5.82781E-05	0.004319142
2310003H01Rik	781.94	508.14	0.65	-0.62	1.05113E-05	0.001244539
Six5	289.85	188.70	0.65	-0.62	1.22557E-05	0.001401154

Hhipl1	185.23	120.63	0.65	-0.62	5.65977E-05	0.00426554
Mdn1	2924.59	1907.07	0.65	-0.62	3.31824E-12	5.96862E-09
Zfp28	220.29	144.11	0.65	-0.61	9.07166E-05	0.005873082
Micall1	1524.69	997.53	0.65	-0.61	1.84185E-13	4.14124E-10
Nagk	273.10	178.72	0.65	-0.61	1.41738E-05	0.001549862
Syngap1	414.43	272.38	0.66	-0.61	0.000562593	0.020540342
Tiam1	841.49	554.16	0.66	-0.60	2.26003E-10	1.90556E-07
Jade2	441.00	290.75	0.66	-0.60	0.000161029	0.008794976
1700007J10Rik	471.52	310.99	0.66	-0.60	0.000528735	0.020036232
Rapgef3	292.14	193.00	0.66	-0.60	3.20557E-06	0.000483181
Unkl	148.75	98.28	0.66	-0.60	0.000415514	0.016858627
Ubr4	6234.97	4120.79	0.66	-0.60	2.7191E-05	0.002521099
Cdh24	468.74	310.97	0.66	-0.59	2.1268E-07	5.31325E-05
Sash1	122.55	81.41	0.66	-0.59	0.00043247	0.017363812
Syne1	939.64	624.41	0.66	-0.59	1.25371E-05	0.001421279
Kmt2d	4234.24	2815.20	0.66	-0.59	2.93534E-08	1.18206E-05
Plekhg2	824.40	548.12	0.66	-0.59	9.85516E-10	6.55533E-07
Vgll4	249.79	166.27	0.67	-0.59	0.000176036	0.009423887
Tmem151a	186.35	124.15	0.67	-0.59	0.000540791	0.020236799
Ankrd52	2896.22	1933.77	0.67	-0.58	1.60622E-07	4.56183E-05
Kmt2a	3226.22	2157.98	0.67	-0.58	7.38908E-10	5.53791E-07
Mlxip	461.39	308.83	0.67	-0.58	0.000159666	0.008755974
Rassf3	177.77	119.29	0.67	-0.58	0.001130649	0.032872882
Ap3s1	197.87	132.81	0.67	-0.58	0.001313144	0.036338387
Dopey2	337.52	226.60	0.67	-0.57	0.00070721	0.023762419
Ccdc120	276.27	185.63	0.67	-0.57	2.91217E-05	0.002645568
Mapk11	362.26	243.56	0.67	-0.57	2.40703E-06	0.000384104
Ksr1	248.40	167.07	0.67	-0.57	0.00101706	0.030902366
Slc27a1	431.33	290.24	0.67	-0.57	7.08624E-05	0.004953208
Pik3cd	221.95	149.60	0.67	-0.57	0.000125623	0.007320577
Inpp4a	250.12	168.97	0.68	-0.57	0.001908794	0.046272401
Setd1b	2097.16	1417.02	0.68	-0.57	5.64551E-13	1.1717E-09
Cand2	844.89	572.34	0.68	-0.56	2.23042E-09	1.39951E-06
Tead4	718.96	487.62	0.68	-0.56	3.21611E-09	1.84625E-06
Plekhg4	189.94	128.90	0.68	-0.56	0.000381926	0.016051026
Fam13b	1765.62	1198.29	0.68	-0.56	6.81417E-07	0.000141425
Klc2	830.87	565.79	0.68	-0.55	8.82324E-09	4.4917E-06
Plcd1	328.15	223.60	0.68	-0.55	2.33725E-05	0.002276583
Aff1	1827.98	1245.77	0.68	-0.55	1.90687E-06	0.000315639
D11Wsu47e	453.13	308.83	0.68	-0.55	6.53766E-07	0.000136738
Arhgap23	1128.48	769.23	0.68	-0.55	4.57624E-10	3.52776E-07
Usp28	545.88	373.07	0.68	-0.55	2.36952E-07	5.86532E-05
Vstm5	206.37	141.06	0.68	-0.55	0.000110122	0.0067374
Slc35e3	639.62	437.28	0.68	-0.55	1.06877E-08	4.9718E-06
Mov10	531.02	363.56	0.68	-0.55	7.68627E-05	0.005303918
Map4k3	727.89	498.57	0.68	-0.55	1.45509E-08	6.13436E-06
Dclk2	636.63	436.72	0.69	-0.54	1.38219E-08	5.91951E-06
Ulk3	253.85	174.40	0.69	-0.54	0.000120354	0.007152602
A930019D19Rik	167.27	115.02	0.69	-0.54	0.001087103	0.031930872
Phf13	707.16	487.13	0.69	-0.54	5.12907E-07	0.000109831
Clcn6	1095.39	754.82	0.69	-0.54	0.000242196	0.011606911
Hic2	224.64	154.80	0.69	-0.54	0.000218859	0.010997609
Fdps	274.91	189.58	0.69	-0.54	7.06949E-05	0.004953208
Tmc6	168.36	116.29	0.69	-0.53	0.001292875	0.035999037
Pak4	779.66	539.42	0.69	-0.53	6.98176E-07	0.000143218
Lrsam1	200.18	139.02	0.69	-0.53	0.000518043	0.019769883
Arl10	295.46	205.25	0.69	-0.53	4.20691E-05	0.003398404
2610028E06Rik	194.09	134.86	0.69	-0.53	0.000555021	0.020429778
Afmid	293.79	204.29	0.70	-0.52	8.08526E-05	0.005501124
Mast1	194.17	135.15	0.70	-0.52	0.001243486	0.035168226
Pdia5	2791.31	1943.49	0.70	-0.52	5.76876E-06	0.000755568
Rhbdf2	358.85	249.88	0.70	-0.52	1.59094E-05	0.001670243
Tubb3	163.94	114.21	0.70	-0.52	0.000890705	0.027982051
Tnrc18	2537.91	1771.07	0.70	-0.52	0.002058315	0.048843801
Gigyf1	1283.82	897.85	0.70	-0.52	2.4405E-09	1.46629E-06
Sept5	1054.54	737.57	0.70	-0.52	3.53849E-08	1.33296E-05
Pou6f1	310.16	217.17	0.70	-0.51	5.26098E-05	0.003998491
Fzd5	217.05	151.99	0.70	-0.51	0.00062661	0.021928097
Mfsd6	283.59	198.74	0.70	-0.51	0.000217859	0.010987041
Ppp1r13b	435.72	305.63	0.70	-0.51	1.29785E-05	0.001452947
Psd3	206.15	144.63	0.70	-0.51	0.000293677	0.013228218
Tbc1d22a	628.91	442.00	0.70	-0.51	5.68428E-07	0.000120762
Snx30	635.09	446.51	0.70	-0.51	0.001575582	0.041112933
Trerf1	388.79	274.28	0.71	-0.50	0.000111199	0.006772595
2410076I21Rik	282.72	199.52	0.71	-0.50	0.000218884	0.010997609

Foxo3	231.71	163.56	0.71	-0.50	0.000610302	0.021581324
Bcl9	573.22	404.79	0.71	-0.50	1.06195E-06	0.000194914
Tnk2os	286.02	202.10	0.71	-0.50	0.000115313	0.006960322
D630045J12Rik	800.71	566.58	0.71	-0.50	6.17084E-08	2.03043E-05
Tbc1d24	787.23	557.19	0.71	-0.50	6.9584E-08	2.23505E-05
Birc3	192.56	136.30	0.71	-0.50	0.001264511	0.035428642
Map1b	8197.68	5805.43	0.71	-0.50	1.3204E-06	0.00022837
Spred3	304.75	215.88	0.71	-0.50	0.000104871	0.006508649
Acvr1b	448.82	317.95	0.71	-0.50	2.44885E-05	0.002347037
Map4	405.02	287.06	0.71	-0.50	0.000515444	0.019729724
Fbxl19	865.74	613.89	0.71	-0.50	2.46873E-07	6.04087E-05
Zhx3	348.91	247.65	0.71	-0.49	3.6218E-05	0.002997538
Zfp395	262.62	186.48	0.71	-0.49	0.002045264	0.048695637
Trio	3147.72	2236.05	0.71	-0.49	8.48346E-06	0.001050506
Cchcr1	1105.58	785.50	0.71	-0.49	3.37244E-08	1.33296E-05
Ptprf	3296.48	2344.73	0.71	-0.49	9.25096E-08	2.89831E-05
Lpar2	399.75	284.57	0.71	-0.49	0.000129115	0.007488878
Crtc1	845.60	602.96	0.71	-0.49	8.76563E-05	0.005754393
Mroh1	743.98	530.56	0.71	-0.49	1.50772E-05	0.001595284
Kctd13	457.31	326.34	0.71	-0.49	0.000713142	0.023855453
Ssh1	414.00	296.52	0.72	-0.48	0.001178784	0.033834854
Dync1h1	11129.59	7979.47	0.72	-0.48	0.001773583	0.044228139
Pvrl1	615.00	441.23	0.72	-0.48	4.04453E-06	0.000583559
9930021J03Rik	912.98	657.64	0.72	-0.47	1.62882E-07	4.57784E-05
Tsc1	964.34	695.16	0.72	-0.47	1.37251E-07	4.11464E-05
Ttc3	2951.62	2129.44	0.72	-0.47	2.75689E-10	2.25405E-07
Tnip2	362.72	262.02	0.72	-0.47	0.000155793	0.008631327
Vps33b	299.65	216.61	0.72	-0.47	0.000391591	0.016251367
Fam102a	268.41	194.45	0.72	-0.47	0.000439606	0.017442662
Nav2	2142.37	1552.91	0.72	-0.46	1.92857E-09	1.23892E-06
Nuak1	380.42	276.13	0.73	-0.46	6.37684E-05	0.004600364
Itpkc	261.59	189.99	0.73	-0.46	0.001067862	0.031720225
Dysf	718.29	521.76	0.73	-0.46	7.12104E-06	0.000897817
Hivep1	1104.92	802.80	0.73	-0.46	9.34557E-08	2.89831E-05
Ahdc1	749.58	544.69	0.73	-0.46	1.22368E-05	0.001401154
Tns3	2235.36	1626.02	0.73	-0.46	8.69805E-10	6.34276E-07
Arid3a	531.99	387.60	0.73	-0.46	1.25916E-05	0.001421477
Rab11b	486.44	354.65	0.73	-0.46	1.48221E-05	0.001593288
Kif7	260.93	190.27	0.73	-0.46	0.000579393	0.020871281
Syne2	1790.94	1310.21	0.73	-0.45	0.001349347	0.037024802
Myo1d	660.09	482.97	0.73	-0.45	2.92487E-05	0.002648183
Man1c1	241.22	176.52	0.73	-0.45	0.001694767	0.042895415
Ankrd12	1399.75	1024.51	0.73	-0.45	0.000371315	0.015653843
Hinfp	330.75	242.10	0.73	-0.45	0.000224477	0.011113065
Lrrc1	354.94	259.94	0.73	-0.45	0.000221196	0.011072508
Zfp516	1068.67	783.39	0.73	-0.45	2.70045E-07	6.44786E-05
Gm16386	241.17	176.86	0.73	-0.45	0.001087598	0.031930872
Hspg2	10365.48	7620.63	0.74	-0.44	2.45308E-05	0.002347037
Ccdc136	563.42	414.67	0.74	-0.44	1.30319E-05	0.001452947
Dpy19l3	581.09	428.23	0.74	-0.44	1.54061E-05	0.001623719
Exo5	700.07	516.02	0.74	-0.44	1.10339E-05	0.001283209
Cdc42ep4	659.55	486.38	0.74	-0.44	8.34303E-06	0.001042145
Btbd7	1195.05	881.39	0.74	-0.44	0.000288276	0.013116296
Tyro3	919.17	678.93	0.74	-0.44	2.54465E-06	0.000399169
Bcorl1	264.17	195.19	0.74	-0.44	0.000878627	0.027694209
Pogk	996.68	736.45	0.74	-0.44	1.39307E-06	0.000237889
Smurf1	1956.61	1446.77	0.74	-0.44	3.55706E-08	1.33296E-05
Cspg4	4394.02	3252.35	0.74	-0.43	9.18383E-07	0.000172076
Cmtm3	768.58	569.26	0.74	-0.43	1.06872E-05	0.001253706
Golga4	2370.98	1756.86	0.74	-0.43	6.35777E-06	0.000816852
Pcgf2	770.56	570.99	0.74	-0.43	0.000763433	0.02505863
Fnip2	1461.01	1082.95	0.74	-0.43	7.16592E-07	0.000143218
Zfp202	277.43	205.71	0.74	-0.43	0.000987216	0.030063305
Camk2g	1718.65	1276.45	0.74	-0.43	1.69247E-07	4.61259E-05
Kctd15	556.77	414.17	0.74	-0.43	0.000114836	0.006947046
Dock6	823.14	612.70	0.74	-0.43	8.51176E-06	0.001050506
Slc4a3	342.09	254.90	0.75	-0.42	0.000439025	0.017442662
Slc6a9	2379.03	1772.78	0.75	-0.42	0.000543778	0.020236799
Pcnxl3	2076.16	1547.64	0.75	-0.42	3.48895E-08	1.33296E-05
Il17ra	649.76	484.36	0.75	-0.42	2.45015E-05	0.002347037
Zfp568	909.90	678.75	0.75	-0.42	2.42013E-06	0.000384104
Sh2b2	308.70	230.41	0.75	-0.42	0.001279068	0.035725203
Rnf24	639.47	477.47	0.75	-0.42	3.3073E-05	0.002878529
Rab11fip5	1889.88	1411.81	0.75	-0.42	2.05633E-07	5.18522E-05
Arhgap32	1321.88	988.54	0.75	-0.42	7.61523E-07	0.000147818

S1pr2	534.44	399.84	0.75	-0.42	4.85771E-05	0.003816882
Zbtb34	425.83	318.66	0.75	-0.42	0.000268673	0.01258518
Ppp4r1l-ps	512.17	383.54	0.75	-0.42	6.65811E-05	0.004727434
4930402H24Rik	832.01	623.33	0.75	-0.42	1.24676E-05	0.001419366
Kif3c	1157.31	867.36	0.75	-0.42	0.000911199	0.028323808
Slc4a2	1385.38	1040.08	0.75	-0.41	1.05089E-06	0.000194205
Plxna1	5069.23	3807.86	0.75	-0.41	2.02009E-07	5.18522E-05
Kif16b	270.75	203.39	0.75	-0.41	0.001658372	0.042291633
Trrap	5032.89	3781.28	0.75	-0.41	4.51038E-09	2.48356E-06
Dbn1	1048.27	787.78	0.75	-0.41	0.00059005	0.021114254
Speg	324.00	243.66	0.75	-0.41	0.000506365	0.019461858
Atat1	443.58	333.60	0.75	-0.41	0.000409243	0.016729967
Lrp1	11114.02	8360.72	0.75	-0.41	7.41155E-05	0.005145537
Ezh1	448.60	337.51	0.75	-0.41	0.00017515	0.009413809
Gtf2ird1	724.79	545.43	0.75	-0.41	2.81534E-05	0.002583697
Cic	3293.37	2479.23	0.75	-0.41	5.49381E-08	1.97508E-05
Mex3d	993.97	748.45	0.75	-0.41	4.86112E-06	0.000676589
Spaca6	2058.63	1551.43	0.75	-0.41	1.56928E-07	4.50433E-05
Spire2	523.18	395.46	0.76	-0.40	0.000172285	0.009296862
Bahcc1	1535.26	1160.84	0.76	-0.40	0.000478373	0.018678714
Sh3pxd2b	2125.81	1608.70	0.76	-0.40	2.00153E-07	5.18522E-05
Fnbp1	1109.76	840.81	0.76	-0.40	5.17198E-06	0.000690818
Bahd1	914.83	693.49	0.76	-0.40	8.65656E-06	0.001061649
Arhgef25	753.93	571.52	0.76	-0.40	5.84018E-05	0.004319142
Megf8	2698.24	2045.88	0.76	-0.40	2.85459E-07	6.75612E-05
Gfod1	1054.68	800.11	0.76	-0.40	4.61534E-06	0.000658871
Arhgef40	1930.56	1464.74	0.76	-0.40	4.15014E-07	9.40965E-05
Il1rl1	240.16	182.22	0.76	-0.40	0.000668723	0.02275262
Cpeb2	601.04	456.14	0.76	-0.40	0.001629077	0.041702199
Gmip	804.84	610.99	0.76	-0.40	4.00362E-05	0.00328333
Ldlrad4	491.84	373.37	0.76	-0.40	0.000181329	0.009646246
Anks1	832.68	632.74	0.76	-0.40	1.90597E-05	0.001940564
Tmem63b	1472.54	1118.99	0.76	-0.40	2.29225E-06	0.000372573
Madd	568.47	432.00	0.76	-0.40	0.000143992	0.008093865
Arfgap3	608.23	462.31	0.76	-0.40	0.00013144	0.007561587
Fchsd2	563.86	428.61	0.76	-0.40	0.000184671	0.009769819
Heatr5a	1699.76	1292.05	0.76	-0.40	6.45678E-05	0.004645607
Myo1b	1380.72	1050.10	0.76	-0.39	1.11707E-06	0.000198467
Csk	1124.07	855.32	0.76	-0.39	1.41262E-05	0.001549862
Dip2a	1328.93	1011.68	0.76	-0.39	2.15954E-06	0.000353131
Kdm2b	862.06	656.98	0.76	-0.39	2.03539E-05	0.002056812
Ppp1r13l	518.63	395.27	0.76	-0.39	0.000640313	0.022201249
Mapk7	854.33	651.24	0.76	-0.39	8.40773E-05	0.005573683
Zscan20	371.51	283.30	0.76	-0.39	0.00151873	0.040178494
Mark4	426.17	325.20	0.76	-0.39	0.000836138	0.026870258
Akna	386.03	294.63	0.76	-0.39	0.000864887	0.027583354
Vps9d1	628.39	479.69	0.76	-0.39	0.000195018	0.010256857
Per3	356.17	271.95	0.76	-0.39	0.001202131	0.034197949
Samd4b	2274.28	1736.48	0.76	-0.39	5.84295E-05	0.004319142
Fryl	1555.92	1189.03	0.76	-0.39	7.34115E-05	0.005118129
Tecpr1	438.92	335.63	0.76	-0.39	0.00048526	0.018865689
Rai1	2575.88	1969.95	0.76	-0.39	1.75251E-07	4.72845E-05
Map3k4	1260.02	963.79	0.76	-0.39	5.00366E-06	0.000684481
Cdr2l	2663.14	2039.03	0.77	-0.39	1.86574E-07	4.98411E-05
Tns1	1124.28	861.36	0.77	-0.38	1.42458E-05	0.001549862
Agrn	2210.99	1693.98	0.77	-0.38	4.28978E-07	9.64521E-05
Plekhg5	497.34	381.27	0.77	-0.38	0.000689344	0.023248979
Diap1	1376.80	1056.28	0.77	-0.38	2.67488E-06	0.000417173
Ptgfrn	1339.71	1028.53	0.77	-0.38	6.05587E-06	0.000785545
Uba6	1341.38	1029.92	0.77	-0.38	6.29744E-05	0.004555264
Ttyh3	994.87	764.22	0.77	-0.38	3.30296E-05	0.002878529
Khnyn	589.41	453.07	0.77	-0.38	0.000141316	0.007986525
Ptpn23	2335.66	1796.30	0.77	-0.38	0.000266975	0.012549213
Abca5	728.85	560.59	0.77	-0.38	0.000745335	0.024724455
Myo9a	1505.45	1157.94	0.77	-0.38	0.001860074	0.045535784
Wdr91	861.39	662.73	0.77	-0.38	3.19108E-05	0.002804515
Usp42	771.58	593.71	0.77	-0.38	6.09837E-05	0.004463296
Pkd1	3665.83	2821.96	0.77	-0.38	2.83468E-05	0.002584301
Ttbk2	1026.26	790.68	0.77	-0.38	1.50718E-05	0.001595284
Clcf1	1715.31	1321.67	0.77	-0.38	1.73763E-06	0.000289402
Ehbp1l1	2545.01	1961.43	0.77	-0.38	4.62319E-07	0.000100596
Rfx3	352.82	272.00	0.77	-0.38	0.001249858	0.03527449
Fgfrl1	747.43	576.36	0.77	-0.37	9.33957E-05	0.005971349
Ilf3	2137.27	1650.23	0.77	-0.37	1.70476E-06	0.00028569
Prr12	1535.64	1186.24	0.77	-0.37	8.77085E-06	0.001070797

Nfe2l1	4769.02	3685.87	0.77	-0.37	1.95977E-07	5.13364E-05
Mpc1	363.32	280.89	0.77	-0.37	0.000939476	0.028969142
Fam160b2	412.83	319.17	0.77	-0.37	0.000963542	0.029576016
Ninl	592.42	458.13	0.77	-0.37	0.000236537	0.011445495
Rnf145	560.55	433.50	0.77	-0.37	0.000599451	0.021341317
Ctif	678.08	525.18	0.77	-0.37	0.000158189	0.008710411
Emx2os	430.54	333.59	0.77	-0.37	0.001166381	0.033586053
Akap13	1072.81	831.37	0.77	-0.37	0.000122299	0.007252193
Cdk2ap1	653.83	506.95	0.78	-0.37	0.000210058	0.010815972
Fam171a2	492.13	381.70	0.78	-0.37	0.000625808	0.021928097
Hip1	2007.71	1557.28	0.78	-0.37	5.17701E-05	0.003956967
Fyco1	493.96	383.40	0.78	-0.37	0.000778336	0.02548578
Fbxl18	524.83	407.87	0.78	-0.36	0.000374757	0.015774276
Slc5a3	2627.69	2042.55	0.78	-0.36	0.000515528	0.019729724
Suv420h2	466.27	362.59	0.78	-0.36	0.00089835	0.028019096
Dlg4	748.49	582.23	0.78	-0.36	0.000223377	0.011091017
Ralgapa2	1025.39	797.72	0.78	-0.36	2.63691E-05	0.002470359
Mtss1l	1008.22	784.69	0.78	-0.36	0.000890871	0.027982051
Mkl2	1195.26	930.95	0.78	-0.36	2.62822E-05	0.002470359
Tmem184b	2386.03	1859.37	0.78	-0.36	4.86484E-06	0.000676589
Rptor	2121.19	1653.81	0.78	-0.36	0.00089561	0.028019096
Thra	593.95	463.25	0.78	-0.36	0.000261405	0.012351949
C77080	1687.38	1316.12	0.78	-0.36	1.43162E-05	0.001551271
Vsig10	526.23	410.83	0.78	-0.36	0.001068785	0.031720225
Zfp651	692.24	540.73	0.78	-0.36	0.000278717	0.012902825
Vat1	3822.85	2986.69	0.78	-0.36	0.000176474	0.009428592
Tdrd7	597.78	467.12	0.78	-0.36	0.000342647	0.014791926
Tnfrsf10b	437.15	341.61	0.78	-0.36	0.001213433	0.034462773
4931428F04Rik	550.16	429.99	0.78	-0.36	0.000554839	0.020429778
Emilin1	679.46	531.05	0.78	-0.36	0.000562576	0.020540342
Tyk2	538.82	421.30	0.78	-0.35	0.000684011	0.023098004
Thap4	759.51	594.00	0.78	-0.35	0.000316356	0.013879026
Gdi1	1429.07	1117.77	0.78	-0.35	3.53404E-05	0.002942959
Asap2	669.10	523.50	0.78	-0.35	0.000312066	0.013735492
Vasn	1471.60	1151.87	0.78	-0.35	0.00018162	0.009646246
Fnbp1l	2482.54	1944.63	0.78	-0.35	3.14724E-06	0.000482476
Parp4	539.68	422.86	0.78	-0.35	0.000910065	0.028321187
Smarcc1	2567.54	2012.40	0.78	-0.35	2.00864E-06	0.000330458
Syne3	616.79	483.66	0.78	-0.35	0.000481977	0.018765123
Cep170	4395.97	3447.86	0.78	-0.35	0.000797002	0.025846045
Stk40	977.07	766.47	0.78	-0.35	0.000124826	0.007320577
Rnf169	1049.66	823.73	0.78	-0.35	0.0005164	0.019735115
Slc39a6	2310.57	1813.73	0.78	-0.35	6.7085E-06	0.000853784
Elf4	1946.41	1528.85	0.79	-0.35	9.27272E-06	0.001121916
Rps6kc1	491.50	386.24	0.79	-0.35	0.00088487	0.027858428
Rcan3	729.94	573.80	0.79	-0.35	0.000238516	0.011450896
Dnm1	1141.77	898.47	0.79	-0.35	9.29369E-05	0.005970311
Dgat1	749.93	590.21	0.79	-0.35	0.000322787	0.014138163
Zfp217	591.83	465.79	0.79	-0.35	0.000392111	0.016251367
Arhgef10	761.63	599.55	0.79	-0.35	0.000358193	0.015291775
Hdac6	1176.14	925.97	0.79	-0.35	0.000101441	0.006350286
Slc9a6	1111.85	875.46	0.79	-0.34	4.19849E-05	0.003398404
Ep400	4324.76	3406.28	0.79	-0.34	8.96372E-07	0.000170317
Smg6	1397.98	1101.28	0.79	-0.34	3.04697E-05	0.002740345
Ptprs	5608.26	4418.13	0.79	-0.34	7.12454E-07	0.000143218
Rad54b	535.75	422.14	0.79	-0.34	0.000523733	0.019930646
Ephb3	546.58	430.80	0.79	-0.34	0.001248984	0.03527449
Spen	2085.93	1644.27	0.79	-0.34	5.81002E-06	0.000757296
Wdr81	1016.37	801.67	0.79	-0.34	0.000119077	0.007123788
E2f3	2196.74	1733.00	0.79	-0.34	0.000455853	0.018007858
Erlin2	947.63	747.96	0.79	-0.34	0.000153246	0.00850767
Mboat7	1352.47	1067.86	0.79	-0.34	4.97171E-05	0.003860882
Wdr59	665.24	525.47	0.79	-0.34	0.00062569	0.021928097
Sfxn5	604.25	477.45	0.79	-0.34	0.000449973	0.017827805
Epn2	1290.34	1020.65	0.79	-0.34	4.6817E-05	0.003704306
Tmem201	1081.95	855.88	0.79	-0.34	0.000103798	0.006467847
Tet3	2318.83	1835.88	0.79	-0.34	2.11036E-05	0.002108875
Scrib	2862.22	2266.46	0.79	-0.34	9.10149E-06	0.001106159
Vasp	1286.94	1019.09	0.79	-0.34	8.35547E-05	0.005573683
Mdm1	499.97	395.95	0.79	-0.34	0.001162772	0.033517909
Anks3	837.19	663.06	0.79	-0.34	0.000232639	0.011391709
Scml2	549.32	435.08	0.79	-0.34	0.001776928	0.044228139
Tnks1bp1	2924.67	2316.75	0.79	-0.34	6.50098E-06	0.000831294
Rap2a	911.26	721.85	0.79	-0.34	0.000177008	0.009438423
Fzd7	520.65	412.46	0.79	-0.34	0.001446547	0.039029275

Dvl2	1043.59	826.75	0.79	-0.34	0.000225022	0.011119635
Sh3pxd2a	4879.82	3866.05	0.79	-0.34	5.73081E-06	0.000754961
Wipf2	1010.64	800.79	0.79	-0.34	0.000219651	0.011015614
Man2a2	1225.63	971.48	0.79	-0.34	0.000247279	0.011829483
Arv1	849.46	673.76	0.79	-0.33	0.00046121	0.018192827
E130308A19Rik	563.04	446.59	0.79	-0.33	0.000595449	0.021251059
Myo10	3227.01	2559.76	0.79	-0.33	2.69588E-06	0.000418031
Kalrn	1368.59	1085.68	0.79	-0.33	4.88528E-05	0.003820569
Pcnx	1625.56	1290.32	0.79	-0.33	3.28554E-05	0.002878153
Map4k2	915.14	726.52	0.79	-0.33	0.000365376	0.015476003
Sgpl1	2358.48	1872.76	0.79	-0.33	1.45642E-05	0.001571826
Uhrf1bp1	1828.19	1451.84	0.79	-0.33	1.68961E-05	0.001760133
Zfp609	1535.44	1219.77	0.79	-0.33	3.34584E-05	0.002893398
Kdm3b	1314.47	1044.47	0.79	-0.33	6.2314E-05	0.004531789
Gpi1	1375.02	1093.14	0.80	-0.33	5.81982E-05	0.004319142
Slc9a5	1007.79	801.44	0.80	-0.33	0.000229785	0.011313539
Kdm4b	726.23	578.05	0.80	-0.33	0.000985431	0.030042829
Mrps6	3986.43	3173.69	0.80	-0.33	3.43807E-06	0.000500315
Rasa2	550.58	438.37	0.80	-0.33	0.001507122	0.040102225
Rab11fip3	1943.49	1547.46	0.80	-0.33	2.75806E-05	0.002539765
Msi2	1353.54	1078.26	0.80	-0.33	0.000124808	0.007320577
Nktr	3751.32	2988.81	0.80	-0.33	0.0001054	0.006508649
Chd3	2086.50	1663.00	0.80	-0.33	2.71754E-05	0.002521099
Rab43	569.94	454.26	0.80	-0.33	0.001517393	0.040178494
Dixdc1	555.78	443.00	0.80	-0.33	0.001746899	0.043765745
Agap3	1115.34	889.12	0.80	-0.33	0.000504409	0.019442081
Git1	2076.15	1655.35	0.80	-0.33	6.67676E-05	0.004728234
Lphn1	1922.75	1533.32	0.80	-0.33	2.70011E-05	0.002520823
Mkl1	1581.11	1261.47	0.80	-0.33	0.000113092	0.006872355
Zdhhc18	1218.44	972.21	0.80	-0.33	0.000148562	0.008316093
Klc1	4360.16	3479.04	0.80	-0.33	0.000141025	0.007986525
Irf2bpl	729.99	582.69	0.80	-0.33	0.000527667	0.020023885
Foxj3	1636.93	1308.69	0.80	-0.32	4.86641E-05	0.003816882
Numbl	633.43	506.58	0.80	-0.32	0.001718705	0.043298204
Tstd2	645.22	516.30	0.80	-0.32	0.000928413	0.028660756
Map6	952.64	762.31	0.80	-0.32	0.000430232	0.017351388
Dlg5	2279.59	1824.22	0.80	-0.32	3.07879E-05	0.002750622
F3	684.70	548.00	0.80	-0.32	0.001499458	0.040056314
Unc5b	1323.65	1059.46	0.80	-0.32	0.000159122	0.008743941
Mast4	1831.72	1466.40	0.80	-0.32	9.58629E-05	0.006097323
Usp49	779.62	624.19	0.80	-0.32	0.00061775	0.021787588
Slc12a7	1460.91	1170.17	0.80	-0.32	8.09439E-05	0.005501124
Szt2	1276.22	1023.08	0.80	-0.32	8.45814E-05	0.005579686
Vash2	1553.69	1245.67	0.80	-0.32	0.000141491	0.007986525
Gse1	787.25	631.27	0.80	-0.32	0.000899319	0.028019096
Nipal1	582.87	467.56	0.80	-0.32	0.001775389	0.044228139
Tenc1	1411.99	1132.96	0.80	-0.32	0.000197658	0.010335287
Fam115a	1055.82	847.23	0.80	-0.32	0.000601105	0.021368141
Ppip5k2	1381.60	1108.79	0.80	-0.32	8.91912E-05	0.005822535
Zmiz1	2612.87	2097.01	0.80	-0.32	2.57081E-05	0.002425282
Pias4	568.36	456.42	0.80	-0.32	0.001890849	0.046002712
Dennd2c	552.91	444.11	0.80	-0.32	0.001581573	0.041133713
Zfp687	1571.07	1262.05	0.80	-0.32	0.000116951	0.007043451
Smyd5	1543.63	1241.09	0.80	-0.31	0.000204936	0.010674468
Foxk1	1412.80	1135.95	0.80	-0.31	9.6044E-05	0.006097323
Thrap3	2007.34	1614.56	0.80	-0.31	0.001358669	0.037178761
Itpr3	4260.49	3428.16	0.80	-0.31	8.52677E-06	0.001050506
BC055324	1374.52	1106.03	0.80	-0.31	0.000166548	0.009059746
Leng8	2748.74	2211.96	0.80	-0.31	0.001033851	0.031132082
Cntrob	817.66	658.02	0.80	-0.31	0.00072802	0.024250258
Tanc2	1230.96	991.07	0.81	-0.31	0.000163119	0.00889114
Cyth3	1153.88	929.06	0.81	-0.31	0.000436308	0.017414235
Flnb	9737.39	7840.28	0.81	-0.31	0.000208151	0.010738262
Crebbp	1612.58	1299.20	0.81	-0.31	0.000487458	0.01892389
Prrc2b	5819.24	4691.89	0.81	-0.31	1.0563E-05	0.001244539
Rnf44	1518.15	1224.25	0.81	-0.31	0.000157606	0.008696067
Tspyl2	2331.73	1880.78	0.81	-0.31	0.000110987	0.006772595
Lrfn4	969.72	782.37	0.81	-0.31	0.000828389	0.02667156
Flii	2515.62	2030.03	0.81	-0.31	6.10413E-05	0.004463296
Wdr6	1960.25	1582.23	0.81	-0.31	0.00012461	0.007320577
Ptpn14	2633.12	2125.93	0.81	-0.31	0.000169781	0.009198489
Vps37c	610.81	493.17	0.81	-0.31	0.001751647	0.043793583
Kidins220	2203.76	1779.41	0.81	-0.31	0.000436294	0.017414235
Inppl1	2626.00	2121.24	0.81	-0.31	5.11847E-05	0.003923338
Arhgef17	2000.88	1617.35	0.81	-0.31	5.69612E-05	0.004280978

Rad54l2	1637.09	1324.63	0.81	-0.31	7.83911E-05	0.005368198
Arhgap31	1599.38	1294.37	0.81	-0.31	0.001147558	0.033221323
Gm17359	774.85	627.36	0.81	-0.30	0.001619497	0.041583042
Rnf121	838.70	679.19	0.81	-0.30	0.000826052	0.026628095
Smarcd1	1251.81	1014.16	0.81	-0.30	0.000604804	0.021427013
Zfp219	593.73	481.01	0.81	-0.30	0.001977688	0.047642854
Baz2a	1751.05	1420.66	0.81	-0.30	0.000101965	0.006368309
Fhdc1	1068.35	866.99	0.81	-0.30	0.000678883	0.023011219
Kdm4a	1870.48	1518.30	0.81	-0.30	8.06823E-05	0.005501124
Wasf2	1970.51	1599.98	0.81	-0.30	6.89633E-05	0.004867772
Bend3	675.96	548.87	0.81	-0.30	0.001093282	0.032062869
Sart3	2391.85	1942.35	0.81	-0.30	0.000133297	0.007652121
Dstyk	1259.80	1024.27	0.81	-0.30	0.000263383	0.01242368
1700037H04Rik	886.19	720.65	0.81	-0.30	0.002010253	0.048041306
Fam193b	1375.40	1118.59	0.81	-0.30	0.000419357	0.016988998
Sfxn3	1023.65	832.68	0.81	-0.30	0.001028476	0.031004823
Sesn2	1209.23	983.97	0.81	-0.30	0.000560075	0.020531785
Dtx4	1538.96	1252.38	0.81	-0.30	0.000342119	0.014791926
Sipa1l3	2584.88	2104.35	0.81	-0.30	9.15347E-05	0.005894268
Pxn	1582.51	1288.83	0.81	-0.30	0.000333773	0.014501659
Ercc2	1009.31	822.21	0.81	-0.30	0.001271919	0.035562329
Ube2o	2449.32	1995.45	0.81	-0.30	0.000168621	0.009154073
Hsdl1	967.68	788.36	0.81	-0.30	0.001362349	0.037239234
Sept8	4123.37	3359.59	0.81	-0.30	5.06219E-05	0.003891256
Rdh13	828.73	675.39	0.81	-0.30	0.001798296	0.044513613
Wwp2	1308.22	1066.63	0.82	-0.29	0.00064385	0.022242915
Lasp1	1908.76	1556.45	0.82	-0.29	0.000300559	0.013426117
Numa1	3741.98	3051.79	0.82	-0.29	3.32947E-05	0.002888504
B4galt5	1253.21	1022.15	0.82	-0.29	0.000434468	0.017392241
Strip1	1666.91	1360.87	0.82	-0.29	0.000470664	0.018484704
Exoc6b	1306.55	1066.85	0.82	-0.29	0.000404106	0.016570209
Lamb2	1972.33	1610.48	0.82	-0.29	0.000212809	0.010923221
Wdfy3	3032.29	2477.00	0.82	-0.29	0.000560892	0.020533839
Ankrd11	6177.64	5047.37	0.82	-0.29	0.001752977	0.043793583
Phlpp2	1371.77	1120.83	0.82	-0.29	0.000277943	0.012902825
4931406P16Rik	892.83	729.51	0.82	-0.29	0.001076063	0.031773207
Gga3	1020.76	834.14	0.82	-0.29	0.001435401	0.038767314
Srebf2	4618.89	3776.26	0.82	-0.29	4.57514E-05	0.003652125
Daam1	1080.65	883.95	0.82	-0.29	0.000733002	0.024356082
Trappc10	1760.99	1440.45	0.82	-0.29	0.000152807	0.008500784
Ago1	2441.13	1997.25	0.82	-0.29	0.000117495	0.007051029
Kctd9	1302.28	1065.49	0.82	-0.29	0.000569716	0.020605224
Snx12	1605.01	1313.41	0.82	-0.29	0.000604364	0.021427013
Lrp8	3352.80	2746.72	0.82	-0.29	0.000105659	0.006508649
Raph1	1475.69	1209.16	0.82	-0.29	0.000343749	0.014815801
Clasp1	2360.69	1934.41	0.82	-0.29	0.000237555	0.011445495
Cep250	1245.41	1021.19	0.82	-0.29	0.001478417	0.039651257
Setd1a	2462.67	2019.86	0.82	-0.29	0.000147991	0.008301357
Kmt2b	2134.35	1750.75	0.82	-0.29	0.000130808	0.007541317
Clasrp	900.76	739.00	0.82	-0.29	0.001729143	0.043479964
Pkn1	844.50	692.87	0.82	-0.29	0.001851134	0.045438821
Mettl2	1177.41	966.20	0.82	-0.29	0.001461921	0.03940351
Cds2	1488.99	1221.94	0.82	-0.29	0.000508521	0.019516939
Kif1c	3412.00	2801.50	0.82	-0.28	8.91453E-05	0.005822535
Adcy6	1373.40	1128.60	0.82	-0.28	0.000652682	0.022404595
Pitpnm1	1610.82	1324.52	0.82	-0.28	0.000661135	0.022637168
Myh10	4700.80	3865.47	0.82	-0.28	0.000136189	0.007785008
Helz2	798.11	656.72	0.82	-0.28	0.001988984	0.047818758
Tomm34	854.39	703.10	0.82	-0.28	0.001788365	0.044430835
Prrc1	1075.64	885.46	0.82	-0.28	0.00151548	0.040178494
Kif3a	1166.05	959.98	0.82	-0.28	0.001261606	0.035398512
Bcl9l	1680.10	1383.28	0.82	-0.28	0.000674898	0.02290493
Tmppe	805.32	663.45	0.82	-0.28	0.002026535	0.048387561
Zfp365	1115.69	919.90	0.82	-0.28	0.001373636	0.037419851
Atxn2	2560.70	2111.46	0.82	-0.28	0.000411015	0.016777004
Dock7	3646.14	3009.63	0.83	-0.28	8.95575E-05	0.005822535
Parvb	1566.60	1293.20	0.83	-0.28	0.001096935	0.032135073
Cnst	1522.37	1256.74	0.83	-0.28	0.000869826	0.027624256
Diap3	1540.31	1271.63	0.83	-0.28	0.001829768	0.045044683
Myo9b	2820.34	2328.55	0.83	-0.28	0.001350299	0.037024802
Phactr4	1725.75	1424.93	0.83	-0.28	0.000666121	0.02269321
Mef2d	1328.34	1096.92	0.83	-0.28	0.000643079	0.022242915
Rarg	1813.02	1497.51	0.83	-0.28	0.000640998	0.022201249
Cttn	2082.06	1720.68	0.83	-0.28	0.000370933	0.015653843
Chd4	5481.41	4530.81	0.83	-0.27	9.11608E-05	0.005884236

Lmtk2	1853.73	1532.32	0.83	-0.27	0.000304869	0.01357372
Rnf19b	1544.36	1276.81	0.83	-0.27	0.00119741	0.034197949
Nfat5	5118.91	4232.53	0.83	-0.27	0.001863219	0.045535784
Dhx37	1556.48	1287.44	0.83	-0.27	0.000841286	0.026958132
Plcg1	1971.58	1632.39	0.83	-0.27	0.000432022	0.017363812
Brd4	1794.45	1486.66	0.83	-0.27	0.000392114	0.016251367
Tfdp1	1416.19	1173.36	0.83	-0.27	0.002088232	0.049379998
Lix1l	1462.03	1211.66	0.83	-0.27	0.001023326	0.031004823
Ino80d	1687.19	1398.34	0.83	-0.27	0.000760279	0.024985505
Anapc2	1767.70	1467.43	0.83	-0.27	0.001484803	0.039743518
Pitpnm2	1621.46	1346.09	0.83	-0.27	0.001822508	0.044906928
Taf4a	1245.49	1034.21	0.83	-0.27	0.001332419	0.036721132
Pip4k2c	1007.47	836.60	0.83	-0.27	0.001963885	0.047394974
Tcf20	2567.42	2132.39	0.83	-0.27	0.000223098	0.011091017
Zfhx3	2127.85	1768.04	0.83	-0.27	0.000505263	0.019447229
Rab3gap2	1350.09	1122.61	0.83	-0.27	0.001079817	0.031806272
Zc3h4	2473.05	2056.75	0.83	-0.27	0.000334971	0.014530289
Cdc42bpb	2901.07	2413.67	0.83	-0.27	0.000325951	0.014230563
Coro7	2245.31	1868.16	0.83	-0.27	0.000662742	0.022663411
Slc6a6	2888.98	2404.82	0.83	-0.26	0.000391059	0.016251367
Kat6a	2123.05	1767.37	0.83	-0.26	0.001818713	0.044854379
Aacs	1781.74	1483.76	0.83	-0.26	0.00105443	0.031631158
Rhbdf1	1716.42	1429.61	0.83	-0.26	0.001330575	0.036717071
Kdm2a	3604.92	3003.60	0.83	-0.26	0.000195988	0.010270879
Tnpo2	3779.85	3149.59	0.83	-0.26	0.000336706	0.014582125
Gfpt1	1894.76	1579.15	0.83	-0.26	0.000632125	0.022063867
Hif1an	1569.45	1309.21	0.83	-0.26	0.001172444	0.033724641
Pcnt	1297.23	1082.61	0.83	-0.26	0.000709173	0.023769195
Sbf2	1614.44	1347.49	0.83	-0.26	0.001180501	0.03384815
Gjc1	1461.66	1220.09	0.83	-0.26	0.001298542	0.036082342
Dnajc13	2585.30	2158.18	0.83	-0.26	0.000385768	0.016112086
Fus	2070.30	1728.66	0.83	-0.26	0.001026314	0.031004823
Ehd1	3086.66	2581.30	0.84	-0.26	0.000745921	0.024724455
Pi4ka	1955.41	1635.46	0.84	-0.26	0.001183109	0.03388691
Arid1a	2284.42	1911.14	0.84	-0.26	0.001064176	0.031691528
Ncoa2	1266.52	1060.02	0.84	-0.26	0.00166551	0.04231367
Phldb1	1717.87	1438.42	0.84	-0.26	0.001191588	0.034093575
A830080D01Rik	2411.97	2019.70	0.84	-0.26	0.000792732	0.025828201
Mfn2	1989.88	1667.26	0.84	-0.26	0.001602737	0.041381281
Piezo1	6847.22	5740.34	0.84	-0.25	0.000232479	0.011391709
Ralbp1	2098.60	1760.23	0.84	-0.25	0.001702641	0.042939487
Ptpn9	1414.61	1187.11	0.84	-0.25	0.001947462	0.047040704
Midn	1662.72	1395.57	0.84	-0.25	0.001544431	0.040627552
Erc1	1564.82	1313.68	0.84	-0.25	0.001146205	0.033217783
Brd1	1998.54	1684.04	0.84	-0.25	0.00085176	0.027261361
U2af1	1560.54	1315.07	0.84	-0.25	0.001602092	0.041381281
Ylpm1	2075.55	1749.63	0.84	-0.25	0.00091941	0.028513342
Zbtb7a	1736.06	1463.46	0.84	-0.25	0.001544934	0.040627552
Dot1l	2001.50	1688.17	0.84	-0.25	0.000872663	0.027667816
1700021K19Rik	2342.28	1976.82	0.84	-0.24	0.001285171	0.035821495
Dcp2	2190.62	1853.60	0.85	-0.24	0.001126597	0.032825812
Eea1	1811.50	1533.11	0.85	-0.24	0.001059386	0.031691528
Ncor2	4027.80	3409.89	0.85	-0.24	0.001064075	0.031691528
Zfp462	2126.43	1800.93	0.85	-0.24	0.001055114	0.031631158
Zfp740	2443.93	2072.12	0.85	-0.24	0.001608922	0.041399142
Pgs1	3027.64	2570.05	0.85	-0.24	0.001302612	0.036158217
Nfic	3717.29	3164.59	0.85	-0.23	0.002010072	0.048041306
Ubqln4	3966.40	3378.69	0.85	-0.23	0.001646887	0.042038466
Dnajc10	2016.66	2386.60	1.18	0.24	0.001619798	0.041583042
Poglut1	1567.93	1857.60	1.18	0.24	0.001997699	0.047911026
Trip4	1911.21	2264.51	1.18	0.24	0.001920195	0.046506983
Usp39	1269.97	1510.05	1.19	0.25	0.001877587	0.045782072
Thoc1	1295.68	1543.33	1.19	0.25	0.001902851	0.046253004
Ddx52	1401.79	1674.10	1.19	0.26	0.001497914	0.040054715
Gusb	1333.68	1597.50	1.20	0.26	0.001026102	0.031004823
Mrpl9	1205.13	1443.63	1.20	0.26	0.001567211	0.040959121
Wdr74	964.51	1159.41	1.20	0.27	0.001433166	0.038767314
Emg1	1108.86	1333.10	1.20	0.27	0.001519583	0.040178494
Trnt1	1237.06	1487.84	1.20	0.27	0.001232255	0.034923827
Orc2	1747.28	2103.55	1.20	0.27	0.000568995	0.020605224
Arfip2	960.03	1155.94	1.20	0.27	0.001347906	0.037024802
Lypla1	1231.33	1482.99	1.20	0.27	0.001107797	0.032382957
Farsb	1263.27	1524.23	1.21	0.27	0.000757968	0.024985505
Rnf146	920.45	1110.65	1.21	0.27	0.001524701	0.040178494
Wdr55	760.42	917.88	1.21	0.27	0.001846351	0.04537012

Igbp1	871.77	1052.38	1.21	0.27	0.001809558	0.044671176
Tspan3	1120.53	1355.37	1.21	0.27	0.000776864	0.025468494
Commd8	867.28	1049.60	1.21	0.28	0.001973305	0.047579754
Pus3	925.80	1120.71	1.21	0.28	0.001790072	0.044432318
Mat2b	938.70	1136.76	1.21	0.28	0.001681559	0.042601062
Ltv1	880.46	1067.52	1.21	0.28	0.001555093	0.040775467
Slc38a4	1778.04	2156.60	1.21	0.28	0.001238271	0.035057491
Trmt2a	1315.47	1595.87	1.21	0.28	0.00053264	0.020099517
Qars	1565.97	1899.76	1.21	0.28	0.000402494	0.016529213
Usp16	1552.02	1885.70	1.22	0.28	0.000542062	0.020236799
Cenpq	716.52	870.90	1.22	0.28	0.001987799	0.047818758
Ccne1	716.33	870.75	1.22	0.28	0.001990307	0.047818758
Idh3a	1749.03	2127.62	1.22	0.28	0.000266753	0.012549213
2700089E24Rik	1417.20	1724.69	1.22	0.28	0.000520981	0.019853925
Ifngr1	628.86	766.15	1.22	0.28	0.001521608	0.040178494
C1d	795.90	970.91	1.22	0.29	0.001356131	0.037146974
Fam149a	1059.74	1292.86	1.22	0.29	0.000537281	0.020236799
Dcun1d5	1083.60	1322.66	1.22	0.29	0.000605144	0.021427013
Thyn1	730.48	892.08	1.22	0.29	0.001002455	0.030492949
Dusp14	803.68	981.89	1.22	0.29	0.001410122	0.038314702
Pop5	637.02	778.95	1.22	0.29	0.001564752	0.040949146
Tmem69	617.68	756.35	1.22	0.29	0.002045589	0.048695637
Snhg6	716.81	879.02	1.23	0.29	0.001297318	0.036082342
Sf3b5	559.40	686.02	1.23	0.29	0.001745474	0.043765745
Pdcd2	637.62	782.04	1.23	0.29	0.001634594	0.041803766
Vimp	764.14	937.38	1.23	0.29	0.000868353	0.027624256
Exosc9	2154.36	2642.90	1.23	0.29	7.66063E-05	0.005299781
Mrpl50	607.78	745.62	1.23	0.29	0.001463338	0.03940351
Trappc13	1216.71	1492.91	1.23	0.30	0.00029944	0.013398329
Sar1b	869.05	1066.44	1.23	0.30	0.000628619	0.021969895
Ptpmt1	646.05	793.20	1.23	0.30	0.001582476	0.041133713
Fam45a	636.83	783.85	1.23	0.30	0.001699954	0.042939487
Timmdc1	560.87	690.44	1.23	0.30	0.001809629	0.044671176
Dclre1c	643.17	792.75	1.23	0.30	0.001426715	0.0386488
Eif2b1	1082.84	1335.15	1.23	0.30	0.000271857	0.012668353
Nup37	559.63	690.81	1.23	0.30	0.001071947	0.031747761
Cuta	639.24	789.55	1.24	0.30	0.0014842	0.039743518
Ccdc104	816.39	1008.69	1.24	0.31	0.000637601	0.022168963
Prdx3	1405.50	1738.50	1.24	0.31	0.000120252	0.007152602
Yipf6	808.73	1000.78	1.24	0.31	0.000469071	0.018448989
Rnft1	850.56	1052.75	1.24	0.31	0.000500993	0.019338053
Mis18bp1	995.45	1232.49	1.24	0.31	0.001260986	0.035398512
Rfc4	684.24	848.09	1.24	0.31	0.001026673	0.031004823
Mrps23	855.86	1060.94	1.24	0.31	0.000302549	0.01349269
Pex2	1078.20	1337.49	1.24	0.31	0.000284063	0.012968365
Guf1	811.53	1007.01	1.24	0.31	0.000616073	0.02175691
Mios	593.24	736.15	1.24	0.31	0.001312462	0.036338387
Ftsj1	647.86	803.99	1.24	0.31	0.000795494	0.025828201
Mrps17	1057.44	1312.61	1.24	0.31	0.000176017	0.009423887
Ciao1	575.69	715.45	1.24	0.31	0.001111365	0.032452106
Tmf1	997.36	1239.73	1.24	0.31	0.001663454	0.04231367
Bcap29	621.03	772.16	1.24	0.31	0.000817867	0.026395785
Zfp961	756.44	940.63	1.24	0.31	0.000450866	0.017836985
Tmem147	695.36	864.94	1.24	0.31	0.000571667	0.020648117
Tex30	742.01	924.03	1.25	0.32	0.000393108	0.016258823
Caap1	475.75	592.60	1.25	0.32	0.002062286	0.048895023
Sgpp1	1311.16	1633.51	1.25	0.32	0.000114567	0.006946352
5430417L22Rik	900.45	1122.74	1.25	0.32	0.000249026	0.01189199
Ift74	960.46	1198.70	1.25	0.32	0.000214028	0.010923221
Ccnc	648.92	810.06	1.25	0.32	0.000780661	0.025500018
Ncapg	2319.03	2895.29	1.25	0.32	2.83515E-05	0.002584301
Gins4	655.30	818.62	1.25	0.32	0.000586369	0.021066336
Mrps2	983.85	1229.46	1.25	0.32	0.000101094	0.006350286
Eci1	557.57	697.13	1.25	0.32	0.000656069	0.022492232
Scrn3	470.13	588.16	1.25	0.32	0.002046657	0.048695637
Tmco1	759.97	950.78	1.25	0.32	0.000361615	0.015413485
Gtf2h5	718.71	899.66	1.25	0.32	0.000398504	0.016415324
Phax	777.96	974.28	1.25	0.32	0.000269886	0.012620079
Tigd2	406.04	508.51	1.25	0.32	0.001660844	0.04231367
Rnf34	496.12	623.15	1.26	0.33	0.001380119	0.03753729
Acot13	475.05	596.95	1.26	0.33	0.001114462	0.03250734
Gtf2b	501.56	630.86	1.26	0.33	0.001269374	0.035527982
Tmem184c	959.03	1206.52	1.26	0.33	9.5356E-05	0.006082269
Mrpl15	973.97	1226.22	1.26	0.33	6.561E-05	0.00468313
Snhg5	843.14	1061.65	1.26	0.33	0.000149406	0.008346033

Mrps34	484.47	611.19	1.26	0.34	0.000673191	0.022875764
Fam189a1	603.48	761.85	1.26	0.34	0.000287513	0.013103677
Wdr92	507.88	641.60	1.26	0.34	0.000724913	0.024176625
Zmat2	849.12	1072.85	1.26	0.34	7.74737E-05	0.005332441
Slc25a16	383.25	484.95	1.27	0.34	0.001255647	0.035398512
Slc43a3	362.90	459.29	1.27	0.34	0.001558739	0.040831388
Hltf	759.74	962.26	1.27	0.34	0.00027928	0.012902825
Angptl4	564.29	715.03	1.27	0.34	0.001577701	0.041128463
Fam92a	631.48	800.77	1.27	0.34	0.000223621	0.011091017
Extl2	633.84	805.12	1.27	0.35	0.000236595	0.011445495
Casp6	405.27	515.05	1.27	0.35	0.000839842	0.026943858
Nxt2	491.53	624.69	1.27	0.35	0.00059956	0.021341317
Snrpb2	433.49	551.04	1.27	0.35	0.0011061	0.032368423
Wdr12	450.94	573.33	1.27	0.35	0.000836552	0.026870258
Exosc3	356.48	453.98	1.27	0.35	0.00154867	0.040686133
Rnaseh2c	408.50	520.45	1.27	0.35	0.000973612	0.029783487
Edn1	519.68	663.26	1.28	0.35	0.000475831	0.018660473
Ccnb2	341.44	436.18	1.28	0.35	0.001374414	0.037419851
Zfp958	315.39	402.99	1.28	0.35	0.002039252	0.048648153
Fpgt	448.75	574.25	1.28	0.36	0.000876556	0.027693639
Ndnl2	543.18	695.10	1.28	0.36	0.000188675	0.009942654
Thg1l	330.29	422.68	1.28	0.36	0.001926947	0.04662865
Echdc1	644.03	825.33	1.28	0.36	0.000105296	0.006508649
Mrps22	627.05	803.69	1.28	0.36	0.0001176	0.007051029
Selm	310.21	397.67	1.28	0.36	0.001310177	0.036330821
Irak1bp1	390.49	500.97	1.28	0.36	0.000962311	0.029571881
Mum1l1	860.87	1104.61	1.28	0.36	0.000898315	0.028019096
Tceal8	767.56	985.62	1.28	0.36	0.000875557	0.027693639
Ptcd2	664.50	853.58	1.28	0.36	9.07704E-05	0.005873082
Mrpl36	501.57	645.05	1.29	0.36	0.00027095	0.012647927
Dph5	524.30	674.34	1.29	0.36	0.000236729	0.011445495
Tmem173	520.16	669.07	1.29	0.36	0.000216189	0.010923221
Cdc20b	897.09	1154.09	1.29	0.36	3.40093E-05	0.002902154
Taf9b	306.40	394.68	1.29	0.37	0.00193248	0.046720649
Nme7	363.69	469.42	1.29	0.37	0.000854135	0.027272678
Gpx8	883.46	1142.56	1.29	0.37	2.36195E-05	0.002292361
C230052I12Rik	372.90	482.67	1.29	0.37	0.001554781	0.040775467
Rhoj	386.31	500.64	1.30	0.37	0.000399338	0.016424617
Stk17b	417.15	540.70	1.30	0.37	0.000480087	0.018718521
Exosc6	598.34	775.64	1.30	0.37	0.00104908	0.031520313
Msrb1	445.17	577.77	1.30	0.38	0.000253073	0.012042626
Taf4b	556.98	722.95	1.30	0.38	0.000295575	0.013291529
Ostm1	680.79	885.23	1.30	0.38	5.20824E-05	0.003969592
Ndufa3	257.78	335.23	1.30	0.38	0.001852515	0.045438821
Acaa2	326.57	424.92	1.30	0.38	0.000720065	0.024044653
Rabepk	430.24	560.05	1.30	0.38	0.000251089	0.011969301
Foxc1	383.47	499.44	1.30	0.38	0.000422274	0.017055959
Fkbp11	231.56	301.97	1.30	0.38	0.001506467	0.040102225
Kdelc1	833.95	1089.48	1.31	0.39	1.3585E-05	0.001508377
Tasp1	379.18	495.64	1.31	0.39	0.000543037	0.020236799
Mab21l1	249.06	325.65	1.31	0.39	0.001803349	0.044597767
Pttg1	480.39	629.60	1.31	0.39	7.78006E-05	0.00534132
Gja1	1660.88	2179.14	1.31	0.39	0.000128613	0.007478684
Ndufaf4	474.80	623.84	1.31	0.39	5.82795E-05	0.004319142
2610305D13Rik	381.03	500.70	1.31	0.39	0.000199962	0.010435546
Rbbp9	255.90	336.80	1.32	0.40	0.00133091	0.036717071
Tefm	241.12	317.37	1.32	0.40	0.001740612	0.043727611
Zfp707	241.73	318.89	1.32	0.40	0.001134157	0.032939379
Lctl	276.55	364.89	1.32	0.40	0.000713515	0.023855453
Gulp1	218.68	288.65	1.32	0.40	0.001746996	0.043765745
Rgs2	357.20	471.92	1.32	0.40	0.000119933	0.007152602
Itgb3bp	297.36	393.19	1.32	0.40	0.001505575	0.040102225
Pnrc2	657.33	870.02	1.32	0.40	1.18537E-05	0.001372643
Tmem179b	290.11	384.12	1.32	0.40	0.000651262	0.022404595
Ccdc32	221.89	294.04	1.33	0.41	0.001890347	0.046002712
Gm10033	296.05	392.67	1.33	0.41	0.00059326	0.021200989
Snupn	225.55	299.18	1.33	0.41	0.001702874	0.042939487
Larp1b	276.32	366.67	1.33	0.41	0.000965837	0.029596102
Tex9	510.19	677.91	1.33	0.41	3.7422E-05	0.003087717
Orc5	508.46	676.32	1.33	0.41	0.000387617	0.016164273
Cetn2	543.73	723.30	1.33	0.41	2.01482E-05	0.002043675
Phospho2	344.22	457.90	1.33	0.41	0.000277392	0.012902825
BC031181	270.59	360.12	1.33	0.41	0.000698833	0.023510246
Hmgn5	282.99	376.82	1.33	0.41	0.000666136	0.02269321
AW209491	295.34	393.57	1.33	0.41	0.000394102	0.016258823

Spc25	609.05	811.79	1.33	0.41	1.01447E-05	0.001211125
Gla	276.45	368.49	1.33	0.41	0.000499701	0.019315815
Scnm1	251.80	335.82	1.33	0.42	0.000870265	0.027624256
Psmc3ip	326.97	436.65	1.34	0.42	0.000316046	0.013879026
Frk	377.63	508.17	1.35	0.43	4.20552E-05	0.003398404
Osgepl1	242.50	327.34	1.35	0.43	0.000927316	0.028659697
Elavl2	305.63	414.54	1.36	0.44	0.000232571	0.011391709
C030006K11Rik	263.83	358.28	1.36	0.44	0.000290982	0.013128734
Rpp38	270.58	368.85	1.36	0.45	0.00022737	0.011215137
C630043F03Rik	242.42	331.01	1.37	0.45	0.000494117	0.019127373
0610011F06Rik	368.29	504.01	1.37	0.45	0.001177293	0.033828049
Commd5	202.32	277.14	1.37	0.45	0.000568574	0.020605224
B230118H07Rik	233.14	320.08	1.37	0.46	0.000356384	0.015262833
Gpr155	192.76	264.78	1.37	0.46	0.001077517	0.031773207
1810043G02Rik	331.27	456.46	1.38	0.46	1.7027E-05	0.001766948
F8a	152.78	210.75	1.38	0.46	0.001728864	0.043479964
4930430F08Rik	329.75	455.45	1.38	0.47	2.37396E-05	0.002295761
Map2k6	159.46	220.39	1.38	0.47	0.000799323	0.025890206
AA987161	206.35	285.74	1.38	0.47	0.002072914	0.049103859
Lpar6	218.75	302.95	1.38	0.47	0.000344575	0.014827702
2610301B20Rik	259.96	361.71	1.39	0.48	5.71238E-05	0.004281273
Tctn2	295.57	414.24	1.40	0.49	3.76598E-05	0.003097864
Dnajc19	140.20	196.75	1.40	0.49	0.00152488	0.040178494
Arxes2	349.13	495.60	1.42	0.51	3.39076E-06	0.000500315
Rilpl2	291.08	413.73	1.42	0.51	7.81818E-06	0.000981127
Mitd1	321.81	459.74	1.43	0.51	4.98584E-06	0.000684481
Zfp930	438.22	629.71	1.44	0.52	6.1177E-07	0.000128954
Ccnb1ip1	113.47	163.44	1.44	0.53	0.000434448	0.017392241
Cdkn3	192.32	283.17	1.47	0.56	4.0526E-05	0.003313433
Hoxa2	71.55	108.71	1.52	0.60	0.001680574	0.042601062
6720489N17Rik	99.08	150.55	1.52	0.60	0.000652424	0.022404595
Arxes1	64.77	102.75	1.59	0.67	0.000548112	0.020323042
Enpp3	46.29	78.96	1.71	0.77	0.000916559	0.028457632
Tfpi	7.88	22.61	2.87	1.52	0.001069842	0.031720225

Supplemental Table 2.3. All Klf9 ChSP peaks, coordinates, distance to nearest TSS, name of nearest gene and peak height.

Chr	Start	End	Distance to	Gene Name	Gene Description	Average tag
chr2	33274101	33274740	16121	Zbtb43	zinc finger and BTB domain containing 43	11.664
chr7	30030161	30030840	635	Sdhaf1	succinate dehydrogenase complex assembly factor 1	13.601
chr15	99325221	99325900	-22796	Bcdin3d	BCDIN3 domain containing	21.963
chr6	1.2E+08	120448881	10955	Cecr6	cat eye syndrome chromosome region, candidate 6	14.537
chr16	38167721	38168400	46003	Nr1i2	nuclear receptor subfamily 1, group I, member 2	10.14
chr3	10372742	10373400	23566	Chmp4c	charged multivesicular body protein 4C	12.184
chr11	97904082	97904930	-34954	Stac2	SH3 and cysteine rich domain 2	21.364
chr9	57398542	57399140	5577	Cplx3	complexin 3	13.766
chr17	65975822	65977130	113	Ankrd12	ankyrin repeat domain 12	28.726
chr3	96189741	96190420	148	Otud7b	OTU domain containing 7B	17.549
chr13	43314172	43314980	568	Gfod1	glucose-fructose oxidoreductase domain containing 1	26.114
chr11	45694982	45696000	104	Clint1	clathrin interactor 1	18.415
chr4	82996381	82997400	114	Ccdc171	coiled-coil domain containing 171	21.987
chr10	1.28E+08	127772340	986	Coq10a	coenzyme Q10 homolog A (yeast)	18.371
chr13	17589832	17590240	203	Cdk13	cyclin-dependent kinase 13	14.667
chr19	44984041	44985060	120	Fam178a	family with sequence similarity 178, member A	22.075
chr10	67374741	67375420	125	Rtkn2	rhotekin 2	19.057
chr15	38022541	38023560	393	Ubr5	ubiquitin protein ligase E3 component n-recognin 5	17.7
chr10	39059201	39059880	325	Fyn	Fyn proto-oncogene	20.542
chr6	90681401	90682331	167	Iqsec1	IQ motif and Sec7 domain 1	18.914
chr15	99866501	99867180	142	Dip2b	DIP2 disco-interacting protein 2 homolog B (Drosophila)	15.757
chr12	50259481	50260360	786	Foxg1	forkhead box G1	14.978
chr9	1.01E+08	101108690	170	Ppp2r3a	protein phosphatase 2, regulatory subunit B'', alpha	20.218
chr10	1.22E+08	122479900	174	Mon2	MON2 homolog (yeast)	24.328
chr19	53195721	53196740	162	Add3	adducin 3 (gamma)	20.108
chr6	83760361	83761690	209	Nagk	N-acetylglucosamine kinase	26.65
chr11	51847281	51848300	146	Cdkl3	cyclin-dependent kinase-like 3	22.987
chr17	78821181	78822180	123	Cebpzos	CCAAT/enhancer binding protein (C/EBP), zeta, opposite strand	14.128
chr17	24999861	25000521	840	Ube2i	ubiquitin-conjugating enzyme E2I	13.621
chr18	50104441	50105460	193	Tnfaip8	tumor necrosis factor, alpha-induced protein 8	15.855
chr2	71012401	71013420	125	Dync1i2	dynein cytoplasmic 1 intermediate chain 2	20.961
chr6	1.2E+08	120004700	254	Wnk1	WNK lysine deficient protein kinase 1	26.217
chr10	25048821	25049840	116	Epb41l2	erythrocyte membrane protein band 4.1 like 2	17.272
chr11	54799161	54799840	6863	Tnip1	TNFAIP3 interacting protein 1	15.281
chr5	1.17E+08	117381600	101	Taok3	TAO kinase 3	18.199
chr5	1.38E+08	137830771	125	Mospd3	motile sperm domain containing 3	19.034
chr5	1.47E+08	147274060	426	Mtif3	mitochondrial translational initiation factor 3	16.622
chr11	5420621	5421300	316	Xbp1	X-box binding protein 1	15.689
chr4	1.41E+08	141066000	203	Casp9	caspase 9	19.647
chr7	45083412	45084391	106	Tead2	TEA domain family member 2	14.043
chr15	98361692	98362340	287	Kansl2	KAT8 regulatory NSL complex subunit 2	18.02
chr7	28080762	28080940	571	Plekhg2	pleckstrin homology domain containing, family G (with RhoGef	11.86
chr7	28080072	28080751	1011	Plekhg2	pleckstrin homology domain containing, family G (with RhoGef	16.037
chr11	61309481	61310840	301	Mapk7	mitogen-activated protein kinase 7	22.474
chr2	1.32E+08	131955360	261	Cds2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase)	12.111
chr13	12515402	12516420	160	Lgals8	lectin, galactose binding, soluble 8	16.258
chr13	55609381	55610060	202			14.513
chr12	55780401	55781420	102	Cfl2	cofilin 2, muscle	13.074
chr11	1.18E+08	117785711	180	Socs3	suppressor of cytokine signaling 3	18.529
chr3	89250681	89251360	298	Clk2	CDC-like kinase 2	14.865
chr16	94634682	94635940	116	Dscr3	Down syndrome critical region gene 3	28.63
chr4	1.09E+08	109175020	121	Faf1	Fas-associated factor 1	16.71
chr3	69214481	69215160	201	Kpna4	karyopherin (importin) alpha 4	17.358
chr1	1.33E+08	132925720	179	Mapkapk2	MAP kinase-activated protein kinase 2	14.832
chr12	8947781	8948131	641	Laptm4a	lysosomal-associated protein transmembrane 4A	12.6
chr19	5637672	5637880	286	Rela	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	14.712
chr12	59929421	59930430	104	Sec23a	SEC23 homolog A, COPII coat complex component	16.584
chr17	80388241	80388920	199	Sos1	son of sevenless homolog 1 (Drosophila)	16.003
chr10	18704152	18705100	200	Tnfaip3	tumor necrosis factor, alpha-induced protein 3	18.586
chr15	98857721	98858400	135	Tuba1c	tubulin, alpha 1C	16.426
chr8	1.23E+08	122797120	319			22.364
chr7	44421072	44422360	291	Nr1h2	nuclear receptor subfamily 1, group H, member 2	15.973
chr7	1.1E+08	109914520	264	Wee1	WEE 1 homolog 1 (S. pombe)	24.246
chr5	1.22E+08	121854640	141	Aldh2	aldehyde dehydrogenase 2, mitochondrial	11.969
chr14	19267882	19269080	204	Anxa7	annexin A7	17.715
chr17	25865912	25867200	270	Axin1	axin 1	19.022
chr2	1.18E+08	118290300	198	Bub1b	budding uninhibited by benzimidazoles 1 homolog, beta (S.	12.642
chr16	20629501	20630520	169	Clcn2	chloride channel, voltage-sensitive 2	15.922
chr7	24958721	24960080	118	Erf	Ets2 repressor factor	15.24
chr8	73627001	73628291	918	Jund	jun D proto-oncogene	27.078
chr19	23208292	23208921	283	Klf9	Kruppel-like factor 9	21.793
chr8	13159021	13159651	224	Lamp1	lysosomal-associated membrane protein 1	12.714
chr11	49088522	49089540	1417	Mgat1	mannoside acetylglucosaminyltransferase 1	31.924
chr3	90698741	90699420	259	S100a6	S100 calcium binding protein A6 (calcyclin)	19.183
chr4	43463561	43464920	863	Tesk1	testis specific protein kinase 1	19.7
chr7	11924141	11924861	170	Trim28	tripartite motif-containing 28	16.347
chr12	21663472	21664120	130	Ywhaq	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	14.884
chr8	1.09E+08	109305240	262	Zfp90	zinc finger protein 90	23.236
chr15	99479241	99479920	110	Racgap1	Rac GTPase-activating protein 1	21.53

chr5	97033392	97034300	159	Anxa3	annexin A3	18.439
chr10	79802081	79802760	240	Mbd3	methyl-CpG binding domain protein 3	23.554
chr7	80071701	80072380	11686	Sema4b	sema domain, immunoglobulin domain (Ig), transmembrane	12.258
chr9	1.08E+08	107861260	171	Ip6k1	inositol hexaphosphate kinase 1	14.703
chr11	61670561	61671181	416	Ulk2	unc-51 like kinase 2	14.613
chr7	80676221	80677240	114	Iqgap1	IQ motif containing GTPase activating protein 1	18.69
chr6	51941202	51942820	121	Skap2	src family associated phosphoprotein 2	20.768
chr3	57934641	57936231	250	Pfn2	profilin 2	15.962
chr17	36654041	36654321	162	Gabbr1	gamma-aminobutyric acid (GABA) B receptor, 1	15.893
chr14	54675741	54676420	167	Rabggta	Rab geranylgeranyl transferase, a subunit	17.339
chr5	1.47E+08	147143840	102	Rpl21	ribosomal protein L21	17.904
chr11	79070061	79071321	199	Wsb1	WD repeat and SOCS box-containing 1	21.111
chr5	4109921	4110940	273	Cyp51	cytochrome P450, family 51	24.087
chr11	99046421	99047100	347	Smarce1	SWI/SNF related, matrix associated, actin dependent regulator of	18.161
chr12	33405022	33406360	109	Nampt	nicotinamide phosphoribosyltransferase	13.821
chr5	1.18E+08	117618920	136	Wsb2	WD repeat and SOCS box-containing 2	14.127
chr19	5689561	5690401	850	Map3k11	mitogen-activated protein kinase kinase kinase 11	15.155
chr4	41042421	41043340	328	B4galt1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide	13.517
chr14	53417892	53419100	144	Lrp10	low-density lipoprotein receptor-related protein 10	16.691
chr3	90595041	90595261	274	Chtop	chromatin target of PRMT1	17.864
chr8	49173521	49174200	116	Ing2	inhibitor of growth family, member 2	15.212
chr3	1.27E+08	126589820	443	Camk2d	calcium/calmodulin-dependent protein kinase II, delta	18.27
chr11	51478721	51479400	259	Rmnd5b	required for meiotic nuclear division 5 homolog B (S. cerevisiae)	13.658
chr19	4756261	4757041	126	Rbm4b	RNA binding motif protein 4B	27.128
chr8	89513662	89514860	113	Lonp2	lon peptidase 2, peroxisomal	16.097
chr5	3653672	3653980	116	Gatad1	GATA zinc finger domain containing 1	15.383
chr2	1.19E+08	119168980	129	Ino80	INO80 homolog (S. cerevisiae)	12.397
chr14	35879521	35880200	145	Ccser2	coiled-coil serine rich 2	12.985
chr8	1.2E+08	119865300	130	1700030J22Rik	RIKEN cDNA 1700030J22 gene	20.837
chr1	87895441	87896460	160	Psmd1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	17.4
chr7	24990902	24991980	502	Cic	capicua homolog (Drosophila)	16.963
chr6	1.16E+08	116304140	159	March8	membrane-associated ring finger (C3HC4) 8	16.845
chr18	57479721	57480740	128	Prrc1	proline-rich coiled-coil 1	18.444
chr7	92511782	92512671	108	Ankrd42	ankyrin repeat domain 42	16.847
chr9	18223321	18224340	131	Zfp558	zinc finger protein 558	25.228
chr19	34258452	34258740	329	Stambpl1	STAM binding protein like 1	15.812
chr7	83759341	83760451	630	Mesdc1	mesoderm development candidate 1	17.495
chr11	53193681	53194921	111	Aff4	AF4/FMR2 family, member 4	18.508
chr9	70302141	70303160	239	Rnf111	ring finger 111	19.15
chr11	62636161	62637180	222	Trim16	tripartite motif-containing 16	14.473
chr5	1.09E+08	108934911	180	Fgfrl1	fibroblast growth factor receptor-like 1	16.043
chr7	1.13E+08	113161180	109	Btbd10	BTB (POZ) domain containing 10	21.198
chr17	24743501	24744520	324	Ift140	intraflagellar transport 140	12.367
chr11	75302861	75303540	228	Prpf8	pre-mRNA processing factor 8	14.009
chr16	4554981	4555660	147	Vasn	vasorin	17.825
chr17	21240141	21240581	125	Zfp52	zinc finger protein 52	15.636
chr15	63889401	63890420	211	Fam49b	family with sequence similarity 49, member B	14.566
chr5	1.38E+08	138016201	288	Mepce	methylphosphate capping enzyme	
chr10	80059801	80060310	145	Btbd2	BTB (POZ) domain containing 2	15.075
chr12	1.13E+08	113257400	277	BC022687	cDNA sequence BC022687	18.432
chr2	1.55E+08	155421140	116	Edem2	ER degradation enhancer, mannosidase alpha-like 2	17.021
chr6	56726621	56727640	261	Kbtbd2	kelch repeat and BTB (POZ) domain containing 2	20.318
chr15	58245401	58246080	189	D15Ertd621e	DNA segment, Chr 15, ERATO Doi 621, expressed	16.834
chr9	79852401	79853080	153	Senp6	SUMO/sentrin specific peptidase 6	13.006
chr13	74069722	74070700	207	Clptm1l	CLPTM1-like	16.853
chr19	7561261	7561940	118	Atl3	atlastin GTPase 3	19.654
chr7	45901361	45902380	132	Nomo1	nodal modulator 1	16.332
chr19	4614821	4616180	167	Lrfn4	leucine rich repeat and fibronectin type III domain containing 4	24.946
chr11	1.1E+08	109538171	530	Fam20a	family with sequence similarity 20, member A	17.366
chr8	49211941	49213300	128	Cdkn2aip	CDKN2A interacting protein	15.187
chr19	12568192	12568780	555	Dtx4	deltex 4 homolog (Drosophila)	18.952
chr12	72749461	72750051	111	Daam1	dishevelled associated activator of morphogenesis 1	14.78
chrX	44452672	44453640	173	Zdhhc9	zinc finger, DHHC domain containing 9	10.418
chr4	59899161	59900520	136	Snx30	sorting nexin family member 30	21.846
chr5	1.43E+08	142717030	120	Ap5z1	adaptor-related protein complex 5, zeta 1 subunit	18.816
chr7	1.27E+08	126720710	114	Kctd13	potassium channel tetramerisation domain containing 13	22.957
chr7	80243832	80244760	592	Man2a2	mannosidase 2, alpha 2	17.112
chr6	90334601	90335620	112	Zxdc	ZXD family zinc finger C	23.963
chr19	16847341	16848360	102	Vps13a	vacuolar protein sorting 13A (yeast)	21.313
chr5	1.11E+08	111011360	169	Ep400	E1A binding protein p400	19.562
chr8	18594941	18595960	300	Mcph1	microcephaly, primary autosomal recessive 1	14.246
chr1	1.84E+08	184246340	158	Trp53bp2	transformation related protein 53 binding protein 2	19.517
chr8	1.28E+08	127549970	164	2310022B05Rik	RIKEN cDNA 2310022B05 gene	19.381
chr1	1.68E+08	168246280	563	Pogk	pogo transposable element with KRAB domain	12.629
chr7	49114701	49114711	496	Nav2	neuron navigator 2	7
chr15	77133421	77134440	378	Rbfox2	RNA binding protein, fox-1 homolog (C. elegans) 2	24.909
chr11	1.02E+08	102006460	161	G6pc3	glucose 6 phosphatase, catalytic, 3	17.715
chr16	31922261	31923280	264	Senp5	SUMO/sentrin specific peptidase 5	23.162
chr2	1.61E+08	160565000	111	Zhx3	zinc fingers and homeoboxes 3	18.935
chr1	90532481	90533840	202	Arl4c	ADP-ribosylation factor-like 4C	20.705
chr2	34228821	34229500	300	Mapkap1	mitogen-activated protein kinase associated protein 1	14.515
chr11	1.15E+08	115292640	193	Armc7	armadillo repeat containing 7	42.69
chr7	80143101	80143780	272	Vps33b	vacuolar protein sorting 33B (yeast)	15.386
chr12	25239901	25241260	130	Klf11	Kruppel-like factor 11	20.596
chr10	1.1E+08	110149960	135	E2f7	E2F transcription factor 7	11.834
chr5	67585881	67586560	130			22.971
chr7	11866001	11866680	297	Zfp324	zinc finger protein 324	15.459
chr7	28879572	28879940	606	Ggn	gametogenetin	22.188
chr3	97743201	97744311	139	Prkab2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	17.883
chr10	50280901	50281580	156	Ascc3	activating signal cointegrator 1 complex subunit 3	22.598

chr8	72737382	72738190	110	Gmip	Gem-interacting protein	20.583
chr11	59478581	59479041	121	Mprip	myosin phosphatase Rho interacting protein	17.783
chr3	1.3E+08	130053060	209	Sec24b	Sec24 related gene family, member B (S. cerevisiae)	12.692
chr11	74454221	74454900	-11130	Cluh	clustered mitochondria (cluA/CLU1) homolog	20.862
chr7	18116262	18116971	-29430	Nanos2	nanos homolog 2 (Drosophila)	12.818
chr2	25186861	25188020	195	Uap1l1	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	22.251
chr5	1.37E+08	137318100	2538	Vgf	VGF nerve growth factor inducible	24.155
chr3	1.07E+08	106850440	363	Lrif1	ligand dependent nuclear receptor interacting factor 1	19.649
chr5	1.23E+08	123082040	338	Anapc5	anaphase-promoting complex subunit 5	22.493
chr3	1.07E+08	107460400	1149	Rbm15	RNA binding motif protein 15	15.814
chr19	6076212	6077810	176	Vps51	vacuolar protein sorting 51 homolog (S. cerevisiae)	23.907
chr9	1.1E+08	110253840	161	Ptpn23	protein tyrosine phosphatase, non-receptor type 23	22.707
chr13	17588881	17589821	888	Cdk13	cyclin-dependent kinase 13	15.128
chr3	1.46E+08	145514560	187	Znhit6	zinc finger, HIT type 6	23.878
chr8	37717302	37718480	142	Lonrf1	LON peptidase N-terminal domain and ring finger 1	26.637
chrX	1.01E+08	100686580	475	Uprt	uracil phosphoribosyltransferase (FUR1) homolog (S. cerevisiae)	18.064
chr10	82128361	82129570	159	Hcfc2	host cell factor C2	18.099
chr3	58504492	58505500	1378	Tsc22d2	TSC22 domain family, member 2	14.262
chr6	83067781	83068460	946	Ccdc142	coiled-coil domain containing 142	23.554
chr10	75788381	75789400	117	Dip2a	DIP2 disco-interacting protein 2 homolog A (Drosophila)	16.088
chr16	96187021	96187111	272	Brwd1	bromodomain and WD repeat domain containing 1	5.889
chr8	1.25E+08	124878260	13636	Mir7237	microRNA 7237	35.803
chr17	5931672	5933000	268	Synj2	synaptojanin 2	16.476
chr4	1.51E+08	151030091	132	Acot7	acyl-CoA thioesterase 7	6.8
chr10	1.26E+08	126304590	255	Xrcc6bp1	XRCC6 binding protein 1	25.643
chr3	96686141	96687160	112	Lix1l	Lix1-like	20.891
chr8	91090081	91091100	1272	Papd5	PAP associated domain containing 5	16.943
chr8	1.29E+08	129479480	556	Irf2bp2	interferon regulatory factor 2 binding protein 2	12.06
chr11	1.2E+08	119967640	311	Slc38a10	solute carrier family 38, member 10	14.947
chr3	1.46E+08	145926291	700	Syde2	synapse defective 1, Rho GTPase, homolog 2 (C. elegans)	12.075
chr15	57742022	57742880	169	Tbc1d31	TBC1 domain family, member 31	23.044
chr10	6239732	6240360	133420	Mthfd1l	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-	11.142
chr16	32787561	32788240	213	Rubcn	RUN domain and cysteine-rich domain containing, Beclin 1-	19.539
chr11	58979121	58980291	234	Iba57	IBA57, iron-sulfur cluster assembly homolog (S. cerevisiae)	21.274
chr8	1.08E+08	108144140	736	B3gnt9	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9	25.663
chr15	76483681	76483781	425	Cyhr1	cysteine and histidine rich 1	6.7
chr17	78322401	78323420	300	Fez2	fasciculation and elongation protein zeta 2 (zygin II)	24.695
chr2	1.53E+08	152521520	1268	Bcl2l1	BCL2-like 1	16.084
chr4	98612241	98613260	183	Dock7	dedicator of cytokinesis 7	31.681
chrX	7300481	7301160	-1566	Rbm3os	RNA binding motif protein 3, opposite strand	10.242
chr5	3601961	3602830	158	Rbm48	RNA binding motif protein 48	17.495
chr6	1.25E+08	124775580	533			18.719
chr1	36389181	36390080	187			14.874
chr5	1.23E+08	122968820	149	P2rx4	purinergic receptor P2X, ligand-gated ion channel 4	17.573
chr13	55632501	55633180	213	Caml	calcium modulating ligand	13.324
chr11	94753982	94755280	2317	Col1a1	collagen, type I, alpha 1	15.881
chr16	91446412	91447390	10948	Ifngr2	interferon gamma receptor 2	12.264
chr10	80695941	80696620	188	Pip5k1c	phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma	19.433
chr19	7036301	7036980	218	Plcb3	phospholipase C, beta 3	20.462
chr2	1.05E+08	105200080	222	Rcn1	reticulocalbin 1	7.562
chr7	18787041	18788400	240	Relb	avian reticuloendotheliosis viral (v-rel) oncogene related B	23.322
chr13	21187822	21188750	890	Trim27	tripartite motif-containing 27	17.708
chr9	1.1E+08	109978100	220	Smarcc1	SWI/SNF related, matrix associated, actin dependent regulator of	35.704
chr19	6276401	6277760	184	Ehd1	EH-domain containing 1	27.475
chr2	38747761	38748571	304	Nr6a1	nuclear receptor subfamily 6, group A, member 1	20.333
chr15	76158972	76159660	767	Gpaa1	GPI anchor attachment protein 1	17.804
chr11	1.02E+08	102272680	-8247	Fam171a2	family with sequence similarity 171, member A2	24.841
chr14	53530542	53530620	1285	Ajuba	ajuba LIM protein	6.385
chr5	34503881	34504560	347	Mxd4	Max dimerization protein 4	14.894
chr7	1.27E+08	126817841	236	Maz	MYC-associated zinc finger protein (purine-binding transcription	13.778
chr17	87882861	87884560	334	Msh6	mutS homolog 6 (E. coli)	21.232
chr17	34194821	34196040	-2432	Gpsm3	G-protein signalling modulator 3 (AGS3-like, C. elegans)	17.242
chr11	50053441	50054800	123	Sqstm1	sequestosome 1	13.775
chr3	40841821	40842840	168	Hspa4l	heat shock protein 4 like	15.5
chr11	1.08E+08	108159780	342	Prkca	protein kinase C, alpha	8.003
chr11	1.17E+08	116669071	168	Srsf2	serine/arginine-rich splicing factor 2	9.273
chr18	60973561	60974710	198	Tcof1	Treacher Collins Franceschetti syndrome 1, homolog	17.324
chr7	44820501	44821180	9558	Tsks	testis-specific serine kinase substrate	18.193
chr2	13492402	13492560	317	Vim	vimentin	10.063
chr7	62298382	62299220	288	Mkrn3	makorin, ring finger protein, 3	21.342
chr8	96900681	96902380	239	Amfr	autocrine motility factor receptor	27.92
chr11	1.01E+08	101282600	218	Vat1	vesicle amine transport protein 1 homolog (T californica)	33.143
chr6	56761422	56762190	169	Fkbp9	FK506 binding protein 9	11.21
chr12	85674221	85674900	11542	Isca2	iron-sulfur cluster assembly 2 homolog (S. cerevisiae)	15.308
chr3	89299632	89300320	286	Mtx1	metaxin 1	30.246
chr17	12850641	12851320	209	Sod2	superoxide dismutase 2, mitochondrial	16.059
chr16	18339622	18340620	141	Txnrd2	thioredoxin reductase 2	24.157
chr11	5695001	5696020	7024	Dbnl	drebrin-like	15.033
chr3	96142821	96143511	694	Vps45	vacuolar protein sorting 45 (yeast)	16.826
chr17	63185012	63185260	906	Fbxl17	F-box and leucine-rich repeat protein 17	8.028
chr17	63184241	63185001	1421	Fbxl17	F-box and leucine-rich repeat protein 17	16.105
chr12	80090412	80091760	212	Vti1b	vesicle transport through interaction with t-SNAREs 1B	20.704
chr6	17231201	17231541	186	Cav2	caveolin 2	14.118
chr7	45574621	45575231	1637	Dbp	D site albumin promoter binding protein	18.279
chr15	81638812	81639100	287	Tef	thyrotroph embryonic factor	27.483
chr9	64535102	64536080	171	Rab11a	RAB11A, member RAS oncogene family	12.39
chr5	1.36E+08	136219631	312	Ywhag	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	19.052
chr11	70660841	70661520	224	Rabep1	rabaptin, RAB GTPase binding effector protein 1	15.454
chr17	29074421	29075100	156	Mtch1	mitochondrial carrier homolog 1 (C. elegans)	18.222
chr7	1.21E+08	120826670	471	Mettl9	methyltransferase like 9	17.217

chr1	1.73E+08	172722350	360	Dusp12	dual specificity phosphatase 12	20.371
chr15	98555352	98556140	486	Fkbp11	FK506 binding protein 11	19.839
chr2	1.52E+08	151986050	118	Tbc1d20	TBC1 domain family, member 20	14.644
chr11	59024341	59025360	294	2310033P09Rik	RIKEN cDNA 2310033P09 gene	15.352
chr11	70267801	70269120	334	Med11	mediator complex subunit 11	28.057
chr7	92436152	92437500	485	Ccdc90b	coiled-coil domain containing 90B	44.279
chr6	82617621	82618980	223	Pole4	polymerase (DNA-directed), epsilon 4 (p12 subunit)	49.575
chr5	1.23E+08	123489250	123	Psmd9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	14.657
chr6	56852852	56853780	194	Nt5c3	5'-nucleotidase, cytosolic III	15.345
chr11	86623161	86624180	185	Dhx40	DEAH (Asp-Glu-Ala-His) box polypeptide 40	16.419
chr16	57152112	57153320	109	Tbc1d23	TBC1 domain family, member 23	18.471
chr4	1.53E+08	153004621	293	Tprgl	transformation related protein 63 regulated like	13.743
chr2	1.19E+08	118505980	222	Knstrn	kinetochore-localized astrin/SPAG5 binding	17.318
chr17	74394381	74395060	245	Yipf4	Yip1 domain family, member 4	14.779
chr8	87950022	87950860	124	A230103J11Rik	RIKEN cDNA A230103J11 gene	36.184
chr15	1.02E+08	102154700	136	Pfdn5	prefoldin 5	20.083
chr5	1.3E+08	130227140	219	Vkorc1l1	vitamin K epoxide reductase complex, subunit 1-like 1	8.858
chr10	70743121	70743451	193	Ipmk	inositol polyphosphate multikinase	12.727
chr11	4034781	4035800	127	Rnf215	ring finger protein 215	14.469
chr17	46214522	46215860	214			20.254
chr4	99426902	99428580	358	Pgm2	phosphoglucomutase 2	19.649
chr5	53029461	53030480	148	Pi4k2b	phosphatidylinositol 4-kinase type 2 beta	15.226
chr4	1.07E+08	107388650	210	0610037L13Rik	RIKEN cDNA 0610037L13 gene	30.411
chr11	1.19E+08	119474300	54796	Rptor	regulatory associated protein of MTOR, complex 1	13.932
chr8	1.27E+08	127407480	133	Cog2	component of oligomeric golgi complex 2	12.049
chr5	1.26E+08	125731660	206	Bri3bp	Bri3 binding protein	14.829
chr8	40474281	40474960	236	Tusc3	tumor suppressor candidate 3	17.611
chr8	89774542	89775630	277	N4bp1	NEDD4 binding protein 1	16.755
chr11	68938401	68939420	2262	Hes7	hairy and enhancer of split 7 (Drosophila)	18.554
chr18	67414181	67415540	268	Impa2	inositol (myo)-1(or 4)-monophosphatase 2	18.753
chr19	41317082	41317140	204	Tm9sf3	transmembrane 9 superfamily member 3	7.017
chr17	35429361	35430601	215	Ier3	immediate early response 3	16.016
chr19	46381441	46382800	625	Fbxl15	F-box and leucine-rich repeat protein 15	24.165
chr2	1.64E+08	164188981	121	Pigt	phosphatidylinositol glycan anchor biosynthesis, class T	22.462
chr5	29899692	29900960	297	Ube3c	ubiquitin protein ligase E3C	20.431
chr5	1.41E+08	140672280	161	Eif3b	eukaryotic translation initiation factor 3, subunit B	21.775
chr8	4252392	4254080	134	Snapc2	small nuclear RNA activating complex, polypeptide 2	23.669
chrX	6999202	6999920	520	Otud5	OTU domain containing 5	16.915
chr1	51233932	51234600	595	Sdpr	serum deprivation response	12.626
chr13	38642021	38642900	115	Bloc1s5	biogenesis of lysosomal organelles complex-1, subunit 5, muted	18.573
chr8	1.27E+08	127117840	192	Galnt2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-	17.22
chr11	22881661	22882630	139	Commd1	COMM domain containing 1	13.492
chr11	1.22E+08	121519400	203	Metrnl	meteorin, glial cell differentiation regulator-like	21.714
chr5	1.38E+08	138015860	969	Mepce	methylphosphate capping enzyme	13.323
chr6	85553181	85554040	421	Alms1	Alstrom syndrome 1	14.229
chr10	7470481	7471500	117	Ginm1	glycoprotein integral membrane 1	16.337
chr15	88690772	88691311	1081	Pim3	proviral integration site 3	18.152
chr19	42143681	42144360	274	Pi4k2a	phosphatidylinositol 4-kinase type 2 alpha	18.287
chr2	1.22E+08	121809760	241	Spg11	spastic paraplegia 11	20.011
chr10	7357422	7358280	157	Nup43	nucleoporin 43	22.061
chr12	87771832	87772700	1651	Irf2bpl	interferon regulatory factor 2 binding protein-like	22.826
chr12	87771112	87771821	2451	Irf2bpl	interferon regulatory factor 2 binding protein-like	20.08
chr10	77025301	77025980	157	Pttg1ip	pituitary tumor-transforming 1 interacting protein	27.27
chr13	32345561	32346240	109	Gmds	GDP-mannose 4, 6-dehydratase	11.869
chr7	1.28E+08	128035840	-2504	Tgfb1i1	transforming growth factor beta 1 induced transcript 1	17.521
chr5	1.36E+08	135679380	303	Pom121	nuclear pore membrane protein 121	17.343
chr18	23946712	23947560	156	Mapre2	microtubule-associated protein, RP/EB family, member 2	13.715
chr11	3812081	3813100	2077	Slc35e4	solute carrier family 35, member E4	20.237
chr6	89609041	89610740	261	Txnrd3	thioredoxin reductase 3	21.436
chr2	1.5E+08	150478900	153	Pygb	brain glycogen phosphorylase	14.216
chr11	95880341	95881960	304	Ube2z	ubiquitin-conjugating enzyme E2Z (putative)	14.784
chr11	1.05E+08	104943310	150	Mettl2	methyltransferase like 2	22.784
chr4	94094661	94095340	265	Plaa	phospholipase A2, activating protein	15.482
chr4	1.51E+08	150840660	339	Phf13	PHD finger protein 13	17.665
chr16	32982041	32982720	112	Lmln	leishmanolysin-like (metallopeptidase M8 family)	17.736
chr19	29870701	29871911	700	9930021J03Rik	RIKEN cDNA 9930021J03 gene	30.744
chr4	1.28E+08	128450001	14948	Azin2	antizyme inhibitor 2	14.553
chr9	66718201	66719220	139	Rab8b	RAB8B, member RAS oncogene family	15.061
chr12	85982941	85983620	12254	Prox2	prospero homeobox 2	15.766
chr7	49114722	49115601	951	Nav2	neuron navigator 2	21.403
chr2	1.58E+08	158317260	396	Actr5	ARP5 actin-related protein 5	11.841
chr10	79363141	79363820	199	Wdr18	WD repeat domain 18	15.052
chr4	57040441	57041800	363	Tmem245	transmembrane protein 245	18.33
chr19	44615821	44616840	165	Hif1an	hypoxia-inducible factor 1, alpha subunit inhibitor	20.791
chr6	85034341	85035670	166	Exoc6b	exocyst complex component 6B	24.226
chr8	1.09E+08	108741520	127	Cenpt	centromere protein T	16.047
chr19	47121281	47121291	227	Taf5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-	7
chr7	1.27E+08	127046061	6074	Dctpp1	dCTP pyrophosphatase 1	17.281
chr11	70820052	70820980	111	Dhx33	DEAH (Asp-Glu-Ala-His) box polypeptide 33	16.943
chr1	1.93E+08	192612720	175	Rps6kc1	ribosomal protein S6 kinase polypeptide 1	17.103
chr8	1.23E+08	123475080	266	Gins2	GINS complex subunit 2 (Psf2 homolog)	16.9
chr6	39504272	39504971	1138	Adck2	aarF domain containing kinase 2	12.694
chr7	26936632	26937810	136	Itpkc	inositol 1,4,5-trisphosphate 3-kinase C	18.657
chr15	83422412	83423080	177	Ttll12	tubulin tyrosine ligase-like family, member 12	14.88
chr6	1.42E+08	142303490	102	Pyroxd1	pyridine nucleotide-disulphide oxidoreductase domain 1	18.375
chr6	17014621	17015960	141	Tes	testis derived transcript	20.55
chr3	50097652	50098081	-244355	Pcdh18	protocadherin 18	20.41
chr18	5819441	5820380	-227475	Gm10125	predicted gene 10125	13.241
chr13	60419021	60419930	-192095	Dapk1	death associated protein kinase 1	14.435
chr4	54782161	54783140	-186395	Zfp462	zinc finger protein 462	15.469

chr4	32567241	32567941	-178457	Bach2	BTB and CNC homology 2	12.814
chr4	32578461	32579480	-167078	Bach2	BTB and CNC homology 2	21.566
chr3	1.04E+08	104489140	-139214	Magi3	membrane associated guanylate kinase, WW and PDZ domain	17.403
chr10	1.2E+08	120013800	-133335	Hmga2	high mobility group AT-hook 2	13.535
chr5	1.12E+08	112119251	-116965	E130006D01Rik	RIKEN cDNA E130006D01 gene	14.098
chr8	1.25E+08	125060840	-107740	Zfpm1	zinc finger protein, multitype 1	21.953
chr3	58398112	58399080	-105022	Tsc22d2	TSC22 domain family, member 2	12.898
chr5	1.19E+08	118726980	-95279	Med13l	mediator complex subunit 13-like	18.524
chr10	5056821	5057500	-94674	Syne1	spectrin repeat containing, nuclear envelope 1	13.465
chr1	92349441	92350330	-83944	Cops8	COP9 (constitutive photomorphogenic) homolog, subunit 8	19.323
chr15	1.03E+08	102668440	-81219	Hoxc13	homeobox C13	21.044
chr8	1.07E+08	106912910	-78309	Cdh5	cadherin 5	16.048
chrX	73686142	73686500	-77625	Tbl1x	transducin (beta)-like 1 X-linked	14.615
chr17	13420141	13420820	-73987	2700054A10Rik	RIKEN cDNA 2700054A10 gene	15.177
chr16	31511541	31512220	-71310	Dlg1	discs, large homolog 1 (Drosophila)	15.027
chr15	66868821	66869650	-69925	Ndrg1	N-myc downstream regulated gene 1	29.557
chr19	41535761	41536440	-66850	Lcor	ligand dependent nuclear receptor corepressor	12.758
chr11	20377221	20378240	-65526	Sertad2	SERTA domain containing 2	27.278
chr13	1.12E+08	112089160	-64096			16.648
chr1	1.59E+08	158834851	-58308	Ralgps2	Ral GEF with PH domain and SH3 binding motif 2	17.05
chr8	1.29E+08	129418960	-57465	Gm17296	predicted gene, 17296	20.227
chr11	1.02E+08	101656260	-54391	Etv4	ets variant 4	12.716
chr3	1.46E+08	145640020	-52309	Cyr61	cysteine rich protein 61	12.189
chr11	51759062	51759991	-51528	Cdkn2aipnl	CDKN2A interacting protein N-terminal like	16.841
chr11	51760002	51760920	-50593	Cdkn2aipnl	CDKN2A interacting protein N-terminal like	16.679
chr7	97663301	97664660	-50541	Aqp11	aquaporin 11	18.033
chr8	1.23E+08	123162881	-48204	A330074K22Rik	RIKEN cDNA A330074K22 gene	16.957
chr11	30167521	30168151	-48064	Sptbn1	spectrin beta, non-erythrocytic 1	14.714
chr17	13266801	13267820	-46545	Smok4a	sperm motility kinase 4A	25.047
chr11	57778581	57779260	-46339	Larp1	La ribonucleoprotein domain family, member 1	20.959
chr10	76654472	76655040	-44510	Col18a1	collagen, type XVIII, alpha 1	12.053
chr2	1.53E+08	153265200	-43344	Nol4l	nucleolar protein 4-like	12.97
chr9	69879282	69880380	-42579	Gcnt3	glucosaminyl (N-acetyl) transferase 3, mucin type	13.334
chr10	1.11E+08	110527820	-41551	Osbpl8	oxysterol binding protein-like 8	15.528
chr1	1.93E+08	192926150	-41547	Atf3	activating transcription factor 3	22.889
chr19	43624042	43624950	-41140	Nkx2-3	NK2 homeobox 3	14.433
chr1	1.38E+08	137504840	-41108	Csrp1	cysteine and glycine-rich protein 1	16.75
chr5	1.49E+08	149012810	-39713	2210417A02Rik	RIKEN cDNA 2210417A02 gene	9.711
chr9	78306542	78306760	-39243	Eef1a1	eukaryotic translation elongation factor 1 alpha 1	12.734
chr17	3244822	3245300	-37994	Tiam2	T cell lymphoma invasion and metastasis 2	20.889
chr15	31133222	31134020	-35353	Dap	death-associated protein	22.761
chr19	37579732	37580730	-35331	Exoc6	exocyst complex component 6	16.768
chr11	97231501	97231841	-34579	Arhgap23	Rho GTPase activating protein 23	21.559
chr11	97231852	97232520	-34064	Arhgap23	Rho GTPase activating protein 23	16.624
chr6	72402661	72403340	-33933	Mat2a	methionine adenosyltransferase II, alpha	22.041
chr3	1.08E+08	107922380	-33215	Csf1	colony stimulating factor 1 (macrophage)	19.794
chr17	45230201	45230880	-33115	1600014C23Rik	RIKEN cDNA 1600014C23 gene	11.389
chr17	26612532	26613500	-31664	Kifc5b	kinesin family member C5B	20.123
chr6	72441972	72442690	-31569	Capg	capping protein (actin filament), gelsolin-like	23.694
chr7	81055802	81056680	-31076	Pde8a	phosphodiesterase 8A	13.763
chr9	35170621	35171300	-30787	Cdon	cell adhesion molecule-related/down-regulated by oncogenes	11.931
chr19	36413321	36414000	-30551	Pcgf5	polycomb group ring finger 5	17.196
chr7	80029892	80030900	-29958	Sema4b	sema domain, immunoglobulin domain (Ig), transmembrane	25.473
chr8	1.27E+08	126511280	-29223	Rhou	ras homolog gene family, member U	40.939
chr17	28121432	28122080	-29024	Tulp1	tubby like protein 1	18.483
chr17	88505542	88506370	-28925	Ston1	stonin 1	12.444
chr6	86565021	86565311	-28642	Asprv1	aspartic peptidase, retroviral-like 1	12.448
chr18	82921682	82922260	-28504	2210420H20Rik	RIKEN cDNA 2210420H20 gene	11.478
chr6	86565322	86566380	-27957	Asprv1	aspartic peptidase, retroviral-like 1	28.101
chr7	34021421	34022780	-27731	4931406P16Rik	RIKEN cDNA 4931406P16 gene	23.802
chr4	1.35E+08	134572680	-27520	Clic4	chloride intracellular channel 4 (mitochondrial)	9.125
chr6	72855881	72856560	-26732	Kcmf1	potassium channel modulatory factor 1	15.39
chr11	1.05E+08	104969220	-26017	Tlk2	tousled-like kinase 2 (Arabidopsis)	10.599
chr3	1.03E+08	103232160	-25131	Dennd2c	DENN/MADD domain containing 2C	37.616
chr17	29706481	29707500	-25109	Zfand3	zinc finger, AN1-type domain 3	31.045
chr11	94690341	94691010	-24992	Gm11544	predicted gene 11544	12.296
chr5	1.43E+08	143197120	-24892	Actb	actin, beta	12.361
chr15	6501821	6502531	-24886	Fyb	FYN binding protein	18.07
chr4	1.29E+08	128536301	-24604	Rnf19b	ring finger protein 19B	30.152
chr4	57637492	57638500	-24306			16.334
chr5	1.06E+08	105736260	-24023	Lrrc8c	leucine rich repeat containing 8 family, member C	14.567
chr13	1.14E+08	113561700	-23922	Il6st	interleukin 6 signal transducer	18.614
chr5	65386421	65387100	-23606	Klhl5	kelch-like 5	15.465
chr19	57292381	57293060	-23438	Ablim1	actin-binding LIM protein 1	14.144
chr3	96586861	96587540	-23390	Hfe2	hemochromatosis type 2 (juvenile) (human homolog)	18.417
chr4	1.32E+08	132380360	-22683	Wasf2	WAS protein family, member 2	15.576
chr15	68192781	68193750	-22307	Mir30d	microRNA 30d	16.22
chr15	85431121	85431800	-21873	Wnt7b	wingless-type MMTV integration site family, member 7B	15.791
chr5	1.14E+08	114191720	-21505	Coro1c	coronin, actin binding protein 1C	14.058
chr11	95461522	95462231	-21171	Phb	prohibitin	11.942
chr14	31321342	31322160	-20779	Ercc6	excision repair cross-complementing rodent repair deficiency,	21.174
chr18	61016741	61017420	-20529	Arsi	arylsulfatase i	14.831
chr11	72386352	72387020	-20245	Spns3	spinster homolog 3	14.57
chr5	1.06E+08	105740131	-20047	Lrrc8c	leucine rich repeat containing 8 family, member C	14.543
chr7	80040081	80041060	-19784	Sema4b	sema domain, immunoglobulin domain (Ig), transmembrane	25.217
chr5	1.26E+08	125699700	-19382	Ubc	ubiquitin C	16.031
chr5	1.36E+08	135955090	-19281	Por	P450 (cytochrome) oxidoreductase	13.302
chr11	43610352	43610980	-19270	Ttc1	tetratricopeptide repeat domain 1	14.949
chr4	44302682	44303020	-19166	Melk	maternal embryonic leucine zipper kinase	15.133
chr12	1.06E+08	105945360	-19156	Bdkrb2	bradykinin receptor, beta 2	10.963

chr19	5529081	5530100	-19101	Snx32	sorting nexin 32	22.109
chr7	15211002	15212140	-18893	Zfp541	zinc finger protein 541	16.929
chr3	96591662	96592300	-18609	Hfe2	hemochromatosis type 2 (juvenile) (human homolog)	16.351
chr13	21168741	21169300	-18376	Trim27	tripartite motif-containing 27	13.623
chr17	33496461	33497140	-18310	Platr17	pluripotency associated transcript 17	16.277
chr5	37001181	37002160	-17400	D5Ertd579e	DNA segment, Chr 5, ERATO Doi 579, expressed	17.714
chr10	12568781	12569670	-17300	Utrn	utrophin	18.399
chr2	27923692	27924540	-17229	Fcnb	ficolin B	13.679
chr8	47650832	47651680	-17117	Cfap97	cilia and flagella associated protein 97	16.923
chr8	1.25E+08	124555260	-16897	Zcchc14	zinc finger, CCHC domain containing 14	14.374
chr10	82209961	82210640	-16360	Nfyb	nuclear transcription factor-Y beta	16.518
chr16	17949961	17950640	-16123	Dgcr6	DiGeorge syndrome critical region gene 6	14.548
chr11	51795192	51795860	-15528	Cdkn2aipnl	CDKN2A interacting protein N-terminal like	11.398
chr19	5817741	5818420	-15409	Malat1	metastasis associated lung adenocarcinoma transcript 1 (non-	19.523
chr2	37525461	37525691	-15283	Mir5128	microRNA 5128	15.087
chr17	83891261	83891940	-15278			14.529
chr9	44234681	44235360	-15111	Bcl9l	B cell CLL/lymphoma 9-like	21.324
chr8	42887941	42888620	-14766	Asah1	N-acylsphingosine amidohydrolase 1	12.131
chr18	60773981	60774980	-14299	G630071F17Rik	RIKEN cDNA G630071F17 gene	14.091
chr6	31007042	31008000	-14265	Mir29b-1	microRNA 29b-1	20.294
chr16	17658581	17659260	-14264	Klhl22	kelch-like 22	9.745
chr5	1.43E+08	143186580	-14176	Actb	actin, beta	28.364
chr11	1.04E+08	103935240	-14090			12.178
chr8	87082501	87083180	-13774	Mir181c	microRNA 181c	16.711
chr7	29227081	29228100	-13370	Sipa1l3	signal-induced proliferation-associated 1 like 3	22.386
chr17	88521112	88522060	-13295	Ston1	stonin 1	12.985
chr12	1.13E+08	113244140	-13153	BC022687	cDNA sequence BC022687	15.322
chr4	44255081	44255710	-13028	Mir5106	microRNA 5106	14.269
chr2	1.7E+08	169847340	-12950	Zfp217	zinc finger protein 217	17.848
chr17	87367761	87368091	-12665	Calm2	calmodulin 2	18.697
chr15	78642341	78643031	-12389	Card10	caspase recruitment domain family, member 10	22.551
chr7	19091462	19092360	-12246	Pvr	poliovirus receptor	12.077
chr9	1.09E+08	108641440	-12221	Ip6k2	inositol hexaphosphate kinase 2	11.973
chr4	44254061	44254740	-12033	Mir5106	microRNA 5106	12.72
chr9	44237862	44238760	-11820	Bcl9l	B cell CLL/lymphoma 9-like	20.864
chr2	27259841	27261100	-11636	Vav2	vav 2 oncogene	34.192
chr11	61094601	61095280	-11559	Aldh3a2	aldehyde dehydrogenase family 3, subfamily A2	14.545
chr9	1.15E+08	114704440	-11250	Cmtm8	CKLF-like MARVEL transmembrane domain containing 8	14.511
chr10	1.28E+08	128183030	-11154	Mmp19	matrix metallopeptidase 19	12.146
chr10	1.17E+08	117125160	-11109	Mdm2	transformed mouse 3T3 cell double minute 2	15.087
chr6	29257762	29258550	-10994	Fam71f1	family with sequence similarity 71, member F1	8.923
chr1	33653972	33654560	-10176	Rab23	RAB23, member RAS oncogene family	15.731
chr4	1.37E+08	136640410	-10140	Cdc42	cell division cycle 42	11.125
chr15	83301642	83302720	-9809	Pacsin2	protein kinase C and casein kinase substrate in neurons 2	40.125
chr3	88598561	88599580	-9791	Lmna	lamin A	22.208
chr2	30533701	30534380	-9179	Mir3089	microRNA 3089	13.138
chr11	1E+08	100353260	-8720	Acly	ATP citrate lyase	12.143
chr7	15453681	15454360	-8703	Ccdc9	coiled-coil domain containing 9	13.467
chr17	26869212	26870540	-8396	Uqcc2	ubiquinol-cytochrome c reductase complex assembly factor 2	28.32
chr4	1.38E+08	138194501	-8123	Otud3	OTU domain containing 3	13.255
chr11	98599122	98600000	-8094	Nr1d1	nuclear receptor subfamily 1, group D, member 1	16.281
chr15	99122921	99123600	-8046	Fam186b	family with sequence similarity 186, member B	17.994
chr18	32290141	32290990	-7985	Proc	protein C	16.217
chr8	87090402	87091000	-7922	Mir23a	microRNA 23a	14.674
chr10	79562721	79563740	-7740	Cirbp	cold inducible RNA binding protein	26.383
chr7	1.27E+08	126600630	-7722	Fam57b	family with sequence similarity 57, member B	13.922
chr3	95735982	95736860	-7704	Mcl1	myeloid cell leukemia sequence 1	24.32
chr17	47305221	47305900	-7678	Mdfi	MyoD family inhibitor	21.432
chr5	1.16E+08	115753680	-7598	Sirt4	sirtuin 4	18.283
chr10	12559402	12559600	-7576	Utrn	utrophin	17.884
chr15	76903581	76904600	-7563	1700109K24Rik	RIKEN cDNA 1700109K24 gene	21.418
chr11	94744741	94745421	-7233	Col1a1	collagen, type I, alpha 1	15.471
chr10	12558712	12559391	-7126	Utrn	utrophin	17.894
chr19	5809292	5810260	-7105	Malat1	metastasis associated lung adenocarcinoma transcript 1 (non-	14.41
chr2	1.66E+08	166478470	-6921	Trp53rkb	transformation related protein 53 regulating kinase B	12.573
chr7	46882941	46883620	-6844	Spty2d1	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae)	13.817
chr5	1.13E+08	112560400	-6746	Tfip11	tuftelin interacting protein 11	10.692
chr3	88595501	88596520	-6731	Lmna	lamin A	21.583
chr8	87091681	87092271	-6647	Mir23a	microRNA 23a	22.831
chr11	98604761	98605780	-6589	Msl1	male-specific lethal 1 homolog (Drosophila)	18.836
chr10	12558152	12558701	-6501	Utrn	utrophin	22.157
chr10	39953061	39953740	-6319	Gtf3c6	general transcription factor IIIC, polypeptide 6, alpha	11.146
chr15	97742181	97742971	-6246	Vdr	vitamin D receptor	14.519
chr19	23201642	23202581	-6212	Klf9	Kruppel-like factor 9	12.677
chr7	1.27E+08	127270500	-6209	Fbrs	fibrosin	15.003
chr9	58012841	58013520	-6107	Mir6385	microRNA 6385	12.398
chr10	12557901	12558141	-6096	Utrn	utrophin	15.542
chr15	98453812	98454820	-6046	Cacnb3	calcium channel, voltage-dependent, beta 3 subunit	16.123
chr6	85345781	85346800	-5998	Rab11fip5	RAB11 family interacting protein 5 (class I)	26.127
chr5	1.43E+08	143089000	-5864	Tnrc18	trinucleotide repeat containing 18	17.809
chr8	87092282	87093371	-5797	Mir23a	microRNA 23a	20.174
chr17	27553261	27554541	-5770	D17Wsu92e	DNA segment, Chr 17, Wayne State University 92, expressed	40.312
chr7	1.41E+08	140975220	-5754	Ano9	anoctamin 9	11.043
chr7	1.42E+08	142203300	-5700	Ctsd	cathepsin D	17.237
chr18	13090341	13091020	-5670	Osbpl1a	oxysterol binding protein-like 1A	15.816
chr17	26778741	26779760	-5643	Itpr3	inositol 1,4,5-triphosphate receptor 3	12.447
chr3	96183961	96184640	-5632	Otud7b	OTU domain containing 7B	17.376
chr4	1.48E+08	148016361	-5619	Pgd	phosphogluconate dehydrogenase	28.39
chr10	75270962	75271870	-5157	Gstt4	glutathione S-transferase, theta 4	11.74
chr14	54747662	54748351	-5078	Ripk3	receptor-interacting serine-threonine kinase 3	16.293

chr4	1.48E+08	148015881	-5064	Pgd	phosphogluconate dehydrogenase	17.726
chr15	97677241	97677920	-5044	Hdac7	histone deacetylase 7	16.982
chr11	83351341	83351950	-4932	Ccl5	chemokine (C-C motif) ligand 5	19.878
chr3	58256152	58256960	-4820	1700007F19Rik	RIKEN cDNA 1700007F19 gene	18.469
chr8	87875381	87876400	-4810	Hook2	hook homolog 2 (Drosophila)	14.535
chr10	1.28E+08	127588060	-4304	Rbms2	RNA binding motif, single stranded interacting protein 2	15.09
chr9	1.08E+08	107573280	-4194	Sema3f	sema domain, immunoglobulin domain (Ig), short basic domain,	12.142
chr11	69233521	69234540	-4160	Kdm6b	KDM1 lysine (K)-specific demethylase 6B	27.02
chr8	1.27E+08	126536390	-4114	Rhou	ras homolog gene family, member U	14.183
chr5	1.23E+08	123398831	-4104	Setd1b	SET domain containing 1B	11
chr12	1.12E+08	111861700	-4048	Exoc3l4	exocyst complex component 3-like 4	16.018
chr8	13204241	13204920	-3979	Grtp1	GH regulated TBC protein 1	17.074
chr18	39616612	39617770	-3972	Nr3c1	nuclear receptor subfamily 3, group C, member 1	15.3
chr5	91839441	91840120	-3938	Ppbp	pro-platelet basic protein	15.009
chr2	26120122	26120840	-3915	Ccdc187	coiled-coil domain containing 187	18.561
chr7	28091572	28092160	-3878	Zfp36	zinc finger protein 36	11.861
chr19	5806181	5806860	-3849	Malat1	metastasis associated lung adenocarcinoma transcript 1 (non-	14.11
chr2	30538801	30540100	-3769	Mir3089	microRNA 3089	24.526
chr15	78633501	78634520	-3713	Card10	caspase recruitment domain family, member 10	14.046
chr5	1.23E+08	123399600	-3589	Setd1b	SET domain containing 1B	14.831
chr3	1.46E+08	145591400	-3519	Cyr61	cysteine rich protein 61	27.987
chr7	28091481	28091520	-3512	Zfp36	zinc finger protein 36	6
chr14	6967621	6968300	-3433	Pdhb	pyruvate dehydrogenase (lipoamide) beta	11.219
chr1	1.58E+08	157578920	-3404	Qsox1	quiescin Q6 sulfhydryl oxidase 1	11.222
chr17	17530741	17532091	-3390	Mir99b	microRNA 99b	14.615
chr4	1.32E+08	131786250	-3273	Sesn2	sestrin 2	16.363
chr3	1.45E+08	145040090	-3238	Clca2	chloride channel accessory 2	20.181
chr9	1.2E+08	119920700	-3237	Cx3cr1	chemokine (C-X3-C motif) receptor 1	14.063
chr14	49818042	49818770	-3200	Klhl33	kelch-like 33	12.202
chr17	56960652	56961860	-3179	Vav1	vav 1 oncogene	19.021
chr5	1.35E+08	134840600	-3065	Clip2	CAP-GLY domain containing linker protein 2	14.727
chr10	1.27E+08	126915200	-3028	Ndufa4l2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	13.691
chr13	23708541	23709140	-2917	Hist1h4c	histone cluster 1, H4c	11.13
chrX	69292341	69293020	-2857	Pnma5	paraneoplastic antigen family 5	14.412
chr9	21605122	21605920	-2484	Dock6	dedicator of cytokinesis 6	11.303
chr10	80832282	80833291	-2484	Nfic	nuclear factor I/C	15.296
chr4	1.29E+08	128766511	-2288	C77080	expressed sequence C77080	36.65
chr15	1.02E+08	101929280	-2252	Tns2	tensin 2	25.553
chr2	84543721	84544740	-2213	Mir130a	microRNA 130a	15.518
chrX	6907441	6908360	-2148	Mir684-1	microRNA 684-1	11.357
chr2	84848701	84849720	-2089	Tnks1bp1	tankyrase 1 binding protein 1	14.781
chr10	80782981	80783990	-1986	Fzr1	fizzy/cell division cycle 20 related 1 (Drosophila)	16.01
chr17	56111561	56112580	-1882	Ptprs	protein tyrosine phosphatase, receptor type, S	17.363
chr10	79388981	79389660	-1861	Tmem259	transmembrane protein 259	18.965
chr17	17532441	17533460	-1856	Mir99b	microRNA 99b	14.959
chr10	69490221	69491240	-1748	Ccdc6	coiled-coil domain containing 6	14.763
chr7	1.28E+08	127536701	-1722	Fbxl19	F-box and leucine-rich repeat protein 19	13.93
chr13	93632941	93633620	-1717	Zfyve16	zinc finger, FYVE domain containing 16	10.595
chr18	39614421	39615440	-1711	Nr3c1	nuclear receptor subfamily 3, group C, member 1	32.653
chr6	1.14E+08	113569180	-1709	Brk1	BRICK1, SCAR/WAVE actin-nucleating complex subunit	16.109
chr11	77307642	77308180	-1696	Git1	G protein-coupled receptor kinase-interactor 1	19.372
chr9	61168381	61169060	-1652	Tle3	transducin-like enhancer of split 3, homolog of Drosophila E(spl)	11.573
chr7	18982541	18983220	-1603	Bcl3	B cell leukemia/lymphoma 3	18.189
chr17	62567821	62568840	-1551	Efna5	ephrin A5	34.833
chr8	73466861	73467481	-1493	Ell	elongation factor RNA polymerase II	17.177
chr19	7121981	7122660	-1492	Macrod1	MACRO domain containing 1	20.801
chr1	1.82E+08	181796640	-1464	Cdc42bpa	CDC42 binding protein kinase alpha	13.169
chr10	98691121	98691800	-1459	Dusp6	dual specificity phosphatase 6	13.442
chr7	67823881	67824771	-1444	Igf1r	insulin-like growth factor I receptor	24.079
chr11	68913241	68914260	-1401	Per1	period circadian clock 1	22.308
chr17	86074401	86075080	-1371	Prkce	protein kinase C, epsilon	18.673
chr5	1.38E+08	137971660	-1364	Nyap1	neuronal tyrosine-phosphorylated phosphoinositide 3-kinase	16.389
chr9	22140461	22141450	-1347	Anln	anillin, actin binding protein	15.497
chr10	41965861	41967140	-1343	Foxo3	forkhead box O3	16.55
chr5	65715832	65716790	-1334	Ugdh	UDP-glucose dehydrogenase	18.513
chr14	54777061	54778080	-1296	Nfatc4	nuclear factor of activated T cells, cytoplasmic, calcineurin	12.419
chr4	1.3E+08	129679151	-1295	Tinagl1	tubulointerstitial nephritis antigen-like 1	30.095
chr3	84899712	84900720	-1288	Fbxw7	F-box and WD-40 domain protein 7	13.086
chr1	90900021	90900700	-1273	Sh3bp4	SH3-domain binding protein 4	14.865
chr19	46553141	46554291	-1243	Trim8	tripartite motif-containing 8	19.948
chr10	75789741	75790720	-1223	Dip2a	DIP2 disco-interacting protein 2 homolog A (Drosophila)	15.022
chr7	1.28E+08	127536720	-1207	Fbxl19	F-box and leucine-rich repeat protein 19	5
chr9	63820752	63821720	-1171	Smad6	SMAD family member 6	15.959
chr3	1.04E+08	103961120	-1147	Bcl2l15	BCLl2-like 15	15.402
chr10	80571802	80572180	-1142	Pias4	protein inhibitor of activated STAT 4	22.802
chr4	1.16E+08	115719000	-1135	Pik3r3	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3	16.654
chr2	91983601	91984280	-1081	Phf21a	PHD finger protein 21A	13.323
chr3	61450921	61451931	-1010	Rap2b	RAP2B, member of RAS oncogene family	19.871
chr11	79530081	79531100	2426	Mir193a	microRNA 193a	18.752
chr3	90701121	90701800	2639	S100a6	S100 calcium binding protein A6 (calcyclin)	24.58
chr2	1.52E+08	152431180	2978	Id1	inhibitor of DNA binding 1	18.858
chr10	80336322	80337240	3561	Gadd45b	growth arrest and DNA-damage-inducible 45 beta	18.611
chr19	5571921	5572940	4356	Ap5b1	adaptor-related protein complex 5, beta 1 subunit	27.67
chr19	9149061	9150080	5431	Scgb1a1	secretoglobin, family 1A, member 1 (uteroglobin)	16.27
chr15	88695121	88696140	5670	Pim3	proviral integration site 3	19.684
chr11	1.18E+08	117780080	5886	Socs3	suppressor of cytokine signaling 3	25.84
chr17	34573581	34574260	6292	Hspa1a	heat shock protein 1A	15.389
chr17	84088801	84089820	6963	Zfp36l2	zinc finger protein 36, C3H type-like 2	16.687
chr9	1.23E+08	123102051	7751	Tmem158	transmembrane protein 158	18.54
chr16	35420861	35421540	7966	1600019K03Rik	RIKEN cDNA 1600019K03 gene	12.644

chr19	5058521	5059361	8133	Rin1	Ras and Rab interactor 1	12.155
chr11	98422872	98423490	8800	Lrrc3c	leucine rich repeat containing 3C	11.641
chr6	1.46E+08	145813420	9553	Bhlhe41	basic helix-loop-helix family, member e41	18.928
chr10	80342341	80343360	9630	Gadd45b	growth arrest and DNA-damage-inducible 45 beta	17.451
chr16	21159561	21160540	9999	Mir7680	microRNA 7680	18.044
chr19	45111201	45112051	10739	Sfxn3	sideroflexin 3	16.282
chr5	1.37E+08	137388220	12954	Trim56	tripartite motif-containing 56	26.047
chr12	98683532	98684320	14241	Gpr65	G-protein coupled receptor 65	13.61
chr6	83422061	83422740	14987	B230319C09Rik	RIKEN cDNA B230319C09 gene	15.669
chr14	19428961	19429910	15657	Myoz1	myozenin 1	19.655
chr6	1.18E+08	117845700	16560	Zfp239	zinc finger protein 239	15.304
chr15	38417961	38418640	16836	Mir6951	microRNA 6951	24.663
chr4	1.41E+08	140532780	17360	Arhgef19	Rho guanine nucleotide exchange factor (GEF) 19	12.16
chr15	88664861	88665880	17958	Creld2	cysteine-rich with EGF-like domains 2	21.914
chr5	1.36E+08	136191030	18175	Hspb1	heat shock protein 1	13.083
chr4	1.08E+08	107845930	19351	Coa7	cytochrome c oxidase assembly factor 7	25.118
chr15	38414652	38415580	20020	Mir6951	microRNA 6951	14.774
chr13	23410021	23410700	20971	Abt1	activator of basal transcription 1	14.501
chr7	34338641	34339991	22285	Kctd15	potassium channel tetramerisation domain containing 15	24.363
chr7	37793381	37794400	22360	Ccne1	cyclin E1	29.176
chr11	52262472	52263100	22935	9530068E07Rik	RIKEN cDNA 9530068E07 gene	9.761
chr19	46577482	46578640	23102	Trim8	tripartite motif-containing 8	25.983
chr2	1.44E+08	143857400	23755	Gm5535	predicted gene 5535	11.639
chr16	21731932	21732621	23946	1300002E11Rik	RIKEN cDNA 1300002E11 gene	14.627
chr15	79880961	79881980	24364	Snord83b	small nucleolar RNA, C/D box 83B	17.216
chr5	1.35E+08	134635920	24415	Mir3965	microRNA 3965	18.8
chr16	33049701	33050380	24932	Mir1947	microRNA 1947	17.773
chr19	12077141	12077820	26305	Olfr1423	olfactory receptor 1423	18.224
chr12	56383561	56384240	26877	Nfkbia	nuclear factor of kappa light polypeptide gene enhancer in B cells	11.303
chr15	36706401	36707080	28781	Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	13.551
chr6	1.47E+08	146644110	29347	4930479D17Rik	RIKEN cDNA 4930479D17 gene	10.745
chr10	59316061	59317080	30557	Ddit4	DNA-damage-inducible transcript 4	14.805
chr3	86056721	86057400	31358	Prss48	protease, serine 48	16.947
chr4	1.15E+08	115483720	32603	Faah	fatty acid amide hydrolase	13.13
chr15	38401301	38402320	33326	Mir6951	microRNA 6951	22.872
chr17	84020461	84021231	33860	4933433H22Rik	RIKEN cDNA 4933433H22 gene	17.532
chr11	1.04E+08	103817640	34339	Arf2	ADP-ribosylation factor 2	12.733
chr5	23187321	23188340	36661	AI506816	expressed sequence AI506816	15.689
chr11	97216201	97217021	37970	Socs7	suppressor of cytokine signaling 7	18.841
chr6	84351032	84351950	38005	Gm10445	predicted gene 10445	12.371
chr11	97217032	97217220	38485	Socs7	suppressor of cytokine signaling 7	7.048
chr17	84056841	84057800	38953	Zfp36l2	zinc finger protein 36, C3H type-like 2	19.574
chr15	44497252	44497840	39016	Sybu	syntabulin (syntaxin-interacting)	17.697
chr13	1.13E+08	112846680	39114	Mier3	mesoderm induction early response 1, family member 3	15.028
chr11	1.22E+08	121558160	39133	Metrnl	meteorin, glial cell differentiation regulator-like	24.481
chr5	1.44E+08	143669241	39853	Grid2ip	glutamate receptor, ionotropic, delta 2 (Grid2) interacting protein 1	27.758
chr12	16875901	16876750	39880	E2f6	E2F transcription factor 6	19.064
chr9	1.03E+08	102638180	40093	Gm5627	predicted gene 5627	16.858
chr5	1.44E+08	143669931	40543	Grid2ip	glutamate receptor, ionotropic, delta 2 (Grid2) interacting protein 1	32.091
chr2	1.2E+08	120344310	42945	Haus2	HAUS augmin-like complex, subunit 2	12.801
chr8	25861081	25861670	43116	1810011O10Rik	RIKEN cDNA 1810011O10 gene	16.684
chr1	88301741	88302760	44750	1700019O17Rik	RIKEN cDNA 1700019O17 gene	22.154
chr12	56361461	56362140	44845	Psma6	proteasome (prosome, macropain) subunit, alpha type 6	14.383
chr8	28244032	28244820	45933	2310008N11Rik	RIKEN cDNA 2310008N11 gene	10.133
chr17	71155552	71156220	46375	Lpin2	lipin 2	22.359
chr1	88303441	88304620	46530	1700019O17Rik	RIKEN cDNA 1700019O17 gene	29.667
chr15	36904621	36905640	46861	Zfp706	zinc finger protein 706	18.033
chr15	38654261	38654940	48107	Atp6v1c1	ATPase, H+ transporting, lysosomal V1 subunit C1	21.128
chr12	87713881	87714850	59552	Irf2bpl	interferon regulatory factor 2 binding protein-like	19.736
chr8	4678061	4679080	65400	Zfp958	zinc finger protein 958	22.982
chr10	67241121	67242140	66389	Zfp365	zinc finger protein 365	12.658
chr5	1.26E+08	125563360	67152	Scarb1	scavenger receptor class B, member 1	19.574
chr6	88937312	88937880	69704	Tpra1	transmembrane protein, adipocyte asscociated 1	11.357
chr16	95924881	95925560	78403	1600002D24Rik	RIKEN cDNA 1600002D24 gene	12.574
chr2	45599101	45600120	80996	1700019E08Rik	RIKEN cDNA 1700019E08 gene	18.641
chr2	1.66E+08	166049540	83918	Gm11468	predicted gene 11468	21.583
chr9	30270541	30271220	93984	Snx19	sorting nexin 19	10.01
chr18	5141141	5142110	95038	Svil	supervillin	14.331
chr4	1.51E+08	151428120	105774	Nphp4	nephronophthisis 4 (juvenile) homolog (human)	9.325
chr8	1.3E+08	129712720	119631	Tomm20	translocase of outer mitochondrial membrane 20 homolog (yeast)	11.863
chr13	84820832	84821500	125760	Tmem161b	transmembrane protein 161B	11.987
chr12	27184792	27185430	129628	Cmpk2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	12.107
chr8	1.25E+08	124996920	132342	Mir7237	microRNA 7237	12.325
chr5	1.19E+08	118643000	136233	2410131K14Rik	RIKEN cDNA 2410131K14 gene	14.016
chr18	5989152	5990120	146460	Arhgap12	Rho GTPase activating protein 12	11.745
chr19	32970481	32971160	147246	Pten	phosphatase and tensin homolog	11.293
chr16	30691052	30691800	171956	Fam43a	family with sequence similarity 43, member A	15.643
chr17	85870061	85870720	183111	Srbd1	S1 RNA binding domain 1	12.649
chr5	50049361	50050040	297544	Adgra3	adhesion G protein-coupled receptor A3	18.009
chr1	7387202	7388540	308870	Pcmtd1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain	20.451
chr13	6192761	6193440	332365	Klf6	Kruppel-like factor 6	13.574
chr1	77743041	77743720	336903	Pax3	paired box 3	16.781
chr8	75064181	75064740	179	Tpm4	tropomyosin 4	11.401
chr8	75075222	75076080	11370	Tpm4	tropomyosin 4	11.878
chr19	47970582	47971161	1739	Itprip	inositol 1,4,5-triphosphate receptor interacting protein	17.193
chr10	95370562	95371360	610	Eea1	early endosome antigen 1	19.97
chr8	23650822	23651080	413	Ckap2	cytoskeleton associated protein 2	11.438
chr8	23650401	23650811	758	Ckap2	cytoskeleton associated protein 2	14.659
chr11	60990232	60991051	613	Usp22	ubiquitin specific peptidase 22	15.126
chr11	77309652	77310220	329	Git1	G protein-coupled receptor kinase-interactor 1	14.775

chr11	77313621	77314270	4338	Git1	G protein-coupled receptor kinase-interactor 1	16.529
chr10	83821561	83822321	48329	Nuak1	NUAK family, SNF1-like kinase, 1	17.434
chr7	44883401	44884760	211	Scaf1	SR-related CTD-associated factor 1	19.812
chr17	35449532	35450121	275	Mdc1	mediator of DNA damage checkpoint 1	26.178
chr7	5758581	5759051	242	Zfp787	zinc finger protein 787	15.362
chr4	59877061	59878340	209	Inip	INTS3 and NABP interacting protein	22.959
chr16	10359801	10360480	788	Tvp23a	trans-golgi network vesicle protein 23A	12.035
chr11	69227061	69228420	2130	Kdm6b	KDM1 lysine (K)-specific demethylase 6B	18.043
chr4	1.33E+08	132886960	-12206	Sfn	stratifin	13.638
chr15	78810301	78811641	660	Triobp	TRIO and F-actin binding protein	31.873
chr5	66043322	66044341	1175	N4bp2	NEDD4 binding protein 2	34.068
chr18	82656721	82657730	-31666	Mbp	myelin basic protein	15.386
chr17	45490981	45491920	-2706	Vegfa	vascular endothelial growth factor A	18.691
chr12	65836482	65837260	355	Gm527	predicted gene 527	20.392
chr8	74594301	74595320	5936	Unc13a	unc-13 homolog A (C. elegans)	19.396
chr3	88618562	88619300	609	Mex3a	mex3 homolog A (C. elegans)	12.148
chr10	58972772	58973680	38823	Mcu	mitochondrial calcium uniporter	15.672
chr15	98697241	98698560	1339	Kmt2d	lysine (K)-specific methyltransferase 2D	13.095
chr2	25185232	25186180	1929	Uap1l1	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	12.089
chr4	45534632	45535520	16852	Shb	src homology 2 domain-containing transforming protein B	13.171
chr13	43313281	43314161	1423	Gfod1	glucose-fructose oxidoreductase domain containing 1	14.545
chr13	43272902	43273500	41943	Gfod1	glucose-fructose oxidoreductase domain containing 1	12.794
chr10	5958501	5960200	917	Zbtb2	zinc finger and BTB domain containing 2	16.16
chr11	23157061	23157740	1359	Xpo1	exportin 1, CRM1 homolog (yeast)	17.009
chr17	63549532	63549740	193	Fer	fer (fms/fps related) protein kinase	17.707
chr5	1.45E+08	145219100	386	Smurf1	SMAD specific E3 ubiquitin protein ligase 1	19.872
chr5	1.45E+08	145218831	836	Smurf1	SMAD specific E3 ubiquitin protein ligase 1	25.914
chr5	1.45E+08	145218201	1386	Smurf1	SMAD specific E3 ubiquitin protein ligase 1	14.435
chr5	1.45E+08	145152460	-1643	Mir7039	microRNA 7039	21.008
chr10	80363872	80364780	31106	Gadd45b	growth arrest and DNA-damage-inducible 45 beta	17.888
chr14	19581282	19582681	659	Camk2g	calcium/calmodulin-dependent protein kinase II gamma	19.31
chr15	78786841	78788200	12541	Triobp	TRIO and F-actin binding protein	27.031
chr5	1.23E+08	123404700	1380	Setd1b	SET domain containing 1B	14.614
chr9	59861112	59861940	77700	Thsd4	thrombospondin, type I, domain containing 4	11.984
chr7	46825832	46826840	204	Uevld	UEV and lactate/malate dehyrogenase domains	11.133
chr1	1.36E+08	136178500	250	Tmem183a	transmembrane protein 183A	14.951
chr13	63440261	63440890	392	Fancc	Fanconi anemia, complementation group C	16.1
chr7	99143321	99144340	1401	Map6	microtubule-associated protein 6	15.716
chr5	1E+08	100218991	884	Hnrnpd	heterogeneous nuclear ribonucleoprotein D	15.827
chr10	75680632	75681960	285			35.554
chr11	1.03E+08	102991100	3532	Fmnl1	formin-like 1	12.607
chr6	6905741	6906710	207	Sdhaf3	succinate dehydrogenase complex assembly factor 3	13.655
chr4	1.35E+08	135129260	433	Srsf10	serine/arginine-rich splicing factor 10	21.029
chr6	1.35E+08	135216640	-2554	Gsg1	germ cell-specific gene 1	16.074
chr2	1.68E+08	167697390	4827	Fam65c	family with sequence similarity 65, member C	13.958
chr11	75472181	75472860	310	Myo1c	myosin IC	17.698
chr3	1.16E+08	116415451	820	Cdc14a	CDC14 cell division cycle 14A	17.043
chr7	29830241	29831450	137	Zfp382	zinc finger protein 382	17.141
chr17	73012961	73013980	603	Lclat1	lysocardiolipin acyltransferase 1	23.294
chr3	84667821	84668500	392	Arfip1	ADP-ribosylation factor interacting protein 1	10.589
chr3	96764341	96765520	9394	Ankrd35	ankyrin repeat domain 35	18.325
chr8	37716272	37717291	1252	Lonrf1	LON peptidase N-terminal domain and ring finger 1	13.225
chr8	1.2E+08	120083140	38568	Gan	giant axonal neuropathy	13.638
chr11	74465441	74466800	430	Cluh	clustered mitochondria (cluA/CLU1) homolog	20.017
chr10	1.2E+08	120380681	2019	Lemd3	LEM domain containing 3	13.323
chr5	72926941	72927960	519	Nipal1	NIPA-like domain containing 1	16.797
chr8	10993352	10993900	-14196	9530052E02Rik	RIKEN cDNA 9530052E02 gene	11.465
chr19	46110121	46111140	780	Pprc1	peroxisome proliferative activated receptor, gamma, coactivator-	30.612
chr18	10609701	10610121	439	Esco1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	19.262
chr2	84861281	84862220	10451	Tnks1bp1	tankyrase 1 binding protein 1	15.55
chr15	27968741	27969760	1187	Trio	triple functional domain (PTPRF interacting)	24.125
chr1	1.91E+08	191389060	133	Cenpf	centromere protein F	15.125
chr17	46970812	46971680	3004	Ccnd3	cyclin D3	13.907
chr17	46973822	46974740	6039	Ccnd3	cyclin D3	18.944
chr8	87689401	87690080	703	Nfix	nuclear factor I/X	13.923
chr3	94666881	94668240	560	Snx27	sorting nexin family member 27	17.478
chr18	69471562	69472200	791	Tcf4	transcription factor 4	11.406
chr11	1.2E+08	119730660	250	Chmp6	charged multivesicular body protein 6	18.985
chr12	21382261	21383270	24519	Asap2	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2	17.644
chr11	1.02E+08	102112671	283	Atxn7l3	ataxin 7-like 3	18.234
chr7	1.26E+08	125690860	183039	Gsg1l	GSG1-like	14.648
chr2	22890841	22891860	269	Acbd5	acyl-Coenzyme A binding domain containing 5	15.256
chr4	32794652	32795380	48968	Bach2	BTB and CNC homology 2	15.405
chr11	49087161	49088511	222	Mgat1	mannoside acetylglucosaminyltransferase 1	20.126
chr10	1.22E+08	122316360	72764	Mirlet7i	microRNA let7i	16.433
chrX	97424621	97425300	322	Snx12	sorting nexin 12	14.52
chr9	56874181	56875880	517	Sin3a	transcriptional regulator, SIN3A (yeast)	31.168
chr9	56870781	56872140	1283	Sin3a	transcriptional regulator, SIN3A (yeast)	21.142
chr11	50168021	50169380	396	Canx	calnexin	17.697
chr14	19267801	19267871	849	Anxa7	annexin A7	5.714
chr17	47386821	47387500	663	Foxp4	forkhead box P4	17.427
chr3	88578161	88579520	399	Lmna	lamin A	35.312
chr7	27397881	27398770	225	C030039L03Rik	RIKEN cDNA C030039L03 gene	16.948
chr5	36898502	36899520	481	Tbc1d14	TBC1 domain family, member 14	20.42
chr6	1.49E+08	149146100	292	Amn1	antagonist of mitotic exit network 1	14.862
chr11	1.17E+08	117033440	17349	Sept9	septin 9	15.106
chr11	1.17E+08	117048740	32479	Sept9	septin 9	14.712
chr3	1.08E+08	107887100	1765	Csf1	colony stimulating factor 1 (macrophage)	15.115
chr15	99675212	99675760	-27303	Lima1	LIM domain and actin binding 1	17.538
chr17	65683241	65683920	682	Ppp4r1	protein phosphatase 4, regulatory subunit 1	18.944

chr18	65013292	65014790	916	Nedd4l	neural precursor cell expressed, developmentally down-regulated	15.224
chr18	65045762	65046760	33136	Nedd4l	neural precursor cell expressed, developmentally down-regulated	18.964
chr19	5724241	5725260	1567	Ehbp1l1	EH domain binding protein 1-like 1	29.458
chr3	1.23E+08	122611140	755	Fnbp1l	formin binding protein 1-like	11.214
chr3	1.23E+08	122610811	1270	Fnbp1l	formin binding protein 1-like	15.101
chr5	1.11E+08	110849180	5033	Galnt9	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-	14.368
chr5	1.43E+08	143079480	3081	Tnrc18	trinucleotide repeat containing 18	10.897
chr1	66749481	66751180	473	Kansl1l	KAT8 regulatory NSL complex subunit 1-like	15.477
chr5	73011032	73011850	4296	Txk	TXK tyrosine kinase	13.556
chr3	10421742	10422700	441	Snx16	sorting nexin 16	13.348
chr3	41661221	41661900	131	Jade1	jade family PHD finger 1	14.38
chr8	74296121	74296800	254	Use1	unconventional SNARE in the ER 1 homolog (S. cerevisiae)	24.305
chr1	1.34E+08	133739340	996	Nucks1	nuclear casein kinase and cyclin-dependent kinase substrate 1	14.115
chr8	1.23E+08	123450940	24501	Gins2	GINS complex subunit 2 (Psf2 homolog)	18.942
chr8	1.23E+08	123450151	25016	Gins2	GINS complex subunit 2 (Psf2 homolog)	19.957
chr4	1.33E+08	132945100	473	Pigv	phosphatidylinositol glycan anchor biosynthesis, class V	27.756
chr4	1.51E+08	151030720	477	Acot7	acyl-CoA thioesterase 7	12.756
chr15	1E+08	100239970	11704	Slc11a2	solute carrier family 11 (proton-coupled divalent metal ion	64.82
chr17	34647701	34648380	6638	Msh5	mutS homolog 5 (E. coli)	18.789
chr11	5688201	5689140	184	Dbnl	drebrin-like	16.113
chr15	83291501	83292860	192	Pacsin2	protein kinase C and casein kinase substrate in neurons 2	17.291
chr2	1.52E+08	152362160	824	H13	histocompatibility 13	23.302
chr5	73571921	73572570	316	Ociad1	OCIA domain containing 1	16.416
chr5	1E+08	100281300	665	Enoph1	enolase-phosphatase 1	14.183
chr11	97514502	97515691	378	Pcgf2	polycomb group ring finger 2	17.812
chr13	78626361	78627040	-34864	A830082K12Rik	RIKEN cDNA A830082K12 gene	13.764
chr7	24080841	24081860	2327	Kcnn4	potassium intermediate/small conductance calcium-activated	20.528
chr15	76032122	76033191	920	Plec	plectin	22.137
chr15	76031141	76032111	1950	Plec	plectin	28.598
chr7	46971792	46972700	-21000	Mir7056	microRNA 7056	14.869
chr7	45377761	45378780	180	Nucb1	nucleobindin 1	16.91
chr7	45376401	45377080	1710	Nucb1	nucleobindin 1	11.258
chr13	56713062	56714040	261	Smad5	SMAD family member 5	14.201
chr6	1.25E+08	124931460	146	Cops7a	COP9 (constitutive photomorphogenic) homolog, subunit 7a	19.076
chr5	1.09E+08	108935320	590	Fgfrl1	fibroblast growth factor receptor-like 1	17.048
chr19	47015201	47015471	326	Nt5c2	5'-nucleotidase, cytosolic II	17.815
chr15	72769552	72770540	113022	Trappc9	trafficking protein particle complex 9	14.893
chr15	72887501	72888520	450	Trappc9	trafficking protein particle complex 9	30.487
chr9	1.14E+08	113556940	421	Pdcd6ip	programmed cell death 6 interacting protein	15.375
chr19	47399112	47400080	-72696	Mir6995	microRNA 6995	23.029
chr19	47368432	47369480	-42056	Mir6995	microRNA 6995	22.578
chr19	47368121	47368421	-41371	Mir6995	microRNA 6995	17.167
chr6	50040181	50040830	678	Mpp6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily	13.508
chr9	85639881	85640560	650	Tpbg	trophoblast glycoprotein	14.027
chr10	1.27E+08	126591860	1051	Arhgef25	Rho guanine nucleotide exchange factor (GEF) 25	12.446
chr10	1.27E+08	126591571	1396	Arhgef25	Rho guanine nucleotide exchange factor (GEF) 25	16.359
chr10	24559221	24560240	328	Med23	mediator complex subunit 23	16.5
chr6	1.18E+08	117873920	138	Hnrnpf	heterogeneous nuclear ribonucleoprotein F	21.635
chr9	1.22E+08	121610520	1279	Zfp651	zinc finger protein 651	14.744
chr7	29692541	29693520	315	Zfp568	zinc finger protein 568	20.016
chr12	83088861	83089500	316	Sipa1l1	signal-induced proliferation-associated 1 like 1	11.919
chr4	1.3E+08	129670900	6520	Tinagl1	tubulointerstitial nephritis antigen-like 1	10.529
chr19	53956222	53957600	248	Pdcd4	programmed cell death 4	19.666
chr7	98234841	98235520	1300	Tsku	tsukushi, small leucine rich proteoglycan	12.564
chr8	86221621	86222640	461	Elmod2	ELMO/CED-12 domain containing 2	22.176
chr6	38481541	38482540	988	Luc7l2	LUC7-like 2 (S. cerevisiae)	19.303
chr3	87258022	87258960	2183	Kirrel	kin of IRRE like (Drosophila)	17.82
chr4	12833642	12834660	167	Triqk	triple QxxK/R motif containing	16.64
chr5	1.21E+08	120776100	3837	Slc8b1	solute carrier family 8 (sodium/lithium/calcium exchanger),	16.072
chr17	25000532	25000540	495	Ube2i	ubiquitin-conjugating enzyme E2I	7
chr19	8852642	8853600	240	Taf6l	TAF6-like RNA polymerase II, p300/CBP-associated factor	18.028
chr19	45101001	45101980	603	Sfxn3	sideroflexin 3	19.946
chr17	34667421	34668380	809	Ddah2	dimethylarginine dimethylaminohydrolase 2	20.478
chr3	1.42E+08	142270620	58956	Pdlim5	PDZ and LIM domain 5	18.651
chr9	34719132	34720090	-146788	4930581F22Rik	RIKEN cDNA 4930581F22 gene	23.718
chr7	25489932	25491160	6947	Axl	AXL receptor tyrosine kinase	13.673
chr7	25489461	25489921	7802	Axl	AXL receptor tyrosine kinase	18.609
chr2	1.53E+08	153324360	286	Commd7	COMM domain containing 7	22.68
chr17	34772232	34773231	202	Prrc2a	proline-rich coiled-coil 2A	31.876
chr2	26137501	26138720	568	Gpsm1	G-protein signalling modulator 1 (AGS3-like, C. elegans)	15.82
chr11	93812801	93813820	1129	Spag9	sperm associated antigen 9	24.942
chr2	29889061	29890080	1087	Set	SET nuclear oncogene	24.805
chr7	4665232	4666160	466	U2af2	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 2	11.593
chr15	85894881	85895900	8897	Gramd4	GRAM domain containing 4	21.751
chr2	35078152	35078820	118	Gsn	gelsolin	18.666
chr10	1.21E+08	121256920	113583	BC048403	cDNA sequence BC048403	13.807
chr7	29617061	29618050	278	Zfp383	zinc finger protein 383	19.842
chr11	61395162	61396180	211	Epn2	epsin 2	19.507
chr11	33061892	33062991	765	Npm1	nucleophosmin 1	28.877
chr17	45745981	45746660	287	Tjap1	tight junction associated protein 1	15.295
chr3	90165762	90166300	583	Tpm3	tropomyosin 3, gamma	18.035
chr15	36736661	36737680	-1649	Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	31.954
chr9	59457501	59458370	3561	Pkm	pyruvate kinase, muscle	15.222
chr4	11485881	11486900	323	Rad54b	RAD54 homolog B (S. cerevisiae)	15.424
chr5	1.11E+08	111120840	395	Ttc28	tetratricopeptide repeat domain 28	20.932
chr5	1.11E+08	111480140	-91319			11.068
chr6	1.21E+08	120983900	63856	Mical3	microtubule associated monooxygenase, calponin and LIM	14.451
chr19	7549361	7550380	465	Rtn3	reticulon 3	20.484
chr16	10698101	10699800	164	Socs1	suppressor of cytokine signaling 1	24.769
chr11	1.18E+08	117639660	-2689	Afmid	arylformamidase	16.158

chr16	18270292	18271240	9021	Arvcf	armadillo repeat gene deleted in velo-cardio-facial syndrome	11.699
chr3	9995292	9996680	869	Fabp5	fatty acid binding protein 5, epidermal	20.468
chr19	4120572	4121140	719	Aip	aryl-hydrocarbon receptor-interacting protein	11.678
chr1	34072421	34073100	10855	Mir6896	microRNA 6896	13.296
chr6	17231552	17231880	531	Cav2	caveolin 2	16.155
chr10	92717321	92718340	23128	Elk3	ELK3, member of ETS oncogene family	20.509
chr4	1.16E+08	116125300	639	Nasp	nuclear autoantigenic sperm protein (histone-binding)	27.138
chr7	45084402	45084680	746	Tead2	TEA domain family member 2	12.586
chr4	1.18E+08	117514241	-86206	Artn	artemin	17.152
chr4	1.29E+08	128759700	4307	C77080	expressed sequence C77080	15.112
chr7	15545582	15546500	377	Sae1	SUMO1 activating enzyme subunit 1	13.955
chr16	21337041	21337720	279	Vps8	vacuolar protein sorting 8 homolog (S. cerevisiae)	14.701
chr4	81871321	81872340	105180	Nfib	nuclear factor I/B	32.172
chr15	8998441	8999481	819	Nadk2	NAD kinase 2, mitochondrial	37.981
chr15	8999492	9000140	1674	Nadk2	NAD kinase 2, mitochondrial	16.546
chr8	1.1E+08	110183460	762	Nfat5	nuclear factor of activated T cells 5	14.076
chr8	1.26E+08	126261040	730	Tcf25	transcription factor 25 (basic helix-loop-helix)	20.033
chr5	74566761	74567670	90192	Rasl11b	RAS-like, family 11, member B	19.333
chr19	9056642	9057841	912	Ahnak	AHNAK nucleoprotein (desmoyokin)	15.23
chr19	9127982	9128980	26520	Scgb1a1	secretoglobin, family 1A, member 1 (uteroglobin)	19.624
chr17	23868681	23869360	196	Pdpk1	3-phosphoinositide dependent protein kinase 1	18.859
chr3	65440282	65441160	-3363	A730090N16Rik	RIKEN cDNA A730090N16 gene	20.795
chr2	28463441	28464120	538	Tsc1	tuberous sclerosis 1	12.426
chr6	42281381	42282060	2285	Zyx	zyxin	20.518
chr3	30793122	30794390	831	Mynn	myoneurin	17.892
chr6	34726921	34727600	16676	Agbl3	ATP/GTP binding protein-like 3	13.708
chr5	77603981	77605190	499	Exoc1	exocyst complex component 1	16.442
chr5	89639981	89641000	889	Rufy3	RUN and FYVE domain containing 3	18.628
chr11	59861952	59862780	318	Pemt	phosphatidylethanolamine N-methyltransferase	13.146
chr10	1.27E+08	126694880	288	Ddit3	DNA-damage inducible transcript 3	39.899
chr7	43333341	43334020	2527	Vsig10l	V-set and immunoglobulin domain containing 10 like	15.047
chr2	33025002	33025900	-12519	Angptl2	angiopoietin-like 2	11.428
chr4	1.19E+08	119038760	793	Foxj3	forkhead box J3	28.985
chr11	53410601	53411500	258	Kif3a	kinesin family member 3A	17.604
chr19	57204342	57205320	-32557	Ablim1	actin-binding LIM protein 1	13.819
chr1	51859521	51860101	712	Myo1b	myosin IB	12.293
chr1	53296762	53297380	226	Asnsd1	asparagine synthetase domain containing 1	10.673
chr4	1.49E+08	148832960	14375	H6pd	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	13.463
chr2	1.51E+08	151186590	552	Nsfl1c	NSFL1 (p97) cofactor (p47)	19.152
chr18	43562501	43563520	607	Dpysl3	dihydropyrimidinase-like 3	21.472
chr11	32121841	32121951	397	Rhbdf1	rhomboid family 1 (Drosophila)	8.909
chr11	32120982	32121500	1052	Rhbdf1	rhomboid family 1 (Drosophila)	13.467
chr11	5762592	5763340	1097	Aebp1	AE binding protein 1	20.451
chr12	21619082	21620260	451	Adam17	a disintegrin and metallopeptidase domain 17	23.705
chr3	1.37E+08	136642600	34807	Ppp3ca	protein phosphatase 3, catalytic subunit, alpha isoform	18.515
chr14	46571501	46572180	652	Ktn1	kinectin 1	14.571
chr10	80229922	80230820	546	Oaz1-ps	ornithine decarboxylase antizyme 1, pseudogene	24.224
chr3	95772221	95773071	676	Adamtsl4	ADAMTS-like 4	16.506
chr19	38023962	38024920	84280	Myof	myoferlin	21.022
chr19	38080341	38081360	27871	Myof	myoferlin	20.203
chr11	60542441	60543181	647	Flii	flightless I homolog (Drosophila)	19.068
chr6	8295352	8296170	86473			21.226
chr1	1.35E+08	134855900	2492			12.515
chr7	24987961	24988980	-2469	Cic	capicua homolog (Drosophila)	12.815
chr1	36500732	36501591	942			10.533
chr1	36501602	36501720	442			9.661
chr4	57866641	57867320	-72322	Akap2	A kinase (PRKA) anchor protein 2	15.208
chr4	1.14E+08	114498740	350			13.842
chr9	57442782	57443000	899	Csk	c-src tyrosine kinase	16.087
chr9	57442292	57442771	1259	Csk	c-src tyrosine kinase	13.724
chr11	94891621	94892241	873	Itga3	integrin alpha 3	14.823
chr19	4214981	4216000	1101			17.202
chr14	32275521	32276141	419			19.339
chr8	74335561	74336440	999	Ankle1	ankyrin repeat and LEM domain containing 1	25.697
chr3	88228892	88228980	637			9.455
chr3	88231701	88232680	3891			18.772
chr5	94202781	94203760	34650			16.111
chr9	49549222	49550580	1398	Ncam1	neural cell adhesion molecule 1	21.217
chr9	49548881	49549211	2253	Ncam1	neural cell adhesion molecule 1	23.515
chr6	29384161	29384831	1138			15.567
chr9	96286981	96288000	537	Rnf7	ring finger protein 7	19.184
chr2	1.31E+08	130851231	595	1700037H04Rik	RIKEN cDNA 1700037H04 gene	24.125
chr1	1.83E+08	182853700	813	Ephx1	epoxide hydrolase 1, microsomal	16.273
chr11	1.09E+08	109468100	579			13.789
chr3	1.22E+08	122080740	43748	Abca4	ATP-binding cassette, sub-family A (ABC1), member 4	19.176
chr3	1.22E+08	122115050	78243	Abca4	ATP-binding cassette, sub-family A (ABC1), member 4	19.419
chr5	1.43E+08	143171280	954	Actb	actin, beta	32.987
chr15	1.01E+08	101020120	-2123	Mir6962	microRNA 6962	19.579
chr11	62067001	62067680	2161	Adora2b	adenosine A2b receptor	17.853
chr8	75168901	75169580	119	Ap1m1	adaptor-related protein complex AP-1, mu subunit 1	15.252
chr7	84256802	84257730	28957	Arnt2	aryl hydrocarbon receptor nuclear translocator 2	11.617
chr8	1.12E+08	111613110	8808	Zfhx3	zinc finger homeobox 3	22.798
chr5	1.49E+08	148709291	1347	Slc7a1	solute carrier family 7 (cationic amino acid transporter, y+ system),	13.9
chr17	35307641	35308421	612	Ddr1	discoidin domain receptor family, member 1	18.474
chr9	69252561	69253901	384	Anxa2	annexin A2	22.821
chr9	69256981	69258061	1413	Mir3109	microRNA 3109	58.602
chr9	69253912	69254940	1579	Anxa2	annexin A2	11.932
chr9	69258072	69258340	2098	Mir3109	microRNA 3109	16.843
chr17	87353481	87354160	1441	Calm2	calmodulin 2	21.514
chr11	96605221	96605811	290	Cbx1	chromobox 1	24.932

chr5	94342181	94343880	253	Ccng2	cyclin G2	16.974
chr19	5490321	5491340	375	Cfl1	cofilin 1, non-muscle	17.169
chr9	36475881	36476560	109	Chek1	checkpoint kinase 1	13.105
chr10	79570881	79572240	590	Cirbp	cold inducible RNA binding protein	28.65
chr10	79391701	79392720	481	Cnn2	calponin 2	21.154
chr11	94752901	94753971	1122	Col1a1	collagen, type I, alpha 1	21.047
chr5	1.3E+08	130314720	271	Crcp	calcitonin gene-related peptide-receptor component protein	20.268
chr7	1.44E+08	144280020	815	Cttn	cortactin	16.221
chr1	1.55E+08	155250120	268	Dhx9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	11.735
chr11	69837361	69838040	2900	Dlg4	discs, large homolog 4 (Drosophila)	14.89
chr11	69842612	69843780	8396	Dlg4	discs, large homolog 4 (Drosophila)	14.652
chr11	69845181	69846190	10885	Dlg4	discs, large homolog 4 (Drosophila)	12.674
chr9	44077452	44078960	366	Dpagt1	dolichyl-phosphate (UDP-N-acetylglucosamine)	23.166
chr8	1.26E+08	126083830	10991	Dpep1	dipeptidase 1 (renal)	12.538
chr6	1.25E+08	124722200	545	Atn1	atrophin 1	14.798
chr2	1.53E+08	153433500	262	Mapre1	microtubule-associated protein, RP/EB family, member 1	14.368
chr1	1.34E+08	133836170	575	Elk4	ELK4, member of ETS oncogene family	18.749
chr5	1.08E+08	108110140	5779	Evi5	ecotropic viral integration site 5	13.784
chr11	1.01E+08	101042900	322	Ezh1	enhancer of zeste 1 polycomb repressive complex 2 subunit	23.931
chr15	73248581	73249600	1357	Ptk2	PTK2 protein tyrosine kinase 2	20.433
chr5	1.43E+08	143227720	1545	Fscn1	fascin homolog 1, actin bundling protein (Strongylocentrotus	20.396
chr5	1.43E+08	143228071	2571	Fscn1	fascin homolog 1, actin bundling protein (Strongylocentrotus	6
chr5	1.43E+08	143229131	3111	Fscn1	fascin homolog 1, actin bundling protein (Strongylocentrotus	49.28
chr5	1.43E+08	143230060	4106	Fscn1	fascin homolog 1, actin bundling protein (Strongylocentrotus	34.841
chr7	27878641	27879540	582	Fbl	fibrillarin	17.65
chr6	34284241	34284730	163	Akr1b8	aldo-keto reductase family 1, member B8	14.8
chr9	32268041	32268720	22637	Fli1	Friend leukemia integration 1	13.591
chr14	33140792	33141160	1157	Glud1	glutamate dehydrogenase 1	14.125
chr4	1.17E+08	117333661	471	Slc6a9	solute carrier family 6 (neurotransmitter transporter, glycine),	
chr4	1.17E+08	117335020	1156	Slc6a9	solute carrier family 6 (neurotransmitter transporter, glycine),	50.803
chr4	1.17E+08	117364750	6067	Ccdc24	coiled-coil domain containing 24	17.82
chr9	1.07E+08	107492360	1763	Gnai2	guanine nucleotide binding protein (G protein), alpha inhibiting 2	25.688
chr11	59007681	59007861	376	Guk1	guanylate kinase 1	11.833
chr3	87996421	87997100	4512	Hdgf	hepatoma-derived growth factor	23.688
chr11	54709741	54710760	389	Hint1	histidine triad nucleotide binding protein 1	14.794
chr11	53142681	53144040	542	Hspa4	heat shock protein 4	15.719
chr4	1.37E+08	136746640	5317	Hspg2	perlecan (heparan sulfate proteoglycan 2)	11.902
chr16	91435521	91436731	173	Ifngr2	interferon gamma receptor 2	11.983
chr16	91436742	91437560	1198	Ifngr2	interferon gamma receptor 2	17.677
chr18	13115841	13116520	759	Impact	impact, RWD domain protein	15.442
chr18	13117472	13117880	2255	Impact	impact, RWD domain protein	19.142
chr11	97003021	97003700	622	Kpnb1	karyopherin (importin) beta 1	19.116
chr2	1.53E+08	153002040	18843	Kif3b	kinesin family member 3B	14.651
chr16	35903062	35904260	551	Kpna1	karyopherin (importin) alpha 1	12.157
chr5	1.41E+08	140864380	4225	Lfng	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	21.436
chr15	78753861	78756220	1060	Lgals1	lectin, galactose binding, soluble 1	24.955
chr10	1.27E+08	127023741	736	Lrp1	low density lipoprotein receptor-related protein 1	21.974
chr10	36826172	36827440	1536	Marcks	myristoylated alanine rich protein kinase C substrate	18.013
chr18	73827662	73828280	1139	Smad4	SMAD family member 4	10.736
chr2	1.28E+08	128430990	40177	Mertk	c-mer proto-oncogene tyrosine kinase	14.096
chr3	1.05E+08	104946091	435	Mov10	Moloney leukemia virus 10	13.939
chr9	99197722	99198740	-30349	Esyt3	extended synaptotagmin-like protein 3	16.347
chr9	1.1E+08	109778860	1461	Map4	microtubule-associated protein 4	18.497
chr13	1.01E+08	100616540	393	Map1b	microtubule-associated protein 1B	12.897
chr13	1.01E+08	100616181	1078	Map1b	microtubule-associated protein 1B	13.42
chr6	83282092	83283440	496	Mthfd2	methylenetetrahydrofolate dehydrogenase (NAD+ dependent),	34.164
chr12	8948142	8948800	1156	Laptm4a	lysosomal-associated protein transmembrane 4A	16.388
chr10	80334181	80334860	1300	Gadd45b	growth arrest and DNA-damage-inducible 45 beta	14.717
chr15	66798441	66798991	594	Ndrg1	N-myc downstream regulated gene 1	37.182
chr10	80812312	80812900	6820	Mir1191b	microRNA 1191b	13.713
chr7	1.42E+08	141893761	11183	Dusp8	dual specificity phosphatase 8	14.389
chr11	76214061	76214911	850	Nxn	nucleoredoxin	15.588
chr7	25005641	25007000	395	Pafah1b3	platelet-activating factor acetylhydrolase, isoform 1b, subunit 3	30.617
chr5	1.38E+08	137840811	406	Pcolce	procollagen C-endopeptidase enhancer protein	10
chr10	79726261	79727280	-3093	2310011J03Rik	RIKEN cDNA 2310011J03 gene	22.175
chr5	1.39E+08	139248271	789	Pdgfa	platelet derived growth factor, alpha	15.935
chr7	34620841	34621860	183	Pepd	peptidase D	16.387
chr10	77411881	77413240	365	Pfkl	phosphofructokinase, liver, B-type	25.233
chr3	31186841	31187520	531	Prkci	protein kinase C, iota	11.642
chr6	89327652	89328200	328	Plxna1	plexin A1	14.641
chr6	89326532	89327641	1168	Plxna1	plexin A1	29.024
chr1	1.96E+08	196377200	56248	Plxna2	plexin A2	14.965
chr19	5962241	5962920	1626	Pola2	polymerase (DNA directed), alpha 2	13.903
chr19	5945662	5945920	18415	Pola2	polymerase (DNA directed), alpha 2	15.942
chr19	5944901	5945651	18930	Pola2	polymerase (DNA directed), alpha 2	24.853
chr13	1.14E+08	113923080	595	Plpp1	phospholipid phosphatase 1	20.481
chr11	60749652	60750180	1664	Map2k3	mitogen-activated protein kinase kinase 3	15.013
chr11	97096181	97096391	380	Npepps	aminopeptidase puromycin sensitive	18.476
chr1	88359541	88360440	2083	Ptma	prothymosin alpha	12.84
chr17	33366241	33367260	616	Rab11b	RAB11B, member RAS oncogene family	27.64
chr11	53549661	53550680	572	Rad50	RAD50 homolog (S. cerevisiae)	17.259
chr12	80352201	80353100	136459	Rad51b	RAD51 homolog B	18.15
chr11	98753992	98754990	683	Rara	retinoic acid receptor, alpha	33.198
chr2	1.05E+08	105199781	692	Rcn1	reticulocalbin 1	11.967
chr17	65783541	65784900	246	Ralbp1	ralA binding protein 1	28.009
chr6	70720872	70721700	468	Rpia	ribose 5-phosphate isomerase A	16.671
chr6	70720132	70720861	1258	Rpia	ribose 5-phosphate isomerase A	15.85
chr7	81216481	81217810	1602	Rps17	ribosomal protein S17	18.798
chr2	13188601	13189280	328	Rsu1	Ras suppressor protein 1	12.202
chr10	60541132	60542611	1151	Sgpl1	sphingosine phosphate lyase 1	26.399

chr1	1.09E+08	108624330	326	Vps4b	vacuolar protein sorting 4b (yeast)	13.803
chr7	15941581	15942940	2392	Slc1a5	solute carrier family 1 (neutral amino acid transporter), member 5	23.489
chr11	32433621	32433631	360	Stk10	serine/threonine kinase 10	4
chr11	32433642	32434300	705	Stk10	serine/threonine kinase 10	17.953
chr13	34084932	34085680	167	Tubb2a	tubulin, beta 2A class IIA	18.501
chr13	34084321	34084921	852	Tubb2a	tubulin, beta 2A class IIA	12.433
chr11	68904892	68905080	263	Vamp2	vesicle-associated membrane protein 2	10.84
chr4	43020302	43021420	746	Vcp	valosin containing protein	23.773
chr15	97735721	97736400	270	Vdr	vitamin D receptor	18.635
chr11	75549701	75550370	953	Ywhae	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	11.531
chr11	49046701	49047380	117	Zfp62	zinc finger protein 62	18.309
chr5	21295622	21296491	933	Dnajc2	DnaJ (Hsp40) homolog, subfamily C, member 2	16.19
chr12	1.13E+08	113121400	1194	Akt1	thymoma viral proto-oncogene 1	24.997
chr3	1.46E+08	145862720	708	Bcl10	B cell leukemia/lymphoma 10	23.162
chr15	83391882	83392721	962	Tspo	translocator protein	22.049
chr1	1.62E+08	162049780	398	Cacybp	calcyclin binding protein	20.805
chr1	1.41E+08	141272380	686	Aspm	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	13.838
chr7	29902321	29903421	937	Capns1	calpain, small subunit 1	18.491
chr18	35244741	35245561	265	Ctnna1	catenin (cadherin associated protein), alpha 1	13.134
chr18	35245572	35245760	780	Ctnna1	catenin (cadherin associated protein), alpha 1	12.059
chr11	22890632	22891520	483	Cct4	chaperonin containing Tcp1, subunit 4 (delta)	32.979
chr7	1.41E+08	141319640	278	Cd151	CD151 antigen	16.983
chr8	1.1E+08	109515360	22604	Cdh1	cadherin 1	12.396
chr2	1.81E+08	180530620	2626	Col9a3	collagen, type IX, alpha 3	13.386
chr11	95821132	95821520	708	Igf2bp1	insulin-like growth factor 2 mRNA binding protein 1	10.237
chr11	95820501	95821121	1223	Igf2bp1	insulin-like growth factor 2 mRNA binding protein 1	13.823
chr8	1.15E+08	114618651	613	Bcar1	breast cancer anti-estrogen resistance 1	30.33
chr14	65820941	65821620	1430	Dpysl2	dihydropyrimidinase-like 2	15.334
chr16	17804242	17805460	440	Dgcr2	DiGeorge syndrome critical region gene 2	11.076
chr13	93456821	93457500	-1404	Msh3	mutS homolog 3 (E. coli)	14.311
chr2	13461662	13462640	366	Trdmt1	tRNA aspartic acid methyltransferase 1	13.648
chr19	6278101	6278131	1220	Ehd1	EH-domain containing 1	7.333
chr19	6278142	6278780	1565	Ehd1	EH-domain containing 1	15.013
chr6	1.35E+08	135330540	1406	Emp1	epithelial membrane protein 1	15.363
chr4	1.41E+08	140583880	10243	Epha2	Eph receptor A2	15.001
chr4	1.36E+08	136081260	27168	Ephb2	Eph receptor B2	13.426
chr4	1.36E+08	136008800	99608	Ephb2	Eph receptor B2	12.577
chr7	1.44E+08	144391880	456	Fadd	Fas (TNFRSF6)-associated via death domain	31.553
chr7	80259472	80260400	1523	Fes	feline sarcoma oncogene	16.962
chr17	28212861	28213540	538	Fkbp5	FK506 binding protein 5	23.585
chr19	10050061	10050411	545	Fth1	ferritin heavy polypeptide 1	15.2
chr5	1.41E+08	141082681	564	Gna12	guanine nucleotide binding protein, alpha 12	17.536
chr3	1.08E+08	108274360	358	Gnai3	guanine nucleotide binding protein (G protein), alpha inhibiting 3	21.234
chr5	1.38E+08	137763240	117	Gnb2	guanine nucleotide binding protein (G protein), beta 2	13.062
chr5	1.38E+08	137761540	1817	Gnb2	guanine nucleotide binding protein (G protein), beta 2	26.128
chr11	1.02E+08	102026520	20194	Mir8101	microRNA 8101	19.55
chr3	89998341	89998931	487			14.034
chr7	1.02E+08	101711951	169	Inppl1	inositol polyphosphate phosphatase-like 1	17.653
chr14	53529292	53530531	1955	Ajuba	ajuba LIM protein	18.738
chr19	23208932	23210501	1393	Klf9	Kruppel-like factor 9	22.793
chr19	23210512	23210991	2428	Klf9	Kruppel-like factor 9	15.681
chr4	1.19E+08	119431370	118422	Hivep3	human immunodeficiency virus type I enhancer binding protein 3	19.493
chr11	97615862	97617060	699	Lasp1	LIM and SH3 protein 1	20.553
chr4	1.29E+08	129059240	1215	Mir8119	microRNA 8119	19.873
chr9	58097222	58098410	13533	Loxl1	lysyl oxidase-like 1	19.251
chr10	80546001	80547260	7230	Zbtb7a	zinc finger and BTB domain containing 7a	21.133
chr17	34793752	34794630	2301	Lst1	leukocyte specific transcript 1	23.615
chr18	76367442	76368080	695	Smad2	SMAD family member 2	14.842
chr11	1.2E+08	120449080	897	Mafg	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein	15.141
chr10	1.17E+08	117113680	411	Mdm2	transformed mouse 3T3 cell double minute 2	14.58
chr11	74647432	74648700	947	Mnt	max binding protein	23.986
chr11	74654492	74655160	7707	Mnt	max binding protein	18.228
chr9	1E+08	100355760	109	Nck1	non-catalytic region of tyrosine kinase adaptor protein 1	13.029
chr1	1.94E+08	193523130	587	Nek2	NIMA (never in mitosis gene a)-related expressed kinase 2	20.652
chr12	56409741	56410451	681	Nfkbia	nuclear factor of kappa light polypeptide gene enhancer in B cells	21.155
chr9	1.22E+08	121568570	246	Nktr	natural killer tumor recognition sequence	14.474
chr3	98099152	98099520	393	Notch2	notch 2	13.562
chr1	93288521	93289321	813	Per2	period circadian clock 2	15.238
chr11	70469761	70470780	575	Pfn1	profilin 1	22.182
chr5	8804332	8804980	503	Abcb1b	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	16.755
chr14	29454881	29454931	311	Prkcd	protein kinase C, delta	4.4
chr7	24171281	24171960	360	Plaur	plasminogen activator, urokinase receptor	12.445
chr15	1.02E+08	102084660	1406	Rarg	retinoic acid receptor, gamma	21.345
chr15	1.02E+08	102074091	938	Rarg	retinoic acid receptor, gamma	14.051
chr2	1.57E+08	156896060	255	Rbl1	retinoblastoma-like 1 (p107)	16.486
chr15	11939781	11940800	442	Sub1	SUB1 homolog (S. cerevisiae)	23.789
chr4	1.29E+08	129244091	801	Khdrbs1	KH domain containing, RNA binding, signal transduction	19.614
chr11	1.17E+08	116668620	1244	Srsf2	serine/arginine-rich splicing factor 2	15.067
chr7	18253921	18254600	1194	Six5	sine oculis-related homeobox 5	19.691
chr4	1.54E+08	154017810	48960	Ski	ski sarcoma viral oncogene homolog (avian)	28.375
chr4	1.19E+08	118607300	444	Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1	22.212
chr8	1.25E+08	124785100	9186	Slc7a5	solute carrier family 7 (cationic amino acid transporter, y+ system),	21.149
chr10	75364262	75365760	319	Smarcb1	SWI/SNF related, matrix associated, actin dependent regulator of	40.386
chr5	1.25E+08	125430420	38283	Ncor2	nuclear receptor co-repressor 2	15.552
chr11	1.13E+08	112599840	1030	Sox9	SRY (sex determining region Y)-box 9	16.166
chr15	81874202	81874751	377	Nhp2l1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	15.678
chr3	1.09E+08	108968640	428	Stxbp3	syntaxin binding protein 3	22.744
chr11	1E+08	100136771	360	Eif1	eukaryotic translation initiation factor 1	16.354
chr7	1.41E+08	141246800	2850	Taldo1	transaldolase 1	17.164
chr6	1.28E+08	128266360	752	Tead4	TEA domain family member 4	20.55

chr7	11924872	11925760	985	Trim28	tripartite motif-containing 28	12.304
chr11	1.18E+08	118143880	15254	BC100451	cDNA sequence BC100451	24.433
chr10	85732392	85733040	2505	Timp3	tissue inhibitor of metalloproteinase 3	15.068
chr4	43581292	43581880	2097	Tln1	talin 1	16.871
chr15	98780612	98781560	449	Tuba1a	tubulin, alpha 1A	21.345
chr15	98779861	98780601	1304	Tuba1a	tubulin, alpha 1A	14.581
chr17	35444321	35445680	1354	Tubb5	tubulin, beta 5 class I	20.854
chr5	1.47E+08	147105181	684	Usp12	ubiquitin specific peptidase 12	16.429
chr17	34609852	34609960	943	Vars	valyl-tRNA synthetase	12.889
chr5	38849492	38849760	218	Wdr1	WD repeat domain 1	8.989
chr5	38848741	38849481	733	Wdr1	WD repeat domain 1	17.635
chr4	1.19E+08	118792291	679	Ybx1	Y box protein 1	35.562
chr8	1.15E+08	114531040	584	Zfp1	zinc finger protein 1	22.571
chr8	1.15E+08	114741160	333	Cfdp1	craniofacial development protein 1	19.443
chr17	8694481	8695160	54901	Pde10a	phosphodiesterase 10A	20.831
chr3	57823461	57824820	149			39.192
chr5	34842432	34843200	175	Sh3bp2	SH3-domain binding protein 2	12.954
chr8	74507642	74508560	10185	Slc27a1	solute carrier family 27 (fatty acid transporter), member 1	10.786
chr2	34931261	34932170	214	Cntrl	centriolin	12.856
chr11	1.01E+08	101281531	1243	Vat1	vesicle amine transport protein 1 homolog (T californica)	37.639
chr19	3323841	3324520	879	Cpt1a	carnitine palmitoyltransferase 1a, liver	11.402
chr19	3324861	3326100	2179	Cpt1a	carnitine palmitoyltransferase 1a, liver	20.495
chr6	87008041	87009640	360	Gfpt1	glutamine fructose-6-phosphate transaminase 1	16.752
chr17	24277772	24278720	696	Pkd1	polycystic kidney disease 1 homolog	17.523
chr8	1.09E+08	108826520	1341	Psmb10	proteasome (prosome, macropain) subunit, beta type 10	21.906
chr15	1.02E+08	102234940	250	Sp1	trans-acting transcription factor 1	16.647
chr15	38243201	38244560	1420	Klf10	Kruppel-like factor 10	18.414
chr11	1.2E+08	120309000	414	Slc25a10	solute carrier family 25 (mitochondrial carrier, dicarboxylate	16.926
chr16	20327581	20328260	12017	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	13.792
chr17	69062161	69063100	918	Epb41l3	erythrocyte membrane protein band 4.1 like 3	14.717
chr6	82738702	82739851	836	Hk2	hexokinase 2	17.758
chr2	1.37E+08	136806480	1660	Jag1	jagged 1	15.388
chr2	1.37E+08	136806111	2170	Jag1	jagged 1	21.72
chr3	1.22E+08	122490100	43943	Mir7657	microRNA 7657	25.227
chr4	1.09E+08	108959120	15827	Rnf11	ring finger protein 11	22.338
chr7	81807061	81807721	581	Hdgfrp3	hepatoma-derived growth factor, related protein 3	12.652
chr11	1.19E+08	118856520	823	Cbx8	chromobox 8	17.467
chr17	65510861	65511540	1898	Vapa	vesicle-associated membrane protein, associated protein A	9.725
chr6	6166581	6167380	193	Slc25a13	solute carrier family 25 (mitochondrial carrier, adenine nucleotide	15.513
chr11	87884742	87885860	827	Vezf1	vascular endothelial zinc finger 1	18.708
chr7	80659992	80660920	16388	Iqgap1	IQ motif containing GTPase activating protein 1	18.714
chr14	1.01E+08	100541400	564	Uchl3	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	16.849
chr2	1.04E+08	103597480	1027	Caprin1	cell cycle associated protein 1	21.673
chr5	1.26E+08	125593960	36453	Scarb1	scavenger receptor class B, member 1	9.541
chr16	32564861	32565540	810	Tnk2	tyrosine kinase, non-receptor, 2	21.592
chr17	28349541	28350220	163	Srpk1	serine/arginine-rich protein specific kinase 1	18.859
chr15	85163881	85165240	413	Atxn10	ataxin 10	16.367
chr1	1.54E+08	154299480	88189	Rgl1	ral guanine nucleotide dissociation stimulator,-like 1	19.465
chr3	1.52E+08	152060920	42835	Gipc2	GIPC PDZ domain containing family, member 2	27.631
chr5	1.14E+08	114032600	388	Sart3	squamous cell carcinoma antigen recognized by T cells 3	16.122
chr9	75345352	75345360	210	Tmod3	tropomodulin 3	8
chr9	75344681	75345341	555	Tmod3	tropomodulin 3	17.712
chr3	98423881	98424900	984	Phgdh	3-phosphoglycerate dehydrogenase	21.833
chr7	45573712	45574280	707	Dbp	D site albumin promoter binding protein	19.31
chr7	45575242	45575300	1982	Dbp	D site albumin promoter binding protein	7.155
chr13	52990701	52991380	2431	Nfil3	nuclear factor, interleukin 3, regulated	13.567
chr9	1.18E+08	118356350	839	Golga4	golgi autoantigen, golgin subfamily a, 4	15.293
chr1	1.33E+08	133012380	15815			17.019
chr9	1.1E+08	109690800	260	Nme6	NME/NM23 nucleoside diphosphate kinase 6	17.311
chr3	96782082	96783380	250	Pias3	protein inhibitor of activated STAT 3	21.625
chr7	27195581	27196260	207	Sertad1	SERTA domain containing 1	19.019
chr7	27216702	27217570	9052	Prx	periaxin	21.145
chr7	1.31E+08	130756860	29169	Htra1	HtrA serine peptidase 1	12.86
chr5	64577221	64577900	68068	Tbc1d1	TBC1 domain family, member 1	14.44
chr4	1.34E+08	133741720	644	Stmn1	stathmin 1	24.38
chr9	56793261	56794620	835	Ptpn9	protein tyrosine phosphatase, non-receptor type 9	26.791
chrX	44696502	44697420	10798	Elf4	E74-like factor 4 (ets domain transcription factor)	17.781
chr6	72810661	72811680	18318	Kcmf1	potassium channel modulatory factor 1	16.824
chr19	6140602	6141420	126	Arl2	ADP-ribosylation factor-like 2	23.203
chr9	65922012	65922940	416	Snx1	sorting nexin 1	21.997
chr10	41964161	41965481	336	Foxo3	forkhead box O3	14.424
chrX	6827201	6828220	639	Plp2	proteolipid protein 2	13.165
chr9	1.03E+08	102582960	4290	Amotl2	angiomotin-like 2	19.586
chr9	1.03E+08	102584800	6230	Amotl2	angiomotin-like 2	20.016
chr4	1.48E+08	147943761	141	Pex14	peroxisomal biogenesis factor 14	13.741
chr19	4810372	4811680	608	Gm21992	predicted gene 21992	16.743
chr3	1.38E+08	137856400	118	Lamtor3	late endosomal/lysosomal adaptor, MAPK and MTOR activator 3	13.803
chr19	6906472	6907440	715	Rps6ka4	ribosomal protein S6 kinase, polypeptide 4	15.142
chr8	87811461	87812480	8530	Gm38426	predicted gene, 38426	13.147
chr3	55330241	55331260	295	Dclk1	doublecortin-like kinase 1	18.232
chr17	53032861	53033800	1430	Kat2b	K(lysine) acetyltransferase 2B	15.628
chr17	46017652	46018660	-1078	Mir6976	microRNA 6976	12.534
chr3	37611552	37612820	687	Spata5	spermatogenesis associated 5	35.661
chr7	63815912	63817391	1214	Klf13	Kruppel-like factor 13	37.972
chr7	63815242	63815901	2294	Klf13	Kruppel-like factor 13	27.822
chr9	44130301	44131320	325	Hyou1	hypoxia up-regulated 1	16.288
chr19	5460252	5461380	209	Fibp	fibroblast growth factor (acidic) intracellular binding protein	24.984
chr10	82502732	82503380	87760	Chst11	carbohydrate sulfotransferase 11	12.875
chr11	97266622	97267540	831	Arhgap23	Rho GTPase activating protein 23	29.874
chr5	33652232	33653200	287	Maea	macrophage erythroblast attacher	16.134

chr10	79550821	79552331	175	Midn	midnolin	19.291
chr9	1.06E+08	106312900	281	Pcbp4	poly(rC) binding protein 4	16.591
chr12	52656272	52657150	-43177	Strn3	striatin, calmodulin binding protein 3	13.866
chr19	10108881	10110240	967	Fads3	fatty acid desaturase 3	18.776
chr1	1.53E+08	153448460	-69521			15.185
chr8	97276041	97277060	921	Herpud1	homocysteine-inducible, endoplasmic reticulum stress-inducible,	24.879
chr9	57359021	57359980	419	Scamp2	secretory carrier membrane protein 2	21.384
chr17	23453782	23454900	383	Pkmyt1	protein kinase, membrane associated tyrosine/threonine 1	19.568
chr4	1.49E+08	149081841	674	Eno1	enolase 1, alpha non-neuron	10.853
chr10	80508601	80510290	369	Map2k2	mitogen-activated protein kinase kinase 2	35.521
chr17	71430832	71431960	318	Ndc80	NDC80 homolog, kinetochore complex component (S. cerevisiae)	17.629
chr4	1.4E+08	140235710	1864	Sdhb	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	17.219
chr19	41967221	41967900	2378	Pgam1	phosphoglycerate mutase 1	13.041
chr8	49172402	49173180	1185	Ing2	inhibitor of growth family, member 2	16.329
chr6	49142581	49143940	1280	Igf2bp3	insulin-like growth factor 2 mRNA binding protein 3	22.533
chr5	1.13E+08	112500900	4437			15.839
chr1	75062141	75062971	983	Abcb6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	18.012
chr19	45835762	45836601	421	Mgea5	meningioma expressed antigen 5 (hyaluronidase)	18.601
chr9	61743662	61744680	634	Kif23	kinesin family member 23	21.575
chr17	55667352	55668540	336	Ubxn6	UBX domain protein 6	21.957
chr17	66414921	66415600	9355	Rab12	RAB12, member RAS oncogene family	12.284
chr12	4832472	4832760	347	Sf3b6	splicing factor 3B, subunit 6	15.663
chr16	32339781	32340460	671	Tctex1d2	Tctex1 domain containing 2	17.897
chr15	1.02E+08	102289680	1966	Prr13	proline rich 13	31.097
chr16	56000612	56001340	545			13.563
chr3	1.31E+08	130698191	823	Ostc	oligosaccharyltransferase complex subunit	21.012
chr10	79442021	79443320	118	Polr2e	polymerase (RNA) II (DNA directed) polypeptide E	19.15
chr8	73434901	73435920	318	2810428I15Rik	RIKEN cDNA 2810428I15 gene	18.574
chr4	53032861	53033880	346	Nipsnap3b	nipsnap homolog 3B (C. elegans)	19.947
chr4	1.14E+08	114485480	454	Cmpk1	cytidine monophosphate (UMP-CMP) kinase 1	17.745
chr11	98402442	98403140	544	Ormdl3	ORM1-like 3 (S. cerevisiae)	12.401
chr3	1.03E+08	103125400	259	Sike1	suppressor of IKBKE 1	20.054
chr2	1.63E+08	163110921	500	Oser1	oxidative stress responsive serine rich 1	24.627
chr3	1.3E+08	129929980	32442	Ccdc109b	coiled-coil domain containing 109B	15.771
chr3	1.3E+08	129929581	32787	Ccdc109b	coiled-coil domain containing 109B	15.357
chr16	8586701	8587720	264	Carhsp1	calcium regulated heat stable protein 1	18.572
chr8	1.1E+08	110326600	409	Wwp2	WW domain containing E3 ubiquitin protein ligase 2	26.115
chr3	69131861	69133220	131	Trim59	tripartite motif-containing 59	16.712
chr7	44114902	44115340	357	2410002F23Rik	RIKEN cDNA 2410002F23 gene	16.568
chr7	34096561	34097240	1400	Lsm14a	LSM14 homolog A (SCD6, S. cerevisiae)	16.016
chrX	1.08E+08	107581040	74317	Rps6ka6	ribosomal protein S6 kinase polypeptide 6	11.499
chr11	72423732	72424760	790	Ube2g1	ubiquitin-conjugating enzyme E2G 1	18.196
chr4	1.24E+08	124196220	148	Utp11l	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	16.718
chr9	1.15E+08	114580340	335	Cmtm6	CKLF-like MARVEL transmembrane domain containing 6	15.981
chr12	72750582	72751500	1396	Daam1	dishevelled associated activator of morphogenesis 1	24.627
chr16	90932321	90933000	578	Paxbp1	PAX3 and PAX7 binding protein 1	15.68
chr10	39945921	39946691	775	Gtf3c6	general transcription factor IIIC, polypeptide 6, alpha	16.182
chr12	45139081	45140100	150	Pnpla8	patatin-like phospholipase domain containing 8	17.076
chr17	26328241	26329260	39638	Ergic1	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	14.468
chr3	53104601	53105280	212	Cog6	component of oligomeric golgi complex 6	15.168
chr9	1.2E+08	119744600	638	Wdr48	WD repeat domain 48	17.476
chr11	1.21E+08	121053940	260	Narf	nuclear prelamin A recognition factor	15.811
chr7	1.25E+08	125282520	510	Nsmce1	non-SMC element 1 homolog (S. cerevisiae)	15.427
chr16	87243321	87244000	279	N6amt1	N-6 adenine-specific DNA methyltransferase 1 (putative)	11.568
chr19	4097102	4098210	305	Cdk2ap2	CDK2-associated protein 2	23.878
chr1	54997381	54998060	405	Coq10b	coenzyme Q10 homolog B (S. cerevisiae)	18.128
chr1	10024901	10025580	1808	Cspp1	centrosome and spindle pole associated protein 1	19.028
chr17	79255732	79256380	4082	Cdc42ep3	CDC42 effector protein (Rho GTPase binding) 3	14.781
chr2	1.19E+08	119168891	644	Ino80	INO80 homolog (S. cerevisiae)	18
chr11	75896222	75897130	-52699	Fam101b	family with sequence similarity 101, member B	13.374
chr17	33235532	33236471	221	Zfp414	zinc finger protein 414	31.192
chr19	5924161	5925180	146	Cdc42ep2	CDC42 effector protein (Rho GTPase binding) 2	25.606
chr4	1.34E+08	134204020	550	Syf2	SYF2 homolog, RNA splicing factor (S. cerevisiae)	13.514
chr1	1.92E+08	191623290	281	Smyd2	SET and MYND domain containing 2	14.067
chr11	1.2E+08	120489880	307	Aspscr1	alveolar soft part sarcoma chromosome region, candidate 1	22.688
chr1	37828741	37829420	5877	Mitd1	MIT, microtubule interacting and transport, domain containing 1	18.865
chr2	83445712	83445860	369	Zc3h15	zinc finger CCCH-type containing 15	17.182
chr17	26666541	26667220	167	Cuta	cutA divalent cation tolerance homolog (E. coli)	18.334
chr15	98708801	98709480	308	Rhebl1	Ras homolog enriched in brain like 1	14.445
chr13	8994021	8994971	762	Gtpbp4	GTP binding protein 4	17.779
chr5	1.52E+08	151919820	447	Rfc3	replication factor C (activator 1) 3	27.575
chr3	1.06E+08	106022451	-10451	Adora3	adenosine A3 receptor	13.543
chr2	74378752	74379760	531	Lnp	limb and neural patterns	13.744
chr3	1.23E+08	123331260	47186	Mettl14	methyltransferase like 14	15.325
chr10	70743462	70744480	878	Ipmk	inositol polyphosphate multikinase	16.605
chr1	1.81E+08	181354300	718	Smyd3	SET and MYND domain containing 3	12.277
chr15	52542581	52543370	447	Med30	mediator complex subunit 30	12.873
chr11	1.13E+08	113382180	235	Slc39a11	solute carrier family 39 (metal ion transporter), member 11	15.115
chr11	1.13E+08	113353280	28965	Slc39a11	solute carrier family 39 (metal ion transporter), member 11	13.502
chr11	1.13E+08	113286910	95470	Slc39a11	solute carrier family 39 (metal ion transporter), member 11	13.37
chr15	78670142	78670220	279	Cdc42ep1	CDC42 effector protein (Rho GTPase binding) 1	8.769
chr4	82794761	82795780	150	Ttc39b	tetratricopeptide repeat domain 39B	18.244
chr4	82773622	82774360	21429	Ttc39b	tetratricopeptide repeat domain 39B	21.05
chr4	1.48E+08	147981450	215	Apitd1	apoptosis-inducing, TAF9-like domain 1	17.957
chr7	43180681	43181051	315	Zfp715	zinc finger protein 715	14.135
chr3	1.46E+08	146458910	388	Rpf1	ribosome production factor 1 homolog (S. cerevisiae)	29.318
chr15	25357541	25357911	763	Basp1	brain abundant, membrane attached signal protein 1	18.568
chr7	28306021	28307380	244	Pak4	p21 protein (Cdc42/Rac)-activated kinase 4	22.631
chr4	1.03E+08	102763830	25400	4921539E11Rik	RIKEN cDNA 4921539E11 gene	15.497
chr5	30571202	30572040	8205	Ept1	ethanolaminephosphotransferase 1 (CDP-ethanolamine-specific)	13.897

chr18	75144081	75144760	283	Dym	dymeclin	16.046
chr9	1.11E+08	110963760	529	Lrrfip2	leucine rich repeat (in FLII) interacting protein 2	16.171
chr11	1.18E+08	117648500	-6056	Tk1	thymidine kinase 1	13.828
chr10	77993621	77994500	1033	Syde1	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	15.056
chr11	83118922	83119800	469	Ap2b1	adaptor-related protein complex 2, beta 1 subunit	15.362
chr11	1.06E+08	105853900	474	Dcaf7	DDB1 and CUL4 associated factor 7	15.669
chr11	1.2E+08	120194621	545	Faap100	Fanconi anemia core complex associated protein 100	36.413
chr15	99599941	99600001	578	Cers5	ceramide synthase 5	9.5
chr5	1.22E+08	121884520	-4486	Acad12	acyl-Coenzyme A dehydrogenase family, member 12	17.07
chr1	1.36E+08	136223040	129	Cyb5r1	cytochrome b5 reductase 1	12.4
chr6	85926501	85927520	291	Dusp11	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	14.538
chr16	35409301	35410660	640	Pdia5	protein disulfide isomerase associated 5	20.757
chr15	75907041	75908400	405	Puf60	poly-U binding splicing factor 60	18.708
chr5	21248981	21249660	336	Pmpcb	peptidase (mitochondrial processing) beta	15.474
chr11	57825501	57826520	751	Larp1	La ribonucleoprotein domain family, member 1	16.316
chr5	1.4E+08	139626440	-2543	Mir339	microRNA 339	33.484
chr2	1.81E+08	180512411	1244	Mrgbp	MRG/MORF4L binding protein	14.563
chr9	50609001	50610000	346	Ppp2r1b	protein phosphatase 2, regulatory subunit A, beta	15.249
chr17	87191981	87192660	1108	Ttc7	tetratricopeptide repeat domain 7	13.776
chr14	56952782	56953400	281	Micu2	mitochondrial calcium uptake 2	21.34
chr5	1.2E+08	120391280	8940	Gm10390	predicted gene 10390	13.029
chr6	91439322	91440590	701	Tmem43	transmembrane protein 43	16.091
chr17	29396532	29397420	9369	Cmtr1	cap methyltransferase 1	13.352
chr4	1.26E+08	125607220	280	Stk40	serine/threonine kinase 40	23.711
chr4	1.26E+08	125613571	7025	Stk40	serine/threonine kinase 40	17.544
chr13	54798821	54799840	303	Tspan17	tetraspanin 17	16.415
chr2	30807142	30807820	3193	Usp20	ubiquitin specific peptidase 20	12.975
chr14	30324941	30325960	1362	Eaf1	ELL associated factor 1	20.572
chr11	96592981	96594000	155	Snx11	sorting nexin 11	26.621
chr15	98745181	98746540	272	Lmbr1l	limb region 1 like	28.638
chr9	1.08E+08	107731040	220	Rbm6	RNA binding motif protein 6	18.146
chr4	1.29E+08	128561981	741	Rnf19b	ring finger protein 19B	34.81
chr4	1.29E+08	128562160	1501	Rnf19b	ring finger protein 19B	11.167
chr15	99301862	99302780	443	Bcdin3d	BCDIN3 domain containing	16.658
chr18	38326161	38326780	9266	Pcdh1	protocadherin 1	14.065
chr19	58576901	58577580	11988	Ccdc172	coiled-coil domain containing 172	18.965
chr15	57863402	57864830	261	9130401M01Rik	RIKEN cDNA 9130401M01 gene	26.957
chr16	20011041	20012060	453	Klhl24	kelch-like 24	17.698
chr13	1.05E+08	105229320	935	Nln	neurolysin (metallopeptidase M3 family)	16.477
chr7	92617982	92618720	1445	Rab30	RAB30, member RAS oncogene family	19.214
chr19	36474181	36475200	30479	Pcgf5	polycomb group ring finger 5	29.3
chr10	77587321	77588000	618	Pwp2	PWP2 periodic tryptophan protein homolog (yeast)	13.626
chr13	60747302	60748140	48266	BC051665	cDNA sequence BC051665	15.436
chr11	62125141	62125820	27812	Ttc19	tetratricopeptide repeat domain 19	11.667
chr5	1.44E+08	143987620	619	Usp42	ubiquitin specific peptidase 42	18.954
chr4	1.34E+08	133807111	628	Mtfr1l	mitochondrial fission regulator 1-like	12.443
chr10	60209581	60210260	17018	Unc5b	unc-5 homolog B (C. elegans)	14.829
chr15	82999101	83000460	194	Cyb5r3	cytochrome b5 reductase 3	22.85
chr15	82992641	82993071	7118	Cyb5r3	cytochrome b5 reductase 3	21.674
chr15	82984821	82985740	7869	Rnu12	RNA U12, small nuclear	15.305
chr3	95401092	95401280	530	Cers2	ceramide synthase 2	13.511
chr17	88537361	88538040	2819	Ston1	stonin 1	12.775
chr17	26442522	26444790	416	Crebrf	CREB3 regulatory factor	31.787
chr13	1.13E+08	113433180	23340	Ankrd55	ankyrin repeat domain 55	14.899
chr16	91476661	91477340	9539	Tmem50b	transmembrane protein 50B	13.648
chr3	95099701	95100720	432	Zfp687	zinc finger protein 687	21.333
chr15	51707881	51708390	620	Utp23	UTP23, small subunit (SSU) processome component, homolog	12.811
chr11	96792901	96793580	538	Sp2	Sp2 transcription factor	15.445
chr6	56644681	56645700	707	Avl9	AVL9 homolog (S. cerevisiase)	21.494
chr12	1.11E+08	111050800	1099	Dync1h1	dynein cytoplasmic 1 heavy chain 1	24.949
chr12	84409862	84410990	212	Dcaf4	DDB1 and CUL4 associated factor 4	16.27
chr3	1.05E+08	105180541	898	Cttnbp2nl	CTTNBP2 N-terminal like	13.814
chr8	89773941	89774531	1127	N4bp1	NEDD4 binding protein 1	18.627
chr7	1.26E+08	126220920	495	Rabep2	rabaptin, RAB GTPase binding effector protein 2	35.119
chr5	1.17E+08	116682390	2032	Hspb8	heat shock protein 8	22.624
chr9	39942532	39943540	149	Zfp202	zinc finger protein 202	14.55
chr9	66773621	66774341	647	Lactb	lactamase, beta	23.306
chr2	1.67E+08	167194891	-10527	Spata2	spermatogenesis associated 2	19.491
chr2	1.67E+08	167195680	-11212	Spata2	spermatogenesis associated 2	14.468
chr15	75756421	75757100	225	Tsta3	tissue specific transplantation antigen P35B	16.786
chr11	5144541	5145560	16563	Kremen1	kringle containing transmembrane protein 1	16.637
chr15	11343421	11344100	623	Tars	threonyl-tRNA synthetase	12.483
chr11	53364021	53364700	1201	Sept8	septin 8	17.016
chr16	18201901	18202920	321	Dgcr8	DiGeorge syndrome critical region gene 8	14.621
chr17	34658921	34658960	641	Clic1	chloride intracellular channel 1	6.282
chr17	34659062	34659940	1202	Clic1	chloride intracellular channel 1	26.63
chr15	34189721	34190400	7445	Laptm4b	lysosomal-associated protein transmembrane 4B	12.043
chr11	19825401	19826080	1295	Spred2	sprouty-related, EVH1 domain containing 2	18.007
chr7	18976552	18977410	4296	Bcl3	B cell leukemia/lymphoma 3	9.382
chr7	1.4E+08	139967460	717	Echs1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	19.886
chr11	48681272	48681880	12015	Trim7	tripartite motif-containing 7	19.704
chr4	46510301	46510980	211	Nans	N-acetylneuraminic acid synthase (sialic acid synthase)	16.415
chr7	26874632	26875640	426	Egln2	egl-9 family hypoxia-inducible factor 2	12.594
chr9	96439981	96440660	535	Rasa2	RAS p21 protein activator 2	14.296
chr4	1.06E+08	106059940	630	Dhcr24	24-dehydrocholesterol reductase	16.468
chr17	6128562	6129520	34411	Tulp4	tubby like protein 4	18.456
chr11	88314661	88315340	-120341			15.116
chr10	1.27E+08	127498220	2018	Baz2a	bromodomain adjacent to zinc finger domain, 2A	23.754
chr10	1.27E+08	126614940	290	Pip4k2c	phosphatidylinositol-5-phosphate 4-kinase, type II, gamma	19.254
chr10	79978881	79980231	869	Klf16	Kruppel-like factor 16	45.415

chr16	91946541	91948240	195	Mrps6	mitochondrial ribosomal protein S6	30.177
chr17	26800572	26801390	16088	Itpr3	inositol 1,4,5-triphosphate receptor 3	18.67
chr16	33171081	33172000	337	Snx4	sorting nexin 4	13.992
chr11	77992261	77992940	261	Nek8	NIMA (never in mitosis gene a)-related expressed kinase 8	19.14
chr3	1.3E+08	129581140	56392	Elovl6	ELOVL family member 6, elongation of long chain fatty acids	18.647
chr11	1.2E+08	119796620	-34747	Mir3065	microRNA 3065	14.184
chr11	1.2E+08	119792540	32848	Baiap2	brain-specific angiogenesis inhibitor 1-associated protein 2	18.594
chr7	15468482	15469320	796	Bbc3	BCL2 binding component 3	16.63
chr7	15470292	15472720	3401	Bbc3	BCL2 binding component 3	20.118
chr18	61524021	61524910	-1196	Mir378a	microRNA 378a	12.053
chr8	87880481	87881500	290	Hook2	hook homolog 2 (Drosophila)	15.902
chr6	1.25E+08	125005991	184	Ing4	inhibitor of growth family, member 4	18.287
chr19	41316121	41317071	719	Tm9sf3	transmembrane 9 superfamily member 3	17.926
chr19	6116982	6117620	1285	Sac3d1	SAC3 domain containing 1	15.994
chr18	35965642	35966780	10419	Cxxc5	CXXC finger 5	17.646
chr7	99995021	99995700	223	Pold3	polymerase (DNA-directed), delta 3, accessory subunit	18.031
chr7	49646801	49647201	622	Prmt3	protein arginine N-methyltransferase 3	8.575
chr8	1.24E+08	124460060	5308	Fbxo31	F-box protein 31	30.329
chr2	1.64E+08	164189591	561	Pigt	phosphatidylinositol glycan anchor biosynthesis, class T	23.84
chr15	78761782	78762940	173	Nol12	nucleolar protein 12	22.197
chr11	94445881	94447240	646	Lrrc59	leucine rich repeat containing 59	27.289
chr1	99491821	99492500	264	D1Ertd622e	DNA segment, Chr 1, ERATO Doi 622, expressed	12.563
chr4	53467132	53468020	6063	Slc44a1	solute carrier family 44, member 1	9.519
chr5	1.14E+08	114437200	10343	Acacb	acetyl-Coenzyme A carboxylase beta	11.583
chr7	1.02E+08	101844521	227	Numa1	nuclear mitotic apparatus protein 1	34.302
chr7	1.02E+08	101844620	912	Numa1	nuclear mitotic apparatus protein 1	10.307
chr7	44736861	44737581	609	Ptov1	prostate tumor over expressed gene 1	22.597
chr14	6609392	6610510	1585	Flnb	filamin, beta	20.789
chr15	87492201	87493220	39714	Fam19a5	family with sequence similarity 19, member A5	14.217
chr15	1.02E+08	102108120	290	Mfsd5	major facilitator superfamily domain containing 5	18.532
chr19	7124502	7125380	1129	Macrod1	MACRO domain containing 1	14.428
chr12	81177802	81179041	790	Actn1	actinin, alpha 1	12.739
chr4	1.17E+08	116680860	206	Kif2c	kinesin family member 2C	19.09
chr9	65258581	65259830	262	Spg21	spastic paraplegia 21 homolog (human)	23.102
chr9	56663381	56663681	290	Cspg4	chondroitin sulfate proteoglycan 4	9.133
chr9	56663692	56664740	975	Cspg4	chondroitin sulfate proteoglycan 4	18.436
chr11	1.21E+08	120806760	1003	Csnk1d	casein kinase 1, delta	15.334
chr18	24745302	24746221	1066	Slc39a6	solute carrier family 39 (metal ion transporter), member 6	27.711
chr7	1.28E+08	127760030	829	Fus	fused in sarcoma	18.77
chr19	32453341	32454311	625	Sgms1	sphingomyelin synthase 1	18.845
chr9	1.2E+08	119959820	213	Slc25a38	solute carrier family 25, member 38	17.472
chr11	77422761	77423641	809	Taok1	TAO kinase 1	19.193
chr11	79777261	79778091	906	Utp6	UTP6, small subunit (SSU) processome component, homolog	13.843
chr11	79759581	79760590	18497	Utp6	UTP6, small subunit (SSU) processome component, homolog	20.65
chr15	63827181	63828480	62291	Fam49b	family with sequence similarity 49, member B	18.512
chr17	93072132	93072960	370	Pja2	praja 2, RING-H2 motif containing	13.643
chr3	88143641	88144860	172	Apoa1bp	apolipoprotein A-I binding protein	21.967
chr3	1.17E+08	116704320	363	Slc35a3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc)	19.482
chr4	59642461	59643820	278	Ptbp3	polypyrimidine tract binding protein 3	24.193
chr4	1.32E+08	131782280	752	Sesn2	sestrin 2	17.011
chr5	96401221	96402101	188	Cnot6l	CCR4-NOT transcription complex, subunit 6-like	14.511
chr6	85397121	85398480	166	Smyd5	SET and MYND domain containing 5	46.78
chr6	1.41E+08	140510331	-74933	Aebp2	AE binding protein 2	18.733
chr15	78919172	78920120	-16592	Micall1	microtubule associated monooxygenase, calponin and LIM	12.818
chr5	1.21E+08	121036140	2580	Oas3	2'-5' oligoadenylate synthetase 3	14.334
chr18	76016861	76017880	71827	Zbtb7c	zinc finger and BTB domain containing 7C	17.829
chr7	1.45E+08	145112680	1871	Mrgprf	MAS-related GPR, member F	16.312
chr11	77931401	77932380	21022	Fam222b	family with sequence similarity 222, member B	15.633
chr11	98589602	98590820	1256	Nr1d1	nuclear receptor subfamily 1, group D, member 1	17.502
chr11	98589461	98589591	1941	Nr1d1	nuclear receptor subfamily 1, group D, member 1	5
chr11	98588441	98589120	2687	Nr1d1	nuclear receptor subfamily 1, group D, member 1	11.183
chr11	1.18E+08	117596431	680	Tmc6	transmembrane channel-like gene family 6	16.997
chr11	1.18E+08	117595621	1170	Tmc6	transmembrane channel-like gene family 6	14.938
chr15	88690361	88690761	601	Pim3	proviral integration site 3	8.8
chr15	88691322	88691380	1391	Pim3	proviral integration site 3	6.19
chr1	95342121	95343140	120	Farp2	FERM, RhoGEF and pleckstrin domain protein 2	14.421
chr2	1.22E+08	121809401	846	Spg11	spastic paraplegia 11	18.039
chr6	83291501	83292520	313	Mob1a	MOB kinase activator 1A	17.371
chr7	1.2E+08	119511940	396	Thumpd1	THUMP domain containing 1	13.463
chr9	21547912	21548671	657	Kank2	KN motif and ankyrin repeat domains 2	11.642
chr9	21542792	21543760	5672	Kank2	KN motif and ankyrin repeat domains 2	18.041
chr9	21542401	21542781	6357	Kank2	KN motif and ankyrin repeat domains 2	13.974
chrX	19861101	19861780	572	Usp11	ubiquitin specific peptidase 11	15.754
chr10	77026952	77028020	2003	Pttg1ip	pituitary tumor-transforming 1 interacting protein	14.282
chr16	11088802	11089780	680	Zc3h7a	zinc finger CCCH type containing 7 A	14.77
chr11	35613301	35613980	722	Pank3	pantothenate kinase 3	16.028
chr9	44517901	44518771	467	Arcn1	archain 1	12.943
chr17	80114201	80115560	751	Srsf7	serine/arginine-rich splicing factor 7	19.333
chr18	34630361	34632060	414	Fam13b	family with sequence similarity 13, member B	35.624
chr2	1.52E+08	151670200	1940	Fam110a	family with sequence similarity 110, member A	19.432
chr4	45992922	45994180	154	Tdrd7	tudor domain containing 7	18.737
chr4	1.17E+08	117412200	1241	Ipo13	importin 13	17.706
chr7	29988012	29989511	420	Wdr62	WD repeat domain 62	20.047
chr9	37239181	37240200	698	Msantd2	Myb/SANT-like DNA-binding domain containing 2	19.445
chr5	31517321	31518340	331	Nrbp1	nuclear receptor binding protein 1	25.333
chr11	1.03E+08	102910520	7568	Plcd3	phospholipase C, delta 3	16.102
chr4	59720762	59721000	616	E130308A19Rik	RIKEN cDNA E130308A19 gene	19.71
chr4	1.25E+08	124629951	349	Zc3h12a	zinc finger CCCH type containing 12A	18.913
chr15	72981681	72982700	30013	Ago2	argonaute RISC catalytic subunit 2	15.95
chr9	1.2E+08	119832660	1135	Csrnp1	cysteine-serine-rich nuclear protein 1	15.082

chr9	1.2E+08	119831771	1915	Csrnp1	cysteine-serine-rich nuclear protein 1	15.56
chr9	1.2E+08	119831101	2325	Csrnp1	cysteine-serine-rich nuclear protein 1	8.214
chr9	1.2E+08	119830620	3185	Csrnp1	cysteine-serine-rich nuclear protein 1	16.521
chr4	1.26E+08	125970571	439	Ago1	argonaute RISC catalytic subunit 1	17.526
chr11	1.02E+08	102065960	679	BC030867	cDNA sequence BC030867	17.767
chr3	1.08E+08	107759431	590	Strip1	striatin interacting protein 1	12.098
chr11	22412121	22413080	314	Tmem17	transmembrane protein 17	17.221
chr6	72163301	72163980	1446	Atoh8	atonal homolog 8 (Drosophila)	12.929
chr7	1.18E+08	117907240	396	Rps15a	ribosomal protein S15A	14.43
chr2	1.67E+08	167177851	-6434	Rnf114	ring finger protein 114	21.138
chr2	1.67E+08	167178340	-5749	Rnf114	ring finger protein 114	10.774
chr7	4518602	4519280	637	Zfp628	zinc finger protein 628	12.537
chr11	35814921	35815600	8252	Wwc1	WW, C2 and coiled-coil domain containing 1	14.542
chr17	26508781	26509670	423	Bnip1	BCL2/adenovirus E1B interacting protein 1	19.441
chr11	94808661	94809680	1868	Ppp1r9b	protein phosphatase 1, regulatory subunit 9B	18.945
chr7	98530641	98531660	611	Emsy	EMSY, BRCA2-interacting transcriptional repressor	20.097
chr8	97103321	97104670	265	Nup93	nucleoporin 93	28.602
chr15	81955392	81955980	509	Ccdc134	coiled-coil domain containing 134	15.287
chr11	1.19E+08	119031960	13063	Tbc1d16	TBC1 domain family, member 16	15.843
chr1	95102761	95103440	-1855	Mir6901	microRNA 6901	20.272
chr5	52957422	52958060	208	Sepsecs	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA	21.544
chr12	1.05E+08	105410540	343	Syne3	spectrin repeat containing, nuclear envelope family member 3	7.375
chr12	1.05E+08	105410481	838	Syne3	spectrin repeat containing, nuclear envelope family member 3	20.584
chr8	86994101	86994780	427	Dcaf15	DDB1 and CUL4 associated factor 15	16.946
chr9	65624761	65625241	569	Zfp609	zinc finger protein 609	17.792
chr5	1.36E+08	136029240	239	Tmem120a	transmembrane protein 120A	20.634
chr10	75110761	75111440	-23376	Susd2	sushi domain containing 2	16.817
chr10	79148941	79149620	430	Polrmt	polymerase (RNA) mitochondrial (DNA directed)	15.074
chr11	50270772	50271890	3203	Rufy1	RUN and FYVE domain containing 1	18.273
chr11	1.16E+08	115926061	944	Trim47	tripartite motif-containing 47	18.691
chr12	85256622	85257340	5265	Coq6	coenzyme Q6 homolog (yeast)	13.74
chr15	79218462	79219660	11113	Tmem184b	transmembrane protein 184b	15.81
chr15	79217352	79218451	12273	Tmem184b	transmembrane protein 184b	26.592
chr19	11979561	11980760	716	Patl1	protein associated with topoisomerase II homolog 1 (yeast)	30.315
chr1	1.64E+08	163970100	-84704	Dnm3os	dynamin 3, opposite strand	11.304
chr5	87246381	87247740	244	Uba6	ubiquitin-like modifier activating enzyme 6	29.307
chr12	1.03E+08	103279420	376	Btbd7	BTB (POZ) domain containing 7	15.184
chr14	60126621	60127300	34393	Sacs	sacsin	14.513
chr17	17328441	17329460	157	Lnpep	leucyl/cystinyl aminopeptidase	18.056
chr18	31777081	31778350	322	Sap130	Sin3A associated protein	25.001
chr7	79987381	79988060	1143	Idh2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	17.912
chr11	3248361	3249380	7274	Limk2	LIM motif-containing protein kinase 2	18.563
chr3	7486121	7487140	131	Zc2hc1a	zinc finger, C2HC-type containing 1A	18.175
chr8	91586821	91587840	197	Cyld	cylindromatosis (turban tumor syndrome)	17.067
chr1	1.37E+08	137283840	-36598	Ipo9	importin 9	18
chr1	60124921	60125940	285	Nbeal1	neurobeachin like 1	20.177
chr7	80196821	80197411	851	Rccd1	RCC1 domain containing 1	25.695
chr11	6099002	6100280	813	Nudcd3	NudC domain containing 3	17.29
chr10	77977612	77978660	507	Ilvbl	ilvB (bacterial acetolactate synthase)-like	28.063
chr11	32388752	32389760	33884	Ubtd2	ubiquitin domain containing 2	20.32
chr8	1.28E+08	128140220	199425	Disc1	disrupted in schizophrenia 1	30.466
chr7	44919781	44920761	652	Prr12	proline rich 12	20.663
chr18	80312492	80313440	575	Adnp2	ADNP homeobox 2	12.685
chr4	1.01E+08	101146260	205	Leprot	leptin receptor overlapping transcript	23.032
chr2	1.73E+08	172643840	274	Rae1	RAE1 RNA export 1 homolog (S. pombe)	14.107
chr15	96527021	96527561	441	Slc38a2	solute carrier family 38, member 2	15.037
chr9	1.08E+08	108376020	490	Qrich1	glutamine-rich 1	13.434
chr8	1.28E+08	127530600	19293	2310022B05Rik	RIKEN cDNA 2310022B05 gene	14.954
chr8	1.28E+08	127529721	19808	2310022B05Rik	RIKEN cDNA 2310022B05 gene	8.571
chr7	49117802	49118440	3911	Nav2	neuron navigator 2	22.461
chr4	1.32E+08	131670780	24091	Phactr4	phosphatase and actin regulator 4	15.33
chr4	1.15E+08	115326980	276	Mob3c	MOB kinase activator 3C	21.031
chr15	95618922	95619560	364	Ano6	anoctamin 6	15.053
chr17	12834492	12835000	445	Wtap	Wilms tumour 1-associating protein	14.321
chr17	12833981	12834481	960	Wtap	Wilms tumour 1-associating protein	16.22
chr4	1.08E+08	107958840	802	Zcchc11	zinc finger, CCHC domain containing 11	15.018
chr5	1.22E+08	122110270	140	Fam109a	family with sequence similarity 109, member A	14.455
chr7	18289642	18290840	11860	Fbxo46	F-box protein 46	24.927
chr6	38363901	38365140	987	Ubn2	ubinuclein 2	22.232
chr8	93798181	93799200	-23664			13.868
chr5	1.23E+08	122549260	3905	Pptc7	PTC7 protein phosphatase homolog (S. cerevisiae)	12.258
chr7	1.1E+08	110406160	447	Sbf2	SET binding factor 2	16.858
chr19	47121302	47122300	742	Taf5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-	14.381
chr11	32247641	32248320	169	Sh3pxd2b	SH3 and PX domains 2B	16.591
chr11	80315662	80316160	9390			19.661
chr1	20999532	21000100	63039	Efhc1	EF-hand domain (C-terminal) containing 1	14.516
chr19	15990902	15991220	580	Psat1	phosphoserine aminotransferase 1	8.95
chr19	15989861	15990891	1265	Psat1	phosphoserine aminotransferase 1	27.34
chr15	78958541	78959220	9626			17.106
chr5	1.24E+08	123656640	730	Mlxip	MLX interacting protein	13.342
chr16	32252061	32252740	401	Ubxn7	UBX domain protein 7	15.832
chr6	1.15E+08	114841120	46591	Vgll4	vestigial like 4 (Drosophila)	14.495
chr8	1.08E+08	108236620	963	Fhod1	formin homology 2 domain containing 1	14.471
chr4	1.28E+08	128112000	742	Zscan20	zinc finger and SCAN domains 20	16.138
chr16	20535632	20536560	-1275	Camk2n2	calcium/calmodulin-dependent protein kinase II inhibitor 2	17.866
chr11	98558861	98559540	1325			11.437
chr11	3231701	3233060	1646	Pik3ip1	phosphoinositide-3-kinase interacting protein 1	22.452
chr11	70819961	70820041	626	Dhx33	DEAH (Asp-Glu-Ala-His) box polypeptide 33	6.25
chr18	47083881	47084900	183	Commd10	COMM domain containing 10	19.191
chr1	1.74E+08	174340830	3530	Tagln2	transgelin 2	17.817

chr2	1.31E+08	131044820	183	Rnf24	ring finger protein 24	17.18
chr10	1.1E+08	110154450	4616	E2f7	E2F transcription factor 7	22.344
chr11	54630521	54631200	266	Cdc42se2	CDC42 small effector 2	13.661
chr6	85298181	85298860	560	Sfxn5	sideroflexin 5	15.386
chr3	1.43E+08	142764880	54970	Pkn2	protein kinase N2	16.003
chr9	1.22E+08	121554080	157	Sec22c	SEC22 homolog C, vesicle trafficking protein	13.919
chr5	48273201	48274220	2307	Slit2	slit homolog 2 (Drosophila)	17.537
chr2	1.53E+08	152706920	244	Pdrg1	p53 and DNA damage regulated 1	17.968
chr17	88349341	88350020	642	Foxn2	forkhead box N2	12.283
chr9	70008422	70009400	2397	Myo1e	myosin IE	14.625
chr8	1.09E+08	108526300	293	Ctcf	CCCTC-binding factor	16.626
chr19	17078122	17078880	55364	Prune2	prune homolog 2 (Drosophila)	21.81
chr19	10755561	10756580	210	Vps37c	vacuolar protein sorting 37C (yeast)	17.244
chr19	57711601	57712550	47791	Atrnl1	attractin like 1	16.415
chr12	1.12E+08	111802190	23865	Cdc42bpb	CDC42 binding protein kinase beta	28.698
chr7	1.26E+08	126293761	1069	Atxn2l	ataxin 2-like	11.855
chr1	75341122	75341620	7713	Asic4	acid-sensing (proton-gated) ion channel family member 4	10.894
chr17	24399421	24400281	2499	Zfp598	zinc finger protein 598	19.767
chr7	70235212	70235980	-1490	Nr2f2	nuclear receptor subfamily 2, group F, member 2	15.917
chr5	1.22E+08	122392860	3160	Ccdc63	coiled-coil domain containing 63	23.831
chr10	79505261	79506131	135	Sbno2	strawberry notch homolog 2 (Drosophila)	15.563
chr11	74712162	74713640	374	Sgsm2	small G protein signaling modulator 2	30.404
chr1	1.54E+08	153849660	3218	1700025G04Rik	RIKEN cDNA 1700025G04 gene	9.437
chr10	79311332	79312140	331	Med16	mediator complex subunit 16	26.385
chr5	1.14E+08	114251220	4046	Ssh1	slingshot homolog 1 (Drosophila)	28.663
chr5	1.14E+08	114237280	17986	Ssh1	slingshot homolog 1 (Drosophila)	18.972
chr12	53740061	53740740	119397	Akap6	A kinase (PRKA) anchor protein 6	15.594
chr19	10364221	10364900	7362	Dagla	diacylglycerol lipase, alpha	15.545
chr19	46051301	46051980	159	9130011E15Rik	RIKEN cDNA 9130011E15 gene	16.946
chr5	1.11E+08	110806000	21004	Galnt9	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-	16.37
chr11	1.2E+08	120069300	19753	Bahcc1	BAH domain and coiled-coil containing 1	17.699
chr11	1.2E+08	120079160	29613	Bahcc1	BAH domain and coiled-coil containing 1	31.512
chr6	1.25E+08	125344060	2403	Plekhg6	pleckstrin homology domain containing, family G (with RhoGef	11.459
chr10	79788481	79789840	1620	Mex3d	mex3 homolog D (C. elegans)	16.976
chr6	1.2E+08	120003000	1784	Wnk1	WNK lysine deficient protein kinase 1	16.935
chr17	34502181	34503790	370	Zbtb12	zinc finger and BTB domain containing 12	27.15
chr11	51699041	51700400	1184	Jade2	jade family PHD finger 2	36.019
chr4	1.29E+08	129199320	502	Tmem39b	transmembrane protein 39b	23.614
chr4	1.37E+08	137203830	-62306	Eif4g3	eukaryotic translation initiation factor 4 gamma, 3	18.377
chr4	1.53E+08	152857100	1038	Lrrc47	leucine rich repeat containing 47	10.927
chr17	79523281	79523960	394	Rmdn2	regulator of microtubule dynamics 2	12.616
chr17	45960922	45961880	1423	Dnph1	2'-deoxynucleoside 5'-phosphate N-hydrolase 1	18.834
chr7	18386861	18387880	459	Opa3	optic atrophy 3	14.763
chr17	32971562	32972520	313	Zfp81	zinc finger protein 81	17.722
chr11	49555001	49556360	465	Cnot6	CCR4-NOT transcription complex, subunit 6	12.668
chr7	1E+08	100457420	307	Mrpl48	mitochondrial ribosomal protein L48	29.876
chr7	1.11E+08	110914071	410	1700012D14Rik	RIKEN cDNA 1700012D14 gene	22.878
chr6	1.13E+08	113042731	905	Gt(ROSA)26Sor	gene trap ROSA 26, Philippe Soriano	22.846
chr4	1.07E+08	107306380	5735	Lrp8	low density lipoprotein receptor-related protein 8, apolipoprotein e	24.307
chr17	32095312	32095781	-13347	Akap8l	A kinase (PRKA) anchor protein 8-like	17.495
chr8	1.09E+08	108750360	231	Nutf2-ps1	nuclear transport factor 2, pseudogene 1	19.769
chr6	34246841	34247860	251	Gm6644	Akr1b3 pseudogene	17.659
chr17	33728341	33729360	1504	Brd2	bromodomain containing 2	17.631
chr11	1.2E+08	120167220	2013	0610009L18Rik	RIKEN cDNA 0610009L18 gene	37.707
chr3	89481332	89482220	1559	Gm15417	predicted gene 15417	16.999
chr4	1.5E+08	149681131	18003	1700045H11Rik	RIKEN cDNA 1700045H11 gene	15.616
chr5	73559482	73560360	3398	1700025M24Rik	RIKEN cDNA 1700025M24 gene	14.081
chr9	63847482	63848600	206	1110036E04Rik	RIKEN cDNA 1110036E04 gene	16.085
chr9	61087572	61088410	3824	B930092H01Rik	RIKEN cDNA B930092H01 gene	13.717
chr17	56359081	56359760	1071	Ranbp3	RAN binding protein 3	13.057
chr3	40896561	40897580	570	Plk4	polo-like kinase 4	16.159
chr12	1.01E+08	100678420	421	Gm10432	predicted gene 10432	10.817
chr5	1.12E+08	111998700	3995	E130006D01Rik	RIKEN cDNA E130006D01 gene	17.988
chr14	46833592	46834320	13141	4930447J18Rik	RIKEN cDNA 4930447J18 gene	15.569
chr3	1.23E+08	122880760	-6653	Fabp2	fatty acid binding protein 2, intestinal	19.918
chr15	76403112	76404460	172	Adck5	aarF domain containing kinase 5	22.387
chr10	80964162	80964790	1903	Aes	amino-terminal enhancer of split	14.025
chr11	31708061	31708630	16202	D630024D03Rik	RIKEN cDNA D630024D03 gene	22.404
chr10	41138641	41139320	207	Zbtb24	zinc finger and BTB domain containing 24	15.432
chr11	26287101	26287980	456	Fancl	Fanconi anemia, complementation group L	14.842
chr7	18429442	18429700	805	Vasp	vasodilator-stimulated phosphoprotein	6.465
chr7	18428762	18429431	1280	Vasp	vasodilator-stimulated phosphoprotein	13.105
chr15	1E+08	100455611	8267	Smagp	small cell adhesion glycoprotein	19.772
chr6	1.09E+08	108625580	-1166	Bhlhe40	basic helix-loop-helix family, member e40	20.529
chr2	1.55E+08	154934260	5792	Dynlrb1	dynein light chain roadblock-type 1	17.159
chr2	1.81E+08	181427560	591	Tpd52l2	tumor protein D52-like 2	12.869
chr3	1.39E+08	138702880	22835	Tspan5	tetraspanin 5	17.791
chr3	1.39E+08	138709460	29411	Tspan5	tetraspanin 5	16.703
chr15	38462841	38463581	644			20.959
chr17	24182161	24183180	322			15.613
chr2	1.51E+08	151234720	456			12.496
chr10	1.16E+08	116137880	4278			11.818
chr15	38871672	38872750	-34795	Cthrc1	collagen triple helix repeat containing 1	22.737
chr4	1.19E+08	118565820	1563			15.854
chr5	45580512	45581121	131832			17.057
chr15	61908901	61909580	40317			20.364
chr1	94764461	94765450	141	Capn10	calpain 10	12.089
chr7	1.27E+08	127303821	180			12.873
chr16	50651501	50652520	111	Dubr	Dppa2 upstream binding RNA	13.331
chr4	1.41E+08	140819500	752	B330016D10Rik	RIKEN cDNA B330016D10 gene	22.32

chr5	5579741	5580420	275	Gm8773	predicted gene 8773	15.75
chr5	1.35E+08	135295180	587	Abhd11	abhydrolase domain containing 11	15.145
chr10	79541981	79542660	176	Cbarp	calcium channel, voltage-dependent, beta subunit associated	20.498
chrX	49301021	49301691	461	C430049B03Rik	RIKEN cDNA C430049B03 gene	15.522
chr3	89477461	89478480	179	Gm15417	predicted gene 15417	14.585
chr19	5117562	5118920	167	Klc2	kinesin light chain 2	21.824
chr9	50527401	50528001	246	Alg9	asparagine-linked glycosylation 9 (alpha 1,2 mannosyltransferase)	20.1
chr9	56928581	56929600	176	Man2c1	mannosidase, alpha, class 2C, member 1	13.702
chr2	75504821	75505840	172			14.375
chr9	64138961	64139640	-37	Dis3l	DIS3 mitotic control homolog (S. cerevisiae)-like	15.194
chr17	84095812	84097300	-283	Zfp36l2	zinc finger protein 36, C3H type-like 2	15.999
chr15	99285441	99286460	-168	Nckap5l	NCK-associated protein 5-like	18.911
chr10	95370341	95370551	95	Eea1	early endosome antigen 1	24
chr19	4396982	4397900	-364	Kdm2a	lysine (K)-specific demethylase 2A	13.668
chr11	78077601	78078251	-23	2610507B11Rik	RIKEN cDNA 2610507B11 gene	12.646
chr17	21271421	21272100	17	Zfp948	zinc finger protein 948	24.596
chr3	88589381	88590400	-611	Lmna	lamin A	20.364
chr11	86573552	86573860	-19	Cltc	clathrin, heavy polypeptide (Hc)	16.529
chr10	86134581	86135940	-17	Hsp90b1	heat shock protein 90, beta (Grp94), member 1	18.073
chr6	85340001	85341020	-218	Rab11fip5	RAB11 family interacting protein 5 (class I)	20.694
chr16	56000041	56000601	-34	Senp7	SUMO1/sentrin specific peptidase 7	15.589
chr11	60991062	60992130	-342	Usp22	ubiquitin specific peptidase 22	20.037
chr11	77309541	77309641	-16	Git1	G protein-coupled receptor kinase-interactor 1	4.1
chr14	68894201	68894880	42	9930012K11Rik	RIKEN cDNA 9930012K11 gene	12.498
chr4	1.19E+08	119038001	108	Foxj3	forkhead box J3	14.867
chr10	83870181	83870860	-250	Nuak1	NUAK family, SNF1-like kinase, 1	19.604
chr12	21357832	21358560	-50	Asap2	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2	16.368
chr5	1.38E+08	138017220	-227	Mepce	methylphosphate capping enzyme	16.45
chr12	76736732	76737320	-132	Syne2	spectrin repeat containing, nuclear envelope 2	11.861
chr5	1.24E+08	124010580	-104	Kntc1	kinetochore associated 1	22.333
chr4	1.2E+08	120449741	-75	Zfp69	zinc finger protein 69	26.121
chr17	26700201	26701450	57	Zbtb9	zinc finger and BTB domain containing 9	23.043
chr17	23401181	23401860	-128	Thoc6	THO complex 6 homolog (Drosophila)	17.144
chr2	29870701	29871320	-122	Wdr34	WD repeat domain 34	13.384
chr7	43429901	43430790	-67	Zfp658	zinc finger protein 658	14.234
chr11	60543782	60545160	-122	Mief2	mitochondrial elongation factor 2	22.957
chr4	45429482	45430371	-60	Slc25a51	solute carrier family 25, member 51	13.423
chr17	35448782	35449521	-400	Mdc1	mediator of DNA damage checkpoint 1	19.754
chr7	18518202	18519361	-776	Cd3eap	CD3E antigen, epsilon polypeptide associated protein	19.003
chr7	18519372	18520140	18	Ppp1r13l	protein phosphatase 1, regulatory (inhibitor) subunit 13 like	19.764
chr6	39740232	39740900	-23	Mrps33	mitochondrial ribosomal protein S33	22.193
chr11	1.18E+08	117666170	-2	Birc5	baculoviral IAP repeat-containing 5	23.125
chr4	33279201	33279790	-56	Ankrd6	ankyrin repeat domain 6	10.961
chr7	5759062	5759600	-273	Zfp787	zinc finger protein 787	15.699
chr1	43042981	43043990	229	AI597479	expressed sequence AI597479	15.053
chr3	1.01E+08	101099330	-252	Ttf2	transcription termination factor, RNA polymerase II	13.162
chr15	5090481	5091500	-86	Prkaa1	protein kinase, AMP-activated, alpha 1 catalytic subunit	14.333
chr7	48749201	48749880	-478	E2f8	E2F transcription factor 8	11.888
chr11	93701732	93703650	382	Mbtd1	mbt domain containing 1	26.081
chr2	1.22E+08	122061020	-151	Shf	Src homology 2 domain containing F	16.233
chr10	1.18E+08	118273080	-844	Dyrk2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	15.789
chr4	59719732	59720751	-24	E130308A19Rik	RIKEN cDNA E130308A19 gene	20.466
chr14	30658821	30659840	94	Ankrd28	ankyrin repeat domain 28	13.667
chr11	77328921	77329940	38	Trp53i13	transformation related protein 53 inducible protein 13	14.568
chr3	1.05E+08	104641460	29			18.183
chr2	73692961	73693980	8	Atf2	activating transcription factor 2	19.18
chr17	93070921	93072121	-655	Pja2	praja 2, RING-H2 motif containing	21.567
chr17	33529441	33530460	18	Tapbp	TAP binding protein	16.513
chr2	1.21E+08	121149140	101	Hypk	huntingtin interacting protein K	11.371
chr17	27282572	27283791	-982	Hmga1	high mobility group AT-hook 1	17.174
chr17	27283802	27284660	-11	Hmga1-rs1	high mobility group AT-hook I, related sequence 1	15.994
chr17	36443921	36444940	-769	Trim26	tripartite motif-containing 26	22.376
chr12	65835922	65836471	-320	Gm527	predicted gene 527	16.464
chr4	1.4E+08	140412161	41	Szrd1	SUZ RNA binding domain containing 1	22.318
chr11	98723421	98724100	-219	Cdc6	cell division cycle 6	15.034
chr3	88617261	88618550	-417	Mex3a	mex3 homolog A (C. elegans)	20.681
chr11	84955801	84956820	-160	Usp32	ubiquitin specific peptidase 32	19.184
chr11	61892581	61893600	-129	Specc1	sperm antigen with calponin homology and coiled-coil domains 1	26.158
chr7	1.18E+08	118035080	30	Smg1	SMG1 homolog, phosphatidylinositol 3-kinase-related kinase (C.	13.424
chr1	39521472	39522530	-108	Rnf149	ring finger protein 149	17.449
chr8	1.25E+08	125362641	-37	Rnf166	ring finger protein 166	21.5
chr9	94347372	94347960	-233	1190002N15Rik	RIKEN cDNA 1190002N15 gene	12.247
chr4	59096761	59097780	23	Dnajc25	DnaJ (Hsp40) homolog, subfamily C, member 25	25.7
chr7	1.21E+08	121499000	-259	Usp31	ubiquitin specific peptidase 31	12.966
chr4	1.29E+08	128751200	-113	C77080	expressed sequence C77080	12.766
chr12	70501041	70502060	83	Vcpkmt	valosin containing protein lysine (K) methyltransferase	21.602
chr14	13495672	13496640	-136	Slc4a7	solute carrier family 4, sodium bicarbonate cotransporter, member	14.699
chr15	88561822	88562520	-186	Brd1	bromodomain containing 1	14.961
chr15	93103142	93103891	-252	Gxylt1	glucoside xylosyltransferase 1	19.852
chr15	98699281	98700300	-551	Kmt2d	lysine (K)-specific methyltransferase 2D	15.948
chr15	1.02E+08	101964980	-51	Spryd3	SPRY domain containing 3	19.004
chr2	1.7E+08	169823160	-236	Zfp217	zinc finger protein 217	21.032
chr3	84566012	84566840	-60	Fhdc1	FH2 domain containing 1	20.04
chr4	45551501	45552520	-82	Shb	src homology 2 domain-containing transforming protein B	13.653
chr5	1.43E+08	143160910	22	Fbxl18	F-box and leucine-rich repeat protein 18	22.475
chr5	1.45E+08	145393860	96	Pdap1	PDGFA associated protein 1	17.962
chr7	18068621	18069300	-34	Ccdc61	coiled-coil domain containing 61	18.037
chr7	4622641	4623920	-183	Zfp865	zinc finger protein 865	21.966
chr19	5567501	5568520	-64	Ap5b1	adaptor-related protein complex 5, beta 1 subunit	17.317
chr2	91450152	91451500	-131	Arhgap1	Rho GTPase activating protein 1	24.473

chr6	1.14E+08	113663020	-596	Tatdn2	TatD DNase domain containing 2	17.013
chr8	1.25E+08	124794280	78	BC048644	cDNA sequence BC048644	24.97
chr8	1.25E+08	124793711	120	Slc7a5	solute carrier family 7 (cationic amino acid transporter, y+ system),	10.182
chr9	72330162	72331240	-106	Rfx7	regulatory factor X, 7	23.925
chr17	35505162	35505520	90	2310061I04Rik	RIKEN cDNA 2310061I04 gene	14.723
chr4	1.08E+08	107799670	-74	Zyg11b	zyg-ll family member B, cell cycle regulator	16.466
chr2	26732161	26733180	-19	Med22	mediator complex subunit 22	16.415
chr8	1.25E+08	125437881	38	Piezo1	piezo-type mechanosensitive ion channel component 1	15.62
chr8	1.15E+08	114530020	-255	Zfp1	zinc finger protein 1	14.538
chr4	43402701	43403380	-42	Rusc2	RUN and SH3 domain containing 2	18.392
chr1	59857001	59857680	-212	Fam117b	family with sequence similarity 117, member B	12.781
chr11	1.2E+08	119759560	-132	Baiap2	brain-specific angiogenesis inhibitor 1-associated protein 2	16.684
chr17	66010661	66011830	57	Wash1	WAS protein family homolog 1	22.235
chr10	1.16E+08	115986520	-419	Cnot2	CCR4-NOT transcription complex, subunit 2	16.654
chr4	43513881	43514900	-75	Ccdc107	coiled-coil domain containing 107	26.637
chr17	63548562	63549521	-402	Fer	fer (fms/fps related) protein kinase	20.895
chr19	5365881	5366900	-27	Banf1	barrier to autointegration factor 1	17.821
chr6	71561841	71563200	-94	Kdm3a	lysine (K)-specific demethylase 3A	16.107
chr3	95313561	95314580	11	Mllt11	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog,	18.08
chr4	44189121	44189800	-77	Rnf38	ring finger protein 38	17.86
chr7	97207021	97208040	15	Kctd21	potassium channel tetramerisation domain containing 21	13.321
chr4	1.03E+08	102617651	-91	Mier1	mesoderm induction early response 1 homolog (Xenopus laevis	13.395
chr1	93370461	93371501	10	Asb1	ankyrin repeat and SOCS box-containing 1	25.635
chr4	1.18E+08	117926620	85	Elovl1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3,	20.755
chr5	1.37E+08	137315120	-142	Vgf	VGF nerve growth factor inducible	15.89
chr6	72887262	72888180	20	Tmsb10	thymosin, beta 10	15.559
chr6	87777121	87777800	-40	Rab43	RAB43, member RAS oncogene family	15.567
chr9	75226782	75227720	-182	Leo1	Leo1, Paf1/RNA polymerase II complex component, homolog (S.	17.336
chr19	9055901	9056631	-63	Ahnak	AHNAK nucleoprotein (desmoyokin)	20.329
chr7	1.01E+08	101222420	36	Arap1	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 1	14.386
chr11	77853541	77854560	-86	Flot2	flotillin 2	16.059
chr15	57906081	57907440	-169	Zhx1	zinc fingers and homeoboxes 1	34.994
chr2	1.56E+08	156412580	110	4930405A21Rik	RIKEN cDNA 4930405A21 gene	16.159
chr7	44716962	44717381	-50	Tbc1d17	TBC1 domain family, member 17	18.709
chr7	44717392	44718181	45	Mir707	microRNA 707	16.948
chr15	1.02E+08	102075480	-257	Rarg	retinoic acid receptor, gamma	20.513
chr15	75443281	75444230	-184	Zfp41	zinc finger protein 41	14.756
chr17	27547821	27548840	-199	D17Wsu92e	DNA segment, Chr 17, Wayne State University 92, expressed	10.858
chr2	1.81E+08	181294800	-102	Zgpat	zinc finger, CCCH-type with G patch domain	23.438
chr19	29317181	29318200	-110	Jak2	Janus kinase 2	18.473
chr18	32702561	32703490	19	Gypc	glycophorin C	13.975
chr1	1.52E+08	152155780	3	BC003331	cDNA sequence BC003331	15.888
chr11	93771661	93772670	181	Nme2	NME/NM23 nucleoside diphosphate kinase 2	20.08
chr10	62418901	62419920	-204	Hnrnph3	heterogeneous nuclear ribonucleoprotein H3	33.011
chr11	98009081	98009690	-2	Med1	mediator complex subunit 1	13.023
chr15	82071581	82072600	11	Cenpm	centromere protein M	18.883
chr6	72309841	72310480	-183	Vamp5	vesicle-associated membrane protein 5	10.343
chr17	27583592	27584540	-30	Uhrf1bp1	UHRF1 (ICBP90) binding protein 1	15.611
chr11	75467832	75468440	-209	Myo1c	myosin IC	22.294
chr1	1.33E+08	133356160	285	Fam72a	family with sequence similarity 72, member A	15.632
chr15	89142901	89143580	-162	Sbf1	SET binding factor 1	19.638
chr9	44631801	44633160	-211	Kmt2a	lysine (K)-specific methyltransferase 2A	22.416
chr10	77647161	77648520	-69	Trappc10	trafficking protein particle complex 10	17.979
chr10	1.21E+08	121030140	-84	Xpot	exportin, tRNA (nuclear export receptor for tRNAs)	25.893
chr19	38288761	38289780	6	Fra10ac1	FRA10AC1 homolog (human)	15.158
chr7	1.01E+08	100807280	-268	Arhgef17	Rho guanine nucleotide exchange factor (GEF) 17	22.056
chr7	65987541	65988560	-415	Chsy1	chondroitin sulfate synthase 1	21.655
chr13	82188582	82189400	237	Mblac2	metallo-beta-lactamase domain containing 2	25.839
chr14	63606181	63607090	-6	Kif13b	kinesin family member 13B	10.58
chr12	71933121	71934670	533	3110056K07Rik	RIKEN cDNA 3110056K07 gene	28.952
chr19	8885561	8886711	203	Ttc9c	tetratricopeptide repeat domain 9C	31.687
chr4	11248901	11249740	-42	Dpy19l4	dpy-19-like 4 (C. elegans)	15.458
chr18	10610132	10610850	-141	Esco1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	15.357
chr18	11800412	11801400	21	Rbbp8	retinoblastoma binding protein 8	17.588
chr3	95904141	95904820	-122	Rprd2	regulation of nuclear pre-mRNA domain containing 2	15.34
chr15	27970142	27971120	-194	Trio	triple functional domain (PTPRF interacting)	14.625
chr17	28528381	28528821	-114	Brpf3	bromodomain and PHD finger containing, 3	13.295
chr3	1.17E+08	116800880	-30	Agl	amylo-1,6-glucosidase, 4-alpha-glucanotransferase	28.179
chr9	1.1E+08	110377260	-493	Setd2	SET domain containing 2	17.52
chr9	55735861	55736540	52	Scaper	S phase cyclin A-associated protein in the ER	16.568
chr4	35414401	35415080	27	3110043O21Rik	RIKEN cDNA 3110043O21 gene	10.508
chr5	1.45E+08	145021991	-643	Trrap	transformation/transcription domain-associated protein	26.898
chr5	1.45E+08	145022820	92	Trrap	transformation/transcription domain-associated protein	16.633
chr4	32985202	32986460	99	Mdn1	midasin homolog (yeast)	29.327
chr16	8744801	8745621	-759	1810013L24Rik	RIKEN cDNA 1810013L24 gene	12.988
chr16	8745632	8746160	-74	1810013L24Rik	RIKEN cDNA 1810013L24 gene	17.119
chr12	70086581	70088230	-14	Lrr1	leucine rich repeat protein 1	33.346
chr10	74504052	74504540	-316	Bcr	breakpoint cluster region	20.246
chr1	54870561	54871580	-138	Ankrd44	ankyrin repeat domain 44	13.459
chr9	1.07E+08	106544390	-22	Tex264	testis expressed gene 264	15.48
chr7	16033381	16034060	-119	Dact3	dapper homolog 3, antagonist of beta-catenin (xenopus)	20.068
chr5	1.25E+08	125151960	-64	Zfp664	zinc finger protein 664	14.632
chr2	26210941	26211620	45	Sdccag3	serologically defined colon cancer antigen 3	17.729
chr11	1.02E+08	102112880	-62	Atxn7l3	ataxin 7-like 3	17.51
chr4	1.27E+08	126628910	58	Gm12942	predicted gene 12942	18.916
chr19	38108221	38109460	-119			23.565
chr9	1.01E+08	100887470	-264	Msl2	male-specific lethal 2 homolog (Drosophila)	12.776
chr10	80005562	80006420	-18	Adat3	adenosine deaminase, tRNA-specific 3	15.477
chr1	10218021	10218960	-606	Arfgef1	ADP-ribosylation factor guanine nucleotide-exchange factor	15.257
chr5	34890121	34891140	59	Add1	adducin 1 (alpha)	15.392

chr16	96187122	96188020	-233	Brwd1	bromodomain and WD repeat domain containing 1	10.634
chr16	32563501	32564180	-550	Tnk2	tyrosine kinase, non-receptor, 2	15.566
chr15	76980761	76981440	-33	Rbfox2	RNA binding protein, fox-1 homolog (C. elegans) 2	16.149
chr17	55937392	55938500	-76	Uhrf1	ubiquitin-like, containing PHD and RING finger domains, 1	29.478
chr1	92883241	92884260	-100			14.182
chr8	72902801	72904080	-68	Gatad2a	GATA zinc finger domain containing 2A	20.067
chr10	61881701	61883060	-218	Vps26a	vacuolar protein sorting 26 homolog A (yeast)	24.605
chr16	36747541	36748220	241	Iqcb1	IQ calmodulin-binding motif containing 1	18.105
chr10	1.26E+08	126382121	-245	Ctdsp2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A)	41.229
chr11	1.17E+08	117082740	-106	Sept9	septin 9	14.805
chr15	99703301	99704250	-285	Lima1	LIM domain and actin binding 1	18.884
chr18	65012421	65013281	-274	Nedd4l	neural precursor cell expressed, developmentally down-regulated	20.267
chr4	1.26E+08	126470820	-83	Zmym4	zinc finger, MYM-type 4	20.502
chr5	1.01E+08	100739431	-141	Lin54	lin-54 homolog (C. elegans)	17.59
chr5	1.49E+08	149495620	31	Uspl1	ubiquitin specific peptidase like 1	14.591
chr8	1.13E+08	112758280	38	Phlpp2	PH domain and leucine rich repeat protein phosphatase 2	15.553
chr8	1.3E+08	129950340	-466	Pard3	par-3 family cell polarity regulator	19.464
chr9	98795212	98796410	86	Faim	Fas apoptotic inhibitory molecule	14.486
chr4	1.37E+08	137489540	183	Hp1bp3	heterochromatin protein 1, binding protein 3	15.778
chr17	3282701	3283561	76	Tiam2	T cell lymphoma invasion and metastasis 2	18.105
chr1	1.82E+08	182093460	25	Psen2	presenilin 2	22.23
chr7	24612601	24613550	-31	Arhgef1	Rho guanine nucleotide exchange factor (GEF) 1	14.021
chr11	96645062	96646360	-119	Nfe2l1	nuclear factor, erythroid derived 2,-like 1	26.654
chr11	96640581	96641260	-703	Nfe2l1	nuclear factor, erythroid derived 2,-like 1	11.13
chr11	6525652	6526640	-76	Tbrg4	transforming growth factor beta regulated gene 4	12.483
chr19	45071172	45071721	0	Lzts2	leucine zipper, putative tumor suppressor 2	19.845
chr9	1.03E+08	103224570	-241	Cdv3	carnitine deficiency-associated gene expressed in ventricle 3	12.846
chr16	45929241	45930260	0	Plcxd2	phosphatidylinositol-specific phospholipase C, X domain	12.274
chr12	1.11E+08	110894740	-645	Ppp2r5c	protein phosphatase 2, regulatory subunit B', gamma	14.074
chr14	69086032	69086930	23	Slc39a14	solute carrier family 39 (zinc transporter), member 14	13.266
chr10	1.28E+08	127635561	89	Timeless	timeless circadian clock 1	17.076
chrX	19819382	19820300	-14	Uba1	ubiquitin-like modifier activating enzyme 1	14.479
chr2	1.56E+08	155699940	34	Ergic3	ERGIC and golgi 3	18.928
chr4	1.17E+08	116750560	167	Tmem53	transmembrane protein 53	28.244
chr2	28354981	28356000	17	Ralgds	ral guanine nucleotide dissociation stimulator	15.684
chr4	1.4E+08	140333530	-300	Crocc	ciliary rootlet coiled-coil, rootletin	18.303
chr17	45624261	45624940	-13	Gtpbp2	GTP binding protein 2	16.353
chr7	1.01E+08	100983400	-142	Fchsd2	FCH and double SH3 domains 2	18.542
chr9	77330272	77330960	-71	Lrrc1	leucine rich repeat containing 1	21.581
chr4	1.51E+08	151029700	-744	Acot7	acyl-CoA thioesterase 7	23.08
chr17	74220981	74221660	56	Dpy30	dpy-30 homolog (C. elegans)	14.859
chr7	45788821	45789500	-269	Emp3	epithelial membrane protein 3	12.193
chr17	35474232	35474240	55	Ppp1r18	protein phosphatase 1, regulatory subunit 18	7
chr17	35472881	35474221	-97	Ppp1r18	protein phosphatase 1, regulatory subunit 18	17.881
chr11	1.2E+08	120284180	11	Hgs	HGF-regulated tyrosine kinase substrate	13.735
chr16	32796892	32797760	-205	Fyttd1	forty-two-three domain containing 1	28.381
chr11	68915362	68916300	-522	Per1	period circadian clock 1	19.865
chr11	53612902	53614260	144	Irf1	interferon regulatory factor 1	18.266
chr1	1.74E+08	173963670	-244	Pex19	peroxisomal biogenesis factor 19	12.125
chr16	94479362	94480560	-148	Pigp	phosphatidylinositol glycan anchor biosynthesis, class P	38.414
chr4	1.54E+08	154408280	-15	Nadk	NAD kinase	15.079
chr1	57914582	57914920	-121	Kctd18	potassium channel tetramerisation domain containing 18	13.654
chr12	1.09E+08	108723840	-106	Ccdc85c	coiled-coil domain containing 85C	18.398
chr5	1.15E+08	114641880	-36	Kctd10	potassium channel tetramerisation domain containing 10	17.015
chr4	1.54E+08	154335501	10	Gnb1	guanine nucleotide binding protein (G protein), beta 1	16.955
chr12	99147422	99148311	-152	Zc3h14	zinc finger CCCH type containing 14	13.367
chr8	1.08E+08	108060160	17	Cbfb	core binding factor beta	14.672
chr8	49608381	49609400	60	Dctd	dCMP deaminase	14.713
chr1	1.8E+08	180365240	-804	Kif26b	kinesin family member 26B	12.105
chr6	83472041	83473310	-48	Dguok	deoxyguanosine kinase	18.332
chr17	74243421	74244361	-78	Spast	spastin	17.67
chr11	1.16E+08	116123260	-43	Exoc7	exocyst complex component 7	18.999
chr15	8115801	8116820	-11	2410089E03Rik	RIKEN cDNA 2410089E03 gene	16.304
chr13	93945061	93945950	-35	Mtx3	metaxin 3	16.519
chr19	4509842	4511240	69	Pcx	pyruvate carboxylase	18.092
chr7	1.02E+08	101808240	-288	Lrrc51	leucine rich repeat containing 51	16.197
chr3	79653161	79654180	-64	Fnip2	folliculin interacting protein 2	18.616
chr9	1.04E+08	104121940	-6	Dnajc13	DnaJ (Hsp40) homolog, subfamily C, member 13	20.831
chr4	1.26E+08	125599400	34	Lsm10	U7 snRNP-specific Sm-like protein LSM10	20.73
chr4	45033001	45033930	47	Zbtb5	zinc finger and BTB domain containing 5	16.036
chr11	97515702	97516080	-153	Pcgf2	polycomb group ring finger 2	19.071
chr3	1.05E+08	105181380	43	Cttnbp2nl	CTTNBP2 N-terminal like	28.378
chr4	41948602	41949500	97	Il11ra1	interleukin 11 receptor, alpha chain 1	11.043
chr3	1.05E+08	104947120	8	Mov10	Moloney leukemia virus 10	22.511
chr2	1.55E+08	155384080	85	Trpc4ap	transient receptor potential cation channel, subfamily C, member 4	15.579
chr2	1.51E+08	150601640	95	Gins1	GINS complex subunit 1 (Psf1 homolog)	17.388
chr15	34387601	34388620	-245	Rpl30	ribosomal protein L30	20.069
chr15	76033202	76035560	-805	Plec	plectin	31.37
chr8	69788942	69789610	70	Naf1	nuclear assembly factor 1 homolog (S. cerevisiae)	14.394
chr3	1.09E+08	109156320	-348	Fam102b	family with sequence similarity 102, member B	18.604
chr8	67875662	67876580	-53	Tmem192	transmembrane protein 192	25.541
chr17	35124721	35125740	61	Cchcr1	coiled-coil alpha-helical rod protein 1	22.223
chr4	1.34E+08	133560160	-152	Pdik1l	PDLIM1 interacting kinase 1 like	29.913
chr17	23932601	23933620	52	Tbc1d24	TBC1 domain family, member 24	18.794
chr19	5963601	5964960	-74	Pola2	polymerase (DNA directed), alpha 2	18.913
chr14	69178101	69179120	20	Mir320	microRNA 320	18.063
chr10	79836421	79837100	22	Tcf3	transcription factor 3	20.792
chr7	3295621	3296591	506	Mboat7	membrane bound O-acyltransferase domain containing 7	19.825
chr11	61578081	61579020	-267	Prpsap2	phosphoribosyl pyrophosphate synthetase-associated protein 2	27.676
chr2	1.2E+08	119589220	41	Mga	MAX gene associated	17.697

chr19	44122481	44123500	7	Erlin1	ER lipid raft associated 1	23.731
chr6	54524242	54525120	-8	Plekha8	pleckstrin homology domain containing, family A (phosphoinositide	12.017
chr8	87578902	87579920	59	Trmt1	tRNA methyltransferase 1	16.476
chr19	41986601	41987250	142	Zdhhc16	zinc finger, DHHC domain containing 16	13.75
chr11	82686981	82687660	85	Rffl	ring finger and FYVE like domain containing protein	13.903
chr16	17532441	17533460	33	Smpd4	sphingomyelin phosphodiesterase 4	32.529
chr19	6046561	6047580	-75	Syvn1	synovial apoptosis inhibitor 1, synoviolin	18.764
chr9	1.11E+08	110963141	-271	Lrrfip2	leucine rich repeat (in FLII) interacting protein 2	16.24
chr17	35587121	35588820	-38	Gnl1	guanine nucleotide binding protein-like 1	24.832
chr3	96781681	96782071	96	Pias3	protein inhibitor of activated STAT 3	16.231
chr3	90137741	90139100	-18	Ubap2l	ubiquitin-associated protein 2-like	15.676
chr2	28662001	28663271	221	Ddx31	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 31	21.677
chr19	6976461	6977140	58	Trmt112	tRNA methyltransferase 11-2	20.828
chrX	44867761	44868440	-105	Slc25a14	solute carrier family 25 (mitochondrial carrier, brain), member 14	13.566
chr11	1.16E+08	116441160	-138	Rhbdf2	rhomboid 5 homolog 2 (Drosophila)	25.719
chr6	89560761	89561780	23	Chchd6	coiled-coil-helix-coiled-coil-helix domain containing 6	21.936
chr19	3906601	3907521	72	Tcirg1	T cell, immune regulator 1, ATPase, H+ transporting, lysosomal	16.783
chr3	38676021	38677040	-165	Ankrd50	ankyrin repeat domain 50	15.578
chr4	1.3E+08	129677481	-70	Tinagl1	tubulointerstitial nephritis antigen-like 1	16.722
chr7	98236201	98237070	-115	Tsku	tsukushi, small leucine rich proteoglycan	14.921
chr6	87637381	87638280	-21	Aplf	aprataxin and PNKP like factor	17.334
chr5	3808122	3809951	94	Ankib1	ankyrin repeat and IBR domain containing 1	20.829
chr15	99220161	99221180	-311	Tmbim6	transmembrane BAX inhibitor motif containing 6	20.358
chr7	1.41E+08	141020780	-14	Rnh1	ribonuclease/angiogenin inhibitor 1	31.154
chr11	98775441	98776120	-781	Rara	retinoic acid receptor, alpha	13.027
chr19	7008421	7009440	25	Bad	BCL2-associated agonist of cell death	30.494
chr19	46357641	46358421	-17	Nfkb2	nuclear factor of kappa light polypeptide gene enhancer in B cells	14.705
chr18	83048401	83049760	20	Zfp516	zinc finger protein 516	13.263
chr3	27344892	27345520	107	1700125G22Rik	RIKEN cDNA 1700125G22 gene	26.745
chr13	23628641	23629660	-561	Hist1h2be	histone cluster 1, H2be	18.644
chr15	97595301	97596320	-110	Rapgef3	Rap guanine nucleotide exchange factor (GEF) 3	20.579
chr11	1.21E+08	120600720	18	Gps1	G protein pathway suppressor 1	16.305
chr19	7053981	7055290	60	Vegfb	vascular endothelial growth factor B	17.613
chr11	6446401	6447420	20	Ccm2	cerebral cavernous malformation 2	23.132
chr11	4964681	4966170	-95	Gas2l1	growth arrest-specific 2 like 1	35.243
chr17	24915541	24916220	-120	Unkl	unkempt-like (Drosophila)	29.583
chr17	35308432	35309290	-218	Ddr1	discoidin domain receptor family, member 1	15.477
chr8	1.15E+08	114619440	-242	Bcar1	breast cancer anti-estrogen resistance 1	35.087
chr12	1.03E+08	102870680	37	Golga5	golgi autoantigen, golgin subfamily a, 5	15.33
chr14	54514241	54514920	-414	Dcaf11	DDB1 and CUL4 associated factor 11	19.845
chr9	21070821	21071500	39	Slc44a2	solute carrier family 44, member 2	17.214
chr11	1E+08	100344540	60	Acly	ATP citrate lyase	24.465
chr9	20702941	20703620	101	Dnmt1	DNA methyltransferase (cytosine-5) 1	15.9
chr5	1.23E+08	123040560	-193	Camkk2	calcium/calmodulin-dependent protein kinase kinase 2, beta	14.158
chr17	28077881	28078900	4	Tead3	TEA domain family member 3	18.542
chr2	29888041	29888720	-103	Set	SET nuclear oncogene	14.001
chr12	4241161	4241840	-159	Ptrhd1	peptidyl-tRNA hydrolase domain containing 1	15.085
chr17	33732761	33733780	-16	H2-DMa	histocompatibility 2, class II, locus DMa	22.917
chr3	1.09E+08	108573771	-91	Sars	seryl-aminoacyl-tRNA synthetase	21.348
chr12	86487841	86488770	97	Jdp2	Jun dimerization protein 2	14.553
chr12	73003441	73004800	-223	L3hypdh	L-3-hydroxyproline dehydratase (trans-)	17.283
chr11	1.16E+08	115927080	-251	Trim47	tripartite motif-containing 47	26.42
chr5	1.26E+08	125630340	73	Scarb1	scavenger receptor class B, member 1	17.286
chr4	1.39E+08	138847160	24	Iffo2	intermediate filament family orphan 2	14.358
chr3	84565821	84566001	455	Fhdc1	FH2 domain containing 1	8.278
chr12	81708852	81709820	-44	Susd6	sushi domain containing 6	15.043
chr6	17257062	17258400	91	Cav1	caveolin 1, caveolae protein	17.014
chr5	34686461	34686980	-70	Fam193a	family with sequence similarity 193, member A	15.141
chr9	1.07E+08	107410080	-60	Rassf1	Ras association (RalGDS/AF-6) domain family member 1	20.732
chr15	97791821	97792840	67	Tmem106c	transmembrane protein 106C	17.382
chr11	33063002	33063300	55	Npm1	nucleophosmin 1	14.906
chr11	53362682	53363680	22	Sept8	septin 8	16.196
chr17	56095672	56097280	-547	Ptprs	protein tyrosine phosphatase, receptor type, S	33.022
chr17	34849972	34850680	528	Ddx39b	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B	18.688
chr11	20641061	20642000	29	Aftph	aftiphilin	13.905
chr7	90004801	90005820	-114	Picalm	phosphatidylinositol binding clathrin assembly protein	12.526
chrX	7056132	7056700	121			17.699
chr2	1.65E+08	164979420	12	Slc35c2	solute carrier family 35, member C2	17.239
chr4	43061001	43062020	-109	Fam214b	family with sequence similarity 214, member B	22.691
chr10	1.28E+08	128151780	36	Pym1	PYM homolog 1, exon junction complex associated factor	23.01
chr15	79229521	79230880	-26	Tmem184b	transmembrane protein 184b	28.88
chr5	1.08E+08	107678680	41	Btbd8	BTB (POZ) domain containing 8	18.779
chr5	1.47E+08	146526060	141	Rnf6	ring finger protein (C3H2C3 type) 6	11.584
chr4	1.55E+08	154513890	-391	Mib2	mindbomb homolog 2 (Drosophila)	15.955
chr5	1.39E+08	139454400	-463	Sun1	Sad1 and UNC84 domain containing 1	19.074
chr5	23961382	23962180	-461	Agap3	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	19.425
chr11	58146801	58147480	155			15.05
chr7	1.21E+08	120635060	-63	Eef2k	eukaryotic elongation factor-2 kinase	12.297
chr11	58980302	58980480	-451	Iba57	IBA57, iron-sulfur cluster assembly homolog (S. cerevisiae)	14.343
chr6	72478212	72479500	74	Capg	capping protein (actin filament), gelsolin-like	24.828
chr13	49664382	49665430	-109	Nol8	nucleolar protein 8	16.665
chr2	93263022	93263700	-20	Cd82	CD82 antigen	13.177
chr9	95667332	95668180	-522	1700065D16Rik	RIKEN cDNA 1700065D16 gene	19.669
chr9	95667161	95667321	-7	1700065D16Rik	RIKEN cDNA 1700065D16 gene	10.812
chr16	4878442	4880020	327	Anks3	ankyrin repeat and sterile alpha motif domain containing 3	17.613
chr19	10271061	10272080	323	Tmem258	transmembrane protein 258	18.845
chr3	90164941	90165751	-102	Tpm3	tropomyosin 3, gamma	13.753
chr15	76483792	76484700	-90	Cyhr1	cysteine and histidine rich 1	16.472
chr2	25804992	25805961	-185	Camsap1	calmodulin regulated spectrin-associated protein 1	20.706
chr13	49432632	49433590	-49	Ippk	inositol 1,3,4,5,6-pentakisphosphate 2-kinase	14.147

chr4	62005801	62006820	-40	Alad	aminolevulinate, delta-, dehydratase	48.675
chr15	64141681	64142970	21	Asap1	ArfGAP with SH3 domain, ankyrin repeat and PH domain1	23.153
chr9	21118081	21119451	-168	Ilf3	interleukin enhancer binding factor 3	29.38
chr19	10622621	10623300	-152	Tmem216	transmembrane protein 216	15.57
chr4	1.41E+08	141065771	-172	Casp9	caspase 9	13.568
chr7	18430041	18431580	-434	Vasp	vasodilator-stimulated phosphoprotein	19.882
chr3	1.45E+08	144658230	66	Sh3glb1	SH3-domain GRB2-like B1 (endophilin)	20.744
chr3	68581401	68582420	-200	Schip1	schwannomin interacting protein 1	15.618
chr6	1.13E+08	113273040	-214	Brpf1	bromodomain and PHD finger containing, 1	14.779
chr4	1.07E+08	107378120	-77	Magoh	mago homolog, exon junction complex core component	29.936
chr4	1.49E+08	148582040	-16	Tmem201	transmembrane protein 201	18.292
chr8	48115441	48116800	12	Casp3	caspase 3	33.473
chr2	1.28E+08	127819260	-96	Bcl2l11	BCL2-like 11 (apoptosis facilitator)	12.227
chr7	1.43E+08	143358620	-62	Nap1l4	nucleosome assembly protein 1-like 4	13.648
chr5	96402112	96403560	-544	Cnot6l	CCR4-NOT transcription complex, subunit 6-like	13.472
chr4	1.27E+08	126579960	-161	Zmym6	zinc finger, MYM-type 6	26.475
chr14	66668272	66669061	274	Cdca2	cell division cycle associated 2	15.854
chr7	1.34E+08	133615580	6	Fank1	fibronectin type 3 and ankyrin repeat domains 1	11.32
chr17	27636221	27637580	5	Anks1	ankyrin repeat and SAM domain containing 1	27.664
chr3	1.52E+08	152333940	211	Zzz3	zinc finger, ZZ domain containing 3	23.194
chr10	79329481	79330160	-352	Arid3a	AT rich interactive domain 3A (BRIGHT-like)	15.308
chr15	38245241	38246940	-790	Klf10	Kruppel-like factor 10	28.416
chr2	1.8E+08	179972880	315	Ss18l1	synovial sarcoma translocation gene on chromosome 18-like 1	16.429
chr3	1.32E+08	131502720	356	Papss1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	15.432
chr17	47875061	47876080	3	Oard1	O-acyl-ADP-ribose deacylase 1	20.613
chr5	64508892	64509900	-96	Tbc1d1	TBC1 domain family, member 1	14.534
chr16	13816302	13816920	112	Pdxdc1	pyridoxal-dependent decarboxylase domain containing 1	13.612
chr16	13816241	13816291	457	Pdxdc1	pyridoxal-dependent decarboxylase domain containing 1	8.2
chr3	87854492	87855320	-26	Pear1	platelet endothelial aggregation receptor 1	14.447
chr6	42278661	42279891	-159	Zyx	zyxin	20.935
chr2	1.81E+08	180640011	80	Gid8	GID complex subunit 8 homolog (S. cerevisiae)	15.564
chr15	1.02E+08	102032820	-385	Zfp740	zinc finger protein 740	20.238
chr2	30180782	30181760	54	Sh3glb2	SH3-domain GRB2-like endophilin B2	13.725
chr3	1.08E+08	108215200	32	Ampd2	adenosine monophosphate deaminase 2	28.296
chr2	1.53E+08	152522640	37	Bcl2l1	BCL2-like 1	14.643
chr16	17979541	17980510	59	Dgcr6	DiGeorge syndrome critical region gene 6	17.599
chr17	80635761	80636780	81	Map4k3	mitogen-activated protein kinase kinase kinase kinase 3	18.512
chr7	25327622	25328300	-213	Atp5sl	ATP5S-like	17.354
chr11	4999361	5000720	-128	Rhbdd3	rhomboid domain containing 3	31.194
chr2	29946181	29946860	100	Zer1	zyg-11 related, cell cycle regulator	15.761
chr2	31394241	31394920	-80	Fubp3	far upstream element (FUSE) binding protein 3	13.158
chr3	37611141	37611541	-158			19.175
chr11	69812912	69814070	-166	Phf23	PHD finger protein 23	15.563
chr7	1.02E+08	102084230	52	Nup98	nucleoporin 98	22.578
chr3	1.05E+08	104917200	-289	Rhoc	ras homolog gene family, member C	16.759
chr8	35575962	35576920	-110	Dctn6	dynactin 6	11.57
chr8	64483041	64483940	-179	Palld	palladin, cytoskeletal associated protein	16.2
chr5	31165421	31166100	-155	Agbl5	ATP/GTP binding protein-like 5	14.923
chr4	1.09E+08	109165160	38	Cdkn2c	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	20.563
chr10	1.23E+08	122600940	-167			22.889
chr11	62946921	62947341	-521	Pmp22	peripheral myelin protein 22	15
chr11	62947352	62948280	164			17.328
chr8	94023601	94024590	37			19.642
chr4	1.55E+08	154836570	357	B3galt6	UDP-Gal:betaGal beta 1,3-galactosyltransferase, polypeptide 6	15.401
chr5	1.37E+08	136530640	-544			18.763
chr18	21144261	21145280	-197			18.686
chr18	46866281	46867980	-77	Ap3s1	adaptor-related protein complex 3, sigma 1 subunit	18.426
chr17	55671652	55672620	-788			14.9
chr15	79174441	79175460	175	Maff	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein	20.046
chr17	45018721	45019820	-11	Nfkbie	nuclear factor of kappa light polypeptide gene enhancer in B cells	23.807
chr10	79552342	79552860	-210			21.909
chr18	38060961	38061640	97			14.567
chr5	1.22E+08	122098171	-310			32.455
chr12	52298461	52299480	-163			16.508
chr12	59979061	59979740	84			11.308
chr8	86498572	86498720	-7			10.446
chr14	29957741	29958660	-261			15.081
chr5	23540581	23541260	-165	Fam126a	family with sequence similarity 126, member A	15.227
chr5	33591661	33592340	-139	Ctbp1	C-terminal binding protein 1	14.878
chr1	51422621	51423300	-16			17.591
chr3	88227621	88228881	-48			23.325
chr14	60510481	60511500	6	Spryd7	SPRY domain containing 7	19.557
chr1	74439282	74439600	174	Rqcd1	rcd1 (required for cell differentiation) homolog 1 (S. pombe)	18.726
chr5	94167761	94168780	-350	Sept11	septin 11	14.825
chr16	32833461	32834111	-61			17.892
chr3	89998942	89999360	-28	Il6ra	interleukin 6 receptor, alpha	17.316
chr5	1.25E+08	124707240	549			37.135
chr4	1.17E+08	116788300	-573			12.124
chr9	20394122	20394900	658	Fbxl12	F-box and leucine-rich repeat protein 12	14.722
chr9	1.19E+08	119251190	-161			13.818
chr4	69896521	69897051	10			28.057
chr11	1.2E+08	120166331	648	0610009L18Rik	RIKEN cDNA 0610009L18 gene	29.12
chr11	78159242	78160220	41	Unc119	unc-119 homolog (C. elegans)	12.828
chr5	1.15E+08	115380910	50	Acads	acyl-Coenzyme A dehydrogenase, short chain	36.834
chr2	48635641	48636320	-138	Acvr2a	activin receptor IIA	19.966
chr4	86140892	86141720	-16	Plin2	perilipin 2	20.797
chr3	1.38E+08	138380340	-480	Adh5	alcohol dehydrogenase 5 (class III), chi polypeptide	20.723
chr11	62064621	62065640	-49	Adora2b	adenosine A2b receptor	37.302
chr1	1.82E+08	182406260	100	Parp1	poly (ADP-ribose) polymerase family, member 1	13.354
chr1	1.8E+08	179633560	-36	Adss	adenylosuccinate synthetase, non muscle	24.638

chr7	1.27E+08	126590840	-309	Aldoa	aldolase A, fructose-bisphosphate	8.488
chr7	1.27E+08	126590571	10	Aldoa	aldolase A, fructose-bisphosphate	15.194
chr11	4886481	4887021	-76	Ap1b1	adaptor protein complex AP-1, beta 1 subunit	16.944
chr5	1.37E+08	137331100	97	Ap1s1	adaptor protein complex AP-1, sigma 1	14.545
chr10	80144801	80146160	-140	Ap3d1	adaptor-related protein complex 3, delta 1 subunit	26.411
chr14	25471101	25471780	59	Arf4	ADP-ribosylation factor 4	17.113
chr5	1E+08	100219991	-256	Hnrnpd	heterogeneous nuclear ribonucleoprotein D	24.524
chr16	87587741	87588420	-70	Bach1	BTB and CNC homology 1	13.844
chr7	25367401	25368400	-13	Exosc5	exosome component 5	18.171
chr1	59707741	59708420	-745	Bmpr2	bone morphogenetic protein receptor, type II (serine/threonine	15.029
chr10	96046261	96046741	-188	Btg1	B cell translocation gene 1, anti-proliferative	23.917
chr15	98462301	98463320	9	Cacnb3	calcium channel, voltage-dependent, beta 3 subunit	17.087
chr8	87736321	87737680	36	Calr	calreticulin	21.826
chr7	37816161	37816840	-250	Ccne1	cyclin E1	16.113
chr17	23978592	23979520	-47	Ccnf	cyclin F	22.023
chr10	1.16E+08	116468020	23	Cct2	chaperonin containing Tcp1, subunit 2 (beta)	17.034
chr10	1.28E+08	128313280	-45	Cd63	CD63 antigen	16.214
chr9	1.1E+08	109733640	21	Cdc25a	cell division cycle 25A	15.647
chr17	28820781	28821800	-143	Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	16.056
chr7	1.21E+08	120773780	21	Cdr2	cerebellar degeneration-related 2	13.923
chr17	15409192	15409971	-76	Chd1	chromodomain helicase DNA binding protein 1	22.525
chr9	57563582	57564380	16	Clk3	CDC-like kinase 3	16.095
chr2	30237901	30238061	-78	Ppp2r4	protein phosphatase 2A activator, regulatory subunit B	8
chr2	30238072	30238850	402	Ppp2r4	protein phosphatase 2A activator, regulatory subunit B	13.639
chr13	42062421	42063440	-63	Hivep1	human immunodeficiency virus type I enhancer binding protein 1	16.547
chr9	57443341	57444101	69	Csk	c-src tyrosine kinase	38.882
chr10	1.1E+08	110324770	39	Csrp2	cysteine and glycine-rich protein 2	15.688
chr14	62076222	62076860	-31	Ctsb	cathepsin B	10.006
chr11	69816282	69817300	-30	Dvl2	dishevelled 2, dsh homolog (Drosophila)	25.04
chr3	14554832	14555740	-129	E2f5	E2F transcription factor 5	17.619
chr10	80579321	80580000	-100	Eef2	eukaryotic translation elongation factor 2	15.996
chr18	34986242	34987020	-550	Egr1	early growth response 1	14.314
chr8	28725921	28726600	-3	Eif4ebp1	eukaryotic translation initiation factor 4E binding protein 1	17.066
chr1	1.34E+08	133835271	95	Elk4	ELK4, member of ETS oncogene family	9.4
chr8	73467492	73468291	-773	Ell	elongation factor RNA polymerase II	15.181
chr8	73468302	73468900	-63	Ell	elongation factor RNA polymerase II	23.109
chr19	7408261	7409620	-36	Mark2	MAP/microtubule affinity regulating kinase 2	22.059
chr7	18540002	18541220	50	Ercc2	excision repair cross-complementing rodent repair deficiency,	27.766
chr19	6988361	6989380	-18	Esrra	estrogen related receptor, alpha	17.833
chr8	47969302	47969920	-243	Acsl1	acyl-CoA synthetase long-chain family member 1	16.814
chr19	34355981	34357221	-55	Fas	Fas (TNF receptor superfamily member 6)	19.613
chr5	31496921	31497740	-204	Ppm1g	protein phosphatase 1G (formerly 2C), magnesium-dependent,	23.232
chr17	35430612	35431740	-234	Flot1	flotillin 1	15.523
chr7	18468461	18469120	-223	Fosb	FBJ osteosarcoma oncogene B	14.882
chr1	59426221	59427070	-48	Fzd7	frizzled homolog 7 (Drosophila)	14.751
chr19	8964592	8965460	-76	Ganab	alpha glucosidase 2 alpha neutral subunit	13.111
chr5	1.3E+08	130040140	17	Gbas	glioblastoma amplified sequence	18.498
chr14	46111141	46111820	-201	Gch1	GTP cyclohydrolase 1	16.975
chr19	16199142	16200240	-159	Gnaq	guanine nucleotide binding protein, alpha q polypeptide	14.066
chr11	48643352	48643800	-207	Gnb2l1	guanine nucleotide binding protein (G protein), beta polypeptide 2	16.877
chr5	1.1E+08	110417380	37	Golga3	golgi autoantigen, golgin subfamily a, 3	19.985
chr7	46663301	46664320	113	Hps5	Hermansky-Pudlak syndrome 5 homolog (human)	21.776
chr8	98323581	98324260	78	Cfap20	cilia and flagella associated protein 20	26.404
chr6	1.13E+08	113012600	-14	Thumpd3	THUMP domain containing 3	19.29
chr11	59007872	59008700	-139	Guk1	guanylate kinase 1	27.304
chrX	70219521	70220540	-953	Hcfc1	host cell factor C1	12.852
chr3	1.17E+08	116655290	36	Hiat1	hippocampus abundant gene transcript 1	22.906
chr17	45036401	45037760	-238	Hsp90ab1	heat shock protein 90 alpha (cytosolic), class B member 1	18.279
chr1	55032192	55032951	-94	Hspd1	heat shock protein 1 (chaperonin)	16.489
chr9	20781481	20782840	-280	Icam5	intercellular adhesion molecule 5, telencephalin	17.472
chr4	1.35E+08	135416220	-172	Id3	inhibitor of DNA binding 3	20.483
chr5	1.09E+08	108900980	7	Idua	iduronidase, alpha-L-	11.015
chr19	34706521	34707200	-26	Ifit1	interferon-induced protein with tetratricopeptide repeats 1	13.155
chr15	1.02E+08	101971991	-674	Igfbp6	insulin-like growth factor binding protein 6	19.449
chr15	1.02E+08	101972120	-159	Igfbp6	insulin-like growth factor binding protein 6	9.432
chr8	85298022	85298810	-83	Il15	interleukin 15	13.129
chr6	94666092	94666880	-878	Lrig1	leucine-rich repeats and immunoglobulin-like domains 1	34.977
chr6	94665412	94666081	-138	Lrig1	leucine-rich repeats and immunoglobulin-like domains 1	28.511
chr11	97004381	97005060	-738	Kpnb1	karyopherin (importin) beta 1	21.901
chr2	71587341	71588020	-98	Itga6	integrin alpha 6	15.364
chr12	21532541	21532951	-19	Itgb1bp1	integrin beta 1 binding protein 1	14.098
chr9	36516681	36517660	79	Stt3a	STT3, subunit of the oligosaccharyltransferase complex, homolog	17.092
chr5	65081862	65082800	-327	Klf3	Kruppel-like factor 3 (basic)	15.748
chr4	1.29E+08	129175520	61	Kpna6	karyopherin (importin) alpha 6	27.689
chr11	60514901	60515920	-475	Llgl1	lethal giant larvae homolog 1 (Drosophila)	14.164
chr10	1.27E+08	127025360	-799	Lrp1	low density lipoprotein receptor-related protein 1	22.103
chr10	1.27E+08	127024421	11	Lrp1	low density lipoprotein receptor-related protein 1	20.852
chr15	10926241	10926920	99	Amacr	alpha-methylacyl-CoA racemase	16.265
chr9	63820041	63820741	-326	Smad6	SMAD family member 6	17.857
chr12	77881081	77882050	-477	Max	Max protein	15.83
chr10	75375961	75376640	-82	Mmp11	matrix metallopeptidase 11	20.177
chr8	97061161	97062180	-77	Mt2	metallothionein 2	22.487
chr4	1.16E+08	115962780	-348	Mast2	microtubule associated serine/threonine kinase 2	22.119
chr1	9685241	9686260	-327	Mybl1	myeloblastosis oncogene-like 1	21.581
chr11	75467421	75467821	-83	Myo1c	myosin IC	15.55
chr10	1.27E+08	127070240	-172	1700012D01Rik	RIKEN cDNA 1700012D01 gene	20.007
chr2	1.66E+08	165684250	-46	Ncoa3	nuclear receptor coactivator 3	27.93
chr15	66799002	66800140	-261	Ndrg1	N-myc downstream regulated gene 1	51.907
chr4	81977342	81978261	-791	Nfib	nuclear factor I/B	22.254
chr4	81977061	81977331	-186	Nfib	nuclear factor I/B	15.852

chr1	39844941	39845960	-9	Map4k4	mitogen-activated protein kinase kinase kinase kinase 4	12.505
chr2	3200502	3202120	-173	Nmt2	N-myristoyltransferase 2	34.064
chr13	1.21E+08	120528640	-76	Nnt	nicotinamide nucleotide transhydrogenase	20.157
chr15	1E+08	100251680	-37	Gm5475	predicted gene 5475	15.444
chr11	76214922	76215760	-5	Nxn	nucleoredoxin	27.257
chr10	80229461	80229911	-99	Oaz1	ornithine decarboxylase antizyme 1	16.711
chr15	36553401	36554420	-348	Pabpc1	poly(A) binding protein, cytoplasmic 1	21.971
chr5	1.38E+08	137841710	-74	Pcolce	procollagen C-endopeptidase enhancer protein	17.551
chr5	1.39E+08	139249040	-66	Pdgfa	platelet derived growth factor, alpha	17.449
chr19	4099381	4100740	62	Pitpnm1	phosphatidylinositol transfer protein, membrane-associated 1	19.167
chr8	86862521	86863200	-223	Prkaca	protein kinase, cAMP dependent, catalytic, alpha	17.027
chrX	70580962	70582180	-215	Plxna3	plexin A3	24.24
chr19	7041061	7042430	-347	Ppp1r14b	protein phosphatase 1, regulatory (inhibitor) subunit 14B	31.92
chr5	1.36E+08	135974160	-261	Por	P450 (cytochrome) oxidoreductase	19.854
chr4	1.22E+08	122338851	-44	Ppt1	palmitoyl-protein thioesterase 1	31.726
chr11	97096402	97097041	-55	Npepps	aminopeptidase puromycin sensitive	15.948
chr19	32822241	32822920	-994	Pten	phosphatase and tensin homolog	16.056
chr15	5191461	5192430	-543	Ptger4	prostaglandin E receptor 4 (subtype EP4)	25.363
chr1	1.91E+08	191428591	-785	Ptpn14	protein tyrosine phosphatase, non-receptor type 14	12.925
chr18	67849381	67850660	-30	Ptpn2	protein tyrosine phosphatase, non-receptor type 2	22.46
chr7	18907741	18908760	-155	Pvrl2	poliovirus receptor-related 2	40.769
chr5	1.11E+08	110526860	-50	Pxmp2	peroxisomal membrane protein 2	16.306
chr18	34748472	34750040	-169	Kif20a	kinesin family member 20A	24.221
chr11	98752602	98753981	-495	Rara	retinoic acid receptor, alpha	22.606
chr19	5637201	5637661	-59	Rela	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	15.696
chr13	21187101	21187811	60	Trim27	tripartite motif-containing 27	21.817
chr13	34009861	34010540	59	Serpinb6a	serine (or cysteine) peptidase inhibitor, clade B, member 6a	19.417
chr2	32783141	32784160	-71	Rpl12	ribosomal protein L12	14.682
chr5	1.47E+08	147388300	95	Polr1d	polymerase (RNA) I polypeptide D	16.606
chr10	79694981	79696000	-70	Rps15	ribosomal protein S15	15.673
chr10	61075221	61076240	52	Sar1a	SAR1 gene homolog A (S. cerevisiae)	18.218
chr11	65604202	65604980	-99	Map2k4	mitogen-activated protein kinase kinase 4	19.242
chr10	60542622	60543460	-19	Sgpl1	sphingosine phosphate lyase 1	21.401
chr7	1.02E+08	101537940	-159	Clpb	ClpB caseinolytic peptidase B	17.992
chr18	58002981	58004151	-481	Slc12a2	solute carrier family 12, member 2	21.701
chr3	1.05E+08	104768280	45	Slc16a1	solute carrier family 16 (monocarboxylic acid transporters),	16.173
chr8	1.1E+08	109825440	-48	Sntb2	syntrophin, basic 2	28.461
chr2	69662022	69662940	80	Ssb	Sjogren syndrome antigen B	19.883
chr7	1.1E+08	110013460	-69	Swap70	SWA-70 protein	21.825
chr13	95889212	95890200	64	Tbca	tubulin cofactor A	14.048
chr19	55794162	55795360	-299	Tcf7l2	transcription factor 7 like 2, T cell specific, HMG box	19.271
chr4	47373561	47374580	-252			14.716
chr11	77981381	77982400	-145	Traf4	TNF receptor associated factor 4	22.669
chr7	1.11E+08	110820620	-22	Ctr9	Ctr9, Paf1/RNA polymerase II complex component, homolog (S.	22.81
chr15	78232641	78233660	-36	Tst	thiosulfate sulfurtransferase, mitochondrial	23.333
chr11	51843541	51844560	-161	Ube2b	ubiquitin-conjugating enzyme E2B	19.632
chr7	25497281	25497820	-57	Axl	AXL receptor tyrosine kinase	11.978
chr5	65714521	65715821	-194	Ugdh	UDP-glucose dehydrogenase	21.3
chr11	68904152	68904881	-207	Vamp2	vesicle-associated membrane protein 2	16.414
chr4	1.5E+08	149902260	3	Vamp3	vesicle-associated membrane protein 3	24.009
chr2	27248621	27249640	-296	Vav2	vav 2 oncogene	19.258
chr6	1.14E+08	113590260	-7	Vhl	von Hippel-Lindau tumor suppressor	17.517
chr12	1.09E+08	109240640	-818	Yy1	YY1 transcription factor	17.564
chr11	88815141	88815820	-13	Trim25	tripartite motif-containing 25	17.088
chr7	80734701	80735250	-646	Zscan2	zinc finger and SCAN domain containing 2	11.413
chr1	1.94E+08	193607781	35	Slc30a1	solute carrier family 30 (zinc transporter), member 1	13.608
chr4	1.01E+08	100918120	-25	Ak4	adenylate kinase 4	20.365
chr11	1.01E+08	101284300	-468	Rnd2	Rho family GTPase 2	19.882
chr13	94871692	94872580	-296	Arsb	arylsulfatase B	15.019
chr17	23897241	23897920	-551	Atp6v0c	ATPase, H+ transporting, lysosomal V0 subunit C	13.554
chr2	1.31E+08	130598080	97	A730017L22Rik	RIKEN cDNA A730017L22 gene	17.784
chr3	1.46E+08	145861981	23	Bcl10	B cell leukemia/lymphoma 10	18.484
chr7	1.27E+08	127500340	84	Bcl7c	B cell CLL/lymphoma 7C	15.62
chr7	1.39E+08	138748560	-201	Bnip3	BCL2/adenovirus E1B interacting protein 3	15.677
chr14	65962721	65963650	-198	Bnip3l	BCL2/adenovirus E1B interacting protein 3-like	13.942
chr15	83390441	83391871	-183	Tspo	translocator protein	28.441
chr7	29903432	29904310	-63	Capns1	calpain, small subunit 1	12.765
chr14	30165481	30166160	87	Capn7	calpain 7	18.28
chr4	1.38E+08	138465340	-145	Capzb	capping protein (actin filament) muscle Z-line, beta	14.396
chr2	1.54E+08	154128460	25	Cbfa2t2	core-binding factor, runt domain, alpha subunit 2, translocated to,	24.114
chr11	22889832	22890621	-367	Cct4	chaperonin containing Tcp1, subunit 4 (delta)	28.346
chr10	1.26E+08	126467080	-86	Cdk4	cyclin-dependent kinase 4	32.591
chr5	3349341	3350360	-49	Cdk6	cyclin-dependent kinase 6	20.775
chr7	34765072	34765950	-185	Cebpg	CCAAT/enhancer binding protein (C/EBP), gamma	20.718
chr4	1.07E+08	107421980	51	Cpt2	carnitine palmitoyltransferase 2	31.597
chr5	1.35E+08	134837540	31	Clip2	CAP-GLY domain containing linker protein 2	18.344
chr9	1.08E+08	108122380	46	Dag1	dystroglycan 1	16.852
chr15	76338501	76339520	63	Dgat1	diacylglycerol O-acyltransferase 1	26.333
chr8	87798201	87798880	-189	Dnase2a	deoxyribonuclease II alpha	14.523
chr11	32121962	32122820	-98	Rhbdf1	rhomboid family 1 (Drosophila)	20.159
chr18	46722461	46723480	-65	Eif1a	eukaryotic translation initiation factor 1A	19.581
chr8	74310401	74311760	-139	Nr2f6	nuclear receptor subfamily 2, group F, member 6	17.203
chr10	1.28E+08	127993000	-210	Erbb3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	17.697
chr3	1.22E+08	121715920	-139	F3	coagulation factor III	19.742
chr7	44971801	44972480	-276	Fcgrt	Fc receptor, IgG, alpha chain transporter	12.669
chr4	1.24E+08	124203700	17	Fhl3	four and a half LIM domains 3	23.16
chr10	84532161	84532840	74	Tmem263	transmembrane protein 263	15.38
chr19	5447141	5448160	-48	Fosl1	fos-like antigen 1	28.936
chr7	96956262	96957120	-252	Gab2	growth factor receptor bound protein 2-associated protein 2	13.534
chr10	79664041	79664720	-283	Gamt	guanidinoacetate methyltransferase	23.493

chr2	38748582	38749450	-546	Nr6a1	nuclear receptor subfamily 6, group A, member 1	17.175
chr15	3532941	3533620	72	Ghr	growth hormone receptor	16.277
chr5	1.41E+08	141083000	59	Gna12	guanine nucleotide binding protein, alpha 12	12.062
chr7	16049782	16050720	-57	Gng8	guanine nucleotide binding protein (G protein), gamma 8	15.037
chr15	76157972	76158961	-83	Gpaa1	GPI anchor attachment protein 1	19.553
chr9	20726741	20727730	-40	S1pr2	sphingosine-1-phosphate receptor 2	13.37
chr19	47907701	47908711	-94	Gsto1	glutathione S-transferase omega 1	18.693
chr17	33551201	33552170	508	Wdr46	WD repeat domain 46	18.764
chr18	36641461	36642140	-21	Hbegf	heparin-binding EGF-like growth factor	18.524
chr9	44085092	44086100	-114	H2afx	H2A histone family, member X	15.26
chr1	55032962	55033420	498	Hspe1	heat shock protein 1 (chaperonin 10)	17.356
chr9	1.07E+08	107427851	32	Hyal2	hyaluronoglucosaminidase 2	18.946
chr7	67824782	67825580	-589	Igf1r	insulin-like growth factor I receptor	19.925
chr7	1.02E+08	101712421	-144	Inppl1	inositol polyphosphate phosphatase-like 1	26.2
chr14	53531301	53532320	56	Ajuba	ajuba LIM protein	16.741
chr19	23207402	23208281	-482	Klf9	Kruppel-like factor 9	17.765
chr1	1.55E+08	155095760	-246	Lamc1	laminin, gamma 1	21.878
chr11	97615082	97615851	-296	Lasp1	LIM and SH3 protein 1	25.589
chr11	82596881	82597900	86	Lig3	ligase III, DNA, ATP-dependent	24.113
chr5	1.35E+08	134974220	-323	Limk1	LIM-domain containing, protein kinase	26.134
chr11	3308862	3309560	30	Limk2	LIM motif-containing protein kinase 2	15.825
chr7	25104241	25105260	-3	Lipe	lipase, hormone sensitive	19.246
chr18	56832472	56833610	-141	Lmnb1	lamin B1	18.861
chr9	58110822	58111720	78	Loxl1	lysyl oxidase-like 1	12.972
chr18	76366272	76367060	-400	Smad2	SMAD family member 2	19.617
chr5	1.4E+08	140044300	-220	Mafk	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein	26.644
chr2	1.21E+08	120700260	-59	Ccndbp1	cyclin D-type binding-protein 1	18.088
chr18	70693141	70694110	-36			12.141
chr4	44321721	44322400	43	Melk	maternal embryonic leucine zipper kinase	14.557
chr17	13496301	13497101	-380	Mllt4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog,	24.062
chr11	74646661	74647421	-78	Mnt	max binding protein	24.039
chr4	1.47E+08	146883060	-107	Clcn6	chloride channel, voltage-sensitive 6	17.596
chr1	95308801	95309820	13	Hdlbp	high density lipoprotein (HDL) binding protein	20.773
chr7	28475001	28475680	64			13.309
chr3	98098501	98099141	-122	Notch2	notch 2	15.5
chr16	13732282	13733280	-74	Ntan1	N-terminal Asn amidase	15.646
chr7	26966862	26967970	-105	Numbl	numb-like	14.998
chr11	6191092	6192080	-14	Ogdh	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	14.803
chr6	1.13E+08	113293100	-163	Ogg1	8-oxoguanine DNA-glycosylase 1	17.687
chr11	68914941	68915351	-5	Per1	period circadian clock 1	20.707
chr4	1.5E+08	149889210	-300	Per3	period circadian clock 3	15.193
chr11	70471121	70472140	-785	Pfn1	profilin 1	15.55
chr3	1.47E+08	146750800	42	Prkacb	protein kinase, cAMP dependent, catalytic, beta	18.47
chr14	29454942	29455560	-34	Prkcd	protein kinase C, delta	16.421
chr12	1.06E+08	106186020	-212	Papola	poly (A) polymerase alpha	18.046
chr10	1.28E+08	127969680	-387	Pa2g4	proliferation-associated 2G4	17.19
chr17	78787181	78788200	-60	Eif2ak2	eukaryotic translation initiation factor 2-alpha kinase 2	13.349
chr2	1.32E+08	131601760	51	Prnp	prion protein	13.277
chr11	1.18E+08	118065340	22	Cyth1	cytohesin 1	18.377
chr5	1.44E+08	143878480	-30	Cyth3	cytohesin 3	17.162
chr5	20567432	20568300	-245	Ptpn12	protein tyrosine phosphatase, non-receptor type 12	12.509
chr9	50280302	50281240	100	Pts	6-pyruvoyl-tetrahydropterin synthase	18.394
chr11	6375872	6376360	-37	Purb	purine rich element binding protein B	14.529
chr8	11478142	11479080	-140	Rab20	RAB20, member RAS oncogene family	13.516
chr19	4201381	4202060	-117	Rad9a	RAD9 homolog A	18.947
chr15	1.02E+08	102086020	46	Rarg	retinoic acid receptor, gamma	16.401
chr5	78339562	78341100	62	Rest	RE1-silencing transcription factor	27.475
chr10	39420281	39421640	463	E130307A14Rik	RIKEN cDNA E130307A14 gene	18.876
chr1	1.53E+08	153263471	-105	Rnf2	ring finger protein 2	14.877
chr11	1.01E+08	101258460	-199	Rpl27	ribosomal protein L27	23.778
chr13	1.01E+08	101208820	34	Serf1	small EDRK-rich factor 1	17.024
chr2	1.21E+08	121140980	1	Serf2	small EDRK-rich factor 2	15.925
chr11	1.17E+08	116670320	-404	Mfsd11	major facilitator superfamily domain containing 11	26.018
chr3	89504321	89504401	-117	Shc1	src homology 2 domain-containing transforming protein C1	14.5
chr6	72026621	72027640	13	St3gal5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	13.708
chr7	18252221	18253061	-425	Six5	sine oculis-related homeobox 5	12.607
chr13	74229152	74229991	-128	Slc12a7	solute carrier family 12, member 7	18.483
chr8	23941781	23942800	45	Slc20a2	solute carrier family 20, member 2	12.184
chr11	53734802	53735640	-95	Slc22a5	solute carrier family 22 (organic cation transporter), member 5	17.937
chr4	1.19E+08	118606931	-71	Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1	20.492
chr2	1.67E+08	167229711	-76	Snai1	snail family zinc finger 1	20.437
chr16	90108912	90110200	-45	Sod1	superoxide dismutase 1, soluble	16.185
chr12	88277261	88277790	-67	Sptlc2	serine palmitoyltransferase, long chain base subunit 2	13.698
chr15	81874762	81875300	-178	Nhp2l1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	13.786
chr10	79518521	79519321	-11			26.613
chr12	8797161	8797840	96	Sdc1	syndecan 1	22.15
chr2	1.64E+08	164134980	-113	Sdc4	syndecan 4	11.152
chr11	1.2E+08	120415080	118	Anapc11	anaphase promoting complex subunit 11	14.389
chr8	1.1E+08	109782731	226	Chtf8	CTF8, chromosome transmission fidelity factor 8	18.021
chr14	17031972	17032640	-79	Nr1d2	nuclear receptor subfamily 1, group D, member 2	19.689
chr11	1.18E+08	118171760	81	Timp2	tissue inhibitor of metalloproteinase 2	16.975
chr5	1.25E+08	124889931	-641	Atp6v0a2	ATPase, H+ transporting, lysosomal V0 subunit A2	21.47
chr5	1.25E+08	124890500	-21	Atp6v0a2	ATPase, H+ transporting, lysosomal V0 subunit A2	26.24
chr1	1.94E+08	193793880	-164	Traf5	TNF receptor-associated factor 5	24.333
chr16	32528141	32529160	7	Tfrc	transferrin receptor	20.023
chr15	98762521	98762951	-312	Tuba1b	tubulin, alpha 1B	27.674
chr4	58049901	58050920	55	Txn1	thioredoxin 1	20.992
chr5	1.47E+08	147105840	-211	Usp12	ubiquitin specific peptidase 12	19.886
chr4	59283081	59283760	-184	Ugcg	UDP-glucose ceramide glucosyltransferase	18.376
chr9	1.08E+08	108206360	20	Usp4	ubiquitin specific peptidase 4 (proto-oncogene)	23.838

chr11	52203941	52204620	-5	Vdac1	voltage-dependent anion channel 1	13.135
chr2	13491201	13492391	-368	Vim	vimentin	41.076
chr15	99198061	99198940	16			21.032
chr5	37276921	37277600	-29	Wfs1	Wolfram syndrome 1 homolog (human)	12.473
chr17	32120481	32121160	-193	Wiz	widely-interspaced zinc finger motifs	14.374
chr7	28087602	28088420	-23	Zfp36	zinc finger protein 36	18.96
chr2	1.22E+08	122394560	-116	Slc30a4	solute carrier family 30 (zinc transporter), member 4	17.511
chr19	4148082	4149020	-112	Coro1b	coronin, actin binding protein 1B	14.606
chr5	1.14E+08	114170300	-85	Coro1c	coronin, actin binding protein 1C	22.195
chr1	1.68E+08	167600620	-175	Creg1	cellular repressor of E1A-stimulated genes 1	16.781
chr5	93158382	93159320	-53	G3bp2	GTPase activating protein (SH3 domain) binding protein 2	21.123
chr6	86698301	86699620	52	Gmcl1	germ cell-less homolog 1 (Drosophila)	22.998
chr6	29162141	29162820	-173	Impdh1	inosine 5'-phosphate dehydrogenase 1	19.901
chr10	7415741	7416760	60	Katna1	katanin p60 (ATPase-containing) subunit A1	22.532
chr8	23631701	23632380	-60	Nek3	NIMA (never in mitosis gene a)-related expressed kinase 3	13.161
chr2	76448321	76449340	3	Prkra	protein kinase, interferon inducible double stranded RNA	18.423
chr15	1E+08	100443140	344	C330013E15Rik	RIKEN cDNA C330013E15 gene	13.485
chr6	1.21E+08	121212030	0	Usp18	ubiquitin specific peptidase 18	19.907
chr8	11555581	11556931	-173	Ing1	inhibitor of growth family, member 1	20.393
chr2	33037801	33038281	71	Angptl2	angiopoietin-like 2	17.375
chr13	55454001	55454680	-354	Grk6	G protein-coupled receptor kinase 6	16.7
chr17	12161461	12162480	48	Map3k4	mitogen-activated protein kinase kinase kinase 4	23.873
chr7	1.27E+08	126551060	-54	Mapk3	mitogen-activated protein kinase 3	14.489
chr2	91824882	91825750	-307	Creb3l1	cAMP responsive element binding protein 3-like 1	17.681
chr7	1.14E+08	114067910	-154	Psma1	proteasome (prosome, macropain) subunit, alpha type 1	12.488
chr13	94404401	94405080	-508	Homer1	homer homolog 1 (Drosophila)	18.406
chr4	1.26E+08	126257200	496	AU040320	expressed sequence AU040320	19.779
chr5	1.38E+08	138391560	31	Cops6	COP9 (constitutive photomorphogenic) homolog, subunit 6	17.714
chr1	1.73E+08	173182960	136	Pfdn2	prefoldin 2	15.634
chr6	86758821	86759500	58	Anxa4	annexin A4	22.184
chr15	76303821	76305860	140	Hsf1	heat shock factor 1	22.361
chr2	35158721	35159610	-147	Stom	stomatin	17.687
chr6	1.25E+08	124678340	92	Phb2	prohibitin 2	15.231
chr17	33637901	33639200	-41	H2-Ke6	H2-K region expressed gene 6	26.085
chr5	1.44E+08	144073640	-220	Eif2ak1	eukaryotic translation initiation factor 2 alpha kinase 1	16.837
chr10	99444901	99445920	-102	Kitl	kit ligand	18.064
chr17	24277062	24277761	-139	Pkd1	polycystic kidney disease 1 homolog	13.187
chr8	1.09E+08	108828190	-4	Psmb10	proteasome (prosome, macropain) subunit, beta type 10	29.71
chr17	26235832	26237120	-404	Dusp1	dual specificity phosphatase 1	21.523
chr6	1.25E+08	124796320	176	Cdca3	cell division cycle associated 3	14.314
chr2	1.18E+08	118080300	-98	Eif2ak4	eukaryotic translation initiation factor 2 alpha kinase 4	14.772
chr5	8428261	8429280	-48	Dbf4	DBF4 homolog (S. cerevisiae)	23.733
chr2	1.21E+08	120963410	37	Trp53bp1	transformation related protein 53 binding protein 1	21.119
chr4	1.35E+08	135294500	-116	Tceb3	transcription elongation factor B (SIII), polypeptide 3	20.675
chr7	1.43E+08	143409960	-140	Cars	cysteinyl-tRNA synthetase	12.809
chr10	60778401	60779420	-30	Pald1	phosphatase domain containing, paladin 1	17.423
chr19	29390972	29391641	9	Insl6	insulin-like 6	13.988
chr15	9067461	9068140	348	Lmbrd2	LMBR1 domain containing 2	20.324
chr6	82739862	82740700	-169	Hk2	hexokinase 2	14.389
chr16	20461352	20462480	183	Gm15760	mitochondrial ribosomal protein S18B pseudogene	15.861
chr17	35577261	35578520	-87	Abcf1	ATP-binding cassette, sub-family F (GCN20), member 1	22.205
chr15	81787681	81788700	-5	Pmm1	phosphomannomutase 1	18.457
chr4	1.09E+08	108975100	-153	Rnf11	ring finger protein 11	22.456
chr4	1.35E+08	134545480	-175	Clic4	chloride intracellular channel 4 (mitochondrial)	14.172
chr5	1.23E+08	123161461	-149	Kdm2b	lysine (K)-specific demethylase 2B	21.213
chr17	65512901	65514180	-442	Vapa	vesicle-associated membrane protein, associated protein A	17.923
chr11	1.16E+08	116015820	-5	Acox1	acyl-Coenzyme A oxidase 1, palmitoyl	21.975
chr10	98536761	98537780	411	Poc1b	POC1 centriolar protein homolog B (Chlamydomonas)	19.951
chr8	82607761	82608330	153	Anapc10	anaphase promoting complex subunit 10	14.406
chr17	63185601	63186520	-18	Fbxl17	F-box and leucine-rich repeat protein 17	17.982
chr8	73601841	73602520	-40	Lsm4	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	13.295
chr8	1.08E+08	108154340	63	Tradd	TNFRSF1A-associated via death domain	15.43
chr9	98372541	98373220	83	4930579K19Rik	RIKEN cDNA 4930579K19 gene	17.352
chr13	55339421	55340100	-408	Mxd3	Max dimerization protein 3	18.216
chr19	4125561	4126441	41	Tmem134	transmembrane protein 134	19
chr12	17715701	17716720	-84	Hpcal1	hippocalcin-like 1	13.742
chr11	87884221	87884731	2	Vezf1	vascular endothelial zinc finger 1	17.059
chr14	32276152	32276880	-266	Mapk8	mitogen-activated protein kinase 8	18.519
chr5	24195421	24196440	50			16.562
chr9	20899801	20900820	-2	Cdc37	cell division cycle 37	18.798
chr15	99079582	99080601	-96	Mcrs1	microspherule protein 1	23.473
chr10	1.27E+08	127486740	-26	Atp5b	ATP synthase, H+ transporting mitochondrial F1 complex, beta	14.173
chr17	47074021	47075380	-17	Bysl	bystin-like	21.342
chr2	1.64E+08	163512800	15	Wisp2	WNT1 inducible signaling pathway protein 2	26.955
chr11	1.03E+08	103084260	5	Map3k14	mitogen-activated protein kinase kinase kinase 14	20.429
chr3	89504412	89505680	568	Shc1	src homology 2 domain-containing transforming protein C1	21.675
chr5	93117841	93118460	92	Cdkl2	cyclin-dependent kinase-like 2 (CDC2-related kinase)	11.042
chr2	1.57E+08	157258160	46	Blcap	bladder cancer associated protein homolog (human)	20.54
chr15	81637401	81638801	-568	Tef	thyrotroph embryonic factor	39.979
chr11	78117381	78118060	-66	Spag5	sperm associated antigen 5	24.723
chr4	1.23E+08	123420340	94	Rragc	Ras-related GTP binding C	19.132
chr6	30826441	30827460	5	Copg2	coatomer protein complex, subunit gamma 2	27.747
chr9	22218321	22219340	-72	Rp9	retinitis pigmentosa 9 (human)	26.937
chr8	24673801	24674820	-312	Gpat4	glycerol-3-phosphate acyltransferase 4	21.244
chr15	38463592	38464500	-191	Azin1	antizyme inhibitor 1	20.458
chr5	1.06E+08	106117400	46	Zfp326	zinc finger protein 326	15.039
chr6	50191141	50191820	-125	Dfna5	deafness, autosomal dominant 5 (human)	12.722
chr5	1.45E+08	144509180	-31	Bri3	brain protein I3	14.145
chr5	1.13E+08	112566081	-711	Tfip11	tuftelin interacting protein 11	6.458
chr5	1.13E+08	112567180	-36	Tfip11	tuftelin interacting protein 11	35.5

chr8	86497701	86498561	-149	Dnajb1	DnaJ (Hsp40) homolog, subfamily B, member 1	21.779
chr17	8121552	8121920	-251	Mpc1	mitochondrial pyruvate carrier 1	17.071
chr11	78351981	78353000	-35	Tnfaip1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	21.535
chr11	20232721	20233740	-514	Slc1a4	solute carrier family 1 (glutamate/neutral amino acid transporter),	15.755
chr5	1.36E+08	136220320	-713	Ywhag	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	19.534
chr1	36883881	36884900	-317	Tmem131	transmembrane protein 131	16.433
chr9	1.07E+08	107400560	-90	Nprl2	nitrogen permease regulator-like 2	23.798
chr17	43129681	43130680	-110	Slc25a27	solute carrier family 25, member 27	14.468
chr19	46358432	46359340	-120	Nfkb2	nuclear factor of kappa light polypeptide gene enhancer in B cells	21.96
chr17	33448861	33449540	-14	Cd320	CD320 antigen	18.022
chr5	93212412	93213720	-72	Uso1	USO1 vesicle docking factor	26.193
chr5	34976481	34977490	20	Nop14	NOP14 nucleolar protein	17.378
chr16	96095352	96096240	17	Psmg1	proteasome (prosome, macropain) assembly chaperone 1	19.101
chr2	1.73E+08	172665260	-15	Rbm38	RNA binding motif protein 38	22.51
chr7	1.02E+08	102124780	-161	Rhog	ras homolog gene family, member G	20.964
chr15	35099901	35100920	-15	Stk3	serine/threonine kinase 3	19.546
chr6	1.49E+08	148904340	-369	Fam60a	family with sequence similarity 60, member A	11.602
chr7	18823081	18824440	-208	Clptm1	cleft lip and palate associated transmembrane protein 1	21.188
chr17	87015521	87016200	-145	Socs5	suppressor of cytokine signaling 5	15.891
chr19	53997441	53998790	-73	Shoc2	soc-2 (suppressor of clear) homolog (C. elegans)	13.764
chr4	1.23E+08	123407760	-125	Mycbp	c-myc binding protein	21.564
chr9	88280321	88281000	-370	Syncrip	synaptotagmin binding, cytoplasmic RNA interacting protein	15.92
chr14	85972401	85973400	-39	Diaph3	diaphanous related formin 3	15.522
chrX	44707281	44708300	-31	Elf4	E74-like factor 4 (ets domain transcription factor)	11.882
chr17	34848981	34849961	-327	Ddx39b	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B	20.592
chr15	81292981	81294000	-81	Rbx1	ring-box 1	18.224
chr10	41965492	41965520	-349	Foxo3	forkhead box O3	5.679
chr11	69807101	69807780	-125	Gabarap	gamma-aminobutyric acid receptor associated protein	17.482
chr10	80780941	80782300	-121	Fzr1	fizzy/cell division cycle 20 related 1 (Drosophila)	32.445
chr6	28429441	28430120	-578	Snd1	staphylococcal nuclease and tudor domain containing 1	14.854
chr4	1.19E+08	118731171	-71	P3h1	prolyl 3-hydroxylase 1	23.266
chr12	71856172	71856620	-66	Actr10	ARP10 actin-related protein 10	13.163
chr5	1.23E+08	122683560	-181	Anapc7	anaphase promoting complex subunit 7	37.464
chr2	1.55E+08	155209660	-164	Acss2	acyl-CoA synthetase short-chain family member 2	11.959
chr19	8808232	8809060	177	Stx5a	syntaxin 5A	22.748
chr5	78384281	78385300	71	Noa1	nitric oxide associated 1	15.286
chr9	1.14E+08	114239661	-1	Crtap	cartilage associated protein	18.068
chr9	59284101	59285120	-230	Arih1	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog	18.068
chr13	54584281	54585170	90	Arl10	ADP-ribosylation factor-like 10	14.835
chr14	30469781	30470720	184	Btd	biotinidase	24.924
chr1	1.69E+08	169187060	54	Aldh9a1	aldehyde dehydrogenase 9, subfamily A1	18.165
chr3	54780461	54781140	-234	Supt20	suppressor of Ty 20	24.124
chr11	1.14E+08	113568160	-230	Cdc42ep4	CDC42 effector protein (Rho GTPase binding) 4	22.974
chr7	45582781	45583800	-41	Sphk2	sphingosine kinase 2	15.473
chr19	5731172	5732400	-54	Sssca1	Sjogren's syndrome/scleroderma autoantigen 1 homolog (human)	30.496
chr8	1.26E+08	126140850	-294	Zfp276	zinc finger protein (C2H2 type) 276	18.105
chr9	1.09E+08	108519840	29	Slc25a20	solute carrier family 25 (mitochondrial carnitine/acylcarnitine	15.359
chr19	7059202	7060100	-335	Dnajc4	DnaJ (Hsp40) homolog, subfamily C, member 4	13.389
chr2	1.04E+08	103829090	-3	Fbxo3	F-box protein 3	14.252
chr6	83080732	83081720	62	Mogs	mannosyl-oligosaccharide glucosidase	20.159
chr2	1.6E+08	160423220	-10	Plcg1	phospholipase C, gamma 1	13.843
chr14	68834892	68835570	6	Bin3	bridging integrator 3	14.965
chr7	63817402	63818680	-176	Klf13	Kruppel-like factor 13	28.439
chr11	20442161	20442840	-756	Sertad2	SERTA domain containing 2	15.595
chr1	74438262	74439271	262			17.441
chr4	1.16E+08	116150090	11	Akr1a1	aldo-keto reductase family 1, member A1 (aldehyde reductase)	16.454
chr11	97265841	97266611	-24	Arhgap23	Rho GTPase activating protein 23	27.455
chr16	46416252	46417030	-337	Pvrl3	poliovirus receptor-related 3	13.486
chr10	80571402	80571791	-747	Pias4	protein inhibitor of activated STAT 4	18.429
chr10	80570481	80571391	-87	Pias4	protein inhibitor of activated STAT 4	26.11
chr8	64115612	64116520	-247	Sh3rf1	SH3 domain containing ring finger 1	13.377
chr11	50220381	50222080	88	Hnrnph1	heterogeneous nuclear ribonucleoprotein H1	17.115
chr5	1.41E+08	140758640	-7	Chst12	carbohydrate sulfotransferase 12	24.812
chr9	21296241	21297260	-546	Carm1	coactivator-associated arginine methyltransferase 1	22.213
chr15	76195701	76196380	-113	Hgh1	HGH1 homolog	20.85
chr8	60380261	60380371	211			5.182
chr8	60380382	60381280	726			11.37
chr13	1.02E+08	101876580	86	Cenph	centromere protein H	12.244
chr11	60543192	60543771	-23			18.584
chr19	5687861	5688791	582	Pcnxl3	pecanex-like 3 (Drosophila)	30.484
chr1	1.86E+08	185735200	408	1700056E22Rik	RIKEN cDNA 1700056E22 gene	23.328
chr4	1.48E+08	148270940	-169	Ube4b	ubiquitination factor E4B	24.82
chr11	77896381	77897400	-312	Eral1	Era (G-protein)-like 1 (E. coli)	16.823
chr1	1.21E+08	121332740	98	Ralb	v-ral simian leukemia viral oncogene homolog B (ras related)	17.402
chr4	45039192	45040010	-108	Polr1e	polymerase (RNA) I polypeptide E	10.984
chr17	24423221	24424580	66	Noxo1	NADPH oxidase organizer 1	22.386
chr17	65850181	65851200	40	Twsg1	twisted gastrulation homolog 1 (Drosophila)	23.859
chr17	23453541	23453771	-302	Pkmyt1	protein kinase, membrane associated tyrosine/threonine 1	10.435
chr6	88411682	88412580	49	Eefsec	eukaryotic elongation factor, selenocysteine-tRNA-specific	25.571
chr8	73695412	73696020	-64	Ifi30	interferon gamma inducible protein 30	16.576
chr16	18412021	18413040	96	Gnb1l	guanine nucleotide binding protein (G protein), beta polypeptide 1-	22.113
chr2	1.54E+08	154482740	-151	Raly	hnRNP-associated with lethal yellow	10.733
chr5	1.45E+08	145368360	-17	Arpc1b	actin related protein 2/3 complex, subunit 1B	27.924
chr1	95173141	95173820	-286	Pask	PAS domain containing serine/threonine kinase	14.477
chr3	90595272	90596060	-241	Chtop	chromatin target of PRMT1	14.506
chr8	73588262	73589260	-34	Pgpep1	pyroglutamyl-peptidase I	21.485
chr5	1.24E+08	123785500	-208	Diablo	diablo homolog (Drosophila)	31.063
chr14	60553321	60554000	38	Trim13	tripartite motif-containing 13	11.944
chr13	85662082	85662660	-216	Ccnh	cyclin H	15.711
chr9	1.08E+08	108426000	-45	Ndufaf3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex,	18.701

chr4	1.48E+08	148362400	-151	Ctnnbip1	catenin beta interacting protein 1	18.753
chr4	1.3E+08	129678281	-735	Tinagl1	tubulointerstitial nephritis antigen-like 1	8.667
chr4	1.3E+08	129677700	-170	Tinagl1	tubulointerstitial nephritis antigen-like 1	15.322
chr11	69662261	69663280	-42	Plscr3	phospholipid scramblase 3	16.034
chr14	1.2E+08	120046520	-194	Ipo5	importin 5	11.919
chr10	60147701	60148590	-6	Slc29a3	solute carrier family 29 (nucleoside transporters), member 3	11.963
chr11	23565401	23566420	25	Pex13	peroxisomal biogenesis factor 13	22.879
chr3	96642621	96643481	-311	Txnip	thioredoxin interacting protein	21.221
chr3	1.27E+08	126589001	-552	Camk2d	calcium/calmodulin-dependent protein kinase II, delta	18.632
chr9	99052201	99053560	60	Cep70	centrosomal protein 70	18.43
chr11	1.06E+08	106304240	15	Ern1	endoplasmic reticulum (ER) to nucleus signalling 1	13.851
chr4	47495282	47495951	-145	Sec61b	Sec61 beta subunit	10.383
chr7	4288081	4288760	-370	Hspbp1	HSPA (heat shock 70kDa) binding protein, cytoplasmic	12.632
chr17	15100761	15101780	61	Fam120b	family with sequence similarity 120, member B	14.629
chr2	6129861	6130880	-104	Echdc3	enoyl Coenzyme A hydratase domain containing 3	17.04
chr5	53121052	53121731	-992	Anapc4	anaphase promoting complex subunit 4	13.459
chr8	1.07E+08	107230220	-13	Cmtm3	CKLF-like MARVEL transmembrane domain containing 3	14.932
chr5	45738292	45739080	-209	Qdpr	quinoid dihydropteridine reductase	17.02
chr6	83537661	83538660	2	Stambp	STAM binding protein	24.171
chr4	1.55E+08	154683680	-94	Mxra8	matrix-remodelling associated 8	15.364
chr9	44157502	44158860	362	Trappc4	trafficking protein particle complex 4	18.032
chr13	36124602	36125540	-37	Fars2	phenylalanine-tRNA synthetase 2 (mitochondrial)	15.854
chr5	45781252	45782020	14	Lap3	leucine aminopeptidase 3	19.126
chr2	1.73E+08	173303100	-13	Ppp4r1l-ps	protein phosphatase 4, regulatory subunit 1-like, pseudogene	17.214
chr3	1.23E+08	122916780	-118	1810037I17Rik	RIKEN cDNA 1810037I17 gene	11.734
chr13	24808101	24808780	-682	BC005537	cDNA sequence BC005537	12.234
chr5	38508412	38509240	95	Lyar	Ly1 antibody reactive clone	18.335
chr11	60729441	60730460	37	Natd1	N-acetyltransferase domain containing 1	18.698
chr17	46108421	46109440	-507	Mrpl2	mitochondrial ribosomal protein L2	24.535
chr11	1.15E+08	115420140	206	Gga3	golgi associated, gamma adaptin ear containing, ARF binding	22.87
chr11	72993582	72994260	643	Tax1bp3	Tax1 (human T cell leukemia virus type I) binding protein 3	24.848
chr12	4831741	4832461	-168	Sf3b6	splicing factor 3B, subunit 6	19.542
chr19	10592042	10593380	422	Cpsf7	cleavage and polyadenylation specific factor 7	16.234
chr15	76178361	76179040	151	Maf1	MAF1 homolog (S. cerevisiae)	15.274
chr3	1.35E+08	135376440	122	4930539J05Rik	RIKEN cDNA 4930539J05 gene	17.875
chr9	1.06E+08	106296920	-243	Acy1	aminoacylase 1	16.371
chr4	1.34E+08	134126600	-675	Tmem57	transmembrane protein 57	17.551
chr9	20392521	20394111	-108	Fbxl12	F-box and leucine-rich repeat protein 12	24.698
chr11	1.21E+08	121021630	-47	Ogfod3	2-oxoglutarate and iron-dependent oxygenase domain containing	23.33
chr15	75748292	75749250	44	Pycrl	pyrroline-5-carboxylate reductase-like	18.049
chr11	84695542	84697060	89	Pigw	phosphatidylinositol glycan anchor biosynthesis, class W	13.035
chr10	1.2E+08	119630360	-100	Llph	LLP homolog, long-term synaptic facilitation (Aplysia)	18.01
chr14	19181781	19182460	-13	Mrps16	mitochondrial ribosomal protein S16	15.18
chr15	83177601	83178280	73	Arfgap3	ADP-ribosylation factor GTPase activating protein 3	21.125
chr1	95633501	95635140	-51	Ing5	inhibitor of growth family, member 5	31.718
chr18	65925321	65926340	-117	Sec11c	SEC11 homolog C, signal peptidase complex subunit	19.418
chr7	30271561	30272920	140	U2af1l4	U2 small nuclear RNA auxiliary factor 1-like 4	16.891
chr3	1.31E+08	130699060	-32	Ostc	oligosaccharyltransferase complex subunit	18.351
chr11	66868481	66869311	31	Sco1	SCO cytochrome oxidase deficient homolog 1 (yeast)	16.518
chr11	66869322	66870180	886	Sco1	SCO cytochrome oxidase deficient homolog 1 (yeast)	16.252
chr10	59398001	59399020	-41	Anapc16	anaphase promoting complex subunit 16	24.77
chr5	1.14E+08	114033331	-505	Iscu	IscU iron-sulfur cluster scaffold homolog (E. coli)	8.8
chr5	1.14E+08	114034130	-75	Iscu	IscU iron-sulfur cluster scaffold homolog (E. coli)	28.286
chr19	3999761	4000780	-310	Nudt8	nudix (nucleoside diphosphate linked moiety X)-type motif 8	14.652
chr17	56681822	56683100	-2	Alkbh7	alkB, alkylation repair homolog 7 (E. coli)	26.753
chr10	53284461	53285660	-316	Asf1a	anti-silencing function 1A histone chaperone	18.795
chr4	40891121	40892110	-28	Aptx	aprataxin	12.017
chr8	13889681	13890840	-12	Coprs	coordinator of PRMT5, differentiation stimulator	25.302
chr11	98254602	98255580	-13	Mien1	migration and invasion enhancer 1	18.242
chr1	74216922	74217891	539	Aamp	angio-associated migratory protein	20.531
chr6	86330842	86331780	-6	Fam136a	family with sequence similarity 136, member A	14.806
chr6	1.25E+08	125157740	-31	Ncapd2	non-SMC condensin I complex, subunit D2	13.838
chr16	57527661	57528550	-92	Cmss1	cms small ribosomal subunit 1	25.495
chr2	1.25E+08	125365140	89	Eid1	EP300 interacting inhibitor of differentiation 1	13.815
chr7	28020542	28021440	-185	Timm50	translocase of inner mitochondrial membrane 50	28.374
chr5	1.48E+08	148171320	-106	Pomp	proteasome maturation protein	23.323
chr2	3630181	3631091	-94	Fam107b	family with sequence similarity 107, member B	23.978
chr3	1.21E+08	121164100	-42	Rwdd3	RWD domain containing 3	17.797
chr16	90616612	90616800	-476	Mis18a	MIS18 kinetochore protein homolog A (S. pombe)	12.527
chr9	1.05E+08	105253460	236	Nek11	NIMA (never in mitosis gene a)-related expressed kinase 11	14.613
chr11	98403972	98404500	-901	Ormdl3	ORM1-like 3 (S. cerevisiae)	19.396
chr11	98403821	98403961	-556	Ormdl3	ORM1-like 3 (S. cerevisiae)	8.571
chr5	1.24E+08	124373020	-446	Ogfod2	2-oxoglutarate and iron-dependent oxygenase domain containing	22.583
chr15	12265501	12266520	-211	Golph3	golgi phosphoprotein 3	17.588
chr1	1.54E+08	154149400	-60	Tsen15	tRNA splicing endonuclease 15 homolog (S. cerevisiae)	14.339
chr9	70341241	70342940	56	Sltm	SAFB-like, transcription modulator	26.396
chr9	1.04E+08	103922360	-214	Uba5	ubiquitin-like modifier activating enzyme 5	35.117
chr2	1.63E+08	163111600	-355	Oser1	oxidative stress responsive serine rich 1	21.787
chr10	51921741	51922420	46	Dcbld1	discoidin, CUB and LCCL domain containing 1	12.862
chr10	1.28E+08	127615260	-78	Spryd4	SPRY domain containing 4	19.803
chr8	88322481	88323500	-44	4921524J17Rik	RIKEN cDNA 4921524J17 gene	18.339
chrX	81826441	81826951	-45	Tab3	TGF-beta activated kinase 1/MAP3K7 binding protein 3	11.824
chr10	13242722	13243680	96	Adat2	adenosine deaminase, tRNA-specific 2	15.334
chr13	45012601	45013560	-12	Dtnbp1	dystrobrevin binding protein 1	12.647
chr11	1.21E+08	121170900	-23	Wdr45b	WD repeat domain 45B	16.604
chr6	52642881	52643560	-87	Tax1bp1	Tax1 (human T cell leukemia virus type I) binding protein 1	19.611
chr6	86362041	86363400	64	Pcyox1	prenylcysteine oxidase 1	18.176
chr18	80417821	80418500	-125	Pqlc1	PQ loop repeat containing 1	16.963
chr2	84479461	84480140	-133	Tmx2	thioredoxin-related transmembrane protein 2	19.698
chr7	44114321	44114891	-158	2410002F23Rik	RIKEN cDNA 2410002F23 gene	15.333

chr17	52943101	52944701	-262	Rab5a	RAB5A, member RAS oncogene family	25.413
chr17	28679782	28680700	-564	Kctd20	potassium channel tetramerisation domain containing 20	18.297
chr5	24112152	24113130	-574	Smarcd3	SWI/SNF related, matrix associated, actin dependent regulator of	13.17
chr7	15256481	15257500	-175	Napa	N-ethylmaleimide sensitive fusion protein attachment protein alpha	12.929
chr10	89161602	89162580	3	Actr6	ARP6 actin-related protein 6	21.365
chr17	17078302	17079220	-189	Riok2	RIO kinase 2 (yeast)	20.147
chr6	1.16E+08	115740041	-455	Cand2	cullin-associated and neddylation-dissociated 2 (putative)	16.688
chr17	27362521	27363460	-159	Rps10	ribosomal protein S10	19.88
chr17	46235292	46235920	-220	2310039H08Rik	RIKEN cDNA 2310039H08 gene	19.525
chr4	1.29E+08	128837900	114	Rbbp4	retinoblastoma binding protein 4	20.869
chr11	72423061	72423721	-65	Ube2g1	ubiquitin-conjugating enzyme E2G 1	15.985
chr11	70834921	70835600	238	Derl2	Der1-like domain family, member 2	16.713
chr7	81635701	81636860	-186	Fam103a1	family with sequence similarity 103, member A1	18.632
chr11	1.06E+08	106033760	-106	Ddx42	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	13.229
chr9	1.1E+08	110469740	-122	Nradd	neurotrophin receptor associated death domain	20.165
chr11	69796221	69797240	-205	Elp5	elongator acetyltransferase complex subunit 5	19.738
chr11	76059482	76060370	-5	Rnmtl1	RNA methyltransferase like 1	16.983
chr8	27250321	27251650	-151	Lsm1	LSM1 homolog, U6 small nuclear RNA associated (S. cerevisiae)	14.843
chr11	59018221	59019130	-6			12.087
chr9	1.15E+08	114580121	-180	Cmtm6	CKLF-like MARVEL transmembrane domain containing 6	23.062
chr18	52590532	52591540	-26	Srfbp1	serum response factor binding protein 1	16.964
chr8	36963612	36964460	14	Eri1	exoribonuclease 1	16.353
chr4	56895941	56897230	-200	Ikbkap	inhibitor of kappa light polypeptide enhancer in B cells, kinase	26.503
chr2	1.31E+08	130851761	21			30.869
chr10	39946702	39947960	-250	Gtf3c6	general transcription factor IIIC, polypeptide 6, alpha	22.003
chr1	37373821	37375180	149	Coa5	cytochrome C oxidase assembly factor 5	27.344
chr7	1.22E+08	121858781	-7	Ears2	glutamyl-tRNA synthetase 2 (mitochondrial)(putative)	18.231
chr10	57718401	57719420	87	Lims1	LIM and senescent cell antigen-like domains 1	27.032
chr19	5874861	5875540	8	Frmd8	FERM domain containing 8	15.454
chr15	1.03E+08	102550800	-78	Calcoco1	calcium binding and coiled coil domain 1	20.093
chr11	74586481	74587500	-68	Mettl16	methyltransferase like 16	26.798
chr11	62695232	62696000	-69	Tvp23b	trans-golgi network vesicle protein 23B	19.16
chr9	1.2E+08	119743851	-47	Wdr48	WD repeat domain 48	20.377
chr10	1.28E+08	127814840	-235	Rnf41	ring finger protein 41	16.979
chr6	1.23E+08	122840640	5	Necap1	NECAP endocytosis associated 1	11.349
chr7	44716121	44716951	585	Tbc1d17	TBC1 domain family, member 17	23.843
chr11	1.21E+08	121053221	-255	Narf	nuclear prelamin A recognition factor	14.333
chr18	80631341	80632360	-124	Ctdp1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A)	15.039
chr11	94137501	94138520	-9	Luc7l3	LUC7-like 3 (S. cerevisiae)	20.022
chr4	48145472	48146350	-108	Stx17	syntaxin 17	13.76
chr6	1.16E+08	115961080	-127	Plxnd1	plexin D1	20.258
chr4	1.53E+08	153004760	-212	Tprgl	transformation related protein 63 regulated like	10.828
chr11	78328181	78328860	29	Poldip2	polymerase (DNA-directed), delta interacting protein 2	21.866
chr1	1.3E+08	130071760	-307	Ubxn4	UBX domain protein 4	18.406
chr19	6084301	6084980	251	Zfpl1	zinc finger like protein 1	18.299
chr18	35724162	35724820	-150	Paip2	polyadenylate-binding protein-interacting protein 2	13.599
chr5	1E+08	100280611	-185	Enoph1	enolase-phosphatase 1	17.048
chr5	1E+08	100279601	-77	Hnrnpdl	heterogeneous nuclear ribonucleoprotein D-like	
chr11	1.21E+08	120543900	-209	Dcxr	dicarbonyl L-xylulose reductase	14.754
chr1	43771702	43772780	13	Uxs1	UDP-glucuronate decarboxylase 1	13.748
chr18	68425001	68426020	192	Fam210a	family with sequence similarity 210, member A	21.184
chr9	1.18E+08	117999350	-131	Cmc1	COX assembly mitochondrial protein 1	13.493
chr8	97726572	97727560	403	Ciapin1	cytokine induced apoptosis inhibitor 1	14.089
chr18	36885921	36886600	47	Wdr55	WD repeat domain 55	11.669
chr4	1.11E+08	111218521	39	Spata6	spermatogenesis associated 6	16.671
chr10	98344321	98345000	-180	Atp2b1	ATPase, Ca++ transporting, plasma membrane 1	16.649
chr15	88902861	88904031	174	1810021B22Rik	RIKEN cDNA 1810021B22 gene	18.615
chr3	28996042	28996651	-238	Rpl22l1	ribosomal protein L22 like 1	15.795
chr11	1.02E+08	102224060	-113	Slc25a39	solute carrier family 25, member 39	18.427
chr13	41011481	41012500	6	Pak1ip1	PAK1 interacting protein 1	15.229
chr11	1.03E+08	102833691	61	Dcakd	dephospho-CoA kinase domain containing	40.67
chr5	93037941	93038960	-182	Rchy1	ring finger and CHY zinc finger domain containing 1	17.728
chr11	72023221	72024240	-19	Txndc17	thioredoxin domain containing 17	24.045
chr3	1.3E+08	129823900	-142	Gar1	GAR1 ribonucleoprotein homolog (yeast)	18.801
chr10	82789321	82790000	-360	D10Wsu102e	DNA segment, Chr 10, Wayne State University 102, expressed	21.711
chr9	1.08E+08	107844600	97	Fam212a	family with sequence similarity 212, member A	32.035
chr5	1.24E+08	124168340	-63	Denr	density-regulated protein	24.065
chr8	35615142	35615340	15	Leprotl1	leptin receptor overlapping transcript-like 1	18.49
chr6	8209301	8209980	352			14.975
chr17	25595652	25596840	92	Fam195a	family with sequence similarity 195, member A	22.677
chr19	12639841	12640860	-220	Fam111a	family with sequence similarity 111, member A	31.945
chr8	1.22E+08	122461540	141	Hsdl1	hydroxysteroid dehydrogenase like 1	13.451
chr5	34953701	34954380	-69	Mfsd10	major facilitator superfamily domain containing 10	13.496
chr4	1.27E+08	126563980	-34	Zmym1	zinc finger, MYM domain containing 1	24.321
chr7	43311241	43311920	-412	Etfb	electron transferring flavoprotein, beta polypeptide	13.916
chr5	1.15E+08	115036620	-28	Ankrd13a	ankyrin repeat domain 13a	19.49
chr8	1.08E+08	107531460	-93	Fam96b	family with sequence similarity 96, member B	18.147
chr4	1.34E+08	134203181	85	Syf2	SYF2 homolog, RNA splicing factor (S. cerevisiae)	7.75
chr2	1.64E+08	164461060	-414	Ube2c	ubiquitin-conjugating enzyme E2C	20.309
chr7	65571721	65572930	-42	Tm2d3	TM2 domain containing 3	20.036
chr14	74744652	74745600	-106	Gtf2f2	general transcription factor IIF, polypeptide 2	21.956
chr15	89419321	89420000	30	Rabl2	RAB, member RAS oncogene family-like 2	14.365
chr1	1.37E+08	136963551	-29	Arl8a	ADP-ribosylation factor-like 8A	15.896
chr8	1.2E+08	119808480	103	Cenpn	centromere protein N	14.392
chr14	53380681	53381700	76	Mrpl52	mitochondrial ribosomal protein L52	32.963
chr6	1.15E+08	115003980	22	Tamm41	TAM41, mitochondrial translocator assembly and maintenance	17.21
chr19	6127821	6128810	-100	Snx15	sorting nexin 15	23.623
chr4	1.18E+08	118119400	-11	Ebna1bp2	EBNA1 binding protein 2	24.459
chr2	83444841	83445701	-146	Zc3h15	zinc finger CCCH-type containing 15	17.419
chr7	18307641	18308320	-262	Qpctl	glutaminyl-peptide cyclotransferase-like	20.1

chr5	1.01E+08	100657000	46	Sec31a	Sec31 homolog A (S. cerevisiae)	27.774
chr1	75025522	75025891	-127	Cnppd1	cyclin Pas1/PHO80 domain containing 1	18.762
chr1	75025902	75026780	-28			22.256
chr11	69653761	69654440	-620	Tmem256	transmembrane protein 256	19.543
chr7	1.27E+08	127213720	-28	Zfp688	zinc finger protein 688	19.359
chr11	96857161	96858170	-11	Mrpl10	mitochondrial ribosomal protein L10	18.43
chr6	30459372	30460260	-23			13.264
chr10	90512081	90513390	-103	Ikbip	IKBKB interacting protein	18.506
chr19	42181761	42183050	-101	Avpi1	arginine vasopressin-induced 1	14.952
chr7	1.39E+08	138685320	251	Ppp2r2d	protein phosphatase 2, regulatory subunit B, delta	12.337
chr5	1.3E+08	130226910	-467	Vkorc1l1	vitamin K epoxide reductase complex, subunit 1-like 1	19.849
chr12	1.11E+08	111186120	-125	Wdr20	WD repeat domain 20	15.048
chr17	72740961	72742320	-64	Ypel5	yippee-like 5 (Drosophila)	19.232
chr13	74403561	74404500	217			15.536
chr7	18731281	18732300	75	Gemin7	gem (nuclear organelle) associated protein 7	14.589
chr15	78669201	78670131	-236	Cdc42ep1	CDC42 effector protein (Rho GTPase binding) 1	18.29
chr5	1.38E+08	138009060	-156	Ppp1r35	protein phosphatase 1, regulatory subunit 35	21.282
chr7	97355601	97355771	-462	Ints4	integrator complex subunit 4	18.824
chr7	97355782	97356620	53	Ints4	integrator complex subunit 4	19.48
chr11	1.16E+08	116229870	-483	Rnf157	ring finger protein 157	12.204
chr7	29939721	29940740	559	Tbcb	tubulin folding cofactor B	21.573
chr1	1.66E+08	165831940	140	BC055324	cDNA sequence BC055324	23.473
chr16	93599621	93600640	-317	Dopey2	dopey family member 2	24.054
chr3	89544781	89545460	75	Pmvk	phosphomevalonate kinase	11.402
chr7	1.13E+08	113305340	-15	Far1	fatty acyl CoA reductase 1	15.44
chr10	80723141	80724500	-412	Cactin	cactin, spliceosome C complex subunit	16.979
chr19	8886722	8887600	715	Hnrnpul2	heterogeneous nuclear ribonucleoprotein U-like 2	19.388
chr10	84051741	84052760	14	Polr3b	polymerase (RNA) III (DNA directed) polypeptide B	14.904
chr3	1.06E+08	106088160	96	Wdr77	WD repeat domain 77	16.547
chr11	70462961	70463791	-142	Slc25a11	solute carrier family 25 (mitochondrial carrier oxoglutarate carrier),	16.494
chr4	1.08E+08	108332160	-134	Btf3l4	basic transcription factor 3-like 4	15.149
chr8	1.09E+08	108648121	-40	Gfod2	glucose-fructose oxidoreductase domain containing 2	22.068
chr8	72971141	72971820	243	Mau2	MAU2 chromatid cohesion factor homolog (C. elegans)	22.766
chr3	1.28E+08	127888620	65	5730508B09Rik	RIKEN cDNA 5730508B09 gene	17.661
chr8	75476941	75477960	-151	Med26	mediator complex subunit 26	20.095
chr18	44505372	44506340	25	Dcp2	DCP2 decapping enzyme homolog (S. cerevisiae)	12.292
chr6	35107381	35108060	-48	Nup205	nucleoporin 205	18.24
chr5	1.5E+08	149680301	-119	Medag	mesenteric estrogen dependent adipogenesis	16.475
chr3	41179101	41180120	-15	Pgrmc2	progesterone receptor membrane component 2	19.795
chr3	1.46E+08	146438000	98	Gng5	guanine nucleotide binding protein (G protein), gamma 5	15.485
chr19	7307712	7308640	90	Naa40	N(alpha)-acetyltransferase 40, NatD catalytic subunit, homolog (S.	18.73
chr7	1.2E+08	119585780	124	2610020H08Rik	RIKEN cDNA 2610020H08 gene	12.726
chr13	38043962	38045190	121	Riok1	RIO kinase 1 (yeast)	28.972
chr4	19496961	19497640	-49	Cpne3	copine III	12.882
chr10	80104352	80105700	-77	Mob3a	MOB kinase activator 3A	27.67
chr9	59548281	59549930	-75	Myo9a	myosin IXa	21.337
chr11	1.15E+08	115236880	324	Kctd2	potassium channel tetramerisation domain containing 2	18.353
chr4	1.47E+08	147289020	40	Ubiad1	UbiA prenyltransferase domain containing 1	22.873
chr7	24990681	24990891	-153	Cic	capicua homolog (Drosophila)	17.476
chr17	46143781	46145140	89	Mea1	male enhanced antigen 1	20.208
chr4	1.34E+08	134187481	-139	Tmem50a	transmembrane protein 50A	18.157
chr11	1.06E+08	105852961	-211	Dcaf7	DDB1 and CUL4 associated factor 7	14.81
chr14	30080192	30080820	8	Bap1	Brca1 associated protein 1	11.1
chr12	17291382	17292400	-184	Pdia6	protein disulfide isomerase associated 6	15.634
chr11	1.2E+08	120195440	-200	Faap100	Fanconi anemia core complex associated protein 100	32.491
chr4	1.47E+08	146984720	91	Mad2l2	MAD2 mitotic arrest deficient-like 2	12.829
chr8	88730481	88731500	64	Itfg1	integrin alpha FG-GAP repeat containing 1	19.354
chr15	99600012	99601240	-77	Cers5	ceramide synthase 5	30.95
chr8	1.13E+08	112582840	93	Ist1	increased sodium tolerance 1 homolog (yeast)	14.517
chr11	4117742	4118710	-28	Gatsl3	GATS protein-like 3	19.307
chr12	1.13E+08	113277950	-168	Cdca4	cell division cycle associated 4	14.146
chr7	80774481	80775160	-38	Wdr73	WD repeat domain 73	18.596
chr9	35017042	35017960	-25	Fam118b	family with sequence similarity 118, member B	16.033
chr13	1.09E+08	109279740	-28	Ndufaf2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex,	19.135
chr1	39479781	39480460	-228	Cnot11	CCR4-NOT transcription complex, subunit 11	13.147
chr18	67899701	67900720	-35	Seh1l	SEH1-like (S. cerevisiae	15.372
chr2	59683261	59683860	-115	Wdsub1	WD repeat, SAM and U-box domain containing 1	17.424
chr15	96288681	96289700	-313	Scaf11	SR-related CTD-associated factor 11	14.224
chr11	97966072	97967210	-935	Fbxl20	F-box and leucine-rich repeat protein 20	22.826
chr11	97965901	97966061	-275	Fbxl20	F-box and leucine-rich repeat protein 20	10.375
chr19	42034742	42035450	22	Ubtd1	ubiquitin domain containing 1	18.46
chr3	36666621	36667980	136	Anxa5	annexin A5	29.219
chr11	45787801	45788750	83	Lsm11	U7 snRNP-specific Sm-like protein LSM11	19.123
chr5	73535262	73536220	12	Fryl	furry homolog-like (Drosophila)	17.264
chr17	45666081	45666760	-16	Xpo5	exportin 5	12.773
chr2	1.29E+08	128510480	56	Tmem87b	transmembrane protein 87B	17.002
chr12	1.09E+08	108627960	-189	Setd3	SET domain containing 3	15.443
chr4	1.3E+08	129550540	56	Col16a1	collagen, type XVI, alpha 1	18.538
chr19	38119101	38120460	-389	Cep55	centrosomal protein 55	28.842
chr5	1.45E+08	145485660	34	Zfp655	zinc finger protein 655	12.773
chrX	96828941	96829910	641	Kif4	kinesin family member 4	13.785
chr3	1.17E+08	116587300	-142	Sass6	spindle assembly 6 homolog (C. elegans)	20.693
chr13	82188201	82188571	-36	Polr3g	polymerase (RNA) III (DNA directed) polypeptide G	19.378
chr6	1.13E+08	113043540	-120	Gt(ROSA)26Sor	gene trap ROSA 26, Philippe Soriano	18.001
chr17	66000801	66001480	-38	Ndufv2	NADH dehydrogenase (ubiquinone) flavoprotein 2	13.308
chr9	22139101	22140120	-2	Anln	anillin, actin binding protein	17.209
chr4	1.07E+08	106752180	135	Lrrc42	leucine rich repeat containing 42	20.03
chr16	20534641	20535621	-310	Camk2n2	calcium/calmodulin-dependent protein kinase II inhibitor 2	13.714
chr4	1.2E+08	120423240	80	Exo5	exonuclease 5	30.863
chr17	48893361	48894380	-61	Mocs1	molybdenum cofactor synthesis 1	21.502

chr5	1.08E+08	108373640	-86	Ccdc18	coiled-coil domain containing 18	22.311
chr7	27637921	27638600	-70	1700049G17Rik	RIKEN cDNA 1700049G17 gene	14.077
chr7	64271352	64271900	-95	Mcee	methylmalonyl CoA epimerase	16.25
chrX	69711561	69712240	-151	Haus7	HAUS augmin-like complex, subunit 7	12.953
chr17	87190621	87191300	180	4833418N02Rik	RIKEN cDNA 4833418N02 gene	17.601
chr3	61451942	61452960	15	Rap2b	RAP2B, member of RAS oncogene family	23.507
chr1	93324561	93325440	-74	Traf3ip1	TRAF3 interacting protein 1	14.542
chr16	4965701	4966720	821	Ubn1	ubinuclein 1	14.678
chr5	1.38E+08	137732980	-83	Pop7	processing of precursor 7, ribonuclease P family, (S. cerevisiae)	20.164
chr7	1.22E+08	121812790	-130	Gga2	golgi associated, gamma adaptin ear containing, ARF binding	11.201
chr5	1.2E+08	120377680	46	Rbm19	RNA binding motif protein 19	13.274
chr6	91438241	91439311	151	Chchd4	coiled-coil-helix-coiled-coil-helix domain containing 4	20.196
chr17	47387841	47387991	-93	Foxp4	forkhead box P4	8.067
chr17	56311652	56312840	-223	Lonp1	lon peptidase 1, mitochondrial	27.47
chr1	1.27E+08	127389160	-82	Slc35f5	solute carrier family 35, member F5	18.781
chr15	79514441	79515770	22	Josd1	Josephin domain containing 1	21.282
chr4	1.26E+08	125605851	-915	Stk40	serine/threonine kinase 40	27.03
chr11	4494461	4495140	18	Mtmr3	myotubularin related protein 3	17.867
chr4	1.36E+08	135583160	-322	Hnrnpr	heterogeneous nuclear ribonucleoprotein R	16.217
chr4	1.49E+08	148799590	-299	Spsb1	splA/ryanodine receptor domain and SOCS box containing 1	19.798
chr10	12654121	12655140	-173	Stx11	syntaxin 11	24.335
chr10	59346882	59348020	-324	Ddit4	DNA-damage-inducible transcript 4	31.018
chr9	98949181	98949860	43	Pik3cb	phosphatidylinositol 3-kinase, catalytic, beta polypeptide	13.306
chr10	82120201	82120880	-91	Glt8d2	glycosyltransferase 8 domain containing 2	19.916
chr10	41498021	41499380	-289	Sesn1	sestrin 1	17.584
chr11	70225981	70227000	-264	Pelp1	proline, glutamic acid and leucine rich protein 1	22.581
chr9	15056292	15056900	-11	Taf1d	TATA box binding protein (Tbp)-associated factor, RNA	16.809
chr11	4536992	4537980	-310	Ascc2	activating signal cointegrator 1 complex subunit 2	18.854
chr14	97982221	97982900	2	Pibf1	progesterone immunomodulatory binding factor 1	15.741
chr1	1.07E+08	107491680	53	Pign	phosphatidylinositol glycan anchor biosynthesis, class N	16.11
chr5	94280641	94281320	719	Ccni	cyclin I	13.106
chr2	1.31E+08	130532120	-24	4930402H24Rik	RIKEN cDNA 4930402H24 gene	18.171
chr13	1.05E+08	105230680	-2	Sgtb	small glutamine-rich tetratricopeptide repeat (TPR)-containing,	17.444
chr18	21039201	21039880	-452	Trappc8	trafficking protein particle complex 8	16.72
chr16	90699081	90699760	-148	Urb1	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	17.8
chr11	1.16E+08	115631280	72	Tsen54	tRNA splicing endonuclease 54 homolog (S. cerevisiae)	19.166
chr3	35945252	35946160	19	Atp11b	ATPase, class VI, type 11B	11.468
chr14	1.17E+08	117015740	-184	Tgds	TDP-glucose 4,6-dehydratase	11.39
chr7	78720412	78720880	78	Det1	de-etiolated homolog 1 (Arabidopsis)	15.882
chr17	25306201	25307091	-128	Lmf1	lipase maturation factor 1	19.022
chr15	76365361	76366720	-39	Fbxl6	F-box and leucine-rich repeat protein 6	31.63
chr19	34257892	34258441	-101	Stambpl1	STAM binding protein like 1	11.763
chr8	56028261	56029210	-40	Spcs3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	20.512
chr1	74169301	74170320	53	Arpc2	actin related protein 2/3 complex, subunit 2	17.49
chr15	57971021	57972020	1	Wdyhv1	WDYHV motif containing 1	21.778
chr1	1.79E+08	178651300	-375	Sdccag8	serologically defined colon cancer antigen 8	15.82
chr4	1.34E+08	133807680	-57	Mtfr1l	mitochondrial fission regulator 1-like	20.898
chr9	35319541	35320220	-140	Hyls1	hydrolethalus syndrome 1	18.654
chr3	95400261	95401081	15	Cers2	ceramide synthase 2	15.366
chr2	38887161	38887840	50	Golga1	golgi autoantigen, golgin subfamily a, 1	13.582
chr17	33291781	33292460	25	Hnrnpm	heterogeneous nuclear ribonucleoprotein M	23.409
chr7	79533141	79534110	-84	Ticrr	TOPBP1-interacting checkpoint and replication regulator	22.183
chr4	1.16E+08	116055940	-229	Gpbp1l1	GC-rich promoter binding protein 1-like 1	23.274
chr11	1.21E+08	121268480	-48	Tbcd	tubulin-specific chaperone d	17.289
chr3	97312432	97313440	-167	Bcl9	B cell CLL/lymphoma 9	15.353
chr7	3296602	3297831	-379	Tsen34	tRNA splicing endonuclease 34 homolog (S. cerevisiae)	16.378
chr9	53010081	53011100	-83	Ddx10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	15.989
chr11	6343721	6345080	46	H2afv	H2A histone family, member V	21.029
chr11	51810732	51811240	-68	Cdkn2aipnl	CDKN2A interacting protein N-terminal like	17.98
chr5	1.38E+08	137831240	-164	Mospd3	motile sperm domain containing 3	13.651
chr2	73014792	73015680	50	Ola1	Obg-like ATPase 1	18.283
chr15	6654821	6655840	-266	Rictor	RPTOR independent companion of MTOR, complex 2	15.714
chr16	4594482	4595430	-8	Coro7	coronin 7	12.821
chr5	1.26E+08	125766000	-14	Aacs	acetoacetyl-CoA synthetase	32.614
chr6	88807112	88808340	-150	Abtb1	ankyrin repeat and BTB (POZ) domain containing 1	22.575
chr9	44249301	44250581	-190	Bcl9l	B cell CLL/lymphoma 9-like	20.195
chr5	1.4E+08	139634600	-48	Gpr146	G protein-coupled receptor 146	18.093
chr9	14026361	14027040	2	Sesn3	sestrin 3	19.437
chr10	76702302	76703311	133	Gm10941	predicted gene 10941	28.737
chr1	37243941	37244620	-104	Inpp4a	inositol polyphosphate-4-phosphatase, type I	14.698
chr5	1.23E+08	123110940	-205	Rnf34	ring finger protein 34	22.271
chr9	1.23E+08	123378211	-894	Sacm1l	SAC1 (suppressor of actin mutations 1, homolog)-like (S.	13.114
chr9	1.23E+08	123378860	-39	Sacm1l	SAC1 (suppressor of actin mutations 1, homolog)-like (S.	17.599
chr3	86310302	86310700	-116	Lrba	LPS-responsive beige-like anchor	13.101
chr7	83760462	83760700	-55	Mesdc1	mesoderm development candidate 1	14.58
chr9	66774352	66774980	-38	Lactb	lactamase, beta	18.162
chr12	8699921	8700940	163	Pum2	pumilio RNA-binding family member 2	15.234
chr16	4509081	4509760	-521	Glis2	GLIS family zinc finger 2	14.501
chr3	88639361	88640040	57	Ubqln4	ubiquilin 4	21.647
chr2	1.81E+08	180518920	-229	Ogfr	opioid growth factor receptor	12.099
chr12	91995161	91995840	-294	Gtf2a1	general transcription factor II A, 1	14.63
chr5	1.38E+08	137564000	-290	Slc12a9	solute carrier family 12 (potassium/chloride transporters), member	27.859
chr15	99529901	99530920	89	Smarcd1	SWI/SNF related, matrix associated, actin dependent regulator of	21.277
chr9	21668201	21669140	-147	Rab3d	RAB3D, member RAS oncogene family	15.021
chr10	1.27E+08	126692500	-270	Mbd6	methyl-CpG binding domain protein 6	21.483
chr17	34608941	34609841	428	Vars	valyl-tRNA synthetase	15.867
chr15	81974001	81975020	-14	Srebf2	sterol regulatory element binding factor 2	31.3
chr15	76498382	76499630	71	Ppp1r16a	protein phosphatase 1, regulatory (inhibitor) subunit 16A	18.254
chr16	18261401	18262080	-5	Arvcf	armadillo repeat gene deleted in velo-cardio-facial syndrome	12.773
chr8	42009982	42010851	155	Cnot7	CCR4-NOT transcription complex, subunit 7	13.157

chr8	42009402	42009971	885	Cnot7	CCR4-NOT transcription complex, subunit 7	11.211
chr1	36415701	36416660	37	Cnnm4	cyclin M4	16.272
chr8	1.15E+08	114899260	888	Terf2ip	telomeric repeat binding factor 2, interacting protein	24.543
chr3	1.45E+08	144507820	122	Hs2st1	heparan sulfate 2-O-sulfotransferase 1	17.644
chr10	62045921	62047400	-105	Ddx50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	19.341
chr8	97764972	97765980	-35	Dok4	docking protein 4	21.305
chr11	1.14E+08	114491940	-128	Ttyh2	tweety homolog 2 (Drosophila)	31.085
chr11	88533961	88534980	-113	Msi2	musashi RNA-binding protein 2	14.67
chr11	97560812	97561640	239	Mir8102	microRNA 8102	25.211
chr5	1.09E+08	108934501	-225	Fgfrl1	fibroblast growth factor receptor-like 1	13.645
chr1	1.66E+08	166086170	-16	Slc19a2	solute carrier family 19 (thiamine transporter), member 2	16.217
chr1	1.53E+08	153107050	19	Ivns1abp	influenza virus NS1A binding protein	14.76
chr17	34742901	34743580	6	Bag6	BCL2-associated athanogene 6	17.056
chr10	79980242	79981940	-666	Klf16	Kruppel-like factor 16	56.747
chr2	1.53E+08	152933020	13	Plagl2	pleiomorphic adenoma gene-like 2	20.932
chr2	1.53E+08	152932541	633	Plagl2	pleiomorphic adenoma gene-like 2	15.186
chr17	26784181	26785200	-203	Itpr3	inositol 1,4,5-triphosphate receptor 3	21.785
chr2	79435712	79436580	-118	Ssfa2	sperm specific antigen 2	21.203
chr3	20226941	20227860	61	Hps3	Hermansky-Pudlak syndrome 3 homolog (human)	15.972
chr5	97237281	97238300	-201	Bmp2k	BMP2 inducible kinase	25.412
chr3	51648512	51649400	-204	Setd7	SET domain containing (lysine methyltransferase) 7	13.466
chr8	1.1E+08	109920640	-155	Vps4a	vacuolar protein sorting 4a (yeast)	18.297
chr10	43589701	43590380	111	Qrsl1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	19.415
chr15	76349381	76350060	-336	Scrt1	scratch homolog 1, zinc finger protein (Drosophila)	14.557
chr7	27181682	27182660	-429	Sertad3	SERTA domain containing 3	13.829
chr19	53091681	53092550	-149	Xpnpep1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	16.129
chr1	1.83E+08	182563340	-58	Acbd3	acyl-Coenzyme A binding domain containing 3	28.152
chr7	15467621	15468471	-59	Bbc3	BCL2 binding component 3	17.659
chr5	1.08E+08	107838480	-28	Rpap2	RNA polymerase II associated protein 2	16.952
chr6	83102121	83102561	-401	Rtkn	rhotekin	17.25
chr6	83102572	83102800	-56	Rtkn	rhotekin	11.873
chr5	65771641	65772660	-180	Smim14	small integral membrane protein 14	20.197
chr11	78366732	78367540	-206	Tmem97	transmembrane protein 97	15.557
chr9	1.19E+08	118775471	-208	Ctdspl	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A)	23.101
chr4	1.21E+08	120515660	-128	Smap2	small ArfGAP 2	17.534
chr9	7763922	7764920	-177	Tmem123	transmembrane protein 123	16.114
chr5	31770762	31771930	4	Gpn1	GPN-loop GTPase 1	24.711
chr5	1.3E+08	130309420	-46	Asl	argininosuccinate lyase	14.003
chr17	74199901	74200571	-391	Memo1	mediator of cell motility 1	15.403
chr2	32217381	32218060	-179	Ptges2	prostaglandin E synthase 2	16.76
chr1	1.08E+08	107999300	80	Gm20753	predicted gene, 20753	11.503
chr2	84527772	84528710	-134	Clp1	CLP1, cleavage and polyadenylation factor I subunit	13.875
chr2	1.53E+08	152853120	38	Tm9sf4	transmembrane 9 superfamily protein member 4	13.312
chr3	1.04E+08	104350420	-273	Magi3	membrane associated guanylate kinase, WW and PDZ domain	21.313
chr4	1.09E+08	108700720	-6	Osbpl9	oxysterol binding protein-like 9	21.59
chr4	1.29E+08	128964380	-113	Bsdc1	BSD domain containing 1	31.795
chr5	50346962	50347780	-127	Adgra3	adhesion G protein-coupled receptor A3	15.088
chr5	1.24E+08	123655641	-295	Mlxip	MLX interacting protein	18.865
chr5	72838602	72839490	-266	Nfxl1	nuclear transcription factor, X-box binding-like 1	19.152
chr2	1.64E+08	164477720	-16	Snx21	sorting nexin family member 21	20.221
chr6	1.13E+08	113343741	41	Tada3	transcriptional adaptor 3	16.867
chr6	88049801	88050361	-33	Rpn1	ribophorin I	15.786
chr6	1.19E+08	119445060	-736	Fbxl14	F-box and leucine-rich repeat protein 14	19.421
chr7	44737592	44738530	-231	Ptov1	prostate tumor over expressed gene 1	20.249
chr8	98220221	98221580	179	Zfp319	zinc finger protein 319	18.074
chr8	1.1E+08	110183251	77	Nfat5	nuclear factor of activated T cells 5	21.243
chr8	11636232	11637000	-887	Ankrd10	ankyrin repeat domain 10	21
chr8	73163382	73164260	-410	Armc6	armadillo repeat containing 6	20.62
chr9	1.22E+08	122143810	-94	Ano10	anoctamin 10	17.421
chr10	80025121	80026140	-279	Csnk1g2	casein kinase 1, gamma 2	23.511
chr11	93700941	93701721	525	Utp18	UTP18, small subunit (SSU) processome component, homolog	21.218
chr11	23155092	23156040	-475	Xpo1	exportin 1, CRM1 homolog (yeast)	18.44
chr11	1.01E+08	100936140	114	Fam134c	family with sequence similarity 134, member C	16.99
chr14	19177042	19178000	-59	Dnajc9	DnaJ (Hsp40) homolog, subfamily C, member 9	11.143
chr14	24526782	24527940	7	Ppif	peptidylprolyl isomerase F (cyclophilin F)	19.852
chr15	81843101	81844120	-14	Xrcc6	X-ray repair complementing defective repair in Chinese hamster	37.601
chr17	35468801	35470080	69	Nrm	nurim (nuclear envelope membrane protein)	20.381
chr17	56934361	56935380	84	Trip10	thyroid hormone receptor interactor 10	20.375
chr19	5424021	5425720	109	Drap1	Dr1 associated protein 1 (negative cofactor 2 alpha)	27.127
chr4	1.29E+08	128692720	-59	Yars	tyrosyl-tRNA synthetase	20.724
chr19	5040841	5041520	-224	Brms1	breast cancer metastasis-suppressor 1	14.635
chr12	81179052	81179760	-195	Actn1	actinin, alpha 1	14.225
chr3	89187202	89188460	63	Fdps	farnesyl diphosphate synthetase	30.514
chr2	91763961	91764980	-68	Dgkz	diacylglycerol kinase zeta	17.028
chr17	34457662	34459000	-71	Skiv2l	superkiller viralicidic activity 2-like (S. cerevisiae)	28.244
chr11	1.14E+08	113501500	409	D11Wsu47e	DNA segment, Chr 11, Wayne State University 47, expressed	43.587
chrX	6998272	6999191	-59	Otud5	OTU domain containing 5	13.427
chr10	7646052	7647540	-483	Tab2	TGF-beta activated kinase 1/MAP3K7 binding protein 2	21.565
chr12	77173542	77174220	-191	Mthfd1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent),	12.465
chr6	1.25E+08	125097900	-96	Nop2	NOP2 nucleolar protein	20.735
chr15	89008261	89009280	-216	Plxnb2	plexin B2	23.572
chr5	34830621	34831270	-109	Tnip2	TNFAIP3 interacting protein 2	22.692
chr18	24746232	24747240	91	Slc39a6	solute carrier family 39 (metal ion transporter), member 6	24.593
chr7	1.28E+08	127758871	-161	Fus	fused in sarcoma	15.63
chr2	1.8E+08	180049040	-74	Osbpl2	oxysterol binding protein-like 2	16.14
chr7	1.27E+08	126999961	45	Tbc1d10b	TBC1 domain family, member 10b	13.141
chr15	25928442	25929420	-160	Zfp622	zinc finger protein 622	34.355
chr11	71857981	71859000	-207	Fam64a	family with sequence similarity 64, member A	16.923
chr9	98105641	98106320	45	Nmnat3	nicotinamide nucleotide adenylyltransferase 3	13.169
chr15	59477221	59478580	-435	Trib1	tribbles homolog 1 (Drosophila)	21.495

chr19	32454322	32455380	-362	2700046G09Rik	RIKEN cDNA 2700046G09 gene	16.166
chr15	80537841	80538860	-218	Tnrc6b	trinucleotide repeat containing 6b	19.342
chr10	59097441	59098410	5	Micu1	mitochondrial calcium uptake 1	19.387
chr11	79778102	79779300	-119	Utp6	UTP6, small subunit (SSU) processome component, homolog	12.772
chr13	71105422	71105900	-655	Ice1	interactor of little elongation complex ELL subunit 1	11.837
chr13	71104962	71105411	-180	Ice1	interactor of little elongation complex ELL subunit 1	19.59
chr19	5688802	5689220	-103	Pcnxl3	pecanex-like 3 (Drosophila)	22.612
chr19	8996092	8996831	-60	Rom1	rod outer segment membrane protein 1	14.217
chr2	30803682	30804680	-107	Usp20	ubiquitin specific peptidase 20	17.818
chr3	88999761	89000410	-208	Msto1	misato homolog 1 (Drosophila)	15.917
chr5	1.23E+08	122615560	20	Vps29	vacuolar protein sorting 29 (S. pombe)	18.567
chr6	72284352	72285360	-136	Tmem150a	transmembrane protein 150A	16.863
chr7	27156141	27157160	-88	Blvrb	biliverdin reductase B (flavin reductase (NADPH))	22.534
chr9	66390781	66391990	-264			20.913
chr17	47157661	47158600	-203	Prickle4	prickle homolog 4 (Drosophila)	15.832
chr13	23542582	23542960	-112	Hist1h3g	histone cluster 1, H3g	18.577
chr11	97838741	97839400	-353	Cacnb1	calcium channel, voltage-dependent, beta 1 subunit	15.367
chr6	1.25E+08	124629040	-23	Lpcat3	lysophosphatidylcholine acyltransferase 3	15.158
chr4	1.39E+08	138583660	500	Akr7a5	aldo-keto reductase family 7, member A5 (aflatoxin aldehyde	12.446
chr7	1.41E+08	140793320	-60	Athl1	ATH1, acid trehalase-like 1 (yeast)	11.22
chr9	44716461	44717110	-190	Ube4a	ubiquitination factor E4A	13.495
chr8	1.09E+08	109099880	306	Slc7a6os	solute carrier family 7, member 6 opposite strand	12.395
chr8	1.09E+08	109099621	821	Slc7a6os	solute carrier family 7, member 6 opposite strand	14.303
chrX	70620721	70621740	38	Ubl4a	ubiquitin-like 4A	17.807
chr8	1.1E+08	109782940	72	Cirh1a	cirrhosis, autosomal recessive 1A (human)	17.263
chr1	1.59E+08	158556280	-19	Fam20b	family with sequence similarity 20, member B	19.242
chr9	21037862	21038860	10	Kri1	KRI1 homolog (S. cerevisiae)	20.195
chr11	60232832	60233941	46	Gid4	GID complex subunit 4, VID24 homolog (S. cerevisiae)	22.808
chr11	60233952	60234400	836	Gid4	GID complex subunit 4, VID24 homolog (S. cerevisiae)	13.962
chr13	85762281	85762960	-24	Rasa1	RAS p21 protein activator 1	26.458
chr13	1.09E+08	109011820	-499	Zswim6	zinc finger SWIM-type containing 6	13.202
chr14	53508181	53509120	-84	Haus4	HAUS augmin-like complex, subunit 4	10.999
chr15	86041842	86042780	86	Tbc1d22a	TBC1 domain family, member 22a	27.767
chr15	88646841	88648200	108	Creld2	cysteine-rich with EGF-like domains 2	18.625
chr17	46174192	46175060	-28	Pex6	peroxisomal biogenesis factor 6	20.067
chr19	5050021	5051380	-108	Rin1	Ras and Rab interactor 1	16.166
chr19	42033861	42034731	151	Mms19	MMS19 (MET18 S. cerevisiae)	19.011
chr19	45068361	45068791	55	Lzts2	leucine zipper, putative tumor suppressor 2	14.605
chr2	1.04E+08	104391900	68	Cstf3	cleavage stimulation factor, 3' pre-RNA, subunit 3	21.098
chr3	1.06E+08	105929720	57	Rap1a	RAS-related protein-1a	16.81
chr4	1.34E+08	134040580	-160	Ldlrap1	low density lipoprotein receptor adaptor protein 1	13.91
chr6	52569441	52570460	-72	Hibadh	3-hydroxyisobutyrate dehydrogenase	12.057
chr8	1.28E+08	127609140	61	Arv1	ARV1 homolog (yeast)	28.68
chr9	21548682	21549540	-163	Kank2	KN motif and ankyrin repeat domains 2	26.803
chr9	55310102	55310860	-101	Etfa	electron transferring flavoprotein, alpha polypeptide	12.975
chr9	66147632	66148700	-290	Herc1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus)	19.646
chr9	1.06E+08	106335680	-70	Rrp9	RRP9, small subunit (SSU) processome component, homolog	15.507
chr15	1.02E+08	101902420	-67	Eif4b	eukaryotic translation initiation factor 4B	17.357
chr10	42166801	42167480	-160	Lace1	lactation elevated 1	17.604
chr7	18517761	18518191	29	Cd3eap	CD3E antigen, epsilon polypeptide associated protein	15.419
chr17	34506261	34507480	-160	Ehmt2	euchromatic histone lysine N-methyltransferase 2	18.286
chr5	64247761	64248440	-68	Rell1	RELT-like 1	24.013
chr11	50067721	50069420	-188	Mgat4b	mannoside acetylglucosaminyltransferase 4, isoenzyme B	21.78
chr14	39875201	39876220	-190	Tspan14	tetraspanin 14	15.307
chr11	1.09E+08	109428320	-501	Wipi1	WD repeat domain, phosphoinositide interacting 1	14.882
chr7	45022121	45022991	24	Aldh16a1	aldehyde dehydrogenase 16 family, member A1	16.057
chr7	1.29E+08	128531900	17	Mcmbp	MCM (minichromosome maintenance deficient) binding protein	14.591
chr3	1.28E+08	127830140	54	Ap1ar	adaptor-related protein complex 1 associated regulatory protein	23.503
chr6	1.25E+08	125061951	-216	Chd4	chromodomain helicase DNA binding protein 4	12.987
chr9	44518782	44518920	-48	Arcn1	archain 1	20.341
chr5	1.36E+08	135917720	99	Rhbdd2	rhomboid domain containing 2	16.848
chr10	75974701	75975720	-111	Lss	lanosterol synthase	19.789
chr10	84005602	84006631	-630	Tcp11l2	t-complex 11 (mouse) like 2	15.742
chr10	84006642	84006860	5	Tcp11l2	t-complex 11 (mouse) like 2	13.546
chr11	94824981	94826311	-323	Samd14	sterile alpha motif domain containing 14	21.218
chr11	96845722	96846510	74	Scrn2	secernin 2	10.826
chr11	1.01E+08	100988840	-938	Plekhh3	pleckstrin homology domain containing, family H (with MyTH4	12.902
chr12	70102592	70102931	-2	Mgat2	mannoside acetylglucosaminyltransferase 2	12.26
chr15	31168141	31169500	-154	Dap	death-associated protein	26.313
chr17	3513742	3514580	34	Tfb1m	transcription factor B1, mitochondrial	26.953
chr18	61680152	61681010	-370	Csnk1a1	casein kinase 1, alpha 1	11.597
chr19	8937942	8938940	-163	Ubxn1	UBX domain protein 1	25.63
chr1	74217902	74218600	10	Pnkd	paroxysmal nonkinesiogenic dyskinesia	25.436
chr1	89157861	89158401	-38	Gigyf2	GRB10 interacting GYF protein 2	17.778
chr4	98415381	98416060	-108	Usp1	ubiquitin specific peptidase 1	20.642
chr4	1.16E+08	116219140	-87	Tesk2	testis-specific kinase 2	17.306
chr4	1.26E+08	125705820	44	Thrap3	thyroid hormone receptor associated protein 3	17.871
chr7	29989522	29990260	-710	Wdr62	WD repeat domain 62	13.943
chr7	1.26E+08	126357940	-2	Eif3c	eukaryotic translation initiation factor 3, subunit C	12.061
chr7	1.27E+08	127137001	-139	Zfp768	zinc finger protein 768	28.938
chr8	1.13E+08	113107460	31	Cmtr2	cap methyltransferase 2	21.234
chr8	1.23E+08	122748500	-122	Klhl36	kelch-like 36	14.393
chr9	37237982	37238840	-581	Msantd2	Myb/SANT-like DNA-binding domain containing 2	25.42
chr10	92590161	92590840	-175	Cdk17	cyclin-dependent kinase 17	13.081
chr2	29955361	29956380	-10	Tbc1d13	TBC1 domain family, member 13	15.368
chr4	1.03E+08	102613020	358	Mier1	mesoderm induction early response 1 homolog (Xenopus laevis	19.171
chr2	24771381	24772400	104	Zmynd19	zinc finger, MYND domain containing 19	22.081
chr11	1.1E+08	110154220	96	Abca5	ATP-binding cassette, sub-family A (ABC1), member 5	17.875
chr17	44897092	44898020	144			16.001
chr18	7868621	7869410	-180	Wac	WW domain containing adaptor with coiled-coil	11.29

chr11	52239641	52240051	-5	9530068E07Rik	RIKEN cDNA 9530068E07 gene	12.561
chr2	26266701	26268060	-155	Sec16a	SEC16 homolog A, endoplasmic reticulum export factor	21.736
chr19	5272381	5273740	59	Pacs1	phosphofurin acidic cluster sorting protein 1	26.276
chr16	17841501	17842180	-58	Slc25a1	solute carrier family 25 (mitochondrial carrier, citrate transporter),	16.325
chr4	1.25E+08	124630740	-166	Zc3h12a	zinc finger CCCH type containing 12A	23.733
chr5	1.38E+08	138494240	-22	6330418K02Rik	RIKEN cDNA 6330418K02 gene	12.262
chrX	90487032	90487940	-163	Klhl15	kelch-like 15	11.812
chr4	1.26E+08	125932600	-244	Ago3	argonaute RISC catalytic subunit 3	20.179
chr4	1.26E+08	125970680	94	Ago1	argonaute RISC catalytic subunit 1	11.704
chr7	1.1E+08	109778040	-159	Tmem41b	transmembrane protein 41B	27.377
chr13	36742572	36743120	-903	Nrn1	neuritin 1	15.544
chr13	36742101	36742561	-388	Nrn1	neuritin 1	19.978
chr10	82963622	82964080	88	Aldh1l2	aldehyde dehydrogenase 1 family, member L2	27.559
chr3	1.08E+08	107759940	75	Strip1	striatin interacting protein 1	19.837
chr5	73192502	73193840	-326	Slain2	SLAIN motif family, member 2	28.561
chr12	1.01E+08	101126880	-292	Rps6ka5	ribosomal protein S6 kinase, polypeptide 5	18.085
chr8	28489302	28490300	66	Erlin2	ER lipid raft associated 2	26.926
chr11	1.1E+08	109538480	15	Fam20a	family with sequence similarity 20, member A	16.433
chr18	38080681	38081360	-58	Hdac3	histone deacetylase 3	15.144
chr2	29899601	29900960	-495	Pkn3	protein kinase N3	13.773
chr9	44056192	44057200	-30	Hinfp	histone H4 transcription factor	24.843
chr5	1.41E+08	140642280	-89	Snx8	sorting nexin 8	25.481
chr8	13287201	13288021	-379	Tmco3	transmembrane and coiled-coil domains 3	12.744
chr8	1.26E+08	126219331	-37	Spire2	spire homolog 2 (Drosophila)	29.469
chr8	1.27E+08	126835980	-115	Nup133	nucleoporin 133	16.541
chr2	26202441	26203120	-118	Snapc4	small nuclear RNA activating complex, polypeptide 4	24.754
chr11	23397441	23398460	89	Ahsa2	AHA1, activator of heat shock protein ATPase 2	17.941
chr8	75499542	75500400	66	Smim7	small integral membrane protein 7	18.322
chr2	30027482	30028371	-218	Ccbl1	cysteine conjugate-beta lyase 1	16.169
chr1	58917921	58918600	143	Stradb	STE20-related kinase adaptor beta	14.451
chr10	42366802	42367400	-230	Ostm1	osteopetrosis associated transmembrane protein 1	16.985
chr2	71168121	71168961	-148	Slc25a12	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	14.512
chr9	65384432	65385630	-180	Pif1	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae)	28.07
chrX	6919001	6920020	-110	Tfe3	transcription factor E3	15.056
chr1	40734721	40735740	-27	Mfsd9	major facilitator superfamily domain containing 9	25.079
chr12	1.05E+08	105411560	-361	Syne3	spectrin repeat containing, nuclear envelope family member 3	17.293
chr10	3133812	3134781	-8	Cnksr3	Cnksr family member 3	18.388
chr10	1.1E+08	110414660	-225	Zdhhc17	zinc finger, DHHC domain containing 17	15.035
chr11	23794901	23795750	-55	Papolg	poly(A) polymerase gamma	18.277
chr12	85250921	85252280	-31	Fam161b	family with sequence similarity 161, member B	22.508
chr1	1.63E+08	162908280	242			22.997
chr1	1.64E+08	163714080	77	Suco	SUN domain containing ossification factor	18.129
chr2	71673361	71674380	-193	Pdk1	pyruvate dehydrogenase kinase, isoenzyme 1	19.479
chr2	1.56E+08	155888300	-128	Phf20	PHD finger protein 20	23.08
chr3	84125612	84126540	12	D930015E06Rik	RIKEN cDNA D930015E06 gene	18.474
chr4	32292222	32293200	-9	Map3k7	mitogen-activated protein kinase kinase kinase 7	12.724
chr4	1.15E+08	115236200	-145	Efcab14	EF-hand calcium binding domain 14	15.728
chr5	1.01E+08	101086760	-111	Agpat9	1-acylglycerol-3-phosphate O-acyltransferase 9	24.081
chr5	1.09E+08	108701740	-234	Pcgf3	polycomb group ring finger 3	16.773
chr5	1.18E+08	118417050	12	Fbxw8	F-box and WD-40 domain protein 8	27.098
chr5	1.22E+08	121659140	72	Naa25	N(alpha)-acetyltransferase 25, NatB auxiliary subunit	17.688
chr7	1.28E+08	127538080	-353	Fbxl19	F-box and leucine-rich repeat protein 19	14.116
chr8	73162602	73163371	-229	Sugp2	SURP and G patch domain containing 2	15.797
chr8	1.3E+08	129857800	-171	Rbm34	RNA binding motif protein 34	26.82
chr9	78373401	78374420	-181	Slc17a5	solute carrier family 17 (anion/sugar transporter), member 5	14.48
chr10	1.28E+08	127780500	-83	Ankrd52	ankyrin repeat domain 52	15.212
chr11	83278921	83279600	-104	Mmp28	matrix metallopeptidase 28 (epilysin)	16.224
chr12	40955381	40956151	447	Zfp277	zinc finger protein 277	19.987
chr19	29871922	29872740	-325	9930021J03Rik	RIKEN cDNA 9930021J03 gene	20.572
chr4	43599561	43600240	64	Gba2	glucosidase beta 2	13.343
chr10	58616142	58617700	283	Sept10	septin 10	36.18
chr15	12149232	12150240	-83	Mtmr12	myotubularin related protein 12	25.04
chr17	67908541	67909900	-167	Arhgap28	Rho GTPase activating protein 28	39.703
chr9	1.09E+08	108848960	-158	Pfkfb4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	18.247
chr4	46158912	46160100	69	Tstd2	thiosulfate sulfurtransferase (rhodanese)-like domain containing 2	17.131
chr3	27902042	27902440	-729	Fndc3b	fibronectin type III domain containing 3B	14.274
chr3	27901081	27902031	-44	Fndc3b	fibronectin type III domain containing 3B	18.747
chr13	93630922	93632100	52	Zfyve16	zinc finger, FYVE domain containing 16	21.941
chr5	35265592	35266770	-124	Rgs12	regulator of G-protein signaling 12	16.928
chr4	5570901	5571580	-86	Fam110b	family with sequence similarity 110, member B	15.58
chr16	32166381	32167340	-88	Fbxo45	F-box protein 45	24.544
chr10	1.28E+08	128077320	-113	Suox	sulfite oxidase	18.809
chr10	77977142	77977601	-258	Ilvbl	ilvB (bacterial acetolactate synthase)-like	48.209
chr11	1.16E+08	116397980	-103	Ube2o	ubiquitin-conjugating enzyme E2O	16.901
chr1	99599941	99600950	53	Ppip5k2	diphosphoinositol pentakisphosphate kinase 2	18.945
chr11	32354401	32354911	-716	Ubtd2	ubiquitin domain containing 2	23.588
chr11	32354922	32355760	-31	Ubtd2	ubiquitin domain containing 2	24.358
chr8	88381992	88383000	-226	Gpt2	glutamic pyruvate transaminase (alanine aminotransferase) 2	16.643
chr5	1.4E+08	139989440	-13	Micall2	MICAL-like 2	37.592
chr1	95584201	95585560	364	Thap4	THAP domain containing 4	24.83
chr11	62464121	62464800	258	Lrrc75a	leucine rich repeat containing 75A	14.443
chr7	44920772	44921140	-33	Prr12	proline rich 12	12.984
chr1	74533441	74534361	703	Rnf25	ring finger protein 25	18.348
chr9	82943001	82943680	-15	Hmgn3	high mobility group nucleosomal binding domain 3	13.345
chr8	36434061	36434690	-168	Tnks	tankyrase, TRF1-interacting ankyrin-related ADP-ribose	10.277
chr15	80091081	80092100	-29	Rps19bp1	ribosomal protein S19 binding protein 1	32.232
chr16	35689542	35690820	48	Hspbap1	Hspb associated protein 1	18.454
chr7	1.31E+08	131202260	1	Acadsb	acyl-Coenzyme A dehydrogenase, short/branched chain	15.797
chr15	96527572	96528380	-244	Slc38a2	solute carrier family 38, member 2	19.365
chr17	14679172	14680180	24	Wdr27	WD repeat domain 27	22.556

chr13	84694742	84695360	-355	Tmem161b	transmembrane protein 161B	14.118
chr10	62315422	62316490	-34	Slc25a16	solute carrier family 25 (mitochondrial carrier, Graves disease	14.562
chr15	58653061	58654080	-60	Tmem65	transmembrane protein 65	16.573
chr4	1.25E+08	124569420	-111	Snip1	Smad nuclear interacting protein 1	20.452
chr3	1.38E+08	138427260	19	Metap1	methionyl aminopeptidase 1	28.362
chr2	51894202	51895220	-135	Rif1	Rap1 interacting factor 1 homolog (yeast)	15.388
chr7	5986782	5988000	71	Zfp28	zinc finger protein 28	23.304
chr11	68507621	68508300	-150	Myh10	myosin, heavy polypeptide 10, non-muscle	19.698
chr14	97929072	97929520	-26	Mzt1	mitotic spindle organizing protein 1	17.812
chr14	97928202	97929061	639	Mzt1	mitotic spindle organizing protein 1	13.594
chr2	25084181	25085200	83	Tprn	taperin	34.351
chr4	1.33E+08	132752660	-59	Fam46b	family with sequence similarity 46, member B	15.747
chr11	50135381	50136060	39	Maml1	mastermind like 1 (Drosophila)	16.096
chr15	95618881	95618911	19	Ano6	anoctamin 6	8.333
chr19	7483752	7484760	-413	2700081O15Rik	RIKEN cDNA 2700081O15 gene	15.77
chr14	66669602	66670510	628	Kctd9	potassium channel tetramerisation domain containing 9	12.238
chr9	1.07E+08	106745960	-399	Rbm15b	RNA binding motif protein 15B	24.308
chr5	1.15E+08	115419800	-115	Mlec	malectin	17.711
chr5	1.23E+08	123276180	-21	Orai1	ORAI calcium release-activated calcium modulator 1	19.91
chr9	48736672	48737950	-6	Usp28	ubiquitin specific peptidase 28	22.34
chr10	1.11E+08	110569020	-232	Osbpl8	oxysterol binding protein-like 8	15.268
chr11	60592761	60593440	460	Top3a	topoisomerase (DNA) III alpha	18.847
chr4	43690001	43691020	439	Tmem8b	transmembrane protein 8B	12.205
chr14	61791261	61791521	-409	Wdfy2	WD repeat and FYVE domain containing 2	15.577
chr6	1.25E+08	124975500	133	Zfp384	zinc finger protein 384	15.053
chr13	23588521	23589271	-171	Hist1h4d	histone cluster 1, H4d	18.187
chr18	38094961	38096250	100	Fchsd1	FCH and double SH3 domains 1	16.419
chr15	76550672	76551680	-76	C030006K11Rik	RIKEN cDNA C030006K11 gene	18.384
chr6	85880941	85881690	-4	Cml1	camello-like 1	13.523
chr11	1.07E+08	106949040	-688	Bptf	bromodomain PHD finger transcription factor	27.956
chr17	95053801	95055090	236	2700099C18Rik	NDC80 homolog, kinetochore complex component pseudogene	17.793
chr8	1.14E+08	114409320	-30	Wdr59	WD repeat domain 59	27.213
chr9	1.03E+08	103163820	-141	Topbp1	topoisomerase (DNA) II binding protein 1	15.106
chr7	1.28E+08	128030320	-501	9130023H24Rik	RIKEN cDNA 9130023H24 gene	28.923
chr4	1.08E+08	108118300	-98	Cc2d1b	coiled-coil and C2 domain containing 1B	23.32
chr1	75361681	75363030	264	Chpf	chondroitin polymerizing factor	17.181
chr11	1.07E+08	106605300	-206	Ddx5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	25.665
chr4	43287852	43288460	-103	Atp8b5	ATPase, class I, type 8B, member 5	12.735
chr4	1.55E+08	154953600	-537	9430015G10Rik	RIKEN cDNA 9430015G10 gene	17.004
chr8	86588821	86589840	-46	Pkn1	protein kinase N1	13.391
chr5	33102061	33103010	-52	Pisd	phosphatidylserine decarboxylase	23.827
chr15	81226352	81227360	93	St13	suppression of tumorigenicity 13	23.965
chr11	68248032	68248751	71	Pik3r5	phosphoinositide-3-kinase, regulatory subunit 5, p101	20.288
chr13	74674201	74675100	52	Exoc3	exocyst complex component 3	17.944
chr11	1.19E+08	119308370	-15	Endov	endonuclease V	26.468
chr1	21064022	21065040	-155	Tram2	translocating chain-associating membrane protein 2	21.702
chr6	1.16E+08	116159640	-137	Tmcc1	transmembrane and coiled coil domains 1	18.289
chr15	78935421	78936780	-138	Micall1	microtubule associated monooxygenase, calponin and LIM	22.223
chr5	74350181	74350860	-412	Usp46	ubiquitin specific peptidase 46	17.842
chr11	84644701	84645880	-83	4930502E09Rik	RIKEN cDNA 4930502E09 gene	23.237
chr19	41901261	41902170	-272	Frat2	frequently rearranged in advanced T cell lymphomas 2	17.897
chr2	30107942	30109040	49	Nup188	nucleoporin 188	27.434
chr6	1.35E+08	134796400	-2	Crebl2	cAMP responsive element binding protein-like 2	18.318
chr7	80119352	80120320	-53	Ttll13	tubulin tyrosine ligase-like family, member 13	17.08
chr8	75421282	75422420	-248	Slc35e1	solute carrier family 35, member E1	17.728
chr11	1.13E+08	113500311	265	Fam104a	family with sequence similarity 104, member A	34.966
chr10	1.17E+08	116553360	-96	Frs2	fibroblast growth factor receptor substrate 2	28.428
chr5	31324282	31325560	222	Slc5a6	solute carrier family 5 (sodium-dependent vitamin transporter),	19.171
chr3	1.53E+08	152651840	-100	Pigk	phosphatidylinositol glycan anchor biosynthesis, class K	25.847
chr9	1.07E+08	107439320	-416	Hyal3	hyaluronoglucosaminidase 3	15.33
chr17	79804121	79805070	-146	Atl2	atlastin GTPase 2	20.667
chr10	61110241	61110920	-40	Aifm2	apoptosis-inducing factor, mitochondrion-associated 2	17.378
chr6	1.2E+08	119814640	318	3110021A11Rik	RIKEN cDNA 3110021A11 gene	23.439
chr7	30243341	30244700	-200	Arhgap33	Rho GTPase activating protein 33	19.789
chr5	33946281	33947640	-468	Fam53a	family with sequence similarity 53, member A	20.548
chr5	1.43E+08	142882620	52	Wipi2	WD repeat domain, phosphoinositide interacting 2	19.048
chr9	22225492	22226320	-211	Bbs9	Bardet-Biedl syndrome 9 (human)	10.659
chr12	1.06E+08	106086800	-31	Gskip	GSK3B interacting protein	15.164
chr1	1.93E+08	193276060	493			16.959
chr7	99016501	99017180	-504	Uvrag	UV radiation resistance associated gene	21.24
chr13	13746201	13747220	-90	B3galnt2	UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase,	17.294
chr15	75736622	75737380	11	Tigd5	tigger transposable element derived 5	28.131
chr15	75735492	75736611	548	Eef1d	eukaryotic translation elongation factor 1 delta (guanine nucleotide	23.823
chr17	44239441	44240800	-106	Supt3	suppressor of Ty 3	30.734
chr1	1.82E+08	181505600	85	Sccpdh	saccharopine dehydrogenase (putative)	41.436
chr3	1.43E+08	142820390	-325	Pkn2	protein kinase N2	24.711
chr11	59265741	59266760	10	Jmjd4	jumonji domain containing 4	12.434
chr7	80866692	80867640	-31	Zfp592	zinc finger protein 592	11.621
chr15	80060821	80061500	-175	Mief1	mitochondrial elongation factor 1	18.679
chr7	80106041	80106710	-31	Gdpgp1	GDP-D-glucose phosphorylase 1	14.311
chr2	30973661	30974680	130	D330023K18Rik	RIKEN cDNA D330023K18 gene	22.809
chr12	40956162	40956740	-25	Dock4	dedicator of cytokinesis 4	14.723
chr15	83338421	83339100	-87	Ttll1	tubulin tyrosine ligase-like 1	21.775
chr5	1.31E+08	130540540	-75	Sbds	Shwachman-Bodian-Diamond syndrome homolog (human)	15.04
chr12	65993712	65994680	-15	Fancm	Fanconi anemia, complementation group M	12.97
chr17	56401581	56402971	-231	Vmac	vimentin-type intermediate filament associated coiled-coil protein	30.727
chr19	46204981	46205911	-423	Gbf1	golgi-specific brefeldin A-resistance factor 1	16.419
chr11	1.05E+08	105406460	-175	Tanc2	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	19.192
chr11	1.18E+08	117597500	-198	Tmc6	transmembrane channel-like gene family 6	22.508
chr19	17022532	17023740	-1	Prune2	prune homolog 2 (Drosophila)	20.05

chr6	1.27E+08	127419760	78	Parp11	poly (ADP-ribose) polymerase family, member 11	15.655
chr3	96246861	96247820	-35	Mtmr11	myotubularin related protein 11	13.458
chr11	1.21E+08	121237880	23	Fn3krp	fructosamine 3 kinase related protein	17.803
chr2	1.8E+08	180000420	79	Mtg2	mitochondrial ribosome associated GTPase 2	16.713
chr2	4981001	4981680	-130	Optn	optineurin	15.131
chr7	28878921	28879251	-64	Ggn	gametogenetin	10.455
chr19	34987742	34988720	-124	Kif20b	kinesin family member 20B	14.988
chr5	1.3E+08	130180900	-206	Zbed5	zinc finger, BED type containing 5	35.155
chr15	54919861	54921220	21	Dscc1	defective in sister chromatid cohesion 1 homolog (S. cerevisiae)	31.902
chr15	76466681	76467640	24	Tonsl	tonsoku-like, DNA repair protein	21.851
chr11	1.2E+08	119915960	256	1810043H04Rik	RIKEN cDNA 1810043H04 gene	26.884
chr2	93650302	93650960	7	Accs	1-aminocyclopropane-1-carboxylate synthase (non-functional)	14.723
chr4	1.06E+08	105814120	-365	Usp24	ubiquitin specific peptidase 24	14.697
chr11	77847761	77848780	-238	Dhrs13	dehydrogenase/reductase (SDR family) member 13	30.63
chr7	30260681	30261360	12	Proser3	proline and serine rich 3	12.826
chr5	93509861	93510880	29	Nup54	nucleoporin 54	18.852
chr11	29593332	29594041	-88	Rtn4	reticulon 4	24.403
chr11	29593261	29593321	393	Rtn4	reticulon 4	8.667
chr14	54544501	54545441	121	Psme2	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	21.021
chr19	6241381	6242060	52	Atg2a	autophagy related 2A	17.037
chr11	98679292	98680240	78	Wipf2	WAS/WASL interacting protein family, member 2	16.507
chr2	1.3E+08	130334900	55	Lzts3	leucine zipper, putative tumor suppressor family member 3	19.96
chr8	86604832	86605820	44	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	12.543
chr11	86942602	86943551	-194	Trim37	tripartite motif-containing 37	21.533
chr11	78567392	78568430	13	Fam58b	family with sequence similarity 58, member B	26.452
chr13	58166861	58167540	-72	Idnk	idnK gluconokinase homolog (E. coli)	14.001
chr7	30017022	30018010	3	Alkbh6	alkB, alkylation repair homolog 6 (E. coli)	15.033
chr2	28946581	28947600	89	Setx	senataxin	19.093
chr11	1.06E+08	106429520	10	Tex2	testis expressed gene 2	13.97
chr12	1.13E+08	113037080	59	Inf2	inverted formin, FH2 and WH2 domain containing	16.657
chr15	76644812	76645860	89	Arhgap39	Rho GTPase activating protein 39	17.103
chr17	47092041	47093730	-996	Usp49	ubiquitin specific peptidase 49	23.858
chr4	1.06E+08	106409460	-282	Ssbp3	single-stranded DNA binding protein 3	16.308
chr10	79790682	79791470	-296	Mex3d	mex3 homolog D (C. elegans)	18.44
chr1	1.87E+08	187030490	-16	Iars2	isoleucine-tRNA synthetase 2, mitochondrial	12.754
chr12	33538621	33539980	108	Sypl	synaptophysin-like protein	23.465
chr15	76283761	76284440	-593	Scx	scleraxis	20.677
chr17	24687741	24688740	-17	Hn1l	hematological and neurological expressed 1-like	21.54
chr1	57940112	57941100	86	Sgol2a	shugoshin-like 2a (S. pombe)	20.881
chr2	37264681	37265700	-60	Zbtb26	zinc finger and BTB domain containing 26	15.229
chr5	1.43E+08	142654140	-171	Foxk1	forkhead box K1	14.05
chr18	80362401	80363080	-62	Rbfa	ribosome binding factor A	18.345
chr8	73720942	73721860	21	Mast3	microtubule associated serine/threonine kinase 3	17.132
chr10	80158061	80158740	65	Dot1l	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	21.342
chr15	76056312	76057660	-234	Plec	plectin	20.519
chr15	76026412	76027400	184	Plec	plectin	20.957
chr15	76024681	76026401	-77	Plec	plectin	29.413
chr15	76022301	76023660	-15	Plec	plectin	26.15
chr3	90351601	90352280	-501	Dennd4b	DENN/MADD domain containing 4B	12.745
chr5	1.26E+08	125723840	94	Dhx37	DEAH (Asp-Glu-Ala-His) box polypeptide 37	22.127
chr2	1.51E+08	150701260	58	Ninl	ninein-like	14.714
chr17	25971241	25972260	92	Fam234a	family with sequence similarity 234, member A	28.183
chr1	94011042	94011700	-624	Hdac4	histone deacetylase 4	18.198
chr4	1.34E+08	133976960	-274	Man1c1	mannosidase, alpha, class 1C, member 1	12.311
chr2	1.15E+08	115273260	-237	BC052040	cDNA sequence BC052040	21.862
chr18	13084561	13085580	-60	Osbpl1a	oxysterol binding protein-like 1A	24.777
chr17	45846281	45847550	-40	Zfp318	zinc finger protein 318	22.677
chr1	1.63E+08	162872210	-392	Gas5	growth arrest specific 5	29.913
chr19	59512312	59513260	846	Emx2	empty spiracles homeobox 2	11.617
chr17	3040281	3041290	-120	Pisd-ps2	phosphatidylserine decarboxylase, pseudogene 2	15.326
chr1	88189541	88190900	406	Ncl	nucleolin	16.063
chr7	1.43E+08	142863580	6	R74862	expressed sequence R74862	13.077
chr8	98695541	98696220	-79	4930513N10Rik	RIKEN cDNA 4930513N10 gene	12.909
chr15	81017581	81018600	-18	4930483J18Rik	RIKEN cDNA 4930483J18 gene	25.921
chr7	1.27E+08	127304451	-124	1700008J07Rik	RIKEN cDNA 1700008J07 gene	18.065
chr15	25357922	25358220	418	Basp1	brain abundant, membrane attached signal protein 1	13.544
chr13	54703012	54704300	-74	Rnf44	ring finger protein 44	33.92
chr10	93095741	93096760	-597	Gm8580	ribosomal protein L29 pseudogene	21.321
chr1	57914241	57914571	224	Kctd18	potassium channel tetramerisation domain containing 18	14.939
chr2	94206861	94207540	328	Ttc17	tetratricopeptide repeat domain 17	13.691
chr16	55899092	55900080	-18	Zbtb11os1	zinc finger and BTB domain containing 11, opposite strand 1	20.268
chr4	1.55E+08	154605480	-22	Atad3aos	ATPase family, AAA domain containing 3A, opposite strand	36.601
chr15	3976981	3977660	86	BC037032	cDNA Sequence BC037032	14.243
chr8	88189201	88190160	-57	Orc6	origin recognition complex, subunit 6	17.39
chr11	85050321	85051340	485	Appbp2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	19.054
chr19	47015482	47016220	-189	Nt5c2	5'-nucleotidase, cytosolic II	25.232
chr18	74904041	74904671	-221	Acaa2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-	17.587
chr10	79258081	79258701	-291	E130317F20Rik	RIKEN cDNA E130317F20 gene	14.839
chr11	1.17E+08	116931780	-216	Sec14l1	SEC14-like lipid binding 1	20.073
chr1	23225401	23226080	-804	Mir30a	microRNA 30a	16.468
chr11	75278332	75279740	-875	Mir22	microRNA 22	33.522
chr7	1.41E+08	141073820	-497	Mir210	microRNA 210	11.269
chr16	14072601	14073620	-94	Mir484	microRNA 484	16.011
chr5	65248532	65249400	-244	Fam114a1	family with sequence similarity 114, member A1	15.325
chr10	81008741	81009420	-357	BC025920	zinc finger protein pseudogene	18.315
chr11	1.2E+08	120006400	56	2810410L24Rik	RIKEN cDNA 2810410L24 gene	18.441
chr10	7352501	7353520	-551	A630066F11Rik	RIKEN cDNA A630066F11 gene	18.694
chr11	75277202	75278321	27	Mir22hg	Mir22 host gene (non-protein coding)	25.553
chr2	1.55E+08	155314600	-115	Mir499	microRNA 499	10.108
chr19	5387792	5389000	60	D330050I16Rik	RIKEN cDNA D330050I16 gene	18.094

chr7	3740001	3740860	287	Leng8	leukocyte receptor cluster (LRC) member 8	16.203
chr19	25028421	25029370	-182	Cbwd1	COBW domain containing 1	28.426
chr8	1.27E+08	126908400	-575	Mir1967	microRNA 1967	25.109
chr8	1.27E+08	126907901	-412	Taf5l	TAF5-like RNA polymerase II, p300/CBP-associated factor	9.167
chr4	1.51E+08	151141151	-333	Icmt	isoprenylcysteine carboxyl methyltransferase	14.609
chr1	16641981	16643000	-157			26.734
chr1	57321961	57322640	134	1700066M21Rik	RIKEN cDNA 1700066M21 gene	19.598
chr10	61735161	61736180	108	Hk1	hexokinase 1	22.043
chr9	59415001	59415680	50	Parp6	poly (ADP-ribose) polymerase family, member 6	20.178
chrX	49301702	49302290	-179	C430049B03Rik	RIKEN cDNA C430049B03 gene	15.866
chr15	32188821	32189551	65	Snhg18	small nucleolar RNA host gene 18	19.712
chr2	1.21E+08	120541900	448	Ttbk2	tau tubulin kinase 2	17.301
chr14	44579781	44580460	-100	Ddhd1	DDHD domain containing 1	15.747
chr2	1.53E+08	153038420	330	Asxl1	additional sex combs like 1	22.992
chr15	88904042	88904220	301	Trabd	TraB domain containing	7.82
chr4	1.16E+08	116184460	-166	AV051173	expressed sequence AV051173	17.352
chr16	10921481	10922221	-625	Gm4262	predicted gene 4262	20.338
chr16	10922232	10922840	60	Gm4262	predicted gene 4262	17.158
chr16	42794781	42794921	68	4932412D23Rik	RIKEN cDNA 4932412D23 gene	11.286
chr16	42794932	42795781	-262	4932412D23Rik	RIKEN cDNA 4932412D23 gene	14.138
chr3	27343892	27344881	541	Ect2	ect2 oncogene	20.173
chr4	11893002	11894220	-14	Pdp1	pyruvate dehyrogenase phosphatase catalytic subunit 1	14.419
chr9	75195081	75196440	165	Mapk6	mitogen-activated protein kinase 6	29.554
chr9	79578032	79579380	408	Tmem30a	transmembrane protein 30A	25.522
chr4	1.29E+08	129245560	-224	Khdrbs1	KH domain containing, RNA binding, signal transduction	29.443
chr17	33520261	33520940	545	Daxx	Fas death domain-associated protein	14.923
chr3	58779692	58780900	21	Siah2	seven in absentia 2	28.441
chr7	44853481	44854500	472	Prmt1	protein arginine N-methyltransferase 1	28.003
chr11	59764181	59765200	281	Med9	mediator complex subunit 9	17.447
chr18	67925201	67925880	64	Cep192	centrosomal protein 192	17.713
chr11	98174321	98175000	202	Stard3	START domain containing 3	13.947
chr13	59594521	59595540	74	Naa35	N(alpha)-acetyltransferase 35, NatC auxiliary subunit	26.308
chr19	43727741	43728760	-58	Slc25a28	solute carrier family 25, member 28	14.584
chr8	1.08E+08	108159440	0	Hsf4	heat shock transcription factor 4	12.974
chr5	1.52E+08	151637590	41	1700028E10Rik	RIKEN cDNA 1700028E10 gene	15.053
chr10	14394982	14395940	226	Vta1	Vps20-associated 1 homolog (S. cerevisiae)	17.614
chr17	8148781	8149800	2	4930506C21Rik	RIKEN cDNA 4930506C21 gene	28.034
chr6	1.25E+08	125062200	299	Chd4	chromodomain helicase DNA binding protein 4	14.298
chr6	1.16E+08	115740760	230	Cand2	cullin-associated and neddylation-dissociated 2 (putative)	21.212
chr10	80819362	80820720	-615	Mir1191b	microRNA 1191b	19.716
chr11	97559972	97560801	408	Pip4k2b	phosphatidylinositol-5-phosphate 4-kinase, type II, beta	15.123
chr8	86894481	86895311	-837	Mir8111	microRNA 8111	17.06
chr8	95244541	95245900	28	Crnde	colorectal neoplasia differentially expressed (non-protein coding)	27.955
chr19	21171192	21171800	-311			14.801
chr2	1.61E+08	160801051	-139			16.221
chr14	68467332	68468170	-101	Chmp7	charged multivesicular body protein 7	12.481
chr17	44896321	44897081	587	Cdc5l	cell division cycle 5-like (S. pombe)	14.974
chr10	1.28E+08	127902220	-127	Myl6b	myosin, light polypeptide 6B	18.692
chr19	5845281	5846191	-256	Neat1	nuclear paraspeckle assembly transcript 1 (non-protein coding)	14.374
chr19	8823382	8824700	-27			19.53
chr17	84091521	84092360	4333	Zfp36l2	zinc finger protein 36, C3H type-like 2	27.019
chr19	4624681	4626040	257	Rce1	RCE1 homolog, prenyl protein peptidase (S. cerevisiae)	25.327
chr5	31183441	31184800	249	Ost4	oligosaccharyltransferase 4 homolog (S. cerevisiae)	13.706
chr7	18314441	18315450	6585	Snrpd2	small nuclear ribonucleoprotein D2	20.121
chr7	15431241	15432600	294	Inafm1	InaF motif containing 1	17.62
chr17	35504572	35505151	570	2310061I04Rik	RIKEN cDNA 2310061I04 gene	19.964
chr3	1.03E+08	103187960	104	Nras	neuroblastoma ras oncogene	18.227
chr19	5940552	5941350	-16135	Cdc42ep2	CDC42 effector protein (Rho GTPase binding) 2	12.777
chr1	75062982	75063160	468	Abcb6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	11.831
chr19	7018552	7019300	9320	Bad	BCL2-associated agonist of cell death	17.203
chr17	33526432	33527370	271	Zbtb22	zinc finger and BTB domain containing 22	12.717
chr8	87865912	87867220	2287	Junb	jun B proto-oncogene	15.261
chr19	6341001	6341680	180	Map4k2	mitogen-activated protein kinase kinase kinase kinase 2	14.465
chr10	79723201	79723880	137	2310011J03Rik	RIKEN cDNA 2310011J03 gene	15.181
chr3	90611021	90611950	-1291	S100a14	S100 calcium binding protein A14	11.499
chr15	99553342	99554380	209	Cox14	cytochrome c oxidase assembly protein 14	16.566
chr10	80351302	80352200	18531	Gadd45b	growth arrest and DNA-damage-inducible 45 beta	22.795
chr8	73629721	73630400	3332	Jund	jun D proto-oncogene	14.452
chr4	1.26E+08	125824140	291	Adprhl2	ADP-ribosylhydrolase like 2	34.251
chr1	1.73E+08	173118091	215	Ppox	protoporphyrinogen oxidase	17.247
chr2	1.55E+08	154742840	23582	Ahcy	S-adenosylhomocysteine hydrolase	14.279
chr13	23746621	23747550	813	Hist1h1c	histone cluster 1, H1c	14.78
chr17	34263161	34263840	8298	Atf6b	activating transcription factor 6 beta	15.191
chr7	26887201	26887880	103	Rab4b	RAB4B, member RAS oncogene family	16.725
chr8	1.26E+08	126028480	11805	Mir7080	microRNA 7080	17.388
chr10	80068072	80068640	-8156	Btbd2	BTB (POZ) domain containing 2	18.421
chr10	80067621	80068061	-7641	Btbd2	BTB (POZ) domain containing 2	21.932
chr9	57387241	57388500	281	Ulk3	unc-51-like kinase 3	17.041
chr19	45802421	45803100	114	Npm3	nucleoplasmin 3	15.518
chr17	46113402	46114200	272	Cul7	cullin 7	33.415
chr17	35517421	35518470	176	Atat1	alpha tubulin acetyltransferase 1	33.984
chr5	33968721	33969740	201	Slbp	stem-loop binding protein	22.463
chr3	96662341	96663700	-10814	Gm15441	predicted gene 15441	18.282
chr17	46136712	46137660	260	Rrp36	ribosomal RNA processing 36 homolog (S. cerevisiae)	17.472
chr9	20823301	20824300	116	Fdx1l	ferredoxin 1-like	14.46
chr17	25559841	25560860	611	Stub1	STIP1 homology and U-Box containing protein 1	22.048
chr7	25510732	25511560	-13653	Axl	AXL receptor tyrosine kinase	19.171
chr6	1.15E+08	114827450	60566	Vgll4	vestigial like 4 (Drosophila)	25.724
chr9	1.08E+08	108436880	499	Wdr6	WD repeat domain 6	19.036
chr7	1.41E+08	140806920	1041	Ifitm2	interferon induced transmembrane protein 2	11.803

chr5	1.38E+08	137544590	104	Trip6	thyroid hormone receptor interactor 6	14.993
chr17	26660081	26661780	214			27.059
chr15	75896161	75897180	369	Scrib	scribbled homolog (Drosophila)	24.807
chr13	23563361	23564040	1203	Hist1h1d	histone cluster 1, H1d	11.359
chr11	35681402	35682320	-3910	Rars	arginyl-tRNA synthetase	14.686
chr4	1.33E+08	132857380	362	Gpn2	GPN-loop GTPase 2	20.895
chr8	1.08E+08	108179160	276	4931428F04Rik	RIKEN cDNA 4931428F04 gene	23.698
chr17	23402881	23403560	-1828	Thoc6	THO complex 6 homolog (Drosophila)	17.695
chr19	9033801	9034691	160	Eef1g	eukaryotic translation elongation factor 1 gamma	19.067
chr8	72751501	72752070	231	Lpar2	lysophosphatidic acid receptor 2	14.063
chr11	1.16E+08	116489440	341	Snord1c	small nucleolar RNA, C/D box 1C	22.13
chr2	1.55E+08	155048840	168	Mir695	microRNA 695	18.795
chr9	61919472	61920120	804	Mir5133	microRNA 5133	12.401
chr14	50907521	50908200	1076	Arhgef40	Rho guanine nucleotide exchange factor (GEF) 40	13.215
chr4	1.4E+08	140219430	11012	Gm13031	predicted gene 13031	21.137
chr5	1.35E+08	134857260	217	Mir7228	microRNA 7228	13.854
chr14	61791532	61792510	190	Mir8098	microRNA 8098	18.669

Chr	Start	End	Distance to	Gene Name	Gene Description	Average
chr2	33274101	33274740	16121	Zbtb43	zinc finger and BTB domain containing 43	11.664
chr7	30030161	30030840	635	Sdhaf1	succinate dehydrogenase complex assembly	13.601
chr15	99325221	99325900	-22796	Bcdin3d	BCDIN3 domain containing	21.963
chr6	1.2E+08	120448881	10955	Cecr6	cat eye syndrome chromosome region,	14.537
chr16	38167721	38168400	46003	Nr1i2	nuclear receptor subfamily 1, group I, member	10.14
chr3	10372742	10373400	23566	Chmp4c	charged multivesicular body protein 4C	12.184
chr11	97904082	97904930	-34954	Stac2	SH3 and cysteine rich domain 2	21.364
chr9	57398542	57399140	5577	Cplx3	complexin 3	13.766
chr17	65975822	65977130	113	Ankrd12	ankyrin repeat domain 12	28.726
chr3	96189741	96190420	148	Otud7b	OTU domain containing 7B	17.549
chr13	43314172	43314980	568	Gfod1	glucose-fructose oxidoreductase domain	26.114
chr11	45694982	45696000	104	Clint1	clathrin interactor 1	18.415
chr4	82996381	82997400	114	Ccdc171	coiled-coil domain containing 171	21.987
chr10	1.28E+08	127772340	986	Coq10a	coenzyme Q10 homolog A (yeast)	18.371
chr13	17589832	17590240	203	Cdk13	cyclin-dependent kinase 13	14.667
chr19	44984041	44985060	120	Fam178a	family with sequence similarity 178, member	22.075
chr10	67374741	67375420	125	Rtkn2	rhotekin 2	19.057
chr15	38022541	38023560	393	Ubr5	ubiquitin protein ligase E3 component n-	17.7
chr10	39059201	39059880	325	Fyn	Fyn proto-oncogene	20.542
chr6	90681401	90682331	167	Iqsec1	IQ motif and Sec7 domain 1	18.914
chr15	99866501	99867180	142	Dip2b	DIP2 disco-interacting protein 2 homolog B	15.757
chr12	50259481	50260360	786	Foxg1	forkhead box G1	14.978
chr9	1.01E+08	101108690	170	Ppp2r3a	protein phosphatase 2, regulatory subunit B'',	20.218
chr10	1.22E+08	122479900	174	Mon2	MON2 homolog (yeast)	24.328
chr19	53195721	53196740	162	Add3	adducin 3 (gamma)	20.108
chr6	83760361	83761690	209	Nagk	N-acetylglucosamine kinase	26.65
chr11	51847281	51848300	146	Cdkl3	cyclin-dependent kinase-like 3	22.987
chr17	78821181	78822180	123	Cebpzos	CCAAT/enhancer binding protein (C/EBP),	14.128
chr17	24999861	25000521	840	Ube2i	ubiquitin-conjugating enzyme E2I	13.621
chr18	50104441	50105460	193	Tnfaip8	tumor necrosis factor, alpha-induced protein 8	15.855
chr2	71012401	71013420	125	Dync1i2	dynein cytoplasmic 1 intermediate chain 2	20.961
chr6	1.2E+08	120004700	254	Wnk1	WNK lysine deficient protein kinase 1	26.217
chr10	25048821	25049840	116	Epb41l2	erythrocyte membrane protein band 4.1 like 2	17.272
chr11	54799161	54799840	6863	Tnip1	TNFAIP3 interacting protein 1	15.281
chr5	1.17E+08	117381600	101	Taok3	TAO kinase 3	18.199
chr5	1.38E+08	137830771	125	Mospd3	motile sperm domain containing 3	19.034
chr5	1.47E+08	147274060	426	Mtif3	mitochondrial translational initiation factor 3	16.622
chr11	5420621	5421300	316	Xbp1	X-box binding protein 1	15.689
chr4	1.41E+08	141066000	203	Casp9	caspase 9	19.647
chr7	45083412	45084391	106	Tead2	TEA domain family member 2	14.043
chr15	98361692	98362340	287	Kansl2	KAT8 regulatory NSL complex subunit 2	18.02
chr7	28080762	28080940	571	Plekhg2	pleckstrin homology domain containing, family	11.86
chr7	28080072	28080751	1011	Plekhg2	pleckstrin homology domain containing, family	16.037
chr11	61309481	61310840	301	Mapk7	mitogen-activated protein kinase 7	22.474
chr2	1.32E+08	131955360	261	Cds2	CDP-diacylglycerol synthase (phosphatidate	12.111
chr13	12515402	12516420	160	Lgals8	lectin, galactose binding, soluble 8	16.258
chr13	55609381	55610060	202			14.513
chr12	55780401	55781420	102	Cfl2	cofilin 2, muscle	13.074
chr11	1.18E+08	117785711	180	Socs3	suppressor of cytokine signaling 3	18.529
chr3	89250681	89251360	298	Clk2	CDC-like kinase 2	14.865
chr16	94634682	94635940	116	Dscr3	Down syndrome critical region gene 3	28.63
chr4	1.09E+08	109175020	121	Faf1	Fas-associated factor 1	16.71
chr3	69214481	69215160	201	Kpna4	karyopherin (importin) alpha 4	17.358
chr1	1.33E+08	132925720	179	Mapkapk2	MAP kinase-activated protein kinase 2	14.832
chr12	8947781	8948131	641	Laptm4a	lysosomal-associated protein transmembrane	12.6
chr19	5637672	5637880	286	Rela	v-rel reticuloendotheliosis viral oncogene	14.712
chr12	59929421	59930430	104	Sec23a	SEC23 homolog A, COPII coat complex	16.584
chr17	80388241	80388920	199	Sos1	son of sevenless homolog 1 (Drosophila)	16.003
chr10	18704152	18705100	200	Tnfaip3	tumor necrosis factor, alpha-induced protein 3	18.586
chr15	98857721	98858400	135	Tuba1c	tubulin, alpha 1C	16.426
chr8	1.23E+08	122797120	319			22.364
chr7	44421072	44422360	291	Nr1h2	nuclear receptor subfamily 1, group H,	15.973
chr7	1.1E+08	109914520	264	Wee1	WEE 1 homolog 1 (S. pombe)	24.246
chr5	1.22E+08	121854640	141	Aldh2	aldehyde dehydrogenase 2, mitochondrial	11.969
chr14	19267882	19269080	204	Anxa7	annexin A7	17.715
chr17	25865912	25867200	270	Axin1	axin 1	19.022
chr2	1.18E+08	118290300	198	Bub1b	budding uninhibited by benzimidazoles 1	12.642
chr16	20629501	20630520	169	Clcn2	chloride channel, voltage-sensitive 2	15.922
chr7	24958721	24960080	118	Erf	Ets2 repressor factor	15.24
chr8	73627001	73628291	918	Jund	jun D proto-oncogene	27.078
chr19	23208292	23208921	283	Klf9	Kruppel-like factor 9	21.793
chr8	13159021	13159651	224	Lamp1	lysosomal-associated membrane protein 1	12.714

chr11	49088522	49089540	1417	Mgat1	mannoside acetylglucosaminyltransferase 1	31.924
chr3	90698741	90699420	259	S100a6	S100 calcium binding protein A6 (calcyclin)	19.183
chr4	43463561	43464920	863	Tesk1	testis specific protein kinase 1	19.7
chr7	11924141	11924861	170	Trim28	tripartite motif-containing 28	16.347
chr12	21663472	21664120	130	Ywhaq	tyrosine 3-monooxygenase/tryptophan 5-	14.884
chr8	1.09E+08	109305240	262	Zfp90	zinc finger protein 90	23.236
chr15	99479241	99479920	110	Racgap1	Rac GTPase-activating protein 1	21.53
chr5	97033392	97034300	159	Anxa3	annexin A3	18.439
chr10	79802081	79802760	240	Mbd3	methyl-CpG binding domain protein 3	23.554
chr7	80071701	80072380	11686	Sema4b	sema domain, immunoglobulin domain (Ig),	12.258
chr9	1.08E+08	107861260	171	Ip6k1	inositol hexaphosphate kinase 1	14.703
chr11	61670561	61671181	416	Ulk2	unc-51 like kinase 2	14.613
chr7	80676221	80677240	114	Iqgap1	IQ motif containing GTPase activating protein	18.69
chr6	51941202	51942820	121	Skap2	src family associated phosphoprotein 2	20.768
chr3	57934641	57936231	250	Pfn2	profilin 2	15.962
chr17	36654041	36654321	162	Gabbr1	gamma-aminobutyric acid (GABA) B receptor,	15.893
chr14	54675741	54676420	167	Rabggta	Rab geranylgeranyl transferase, a subunit	17.339
chr5	1.47E+08	147143840	102	Rpl21	ribosomal protein L21	17.904
chr11	79070061	79071321	199	Wsb1	WD repeat and SOCS box-containing 1	21.111
chr5	4109921	4110940	273	Cyp51	cytochrome P450, family 51	24.087
chr11	99046421	99047100	347	Smarce1	SWI/SNF related, matrix associated, actin	18.161
chr12	33405022	33406360	109	Nampt	nicotinamide phosphoribosyltransferase	13.821
chr5	1.18E+08	117618920	136	Wsb2	WD repeat and SOCS box-containing 2	14.127
chr19	5689561	5690401	850	Map3k11	mitogen-activated protein kinase kinase	15.155
chr4	41042421	41043340	328	B4galt1	UDP-Gal:betaGlcNAc beta 1,4-	13.517
chr14	53417892	53419100	144	Lrp10	low-density lipoprotein receptor-related	16.691
chr3	90595041	90595261	274	Chtop	chromatin target of PRMT1	17.864
chr8	49173521	49174200	116	Ing2	inhibitor of growth family, member 2	15.212
chr3	1.27E+08	126589820	443	Camk2d	calcium/calmodulin-dependent protein kinase	18.27
chr11	51478721	51479400	259	Rmnd5b	required for meiotic nuclear division 5	13.658
chr19	4756261	4757041	126	Rbm4b	RNA binding motif protein 4B	27.128
chr8	89513662	89514860	113	Lonp2	lon peptidase 2, peroxisomal	16.097
chr5	3653672	3653980	116	Gatad1	GATA zinc finger domain containing 1	15.383
chr2	1.19E+08	119168980	129	Ino80	INO80 homolog (S. cerevisiae)	12.397
chr14	35879521	35880200	145	Ccser2	coiled-coil serine rich 2	12.985
chr8	1.2E+08	119865300	130	1700030J22Rik	RIKEN cDNA 1700030J22 gene	20.837
chr1	87895441	87896460	160	Psmd1	proteasome (prosome, macropain) 26S	17.4
chr7	24990902	24991980	502	Cic	capicua homolog (Drosophila)	16.963
chr6	1.16E+08	116304140	159	March8	membrane-associated ring finger (C3HC4) 8	16.845
chr18	57479721	57480740	128	Prrc1	proline-rich coiled-coil 1	18.444
chr7	92511782	92512671	108	Ankrd42	ankyrin repeat domain 42	16.847
chr9	18223321	18224340	131	Zfp558	zinc finger protein 558	25.228
chr19	34258452	34258740	329	Stambpl1	STAM binding protein like 1	15.812
chr7	83759341	83760451	630	Mesdc1	mesoderm development candidate 1	17.495
chr11	53193681	53194921	111	Aff4	AF4/FMR2 family, member 4	18.508
chr9	70302141	70303160	239	Rnf111	ring finger 111	19.15
chr11	62636161	62637180	222	Trim16	tripartite motif-containing 16	14.473
chr5	1.09E+08	108934911	180	Fgfrl1	fibroblast growth factor receptor-like 1	16.043
chr7	1.13E+08	113161180	109	Btbd10	BTB (POZ) domain containing 10	21.198
chr17	24743501	24744520	324	Ift140	intraflagellar transport 140	12.367
chr11	75302861	75303540	228	Prpf8	pre-mRNA processing factor 8	14.009
chr16	4554981	4555660	147	Vasn	vasorin	17.825
chr17	21240141	21240581	125	Zfp52	zinc finger protein 52	15.636
chr15	63889401	63890420	211	Fam49b	family with sequence similarity 49, member B	14.566
chr5	1.38E+08	138016201	288	Mepce	methylphosphate capping enzyme	
chr10	80059801	80060310	145	Btbd2	BTB (POZ) domain containing 2	15.075
chr12	1.13E+08	113257400	277	BC022687	cDNA sequence BC022687	18.432
chr2	1.55E+08	155421140	116	Edem2	ER degradation enhancer, mannosidase	17.021
chr6	56726621	56727640	261	Kbtbd2	kelch repeat and BTB (POZ) domain	20.318
chr15	58245401	58246080	189	D15Ertd621e	DNA segment, Chr 15, ERATO Doi 621,	16.834
chr9	79852401	79853080	153	Senp6	SUMO/sentrin specific peptidase 6	13.006
chr13	74069722	74070700	207	Clptm1l	CLPTM1-like	16.853
chr19	7561261	7561940	118	Atl3	atlastin GTPase 3	19.654
chr7	45901361	45902380	132	Nomo1	nodal modulator 1	16.332
chr19	4614821	4616180	167	Lrfn4	leucine rich repeat and fibronectin type III	24.946
chr11	1.1E+08	109538171	530	Fam20a	family with sequence similarity 20, member A	17.366
chr8	49211941	49213300	128	Cdkn2aip	CDKN2A interacting protein	15.187
chr19	12568192	12568780	555	Dtx4	deltex 4 homolog (Drosophila)	18.952
chr12	72749461	72750051	111	Daam1	dishevelled associated activator of	14.78
chrX	44452672	44453640	173	Zdhhc9	zinc finger, DHHC domain containing 9	10.418
chr4	59899161	59900520	136	Snx30	sorting nexin family member 30	21.846
chr5	1.43E+08	142717030	120	Ap5z1	adaptor-related protein complex 5, zeta 1	18.816
chr7	1.27E+08	126720710	114	Kctd13	potassium channel tetramerisation domain	22.957
chr7	80243832	80244760	592	Man2a2	mannosidase 2, alpha 2	17.112
chr6	90334601	90335620	112	Zxdc	ZXD family zinc finger C	23.963
chr19	16847341	16848360	102	Vps13a	vacuolar protein sorting 13A (yeast)	21.313
chr5	1.11E+08	111011360	169	Ep400	E1A binding protein p400	19.562
chr8	18594941	18595960	300	Mcph1	microcephaly, primary autosomal recessive 1	14.246
chr1	1.84E+08	184246340	158	Trp53bp2	transformation related protein 53 binding	19.517
chr8	1.28E+08	127549970	164	2310022B05Rik	RIKEN cDNA 2310022B05 gene	19.381
chr1	1.68E+08	168246280	563	Pogk	pogo transposable element with KRAB	12.629
chr7	49114701	49114711	496	Nav2	neuron navigator 2	7
chr15	77133421	77134440	378	Rbfox2	RNA binding protein, fox-1 homolog (C.	24.909
chr11	1.02E+08	102006460	161	G6pc3	glucose 6 phosphatase, catalytic, 3	17.715
chr16	31922261	31923280	264	Senp5	SUMO/sentrin specific peptidase 5	23.162
chr2	1.61E+08	160565000	111	Zhx3	zinc fingers and homeoboxes 3	18.935
chr1	90532481	90533840	202	Arl4c	ADP-ribosylation factor-like 4C	20.705
chr2	34228821	34229500	300	Mapkap1	mitogen-activated protein kinase associated	14.515
chr11	1.15E+08	115292640	193	Armc7	armadillo repeat containing 7	42.69
chr7	80143101	80143780	272	Vps33b	vacuolar protein sorting 33B (yeast)	15.386

chr12	25239901	25241260	130	Klf11	Kruppel-like factor 11	20.596
chr10	1.1E+08	110149960	135	E2f7	E2F transcription factor 7	11.834
chr5	67585881	67586560	130			22.971
chr7	11866001	11866680	297	Zfp324	zinc finger protein 324	15.459
chr7	28879572	28879940	606	Ggn	gametogenetin	22.188
chr3	97743201	97744311	139	Prkab2	protein kinase, AMP-activated, beta 2 non-	17.883
chr10	50280901	50281580	156	Ascc3	activating signal cointegrator 1 complex	22.598
chr8	72737382	72738190	110	Gmip	Gem-interacting protein	20.583
chr11	59478581	59479041	121	Mprip	myosin phosphatase Rho interacting protein	17.783
chr3	1.3E+08	130053060	209	Sec24b	Sec24 related gene family, member B (S.	12.692
chr11	74454221	74454900	-11130	Cluh	clustered mitochondria (cluA/CLU1) homolog	20.862
chr7	18116262	18116971	-29430	Nanos2	nanos homolog 2 (Drosophila)	12.818
chr2	25186861	25188020	195	Uap1l1	UDP-N-acteylglucosamine pyrophosphorylase	22.251
chr5	1.37E+08	137318100	2538	Vgf	VGF nerve growth factor inducible	24.155
chr3	1.07E+08	106850440	363	Lrif1	ligand dependent nuclear receptor interacting	19.649
chr5	1.23E+08	123082040	338	Anapc5	anaphase-promoting complex subunit 5	22.493
chr3	1.07E+08	107460400	1149	Rbm15	RNA binding motif protein 15	15.814
chr19	6076212	6077810	176	Vps51	vacuolar protein sorting 51 homolog (S.	23.907
chr9	1.1E+08	110253840	161	Ptpn23	protein tyrosine phosphatase, non-receptor	22.707
chr13	17588881	17589821	888	Cdk13	cyclin-dependent kinase 13	15.128
chr3	1.46E+08	145514560	187	Znhit6	zinc finger, HIT type 6	23.878
chr8	37717302	37718480	142	Lonrf1	LON peptidase N-terminal domain and ring	26.637
chrX	1.01E+08	100686580	475	Uprt	uracil phosphoribosyltransferase (FUR1)	18.064
chr10	82128361	82129570	159	Hcfc2	host cell factor C2	18.099
chr3	58504492	58505500	1378	Tsc22d2	TSC22 domain family, member 2	14.262
chr6	83067781	83068460	946	Ccdc142	coiled-coil domain containing 142	23.554
chr10	75788381	75789400	117	Dip2a	DIP2 disco-interacting protein 2 homolog A	16.088
chr16	96187021	96187111	272	Brwd1	bromodomain and WD repeat domain	5.889
chr8	1.25E+08	124878260	13636	Mir7237	microRNA 7237	35.803
chr17	5931672	5933000	268	Synj2	synaptojanin 2	16.476
chr4	1.51E+08	151030091	132	Acot7	acyl-CoA thioesterase 7	6.8
chr10	1.26E+08	126304590	255	Xrcc6bp1	XRCC6 binding protein 1	25.643
chr3	96686141	96687160	112	Lix1l	Lix1-like	20.891
chr8	91090081	91091100	1272	Papd5	PAP associated domain containing 5	16.943
chr8	1.29E+08	129479480	556	Irf2bp2	interferon regulatory factor 2 binding protein 2	12.06
chr11	1.2E+08	119967640	311	Slc38a10	solute carrier family 38, member 10	14.947
chr3	1.46E+08	145926291	700	Syde2	synapse defective 1, Rho GTPase, homolog 2	12.075
chr15	57742022	57742880	169	Tbc1d31	TBC1 domain family, member 31	23.044
chr10	6239732	6240360	133420	Mthfd1l	methylenetetrahydrofolate dehydrogenase	11.142
chr16	32787561	32788240	213	Rubcn	RUN domain and cysteine-rich domain	19.539
chr11	58979121	58980291	234	Iba57	IBA57, iron-sulfur cluster assembly homolog	21.274
chr8	1.08E+08	108144140	736	B3gnt9	UDP-GlcNAc:betaGal beta-1,3-N-	25.663
chr15	76483681	76483781	425	Cyhr1	cysteine and histidine rich 1	6.7
chr17	78322401	78323420	300	Fez2	fasciculation and elongation protein zeta 2	24.695
chr2	1.53E+08	152521520	1268	Bcl2l1	BCL2-like 1	16.084
chr4	98612241	98613260	183	Dock7	dedicator of cytokinesis 7	31.681
chrX	7300481	7301160	-1566	Rbm3os	RNA binding motif protein 3, opposite strand	10.242
chr5	3601961	3602830	158	Rbm48	RNA binding motif protein 48	17.495
chr6	1.25E+08	124775580	533			18.719
chr1	36389181	36390080	187			14.874
chr5	1.23E+08	122968820	149	P2rx4	purinergic receptor P2X, ligand-gated ion	17.573
chr13	55632501	55633180	213	Caml	calcium modulating ligand	13.324
chr11	94753982	94755280	2317	Col1a1	collagen, type I, alpha 1	15.881
chr16	91446412	91447390	10948	Ifngr2	interferon gamma receptor 2	12.264
chr10	80695941	80696620	188	Pip5k1c	phosphatidylinositol-4-phosphate 5-kinase,	19.433
chr19	7036301	7036980	218	Plcb3	phospholipase C, beta 3	20.462
chr2	1.05E+08	105200080	222	Rcn1	reticulocalbin 1	7.562
chr7	18787041	18788400	240	Relb	avian reticuloendotheliosis viral (v-rel)	23.322
chr13	21187822	21188750	890	Trim27	tripartite motif-containing 27	17.708
chr9	1.1E+08	109978100	220	Smarcc1	SWI/SNF related, matrix associated, actin	35.704
chr19	6276401	6277760	184	Ehd1	EH-domain containing 1	27.475
chr2	38747761	38748571	304	Nr6a1	nuclear receptor subfamily 6, group A,	20.333
chr15	76158972	76159660	767	Gpaa1	GPI anchor attachment protein 1	17.804
chr11	1.02E+08	102272680	-8247	Fam171a2	family with sequence similarity 171, member	24.841
chr14	53530542	53530620	1285	Ajuba	ajuba LIM protein	6.385
chr5	34503881	34504560	347	Mxd4	Max dimerization protein 4	14.894
chr7	1.27E+08	126817841	236	Maz	MYC-associated zinc finger protein (purine-	13.778
chr17	87882861	87884560	334	Msh6	mutS homolog 6 (E. coli)	21.232
chr17	34194821	34196040	-2432	Gpsm3	G-protein signalling modulator 3 (AGS3-like,	17.242
chr11	50053441	50054800	123	Sqstm1	sequestosome 1	13.775
chr3	40841821	40842840	168	Hspa4l	heat shock protein 4 like	15.5
chr11	1.08E+08	108159780	342	Prkca	protein kinase C, alpha	8.003
chr11	1.17E+08	116669071	168	Srsf2	serine/arginine-rich splicing factor 2	9.273
chr18	60973561	60974710	198	Tcof1	Treacher Collins Franceschetti syndrome 1,	17.324
chr7	44820501	44821180	9558	Tsks	testis-specific serine kinase substrate	18.193
chr2	13492402	13492560	317	Vim	vimentin	10.063
chr7	62298382	62299220	288	Mkrn3	makorin, ring finger protein, 3	21.342
chr8	96900681	96902380	239	Amfr	autocrine motility factor receptor	27.92
chr11	1.01E+08	101282600	218	Vat1	vesicle amine transport protein 1 homolog (T	33.143
chr6	56761422	56762190	169	Fkbp9	FK506 binding protein 9	11.21
chr12	85674221	85674900	11542	Isca2	iron-sulfur cluster assembly 2 homolog (S.	15.308
chr3	89299632	89300320	286	Mtx1	metaxin 1	30.246
chr17	12850641	12851320	209	Sod2	superoxide dismutase 2, mitochondrial	16.059
chr16	18339622	18340620	141	Txnrd2	thioredoxin reductase 2	24.157
chr11	5695001	5696020	7024	Dbnl	drebrin-like	15.033
chr3	96142821	96143511	694	Vps45	vacuolar protein sorting 45 (yeast)	16.826
chr17	63185012	63185260	906	Fbxl17	F-box and leucine-rich repeat protein 17	8.028
chr17	63184241	63185001	1421	Fbxl17	F-box and leucine-rich repeat protein 17	16.105
chr12	80090412	80091760	212	Vti1b	vesicle transport through interaction with t-	20.704
chr6	17231201	17231541	186	Cav2	caveolin 2	14.118

chr7	45574621	45575231	1637	Dbp	D site albumin promoter binding protein	18.279
chr15	81638812	81639100	287	Tef	thyrotroph embryonic factor	27.483
chr9	64535102	64536080	171	Rab11a	RAB11A, member RAS oncogene family	12.39
chr5	1.36E+08	136219631	312	Ywhag	tyrosine 3-monooxygenase/tryptophan 5-	19.052
chr11	70660841	70661520	224	Rabep1	rabaptin, RAB GTPase binding effector	15.454
chr17	29074421	29075100	156	Mtch1	mitochondrial carrier homolog 1 (C. elegans)	18.222
chr7	1.21E+08	120826670	471	Mettl9	methyltransferase like 9	17.217
chr1	1.73E+08	172722350	360	Dusp12	dual specificity phosphatase 12	20.371
chr15	98555352	98556140	486	Fkbp11	FK506 binding protein 11	19.839
chr2	1.52E+08	151986050	118	Tbc1d20	TBC1 domain family, member 20	14.644
chr11	59024341	59025360	294	2310033P09Rik	RIKEN cDNA 2310033P09 gene	15.352
chr11	70267801	70269120	334	Med11	mediator complex subunit 11	28.057
chr7	92436152	92437500	485	Ccdc90b	coiled-coil domain containing 90B	44.279
chr6	82617621	82618980	223	Pole4	polymerase (DNA-directed), epsilon 4 (p12	49.575
chr5	1.23E+08	123489250	123	Psmd9	proteasome (prosome, macropain) 26S	14.657
chr6	56852852	56853780	194	Nt5c3	5'-nucleotidase, cytosolic III	15.345
chr11	86623161	86624180	185	Dhx40	DEAH (Asp-Glu-Ala-His) box polypeptide 40	16.419
chr16	57152112	57153320	109	Tbc1d23	TBC1 domain family, member 23	18.471
chr4	1.53E+08	153004621	293	Tprgl	transformation related protein 63 regulated	13.743
chr2	1.19E+08	118505980	222	Knstrn	kinetochore-localized astrin/SPAG5 binding	17.318
chr17	74394381	74395060	245	Yipf4	Yip1 domain family, member 4	14.779
chr8	87950022	87950860	124	A230103J11Rik	RIKEN cDNA A230103J11 gene	36.184
chr15	1.02E+08	102154700	136	Pfdn5	prefoldin 5	20.083
chr5	1.3E+08	130227140	219	Vkorc1l1	vitamin K epoxide reductase complex, subunit	8.858
chr10	70743121	70743451	193	Ipmk	inositol polyphosphate multikinase	12.727
chr11	4034781	4035800	127	Rnf215	ring finger protein 215	14.469
chr17	46214522	46215860	214			20.254
chr4	99426902	99428580	358	Pgm2	phosphoglucomutase 2	19.649
chr5	53029461	53030480	148	Pi4k2b	phosphatidylinositol 4-kinase type 2 beta	15.226
chr4	1.07E+08	107388650	210	0610037L13Rik	RIKEN cDNA 0610037L13 gene	30.411
chr11	1.19E+08	119474300	54796	Rptor	regulatory associated protein of MTOR,	13.932
chr8	1.27E+08	127407480	133	Cog2	component of oligomeric golgi complex 2	12.049
chr5	1.26E+08	125731660	206	Bri3bp	Bri3 binding protein	14.829
chr8	40474281	40474960	236	Tusc3	tumor suppressor candidate 3	17.611
chr8	89774542	89775630	277	N4bp1	NEDD4 binding protein 1	16.755
chr11	68938401	68939420	2262	Hes7	hairy and enhancer of split 7 (Drosophila)	18.554
chr18	67414181	67415540	268	Impa2	inositol (myo)-1(or 4)-monophosphatase 2	18.753
chr19	41317082	41317140	204	Tm9sf3	transmembrane 9 superfamily member 3	7.017
chr17	35429361	35430601	215	Ier3	immediate early response 3	16.016
chr19	46381441	46382800	625	Fbxl15	F-box and leucine-rich repeat protein 15	24.165
chr2	1.64E+08	164188981	121	Pigt	phosphatidylinositol glycan anchor	22.462
chr5	29899692	29900960	297	Ube3c	ubiquitin protein ligase E3C	20.431
chr5	1.41E+08	140672280	161	Eif3b	eukaryotic translation initiation factor 3,	21.775
chr8	4252392	4254080	134	Snapc2	small nuclear RNA activating complex,	23.669
chrX	6999202	6999920	520	Otud5	OTU domain containing 5	16.915
chr1	51233932	51234600	595	Sdpr	serum deprivation response	12.626
chr13	38642021	38642900	115	Bloc1s5	biogenesis of lysosomal organelles complex-	18.573
chr8	1.27E+08	127117840	192	Galnt2	UDP-N-acetyl-alpha-D-	17.22
chr11	22881661	22882630	139	Commd1	COMM domain containing 1	13.492
chr11	1.22E+08	121519400	203	Metrnl	meteorin, glial cell differentiation regulator-like	21.714
chr5	1.38E+08	138015860	969	Mepce	methylphosphate capping enzyme	13.323
chr6	85553181	85554040	421	Alms1	Alstrom syndrome 1	14.229
chr10	7470481	7471500	117	Ginm1	glycoprotein integral membrane 1	16.337
chr15	88690772	88691311	1081	Pim3	proviral integration site 3	18.152
chr19	42143681	42144360	274	Pi4k2a	phosphatidylinositol 4-kinase type 2 alpha	18.287
chr2	1.22E+08	121809760	241	Spg11	spastic paraplegia 11	20.011
chr10	7357422	7358280	157	Nup43	nucleoporin 43	22.061
chr12	87771832	87772700	1651	Irf2bpl	interferon regulatory factor 2 binding protein-	22.826
chr12	87771112	87771821	2451	Irf2bpl	interferon regulatory factor 2 binding protein-	20.08
chr10	77025301	77025980	157	Pttg1ip	pituitary tumor-transforming 1 interacting	27.27
chr13	32345561	32346240	109	Gmds	GDP-mannose 4, 6-dehydratase	11.869
chr7	1.28E+08	128035840	-2504	Tgfb1i1	transforming growth factor beta 1 induced	17.521
chr5	1.36E+08	135679380	303	Pom121	nuclear pore membrane protein 121	17.343
chr18	23946712	23947560	156	Mapre2	microtubule-associated protein, RP/EB family,	13.715
chr11	3812081	3813100	2077	Slc35e4	solute carrier family 35, member E4	20.237
chr6	89609041	89610740	261	Txnrd3	thioredoxin reductase 3	21.436
chr2	1.5E+08	150478900	153	Pygb	brain glycogen phosphorylase	14.216
chr11	95880341	95881960	304	Ube2z	ubiquitin-conjugating enzyme E2Z (putative)	14.784
chr11	1.05E+08	104943310	150	Mettl2	methyltransferase like 2	22.784
chr4	94094661	94095340	265	Plaa	phospholipase A2, activating protein	15.482
chr4	1.51E+08	150840660	339	Phf13	PHD finger protein 13	17.665
chr16	32982041	32982720	112	Lmln	leishmanolysin-like (metallopeptidase M8	17.736
chr19	29870701	29871911	700	9930021J03Rik	RIKEN cDNA 9930021J03 gene	30.744
chr4	1.28E+08	128450001	14948	Azin2	antizyme inhibitor 2	14.553
chr9	66718201	66719220	139	Rab8b	RAB8B, member RAS oncogene family	15.061
chr12	85982941	85983620	12254	Prox2	prospero homeobox 2	15.766
chr7	49114722	49115601	951	Nav2	neuron navigator 2	21.403
chr2	1.58E+08	158317260	396	Actr5	ARP5 actin-related protein 5	11.841
chr10	79363141	79363820	199	Wdr18	WD repeat domain 18	15.052
chr4	57040441	57041800	363	Tmem245	transmembrane protein 245	18.33
chr19	44615821	44616840	165	Hif1an	hypoxia-inducible factor 1, alpha subunit	20.791
chr6	85034341	85035670	166	Exoc6b	exocyst complex component 6B	24.226
chr8	1.09E+08	108741520	127	Cenpt	centromere protein T	16.047
chr19	47121281	47121291	227	Taf5	TAF5 RNA polymerase II, TATA box binding	7
chr7	1.27E+08	127046061	6074	Dctpp1	dCTP pyrophosphatase 1	17.281
chr11	70820052	70820980	111	Dhx33	DEAH (Asp-Glu-Ala-His) box polypeptide 33	16.943
chr1	1.93E+08	192612720	175	Rps6kc1	ribosomal protein S6 kinase polypeptide 1	17.103
chr8	1.23E+08	123475080	266	Gins2	GINS complex subunit 2 (Psf2 homolog)	16.9
chr6	39504272	39504971	1138	Adck2	aarF domain containing kinase 2	12.694
chr7	26936632	26937810	136	Itpkc	inositol 1,4,5-trisphosphate 3-kinase C	18.657

chr15	83422412	83423080	177	Ttll12	tubulin tyrosine ligase-like family, member 12	14.88
chr6	1.42E+08	142303490	102	Pyroxd1	pyridine nucleotide-disulphide oxidoreductase	18.375
chr6	17014621	17015960	141	Tes	testis derived transcript	20.55
chr3	50097652	50098081	-244355	Pcdh18	protocadherin 18	20.41
chr18	5819441	5820380	-227475	Gm10125	predicted gene 10125	13.241
chr13	60419021	60419930	-192095	Dapk1	death associated protein kinase 1	14.435
chr4	54782161	54783140	-186395	Zfp462	zinc finger protein 462	15.469
chr4	32567241	32567941	-178457	Bach2	BTB and CNC homology 2	12.814
chr4	32578461	32579480	-167078	Bach2	BTB and CNC homology 2	21.566
chr3	1.04E+08	104489140	-139214	Magi3	membrane associated guanylate kinase, WW	17.403
chr10	1.2E+08	120013800	-133335	Hmga2	high mobility group AT-hook 2	13.535
chr5	1.12E+08	112119251	-116965	E130006D01Rik	RIKEN cDNA E130006D01 gene	14.098
chr8	1.25E+08	125060840	-107740	Zfpm1	zinc finger protein, multitype 1	21.953
chr3	58398112	58399080	-105022	Tsc22d2	TSC22 domain family, member 2	12.898
chr5	1.19E+08	118726980	-95279	Med13l	mediator complex subunit 13-like	18.524
chr10	5056821	5057500	-94674	Syne1	spectrin repeat containing, nuclear envelope 1	13.465
chr1	92349441	92350330	-83944	Cops8	COP9 (constitutive photomorphogenic)	19.323
chr15	1.03E+08	102668440	-81219	Hoxc13	homeobox C13	21.044
chr8	1.07E+08	106912910	-78309	Cdh5	cadherin 5	16.048
chrX	73686142	73686500	-77625	Tbl1x	transducin (beta)-like 1 X-linked	14.615
chr17	13420141	13420820	-73987	2700054A10Rik	RIKEN cDNA 2700054A10 gene	15.177
chr16	31511541	31512220	-71310	Dlg1	discs, large homolog 1 (Drosophila)	15.027
chr15	66868821	66869650	-69925	Ndrg1	N-myc downstream regulated gene 1	29.557
chr19	41535761	41536440	-66850	Lcor	ligand dependent nuclear receptor	12.758
chr11	20377221	20378240	-65526	Sertad2	SERTA domain containing 2	27.278
chr13	1.12E+08	112089160	-64096			16.648
chr1	1.59E+08	158834851	-58308	Ralgps2	Ral GEF with PH domain and SH3 binding	17.05
chr8	1.29E+08	129418960	-57465	Gm17296	predicted gene, 17296	20.227
chr11	1.02E+08	101656260	-54391	Etv4	ets variant 4	12.716
chr3	1.46E+08	145640020	-52309	Cyr61	cysteine rich protein 61	12.189
chr11	51759062	51759991	-51528	Cdkn2aipnl	CDKN2A interacting protein N-terminal like	16.841
chr11	51760002	51760920	-50593	Cdkn2aipnl	CDKN2A interacting protein N-terminal like	16.679
chr7	97663301	97664660	-50541	Aqp11	aquaporin 11	18.033
chr8	1.23E+08	123162881	-48204	A330074K22Rik	RIKEN cDNA A330074K22 gene	16.957
chr11	30167521	30168151	-48064	Sptbn1	spectrin beta, non-erythrocytic 1	14.714
chr17	13266801	13267820	-46545	Smok4a	sperm motility kinase 4A	25.047
chr11	57778581	57779260	-46339	Larp1	La ribonucleoprotein domain family, member	20.959
chr10	76654472	76655040	-44510	Col18a1	collagen, type XVIII, alpha 1	12.053
chr2	1.53E+08	153265200	-43344	Nol4l	nucleolar protein 4-like	12.97
chr9	69879282	69880380	-42579	Gcnt3	glucosaminyl (N-acetyl) transferase 3, mucin	13.334
chr10	1.11E+08	110527820	-41551	Osbpl8	oxysterol binding protein-like 8	15.528
chr1	1.93E+08	192926150	-41547	Atf3	activating transcription factor 3	22.889
chr19	43624042	43624950	-41140	Nkx2-3	NK2 homeobox 3	14.433
chr1	1.38E+08	137504840	-41108	Csrp1	cysteine and glycine-rich protein 1	16.75
chr5	1.49E+08	149012810	-39713	2210417A02Rik	RIKEN cDNA 2210417A02 gene	9.711
chr9	78306542	78306760	-39243	Eef1a1	eukaryotic translation elongation factor 1	12.734
chr17	3244822	3245300	-37994	Tiam2	T cell lymphoma invasion and metastasis 2	20.889
chr15	31133222	31134020	-35353	Dap	death-associated protein	22.761
chr19	37579732	37580730	-35331	Exoc6	exocyst complex component 6	16.768
chr11	97231501	97231841	-34579	Arhgap23	Rho GTPase activating protein 23	21.559
chr11	97231852	97232520	-34064	Arhgap23	Rho GTPase activating protein 23	16.624
chr6	72402661	72403340	-33933	Mat2a	methionine adenosyltransferase II, alpha	22.041
chr3	1.08E+08	107922380	-33215	Csf1	colony stimulating factor 1 (macrophage)	19.794
chr17	45230201	45230880	-33115	1600014C23Rik	RIKEN cDNA 1600014C23 gene	11.389
chr17	26612532	26613500	-31664	Kifc5b	kinesin family member C5B	20.123
chr6	72441972	72442690	-31569	Capg	capping protein (actin filament), gelsolin-like	23.694
chr7	81055802	81056680	-31076	Pde8a	phosphodiesterase 8A	13.763
chr9	35170621	35171300	-30787	Cdon	cell adhesion molecule-related/down-	11.931
chr19	36413321	36414000	-30551	Pcgf5	polycomb group ring finger 5	17.196
chr7	80029892	80030900	-29958	Sema4b	sema domain, immunoglobulin domain (Ig),	25.473
chr8	1.27E+08	126511280	-29223	Rhou	ras homolog gene family, member U	40.939
chr17	28121432	28122080	-29024	Tulp1	tubby like protein 1	18.483
chr17	88505542	88506370	-28925	Ston1	stonin 1	12.444
chr6	86565021	86565311	-28642	Asprv1	aspartic peptidase, retroviral-like 1	12.448
chr18	82921682	82922260	-28504	2210420H20Rik	RIKEN cDNA 2210420H20 gene	11.478
chr6	86565322	86566380	-27957	Asprv1	aspartic peptidase, retroviral-like 1	28.101
chr7	34021421	34022780	-27731	4931406P16Rik	RIKEN cDNA 4931406P16 gene	23.802
chr4	1.35E+08	134572680	-27520	Clic4	chloride intracellular channel 4 (mitochondrial)	9.125
chr6	72855881	72856560	-26732	Kcmf1	potassium channel modulatory factor 1	15.39
chr11	1.05E+08	104969220	-26017	Tlk2	tousled-like kinase 2 (Arabidopsis)	10.599
chr3	1.03E+08	103232160	-25131	Dennd2c	DENN/MADD domain containing 2C	37.616
chr17	29706481	29707500	-25109	Zfand3	zinc finger, AN1-type domain 3	31.045
chr11	94690341	94691010	-24992	Gm11544	predicted gene 11544	12.296
chr5	1.43E+08	143197120	-24892	Actb	actin, beta	12.361
chr15	6501821	6502531	-24886	Fyb	FYN binding protein	18.07
chr4	1.29E+08	128536301	-24604	Rnf19b	ring finger protein 19B	30.152
chr4	57637492	57638500	-24306			16.334
chr5	1.06E+08	105736260	-24023	Lrrc8c	leucine rich repeat containing 8 family,	14.567
chr13	1.14E+08	113561700	-23922	Il6st	interleukin 6 signal transducer	18.614
chr5	65386421	65387100	-23606	Klhl5	kelch-like 5	15.465
chr19	57292381	57293060	-23438	Ablim1	actin-binding LIM protein 1	14.144
chr3	96586861	96587540	-23390	Hfe2	hemochromatosis type 2 (juvenile) (human	18.417
chr4	1.32E+08	132380360	-22683	Wasf2	WAS protein family, member 2	15.576
chr15	68192781	68193750	-22307	Mir30d	microRNA 30d	16.22
chr15	85431121	85431800	-21873	Wnt7b	wingless-type MMTV integration site family,	15.791
chr5	1.14E+08	114191720	-21505	Coro1c	coronin, actin binding protein 1C	14.058
chr11	95461522	95462231	-21171	Phb	prohibitin	11.942
chr14	31321342	31322160	-20779	Ercc6	excision repair cross-complementing rodent	21.174
chr18	61016741	61017420	-20529	Arsi	arylsulfatase i	14.831
chr11	72386352	72387020	-20245	Spns3	spinster homolog 3	14.57

chr5	1.06E+08	105740131	-20047	Lrrc8c	leucine rich repeat containing 8 family,	14.543
chr7	80040081	80041060	-19784	Sema4b	sema domain, immunoglobulin domain (Ig),	25.217
chr5	1.26E+08	125699700	-19382	Ubc	ubiquitin C	16.031
chr5	1.36E+08	135955090	-19281	Por	P450 (cytochrome) oxidoreductase	13.302
chr11	43610352	43610980	-19270	Ttc1	tetratricopeptide repeat domain 1	14.949
chr4	44302682	44303020	-19166	Melk	maternal embryonic leucine zipper kinase	15.133
chr12	1.06E+08	105945360	-19156	Bdkrb2	bradykinin receptor, beta 2	10.963
chr19	5529081	5530100	-19101	Snx32	sorting nexin 32	22.109
chr7	15211002	15212140	-18893	Zfp541	zinc finger protein 541	16.929
chr3	96591662	96592300	-18609	Hfe2	hemochromatosis type 2 (juvenile) (human	16.351
chr13	21168741	21169300	-18376	Trim27	tripartite motif-containing 27	13.623
chr17	33496461	33497140	-18310	Platr17	pluripotency associated transcript 17	16.277
chr5	37001181	37002160	-17400	D5Ertd579e	DNA segment, Chr 5, ERATO Doi 579,	17.714
chr10	12568781	12569670	-17300	Utrn	utrophin	18.399
chr2	27923692	27924540	-17229	Fcnb	ficolin B	13.679
chr8	47650832	47651680	-17117	Cfap97	cilia and flagella associated protein 97	16.923
chr8	1.25E+08	124555260	-16897	Zcchc14	zinc finger, CCHC domain containing 14	14.374
chr10	82209961	82210640	-16360	Nfyb	nuclear transcription factor-Y beta	16.518
chr16	17949961	17950640	-16123	Dgcr6	DiGeorge syndrome critical region gene 6	14.548
chr11	51795192	51795860	-15528	Cdkn2aipnl	CDKN2A interacting protein N-terminal like	11.398
chr19	5817741	5818420	-15409	Malat1	metastasis associated lung adenocarcinoma	19.523
chr2	37525461	37525691	-15283	Mir5128	microRNA 5128	15.087
chr17	83891261	83891940	-15278			14.529
chr9	44234681	44235360	-15111	Bcl9l	B cell CLL/lymphoma 9-like	21.324
chr8	42887941	42888620	-14766	Asah1	N-acylsphingosine amidohydrolase 1	12.131
chr18	60773981	60774980	-14299	G630071F17Rik	RIKEN cDNA G630071F17 gene	14.091
chr6	31007042	31008000	-14265	Mir29b-1	microRNA 29b-1	20.294
chr16	17658581	17659260	-14264	Klhl22	kelch-like 22	9.745
chr5	1.43E+08	143186580	-14176	Actb	actin, beta	28.364
chr11	1.04E+08	103935240	-14090			12.178
chr8	87082501	87083180	-13774	Mir181c	microRNA 181c	16.711
chr7	29227081	29228100	-13370	Sipa1l3	signal-induced proliferation-associated 1 like	22.386
chr17	88521112	88522060	-13295	Ston1	stonin 1	12.985
chr12	1.13E+08	113244140	-13153	BC022687	cDNA sequence BC022687	15.322
chr4	44255081	44255710	-13028	Mir5106	microRNA 5106	14.269
chr2	1.7E+08	169847340	-12950	Zfp217	zinc finger protein 217	17.848
chr17	87367761	87368091	-12665	Calm2	calmodulin 2	18.697
chr15	78642341	78643031	-12389	Card10	caspase recruitment domain family, member	22.551
chr7	19091462	19092360	-12246	Pvr	poliovirus receptor	12.077
chr9	1.09E+08	108641440	-12221	Ip6k2	inositol hexaphosphate kinase 2	11.973
chr4	44254061	44254740	-12033	Mir5106	microRNA 5106	12.72
chr9	44237862	44238760	-11820	Bcl9l	B cell CLL/lymphoma 9-like	20.864
chr2	27259841	27261100	-11636	Vav2	vav 2 oncogene	34.192
chr11	61094601	61095280	-11559	Aldh3a2	aldehyde dehydrogenase family 3, subfamily	14.545
chr9	1.15E+08	114704440	-11250	Cmtm8	CKLF-like MARVEL transmembrane domain	14.511
chr10	1.28E+08	128183030	-11154	Mmp19	matrix metallopeptidase 19	12.146
chr10	1.17E+08	117125160	-11109	Mdm2	transformed mouse 3T3 cell double minute 2	15.087
chr6	29257762	29258550	-10994	Fam71f1	family with sequence similarity 71, member F1	8.923
chr1	33653972	33654560	-10176	Rab23	RAB23, member RAS oncogene family	15.731
chr4	1.37E+08	136640410	-10140	Cdc42	cell division cycle 42	11.125
chr15	83301642	83302720	-9809	Pacsin2	protein kinase C and casein kinase substrate	40.125
chr3	88598561	88599580	-9791	Lmna	lamin A	22.208
chr2	30533701	30534380	-9179	Mir3089	microRNA 3089	13.138
chr11	1E+08	100353260	-8720	Acly	ATP citrate lyase	12.143
chr7	15453681	15454360	-8703	Ccdc9	coiled-coil domain containing 9	13.467
chr17	26869212	26870540	-8396	Uqcc2	ubiquinol-cytochrome c reductase complex	28.32
chr4	1.38E+08	138194501	-8123	Otud3	OTU domain containing 3	13.255
chr11	98599122	98600000	-8094	Nr1d1	nuclear receptor subfamily 1, group D,	16.281
chr15	99122921	99123600	-8046	Fam186b	family with sequence similarity 186, member	17.994
chr18	32290141	32290990	-7985	Proc	protein C	16.217
chr8	87090402	87091000	-7922	Mir23a	microRNA 23a	14.674
chr10	79562721	79563740	-7740	Cirbp	cold inducible RNA binding protein	26.383
chr7	1.27E+08	126600630	-7722	Fam57b	family with sequence similarity 57, member B	13.922
chr3	95735982	95736860	-7704	Mcl1	myeloid cell leukemia sequence 1	24.32
chr17	47305221	47305900	-7678	Mdfi	MyoD family inhibitor	21.432
chr5	1.16E+08	115753680	-7598	Sirt4	sirtuin 4	18.283
chr10	12559402	12559600	-7576	Utrn	utrophin	17.884
chr15	76903581	76904600	-7563	1700109K24Rik	RIKEN cDNA 1700109K24 gene	21.418
chr11	94744741	94745421	-7233	Col1a1	collagen, type I, alpha 1	15.471
chr10	12558712	12559391	-7126	Utrn	utrophin	17.894
chr19	5809292	5810260	-7105	Malat1	metastasis associated lung adenocarcinoma	14.41
chr2	1.66E+08	166478470	-6921	Trp53rkb	transformation related protein 53 regulating	12.573
chr7	46882941	46883620	-6844	Spty2d1	SPT2, Suppressor of Ty, domain containing 1	13.817
chr5	1.13E+08	112560400	-6746	Tfip11	tuftelin interacting protein 11	10.692
chr3	88595501	88596520	-6731	Lmna	lamin A	21.583
chr8	87091681	87092271	-6647	Mir23a	microRNA 23a	22.831
chr11	98604761	98605780	-6589	Msl1	male-specific lethal 1 homolog (Drosophila)	18.836
chr10	12558152	12558701	-6501	Utrn	utrophin	22.157
chr10	39953061	39953740	-6319	Gtf3c6	general transcription factor IIIC, polypeptide 6,	11.146
chr15	97742181	97742971	-6246	Vdr	vitamin D receptor	14.519
chr19	23201642	23202581	-6212	Klf9	Kruppel-like factor 9	12.677
chr7	1.27E+08	127270500	-6209	Fbrs	fibrosin	15.003
chr9	58012841	58013520	-6107	Mir6385	microRNA 6385	12.398
chr10	12557901	12558141	-6096	Utrn	utrophin	15.542
chr15	98453812	98454820	-6046	Cacnb3	calcium channel, voltage-dependent, beta 3	16.123
chr6	85345781	85346800	-5998	Rab11fip5	RAB11 family interacting protein 5 (class I)	26.127
chr5	1.43E+08	143089000	-5864	Tnrc18	trinucleotide repeat containing 18	17.809
chr8	87092282	87093371	-5797	Mir23a	microRNA 23a	20.174
chr17	27553261	27554541	-5770	D17Wsu92e	DNA segment, Chr 17, Wayne State	40.312
chr7	1.41E+08	140975220	-5754	Ano9	anoctamin 9	11.043

chr7	1.42E+08	142203300	-5700	Ctsd	cathepsin D	17.237
chr18	13090341	13091020	-5670	Osbpl1a	oxysterol binding protein-like 1A	15.816
chr17	26778741	26779760	-5643	Itpr3	inositol 1,4,5-triphosphate receptor 3	12.447
chr3	96183961	96184640	-5632	Otud7b	OTU domain containing 7B	17.376
chr4	1.48E+08	148016361	-5619	Pgd	phosphogluconate dehydrogenase	28.39
chr10	75270962	75271870	-5157	Gstt4	glutathione S-transferase, theta 4	11.74
chr14	54747662	54748351	-5078	Ripk3	receptor-interacting serine-threonine kinase 3	16.293
chr4	1.48E+08	148015881	-5064	Pgd	phosphogluconate dehydrogenase	17.726
chr15	97677241	97677920	-5044	Hdac7	histone deacetylase 7	16.982
chr11	83351341	83351950	-4932	Ccl5	chemokine (C-C motif) ligand 5	19.878
chr3	58256152	58256960	-4820	1700007F19Rik	RIKEN cDNA 1700007F19 gene	18.469
chr8	87875381	87876400	-4810	Hook2	hook homolog 2 (Drosophila)	14.535
chr10	1.28E+08	127588060	-4304	Rbms2	RNA binding motif, single stranded interacting	15.09
chr9	1.08E+08	107573280	-4194	Sema3f	sema domain, immunoglobulin domain (Ig),	12.142
chr11	69233521	69234540	-4160	Kdm6b	KDM1 lysine (K)-specific demethylase 6B	27.02
chr8	1.27E+08	126536390	-4114	Rhou	ras homolog gene family, member U	14.183
chr5	1.23E+08	123398831	-4104	Setd1b	SET domain containing 1B	11
chr12	1.12E+08	111861700	-4048	Exoc3l4	exocyst complex component 3-like 4	16.018
chr8	13204241	13204920	-3979	Grtp1	GH regulated TBC protein 1	17.074
chr18	39616612	39617770	-3972	Nr3c1	nuclear receptor subfamily 3, group C,	15.3
chr5	91839441	91840120	-3938	Ppbp	pro-platelet basic protein	15.009
chr2	26120122	26120840	-3915	Ccdc187	coiled-coil domain containing 187	18.561
chr7	28091572	28092160	-3878	Zfp36	zinc finger protein 36	11.861
chr19	5806181	5806860	-3849	Malat1	metastasis associated lung adenocarcinoma	14.11
chr2	30538801	30540100	-3769	Mir3089	microRNA 3089	24.526
chr15	78633501	78634520	-3713	Card10	caspase recruitment domain family, member	14.046
chr5	1.23E+08	123399600	-3589	Setd1b	SET domain containing 1B	14.831
chr3	1.46E+08	145591400	-3519	Cyr61	cysteine rich protein 61	27.987
chr7	28091481	28091520	-3512	Zfp36	zinc finger protein 36	6
chr14	6967621	6968300	-3433	Pdhb	pyruvate dehydrogenase (lipoamide) beta	11.219
chr1	1.58E+08	157578920	-3404	Qsox1	quiescin Q6 sulfhydryl oxidase 1	11.222
chr17	17530741	17532091	-3390	Mir99b	microRNA 99b	14.615
chr4	1.32E+08	131786250	-3273	Sesn2	sestrin 2	16.363
chr3	1.45E+08	145040090	-3238	Clca2	chloride channel accessory 2	20.181
chr9	1.2E+08	119920700	-3237	Cx3cr1	chemokine (C-X3-C motif) receptor 1	14.063
chr14	49818042	49818770	-3200	Klhl33	kelch-like 33	12.202
chr17	56960652	56961860	-3179	Vav1	vav 1 oncogene	19.021
chr5	1.35E+08	134840600	-3065	Clip2	CAP-GLY domain containing linker protein 2	14.727
chr10	1.27E+08	126915200	-3028	Ndufa4l2	NADH dehydrogenase (ubiquinone) 1 alpha	13.691
chr13	23708541	23709140	-2917	Hist1h4c	histone cluster 1, H4c	11.13
chrX	69292341	69293020	-2857	Pnma5	paraneoplastic antigen family 5	14.412
chr9	21605122	21605920	-2484	Dock6	dedicator of cytokinesis 6	11.303
chr10	80832282	80833291	-2484	Nfic	nuclear factor I/C	15.296
chr4	1.29E+08	128766511	-2288	C77080	expressed sequence C77080	36.65
chr15	1.02E+08	101929280	-2252	Tns2	tensin 2	25.553
chr2	84543721	84544740	-2213	Mir130a	microRNA 130a	15.518
chrX	6907441	6908360	-2148	Mir684-1	microRNA 684-1	11.357
chr2	84848701	84849720	-2089	Tnks1bp1	tankyrase 1 binding protein 1	14.781
chr10	80782981	80783990	-1986	Fzr1	fizzy/cell division cycle 20 related 1	16.01
chr17	56111561	56112580	-1882	Ptprs	protein tyrosine phosphatase, receptor type, S	17.363
chr10	79388981	79389660	-1861	Tmem259	transmembrane protein 259	18.965
chr17	17532441	17533460	-1856	Mir99b	microRNA 99b	14.959
chr10	69490221	69491240	-1748	Ccdc6	coiled-coil domain containing 6	14.763
chr7	1.28E+08	127536701	-1722	Fbxl19	F-box and leucine-rich repeat protein 19	13.93
chr13	93632941	93633620	-1717	Zfyve16	zinc finger, FYVE domain containing 16	10.595
chr18	39614421	39615440	-1711	Nr3c1	nuclear receptor subfamily 3, group C,	32.653
chr6	1.14E+08	113569180	-1709	Brk1	BRICK1, SCAR/WAVE actin-nucleating	16.109
chr11	77307642	77308180	-1696	Git1	G protein-coupled receptor kinase-interactor 1	19.372
chr9	61168381	61169060	-1652	Tle3	transducin-like enhancer of split 3, homolog of	11.573
chr7	18982541	18983220	-1603	Bcl3	B cell leukemia/lymphoma 3	18.189
chr17	62567821	62568840	-1551	Efna5	ephrin A5	34.833
chr8	73466861	73467481	-1493	Ell	elongation factor RNA polymerase II	17.177
chr19	7121981	7122660	-1492	Macrod1	MACRO domain containing 1	20.801
chr1	1.82E+08	181796640	-1464	Cdc42bpa	CDC42 binding protein kinase alpha	13.169
chr10	98691121	98691800	-1459	Dusp6	dual specificity phosphatase 6	13.442
chr7	67823881	67824771	-1444	Igf1r	insulin-like growth factor I receptor	24.079
chr11	68913241	68914260	-1401	Per1	period circadian clock 1	22.308
chr17	86074401	86075080	-1371	Prkce	protein kinase C, epsilon	18.673
chr5	1.38E+08	137971660	-1364	Nyap1	neuronal tyrosine-phosphorylated	16.389
chr9	22140461	22141450	-1347	Anln	anillin, actin binding protein	15.497
chr10	41965861	41967140	-1343	Foxo3	forkhead box O3	16.55
chr5	65715832	65716790	-1334	Ugdh	UDP-glucose dehydrogenase	18.513
chr14	54777061	54778080	-1296	Nfatc4	nuclear factor of activated T cells,	12.419
chr4	1.3E+08	129679151	-1295	Tinagl1	tubulointerstitial nephritis antigen-like 1	30.095
chr3	84899712	84900720	-1288	Fbxw7	F-box and WD-40 domain protein 7	13.086
chr1	90900021	90900700	-1273	Sh3bp4	SH3-domain binding protein 4	14.865
chr19	46553141	46554291	-1243	Trim8	tripartite motif-containing 8	19.948
chr10	75789741	75790720	-1223	Dip2a	DIP2 disco-interacting protein 2 homolog A	15.022
chr7	1.28E+08	127536720	-1207	Fbxl19	F-box and leucine-rich repeat protein 19	5
chr9	63820752	63821720	-1171	Smad6	SMAD family member 6	15.959
chr3	1.04E+08	103961120	-1147	Bcl2l15	BCLl2-like 15	15.402
chr10	80571802	80572180	-1142	Pias4	protein inhibitor of activated STAT 4	22.802
chr4	1.16E+08	115719000	-1135	Pik3r3	phosphatidylinositol 3 kinase, regulatory	16.654
chr2	91983601	91984280	-1081	Phf21a	PHD finger protein 21A	13.323
chr3	61450921	61451931	-1010	Rap2b	RAP2B, member of RAS oncogene family	19.871
chr11	79530081	79531100	2426	Mir193a	microRNA 193a	18.752
chr3	90701121	90701800	2639	S100a6	S100 calcium binding protein A6 (calcyclin)	24.58
chr2	1.52E+08	152431180	2978	Id1	inhibitor of DNA binding 1	18.858
chr10	80336322	80337240	3561	Gadd45b	growth arrest and DNA-damage-inducible 45	18.611
chr19	5571921	5572940	4356	Ap5b1	adaptor-related protein complex 5, beta 1	27.67

chr19	9149061	9150080	5431	Scgb1a1	secretoglobin, family 1A, member 1	16.27
chr15	88695121	88696140	5670	Pim3	proviral integration site 3	19.684
chr11	1.18E+08	117780080	5886	Socs3	suppressor of cytokine signaling 3	25.84
chr17	34573581	34574260	6292	Hspa1a	heat shock protein 1A	15.389
chr17	84088801	84089820	6963	Zfp36l2	zinc finger protein 36, C3H type-like 2	16.687
chr9	1.23E+08	123102051	7751	Tmem158	transmembrane protein 158	18.54
chr16	35420861	35421540	7966	1600019K03Rik	RIKEN cDNA 1600019K03 gene	12.644
chr19	5058521	5059361	8133	Rin1	Ras and Rab interactor 1	12.155
chr11	98422872	98423490	8800	Lrrc3c	leucine rich repeat containing 3C	11.641
chr6	1.46E+08	145813420	9553	Bhlhe41	basic helix-loop-helix family, member e41	18.928
chr10	80342341	80343360	9630	Gadd45b	growth arrest and DNA-damage-inducible 45	17.451
chr16	21159561	21160540	9999	Mir7680	microRNA 7680	18.044
chr19	45111201	45112051	10739	Sfxn3	sideroflexin 3	16.282
chr5	1.37E+08	137388220	12954	Trim56	tripartite motif-containing 56	26.047
chr12	98683532	98684320	14241	Gpr65	G-protein coupled receptor 65	13.61
chr6	83422061	83422740	14987	B230319C09Rik	RIKEN cDNA B230319C09 gene	15.669
chr14	19428961	19429910	15657	Myoz1	myozenin 1	19.655
chr6	1.18E+08	117845700	16560	Zfp239	zinc finger protein 239	15.304
chr15	38417961	38418640	16836	Mir6951	microRNA 6951	24.663
chr4	1.41E+08	140532780	17360	Arhgef19	Rho guanine nucleotide exchange factor	12.16
chr15	88664861	88665880	17958	Creld2	cysteine-rich with EGF-like domains 2	21.914
chr5	1.36E+08	136191030	18175	Hspb1	heat shock protein 1	13.083
chr4	1.08E+08	107845930	19351	Coa7	cytochrome c oxidase assembly factor 7	25.118
chr15	38414652	38415580	20020	Mir6951	microRNA 6951	14.774
chr13	23410021	23410700	20971	Abt1	activator of basal transcription 1	14.501
chr7	34338641	34339991	22285	Kctd15	potassium channel tetramerisation domain	24.363
chr7	37793381	37794400	22360	Ccne1	cyclin E1	29.176
chr11	52262472	52263100	22935	9530068E07Rik	RIKEN cDNA 9530068E07 gene	9.761
chr19	46577482	46578640	23102	Trim8	tripartite motif-containing 8	25.983
chr2	1.44E+08	143857400	23755	Gm5535	predicted gene 5535	11.639
chr16	21731932	21732621	23946	1300002E11Rik	RIKEN cDNA 1300002E11 gene	14.627
chr15	79880961	79881980	24364	Snord83b	small nucleolar RNA, C/D box 83B	17.216
chr5	1.35E+08	134635920	24415	Mir3965	microRNA 3965	18.8
chr16	33049701	33050380	24932	Mir1947	microRNA 1947	17.773
chr19	12077141	12077820	26305	Olfr1423	olfactory receptor 1423	18.224
chr12	56383561	56384240	26877	Nfkbia	nuclear factor of kappa light polypeptide gene	11.303
chr15	36706401	36707080	28781	Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-	13.551
chr6	1.47E+08	146644110	29347	4930479D17Rik	RIKEN cDNA 4930479D17 gene	10.745
chr10	59316061	59317080	30557	Ddit4	DNA-damage-inducible transcript 4	14.805
chr3	86056721	86057400	31358	Prss48	protease, serine 48	16.947
chr4	1.15E+08	115483720	32603	Faah	fatty acid amide hydrolase	13.13
chr15	38401301	38402320	33326	Mir6951	microRNA 6951	22.872
chr17	84020461	84021231	33860	4933433H22Rik	RIKEN cDNA 4933433H22 gene	17.532
chr11	1.04E+08	103817640	34339	Arf2	ADP-ribosylation factor 2	12.733
chr5	23187321	23188340	36661	AI506816	expressed sequence AI506816	15.689
chr11	97216201	97217021	37970	Socs7	suppressor of cytokine signaling 7	18.841
chr6	84351032	84351950	38005	Gm10445	predicted gene 10445	12.371
chr11	97217032	97217220	38485	Socs7	suppressor of cytokine signaling 7	7.048
chr17	84056841	84057800	38953	Zfp36l2	zinc finger protein 36, C3H type-like 2	19.574
chr15	44497252	44497840	39016	Sybu	syntabulin (syntaxin-interacting)	17.697
chr13	1.13E+08	112846680	39114	Mier3	mesoderm induction early response 1, family	15.028
chr11	1.22E+08	121558160	39133	Metrnl	meteorin, glial cell differentiation regulator-like	24.481
chr5	1.44E+08	143669241	39853	Grid2ip	glutamate receptor, ionotropic, delta 2 (Grid2)	27.758
chr12	16875901	16876750	39880	E2f6	E2F transcription factor 6	19.064
chr9	1.03E+08	102638180	40093	Gm5627	predicted gene 5627	16.858
chr5	1.44E+08	143669931	40543	Grid2ip	glutamate receptor, ionotropic, delta 2 (Grid2)	32.091
chr2	1.2E+08	120344310	42945	Haus2	HAUS augmin-like complex, subunit 2	12.801
chr8	25861081	25861670	43116	1810011O10Rik	RIKEN cDNA 1810011O10 gene	16.684
chr1	88301741	88302760	44750	1700019O17Rik	RIKEN cDNA 1700019O17 gene	22.154
chr12	56361461	56362140	44845	Psma6	proteasome (prosome, macropain) subunit,	14.383
chr8	28244032	28244820	45933	2310008N11Rik	RIKEN cDNA 2310008N11 gene	10.133
chr17	71155552	71156220	46375	Lpin2	lipin 2	22.359
chr1	88303441	88304620	46530	1700019O17Rik	RIKEN cDNA 1700019O17 gene	29.667
chr15	36904621	36905640	46861	Zfp706	zinc finger protein 706	18.033
chr15	38654261	38654940	48107	Atp6v1c1	ATPase, H+ transporting, lysosomal V1	21.128
chr12	87713881	87714850	59552	Irf2bpl	interferon regulatory factor 2 binding protein-	19.736
chr8	4678061	4679080	65400	Zfp958	zinc finger protein 958	22.982
chr10	67241121	67242140	66389	Zfp365	zinc finger protein 365	12.658
chr5	1.26E+08	125563360	67152	Scarb1	scavenger receptor class B, member 1	19.574
chr6	88937312	88937880	69704	Tpra1	transmembrane protein, adipocyte	11.357
chr16	95924881	95925560	78403	1600002D24Rik	RIKEN cDNA 1600002D24 gene	12.574
chr2	45599101	45600120	80996	1700019E08Rik	RIKEN cDNA 1700019E08 gene	18.641
chr2	1.66E+08	166049540	83918	Gm11468	predicted gene 11468	21.583
chr9	30270541	30271220	93984	Snx19	sorting nexin 19	10.01
chr18	5141141	5142110	95038	Svil	supervillin	14.331
chr4	1.51E+08	151428120	105774	Nphp4	nephronophthisis 4 (juvenile) homolog	9.325
chr8	1.3E+08	129712720	119631	Tomm20	translocase of outer mitochondrial membrane	11.863
chr13	84820832	84821500	125760	Tmem161b	transmembrane protein 161B	11.987
chr12	27184792	27185430	129628	Cmpk2	cytidine monophosphate (UMP-CMP) kinase	12.107
chr8	1.25E+08	124996920	132342	Mir7237	microRNA 7237	12.325
chr5	1.19E+08	118643000	136233	2410131K14Rik	RIKEN cDNA 2410131K14 gene	14.016
chr18	5989152	5990120	146460	Arhgap12	Rho GTPase activating protein 12	11.745
chr19	32970481	32971160	147246	Pten	phosphatase and tensin homolog	11.293
chr16	30691052	30691800	171956	Fam43a	family with sequence similarity 43, member A	15.643
chr17	85870061	85870720	183111	Srbd1	S1 RNA binding domain 1	12.649
chr5	50049361	50050040	297544	Adgra3	adhesion G protein-coupled receptor A3	18.009
chr1	7387202	7388540	308870	Pcmtd1	protein-L-isoaspartate (D-aspartate) O-	20.451
chr13	6192761	6193440	332365	Klf6	Kruppel-like factor 6	13.574
chr1	77743041	77743720	336903	Pax3	paired box 3	16.781
chr8	75064181	75064740	179	Tpm4	tropomyosin 4	11.401

chr8	75075222	75076080	11370	Tpm4	tropomyosin 4	11.878
chr19	47970582	47971161	1739	Itprip	inositol 1,4,5-triphosphate receptor interacting	17.193
chr10	95370562	95371360	610	Eea1	early endosome antigen 1	19.97
chr8	23650822	23651080	413	Ckap2	cytoskeleton associated protein 2	11.438
chr8	23650401	23650811	758	Ckap2	cytoskeleton associated protein 2	14.659
chr11	60990232	60991051	613	Usp22	ubiquitin specific peptidase 22	15.126
chr11	77309652	77310220	329	Git1	G protein-coupled receptor kinase-interactor 1	14.775
chr11	77313621	77314270	4338	Git1	G protein-coupled receptor kinase-interactor 1	16.529
chr10	83821561	83822321	48329	Nuak1	NUAK family, SNF1-like kinase, 1	17.434
chr7	44883401	44884760	211	Scaf1	SR-related CTD-associated factor 1	19.812
chr17	35449532	35450121	275	Mdc1	mediator of DNA damage checkpoint 1	26.178
chr7	5758581	5759051	242	Zfp787	zinc finger protein 787	15.362
chr4	59877061	59878340	209	Inip	INTS3 and NABP interacting protein	22.959
chr16	10359801	10360480	788	Tvp23a	trans-golgi network vesicle protein 23A	12.035
chr11	69227061	69228420	2130	Kdm6b	KDM1 lysine (K)-specific demethylase 6B	18.043
chr4	1.33E+08	132886960	-12206	Sfn	stratifin	13.638
chr15	78810301	78811641	660	Triobp	TRIO and F-actin binding protein	31.873
chr5	66043322	66044341	1175	N4bp2	NEDD4 binding protein 2	34.068
chr18	82656721	82657730	-31666	Mbp	myelin basic protein	15.386
chr17	45490981	45491920	-2706	Vegfa	vascular endothelial growth factor A	18.691
chr12	65836482	65837260	355	Gm527	predicted gene 527	20.392
chr8	74594301	74595320	5936	Unc13a	unc-13 homolog A (C. elegans)	19.396
chr3	88618562	88619300	609	Mex3a	mex3 homolog A (C. elegans)	12.148
chr10	58972772	58973680	38823	Mcu	mitochondrial calcium uniporter	15.672
chr15	98697241	98698560	1339	Kmt2d	lysine (K)-specific methyltransferase 2D	13.095
chr2	25185232	25186180	1929	Uap1l1	UDP-N-acteylglucosamine pyrophosphorylase	12.089
chr4	45534632	45535520	16852	Shb	src homology 2 domain-containing	13.171
chr13	43313281	43314161	1423	Gfod1	glucose-fructose oxidoreductase domain	14.545
chr13	43272902	43273500	41943	Gfod1	glucose-fructose oxidoreductase domain	12.794
chr10	5958501	5960200	917	Zbtb2	zinc finger and BTB domain containing 2	16.16
chr11	23157061	23157740	1359	Xpo1	exportin 1, CRM1 homolog (yeast)	17.009
chr17	63549532	63549740	193	Fer	fer (fms/fps related) protein kinase	17.707
chr5	1.45E+08	145219100	386	Smurf1	SMAD specific E3 ubiquitin protein ligase 1	19.872
chr5	1.45E+08	145218831	836	Smurf1	SMAD specific E3 ubiquitin protein ligase 1	25.914
chr5	1.45E+08	145218201	1386	Smurf1	SMAD specific E3 ubiquitin protein ligase 1	14.435
chr5	1.45E+08	145152460	-1643	Mir7039	microRNA 7039	21.008
chr10	80363872	80364780	31106	Gadd45b	growth arrest and DNA-damage-inducible 45	17.888
chr14	19581282	19582681	659	Camk2g	calcium/calmodulin-dependent protein kinase	19.31
chr15	78786841	78788200	12541	Triobp	TRIO and F-actin binding protein	27.031
chr5	1.23E+08	123404700	1380	Setd1b	SET domain containing 1B	14.614
chr9	59861112	59861940	77700	Thsd4	thrombospondin, type I, domain containing 4	11.984
chr7	46825832	46826840	204	Uevld	UEV and lactate/malate dehyrogenase	11.133
chr1	1.36E+08	136178500	250	Tmem183a	transmembrane protein 183A	14.951
chr13	63440261	63440890	392	Fancc	Fanconi anemia, complementation group C	16.1
chr7	99143321	99144340	1401	Map6	microtubule-associated protein 6	15.716
chr5	1E+08	100218991	884	Hnrnpd	heterogeneous nuclear ribonucleoprotein D	15.827
chr10	75680632	75681960	285			35.554
chr11	1.03E+08	102991100	3532	Fmnl1	formin-like 1	12.607
chr6	6905741	6906710	207	Sdhaf3	succinate dehydrogenase complex assembly	13.655
chr4	1.35E+08	135129260	433	Srsf10	serine/arginine-rich splicing factor 10	21.029
chr6	1.35E+08	135216640	-2554	Gsg1	germ cell-specific gene 1	16.074
chr2	1.68E+08	167697390	4827	Fam65c	family with sequence similarity 65, member C	13.958
chr11	75472181	75472860	310	Myo1c	myosin IC	17.698
chr3	1.16E+08	116415451	820	Cdc14a	CDC14 cell division cycle 14A	17.043
chr7	29830241	29831450	137	Zfp382	zinc finger protein 382	17.141
chr17	73012961	73013980	603	Lclat1	lysocardiolipin acyltransferase 1	23.294
chr3	84667821	84668500	392	Arfip1	ADP-ribosylation factor interacting protein 1	10.589
chr3	96764341	96765520	9394	Ankrd35	ankyrin repeat domain 35	18.325
chr8	37716272	37717291	1252	Lonrf1	LON peptidase N-terminal domain and ring	13.225
chr8	1.2E+08	120083140	38568	Gan	giant axonal neuropathy	13.638
chr11	74465441	74466800	430	Cluh	clustered mitochondria (cluA/CLU1) homolog	20.017
chr10	1.2E+08	120380681	2019	Lemd3	LEM domain containing 3	13.323
chr5	72926941	72927960	519	Nipal1	NIPA-like domain containing 1	16.797
chr8	10993352	10993900	-14196	9530052E02Rik	RIKEN cDNA 9530052E02 gene	11.465
chr19	46110121	46111140	780	Pprc1	peroxisome proliferative activated receptor,	30.612
chr18	10609701	10610121	439	Esco1	establishment of cohesion 1 homolog 1 (S.	19.262
chr2	84861281	84862220	10451	Tnks1bp1	tankyrase 1 binding protein 1	15.55
chr15	27968741	27969760	1187	Trio	triple functional domain (PTPRF interacting)	24.125
chr1	1.91E+08	191389060	133	Cenpf	centromere protein F	15.125
chr17	46970812	46971680	3004	Ccnd3	cyclin D3	13.907
chr17	46973822	46974740	6039	Ccnd3	cyclin D3	18.944
chr8	87689401	87690080	703	Nfix	nuclear factor I/X	13.923
chr3	94666881	94668240	560	Snx27	sorting nexin family member 27	17.478
chr18	69471562	69472200	791	Tcf4	transcription factor 4	11.406
chr11	1.2E+08	119730660	250	Chmp6	charged multivesicular body protein 6	18.985
chr12	21382261	21383270	24519	Asap2	ArfGAP with SH3 domain, ankyrin repeat and	17.644
chr11	1.02E+08	102112671	283	Atxn7l3	ataxin 7-like 3	18.234
chr7	1.26E+08	125690860	183039	Gsg1l	GSG1-like	14.648
chr2	22890841	22891860	269	Acbd5	acyl-Coenzyme A binding domain containing	15.256
chr4	32794652	32795380	48968	Bach2	BTB and CNC homology 2	15.405
chr11	49087161	49088511	222	Mgat1	mannoside acetylglucosaminyltransferase 1	20.126
chr10	1.22E+08	122316360	72764	Mirlet7i	microRNA let7i	16.433
chrX	97424621	97425300	322	Snx12	sorting nexin 12	14.52
chr9	56874181	56875880	517	Sin3a	transcriptional regulator, SIN3A (yeast)	31.168
chr9	56870781	56872140	1283	Sin3a	transcriptional regulator, SIN3A (yeast)	21.142
chr11	50168021	50169380	396	Canx	calnexin	17.697
chr14	19267801	19267871	849	Anxa7	annexin A7	5.714
chr17	47386821	47387500	663	Foxp4	forkhead box P4	17.427
chr3	88578161	88579520	399	Lmna	lamin A	35.312
chr7	27397881	27398770	225	C030039L03Rik	RIKEN cDNA C030039L03 gene	16.948

chr5	36898502	36899520	481	Tbc1d14	TBC1 domain family, member 14	20.42
chr6	1.49E+08	149146100	292	Amn1	antagonist of mitotic exit network 1	14.862
chr11	1.17E+08	117033440	17349	Sept9	septin 9	15.106
chr11	1.17E+08	117048740	32479	Sept9	septin 9	14.712
chr3	1.08E+08	107887100	1765	Csf1	colony stimulating factor 1 (macrophage)	15.115
chr15	99675212	99675760	-27303	Lima1	LIM domain and actin binding 1	17.538
chr17	65683241	65683920	682	Ppp4r1	protein phosphatase 4, regulatory subunit 1	18.944
chr18	65013292	65014790	916	Nedd4l	neural precursor cell expressed,	15.224
chr18	65045762	65046760	33136	Nedd4l	neural precursor cell expressed,	18.964
chr19	5724241	5725260	1567	Ehbp1l1	EH domain binding protein 1-like 1	29.458
chr3	1.23E+08	122611140	755	Fnbp1l	formin binding protein 1-like	11.214
chr3	1.23E+08	122610811	1270	Fnbp1l	formin binding protein 1-like	15.101
chr5	1.11E+08	110849180	5033	Galnt9	UDP-N-acetyl-alpha-D-	14.368
chr5	1.43E+08	143079480	3081	Tnrc18	trinucleotide repeat containing 18	10.897
chr1	66749481	66751180	473	Kansl1l	KAT8 regulatory NSL complex subunit 1-like	15.477
chr5	73011032	73011850	4296	Txk	TXK tyrosine kinase	13.556
chr3	10421742	10422700	441	Snx16	sorting nexin 16	13.348
chr3	41661221	41661900	131	Jade1	jade family PHD finger 1	14.38
chr8	74296121	74296800	254	Use1	unconventional SNARE in the ER 1 homolog	24.305
chr1	1.34E+08	133739340	996	Nucks1	nuclear casein kinase and cyclin-dependent	14.115
chr8	1.23E+08	123450940	24501	Gins2	GINS complex subunit 2 (Psf2 homolog)	18.942
chr8	1.23E+08	123450151	25016	Gins2	GINS complex subunit 2 (Psf2 homolog)	19.957
chr4	1.33E+08	132945100	473	Pigv	phosphatidylinositol glycan anchor	27.756
chr4	1.51E+08	151030720	477	Acot7	acyl-CoA thioesterase 7	12.756
chr15	1E+08	100239970	11704	Slc11a2	solute carrier family 11 (proton-coupled	64.82
chr17	34647701	34648380	6638	Msh5	mutS homolog 5 (E. coli)	18.789
chr11	5688201	5689140	184	Dbnl	drebrin-like	16.113
chr15	83291501	83292860	192	Pacsin2	protein kinase C and casein kinase substrate	17.291
chr2	1.52E+08	152362160	824	H13	histocompatibility 13	23.302
chr5	73571921	73572570	316	Ociad1	OCIA domain containing 1	16.416
chr5	1E+08	100281300	665	Enoph1	enolase-phosphatase 1	14.183
chr11	97514502	97515691	378	Pcgf2	polycomb group ring finger 2	17.812
chr13	78626361	78627040	-34864	A830082K12Rik	RIKEN cDNA A830082K12 gene	13.764
chr7	24080841	24081860	2327	Kcnn4	potassium intermediate/small conductance	20.528
chr15	76032122	76033191	920	Plec	plectin	22.137
chr15	76031141	76032111	1950	Plec	plectin	28.598
chr7	46971792	46972700	-21000	Mir7056	microRNA 7056	14.869
chr7	45377761	45378780	180	Nucb1	nucleobindin 1	16.91
chr7	45376401	45377080	1710	Nucb1	nucleobindin 1	11.258
chr13	56713062	56714040	261	Smad5	SMAD family member 5	14.201
chr6	1.25E+08	124931460	146	Cops7a	COP9 (constitutive photomorphogenic)	19.076
chr5	1.09E+08	108935320	590	Fgfrl1	fibroblast growth factor receptor-like 1	17.048
chr19	47015201	47015471	326	Nt5c2	5'-nucleotidase, cytosolic II	17.815
chr15	72769552	72770540	113022	Trappc9	trafficking protein particle complex 9	14.893
chr15	72887501	72888520	450	Trappc9	trafficking protein particle complex 9	30.487
chr9	1.14E+08	113556940	421	Pdcd6ip	programmed cell death 6 interacting protein	15.375
chr19	47399112	47400080	-72696	Mir6995	microRNA 6995	23.029
chr19	47368432	47369480	-42056	Mir6995	microRNA 6995	22.578
chr19	47368121	47368421	-41371	Mir6995	microRNA 6995	17.167
chr6	50040181	50040830	678	Mpp6	membrane protein, palmitoylated 6 (MAGUK	13.508
chr9	85639881	85640560	650	Tpbg	trophoblast glycoprotein	14.027
chr10	1.27E+08	126591860	1051	Arhgef25	Rho guanine nucleotide exchange factor	12.446
chr10	1.27E+08	126591571	1396	Arhgef25	Rho guanine nucleotide exchange factor	16.359
chr10	24559221	24560240	328	Med23	mediator complex subunit 23	16.5
chr6	1.18E+08	117873920	138	Hnrnpf	heterogeneous nuclear ribonucleoprotein F	21.635
chr9	1.22E+08	121610520	1279	Zfp651	zinc finger protein 651	14.744
chr7	29692541	29693520	315	Zfp568	zinc finger protein 568	20.016
chr12	83088861	83089500	316	Sipa1l1	signal-induced proliferation-associated 1 like	11.919
chr4	1.3E+08	129670900	6520	Tinagl1	tubulointerstitial nephritis antigen-like 1	10.529
chr19	53956222	53957600	248	Pdcd4	programmed cell death 4	19.666
chr7	98234841	98235520	1300	Tsku	tsukushi, small leucine rich proteoglycan	12.564
chr8	86221621	86222640	461	Elmod2	ELMO/CED-12 domain containing 2	22.176
chr6	38481541	38482540	988	Luc7l2	LUC7-like 2 (S. cerevisiae)	19.303
chr3	87258022	87258960	2183	Kirrel	kin of IRRE like (Drosophila)	17.82
chr4	12833642	12834660	167	Triqk	triple QxxK/R motif containing	16.64
chr5	1.21E+08	120776100	3837	Slc8b1	solute carrier family 8 (sodium/lithium/calcium	16.072
chr17	25000532	25000540	495	Ube2i	ubiquitin-conjugating enzyme E2I	7
chr19	8852642	8853600	240	Taf6l	TAF6-like RNA polymerase II, p300/CBP-	18.028
chr19	45101001	45101980	603	Sfxn3	sideroflexin 3	19.946
chr17	34667421	34668380	809	Ddah2	dimethylarginine dimethylaminohydrolase 2	20.478
chr3	1.42E+08	142270620	58956	Pdlim5	PDZ and LIM domain 5	18.651
chr9	34719132	34720090	-146788	4930581F22Rik	RIKEN cDNA 4930581F22 gene	23.718
chr7	25489932	25491160	6947	Axl	AXL receptor tyrosine kinase	13.673
chr7	25489461	25489921	7802	Axl	AXL receptor tyrosine kinase	18.609
chr2	1.53E+08	153324360	286	Commd7	COMM domain containing 7	22.68
chr17	34772232	34773231	202	Prrc2a	proline-rich coiled-coil 2A	31.876
chr2	26137501	26138720	568	Gpsm1	G-protein signalling modulator 1 (AGS3-like,	15.82
chr11	93812801	93813820	1129	Spag9	sperm associated antigen 9	24.942
chr2	29889061	29890080	1087	Set	SET nuclear oncogene	24.805
chr7	4665232	4666160	466	U2af2	U2 small nuclear ribonucleoprotein auxiliary	11.593
chr15	85894881	85895900	8897	Gramd4	GRAM domain containing 4	21.751
chr2	35078152	35078820	118	Gsn	gelsolin	18.666
chr10	1.21E+08	121256920	113583	BC048403	cDNA sequence BC048403	13.807
chr7	29617061	29618050	278	Zfp383	zinc finger protein 383	19.842
chr11	61395162	61396180	211	Epn2	epsin 2	19.507
chr11	33061892	33062991	765	Npm1	nucleophosmin 1	28.877
chr17	45745981	45746660	287	Tjap1	tight junction associated protein 1	15.295
chr3	90165762	90166300	583	Tpm3	tropomyosin 3, gamma	18.035
chr15	36736661	36737680	-1649	Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-	31.954
chr9	59457501	59458370	3561	Pkm	pyruvate kinase, muscle	15.222

chr4	11485881	11486900	323	Rad54b	RAD54 homolog B (S. cerevisiae)	15.424
chr5	1.11E+08	111120840	395	Ttc28	tetratricopeptide repeat domain 28	20.932
chr5	1.11E+08	111480140	-91319			11.068
chr6	1.21E+08	120983900	63856	Mical3	microtubule associated monooxygenase,	14.451
chr19	7549361	7550380	465	Rtn3	reticulon 3	20.484
chr16	10698101	10699800	164	Socs1	suppressor of cytokine signaling 1	24.769
chr11	1.18E+08	117639660	-2689	Afmid	arylformamidase	16.158
chr16	18270292	18271240	9021	Arvcf	armadillo repeat gene deleted in velo-cardio-	11.699
chr3	9995292	9996680	869	Fabp5	fatty acid binding protein 5, epidermal	20.468
chr19	4120572	4121140	719	Aip	aryl-hydrocarbon receptor-interacting protein	11.678
chr1	34072421	34073100	10855	Mir6896	microRNA 6896	13.296
chr6	17231552	17231880	531	Cav2	caveolin 2	16.155
chr10	92717321	92718340	23128	Elk3	ELK3, member of ETS oncogene family	20.509
chr4	1.16E+08	116125300	639	Nasp	nuclear autoantigenic sperm protein (histone-	27.138
chr7	45084402	45084680	746	Tead2	TEA domain family member 2	12.586
chr4	1.18E+08	117514241	-86206	Artn	artemin	17.152
chr4	1.29E+08	128759700	4307	C77080	expressed sequence C77080	15.112
chr7	15545582	15546500	377	Sae1	SUMO1 activating enzyme subunit 1	13.955
chr16	21337041	21337720	279	Vps8	vacuolar protein sorting 8 homolog (S.	14.701
chr4	81871321	81872340	105180	Nfib	nuclear factor I/B	32.172
chr15	8998441	8999481	819	Nadk2	NAD kinase 2, mitochondrial	37.981
chr15	8999492	9000140	1674	Nadk2	NAD kinase 2, mitochondrial	16.546
chr8	1.1E+08	110183460	762	Nfat5	nuclear factor of activated T cells 5	14.076
chr8	1.26E+08	126261040	730	Tcf25	transcription factor 25 (basic helix-loop-helix)	20.033
chr5	74566761	74567670	90192	Rasl11b	RAS-like, family 11, member B	19.333
chr19	9056642	9057841	912	Ahnak	AHNAK nucleoprotein (desmoyokin)	15.23
chr19	9127982	9128980	26520	Scgb1a1	secretoglobin, family 1A, member 1	19.624
chr17	23868681	23869360	196	Pdpk1	3-phosphoinositide dependent protein kinase	18.859
chr3	65440282	65441160	-3363	A730090N16Rik	RIKEN cDNA A730090N16 gene	20.795
chr2	28463441	28464120	538	Tsc1	tuberous sclerosis 1	12.426
chr6	42281381	42282060	2285	Zyx	zyxin	20.518
chr3	30793122	30794390	831	Mynn	myoneurin	17.892
chr6	34726921	34727600	16676	Agbl3	ATP/GTP binding protein-like 3	13.708
chr5	77603981	77605190	499	Exoc1	exocyst complex component 1	16.442
chr5	89639981	89641000	889	Rufy3	RUN and FYVE domain containing 3	18.628
chr11	59861952	59862780	318	Pemt	phosphatidylethanolamine N-	13.146
chr10	1.27E+08	126694880	288	Ddit3	DNA-damage inducible transcript 3	39.899
chr7	43333341	43334020	2527	Vsig10l	V-set and immunoglobulin domain containing	15.047
chr2	33025002	33025900	-12519	Angptl2	angiopoietin-like 2	11.428
chr4	1.19E+08	119038760	793	Foxj3	forkhead box J3	28.985
chr11	53410601	53411500	258	Kif3a	kinesin family member 3A	17.604
chr19	57204342	57205320	-32557	Ablim1	actin-binding LIM protein 1	13.819
chr1	51859521	51860101	712	Myo1b	myosin IB	12.293
chr1	53296762	53297380	226	Asnsd1	asparagine synthetase domain containing 1	10.673
chr4	1.49E+08	148832960	14375	H6pd	hexose-6-phosphate dehydrogenase (glucose	13.463
chr2	1.51E+08	151186590	552	Nsfl1c	NSFL1 (p97) cofactor (p47)	19.152
chr18	43562501	43563520	607	Dpysl3	dihydropyrimidinase-like 3	21.472
chr11	32121841	32121951	397	Rhbdf1	rhomboid family 1 (Drosophila)	8.909
chr11	32120982	32121500	1052	Rhbdf1	rhomboid family 1 (Drosophila)	13.467
chr11	5762592	5763340	1097	Aebp1	AE binding protein 1	20.451
chr12	21619082	21620260	451	Adam17	a disintegrin and metallopeptidase domain 17	23.705
chr3	1.37E+08	136642600	34807	Ppp3ca	protein phosphatase 3, catalytic subunit,	18.515
chr14	46571501	46572180	652	Ktn1	kinectin 1	14.571
chr10	80229922	80230820	546	Oaz1-ps	ornithine decarboxylase antizyme 1,	24.224
chr3	95772221	95773071	676	Adamtsl4	ADAMTS-like 4	16.506
chr19	38023962	38024920	84280	Myof	myoferlin	21.022
chr19	38080341	38081360	27871	Myof	myoferlin	20.203
chr11	60542441	60543181	647	Flii	flightless I homolog (Drosophila)	19.068
chr6	8295352	8296170	86473			21.226
chr1	1.35E+08	134855900	2492			12.515
chr7	24987961	24988980	-2469	Cic	capicua homolog (Drosophila)	12.815
chr1	36500732	36501591	942			10.533
chr1	36501602	36501720	442			9.661
chr4	57866641	57867320	-72322	Akap2	A kinase (PRKA) anchor protein 2	15.208
chr4	1.14E+08	114498740	350			13.842
chr9	57442782	57443000	899	Csk	c-src tyrosine kinase	16.087
chr9	57442292	57442771	1259	Csk	c-src tyrosine kinase	13.724
chr11	94891621	94892241	873	Itga3	integrin alpha 3	14.823
chr19	4214981	4216000	1101			17.202
chr14	32275521	32276141	419			19.339
chr8	74335561	74336440	999	Ankle1	ankyrin repeat and LEM domain containing 1	25.697
chr3	88228892	88228980	637			9.455
chr3	88231701	88232680	3891			18.772
chr5	94202781	94203760	34650			16.111
chr9	49549222	49550580	1398	Ncam1	neural cell adhesion molecule 1	21.217
chr9	49548881	49549211	2253	Ncam1	neural cell adhesion molecule 1	23.515
chr6	29384161	29384831	1138			15.567
chr9	96286981	96288000	537	Rnf7	ring finger protein 7	19.184
chr2	1.31E+08	130851231	595	1700037H04Rik	RIKEN cDNA 1700037H04 gene	24.125
chr1	1.83E+08	182853700	813	Ephx1	epoxide hydrolase 1, microsomal	16.273
chr11	1.09E+08	109468100	579			13.789
chr3	1.22E+08	122080740	43748	Abca4	ATP-binding cassette, sub-family A (ABC1),	19.176
chr3	1.22E+08	122115050	78243	Abca4	ATP-binding cassette, sub-family A (ABC1),	19.419
chr5	1.43E+08	143171280	954	Actb	actin, beta	32.987
chr15	1.01E+08	101020120	-2123	Mir6962	microRNA 6962	19.579
chr11	62067001	62067680	2161	Adora2b	adenosine A2b receptor	17.853
chr8	75168901	75169580	119	Ap1m1	adaptor-related protein complex AP-1, mu	15.252
chr7	84256802	84257730	28957	Arnt2	aryl hydrocarbon receptor nuclear translocator	11.617
chr8	1.12E+08	111613110	8808	Zfhx3	zinc finger homeobox 3	22.798
chr5	1.49E+08	148709291	1347	Slc7a1	solute carrier family 7 (cationic amino acid	13.9

chr17	35307641	35308421	612	Ddr1	discoidin domain receptor family, member 1	18.474
chr9	69252561	69253901	384	Anxa2	annexin A2	22.821
chr9	69256981	69258061	1413	Mir3109	microRNA 3109	58.602
chr9	69253912	69254940	1579	Anxa2	annexin A2	11.932
chr9	69258072	69258340	2098	Mir3109	microRNA 3109	16.843
chr17	87353481	87354160	1441	Calm2	calmodulin 2	21.514
chr11	96605221	96605811	290	Cbx1	chromobox 1	24.932
chr5	94342181	94343880	253	Ccng2	cyclin G2	16.974
chr19	5490321	5491340	375	Cfl1	cofilin 1, non-muscle	17.169
chr9	36475881	36476560	109	Chek1	checkpoint kinase 1	13.105
chr10	79570881	79572240	590	Cirbp	cold inducible RNA binding protein	28.65
chr10	79391701	79392720	481	Cnn2	calponin 2	21.154
chr11	94752901	94753971	1122	Col1a1	collagen, type I, alpha 1	21.047
chr5	1.3E+08	130314720	271	Crcp	calcitonin gene-related peptide-receptor	20.268
chr7	1.44E+08	144280020	815	Cttn	cortactin	16.221
chr1	1.55E+08	155250120	268	Dhx9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	11.735
chr11	69837361	69838040	2900	Dlg4	discs, large homolog 4 (Drosophila)	14.89
chr11	69842612	69843780	8396	Dlg4	discs, large homolog 4 (Drosophila)	14.652
chr11	69845181	69846190	10885	Dlg4	discs, large homolog 4 (Drosophila)	12.674
chr9	44077452	44078960	366	Dpagt1	dolichyl-phosphate (UDP-N-	23.166
chr8	1.26E+08	126083830	10991	Dpep1	dipeptidase 1 (renal)	12.538
chr6	1.25E+08	124722200	545	Atn1	atrophin 1	14.798
chr2	1.53E+08	153433500	262	Mapre1	microtubule-associated protein, RP/EB family,	14.368
chr1	1.34E+08	133836170	575	Elk4	ELK4, member of ETS oncogene family	18.749
chr5	1.08E+08	108110140	5779	Evi5	ecotropic viral integration site 5	13.784
chr11	1.01E+08	101042900	322	Ezh1	enhancer of zeste 1 polycomb repressive	23.931
chr15	73248581	73249600	1357	Ptk2	PTK2 protein tyrosine kinase 2	20.433
chr5	1.43E+08	143227720	1545	Fscn1	fascin homolog 1, actin bundling protein	20.396
chr5	1.43E+08	143228071	2571	Fscn1	fascin homolog 1, actin bundling protein	6
chr5	1.43E+08	143229131	3111	Fscn1	fascin homolog 1, actin bundling protein	49.28
chr5	1.43E+08	143230060	4106	Fscn1	fascin homolog 1, actin bundling protein	34.841
chr7	27878641	27879540	582	Fbl	fibrillarin	17.65
chr6	34284241	34284730	163	Akr1b8	aldo-keto reductase family 1, member B8	14.8
chr9	32268041	32268720	22637	Fli1	Friend leukemia integration 1	13.591
chr14	33140792	33141160	1157	Glud1	glutamate dehydrogenase 1	14.125
chr4	1.17E+08	117333661	471	Slc6a9	solute carrier family 6 (neurotransmitter	
chr4	1.17E+08	117335020	1156	Slc6a9	solute carrier family 6 (neurotransmitter	50.803
chr4	1.17E+08	117364750	6067	Ccdc24	coiled-coil domain containing 24	17.82
chr9	1.07E+08	107492360	1763	Gnai2	guanine nucleotide binding protein (G	25.688
chr11	59007681	59007861	376	Guk1	guanylate kinase 1	11.833
chr3	87996421	87997100	4512	Hdgf	hepatoma-derived growth factor	23.688
chr11	54709741	54710760	389	Hint1	histidine triad nucleotide binding protein 1	14.794
chr11	53142681	53144040	542	Hspa4	heat shock protein 4	15.719
chr4	1.37E+08	136746640	5317	Hspg2	perlecan (heparan sulfate proteoglycan 2)	11.902
chr16	91435521	91436731	173	Ifngr2	interferon gamma receptor 2	11.983
chr16	91436742	91437560	1198	Ifngr2	interferon gamma receptor 2	17.677
chr18	13115841	13116520	759	Impact	impact, RWD domain protein	15.442
chr18	13117472	13117880	2255	Impact	impact, RWD domain protein	19.142
chr11	97003021	97003700	622	Kpnb1	karyopherin (importin) beta 1	19.116
chr2	1.53E+08	153002040	18843	Kif3b	kinesin family member 3B	14.651
chr16	35903062	35904260	551	Kpna1	karyopherin (importin) alpha 1	12.157
chr5	1.41E+08	140864380	4225	Lfng	LFNG O-fucosylpeptide 3-beta-N-	21.436
chr15	78753861	78756220	1060	Lgals1	lectin, galactose binding, soluble 1	24.955
chr10	1.27E+08	127023741	736	Lrp1	low density lipoprotein receptor-related	21.974
chr10	36826172	36827440	1536	Marcks	myristoylated alanine rich protein kinase C	18.013
chr18	73827662	73828280	1139	Smad4	SMAD family member 4	10.736
chr2	1.28E+08	128430990	40177	Mertk	c-mer proto-oncogene tyrosine kinase	14.096
chr3	1.05E+08	104946091	435	Mov10	Moloney leukemia virus 10	13.939
chr9	99197722	99198740	-30349	Esyt3	extended synaptotagmin-like protein 3	16.347
chr9	1.1E+08	109778860	1461	Map4	microtubule-associated protein 4	18.497
chr13	1.01E+08	100616540	393	Map1b	microtubule-associated protein 1B	12.897
chr13	1.01E+08	100616181	1078	Map1b	microtubule-associated protein 1B	13.42
chr6	83282092	83283440	496	Mthfd2	methylenetetrahydrofolate dehydrogenase	34.164
chr12	8948142	8948800	1156	Laptm4a	lysosomal-associated protein transmembrane	16.388
chr10	80334181	80334860	1300	Gadd45b	growth arrest and DNA-damage-inducible 45	14.717
chr15	66798441	66798991	594	Ndrg1	N-myc downstream regulated gene 1	37.182
chr10	80812312	80812900	6820	Mir1191b	microRNA 1191b	13.713
chr7	1.42E+08	141893761	11183	Dusp8	dual specificity phosphatase 8	14.389
chr11	76214061	76214911	850	Nxn	nucleoredoxin	15.588
chr7	25005641	25007000	395	Pafah1b3	platelet-activating factor acetylhydrolase,	30.617
chr5	1.38E+08	137840811	406	Pcolce	procollagen C-endopeptidase enhancer	10
chr10	79726261	79727280	-3093	2310011J03Rik	RIKEN cDNA 2310011J03 gene	22.175
chr5	1.39E+08	139248271	789	Pdgfa	platelet derived growth factor, alpha	15.935
chr7	34620841	34621860	183	Pepd	peptidase D	16.387
chr10	77411881	77413240	365	Pfkl	phosphofructokinase, liver, B-type	25.233
chr3	31186841	31187520	531	Prkci	protein kinase C, iota	11.642
chr6	89327652	89328200	328	Plxna1	plexin A1	14.641
chr6	89326532	89327641	1168	Plxna1	plexin A1	29.024
chr1	1.96E+08	196377200	56248	Plxna2	plexin A2	14.965
chr19	5962241	5962920	1626	Pola2	polymerase (DNA directed), alpha 2	13.903
chr19	5945662	5945920	18415	Pola2	polymerase (DNA directed), alpha 2	15.942
chr19	5944901	5945651	18930	Pola2	polymerase (DNA directed), alpha 2	24.853
chr13	1.14E+08	113923080	595	Plpp1	phospholipid phosphatase 1	20.481
chr11	60749652	60750180	1664	Map2k3	mitogen-activated protein kinase kinase 3	15.013
chr11	97096181	97096391	380	Npepps	aminopeptidase puromycin sensitive	18.476
chr1	88359541	88360440	2083	Ptma	prothymosin alpha	12.84
chr17	33366241	33367260	616	Rab11b	RAB11B, member RAS oncogene family	27.64
chr11	53549661	53550680	572	Rad50	RAD50 homolog (S. cerevisiae)	17.259
chr12	80352201	80353100	136459	Rad51b	RAD51 homolog B	18.15
chr11	98753992	98754990	683	Rara	retinoic acid receptor, alpha	33.198

chr2	1.05E+08	105199781	692	Rcn1	reticulocalbin 1	11.967
chr17	65783541	65784900	246	Ralbp1	ralA binding protein 1	28.009
chr6	70720872	70721700	468	Rpia	ribose 5-phosphate isomerase A	16.671
chr6	70720132	70720861	1258	Rpia	ribose 5-phosphate isomerase A	15.85
chr7	81216481	81217810	1602	Rps17	ribosomal protein S17	18.798
chr2	13188601	13189280	328	Rsu1	Ras suppressor protein 1	12.202
chr10	60541132	60542611	1151	Sgpl1	sphingosine phosphate lyase 1	26.399
chr1	1.09E+08	108624330	326	Vps4b	vacuolar protein sorting 4b (yeast)	13.803
chr7	15941581	15942940	2392	Slc1a5	solute carrier family 1 (neutral amino acid	23.489
chr11	32433621	32433631	360	Stk10	serine/threonine kinase 10	4
chr11	32433642	32434300	705	Stk10	serine/threonine kinase 10	17.953
chr13	34084932	34085680	167	Tubb2a	tubulin, beta 2A class IIA	18.501
chr13	34084321	34084921	852	Tubb2a	tubulin, beta 2A class IIA	12.433
chr11	68904892	68905080	263	Vamp2	vesicle-associated membrane protein 2	10.84
chr4	43020302	43021420	746	Vcp	valosin containing protein	23.773
chr15	97735721	97736400	270	Vdr	vitamin D receptor	18.635
chr11	75549701	75550370	953	Ywhae	tyrosine 3-monooxygenase/tryptophan 5-	11.531
chr11	49046701	49047380	117	Zfp62	zinc finger protein 62	18.309
chr5	21295622	21296491	933	Dnajc2	DnaJ (Hsp40) homolog, subfamily C, member	16.19
chr12	1.13E+08	113121400	1194	Akt1	thymoma viral proto-oncogene 1	24.997
chr3	1.46E+08	145862720	708	Bcl10	B cell leukemia/lymphoma 10	23.162
chr15	83391882	83392721	962	Tspo	translocator protein	22.049
chr1	1.62E+08	162049780	398	Cacybp	calcyclin binding protein	20.805
chr1	1.41E+08	141272380	686	Aspm	asp (abnormal spindle)-like, microcephaly	13.838
chr7	29902321	29903421	937	Capns1	calpain, small subunit 1	18.491
chr18	35244741	35245561	265	Ctnna1	catenin (cadherin associated protein), alpha 1	13.134
chr18	35245572	35245760	780	Ctnna1	catenin (cadherin associated protein), alpha 1	12.059
chr11	22890632	22891520	483	Cct4	chaperonin containing Tcp1, subunit 4 (delta)	32.979
chr7	1.41E+08	141319640	278	Cd151	CD151 antigen	16.983
chr8	1.1E+08	109515360	22604	Cdh1	cadherin 1	12.396
chr2	1.81E+08	180530620	2626	Col9a3	collagen, type IX, alpha 3	13.386
chr11	95821132	95821520	708	Igf2bp1	insulin-like growth factor 2 mRNA binding	10.237
chr11	95820501	95821121	1223	Igf2bp1	insulin-like growth factor 2 mRNA binding	13.823
chr8	1.15E+08	114618651	613	Bcar1	breast cancer anti-estrogen resistance 1	30.33
chr14	65820941	65821620	1430	Dpysl2	dihydropyrimidinase-like 2	15.334
chr16	17804242	17805460	440	Dgcr2	DiGeorge syndrome critical region gene 2	11.076
chr13	93456821	93457500	-1404	Msh3	mutS homolog 3 (E. coli)	14.311
chr2	13461662	13462640	366	Trdmt1	tRNA aspartic acid methyltransferase 1	13.648
chr19	6278101	6278131	1220	Ehd1	EH-domain containing 1	7.333
chr19	6278142	6278780	1565	Ehd1	EH-domain containing 1	15.013
chr6	1.35E+08	135330540	1406	Emp1	epithelial membrane protein 1	15.363
chr4	1.41E+08	140583880	10243	Epha2	Eph receptor A2	15.001
chr4	1.36E+08	136081260	27168	Ephb2	Eph receptor B2	13.426
chr4	1.36E+08	136008800	99608	Ephb2	Eph receptor B2	12.577
chr7	1.44E+08	144391880	456	Fadd	Fas (TNFRSF6)-associated via death domain	31.553
chr7	80259472	80260400	1523	Fes	feline sarcoma oncogene	16.962
chr17	28212861	28213540	538	Fkbp5	FK506 binding protein 5	23.585
chr19	10050061	10050411	545	Fth1	ferritin heavy polypeptide 1	15.2
chr5	1.41E+08	141082681	564	Gna12	guanine nucleotide binding protein, alpha 12	17.536
chr3	1.08E+08	108274360	358	Gnai3	guanine nucleotide binding protein (G	21.234
chr5	1.38E+08	137763240	117	Gnb2	guanine nucleotide binding protein (G	13.062
chr5	1.38E+08	137761540	1817	Gnb2	guanine nucleotide binding protein (G	26.128
chr11	1.02E+08	102026520	20194	Mir8101	microRNA 8101	19.55
chr3	89998341	89998931	487			14.034
chr7	1.02E+08	101711951	169	Inppl1	inositol polyphosphate phosphatase-like 1	17.653
chr14	53529292	53530531	1955	Ajuba	ajuba LIM protein	18.738
chr19	23208932	23210501	1393	Klf9	Kruppel-like factor 9	22.793
chr19	23210512	23210991	2428	Klf9	Kruppel-like factor 9	15.681
chr4	1.19E+08	119431370	118422	Hivep3	human immunodeficiency virus type I	19.493
chr11	97615862	97617060	699	Lasp1	LIM and SH3 protein 1	20.553
chr4	1.29E+08	129059240	1215	Mir8119	microRNA 8119	19.873
chr9	58097222	58098410	13533	Loxl1	lysyl oxidase-like 1	19.251
chr10	80546001	80547260	7230	Zbtb7a	zinc finger and BTB domain containing 7a	21.133
chr17	34793752	34794630	2301	Lst1	leukocyte specific transcript 1	23.615
chr18	76367442	76368080	695	Smad2	SMAD family member 2	14.842
chr11	1.2E+08	120449080	897	Mafg	v-maf musculoaponeurotic fibrosarcoma	15.141
chr10	1.17E+08	117113680	411	Mdm2	transformed mouse 3T3 cell double minute 2	14.58
chr11	74647432	74648700	947	Mnt	max binding protein	23.986
chr11	74654492	74655160	7707	Mnt	max binding protein	18.228
chr9	1E+08	100355760	109	Nck1	non-catalytic region of tyrosine kinase adaptor	13.029
chr1	1.94E+08	193523130	587	Nek2	NIMA (never in mitosis gene a)-related	20.652
chr12	56409741	56410451	681	Nfkbia	nuclear factor of kappa light polypeptide gene	21.155
chr9	1.22E+08	121568570	246	Nktr	natural killer tumor recognition sequence	14.474
chr3	98099152	98099520	393	Notch2	notch 2	13.562
chr1	93288521	93289321	813	Per2	period circadian clock 2	15.238
chr11	70469761	70470780	575	Pfn1	profilin 1	22.182
chr5	8804332	8804980	503	Abcb1b	ATP-binding cassette, sub-family B	16.755
chr14	29454881	29454931	311	Prkcd	protein kinase C, delta	4.4
chr7	24171281	24171960	360	Plaur	plasminogen activator, urokinase receptor	12.445
chr15	1.02E+08	102084660	1406	Rarg	retinoic acid receptor, gamma	21.345
chr15	1.02E+08	102074091	938	Rarg	retinoic acid receptor, gamma	14.051
chr2	1.57E+08	156896060	255	Rbl1	retinoblastoma-like 1 (p107)	16.486
chr15	11939781	11940800	442	Sub1	SUB1 homolog (S. cerevisiae)	23.789
chr4	1.29E+08	129244091	801	Khdrbs1	KH domain containing, RNA binding, signal	19.614
chr11	1.17E+08	116668620	1244	Srsf2	serine/arginine-rich splicing factor 2	15.067
chr7	18253921	18254600	1194	Six5	sine oculis-related homeobox 5	19.691
chr4	1.54E+08	154017810	48960	Ski	ski sarcoma viral oncogene homolog (avian)	28.375
chr4	1.19E+08	118607300	444	Slc2a1	solute carrier family 2 (facilitated glucose	22.212
chr8	1.25E+08	124785100	9186	Slc7a5	solute carrier family 7 (cationic amino acid	21.149
chr10	75364262	75365760	319	Smarcb1	SWI/SNF related, matrix associated, actin	40.386

chr5	1.25E+08	125430420	38283	Ncor2	nuclear receptor co-repressor 2	15.552
chr11	1.13E+08	112599840	1030	Sox9	SRY (sex determining region Y)-box 9	16.166
chr15	81874202	81874751	377	Nhp2l1	NHP2 non-histone chromosome protein 2-like	15.678
chr3	1.09E+08	108968640	428	Stxbp3	syntaxin binding protein 3	22.744
chr11	1E+08	100136771	360	Eif1	eukaryotic translation initiation factor 1	16.354
chr7	1.41E+08	141246800	2850	Taldo1	transaldolase 1	17.164
chr6	1.28E+08	128266360	752	Tead4	TEA domain family member 4	20.55
chr7	11924872	11925760	985	Trim28	tripartite motif-containing 28	12.304
chr11	1.18E+08	118143880	15254	BC100451	cDNA sequence BC100451	24.433
chr10	85732392	85733040	2505	Timp3	tissue inhibitor of metalloproteinase 3	15.068
chr4	43581292	43581880	2097	Tln1	talin 1	16.871
chr15	98780612	98781560	449	Tuba1a	tubulin, alpha 1A	21.345
chr15	98779861	98780601	1304	Tuba1a	tubulin, alpha 1A	14.581
chr17	35444321	35445680	1354	Tubb5	tubulin, beta 5 class I	20.854
chr5	1.47E+08	147105181	684	Usp12	ubiquitin specific peptidase 12	16.429
chr17	34609852	34609960	943	Vars	valyl-tRNA synthetase	12.889
chr5	38849492	38849760	218	Wdr1	WD repeat domain 1	8.989
chr5	38848741	38849481	733	Wdr1	WD repeat domain 1	17.635
chr4	1.19E+08	118792291	679	Ybx1	Y box protein 1	35.562
chr8	1.15E+08	114531040	584	Zfp1	zinc finger protein 1	22.571
chr8	1.15E+08	114741160	333	Cfdp1	craniofacial development protein 1	19.443
chr17	8694481	8695160	54901	Pde10a	phosphodiesterase 10A	20.831
chr3	57823461	57824820	149			39.192
chr5	34842432	34843200	175	Sh3bp2	SH3-domain binding protein 2	12.954
chr8	74507642	74508560	10185	Slc27a1	solute carrier family 27 (fatty acid transporter),	10.786
chr2	34931261	34932170	214	Cntrl	centriolin	12.856
chr11	1.01E+08	101281531	1243	Vat1	vesicle amine transport protein 1 homolog (T	37.639
chr19	3323841	3324520	879	Cpt1a	carnitine palmitoyltransferase 1a, liver	11.402
chr19	3324861	3326100	2179	Cpt1a	carnitine palmitoyltransferase 1a, liver	20.495
chr6	87008041	87009640	360	Gfpt1	glutamine fructose-6-phosphate transaminase	16.752
chr17	24277772	24278720	696	Pkd1	polycystic kidney disease 1 homolog	17.523
chr8	1.09E+08	108826520	1341	Psmb10	proteasome (prosome, macropain) subunit,	21.906
chr15	1.02E+08	102234940	250	Sp1	trans-acting transcription factor 1	16.647
chr15	38243201	38244560	1420	Klf10	Kruppel-like factor 10	18.414
chr11	1.2E+08	120309000	414	Slc25a10	solute carrier family 25 (mitochondrial carrier,	16.926
chr16	20327581	20328260	12017	Abcc5	ATP-binding cassette, sub-family C	13.792
chr17	69062161	69063100	918	Epb41l3	erythrocyte membrane protein band 4.1 like 3	14.717
chr6	82738702	82739851	836	Hk2	hexokinase 2	17.758
chr2	1.37E+08	136806480	1660	Jag1	jagged 1	15.388
chr2	1.37E+08	136806111	2170	Jag1	jagged 1	21.72
chr3	1.22E+08	122490100	43943	Mir7657	microRNA 7657	25.227
chr4	1.09E+08	108959120	15827	Rnf11	ring finger protein 11	22.338
chr7	81807061	81807721	581	Hdgfrp3	hepatoma-derived growth factor, related	12.652
chr11	1.19E+08	118856520	823	Cbx8	chromobox 8	17.467
chr17	65510861	65511540	1898	Vapa	vesicle-associated membrane protein,	9.725
chr6	6166581	6167380	193	Slc25a13	solute carrier family 25 (mitochondrial carrier,	15.513
chr11	87884742	87885860	827	Vezf1	vascular endothelial zinc finger 1	18.708
chr7	80659992	80660920	16388	Iqgap1	IQ motif containing GTPase activating protein	18.714
chr14	1.01E+08	100541400	564	Uchl3	ubiquitin carboxyl-terminal esterase L3	16.849
chr2	1.04E+08	103597480	1027	Caprin1	cell cycle associated protein 1	21.673
chr5	1.26E+08	125593960	36453	Scarb1	scavenger receptor class B, member 1	9.541
chr16	32564861	32565540	810	Tnk2	tyrosine kinase, non-receptor, 2	21.592
chr17	28349541	28350220	163	Srpk1	serine/arginine-rich protein specific kinase 1	18.859
chr15	85163881	85165240	413	Atxn10	ataxin 10	16.367
chr1	1.54E+08	154299480	88189	Rgl1	ral guanine nucleotide dissociation	19.465
chr3	1.52E+08	152060920	42835	Gipc2	GIPC PDZ domain containing family, member	27.631
chr5	1.14E+08	114032600	388	Sart3	squamous cell carcinoma antigen recognized	16.122
chr9	75345352	75345360	210	Tmod3	tropomodulin 3	8
chr9	75344681	75345341	555	Tmod3	tropomodulin 3	17.712
chr3	98423881	98424900	984	Phgdh	3-phosphoglycerate dehydrogenase	21.833
chr7	45573712	45574280	707	Dbp	D site albumin promoter binding protein	19.31
chr7	45575242	45575300	1982	Dbp	D site albumin promoter binding protein	7.155
chr13	52990701	52991380	2431	Nfil3	nuclear factor, interleukin 3, regulated	13.567
chr9	1.18E+08	118356350	839	Golga4	golgi autoantigen, golgin subfamily a, 4	15.293
chr1	1.33E+08	133012380	15815			17.019
chr9	1.1E+08	109690800	260	Nme6	NME/NM23 nucleoside diphosphate kinase 6	17.311
chr3	96782082	96783380	250	Pias3	protein inhibitor of activated STAT 3	21.625
chr7	27195581	27196260	207	Sertad1	SERTA domain containing 1	19.019
chr7	27216702	27217570	9052	Prx	periaxin	21.145
chr7	1.31E+08	130756860	29169	Htra1	HtrA serine peptidase 1	12.86
chr5	64577221	64577900	68068	Tbc1d1	TBC1 domain family, member 1	14.44
chr4	1.34E+08	133741720	644	Stmn1	stathmin 1	24.38
chr9	56793261	56794620	835	Ptpn9	protein tyrosine phosphatase, non-receptor	26.791
chrX	44696502	44697420	10798	Elf4	E74-like factor 4 (ets domain transcription	17.781
chr6	72810661	72811680	18318	Kcmf1	potassium channel modulatory factor 1	16.824
chr19	6140602	6141420	126	Arl2	ADP-ribosylation factor-like 2	23.203
chr9	65922012	65922940	416	Snx1	sorting nexin 1	21.997
chr10	41964161	41965481	336	Foxo3	forkhead box O3	14.424
chrX	6827201	6828220	639	Plp2	proteolipid protein 2	13.165
chr9	1.03E+08	102582960	4290	Amotl2	angiomotin-like 2	19.586
chr9	1.03E+08	102584800	6230	Amotl2	angiomotin-like 2	20.016
chr4	1.48E+08	147943761	141	Pex14	peroxisomal biogenesis factor 14	13.741
chr19	4810372	4811680	608	Gm21992	predicted gene 21992	16.743
chr3	1.38E+08	137856400	118	Lamtor3	late endosomal/lysosomal adaptor, MAPK	13.803
chr19	6906472	6907440	715	Rps6ka4	ribosomal protein S6 kinase, polypeptide 4	15.142
chr8	87811461	87812480	8530	Gm38426	predicted gene, 38426	13.147
chr3	55330241	55331260	295	Dclk1	doublecortin-like kinase 1	18.232
chr17	53032861	53033800	1430	Kat2b	K(lysine) acetyltransferase 2B	15.628
chr17	46017652	46018660	-1078	Mir6976	microRNA 6976	12.534
chr3	37611552	37612820	687	Spata5	spermatogenesis associated 5	35.661

chr7	63815912	63817391	1214	Klf13	Kruppel-like factor 13	37.972
chr7	63815242	63815901	2294	Klf13	Kruppel-like factor 13	27.822
chr9	44130301	44131320	325	Hyou1	hypoxia up-regulated 1	16.288
chr19	5460252	5461380	209	Fibp	fibroblast growth factor (acidic) intracellular	24.984
chr10	82502732	82503380	87760	Chst11	carbohydrate sulfotransferase 11	12.875
chr11	97266622	97267540	831	Arhgap23	Rho GTPase activating protein 23	29.874
chr5	33652232	33653200	287	Maea	macrophage erythroblast attacher	16.134
chr10	79550821	79552331	175	Midn	midnolin	19.291
chr9	1.06E+08	106312900	281	Pcbp4	poly(rC) binding protein 4	16.591
chr12	52656272	52657150	-43177	Strn3	striatin, calmodulin binding protein 3	13.866
chr19	10108881	10110240	967	Fads3	fatty acid desaturase 3	18.776
chr1	1.53E+08	153448460	-69521			15.185
chr8	97276041	97277060	921	Herpud1	homocysteine-inducible, endoplasmic	24.879
chr9	57359021	57359980	419	Scamp2	secretory carrier membrane protein 2	21.384
chr17	23453782	23454900	383	Pkmyt1	protein kinase, membrane associated	19.568
chr4	1.49E+08	149081841	674	Eno1	enolase 1, alpha non-neuron	10.853
chr10	80508601	80510290	369	Map2k2	mitogen-activated protein kinase kinase 2	35.521
chr17	71430832	71431960	318	Ndc80	NDC80 homolog, kinetochore complex	17.629
chr4	1.4E+08	140235710	1864	Sdhb	succinate dehydrogenase complex, subunit B,	17.219
chr19	41967221	41967900	2378	Pgam1	phosphoglycerate mutase 1	13.041
chr8	49172402	49173180	1185	Ing2	inhibitor of growth family, member 2	16.329
chr6	49142581	49143940	1280	Igf2bp3	insulin-like growth factor 2 mRNA binding	22.533
chr5	1.13E+08	112500900	4437			15.839
chr1	75062141	75062971	983	Abcb6	ATP-binding cassette, sub-family B	18.012
chr19	45835762	45836601	421	Mgea5	meningioma expressed antigen 5	18.601
chr9	61743662	61744680	634	Kif23	kinesin family member 23	21.575
chr17	55667352	55668540	336	Ubxn6	UBX domain protein 6	21.957
chr17	66414921	66415600	9355	Rab12	RAB12, member RAS oncogene family	12.284
chr12	4832472	4832760	347	Sf3b6	splicing factor 3B, subunit 6	15.663
chr16	32339781	32340460	671	Tctex1d2	Tctex1 domain containing 2	17.897
chr15	1.02E+08	102289680	1966	Prr13	proline rich 13	31.097
chr16	56000612	56001340	545			13.563
chr3	1.31E+08	130698191	823	Ostc	oligosaccharyltransferase complex subunit	21.012
chr10	79442021	79443320	118	Polr2e	polymerase (RNA) II (DNA directed)	19.15
chr8	73434901	73435920	318	2810428I15Rik	RIKEN cDNA 2810428I15 gene	18.574
chr4	53032861	53033880	346	Nipsnap3b	nipsnap homolog 3B (C. elegans)	19.947
chr4	1.14E+08	114485480	454	Cmpk1	cytidine monophosphate (UMP-CMP) kinase	17.745
chr11	98402442	98403140	544	Ormdl3	ORM1-like 3 (S. cerevisiae)	12.401
chr3	1.03E+08	103125400	259	Sike1	suppressor of IKBKE 1	20.054
chr2	1.63E+08	163110921	500	Oser1	oxidative stress responsive serine rich 1	24.627
chr3	1.3E+08	129929980	32442	Ccdc109b	coiled-coil domain containing 109B	15.771
chr3	1.3E+08	129929581	32787	Ccdc109b	coiled-coil domain containing 109B	15.357
chr16	8586701	8587720	264	Carhsp1	calcium regulated heat stable protein 1	18.572
chr8	1.1E+08	110326600	409	Wwp2	WW domain containing E3 ubiquitin protein	26.115
chr3	69131861	69133220	131	Trim59	tripartite motif-containing 59	16.712
chr7	44114902	44115340	357	2410002F23Rik	RIKEN cDNA 2410002F23 gene	16.568
chr7	34096561	34097240	1400	Lsm14a	LSM14 homolog A (SCD6, S. cerevisiae)	16.016
chrX	1.08E+08	107581040	74317	Rps6ka6	ribosomal protein S6 kinase polypeptide 6	11.499
chr11	72423732	72424760	790	Ube2g1	ubiquitin-conjugating enzyme E2G 1	18.196
chr4	1.24E+08	124196220	148	Utp11l	UTP11-like, U3 small nucleolar	16.718
chr9	1.15E+08	114580340	335	Cmtm6	CKLF-like MARVEL transmembrane domain	15.981
chr12	72750582	72751500	1396	Daam1	dishevelled associated activator of	24.627
chr16	90932321	90933000	578	Paxbp1	PAX3 and PAX7 binding protein 1	15.68
chr10	39945921	39946691	775	Gtf3c6	general transcription factor IIIC, polypeptide 6,	16.182
chr12	45139081	45140100	150	Pnpla8	patatin-like phospholipase domain containing	17.076
chr17	26328241	26329260	39638	Ergic1	endoplasmic reticulum-golgi intermediate	14.468
chr3	53104601	53105280	212	Cog6	component of oligomeric golgi complex 6	15.168
chr9	1.2E+08	119744600	638	Wdr48	WD repeat domain 48	17.476
chr11	1.21E+08	121053940	260	Narf	nuclear prelamin A recognition factor	15.811
chr7	1.25E+08	125282520	510	Nsmce1	non-SMC element 1 homolog (S. cerevisiae)	15.427
chr16	87243321	87244000	279	N6amt1	N-6 adenine-specific DNA methyltransferase	11.568
chr19	4097102	4098210	305	Cdk2ap2	CDK2-associated protein 2	23.878
chr1	54997381	54998060	405	Coq10b	coenzyme Q10 homolog B (S. cerevisiae)	18.128
chr1	10024901	10025580	1808	Cspp1	centrosome and spindle pole associated	19.028
chr17	79255732	79256380	4082	Cdc42ep3	CDC42 effector protein (Rho GTPase binding)	14.781
chr2	1.19E+08	119168891	644	Ino80	INO80 homolog (S. cerevisiae)	18
chr11	75896222	75897130	-52699	Fam101b	family with sequence similarity 101, member	13.374
chr17	33235532	33236471	221	Zfp414	zinc finger protein 414	31.192
chr19	5924161	5925180	146	Cdc42ep2	CDC42 effector protein (Rho GTPase binding)	25.606
chr4	1.34E+08	134204020	550	Syf2	SYF2 homolog, RNA splicing factor (S.	13.514
chr1	1.92E+08	191623290	281	Smyd2	SET and MYND domain containing 2	14.067
chr11	1.2E+08	120489880	307	Aspscr1	alveolar soft part sarcoma chromosome	22.688
chr1	37828741	37829420	5877	Mitd1	MIT, microtubule interacting and transport,	18.865
chr2	83445712	83445860	369	Zc3h15	zinc finger CCCH-type containing 15	17.182
chr17	26666541	26667220	167	Cuta	cutA divalent cation tolerance homolog (E.	18.334
chr15	98708801	98709480	308	Rhebl1	Ras homolog enriched in brain like 1	14.445
chr13	8994021	8994971	762	Gtpbp4	GTP binding protein 4	17.779
chr5	1.52E+08	151919820	447	Rfc3	replication factor C (activator 1) 3	27.575
chr3	1.06E+08	106022451	-10451	Adora3	adenosine A3 receptor	13.543
chr2	74378752	74379760	531	Lnp	limb and neural patterns	13.744
chr3	1.23E+08	123331260	47186	Mettl14	methyltransferase like 14	15.325
chr10	70743462	70744480	878	Ipmk	inositol polyphosphate multikinase	16.605
chr1	1.81E+08	181354300	718	Smyd3	SET and MYND domain containing 3	12.277
chr15	52542581	52543370	447	Med30	mediator complex subunit 30	12.873
chr11	1.13E+08	113382180	235	Slc39a11	solute carrier family 39 (metal ion transporter),	15.115
chr11	1.13E+08	113353280	28965	Slc39a11	solute carrier family 39 (metal ion transporter),	13.502
chr11	1.13E+08	113286910	95470	Slc39a11	solute carrier family 39 (metal ion transporter),	13.37
chr15	78670142	78670220	279	Cdc42ep1	CDC42 effector protein (Rho GTPase binding)	8.769
chr4	82794761	82795780	150	Ttc39b	tetratricopeptide repeat domain 39B	18.244
chr4	82773622	82774360	21429	Ttc39b	tetratricopeptide repeat domain 39B	21.05

chr4	1.48E+08	147981450	215	Apitd1	apoptosis-inducing, TAF9-like domain 1	17.957
chr7	43180681	43181051	315	Zfp715	zinc finger protein 715	14.135
chr3	1.46E+08	146458910	388	Rpf1	ribosome production factor 1 homolog (S.	29.318
chr15	25357541	25357911	763	Basp1	brain abundant, membrane attached signal	18.568
chr7	28306021	28307380	244	Pak4	p21 protein (Cdc42/Rac)-activated kinase 4	22.631
chr4	1.03E+08	102763830	25400	4921539E11Rik	RIKEN cDNA 4921539E11 gene	15.497
chr5	30571202	30572040	8205	Ept1	ethanolaminephosphotransferase 1 (CDP-	13.897
chr18	75144081	75144760	283	Dym	dymeclin	16.046
chr9	1.11E+08	110963760	529	Lrrfip2	leucine rich repeat (in FLII) interacting protein	16.171
chr11	1.18E+08	117648500	-6056	Tk1	thymidine kinase 1	13.828
chr10	77993621	77994500	1033	Syde1	synapse defective 1, Rho GTPase, homolog 1	15.056
chr11	83118922	83119800	469	Ap2b1	adaptor-related protein complex 2, beta 1	15.362
chr11	1.06E+08	105853900	474	Dcaf7	DDB1 and CUL4 associated factor 7	15.669
chr11	1.2E+08	120194621	545	Faap100	Fanconi anemia core complex associated	36.413
chr15	99599941	99600001	578	Cers5	ceramide synthase 5	9.5
chr5	1.22E+08	121884520	-4486	Acad12	acyl-Coenzyme A dehydrogenase family,	17.07
chr1	1.36E+08	136223040	129	Cyb5r1	cytochrome b5 reductase 1	12.4
chr6	85926501	85927520	291	Dusp11	dual specificity phosphatase 11 (RNA/RNP	14.538
chr16	35409301	35410660	640	Pdia5	protein disulfide isomerase associated 5	20.757
chr15	75907041	75908400	405	Puf60	poly-U binding splicing factor 60	18.708
chr5	21248981	21249660	336	Pmpcb	peptidase (mitochondrial processing) beta	15.474
chr11	57825501	57826520	751	Larp1	La ribonucleoprotein domain family, member	16.316
chr5	1.4E+08	139626440	-2543	Mir339	microRNA 339	33.484
chr2	1.81E+08	180512411	1244	Mrgbp	MRG/MORF4L binding protein	14.563
chr9	50609001	50610000	346	Ppp2r1b	protein phosphatase 2, regulatory subunit A,	15.249
chr17	87191981	87192660	1108	Ttc7	tetratricopeptide repeat domain 7	13.776
chr14	56952782	56953400	281	Micu2	mitochondrial calcium uptake 2	21.34
chr5	1.2E+08	120391280	8940	Gm10390	predicted gene 10390	13.029
chr6	91439322	91440590	701	Tmem43	transmembrane protein 43	16.091
chr17	29396532	29397420	9369	Cmtr1	cap methyltransferase 1	13.352
chr4	1.26E+08	125607220	280	Stk40	serine/threonine kinase 40	23.711
chr4	1.26E+08	125613571	7025	Stk40	serine/threonine kinase 40	17.544
chr13	54798821	54799840	303	Tspan17	tetraspanin 17	16.415
chr2	30807142	30807820	3193	Usp20	ubiquitin specific peptidase 20	12.975
chr14	30324941	30325960	1362	Eaf1	ELL associated factor 1	20.572
chr11	96592981	96594000	155	Snx11	sorting nexin 11	26.621
chr15	98745181	98746540	272	Lmbr1l	limb region 1 like	28.638
chr9	1.08E+08	107731040	220	Rbm6	RNA binding motif protein 6	18.146
chr4	1.29E+08	128561981	741	Rnf19b	ring finger protein 19B	34.81
chr4	1.29E+08	128562160	1501	Rnf19b	ring finger protein 19B	11.167
chr15	99301862	99302780	443	Bcdin3d	BCDIN3 domain containing	16.658
chr18	38326161	38326780	9266	Pcdh1	protocadherin 1	14.065
chr19	58576901	58577580	11988	Ccdc172	coiled-coil domain containing 172	18.965
chr15	57863402	57864830	261	9130401M01Rik	RIKEN cDNA 9130401M01 gene	26.957
chr16	20011041	20012060	453	Klhl24	kelch-like 24	17.698
chr13	1.05E+08	105229320	935	Nln	neurolysin (metallopeptidase M3 family)	16.477
chr7	92617982	92618720	1445	Rab30	RAB30, member RAS oncogene family	19.214
chr19	36474181	36475200	30479	Pcgf5	polycomb group ring finger 5	29.3
chr10	77587321	77588000	618	Pwp2	PWP2 periodic tryptophan protein homolog	13.626
chr13	60747302	60748140	48266	BC051665	cDNA sequence BC051665	15.436
chr11	62125141	62125820	27812	Ttc19	tetratricopeptide repeat domain 19	11.667
chr5	1.44E+08	143987620	619	Usp42	ubiquitin specific peptidase 42	18.954
chr4	1.34E+08	133807111	628	Mtfr1l	mitochondrial fission regulator 1-like	12.443
chr10	60209581	60210260	17018	Unc5b	unc-5 homolog B (C. elegans)	14.829
chr15	82999101	83000460	194	Cyb5r3	cytochrome b5 reductase 3	22.85
chr15	82992641	82993071	7118	Cyb5r3	cytochrome b5 reductase 3	21.674
chr15	82984821	82985740	7869	Rnu12	RNA U12, small nuclear	15.305
chr3	95401092	95401280	530	Cers2	ceramide synthase 2	13.511
chr17	88537361	88538040	2819	Ston1	stonin 1	12.775
chr17	26442522	26444790	416	Crebrf	CREB3 regulatory factor	31.787
chr13	1.13E+08	113433180	23340	Ankrd55	ankyrin repeat domain 55	14.899
chr16	91476661	91477340	9539	Tmem50b	transmembrane protein 50B	13.648
chr3	95099701	95100720	432	Zfp687	zinc finger protein 687	21.333
chr15	51707881	51708390	620	Utp23	UTP23, small subunit (SSU) processome	12.811
chr11	96792901	96793580	538	Sp2	Sp2 transcription factor	15.445
chr6	56644681	56645700	707	Avl9	AVL9 homolog (S. cerevisiase)	21.494
chr12	1.11E+08	111050800	1099	Dync1h1	dynein cytoplasmic 1 heavy chain 1	24.949
chr12	84409862	84410990	212	Dcaf4	DDB1 and CUL4 associated factor 4	16.27
chr3	1.05E+08	105180541	898	Cttnbp2nl	CTTNBP2 N-terminal like	13.814
chr8	89773941	89774531	1127	N4bp1	NEDD4 binding protein 1	18.627
chr7	1.26E+08	126220920	495	Rabep2	rabaptin, RAB GTPase binding effector	35.119
chr5	1.17E+08	116682390	2032	Hspb8	heat shock protein 8	22.624
chr9	39942532	39943540	149	Zfp202	zinc finger protein 202	14.55
chr9	66773621	66774341	647	Lactb	lactamase, beta	23.306
chr2	1.67E+08	167194891	-10527	Spata2	spermatogenesis associated 2	19.491
chr2	1.67E+08	167195680	-11212	Spata2	spermatogenesis associated 2	14.468
chr15	75756421	75757100	225	Tsta3	tissue specific transplantation antigen P35B	16.786
chr11	5144541	5145560	16563	Kremen1	kringle containing transmembrane protein 1	16.637
chr15	11343421	11344100	623	Tars	threonyl-tRNA synthetase	12.483
chr11	53364021	53364700	1201	Sept8	septin 8	17.016
chr16	18201901	18202920	321	Dgcr8	DiGeorge syndrome critical region gene 8	14.621
chr17	34658921	34658960	641	Clic1	chloride intracellular channel 1	6.282
chr17	34659062	34659940	1202	Clic1	chloride intracellular channel 1	26.63
chr15	34189721	34190400	7445	Laptm4b	lysosomal-associated protein transmembrane	12.043
chr11	19825401	19826080	1295	Spred2	sprouty-related, EVH1 domain containing 2	18.007
chr7	18976552	18977410	4296	Bcl3	B cell leukemia/lymphoma 3	9.382
chr7	1.4E+08	139967460	717	Echs1	enoyl Coenzyme A hydratase, short chain, 1,	19.886
chr11	48681272	48681880	12015	Trim7	tripartite motif-containing 7	19.704
chr4	46510301	46510980	211	Nans	N-acetylneuraminic acid synthase (sialic acid	16.415
chr7	26874632	26875640	426	Egln2	egl-9 family hypoxia-inducible factor 2	12.594

chr9	96439981	96440660	535	Rasa2	RAS p21 protein activator 2	14.296
chr4	1.06E+08	106059940	630	Dhcr24	24-dehydrocholesterol reductase	16.468
chr17	6128562	6129520	34411	Tulp4	tubby like protein 4	18.456
chr11	88314661	88315340	-120341			15.116
chr10	1.27E+08	127498220	2018	Baz2a	bromodomain adjacent to zinc finger domain,	23.754
chr10	1.27E+08	126614940	290	Pip4k2c	phosphatidylinositol-5-phosphate 4-kinase,	19.254
chr10	79978881	79980231	869	Klf16	Kruppel-like factor 16	45.415
chr16	91946541	91948240	195	Mrps6	mitochondrial ribosomal protein S6	30.177
chr17	26800572	26801390	16088	Itpr3	inositol 1,4,5-triphosphate receptor 3	18.67
chr16	33171081	33172000	337	Snx4	sorting nexin 4	13.992
chr11	77992261	77992940	261	Nek8	NIMA (never in mitosis gene a)-related	19.14
chr3	1.3E+08	129581140	56392	Elovl6	ELOVL family member 6, elongation of long	18.647
chr11	1.2E+08	119796620	-34747	Mir3065	microRNA 3065	14.184
chr11	1.2E+08	119792540	32848	Baiap2	brain-specific angiogenesis inhibitor 1-	18.594
chr7	15468482	15469320	796	Bbc3	BCL2 binding component 3	16.63
chr7	15470292	15472720	3401	Bbc3	BCL2 binding component 3	20.118
chr18	61524021	61524910	-1196	Mir378a	microRNA 378a	12.053
chr8	87880481	87881500	290	Hook2	hook homolog 2 (Drosophila)	15.902
chr6	1.25E+08	125005991	184	Ing4	inhibitor of growth family, member 4	18.287
chr19	41316121	41317071	719	Tm9sf3	transmembrane 9 superfamily member 3	17.926
chr19	6116982	6117620	1285	Sac3d1	SAC3 domain containing 1	15.994
chr18	35965642	35966780	10419	Cxxc5	CXXC finger 5	17.646
chr7	99995021	99995700	223	Pold3	polymerase (DNA-directed), delta 3,	18.031
chr7	49646801	49647201	622	Prmt3	protein arginine N-methyltransferase 3	8.575
chr8	1.24E+08	124460060	5308	Fbxo31	F-box protein 31	30.329
chr2	1.64E+08	164189591	561	Pigt	phosphatidylinositol glycan anchor	23.84
chr15	78761782	78762940	173	Nol12	nucleolar protein 12	22.197
chr11	94445881	94447240	646	Lrrc59	leucine rich repeat containing 59	27.289
chr1	99491821	99492500	264	D1Ertd622e	DNA segment, Chr 1, ERATO Doi 622,	12.563
chr4	53467132	53468020	6063	Slc44a1	solute carrier family 44, member 1	9.519
chr5	1.14E+08	114437200	10343	Acacb	acetyl-Coenzyme A carboxylase beta	11.583
chr7	1.02E+08	101844521	227	Numa1	nuclear mitotic apparatus protein 1	34.302
chr7	1.02E+08	101844620	912	Numa1	nuclear mitotic apparatus protein 1	10.307
chr7	44736861	44737581	609	Ptov1	prostate tumor over expressed gene 1	22.597
chr14	6609392	6610510	1585	Flnb	filamin, beta	20.789
chr15	87492201	87493220	39714	Fam19a5	family with sequence similarity 19, member	14.217
chr15	1.02E+08	102108120	290	Mfsd5	major facilitator superfamily domain	18.532
chr19	7124502	7125380	1129	Macrod1	MACRO domain containing 1	14.428
chr12	81177802	81179041	790	Actn1	actinin, alpha 1	12.739
chr4	1.17E+08	116680860	206	Kif2c	kinesin family member 2C	19.09
chr9	65258581	65259830	262	Spg21	spastic paraplegia 21 homolog (human)	23.102
chr9	56663381	56663681	290	Cspg4	chondroitin sulfate proteoglycan 4	9.133
chr9	56663692	56664740	975	Cspg4	chondroitin sulfate proteoglycan 4	18.436
chr11	1.21E+08	120806760	1003	Csnk1d	casein kinase 1, delta	15.334
chr18	24745302	24746221	1066	Slc39a6	solute carrier family 39 (metal ion transporter),	27.711
chr7	1.28E+08	127760030	829	Fus	fused in sarcoma	18.77
chr19	32453341	32454311	625	Sgms1	sphingomyelin synthase 1	18.845
chr9	1.2E+08	119959820	213	Slc25a38	solute carrier family 25, member 38	17.472
chr11	77422761	77423641	809	Taok1	TAO kinase 1	19.193
chr11	79777261	79778091	906	Utp6	UTP6, small subunit (SSU) processome	13.843
chr11	79759581	79760590	18497	Utp6	UTP6, small subunit (SSU) processome	20.65
chr15	63827181	63828480	62291	Fam49b	family with sequence similarity 49, member B	18.512
chr17	93072132	93072960	370	Pja2	praja 2, RING-H2 motif containing	13.643
chr3	88143641	88144860	172	Apoa1bp	apolipoprotein A-I binding protein	21.967
chr3	1.17E+08	116704320	363	Slc35a3	solute carrier family 35 (UDP-N-	19.482
chr4	59642461	59643820	278	Ptbp3	polypyrimidine tract binding protein 3	24.193
chr4	1.32E+08	131782280	752	Sesn2	sestrin 2	17.011
chr5	96401221	96402101	188	Cnot6l	CCR4-NOT transcription complex, subunit 6-	14.511
chr6	85397121	85398480	166	Smyd5	SET and MYND domain containing 5	46.78
chr6	1.41E+08	140510331	-74933	Aebp2	AE binding protein 2	18.733
chr15	78919172	78920120	-16592	Micall1	microtubule associated monooxygenase,	12.818
chr5	1.21E+08	121036140	2580	Oas3	2'-5' oligoadenylate synthetase 3	14.334
chr18	76016861	76017880	71827	Zbtb7c	zinc finger and BTB domain containing 7C	17.829
chr7	1.45E+08	145112680	1871	Mrgprf	MAS-related GPR, member F	16.312
chr11	77931401	77932380	21022	Fam222b	family with sequence similarity 222, member	15.633
chr11	98589602	98590820	1256	Nr1d1	nuclear receptor subfamily 1, group D,	17.502
chr11	98589461	98589591	1941	Nr1d1	nuclear receptor subfamily 1, group D,	5
chr11	98588441	98589120	2687	Nr1d1	nuclear receptor subfamily 1, group D,	11.183
chr11	1.18E+08	117596431	680	Tmc6	transmembrane channel-like gene family 6	16.997
chr11	1.18E+08	117595621	1170	Tmc6	transmembrane channel-like gene family 6	14.938
chr15	88690361	88690761	601	Pim3	proviral integration site 3	8.8
chr15	88691322	88691380	1391	Pim3	proviral integration site 3	6.19
chr1	95342121	95343140	120	Farp2	FERM, RhoGEF and pleckstrin domain	14.421
chr2	1.22E+08	121809401	846	Spg11	spastic paraplegia 11	18.039
chr6	83291501	83292520	313	Mob1a	MOB kinase activator 1A	17.371
chr7	1.2E+08	119511940	396	Thumpd1	THUMP domain containing 1	13.463
chr9	21547912	21548671	657	Kank2	KN motif and ankyrin repeat domains 2	11.642
chr9	21542792	21543760	5672	Kank2	KN motif and ankyrin repeat domains 2	18.041
chr9	21542401	21542781	6357	Kank2	KN motif and ankyrin repeat domains 2	13.974
chrX	19861101	19861780	572	Usp11	ubiquitin specific peptidase 11	15.754
chr10	77026952	77028020	2003	Pttg1ip	pituitary tumor-transforming 1 interacting	14.282
chr16	11088802	11089780	680	Zc3h7a	zinc finger CCCH type containing 7 A	14.77
chr11	35613301	35613980	722	Pank3	pantothenate kinase 3	16.028
chr9	44517901	44518771	467	Arcn1	archain 1	12.943
chr17	80114201	80115560	751	Srsf7	serine/arginine-rich splicing factor 7	19.333
chr18	34630361	34632060	414	Fam13b	family with sequence similarity 13, member B	35.624
chr2	1.52E+08	151670200	1940	Fam110a	family with sequence similarity 110, member	19.432
chr4	45992922	45994180	154	Tdrd7	tudor domain containing 7	18.737
chr4	1.17E+08	117412200	1241	Ipo13	importin 13	17.706
chr7	29988012	29989511	420	Wdr62	WD repeat domain 62	20.047

chr9	37239181	37240200	698	Msantd2	Myb/SANT-like DNA-binding domain	19.445
chr5	31517321	31518340	331	Nrbp1	nuclear receptor binding protein 1	25.333
chr11	1.03E+08	102910520	7568	Plcd3	phospholipase C, delta 3	16.102
chr4	59720762	59721000	616	E130308A19Rik	RIKEN cDNA E130308A19 gene	19.71
chr4	1.25E+08	124629951	349	Zc3h12a	zinc finger CCCH type containing 12A	18.913
chr15	72981681	72982700	30013	Ago2	argonaute RISC catalytic subunit 2	15.95
chr9	1.2E+08	119832660	1135	Csrnp1	cysteine-serine-rich nuclear protein 1	15.082
chr9	1.2E+08	119831771	1915	Csrnp1	cysteine-serine-rich nuclear protein 1	15.56
chr9	1.2E+08	119831101	2325	Csrnp1	cysteine-serine-rich nuclear protein 1	8.214
chr9	1.2E+08	119830620	3185	Csrnp1	cysteine-serine-rich nuclear protein 1	16.521
chr4	1.26E+08	125970571	439	Ago1	argonaute RISC catalytic subunit 1	17.526
chr11	1.02E+08	102065960	679	BC030867	cDNA sequence BC030867	17.767
chr3	1.08E+08	107759431	590	Strip1	striatin interacting protein 1	12.098
chr11	22412121	22413080	314	Tmem17	transmembrane protein 17	17.221
chr6	72163301	72163980	1446	Atoh8	atonal homolog 8 (Drosophila)	12.929
chr7	1.18E+08	117907240	396	Rps15a	ribosomal protein S15A	14.43
chr2	1.67E+08	167177851	-6434	Rnf114	ring finger protein 114	21.138
chr2	1.67E+08	167178340	-5749	Rnf114	ring finger protein 114	10.774
chr7	4518602	4519280	637	Zfp628	zinc finger protein 628	12.537
chr11	35814921	35815600	8252	Wwc1	WW, C2 and coiled-coil domain containing 1	14.542
chr17	26508781	26509670	423	Bnip1	BCL2/adenovirus E1B interacting protein 1	19.441
chr11	94808661	94809680	1868	Ppp1r9b	protein phosphatase 1, regulatory subunit 9B	18.945
chr7	98530641	98531660	611	Emsy	EMSY, BRCA2-interacting transcriptional	20.097
chr8	97103321	97104670	265	Nup93	nucleoporin 93	28.602
chr15	81955392	81955980	509	Ccdc134	coiled-coil domain containing 134	15.287
chr11	1.19E+08	119031960	13063	Tbc1d16	TBC1 domain family, member 16	15.843
chr1	95102761	95103440	-1855	Mir6901	microRNA 6901	20.272
chr5	52957422	52958060	208	Sepsecs	Sep (O-phosphoserine) tRNA:Sec	21.544
chr12	1.05E+08	105410540	343	Syne3	spectrin repeat containing, nuclear envelope	7.375
chr12	1.05E+08	105410481	838	Syne3	spectrin repeat containing, nuclear envelope	20.584
chr8	86994101	86994780	427	Dcaf15	DDB1 and CUL4 associated factor 15	16.946
chr9	65624761	65625241	569	Zfp609	zinc finger protein 609	17.792
chr5	1.36E+08	136029240	239	Tmem120a	transmembrane protein 120A	20.634
chr10	75110761	75111440	-23376	Susd2	sushi domain containing 2	16.817
chr10	79148941	79149620	430	Polrmt	polymerase (RNA) mitochondrial (DNA	15.074
chr11	50270772	50271890	3203	Rufy1	RUN and FYVE domain containing 1	18.273
chr11	1.16E+08	115926061	944	Trim47	tripartite motif-containing 47	18.691
chr12	85256622	85257340	5265	Coq6	coenzyme Q6 homolog (yeast)	13.74
chr15	79218462	79219660	11113	Tmem184b	transmembrane protein 184b	15.81
chr15	79217352	79218451	12273	Tmem184b	transmembrane protein 184b	26.592
chr19	11979561	11980760	716	Patl1	protein associated with topoisomerase II	30.315
chr1	1.64E+08	163970100	-84704	Dnm3os	dynamin 3, opposite strand	11.304
chr5	87246381	87247740	244	Uba6	ubiquitin-like modifier activating enzyme 6	29.307
chr12	1.03E+08	103279420	376	Btbd7	BTB (POZ) domain containing 7	15.184
chr14	60126621	60127300	34393	Sacs	sacsin	14.513
chr17	17328441	17329460	157	Lnpep	leucyl/cystinyl aminopeptidase	18.056
chr18	31777081	31778350	322	Sap130	Sin3A associated protein	25.001
chr7	79987381	79988060	1143	Idh2	isocitrate dehydrogenase 2 (NADP+),	17.912
chr11	3248361	3249380	7274	Limk2	LIM motif-containing protein kinase 2	18.563
chr3	7486121	7487140	131	Zc2hc1a	zinc finger, C2HC-type containing 1A	18.175
chr8	91586821	91587840	197	Cyld	cylindromatosis (turban tumor syndrome)	17.067
chr1	1.37E+08	137283840	-36598	Ipo9	importin 9	18
chr1	60124921	60125940	285	Nbeal1	neurobeachin like 1	20.177
chr7	80196821	80197411	851	Rccd1	RCC1 domain containing 1	25.695
chr11	6099002	6100280	813	Nudcd3	NudC domain containing 3	17.29
chr10	77977612	77978660	507	Ilvbl	ilvB (bacterial acetolactate synthase)-like	28.063
chr11	32388752	32389760	33884	Ubtd2	ubiquitin domain containing 2	20.32
chr8	1.28E+08	128140220	199425	Disc1	disrupted in schizophrenia 1	30.466
chr7	44919781	44920761	652	Prr12	proline rich 12	20.663
chr18	80312492	80313440	575	Adnp2	ADNP homeobox 2	12.685
chr4	1.01E+08	101146260	205	Leprot	leptin receptor overlapping transcript	23.032
chr2	1.73E+08	172643840	274	Rae1	RAE1 RNA export 1 homolog (S. pombe)	14.107
chr15	96527021	96527561	441	Slc38a2	solute carrier family 38, member 2	15.037
chr9	1.08E+08	108376020	490	Qrich1	glutamine-rich 1	13.434
chr8	1.28E+08	127530600	19293	2310022B05Rik	RIKEN cDNA 2310022B05 gene	14.954
chr8	1.28E+08	127529721	19808	2310022B05Rik	RIKEN cDNA 2310022B05 gene	8.571
chr7	49117802	49118440	3911	Nav2	neuron navigator 2	22.461
chr4	1.32E+08	131670780	24091	Phactr4	phosphatase and actin regulator 4	15.33
chr4	1.15E+08	115326980	276	Mob3c	MOB kinase activator 3C	21.031
chr15	95618922	95619560	364	Ano6	anoctamin 6	15.053
chr17	12834492	12835000	445	Wtap	Wilms tumour 1-associating protein	14.321
chr17	12833981	12834481	960	Wtap	Wilms tumour 1-associating protein	16.22
chr4	1.08E+08	107958840	802	Zcchc11	zinc finger, CCHC domain containing 11	15.018
chr5	1.22E+08	122110270	140	Fam109a	family with sequence similarity 109, member	14.455
chr7	18289642	18290840	11860	Fbxo46	F-box protein 46	24.927
chr6	38363901	38365140	987	Ubn2	ubinuclein 2	22.232
chr8	93798181	93799200	-23664			13.868
chr5	1.23E+08	122549260	3905	Pptc7	PTC7 protein phosphatase homolog (S.	12.258
chr7	1.1E+08	110406160	447	Sbf2	SET binding factor 2	16.858
chr19	47121302	47122300	742	Taf5	TAF5 RNA polymerase II, TATA box binding	14.381
chr11	32247641	32248320	169	Sh3pxd2b	SH3 and PX domains 2B	16.591
chr11	80315662	80316160	9390			19.661
chr1	20999532	21000100	63039	Efhc1	EF-hand domain (C-terminal) containing 1	14.516
chr19	15990902	15991220	580	Psat1	phosphoserine aminotransferase 1	8.95
chr19	15989861	15990891	1265	Psat1	phosphoserine aminotransferase 1	27.34
chr15	78958541	78959220	9626			17.106
chr5	1.24E+08	123656640	730	Mlxip	MLX interacting protein	13.342
chr16	32252061	32252740	401	Ubxn7	UBX domain protein 7	15.832
chr6	1.15E+08	114841120	46591	Vgll4	vestigial like 4 (Drosophila)	14.495
chr8	1.08E+08	108236620	963	Fhod1	formin homology 2 domain containing 1	14.471

chr4	1.28E+08	128112000	742	Zscan20	zinc finger and SCAN domains 20	16.138
chr16	20535632	20536560	-1275	Camk2n2	calcium/calmodulin-dependent protein kinase	17.866
chr11	98558861	98559540	1325			11.437
chr11	3231701	3233060	1646	Pik3ip1	phosphoinositide-3-kinase interacting protein	22.452
chr11	70819961	70820041	626	Dhx33	DEAH (Asp-Glu-Ala-His) box polypeptide 33	6.25
chr18	47083881	47084900	183	Commd10	COMM domain containing 10	19.191
chr1	1.74E+08	174340830	3530	Tagln2	transgelin 2	17.817
chr2	1.31E+08	131044820	183	Rnf24	ring finger protein 24	17.18
chr10	1.1E+08	110154450	4616	E2f7	E2F transcription factor 7	22.344
chr11	54630521	54631200	266	Cdc42se2	CDC42 small effector 2	13.661
chr6	85298181	85298860	560	Sfxn5	sideroflexin 5	15.386
chr3	1.43E+08	142764880	54970	Pkn2	protein kinase N2	16.003
chr9	1.22E+08	121554080	157	Sec22c	SEC22 homolog C, vesicle trafficking protein	13.919
chr5	48273201	48274220	2307	Slit2	slit homolog 2 (Drosophila)	17.537
chr2	1.53E+08	152706920	244	Pdrg1	p53 and DNA damage regulated 1	17.968
chr17	88349341	88350020	642	Foxn2	forkhead box N2	12.283
chr9	70008422	70009400	2397	Myo1e	myosin IE	14.625
chr8	1.09E+08	108526300	293	Ctcf	CCCTC-binding factor	16.626
chr19	17078122	17078880	55364	Prune2	prune homolog 2 (Drosophila)	21.81
chr19	10755561	10756580	210	Vps37c	vacuolar protein sorting 37C (yeast)	17.244
chr19	57711601	57712550	47791	Atrnl1	attractin like 1	16.415
chr12	1.12E+08	111802190	23865	Cdc42bpb	CDC42 binding protein kinase beta	28.698
chr7	1.26E+08	126293761	1069	Atxn2l	ataxin 2-like	11.855
chr1	75341122	75341620	7713	Asic4	acid-sensing (proton-gated) ion channel	10.894
chr17	24399421	24400281	2499	Zfp598	zinc finger protein 598	19.767
chr7	70235212	70235980	-1490	Nr2f2	nuclear receptor subfamily 2, group F,	15.917
chr5	1.22E+08	122392860	3160	Ccdc63	coiled-coil domain containing 63	23.831
chr10	79505261	79506131	135	Sbno2	strawberry notch homolog 2 (Drosophila)	15.563
chr11	74712162	74713640	374	Sgsm2	small G protein signaling modulator 2	30.404
chr1	1.54E+08	153849660	3218	1700025G04Rik	RIKEN cDNA 1700025G04 gene	9.437
chr10	79311332	79312140	331	Med16	mediator complex subunit 16	26.385
chr5	1.14E+08	114251220	4046	Ssh1	slingshot homolog 1 (Drosophila)	28.663
chr5	1.14E+08	114237280	17986	Ssh1	slingshot homolog 1 (Drosophila)	18.972
chr12	53740061	53740740	119397	Akap6	A kinase (PRKA) anchor protein 6	15.594
chr19	10364221	10364900	7362	Dagla	diacylglycerol lipase, alpha	15.545
chr19	46051301	46051980	159	9130011E15Rik	RIKEN cDNA 9130011E15 gene	16.946
chr5	1.11E+08	110806000	21004	Galnt9	UDP-N-acetyl-alpha-D-	16.37
chr11	1.2E+08	120069300	19753	Bahcc1	BAH domain and coiled-coil containing 1	17.699
chr11	1.2E+08	120079160	29613	Bahcc1	BAH domain and coiled-coil containing 1	31.512
chr6	1.25E+08	125344060	2403	Plekhg6	pleckstrin homology domain containing, family	11.459
chr10	79788481	79789840	1620	Mex3d	mex3 homolog D (C. elegans)	16.976
chr6	1.2E+08	120003000	1784	Wnk1	WNK lysine deficient protein kinase 1	16.935
chr17	34502181	34503790	370	Zbtb12	zinc finger and BTB domain containing 12	27.15
chr11	51699041	51700400	1184	Jade2	jade family PHD finger 2	36.019
chr4	1.29E+08	129199320	502	Tmem39b	transmembrane protein 39b	23.614
chr4	1.37E+08	137203830	-62306	Eif4g3	eukaryotic translation initiation factor 4	18.377
chr4	1.53E+08	152857100	1038	Lrrc47	leucine rich repeat containing 47	10.927
chr17	79523281	79523960	394	Rmdn2	regulator of microtubule dynamics 2	12.616
chr17	45960922	45961880	1423	Dnph1	2'-deoxynucleoside 5'-phosphate N-hydrolase	18.834
chr7	18386861	18387880	459	Opa3	optic atrophy 3	14.763
chr17	32971562	32972520	313	Zfp81	zinc finger protein 81	17.722
chr11	49555001	49556360	465	Cnot6	CCR4-NOT transcription complex, subunit 6	12.668
chr7	1E+08	100457420	307	Mrpl48	mitochondrial ribosomal protein L48	29.876
chr7	1.11E+08	110914071	410	1700012D14Rik	RIKEN cDNA 1700012D14 gene	22.878
chr6	1.13E+08	113042731	905	Gt(ROSA)26Sor	gene trap ROSA 26, Philippe Soriano	22.846
chr4	1.07E+08	107306380	5735	Lrp8	low density lipoprotein receptor-related	24.307
chr17	32095312	32095781	-13347	Akap8l	A kinase (PRKA) anchor protein 8-like	17.495
chr8	1.09E+08	108750360	231	Nutf2-ps1	nuclear transport factor 2, pseudogene 1	19.769
chr6	34246841	34247860	251	Gm6644	Akr1b3 pseudogene	17.659
chr17	33728341	33729360	1504	Brd2	bromodomain containing 2	17.631
chr11	1.2E+08	120167220	2013	0610009L18Rik	RIKEN cDNA 0610009L18 gene	37.707
chr3	89481332	89482220	1559	Gm15417	predicted gene 15417	16.999
chr4	1.5E+08	149681131	18003	1700045H11Rik	RIKEN cDNA 1700045H11 gene	15.616
chr5	73559482	73560360	3398	1700025M24Rik	RIKEN cDNA 1700025M24 gene	14.081
chr9	63847482	63848600	206	1110036E04Rik	RIKEN cDNA 1110036E04 gene	16.085
chr9	61087572	61088410	3824	B930092H01Rik	RIKEN cDNA B930092H01 gene	13.717
chr17	56359081	56359760	1071	Ranbp3	RAN binding protein 3	13.057
chr3	40896561	40897580	570	Plk4	polo-like kinase 4	16.159
chr12	1.01E+08	100678420	421	Gm10432	predicted gene 10432	10.817
chr5	1.12E+08	111998700	3995	E130006D01Rik	RIKEN cDNA E130006D01 gene	17.988
chr14	46833592	46834320	13141	4930447J18Rik	RIKEN cDNA 4930447J18 gene	15.569
chr3	1.23E+08	122880760	-6653	Fabp2	fatty acid binding protein 2, intestinal	19.918
chr15	76403112	76404460	172	Adck5	aarF domain containing kinase 5	22.387
chr10	80964162	80964790	1903	Aes	amino-terminal enhancer of split	14.025
chr11	31708061	31708630	16202	D630024D03Rik	RIKEN cDNA D630024D03 gene	22.404
chr10	41138641	41139320	207	Zbtb24	zinc finger and BTB domain containing 24	15.432
chr11	26287101	26287980	456	Fancl	Fanconi anemia, complementation group L	14.842
chr7	18429442	18429700	805	Vasp	vasodilator-stimulated phosphoprotein	6.465
chr7	18428762	18429431	1280	Vasp	vasodilator-stimulated phosphoprotein	13.105
chr15	1E+08	100455611	8267	Smagp	small cell adhesion glycoprotein	19.772
chr6	1.09E+08	108625580	-1166	Bhlhe40	basic helix-loop-helix family, member e40	20.529
chr2	1.55E+08	154934260	5792	Dynlrb1	dynein light chain roadblock-type 1	17.159
chr2	1.81E+08	181427560	591	Tpd52l2	tumor protein D52-like 2	12.869
chr3	1.39E+08	138702880	22835	Tspan5	tetraspanin 5	17.791
chr3	1.39E+08	138709460	29411	Tspan5	tetraspanin 5	16.703
chr15	38462841	38463581	644			20.959
chr17	24182161	24183180	322			15.613
chr2	1.51E+08	151234720	456			12.496
chr10	1.16E+08	116137880	4278			11.818
chr15	38871672	38872750	-34795	Cthrc1	collagen triple helix repeat containing 1	22.737

chr4	1.19E+08	118565820	1563			15.854
chr5	45580512	45581121	131832			17.057
chr15	61908901	61909580	40317			20.364
chr1	94764461	94765450	141	Capn10	calpain 10	12.089
chr7	1.27E+08	127303821	180			12.873
chr16	50651501	50652520	111	Dubr	Dppa2 upstream binding RNA	13.331
chr4	1.41E+08	140819500	752	B330016D10Rik	RIKEN cDNA B330016D10 gene	22.32
chr5	5579741	5580420	275	Gm8773	predicted gene 8773	15.75
chr5	1.35E+08	135295180	587	Abhd11	abhydrolase domain containing 11	15.145
chr10	79541981	79542660	176	Cbarp	calcium channel, voltage-dependent, beta	20.498
chrX	49301021	49301691	461	C430049B03Rik	RIKEN cDNA C430049B03 gene	15.522
chr3	89477461	89478480	179	Gm15417	predicted gene 15417	14.585
chr19	5117562	5118920	167	Klc2	kinesin light chain 2	21.824
chr9	50527401	50528001	246	Alg9	asparagine-linked glycosylation 9 (alpha 1,2	20.1
chr9	56928581	56929600	176	Man2c1	mannosidase, alpha, class 2C, member 1	13.702
chr2	75504821	75505840	172			14.375
chr9	64138961	64139640	-37	Dis3l	DIS3 mitotic control homolog (S. cerevisiae)-	15.194
chr17	84095812	84097300	-283	Zfp36l2	zinc finger protein 36, C3H type-like 2	15.999
chr15	99285441	99286460	-168	Nckap5l	NCK-associated protein 5-like	18.911
chr10	95370341	95370551	95	Eea1	early endosome antigen 1	24
chr19	4396982	4397900	-364	Kdm2a	lysine (K)-specific demethylase 2A	13.668
chr11	78077601	78078251	-23	2610507B11Rik	RIKEN cDNA 2610507B11 gene	12.646
chr17	21271421	21272100	17	Zfp948	zinc finger protein 948	24.596
chr3	88589381	88590400	-611	Lmna	lamin A	20.364
chr11	86573552	86573860	-19	Cltc	clathrin, heavy polypeptide (Hc)	16.529
chr10	86134581	86135940	-17	Hsp90b1	heat shock protein 90, beta (Grp94), member	18.073
chr6	85340001	85341020	-218	Rab11fip5	RAB11 family interacting protein 5 (class I)	20.694
chr16	56000041	56000601	-34	Senp7	SUMO1/sentrin specific peptidase 7	15.589
chr11	60991062	60992130	-342	Usp22	ubiquitin specific peptidase 22	20.037
chr11	77309541	77309641	-16	Git1	G protein-coupled receptor kinase-interactor 1	4.1
chr14	68894201	68894880	42	9930012K11Rik	RIKEN cDNA 9930012K11 gene	12.498
chr4	1.19E+08	119038001	108	Foxj3	forkhead box J3	14.867
chr10	83870181	83870860	-250	Nuak1	NUAK family, SNF1-like kinase, 1	19.604
chr12	21357832	21358560	-50	Asap2	ArfGAP with SH3 domain, ankyrin repeat and	16.368
chr5	1.38E+08	138017220	-227	Mepce	methylphosphate capping enzyme	16.45
chr12	76736732	76737320	-132	Syne2	spectrin repeat containing, nuclear envelope 2	11.861
chr5	1.24E+08	124010580	-104	Kntc1	kinetochore associated 1	22.333
chr4	1.2E+08	120449741	-75	Zfp69	zinc finger protein 69	26.121
chr17	26700201	26701450	57	Zbtb9	zinc finger and BTB domain containing 9	23.043
chr17	23401181	23401860	-128	Thoc6	THO complex 6 homolog (Drosophila)	17.144
chr2	29870701	29871320	-122	Wdr34	WD repeat domain 34	13.384
chr7	43429901	43430790	-67	Zfp658	zinc finger protein 658	14.234
chr11	60543782	60545160	-122	Mief2	mitochondrial elongation factor 2	22.957
chr4	45429482	45430371	-60	Slc25a51	solute carrier family 25, member 51	13.423
chr17	35448782	35449521	-400	Mdc1	mediator of DNA damage checkpoint 1	19.754
chr7	18518202	18519361	-776	Cd3eap	CD3E antigen, epsilon polypeptide associated	19.003
chr7	18519372	18520140	18	Ppp1r13l	protein phosphatase 1, regulatory (inhibitor)	19.764
chr6	39740232	39740900	-23	Mrps33	mitochondrial ribosomal protein S33	22.193
chr11	1.18E+08	117666170	-2	Birc5	baculoviral IAP repeat-containing 5	23.125
chr4	33279201	33279790	-56	Ankrd6	ankyrin repeat domain 6	10.961
chr7	5759062	5759600	-273	Zfp787	zinc finger protein 787	15.699
chr1	43042981	43043990	229	AI597479	expressed sequence AI597479	15.053
chr3	1.01E+08	101099330	-252	Ttf2	transcription termination factor, RNA	13.162
chr15	5090481	5091500	-86	Prkaa1	protein kinase, AMP-activated, alpha 1	14.333
chr7	48749201	48749880	-478	E2f8	E2F transcription factor 8	11.888
chr11	93701732	93703650	382	Mbtd1	mbt domain containing 1	26.081
chr2	1.22E+08	122061020	-151	Shf	Src homology 2 domain containing F	16.233
chr10	1.18E+08	118273080	-844	Dyrk2	dual-specificity tyrosine-(Y)-phosphorylation	15.789
chr4	59719732	59720751	-24	E130308A19Rik	RIKEN cDNA E130308A19 gene	20.466
chr14	30658821	30659840	94	Ankrd28	ankyrin repeat domain 28	13.667
chr11	77328921	77329940	38	Trp53i13	transformation related protein 53 inducible	14.568
chr3	1.05E+08	104641460	29			18.183
chr2	73692961	73693980	8	Atf2	activating transcription factor 2	19.18
chr17	93070921	93072121	-655	Pja2	praja 2, RING-H2 motif containing	21.567
chr17	33529441	33530460	18	Tapbp	TAP binding protein	16.513
chr2	1.21E+08	121149140	101	Hypk	huntingtin interacting protein K	11.371
chr17	27282572	27283791	-982	Hmga1	high mobility group AT-hook 1	17.174
chr17	27283802	27284660	-11	Hmga1-rs1	high mobility group AT-hook I, related	15.994
chr17	36443921	36444940	-769	Trim26	tripartite motif-containing 26	22.376
chr12	65835922	65836471	-320	Gm527	predicted gene 527	16.464
chr4	1.4E+08	140412161	41	Szrd1	SUZ RNA binding domain containing 1	22.318
chr11	98723421	98724100	-219	Cdc6	cell division cycle 6	15.034
chr3	88617261	88618550	-417	Mex3a	mex3 homolog A (C. elegans)	20.681
chr11	84955801	84956820	-160	Usp32	ubiquitin specific peptidase 32	19.184
chr11	61892581	61893600	-129	Specc1	sperm antigen with calponin homology and	26.158
chr7	1.18E+08	118035080	30	Smg1	SMG1 homolog, phosphatidylinositol 3-	13.424
chr1	39521472	39522530	-108	Rnf149	ring finger protein 149	17.449
chr8	1.25E+08	125362641	-37	Rnf166	ring finger protein 166	21.5
chr9	94347372	94347960	-233	1190002N15Rik	RIKEN cDNA 1190002N15 gene	12.247
chr4	59096761	59097780	23	Dnajc25	DnaJ (Hsp40) homolog, subfamily C, member	25.7
chr7	1.21E+08	121499000	-259	Usp31	ubiquitin specific peptidase 31	12.966
chr4	1.29E+08	128751200	-113	C77080	expressed sequence C77080	12.766
chr12	70501041	70502060	83	Vcpkmt	valosin containing protein lysine (K)	21.602
chr14	13495672	13496640	-136	Slc4a7	solute carrier family 4, sodium bicarbonate	14.699
chr15	88561822	88562520	-186	Brd1	bromodomain containing 1	14.961
chr15	93103142	93103891	-252	Gxylt1	glucoside xylosyltransferase 1	19.852
chr15	98699281	98700300	-551	Kmt2d	lysine (K)-specific methyltransferase 2D	15.948
chr15	1.02E+08	101964980	-51	Spryd3	SPRY domain containing 3	19.004
chr2	1.7E+08	169823160	-236	Zfp217	zinc finger protein 217	21.032
chr3	84566012	84566840	-60	Fhdc1	FH2 domain containing 1	20.04

chr4	45551501	45552520	-82	Shb	src homology 2 domain-containing	13.653
chr5	1.43E+08	143160910	22	Fbxl18	F-box and leucine-rich repeat protein 18	22.475
chr5	1.45E+08	145393860	96	Pdap1	PDGFA associated protein 1	17.962
chr7	18068621	18069300	-34	Ccdc61	coiled-coil domain containing 61	18.037
chr7	4622641	4623920	-183	Zfp865	zinc finger protein 865	21.966
chr19	5567501	5568520	-64	Ap5b1	adaptor-related protein complex 5, beta 1	17.317
chr2	91450152	91451500	-131	Arhgap1	Rho GTPase activating protein 1	24.473
chr6	1.14E+08	113663020	-596	Tatdn2	TatD DNase domain containing 2	17.013
chr8	1.25E+08	124794280	78	BC048644	cDNA sequence BC048644	24.97
chr8	1.25E+08	124793711	120	Slc7a5	solute carrier family 7 (cationic amino acid	10.182
chr9	72330162	72331240	-106	Rfx7	regulatory factor X, 7	23.925
chr17	35505162	35505520	90	2310061I04Rik	RIKEN cDNA 2310061I04 gene	14.723
chr4	1.08E+08	107799670	-74	Zyg11b	zyg-ll family member B, cell cycle regulator	16.466
chr2	26732161	26733180	-19	Med22	mediator complex subunit 22	16.415
chr8	1.25E+08	125437881	38	Piezo1	piezo-type mechanosensitive ion channel	15.62
chr8	1.15E+08	114530020	-255	Zfp1	zinc finger protein 1	14.538
chr4	43402701	43403380	-42	Rusc2	RUN and SH3 domain containing 2	18.392
chr1	59857001	59857680	-212	Fam117b	family with sequence similarity 117, member	12.781
chr11	1.2E+08	119759560	-132	Baiap2	brain-specific angiogenesis inhibitor 1-	16.684
chr17	66010661	66011830	57	Wash1	WAS protein family homolog 1	22.235
chr10	1.16E+08	115986520	-419	Cnot2	CCR4-NOT transcription complex, subunit 2	16.654
chr4	43513881	43514900	-75	Ccdc107	coiled-coil domain containing 107	26.637
chr17	63548562	63549521	-402	Fer	fer (fms/fps related) protein kinase	20.895
chr19	5365881	5366900	-27	Banf1	barrier to autointegration factor 1	17.821
chr6	71561841	71563200	-94	Kdm3a	lysine (K)-specific demethylase 3A	16.107
chr3	95313561	95314580	11	Mllt11	myeloid/lymphoid or mixed-lineage leukemia	18.08
chr4	44189121	44189800	-77	Rnf38	ring finger protein 38	17.86
chr7	97207021	97208040	15	Kctd21	potassium channel tetramerisation domain	13.321
chr4	1.03E+08	102617651	-91	Mier1	mesoderm induction early response 1	13.395
chr1	93370461	93371501	10	Asb1	ankyrin repeat and SOCS box-containing 1	25.635
chr4	1.18E+08	117926620	85	Elovl1	elongation of very long chain fatty acids	20.755
chr5	1.37E+08	137315120	-142	Vgf	VGF nerve growth factor inducible	15.89
chr6	72887262	72888180	20	Tmsb10	thymosin, beta 10	15.559
chr6	87777121	87777800	-40	Rab43	RAB43, member RAS oncogene family	15.567
chr9	75226782	75227720	-182	Leo1	Leo1, Paf1/RNA polymerase II complex	17.336
chr19	9055901	9056631	-63	Ahnak	AHNAK nucleoprotein (desmoyokin)	20.329
chr7	1.01E+08	101222420	36	Arap1	ArfGAP with RhoGAP domain, ankyrin repeat	14.386
chr11	77853541	77854560	-86	Flot2	flotillin 2	16.059
chr15	57906081	57907440	-169	Zhx1	zinc fingers and homeoboxes 1	34.994
chr2	1.56E+08	156412580	110	4930405A21Rik	RIKEN cDNA 4930405A21 gene	16.159
chr7	44716962	44717381	-50	Tbc1d17	TBC1 domain family, member 17	18.709
chr7	44717392	44718181	45	Mir707	microRNA 707	16.948
chr15	1.02E+08	102075480	-257	Rarg	retinoic acid receptor, gamma	20.513
chr15	75443281	75444230	-184	Zfp41	zinc finger protein 41	14.756
chr17	27547821	27548840	-199	D17Wsu92e	DNA segment, Chr 17, Wayne State	10.858
chr2	1.81E+08	181294800	-102	Zgpat	zinc finger, CCCH-type with G patch domain	23.438
chr19	29317181	29318200	-110	Jak2	Janus kinase 2	18.473
chr18	32702561	32703490	19	Gypc	glycophorin C	13.975
chr1	1.52E+08	152155780	3	BC003331	cDNA sequence BC003331	15.888
chr11	93771661	93772670	181	Nme2	NME/NM23 nucleoside diphosphate kinase 2	20.08
chr10	62418901	62419920	-204	Hnrnph3	heterogeneous nuclear ribonucleoprotein H3	33.011
chr11	98009081	98009690	-2	Med1	mediator complex subunit 1	13.023
chr15	82071581	82072600	11	Cenpm	centromere protein M	18.883
chr6	72309841	72310480	-183	Vamp5	vesicle-associated membrane protein 5	10.343
chr17	27583592	27584540	-30	Uhrf1bp1	UHRF1 (ICBP90) binding protein 1	15.611
chr11	75467832	75468440	-209	Myo1c	myosin IC	22.294
chr1	1.33E+08	133356160	285	Fam72a	family with sequence similarity 72, member A	15.632
chr15	89142901	89143580	-162	Sbf1	SET binding factor 1	19.638
chr9	44631801	44633160	-211	Kmt2a	lysine (K)-specific methyltransferase 2A	22.416
chr10	77647161	77648520	-69	Trappc10	trafficking protein particle complex 10	17.979
chr10	1.21E+08	121030140	-84	Xpot	exportin, tRNA (nuclear export receptor for	25.893
chr19	38288761	38289780	6	Fra10ac1	FRA10AC1 homolog (human)	15.158
chr7	1.01E+08	100807280	-268	Arhgef17	Rho guanine nucleotide exchange factor	22.056
chr7	65987541	65988560	-415	Chsy1	chondroitin sulfate synthase 1	21.655
chr13	82188582	82189400	237	Mblac2	metallo-beta-lactamase domain containing 2	25.839
chr14	63606181	63607090	-6	Kif13b	kinesin family member 13B	10.58
chr12	71933121	71934670	533	3110056K07Rik	RIKEN cDNA 3110056K07 gene	28.952
chr19	8885561	8886711	203	Ttc9c	tetratricopeptide repeat domain 9C	31.687
chr4	11248901	11249740	-42	Dpy19l4	dpy-19-like 4 (C. elegans)	15.458
chr18	10610132	10610850	-141	Esco1	establishment of cohesion 1 homolog 1 (S.	15.357
chr18	11800412	11801400	21	Rbbp8	retinoblastoma binding protein 8	17.588
chr3	95904141	95904820	-122	Rprd2	regulation of nuclear pre-mRNA domain	15.34
chr15	27970142	27971120	-194	Trio	triple functional domain (PTPRF interacting)	14.625
chr17	28528381	28528821	-114	Brpf3	bromodomain and PHD finger containing, 3	13.295
chr3	1.17E+08	116800880	-30	Agl	amylo-1,6-glucosidase, 4-alpha-	28.179
chr9	1.1E+08	110377260	-493	Setd2	SET domain containing 2	17.52
chr9	55735861	55736540	52	Scaper	S phase cyclin A-associated protein in the ER	16.568
chr4	35414401	35415080	27	3110043O21Rik	RIKEN cDNA 3110043O21 gene	10.508
chr5	1.45E+08	145021991	-643	Trrap	transformation/transcription domain-	26.898
chr5	1.45E+08	145022820	92	Trrap	transformation/transcription domain-	16.633
chr4	32985202	32986460	99	Mdn1	midasin homolog (yeast)	29.327
chr16	8744801	8745621	-759	1810013L24Rik	RIKEN cDNA 1810013L24 gene	12.988
chr16	8745632	8746160	-74	1810013L24Rik	RIKEN cDNA 1810013L24 gene	17.119
chr12	70086581	70088230	-14	Lrr1	leucine rich repeat protein 1	33.346
chr10	74504052	74504540	-316	Bcr	breakpoint cluster region	20.246
chr1	54870561	54871580	-138	Ankrd44	ankyrin repeat domain 44	13.459
chr9	1.07E+08	106544390	-22	Tex264	testis expressed gene 264	15.48
chr7	16033381	16034060	-119	Dact3	dapper homolog 3, antagonist of beta-catenin	20.068
chr5	1.25E+08	125151960	-64	Zfp664	zinc finger protein 664	14.632
chr2	26210941	26211620	45	Sdccag3	serologically defined colon cancer antigen 3	17.729

chr11	1.02E+08	102112880	-62	Atxn7l3	ataxin 7-like 3	17.51
chr4	1.27E+08	126628910	58	Gm12942	predicted gene 12942	18.916
chr19	38108221	38109460	-119			23.565
chr9	1.01E+08	100887470	-264	Msl2	male-specific lethal 2 homolog (Drosophila)	12.776
chr10	80005562	80006420	-18	Adat3	adenosine deaminase, tRNA-specific 3	15.477
chr1	10218021	10218960	-606	Arfgef1	ADP-ribosylation factor guanine nucleotide-	15.257
chr5	34890121	34891140	59	Add1	adducin 1 (alpha)	15.392
chr16	96187122	96188020	-233	Brwd1	bromodomain and WD repeat domain	10.634
chr16	32563501	32564180	-550	Tnk2	tyrosine kinase, non-receptor, 2	15.566
chr15	76980761	76981440	-33	Rbfox2	RNA binding protein, fox-1 homolog (C.	16.149
chr17	55937392	55938500	-76	Uhrf1	ubiquitin-like, containing PHD and RING	29.478
chr1	92883241	92884260	-100			14.182
chr8	72902801	72904080	-68	Gatad2a	GATA zinc finger domain containing 2A	20.067
chr10	61881701	61883060	-218	Vps26a	vacuolar protein sorting 26 homolog A (yeast)	24.605
chr16	36747541	36748220	241	Iqcb1	IQ calmodulin-binding motif containing 1	18.105
chr10	1.26E+08	126382121	-245	Ctdsp2	CTD (carboxy-terminal domain, RNA	41.229
chr11	1.17E+08	117082740	-106	Sept9	septin 9	14.805
chr15	99703301	99704250	-285	Lima1	LIM domain and actin binding 1	18.884
chr18	65012421	65013281	-274	Nedd4l	neural precursor cell expressed,	20.267
chr4	1.26E+08	126470820	-83	Zmym4	zinc finger, MYM-type 4	20.502
chr5	1.01E+08	100739431	-141	Lin54	lin-54 homolog (C. elegans)	17.59
chr5	1.49E+08	149495620	31	Uspl1	ubiquitin specific peptidase like 1	14.591
chr8	1.13E+08	112758280	38	Phlpp2	PH domain and leucine rich repeat protein	15.553
chr8	1.3E+08	129950340	-466	Pard3	par-3 family cell polarity regulator	19.464
chr9	98795212	98796410	86	Faim	Fas apoptotic inhibitory molecule	14.486
chr4	1.37E+08	137489540	183	Hp1bp3	heterochromatin protein 1, binding protein 3	15.778
chr17	3282701	3283561	76	Tiam2	T cell lymphoma invasion and metastasis 2	18.105
chr1	1.82E+08	182093460	25	Psen2	presenilin 2	22.23
chr7	24612601	24613550	-31	Arhgef1	Rho guanine nucleotide exchange factor	14.021
chr11	96645062	96646360	-119	Nfe2l1	nuclear factor, erythroid derived 2,-like 1	26.654
chr11	96640581	96641260	-703	Nfe2l1	nuclear factor, erythroid derived 2,-like 1	11.13
chr11	6525652	6526640	-76	Tbrg4	transforming growth factor beta regulated	12.483
chr19	45071172	45071721	0	Lzts2	leucine zipper, putative tumor suppressor 2	19.845
chr9	1.03E+08	103224570	-241	Cdv3	carnitine deficiency-associated gene	12.846
chr16	45929241	45930260	0	Plcxd2	phosphatidylinositol-specific phospholipase C,	12.274
chr12	1.11E+08	110894740	-645	Ppp2r5c	protein phosphatase 2, regulatory subunit B',	14.074
chr14	69086032	69086930	23	Slc39a14	solute carrier family 39 (zinc transporter),	13.266
chr10	1.28E+08	127635561	89	Timeless	timeless circadian clock 1	17.076
chrX	19819382	19820300	-14	Uba1	ubiquitin-like modifier activating enzyme 1	14.479
chr2	1.56E+08	155699940	34	Ergic3	ERGIC and golgi 3	18.928
chr4	1.17E+08	116750560	167	Tmem53	transmembrane protein 53	28.244
chr2	28354981	28356000	17	Ralgds	ral guanine nucleotide dissociation stimulator	15.684
chr4	1.4E+08	140333530	-300	Crocc	ciliary rootlet coiled-coil, rootletin	18.303
chr17	45624261	45624940	-13	Gtpbp2	GTP binding protein 2	16.353
chr7	1.01E+08	100983400	-142	Fchsd2	FCH and double SH3 domains 2	18.542
chr9	77330272	77330960	-71	Lrrc1	leucine rich repeat containing 1	21.581
chr4	1.51E+08	151029700	-744	Acot7	acyl-CoA thioesterase 7	23.08
chr17	74220981	74221660	56	Dpy30	dpy-30 homolog (C. elegans)	14.859
chr7	45788821	45789500	-269	Emp3	epithelial membrane protein 3	12.193
chr17	35474232	35474240	55	Ppp1r18	protein phosphatase 1, regulatory subunit 18	7
chr17	35472881	35474221	-97	Ppp1r18	protein phosphatase 1, regulatory subunit 18	17.881
chr11	1.2E+08	120284180	11	Hgs	HGF-regulated tyrosine kinase substrate	13.735
chr16	32796892	32797760	-205	Fyttd1	forty-two-three domain containing 1	28.381
chr11	68915362	68916300	-522	Per1	period circadian clock 1	19.865
chr11	53612902	53614260	144	Irf1	interferon regulatory factor 1	18.266
chr1	1.74E+08	173963670	-244	Pex19	peroxisomal biogenesis factor 19	12.125
chr16	94479362	94480560	-148	Pigp	phosphatidylinositol glycan anchor	38.414
chr4	1.54E+08	154408280	-15	Nadk	NAD kinase	15.079
chr1	57914582	57914920	-121	Kctd18	potassium channel tetramerisation domain	13.654
chr12	1.09E+08	108723840	-106	Ccdc85c	coiled-coil domain containing 85C	18.398
chr5	1.15E+08	114641880	-36	Kctd10	potassium channel tetramerisation domain	17.015
chr4	1.54E+08	154335501	10	Gnb1	guanine nucleotide binding protein (G	16.955
chr12	99147422	99148311	-152	Zc3h14	zinc finger CCCH type containing 14	13.367
chr8	1.08E+08	108060160	17	Cbfb	core binding factor beta	14.672
chr8	49608381	49609400	60	Dctd	dCMP deaminase	14.713
chr1	1.8E+08	180365240	-804	Kif26b	kinesin family member 26B	12.105
chr6	83472041	83473310	-48	Dguok	deoxyguanosine kinase	18.332
chr17	74243421	74244361	-78	Spast	spastin	17.67
chr11	1.16E+08	116123260	-43	Exoc7	exocyst complex component 7	18.999
chr15	8115801	8116820	-11	2410089E03Rik	RIKEN cDNA 2410089E03 gene	16.304
chr13	93945061	93945950	-35	Mtx3	metaxin 3	16.519
chr19	4509842	4511240	69	Pcx	pyruvate carboxylase	18.092
chr7	1.02E+08	101808240	-288	Lrrc51	leucine rich repeat containing 51	16.197
chr3	79653161	79654180	-64	Fnip2	folliculin interacting protein 2	18.616
chr9	1.04E+08	104121940	-6	Dnajc13	DnaJ (Hsp40) homolog, subfamily C, member	20.831
chr4	1.26E+08	125599400	34	Lsm10	U7 snRNP-specific Sm-like protein LSM10	20.73
chr4	45033001	45033930	47	Zbtb5	zinc finger and BTB domain containing 5	16.036
chr11	97515702	97516080	-153	Pcgf2	polycomb group ring finger 2	19.071
chr3	1.05E+08	105181380	43	Cttnbp2nl	CTTNBP2 N-terminal like	28.378
chr4	41948602	41949500	97	Il11ra1	interleukin 11 receptor, alpha chain 1	11.043
chr3	1.05E+08	104947120	8	Mov10	Moloney leukemia virus 10	22.511
chr2	1.55E+08	155384080	85	Trpc4ap	transient receptor potential cation channel,	15.579
chr2	1.51E+08	150601640	95	Gins1	GINS complex subunit 1 (Psf1 homolog)	17.388
chr15	34387601	34388620	-245	Rpl30	ribosomal protein L30	20.069
chr15	76033202	76035560	-805	Plec	plectin	31.37
chr8	69788942	69789610	70	Naf1	nuclear assembly factor 1 homolog (S.	14.394
chr3	1.09E+08	109156320	-348	Fam102b	family with sequence similarity 102, member	18.604
chr8	67875662	67876580	-53	Tmem192	transmembrane protein 192	25.541
chr17	35124721	35125740	61	Cchcr1	coiled-coil alpha-helical rod protein 1	22.223
chr4	1.34E+08	133560160	-152	Pdik1l	PDLIM1 interacting kinase 1 like	29.913

chr17	23932601	23933620	52	Tbc1d24	TBC1 domain family, member 24	18.794
chr19	5963601	5964960	-74	Pola2	polymerase (DNA directed), alpha 2	18.913
chr14	69178101	69179120	20	Mir320	microRNA 320	18.063
chr10	79836421	79837100	22	Tcf3	transcription factor 3	20.792
chr7	3295621	3296591	506	Mboat7	membrane bound O-acyltransferase domain	19.825
chr11	61578081	61579020	-267	Prpsap2	phosphoribosyl pyrophosphate synthetase-	27.676
chr2	1.2E+08	119589220	41	Mga	MAX gene associated	17.697
chr19	44122481	44123500	7	Erlin1	ER lipid raft associated 1	23.731
chr6	54524242	54525120	-8	Plekha8	pleckstrin homology domain containing, family	12.017
chr8	87578902	87579920	59	Trmt1	tRNA methyltransferase 1	16.476
chr19	41986601	41987250	142	Zdhhc16	zinc finger, DHHC domain containing 16	13.75
chr11	82686981	82687660	85	Rffl	ring finger and FYVE like domain containing	13.903
chr16	17532441	17533460	33	Smpd4	sphingomyelin phosphodiesterase 4	32.529
chr19	6046561	6047580	-75	Syvn1	synovial apoptosis inhibitor 1, synoviolin	18.764
chr9	1.11E+08	110963141	-271	Lrrfip2	leucine rich repeat (in FLII) interacting protein	16.24
chr17	35587121	35588820	-38	Gnl1	guanine nucleotide binding protein-like 1	24.832
chr3	96781681	96782071	96	Pias3	protein inhibitor of activated STAT 3	16.231
chr3	90137741	90139100	-18	Ubap2l	ubiquitin-associated protein 2-like	15.676
chr2	28662001	28663271	221	Ddx31	DEAD/H (Asp-Glu-Ala-Asp/His) box	21.677
chr19	6976461	6977140	58	Trmt112	tRNA methyltransferase 11-2	20.828
chrX	44867761	44868440	-105	Slc25a14	solute carrier family 25 (mitochondrial carrier,	13.566
chr11	1.16E+08	116441160	-138	Rhbdf2	rhomboid 5 homolog 2 (Drosophila)	25.719
chr6	89560761	89561780	23	Chchd6	coiled-coil-helix-coiled-coil-helix domain	21.936
chr19	3906601	3907521	72	Tcirg1	T cell, immune regulator 1, ATPase, H+	16.783
chr3	38676021	38677040	-165	Ankrd50	ankyrin repeat domain 50	15.578
chr4	1.3E+08	129677481	-70	Tinagl1	tubulointerstitial nephritis antigen-like 1	16.722
chr7	98236201	98237070	-115	Tsku	tsukushi, small leucine rich proteoglycan	14.921
chr6	87637381	87638280	-21	Aplf	aprataxin and PNKP like factor	17.334
chr5	3808122	3809951	94	Ankib1	ankyrin repeat and IBR domain containing 1	20.829
chr15	99220161	99221180	-311	Tmbim6	transmembrane BAX inhibitor motif containing	20.358
chr7	1.41E+08	141020780	-14	Rnh1	ribonuclease/angiogenin inhibitor 1	31.154
chr11	98775441	98776120	-781	Rara	retinoic acid receptor, alpha	13.027
chr19	7008421	7009440	25	Bad	BCL2-associated agonist of cell death	30.494
chr19	46357641	46358421	-17	Nfkb2	nuclear factor of kappa light polypeptide gene	14.705
chr18	83048401	83049760	20	Zfp516	zinc finger protein 516	13.263
chr3	27344892	27345520	107	1700125G22Rik	RIKEN cDNA 1700125G22 gene	26.745
chr13	23628641	23629660	-561	Hist1h2be	histone cluster 1, H2be	18.644
chr15	97595301	97596320	-110	Rapgef3	Rap guanine nucleotide exchange factor	20.579
chr11	1.21E+08	120600720	18	Gps1	G protein pathway suppressor 1	16.305
chr19	7053981	7055290	60	Vegfb	vascular endothelial growth factor B	17.613
chr11	6446401	6447420	20	Ccm2	cerebral cavernous malformation 2	23.132
chr11	4964681	4966170	-95	Gas2l1	growth arrest-specific 2 like 1	35.243
chr17	24915541	24916220	-120	Unkl	unkempt-like (Drosophila)	29.583
chr17	35308432	35309290	-218	Ddr1	discoidin domain receptor family, member 1	15.477
chr8	1.15E+08	114619440	-242	Bcar1	breast cancer anti-estrogen resistance 1	35.087
chr12	1.03E+08	102870680	37	Golga5	golgi autoantigen, golgin subfamily a, 5	15.33
chr14	54514241	54514920	-414	Dcaf11	DDB1 and CUL4 associated factor 11	19.845
chr9	21070821	21071500	39	Slc44a2	solute carrier family 44, member 2	17.214
chr11	1E+08	100344540	60	Acly	ATP citrate lyase	24.465
chr9	20702941	20703620	101	Dnmt1	DNA methyltransferase (cytosine-5) 1	15.9
chr5	1.23E+08	123040560	-193	Camkk2	calcium/calmodulin-dependent protein kinase	14.158
chr17	28077881	28078900	4	Tead3	TEA domain family member 3	18.542
chr2	29888041	29888720	-103	Set	SET nuclear oncogene	14.001
chr12	4241161	4241840	-159	Ptrhd1	peptidyl-tRNA hydrolase domain containing 1	15.085
chr17	33732761	33733780	-16	H2-DMa	histocompatibility 2, class II, locus DMa	22.917
chr3	1.09E+08	108573771	-91	Sars	seryl-aminoacyl-tRNA synthetase	21.348
chr12	86487841	86488770	97	Jdp2	Jun dimerization protein 2	14.553
chr12	73003441	73004800	-223	L3hypdh	L-3-hydroxyproline dehydratase (trans-)	17.283
chr11	1.16E+08	115927080	-251	Trim47	tripartite motif-containing 47	26.42
chr5	1.26E+08	125630340	73	Scarb1	scavenger receptor class B, member 1	17.286
chr4	1.39E+08	138847160	24	Iffo2	intermediate filament family orphan 2	14.358
chr3	84565821	84566001	455	Fhdc1	FH2 domain containing 1	8.278
chr12	81708852	81709820	-44	Susd6	sushi domain containing 6	15.043
chr6	17257062	17258400	91	Cav1	caveolin 1, caveolae protein	17.014
chr5	34686461	34686980	-70	Fam193a	family with sequence similarity 193, member	15.141
chr9	1.07E+08	107410080	-60	Rassf1	Ras association (RalGDS/AF-6) domain	20.732
chr15	97791821	97792840	67	Tmem106c	transmembrane protein 106C	17.382
chr11	33063002	33063300	55	Npm1	nucleophosmin 1	14.906
chr11	53362682	53363680	22	Sept8	septin 8	16.196
chr17	56095672	56097280	-547	Ptprs	protein tyrosine phosphatase, receptor type, S	33.022
chr17	34849972	34850680	528	Ddx39b	DEAD (Asp-Glu-Ala-Asp) box polypeptide	18.688
chr11	20641061	20642000	29	Aftph	aftiphilin	13.905
chr7	90004801	90005820	-114	Picalm	phosphatidylinositol binding clathrin assembly	12.526
chrX	7056132	7056700	121			17.699
chr2	1.65E+08	164979420	12	Slc35c2	solute carrier family 35, member C2	17.239
chr4	43061001	43062020	-109	Fam214b	family with sequence similarity 214, member	22.691
chr10	1.28E+08	128151780	36	Pym1	PYM homolog 1, exon junction complex	23.01
chr15	79229521	79230880	-26	Tmem184b	transmembrane protein 184b	28.88
chr5	1.08E+08	107678680	41	Btbd8	BTB (POZ) domain containing 8	18.779
chr5	1.47E+08	146526060	141	Rnf6	ring finger protein (C3H2C3 type) 6	11.584
chr4	1.55E+08	154513890	-391	Mib2	mindbomb homolog 2 (Drosophila)	15.955
chr5	1.39E+08	139454400	-463	Sun1	Sad1 and UNC84 domain containing 1	19.074
chr5	23961382	23962180	-461	Agap3	ArfGAP with GTPase domain, ankyrin repeat	19.425
chr11	58146801	58147480	155			15.05
chr7	1.21E+08	120635060	-63	Eef2k	eukaryotic elongation factor-2 kinase	12.297
chr11	58980302	58980480	-451	Iba57	IBA57, iron-sulfur cluster assembly homolog	14.343
chr6	72478212	72479500	74	Capg	capping protein (actin filament), gelsolin-like	24.828
chr13	49664382	49665430	-109	Nol8	nucleolar protein 8	16.665
chr2	93263022	93263700	-20	Cd82	CD82 antigen	13.177
chr9	95667332	95668180	-522	1700065D16Rik	RIKEN cDNA 1700065D16 gene	19.669

chr9	95667161	95667321	-7	1700065D16Rik	RIKEN cDNA 1700065D16 gene	10.812
chr16	4878442	4880020	327	Anks3	ankyrin repeat and sterile alpha motif domain	17.613
chr19	10271061	10272080	323	Tmem258	transmembrane protein 258	18.845
chr3	90164941	90165751	-102	Tpm3	tropomyosin 3, gamma	13.753
chr15	76483792	76484700	-90	Cyhr1	cysteine and histidine rich 1	16.472
chr2	25804992	25805961	-185	Camsap1	calmodulin regulated spectrin-associated	20.706
chr13	49432632	49433590	-49	Ippk	inositol 1,3,4,5,6-pentakisphosphate 2-kinase	14.147
chr4	62005801	62006820	-40	Alad	aminolevulinate, delta-, dehydratase	48.675
chr15	64141681	64142970	21	Asap1	ArfGAP with SH3 domain, ankyrin repeat and	23.153
chr9	21118081	21119451	-168	Ilf3	interleukin enhancer binding factor 3	29.38
chr19	10622621	10623300	-152	Tmem216	transmembrane protein 216	15.57
chr4	1.41E+08	141065771	-172	Casp9	caspase 9	13.568
chr7	18430041	18431580	-434	Vasp	vasodilator-stimulated phosphoprotein	19.882
chr3	1.45E+08	144658230	66	Sh3glb1	SH3-domain GRB2-like B1 (endophilin)	20.744
chr3	68581401	68582420	-200	Schip1	schwannomin interacting protein 1	15.618
chr6	1.13E+08	113273040	-214	Brpf1	bromodomain and PHD finger containing, 1	14.779
chr4	1.07E+08	107378120	-77	Magoh	mago homolog, exon junction complex core	29.936
chr4	1.49E+08	148582040	-16	Tmem201	transmembrane protein 201	18.292
chr8	48115441	48116800	12	Casp3	caspase 3	33.473
chr2	1.28E+08	127819260	-96	Bcl2l11	BCL2-like 11 (apoptosis facilitator)	12.227
chr7	1.43E+08	143358620	-62	Nap1l4	nucleosome assembly protein 1-like 4	13.648
chr5	96402112	96403560	-544	Cnot6l	CCR4-NOT transcription complex, subunit 6-	13.472
chr4	1.27E+08	126579960	-161	Zmym6	zinc finger, MYM-type 6	26.475
chr14	66668272	66669061	274	Cdca2	cell division cycle associated 2	15.854
chr7	1.34E+08	133615580	6	Fank1	fibronectin type 3 and ankyrin repeat domains	11.32
chr17	27636221	27637580	5	Anks1	ankyrin repeat and SAM domain containing 1	27.664
chr3	1.52E+08	152333940	211	Zzz3	zinc finger, ZZ domain containing 3	23.194
chr10	79329481	79330160	-352	Arid3a	AT rich interactive domain 3A (BRIGHT-like)	15.308
chr15	38245241	38246940	-790	Klf10	Kruppel-like factor 10	28.416
chr2	1.8E+08	179972880	315	Ss18l1	synovial sarcoma translocation gene on	16.429
chr3	1.32E+08	131502720	356	Papss1	3'-phosphoadenosine 5'-phosphosulfate	15.432
chr17	47875061	47876080	3	Oard1	O-acyl-ADP-ribose deacylase 1	20.613
chr5	64508892	64509900	-96	Tbc1d1	TBC1 domain family, member 1	14.534
chr16	13816302	13816920	112	Pdxdc1	pyridoxal-dependent decarboxylase domain	13.612
chr16	13816241	13816291	457	Pdxdc1	pyridoxal-dependent decarboxylase domain	8.2
chr3	87854492	87855320	-26	Pear1	platelet endothelial aggregation receptor 1	14.447
chr6	42278661	42279891	-159	Zyx	zyxin	20.935
chr2	1.81E+08	180640011	80	Gid8	GID complex subunit 8 homolog (S.	15.564
chr15	1.02E+08	102032820	-385	Zfp740	zinc finger protein 740	20.238
chr2	30180782	30181760	54	Sh3glb2	SH3-domain GRB2-like endophilin B2	13.725
chr3	1.08E+08	108215200	32	Ampd2	adenosine monophosphate deaminase 2	28.296
chr2	1.53E+08	152522640	37	Bcl2l1	BCL2-like 1	14.643
chr16	17979541	17980510	59	Dgcr6	DiGeorge syndrome critical region gene 6	17.599
chr17	80635761	80636780	81	Map4k3	mitogen-activated protein kinase kinase	18.512
chr7	25327622	25328300	-213	Atp5sl	ATP5S-like	17.354
chr11	4999361	5000720	-128	Rhbdd3	rhomboid domain containing 3	31.194
chr2	29946181	29946860	100	Zer1	zyg-11 related, cell cycle regulator	15.761
chr2	31394241	31394920	-80	Fubp3	far upstream element (FUSE) binding protein	13.158
chr3	37611141	37611541	-158			19.175
chr11	69812912	69814070	-166	Phf23	PHD finger protein 23	15.563
chr7	1.02E+08	102084230	52	Nup98	nucleoporin 98	22.578
chr3	1.05E+08	104917200	-289	Rhoc	ras homolog gene family, member C	16.759
chr8	35575962	35576920	-110	Dctn6	dynactin 6	11.57
chr8	64483041	64483940	-179	Palld	palladin, cytoskeletal associated protein	16.2
chr5	31165421	31166100	-155	Agbl5	ATP/GTP binding protein-like 5	14.923
chr4	1.09E+08	109165160	38	Cdkn2c	cyclin-dependent kinase inhibitor 2C (p18,	20.563
chr10	1.23E+08	122600940	-167			22.889
chr11	62946921	62947341	-521	Pmp22	peripheral myelin protein 22	15
chr11	62947352	62948280	164			17.328
chr8	94023601	94024590	37			19.642
chr4	1.55E+08	154836570	357	B3galt6	UDP-Gal:betaGal beta 1,3-	15.401
chr5	1.37E+08	136530640	-544			18.763
chr18	21144261	21145280	-197			18.686
chr18	46866281	46867980	-77	Ap3s1	adaptor-related protein complex 3, sigma 1	18.426
chr17	55671652	55672620	-788			14.9
chr15	79174441	79175460	175	Maff	v-maf musculoaponeurotic fibrosarcoma	20.046
chr17	45018721	45019820	-11	Nfkbie	nuclear factor of kappa light polypeptide gene	23.807
chr10	79552342	79552860	-210			21.909
chr18	38060961	38061640	97			14.567
chr5	1.22E+08	122098171	-310			32.455
chr12	52298461	52299480	-163			16.508
chr12	59979061	59979740	84			11.308
chr8	86498572	86498720	-7			10.446
chr14	29957741	29958660	-261			15.081
chr5	23540581	23541260	-165	Fam126a	family with sequence similarity 126, member	15.227
chr5	33591661	33592340	-139	Ctbp1	C-terminal binding protein 1	14.878
chr1	51422621	51423300	-16			17.591
chr3	88227621	88228881	-48			23.325
chr14	60510481	60511500	6	Spryd7	SPRY domain containing 7	19.557
chr1	74439282	74439600	174	Rqcd1	rcd1 (required for cell differentiation) homolog	18.726
chr5	94167761	94168780	-350	Sept11	septin 11	14.825
chr16	32833461	32834111	-61			17.892
chr3	89998942	89999360	-28	Il6ra	interleukin 6 receptor, alpha	17.316
chr5	1.25E+08	124707240	549			37.135
chr4	1.17E+08	116788300	-573			12.124
chr9	20394122	20394900	658	Fbxl12	F-box and leucine-rich repeat protein 12	14.722
chr9	1.19E+08	119251190	-161			13.818
chr4	69896521	69897051	10			28.057
chr11	1.2E+08	120166331	648	0610009L18Rik	RIKEN cDNA 0610009L18 gene	29.12
chr11	78159242	78160220	41	Unc119	unc-119 homolog (C. elegans)	12.828

chr5	1.15E+08	115380910	50	Acads	acyl-Coenzyme A dehydrogenase, short chain	36.834
chr2	48635641	48636320	-138	Acvr2a	activin receptor IIA	19.966
chr4	86140892	86141720	-16	Plin2	perilipin 2	20.797
chr3	1.38E+08	138380340	-480	Adh5	alcohol dehydrogenase 5 (class III), chi	20.723
chr11	62064621	62065640	-49	Adora2b	adenosine A2b receptor	37.302
chr1	1.82E+08	182406260	100	Parp1	poly (ADP-ribose) polymerase family, member	13.354
chr1	1.8E+08	179633560	-36	Adss	adenylosuccinate synthetase, non muscle	24.638
chr7	1.27E+08	126590840	-309	Aldoa	aldolase A, fructose-bisphosphate	8.488
chr7	1.27E+08	126590571	10	Aldoa	aldolase A, fructose-bisphosphate	15.194
chr11	4886481	4887021	-76	Ap1b1	adaptor protein complex AP-1, beta 1 subunit	16.944
chr5	1.37E+08	137331100	97	Ap1s1	adaptor protein complex AP-1, sigma 1	14.545
chr10	80144801	80146160	-140	Ap3d1	adaptor-related protein complex 3, delta 1	26.411
chr14	25471101	25471780	59	Arf4	ADP-ribosylation factor 4	17.113
chr5	1E+08	100219991	-256	Hnrnpd	heterogeneous nuclear ribonucleoprotein D	24.524
chr16	87587741	87588420	-70	Bach1	BTB and CNC homology 1	13.844
chr7	25367401	25368400	-13	Exosc5	exosome component 5	18.171
chr1	59707741	59708420	-745	Bmpr2	bone morphogenetic protein receptor, type II	15.029
chr10	96046261	96046741	-188	Btg1	B cell translocation gene 1, anti-proliferative	23.917
chr15	98462301	98463320	9	Cacnb3	calcium channel, voltage-dependent, beta 3	17.087
chr8	87736321	87737680	36	Calr	calreticulin	21.826
chr7	37816161	37816840	-250	Ccne1	cyclin E1	16.113
chr17	23978592	23979520	-47	Ccnf	cyclin F	22.023
chr10	1.16E+08	116468020	23	Cct2	chaperonin containing Tcp1, subunit 2 (beta)	17.034
chr10	1.28E+08	128313280	-45	Cd63	CD63 antigen	16.214
chr9	1.1E+08	109733640	21	Cdc25a	cell division cycle 25A	15.647
chr17	28820781	28821800	-143	Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	16.056
chr7	1.21E+08	120773780	21	Cdr2	cerebellar degeneration-related 2	13.923
chr17	15409192	15409971	-76	Chd1	chromodomain helicase DNA binding protein	22.525
chr9	57563582	57564380	16	Clk3	CDC-like kinase 3	16.095
chr2	30237901	30238061	-78	Ppp2r4	protein phosphatase 2A activator, regulatory	8
chr2	30238072	30238850	402	Ppp2r4	protein phosphatase 2A activator, regulatory	13.639
chr13	42062421	42063440	-63	Hivep1	human immunodeficiency virus type I	16.547
chr9	57443341	57444101	69	Csk	c-src tyrosine kinase	38.882
chr10	1.1E+08	110324770	39	Csrp2	cysteine and glycine-rich protein 2	15.688
chr14	62076222	62076860	-31	Ctsb	cathepsin B	10.006
chr11	69816282	69817300	-30	Dvl2	dishevelled 2, dsh homolog (Drosophila)	25.04
chr3	14554832	14555740	-129	E2f5	E2F transcription factor 5	17.619
chr10	80579321	80580000	-100	Eef2	eukaryotic translation elongation factor 2	15.996
chr18	34986242	34987020	-550	Egr1	early growth response 1	14.314
chr8	28725921	28726600	-3	Eif4ebp1	eukaryotic translation initiation factor 4E	17.066
chr1	1.34E+08	133835271	95	Elk4	ELK4, member of ETS oncogene family	9.4
chr8	73467492	73468291	-773	Ell	elongation factor RNA polymerase II	15.181
chr8	73468302	73468900	-63	Ell	elongation factor RNA polymerase II	23.109
chr19	7408261	7409620	-36	Mark2	MAP/microtubule affinity regulating kinase 2	22.059
chr7	18540002	18541220	50	Ercc2	excision repair cross-complementing rodent	27.766
chr19	6988361	6989380	-18	Esrra	estrogen related receptor, alpha	17.833
chr8	47969302	47969920	-243	Acsl1	acyl-CoA synthetase long-chain family	16.814
chr19	34355981	34357221	-55	Fas	Fas (TNF receptor superfamily member 6)	19.613
chr5	31496921	31497740	-204	Ppm1g	protein phosphatase 1G (formerly 2C),	23.232
chr17	35430612	35431740	-234	Flot1	flotillin 1	15.523
chr7	18468461	18469120	-223	Fosb	FBJ osteosarcoma oncogene B	14.882
chr1	59426221	59427070	-48	Fzd7	frizzled homolog 7 (Drosophila)	14.751
chr19	8964592	8965460	-76	Ganab	alpha glucosidase 2 alpha neutral subunit	13.111
chr5	1.3E+08	130040140	17	Gbas	glioblastoma amplified sequence	18.498
chr14	46111141	46111820	-201	Gch1	GTP cyclohydrolase 1	16.975
chr19	16199142	16200240	-159	Gnaq	guanine nucleotide binding protein, alpha q	14.066
chr11	48643352	48643800	-207	Gnb2l1	guanine nucleotide binding protein (G	16.877
chr5	1.1E+08	110417380	37	Golga3	golgi autoantigen, golgin subfamily a, 3	19.985
chr7	46663301	46664320	113	Hps5	Hermansky-Pudlak syndrome 5 homolog	21.776
chr8	98323581	98324260	78	Cfap20	cilia and flagella associated protein 20	26.404
chr6	1.13E+08	113012600	-14	Thumpd3	THUMP domain containing 3	19.29
chr11	59007872	59008700	-139	Guk1	guanylate kinase 1	27.304
chrX	70219521	70220540	-953	Hcfc1	host cell factor C1	12.852
chr3	1.17E+08	116655290	36	Hiat1	hippocampus abundant gene transcript 1	22.906
chr17	45036401	45037760	-238	Hsp90ab1	heat shock protein 90 alpha (cytosolic), class	18.279
chr1	55032192	55032951	-94	Hspd1	heat shock protein 1 (chaperonin)	16.489
chr9	20781481	20782840	-280	Icam5	intercellular adhesion molecule 5,	17.472
chr4	1.35E+08	135416220	-172	Id3	inhibitor of DNA binding 3	20.483
chr5	1.09E+08	108900980	7	Idua	iduronidase, alpha-L-	11.015
chr19	34706521	34707200	-26	Ifit1	interferon-induced protein with	13.155
chr15	1.02E+08	101971991	-674	Igfbp6	insulin-like growth factor binding protein 6	19.449
chr15	1.02E+08	101972120	-159	Igfbp6	insulin-like growth factor binding protein 6	9.432
chr8	85298022	85298810	-83	Il15	interleukin 15	13.129
chr6	94666092	94666880	-878	Lrig1	leucine-rich repeats and immunoglobulin-like	34.977
chr6	94665412	94666081	-138	Lrig1	leucine-rich repeats and immunoglobulin-like	28.511
chr11	97004381	97005060	-738	Kpnb1	karyopherin (importin) beta 1	21.901
chr2	71587341	71588020	-98	Itga6	integrin alpha 6	15.364
chr12	21532541	21532951	-19	Itgb1bp1	integrin beta 1 binding protein 1	14.098
chr9	36516681	36517660	79	Stt3a	STT3, subunit of the	17.092
chr5	65081862	65082800	-327	Klf3	Kruppel-like factor 3 (basic)	15.748
chr4	1.29E+08	129175520	61	Kpna6	karyopherin (importin) alpha 6	27.689
chr11	60514901	60515920	-475	Llgl1	lethal giant larvae homolog 1 (Drosophila)	14.164
chr10	1.27E+08	127025360	-799	Lrp1	low density lipoprotein receptor-related	22.103
chr10	1.27E+08	127024421	11	Lrp1	low density lipoprotein receptor-related	20.852
chr15	10926241	10926920	99	Amacr	alpha-methylacyl-CoA racemase	16.265
chr9	63820041	63820741	-326	Smad6	SMAD family member 6	17.857
chr12	77881081	77882050	-477	Max	Max protein	15.83
chr10	75375961	75376640	-82	Mmp11	matrix metallopeptidase 11	20.177
chr8	97061161	97062180	-77	Mt2	metallothionein 2	22.487
chr4	1.16E+08	115962780	-348	Mast2	microtubule associated serine/threonine	22.119

chr1	9685241	9686260	-327	Mybl1	myeloblastosis oncogene-like 1	21.581
chr11	75467421	75467821	-83	Myo1c	myosin IC	15.55
chr10	1.27E+08	127070240	-172	1700012D01Rik	RIKEN cDNA 1700012D01 gene	20.007
chr2	1.66E+08	165684250	-46	Ncoa3	nuclear receptor coactivator 3	27.93
chr15	66799002	66800140	-261	Ndrg1	N-myc downstream regulated gene 1	51.907
chr4	81977342	81978261	-791	Nfib	nuclear factor I/B	22.254
chr4	81977061	81977331	-186	Nfib	nuclear factor I/B	15.852
chr1	39844941	39845960	-9	Map4k4	mitogen-activated protein kinase kinase	12.505
chr2	3200502	3202120	-173	Nmt2	N-myristoyltransferase 2	34.064
chr13	1.21E+08	120528640	-76	Nnt	nicotinamide nucleotide transhydrogenase	20.157
chr15	1E+08	100251680	-37	Gm5475	predicted gene 5475	15.444
chr11	76214922	76215760	-5	Nxn	nucleoredoxin	27.257
chr10	80229461	80229911	-99	Oaz1	ornithine decarboxylase antizyme 1	16.711
chr15	36553401	36554420	-348	Pabpc1	poly(A) binding protein, cytoplasmic 1	21.971
chr5	1.38E+08	137841710	-74	Pcolce	procollagen C-endopeptidase enhancer	17.551
chr5	1.39E+08	139249040	-66	Pdgfa	platelet derived growth factor, alpha	17.449
chr19	4099381	4100740	62	Pitpnm1	phosphatidylinositol transfer protein,	19.167
chr8	86862521	86863200	-223	Prkaca	protein kinase, cAMP dependent, catalytic,	17.027
chrX	70580962	70582180	-215	Plxna3	plexin A3	24.24
chr19	7041061	7042430	-347	Ppp1r14b	protein phosphatase 1, regulatory (inhibitor)	31.92
chr5	1.36E+08	135974160	-261	Por	P450 (cytochrome) oxidoreductase	19.854
chr4	1.22E+08	122338851	-44	Ppt1	palmitoyl-protein thioesterase 1	31.726
chr11	97096402	97097041	-55	Npepps	aminopeptidase puromycin sensitive	15.948
chr19	32822241	32822920	-994	Pten	phosphatase and tensin homolog	16.056
chr15	5191461	5192430	-543	Ptger4	prostaglandin E receptor 4 (subtype EP4)	25.363
chr1	1.91E+08	191428591	-785	Ptpn14	protein tyrosine phosphatase, non-receptor	12.925
chr18	67849381	67850660	-30	Ptpn2	protein tyrosine phosphatase, non-receptor	22.46
chr7	18907741	18908760	-155	Pvrl2	poliovirus receptor-related 2	40.769
chr5	1.11E+08	110526860	-50	Pxmp2	peroxisomal membrane protein 2	16.306
chr18	34748472	34750040	-169	Kif20a	kinesin family member 20A	24.221
chr11	98752602	98753981	-495	Rara	retinoic acid receptor, alpha	22.606
chr19	5637201	5637661	-59	Rela	v-rel reticuloendotheliosis viral oncogene	15.696
chr13	21187101	21187811	60	Trim27	tripartite motif-containing 27	21.817
chr13	34009861	34010540	59	Serpinb6a	serine (or cysteine) peptidase inhibitor, clade	19.417
chr2	32783141	32784160	-71	Rpl12	ribosomal protein L12	14.682
chr5	1.47E+08	147388300	95	Polr1d	polymerase (RNA) I polypeptide D	16.606
chr10	79694981	79696000	-70	Rps15	ribosomal protein S15	15.673
chr10	61075221	61076240	52	Sar1a	SAR1 gene homolog A (S. cerevisiae)	18.218
chr11	65604202	65604980	-99	Map2k4	mitogen-activated protein kinase kinase 4	19.242
chr10	60542622	60543460	-19	Sgpl1	sphingosine phosphate lyase 1	21.401
chr7	1.02E+08	101537940	-159	Clpb	ClpB caseinolytic peptidase B	17.992
chr18	58002981	58004151	-481	Slc12a2	solute carrier family 12, member 2	21.701
chr3	1.05E+08	104768280	45	Slc16a1	solute carrier family 16 (monocarboxylic acid	16.173
chr8	1.1E+08	109825440	-48	Sntb2	syntrophin, basic 2	28.461
chr2	69662022	69662940	80	Ssb	Sjogren syndrome antigen B	19.883
chr7	1.1E+08	110013460	-69	Swap70	SWA-70 protein	21.825
chr13	95889212	95890200	64	Tbca	tubulin cofactor A	14.048
chr19	55794162	55795360	-299	Tcf7l2	transcription factor 7 like 2, T cell specific,	19.271
chr4	47373561	47374580	-252			14.716
chr11	77981381	77982400	-145	Traf4	TNF receptor associated factor 4	22.669
chr7	1.11E+08	110820620	-22	Ctr9	Ctr9, Paf1/RNA polymerase II complex	22.81
chr15	78232641	78233660	-36	Tst	thiosulfate sulfurtransferase, mitochondrial	23.333
chr11	51843541	51844560	-161	Ube2b	ubiquitin-conjugating enzyme E2B	19.632
chr7	25497281	25497820	-57	Axl	AXL receptor tyrosine kinase	11.978
chr5	65714521	65715821	-194	Ugdh	UDP-glucose dehydrogenase	21.3
chr11	68904152	68904881	-207	Vamp2	vesicle-associated membrane protein 2	16.414
chr4	1.5E+08	149902260	3	Vamp3	vesicle-associated membrane protein 3	24.009
chr2	27248621	27249640	-296	Vav2	vav 2 oncogene	19.258
chr6	1.14E+08	113590260	-7	Vhl	von Hippel-Lindau tumor suppressor	17.517
chr12	1.09E+08	109240640	-818	Yy1	YY1 transcription factor	17.564
chr11	88815141	88815820	-13	Trim25	tripartite motif-containing 25	17.088
chr7	80734701	80735250	-646	Zscan2	zinc finger and SCAN domain containing 2	11.413
chr1	1.94E+08	193607781	35	Slc30a1	solute carrier family 30 (zinc transporter),	13.608
chr4	1.01E+08	100918120	-25	Ak4	adenylate kinase 4	20.365
chr11	1.01E+08	101284300	-468	Rnd2	Rho family GTPase 2	19.882
chr13	94871692	94872580	-296	Arsb	arylsulfatase B	15.019
chr17	23897241	23897920	-551	Atp6v0c	ATPase, H+ transporting, lysosomal V0	13.554
chr2	1.31E+08	130598080	97	A730017L22Rik	RIKEN cDNA A730017L22 gene	17.784
chr3	1.46E+08	145861981	23	Bcl10	B cell leukemia/lymphoma 10	18.484
chr7	1.27E+08	127500340	84	Bcl7c	B cell CLL/lymphoma 7C	15.62
chr7	1.39E+08	138748560	-201	Bnip3	BCL2/adenovirus E1B interacting protein 3	15.677
chr14	65962721	65963650	-198	Bnip3l	BCL2/adenovirus E1B interacting protein 3-	13.942
chr15	83390441	83391871	-183	Tspo	translocator protein	28.441
chr7	29903432	29904310	-63	Capns1	calpain, small subunit 1	12.765
chr14	30165481	30166160	87	Capn7	calpain 7	18.28
chr4	1.38E+08	138465340	-145	Capzb	capping protein (actin filament) muscle Z-line,	14.396
chr2	1.54E+08	154128460	25	Cbfa2t2	core-binding factor, runt domain, alpha	24.114
chr11	22889832	22890621	-367	Cct4	chaperonin containing Tcp1, subunit 4 (delta)	28.346
chr10	1.26E+08	126467080	-86	Cdk4	cyclin-dependent kinase 4	32.591
chr5	3349341	3350360	-49	Cdk6	cyclin-dependent kinase 6	20.775
chr7	34765072	34765950	-185	Cebpg	CCAAT/enhancer binding protein (C/EBP),	20.718
chr4	1.07E+08	107421980	51	Cpt2	carnitine palmitoyltransferase 2	31.597
chr5	1.35E+08	134837540	31	Clip2	CAP-GLY domain containing linker protein 2	18.344
chr9	1.08E+08	108122380	46	Dag1	dystroglycan 1	16.852
chr15	76338501	76339520	63	Dgat1	diacylglycerol O-acyltransferase 1	26.333
chr8	87798201	87798880	-189	Dnase2a	deoxyribonuclease II alpha	14.523
chr11	32121962	32122820	-98	Rhbdf1	rhomboid family 1 (Drosophila)	20.159
chr18	46722461	46723480	-65	Eif1a	eukaryotic translation initiation factor 1A	19.581
chr8	74310401	74311760	-139	Nr2f6	nuclear receptor subfamily 2, group F,	17.203
chr10	1.28E+08	127993000	-210	Erbb3	v-erb-b2 erythroblastic leukemia viral	17.697

chr3	1.22E+08	121715920	-139	F3	coagulation factor III	19.742
chr7	44971801	44972480	-276	Fcgrt	Fc receptor, IgG, alpha chain transporter	12.669
chr4	1.24E+08	124203700	17	Fhl3	four and a half LIM domains 3	23.16
chr10	84532161	84532840	74	Tmem263	transmembrane protein 263	15.38
chr19	5447141	5448160	-48	Fosl1	fos-like antigen 1	28.936
chr7	96956262	96957120	-252	Gab2	growth factor receptor bound protein 2-	13.534
chr10	79664041	79664720	-283	Gamt	guanidinoacetate methyltransferase	23.493
chr2	38748582	38749450	-546	Nr6a1	nuclear receptor subfamily 6, group A,	17.175
chr15	3532941	3533620	72	Ghr	growth hormone receptor	16.277
chr5	1.41E+08	141083000	59	Gna12	guanine nucleotide binding protein, alpha 12	12.062
chr7	16049782	16050720	-57	Gng8	guanine nucleotide binding protein (G	15.037
chr15	76157972	76158961	-83	Gpaa1	GPI anchor attachment protein 1	19.553
chr9	20726741	20727730	-40	S1pr2	sphingosine-1-phosphate receptor 2	13.37
chr19	47907701	47908711	-94	Gsto1	glutathione S-transferase omega 1	18.693
chr17	33551201	33552170	508	Wdr46	WD repeat domain 46	18.764
chr18	36641461	36642140	-21	Hbegf	heparin-binding EGF-like growth factor	18.524
chr9	44085092	44086100	-114	H2afx	H2A histone family, member X	15.26
chr1	55032962	55033420	498	Hspe1	heat shock protein 1 (chaperonin 10)	17.356
chr9	1.07E+08	107427851	32	Hyal2	hyaluronoglucosaminidase 2	18.946
chr7	67824782	67825580	-589	Igf1r	insulin-like growth factor I receptor	19.925
chr7	1.02E+08	101712421	-144	Inppl1	inositol polyphosphate phosphatase-like 1	26.2
chr14	53531301	53532320	56	Ajuba	ajuba LIM protein	16.741
chr19	23207402	23208281	-482	Klf9	Kruppel-like factor 9	17.765
chr1	1.55E+08	155095760	-246	Lamc1	laminin, gamma 1	21.878
chr11	97615082	97615851	-296	Lasp1	LIM and SH3 protein 1	25.589
chr11	82596881	82597900	86	Lig3	ligase III, DNA, ATP-dependent	24.113
chr5	1.35E+08	134974220	-323	Limk1	LIM-domain containing, protein kinase	26.134
chr11	3308862	3309560	30	Limk2	LIM motif-containing protein kinase 2	15.825
chr7	25104241	25105260	-3	Lipe	lipase, hormone sensitive	19.246
chr18	56832472	56833610	-141	Lmnb1	lamin B1	18.861
chr9	58110822	58111720	78	Loxl1	lysyl oxidase-like 1	12.972
chr18	76366272	76367060	-400	Smad2	SMAD family member 2	19.617
chr5	1.4E+08	140044300	-220	Mafk	v-maf musculoaponeurotic fibrosarcoma	26.644
chr2	1.21E+08	120700260	-59	Ccndbp1	cyclin D-type binding-protein 1	18.088
chr18	70693141	70694110	-36			12.141
chr4	44321721	44322400	43	Melk	maternal embryonic leucine zipper kinase	14.557
chr17	13496301	13497101	-380	Mllt4	myeloid/lymphoid or mixed-lineage leukemia	24.062
chr11	74646661	74647421	-78	Mnt	max binding protein	24.039
chr4	1.47E+08	146883060	-107	Clcn6	chloride channel, voltage-sensitive 6	17.596
chr1	95308801	95309820	13	Hdlbp	high density lipoprotein (HDL) binding protein	20.773
chr7	28475001	28475680	64			13.309
chr3	98098501	98099141	-122	Notch2	notch 2	15.5
chr16	13732282	13733280	-74	Ntan1	N-terminal Asn amidase	15.646
chr7	26966862	26967970	-105	Numbl	numb-like	14.998
chr11	6191092	6192080	-14	Ogdh	oxoglutarate (alpha-ketoglutarate)	14.803
chr6	1.13E+08	113293100	-163	Ogg1	8-oxoguanine DNA-glycosylase 1	17.687
chr11	68914941	68915351	-5	Per1	period circadian clock 1	20.707
chr4	1.5E+08	149889210	-300	Per3	period circadian clock 3	15.193
chr11	70471121	70472140	-785	Pfn1	profilin 1	15.55
chr3	1.47E+08	146750800	42	Prkacb	protein kinase, cAMP dependent, catalytic,	18.47
chr14	29454942	29455560	-34	Prkcd	protein kinase C, delta	16.421
chr12	1.06E+08	106186020	-212	Papola	poly (A) polymerase alpha	18.046
chr10	1.28E+08	127969680	-387	Pa2g4	proliferation-associated 2G4	17.19
chr17	78787181	78788200	-60	Eif2ak2	eukaryotic translation initiation factor 2-alpha	13.349
chr2	1.32E+08	131601760	51	Prnp	prion protein	13.277
chr11	1.18E+08	118065340	22	Cyth1	cytohesin 1	18.377
chr5	1.44E+08	143878480	-30	Cyth3	cytohesin 3	17.162
chr5	20567432	20568300	-245	Ptpn12	protein tyrosine phosphatase, non-receptor	12.509
chr9	50280302	50281240	100	Pts	6-pyruvoyl-tetrahydropterin synthase	18.394
chr11	6375872	6376360	-37	Purb	purine rich element binding protein B	14.529
chr8	11478142	11479080	-140	Rab20	RAB20, member RAS oncogene family	13.516
chr19	4201381	4202060	-117	Rad9a	RAD9 homolog A	18.947
chr15	1.02E+08	102086020	46	Rarg	retinoic acid receptor, gamma	16.401
chr5	78339562	78341100	62	Rest	RE1-silencing transcription factor	27.475
chr10	39420281	39421640	463	E130307A14Rik	RIKEN cDNA E130307A14 gene	18.876
chr1	1.53E+08	153263471	-105	Rnf2	ring finger protein 2	14.877
chr11	1.01E+08	101258460	-199	Rpl27	ribosomal protein L27	23.778
chr13	1.01E+08	101208820	34	Serf1	small EDRK-rich factor 1	17.024
chr2	1.21E+08	121140980	1	Serf2	small EDRK-rich factor 2	15.925
chr11	1.17E+08	116670320	-404	Mfsd11	major facilitator superfamily domain	26.018
chr3	89504321	89504401	-117	Shc1	src homology 2 domain-containing	14.5
chr6	72026621	72027640	13	St3gal5	ST3 beta-galactoside alpha-2,3-	13.708
chr7	18252221	18253061	-425	Six5	sine oculis-related homeobox 5	12.607
chr13	74229152	74229991	-128	Slc12a7	solute carrier family 12, member 7	18.483
chr8	23941781	23942800	45	Slc20a2	solute carrier family 20, member 2	12.184
chr11	53734802	53735640	-95	Slc22a5	solute carrier family 22 (organic cation	17.937
chr4	1.19E+08	118606931	-71	Slc2a1	solute carrier family 2 (facilitated glucose	20.492
chr2	1.67E+08	167229711	-76	Snai1	snail family zinc finger 1	20.437
chr16	90108912	90110200	-45	Sod1	superoxide dismutase 1, soluble	16.185
chr12	88277261	88277790	-67	Sptlc2	serine palmitoyltransferase, long chain base	13.698
chr15	81874762	81875300	-178	Nhp2l1	NHP2 non-histone chromosome protein 2-like	13.786
chr10	79518521	79519321	-11			26.613
chr12	8797161	8797840	96	Sdc1	syndecan 1	22.15
chr2	1.64E+08	164134980	-113	Sdc4	syndecan 4	11.152
chr11	1.2E+08	120415080	118	Anapc11	anaphase promoting complex subunit 11	14.389
chr8	1.1E+08	109782731	226	Chtf8	CTF8, chromosome transmission fidelity	18.021
chr14	17031972	17032640	-79	Nr1d2	nuclear receptor subfamily 1, group D,	19.689
chr11	1.18E+08	118171760	81	Timp2	tissue inhibitor of metalloproteinase 2	16.975
chr5	1.25E+08	124889931	-641	Atp6v0a2	ATPase, H+ transporting, lysosomal V0	21.47
chr5	1.25E+08	124890500	-21	Atp6v0a2	ATPase, H+ transporting, lysosomal V0	26.24

chr1	1.94E+08	193793880	-164	Traf5	TNF receptor-associated factor 5	24.333
chr16	32528141	32529160	7	Tfrc	transferrin receptor	20.023
chr15	98762521	98762951	-312	Tuba1b	tubulin, alpha 1B	27.674
chr4	58049901	58050920	55	Txn1	thioredoxin 1	20.992
chr5	1.47E+08	147105840	-211	Usp12	ubiquitin specific peptidase 12	19.886
chr4	59283081	59283760	-184	Ugcg	UDP-glucose ceramide glucosyltransferase	18.376
chr9	1.08E+08	108206360	20	Usp4	ubiquitin specific peptidase 4 (proto-	23.838
chr11	52203941	52204620	-5	Vdac1	voltage-dependent anion channel 1	13.135
chr2	13491201	13492391	-368	Vim	vimentin	41.076
chr15	99198061	99198940	16			21.032
chr5	37276921	37277600	-29	Wfs1	Wolfram syndrome 1 homolog (human)	12.473
chr17	32120481	32121160	-193	Wiz	widely-interspaced zinc finger motifs	14.374
chr7	28087602	28088420	-23	Zfp36	zinc finger protein 36	18.96
chr2	1.22E+08	122394560	-116	Slc30a4	solute carrier family 30 (zinc transporter),	17.511
chr19	4148082	4149020	-112	Coro1b	coronin, actin binding protein 1B	14.606
chr5	1.14E+08	114170300	-85	Coro1c	coronin, actin binding protein 1C	22.195
chr1	1.68E+08	167600620	-175	Creg1	cellular repressor of E1A-stimulated genes 1	16.781
chr5	93158382	93159320	-53	G3bp2	GTPase activating protein (SH3 domain)	21.123
chr6	86698301	86699620	52	Gmcl1	germ cell-less homolog 1 (Drosophila)	22.998
chr6	29162141	29162820	-173	Impdh1	inosine 5'-phosphate dehydrogenase 1	19.901
chr10	7415741	7416760	60	Katna1	katanin p60 (ATPase-containing) subunit A1	22.532
chr8	23631701	23632380	-60	Nek3	NIMA (never in mitosis gene a)-related	13.161
chr2	76448321	76449340	3	Prkra	protein kinase, interferon inducible double	18.423
chr15	1E+08	100443140	344	C330013E15Rik	RIKEN cDNA C330013E15 gene	13.485
chr6	1.21E+08	121212030	0	Usp18	ubiquitin specific peptidase 18	19.907
chr8	11555581	11556931	-173	Ing1	inhibitor of growth family, member 1	20.393
chr2	33037801	33038281	71	Angptl2	angiopoietin-like 2	17.375
chr13	55454001	55454680	-354	Grk6	G protein-coupled receptor kinase 6	16.7
chr17	12161461	12162480	48	Map3k4	mitogen-activated protein kinase kinase	23.873
chr7	1.27E+08	126551060	-54	Mapk3	mitogen-activated protein kinase 3	14.489
chr2	91824882	91825750	-307	Creb3l1	cAMP responsive element binding protein 3-	17.681
chr7	1.14E+08	114067910	-154	Psma1	proteasome (prosome, macropain) subunit,	12.488
chr13	94404401	94405080	-508	Homer1	homer homolog 1 (Drosophila)	18.406
chr4	1.26E+08	126257200	496	AU040320	expressed sequence AU040320	19.779
chr5	1.38E+08	138391560	31	Cops6	COP9 (constitutive photomorphogenic)	17.714
chr1	1.73E+08	173182960	136	Pfdn2	prefoldin 2	15.634
chr6	86758821	86759500	58	Anxa4	annexin A4	22.184
chr15	76303821	76305860	140	Hsf1	heat shock factor 1	22.361
chr2	35158721	35159610	-147	Stom	stomatin	17.687
chr6	1.25E+08	124678340	92	Phb2	prohibitin 2	15.231
chr17	33637901	33639200	-41	H2-Ke6	H2-K region expressed gene 6	26.085
chr5	1.44E+08	144073640	-220	Eif2ak1	eukaryotic translation initiation factor 2 alpha	16.837
chr10	99444901	99445920	-102	Kitl	kit ligand	18.064
chr17	24277062	24277761	-139	Pkd1	polycystic kidney disease 1 homolog	13.187
chr8	1.09E+08	108828190	-4	Psmb10	proteasome (prosome, macropain) subunit,	29.71
chr17	26235832	26237120	-404	Dusp1	dual specificity phosphatase 1	21.523
chr6	1.25E+08	124796320	176	Cdca3	cell division cycle associated 3	14.314
chr2	1.18E+08	118080300	-98	Eif2ak4	eukaryotic translation initiation factor 2 alpha	14.772
chr5	8428261	8429280	-48	Dbf4	DBF4 homolog (S. cerevisiae)	23.733
chr2	1.21E+08	120963410	37	Trp53bp1	transformation related protein 53 binding	21.119
chr4	1.35E+08	135294500	-116	Tceb3	transcription elongation factor B (SIII),	20.675
chr7	1.43E+08	143409960	-140	Cars	cysteinyl-tRNA synthetase	12.809
chr10	60778401	60779420	-30	Pald1	phosphatase domain containing, paladin 1	17.423
chr19	29390972	29391641	9	Insl6	insulin-like 6	13.988
chr15	9067461	9068140	348	Lmbrd2	LMBR1 domain containing 2	20.324
chr6	82739862	82740700	-169	Hk2	hexokinase 2	14.389
chr16	20461352	20462480	183	Gm15760	mitochondrial ribosomal protein S18B	15.861
chr17	35577261	35578520	-87	Abcf1	ATP-binding cassette, sub-family F (GCN20),	22.205
chr15	81787681	81788700	-5	Pmm1	phosphomannomutase 1	18.457
chr4	1.09E+08	108975100	-153	Rnf11	ring finger protein 11	22.456
chr4	1.35E+08	134545480	-175	Clic4	chloride intracellular channel 4 (mitochondrial)	14.172
chr5	1.23E+08	123161461	-149	Kdm2b	lysine (K)-specific demethylase 2B	21.213
chr17	65512901	65514180	-442	Vapa	vesicle-associated membrane protein,	17.923
chr11	1.16E+08	116015820	-5	Acox1	acyl-Coenzyme A oxidase 1, palmitoyl	21.975
chr10	98536761	98537780	411	Poc1b	POC1 centriolar protein homolog B	19.951
chr8	82607761	82608330	153	Anapc10	anaphase promoting complex subunit 10	14.406
chr17	63185601	63186520	-18	Fbxl17	F-box and leucine-rich repeat protein 17	17.982
chr8	73601841	73602520	-40	Lsm4	LSM4 homolog, U6 small nuclear RNA	13.295
chr8	1.08E+08	108154340	63	Tradd	TNFRSF1A-associated via death domain	15.43
chr9	98372541	98373220	83	4930579K19Rik	RIKEN cDNA 4930579K19 gene	17.352
chr13	55339421	55340100	-408	Mxd3	Max dimerization protein 3	18.216
chr19	4125561	4126441	41	Tmem134	transmembrane protein 134	19
chr12	17715701	17716720	-84	Hpcal1	hippocalcin-like 1	13.742
chr11	87884221	87884731	2	Vezf1	vascular endothelial zinc finger 1	17.059
chr14	32276152	32276880	-266	Mapk8	mitogen-activated protein kinase 8	18.519
chr5	24195421	24196440	50			16.562
chr9	20899801	20900820	-2	Cdc37	cell division cycle 37	18.798
chr15	99079582	99080601	-96	Mcrs1	microspherule protein 1	23.473
chr10	1.27E+08	127486740	-26	Atp5b	ATP synthase, H+ transporting mitochondrial	14.173
chr17	47074021	47075380	-17	Bysl	bystin-like	21.342
chr2	1.64E+08	163512800	15	Wisp2	WNT1 inducible signaling pathway protein 2	26.955
chr11	1.03E+08	103084260	5	Map3k14	mitogen-activated protein kinase kinase	20.429
chr3	89504412	89505680	568	Shc1	src homology 2 domain-containing	21.675
chr5	93117841	93118460	92	Cdkl2	cyclin-dependent kinase-like 2 (CDC2-related	11.042
chr2	1.57E+08	157258160	46	Blcap	bladder cancer associated protein homolog	20.54
chr15	81637401	81638801	-568	Tef	thyrotroph embryonic factor	39.979
chr11	78117381	78118060	-66	Spag5	sperm associated antigen 5	24.723
chr4	1.23E+08	123420340	94	Rragc	Ras-related GTP binding C	19.132
chr6	30826441	30827460	5	Copg2	coatomer protein complex, subunit gamma 2	27.747
chr9	22218321	22219340	-72	Rp9	retinitis pigmentosa 9 (human)	26.937

chr8	24673801	24674820	-312	Gpat4	glycerol-3-phosphate acyltransferase 4	21.244
chr15	38463592	38464500	-191	Azin1	antizyme inhibitor 1	20.458
chr5	1.06E+08	106117400	46	Zfp326	zinc finger protein 326	15.039
chr6	50191141	50191820	-125	Dfna5	deafness, autosomal dominant 5 (human)	12.722
chr5	1.45E+08	144509180	-31	Bri3	brain protein I3	14.145
chr5	1.13E+08	112566081	-711	Tfip11	tuftelin interacting protein 11	6.458
chr5	1.13E+08	112567180	-36	Tfip11	tuftelin interacting protein 11	35.5
chr8	86497701	86498561	-149	Dnajb1	DnaJ (Hsp40) homolog, subfamily B, member	21.779
chr17	8121552	8121920	-251	Mpc1	mitochondrial pyruvate carrier 1	17.071
chr11	78351981	78353000	-35	Tnfaip1	tumor necrosis factor, alpha-induced protein 1	21.535
chr11	20232721	20233740	-514	Slc1a4	solute carrier family 1 (glutamate/neutral	15.755
chr5	1.36E+08	136220320	-713	Ywhag	tyrosine 3-monooxygenase/tryptophan 5-	19.534
chr1	36883881	36884900	-317	Tmem131	transmembrane protein 131	16.433
chr9	1.07E+08	107400560	-90	Nprl2	nitrogen permease regulator-like 2	23.798
chr17	43129681	43130680	-110	Slc25a27	solute carrier family 25, member 27	14.468
chr19	46358432	46359340	-120	Nfkb2	nuclear factor of kappa light polypeptide gene	21.96
chr17	33448861	33449540	-14	Cd320	CD320 antigen	18.022
chr5	93212412	93213720	-72	Uso1	USO1 vesicle docking factor	26.193
chr5	34976481	34977490	20	Nop14	NOP14 nucleolar protein	17.378
chr16	96095352	96096240	17	Psmg1	proteasome (prosome, macropain) assembly	19.101
chr2	1.73E+08	172665260	-15	Rbm38	RNA binding motif protein 38	22.51
chr7	1.02E+08	102124780	-161	Rhog	ras homolog gene family, member G	20.964
chr15	35099901	35100920	-15	Stk3	serine/threonine kinase 3	19.546
chr6	1.49E+08	148904340	-369	Fam60a	family with sequence similarity 60, member A	11.602
chr7	18823081	18824440	-208	Clptm1	cleft lip and palate associated transmembrane	21.188
chr17	87015521	87016200	-145	Socs5	suppressor of cytokine signaling 5	15.891
chr19	53997441	53998790	-73	Shoc2	soc-2 (suppressor of clear) homolog (C.	13.764
chr4	1.23E+08	123407760	-125	Mycbp	c-myc binding protein	21.564
chr9	88280321	88281000	-370	Syncrip	synaptotagmin binding, cytoplasmic RNA	15.92
chr14	85972401	85973400	-39	Diaph3	diaphanous related formin 3	15.522
chrX	44707281	44708300	-31	Elf4	E74-like factor 4 (ets domain transcription	11.882
chr17	34848981	34849961	-327	Ddx39b	DEAD (Asp-Glu-Ala-Asp) box polypeptide	20.592
chr15	81292981	81294000	-81	Rbx1	ring-box 1	18.224
chr10	41965492	41965520	-349	Foxo3	forkhead box O3	5.679
chr11	69807101	69807780	-125	Gabarap	gamma-aminobutyric acid receptor associated	17.482
chr10	80780941	80782300	-121	Fzr1	fizzy/cell division cycle 20 related 1	32.445
chr6	28429441	28430120	-578	Snd1	staphylococcal nuclease and tudor domain	14.854
chr4	1.19E+08	118731171	-71	P3h1	prolyl 3-hydroxylase 1	23.266
chr12	71856172	71856620	-66	Actr10	ARP10 actin-related protein 10	13.163
chr5	1.23E+08	122683560	-181	Anapc7	anaphase promoting complex subunit 7	37.464
chr2	1.55E+08	155209660	-164	Acss2	acyl-CoA synthetase short-chain family	11.959
chr19	8808232	8809060	177	Stx5a	syntaxin 5A	22.748
chr5	78384281	78385300	71	Noa1	nitric oxide associated 1	15.286
chr9	1.14E+08	114239661	-1	Crtap	cartilage associated protein	18.068
chr9	59284101	59285120	-230	Arih1	ariadne ubiquitin-conjugating enzyme E2	18.068
chr13	54584281	54585170	90	Arl10	ADP-ribosylation factor-like 10	14.835
chr14	30469781	30470720	184	Btd	biotinidase	24.924
chr1	1.69E+08	169187060	54	Aldh9a1	aldehyde dehydrogenase 9, subfamily A1	18.165
chr3	54780461	54781140	-234	Supt20	suppressor of Ty 20	24.124
chr11	1.14E+08	113568160	-230	Cdc42ep4	CDC42 effector protein (Rho GTPase binding)	22.974
chr7	45582781	45583800	-41	Sphk2	sphingosine kinase 2	15.473
chr19	5731172	5732400	-54	Sssca1	Sjogren's syndrome/scleroderma autoantigen	30.496
chr8	1.26E+08	126140850	-294	Zfp276	zinc finger protein (C2H2 type) 276	18.105
chr9	1.09E+08	108519840	29	Slc25a20	solute carrier family 25 (mitochondrial	15.359
chr19	7059202	7060100	-335	Dnajc4	DnaJ (Hsp40) homolog, subfamily C, member	13.389
chr2	1.04E+08	103829090	-3	Fbxo3	F-box protein 3	14.252
chr6	83080732	83081720	62	Mogs	mannosyl-oligosaccharide glucosidase	20.159
chr2	1.6E+08	160423220	-10	Plcg1	phospholipase C, gamma 1	13.843
chr14	68834892	68835570	6	Bin3	bridging integrator 3	14.965
chr7	63817402	63818680	-176	Klf13	Kruppel-like factor 13	28.439
chr11	20442161	20442840	-756	Sertad2	SERTA domain containing 2	15.595
chr1	74438262	74439271	262			17.441
chr4	1.16E+08	116150090	11	Akr1a1	aldo-keto reductase family 1, member A1	16.454
chr11	97265841	97266611	-24	Arhgap23	Rho GTPase activating protein 23	27.455
chr16	46416252	46417030	-337	Pvrl3	poliovirus receptor-related 3	13.486
chr10	80571402	80571791	-747	Pias4	protein inhibitor of activated STAT 4	18.429
chr10	80570481	80571391	-87	Pias4	protein inhibitor of activated STAT 4	26.11
chr8	64115612	64116520	-247	Sh3rf1	SH3 domain containing ring finger 1	13.377
chr11	50220381	50222080	88	Hnrnph1	heterogeneous nuclear ribonucleoprotein H1	17.115
chr5	1.41E+08	140758640	-7	Chst12	carbohydrate sulfotransferase 12	24.812
chr9	21296241	21297260	-546	Carm1	coactivator-associated arginine	22.213
chr15	76195701	76196380	-113	Hgh1	HGH1 homolog	20.85
chr8	60380261	60380371	211			5.182
chr8	60380382	60381280	726			11.37
chr13	1.02E+08	101876580	86	Cenph	centromere protein H	12.244
chr11	60543192	60543771	-23			18.584
chr19	5687861	5688791	582	Pcnxl3	pecanex-like 3 (Drosophila)	30.484
chr1	1.86E+08	185735200	408	1700056E22Rik	RIKEN cDNA 1700056E22 gene	23.328
chr4	1.48E+08	148270940	-169	Ube4b	ubiquitination factor E4B	24.82
chr11	77896381	77897400	-312	Eral1	Era (G-protein)-like 1 (E. coli)	16.823
chr1	1.21E+08	121332740	98	Ralb	v-ral simian leukemia viral oncogene homolog	17.402
chr4	45039192	45040010	-108	Polr1e	polymerase (RNA) I polypeptide E	10.984
chr17	24423221	24424580	66	Noxo1	NADPH oxidase organizer 1	22.386
chr17	65850181	65851200	40	Twsg1	twisted gastrulation homolog 1 (Drosophila)	23.859
chr17	23453541	23453771	-302	Pkmyt1	protein kinase, membrane associated	10.435
chr6	88411682	88412580	49	Eefsec	eukaryotic elongation factor, selenocysteine-	25.571
chr8	73695412	73696020	-64	Ifi30	interferon gamma inducible protein 30	16.576
chr16	18412021	18413040	96	Gnb1l	guanine nucleotide binding protein (G	22.113
chr2	1.54E+08	154482740	-151	Raly	hnRNP-associated with lethal yellow	10.733
chr5	1.45E+08	145368360	-17	Arpc1b	actin related protein 2/3 complex, subunit 1B	27.924

chr1	95173141	95173820	-286	Pask	PAS domain containing serine/threonine	14.477
chr3	90595272	90596060	-241	Chtop	chromatin target of PRMT1	14.506
chr8	73588262	73589260	-34	Pgpep1	pyroglutamyl-peptidase I	21.485
chr5	1.24E+08	123785500	-208	Diablo	diablo homolog (Drosophila)	31.063
chr14	60553321	60554000	38	Trim13	tripartite motif-containing 13	11.944
chr13	85662082	85662660	-216	Ccnh	cyclin H	15.711
chr9	1.08E+08	108426000	-45	Ndufaf3	NADH dehydrogenase (ubiquinone) 1 alpha	18.701
chr4	1.48E+08	148362400	-151	Ctnnbip1	catenin beta interacting protein 1	18.753
chr4	1.3E+08	129678281	-735	Tinagl1	tubulointerstitial nephritis antigen-like 1	8.667
chr4	1.3E+08	129677700	-170	Tinagl1	tubulointerstitial nephritis antigen-like 1	15.322
chr11	69662261	69663280	-42	Plscr3	phospholipid scramblase 3	16.034
chr14	1.2E+08	120046520	-194	Ipo5	importin 5	11.919
chr10	60147701	60148590	-6	Slc29a3	solute carrier family 29 (nucleoside	11.963
chr11	23565401	23566420	25	Pex13	peroxisomal biogenesis factor 13	22.879
chr3	96642621	96643481	-311	Txnip	thioredoxin interacting protein	21.221
chr3	1.27E+08	126589001	-552	Camk2d	calcium/calmodulin-dependent protein kinase	18.632
chr9	99052201	99053560	60	Cep70	centrosomal protein 70	18.43
chr11	1.06E+08	106304240	15	Ern1	endoplasmic reticulum (ER) to nucleus	13.851
chr4	47495282	47495951	-145	Sec61b	Sec61 beta subunit	10.383
chr7	4288081	4288760	-370	Hspbp1	HSPA (heat shock 70kDa) binding protein,	12.632
chr17	15100761	15101780	61	Fam120b	family with sequence similarity 120, member	14.629
chr2	6129861	6130880	-104	Echdc3	enoyl Coenzyme A hydratase domain	17.04
chr5	53121052	53121731	-992	Anapc4	anaphase promoting complex subunit 4	13.459
chr8	1.07E+08	107230220	-13	Cmtm3	CKLF-like MARVEL transmembrane domain	14.932
chr5	45738292	45739080	-209	Qdpr	quinoid dihydropteridine reductase	17.02
chr6	83537661	83538660	2	Stambp	STAM binding protein	24.171
chr4	1.55E+08	154683680	-94	Mxra8	matrix-remodelling associated 8	15.364
chr9	44157502	44158860	362	Trappc4	trafficking protein particle complex 4	18.032
chr13	36124602	36125540	-37	Fars2	phenylalanine-tRNA synthetase 2	15.854
chr5	45781252	45782020	14	Lap3	leucine aminopeptidase 3	19.126
chr2	1.73E+08	173303100	-13	Ppp4r1l-ps	protein phosphatase 4, regulatory subunit 1-	17.214
chr3	1.23E+08	122916780	-118	1810037I17Rik	RIKEN cDNA 1810037I17 gene	11.734
chr13	24808101	24808780	-682	BC005537	cDNA sequence BC005537	12.234
chr5	38508412	38509240	95	Lyar	Ly1 antibody reactive clone	18.335
chr11	60729441	60730460	37	Natd1	N-acetyltransferase domain containing 1	18.698
chr17	46108421	46109440	-507	Mrpl2	mitochondrial ribosomal protein L2	24.535
chr11	1.15E+08	115420140	206	Gga3	golgi associated, gamma adaptin ear	22.87
chr11	72993582	72994260	643	Tax1bp3	Tax1 (human T cell leukemia virus type I)	24.848
chr12	4831741	4832461	-168	Sf3b6	splicing factor 3B, subunit 6	19.542
chr19	10592042	10593380	422	Cpsf7	cleavage and polyadenylation specific factor 7	16.234
chr15	76178361	76179040	151	Maf1	MAF1 homolog (S. cerevisiae)	15.274
chr3	1.35E+08	135376440	122	4930539J05Rik	RIKEN cDNA 4930539J05 gene	17.875
chr9	1.06E+08	106296920	-243	Acy1	aminoacylase 1	16.371
chr4	1.34E+08	134126600	-675	Tmem57	transmembrane protein 57	17.551
chr9	20392521	20394111	-108	Fbxl12	F-box and leucine-rich repeat protein 12	24.698
chr11	1.21E+08	121021630	-47	Ogfod3	2-oxoglutarate and iron-dependent oxygenase	23.33
chr15	75748292	75749250	44	Pycrl	pyrroline-5-carboxylate reductase-like	18.049
chr11	84695542	84697060	89	Pigw	phosphatidylinositol glycan anchor	13.035
chr10	1.2E+08	119630360	-100	Llph	LLP homolog, long-term synaptic facilitation	18.01
chr14	19181781	19182460	-13	Mrps16	mitochondrial ribosomal protein S16	15.18
chr15	83177601	83178280	73	Arfgap3	ADP-ribosylation factor GTPase activating	21.125
chr1	95633501	95635140	-51	Ing5	inhibitor of growth family, member 5	31.718
chr18	65925321	65926340	-117	Sec11c	SEC11 homolog C, signal peptidase complex	19.418
chr7	30271561	30272920	140	U2af1l4	U2 small nuclear RNA auxiliary factor 1-like 4	16.891
chr3	1.31E+08	130699060	-32	Ostc	oligosaccharyltransferase complex subunit	18.351
chr11	66868481	66869311	31	Sco1	SCO cytochrome oxidase deficient homolog 1	16.518
chr11	66869322	66870180	886	Sco1	SCO cytochrome oxidase deficient homolog 1	16.252
chr10	59398001	59399020	-41	Anapc16	anaphase promoting complex subunit 16	24.77
chr5	1.14E+08	114033331	-505	Iscu	IscU iron-sulfur cluster scaffold homolog (E.	8.8
chr5	1.14E+08	114034130	-75	Iscu	IscU iron-sulfur cluster scaffold homolog (E.	28.286
chr19	3999761	4000780	-310	Nudt8	nudix (nucleoside diphosphate linked moiety	14.652
chr17	56681822	56683100	-2	Alkbh7	alkB, alkylation repair homolog 7 (E. coli)	26.753
chr10	53284461	53285660	-316	Asf1a	anti-silencing function 1A histone chaperone	18.795
chr4	40891121	40892110	-28	Aptx	aprataxin	12.017
chr8	13889681	13890840	-12	Coprs	coordinator of PRMT5, differentiation	25.302
chr11	98254602	98255580	-13	Mien1	migration and invasion enhancer 1	18.242
chr1	74216922	74217891	539	Aamp	angio-associated migratory protein	20.531
chr6	86330842	86331780	-6	Fam136a	family with sequence similarity 136, member	14.806
chr6	1.25E+08	125157740	-31	Ncapd2	non-SMC condensin I complex, subunit D2	13.838
chr16	57527661	57528550	-92	Cmss1	cms small ribosomal subunit 1	25.495
chr2	1.25E+08	125365140	89	Eid1	EP300 interacting inhibitor of differentiation 1	13.815
chr7	28020542	28021440	-185	Timm50	translocase of inner mitochondrial membrane	28.374
chr5	1.48E+08	148171320	-106	Pomp	proteasome maturation protein	23.323
chr2	3630181	3631091	-94	Fam107b	family with sequence similarity 107, member	23.978
chr3	1.21E+08	121164100	-42	Rwdd3	RWD domain containing 3	17.797
chr16	90616612	90616800	-476	Mis18a	MIS18 kinetochore protein homolog A (S.	12.527
chr9	1.05E+08	105253460	236	Nek11	NIMA (never in mitosis gene a)-related	14.613
chr11	98403972	98404500	-901	Ormdl3	ORM1-like 3 (S. cerevisiae)	19.396
chr11	98403821	98403961	-556	Ormdl3	ORM1-like 3 (S. cerevisiae)	8.571
chr5	1.24E+08	124373020	-446	Ogfod2	2-oxoglutarate and iron-dependent oxygenase	22.583
chr15	12265501	12266520	-211	Golph3	golgi phosphoprotein 3	17.588
chr1	1.54E+08	154149400	-60	Tsen15	tRNA splicing endonuclease 15 homolog (S.	14.339
chr9	70341241	70342940	56	Sltm	SAFB-like, transcription modulator	26.396
chr9	1.04E+08	103922360	-214	Uba5	ubiquitin-like modifier activating enzyme 5	35.117
chr2	1.63E+08	163111600	-355	Oser1	oxidative stress responsive serine rich 1	21.787
chr10	51921741	51922420	46	Dcbld1	discoidin, CUB and LCCL domain containing	12.862
chr10	1.28E+08	127615260	-78	Spryd4	SPRY domain containing 4	19.803
chr8	88322481	88323500	-44	4921524J17Rik	RIKEN cDNA 4921524J17 gene	18.339
chrX	81826441	81826951	-45	Tab3	TGF-beta activated kinase 1/MAP3K7 binding	11.824
chr10	13242722	13243680	96	Adat2	adenosine deaminase, tRNA-specific 2	15.334

chr13	45012601	45013560	-12	Dtnbp1	dystrobrevin binding protein 1	12.647
chr11	1.21E+08	121170900	-23	Wdr45b	WD repeat domain 45B	16.604
chr6	52642881	52643560	-87	Tax1bp1	Tax1 (human T cell leukemia virus type I)	19.611
chr6	86362041	86363400	64	Pcyox1	prenylcysteine oxidase 1	18.176
chr18	80417821	80418500	-125	Pqlc1	PQ loop repeat containing 1	16.963
chr2	84479461	84480140	-133	Tmx2	thioredoxin-related transmembrane protein 2	19.698
chr7	44114321	44114891	-158	2410002F23Rik	RIKEN cDNA 2410002F23 gene	15.333
chr17	52943101	52944701	-262	Rab5a	RAB5A, member RAS oncogene family	25.413
chr17	28679782	28680700	-564	Kctd20	potassium channel tetramerisation domain	18.297
chr5	24112152	24113130	-574	Smarcd3	SWI/SNF related, matrix associated, actin	13.17
chr7	15256481	15257500	-175	Napa	N-ethylmaleimide sensitive fusion protein	12.929
chr10	89161602	89162580	3	Actr6	ARP6 actin-related protein 6	21.365
chr17	17078302	17079220	-189	Riok2	RIO kinase 2 (yeast)	20.147
chr6	1.16E+08	115740041	-455	Cand2	cullin-associated and neddylation-dissociated	16.688
chr17	27362521	27363460	-159	Rps10	ribosomal protein S10	19.88
chr17	46235292	46235920	-220	2310039H08Rik	RIKEN cDNA 2310039H08 gene	19.525
chr4	1.29E+08	128837900	114	Rbbp4	retinoblastoma binding protein 4	20.869
chr11	72423061	72423721	-65	Ube2g1	ubiquitin-conjugating enzyme E2G 1	15.985
chr11	70834921	70835600	238	Derl2	Der1-like domain family, member 2	16.713
chr7	81635701	81636860	-186	Fam103a1	family with sequence similarity 103, member	18.632
chr11	1.06E+08	106033760	-106	Ddx42	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	13.229
chr9	1.1E+08	110469740	-122	Nradd	neurotrophin receptor associated death	20.165
chr11	69796221	69797240	-205	Elp5	elongator acetyltransferase complex subunit 5	19.738
chr11	76059482	76060370	-5	Rnmtl1	RNA methyltransferase like 1	16.983
chr8	27250321	27251650	-151	Lsm1	LSM1 homolog, U6 small nuclear RNA	14.843
chr11	59018221	59019130	-6			12.087
chr9	1.15E+08	114580121	-180	Cmtm6	CKLF-like MARVEL transmembrane domain	23.062
chr18	52590532	52591540	-26	Srfbp1	serum response factor binding protein 1	16.964
chr8	36963612	36964460	14	Eri1	exoribonuclease 1	16.353
chr4	56895941	56897230	-200	Ikbkap	inhibitor of kappa light polypeptide enhancer	26.503
chr2	1.31E+08	130851761	21			30.869
chr10	39946702	39947960	-250	Gtf3c6	general transcription factor IIIC, polypeptide 6,	22.003
chr1	37373821	37375180	149	Coa5	cytochrome C oxidase assembly factor 5	27.344
chr7	1.22E+08	121858781	-7	Ears2	glutamyl-tRNA synthetase 2	18.231
chr10	57718401	57719420	87	Lims1	LIM and senescent cell antigen-like domains	27.032
chr19	5874861	5875540	8	Frmd8	FERM domain containing 8	15.454
chr15	1.03E+08	102550800	-78	Calcoco1	calcium binding and coiled coil domain 1	20.093
chr11	74586481	74587500	-68	Mettl16	methyltransferase like 16	26.798
chr11	62695232	62696000	-69	Tvp23b	trans-golgi network vesicle protein 23B	19.16
chr9	1.2E+08	119743851	-47	Wdr48	WD repeat domain 48	20.377
chr10	1.28E+08	127814840	-235	Rnf41	ring finger protein 41	16.979
chr6	1.23E+08	122840640	5	Necap1	NECAP endocytosis associated 1	11.349
chr7	44716121	44716951	585	Tbc1d17	TBC1 domain family, member 17	23.843
chr11	1.21E+08	121053221	-255	Narf	nuclear prelamin A recognition factor	14.333
chr18	80631341	80632360	-124	Ctdp1	CTD (carboxy-terminal domain, RNA	15.039
chr11	94137501	94138520	-9	Luc7l3	LUC7-like 3 (S. cerevisiae)	20.022
chr4	48145472	48146350	-108	Stx17	syntaxin 17	13.76
chr6	1.16E+08	115961080	-127	Plxnd1	plexin D1	20.258
chr4	1.53E+08	153004760	-212	Tprgl	transformation related protein 63 regulated	10.828
chr11	78328181	78328860	29	Poldip2	polymerase (DNA-directed), delta interacting	21.866
chr1	1.3E+08	130071760	-307	Ubxn4	UBX domain protein 4	18.406
chr19	6084301	6084980	251	Zfpl1	zinc finger like protein 1	18.299
chr18	35724162	35724820	-150	Paip2	polyadenylate-binding protein-interacting	13.599
chr5	1E+08	100280611	-185	Enoph1	enolase-phosphatase 1	17.048
chr5	1E+08	100279601	-77	Hnrnpdl	heterogeneous nuclear ribonucleoprotein D-	
chr11	1.21E+08	120543900	-209	Dcxr	dicarbonyl L-xylulose reductase	14.754
chr1	43771702	43772780	13	Uxs1	UDP-glucuronate decarboxylase 1	13.748
chr18	68425001	68426020	192	Fam210a	family with sequence similarity 210, member	21.184
chr9	1.18E+08	117999350	-131	Cmc1	COX assembly mitochondrial protein 1	13.493
chr8	97726572	97727560	403	Ciapin1	cytokine induced apoptosis inhibitor 1	14.089
chr18	36885921	36886600	47	Wdr55	WD repeat domain 55	11.669
chr4	1.11E+08	111218521	39	Spata6	spermatogenesis associated 6	16.671
chr10	98344321	98345000	-180	Atp2b1	ATPase, Ca++ transporting, plasma	16.649
chr15	88902861	88904031	174	1810021B22Rik	RIKEN cDNA 1810021B22 gene	18.615
chr3	28996042	28996651	-238	Rpl22l1	ribosomal protein L22 like 1	15.795
chr11	1.02E+08	102224060	-113	Slc25a39	solute carrier family 25, member 39	18.427
chr13	41011481	41012500	6	Pak1ip1	PAK1 interacting protein 1	15.229
chr11	1.03E+08	102833691	61	Dcakd	dephospho-CoA kinase domain containing	40.67
chr5	93037941	93038960	-182	Rchy1	ring finger and CHY zinc finger domain	17.728
chr11	72023221	72024240	-19	Txndc17	thioredoxin domain containing 17	24.045
chr3	1.3E+08	129823900	-142	Gar1	GAR1 ribonucleoprotein homolog (yeast)	18.801
chr10	82789321	82790000	-360	D10Wsu102e	DNA segment, Chr 10, Wayne State	21.711
chr9	1.08E+08	107844600	97	Fam212a	family with sequence similarity 212, member	32.035
chr5	1.24E+08	124168340	-63	Denr	density-regulated protein	24.065
chr8	35615142	35615340	15	Leprotl1	leptin receptor overlapping transcript-like 1	18.49
chr6	8209301	8209980	352			14.975
chr17	25595652	25596840	92	Fam195a	family with sequence similarity 195, member	22.677
chr19	12639841	12640860	-220	Fam111a	family with sequence similarity 111, member	31.945
chr8	1.22E+08	122461540	141	Hsdl1	hydroxysteroid dehydrogenase like 1	13.451
chr5	34953701	34954380	-69	Mfsd10	major facilitator superfamily domain	13.496
chr4	1.27E+08	126563980	-34	Zmym1	zinc finger, MYM domain containing 1	24.321
chr7	43311241	43311920	-412	Etfb	electron transferring flavoprotein, beta	13.916
chr5	1.15E+08	115036620	-28	Ankrd13a	ankyrin repeat domain 13a	19.49
chr8	1.08E+08	107531460	-93	Fam96b	family with sequence similarity 96, member B	18.147
chr4	1.34E+08	134203181	85	Syf2	SYF2 homolog, RNA splicing factor (S.	7.75
chr2	1.64E+08	164461060	-414	Ube2c	ubiquitin-conjugating enzyme E2C	20.309
chr7	65571721	65572930	-42	Tm2d3	TM2 domain containing 3	20.036
chr14	74744652	74745600	-106	Gtf2f2	general transcription factor IIF, polypeptide 2	21.956
chr15	89419321	89420000	30	Rabl2	RAB, member RAS oncogene family-like 2	14.365
chr1	1.37E+08	136963551	-29	Arl8a	ADP-ribosylation factor-like 8A	15.896

chr8	1.2E+08	119808480	103	Cenpn	centromere protein N	14.392
chr14	53380681	53381700	76	Mrpl52	mitochondrial ribosomal protein L52	32.963
chr6	1.15E+08	115003980	22	Tamm41	TAM41, mitochondrial translocator assembly	17.21
chr19	6127821	6128810	-100	Snx15	sorting nexin 15	23.623
chr4	1.18E+08	118119400	-11	Ebna1bp2	EBNA1 binding protein 2	24.459
chr2	83444841	83445701	-146	Zc3h15	zinc finger CCCH-type containing 15	17.419
chr7	18307641	18308320	-262	Qpctl	glutaminyl-peptide cyclotransferase-like	20.1
chr5	1.01E+08	100657000	46	Sec31a	Sec31 homolog A (S. cerevisiae)	27.774
chr1	75025522	75025891	-127	Cnppd1	cyclin Pas1/PHO80 domain containing 1	18.762
chr1	75025902	75026780	-28			22.256
chr11	69653761	69654440	-620	Tmem256	transmembrane protein 256	19.543
chr7	1.27E+08	127213720	-28	Zfp688	zinc finger protein 688	19.359
chr11	96857161	96858170	-11	Mrpl10	mitochondrial ribosomal protein L10	18.43
chr6	30459372	30460260	-23			13.264
chr10	90512081	90513390	-103	Ikbip	IKBKB interacting protein	18.506
chr19	42181761	42183050	-101	Avpi1	arginine vasopressin-induced 1	14.952
chr7	1.39E+08	138685320	251	Ppp2r2d	protein phosphatase 2, regulatory subunit B,	12.337
chr5	1.3E+08	130226910	-467	Vkorc1l1	vitamin K epoxide reductase complex, subunit	19.849
chr12	1.11E+08	111186120	-125	Wdr20	WD repeat domain 20	15.048
chr17	72740961	72742320	-64	Ypel5	yippee-like 5 (Drosophila)	19.232
chr13	74403561	74404500	217			15.536
chr7	18731281	18732300	75	Gemin7	gem (nuclear organelle) associated protein 7	14.589
chr15	78669201	78670131	-236	Cdc42ep1	CDC42 effector protein (Rho GTPase binding)	18.29
chr5	1.38E+08	138009060	-156	Ppp1r35	protein phosphatase 1, regulatory subunit 35	21.282
chr7	97355601	97355771	-462	Ints4	integrator complex subunit 4	18.824
chr7	97355782	97356620	53	Ints4	integrator complex subunit 4	19.48
chr11	1.16E+08	116229870	-483	Rnf157	ring finger protein 157	12.204
chr7	29939721	29940740	559	Tbcb	tubulin folding cofactor B	21.573
chr1	1.66E+08	165831940	140	BC055324	cDNA sequence BC055324	23.473
chr16	93599621	93600640	-317	Dopey2	dopey family member 2	24.054
chr3	89544781	89545460	75	Pmvk	phosphomevalonate kinase	11.402
chr7	1.13E+08	113305340	-15	Far1	fatty acyl CoA reductase 1	15.44
chr10	80723141	80724500	-412	Cactin	cactin, spliceosome C complex subunit	16.979
chr19	8886722	8887600	715	Hnrnpul2	heterogeneous nuclear ribonucleoprotein U-	19.388
chr10	84051741	84052760	14	Polr3b	polymerase (RNA) III (DNA directed)	14.904
chr3	1.06E+08	106088160	96	Wdr77	WD repeat domain 77	16.547
chr11	70462961	70463791	-142	Slc25a11	solute carrier family 25 (mitochondrial carrier	16.494
chr4	1.08E+08	108332160	-134	Btf3l4	basic transcription factor 3-like 4	15.149
chr8	1.09E+08	108648121	-40	Gfod2	glucose-fructose oxidoreductase domain	22.068
chr8	72971141	72971820	243	Mau2	MAU2 chromatid cohesion factor homolog (C.	22.766
chr3	1.28E+08	127888620	65	5730508B09Rik	RIKEN cDNA 5730508B09 gene	17.661
chr8	75476941	75477960	-151	Med26	mediator complex subunit 26	20.095
chr18	44505372	44506340	25	Dcp2	DCP2 decapping enzyme homolog (S.	12.292
chr6	35107381	35108060	-48	Nup205	nucleoporin 205	18.24
chr5	1.5E+08	149680301	-119	Medag	mesenteric estrogen dependent adipogenesis	16.475
chr3	41179101	41180120	-15	Pgrmc2	progesterone receptor membrane component	19.795
chr3	1.46E+08	146438000	98	Gng5	guanine nucleotide binding protein (G	15.485
chr19	7307712	7308640	90	Naa40	N(alpha)-acetyltransferase 40, NatD catalytic	18.73
chr7	1.2E+08	119585780	124	2610020H08Rik	RIKEN cDNA 2610020H08 gene	12.726
chr13	38043962	38045190	121	Riok1	RIO kinase 1 (yeast)	28.972
chr4	19496961	19497640	-49	Cpne3	copine III	12.882
chr10	80104352	80105700	-77	Mob3a	MOB kinase activator 3A	27.67
chr9	59548281	59549930	-75	Myo9a	myosin IXa	21.337
chr11	1.15E+08	115236880	324	Kctd2	potassium channel tetramerisation domain	18.353
chr4	1.47E+08	147289020	40	Ubiad1	UbiA prenyltransferase domain containing 1	22.873
chr7	24990681	24990891	-153	Cic	capicua homolog (Drosophila)	17.476
chr17	46143781	46145140	89	Mea1	male enhanced antigen 1	20.208
chr4	1.34E+08	134187481	-139	Tmem50a	transmembrane protein 50A	18.157
chr11	1.06E+08	105852961	-211	Dcaf7	DDB1 and CUL4 associated factor 7	14.81
chr14	30080192	30080820	8	Bap1	Brca1 associated protein 1	11.1
chr12	17291382	17292400	-184	Pdia6	protein disulfide isomerase associated 6	15.634
chr11	1.2E+08	120195440	-200	Faap100	Fanconi anemia core complex associated	32.491
chr4	1.47E+08	146984720	91	Mad2l2	MAD2 mitotic arrest deficient-like 2	12.829
chr8	88730481	88731500	64	Itfg1	integrin alpha FG-GAP repeat containing 1	19.354
chr15	99600012	99601240	-77	Cers5	ceramide synthase 5	30.95
chr8	1.13E+08	112582840	93	Ist1	increased sodium tolerance 1 homolog	14.517
chr11	4117742	4118710	-28	Gatsl3	GATS protein-like 3	19.307
chr12	1.13E+08	113277950	-168	Cdca4	cell division cycle associated 4	14.146
chr7	80774481	80775160	-38	Wdr73	WD repeat domain 73	18.596
chr9	35017042	35017960	-25	Fam118b	family with sequence similarity 118, member	16.033
chr13	1.09E+08	109279740	-28	Ndufaf2	NADH dehydrogenase (ubiquinone) 1 alpha	19.135
chr1	39479781	39480460	-228	Cnot11	CCR4-NOT transcription complex, subunit 11	13.147
chr18	67899701	67900720	-35	Seh1l	SEH1-like (S. cerevisiae	15.372
chr2	59683261	59683860	-115	Wdsub1	WD repeat, SAM and U-box domain	17.424
chr15	96288681	96289700	-313	Scaf11	SR-related CTD-associated factor 11	14.224
chr11	97966072	97967210	-935	Fbxl20	F-box and leucine-rich repeat protein 20	22.826
chr11	97965901	97966061	-275	Fbxl20	F-box and leucine-rich repeat protein 20	10.375
chr19	42034742	42035450	22	Ubtd1	ubiquitin domain containing 1	18.46
chr3	36666621	36667980	136	Anxa5	annexin A5	29.219
chr11	45787801	45788750	83	Lsm11	U7 snRNP-specific Sm-like protein LSM11	19.123
chr5	73535262	73536220	12	Fryl	furry homolog-like (Drosophila)	17.264
chr17	45666081	45666760	-16	Xpo5	exportin 5	12.773
chr2	1.29E+08	128510480	56	Tmem87b	transmembrane protein 87B	17.002
chr12	1.09E+08	108627960	-189	Setd3	SET domain containing 3	15.443
chr4	1.3E+08	129550540	56	Col16a1	collagen, type XVI, alpha 1	18.538
chr19	38119101	38120460	-389	Cep55	centrosomal protein 55	28.842
chr5	1.45E+08	145485660	34	Zfp655	zinc finger protein 655	12.773
chrX	96828941	96829910	641	Kif4	kinesin family member 4	13.785
chr3	1.17E+08	116587300	-142	Sass6	spindle assembly 6 homolog (C. elegans)	20.693
chr13	82188201	82188571	-36	Polr3g	polymerase (RNA) III (DNA directed)	19.378

chr6	1.13E+08	113043540	-120	Gt(ROSA)26Sor	gene trap ROSA 26, Philippe Soriano	18.001
chr17	66000801	66001480	-38	Ndufv2	NADH dehydrogenase (ubiquinone)	13.308
chr9	22139101	22140120	-2	Anln	anillin, actin binding protein	17.209
chr4	1.07E+08	106752180	135	Lrrc42	leucine rich repeat containing 42	20.03
chr16	20534641	20535621	-310	Camk2n2	calcium/calmodulin-dependent protein kinase	13.714
chr4	1.2E+08	120423240	80	Exo5	exonuclease 5	30.863
chr17	48893361	48894380	-61	Mocs1	molybdenum cofactor synthesis 1	21.502
chr5	1.08E+08	108373640	-86	Ccdc18	coiled-coil domain containing 18	22.311
chr7	27637921	27638600	-70	1700049G17Rik	RIKEN cDNA 1700049G17 gene	14.077
chr7	64271352	64271900	-95	Mcee	methylmalonyl CoA epimerase	16.25
chrX	69711561	69712240	-151	Haus7	HAUS augmin-like complex, subunit 7	12.953
chr17	87190621	87191300	180	4833418N02Rik	RIKEN cDNA 4833418N02 gene	17.601
chr3	61451942	61452960	15	Rap2b	RAP2B, member of RAS oncogene family	23.507
chr1	93324561	93325440	-74	Traf3ip1	TRAF3 interacting protein 1	14.542
chr16	4965701	4966720	821	Ubn1	ubinuclein 1	14.678
chr5	1.38E+08	137732980	-83	Pop7	processing of precursor 7, ribonuclease P	20.164
chr7	1.22E+08	121812790	-130	Gga2	golgi associated, gamma adaptin ear	11.201
chr5	1.2E+08	120377680	46	Rbm19	RNA binding motif protein 19	13.274
chr6	91438241	91439311	151	Chchd4	coiled-coil-helix-coiled-coil-helix domain	20.196
chr17	47387841	47387991	-93	Foxp4	forkhead box P4	8.067
chr17	56311652	56312840	-223	Lonp1	lon peptidase 1, mitochondrial	27.47
chr1	1.27E+08	127389160	-82	Slc35f5	solute carrier family 35, member F5	18.781
chr15	79514441	79515770	22	Josd1	Josephin domain containing 1	21.282
chr4	1.26E+08	125605851	-915	Stk40	serine/threonine kinase 40	27.03
chr11	4494461	4495140	18	Mtmr3	myotubularin related protein 3	17.867
chr4	1.36E+08	135583160	-322	Hnrnpr	heterogeneous nuclear ribonucleoprotein R	16.217
chr4	1.49E+08	148799590	-299	Spsb1	splA/ryanodine receptor domain and SOCS	19.798
chr10	12654121	12655140	-173	Stx11	syntaxin 11	24.335
chr10	59346882	59348020	-324	Ddit4	DNA-damage-inducible transcript 4	31.018
chr9	98949181	98949860	43	Pik3cb	phosphatidylinositol 3-kinase, catalytic, beta	13.306
chr10	82120201	82120880	-91	Glt8d2	glycosyltransferase 8 domain containing 2	19.916
chr10	41498021	41499380	-289	Sesn1	sestrin 1	17.584
chr11	70225981	70227000	-264	Pelp1	proline, glutamic acid and leucine rich protein	22.581
chr9	15056292	15056900	-11	Taf1d	TATA box binding protein (Tbp)-associated	16.809
chr11	4536992	4537980	-310	Ascc2	activating signal cointegrator 1 complex	18.854
chr14	97982221	97982900	2	Pibf1	progesterone immunomodulatory binding	15.741
chr1	1.07E+08	107491680	53	Pign	phosphatidylinositol glycan anchor	16.11
chr5	94280641	94281320	719	Ccni	cyclin I	13.106
chr2	1.31E+08	130532120	-24	4930402H24Rik	RIKEN cDNA 4930402H24 gene	18.171
chr13	1.05E+08	105230680	-2	Sgtb	small glutamine-rich tetratricopeptide repeat	17.444
chr18	21039201	21039880	-452	Trappc8	trafficking protein particle complex 8	16.72
chr16	90699081	90699760	-148	Urb1	URB1 ribosome biogenesis 1 homolog (S.	17.8
chr11	1.16E+08	115631280	72	Tsen54	tRNA splicing endonuclease 54 homolog (S.	19.166
chr3	35945252	35946160	19	Atp11b	ATPase, class VI, type 11B	11.468
chr14	1.17E+08	117015740	-184	Tgds	TDP-glucose 4,6-dehydratase	11.39
chr7	78720412	78720880	78	Det1	de-etiolated homolog 1 (Arabidopsis)	15.882
chr17	25306201	25307091	-128	Lmf1	lipase maturation factor 1	19.022
chr15	76365361	76366720	-39	Fbxl6	F-box and leucine-rich repeat protein 6	31.63
chr19	34257892	34258441	-101	Stambpl1	STAM binding protein like 1	11.763
chr8	56028261	56029210	-40	Spcs3	signal peptidase complex subunit 3 homolog	20.512
chr1	74169301	74170320	53	Arpc2	actin related protein 2/3 complex, subunit 2	17.49
chr15	57971021	57972020	1	Wdyhv1	WDYHV motif containing 1	21.778
chr1	1.79E+08	178651300	-375	Sdccag8	serologically defined colon cancer antigen 8	15.82
chr4	1.34E+08	133807680	-57	Mtfr1l	mitochondrial fission regulator 1-like	20.898
chr9	35319541	35320220	-140	Hyls1	hydrolethalus syndrome 1	18.654
chr3	95400261	95401081	15	Cers2	ceramide synthase 2	15.366
chr2	38887161	38887840	50	Golga1	golgi autoantigen, golgin subfamily a, 1	13.582
chr17	33291781	33292460	25	Hnrnpm	heterogeneous nuclear ribonucleoprotein M	23.409
chr7	79533141	79534110	-84	Ticrr	TOPBP1-interacting checkpoint and	22.183
chr4	1.16E+08	116055940	-229	Gpbp1l1	GC-rich promoter binding protein 1-like 1	23.274
chr11	1.21E+08	121268480	-48	Tbcd	tubulin-specific chaperone d	17.289
chr3	97312432	97313440	-167	Bcl9	B cell CLL/lymphoma 9	15.353
chr7	3296602	3297831	-379	Tsen34	tRNA splicing endonuclease 34 homolog (S.	16.378
chr9	53010081	53011100	-83	Ddx10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	15.989
chr11	6343721	6345080	46	H2afv	H2A histone family, member V	21.029
chr11	51810732	51811240	-68	Cdkn2aipnl	CDKN2A interacting protein N-terminal like	17.98
chr5	1.38E+08	137831240	-164	Mospd3	motile sperm domain containing 3	13.651
chr2	73014792	73015680	50	Ola1	Obg-like ATPase 1	18.283
chr15	6654821	6655840	-266	Rictor	RPTOR independent companion of MTOR,	15.714
chr16	4594482	4595430	-8	Coro7	coronin 7	12.821
chr5	1.26E+08	125766000	-14	Aacs	acetoacetyl-CoA synthetase	32.614
chr6	88807112	88808340	-150	Abtb1	ankyrin repeat and BTB (POZ) domain	22.575
chr9	44249301	44250581	-190	Bcl9l	B cell CLL/lymphoma 9-like	20.195
chr5	1.4E+08	139634600	-48	Gpr146	G protein-coupled receptor 146	18.093
chr9	14026361	14027040	2	Sesn3	sestrin 3	19.437
chr10	76702302	76703311	133	Gm10941	predicted gene 10941	28.737
chr1	37243941	37244620	-104	Inpp4a	inositol polyphosphate-4-phosphatase, type I	14.698
chr5	1.23E+08	123110940	-205	Rnf34	ring finger protein 34	22.271
chr9	1.23E+08	123378211	-894	Sacm1l	SAC1 (suppressor of actin mutations 1,	13.114
chr9	1.23E+08	123378860	-39	Sacm1l	SAC1 (suppressor of actin mutations 1,	17.599
chr3	86310302	86310700	-116	Lrba	LPS-responsive beige-like anchor	13.101
chr7	83760462	83760700	-55	Mesdc1	mesoderm development candidate 1	14.58
chr9	66774352	66774980	-38	Lactb	lactamase, beta	18.162
chr12	8699921	8700940	163	Pum2	pumilio RNA-binding family member 2	15.234
chr16	4509081	4509760	-521	Glis2	GLIS family zinc finger 2	14.501
chr3	88639361	88640040	57	Ubqln4	ubiquilin 4	21.647
chr2	1.81E+08	180518920	-229	Ogfr	opioid growth factor receptor	12.099
chr12	91995161	91995840	-294	Gtf2a1	general transcription factor II A, 1	14.63
chr5	1.38E+08	137564000	-290	Slc12a9	solute carrier family 12 (potassium/chloride	27.859
chr15	99529901	99530920	89	Smarcd1	SWI/SNF related, matrix associated, actin	21.277

chr9	21668201	21669140	-147	Rab3d	RAB3D, member RAS oncogene family	15.021
chr10	1.27E+08	126692500	-270	Mbd6	methyl-CpG binding domain protein 6	21.483
chr17	34608941	34609841	428	Vars	valyl-tRNA synthetase	15.867
chr15	81974001	81975020	-14	Srebf2	sterol regulatory element binding factor 2	31.3
chr15	76498382	76499630	71	Ppp1r16a	protein phosphatase 1, regulatory (inhibitor)	18.254
chr16	18261401	18262080	-5	Arvcf	armadillo repeat gene deleted in velo-cardio-	12.773
chr8	42009982	42010851	155	Cnot7	CCR4-NOT transcription complex, subunit 7	13.157
chr8	42009402	42009971	885	Cnot7	CCR4-NOT transcription complex, subunit 7	11.211
chr1	36415701	36416660	37	Cnnm4	cyclin M4	16.272
chr8	1.15E+08	114899260	888	Terf2ip	telomeric repeat binding factor 2, interacting	24.543
chr3	1.45E+08	144507820	122	Hs2st1	heparan sulfate 2-O-sulfotransferase 1	17.644
chr10	62045921	62047400	-105	Ddx50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	19.341
chr8	97764972	97765980	-35	Dok4	docking protein 4	21.305
chr11	1.14E+08	114491940	-128	Ttyh2	tweety homolog 2 (Drosophila)	31.085
chr11	88533961	88534980	-113	Msi2	musashi RNA-binding protein 2	14.67
chr11	97560812	97561640	239	Mir8102	microRNA 8102	25.211
chr5	1.09E+08	108934501	-225	Fgfrl1	fibroblast growth factor receptor-like 1	13.645
chr1	1.66E+08	166086170	-16	Slc19a2	solute carrier family 19 (thiamine transporter),	16.217
chr1	1.53E+08	153107050	19	Ivns1abp	influenza virus NS1A binding protein	14.76
chr17	34742901	34743580	6	Bag6	BCL2-associated athanogene 6	17.056
chr10	79980242	79981940	-666	Klf16	Kruppel-like factor 16	56.747
chr2	1.53E+08	152933020	13	Plagl2	pleiomorphic adenoma gene-like 2	20.932
chr2	1.53E+08	152932541	633	Plagl2	pleiomorphic adenoma gene-like 2	15.186
chr17	26784181	26785200	-203	Itpr3	inositol 1,4,5-triphosphate receptor 3	21.785
chr2	79435712	79436580	-118	Ssfa2	sperm specific antigen 2	21.203
chr3	20226941	20227860	61	Hps3	Hermansky-Pudlak syndrome 3 homolog	15.972
chr5	97237281	97238300	-201	Bmp2k	BMP2 inducible kinase	25.412
chr3	51648512	51649400	-204	Setd7	SET domain containing (lysine	13.466
chr8	1.1E+08	109920640	-155	Vps4a	vacuolar protein sorting 4a (yeast)	18.297
chr10	43589701	43590380	111	Qrsl1	glutaminyl-tRNA synthase (glutamine-	19.415
chr15	76349381	76350060	-336	Scrt1	scratch homolog 1, zinc finger protein	14.557
chr7	27181682	27182660	-429	Sertad3	SERTA domain containing 3	13.829
chr19	53091681	53092550	-149	Xpnpep1	X-prolyl aminopeptidase (aminopeptidase P)	16.129
chr1	1.83E+08	182563340	-58	Acbd3	acyl-Coenzyme A binding domain containing	28.152
chr7	15467621	15468471	-59	Bbc3	BCL2 binding component 3	17.659
chr5	1.08E+08	107838480	-28	Rpap2	RNA polymerase II associated protein 2	16.952
chr6	83102121	83102561	-401	Rtkn	rhotekin	17.25
chr6	83102572	83102800	-56	Rtkn	rhotekin	11.873
chr5	65771641	65772660	-180	Smim14	small integral membrane protein 14	20.197
chr11	78366732	78367540	-206	Tmem97	transmembrane protein 97	15.557
chr9	1.19E+08	118775471	-208	Ctdspl	CTD (carboxy-terminal domain, RNA	23.101
chr4	1.21E+08	120515660	-128	Smap2	small ArfGAP 2	17.534
chr9	7763922	7764920	-177	Tmem123	transmembrane protein 123	16.114
chr5	31770762	31771930	4	Gpn1	GPN-loop GTPase 1	24.711
chr5	1.3E+08	130309420	-46	Asl	argininosuccinate lyase	14.003
chr17	74199901	74200571	-391	Memo1	mediator of cell motility 1	15.403
chr2	32217381	32218060	-179	Ptges2	prostaglandin E synthase 2	16.76
chr1	1.08E+08	107999300	80	Gm20753	predicted gene, 20753	11.503
chr2	84527772	84528710	-134	Clp1	CLP1, cleavage and polyadenylation factor I	13.875
chr2	1.53E+08	152853120	38	Tm9sf4	transmembrane 9 superfamily protein member	13.312
chr3	1.04E+08	104350420	-273	Magi3	membrane associated guanylate kinase, WW	21.313
chr4	1.09E+08	108700720	-6	Osbpl9	oxysterol binding protein-like 9	21.59
chr4	1.29E+08	128964380	-113	Bsdc1	BSD domain containing 1	31.795
chr5	50346962	50347780	-127	Adgra3	adhesion G protein-coupled receptor A3	15.088
chr5	1.24E+08	123655641	-295	Mlxip	MLX interacting protein	18.865
chr5	72838602	72839490	-266	Nfxl1	nuclear transcription factor, X-box binding-like	19.152
chr2	1.64E+08	164477720	-16	Snx21	sorting nexin family member 21	20.221
chr6	1.13E+08	113343741	41	Tada3	transcriptional adaptor 3	16.867
chr6	88049801	88050361	-33	Rpn1	ribophorin I	15.786
chr6	1.19E+08	119445060	-736	Fbxl14	F-box and leucine-rich repeat protein 14	19.421
chr7	44737592	44738530	-231	Ptov1	prostate tumor over expressed gene 1	20.249
chr8	98220221	98221580	179	Zfp319	zinc finger protein 319	18.074
chr8	1.1E+08	110183251	77	Nfat5	nuclear factor of activated T cells 5	21.243
chr8	11636232	11637000	-887	Ankrd10	ankyrin repeat domain 10	21
chr8	73163382	73164260	-410	Armc6	armadillo repeat containing 6	20.62
chr9	1.22E+08	122143810	-94	Ano10	anoctamin 10	17.421
chr10	80025121	80026140	-279	Csnk1g2	casein kinase 1, gamma 2	23.511
chr11	93700941	93701721	525	Utp18	UTP18, small subunit (SSU) processome	21.218
chr11	23155092	23156040	-475	Xpo1	exportin 1, CRM1 homolog (yeast)	18.44
chr11	1.01E+08	100936140	114	Fam134c	family with sequence similarity 134, member	16.99
chr14	19177042	19178000	-59	Dnajc9	DnaJ (Hsp40) homolog, subfamily C, member	11.143
chr14	24526782	24527940	7	Ppif	peptidylprolyl isomerase F (cyclophilin F)	19.852
chr15	81843101	81844120	-14	Xrcc6	X-ray repair complementing defective repair in	37.601
chr17	35468801	35470080	69	Nrm	nurim (nuclear envelope membrane protein)	20.381
chr17	56934361	56935380	84	Trip10	thyroid hormone receptor interactor 10	20.375
chr19	5424021	5425720	109	Drap1	Dr1 associated protein 1 (negative cofactor 2	27.127
chr4	1.29E+08	128692720	-59	Yars	tyrosyl-tRNA synthetase	20.724
chr19	5040841	5041520	-224	Brms1	breast cancer metastasis-suppressor 1	14.635
chr12	81179052	81179760	-195	Actn1	actinin, alpha 1	14.225
chr3	89187202	89188460	63	Fdps	farnesyl diphosphate synthetase	30.514
chr2	91763961	91764980	-68	Dgkz	diacylglycerol kinase zeta	17.028
chr17	34457662	34459000	-71	Skiv2l	superkiller viralicidic activity 2-like (S.	28.244
chr11	1.14E+08	113501500	409	D11Wsu47e	DNA segment, Chr 11, Wayne State	43.587
chrX	6998272	6999191	-59	Otud5	OTU domain containing 5	13.427
chr10	7646052	7647540	-483	Tab2	TGF-beta activated kinase 1/MAP3K7 binding	21.565
chr12	77173542	77174220	-191	Mthfd1	methylenetetrahydrofolate dehydrogenase	12.465
chr6	1.25E+08	125097900	-96	Nop2	NOP2 nucleolar protein	20.735
chr15	89008261	89009280	-216	Plxnb2	plexin B2	23.572
chr5	34830621	34831270	-109	Tnip2	TNFAIP3 interacting protein 2	22.692
chr18	24746232	24747240	91	Slc39a6	solute carrier family 39 (metal ion transporter),	24.593

chr7	1.28E+08	127758871	-161	Fus	fused in sarcoma	15.63
chr2	1.8E+08	180049040	-74	Osbpl2	oxysterol binding protein-like 2	16.14
chr7	1.27E+08	126999961	45	Tbc1d10b	TBC1 domain family, member 10b	13.141
chr15	25928442	25929420	-160	Zfp622	zinc finger protein 622	34.355
chr11	71857981	71859000	-207	Fam64a	family with sequence similarity 64, member A	16.923
chr9	98105641	98106320	45	Nmnat3	nicotinamide nucleotide adenylyltransferase 3	13.169
chr15	59477221	59478580	-435	Trib1	tribbles homolog 1 (Drosophila)	21.495
chr19	32454322	32455380	-362	2700046G09Rik	RIKEN cDNA 2700046G09 gene	16.166
chr15	80537841	80538860	-218	Tnrc6b	trinucleotide repeat containing 6b	19.342
chr10	59097441	59098410	5	Micu1	mitochondrial calcium uptake 1	19.387
chr11	79778102	79779300	-119	Utp6	UTP6, small subunit (SSU) processome	12.772
chr13	71105422	71105900	-655	Ice1	interactor of little elongation complex ELL	11.837
chr13	71104962	71105411	-180	Ice1	interactor of little elongation complex ELL	19.59
chr19	5688802	5689220	-103	Pcnxl3	pecanex-like 3 (Drosophila)	22.612
chr19	8996092	8996831	-60	Rom1	rod outer segment membrane protein 1	14.217
chr2	30803682	30804680	-107	Usp20	ubiquitin specific peptidase 20	17.818
chr3	88999761	89000410	-208	Msto1	misato homolog 1 (Drosophila)	15.917
chr5	1.23E+08	122615560	20	Vps29	vacuolar protein sorting 29 (S. pombe)	18.567
chr6	72284352	72285360	-136	Tmem150a	transmembrane protein 150A	16.863
chr7	27156141	27157160	-88	Blvrb	biliverdin reductase B (flavin reductase	22.534
chr9	66390781	66391990	-264			20.913
chr17	47157661	47158600	-203	Prickle4	prickle homolog 4 (Drosophila)	15.832
chr13	23542582	23542960	-112	Hist1h3g	histone cluster 1, H3g	18.577
chr11	97838741	97839400	-353	Cacnb1	calcium channel, voltage-dependent, beta 1	15.367
chr6	1.25E+08	124629040	-23	Lpcat3	lysophosphatidylcholine acyltransferase 3	15.158
chr4	1.39E+08	138583660	500	Akr7a5	aldo-keto reductase family 7, member A5	12.446
chr7	1.41E+08	140793320	-60	Athl1	ATH1, acid trehalase-like 1 (yeast)	11.22
chr9	44716461	44717110	-190	Ube4a	ubiquitination factor E4A	13.495
chr8	1.09E+08	109099880	306	Slc7a6os	solute carrier family 7, member 6 opposite	12.395
chr8	1.09E+08	109099621	821	Slc7a6os	solute carrier family 7, member 6 opposite	14.303
chrX	70620721	70621740	38	Ubl4a	ubiquitin-like 4A	17.807
chr8	1.1E+08	109782940	72	Cirh1a	cirrhosis, autosomal recessive 1A (human)	17.263
chr1	1.59E+08	158556280	-19	Fam20b	family with sequence similarity 20, member B	19.242
chr9	21037862	21038860	10	Kri1	KRI1 homolog (S. cerevisiae)	20.195
chr11	60232832	60233941	46	Gid4	GID complex subunit 4, VID24 homolog (S.	22.808
chr11	60233952	60234400	836	Gid4	GID complex subunit 4, VID24 homolog (S.	13.962
chr13	85762281	85762960	-24	Rasa1	RAS p21 protein activator 1	26.458
chr13	1.09E+08	109011820	-499	Zswim6	zinc finger SWIM-type containing 6	13.202
chr14	53508181	53509120	-84	Haus4	HAUS augmin-like complex, subunit 4	10.999
chr15	86041842	86042780	86	Tbc1d22a	TBC1 domain family, member 22a	27.767
chr15	88646841	88648200	108	Creld2	cysteine-rich with EGF-like domains 2	18.625
chr17	46174192	46175060	-28	Pex6	peroxisomal biogenesis factor 6	20.067
chr19	5050021	5051380	-108	Rin1	Ras and Rab interactor 1	16.166
chr19	42033861	42034731	151	Mms19	MMS19 (MET18 S. cerevisiae)	19.011
chr19	45068361	45068791	55	Lzts2	leucine zipper, putative tumor suppressor 2	14.605
chr2	1.04E+08	104391900	68	Cstf3	cleavage stimulation factor, 3' pre-RNA,	21.098
chr3	1.06E+08	105929720	57	Rap1a	RAS-related protein-1a	16.81
chr4	1.34E+08	134040580	-160	Ldlrap1	low density lipoprotein receptor adaptor	13.91
chr6	52569441	52570460	-72	Hibadh	3-hydroxyisobutyrate dehydrogenase	12.057
chr8	1.28E+08	127609140	61	Arv1	ARV1 homolog (yeast)	28.68
chr9	21548682	21549540	-163	Kank2	KN motif and ankyrin repeat domains 2	26.803
chr9	55310102	55310860	-101	Etfa	electron transferring flavoprotein, alpha	12.975
chr9	66147632	66148700	-290	Herc1	hect (homologous to the E6-AP (UBE3A)	19.646
chr9	1.06E+08	106335680	-70	Rrp9	RRP9, small subunit (SSU) processome	15.507
chr15	1.02E+08	101902420	-67	Eif4b	eukaryotic translation initiation factor 4B	17.357
chr10	42166801	42167480	-160	Lace1	lactation elevated 1	17.604
chr7	18517761	18518191	29	Cd3eap	CD3E antigen, epsilon polypeptide associated	15.419
chr17	34506261	34507480	-160	Ehmt2	euchromatic histone lysine N-	18.286
chr5	64247761	64248440	-68	Rell1	RELT-like 1	24.013
chr11	50067721	50069420	-188	Mgat4b	mannoside acetylglucosaminyltransferase 4,	21.78
chr14	39875201	39876220	-190	Tspan14	tetraspanin 14	15.307
chr11	1.09E+08	109428320	-501	Wipi1	WD repeat domain, phosphoinositide	14.882
chr7	45022121	45022991	24	Aldh16a1	aldehyde dehydrogenase 16 family, member	16.057
chr7	1.29E+08	128531900	17	Mcmbp	MCM (minichromosome maintenance	14.591
chr3	1.28E+08	127830140	54	Ap1ar	adaptor-related protein complex 1 associated	23.503
chr6	1.25E+08	125061951	-216	Chd4	chromodomain helicase DNA binding protein	12.987
chr9	44518782	44518920	-48	Arcn1	archain 1	20.341
chr5	1.36E+08	135917720	99	Rhbdd2	rhomboid domain containing 2	16.848
chr10	75974701	75975720	-111	Lss	lanosterol synthase	19.789
chr10	84005602	84006631	-630	Tcp11l2	t-complex 11 (mouse) like 2	15.742
chr10	84006642	84006860	5	Tcp11l2	t-complex 11 (mouse) like 2	13.546
chr11	94824981	94826311	-323	Samd14	sterile alpha motif domain containing 14	21.218
chr11	96845722	96846510	74	Scrn2	secernin 2	10.826
chr11	1.01E+08	100988840	-938	Plekhh3	pleckstrin homology domain containing, family	12.902
chr12	70102592	70102931	-2	Mgat2	mannoside acetylglucosaminyltransferase 2	12.26
chr15	31168141	31169500	-154	Dap	death-associated protein	26.313
chr17	3513742	3514580	34	Tfb1m	transcription factor B1, mitochondrial	26.953
chr18	61680152	61681010	-370	Csnk1a1	casein kinase 1, alpha 1	11.597
chr19	8937942	8938940	-163	Ubxn1	UBX domain protein 1	25.63
chr1	74217902	74218600	10	Pnkd	paroxysmal nonkinesiogenic dyskinesia	25.436
chr1	89157861	89158401	-38	Gigyf2	GRB10 interacting GYF protein 2	17.778
chr4	98415381	98416060	-108	Usp1	ubiquitin specific peptidase 1	20.642
chr4	1.16E+08	116219140	-87	Tesk2	testis-specific kinase 2	17.306
chr4	1.26E+08	125705820	44	Thrap3	thyroid hormone receptor associated protein 3	17.871
chr7	29989522	29990260	-710	Wdr62	WD repeat domain 62	13.943
chr7	1.26E+08	126357940	-2	Eif3c	eukaryotic translation initiation factor 3,	12.061
chr7	1.27E+08	127137001	-139	Zfp768	zinc finger protein 768	28.938
chr8	1.13E+08	113107460	31	Cmtr2	cap methyltransferase 2	21.234
chr8	1.23E+08	122748500	-122	Klhl36	kelch-like 36	14.393
chr9	37237982	37238840	-581	Msantd2	Myb/SANT-like DNA-binding domain	25.42

chr10	92590161	92590840	-175	Cdk17	cyclin-dependent kinase 17	13.081
chr2	29955361	29956380	-10	Tbc1d13	TBC1 domain family, member 13	15.368
chr4	1.03E+08	102613020	358	Mier1	mesoderm induction early response 1	19.171
chr2	24771381	24772400	104	Zmynd19	zinc finger, MYND domain containing 19	22.081
chr11	1.1E+08	110154220	96	Abca5	ATP-binding cassette, sub-family A (ABC1),	17.875
chr17	44897092	44898020	144			16.001
chr18	7868621	7869410	-180	Wac	WW domain containing adaptor with coiled-	11.29
chr11	52239641	52240051	-5	9530068E07Rik	RIKEN cDNA 9530068E07 gene	12.561
chr2	26266701	26268060	-155	Sec16a	SEC16 homolog A, endoplasmic reticulum	21.736
chr19	5272381	5273740	59	Pacs1	phosphofurin acidic cluster sorting protein 1	26.276
chr16	17841501	17842180	-58	Slc25a1	solute carrier family 25 (mitochondrial carrier,	16.325
chr4	1.25E+08	124630740	-166	Zc3h12a	zinc finger CCCH type containing 12A	23.733
chr5	1.38E+08	138494240	-22	6330418K02Rik	RIKEN cDNA 6330418K02 gene	12.262
chrX	90487032	90487940	-163	Klhl15	kelch-like 15	11.812
chr4	1.26E+08	125932600	-244	Ago3	argonaute RISC catalytic subunit 3	20.179
chr4	1.26E+08	125970680	94	Ago1	argonaute RISC catalytic subunit 1	11.704
chr7	1.1E+08	109778040	-159	Tmem41b	transmembrane protein 41B	27.377
chr13	36742572	36743120	-903	Nrn1	neuritin 1	15.544
chr13	36742101	36742561	-388	Nrn1	neuritin 1	19.978
chr10	82963622	82964080	88	Aldh1l2	aldehyde dehydrogenase 1 family, member	27.559
chr3	1.08E+08	107759940	75	Strip1	striatin interacting protein 1	19.837
chr5	73192502	73193840	-326	Slain2	SLAIN motif family, member 2	28.561
chr12	1.01E+08	101126880	-292	Rps6ka5	ribosomal protein S6 kinase, polypeptide 5	18.085
chr8	28489302	28490300	66	Erlin2	ER lipid raft associated 2	26.926
chr11	1.1E+08	109538480	15	Fam20a	family with sequence similarity 20, member A	16.433
chr18	38080681	38081360	-58	Hdac3	histone deacetylase 3	15.144
chr2	29899601	29900960	-495	Pkn3	protein kinase N3	13.773
chr9	44056192	44057200	-30	Hinfp	histone H4 transcription factor	24.843
chr5	1.41E+08	140642280	-89	Snx8	sorting nexin 8	25.481
chr8	13287201	13288021	-379	Tmco3	transmembrane and coiled-coil domains 3	12.744
chr8	1.26E+08	126219331	-37	Spire2	spire homolog 2 (Drosophila)	29.469
chr8	1.27E+08	126835980	-115	Nup133	nucleoporin 133	16.541
chr2	26202441	26203120	-118	Snapc4	small nuclear RNA activating complex,	24.754
chr11	23397441	23398460	89	Ahsa2	AHA1, activator of heat shock protein ATPase	17.941
chr8	75499542	75500400	66	Smim7	small integral membrane protein 7	18.322
chr2	30027482	30028371	-218	Ccbl1	cysteine conjugate-beta lyase 1	16.169
chr1	58917921	58918600	143	Stradb	STE20-related kinase adaptor beta	14.451
chr10	42366802	42367400	-230	Ostm1	osteopetrosis associated transmembrane	16.985
chr2	71168121	71168961	-148	Slc25a12	solute carrier family 25 (mitochondrial carrier,	14.512
chr9	65384432	65385630	-180	Pif1	PIF1 5'-to-3' DNA helicase homolog (S.	28.07
chrX	6919001	6920020	-110	Tfe3	transcription factor E3	15.056
chr1	40734721	40735740	-27	Mfsd9	major facilitator superfamily domain	25.079
chr12	1.05E+08	105411560	-361	Syne3	spectrin repeat containing, nuclear envelope	17.293
chr10	3133812	3134781	-8	Cnksr3	Cnksr family member 3	18.388
chr10	1.1E+08	110414660	-225	Zdhhc17	zinc finger, DHHC domain containing 17	15.035
chr11	23794901	23795750	-55	Papolg	poly(A) polymerase gamma	18.277
chr12	85250921	85252280	-31	Fam161b	family with sequence similarity 161, member	22.508
chr1	1.63E+08	162908280	242			22.997
chr1	1.64E+08	163714080	77	Suco	SUN domain containing ossification factor	18.129
chr2	71673361	71674380	-193	Pdk1	pyruvate dehydrogenase kinase, isoenzyme 1	19.479
chr2	1.56E+08	155888300	-128	Phf20	PHD finger protein 20	23.08
chr3	84125612	84126540	12	D930015E06Rik	RIKEN cDNA D930015E06 gene	18.474
chr4	32292222	32293200	-9	Map3k7	mitogen-activated protein kinase kinase	12.724
chr4	1.15E+08	115236200	-145	Efcab14	EF-hand calcium binding domain 14	15.728
chr5	1.01E+08	101086760	-111	Agpat9	1-acylglycerol-3-phosphate O-acyltransferase	24.081
chr5	1.09E+08	108701740	-234	Pcgf3	polycomb group ring finger 3	16.773
chr5	1.18E+08	118417050	12	Fbxw8	F-box and WD-40 domain protein 8	27.098
chr5	1.22E+08	121659140	72	Naa25	N(alpha)-acetyltransferase 25, NatB auxiliary	17.688
chr7	1.28E+08	127538080	-353	Fbxl19	F-box and leucine-rich repeat protein 19	14.116
chr8	73162602	73163371	-229	Sugp2	SURP and G patch domain containing 2	15.797
chr8	1.3E+08	129857800	-171	Rbm34	RNA binding motif protein 34	26.82
chr9	78373401	78374420	-181	Slc17a5	solute carrier family 17 (anion/sugar	14.48
chr10	1.28E+08	127780500	-83	Ankrd52	ankyrin repeat domain 52	15.212
chr11	83278921	83279600	-104	Mmp28	matrix metallopeptidase 28 (epilysin)	16.224
chr12	40955381	40956151	447	Zfp277	zinc finger protein 277	19.987
chr19	29871922	29872740	-325	9930021J03Rik	RIKEN cDNA 9930021J03 gene	20.572
chr4	43599561	43600240	64	Gba2	glucosidase beta 2	13.343
chr10	58616142	58617700	283	Sept10	septin 10	36.18
chr15	12149232	12150240	-83	Mtmr12	myotubularin related protein 12	25.04
chr17	67908541	67909900	-167	Arhgap28	Rho GTPase activating protein 28	39.703
chr9	1.09E+08	108848960	-158	Pfkfb4	6-phosphofructo-2-kinase/fructose-2,6-	18.247
chr4	46158912	46160100	69	Tstd2	thiosulfate sulfurtransferase (rhodanese)-like	17.131
chr3	27902042	27902440	-729	Fndc3b	fibronectin type III domain containing 3B	14.274
chr3	27901081	27902031	-44	Fndc3b	fibronectin type III domain containing 3B	18.747
chr13	93630922	93632100	52	Zfyve16	zinc finger, FYVE domain containing 16	21.941
chr5	35265592	35266770	-124	Rgs12	regulator of G-protein signaling 12	16.928
chr4	5570901	5571580	-86	Fam110b	family with sequence similarity 110, member	15.58
chr16	32166381	32167340	-88	Fbxo45	F-box protein 45	24.544
chr10	1.28E+08	128077320	-113	Suox	sulfite oxidase	18.809
chr10	77977142	77977601	-258	Ilvbl	ilvB (bacterial acetolactate synthase)-like	48.209
chr11	1.16E+08	116397980	-103	Ube2o	ubiquitin-conjugating enzyme E2O	16.901
chr1	99599941	99600950	53	Ppip5k2	diphosphoinositol pentakisphosphate kinase 2	18.945
chr11	32354401	32354911	-716	Ubtd2	ubiquitin domain containing 2	23.588
chr11	32354922	32355760	-31	Ubtd2	ubiquitin domain containing 2	24.358
chr8	88381992	88383000	-226	Gpt2	glutamic pyruvate transaminase (alanine	16.643
chr5	1.4E+08	139989440	-13	Micall2	MICAL-like 2	37.592
chr1	95584201	95585560	364	Thap4	THAP domain containing 4	24.83
chr11	62464121	62464800	258	Lrrc75a	leucine rich repeat containing 75A	14.443
chr7	44920772	44921140	-33	Prr12	proline rich 12	12.984
chr1	74533441	74534361	703	Rnf25	ring finger protein 25	18.348

chr9	82943001	82943680	-15	Hmgn3	high mobility group nucleosomal binding	13.345
chr8	36434061	36434690	-168	Tnks	tankyrase, TRF1-interacting ankyrin-related	10.277
chr15	80091081	80092100	-29	Rps19bp1	ribosomal protein S19 binding protein 1	32.232
chr16	35689542	35690820	48	Hspbap1	Hspb associated protein 1	18.454
chr7	1.31E+08	131202260	1	Acadsb	acyl-Coenzyme A dehydrogenase,	15.797
chr15	96527572	96528380	-244	Slc38a2	solute carrier family 38, member 2	19.365
chr17	14679172	14680180	24	Wdr27	WD repeat domain 27	22.556
chr13	84694742	84695360	-355	Tmem161b	transmembrane protein 161B	14.118
chr10	62315422	62316490	-34	Slc25a16	solute carrier family 25 (mitochondrial carrier,	14.562
chr15	58653061	58654080	-60	Tmem65	transmembrane protein 65	16.573
chr4	1.25E+08	124569420	-111	Snip1	Smad nuclear interacting protein 1	20.452
chr3	1.38E+08	138427260	19	Metap1	methionyl aminopeptidase 1	28.362
chr2	51894202	51895220	-135	Rif1	Rap1 interacting factor 1 homolog (yeast)	15.388
chr7	5986782	5988000	71	Zfp28	zinc finger protein 28	23.304
chr11	68507621	68508300	-150	Myh10	myosin, heavy polypeptide 10, non-muscle	19.698
chr14	97929072	97929520	-26	Mzt1	mitotic spindle organizing protein 1	17.812
chr14	97928202	97929061	639	Mzt1	mitotic spindle organizing protein 1	13.594
chr2	25084181	25085200	83	Tprn	taperin	34.351
chr4	1.33E+08	132752660	-59	Fam46b	family with sequence similarity 46, member B	15.747
chr11	50135381	50136060	39	Maml1	mastermind like 1 (Drosophila)	16.096
chr15	95618881	95618911	19	Ano6	anoctamin 6	8.333
chr19	7483752	7484760	-413	2700081O15Rik	RIKEN cDNA 2700081O15 gene	15.77
chr14	66669602	66670510	628	Kctd9	potassium channel tetramerisation domain	12.238
chr9	1.07E+08	106745960	-399	Rbm15b	RNA binding motif protein 15B	24.308
chr5	1.15E+08	115419800	-115	Mlec	malectin	17.711
chr5	1.23E+08	123276180	-21	Orai1	ORAI calcium release-activated calcium	19.91
chr9	48736672	48737950	-6	Usp28	ubiquitin specific peptidase 28	22.34
chr10	1.11E+08	110569020	-232	Osbpl8	oxysterol binding protein-like 8	15.268
chr11	60592761	60593440	460	Top3a	topoisomerase (DNA) III alpha	18.847
chr4	43690001	43691020	439	Tmem8b	transmembrane protein 8B	12.205
chr14	61791261	61791521	-409	Wdfy2	WD repeat and FYVE domain containing 2	15.577
chr6	1.25E+08	124975500	133	Zfp384	zinc finger protein 384	15.053
chr13	23588521	23589271	-171	Hist1h4d	histone cluster 1, H4d	18.187
chr18	38094961	38096250	100	Fchsd1	FCH and double SH3 domains 1	16.419
chr15	76550672	76551680	-76	C030006K11Rik	RIKEN cDNA C030006K11 gene	18.384
chr6	85880941	85881690	-4	Cml1	camello-like 1	13.523
chr11	1.07E+08	106949040	-688	Bptf	bromodomain PHD finger transcription factor	27.956
chr17	95053801	95055090	236	2700099C18Rik	NDC80 homolog, kinetochore complex	17.793
chr8	1.14E+08	114409320	-30	Wdr59	WD repeat domain 59	27.213
chr9	1.03E+08	103163820	-141	Topbp1	topoisomerase (DNA) II binding protein 1	15.106
chr7	1.28E+08	128030320	-501	9130023H24Rik	RIKEN cDNA 9130023H24 gene	28.923
chr4	1.08E+08	108118300	-98	Cc2d1b	coiled-coil and C2 domain containing 1B	23.32
chr1	75361681	75363030	264	Chpf	chondroitin polymerizing factor	17.181
chr11	1.07E+08	106605300	-206	Ddx5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	25.665
chr4	43287852	43288460	-103	Atp8b5	ATPase, class I, type 8B, member 5	12.735
chr4	1.55E+08	154953600	-537	9430015G10Rik	RIKEN cDNA 9430015G10 gene	17.004
chr8	86588821	86589840	-46	Pkn1	protein kinase N1	13.391
chr5	33102061	33103010	-52	Pisd	phosphatidylserine decarboxylase	23.827
chr15	81226352	81227360	93	St13	suppression of tumorigenicity 13	23.965
chr11	68248032	68248751	71	Pik3r5	phosphoinositide-3-kinase, regulatory subunit	20.288
chr13	74674201	74675100	52	Exoc3	exocyst complex component 3	17.944
chr11	1.19E+08	119308370	-15	Endov	endonuclease V	26.468
chr1	21064022	21065040	-155	Tram2	translocating chain-associating membrane	21.702
chr6	1.16E+08	116159640	-137	Tmcc1	transmembrane and coiled coil domains 1	18.289
chr15	78935421	78936780	-138	Micall1	microtubule associated monooxygenase,	22.223
chr5	74350181	74350860	-412	Usp46	ubiquitin specific peptidase 46	17.842
chr11	84644701	84645880	-83	4930502E09Rik	RIKEN cDNA 4930502E09 gene	23.237
chr19	41901261	41902170	-272	Frat2	frequently rearranged in advanced T cell	17.897
chr2	30107942	30109040	49	Nup188	nucleoporin 188	27.434
chr6	1.35E+08	134796400	-2	Crebl2	cAMP responsive element binding protein-like	18.318
chr7	80119352	80120320	-53	Ttll13	tubulin tyrosine ligase-like family, member 13	17.08
chr8	75421282	75422420	-248	Slc35e1	solute carrier family 35, member E1	17.728
chr11	1.13E+08	113500311	265	Fam104a	family with sequence similarity 104, member	34.966
chr10	1.17E+08	116553360	-96	Frs2	fibroblast growth factor receptor substrate 2	28.428
chr5	31324282	31325560	222	Slc5a6	solute carrier family 5 (sodium-dependent	19.171
chr3	1.53E+08	152651840	-100	Pigk	phosphatidylinositol glycan anchor	25.847
chr9	1.07E+08	107439320	-416	Hyal3	hyaluronoglucosaminidase 3	15.33
chr17	79804121	79805070	-146	Atl2	atlastin GTPase 2	20.667
chr10	61110241	61110920	-40	Aifm2	apoptosis-inducing factor, mitochondrion-	17.378
chr6	1.2E+08	119814640	318	3110021A11Rik	RIKEN cDNA 3110021A11 gene	23.439
chr7	30243341	30244700	-200	Arhgap33	Rho GTPase activating protein 33	19.789
chr5	33946281	33947640	-468	Fam53a	family with sequence similarity 53, member A	20.548
chr5	1.43E+08	142882620	52	Wipi2	WD repeat domain, phosphoinositide	19.048
chr9	22225492	22226320	-211	Bbs9	Bardet-Biedl syndrome 9 (human)	10.659
chr12	1.06E+08	106086800	-31	Gskip	GSK3B interacting protein	15.164
chr1	1.93E+08	193276060	493			16.959
chr7	99016501	99017180	-504	Uvrag	UV radiation resistance associated gene	21.24
chr13	13746201	13747220	-90	B3galnt2	UDP-GalNAc:betaGlcNAc beta 1,3-	17.294
chr15	75736622	75737380	11	Tigd5	tigger transposable element derived 5	28.131
chr15	75735492	75736611	548	Eef1d	eukaryotic translation elongation factor 1 delta	23.823
chr17	44239441	44240800	-106	Supt3	suppressor of Ty 3	30.734
chr1	1.82E+08	181505600	85	Sccpdh	saccharopine dehydrogenase (putative)	41.436
chr3	1.43E+08	142820390	-325	Pkn2	protein kinase N2	24.711
chr11	59265741	59266760	10	Jmjd4	jumonji domain containing 4	12.434
chr7	80866692	80867640	-31	Zfp592	zinc finger protein 592	11.621
chr15	80060821	80061500	-175	Mief1	mitochondrial elongation factor 1	18.679
chr7	80106041	80106710	-31	Gdpgp1	GDP-D-glucose phosphorylase 1	14.311
chr2	30973661	30974680	130	D330023K18Rik	RIKEN cDNA D330023K18 gene	22.809
chr12	40956162	40956740	-25	Dock4	dedicator of cytokinesis 4	14.723
chr15	83338421	83339100	-87	Ttll1	tubulin tyrosine ligase-like 1	21.775

chr5	1.31E+08	130540540	-75	Sbds	Shwachman-Bodian-Diamond syndrome	15.04
chr12	65993712	65994680	-15	Fancm	Fanconi anemia, complementation group M	12.97
chr17	56401581	56402971	-231	Vmac	vimentin-type intermediate filament	30.727
chr19	46204981	46205911	-423	Gbf1	golgi-specific brefeldin A-resistance factor 1	16.419
chr11	1.05E+08	105406460	-175	Tanc2	tetratricopeptide repeat, ankyrin repeat and	19.192
chr11	1.18E+08	117597500	-198	Tmc6	transmembrane channel-like gene family 6	22.508
chr19	17022532	17023740	-1	Prune2	prune homolog 2 (Drosophila)	20.05
chr6	1.27E+08	127419760	78	Parp11	poly (ADP-ribose) polymerase family, member	15.655
chr3	96246861	96247820	-35	Mtmr11	myotubularin related protein 11	13.458
chr11	1.21E+08	121237880	23	Fn3krp	fructosamine 3 kinase related protein	17.803
chr2	1.8E+08	180000420	79	Mtg2	mitochondrial ribosome associated GTPase 2	16.713
chr2	4981001	4981680	-130	Optn	optineurin	15.131
chr7	28878921	28879251	-64	Ggn	gametogenetin	10.455
chr19	34987742	34988720	-124	Kif20b	kinesin family member 20B	14.988
chr5	1.3E+08	130180900	-206	Zbed5	zinc finger, BED type containing 5	35.155
chr15	54919861	54921220	21	Dscc1	defective in sister chromatid cohesion 1	31.902
chr15	76466681	76467640	24	Tonsl	tonsoku-like, DNA repair protein	21.851
chr11	1.2E+08	119915960	256	1810043H04Rik	RIKEN cDNA 1810043H04 gene	26.884
chr2	93650302	93650960	7	Accs	1-aminocyclopropane-1-carboxylate synthase	14.723
chr4	1.06E+08	105814120	-365	Usp24	ubiquitin specific peptidase 24	14.697
chr11	77847761	77848780	-238	Dhrs13	dehydrogenase/reductase (SDR family)	30.63
chr7	30260681	30261360	12	Proser3	proline and serine rich 3	12.826
chr5	93509861	93510880	29	Nup54	nucleoporin 54	18.852
chr11	29593332	29594041	-88	Rtn4	reticulon 4	24.403
chr11	29593261	29593321	393	Rtn4	reticulon 4	8.667
chr14	54544501	54545441	121	Psme2	proteasome (prosome, macropain) activator	21.021
chr19	6241381	6242060	52	Atg2a	autophagy related 2A	17.037
chr11	98679292	98680240	78	Wipf2	WAS/WASL interacting protein family,	16.507
chr2	1.3E+08	130334900	55	Lzts3	leucine zipper, putative tumor suppressor	19.96
chr8	86604832	86605820	44	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	12.543
chr11	86942602	86943551	-194	Trim37	tripartite motif-containing 37	21.533
chr11	78567392	78568430	13	Fam58b	family with sequence similarity 58, member B	26.452
chr13	58166861	58167540	-72	Idnk	idnK gluconokinase homolog (E. coli)	14.001
chr7	30017022	30018010	3	Alkbh6	alkB, alkylation repair homolog 6 (E. coli)	15.033
chr2	28946581	28947600	89	Setx	senataxin	19.093
chr11	1.06E+08	106429520	10	Tex2	testis expressed gene 2	13.97
chr12	1.13E+08	113037080	59	Inf2	inverted formin, FH2 and WH2 domain	16.657
chr15	76644812	76645860	89	Arhgap39	Rho GTPase activating protein 39	17.103
chr17	47092041	47093730	-996	Usp49	ubiquitin specific peptidase 49	23.858
chr4	1.06E+08	106409460	-282	Ssbp3	single-stranded DNA binding protein 3	16.308
chr10	79790682	79791470	-296	Mex3d	mex3 homolog D (C. elegans)	18.44
chr1	1.87E+08	187030490	-16	Iars2	isoleucine-tRNA synthetase 2, mitochondrial	12.754
chr12	33538621	33539980	108	Sypl	synaptophysin-like protein	23.465
chr15	76283761	76284440	-593	Scx	scleraxis	20.677
chr17	24687741	24688740	-17	Hn1l	hematological and neurological expressed 1-	21.54
chr1	57940112	57941100	86	Sgol2a	shugoshin-like 2a (S. pombe)	20.881
chr2	37264681	37265700	-60	Zbtb26	zinc finger and BTB domain containing 26	15.229
chr5	1.43E+08	142654140	-171	Foxk1	forkhead box K1	14.05
chr18	80362401	80363080	-62	Rbfa	ribosome binding factor A	18.345
chr8	73720942	73721860	21	Mast3	microtubule associated serine/threonine	17.132
chr10	80158061	80158740	65	Dot1l	DOT1-like, histone H3 methyltransferase (S.	21.342
chr15	76056312	76057660	-234	Plec	plectin	20.519
chr15	76026412	76027400	184	Plec	plectin	20.957
chr15	76024681	76026401	-77	Plec	plectin	29.413
chr15	76022301	76023660	-15	Plec	plectin	26.15
chr3	90351601	90352280	-501	Dennd4b	DENN/MADD domain containing 4B	12.745
chr5	1.26E+08	125723840	94	Dhx37	DEAH (Asp-Glu-Ala-His) box polypeptide 37	22.127
chr2	1.51E+08	150701260	58	Ninl	ninein-like	14.714
chr17	25971241	25972260	92	Fam234a	family with sequence similarity 234, member	28.183
chr1	94011042	94011700	-624	Hdac4	histone deacetylase 4	18.198
chr4	1.34E+08	133976960	-274	Man1c1	mannosidase, alpha, class 1C, member 1	12.311
chr2	1.15E+08	115273260	-237	BC052040	cDNA sequence BC052040	21.862
chr18	13084561	13085580	-60	Osbpl1a	oxysterol binding protein-like 1A	24.777
chr17	45846281	45847550	-40	Zfp318	zinc finger protein 318	22.677
chr1	1.63E+08	162872210	-392	Gas5	growth arrest specific 5	29.913
chr19	59512312	59513260	846	Emx2	empty spiracles homeobox 2	11.617
chr17	3040281	3041290	-120	Pisd-ps2	phosphatidylserine decarboxylase,	15.326
chr1	88189541	88190900	406	Ncl	nucleolin	16.063
chr7	1.43E+08	142863580	6	R74862	expressed sequence R74862	13.077
chr8	98695541	98696220	-79	4930513N10Rik	RIKEN cDNA 4930513N10 gene	12.909
chr15	81017581	81018600	-18	4930483J18Rik	RIKEN cDNA 4930483J18 gene	25.921
chr7	1.27E+08	127304451	-124	1700008J07Rik	RIKEN cDNA 1700008J07 gene	18.065
chr15	25357922	25358220	418	Basp1	brain abundant, membrane attached signal	13.544
chr13	54703012	54704300	-74	Rnf44	ring finger protein 44	33.92
chr10	93095741	93096760	-597	Gm8580	ribosomal protein L29 pseudogene	21.321
chr1	57914241	57914571	224	Kctd18	potassium channel tetramerisation domain	14.939
chr2	94206861	94207540	328	Ttc17	tetratricopeptide repeat domain 17	13.691
chr16	55899092	55900080	-18	Zbtb11os1	zinc finger and BTB domain containing 11,	20.268
chr4	1.55E+08	154605480	-22	Atad3aos	ATPase family, AAA domain containing 3A,	36.601
chr15	3976981	3977660	86	BC037032	cDNA Sequence BC037032	14.243
chr8	88189201	88190160	-57	Orc6	origin recognition complex, subunit 6	17.39
chr11	85050321	85051340	485	Appbp2	amyloid beta precursor protein (cytoplasmic	19.054
chr19	47015482	47016220	-189	Nt5c2	5'-nucleotidase, cytosolic II	25.232
chr18	74904041	74904671	-221	Acaa2	acetyl-Coenzyme A acyltransferase 2	17.587
chr10	79258081	79258701	-291	E130317F20Rik	RIKEN cDNA E130317F20 gene	14.839
chr11	1.17E+08	116931780	-216	Sec14l1	SEC14-like lipid binding 1	20.073
chr1	23225401	23226080	-804	Mir30a	microRNA 30a	16.468
chr11	75278332	75279740	-875	Mir22	microRNA 22	33.522
chr7	1.41E+08	141073820	-497	Mir210	microRNA 210	11.269
chr16	14072601	14073620	-94	Mir484	microRNA 484	16.011

chr5	65248532	65249400	-244	Fam114a1	family with sequence similarity 114, member	15.325
chr10	81008741	81009420	-357	BC025920	zinc finger protein pseudogene	18.315
chr11	1.2E+08	120006400	56	2810410L24Rik	RIKEN cDNA 2810410L24 gene	18.441
chr10	7352501	7353520	-551	A630066F11Rik	RIKEN cDNA A630066F11 gene	18.694
chr11	75277202	75278321	27	Mir22hg	Mir22 host gene (non-protein coding)	25.553
chr2	1.55E+08	155314600	-115	Mir499	microRNA 499	10.108
chr19	5387792	5389000	60	D330050I16Rik	RIKEN cDNA D330050I16 gene	18.094
chr7	3740001	3740860	287	Leng8	leukocyte receptor cluster (LRC) member 8	16.203
chr19	25028421	25029370	-182	Cbwd1	COBW domain containing 1	28.426
chr8	1.27E+08	126908400	-575	Mir1967	microRNA 1967	25.109
chr8	1.27E+08	126907901	-412	Taf5l	TAF5-like RNA polymerase II, p300/CBP-	9.167
chr4	1.51E+08	151141151	-333	Icmt	isoprenylcysteine carboxyl methyltransferase	14.609
chr1	16641981	16643000	-157			26.734
chr1	57321961	57322640	134	1700066M21Rik	RIKEN cDNA 1700066M21 gene	19.598
chr10	61735161	61736180	108	Hk1	hexokinase 1	22.043
chr9	59415001	59415680	50	Parp6	poly (ADP-ribose) polymerase family, member	20.178
chrX	49301702	49302290	-179	C430049B03Rik	RIKEN cDNA C430049B03 gene	15.866
chr15	32188821	32189551	65	Snhg18	small nucleolar RNA host gene 18	19.712
chr2	1.21E+08	120541900	448	Ttbk2	tau tubulin kinase 2	17.301
chr14	44579781	44580460	-100	Ddhd1	DDHD domain containing 1	15.747
chr2	1.53E+08	153038420	330	Asxl1	additional sex combs like 1	22.992
chr15	88904042	88904220	301	Trabd	TraB domain containing	7.82
chr4	1.16E+08	116184460	-166	AV051173	expressed sequence AV051173	17.352
chr16	10921481	10922221	-625	Gm4262	predicted gene 4262	20.338
chr16	10922232	10922840	60	Gm4262	predicted gene 4262	17.158
chr16	42794781	42794921	68	4932412D23Rik	RIKEN cDNA 4932412D23 gene	11.286
chr16	42794932	42795781	-262	4932412D23Rik	RIKEN cDNA 4932412D23 gene	14.138
chr3	27343892	27344881	541	Ect2	ect2 oncogene	20.173
chr4	11893002	11894220	-14	Pdp1	pyruvate dehyrogenase phosphatase catalytic	14.419
chr9	75195081	75196440	165	Mapk6	mitogen-activated protein kinase 6	29.554
chr9	79578032	79579380	408	Tmem30a	transmembrane protein 30A	25.522
chr4	1.29E+08	129245560	-224	Khdrbs1	KH domain containing, RNA binding, signal	29.443
chr17	33520261	33520940	545	Daxx	Fas death domain-associated protein	14.923
chr3	58779692	58780900	21	Siah2	seven in absentia 2	28.441
chr7	44853481	44854500	472	Prmt1	protein arginine N-methyltransferase 1	28.003
chr11	59764181	59765200	281	Med9	mediator complex subunit 9	17.447
chr18	67925201	67925880	64	Cep192	centrosomal protein 192	17.713
chr11	98174321	98175000	202	Stard3	START domain containing 3	13.947
chr13	59594521	59595540	74	Naa35	N(alpha)-acetyltransferase 35, NatC auxiliary	26.308
chr19	43727741	43728760	-58	Slc25a28	solute carrier family 25, member 28	14.584
chr8	1.08E+08	108159440	0	Hsf4	heat shock transcription factor 4	12.974
chr5	1.52E+08	151637590	41	1700028E10Rik	RIKEN cDNA 1700028E10 gene	15.053
chr10	14394982	14395940	226	Vta1	Vps20-associated 1 homolog (S. cerevisiae)	17.614
chr17	8148781	8149800	2	4930506C21Rik	RIKEN cDNA 4930506C21 gene	28.034
chr6	1.25E+08	125062200	299	Chd4	chromodomain helicase DNA binding protein	14.298
chr6	1.16E+08	115740760	230	Cand2	cullin-associated and neddylation-dissociated	21.212
chr10	80819362	80820720	-615	Mir1191b	microRNA 1191b	19.716
chr11	97559972	97560801	408	Pip4k2b	phosphatidylinositol-5-phosphate 4-kinase,	15.123
chr8	86894481	86895311	-837	Mir8111	microRNA 8111	17.06
chr8	95244541	95245900	28	Crnde	colorectal neoplasia differentially expressed	27.955
chr19	21171192	21171800	-311			14.801
chr2	1.61E+08	160801051	-139			16.221
chr14	68467332	68468170	-101	Chmp7	charged multivesicular body protein 7	12.481
chr17	44896321	44897081	587	Cdc5l	cell division cycle 5-like (S. pombe)	14.974
chr10	1.28E+08	127902220	-127	Myl6b	myosin, light polypeptide 6B	18.692
chr19	5845281	5846191	-256	Neat1	nuclear paraspeckle assembly transcript 1	14.374
chr19	8823382	8824700	-27			19.53
chr17	84091521	84092360	4333	Zfp36l2	zinc finger protein 36, C3H type-like 2	27.019
chr19	4624681	4626040	257	Rce1	RCE1 homolog, prenyl protein peptidase (S.	25.327
chr5	31183441	31184800	249	Ost4	oligosaccharyltransferase 4 homolog (S.	13.706
chr7	18314441	18315450	6585	Snrpd2	small nuclear ribonucleoprotein D2	20.121
chr7	15431241	15432600	294	Inafm1	InaF motif containing 1	17.62
chr17	35504572	35505151	570	2310061I04Rik	RIKEN cDNA 2310061I04 gene	19.964
chr3	1.03E+08	103187960	104	Nras	neuroblastoma ras oncogene	18.227
chr19	5940552	5941350	-16135	Cdc42ep2	CDC42 effector protein (Rho GTPase binding)	12.777
chr1	75062982	75063160	468	Abcb6	ATP-binding cassette, sub-family B	11.831
chr19	7018552	7019300	9320	Bad	BCL2-associated agonist of cell death	17.203
chr17	33526432	33527370	271	Zbtb22	zinc finger and BTB domain containing 22	12.717
chr8	87865912	87867220	2287	Junb	jun B proto-oncogene	15.261
chr19	6341001	6341680	180	Map4k2	mitogen-activated protein kinase kinase	14.465
chr10	79723201	79723880	137	2310011J03Rik	RIKEN cDNA 2310011J03 gene	15.181
chr3	90611021	90611950	-1291	S100a14	S100 calcium binding protein A14	11.499
chr15	99553342	99554380	209	Cox14	cytochrome c oxidase assembly protein 14	16.566
chr10	80351302	80352200	18531	Gadd45b	growth arrest and DNA-damage-inducible 45	22.795
chr8	73629721	73630400	3332	Jund	jun D proto-oncogene	14.452
chr4	1.26E+08	125824140	291	Adprhl2	ADP-ribosylhydrolase like 2	34.251
chr1	1.73E+08	173118091	215	Ppox	protoporphyrinogen oxidase	17.247
chr2	1.55E+08	154742840	23582	Ahcy	S-adenosylhomocysteine hydrolase	14.279
chr13	23746621	23747550	813	Hist1h1c	histone cluster 1, H1c	14.78
chr17	34263161	34263840	8298	Atf6b	activating transcription factor 6 beta	15.191
chr7	26887201	26887880	103	Rab4b	RAB4B, member RAS oncogene family	16.725
chr8	1.26E+08	126028480	11805	Mir7080	microRNA 7080	17.388
chr10	80068072	80068640	-8156	Btbd2	BTB (POZ) domain containing 2	18.421
chr10	80067621	80068061	-7641	Btbd2	BTB (POZ) domain containing 2	21.932
chr9	57387241	57388500	281	Ulk3	unc-51-like kinase 3	17.041
chr19	45802421	45803100	114	Npm3	nucleoplasmin 3	15.518
chr17	46113402	46114200	272	Cul7	cullin 7	33.415
chr17	35517421	35518470	176	Atat1	alpha tubulin acetyltransferase 1	33.984
chr5	33968721	33969740	201	Slbp	stem-loop binding protein	22.463
chr3	96662341	96663700	-10814	Gm15441	predicted gene 15441	18.282

chr17	46136712	46137660	260	Rrp36	ribosomal RNA processing 36 homolog (S.	17.472
chr9	20823301	20824300	116	Fdx1l	ferredoxin 1-like	14.46
chr17	25559841	25560860	611	Stub1	STIP1 homology and U-Box containing	22.048
chr7	25510732	25511560	-13653	Axl	AXL receptor tyrosine kinase	19.171
chr6	1.15E+08	114827450	60566	Vgll4	vestigial like 4 (Drosophila)	25.724
chr9	1.08E+08	108436880	499	Wdr6	WD repeat domain 6	19.036
chr7	1.41E+08	140806920	1041	Ifitm2	interferon induced transmembrane protein 2	11.803
chr5	1.38E+08	137544590	104	Trip6	thyroid hormone receptor interactor 6	14.993
chr17	26660081	26661780	214			27.059
chr15	75896161	75897180	369	Scrib	scribbled homolog (Drosophila)	24.807
chr13	23563361	23564040	1203	Hist1h1d	histone cluster 1, H1d	11.359
chr11	35681402	35682320	-3910	Rars	arginyl-tRNA synthetase	14.686
chr4	1.33E+08	132857380	362	Gpn2	GPN-loop GTPase 2	20.895
chr8	1.08E+08	108179160	276	4931428F04Rik	RIKEN cDNA 4931428F04 gene	23.698
chr17	23402881	23403560	-1828	Thoc6	THO complex 6 homolog (Drosophila)	17.695
chr19	9033801	9034691	160	Eef1g	eukaryotic translation elongation factor 1	19.067
chr8	72751501	72752070	231	Lpar2	lysophosphatidic acid receptor 2	14.063
chr11	1.16E+08	116489440	341	Snord1c	small nucleolar RNA, C/D box 1C	22.13
chr2	1.55E+08	155048840	168	Mir695	microRNA 695	18.795
chr9	61919472	61920120	804	Mir5133	microRNA 5133	12.401
chr14	50907521	50908200	1076	Arhgef40	Rho guanine nucleotide exchange factor	13.215
chr4	1.4E+08	140219430	11012	Gm13031	predicted gene 13031	21.137
chr5	1.35E+08	134857260	217	Mir7228	microRNA 7228	13.854
chr14	61791532	61792510	190	Mir8098	microRNA 8098	18.669

Supplemental Table 2.4: Additional GC-rich motifs identified in Klf9 peaks

	$1*10^{-537}$	70.37	29.68
	$1*10^{-353}$	69.71	36.26
	$1*10^{-334}$	74.92	42.39
	$1*10^{-294}$	63.11	32.80
	$1*10^{-151}$	61.29	39.31
	$1*10^{-107}$	19.73	7.94
	$1*10^{-84}$	54.43	38.09
	$1*10^{-71}$	22	11.35
	$1*10^{-51}$	47.68	35.14
	$1*10^{-43}$	6.18	2.04
	$1*10^{-43}$	44.63	33.30
	$1*10^{-35}$	5.10	1.71
	$1*10^{-31}$	29.92	21.42
	$1*10-^{18}$	4.9	2.28

	$1*10^{-18}$	20.98	15.28
	$1*10^{-18}$	14.52	9.82
	$1*10^{-16}$	8.31	5
	$1*10^{-8}$	3.76	2.17

Supplemental Figure 2.5: All GO:PANTHER pathways enriched in genes with Klf9 peaks associated

Id	Items	Items_Details	Support	List size	Reference Support	Reference size	Hyp_c
32	Panther:P00006	Apoptosis signaling pathway	31	2870	93	37681	8.67E-11
23	Panther:P00034	Integrin signalling pathway	36	2870	131	37681	2.79E-10
0	Panther:P00031	Inflammation mediated by chemokine and cytokine signaling pathway	46	2870	197	37681	3.16E-10
19	Panther:P00016	Cytoskeletal regulation by Rho GTPase	23	2870	62	37681	1.28E-09
18	Panther:P00005	Angiogenesis	33	2870	120	37681	1.51E-09
1	Panther:P00057	Wnt signaling pathway	42	2870	197	37681	1.75E-08
16	Panther:P00056	VEGF signaling pathway	19	2870	50	37681	2.64E-08
17	Panther:P00047	PDGF signaling pathway	28	2870	103	37681	2.82E-08
13	Panther:P04393	Ras Pathway	20	2870	59	37681	7.85E-08
5	Panther:P00021	FGF signaling pathway	24	2870	90	37681	4.71E-07
33	Panther:P00059	p53 pathway	19	2870	60	37681	5.39E-07
6	Panther:P00018	EGF receptor signaling pathway	24	2870	93	37681	7.78E-07
7	Panther:P00049	Parkinson disease	21	2870	75	37681	1.01E-06
31	Panther:P00019	Endothelin signaling pathway	19	2870	63	37681	1.02E-06
30	Panther:P04398	p53 pathway feedback loops 2	14	2870	36	37681	1.24E-06
15	Panther:P00036	Interleukin signaling pathway	20	2870	73	37681	2.40E-06
45	Panther:P00046	Oxidative stress response	14	2870	39	37681	3.13E-06

51	Panther:P00048	PI3 kinase pathway	14	2870	39	37681	3.13E-06
36	Panther:P00053	T cell activation	17	2870	56	37681	3.44E-06
28	Panther:P00030	Hypoxia response via HIF activation	9	2870	19	37681	2.22E-05
54	Panther:P00020	FAS signaling pathway	10	2870	24	37681	2.54E-05
38	Panther:P00029	Huntington disease	22	2870	106	37681	7.04E-05
29	Panther:P00033	Insulin/IGF pathway-protein kinase B signaling cascade	9	2870	24	37681	0.000192
35	Panther:P00009	Axon guidance mediated by netrin	8	2870	20	37681	0.000292
62	Panther:P00042	Muscarinic acetylcholine receptor 1 and 3 signaling pathway	13	2870	50	37681	0.000302
69	Panther:P04391	Oxytocin receptor mediated signaling pathway	13	2870	50	37681	0.000302
41	Panther:P00060	Ubiquitin proteasome pathway	11	2870	39	37681	0.000469
65	Panther:P04394	Thyrotropin-releasing hormone receptor signaling pathway	13	2870	53	37681	0.000535
21	Panther:P00003	Alzheimer disease-amyloid secretase pathway	13	2870	54	37681	0.000634
59	Panther:P00040	Metabotropic glutamate receptor group II pathway	11	2870	41	37681	0.000691
50	Panther:P00052	TGF-beta signaling pathway	16	2870	79	37681	0.000967
48	Panther:P05731	GABA-B receptor II signaling	9	2870	31	37681	0.001307
11	Panther:P04374	5HT2 type receptor mediated signaling pathway	13	2870	60	37681	0.00169

9	Panther:P04373	5HT1 type receptor mediated signaling pathway	10	2870	39	37681	0.001719
66	Panther:P04385	Histamine H1 receptor mediated signaling pathway	10	2870	39	37681	0.001719
64	Panther:P04378	Beta2 adrenergic receptor signaling pathway	9	2870	36	37681	0.003732
71	Panther:P04377	Beta1 adrenergic receptor signaling pathway	9	2870	36	37681	0.003732
86	Panther:P04397	p53 pathway by glucose deprivation	6	2870	18	37681	0.004729
26	Panther:P02738	De novo purine biosynthesis	7	2870	24	37681	0.004816
76	Panther:P00002	Alpha adrenergic receptor signaling pathway	5	2870	14	37681	0.008127
22	Panther:P00027	Heterotrimeric G-protein signaling pathway-Gq alpha and Go alpha mediated pathway	16	2870	98	37681	0.008158
82	Panther:P00015	Circadian clock system	4	2870	9	37681	0.008407
20	Panther:P00043	Muscarinic acetylcholine receptor 2 and 4 signaling pathway	10	2870	50	37681	0.010262
34	Panther:P00010	B cell activation	10	2870	50	37681	0.010262
73	Panther:P04396	Vitamin D metabolism and pathway	4	2870	10	37681	0.012293
68	Panther:P04386	Histamine H2 receptor mediated signaling pathway	6	2870	22	37681	0.012381
37	Panther:P00044	Nicotinic acetylcholine receptor signaling pathway	11	2870	61	37681	0.014006

52	Panther:P02762	Pentose phosphate pathway	2	2870	2	37681	0.014067
63	Panther:P04380	Cortocotropin releasing factor receptor signaling pathway	7	2870	30	37681	0.014688
94	Panther:P04392	P53 pathway feedback loops 1	3	2870	6	37681	0.016557
46	Panther:P00007	Axon guidance mediated by semaphorins	5	2870	17	37681	0.01658
14	Panther:P00026	Heterotrimeric G-protein signaling pathway-Gi alpha and Gs alpha mediated pathway	18	2870	128	37681	0.018464
72	Panther:P04372	5-Hydroxytryptamine degredation	5	2870	18	37681	0.020319
74	Panther:P00032	Insulin/IGF pathway-mitogen activated protein kinase kinase/MAP kinase cascade	6	2870	25	37681	0.020567
24	Panther:P00004	Alzheimer disease-presenilin pathway	15	2870	102	37681	0.021028
3	Panther:P00039	Metabotropic glutamate receptor group III pathway	10	2870	57	37681	0.021273
87	Panther:P00041	Metabotropic glutamate receptor group I pathway	5	2870	19	37681	0.024059
67	Panther:P04379	Beta3 adrenergic receptor signaling pathway	6	2870	27	37681	0.028093
70	Panther:P05730	Endogenous cannabinoid signaling	5	2870	20	37681	0.029085
102	Panther:P02776	Serine glycine biosynthesis	2	2870	3	37681	0.031379
93	Panther:P00014	Cholesterol biosynthesis	3	2870	9	37681	0.048888

49	Panther:P00035	Interferon-gamma signaling pathway	5	2870	23	37681	0.049698