Computational and biological approaches for identification of Hedgehog signaling targets and their application to intestinal visceral smooth muscle development in the mouse

by

Katherine Gurdziel

A dissertation submitted in partial fulfillment
of the requirements for the degree of
Doctor of Philosophy
(Bioinformatics)
in The University of Michigan
2016

Doctoral Committee:

Professor Deborah Gumucio, Chair
Professor Philip Andrews
Associate Professor Jun Li
Associate Research Associate Professor Laura Scott
Associate Professor Trisha Wittkopp

Acknowledgements

I am indebted to several people for their support and help during my time at the University of Michigan. First, I would like to thank the members of my dissertation committee: Deb Gumucio, Phil Andrews, Jun Li, Laura Scott and Trisha Wittkopp. Their expertise has been crucial to the development of this dissertation. In particular, Deb has fostered my ability to conduct independent research. I would also like to thank Lori Longeway and Julia Eussen for their logistical support at various stages of this process.

A number of other people at U of M have contributed to my progress. Fellow lab members Kate Walton, Michelle Muza-Moons, Tracy Qiao and Jierong Lang provided advice on mouse husbandry as well as staining techniques. Members of the Allen lab, especially Jane Song and Irene Althaus, were instrumental in helping me develop web lab skills. I was also fortunate to collaborate with several people on various projects. I am grateful to Ken Krill from the Hammer lab for fostering my knowledge of experimental design and more advanced lab techniques. In addition, Lihong Shi of the Engel lab provided pivotal guidance with preliminary ChIP-seq experiments. I should also thank the following coauthors for their contributions to papers: Ben Allen, Scott Barolo, David Lorberbaum, Neil Richards and Aaron Udager. I am especially grateful to Gary Schneider and Kyle Vogt, two undergraduate students who provided essential assistance with experiments. It has been a great pleasure to mentor them and watch their development.

I am indebted to my previous mentors, Fran Lewitter and George Bell of the Bioinformatics and Research Computing unit at the Whitehead Institute as well as Premananda Indic, formerly of the Department of Sleep Medicine at Brigham and Women's Hospital. All three have provided encouragement at critical points at my career. I continue to benefit greatly from their guidance.

A number of grants have supported my study and research while at U of M, including training grants from both the Bioinformatics Program and Basic and Translational Digestive Sciences. Meetings for the latter were especially useful in advancing my professional development. I also received much-appreciated funding in support of the dissertation from the Rackham Graduate Student Research Grant.

I would also like to thank my family and friends for their support. I am particularly thankful for the friendship of Ellen Barton, Chera Kee, Jose Guzman, John Kee, Lissy Sklar, Simone Chess and Max Matthies. During my time at Sheffield University, Nicky Hallett, Rosie Valerio, and Pete Artymiuk were very welcoming. I would also like to thank Eli for his constant support during the writing process and Chloe for reminding me of what is important. Finally, I would like to thank Jaime. We have always been more than the sum of our parts, and I am grateful every day for the life that we share.

Table of Contents

List of Figures

Figure

List of Tables

Table

List of Abbreviations

BS	binding site
ChIP	Chromatin Immunoprecipitation
DNA	Deoxyribonucleic
ICM	inner circular muscle
ISM	intestinal visceral smooth muscle
OLM	outer longitudinal muscle
RNA	Ribonucleic acid
TF	transcription factor
seq	sequencing
SM	organ affiliated smooth muscle

Abstract

The Hedgehog (Hh) pathway is an evolutionarily conserved cell-cell signaling pathway that controls organ development and homeostasis in embryos and adults. Hh signaling functions in cell fate choice, patterning, cell survival, proliferation and/or differentiation. Several birth defects are known to result from altered Hh signaling and aberrant Hh signaling is also responsible for several cancers. Despite its central role in development and disease, very little is known about the precise genetic targets of Hh signaling or the genomic enhancers that activate those genes. These target genes and associated Hh-responsive enhancers are themselves responsible for disease initiation and progression. A comprehensive effort to identify these signaling targets and to dissect the context specificity that underlies their expression is therefore a high priority. This work was driven by two Aims: 1) to explore novel computational approaches for the identification of Hh-responsive enhancers; and 2) to understand the contribution of Hh-driven gene expression in the context of a single Hh-responsive cell type, intestinal visceral smooth muscle (ISM).

This work comprised a multi-pronged approach, integrating both computational and biological methods in parallel, to achieve these Aims. First, we explored the degree to which clustered binding sites for the Hh transcription factor, ci/GLI, would predict functional enhancers. While this method was somewhat successful in the fly, it could not be applied to the mouse, where Hh enhancers tend not to be homotypically clustered. Therefore, a machine learning strategy was explored with substantial success, resulting in the identification of seven

new enhancers in genes encoding Hh pathway components. Finally, RNA-seq and ChIP-seq data were collected to generate a catalog of smooth muscle genes that are expressed in a specific layer of developing intestinal smooth muscle. Analysis of this data implicated cJUN as a regulatory component in ISM formation and established Hh as an upstream regulator of *cJun* expression in that tissue.

Though this work has focused on Hh signaling, a similar approach could be applied to any transcription factor or signaling pathway to comprehensively analyze the gene regulatory networks governing many normal and disease-related cell states.

Chapter I

Introduction

1.1 Research Overview

1.1.1 Importance of Intestinal Smooth Muscle

The small intestine, consisting of the duodenum, jejunum and ileum is critical to the digestion and absorption of nutrients into the bloodstream. In addition to chemical digestion, begun in the stomach and continued by the intestine, efficient processing and absorption of nutrients also relies on mechanical movement of the food bolus, resulting from the coordinated contraction of the intestinal circular and longitudinal smooth muscle layers. The segmentation contractions of the circular muscle mix partially digested food with enzymes to increase the breakdown into nutrients while the peristaltic contractions of longitudinal muscles direct the movement of material downward through the digestive tract. Despite the critical importance of visceral smooth muscle (ISM) to intestinal function, very little is known about its development or maintenance. For this reason, the ultimate goal of this dissertation was to identify the regulatory programs underlying intestinal smooth muscle development.

Several intestinal diseases result from malformation of, or injury to ISM. Visceral myopathic chronic pseudoobstrution resulting from familial (Anuras et al., 1981; Sipponen et al., 2009) and sporadic cases (Montalvo et al., 2004) have been reported. Infants present with feeding intolerance and absence of bowel motility, causing the appearance of obstruction, but without evidence of bowel narrowing. Only two susceptibility loci, DNA POLG and ACTG2, are currently known (Vissing et al., 2002; Van Goethem et al., 2003; Giordano et al., 2009; Lehtonen et al., 2012; Holla et al., 2014; Thorson et al., 2014; Wangler et al., 2014). However, cases have been reported indicating that the layers of ISM are differently affected, suggesting involvement of multiple loci that have yet to be discovered (Anuras et al., 1983; Alstead et al., 1988; Smith et al., 1992; Donnell et al., 2008). Muscle contractility can also be disrupted in response to gut inflammation (Ohama et al., 2007b) and irritable bowel syndrome (IBS) (Whorwell et al., 1986; Van der Vliet et al., 1992; Abrams et al., 2012). While roughly 30 million patients in the United States suffer from IBS (Occhipinti and Smith, 2012), almost nothing is known about the genes or signaling pathways that may play a role in this malady. In part, this is because so little is known in general about gene networks that control ISM.

1.1.2 Intestinal Development

The luminal surface of the murine intestine arises from a flat sheet of endoderm. Between E7.25 and E9.5, this endodermal sheet recruits lateral plate mesoderm and wraps into a tube that will eventually give rise to the entire gastrointestinal tract (Zorn and Wells, 2009). The stomach and proximal part of the small intestine arise from foregut endoderm. The rest of the small intestine is considered midgut while the large intestine is derived from the hindgut (Zorn and Wells, 2009). By E9.5, the tube is complete and the interior of the midgut consists of a lumen that is encased by endoderm-derived epithelium and surrounded by mesoderm. Between E9.5 and E14.5, the gut tube expands in length and circumference (Noah et al., 2011). At E14.5, a dramatic restructuring of the epithelium begins, which will result in the emergence of villi, finger-like protrusions of the apical surface that serve to increase surface area for food absorption. Establishment of the crypts, which harbor stem cell populations that generate replacement cells for the epithelial layer of the villi begins postnatally and is completed by weaning (Spence et al., 2011).

Crosstalk between the interior endoderm-derived epithelial tissue and the underlying mesenchyme is vital for differentiation of intestinal cell types during development. Roles for multiple signaling pathways, including bone morphogenic protein (BMP), Hedgehog (Hh), platelet derived growth factor (PDGF), TGF-β, and Wnt, among others, have been documented (McLin et al., 2009; Spence et al., 2011). Reliance on epithelial:mesenchymal crosstalk is critical to intestinal homeostasis and persists within adult tissue (Kedinger et al., 1998b). The epithelial tissue progenitor and stem cell populations are directed by BMP and Wnt signals (Madison et al., 2005; Kim et al., 2007) while both PDGF and Hh act by paracrine signaling to direct villus formation (Karlsson et al., 2000; Walton et al., 2012). Hh has multiple roles in cell fate specification in the intestinal mesenchyme and is known to signal to at least seven different cell/tissue targets in the stroma underlying the epithelium (Kolterud et al., 2009). In particular, Hh signaling has been clearly demonstrated to be crucial to the development of ISM (Ramalho-Santos et al., 2000; Kolterud et al., 2009).

Within the adult intestine, there are several subtypes of ISM. Close to the luminal surface within the mucosa, are the muscularis mucosa and villus ISM. The muscularis mucosa is a thin muscular layer that lies directly under the epithelium, while the villus ISM consists of thin strands of muscle that travel vertically up the villi from their origin in the muscularis mucosa. Together, these muscles move the villi and epithelium to churn the gut contents. At the outer side of the intestinal tube is the muscularis externa, comprised of inner circular muscle (ICM) and outer longitudinal muscle (OLM). During development, the ICM forms at E13.5, just prior to the epithelial remodeling of the villi. The OLM forms 48 hours later at E15.5 (Kedinger et al., 1998b; Kolterud et al., 2009; Thomason et al., 2012). ISM strands within the villus cores begin to form at E18, while the final muscle, the muscularis mucosa, develops after birth (Kolterud et al., 2009). All of the ISM populations play roles in gut motility that is required for digestion and absorption of nutrients and all of are known to require Hh signals for development (Ramalho-Santos et al., 2000; Madison et al., 2005; Kolterud et al., 2009; Zacharias et al., 2011). Hh signaling is currently the only known signaling pathway critical to smooth muscle formation.

1.1.3 Hedgehog Signaling

First discovered in the fruit fly (*Drosophila)* (Nusslein-Volhard and Wieschaus, 1980), the Hedgehog (Hh) signaling pathway plays crucial roles in embryonic development in many species, including humans. Predictably, disruption of this pathway is associated with developmental malformations in many tissues; and, since it often regulates cell proliferation, misregulation of the pathway has been shown to cause cancers (Barakat et al., 2010). An important unanswered question is: How does the same Hh signal activate different genes in different cellular contexts? I hypothesized that at least part of this context specificity is accounted for by the distinct regulatory regions that are targeted by Hh signaling.

In *Drosophila*, the hedgehog gene encodes a ligand (hh) that binds to the transmembrane receptor patched (ptc). In the absence of hh ligand, ptc functions to inhibit signaling from its co-receptor, smoothened (smo) and under these conditions, the downstream transcription factor, cubitus interruptus (ci), is phosphorylated and cleaved, generating a repressor protein that goes to the nucleus to suppress target gene activity (Figure 1.1A). However, when the hh ligand binds to ptc, this inhibition is released and smo is then free to interact with the kinesin related protein Costal-2 (Cos2). This interaction in turn activates other cytoplasmic components, fused (fu) and Suppressor of fused (SuFu). As a result of this cascade, ci is no longer phosphorylated and therefore, no longer cleaved. The full-length protein then enters the nucleus, where it acts a transcriptional activator (Figure 1.1B). Therefore, the Hh pathway contains a built-in switch: it activates gene expression in the presence of the ligand and actively represses gene transcription in its absence (Barolo and Posakony, 2002; Robbins et al., 2012).

In mammals, Hh signaling originates with the release of one of the three lipid-modified HH ligands, all homologs of the *Drosophila hh* gene (Sonic hedgehog (*Shh*), Indian hedgehog (*Ihh*) and Desert hedgehog (*Dhh*)) (for Review see (Varjosalo and Taipale, 2008)). Release and diffusion of the Hh ligand in the extracellular space is facilitated by the secreted protein Scube and the transmembrane protein Dispatched (Creanga et al., 2012; Jakobs et al., 2014). Once discharged, Hh ligand can interact with several cell membrane proteins. Binding with the transmembrane receptor protein Patched (PTCH1) as well as the cell membrane co-receptors BOC, CDO and GAS1 initiates Hh signaling within target cells, while binding with the membrane-associated Hedgehog-interacting protein (HHIP) can suppress the Hh signal (Figure 1.1CD) (Chuang and McMahon, 1999). Just as in the *Drosophila*, the binding of HH ligand to PTCH results in de-repression of the Smoothened (SMO) transmembrane protein allowing SMO to activate the downstream portion of the pathway.

A major difference in the Hh pathway in higher organisms compared to *Drosophila* is the importance of cilia to signal transduction. Cilia are microtubule-based organelles that are thought to act as cellular sensors (DeRouen and Oro, 2009). Activation of Hh signaling causes SMO to accumulate within cilia (Allen et al., 2011; Izzi et al., 2011) where the GLI transcription factors (mediators of Hh signaling in vertebrates) are processed (Figure 1.1D) (Kim et al., 2009; Beachy et al., 2010). In contrast, in *Drosophila*, cilia do not seem to play a role in signal reception or processing (Goetz and Anderson, 2010).

The vertebrate Hh pathway relies on three transcription factors for signal transduction; all are homologues of *Drosophila* ci. GLI1 is not appreciably processed and may function primarily to amplify the Hh signal. In addition to its role as a pathway activator, GLI1 is a known target of Hh signaling (Dai et al., 1999). GLI2 is primarily an activator (Pan et al., 2006), but under some conditions, can act as a repressor. GLI3, typically a repressor, can occasionally act as an activator (Wang et al., 2000). Proteolytic processing, which occurs in the absence of Hh ligand, determines whether the GLI proteins act as repressors or activators. In the presence of the Hh ligand, this processing is inhibited (Kim et al., 2009; Beachy et al., 2010), allowing full-length GLI proteins to traffic to the nucleus and activate gene expression (Dai et al., 1999; Sasaki et al., 1999; Shin et al., 1999; Wen et al., 2010).

1.1.4 Roles for Hedgehog Signaling in Muscle Development

Vertebrates contain three distinct types of muscle: cardiac, skeletal, and smooth (subdivided into vascular smooth muscle and organ affiliated smooth muscle typified by involuntary contractions) with distinct structural and functional roles. All three muscle types originate from mesoderm tissue. Cardiac muscle arises from the cardiac lateral splanchnic mesoderm (Nathan et al., 2008), skeletal muscle is from the myotome of paraxial mesoderm (Yoon and Wold, 2000), while smooth muscle has multiple origins, including the splanchic mesoderm (Christ and Ordahl, 1995), neural crest (Le Lievre and Le Douarin, 1975; Etchevers et al., 2001) and local undifferentiated mesenchymal cells (Ruzicka and Schwartz, 1988; Kedinger et al., 1990; McHugh, 1995). Hh signaling has been connected to the development of each of these different types of muscle, as discussed below.

1.1.4.1 Skeletal Muscle

Hedgehog plays an active role in the development and homeostasis of skeletal muscle, both during developmental specification of tissues and in maintenance of the stem cell population. In the mouse, myogenic regulatory factors *MyoD* and *myogenic factor 5* (*Myf5)* control the establishment and maintenance of muscle progenitor cells while *Myogenin (MyoG)* and *Mrf4* facilitate myoblast differentiation (Pownall et al., 2002). Mouse models with deletions of *Myf5* and *MyoD* have demonstrated a redundancy of myogenic function between the two genes (Braun et al., 1992; Rudnicki et al., 1992) and subsequent knockout mouse models have shown that these genes function upstream of *MyoG* and *Mrf4* (Hasty et al., 1993; Kassar-Duchossoy et al., 2004). *MyoD* is activated by the skeletal progenitor factor *Pax-3,* which is regulated by Hh, Wnt, Fgf and BMP signaling (Duprez et al., 1998; Pownall et al., 2002). Downregulation of *Pax-3* by Hh signaling allows the differentiation of *MyoD* and *Myf5* co-expressing cells (Borycki et al., 1998; Hammond et al., 2007). *Shh* null mice exhibit reduced expression of *MyoD* (Borycki et al., 1999) and *Myf5* (Chiang et al., 1996), both of which have been shown to be direct regulatory targets of Hh signaling (Gustafsson, 2002; Borello et al., 2006; Voronova et al., 2013). MYOD and GLI2 form a protein complex with MEF2C, another direct transcriptional target of Hh signaling (Voronova et al., 2012), promoting myogenic activation through the activation of muscle target genes (Voronova et al., 2013). Unlike for *Myf5*, *MyoD* and *Mef2C*, there is currently no evidence to suggest that *MyoG* or *Mrf4* are direct targets of Hh. However, since *Myf5* and *MyoD* are upstream regulators of *MyoG* and *Mrf4*, which act to drive terminal differentiation of myoblasts, Hh may function primarily in regulating the skeletal muscle progenitor population. Interestingly, *Shh* and *Ihh* seem to have partially redundant and partially distinct temporal roles in skeletal muscle formation, since skeletal muscle develops normally in *Ihh* null mice until after cessation of *Shh* expression, at which point muscle mass is lost (Bren-Mattison et al., 2011).

1.1.4.2 Cardiac Muscle

Mice that lack *Shh* exhibit developmental cardiac abnormalities (Chiang et al., 1996; Tsukui et al., 1999; Washington Smoak et al., 2005). The severity of the cardiac defects is increased in mouse models that remove both *Shh* and *Ihh* or that abrogate Hh signaling entirely be removing *Smo* (Zhang et al., 2001). The expression of the cardiac marker *Nkx2-5* is delayed in these mice, while mice that lack *Ptch1* show an expanded *Nkx2-5* expression (Thomas et al., 2008). Consistent with the phenotype for *Ptch1*, loss of *Sufu*, another negative regulator of the Hh pathway, also produces heart defects (Cooper et al., 2005). In addition to upregulation of *Nkx2-5*, *Shh* induces expression of *Gata-4*, *Mef2C*, *Meox1*, and *BMP-4* during cardiomyogenesis. There are several feed forward relationships among the Hh targeted genes. Activation of *Meox1* increases *Gli2*, *BMP-4*, *Gata-4*, *Mef2C* and *Nkx2-5* expression (Gianakopoulos and Skerjanc,

2005) (Petropoulos et al., 2004) while *Mef2C* and *Gli2* activate each other during cardiomygenesis (Voronova et al., 2012).

Comparisons between cardiac and skeletal muscle suggest that some components of the regulatory networks are shared between different types of muscle. In addition to their roles in cardiomygenesis, *Mef2C* and skeletal progenitor factor *Meox1* are both active in skeletal muscle development. Myocardin (*Myocd*), the critical regulator of smooth muscle development (Wang et al., 2003), is also required for cardiomyocyte differentiation (Huang et al., 2009a).

1.1.4.3 Smooth Muscle

Overall, much less is known about smooth muscle formation than either skeletal or cardiac muscle development. However, consistent with other types of muscle development, both vascular and organ affiliated smooth muscle subtypes also require Hh signaling. In developing vertebrates, Hh signaling facilitates vasculogenesis and angiogenesis by targeting vascular growth factors (Byrd and Grabel, 2004) and the lungs of mice that lack *Shh* have decreased vascularization (Pepicelli et al., 1998).

SM subtypes are critical for the function of many organs including respiratory (Tollet et al., 2001; Goyal and Chaudhury, 2008), urogenital (Baker and Gomez, 1998; DiSandro et al., 1998) and gastrointestinal systems. Within bladder, intestine, and ureter, Hh has been shown to function in the ontogeny of SM as well as its homeostasis in the adult (Ramalho-Santos et al., 2000; Caubit et al., 2008; Kolterud et al., 2009; Zacharias et al., 2011). In the intestine, augmenting *Ihh* expression in the epithelium of transgenic mice results in robust expansion of mucosal SM (Madison et al., 2005; Kolterud et al., 2009; Zacharias et al., 2011) while attenuation of epithelial Hh signaling leads to loss of mucosal SM (Madison et al., 2005; Zacharias et al., 2011). Hh is epithelially secreted and acts upstream of the mesenchymal factors, *Foxf2* and *Myocd*, which are both involved in feedback mechanisms that regulate intestinal smooth muscle development by regulating epithelial Hh, emphasizing the complex nature of epithelial:mesenchymal crosstalk in the intestine (Wang et al., 2003; Ormestad et al., 2006). For example, mice with *Foxf2* conditionally deleted in the smooth muscle population exhibit increased HH (an indirect effect since FOXF2 is mesenchymal while HH is expressed only epithelially), and FOXF2 binds to promoters of the MYOCD and FOXF1 genes (both of which are also HH targets) to modulate signaling (Bolte et al., 2015).

1.2 Dissertation Proposal Objective

The ultimate goal of this dissertation was to identify regulatory programs underlying intestinal smooth muscle development. This work integrated computational and biological methods in parallel to achieve this goal. First, because Hh signaling has a documented role as a regulator of ISM development, computational methods were implemented to globally identify Hh enhancer regions that might drive ISM development (Roberts et al., 1995; De Santa Barbara et al., 2005; Madison et al., 2009; Zacharias et al., 2011; van den Brink and Rubin, 2013; Bolte et al., 2015). The advantage of computational prediction methods is that they are unbiased and allow the simultaneous exploration of all possible enhancers, regardless of spatial or temporal timing of target gene expression. This part was addressed in two different stages; a) I explored ways to identify Hh enhancers in genomic DNA based on the clustering of ci/GLI binding sites (presented in Chapter II) and b) I used machine learning to extract sequence information from

GLI bound sequences in ChIP data (Vokes et al., 2007; Vokes et al., 2008; Lee et al., 2010; Peterson et al., 2012) and to predict new Hh enhancers (presented in Chapter III). Finally, I collected biological data to begin to explore the transcriptome of the developing ICM, identifying genes expressed within ISM and thereby allowing prediction of additional regulators of ISM.

Despite the enormous importance of the Hh pathway, little is known about how the Hh signal is transduced into a specific phenotypic response in a given cell type, a key question for elucidating context-specific activation of gene targets. When Hh signals are received by a responsive cell, this results in the binding of ci/GLI transcription factors to genomic enhancers of Hh targeted genes. Since so few Hh-regulated enhancers have been identified and functionally validated to respond to Hh signals (Table 1.1), very little is known about what features these enhancers have in common or about how individual enhancers are activated in different contexts. The first aim of my dissertation work was to implement computational approaches to expand the database of known Hh enhancers and to verify them as GLI dependent.

1.3 Identification of Transcription Factor Binding Sites

1.3.1 Enhancer Background

Enhancers are defined as short regions of DNA that contain binding sites for transcription factors that act in an integrated manner to control gene expression in a specific spatiotemporal context (Martinez-Salas et al., 1988). The combinatorial input of all bound transcription factors (reviewed in (Spitz and Furlong, 2012)), both activators and repressors, determines whether the enhancer, as a protein:DNA complex, interacts with promoters to initiate gene transcription. It has also been shown that enhancers emit transcripts (Kim et al., 2010), which in some cases are required for enhancer function (Melo et al., 2013) and may also serve to perpetuate the openness of the chromatin region. The modular organization of TFBS within enhancers facilitates context dependent initiation of enhancer activity by different combinations of factors. TFs work cooperatively and many have specific interaction partners that result in context specific activation (Lefterova et al., 2008; Bery et al., 2013). For instance, the single zebrafish wnt8a enhancer region is activated via two different combinatorial inputs (Narayanan and Lekven, 2012), exemplifying how enhancers can be employed in multiple contexts. Although some enhancer regions are well conserved across species, new enhancers can arise as the result of duplication events (Kikuta et al., 2007), alterations from mobile elements (Sanges et al., 2006; Lowe et al., 2007) and *de novo* generation from accumulated changes in nucleotide sequence (Eichenlaub and Ettwiller, 2011; Domené et al., 2013; Rubinstein and Souza, 2013). Thus enhancers appear to be highly malleable and rapidly evolving (Villar et al., 2015).

In vertebrates, the relationship between enhancers and their gene targets is complex, since genes that are expressed in the same tissue are seldom located in contiguous chromosome regions (Moltó et al., 2009). Initially thought to reside largely in proximal upstream and intronic regions of genes, vertebrate enhancers have been located in every component of the genomic landscape, including exons (Dong et al., 2010; Birnbaum et al., 2012; Khan et al., 2012; Ritter et al., 2012) and intergenic regions such as CpG islands and repeat regions (McBride et al., 2011). Looping mechanisms (reviewed by (Dean, 2011)) facilitate long range interactions that span large genomic distances (Lettice et al., 2003; Gordon et al., 2009a; El-Kasti et al., 2012; Sakabe et al., 2012; Hill and Lettice, 2013)(reviewed by (Harmston and Lenhard, 2013)), which include upstream and downstream relationships to target genes. Even cross-chromosome interactions have been documented (Spilianakis et al., 2005; Lomvardas et al., 2006).

Individual genes often have several enhancer elements that activate temporal-specific gene expression in different contexts (Gordon et al., 2009a; Hill and Lettice, 2013)(Göttgens et al., 2010). Secondary enhancers can arise from duplication events; these can evolve somewhat divergent functions (Hong et al., 2008), or can provide redundant overlapping expression (Nolte et al., 2013). Others, however, may not be functional in isolation, serving only to augment primary enhancer function (Guerrero et al., 2010). Characterization of the *Pax6* regulatory region by transgenic analysis illuminates how sophisticated enhancer regulation can be; locus expression in the mouse is controlled by several enhancers that facilitate distinct and overlapping gene expression patterns and the locus also contains interdependent enhancer regions that provide protective redundancy (McBride et al., 2011).

1.3.2 Transcription Factor Binding Site Prediction

Over the last decade, largescale genomic studies have provided abundant datasets to start unraveling how enhancers function globally in development and in disease settings (Raney et al., 2011). Computational approaches are well suited for processing and integrating these large datasets in order to identify and predict transcription factor (TF) interactions that result in gene expression within specific cells. Yet despite the increased use of computational methods for these purposes, success rates for predicting enhancer regions remain low. Most problematically, the underlying regulatory logic used by enhancers is still poorly understood.

For some enhancers, multiple copies of a specific transcription factor binding site (TFBS) will be present (Gotea et al., 2010), but the biological function of homotypic clustering is not fully understood. In some instances the presence of multiple copies of the TF is required because multiple proteins are needed to permit activation. For example, the neural crest specific *Sox10* enhancer contains multiple SOX10 binding sites that are required for fully functional enhancer activity (Wahlbuhl et al., 2012). For others, multiple binding sites could serve to maintain the presence of a single TF in the region until it binds to the right site or to preserve enhancer function in the event of mutation.

All enhancers have cofactor relationships (also called heterotypic clustering) that generate combinatorial inputs resulting in cell-specific gene expression (Berman et al., 2004; Morgan et al., 2007; Miller et al., 2012; Wang et al., 2012a). For example, cortical development relies on a cofactor relationship between SOX and POU across multiple enhancers for activation in different cell populations (Bery et al., 2013). Importantly, the organization of TFBS within an enhancer region is modular, and there is evidence that, at least in some cases, the order of binding sites is less important than the presence of these sites (Swanson et al., 2010; Evans et al., 2012; Guo et al., 2012). In contrast, in promoters, the order and distance between binding sites for each factor appears to be more constrained (Hosseinpour et al., 2013). This strict organization of both TF relationships and distances between binding sites makes it easier to mine cell specific cofactor relationships in promoter regions of co-expressed genes compared to the variable proximity relationships between TFBS that occur in most enhancers (Alkema et al., 2004; Gruel et al., 2011; Whitfield et al., 2012). Occasionally, however, it is seen that features found in promoters can be used to find relationships that predict enhancer elements (Nolis et al., 2009).

Another major advantage of promoter mining is that the close proximity to the target gene provides more accurate annotation (Subramanian et al., 2005; Huang et al., 2009b).

Using conservation as a tool for data mining can sometimes be extremely helpful in identifying functional sites, determining whether a TF has multiple TFBS, and establishing the presence of cofactor relationships (Bulyk, 2003). However, some conserved regions exhibit no enhancer activity (Bejerano et al., 2004; Katzman et al., 2007), and deletion of some ultra-conserved regions from genomes can fail to show an obvious phenotype (McLean and Bejerano, 2008). In general, cis-regulatory regions are not stable, and sequence conservation of binding sites is low (Dermitzakis and Clark, 2002). Even among pathways that have strongly conserved functions, rearrangement of TFBS in target enhancers is common (Odom et al., 2007), and this divergent sequence still maintains conserved regulatory function (Göttgens et al., 2010; Taher et al., 2011). Since enhancers are responsible for regulation of conserved functionality as well as diversification, it is not surprising that examples of both positive and negative selection of regulatory regions exist (Smith et al., 2013). Given the apparently rapid evolution of enhancers (perhaps demanded by the fact that these elements are so important to the modulation of gene activity) (Villar et al., 2015), conservation may not work for some types of enhancers. However, enhancer detection methods that allow alteration in the positioning of TFBS, but require a similar distribution of transcription factors, might be more valuable than direct conservation for discovering trends within others.

Statistical learning approaches are valuable in identifying enhancer function since they attempt to learn features that discriminate functional from non-functional regulatory regions with no prior constraint imposed on the system. Machine learning methods are capable of discriminating sequence characteristics that contribute to TF interaction (Narlikar et al., 2010; Burzynski et al., 2012; Hansen et al., 2012; Lee and Huang, 2012; Ahmad et al., 2014) by deriving an optimal boundary between a training set and a negative set. For example, new regulatory regions have successfully been predicted in human cells by looking for k-mer enrichment against a background set of sequences and using those motifs to predict new regions that contain the same k-mer combinations (Fletez-Brant et al., 2013). One of the challenges in implementing machine learning approaches is that there may not be a good set of known negative regulatory regions for comparison with positive areas, resulting in overfitting. Furthermore, many of these approaches are based exclusively on sequence, but it is possible to integrate multiple datasets in a machine learning approach to extend the information beyond genomic DNA and to incorporate additional regulatory levels that control chromatin access (Yaragatti et al., 2009).

1.3.3 Mining Biological Data Sets for Transcription Factor Binding Sites

Global datasets, including open chromatin regions, chromatin marks associated with enhancers, regions bound by TFs *in vivo* (as determined by DNA protection assays or ChIP-seq), putative DNA motif libraries, and conserved genomic regions provide abundant data to identify genomic regions that are likely to participate functionally in gene regulation. Biologically collected DNA accessible datasets include DNAseI hypersensitivity sites (Neph et al., 2012), FAIRE or Formaldehyde-Assisted Isolation of Regulatory Elements (Song et al., 2011), enhancer transcription (eRNA) (Mousavi et al., 2013), enhancer affiliated markers (CTCF, CBP, and histone modifiers such as P300 and HAT) (Visel et al., 2009) as well as histone marks (H3K4me1, H3K4me2, H3Kac etc) (Jin et al., 2011; Rada-Iglesias et al., 2011) specific enough to differentiate active and poised enhancers. These features are generally seen in regulatory regions and can be used to restrict the organism's genomic DNA to a subset of putative participating regions when computationally mining for putative TFs or context specific enhancer regions.

However, there are some limitations to using such biological datasets to identify enhancers. ChIP-seq studies are known to generate a high level of false positive peaks. An unknown percentage of the data may be background (e.g., from bulk precipitation) or only indirectly related (such as ChIP-seq peaks that do not contain a binding site for the factor in question) or may contain irrelevant information (such cell contamination or spurious TF binding). And, of course, the fact that a TF binds to DNA region does not confirm its regulatory function (Cusanovich et al., 2014). However, it remains to be seen if some of these apparently non-functional regions, tested in a broader context, might act as secondary enhancers to facilitate primary enhancer activity (Maston et al., 2012). At the same time, due to low affinity TF binding or to poor antibody interactions, some truly functional regions may not be captured. Additionally, if the available data contains a mixed population of cells (i.e., is derived from tissue rather than purified cells), it can be difficult to identify enhancer regions involved in context-specific gene activation.

1.3.4 Prediction of Hedgehog Enhancer Regions

To begin to understand the genomic landscape underlying Hh gene activation, my first approach implemented a computational method to examine the distribution of TFBS for the Hh transcription factor *ci* in the fruit fly genome. Using the *Drosophila* model organism was advantageous since the small genome facilitates computational strategies and functional testing of the enhancers in transgenic flies is relatively easy and quick. Nevertheless, in total, only seven Hh enhancers had been functionally verified in *Drosophila* prior to our study. Four (regulating *decapentaplegic*, *knot*, *patch*, *wingless*) were known to contain three or more functional ci sites, while the remainder contained two (*stripe*, *hairy*) or one (*orthodenticle*) ci site (Alexandre et al., 1996; Ohlen and Hooper, 1997; Müller and Basler, 2000; Piepenburg et al., 2000; Kwon et al., 2004; Hersh and Carroll, 2005; Blanco et al., 2009). Since the majority of these characterized *Drosophila* Hh enhancers contained clusters of multiple Hh transcription factor binding sites, the work presented in Chapter II tested whether homotypic clustering of Hh transcription factor sites could be used to predict the location of additional enhancers. A sensitive computational algorithm was developed to identify clustered sites and to measure the probability of finding such clusters by chance. Twenty-two predicted clusters were tested in functional assays. Of these, eight, one previously known and seven new, were found to be Hh enhancers; their function was confirmed by an *in vivo* transgenic fly assay and after electroporation of the chicken neural tube. Importantly, all of these Hh enhancers showed direct Hh response since loss of enhancer activity occurred after mutagenesis of the ci binding sites. Since only 32% of the predicted enhancers were functional, we concluded that while clusters of Hh transcription factor binding sites clearly define some active enhancers in the fly genome, homotypic clustering alone is not sufficient to specify a Hh enhancer region and that other features must be involved. Nevertheless, if this rate of prediction were to hold, the data generated in this study could lead to the identification of a very large number of Hh-regulated enhancers.

In the mouse, unlike the fly, most of the previously characterized and functionally validated Hh enhancers contain only one functional GLI site (*FoxA2* (Sasaki et al., 1997), *Gli1*

(Dai et al., 1999), *Nxk2.9* (Santagati et al., 2003), *Myf5* (Gustafsson, 2002), *Cltb*, *Tle1*, *Ncor2*, *Boc*, *Ptch2* (Lee et al., 2010), *Rab34*, *Nkx2.2* (Vokes et al., 2007), *Ptch1* (Agren et al., 2004)). The remaining contain two (*Sox18*, *Ptch1* (Lee et al., 2010), *Has2* (Liu et al., 2013)). Publically available ChIP datasets from mouse models carrying FLAG-tagged GLI proteins (GLI^{FLAG}) also seem to suggest that regions bound by GLI1 or GLI3 proteins contain only one GLI binding site (Vokes et al., 2007; Lee et al., 2010). Indeed, when the cluster finding algorithm that we developed in *Drosophila* was applied to the mouse, using Chromosome 2 as a test, no Hh enhancers were found after testing 40 predicted putative enhancers. Thus, a different approach was needed.

Chapter III describes a strategy for finding mammalian Hh enhancers that takes advantage of four existing GLI ChIP datasets. Though no ChIP-grade antibody for GLI is available, the generation of mouse lines carrying FLAG-tagged alleles of the GL1 and GLI3 proteins allowed several ChIP analyses to be accomplished in different tissues. I performed a meta-analysis of these datasets in order to capture a library of GLI binding motifs that are representative of possible *in vitro* binding sites (Vokes et al., 2008; Lee et al., 2010; Peterson et al., 2012). Previously, prediction of putative GLI binding motifs relied on *in vitro* binding data which predicted 1,432,161 possible GLI binding sites across the mouse genome (Hallikas et al., 2006). The GLI library based on the *in vivo* meta-analysis, based on GLI motifs enriched in the *in vitro* datasets, suggested substantially fewer, 195,816. Critically, the *in vitro* motifs included predicted binding motifs that did not contain cysteines (C) in the fifth and seventh positions of the binding site; a C in this position is a known requirement for functional GLI binding (Winklmayr et al., 2010). Thus, the putative motifs defined by *in vitro* binding studies likely contains more false positives than in the *in vivo* generated GLI library, which contains C in the critical positions. To determine whether machine learning could be used to reveal genomic features predictive of Hh enhancers, I applied kmer-SVM to this redefined set of *in vivo* binding sequences culled from the GLI^{FLAG} datasets (Fletez-Brant et al., 2013). Classifiers trained on two of the four GLI1^{FLAG} datasets (one done in neural precursor cells and one in the developing limb) were found to be capable of distinguishing members of a positive group from a negative background dataset with high confidence (Vokes et al., 2008; Peterson et al., 2012). Because these datasets were collected from sequences precipitated by two different GLI transcription factors (GLI1 for the neural precursors and GLI3 for the limb), and from different tissues at different time points, we expected that shared targets were most likely to be Hh pathway components, which are active in all contexts. Therefore, both datasets were used to independently predict Hh enhancers across the mouse genome and the resulting predictions were then overlapped and filtered for regions annotated to Hh pathway components. Nine regions annotated to *Boc*, *Dpp6, Gli3*, *Hhip*, *Hipk2*, *Ptch1*, *Scube1*, *Shh*, and *Tgfbr2* were tested and seven (78%) were Hh responsive. To confirm direct Hh interaction, putative enhancer regions were co-transfected with modulators that constitutively activate the Hh pathway (Xie et al., 1998); the Hh response was lost after mutation of GLI-binding sites, proving the Hh-dependent nature of enhancer activity and identifying the precise genomic sequence bound by the GLI proteins responsible for driving gene expression within the enhancer. These results suggest that machine learning methods can be successfully applied to identify sequence features that characterize Hh enhancer regions.

1.4 Intestinal Visceral Smooth Muscle Development

In Chapter IV, I concentrated on analysis of developing intestinal smooth muscle, specifically, the inner circular smooth muscle. In this case, I collected new biological data sets (RNA-seq and ChIP-seq) and used these to determine which muscle genes are expressed in ISM and to identify the regions of DNA that regulate expression of these genes. The first of these techniques, RNA-seq, captures a transcriptome profile by utilizing high throughput sequencing to quantitate RNA levels. RNA-seq of the separated epithelial and mesenchyme populations of E14.5 intestine allowed a comparison between a transcriptome profile with no muscle (epithelium) and the muscle enriched mesenchyme during the formation of inner circular muscle (ICM). Using Gene Set Enrichment Analysis (GSEA) and clustering analysis followed by examination of *in situ* data at E14.5, we identified over 100 genes that are expressed in the ICM (Visel et al., 2004; Subramanian et al., 2005; Diez-Roux et al., 2011). The promoters of these genes were then analyzed to determine putative transcription factors involved in the regulation of ISM genes (Gotea and Ovcharenko, 2008). This analysis showed enrichment for cJUN, which was further shown to be expressed exclusively within the ICM. To examine the genomic regions bound by cJUN, ChIP-seq, a method for determining the location of transcription factor binding sites on DNA *in vivo*, was performed. ChIP-seq relies on cross-linking the transcription factor to the DNA in the nucleus, breaking DNA into small pieces, and then using an antibody to capture the segments of DNA bound by transcription factor. These regions are then sequenced to determine the enriched regions. We found that genomic regions bound by cJUN at E14.5 contained characteristics of muscle enhancers, indicating a previously unknown regulatory role for cJUN in ISM. Since previous studies had shown that Hh signaling is also important in the regulation of ISM gene expression in the intestine and that cJUN and GLI have a cofactor relationship in other conditions (Laner-Plamberger et al., 2009), we examined the regulatory relationship between cJUN and GLI. We found no evidence for co-binding of these factors at cJUN immunoprecipitated regions. However, we established cJUN as a Hh target gene. Additionally, we established that at least some of the genes that had previously been shown to be regulated by Hh in skeletal muscle are also regulated by Hh in ISM.

1.5 Significance of This Work

The Hedgehog signaling pathway is critical for embryonic organ development and adult tissue homeostasis across animal phyla (McMahon et al., 2003; Jiang and Hui, 2008; Briscoe and Thérond, 2013). Additionally, misregulation of this pathway causes a number of developmental malformations as well as adult human diseases, including cancer (Barakat et al., 2010). Thus, there is great interest in determining which genes are regulated by the Hh pathway and which *cis* elements direct this regulation. To answer this question in the context of intestinal inner circular muscle, computation methods to globally predict Hh enhancer regions were implemented in parallel with biological data collection (ChIP-seq, and expression profiling using RNA-seq) to identify Hh target genes and regulatory regions responsible for activating ISM genes. Though this project focused on Hh signaling, this multi-pronged approach could be applied to any transcription factor or signaling pathway to comprehensively analyze the gene regulatory networks governing many normal and disease-related cell states resulting from dysregulation of signaling pathways. This type of knowledge is important in disease settings both acutely (targets may provide effective biomarkers for disease initiation) and chronically (such targets can be used as disease monitors and/or therapeutics). Moreover, the whole genome analysis could have a major impact on the interpretation of Genome Wide Association Studies that identify variations in DNA regions (often regulatory) linked to disease phenotypes, since many new functional genomic regions are annotated.

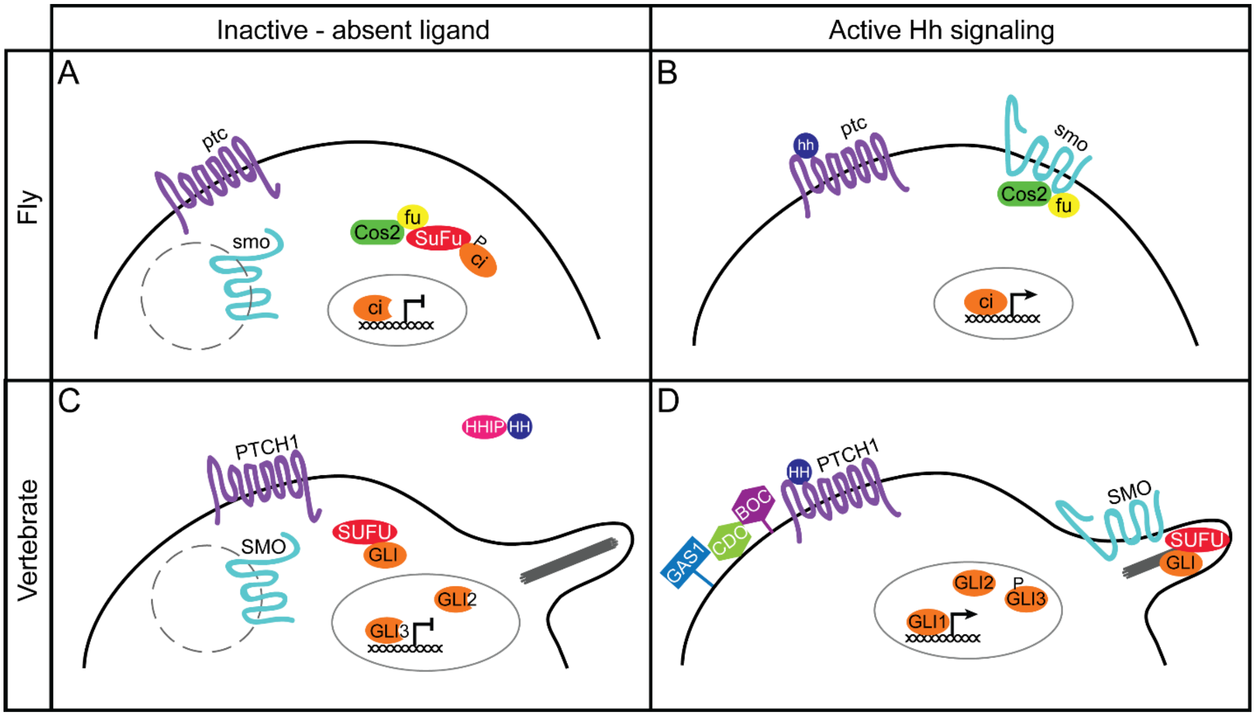


Figure 1.1. Schematic of Hh signaling in Fly and Vertebrate. (A) In the absence of hh ligand, the transmembrane protein ptc inhibits smo, preventing it from engaging the downstream signal transduction pathway. This may involve the sequestration of smo in intracellular vesicles. The Cos2, fu, and SuFu complex phosphorylates ci, which is subsequently cleaved and translocated to the nucleus, where it acts as a repressor. **(B)** Binding of hh to ptc relieves smo inhibition, allowing it to interact with Cos2 and fu; as a result ci is neither phosphorylated nor cleaved. The full length ci enters the nucleus where it acts as a transcriptional activator. In vertebrates, the Hh signaling pathway relies on cilia. **(C)** Without HH interaction with PTCH1, either in the absence of HH or when HH is sequestered by HHIP, SMO is inhibited and GLI2 and GLI3 proteins are cleaved into transcriptional repressors. **(D)** In the presence of HH, several co-receptors (BOC, CDO, GAS1) facilitate binding to PTCH1. SMO then localizes to the cilia where the SUFU GLI complex is trafficked along the microtubules. GLI1 or active forms of GLI2 and GLI3 are not cleaved under these conditions and can enter the nucleus to activate transcription.

Enhancer Gene Target	**Organism**	**Reference**
decapentaplegic	*Drosophila*	Muller et al., 2000
knot	*Drosophila*	Hersh et al., 2005
hairy	*Drosophila*	Kwon et al., 2004
orthodenticle	*Drosophila*	Blanco et al., 2009
patch	*Drosophila*	Alexandre et al., 1996
stripe	*Drosophila*	Piepenburg et al., 2000
wingless	*Drosophila*	Ohlen et al., 1997
Boc	Mouse	Lee et al., 2010
Cltb	Mouse	Lee et al., 2010
FoxA2	Mouse	Sasaki et al., 1997
Gli1	Mouse	Dai et al., 1999
Has2	Mouse	Liu et al., 2013
Myf5	Mouse	Gustafsson et al., 2002
Ncor2	Mouse	Lee et al., 2010
Nkx2.2	Mouse	Vokes et al., 2007
Nxk2.9	Mouse	Santagati et al., 2003
Ptch1	Mouse	Agren et al., 2004; Lee et al., 2010
Ptch2	Mouse	Lee et al., 2010
Rab34	Mouse	Vokes et al., 2007
Sox18	Mouse	Lee et al., 2010
Tle1	Mouse	Lee et al., 2010

Table 1.1. Functionally verified Hh enhancers identified at the time this work was started. This list includes enhancers from *Drosophila* or mouse for which response to Hh was functionally verified and ci/GLI binding dependence was confirmed by mutagenesis of the TFBS.

Chapter II

Identification and validation of novel Hedgehog-responsive enhancers predicted by computational analysis of ci/GLI binding site density

2.1 Abstract

The Hedgehog (Hh) signaling pathway directs a multitude of cellular responses during embryogenesis and adult tissue homeostasis. Stimulation of the pathway results in activation of Hh target genes by the transcription factor ci/GLI, which binds to specific motifs in genomic enhancers. In *Drosophila,* only a few enhancers (*patched*, *decapentaplegic*, *wingless*, *stripe*, *knot*, *hairy*, *orthodenticle*) have been shown by *in vivo* functional assays to depend on direct ci/GLI regulation. All but one (*orthodenticle*) contain more than one ci/GLI site, prompting us to directly test whether homotypic clustering of ci/GLI binding sites is sufficient to define a Hh-regulated enhancer. We therefore developed a computational algorithm to identify ci/GLI clusters that are enriched over random expectation, within a given region of the genome. Candidate genomic regions containing ci/GLI clusters were functionally tested in chicken neural tube electroporation assays and in transgenic flies. Of the 22 ci/GLI clusters tested, seven novel enhancers (and the previously known *patched* enhancer) were identified as Hh-responsive and ci/GLI-dependent in one or both of these assays, including: *Cuticular protein 100A* (*Cpr100A*); *invected* (*inv*), which encodes an *engrailed*-related transcription factor expressed at the

Gurdziel K*, Lorberbaum DS*, Udager AM*, Song JY*, Richards N, Parker DS, Johnson LA, Allen BL, Barolo S, Gumucio DL. *Identification and validation of novel Hedgehog-responsive enhancers predicted by computational analysis of Ci/Gli binding site density.* PLOS One.

anterior/posterior wing disc boundary; *roadkill (rdx)*, the fly homolog of vertebrate *Spop*; the segment polarity gene *gooseberry (gsb)*; and two previously untested regions of the Hh receptor encoding *patched (ptc)* gene. We conclude that homotypic ci/GLI clustering is not sufficient information to ensure Hh-responsiveness; however, it can provide a clue for enhancer recognition within putative Hedgehog target gene loci.

2.2 Introduction

The Hedgehog (Hh) signaling pathway plays multiple roles in embryonic organ development and adult tissue homeostasis across animal phyla (McMahon et al., 2003; Jiang and Hui, 2008; Briscoe and Thérond, 2013). Hh signaling directs specific cell fate choices, controls tissue patterning and governs cell proliferation. Several human developmental diseases are caused by altered Hh signaling, including spina bifida, exencephaly (Murdoch and Copp, 2010), holoprosencephaly (Schachter and Krauss, 2008), cleft lip/palate (Lipinski et al., 2010), and a host of malformations in vertebral, anal, cardiac, tracheal, esophageal, renal, and limb tissues (together known as VACTERL Association (Ngan et al., 2013)). Aberrant Hh signaling is also responsible for several cancers, including basal cell carcinoma, medulloblastoma and rhabdomyosarcoma (Teglund and Toftgard, 2010). Recently, cancers of the pancreas, colon, ovary, stomach and lung have also been associated with increased Hh signaling (Barakat et al., 2010; Teglund and Toftgard, 2010), prompting initiation of clinical trials with Hh antagonists for some of these conditions (de Sauvage, 2007; Scales and de Sauvage, 2009; Sekulic et al., 2012; Tang et al., 2012).

The Hh-regulated GLI family transcription factors (including cubitus interruptus (ci) in the fly and GLI1-3 in mammals) are highly conserved across metazoans, as is the sequence of the preferred consensus ci/GLI binding site (Hallikas et al., 2006; Winklmayr et al., 2010). Despite the functional importance and high conservation of the Hh pathway, surprisingly little is known about its target genes in any organism. These target genes and their associated enhancers, which are responsible for the genomic response to Hh in development and disease, have significant potential therapeutic and diagnostic value.

One method for identifying putative enhancers is chromatin immunoprecipitation (ChIP) (Vokes et al., 2007; Vokes et al., 2008; Lee et al., 2010; Peterson et al., 2012), though such data are subject to the spatiotemporal limitations of the analyzed cells or tissues and can be diluted by a high number of false positive binding sites. While many potential murine Hedgehog-responsive enhancers have been pinpointed in this manner, relatively few have been functionally verified by mutagenesis of transcription factor binding sites (Vokes et al., 2007; Vokes et al., 2008; Lee et al., 2010; Peterson et al., 2012). In *Drosophila*, an alternative approach, DamID which fuses a DNA interacting protein to DNA adenine methyltransferase leading to methylation near binding locations, identified 52 potential ci/GLI target enhancers, though none of these were functionally verified by mutagenesis of ci/GLI sites (Biehs et al., 2010). To date, only seven *Drosophila* enhancers have been shown by mutational analysis to be ci/GLI-dependent (Alexandre et al., 1996; Ohlen and Hooper, 1997; Müller and Basler, 2000; Piepenburg et al., 2000; Hersh and Carroll, 2005; Blanco et al., 2009; Ramos and Barolo, 2013), which limits our understanding of the basic rules that govern their activity and context specificity. Analysis of the known *Drosophila* Hh enhancers reveals that three (regulating *ptc, wg,* and *knot*) contain clusters of three or more ci/GLI binding sites, while the remaining enhancers (of the *dpp, stripe* and *hairy* genes) contain two sites (Alexandre et al., 1996; Ohlen and Hooper, 1997; Müller and Basler, 2000; Piepenburg et al., 2000; Hersh and Carroll, 2005; Blanco et al., 2009; Ramos and Barolo, 2013). These examples, and findings in other systems (Markstein, 2001; Berman et al., 2002; Rebeiz et al., 2002; Lifanov, 2003; Gotea et al., 2010) suggest that homotypic clustering might be a relevant indicator of Hh enhancer activity in the fly. To test this, we computationally identified regions of the fly genome in which the density of ci/GLI binding sites is enriched relative to chance expectation. We then tested the ability of these regions to: 1) drive Hh-dependent activity in the developing chicken neural tube, and 2) direct tissue-specific gene expression in a *Drosophila* transgenic reporter model. Importantly, the functional significance of the ci/GLI binding motifs was also tested by mutation of these sites within each active enhancer. Of the 17 top clusters, four (23%) drove reporter expression in a known Hh domain and/or in a ci/GLI-dependent fashion in one or both assays. Thus, while some Hh-regulated enhancers indeed contain homotypic clusters of ci/GLI motifs, not all such clusters function as enhancers *in vivo.*

We also asked whether ci/GLI site clustering could be used to predict the location of enhancers in genes that are known or putative targets of Hh signaling. We identified five such ci/GLI site clusters, four of which were subsequently validated as Hh enhancers by functional assays (80%). Thus, altogether, our analysis of clustered ci/GLI sites identified eight Hh enhancers, including seven novel enhancers and one previously identified *ptc* enhancer. These findings double the number of functionally verified Hh enhancers.

2.3 Materials and Methods

2.3.1 Computing Resources

Except where otherwise indicated, all computational steps were performed using custom Perl scripts, which are available for download at https://github.com/um-gurdziel/GurdzielUdagerLorberbaum2015. Overlap between coordinates in bed file format were performed using the UCSC Table Browser.

2.3.2 Definition of Putative ci/GLI Binding Sites

A mono-nucleotide distribution matrix for ci binding sites, derived from *in vitro* competitive DNA binding assays with recombinant ci protein and labeled oligonucleotides, was obtained via the Genomatix Software Suite (www.genomatix.de; Genomatix, Germany) (Hallikas et al., 2006). The consensus index vector for such a matrix reflects the degree of nucleotide preference at each position; values range from 0, indicating equal preference for any of the four nucleotides, to 100, indicating strict preference for a single nucleotide (Quandt et al., 1995). The matrix similarity score (MSS) for a given site is calculated as the ratio of its matrix-vector product to that of the consensus site, as described previously (Quandt et al., 1995), and MSS values range from 0 to 1 (where 1 equals an exact match to the consensus site). The first nine of the eleven positions in the ci matrix have consensus index vector values greater than 70, suggesting that they contain a high degree of specific information about potential ci binding. Thus, these matrix positions were used to define a set of 211 9-mers (422 in sense and antisense directions) that pass a minimum level (0.75) of overall matrix similarity (i.e. with a MSS ≥ 0.75) to the optimal consensus ci site (GACCACCCA) (Table S2.1) (Quandt et al., 1995; Hallikas et al., 2006) and also contain concordant (C and C or G and G) nucleotides in the 4th and 6th position, which are critical for ci binding (Winklmayr et al., 2010).

2.3.3 Identification and Annotation of Predicted ci Binding Sites in Genomic Sequence

Genomic sequence files (chromFa) for *D. melanogaster* (Dm) and *D. pseudoobscura* (Dp) were downloaded from UCSC Genome browser (genome.ucsc.edu) build dm3 (Celniker et al., 2002; Richards et al., 2005; Fujita et al., 2011). The genomic coordinates of predicted ci/GLI binding sites were identified for chr2R, chr2L, chr3R, chr3L, chr4, and chrX (build dm3); and chr2, chr3, chr4 and chrX (build dp3). Each putative ci/GLI binding site was annotated for nearest gene/transcript, distance to nearest gene/transcript, and associated gene/transcript feature transcript using refFlat files obtained from UCSC Genome Bioinformatics. ci/GLI clusters were defined as regions containing at least three and at most ten putative ci/GLI binding sites within a maximum distance of 1000 base pairs (bp) (measured from the outside ends of the flanking sites (Fujita et al., 2011; McQuilton et al., 2012). Predicted sites were also annotated with respect to the nearest CTCF boundary region (Holohan et al., 2007). Cluster regions that contained predicted ci binding sites that mapped to exons or repeat regions were excluded. Repeat regions often have regulatory function (Sawaya et al., 2013; Taher et al., 2015). If clustered regions were identified within repetitive regions and found to be positive we would not know if the activity was dependent on clustering or features of the repetitive sequence.

2.3.4 Background Modeling

To identify regions of the genome that exhibit a higher density of ci/GLI sites than would be expected by chance, we compared the actual distribution of ci/GLI sites to a randomized background model. Three different modes of background modeling were examined. For Model 1

(Random), all bases in the genome were randomized, as was done in a previous analysis of clustered binding sites for Suppressor of Hairless (Rebeiz et al., 2002). For Model 2 (Shuffle 3mer), the genome was parsed into contiguous 3-mers and these were then shuffled to create the background. In Model 3 (Flip GC/AT), each base was randomly flipped between itself and its complementary base pair (e.g., G will randomly become G or C; A will become A or T; C will become C or G; T will become T or A). On the basis of the data shown in Results (Figure S2.1), only the Flip GC/AT model generates background genomes that most closely represent the GC content surrounding ci/GLI sites in the native genome. Since GC rich ci/GLI sites will occur by chance more often in GC rich than AT rich regions, use of a randomization model that homogenizes the AT/GC landscape would artificially reduce the density of expected ci/GLI sites in GC rich areas and increase this density in AT rich regions. Therefore, using the Flip GC/AT strategy, background models were generated separately for the Dm and Dp genomes for comparison to each native genome.

2.3.5 Generation of Artificial Genomic Sequence and Random Genomic Distributions of Binding Sites

On a chromosome-by-chromosome basis, 1000 sets of background genomic sequences were generated using the Flip GC/AT method. However, base flipping resulted in fewer ci/GLI sites in the randomized chromosomes, relative to the native Dm or Dp genome. To correct for this, putative ci/GLI binding sites were identified in each of the 1000 background genomic sequences and the genomic coordinates of each site was recorded. Site motifs, tagged with their location coordinates, were pooled into a master list of possible site positions. This master list was used to re-create 100 background chromosomes for each chromosome, such that each background chromosome contained the same composition of ci/GLI sites (overall number and motif) as the native Dm or Dp chromosome (see Results).

2.3.6 Assessment of Relative ci/GLI Binding Site Clustering

ci/GLI site clusters were defined as regions containing at least three and at most ten putative ci/GLI sites within a maximum distance of 1000 base pairs (bp; measured from the outside ends of the flanking sites). The genomic coordinates of each cluster were cataloged, and clusters were subsequently filtered for the presence of at least one predicted binding site with a MSS $\geq$0.81. This was done to decrease the number of clusters comprised entirely of low scoring sites, substantial portions of which are predicted to be non-functional. Clusters that contained exon or repeat elements were excluded. Clusters for which the ci/GLI binding sites themselves accounted for more than 25% of the end-to-end cluster length were also excluded, since the majority of such clusters were composed of repetitive sequence. For each cluster, the number of binding sites expected to be present by chance for that specific genomic region was determined from 100 control reconstructed genomes as described in Results. A clustering coefficient (CC) was defined as the number of ci/GLI sites observed in a given interval of the native genome (at a given location) divided by the average number of ci/GLI sites in the same region of the background genome (at the same location). To enrich for clusters likely to represent enhancers, we selected a CC cutoff of four which captured all of the previously known clustered Hh enhancers. Importantly, the CC score was used as a filter, and not as a ranking tool.

2.3.7 Orthologous Enrichment of ci/GLI Clusters

Clusters were identified and annotated in the Dp genome exactly as described above for Dm. Background modeling for the Dp genome was done by Flip GC/AT; 1000 randomized genomes were generated and corrected as outlined above for number and affinity class to make 100 randomized, corrected Dp genomes for comparison to the native Dp genome. Clusters identified in the Dp genome were selected according to the same criteria as for the Dm genome (cluster size ≤ 1000; 3-10 ci/GLI sites; CC ≥ 4; at least one site with MSS ≥ 0.81). The coordinates for enriched clusters of ci/GLI binding sites (CC ≥ 4) were determined for Dm and Dp and compared using the LiftOver tool available from UCSC Genome Bioinformatics (Fujita et al., 2011). All clusters that were present in orthologous positions of the Dm and Dp genomes (i.e., with an overlap of one or more bases, irrespective of sequence identity) were selected for further analysis.

2.3.8 Cloning of Putative Enhancer Regions for Testing

Putative enhancer regions in the Dm genome were visualized in the UCSC Genome Browser, and using the Conservation track (12 Flies, Mosquito, Honeybee, Beetle Multiz Alignments & phastCons Scores), the ends of an individual enhancer element were extended to include contiguous highly conserved sequence (Blanchette et al., 2004). Putative enhancers were amplified from w^{1118} genomic DNA using template-specific PCR primers (Table S2.2). A CACC extension was added to the end of one primer to facilitate directional cloning. PCR fragments were cloned into the pENTR/D-TOPO vector using the standard kit (Invitrogen) and then shuttled into either Ganesh-G2 (Swanson et al., 2008) or HP-desteGFP (Boy et al., 2010) vectors using the Gateway® cloning system (Invitrogen). ci binding site mutations (C4A) were introduced by overlap extension PCR, as previously described (Swanson et al., 2010).

QuikChange mutagenesis (Stratagene) was also used to mutate some ci binding sites. pCIT was generated by replacing eGFP in pCIG (Megason and McMahon, 2002) with TdTOMATO, which was cloned into the location between the third PmlI site and the NotI site in pCIG. *SmoM2*-pCIT was generated by cloning rat *SmoM2* into the XhoI and ClaI sites of pCIT.

2.3.9 *Drosophila* Transgenesis

Transformation was achieved by injection of *w*^{1118} or *ZH-attP-86Fb* embryos, essentially as described previously (Rubin and Spradling, 1982; Bischof et al., 2007). A current protocol is available at: http://sitemaker.umich.edu/barolo/injection. For *w*^{1118} transgenesis, at least three independent lines were examined; one or more lines were examined for *ZH-attP-86Fb* transgenesis.

2.3.10 *Drosophila* Tissue Analysis

Since Hh is active in a variety of tissue contexts in the embryo (brain, gut, muscle, segmental stripes etc.), we utilized embryos at stages 9-13 to gain an unbiased view of all of these contexts. Additionally, we specifically examined the wing imaginal disc since this is a well-known and well-characterized expression domain for Hh signaling. Of the 22 genes selected for analysis (Table 2.1), 17 are expressed in the embryo or imaginal disc (Tomancak et al., 2002; Tomancak et al., 2007; Hammonds et al., 2013). There are no data on two (CG5475, CG4704) and three others (beat-IV, BDGP, HGTX) are not reported to be expressed in these sites, but these have been incompletely studied. For imaginal disc analysis, 3rd instar wandering larvae were collected from vials, and discs were dissected fresh and fixed in 4% paraformaldehyde. For embryo analysis, embryos were collected in 6-hour batches at 25°C, dechorionated in 100% bleach, fixed in 4% paraformaldehyde, and devitellinized by shaking in methanol and heptane.

2.3.11 Chicken *in ovo* Electroporations

Chicken neural tube electroporations were performed essentially as described previously (Tenzen et al., 2006). Briefly, 500 ng/μl of reporter vector and 500 ng/μl of either pCIT or *SmoM2*-pCIT was dissolved in PBS with 50 ng/μl of Fast Green and injected into the neural tubes of Hamburger-Hamilton stage 10–12 chicken embryos. Approximately 48 hours following electroporation embryos were recovered and fixed in 4% paraformaldehyde for subsequent immunofluorescent analysis. Fertile eggs were obtained from the Michigan State University Poultry Farm.

2.3.12 Immunofluorescence and Microscopy

Drosophila embryos and imaginal discs were blocked with 10% BSA in phosphate-buffered saline (PBS) with 0.1% Triton X-100. The following primary antibodies were used overnight at 4°C: rabbit anti-GFP IgG antibody (1:200; Life Technologies A11122), mouse anti-Ptc (1:50, DSHB; APA1) and mouse anti-En (1:50, DSHB; 4D9). Samples were then incubated in the following secondary antibodies for 2 hours at room temperatures, Alexa Fluor 488-conjugated goat anti-rabbit IgG antibody (1:2,000; Life Technologies A11008) and/or Alexa Fluor 468-conjugated goat anti-mouse IgG antibody (1:2,000; Life Technologies A11004). Embryos and imaginal discs were mounted on glass slides using ProLong Gold with DAPI and imaged on an Olympus BX-51 upright microscope, Nikon A1 confocal with Ti-E microscope or Olympus FluoView 500 Laser Scanning Confocal Microscope. For direct comparisons, wild type and mutant constructs were processed in parallel including being imaged on the same day, using the same exposure settings.Immunofluorescent analyses of chicken neural tubes were performed essentially as described previously (Jeong and McMahon, 2005). The antibodies used were as follows: 1:20 Mouse IgG1 anti-NKX6.1 (DSHB; F55A10). DAPI (Life Technologies) was used at a dilution of 1:30,000. All secondary antibodies (Alexa Fluor; Life Technologies) were used at a dilution of 1:500. Primary antibodies were incubated overnight at 4°C, followed by incubation with secondary antibodies for one hour at room temperature. Images were collected with a Leica SP5X confocal microscope.

2.4 Results

2.4.1 Computational Identification of Clustered ci/GLI Sites Across the *Drosophila* Genome

To test if clustering of ci/GLI sites could be used to predicted Hh enhancers, we developed a computational strategy to identify all regions of the genome that contain clusters of 3-10 ci/GLI sites that are enriched above chance expectation. Since the ci/GLI binding sequence is highly GC rich, these sites are more likely to occur by chance in GC rich regions of the genome. Thus, to achieve an unbiased assessment of clustering likelihood, it was important to utilize a background model with a GC landscape similar to that of the native genome. Three different background models were examined (see Materials and Methods for details). The three models were compared by mapping all predicted ci/GLI sites (MSS ≥ 0.75) and examining the GC content of the genomic sequence surrounding each predicted ci/GLI site (Figure S2.1). Importantly, the randomized (Model 1) and shuffled 3-mer (Model 2) strategies significantly change (i.e., homogenize) the GC context around ci/GLI sites, while the Flip GC/AT model (Model 3), by its nature, faithfully replicates the GC context of ci/GLI sites in the real genome; thus, this model was selected for use.

An accurate assessment of the relative density of ci/GLI clusters found in the native genome also requires that the background genomes contain a similar composition (number and type) of ci sites as the native genome. After generating background genomes using the Flip GC/AT method, we noticed that the total number of predicted ci/GLI binding sites on each chromosome was consistently reduced compared to the native Dm genome (Figure S2.2A). Left uncorrected, this deficit in total sites would lead to an artificial enrichment of clusters of ci/GLI sites in the Dm genome when compared to the background model. To correct for this discrepancy, we re-built background chromosomes (see detail in Materials and Methods) so that they contained the same number of each type of ci/GLI binding site (based on matrix similarity score) found in the Dm genome (Figure S2.2B). Relative enrichment of ci/GLI clusters in each genomic region was then assessed across the native genome by direct comparison to the 100 rebuilt background chromosomes (Figure S2.2C).

2.4.2 ci/GLI Cluster Analysis in *Drosophila melanogaster* (Dm)

The complete pipeline for identification of enriched clusters of ci/GLI sites and examination of their potential as Hh enhancers is provided in Figure 2.1. Clusters of 3-10 ci/GLI sites (maximum end-to-end distance 1000 bp) were identified in the native Dm and Dp genomes. Background modeling and background correction was performed separately for Dm and Dp. For each putative cluster, a cluster coefficient (CC) was defined as the number of ci/GLI sites in a given genomic region divided by the average number of ci/GLI sites in the same genomic location in 100 control genomes (schematically illustrated in Figure S2.2C). Only clusters with a CC of greater than or equal to 4 and at least one ci/GLI site with a MSS of 0.81 or greater were chosen for subsequent analysis. These filters (1kb length; CC ≥ 4; one site ≥ MSS of 0.81) were designed to increase the likelihood that functional enhancers would be identified. As an additional stringency filter, we required that ci/GLI site clusters be present in orthologous regions of both Dp and Dm genomes (see Materials and Methods for details). Table S2.4 lists all selected Dm clusters with a CC greater than or equal to 4 (ranked by order of ci/GLI site density and average MSS). When we sorted these results by average MSS (high to low), to strengthen the likelihood that all of the ci/GLI sites located within any putative cluster were capable of binding ci/GLI, a known Hh-regulated enhancer of the *ptc* gene (Alexandre et al., 1996) appeared at the top of the list. In addition to this known enhancer region, we selected the next 16 putative Hh enhancer regions for functional validation (Table 2.1).

2.4.3 Functional Verification of ci/GLI-Driven Enhancers in a Chicken Neural Tube Assay

We first screened for possible enhancer function of the 16 novel genomic regions (Table 2.1) in the developing chicken neural tube, one of the best-studied sites of Hh signaling (Dessaud et al., 2008). In this assay, Hamburger-Hamilton stage 11 embryos are electroporated with DNA reporter constructs in which the putative enhancer is cloned upstream of a minimal promoter driving EGFP expression (see Materials and Methods). This assay has been previously used to validate enhancers for multiple signaling pathways (Timmer et al., 2001; Uchikawa et al., 2003;

Lei et al., 2006; Lang et al., 2010; Wang et al., 2011; Oosterveen et al., 2012; Peterson et al., 2012; Vadasz et al., 2013). Endogenous Sonic Hedgehog (SHH) produced by the notochord and floorplate drives expression of Hh-dependent enhancers in the ventral half of the neural tube (Dessaud et al., 2008). Additionally, to further increase the sensitivity of our assay, we co-electroporated a constitutively active form of *Smoothened* (*SmoM2*) (Xie et al., 1998), which activates Hh signaling throughout the neural tube. Successful activation of Hh signaling by *SmoM2* is readily detectable as an expansion of the expression domain of the known Hh target gene, NKX6.1 (Oosterveen et al., 2012; Peterson et al., 2012), on the electroporated side of the neural tube. An RFP-expressing plasmid (pCIT) was co-electroporated to confirm the success of the electroporation. For those enhancers that demonstrated apparent Hh activation (expression of the enhancer-containing construct, but not the enhancer-less construct, in the presence of *SmoM2*), ci/GLI-dependent activity was further confirmed by mutagenesis of the ci/GLI binding sites.

Of the 16 computationally predicted enhancers tested in this way, four drove Hh-enhancer dependent expression in the chicken neural tube assay (Figure 2.2). An intronic sequence of the *invected* (*inv*) gene harbors two of these active regions, each containing a cluster of four ci/GLI sites with MSS ≥0.81. Both regions drive expression in the presence of co-electroporated *SmoM2* and mutagenesis of the ci/GLI binding sites abrogates this response in both cases (Figure 2.2BC).

Two additional predicted enhancers, located near the genes *Cpr100A* and *Plc21C*, also showed expression in the chicken neural tube assay (Figure 2.2DE). However, mutation of the ci/GLI sites abrogated EGFP expression only in the putative *Cpr100A* enhancer (Figure 2.2D), but not in the *Plc21C* enhancer (Figure 2.2E). Thus, only the former behaved as a direct Hh target; the *Plc21C* enhancer is responsive to Hh pathway activation, but this activity does not depend upon the ci/GLI binding sites. Thus, altogether, in addition to the top scoring, previously validated proximal *ptc* enhancer, three of the 16 novel predicted enhancers were validated by the chicken *in ovo* electroporation assay, for an overall success rate of 4/17 or 23%.

We next tested whether additional information would further improve prediction of Hh enhancers. We searched the list of clusters in Table S2.4 for regions that were annotated to known or suspected Hh target genes and tested five additional regions linked to *roadkill* (*rdx*) (Kent et al., 2006), *retinal homeobox* (*Rx*), *gooseberry* (*gsb*) (Li and Noll, 1993; Von Ohlen et al., 1997) and two additional regions of the *patched* receptor ($ptc^{-2.8}$ and $ptc^{+5.3}$). Of these five cluster regions, only *rdx* tested positive in the chicken neural tube assay (Figure 2.2F), reflecting a similar 20% success rate.

To learn more about the sensitivity of the chicken neural tube assay, we also tested 18 clusters with ci/GLI sites of low MSS (0.75-0.8). These may represent clusters of sites of low affinity ci/GLI binding. The regions tested included the known enhancers regulating the *wingless* (*wg)* and *decapentaplegic* (*dpp)* loci (Table S2.5). However, none of these showed activity in the chicken neural tube.

Having identified two closely associated novel regions of the *inv* gene that both act as Hh enhancers in the chicken electroporation assay (Figure 2.2BC), we next utilized this assay to further examine these regions. While both enhancers respond to SmoM2 co-electroporation, only one (*inv*$^{+18.6}$), drives EGFP expression in response to endogenous levels of Hh signaling (i.e. in the absence of *SmoM2* co-electroporation) (Figure 2.3).

Notably, though it is not in the top 16 predictions, Table S2.4 lists a third cluster in this region of the *inv* locus, lying between the two active regions tested above. Thus, we also tested a fragment spanning all three of these predicted *inv* ci/GLI clusters, containing a total of 12 ci/GLI binding sites (*inv*^{long}) (Figure 2.4A). This larger construct is activated both by endogenous SHH in the ventral neural tube and by co-electroporation of *SmoM2* (Figure 2.4B). Furthermore, a construct (*inv*$^{\mathrm{long}}$-ciKO) containing mutations in 10 of the 12 ci/GLI binding sites identified computationally (only the two ci/GLI sites with lowest MSS were left intact) fails to activate EGFP expression, even when co-expressed with *SmoM2* (Figure 2.4C), confirming the Hh-dependent activity of this large complex enhancer. Further selective mutagenesis of ci/GLI sites within the larger fragment demonstrates that, in the absence of the *inv*$^{+16.8}$ and *inv*$^{+18.6}$ ci/GLI clusters, the central cluster of ci/GLI binding sites is unable to drive enhancer activity in the chicken neural tube (Construct D, Figure 2.4C).

2.4.4 Functional Verification of ci-Driven Enhancers in Transgenic *Drosophila*

To further verify enhancer function in *Drosophila*, we generated transgenic reporter flies in which EGFP was driven by predicted enhancers and examined gene expression in two of the best-studied Hh-responsive contexts: the stage 9-13 embryo (when Hh signaling is active during development of a variety of tissues) and the anterior/posterior boundary of the larval wing imaginal disc (Alexandre et al., 1996; Ohlen and Hooper, 1997; Ramos and Barolo, 2013). The top computational hit, upstream of the *ptc* gene (Table 2.1, Figure 2.5A) has three consensus ci/GLI binding sites and was previously shown to harbor enhancer activity (Alexandre et al., 1996). This conserved cluster was examined as a minimal fragment, ($ptc^{-0.6}$), which was able to respond to Hh signaling in the wing (Figure 2.5A). When the three consensus ci/GLI binding sites were mutated, enhancer activity was abrogated (Figure 2.5B), confirming that enhancer activity directly depends upon function of the ci/GLI binding motifs. This region was also found to have enhancer activity in a recent unbiased search for imaginal disc enhancers (Jory et al., 2012).

We next examined the other novel 16 top computationally predicted enhancers in *Drosophila* and found that three regions exhibited enhancer activity in the fly assay. Although $inv^{+16.8}$ and $inv^{+18.6}$ were both active in the chicken neural tube assay when co-electroporated with *SmoM2* (Figure 2.2BC), only $inv^{+18.6}$ responded in the wing imaginal disc (Figure 2.5EG). This $inv^{+18.6}$ enhancer was also the only enhancer to demonstrate positive activity in the chicken ventral neural tube in the absence of *SmoM2*, in response to endogenous Hh expression (Figure 2.3). When the four predicted ci/GLI binding sites with higher MSS were mutated in $inv^{+18.6}$, this enhancer was no longer able to respond to Hh signaling in the wing imaginal disc (Figure 2.5F), demonstrating its Hh-dependent activity. A larger construct (inv^{long}), encompassing the four ci/GLI sites in $inv^{+16.8}$, the four in $inv^{+18.6}$, and the intervening cluster of four predicted sites that was tested in the chicken assay in Figure 2.4A, was also able to drive expression in Hh-responsive cells of the wing imaginal discs of transgenic flies (Figure 2.5C). The *in vivo* activity of this genomic fragment depended on the predicted ci/GLI sites (Figure 2.5D), confirming it as a direct ci/GLI target enhancer.

In addition to confirming direct Hh-responsiveness of the *ptc* and *inv* enhancers, we also examined the other predicted enhancers in Table 2.1 in transgenic fly assays. Both *hth* and *Plc21C* showed enhancer activity in the transgenic fly assay, but neither was Hh-dependent (Figure S2.4). *Hth* exhibited a segmented expression pattern in the fly embryo, which remained unaltered after mutagenesis of the ci/GLI binding sites (Figure S2.3AB). *Plc21C* was expressed in the fly gut and expression persisted after mutation of the ci/GLI binding sites (Figure S2.3CD), consistent with the results in the chicken neural tube assay (Figure 2.2E).

Examination of the five additional ci/GLI clusters selected from known or suspected Hh target genes yielded four potential Hh-responsive enhancers: *rdx*, *ptc*$^{-2.8}$, *ptc*$^{+5.3}$ and *gsb*. A ci/GLI cluster in the intron of *roadkill* (*rdx)* was active at the A/P boundary of the wing imaginal disc in Hh-responsive cells (Figure 2.5H). Mutating the predicted ci/GLI sites within this cluster abrogated its activity (Figure 2.5I). *Rdx* had previously been shown to be genetically downstream of Hh signaling (Kent et al., 2006), but the enhancer that mediates this response had not been identified. The *Rdx* enhancer identified here also responds to Hh in the chicken neural tube assay (Figure 2.2F).

Within the *ptc* locus, two other ci/GLI binding site clusters are computationally predicted in addition to the previously identified promoter-proximal enhancer that topped the list. The first of these, *ptc*$^{-2.8}$, is found 2.8 kb upstream of *ptc*, and contains 5 predicted ci/GLI binding sites. When examined in the wing imaginal disc, *ptc*$^{-2.8}$ responds with a stripe of expression largely overlapping Ptc positive cells (Figure 2.5J). Upon mutation of the predicted ci/GLI binding sites in this novel enhancer, its ability to respond to Hh is greatly reduced (Figure 2.5K). A second cluster of ci/GLI sites in the first intron of *ptc* (*ptc*$^{+5.3}$) is also predicted. This putative enhancer contains 7 predicted ci/GLI binding sites, one of which matches the optimal consensus site recognized by ci/GLI. In flies containing this transgene, *ptc*-like reporter gene expression is seen in the embryo (Figure 2.5L), but not the wing disc (data not shown). Two stripes of enhancer expression are detected, proximal to cells secreting Hh ligand, marked by *En*, in all segments of the embryonic ectoderm. After mutation of the predicted ci/GLI binding sites contained within this enhancer, the segmentally repeated stripes are lost (Figure 2.5M).

Finally, a region with several clusters of ci/GLI binding sites was identified downstream of the *gooseberry (gsb)* coding region. *Gooseberry*, a segment polarity gene, is part of the Hh-Wnt segmentation network, but no direct ci/GLI target enhancer has been identified (Li and Noll, 1993). The only known enhancer of *gsb*, which does not appear to be regulated by ci/GLI, is 5' of the gene (Bouchard et al., 2000). The 3' enhancer identified by our analysis contains five predicted ci/GLI binding sites and is active in segmental stripes in the embryonic ectoderm of transgenic *Drosophila*, posterior to each stripe of Hh-secreting cells at stage 11 (Figure 2.5N). Upon mutation of the ci/GLI binding sites, activity is attenuated, suggesting that the *gsb* enhancer requires direct ci/GLI input in order to respond to Hh signaling in the embryo (Figure 2.5O).

Overall, the fly assay functionally verified six Hh-dependent enhancers out of 22 tested, for a success rate of 27%. The genomic locations of these enhancers, relative to the gene locus, are presented in Figure 2.6. One additional enhancer, *Cpr100A*, was demonstrated to be Hh-dependent in the chicken, but had no activity in the fly assay; thus, it must be considered a potential regulatory element. This result suggested that *Cpr100A* might have been a false-negative in the fly assay, and prompted us to examine it, along with all of the other predicted enhancers, in a third site of Hh signaling, the adult testis. Although the testis depends on Hh signaling, none of the predicted enhancers were active in this tissue. It is possible, however, that the *Cpr100A* cluster (or any other predicted enhancer that is negative in the chicken and/or fly assays) may be active in another tissue that was not examined (Michel et al., 2012). Altogether, both assays established 7/22 (31.8%) of tested ci/GLI clusters as Hh enhancers, six of which are novel (the potential *Cpr100A* element is not included in this count).

2.5 Discussion

Homotypic clustering of transcription factor binding sites has been observed in multiple settings and has been successfully used to identify potential enhancers (Markstein, 2001; Berman et al., 2002; Lifanov, 2003; Gotea et al., 2010; Suryamohan and Halfon, 2014). Since all but one of the known *Drosophila* Hh-driven enhancers contain two or more ci/GLI sites, we assessed the extent to which clustering of ci/GLI sites can be used to predict the location of Hh-dependent enhancers, a question that has not previously been directly tested. To do this, we utilized a background correction method that preserves local nucleotide topography to allow us to identified genomic regions that appear to have unusually dense ci/GLI binding site representation and tested the extent to which these regions can function as Hh-dependent enhancers.

To establish background genomes for comparison of GLI density, we used a strategy that randomly flips each base to its complimentary partner. This approach maintains the GC/AT landscape of the native *Drosophila* chromosomes. Overall, only 43% of the *D. melanogaster* contains G or C bases while the consensus ci/GLI binding site itself is 67% GC rich (Hallikas et al., 2006; Keightley et al., 2009). Distribution of GC content has been strongly correlated with gene density and other genomic features and the importance of maintaining the original properties of the native sequence when generating a background comparison has been discussed previously (Fitch, 1983). Other background generation methods that preserve dinucleotide frequencies also exist (Fitch, 1983; Coward, 1999). Additional comparisons would be needed to determine which background strategy best strengthens enhancer detection.

The success rate of functional enhancer identification based on the approach used here was 23%, suggesting that clustering of ci/GLI sites alone is not sufficient to effectively predict Hh-regulated enhancers. However, this success rate increased to 80% when examining ci/GLI clusters associated with known or suspected Hh target genes. Together, these data indicate that ci/GLI clustering is not, by itself, an effective means to predict Hh-regulated enhancers. While some Hh enhancers can be identified by virtue of ci/GLI homotypic clustering, not all homotypic clusters function as enhancers. Since one of the previously identified Hh enhancers (in orthodenticle) only has one ci/GLI site (Ramos and Barolo, 2013), it is also clear that the presence of clustered ci/GLI sites is not a requirement for functional Hh enhancers. However, in the context of additional information, clustering can be used as one criterion to predict enhancers within a suspected Hh target gene locus. Future studies will be necessary to determine whether the presence of multiple ci/GLI sites are more effective predictors of Hh-regulated enhancers associated with putative Hh target genes, or whether a single ci/GLI site is equally likely to drive Hh-dependent target gene expression. Given that ci/GLI binding site clustering alone is not sufficient to identify Hh-regulated enhancers, this raises the question: what is an effective method to identify Hh-regulated enhancers? One possibility is to pair ci/GLI binding sites with sites for other transcriptional co-activators or co-repressors. *De novo* motif analysis has been performed previously as part of ChIP-chip analysis of GLI repressor binding in the developing limb (Vokes et al., 2008). More recent studies suggest that GLI proteins cooperate with SOXB1 proteins to drive Hh-regulated gene expression during spinal cord development (Oosterveen et al., 2012; Peterson et al., 2012). However, specific co-factor identification may yield only tissue-specific Hh-regulated enhancers. Thus, other approaches include: 1) examining ci/GLI binding site association with active or repressive chromatin modifications, which has been recently used to investigate Hh-regulated enhancers in the developing neural tube (Nishi et al., 2015), and 2) investigating ci/GLI binding site location near sites of open chromatin using techniques such as DNAse I hypersensitivity and FAIRE (Giresi et al., 2007; McKay and Lieb, 2013). It is likely that a combination of these methods will be required to effectively identify a more complete set of Hh-regulated enhancers on a genome wide basis.

One intriguing finding from this work is the identification of multiple discrepancies between the chicken neural tube and transgenic fly assays (Table 2.1). These data emphasize the importance of testing putative enhancers in diverse assay systems to provide several different contexts in which an enhancer can show activity. The chicken neural tube assay is a quick and inexpensive strategy that, in a large-scale study, could improve throughput. It has been successfully used previously to identify Hh-regulated mouse enhancers (Oosterveen et al., 2012; Peterson et al., 2012), and is used here to validate Hh-regulated fly enhancers. However, because some enhancers may require additional species-specific information that is not present in the chicken neural tube, false negative calls are a limitation of this assay. Further, the requirement for context-specific information may also restrict the utility of this assay in the identification of general Hh-regulated enhancers (Vokes et al., 2007). Along these lines, analysis of 18 clusters containing ci/GLI sites of lower predicted affinity, including the known Hh enhancers in the *wg* and *dpp* loci (Ohlen and Hooper, 1997; Müller and Basler, 2000), showed no activity in the chicken neural tube (Table S2.5). Thus, this assay may only detect Hh enhancers with high affinity ci/GLI binding sites, thereby missing some true positives (Ramos and Barolo, 2013). Nevertheless, the assay can be useful to dissect enhancer activity in the context of a complex developing tissue (Figure 2.4).

The computational study presented here can be compared with a recent analysis of potential ci/GLI-driven enhancers in *Drosophila*, by Biehs et al., who fused ci^{ACT} (activator) and ci^{REP} (repressor) proteins with DNA adenine methyltransferase (Dam) domains to define chromatin regions in stage 10-11 embryos that are occupied by ci/GLI *in vivo* (Biehs et al., 2010). That study listed 1743 sites bound by Dam-ci fusion proteins; of these, 55 sites (3%, listed in Table S2.6) were represented in clusters that were selected by our computational analysis. This limited overlap is likely due to two factors. First, since the computational study was limited to analysis of larger clusters, enhancers that are driven by one or two ci/GLI sites were not selected, by design. Second, because the DamID study was performed in 2-6 hour embryos, ci/GLI binding events were likely limited to chromatin regions that were accessible at that developmental stage. Of the seven previously known Hh/GLI-regulated enhancers, the DamID approach identified ci/GLI binding to two (*ptc* and *wg*), while the computational strategy described here detected three (*ptc*, *wg* and *knot*). The other four previously known enhancers (*stripe, hairy*, *dpp* and *orthodenticle*) were not detected computationally because those enhancers have only two ci/GLI sites (our filters selected clusters of 3-10). Of the new enhancers functionally confirmed in our study, none were found to harbor protected regions in the DamID assay. Biehs et al. used expression assays to identify 147 genes whose expression appeared to correlate with Hh signaling activity. They then asked, of these 147 genes, how many had protected regions within or adjacent to the transcription unit? Protected regions were identified as DamAct or DamRep protection and consisted of a total 2108 protected regions. They identified 52 genomic regions that were DamID-protected and showed expression changes when Hh signaling was modulated. Thus, 35% of the genes that appear to be targets (as assessed by their expression modulation) showed some DamID protection, but only 2.5% of the total DamID protected regions were found to be probable Hh targets (Biehs et al., 2010). Four of these 52 can be found in the list of 55 sites common to the two studies.

An important aspect of the present study is that the direct Hh dependency of all enhancers was verified by ci/GLI binding site mutagenesis. While expression assays such as those used by Biehs et al. clearly demonstrate a Hh response, they do not establish whether this response is direct or indirect and do not confirm that the response is mediated through the ci/GLI binding sites in the candidate enhancers. Indeed, of the top 17 clusters detected computationally, we found four direct targets and two additional enhancers that showed apparent expression in *ptc*-expressing cells, but this expression persisted after mutation of the ci/GLI sites (Figure S2.4) suggesting that other factors might be responsible for this enhancer activity. This raises a cautionary note about assigning potential Hh, or any signaling cascade, responsiveness in the absence of functional verification (Halfon et al., 2011).

Using homotypic ci/GLI site clustering as a criterion together with functional analyses, we have doubled the number of previously verified *Drosophila* ci/GLI-dependent enhancers, including multiple distinct enhancers that regulate a single Hh-responsive gene (i.e., *ptc*, *inv*, and *gsb*). Further testing of other candidate clusters identified in this study might further enlarge the pool of known Hh-responsive enhancers that are active in diverse tissues and organs, providing a robust substrate for the future dissection of the rules that underlie context-specific enhancer function.

2.6 Acknowledgements

The NKX6.1 antibody was obtained from the Developmental Studies Hybridoma Bank developed under the auspices of the NICHD and maintained by The University of Iowa, Department of Biological Sciences, Iowa City, IA. Confocal microscopy was performed in the Microscopy and Image Analysis Laboratory at the University of Michigan. Sequencing of enhancer constructs was performed at the University of Michigan Sequencing Core. The authors would like to thank Dr. Mark Rebeiz for generously sharing scripts and Dr. William J. Zacharias for helpful discussions.

2.7 Authors' contributions

KG, AU and DG conceived and designed the computational methods. Biological experiments were devised by SB, BA, DL and JS. KG, DL, JS, NR, DP, LJ and AU performed the experiments and analyzed the data. The paper was written by KG, DL, JS, AU and senior authors DG, SB, and BA.

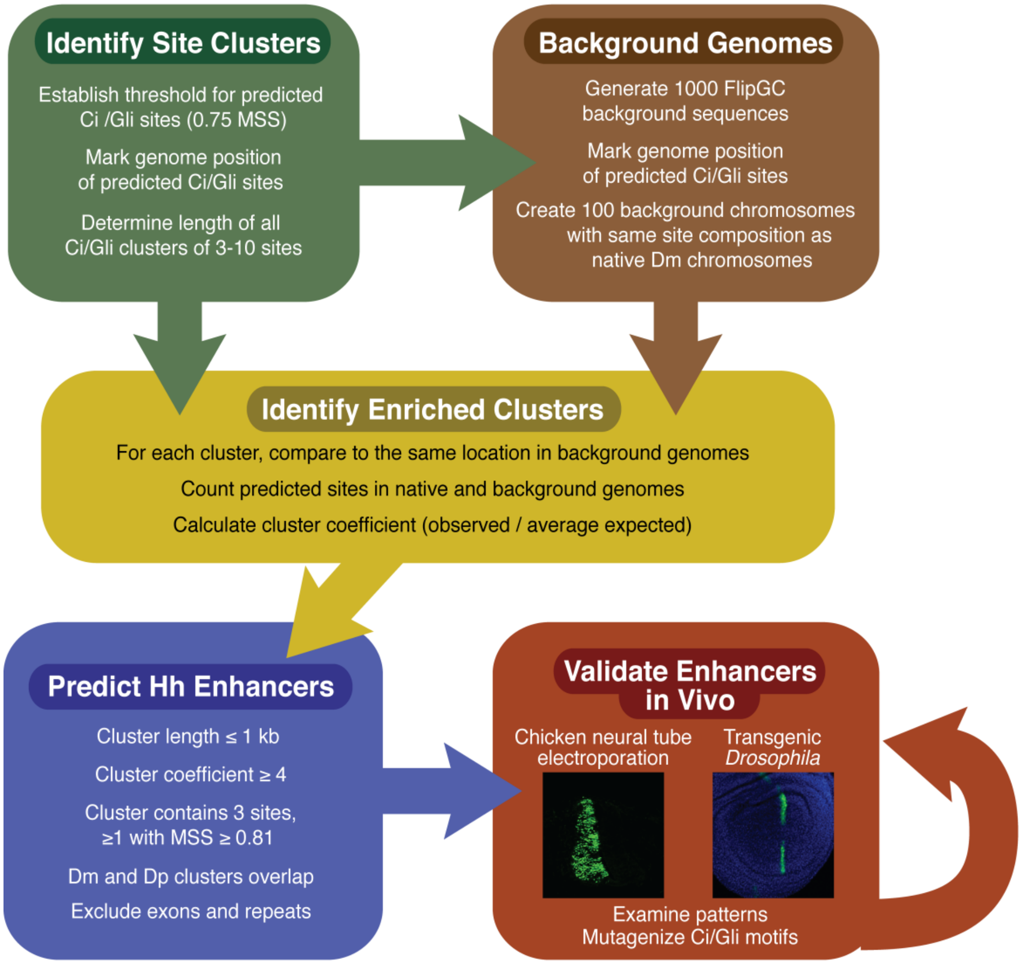


Figure 2.1. Pipeline for detection and validation of Hh-responsive enhancers. ci/GLI cluster identification and background genome generation were performed as outlined in Figure S2.2. The cluster (CC) for a given genomic region was calculated as the total number of sites observed in the Dm or Dp genome (observed) divided by the average number of sites per background genome for that species (expected). Clusters of ci/GLI sites with a (CC) ≥ 4 were further filtered as follows: a) Clusters were required to contain at least one ci/GLI site of ≥0.81 MSS; b) Dm Clusters were required to overlap in position (but not sequence) with a cluster in Dp*;* c) Clusters in exon or repeat regions were excluded. The entire table of selected clusters, sorted by chromosomal location, is provided in Table S2.4**.** The list of clusters was then ranked by average MSS of the predicted ci/GLI sites and the top 17 were examined functionally (these included 16 novel hits and one known enhancer, *ptc*$^{-0.6}$). The Hh-responsive enhancer activity of genomic regions containing selected clusters was functionally evaluated by means of a transgenic fly assay as well as by chicken neural tube electroporation. For genomic regions that showed apparent Hh responsiveness, ci/GLI sites were mutated and re-assayed to confirm direct ci/GLI regulation.

Annotated Gene	Genomic coordinates (dm3)	Number of ci/GLI Sites	Average MSS	Hh Responsive in Chicken Neural Tube	Hh Responsive in Transgenic Fly
ptc$^{-0.6}$	chr2R:4536264-4536572	3	1.000	+	+
inv$^{+16.8}$	chr2R:7378801-7380000	4	0.941	+	-
Sox100B	chr3R:26894840-26896225	3	0.920	-	-
inv$^{+18.6}$	chr2R:7380576-7381900	4	0.903	+	+
beat-IV	chr3R:19385801-19387033	5	0.899	-	-
CG6475	chr3R:17227902-17229095	4	0.898	-	-
CG34139	chr3R:16067525-16068300	3	0.893	-	-
Plc21C	chr2L:308225-309200	4	0.892	-	-
CG4704	chr3R:18671231-18671930	3	0.891	-	-
Bi	chrX:4316001-4317440	4	0.886	-	-
HGTX	chr3L:14583895-14584670	4	0.886	-	-
Cpr100A	chr3R:26692110-26692580	3	0.886	+	-
Ets21C	chr2L:550010-551035	4	0.885	-	-
CG12541	chrX:6927600-6928375	5	0.884	-	-
Sp1	chrX:9613671-9614922	4	0.881	-	-
Hth	chr3R:6433650-6434996	5	0.879	-	-
Ko	chr3L:21072420-21073658	3	0.879	-	-
ptc$^{+5.3}$	chr2R:4542467-4545417	7	0.875	-	+
ptc$^{-2.8}$	chr2R:4531601-4534319	5	0.847	-	+
Rx	chr2R:16820211-16822050	5	0.845	-	-
Rdx	chr3R:9815295-9817061	3	0.838	+	+
Gsb	chr2R:20952400-20953750	7	0.834	-	+

Table 2.1. Assessment of Hh response. The chicken neural tube (CNT) and transgenic fly (TF) assays together identified eight predicted regions as Hh-responsive. Both assays showed positive Hh activity for *inv*$^{+18.6}$ and *rdx* as well as the previously identified *ptc* enhancer region. Five additional regions were positive in only one assay: CNT: *Cpr100A* and *inv*$^{+16.8}$; TF: *gsb* and two *ptc* additional genomic regions (*ptc*$^{+5.3}$ and *ptc*$^{-2.8}$). All enhancer regions were verified by mutagenesis to be ci/GLI binding site dependent.

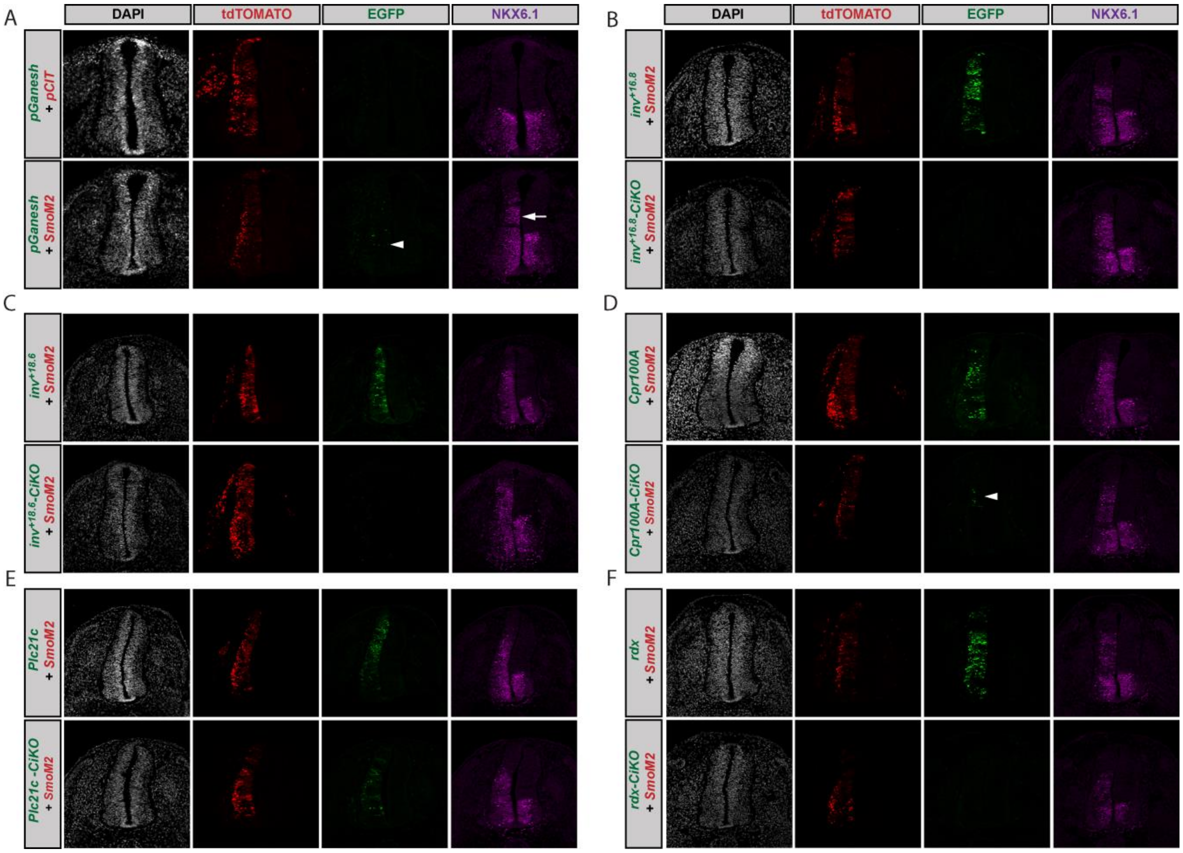


Figure 2.2. Validation of predicted Hh-responsive enhancers in the chicken neural tube. Transverse sections of Hamburger-Hamilton stage 21-22 chicken embryos are shown. DAPI (grayscale, far left column) depicts nuclei. tdTOMATO (red, middle left column) marks cells electroporated with pCIT or *SmoM2*. GFP (green, middle right column) reports enhancer activation. Anti-NKX6.1 antibody staining (magenta, far right column) denotes Hh-responsive cells. (A) Chicken embryos co-electroporated with an enhancer less pGanesh construct (containing only an Hsp70 minimal promoter) and either pCIT or a constitutively active *SmoM2*. An arrowhead (middle right column; bottom row) depicts a few GFP positive cells in pGanesh electroporated embryos. Note the ectopic NKX6.1 expression (far right column) indicative of overactive Hh signaling in electroporated cells (white arrow). (B-E) Candidate Hh-responsive *inv*$^{+16.8}$ (B top row), *inv*$^{+18.6}$ (C top row), *Cpr100A* (D top row), and *Plc21C* (E top row) constructs all exhibit GFP expression in cells in which Hh is activated by co-electroporation of *SmoM2*. However, chicken embryos co-electroporated with *SmoM2* in combination with a ci/GLI-binding deficient mutant (ciKO) of each candidate (bottom rows) show a complete absence of GFP expression in the case of *inv*$^{+16.8}$*-ciKO* (B) and *inv*$^{+18.6}$*-ciKO* (C), despite ectopic NKX6.1 expression in both conditions (far right column). *Cpr100A-ciKO* (D) has a greatly diminished expression pattern with only a few GFP positive cells (white arrowhead) remaining (middle right column; bottom row). *Plc21C-ciKO* (E) does not show loss of GFP expression, indicating that it is not a direct Hh target, since its response to Hh signaling is not ci/GLI dependent. *Rdx* (F top row) GFP expression corresponds to Hh expressing cells and shows no expression once ci/GLI sites are mutated (*rdx-ciKO* bottom row).

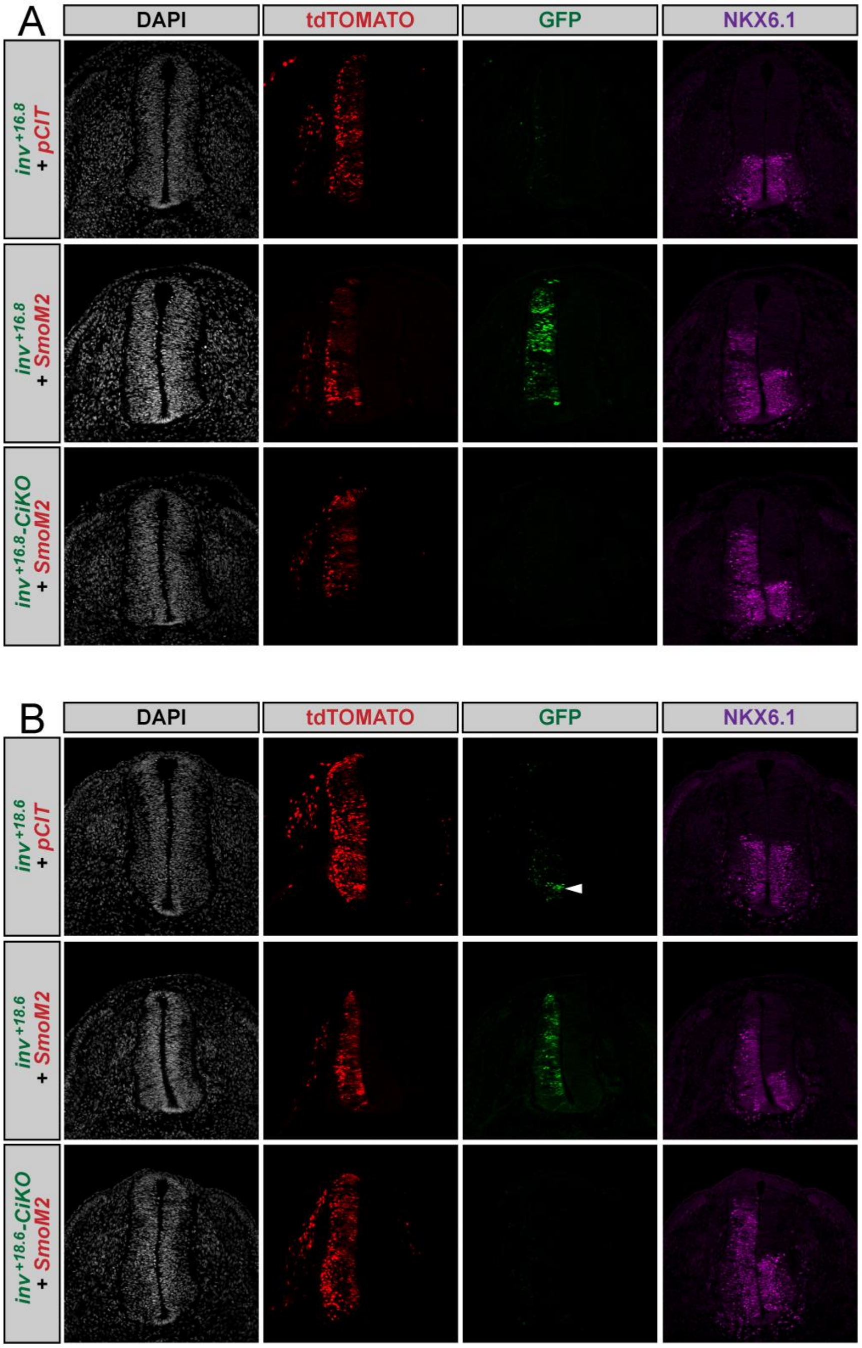
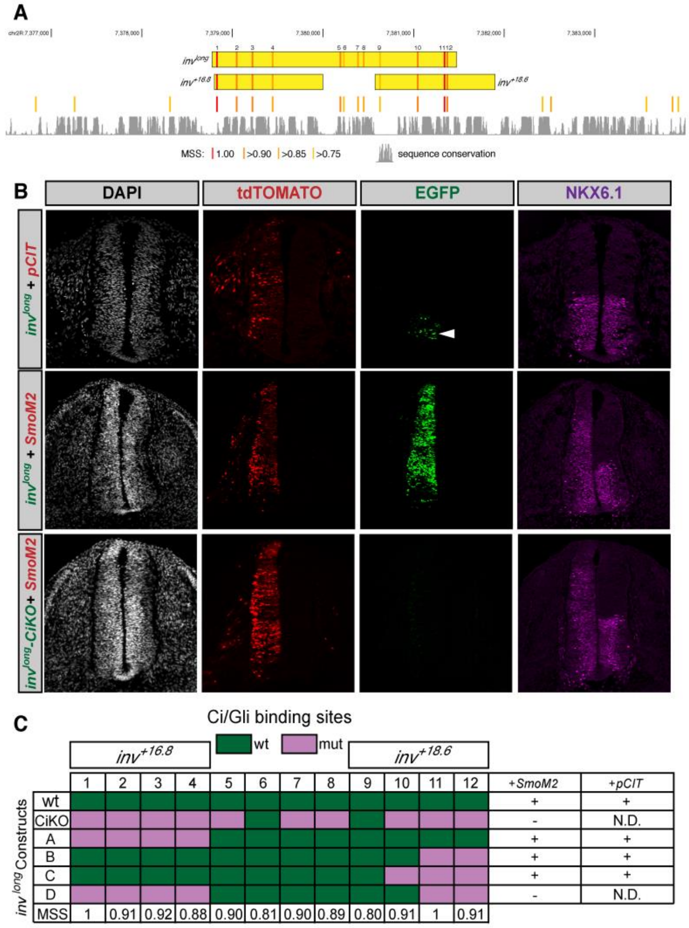


Figure 2.3. Endogenous expression of *inv*$^{+16.8}$ and *inv*$^{+18.6}$ in the chicken neural tube. Transverse sections of Hamburger-Hamilton stage 21-22 chicken embryos are shown. DAPI (grayscale, far left column) depicts nuclei. tdTOMATO (red, middle left column) marks cells electroporated with pCIT. GFP (green, middle right column) reports enhancer activation. Anti-NKX6.1 antibody staining (magenta, far right column) denotes Hh-responsive cells. (A) Chicken embryos electroporated with *inv*$^{+16.8}$ show no GFP expression in the chicken neural tube. (B) Chicken embryos electroporated with *inv*$^{+18.6}$ exhibit GFP expression (white arrowhead).



	1	2	3	4	5	6	7	8	9	10	11	12	+*SmoM2*	+*pCIT*
wt	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	+	+
CiKO	🟪	🟪	🟪	🟪	🟪	🟩	🟪	🟪	🟩	🟪	🟪	🟪	-	N.D.
A	🟪	🟪	🟪	🟪	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	+	+
B	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟪	🟪	+	+
C	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟩	🟪	🟪	🟪	+	+
D	🟪	🟪	🟪	🟪	🟩	🟩	🟩	🟩	🟩	🟩	🟪	🟪	-	N.D.
MSS	1	0.91	0.92	0.88	0.90	0.81	0.90	0.89	0.80	0.91	1	0.91		

Figure 2.4. Expression of a complex *inv* enhancer in the chicken neural tube and *Drosophila* wing imaginal disc.
(A) Genomic landscape of the *inv* locus depicting the *inv*^{long}, *inv*$^{+16.8}$ and *inv*$^{+18.6}$ constructs. ci/GLI binding sites are shown as red/orange bars; the intensity of red coloration indicates the MSS. Sequence conservation is indicated by the track at bottom of the panel. **(B)** Transverse sections of Hamburger-Hamilton stage 21-22 chicken embryos are shown as in Figure 2.5. DAPI (gray, far left column) depicts nuclei. tdTOMATO (red, middle left column) marks cells electroporated with pCIT or *SmoM2*. GFP (green, middle right column) reports enhancer activation. Anti-NKX6.1 antibody staining (magenta, far right column) marks Hh-responsive cells. The *inv*^{long} (top row) enhancer demonstrates GFP expression in the ventral neural tube (white arrowhead). The expression of *inv*^{long} is strengthened and broadened with co-electroporation of *SmoM2* (middle row). Mutagenesis of ci/GLI binding sites demonstrates that enhancer activity is ci/GLI dependent (bottom row). **(C)** Tabulation of activity in the chicken neural tube of *inv*^{long} constructs containing different ci/GLI site compositions. Green boxes indicate wild type ci/GLI sequences; purple boxes indicate mutated ci/GLI sites. Constructs that have functional ci/GLI sites that correspond to *inv*$^{+18.6}$ (Construct A) or *inv*$^{+16.8}$ (Construct B and C) exhibit GFP expression in the neural tube. However, the central ci/GLI binding sites are insufficient to drive enhancer activity alone (construct D).

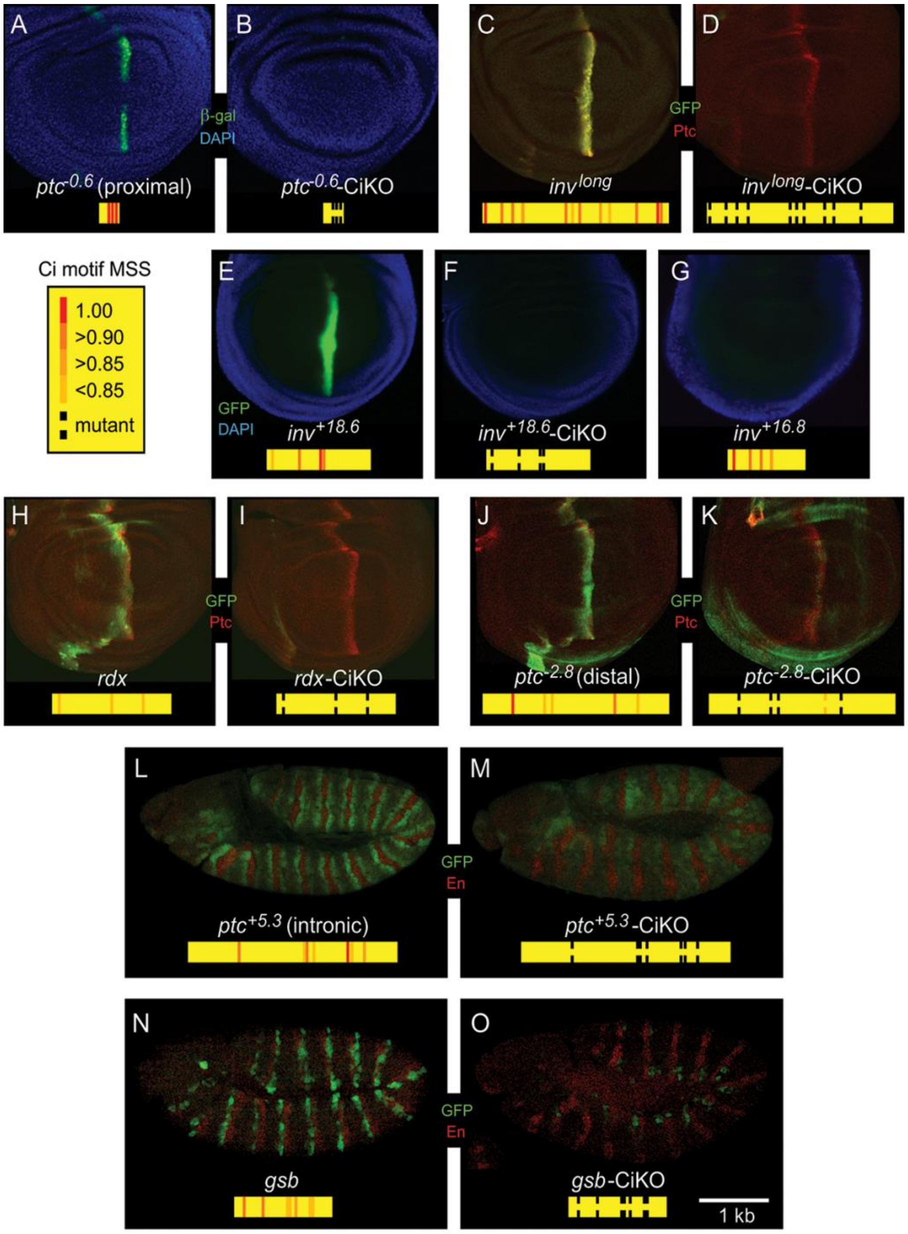


Figure 2.5. Novel enhancers directly respond to Hh signaling in the wing imaginal disc and embryo. (A-K) β-galactosidase or GFP marks the expression of enhancers in the pouch of the wing imaginal disc. A diagram of the fragments tested and location and MSS for all ci/GLI sites is shown for each candidate (yellow rectangles). Each wild type enhancer responds to Hh signaling along the anterior-posterior compartment boundary of the wing disc, with the exception of *inv*$^{+16.8}$**(G)**. Active enhancers lose Hh responsiveness in the wing imaginal disc when predicted ci/GLI binding sites are mutated, as shown in the right of each panel. **(L-O)** GFP marks the expression of the noted enhancers in the embryo. *En* expression (red) marks cells producing Hh ligand. When the predicted ci/GLI binding sites in these enhancers are mutated **(M-O)**, activity in Hh-responsive cells is severely reduced.

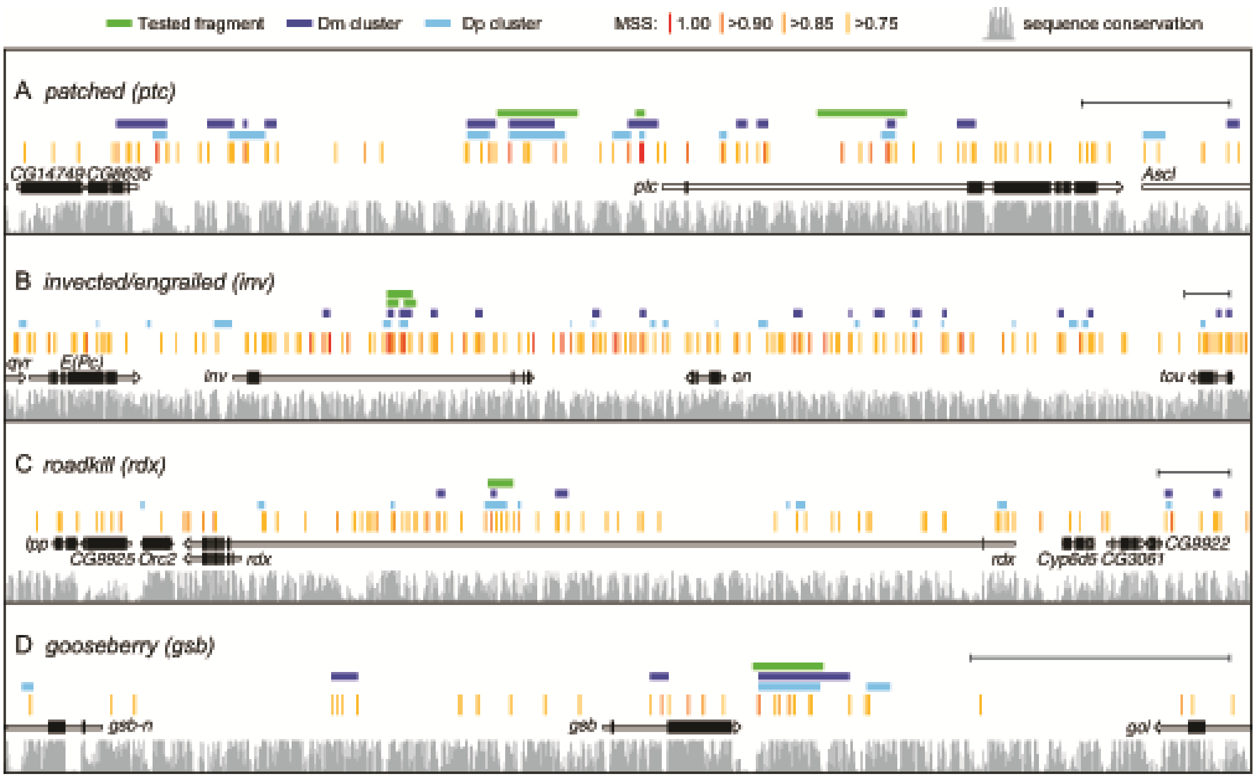


Figure 2.6. Mapping six Hh regulated enhancers in four genetic loci.
(A-D) Genomic landscape of the *ptc*, *inv*, *rdx* and *gsb* loci with fragments tested marked by green bars. All predicted ci/GLI binding sites are highlighted (red/orange tick marks, annotated according to MSS, as noted at top of Figure). The sequence conservation track (gray bars) marks conservation among the 12 sequenced *Drosophila* species, whereas the dark and light blue bars represent clusters of predicted ci/GLI binding sites in Dm and Dp, respectively. Black brackets at right indicate 5Kb.

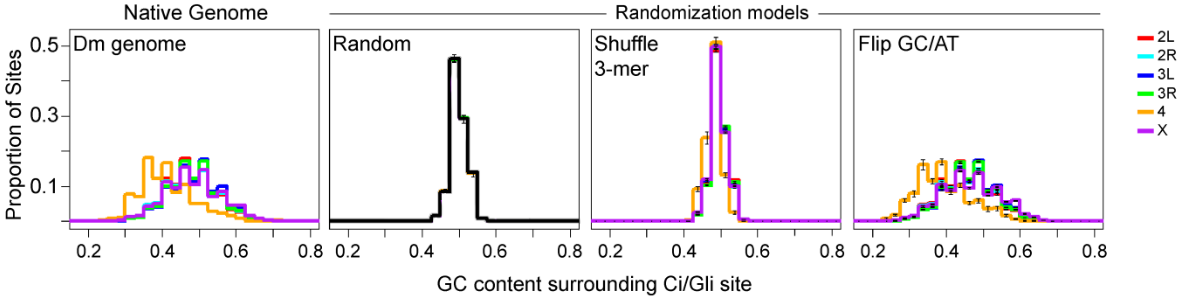


Figure S2.1. Assessment of GC content surrounding ci/GLI sites in the *Drosophila melanogaster* genome.

Forward	Reverse	Matrix Similarity Score (MSS)
GACCACCCA	TGGGTGGTC	1
GACCCCCCA	TGGGGGGTC	0.918
GACCTCCCA	TGGGAGGTC	0.916
GGCCACCCA	TGGGTGGCC	0.915
GCCCACCCA	TGGGTGGGC	0.915
GACCGCCCA	TGGGCGGTC	0.914
GTCCACCCA	TGGGTGGAC	0.91
GACCACACA	TGTGTGGTC	0.907
GACCACGCA	TGCGTGGTC	0.899
GACCACTCA	TGAGTGGTC	0.899
GACCACCTA	TAGGTGGTC	0.897
GACCACCAA	TTGGTGGTC	0.897
GACCACCGA	TCGGTGGTC	0.895
GACCACCCC	GGGGTGGTC	0.889
GACCACCCT	AGGGTGGTC	0.889
GACCACCCG	CGGGTGGTC	0.888
AACCACCCA	TGGGTGGTT	0.882
TACCACCCA	TGGGTGGTA	0.882
CACCACCCA	TGGGTGGTG	0.881
GAACACCCA	TGGGTGTTC	0.879
GAGCACCCA	TGGGTGCTC	0.878
GATCACCCA	TGGGTGATC	0.878
GCCCCCCCA	TGGGGGGGC	0.833
GGCCCCCCA	TGGGGGGCC	0.833
GGCCTCCCA	TGGGAGGCC	0.831
GCCCTCCCA	TGGGAGGGC	0.831
GTCCCCCCA	TGGGGGGAC	0.829
GGCCGCCCA	TGGGCGGCC	0.829
GCCCGCCCA	TGGGCGGGC	0.828
GTCCTCCCA	TGGGAGGAC	0.826
GACCCCACA	TGTGGGGTC	0.825
GTCCGCCCA	TGGGCGGAC	0.824
GACCTCACA	TGTGAGGTC	0.823
GGCCACACA	TGTGTGGCC	0.822
GCCCACACA	TGTGTGGGC	0.822
GACCGCACA	TGTGCGGTC	0.82
GTCCACACA	TGTGTGGAC	0.817

Forward	Reverse	Matrix Similarity Score (MSS)
GACCCCGCA	TGCGGGGTC	0.817
GACCCCTCA	TGAGGGGTC	0.817
GACCTCGCA	TGCGAGGTC	0.815
GACCCCCTA	TAGGGGGTC	0.815
GACCCCCAA	TTGGGGGTC	0.815
GACCTCTCA	TGAGAGGTC	0.815
GGCCACGCA	TGCGTGGCC	0.814
GGCCACTCA	TGAGTGGCC	0.814
GCCCACGCA	TGCGTGGGC	0.814
GCCCACTCA	TGAGTGGGC	0.814
GACCCCCGA	TCGGGGGTC	0.814
GACCTCCTA	TAGGAGGTC	0.813
GACCTCCAA	TTGGAGGTC	0.813
GACCGCGCA	TGCGCGGTC	0.812
GGCCACCTA	TAGGTGGCC	0.812
GGCCACCAA	TTGGTGGCC	0.812
GCCCACCTA	TAGGTGGGC	0.812
GCCCACCAA	TTGGTGGGC	0.812
GACCGCTCA	TGAGCGGTC	0.812
GACCTCCGA	TCGGAGGTC	0.811
GGCCACCGA	TCGGTGGCC	0.81
GCCCACCGA	TCGGTGGGC	0.81
GACCGCCTA	TAGGCGGTC	0.81
GACCGCCAA	TTGGCGGTC	0.81
GTCCACGCA	TGCGTGGAC	0.809
GTCCACTCA	TGAGTGGAC	0.809
GACCGCCGA	TCGGCGGTC	0.809
GTCCACCTA	TAGGTGGAC	0.807
GTCCACCAA	TTGGTGGAC	0.807
GACCCCCCC	GGGGGGGTC	0.807
GACCCCCCT	AGGGGGGTC	0.807
GACCCCCCG	CGGGGGGTC	0.806
GTCCACCGA	TCGGTGGAC	0.805
GACCTCCCC	GGGGAGGTC	0.805
GACCTCCCT	AGGGAGGTC	0.805
GGCCACCCC	GGGGTGGCC	0.804
GGCCACCCT	AGGGTGGCC	0.804

Forward	Reverse	Matrix Similarity Score (MSS)
GCCCACCCC	GGGGTGGGC	0.804
GCCCACCCT	AGGGTGGGC	0.804
GACCACATA	TATGTGGTC	0.804
GACCTCCCG	CGGGAGGTC	0.804
GGCCACCCG	CGGGTGGCC	0.803
GCCCACCCG	CGGGTGGGC	0.803
GACCACAAA	TTTGTGGTC	0.803
GACCACAGA	TCTGTGGTC	0.802
GACCGCCCC	GGGGCGGTC	0.802
GACCGCCCT	AGGGCGGTC	0.802
AACCCCCCA	TGGGGGGTT	0.801
GACCGCCCG	CGGGCGGTC	0.801
TACCCCCCA	TGGGGGGTA	0.8
GTCCACCCC	GGGGTGGAC	0.799
GTCCACCCT	AGGGTGGAC	0.799
CACCCCCCA	TGGGGGGTG	0.799
AACCTCCCA	TGGGAGGTT	0.798
GTCCACCCG	CGGGTGGAC	0.798
GAACCCCCA	TGGGGGTTC	0.798
TACCTCCCA	TGGGAGGTA	0.798
AGCCACCCA	TGGGTGGCT	0.797
ACCCACCCA	TGGGTGGGT	0.797
CACCTCCCA	TGGGAGGTG	0.797
GATCCCCCA	TGGGGGATC	0.797
TGCCACCCA	TGGGTGGCA	0.797
TCCCACCCA	TGGGTGGGA	0.797
GAACTCCCA	TGGGAGTTC	0.796
AACCGCCCA	TGGGCGGTT	0.796
CGCCACCCA	TGGGTGGCG	0.796
CCCCACCCA	TGGGTGGGG	0.796
GAGCCCCCA	TGGGGGCTC	0.796
TACCGCCCA	TGGGCGGTA	0.796
CACCGCCCA	TGGGCGGTG	0.795
GACCACACC	GGTGTGGTC	0.795
GACCACACG	CGTGTGGTC	0.795
GACCACACT	AGTGTGGTC	0.795
GACCACGAA	TTCGTGGTC	0.795

Forward	Reverse	Matrix Similarity Score (MSS)
GACCACTAA	TTAGTGGTC	0.795
GACCACGTA	TACGTGGTC	0.795
GACCACTTA	TAAGTGGTC	0.795
GATCTCCCA	TGGGAGATC	0.794
GAGCTCCCA	TGGGAGCTC	0.794
GGACACCCA	TGGGTGTCC	0.794
GCACACCCA	TGGGTGTGC	0.794
GACCACGGA	TCCGTGGTC	0.794
GACCACTGA	TCAGTGGTC	0.794
GAACGCCCA	TGGGCGTTC	0.793
GGGCACCCA	TGGGTGCCC	0.793
GGTCACCCA	TGGGTGACC	0.793
GCGCACCCA	TGGGTGCGC	0.793
GCTCACCCA	TGGGTGAGC	0.793
GATCGCCCA	TGGGCGATC	0.792
ATCCACCCA	TGGGTGGAT	0.792
TTCCACCCA	TGGGTGGAA	0.792
GAGCGCCCA	TGGGCGCTC	0.791
CTCCACCCA	TGGGTGGAG	0.791
GTACACCCA	TGGGTGTAC	0.79
AACCACACA	TGTGTGGTT	0.789
TACCACACA	TGTGTGGTA	0.789
CACCACACA	TGTGTGGTG	0.788
GTGCACCCA	TGGGTGCAC	0.788
GTTCACCCA	TGGGTGAAC	0.788
GACCACGCC	GGCGTGGTC	0.787
GACCACGCT	AGCGTGGTC	0.787
GACCACTCC	GGAGTGGTC	0.787
GACCACTCT	AGAGTGGTC	0.787
GAACACACA	TGTGTGTTC	0.786
GACCACGCG	CGCGTGGTC	0.786
GACCACTCG	CGAGTGGTC	0.786
GACCACCTG	CAGGTGGTC	0.785
GACCACCAC	GTGGTGGTC	0.785
GACCACCAT	ATGGTGGTC	0.785
GAGCACACA	TGTGTGCTC	0.785
GATCACACA	TGTGTGATC	0.785

Forward	Reverse	Matrix Similarity Score (MSS)
GACCACCTC	GAGGTGGTC	0.785
GACCACCTT	AAGGTGGTC	0.785
GACCACCGC	GCGGTGGTC	0.784
GACCACCGT	ACGGTGGTC	0.784
GACCACCAG	CTGGTGGTC	0.784
GACCACCGG	CCGGTGGTC	0.783
AACCACGCA	TGCGTGGTT	0.781
AACCACTCA	TGAGTGGTT	0.781
TACCACGCA	TGCGTGGTA	0.781
TACCACTCA	TGAGTGGTA	0.781
CACCACGCA	TGCGTGGTG	0.78
CACCACTCA	TGAGTGGTG	0.78
AACCACCTA	TAGGTGGTT	0.779
AACCACCAA	TTGGTGGTT	0.779
TACCACCTA	TAGGTGGTA	0.779
TACCACCAA	TTGGTGGTA	0.779
GAACACGCA	TGCGTGTTC	0.778
CACCACCTA	TAGGTGGTG	0.778
CACCACCAA	TTGGTGGTG	0.778
GAACACTCA	TGAGTGTTC	0.778
GATCACGCA	TGCGTGATC	0.777
GAGCACGCA	TGCGTGCTC	0.777
AACCACCGA	TCGGTGGTT	0.777
GAGCACTCA	TGAGTGCTC	0.777
GATCACTCA	TGAGTGATC	0.777
TACCACCGA	TCGGTGGTA	0.777
CACCACCGA	TCGGTGGTG	0.776
GAACACCTA	TAGGTGTTC	0.776
GAACACCAA	TTGGTGTTC	0.776
GAACACCGA	TCGGTGTTC	0.775
GAGCACCTA	TAGGTGCTC	0.775
GAGCACCAA	TTGGTGCTC	0.775
GATCACCTA	TAGGTGATC	0.775
GATCACCAA	TTGGTGATC	0.775
GAGCACCGA	TCGGTGCTC	0.773
GATCACCGA	TCGGTGATC	0.773
AACCACCCC	GGGGTGGTT	0.771
AACCACCCT	AGGGTGGTT	0.771
TACCACCCC	GGGGTGGTA	0.771
TACCACCCT	AGGGTGGTA	0.771
AACCACCCG	CGGGTGGTT	0.77
CACCACCCC	GGGGTGGTG	0.77
CACCACCCT	AGGGTGGTG	0.77
TACCACCCG	CGGGTGGTA	0.77
CACCACCCG	CGGGTGGTG	0.769
GAACACCCC	GGGGTGTTC	0.768
GAACACCCT	AGGGTGTTC	0.768
GAACACCCG	CGGGTGTTC	0.767
GATCACCCC	GGGGTGATC	0.767
GATCACCCT	AGGGTGATC	0.767
GAGCACCCG	CGGGTGCTC	0.766
GATCACCCG	CGGGTGATC	0.766
GAGCACCCC	GGGGTGCTC	0.766
GAGCACCCT	AGGGTGCTC	0.766
AAACACCCA	TGGGTGTTT	0.762
TAACACCCA	TGGGTGTTA	0.761
AAGCACCCA	TGGGTGCTT	0.76
AATCACCCA	TGGGTGATT	0.76
CAACACCCA	TGGGTGTTG	0.76
TAGCACCCA	TGGGTGCTA	0.76
TATCACCCA	TGGGTGATA	0.76
CAGCACCCA	TGGGTGCTG	0.759
CATCACCCA	TGGGTGATG	0.759

Table S2.1. 9-mers with a minimum level (≥0.75) ci matrix similarity score.

Annotation	Forward primer	Reverse primer	Genomic coordinates (dm3)
ptc -0.6	CACCGGCGCGCCATGCATGCGCAGCCTGCCAC	GTACCGCGGTTTCTATTGTTATTCGCATG	chr2R:4536264-4536572
inv +16.8	CACCTGATATCTTAGGTTAGTAGTAT	AATCTAATTTTGCCCTGATATT	chr2R:7378801-7380000
Sox100B	CACCTAAGCTCGGGATATTTTGCC	AGCTTAGAGGTCCTGCATAG	chr3R:26894840-26896225
inv +18.6	CACCTATGTTATAAAATTTGTAATAT	TTTGGTTATACTGTCTAACAAA	chr2R:7380576-7381900
beat-IV	CACCGTTTTTTTGCATTTCACC	AAACTACACGGCTGCCCTG	chr3R:19385801-19387033
CG6475	CACCGACCACACAACAGACGC	TACTTGAGCACCCGATTGG	chr3R:17227902-17229095
CG34139	CACCCTTTCGTTTTATGTTAACG	TTGTTTTTTTTCTTTTCGCTGTGCG	chr3R:16067525-16068300
Plc21C	CACCTCGTTATGATGTGCCTTAAAAG	AAAATATTAACGCGAAATAGG	chr2L:308225-309200
CG4704	CACCGTCATATTAGGCTATTTC	CATTTTATTAGCCGAATGC	chr3R:18671231-18671930
bi	CACCGAGAGGGAGCGAGTGAGTAAG	TGAGGCAATCGATAAAATTAGC	chrX:4316001-4317440
HGTX	CACCTGCAGCCGCTTAATAATTCC	AGTGCCGTGCTTAACCCG	chr3L:14583895-14584670
Cpr100A	CACCATAATGCCAAAAGTTCTCTG	TGTCTTTTTGATTTTTCCAGTG	chr3R:26692110-26692580
Ets21C	CACCGTTTGTACCCTGTAAAGGG	ACTTAAACGGAGCCACATTTTTCTC	chr2L:550010-551035
CG12541	CACCCAGCAAGAAGCATACCAAAG	ACTATTAGCTACATTTTCTTCC	chrX:6927600-6928375
Sp1	CACCTTCGCCGTGTGTATGTATTAGC	TATCAACGGAAATTCATTAC	chrX:9613671-9614922
hth	CACCTAAAGCCGAAAGCCTAAAATAG	TTTGCTTGTATTTTCCGAAC	chr3R:6433650-6434996
ko	CACCAGGAGACAGGTGGTATGGTC	ATTCACAGTGTAATTTTACAGC	chr3L:21072420-21073658
ptc +5.3	CACCGGCGCGCCGAAGTGCTTAACAAGTTAAC	GTACCGCGGCACGACAACCAATGAGATCG	chr2R:4542467-4545417
ptc -2.8	CACCGGCGCGCCTACGTACTCTTATTACTCCACTC	GTACCGCGGGCTATTGCATTTGTCATTGGC	chr2R:4531601-4534319
Rx	CACCACTCCTTCCCCGACTTAC	GTTTAAACCGAAAAACGTTTAATTTAATCTGG	chr2R:16820211-16822050
Rdx	CACCTTTAGCCAGGTGTGGATTGTG	CCAGCGAAAGCAAACAGAGTAC	chr3R:9815295-9817061
Gsb	CACCGCGAGTCAAACTCATTCCGTG	AAGTGTACGGTGAATTC	chr2R:20952400-20953750

Table S2.2. PCR primers used to amplify genomic DNA from the *D. melanogaster* genome (build Dm3).

	2L	**2R**	**3L**	**3R**	**4**	**X**
MSS ≥ .81	8156	8029	8671	10381	268	8887
MSS ≥ .75	30637	30186	33098	38723	1279	33310
Chromosome length (bp)	23,011,544	21,146,708	24,543,557	27,905,053	1,351,857	22,422,827

Table S2.3. Distribution of predicted ci/GLI sites across chromosomes.

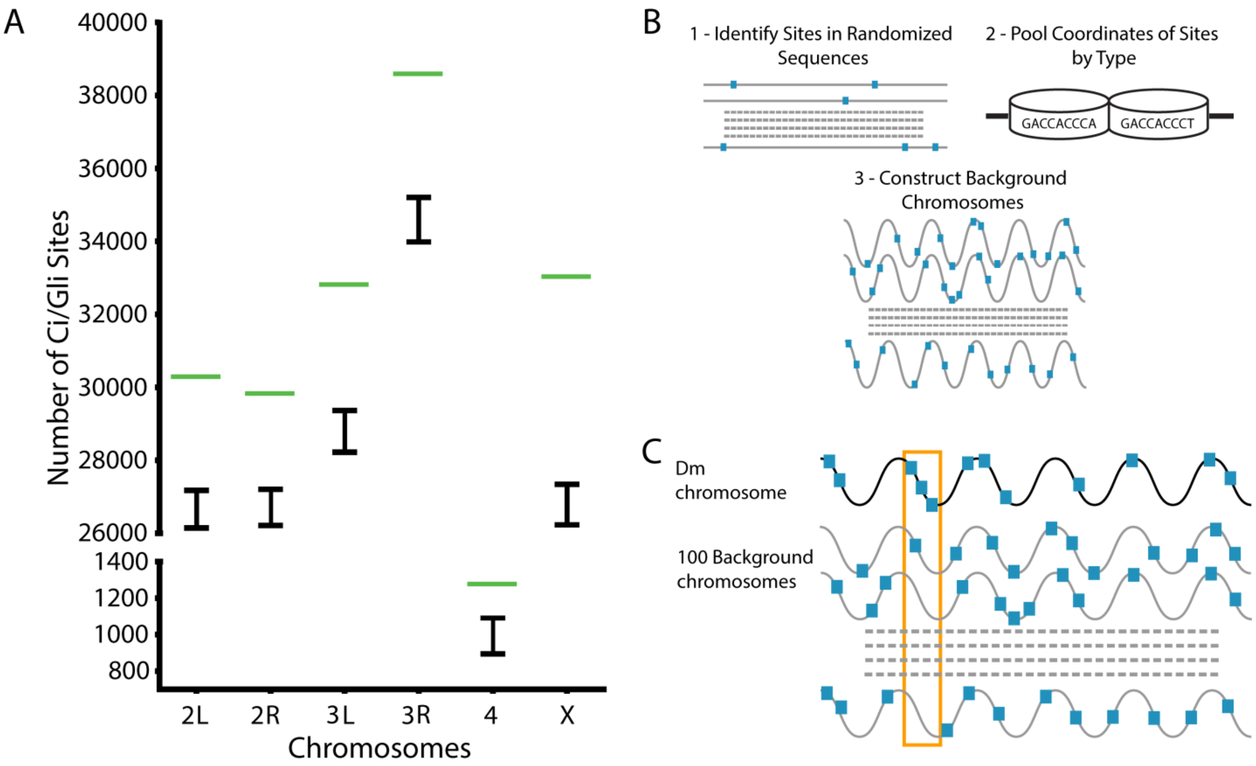


Figure S2.2. Construction of background genomes and determination of cluster enrichment. (A) The actual number of predicted ci/GLI sites (≥0.75 MSS) determined in each Dm chromosome is shown by the green lines. The Flip GC/AT method was used to create 1000 background sequences and the number of predicted ci/GLI sites was tallied for each sequence. Box plots show that randomized chromosomes contain substantially fewer predicted ci/GLI sites. Brackets represent the range in total number of ci/GLI sites across the background sequences for each chromosome. **(B)** To correct for the depleted number of predicted ci/GLI sites and create background chromosomes that would closely mirror the native Dm genome, the location (coordinates) and type (sequence) of all predicted ci/GLI sites in each of the 1000 background sequences were recorded and pooled. Background genomes were then constructed by randomly selecting coordinates from the pools so that the composition (number and site type) matched that of the corresponding Dm chromosome. **(C)** Enrichment of clusters of 3-10 ci/GLI sites relative to the background chromosomes was then determined. The example shows analysis of enrichment for clusters of 3 ci/GLI sites (blue boxes). The Dm chromosome (black line) is compared with 100 background chromosomes (grey lines); the diagram shows only three of the 100 background chromosomes. In a moving window, each group of three ci/GLI sites was delineated in the Dm chromosome (one such cluster is outlined in orange) and the average number of ci/GLI sites was determined within that same genomic space in each of the 100 background chromosomes. The cluster outlined by the orange box is considered enriched if the average number of sites in the Dm chromosome is ≥4 fold more than the average number of ci/GLI sites per background chromosome.

Chromo some	Cluster Start	Cluster End	Nearest Gene	Cluster Coefficient
chr2L	224157	224425	kis	8.85
chr2L	307304	307667	Plc21C	5.54
chr2L	308379	308837	Plc21C	4.695
chr2L	343561	344047	Plc21C	8.639
chr2L	469557	470464	MED15	7.102
chr2L	469557	470477	MED15	7.042
chr2L	470449	471006	MED15	5.083
chr2L	550183	550374	Ets21C	8.811
chr2L	550301	550533	Ets21C	8.811
chr2L	550301	550896	Ets21C	5.045
chr2L	589044	589438	Gsc	7.013
chr2L	589390	589862	Gsc	5.241
chr2L	675840	676572	ds	5.045
chr2L	675840	676768	ds	4.181
chr2L	679538	680264	ds	7.576
chr2L	788590	789216	Pkg21D	4.362
chr2L	895840	896637	Lsp1beta	4.076
chr2L	1076568	1077102	S	4.193
chr2L	1157377	1157954	capt	5.682
chr2L	1207768	1208263	CG14342	4.425
chr2L	1208186	1208449	CG14342	5.27
chr2L	1349318	1349842	CG5556	4.409
chr2L	1417798	1418139	lea	5.27
chr2L	1417798	1418404	lea	4.425
chr2L	1436421	1437406	snRNA:U3:22A	4.537
chr2L	1455873	1456140	snRNA:U3:22A	6.667
chr2L	1538844	1539238	Or22b	4.745
chr2L	1660217	1660479	chinmo	5.083
chr2L	1660446	1660882	chinmo	4
chr2L	1722762	1722944	CG18317	12.346
chr2L	1927228	1928142	CG7337	4.062
chr2L	1928046	1928721	CG7337	4.499
chr2L	2076821	2076968	dpr3	10.811
chr2L	2076821	2077165	dpr3	8.306
chr2L	2076821	2077373	dpr3	5.401
chr2L	2131149	2131543	GlyP	5.141
chr2L	2172681	2173528	aop	7.84
chr2L	2173264	2174038	aop	6.701
chr2L	2327144	2327509	CG9967	8.639
chr2L	2327300	2327600	CG9967	8.811
chr2L	2464347	2464714	dpp	5.398
chr2L	2485523	2486058	CG15393	5.568
chr2L	2633436	2633675	CG9962	6.479
chr2L	2633436	2634110	CG9962	6.452
chr2L	2676728	2677183	CG31690	7.08
chr2L	2706033	2706864	CG31690	4.062
chr2L	2716048	2716410	CG31690	4.355
chr2L	2716378	2717079	CG31690	6.748
chr2L	2748781	2749507	Pgk	8.316
chr2L	2749473	2749751	Pgk	6.427
chr2L	2749473	2749866	Pgk	5.489
chr2L	2757532	2758015	snapin	6.645
chr2L	2796200	2797118	Syt1	4.473
chr2L	2895471	2896008	lilli	5.839
chr2L	2895850	2896246	lilli	6.452
chr2L	3154232	3154808	Mad	5.472
chr2L	3409305	3410047	pgant2	5.141
chr2L	3532301	3532998	CG8853	4.425
chr2L	3600104	3600390	odd	6.897
chr2L	3612212	3612502	odd	8.475
chr2L	3612268	3612775	odd	6.969
chr2L	3664107	3664872	CG34340	6.682
chr2L	3664480	3665127	CG34340	6.135
chr2L	3681011	3681491	CG34340	5.997
chr2L	3681011	3681689	CG34340	5.141
chr2L	3721146	3721682	Shaw	6.925
chr2L	3803866	3804031	l(2)k16918	7.326
chr2L	3829612	3830403	slp1	5.226
chr2L	3829710	3830646	slp1	6.404
chr2L	3830384	3831170	slp1	6.588
chr2L	3989507	3990200	CG34176	5.61
chr2L	4162831	4163050	Or24a	10.791
chr2L	4271949	4272525	Art2	5
chr2L	4299398	4300399	tutl	4.127
chr2L	4300353	4300661	tutl	7.538
chr2L	4621866	4622276	BG642163	5.869

chr2L	4705805	4706494	CG34351	7.859
chr2L	4706417	4706727	CG34351	6.969
chr2L	5094889	5095720	CG5828	4.021
chr2L	5098159	5098686	CG4230	4.077
chr2L	5120002	5120997	Msp-300	4.454
chr2L	5301031	5301420	vri	4.802
chr2L	5301124	5301596	vri	4.036
chr2L	5361619	5362064	nompC	5.764
chr2L	5411889	5412644	H15	6.615
chr2L	5437299	5438000	CG31647	4.41
chr2L	5445064	5445591	CG31647	9.592
chr2L	5445554	5446251	CG31647	4.822
chr2L	5464393	5464800	mid	7.707
chr2L	5509164	5509417	CG14020	13.937
chr2L	5509164	5509869	CG14020	6.502
chr2L	5509164	5510099	CG14020	5.786
chr2L	5617311	5618117	CG14010	4.755
chr2L	5656242	5657211	CG31646	4.528
chr2L	5677620	5678067	CG12511	5.917
chr2L	5732767	5733434	CG11030	4.499
chr2L	5733426	5734412	CG11030	5.472
chr2L	5853722	5854330	CG34381	5.202
chr2L	5853809	5854605	CG34381	5.025
chr2L	5853809	5854808	CG34381	4.188
chr2L	5940796	5941704	Sfp26Ad	4.208
chr2L	6090269	6091255	Kr-h1	4.278
chr2L	6090571	6091556	Kr-h1	4.464
chr2L	6091207	6091658	Kr-h1	6.479
chr2L	6091207	6092139	Kr-h1	5.251
chr2L	6150404	6150603	Muc26B	5.997
chr2L	6150404	6150671	Muc26B	5.4
chr2L	6248734	6249726	Ddr	4.102
chr2L	6252580	6253012	Ddr	8.639
chr2L	6252580	6253354	Ddr	4.438
chr2L	6539285	6539784	eya	5.045
chr2L	6539708	6539924	eya	7.205
chr2L	6539708	6540049	eya	6.818
chr2L	6827632	6828030	sens-2	5.839
chr2L	6832808	6833642	sens-2	4.062
chr2L	7303281	7303496	wg	5.997
chr2L	7303424	7303790	wg	6.925
chr2L	7311767	7312687	wg	4.036
chr2L	7319199	7319903	wg	4.5
chr2L	7319641	7320043	wg	4.193
chr2L	7392657	7393164	CG5160	6.088
chr2L	7417064	7417916	chm	7.825
chr2L	7417064	7418058	chm	7.538
chr2L	7538294	7539165	Rapgap1	7.013
chr2L	7625773	7626160	CG6739	4.695
chr2L	8089867	8090201	Bsg	15.766
chr2L	8103360	8103509	Bsg	7.194
chr2L	8103420	8104130	Bsg	4.745
chr2L	8497224	8497950	Dh31	4.532
chr2L	8511973	8512424	CG13097	10.05
chr2L	8557017	8557734	Sema-1a	4.963
chr2L	8639944	8640535	Sema-1a	5.141
chr2L	8795244	8795688	CG9468	8
chr2L	8973919	8974766	CG9541	8.316
chr2L	8974758	8975016	CG9541	9.195
chr2L	8974939	8975581	CG9541	5.624
chr2L	9111745	9112729	Or30a	5.54
chr2L	9168557	9168972	tai	4.963
chr2L	9445357	9445977	numb	5.61
chr2L	9509985	9510871	CG33298	4.155
chr2L	9510670	9511041	CG33298	6.203
chr2L	9510670	9511480	CG33298	4.38
chr2L	9783289	9783744	IP3K1	5.025
chr2L	9785633	9786483	IP3K1	5.025
chr2L	9894965	9895631	Bka	5.997
chr2L	9905220	9905883	CG13124	4.563
chr2L	10431448	10431754	TfIIB	4.454
chr2L	10562289	10562433	Trim9	6.861
chr2L	10850047	10850463	porin	6.464
chr2L	11033089	11034058	Samuel	5.839
chr2L	11033137	11034134	Samuel	4.115
chr2L	11247749	11247999	ab	6.745
chr2L	11289752	11290286	Osi21	5.36
chr2L	11290100	11290672	Osi21	8.759
chr2L	11347457	11348317	CG14926	5.54
chr2L	11423198	11423454	salm	4.695

chr2L	11436190	11436638	salm	6.452
chr2L	11490514	11491226	sala	8.403
chr2L	11490853	11491330	sala	13.514
chr2L	11490853	11491535	sala	8.13
chr2L	11561853	11562485	Mst33A	5.472
chr2L	11684444	11684719	CG4988	8.85
chr2L	11755495	11756407	Sfp33A1	4.963
chr2L	11761005	11761167	Sfp33A1	10.526
chr2L	11761149	11761414	Sfp33A1	10.292
chr2L	11761149	11761573	Sfp33A1	7.387
chr2L	11865562	11865828	Pde1c	8.432
chr2L	11870723	11871367	Pde1c	5.917
chr2L	12105069	12105432	Aats-thr	6.547
chr2L	12159755	12160504	CG31760	4.077
chr2L	12321237	12321677	aret	7.194
chr2L	12500402	12500911	bun	6.547
chr2L	12673933	12674380	pdm2	8.523
chr2L	12674209	12674524	pdm2	7.444
chr2L	12745734	12746054	MRP	5.141
chr2L	12849933	12850587	kek1	4.154
chr2L	12854258	12855018	kek1	5.144
chr2L	12854798	12855803	kek1	4.362
chr2L	13078471	13078759	CG5142	7.716
chr2L	13099315	13100132	CG5142	4.955
chr2L	13099936	13100679	CG5142	5.192
chr2L	13426441	13426687	Tehao	11.364
chr2L	13426441	13426883	Tehao	6.667
chr2L	13501495	13502045	B4	6.452
chr2L	14179493	14180268	CG32972	5.083
chr2L	14278893	14279299	wb	7.449
chr2L	14407625	14408505	elB	6.667
chr2L	14443028	14443926	CG15283	7.338
chr2L	14444204	14444430	CG15283	15.464
chr2L	14444204	14445160	CG15283	4.545
chr2L	14471825	14472643	noc	5.4
chr2L	14745106	14745927	CG42587	8.316
chr2L	14745619	14746060	CG42587	10.811
chr2L	14773235	14773659	CG4650	4.115
chr2L	14809507	14810378	CG33309	4
chr2L	14934569	14935180	CG42313	4.092

chr2L	15067078	15067481	vas	5.045
chr2L	15104872	15105218	CG15269	13.937
chr2L	15105130	15105703	CG15269	15.432
chr2L	15105130	15106127	CG15269	9.259
chr2L	15106615	15107288	CG15269	6.088
chr2L	15282712	15282916	CG15263	5.398
chr2L	15335739	15336710	esg	7.449
chr2L	15490818	15491648	Tim17b2	4.278
chr2L	15535363	15536353	CG42448	4.32
chr2L	15604901	15605503	CG15255	9.195
chr2L	15936528	15937235	beat-Ib	5.998
chr2L	15937185	15937383	beat-Ib	10.183
chr2L	16007983	16008204	beat-Ic	12.012
chr2L	16008030	16008398	beat-Ic	13.85
chr2L	16523372	16524357	CG5953	8.451
chr2L	16540765	16541091	CG31816	7.319
chr2L	16541032	16542034	CG31816	8.097
chr2L	16547346	16548248	CG42389	7.795
chr2L	16548122	16548832	CG42389	6.818
chr2L	16548122	16548951	CG42389	5.907
chr2L	16570066	16570842	CG42389	4.036
chr2L	16782148	16782965	Mhc	4.37
chr2L	17101764	17102010	CG31784	9.009
chr2L	17209384	17210217	beat-IIIc	4.355
chr2L	17221217	17221771	beat-IIIc	5.807
chr2L	17326866	17327077	CG34170	8.639
chr2L	17346002	17346266	CG31804	9.195
chr2L	17355334	17355882	CG31804	4.193
chr2L	17399685	17400467	CLIP-190	5.27
chr2L	17400908	17401354	CLIP-190	4.193
chr2L	17433182	17433529	CG5043	5.513
chr2L	17578043	17578705	Oli	4.545
chr2L	17584850	17585071	Oli	11.561
chr2L	17584935	17585209	Oli	15.424
chr2L	17584935	17585314	Oli	12.007
chr2L	17584935	17585409	Oli	9.604
chr2L	18004718	18005443	CG5693	7.444
chr2L	18028936	18029643	rdo	4.598
chr2L	18737563	18737995	CG15167	5.839
chr2L	18737823	18738336	CG15167	10.05

chr2L	18814753	18815451	CG17325	4.219
chr2L	18973820	18974787	CG10639	4.092
chr2L	19015688	19015947	robl37BC	5.445
chr2L	19015888	19016804	robl37BC	4.878
chr2L	19020871	19021531	CG15172	5.141
chr2L	19021422	19021718	CG15172	4.963
chr2L	19144519	19145347	brat	6.042
chr2L	19360312	19361151	dnt	4.193
chr2L	19514284	19514674	CG10186	6.349
chr2L	19514284	19514873	CG10186	5.786
chr2L	19629891	19630237	Lar	4.278
chr2L	19824278	19825032	CG13958	4.908
chr2L	19882749	19883355	sick	5.839
chr2L	19883248	19883507	sick	6.745
chr2L	19883248	19883688	sick	4.78
chr2L	20020671	20021345	CG10659	4.839
chr2L	20500026	20500384	CG34007	5.917
chr2L	20500026	20500750	CG34007	5.097
chr2L	20516462	20517339	CG34007	5.907
chr2L	20649717	20650264	CG18810	5.398
chr2L	20845537	20845805	CG31676	8.639
chr2L	21029388	21030096	CG42238	8.316
chr2L	21811017	21811841	tsh	4.963
chr2L	21811017	21811991	tsh	4.5
chr2L	21958680	21958911	CG2528	6.588
chr2L	21958669	21959022	CG2528	5.063
chr2L	21960881	21961186	CG2528	11.583
chr2L	21960881	21961556	CG2528	6.84
chr2L	21960881	21961577	CG2528	6.818
chr2L	21960881	21961713	CG2528	6.05
chr2R	1661799	1662671	CG11163	4.646
chr2R	1662663	1663094	CG11163	4.498
chr2R	2014104	2014214	EcR	12.987
chr2R	2566475	2566947	CG9422	6.088
chr2R	2656051	2656477	Epac	6.969
chr2R	2939493	2939787	lbm	12.987
chr2R	2939714	2940347	lbm	6
chr2R	2965576	2965947	CG12831	61.538
chr2R	2997233	2997608	esn	6
chr2R	3057470	3058313	pk	5.141
chr2R	3057484	3058321	pk	5.141
chr2R	3141403	3142377	Gadd45	7.576
chr2R	3142362	3142697	Gadd45	11.261
chr2R	3344556	3345175	Inos	4.566
chr2R	3345504	3346174	Inos	4.839
chr2R	3345853	3346237	Inos	5.059
chr2R	3652947	3653720	CG30497	13.937
chr2R	3653712	3653895	CG30497	210.526
chr2R	3653746	3654118	CG30497	28.777
chr2R	3653781	3654690	CG30497	4.036
chr2R	3669306	3670079	cn	4.362
chr2R	3887949	3888104	CG11191	4.646
chr2R	3945294	3946197	CG12769	4.695
chr2R	4171505	4171947	CG30371	7.707
chr2R	4180231	4181023	CG30371	4.38
chr2R	4188822	4188966	CG30371	17.964
chr2R	4189031	4189989	CG30371	4.092
chr2R	4260688	4260855	CG8701	18.018
chr2R	4260818	4261362	CG8701	7.326
chr2R	4265757	4265908	CG8701	17.316
chr2R	4265757	4266177	CG8701	9.47
chr2R	4265769	4266394	CG8701	5.297
chr2R	4269955	4270182	pdm3	17.316
chr2R	4334990	4335177	Cyp4e1	9.804
chr2R	4347126	4347551	CG8693	6.897
chr2R	4463778	4464265	CG42326	8.639
chr2R	4464050	4464395	CG42326	7.859
chr2R	4473508	4473691	CG14752	6.237
chr2R	4475772	4476297	CG14752	5.396
chr2R	4475772	4476670	CG14752	4.284
chr2R	4519468	4520108	CG8635	5.226
chr2R	4531060	4531543	ptc	7.08
chr2R	4532024	4532643	ptc	5.083
chr2R	4532518	4532669	ptc	142.857
chr2R	4532631	4533543	ptc	4.237
chr2R	4536026	4536527	ptc	5.083
chr2R	4536453	4537018	ptc	4.208
chr2R	4544755	4545026	ptc	7.371
chr2R	4599045	4599490	CG14743	4.983
chr2R	4619974	4620552	stmA	4.908

chr2R	4620058	4620687	stmA	4.41
chr2R	4620205	4620845	stmA	4.154
chr2R	4643981	4644322	CG8740	4.566
chr2R	4672985	4673404	CG8746	6.173
chr2R	4882942	4883426	CG34350	22.727
chr2R	5084627	5085141	unpg	5.839
chr2R	5090819	5091011	CG8027	8.746
chr2R	5091621	5091764	CG8027	5.226
chr2R	5157261	5158001	Pkn	6.645
chr2R	5235163	5235392	CG13739	10.283
chr2R	5235322	5235475	CG13739	16.598
chr2R	5384155	5384985	Wnt2	5.917
chr2R	5391184	5392138	brp	4.029
chr2R	5397320	5397969	brp	7.496
chr2R	5408548	5408869	brp	7.538
chr2R	5445495	5445946	Or45b	5.141
chr2R	5488211	5488363	CG1902	48.193
chr2R	5488325	5488472	CG1902	23.952
chr2R	5491540	5492043	CG1902	7.576
chr2R	5774661	5775105	CG12923	10.283
chr2R	5788191	5788645	CG1441	5.997
chr2R	5788458	5788939	CG1441	5.839
chr2R	5788467	5789280	CG1441	4.854
chr2R	5798378	5798971	CG12140	14.87
chr2R	5869383	5870077	eve	5.333
chr2R	5906786	5907535	Pka-R2	5.146
chr2R	5989625	5990006	14-3-3zeta	61.538
chr2R	6112204	6112546	Hr46	13.937
chr2R	6112359	6113085	Hr46	10.526
chr2R	6135029	6135681	CG12914	5.78
chr2R	6136569	6136924	CG12914	21.622
chr2R	6136569	6137280	CG12914	5.513
chr2R	6136916	6137462	CG12913	5.396
chr2R	6418353	6418759	lola	8.746
chr2R	6458687	6459675	psq	6.353
chr2R	6461151	6461657	psq	6.748
chr2R	6461161	6461507	psq	7.371
chr2R	6461408	6461657	psq	7.895
chr2R	6461408	6462025	psq	6.349
chr2R	6587668	6588157	stan	6.26
chr2R	6657910	6658335	CG33144	4.41
chr2R	6731066	6731903	CG30015	11.662
chr2R	6741436	6742210	CG30015	4.908
chr2R	7092641	7093475	shn	6.26
chr2R	7123813	7124654	CG13217	4.908
chr2R	7136275	7136805	CG34227	6
chr2R	7162504	7162846	TpnC47D	12.448
chr2R	7162550	7163139	TpnC47D	8.432
chr2R	7200893	7201078	nompA	6.068
chr2R	7262100	7262881	CG13203	4.036
chr2R	7378828	7379226	inv	7.042
chr2R	7379044	7379448	inv	5.495
chr2R	7380187	7380454	inv	7.326
chr2R	7380383	7380632	inv	5.894
chr2R	7380624	7381376	inv	4
chr2R	7455310	7455887	tou	4.104
chr2R	7682102	7682696	ths	8.711
chr2R	7682229	7682570	ths	9.804
chr2R	7687754	7688607	ths	4.907
chr2R	7701704	7702389	ths	9.828
chr2R	7702241	7702627	ths	33.333
chr2R	7734178	7734370	Sln	210.526
chr2R	7734302	7734536	Sln	210.526
chr2R	7734327	7734546	Sln	210.526
chr2R	7855414	7855994	CG8979	10.526
chr2R	8011025	8011915	jeb	4.745
chr2R	8011707	8012076	jeb	27.027
chr2R	8153859	8154063	Cam	9.009
chr2R	8154055	8154361	Cam	8.147
chr2R	8653016	8653886	CG12374	4.575
chr2R	8838792	8839271	CG3884	9.823
chr2R	8838838	8839262	CG3884	10.791
chr2R	8860704	8861146	Psc	4.049
chr2R	8879829	8880583	CG33798	10.05
chr2R	8965690	8966054	Drl-2	17.316
chr2R	8981205	8981375	Drl-2	21.622
chr2R	8985115	8986083	CG13325	10.283
chr2R	8985944	8986186	CG13325	400
chr2R	8989909	8990177	CG13325	7.712
chr2R	9257541	9258057	CG10814	7.905

chr2R	9309045	9309601	CG42321	9.592
chr2R	9688042	9688414	Cpr50Cb	4.983
chr2R	9688042	9688896	Cpr50Cb	4.237
chr2R	9840907	9841682	AGO1	4.545
chr2R	9841497	9842022	AGO1	10.05
chr2R	9955070	9955239	Prosap	19.608
chr2R	10033422	10034046	Rcd1	4
chr2R	10157104	10157811	SelD	17.316
chr2R	10166787	10167355	Ih	4.745
chr2R	10236029	10237011	Shroom	5.202
chr2R	10342729	10343186	Oaz	5.31
chr2R	10540962	10541599	Adgf-E	4.208
chr2R	10674327	10674532	kn	28.777
chr2R	10674327	10674542	kn	14.577
chr2R	10699557	10700017	CG10200 (knot)	5.059
chr2R	10699888	10700190	CG10200	4.762
chr2R	10742561	10743114	Ciao1	4.695
chr2R	10756680	10757391	Pcf11	5.396
chr2R	10758190	10759090	Pcf11	7.895
chr2R	10789959	10790082	CG10249	7.538
chr2R	10800135	10800876	CG10249	4.762
chr2R	10814534	10815122	CG10253	4.91
chr2R	10854025	10854606	CG12424	7.102
chr2R	10854101	10854638	CG12424	8.183
chr2R	10856913	10857173	CG12424	6.479
chr2R	10856967	10857599	CG12424	6.588
chr2R	10875846	10876007	pcs	71.429
chr2R	10875881	10876089	pcs	61.538
chr2R	10875931	10876305	pcs	10.526
chr2R	10875931	10876324	pcs	6.84
chr2R	10876755	10876967	pcs	5.146
chr2R	10888725	10889522	CG10265	7.326
chr2R	10911099	10911471	hbs	13.514
chr2R	10911463	10911962	hbs	6.002
chr2R	10912720	10913010	hbs	8.811
chr2R	10922067	10922364	hbs	4.762
chr2R	10994428	10995433	chn	8.811
chr2R	10994712	10995477	chn	10.05
chr2R	10994748	10995548	chn	10.283
chr2R	10998060	10998943	chn	5.4
chr2R	11003713	11003984	chn	9.311
chr2R	11004180	11005090	chn	6.353
chr2R	11004904	11005421	chn	8.85
chr2R	11038670	11039256	CG7544	8.576
chr2R	11090075	11090569	CG11807	6.757
chr2R	11090432	11091198	CG11807	10.526
chr2R	11093782	11093982	row	9.804
chr2R	11100677	11101193	row	5.997
chr2R	11101185	11102041	row	4.839
chr2R	11135357	11136230	scb	4.049
chr2R	11138385	11139006	scb	4.839
chr2R	11186006	11186788	CG8102	8.711
chr2R	11186239	11186828	CG8102	7.326
chr2R	11186315	11187134	CG8102	6.645
chr2R	11210708	11211466	Arf51F	4.049
chr2R	11218534	11218691	Hr51	4.566
chr2R	11221366	11221772	Hr51	4.498
chr2R	11242649	11242931	unc-5	11.583
chr2R	11242653	11242994	unc-5	9.259
chr2R	11242649	11243535	unc-5	4.252
chr2R	11277182	11277997	SRPK	6.173
chr2R	11279237	11279402	SRPK	5.495
chr2R	11279244	11279463	SRPK	4.695
chr2R	11281951	11282528	SRPK	6.356
chr2R	11300613	11300919	CG34365	4.155
chr2R	11301690	11301953	CG34365	11.364
chr2R	11301875	11302537	CG34365	6.502
chr2R	11305134	11305956	CG34365	8.639
chr2R	11309355	11309910	CG34365	7.707
chr2R	11321080	11321440	CG34365	6.356
chr2R	11321080	11321590	CG34365	5.997
chr2R	11336714	11337271	CG34365	5.4
chr2R	11345054	11345780	CG34365	5.682
chr2R	11345651	11345978	CG34365	12.012
chr2R	11377647	11378213	CG12964	4.104
chr2R	11377929	11378342	CG12964	4.695
chr2R	11380795	11381778	CG12964	4.278
chr2R	11381313	11381965	CG12964	8.811
chr2R	11409951	11410140	Khc-73	12

chr2R	11418890	11419056	Khc-73	5.682
chr2R	11419036	11419862	Khc-73	5.202
chr2R	11420951	11421424	Khc-73	6.356
chr2R	11441137	11442119	CG12963	4.115
chr2R	11441808	11442264	CG12963	6.969
chr2R	11444404	11445150	CG12963	4.839
chr2R	11447113	11447936	CG12963	5.513
chr2R	11484458	11484743	CG42524	18.779
chr2R	11493435	11494048	CG42524	7.449
chr2R	11493919	11494178	CG42524	10.811
chr2R	11503828	11504337	CG42524	5.839
chr2R	11517843	11518614	CG42524	4.655
chr2R	11518505	11518872	CG42524	8
chr2R	11518588	11519347	CG42524	4.854
chr2R	11527076	11527478	CG42524	6.757
chr2R	11536745	11536932	CG42524	12.448
chr2R	11548317	11549179	fus	4.575
chr2R	11548638	11548903	fus	6.356
chr2R	11548890	11549179	fus	7.895
chr2R	11548890	11549461	fus	5.333
chr2R	11563870	11564279	fus	5.31
chr2R	11566797	11567427	Vha14	4.154
chr2R	11575662	11575911	CG8214	11.364
chr2R	11575842	11576719	CG8214	8.316
chr2R	11582841	11583620	CG33461	5.453
chr2R	11590226	11590369	CG30080	11.583
chr2R	11602343	11602564	CG30083	9.804
chr2R	11613150	11613528	CG30089	10.526
chr2R	11659638	11659988	Zasp52	4.104
chr2R	11716587	11717390	Poxn	9.39
chr2R	11716940	11717616	Poxn	11.364
chr2R	11723741	11724197	Poxn	11.662
chr2R	11724394	11724517	Poxn	12.987
chr2R	11728883	11729155	CG8249	4.91
chr2R	11750736	11751297	Gpo-1	16.598
chr2R	11750906	11751628	Gpo-1	6.969
chr2R	11765804	11766000	sli	8.523
chr2R	11781405	11781953	sli	11.364
chr2R	11792774	11793189	sli	4.454
chr2R	11793119	11793308	sli	5.894
chr2R	11800823	11801745	sli	4.854
chr2R	11844565	11845367	CG8366	8.147
chr2R	11844574	11845427	CG8366	7.449
chr2R	11852288	11852849	Strn-Mlck	4.237
chr2R	11853445	11854204	Strn-Mlck	5.61
chr2R	11872593	11873305	Strn-Mlck	5.54
chr2R	11875205	11875406	CG15699	6.11
chr2R	11877665	11877930	CG8314	14.388
chr2R	11877703	11877998	CG8314	14.87
chr2R	11885983	11886882	ATPCL	4.762
chr2R	11899289	11899697	CG8389	5.78
chr2R	11906508	11907159	CG8399	6.645
chr2R	11922534	11922805	SP2353	8.31
chr2R	11924293	11924961	SP2353	18.018
chr2R	11924873	11925542	SP2353	9.828
chr2R	11931092	11931765	SP2353	7.326
chr2R	11933643	11934629	SP2353	6.969
chr2R	11935411	11935606	CG8405	19.108
chr2R	11940620	11940973	CG8405	4.63
chr2R	11940620	11941229	CG8405	4
chr2R	11979617	11980069	Dg	5.917
chr2R	11980009	11980365	Dg	12
chr2R	11983948	11984275	Dg	4.839
chr2R	12020739	12021490	spin	5.27
chr2R	12026380	12026605	Got1	6.237
chr2R	12061469	12061801	Ptp52F	4.261
chr2R	12067735	12068182	Lis-1	27.027
chr2R	12067789	12068288	Lis-1	17.316
chr2R	12068044	12068917	Lis-1	5.333
chr2R	12070403	12071055	Lis-1	12.698
chr2R	12084900	12085115	CG8446	4.839
chr2R	12093494	12093917	mrj	11.152
chr2R	12115105	12116009	CG15706	4.193
chr2R	12118234	12118590	CG15701	6.452
chr2R	12122228	12122535	CG7786	7.042
chr2R	12127968	12128422	krimp	7.538
chr2R	12127968	12128732	krimp	4.695
chr2R	12148759	12148959	fidipidine	5.396
chr2R	12148936	12149225	fidipidine	4.261
chr2R	12177885	12178354	JhI-26	5.682

chr2R	12191454	12192156	Nox	5.917
chr2R	12192114	12192650	Nox	9.39
chr2R	12195766	12196542	Nox	4.802
chr2R	12196305	12196757	Nox	4.908
chr2R	12196534	12197162	Nox	5.398
chr2R	12215782	12216478	Vha44	15.444
chr2R	12216470	12216752	Vha44	11.152
chr2R	12216685	12217690	Vha44	6.745
chr2R	12244917	12245819	CG6262	6.349
chr2R	12245227	12245830	CG6262	8.811
chr2R	12245419	12245845	CG6262	9.39
chr2R	12255922	12256341	CG15711	30.769
chr2R	12256349	12256647	CG15711	14.388
chr2R	12256447	12257279	CG15711	8.475
chr2R	12279256	12279759	CG33960	5.472
chr2R	12279656	12280381	CG33960	4.762
chr2R	12281340	12281607	CG33960	6.897
chr2R	12281599	12281860	CG33960	9.195
chr2R	12281852	12282511	CG33960	5.54
chr2R	12284061	12284394	CG33960	6.237
chr2R	12332423	12333217	CG4409	4.454
chr2R	12332538	12333356	CG4409	4.115
chr2R	12335293	12335640	CG15925	8.31
chr2R	12338151	12338317	CG15925	6
chr2R	12351339	12351638	CheB53a	5.31
chr2R	12358138	12358700	CheB53b	5.146
chr2R	12358453	12358707	CheB53b	6.356
chr2R	12381552	12381825	CG4439	28.777
chr2R	12389087	12389207	Sema-2a	17.964
chr2R	12389087	12389437	Sema-2a	8.85
chr2R	12389192	12389840	Sema-2a	5.624
chr2R	12407530	12407646	Sema-2a	9.524
chr2R	12412235	12412734	Sema-2a	10.05
chr2R	12416993	12417312	Sema-2a	11.364
chr2R	12417225	12417557	Sema-2a	8.108
chr2R	12418572	12419488	Sema-2a	9.592
chr2R	12422283	12423272	loopin-1	6.088
chr2R	12454499	12455492	CG4945	4.438
chr2R	12462190	12463107	CG8317	4.908
chr2R	12491541	12492061	CG8303	8.811
chr2R	12498903	12499084	CG5065	6.356
chr2R	12502325	12502745	CG5065	14.87
chr2R	12502350	12502789	CG5065	14.87
chr2R	12507868	12508551	CG5065	4.598
chr2R	12528359	12528634	gprs	6.645
chr2R	12535593	12536335	gprs	4.41
chr2R	12537034	12538003	gprs	5.31
chr2R	12537601	12538280	Amyrel	7.042
chr2R	12559410	12560295	CG34458	4.077
chr2R	12563219	12563634	CG30463	8.811
chr2R	12563385	12563813	CG30463	6.969
chr2R	12580057	12580981	CG30463	4.646
chr2R	12580702	12581045	CG30463	10.526
chr2R	12591716	12592544	CG30463	8.811
chr2R	12592536	12593427	CG30463	11.08
chr2R	12604435	12605066	CG30463	8.639
chr2R	12619177	12620175	Sfp53D	4.322
chr2R	12643259	12643744	unc-104	27.027
chr2R	12643337	12643851	unc-104	30.769
chr2R	12655982	12656635	unc-104	5.31
chr2R	12659107	12659386	unc-104	4.323
chr2R	12666767	12667111	Vkor	7.895
chr2R	12668783	12669179	resilin	5.025
chr2R	12671147	12671617	CG5522	16
chr2R	12671587	12672041	CG5522	15.444
chr2R	12676473	12676958	CG5522	7.08
chr2R	12676636	12677619	CG5522	4.362
chr2R	12680506	12680857	CG15919	8.639
chr2R	12700969	12701447	CG5550	4
chr2R	12707820	12708002	CG5550	86.957
chr2R	12707823	12708039	CG5550	39.216
chr2R	12751749	12752398	Psi	10.283
chr2R	12752295	12752595	Psi	6.745
chr2R	12768607	12769316	CG8910	6
chr2R	12768947	12769539	CG8910	6.897
chr2R	12769308	12769894	CG8910	5.587
chr2R	12774256	12774986	CG8910	4.049
chr2R	12774968	12775251	CG8910	8.108
chr2R	12775863	12776552	CG8910	4.646
chr2R	12778070	12778667	CG8910	5.396

chr2R	12778070	12778722	CG8910	5.025
chr2R	12788237	12789106	inaC	4.454
chr2R	12802259	12803132	Pkc53E	6.353
chr2R	12802701	12803177	Pkc53E	10
chr2R	12803370	12803696	Pkc53E	7.396
chr2R	12803377	12804009	Pkc53E	6.002
chr2R	12803399	12804072	Pkc53E	4.655
chr2R	12847803	12847918	CG9010	9.524
chr2R	12854974	12855655	Cbp53E	8.811
chr2R	12855516	12855847	Cbp53E	7.371
chr2R	12858167	12858532	Cbp53E	5.682
chr2R	12858520	12859371	Cbp53E	4.323
chr2R	12862997	12863558	Cbp53E	7.194
chr2R	12863405	12863749	Cbp53E	15.464
chr2R	12866743	12867068	Cbp53E	4.695
chr2R	12871345	12871474	Cbp53E	7.538
chr2R	12871345	12871652	Cbp53E	6.969
chr2R	12876736	12877630	Cbp53E	4.545
chr2R	12879141	12879989	Cbp53E	6.757
chr2R	12879915	12880904	Cbp53E	4.41
chr2R	12920927	12921758	RhoGEF2	6.452
chr2R	12953454	12954335	CG6967	5.682
chr2R	12963749	12964333	CG30460	7.326
chr2R	12987166	12987814	GstS1	4.695
chr2R	12987806	12988578	CG30456	4.802
chr2R	12992760	12993169	CG30456	11.08
chr2R	13013371	13013957	Amy-d	4.193
chr2R	13051217	13051370	CG10953	7.371
chr2R	13072472	13072955	CG10950	10.05
chr2R	13072947	13073377	CG10950	17.316
chr2R	13073362	13073564	CG10950	21.622
chr2R	13073369	13074020	CG10950	4.454
chr2R	13088827	13089178	CG10950	5.297
chr2R	13089135	13089485	CG10950	25.478
chr2R	13148307	13148548	mbl	8.432
chr2R	13163618	13164258	mbl	6.11
chr2R	13166630	13167109	mbl	6.608
chr2R	13173214	13174144	mbl	4.695
chr2R	13174116	13174333	mbl	61.538
chr2R	13174123	13174449	mbl	22.727
chr2R	13179535	13180223	mbl	6.356
chr2R	13267222	13267629	Sip1	8
chr2R	13267544	13268149	Sip1	4.237
chr2R	13272752	13273658	Sip1	5.141
chr2R	13288044	13288802	Sip1	4.323
chr2R	13288780	13289540	Sip1	4.566
chr2R	13290583	13291441	Sip1	4.049
chr2R	13297921	13298403	CG30101	4
chr2R	13298105	13298630	CG30101	6
chr2R	13321315	13321773	EDTP	20.619
chr2R	13352840	13353334	CG14478	8.576
chr2R	13394739	13395102	CG4844	9.39
chr2R	13396570	13396807	CG4844	7.194
chr2R	13396768	13397027	CG4844	8.147
chr2R	13427847	13428336	CG18432	8.639
chr2R	13444225	13444679	Klp54D	5.472
chr2R	13472833	13473051	CG14483	6.897
chr2R	13485394	13486197	lack	8
chr2R	13486148	13486321	lack	22.727
chr2R	13509261	13510034	CG10936	4.695
chr2R	13509596	13510178	CG10936	4.839
chr2R	13514476	13514864	CG10936	5.495
chr2R	13514476	13515363	CG10936	4.036
chr2R	13520674	13521524	CG10936	5.61
chr2R	13568765	13569441	Sema-1b	13.937
chr2R	13582492	13583462	swi2	4
chr2R	13604206	13604969	CG10934	10.05
chr2R	13626923	13627181	CG6401	8.108
chr2R	13626923	13627711	CG6401	6.203
chr2R	13646668	13647388	HLH54F	4.104
chr2R	13656907	13657644	CG18635	4
chr2R	13680251	13680868	CG5036	5.141
chr2R	13707725	13708531	grh	5.27
chr2R	13711493	13711618	grh	9.804
chr2R	13711493	13712315	grh	4.908
chr2R	13714618	13715214	grh	11.662
chr2R	13739187	13739887	olf186-F	5.31
chr2R	13744411	13745217	olf186-F	4.154
chr2R	13774619	13775383	elk	5.839
chr2R	13777941	13778084	elk	12.448

chr2R	13824893	13825436	PpY-55A	5.059
chr2R	13828138	13828467	PpY-55A	8.306
chr2R	13834690	13835398	PpY-55A	4.284
chr2R	13843365	13844291	PpY-55A	4.908
chr2R	13852654	13853425	PpY-55A	4.762
chr2R	13857813	13858781	dpr13	4.122
chr2R	13859415	13859910	dpr13	9.592
chr2R	13859898	13860262	dpr13	11.583
chr2R	13867079	13867483	dpr13	6.237
chr2R	13867161	13867889	dpr13	4.261
chr2R	13870544	13871222	dpr13	4.908
chr2R	13870585	13871289	dpr13	5.54
chr2R	13877265	13878137	dpr13	4.854
chr2R	13907192	13907851	CG5084	4.104
chr2R	13924463	13924885	CG5773	7.825
chr2R	13924463	13925026	CG5773	5.297
chr2R	13944802	13945670	CG10912	5.31
chr2R	13958201	13958361	CG34386	9.259
chr2R	13965659	13966038	CG34386	7.194
chr2R	14028253	14029036	pAbp	5.869
chr2R	14028309	14029041	pAbp	6.068
chr2R	14035514	14035706	CG17680	15.464
chr2R	14041906	14042467	lolal	8.811
chr2R	14078946	14079591	CG33958	7.859
chr2R	14079468	14080418	CG33958	6.969
chr2R	14081582	14082117	CG14500	13.072
chr2R	14082035	14082252	CG14500	61.538
chr2R	14082082	14082622	CG14500	18.018
chr2R	14094068	14095069	CG30114	6.547
chr2R	14111491	14111907	fj	5.297
chr2R	14165096	14165842	pen-2	4.38
chr2R	14178483	14178815	sbb	6.757
chr2R	14185007	14185556	sbb	9.524
chr2R	14202577	14203233	sbb	4.104
chr2R	14204726	14205137	sbb	5.587
chr2R	14208115	14208978	sbb	4.049
chr2R	14208818	14209188	sbb	9.804
chr2R	14209631	14210268	sbb	5.146
chr2R	14278499	14278974	CG15068	6.356
chr2R	14280543	14280784	Idgf5	10.811
chr2R	14280776	14280886	Idgf5	12.987
chr2R	14282434	14283094	Idgf5	5.682
chr2R	14290388	14290673	GstE4	11.583
chr2R	14299658	14299934	imd	4.104
chr2R	14301817	14302412	Dp1	4.745
chr2R	14312510	14312722	CG5174	21.583
chr2R	14317852	14318177	CG30118	9.592
chr2R	14405016	14405199	CG5226	9.259
chr2R	14405016	14405734	CG5226	6.088
chr2R	14406048	14406338	CG5226	12.448
chr2R	14406330	14406908	CG5226	7.707
chr2R	14423666	14424058	Pepck	8.639
chr2R	14426693	14427468	Pepck	6.11
chr2R	14427942	14428238	Rgk2	6.088
chr2R	14427963	14428365	Rgk2	6.349
chr2R	14428162	14428609	Rgk2	14.388
chr2R	14428230	14428658	Rgk2	16
chr2R	14428357	14428662	Rgk2	27.027
chr2R	14428601	14428844	Rgk2	13.937
chr2R	14428650	14428967	Rgk2	9.828
chr2R	14428650	14429257	Rgk2	4.252
chr2R	14503648	14504129	CG5327	6.645
chr2R	14557418	14557791	edl	6.349
chr2R	14560090	14560885	edl	6.11
chr2R	14571845	14572163	CG15086	7.042
chr2R	14571971	14572217	CG15086	7.371
chr2R	14599486	14600458	pncr016:2R	4.695
chr2R	14610008	14610522	Hs3st-A	7.08
chr2R	14610323	14610650	Hs3st-A	142.857
chr2R	14627581	14627962	Hs3st-A	9.009
chr2R	14629369	14629836	Hs3st-A	12.987
chr2R	14629760	14630205	Hs3st-A	7.194
chr2R	14653902	14654054	Mctp	27.027
chr2R	14654354	14654955	Mctp	8.811
chr2R	14654376	14655254	Mctp	5.202
chr2R	14656431	14656981	Mctp	7.576
chr2R	14683601	14684243	CG15094	6.452
chr2R	14740539	14741443	Jheh1	4.454
chr2R	14802430	14803437	sano	4.41
chr2R	14802592	14803582	sano	4.646

chr2R	14876769	14877104	abba	14.87
chr2R	14978647	14979529	5-HT1A	7.576
chr2R	15041200	15041634	ena	4.38
chr2R	15058092	15058588	CG10737	7.449
chr2R	15094264	15094528	hppy	28.777
chr2R	15094268	15094549	hppy	28.777
chr2R	15196308	15197315	endoB	6.088
chr2R	15211205	15211546	Rgk1	5.495
chr2R	15319332	15320192	Fak56D	4.575
chr2R	15348836	15349734	par-1	4.38
chr2R	15456684	15456923	sm	7.042
chr2R	15456871	15457106	sm	10.453
chr2R	15456871	15457203	sm	8.147
chr2R	15457098	15457623	sm	7.449
chr2R	15515380	15515518	sm	12.987
chr2R	15563532	15563945	isopeptidase-T-3	7.707
chr2R	15563709	15564596	isopeptidase-T-3	6.26
chr2R	15598399	15598522	Obp56e	10.135
chr2R	15598399	15599266	Obp56e	6.452
chr2R	15613598	15614453	snoRNA:185	5.786
chr2R	15675141	15676010	Obp56g	4.598
chr2R	15680992	15681678	Obp56g	5.917
chr2R	15681187	15682027	Obp56g	5.997
chr2R	15706999	15707450	Obp56h	9.828
chr2R	15743081	15743609	Obp56i	4.077
chr2R	15743458	15743927	Obp56i	5.141
chr2R	16082249	16082501	CG16894	6.356
chr2R	16082952	16083146	CG16894	4.745
chr2R	16115878	16116320	CG11044	10.283
chr2R	16161373	16162286	CG10444	4.077
chr2R	16207636	16208553	CG8920	4.154
chr2R	16233903	16234267	CG16741	8.811
chr2R	16374810	16375635	Obp57c	7.576
chr2R	16433430	16433632	CG30148	11.08
chr2R	16433624	16433832	CG30148	10.526
chr2R	16433624	16434140	CG30148	7.61
chr2R	16478617	16479024	bl	8
chr2R	16479016	16479871	bl	7.576
chr2R	16649188	16649924	CG34202	4.278
chr2R	16702229	16702475	insc	13.514
chr2R	16778526	16778916	otp	11.662
chr2R	16778540	16778960	otp	11.662
chr2R	16805715	16806308	Rx	5.333
chr2R	16809441	16810113	Rx	12.012
chr2R	16809555	16810128	Rx	16.598
chr2R	16809766	16810185	Rx	39.216
chr2R	16835221	16835995	snoRNA:660	6.897
chr2R	16843838	16844242	hbn	9.39
chr2R	16843856	16844249	hbn	9.39
chr2R	16850198	16851047	hbn	7.576
chr2R	16850443	16851167	hbn	9.828
chr2R	16851021	16851517	hbn	16
chr2R	16851039	16851676	hbn	15.444
chr2R	16868353	16868961	CG9313	6.088
chr2R	16884983	16885515	CG10543	8.065
chr2R	16913067	16913404	CG9350	8.639
chr2R	16990641	16990997	king-tubby	6.745
chr2R	17367609	17368319	Sdc	6.356
chr2R	17394863	17395329	MESK2	10.283
chr2R	17529429	17529978	CG10321	9.828
chr2R	17606036	17606670	Tango11	5.61
chr2R	17674352	17675063	lox2	6.135
chr2R	17674981	17675732	lox2	6.427
chr2R	17675702	17675884	lox2	10.453
chr2R	17675702	17676229	lox2	6.502
chr2R	17687946	17688414	CG4386	4.545
chr2R	17729041	17729163	CG4372	23.077
chr2R	17734106	17734504	CG4372	7.371
chr2R	17842591	17842772	CG13494	7.712
chr2R	17853351	17853844	CG34369	7.194
chr2R	17893997	17894425	CG34370	9.009
chr2R	17894273	17894593	CG34370	11.364
chr2R	17894405	17895121	CG34370	5.682
chr2R	17967664	17967998	synj	5.894
chr2R	17997521	17998455	Vrp1	4.036
chr2R	17999646	17999944	Vrp1	48.193
chr2R	18021079	18022021	CG34205	5.31
chr2R	18125135	18125246	dve	11.583
chr2R	18153112	18153392	dve	48.193

chr2R	18153153	18153744	dve	8.475
chr2R	18157402	18158004	dve	4.839
chr2R	18178346	18179014	CG5819	8.147
chr2R	18178524	18179026	CG5819	17.316
chr2R	18226458	18226970	CG11206	39.216
chr2R	18260459	18261287	Rtf1	5.141
chr2R	18260867	18261486	Rtf1	5.472
chr2R	18260997	18261502	Rtf1	6.452
chr2R	18261478	18262039	Rtf1	5.839
chr2R	18432448	18432907	px	10.526
chr2R	18499545	18500177	CG4329	4.41
chr2R	18499744	18500268	CG4329	6.969
chr2R	18544757	18545723	CG13510	4.695
chr2R	18570159	18570746	ppa	6.897
chr2R	18570405	18571188	ppa	4.422
chr2R	18595115	18595517	Obp58d	4.762
chr2R	18795845	18796244	nahoda	4.695
chr2R	18832101	18833083	CG3831	6.068
chr2R	18832161	18833087	CG3831	5.682
chr2R	18834418	18834900	CG32835	7.042
chr2R	19069564	19069732	CG34371	39.216
chr2R	19069590	19069985	CG34371	8.639
chr2R	19069590	19070449	CG34371	4.092
chr2R	19085857	19086498	CG34371	4.362
chr2R	19085984	19086522	CG34371	8.639
chr2R	19086490	19087437	CG34371	4.115
chr2R	19195167	19195584	Prosbeta5R	7.013
chr2R	19295951	19296897	CG9812	4.062
chr2R	19457922	19458495	apt	6.969
chr2R	19458187	19458531	apt	18.018
chr2R	19458398	19458750	apt	8.639
chr2R	19509447	19509966	CG4019	6.135
chr2R	19519133	19519313	retn	5.587
chr2R	19519174	19519928	retn	4.323
chr2R	19530473	19531238	retn	4.41
chr2R	19530562	19531309	retn	4
chr2R	19559659	19560072	Pde8	19.608
chr2R	19582013	19582267	CG30183	8.746
chr2R	19582148	19582278	CG30183	8.523
chr2R	19614486	19614876	CG11299	8.475
chr2R	19614854	19615107	CG11299	25.478
chr2R	19614861	19615391	CG11299	19.608
chr2R	19614868	19615426	CG11299	17.316
chr2R	19650144	19651022	CG9850	4.092
chr2R	19650890	19651069	CG9850	36.036
chr2R	19659936	19660527	CG9850	12.563
chr2R	19660516	19660678	CG9850	12.346
chr2R	19660519	19661041	CG9850	4.695
chr2R	19698670	19699514	CG5543	6.088
chr2R	19898675	19899433	Unc-89	4.499
chr2R	19902967	19903289	CG4324	9.592
chr2R	20106592	20106738	CG30419	5.31
chr2R	20161655	20161919	nvy	39.216
chr2R	20161655	20161940	nvy	5.045
chr2R	20171453	20172288	nvy	5.025
chr2R	20184835	20184987	CG3394	10.135
chr2R	20197767	20198384	betaTub60D	4.91
chr2R	20272357	20273224	mAcR-60C	6.969
chr2R	20293002	20293239	SerT	400
chr2R	20306895	20307072	prom	36.036
chr2R	20428425	20429205	CG4622	4.41
chr2R	20438435	20438743	CG4622	4.762
chr2R	20514402	20514758	CG13594	8.475
chr2R	20579744	20580064	ST6Gal	19.608
chr2R	20628264	20628947	CG30421	4.802
chr2R	20658950	20659309	Eps-15	11.364
chr2R	20741562	20741748	CG3650	142.857
chr2R	20818339	20818958	CG30427	5.997
chr2R	20874493	20875045	CG3829	5.807
chr2R	20952508	20952899	gsb	5.894
chr2R	20952819	20953185	gsb	6.452
chr2R	20952891	20953209	gsb	6.547
chr2R	20953201	20953535	gsb	7.371
chr2R	20953491	20954256	gsb	4
chr2R	20985914	20986866	CG16778	4.153
chr2R	21047715	21048174	CG34038	33.333
chr3L	123151	123670	Pk61C	4.695
chr3L	132868	133548	Pk61C	4.91
chr3L	428959	429081	CG13891	9.524
chr3L	428959	429206	CG13891	6.969

chr3L	590335	591030	CG17181	5.786
chr3L	1128230	1128983	bab2	4.742
chr3L	1132561	1133007	bab2	4.38
chr3L	1218574	1218716	LysP	11.152
chr3L	1549358	1549843	Cct1	6.088
chr3L	1567508	1568458	CG7879	4.261
chr3L	1635809	1635978	n-syb	10.135
chr3L	1942382	1943128	Mfap1	4.029
chr3L	2355306	2355485	CG13801	11.583
chr3L	2355457	2355822	CG13801	9.009
chr3L	2394983	2395782	CG13800	5.059
chr3L	2563000	2563894	msn	4.695
chr3L	2563878	2564126	msn	6.745
chr3L	2584914	2585449	msn	8.147
chr3L	2584914	2585518	msn	7.396
chr3L	2625328	2626167	Pxn	4.655
chr3L	2956236	2956462	CG9965	6.356
chr3L	2956438	2956917	CG9965	4.963
chr3L	2956438	2957204	CG9965	4.909
chr3L	2996409	2996871	CG2113	4.208
chr3L	3508257	3508475	ImpE2	5.682
chr3L	3567178	3568179	Eip63E	4.646
chr3L	3734479	3734690	CG32264	4.208
chr3L	3752678	3753517	CG32264	5.202
chr3L	3841529	3841908	enc	13.514
chr3L	4012349	4012504	CG14985	8.108
chr3L	4097082	4097215	CG14995	19.108
chr3L	4097082	4097372	CG14995	6.353
chr3L	4141753	4142124	Akh	5.587
chr3L	4141753	4142551	Akh	4.499
chr3L	4219852	4220061	CG1332	7.712
chr3L	4240701	4241269	CG14997	4.464
chr3L	4305282	4305581	dyl	10.791
chr3L	4328194	4328521	Cip4	4.438
chr3L	4417001	4417693	CG11347	4.498
chr3L	4431859	4432802	nAcRbeta-64B	4.955
chr3L	4448240	4448713	CG12607	4.208
chr3L	4812025	4812744	Dhc64C	4.155
chr3L	4839719	4839979	CG13707	5.587
chr3L	4839719	4840202	CG13707	5.27
chr3L	4839971	4840334	CG13707	4.762
chr3L	4932084	4932205	Con	5.682
chr3L	4946803	4947509	Con	4.322
chr3L	4955320	4955771	Con	5.226
chr3L	4992738	4993104	CG32232	7.194
chr3L	4993092	4993381	CG32232	7.449
chr3L	5101754	5101939	CG34047	5.146
chr3L	5156549	5157117	shep	4.955
chr3L	5500496	5501244	CG34342	5.396
chr3L	5662047	5662589	sif	4.963
chr3L	5746863	5747235	Ubp64E	8.108
chr3L	5746863	5747406	Ubp64E	5.472
chr3L	5746863	5747675	Ubp64E	4.322
chr3L	5870779	5871060	CG18586	4.566
chr3L	5870989	5871458	CG18586	5.146
chr3L	5887394	5888068	Pole2	4.362
chr3L	5969469	5970058	CG10479	5.333
chr3L	6011737	6012256	CG32406	5.513
chr3L	6081259	6081467	CG13293	17.045
chr3L	6106689	6106807	Ets65A	14.085
chr3L	6298548	6299186	Or65a	4.727
chr3L	6341631	6342268	Sfp65A	4.104
chr3L	6630862	6631481	Glu-RI	6.502
chr3L	6631388	6632018	Glu-RI	7.102
chr3L	6687577	6688325	SP1173	4.91
chr3L	6689026	6689891	SP1173	4.155
chr3L	6690511	6691144	SP1173	4.762
chr3L	6690934	6691377	SP1173	4.983
chr3L	6837019	6837982	vvl	5.059
chr3L	6837722	6838155	vvl	4.762
chr3L	6920529	6920786	CG14820	7.371
chr3L	6937217	6937378	tow	21.583
chr3L	6937217	6937387	tow	20.619
chr3L	7154190	7155092	CG17742	4.615
chr3L	7154929	7155391	CG17742	9.695
chr3L	7154929	7155499	CG17742	7.715
chr3L	7178671	7178806	CG42256	12.987
chr3L	7225536	7225798	CG14826	11.364
chr3L	7225536	7225980	CG14826	8.85
chr3L	7225536	7226217	CG14826	7.042

chr3L	7334727	7335240	lark	4.049
chr3L	7341592	7341945	qm	6.479
chr3L	7462032	7462323	Tsp66A	6.11
chr3L	7481381	7481603	mthl6	5.146
chr3L	7481587	7482122	mthl6	5.869
chr3L	7481587	7482175	mthl6	5.682
chr3L	7506713	7507250	CG7546	4.193
chr3L	7592865	7593067	CG33275	12.987
chr3L	7600452	7601070	CG33275	4.839
chr3L	7784542	7785268	CG32369	7.859
chr3L	7807380	7807688	Pdp1	9.524
chr3L	7852808	7853205	Pdp1	12.285
chr3L	7853159	7853859	Pdp1	6.068
chr3L	7899067	7899483	pbl	7.576
chr3L	7951595	7952209	exex	4.617
chr3L	7951793	7952056	exex	7.895
chr3L	7951956	7952209	exex	10.791
chr3L	7953099	7953586	exex	5.78
chr3L	8052894	8053443	bip1	4.908
chr3L	8053050	8053622	bip1	5.333
chr3L	8053050	8053845	bip1	4.78
chr3L	8204373	8204612	CG8006	4.63
chr3L	8489086	8489428	CG6902	9.009
chr3L	8489086	8489521	CG6902	8.811
chr3L	8518320	8518937	foi	5.102
chr3L	8518901	8519618	foi	5.241
chr3L	8550155	8550753	rhea	6.969
chr3L	8635690	8636354	Cpr66D	4.193
chr3L	8748775	8749219	Fhos	9.009
chr3L	8819157	8819578	dally	4.695
chr3L	8819157	8819815	dally	4
chr3L	9066993	9067647	CG4942	4
chr3L	9282659	9282907	Glu-RIB	7.538
chr3L	9282659	9283201	Glu-RIB	5.472
chr3L	9497273	9497384	path	7.538
chr3L	9497347	9497455	path	6.757
chr3L	9516624	9516931	CG33700	8.639
chr3L	9684740	9684870	CG6767	21.583
chr3L	9831200	9831561	Cdk8	4.566
chr3L	9942787	9943371	CG34356	6.745
chr3L	10051654	10052045	dpr6	7.895
chr3L	10177849	10178654	dpr10	5.917
chr3L	10235128	10235419	Or67c	4.908
chr3L	10272194	10272927	Or67d	4.038
chr3L	10272905	10273498	Or67d	4.323
chr3L	10463258	10463547	CG32063	6.452
chr3L	10660584	10661588	simj	4.468
chr3L	10664830	10665710	simj	5.575
chr3L	10666710	10666936	simj	13.072
chr3L	10666888	10667081	simj	17.045
chr3L	10692837	10693007	NijA	17.316
chr3L	10692837	10693737	NijA	6.748
chr3L	10804364	10805282	CG12523	4.955
chr3L	10804684	10805110	CG12523	9.524
chr3L	10804684	10805282	CG12523	8.639
chr3L	10819153	10819707	tna	7.634
chr3L	10819153	10819958	tna	6.4
chr3L	10949752	10950054	CG34050	4.498
chr3L	10955663	10956218	CG14147	6.11
chr3L	10997695	10998307	klu	4.532
chr3L	11162489	11163213	wls	5.839
chr3L	11172788	11173004	GlcAT-P	6
chr3L	11172949	11173529	GlcAT-P	5.513
chr3L	11359788	11360003	CG6163	7.194
chr3L	11359921	11360726	CG6163	6.452
chr3L	11506977	11507817	Sgs3	4.278
chr3L	11525874	11526578	Mob2	4.208
chr3L	11708399	11708761	CG14132	6.547
chr3L	11864451	11864952	CG5906	6.547
chr3L	11913663	11913958	CG11588	7.194
chr3L	11913756	11914284	CG11588	7.042
chr3L	12117340	12117520	yps	11.494
chr3L	12283596	12283975	CG4328	4.839
chr3L	12300350	12300612	CG4328	4.38
chr3L	12300502	12300954	CG4328	7.194
chr3L	12300502	12301132	CG4328	5.917
chr3L	12305290	12305494	CG4328	11.152
chr3L	12314358	12315199	CG32105	7.08
chr3L	12314712	12315559	CG32105	5.54
chr3L	12315012	12315798	CG32105	4.854

chr3L	12339326	12339581	GRHRII	5.495
chr3L	12420581	12420861	toe	4
chr3L	12457913	12458121	eyg	4.646
chr3L	12464845	12465249	CG10616	4.499
chr3L	12465197	12465851	CG10616	5.764
chr3L	12682342	12682977	mirr	4.104
chr3L	12799269	12800223	CG11006	5.357
chr3L	12821024	12821691	CG10960	7.712
chr3L	12887600	12888065	CG14118	6.11
chr3L	12963758	12964425	CG10748	4.63
chr3L	12967834	12968022	CG10749	5.059
chr3L	13054815	13055253	CG34428	5.931
chr3L	13117123	13117942	trn	5.31
chr3L	13150754	13151412	snky	4.092
chr3L	13182058	13182870	snky	4.963
chr3L	13250734	13251100	caps	4.323
chr3L	13264448	13264649	caps	8.523
chr3L	13659453	13660087	bru-3	5.869
chr3L	13659961	13660551	bru-3	4.464
chr3L	13659961	13660750	bru-3	4.32
chr3L	13743893	13744019	CG34243	5.587
chr3L	13820872	13821069	CG8757	11.152
chr3L	13898946	13899403	Rgl	4.104
chr3L	13930491	13930668	CG32137	12.448
chr3L	13930491	13930702	CG32137	10.283
chr3L	13930491	13931464	CG32137	6.427
chr3L	13930553	13931554	CG32137	5.869
chr3L	13935384	13935775	CG32137	6.479
chr3L	13941029	13941736	CG32137	10.283
chr3L	14034586	14035076	Hsc70Cb	9.259
chr3L	14091870	14092363	Fbp1	6.26
chr3L	14094840	14095082	Sox21a	6.11
chr3L	14095011	14095469	Sox21a	5.587
chr3L	14119150	14119537	Sox21b	4.104
chr3L	14216162	14217158	nuf	4.695
chr3L	14427273	14427944	bbg	5.226
chr3L	14512813	14513154	CG4613	5.894
chr3L	14582204	14582618	HGTX	6.969
chr3L	14583588	14584333	HGTX	4.963
chr3L	14584275	14584525	HGTX	10.135
chr3L	14618308	14619099	CG9628	5.146
chr3L	14618850	14619657	CG9628	4.695
chr3L	14772091	14772601	bmm	5.396
chr3L	14814750	14815713	CG17839	8.403
chr3L	14815520	14815814	CG17839	7.712
chr3L	14847535	14847727	CG17839	9.828
chr3L	14847535	14848333	CG17839	4.955
chr3L	14856183	14856701	CG17839	6.098
chr3L	14856413	14857027	CG17839	5.401
chr3L	14943391	14943737	BobA	5.682
chr3L	14969897	14970681	Ocho	7.282
chr3L	14992693	14993347	Prosbeta2	5.587
chr3L	15328258	15328415	Toll-6	10.453
chr3L	15368407	15368971	CG33259	7.895
chr3L	15458677	15459573	CG7804	4.575
chr3L	15459549	15459818	CG7804	7.576
chr3L	15480209	15480500	ran-like	6.479
chr3L	15480209	15480625	ran-like	5.54
chr3L	15494895	15495370	CG7272	8.993
chr3L	15497021	15497300	CG7857	6.26
chr3L	15559340	15559608	CG6498	4.762
chr3L	15656286	15657242	Eig71Ek	4.655
chr3L	15671721	15671997	CG7304	5.472
chr3L	15671985	15672551	CG7304	4.077
chr3L	15720596	15720887	comm	4.762
chr3L	15738234	15738481	comm	8.996
chr3L	15914284	15914862	Pka-C3	4.104
chr3L	16033745	16033942	th	15.464
chr3L	16033745	16034326	th	7.194
chr3L	16043039	16043629	th	5.764
chr3L	16058400	16059034	Mbs	12
chr3L	16058400	16059376	Mbs	4.854
chr3L	16059026	16059576	Mbs	4.323
chr3L	16275329	16276198	CG13049	5.202
chr3L	16289542	16290168	CG4962	4.323
chr3L	16290100	16290612	CG4962	4.983
chr3L	16328003	16328348	CG13056	4.91
chr3L	16335782	16336166	CG4998	6.84
chr3L	16443644	16443847	CG33158	5.61
chr3L	16504876	16505459	CG42513	7.825

chr3L	16505398	16505711	CG42513	7.013
chr3L	16505398	16505968	CG42513	5.682
chr3L	16651878	16652521	Baldspot	5.472
chr3L	16661018	16661248	Galpha73B	5.396
chr3L	16863689	16864251	Lmpt	4.208
chr3L	16885804	16886319	Lmpt	6.969
chr3L	16886283	16886616	Lmpt	4.963
chr3L	16892859	16893039	Lmpt	10.453
chr3L	16937385	16937810	CG13027	4.63
chr3L	16949801	16950337	Nc73EF	5.587
chr3L	17122035	17122328	Rbp6	6
chr3L	17341139	17341588	Mip	6.203
chr3L	17387044	17387201	blot	5.894
chr3L	17453913	17454874	CG7603	4.252
chr3L	17565342	17565597	Eip74EF	4.104
chr3L	17626325	17626470	CG7497	4.695
chr3L	17663069	17663922	CG34251	4.91
chr3L	17663832	17664446	CG34251	6.237
chr3L	17663914	17664706	CG34251	5.78
chr3L	17697024	17697975	Ccn	4
chr3L	17969143	17969696	Eip75B	6.667
chr3L	17969637	17969929	Eip75B	6.645
chr3L	17969637	17970167	Eip75B	5.489
chr3L	17969637	17970354	Eip75B	4.848
chr3L	18002310	18003000	Eip75B	5.141
chr3L	18002916	18003477	Eip75B	13.072
chr3L	18003457	18004212	Eip75B	4.155
chr3L	18128023	18128467	Cyp312a1	6.502
chr3L	18163344	18163639	W	10.799
chr3L	18163344	18164208	W	5.888
chr3L	18344382	18344631	rpr	11.152
chr3L	18418356	18418736	skl	14.388
chr3L	18418356	18419029	skl	8.183
chr3L	18437461	18437704	skl	10.811
chr3L	18504760	18504927	AlCR2	12.698
chr3L	18548838	18549485	star1	4.438
chr3L	18680018	18680759	Cyp12c1	7.102
chr3L	18748947	18749219	ftz-f1	17.045
chr3L	18802243	18802522	CG14073	5.083
chr3L	18819214	18819652	Cat	4
chr3L	19100342	19100534	CG14082	8.639
chr3L	19101662	19102638	CG14082	6.645
chr3L	19166598	19167178	fz2	4.63
chr3L	19383728	19384039	CG32206	4.049
chr3L	19429378	19429494	Chd3	10.453
chr3L	19429609	19429901	Chd3	9.195
chr3L	19511889	19512682	Cpr76Ba	6.897
chr3L	19517561	19517805	Cpr76Bc	5.839
chr3L	19685192	19685812	verm	4.237
chr3L	19826482	19826739	trc	6.356
chr3L	20245963	20246136	CG13814	12.698
chr3L	20274947	20275570	gogo	7.802
chr3L	20275447	20276156	gogo	6.657
chr3L	20275447	20276226	gogo	6.506
chr3L	20275451	20276382	gogo	4.864
chr3L	20303559	20304264	polo	5.682
chr3L	20519639	20519968	CG4858	7.042
chr3L	20679943	20680222	kni	4.839
chr3L	20692956	20693766	kni	4.049
chr3L	20693687	20694153	kni	10.791
chr3L	20783996	20784488	Six4	5.61
chr3L	20928008	20928737	fng	4.155
chr3L	21041778	21042678	siz	4.735
chr3L	21072572	21072709	ko	14.706
chr3L	21266774	21266985	AcCoAS	9.804
chr3L	21364728	21365283	CG32440	6.479
chr3L	21641930	21642622	CG33291	4.278
chr3L	21762705	21762883	CG7370	7.042
chr3L	21970523	21970740	CG7470	5.839
chr3L	22036327	22036793	TyrR	6.353
chr3L	22036327	22037026	TyrR	4.594
chr3L	22085977	22086938	msopa	4.545
chr3L	22135149	22135557	olf413	5.764
chr3L	22326625	22327028	Ten-m	5.333
chr3L	22446949	22447309	CG11449	5.682
chr3L	22449444	22449852	CG11449	4.735
chr3L	22490509	22490858	CG12377	4.695
chr3L	22536754	22536972	CG11404	7.449
chr3L	22536677	22537535	CG11404	4.024
chr3L	22603902	22604308	CG6914	4.598

chr3L	22643943	22644239	CG33771	5.839
chr3L	22703155	22704024	CG11370	4.38
chr3L	22779743	22780274	SPoCk	7.712
chr3L	22782136	22782916	CG14448	6.479
chr3L	23023493	23024046	nrm	10.135
chr3L	23956132	23956827	CG40470	4.036
chr3R	165870	166119	CG1103	9.009
chr3R	167005	167730	CG1103	4.646
chr3R	261728	262406	CG1074	5.472
chr3R	274370	274850	CG31522	6.349
chr3R	277518	278130	CG31522	4.155
chr3R	277518	278222	CG31522	4
chr3R	660303	661180	CG14659	4.908
chr3R	679576	680011	opa	4.695
chr3R	1101003	1101605	l(3)82Fd	4.695
chr3R	1213109	1213856	kkv	4.208
chr3R	1237319	1238266	Or83b	4.208
chr3R	1238222	1238675	CG14669	4.362
chr3R	1318768	1318914	CG31547	8.31
chr3R	1319023	1319750	CG31547	4.598
chr3R	1367955	1368188	CG2519	23.077
chr3R	1473357	1473704	MTA1-like	5.61
chr3R	1519744	1520464	plx	4.983
chr3R	1597839	1598445	CG2082	6.757
chr3R	1889106	1889512	CG15580	8.646
chr3R	1908527	1908771	Or83c	6.608
chr3R	1998191	1998459	Osi1	9.677
chr3R	1998191	1999037	Osi1	4.799
chr3R	2061822	2062640	Osi6	4.355
chr3R	2130819	2131261	Osi16	4.261
chr3R	2146531	2146754	Osi17	6.427
chr3R	2146742	2146922	Osi17	6.237
chr3R	2146742	2146976	Osi17	4.854
chr3R	2239952	2240168	gpp	9.828
chr3R	2239952	2240374	gpp	5.144
chr3R	2245910	2246216	gpp	5.333
chr3R	2329972	2330257	CG15186	4.38
chr3R	2525381	2526173	pncr002:3R	4.639
chr3R	2565668	2566447	pb	5.931
chr3R	2608915	2609434	Dfd	5.997
chr3R	2745668	2746235	Antp	4.963
chr3R	2937175	2937693	Alh	4.41
chr3R	2938645	2939200	Alh	9.677
chr3R	2968635	2969037	CG14610	12.012
chr3R	2994981	2995707	sas	12.012
chr3R	2995600	2996607	sas	4.049
chr3R	3005820	3006410	sas	4.537
chr3R	3109554	3110428	rn	5.472
chr3R	3151053	3151516	CG10029	6.356
chr3R	3215484	3216317	Ir84a	4.695
chr3R	3331090	3331385	CG1287	10.453
chr3R	3575096	3575785	pyd3	6.757
chr3R	3639325	3639830	CG31473	4.104
chr3R	3851992	3852402	CG2747	5.083
chr3R	3975341	3975522	grn	9.195
chr3R	3975341	3975786	grn	8
chr3R	3978441	3978655	grn	6.237
chr3R	4020770	4021200	CheA84a	5.641
chr3R	4049815	4050363	CG18249	4.077
chr3R	4102638	4102804	ato	9.804
chr3R	4102638	4102927	ato	9.39
chr3R	4338262	4339015	Or85c	4.438
chr3R	4403133	4403663	Cenp-C	6
chr3R	4476135	4477056	Mkk4	4.563
chr3R	4568470	4569005	CG9801	5.202
chr3R	4749838	4750820	pyd	5.78
chr3R	4858119	4859016	neur	4.193
chr3R	5220388	5220996	Fps85D	11.99
chr3R	5268610	5269097	ps	4.323
chr3R	5275729	5276699	CG9362	6.518
chr3R	5277458	5277826	CG9362	5.472
chr3R	5277458	5278023	CG9362	5.453
chr3R	5277458	5278400	CG9362	5.357
chr3R	5307214	5307346	CG16779	12.987
chr3R	5427077	5427227	CG8312	12
chr3R	5427077	5427814	CG8312	6.427
chr3R	5471944	5472295	Dh	14.706
chr3R	5473197	5473592	Dh	4.839
chr3R	5473408	5473833	Dh	6.11
chr3R	5569129	5569665	CG34409	5.78

chr3R	5645486	5645967	CG9458	4.38
chr3R	5677558	5678105	Teh1	6.173
chr3R	5682873	5683180	Teh1	7.716
chr3R	5682873	5683534	Teh1	4.264
chr3R	5688552	5688923	Teh1	4.963
chr3R	5689683	5690190	Teh1	6.417
chr3R	5707220	5707965	CG34360	4.029
chr3R	6092685	6092852	CG11870	5.78
chr3R	6093929	6094123	CG11870	6.356
chr3R	6118388	6118569	CG11870	6.479
chr3R	6258562	6258727	Cyp12e1	17.316
chr3R	6391560	6391829	hth	12.853
chr3R	6416488	6417440	hth	4.036
chr3R	6419496	6420159	hth	4.154
chr3R	6433169	6434025	hth	4.029
chr3R	6433779	6434478	hth	4.464
chr3R	6517123	6517663	Skeletor	4.566
chr3R	6571118	6571523	Takr86C	5.226
chr3R	6840190	6840769	CG34114	7.538
chr3R	6840334	6840501	CG34114	9.804
chr3R	6840357	6840769	CG34114	11.152
chr3R	6845562	6846486	CG34114	4.208
chr3R	7015706	7015986	CG18577	4.695
chr3R	7124382	7124765	CG31386	5.682
chr3R	7124726	7124956	CG31386	4.963
chr3R	7196909	7197346	pros	10.135
chr3R	7214222	7214483	pros	4.91
chr3R	7214448	7214904	pros	5.624
chr3R	7316922	7317150	dpr5	4.91
chr3R	7393135	7393808	CG6783	4.5
chr3R	7417951	7418288	Jupiter	4.908
chr3R	7418187	7418850	Jupiter	4.695
chr3R	7428790	7428943	Jupiter	7.895
chr3R	7556408	7556918	CG12594	4.104
chr3R	7556905	7557515	CG12594	5.059
chr3R	7596614	7596962	l(3)neo38	5.764
chr3R	7678663	7679310	CG6959	5.226
chr3R	7734433	7735140	CG34307	5.396
chr3R	7876818	7877107	CG14739	5.059
chr3R	7927251	7927494	dpr17	20.27
chr3R	7927251	7927735	dpr17	13.85
chr3R	8171724	8172653	CG10038	5.083
chr3R	8172620	8173194	CG10038	12
chr3R	8395821	8396186	Octbeta2R	5.894
chr3R	8557260	8557604	CG5724	6.088
chr3R	8651703	8651915	CG31345	4.839
chr3R	8657679	8658038	beat-Va	8
chr3R	8680509	8681023	CG10126	4.864
chr3R	8680654	8680843	CG10126	5.682
chr3R	8680820	8681023	CG10126	12.448
chr3R	8686732	8687570	CG10126	4.983
chr3R	8691020	8691171	CG10126	10.791
chr3R	8784044	8784280	granny-smith	4.63
chr3R	8928781	8929555	timeout	5.682
chr3R	8964169	8964695	timeout	6.757
chr3R	8964555	8964831	timeout	8.523
chr3R	8998815	8998928	CG8138	46.154
chr3R	9033721	9034020	CG8483	8.306
chr3R	9189968	9190145	poly	8.108
chr3R	9190074	9190766	poly	4.32
chr3R	9201976	9202930	CG9813	4.208
chr3R	9203736	9204027	CG9813	6.897
chr3R	9335368	9335699	CG12538	4.155
chr3R	9362646	9363161	CG31337	5.453
chr3R	9640489	9640644	tal-1A	17.964
chr3R	9670696	9671137	CG31495	5.31
chr3R	9681387	9681751	CG14362	11.583
chr3R	9681457	9681830	CG14362	9.524
chr3R	9681387	9682123	CG14362	5
chr3R	9712680	9712937	E5	6.26
chr3R	9712787	9713452	E5	4.908
chr3R	9742304	9742855	ems	5.146
chr3R	9751645	9752592	Art9	4.454
chr3R	9815059	9815403	rdx	4.323
chr3R	9922789	9923084	CG9920	12
chr3R	9997507	9998317	DopR	5.025
chr3R	10250955	10251272	CG34388	7.538
chr3R	10250955	10251448	CG34388	5.54
chr3R	10466922	10467186	CG7886	5.146
chr3R	10467138	10467327	CG7886	8.31

chr3R	10488088	10488324	Rad17	5.78
chr3R	10872566	10872894	RpL10Aa	11.99
chr3R	10899187	10899615	dpr9	6.042
chr3R	10901485	10901716	dpr9	4.438
chr3R	10901664	10902372	dpr9	4.839
chr3R	11126887	11127353	Tm1	11.152
chr3R	11129501	11129610	Tm1	12.448
chr3R	11136288	11137255	Tm2	5.472
chr3R	11297867	11298371	CG14869	6.452
chr3R	11505946	11506743	pxb	6.281
chr3R	11506717	11506930	pxb	10.453
chr3R	11506717	11506968	pxb	8.811
chr3R	11654376	11654548	rec	6.356
chr3R	11671521	11671839	CG31150	6.757
chr3R	11724417	11725138	glob1	4.802
chr3R	11765177	11766001	Sap47	4.292
chr3R	11821366	11821577	srp	4.438
chr3R	11969307	11969478	Sb	5.495
chr3R	12116724	12117516	gish	5.495
chr3R	12117008	12117798	gish	5.398
chr3R	12216922	12217684	ss	5.059
chr3R	12369565	12370418	CG42342	4.839
chr3R	12370312	12370635	CG42342	7.859
chr3R	12411217	12412034	Scp2	5.022
chr3R	12768569	12768775	Abd-B	4.983
chr3R	12787863	12788455	Abd-B	5.045
chr3R	12798431	12799347	CG14909	4.802
chr3R	12836361	12836995	CG8907	4.63
chr3R	12920356	12921242	cher	4.104
chr3R	13192607	13192948	beat-IIa	4.63
chr3R	13392637	13392937	Hmx	5.61
chr3R	13410168	13410717	CG7587	5.241
chr3R	13727669	13728056	Rim	11.662
chr3R	13852636	13853077	CG7794	4.745
chr3R	13857284	13858056	CG7794	4.745
chr3R	13858042	13858240	CG7794	8.31
chr3R	13858042	13858366	CG7794	6.349
chr3R	13885074	13885464	htl	6.281
chr3R	13885368	13885611	htl	8.316
chr3R	13885368	13885988	htl	5.453
chr3R	13902140	13902464	CG14317	6.757
chr3R	13915032	13915793	sr	5.837
chr3R	13915760	13916140	sr	9.009
chr3R	13915760	13916255	sr	8.475
chr3R	13920475	13920621	sr	11.583
chr3R	13928588	13929035	sr	4.762
chr3R	14070738	14071209	14-3-3epsilon	4.499
chr3R	14071114	14071632	14-3-3epsilon	5.146
chr3R	14119480	14120332	l(3)05822	5.764
chr3R	14161324	14161942	CG31235	5.31
chr3R	14245139	14245561	fru	11.261
chr3R	14245553	14246197	fru	9.592
chr3R	14248598	14248753	fru	9.259
chr3R	14266986	14267256	fru	7.496
chr3R	14266986	14267838	fru	4.874
chr3R	14269942	14270781	fru	6.452
chr3R	14270754	14270915	fru	8.108
chr3R	14712422	14713265	CG14298	4.115
chr3R	14721801	14722128	CG14297	5.146
chr3R	14745641	14745818	Xrp1	8.639
chr3R	14787777	14788468	CG42613	4
chr3R	14793874	14794585	CG42613	6.317
chr3R	14798631	14799000	CG42613	5.764
chr3R	14942629	14943595	CG6040	4.983
chr3R	15071419	15072096	unc79	4.498
chr3R	15164129	15164253	Dl	8.108
chr3R	15313213	15314076	Dys	5.398
chr3R	15313862	15314130	Dys	9.009
chr3R	15324859	15325298	Dys	5.917
chr3R	15495682	15495917	CG7432	7.194
chr3R	15643170	15643820	bnl	4.104
chr3R	15662545	15663159	bnl	6.897
chr3R	15696736	15697471	CG4562	4.802
chr3R	15728209	15728576	CG4538	5.059
chr3R	16063859	16064154	CG34139	4.104
chr3R	16066818	16067752	CG34139	6.349
chr3R	16068036	16069024	CG34139	6.05
chr3R	16157495	16158025	Sirt2	4.802
chr3R	16224877	16225089	mun	8.523
chr3R	16225721	16226191	mun	4.566

chr3R	16491332	16491596	Cpr92F	7.371
chr3R	16509585	16510376	Oamb	9.333
chr3R	16575594	16576513	CG42322	4
chr3R	16576505	16577166	CG42322	16.216
chr3R	16576505	16577320	CG42322	10.811
chr3R	16577475	16577731	CG42322	10.453
chr3R	16577679	16578152	CG42322	7.712
chr3R	16601066	16601460	CG17838	4.762
chr3R	16623355	16623731	CG17838	5.059
chr3R	16625779	16626410	CG17838	4.454
chr3R	16676670	16676847	RpS30	7.194
chr3R	16783534	16783995	Atpalpha	5.682
chr3R	16783724	16784460	Atpalpha	6.281
chr3R	16865998	16866431	Dhc93AB	4.323
chr3R	17114270	17114885	SIFR	7.013
chr3R	17166023	17166816	CG16791	4.155
chr3R	17167092	17167371	CG16791	5.31
chr3R	17219899	17220257	CG6475	9.39
chr3R	17227902	17228674	CG6475	4.155
chr3R	17515932	17516143	CG31176	6.11
chr3R	17516268	17516623	CG31176	5.807
chr3R	17516268	17516937	CG31176	5.109
chr3R	17521863	17522423	CG31176	5.31
chr3R	17521969	17522964	CG31176	4.104
chr3R	17622337	17622762	Caki	6.427
chr3R	17622925	17623370	Caki	6.897
chr3R	17622925	17623641	Caki	4.907
chr3R	17646250	17646385	Caki	7.712
chr3R	17761522	17762330	Eip93F	4.029
chr3R	17789677	17789958	Eip93F	9.576
chr3R	17789812	17790491	Eip93F	5.821
chr3R	17791604	17791870	Eip93F	7.61
chr3R	17842198	17842842	CG6439	5.472
chr3R	18169950	18170434	CG5386	4.362
chr3R	18173135	18173521	CG7077	4.695
chr3R	18229016	18229193	CG13856	20.27
chr3R	18229016	18229910	CG13856	4.362
chr3R	18257944	18258464	CG13847	5.083
chr3R	18308519	18309015	Nrx-1	4
chr3R	18404128	18404698	CG33110	4
chr3R	18576823	18577198	CG7029	7.712
chr3R	18646858	18647331	CG13840	6.745
chr3R	18662696	18663304	CG4704	4.802
chr3R	18669324	18669812	CG4704	4.955
chr3R	18671471	18671742	CG4704	4.208
chr3R	18674304	18675246	CG4704	4.355
chr3R	18783408	18783656	klg	5.587
chr3R	18810681	18811050	Nha2	7.102
chr3R	18810795	18811043	Nha2	7.712
chr3R	18811007	18811642	Nha2	4.092
chr3R	18884197	18885177	sav	4.108
chr3R	19263879	19264407	CG4374	4.566
chr3R	19264362	19264651	CG4374	7.712
chr3R	19316981	19317556	Ir94h	6.925
chr3R	19317490	19317764	Ir94h	5.472
chr3R	19374705	19374956	CG10164	4.566
chr3R	19386168	19386466	beat-IV	8.85
chr3R	19406427	19406572	beat-IV	15.464
chr3R	19406929	19407138	beat-IV	14.388
chr3R	19411574	19411804	CG10182	6.861
chr3R	19420818	19421567	CG16723	4.963
chr3R	19506209	19506541	eIF-3p66	5.025
chr3R	19542573	19542941	nau	4.63
chr3R	19692177	19692408	Pli	8.475
chr3R	19692177	19692436	Pli	7.825
chr3R	19692177	19692876	Pli	5.445
chr3R	19827638	19828089	KrT95D	14.205
chr3R	19900658	19900929	4EHP	7.955
chr3R	20084274	20084955	jar	5.54
chr3R	20306411	20307084	nAcRalpha-96Ab	4.545
chr3R	20315040	20315365	nAcRalpha-96Ab	4.104
chr3R	20434979	20435466	mld	5.396
chr3R	20435243	20435531	mld	4.498
chr3R	20465514	20465646	CG5794	8.746
chr3R	20488179	20488598	Ppox	4.208
chr3R	20530072	20530762	slo	7.042
chr3R	20530430	20531229	slo	6.757
chr3R	20549943	20550067	tok	8.523
chr3R	20595742	20596415	CG13631	4.104

chr3R	20620671	20621114	Ets96B	9.634
chr3R	20620671	20621410	Ets96B	6.098
chr3R	20649591	20649796	niki	8.31
chr3R	20649706	20649836	niki	7.895
chr3R	20723782	20724644	CG13643	4.636
chr3R	20903890	20904872	CG11920	8.216
chr3R	21180942	21181629	Fur1	5.54
chr3R	21181335	21181515	Fur1	19.108
chr3R	21181335	21181629	Fur1	12.853
chr3R	21181335	21181697	Fur1	10.292
chr3R	21181335	21181760	Fur1	8.13
chr3R	21188352	21188646	Fur1	6.925
chr3R	21337084	21337249	CG5111	5.396
chr3R	21543218	21543658	LpR2	5.764
chr3R	21593234	21593900	CG17198	4.468
chr3R	21593778	21593893	CG17198	10.135
chr3R	21593745	21594191	CG17198	7.538
chr3R	21741144	21741478	CG42235	9.195
chr3R	21829198	21829830	HLHmbeta	7.716
chr3R	21841859	21842512	m2	4.38
chr3R	22105129	22105441	CG6154	10.791
chr3R	22105129	22106019	CG6154	4.077
chr3R	22175815	22176001	CG33970	7.538
chr3R	22488463	22488838	beat-VII	4.762
chr3R	22594220	22594589	CG14247	4.049
chr3R	22700735	22701069	Rb97D	5.083
chr3R	22700735	22701187	Rb97D	4.5
chr3R	22701018	22701717	Rb97D	4.036
chr3R	22746703	22746960	sda	6
chr3R	22781437	22782222	CG6330	4.155
chr3R	22794877	22795033	CG5521	16.216
chr3R	22848651	22849035	CG6277	4.762
chr3R	23020862	23021206	Ser	7.371
chr3R	23023485	23023747	Ser	6.452
chr3R	23024121	23024697	Ser	4.908
chr3R	23163337	23163694	CG42534	5.587
chr3R	23263704	23264703	side	4.839
chr3R	23312041	23312878	Gr98a	5.472
chr3R	23441585	23442095	CG5612	7.449
chr3R	23441922	23442232	CG5612	6.608
chr3R	23474018	23474314	tau	4.983
chr3R	23541106	23541290	CG12877	6.897
chr3R	23610222	23610487	CG34353	4.566
chr3R	23614347	23614596	CG34353	17.045
chr3R	23614347	23614927	CG34353	4.193
chr3R	23620770	23621231	CG34353	4.104
chr3R	23754794	23755098	CG5508	9.009
chr3R	23783470	23783832	CG4884	4.049
chr3R	24017535	24017769	CG34354	5.333
chr3R	24100897	24101008	CG34436	11.152
chr3R	24192039	24192379	Or98b	7.013
chr3R	24330924	24331444	Dhc98D	4.438
chr3R	24362969	24363149	Ppn	7.895
chr3R	24510479	24510832	CG9990	8.475
chr3R	24608260	24608415	CG34295	8.108
chr3R	24743976	24744984	Doa	6.757
chr3R	24744923	24745074	Doa	12.448
chr3R	24744923	24745129	Doa	10.283
chr3R	24794749	24795000	CG14521	4.498
chr3R	25030103	25030394	CG14508	10.811
chr3R	25054148	25054472	CG15817	10.799
chr3R	25174633	25175011	Cnx99A	4.036
chr3R	25385815	25386078	Dr	5.495
chr3R	25476851	25477000	DopR2	6.356
chr3R	25476976	25477226	DopR2	5.202
chr3R	25477202	25477929	DopR2	4.32
chr3R	25508461	25509106	Gycalpha99B	4.468
chr3R	25515317	25515538	Obp99c	6.897
chr3R	25515317	25516118	Obp99c	4.154
chr3R	25525960	25526278	dmrt99B	5.78
chr3R	25835709	25836647	Nlp	4.292
chr3R	26085322	26085818	CG18404	4.438
chr3R	26085803	26086001	CG18404	9.804
chr3R	26085803	26086296	CG18404	7.326
chr3R	26085803	26086494	CG18404	5.869
chr3R	26108882	26109633	hdc	4.208
chr3R	26109522	26110017	hdc	5.78
chr3R	26109522	26110191	hdc	4.193
chr3R	26183458	26183626	hdc	4.38
chr3R	26188367	26188684	hdc	5.097

chr3R	26214714	26215533	Fer2LCH	4.049
chr3R	26262374	26262734	CG15537	5.396
chr3R	26546831	26547533	CG1340	4.5
chr3R	26555065	26555263	CG11313	11.583
chr3R	26555065	26555794	CG11313	5.888
chr3R	26661279	26661459	CG15544	9.259
chr3R	26661565	26661687	CG15544	8.746
chr3R	26683550	26684350	tll	4.284
chr3R	26691739	26692188	Cpr100A	7.895
chr3R	26692176	26692520	Cpr100A	12
chr3R	26749747	26750113	Ptx1	4.208
chr3R	26782169	26782745	CG15548	5.398
chr3R	26847475	26848082	CG33773	4.104
chr3R	26866687	26867287	CanA1	11.08
chr3R	26895090	26895679	Sox100B	4.498
chr3R	27062927	27063358	CG31005	5.568
chr3R	27087939	27088272	CG18673	7.712
chr3R	27089150	27089601	CG18673	4.63
chr3R	27094788	27095337	CG15555	4.498
chr3R	27094788	27095518	CG15555	4.036
chr3R	27094788	27095705	CG15555	4.029
chr3R	27114846	27115037	CG11340	18.587
chr3R	27114846	27115598	CG11340	11.561
chr3R	27114846	27115847	CG11340	9.576
chr3R	27192499	27192647	gskt	5.495
chr3R	27192639	27193088	gskt	6.237
chr3R	27196952	27197404	gskt	6.757
chr3R	27436758	27437150	Med	5.682
chr3R	27457913	27458029	pasha	10.135
chr3R	27467495	27467746	kek6	9.195
chr3R	27530248	27530683	CG34046	4.545
chr3R	27648008	27648312	RhoGAP100F	6.645
chr3R	27648232	27648499	RhoGAP100F	7.707
chr3R	27648232	27649091	RhoGAP100F	5.102
chr3R	27775745	27776660	heph	5.682
chr3R	27802020	27802695	heph	4.63
chr3R	27802643	27802842	heph	6
chrX	311157	311412	CG32816	8.108
chrX	404694	405164	arg	6.356
chrX	502406	503089	CG13366	6
chrX	699050	699535	CG13358	4.63
chrX	737955	738428	CG42248	4.91
chrX	850483	851420	CG3690	4.186
chrX	851240	851779	CG3690	4.101
chrX	870800	871012	CG18823	5.333
chrX	1307325	1308304	futsch	4.854
chrX	1440160	1440460	Mur2B	9.39
chrX	1440160	1440622	Mur2B	7.874
chrX	1440160	1440865	Mur2B	6.446
chrX	1441156	1441517	Mur2B	7.595
chrX	1441156	1441768	Mur2B	5.685
chrX	1532678	1533617	br	4.908
chrX	1533609	1534076	br	4.049
chrX	1571335	1571644	CG32809	12.448
chrX	1608725	1608877	CG3795	12.987
chrX	1608725	1609145	CG3795	6.925
chrX	1621058	1621225	CG3795	9.009
chrX	1621058	1621483	CG3795	4.499
chrX	1841463	1841854	CG3600	8.31
chrX	1927139	1927557	Actn	5.587
chrX	1927416	1927685	Actn	11.152
chrX	1927416	1928168	Actn	4.193
chrX	2137156	2137659	fs(1)K10	4.264
chrX	2350394	2350589	boi	7.538
chrX	2350509	2351465	boi	4.41
chrX	2538537	2538727	sgg	9.259
chrX	2538537	2538749	sgg	6.745
chrX	2792414	2793123	CG3526	4.695
chrX	2792852	2792987	CG3526	6.757
chrX	2792979	2793123	CG3526	6.608
chrX	2845399	2845667	rst	5.682
chrX	2851042	2851330	rst	5.059
chrX	2854369	2854566	rst	4.208
chrX	2924312	2925141	kirre	5.226
chrX	3176149	3176935	dnc	4.598
chrX	3262710	3263206	dm	7.895
chrX	3375036	3375847	CG10804	5.297
chrX	3441393	3442125	CG32792	4.049
chrX	3616273	3616761	tlk	4.575
chrX	3698375	3699331	fd3F	5.445

chrX	3719353	3720105	ec	4.874
chrX	3719866	3719984	ec	7.538
chrX	3719976	3720105	ec	10.135
chrX	3719976	3720491	ec	6.281
chrX	3733800	3734008	ec	9.828
chrX	3973166	3973644	CG32790	5.31
chrX	3988556	3989474	CG6379	4.695
chrX	4155773	4156630	CG12691	5.624
chrX	4227747	4228678	norpA	4.498
chrX	4249936	4250271	norpA	9.828
chrX	4256588	4257103	norpA	7.895
chrX	4270820	4270990	CG12688	6.757
chrX	4271464	4271719	CG12688	5.78
chrX	4289214	4289722	CG32773	6.645
chrX	4292327	4292766	CG32773	8.147
chrX	4292753	4292924	CG32773	23.077
chrX	4292753	4293233	CG32773	6.547
chrX	4316564	4316967	bi	13.937
chrX	4316564	4317147	bi	8.576
chrX	4316564	4317378	bi	6.116
chrX	4482563	4482909	CG12684	4.323
chrX	4537020	4537166	CG3062	5.61
chrX	4623909	4624599	Proc-R	4.735
chrX	4671697	4671954	CG2871	7.624
chrX	4743214	4744145	CG12682	4.32
chrX	4744126	4744632	CG12682	7.859
chrX	4744126	4745085	CG12682	4.188
chrX	4978131	4978353	CG32767	11.152
chrX	5098863	5099530	rg	8.058
chrX	5112012	5112211	rg	4.63
chrX	5112177	5112402	rg	5.61
chrX	5112367	5112555	rg	8.108
chrX	5116018	5116402	rg	5.31
chrX	5236033	5236908	SK	5.059
chrX	5247286	5248227	SK	4.049
chrX	5247364	5248331	SK	4.498
chrX	5267054	5267289	SK	5.869
chrX	5267054	5267896	SK	4.271
chrX	5327068	5327416	CG15784	6
chrX	5327401	5327536	CG15784	9.259
chrX	5394207	5394371	CG32762	9.804
chrX	5410399	5410939	CG12730	4.566
chrX	5539617	5540000	CG42492	4.498
chrX	5539974	5540628	CG42492	5.869
chrX	5630409	5631126	CG32758	4.454
chrX	5986995	5987157	Nep1	14.706
chrX	6076385	6076646	CG32750	10
chrX	6202296	6202630	CG3823	4.963
chrX	6202606	6203099	CG3823	6.173
chrX	6285021	6285172	CG33664	7.08
chrX	6296956	6297618	CG33669	5.624
chrX	6364018	6364304	CG42340	9.259
chrX	6550708	6550822	l(1)G0148	7.895
chrX	6639699	6639937	CG14439	9.009
chrX	6639699	6640241	CG14439	4.062
chrX	6645361	6645819	CG14439	5.059
chrX	6777200	6777763	CG33692	4.695
chrX	6777523	6777958	CG33692	5.141
chrX	6843460	6844081	CG4575	7.61
chrX	6844069	6844236	CG4575	9.259
chrX	6844069	6844463	CG4575	6.745
chrX	6896064	6896555	inx7	9.158
chrX	6927682	6927922	CG12541	4.802
chrX	6927682	6928024	CG12541	4.617
chrX	7044452	7045439	CR32730	4.598
chrX	7045288	7045706	CR32730	12.563
chrX	7045288	7045810	CR32730	6.543
chrX	7045980	7046834	CR32730	5.575
chrX	7046259	7046785	CR32730	7.624
chrX	7046566	7046753	CR32730	11.662
chrX	7053628	7053864	CR32730	8.147
chrX	7079903	7080035	CG9650	7.371
chrX	7085026	7085137	CG9650	16.216
chrX	7085784	7086000	CG9650	6.417
chrX	7085946	7086223	CG9650	11.583
chrX	7088623	7088970	CG9650	5.398
chrX	7089826	7089950	CG9650	16.216
chrX	7095907	7096504	CG9650	4.278
chrX	7171647	7172097	CG1677	6.757
chrX	7254677	7255090	CG1999	4.498

chrX	7279347	7280150	CheA7a	4.908
chrX	7309556	7310205	CG34337	5.931
chrX	7326488	7326735	CG32726	7.449
chrX	7346438	7346712	CG11368	5.587
chrX	7389199	7389687	CG32719	8.316
chrX	7396287	7396430	CG32719	13.514
chrX	7400758	7401576	CG32719	4.501
chrX	7400758	7401692	CG32719	4.086
chrX	7419443	7419878	CG32720	10.135
chrX	7425629	7426014	CG32720	8.31
chrX	7437421	7437777	CG32720	4.983
chrX	7460473	7460711	CG11369	10.791
chrX	7460473	7460868	CG11369	8.811
chrX	7506368	7507074	ct	8.31
chrX	7506539	7507474	ct	6.969
chrX	7559248	7559662	ct	5.102
chrX	7612152	7612741	CG15478	4.695
chrX	7613267	7614271	CG15478	4.271
chrX	7613681	7614261	CG15478	6.645
chrX	7614206	7614494	Hira	6.615
chrX	7614206	7614763	Hira	5.686
chrX	7614206	7615181	Hira	4.038
chrX	7655614	7656469	Ir7a	4.38
chrX	7656440	7656644	Ir7a	10.135
chrX	7656636	7657132	Ir7a	9.195
chrX	7668886	7669517	CG32718	5.682
chrX	7907996	7908130	Tbh	7.371
chrX	8129007	8129574	sdt	4.036
chrX	8174077	8174720	nAcRalpha-7E	7.013
chrX	8212775	8213419	nAcRalpha-7E	7.117
chrX	8212775	8213520	nAcRalpha-7E	6.098
chrX	8216496	8216804	nAcRalpha-7E	20.27
chrX	8228956	8229167	nAcRalpha-7E	5.146
chrX	8231998	8232257	nAcRalpha-7E	6
chrX	8231998	8232387	nAcRalpha-7E	5.682
chrX	8279226	8279598	CG1387	4.802
chrX	8369514	8370200	CG33223	5.587
chrX	8375853	8376607	CG33223	4.024
chrX	8503095	8503791	Caf1-180	5.54
chrX	8509894	8510850	Caf1-180	4.955
chrX	8510818	8511123	Caf1-180	4.983
chrX	8546795	8547002	oc	9.259
chrX	8690345	8690999	Lim1	4.537
chrX	9147761	9147923	CG17754	10.453
chrX	9168784	9169201	CG16892	4.155
chrX	9534852	9535748	l(1)G0232	5.025
chrX	9536351	9536666	l(1)G0232	10.283
chrX	9536351	9537227	l(1)G0232	6.502
chrX	9599836	9600677	btd	6.897
chrX	9613824	9614386	Sp1	4.036
chrX	9614371	9614822	Sp1	5.495
chrX	9621433	9621807	Sp1	6.818
chrX	9699819	9700383	CG32698	4.695
chrX	9759446	9760324	Ser7	4.292
chrX	9770756	9771412	CG15247	4.438
chrX	9771299	9771522	CG15247	6.11
chrX	9771404	9771702	CG15247	6
chrX	9771404	9771745	CG15247	5.61
chrX	9855636	9855911	CG1791	6.088
chrX	10254526	10255508	l(1)G0289	5.025
chrX	10291727	10292031	flw	8
chrX	10461749	10462317	CG15296	5.495
chrX	10506502	10506955	CG9817	4.63
chrX	10510012	10510280	CG15295	6.26
chrX	10676100	10676326	Ant2	4.38
chrX	10708160	10708547	Imp	5.587
chrX	10712978	10713427	Imp	5.946
chrX	10732085	10732282	sbr	6
chrX	10784434	10784744	Ork1	11.583
chrX	10850959	10851148	Myo10A	6.356
chrX	10851119	10851755	Myo10A	5.398
chrX	11053231	11053416	Dlic	12.987
chrX	11053995	11054812	Dlic	7.042
chrX	11148599	11149053	CG15198	6.26
chrX	11307286	11307657	Gr10a	6.757
chrX	11343405	11343595	CG11727	5.894
chrX	11343405	11343795	CG11727	4.362
chrX	11421375	11421787	CG32666	9.592
chrX	11636134	11636665	inaF-A	4.38
chrX	11742444	11742688	CG15740	16.216

chrX	11874048	11874641	cac	4
chrX	11966741	11967352	CG12721	6
chrX	11966741	11967366	CG12721	5.472
chrX	11973362	11973549	CG12721	5.78
chrX	11981847	11982013	CR32657	4.38
chrX	12067681	12067895	CG1924	8.31
chrX	12398458	12399312	CG2556	5.045
chrX	12469975	12470965	CG11138	5.348
chrX	12470856	12471787	CG11138	12.698
chrX	12535806	12536350	tomosyn	9.524
chrX	12536201	12536515	tomosyn	11.152
chrX	12538947	12539298	tomosyn	5.78
chrX	12680730	12681196	CG32647	12.012
chrX	13075221	13075333	CG34411	15.464
chrX	13075211	13075562	CG34411	6.353
chrX	13081685	13082036	CG34411	6.84
chrX	13147890	13148111	mew	6.088
chrX	13172860	13173829	HDAC4	4.154
chrX	13174376	13174683	HDAC4	9.823
chrX	13174624	13175150	HDAC4	12.346
chrX	13174611	13175322	HDAC4	8.759
chrX	13216836	13217068	IP3K2	5.839
chrX	13216836	13217699	IP3K2	5.109
chrX	13280499	13280940	Yippee	5.587
chrX	13419065	13419700	CG15753	7.326
chrX	13541445	13541753	NFAT	4.438
chrX	13541648	13542014	NFAT	8.108
chrX	13554716	13554949	NFAT	8.746
chrX	13754142	13754931	CG11071	9.39
chrX	13754406	13755177	CG11071	13.937
chrX	13901702	13902304	Ste12DOR	4.062
chrX	13905574	13906263	Ste12DOR	4
chrX	13964053	13964261	Ste:CG33236	6.479
chrX	14623820	14624121	NetB	9.009
chrX	14758846	14759052	Flo-2	7.371
chrX	14767902	14768311	Flo-2	7.449
chrX	14768217	14768452	Flo-2	6.547
chrX	14770433	14770621	Flo-2	6.479
chrX	14813513	14814454	Flo-2	4.092
chrX	14814116	14814340	Flo-2	6.356
chrX	14814304	14814454	Flo-2	9.804
chrX	14818543	14818942	Flo-2	9.195
chrX	14819822	14820139	Flo-2	14.706
chrX	14824106	14824233	Flo-2	9.259
chrX	14824106	14824744	Flo-2	5.839
chrX	14892992	14893713	eag	6.969
chrX	14892992	14893729	eag	6.75
chrX	15219773	15220026	Top1	4.208
chrX	15228168	15229032	HDAC6	4.498
chrX	15289865	15290159	cngl	15.789
chrX	15289865	15290317	cngl	10.955
chrX	15289865	15290335	cngl	10.796
chrX	15419155	15419537	Ac13E	6.745
chrX	15496287	15496937	sog	4.122
chrX	15537132	15537533	CG8117	6.173
chrX	15537501	15538247	CG8117	6.173
chrX	15545285	15545603	CG8117	9.259
chrX	16017940	16018051	disco-r	8.523
chrX	16224236	16224606	CG9919	11.583
chrX	16224236	16224797	CG9919	10.526
chrX	16336719	16336920	CG4420	5.495
chrX	16336719	16337405	CG4420	4.908
chrX	16662690	16663277	if	8
chrX	17065104	17065830	baz	7.194
chrX	17098306	17098432	CG5070	13.514
chrX	17257031	17257448	B-H1	18.779
chrX	17285901	17286770	B-H1	6.925
chrX	17286069	17286971	B-H1	6.068
chrX	17310658	17310797	CG8611	9.009
chrX	17395644	17396057	CG8557	8.108
chrX	17751152	17751433	CG6762	4.261
chrX	17889456	17889973	Sh	4.695
chrX	17921214	17921708	Sh	4.695
chrX	18014569	18015181	wupA	5.839
chrX	18294850	18295166	CG32549	13.85
chrX	18359402	18359936	CG32547	4
chrX	18360606	18360815	CG32547	8.108
chrX	18375717	18376233	CG6361	5.917
chrX	18431351	18431909	Bx	4.261
chrX	18431557	18431980	Bx	5.396

chrX	18467562	18467785	Bx	7.042
chrX	18636699	18637191	CG6873	4.598
chrX	18779210	18779915	CG7332	4.566
chrX	19066161	19066500	pncr004:X	7.194
chrX	19105597	19105742	CG14195	10.791
chrX	19105597	19105965	CG14195	6.427
chrX	19482442	19483026	CG14219	4.049
chrX	19656576	19657150	CG12702	4.983
chrX	19657246	19657917	CG12702	4.237
chrX	19710922	19711264	skpC	5.568
chrX	19719671	19719926	skpE	6.11
chrX	19837078	19838008	CG12655	4.323
chrX	19873652	19874002	Nep3	7.825
chrX	19908406	19908693	D2R	4.208
chrX	19949512	19950051	CG9570	4
chrX	19952231	19952499	CG9570	6.479
chrX	19963547	19964145	CG9570	5.333
chrX	20143096	20143318	inx6	5.226
chrX	20143831	20144581	inx6	7.895
chrX	20147518	20148336	inx6	4.727
chrX	20429441	20429750	RunxB	5.097
chrX	20429704	20429964	RunxB	6.588
chrX	20435236	20435939	CG42580	6.203
chrX	20435844	20436118	CG42580	4.983
chrX	20455753	20455893	RunxA	27.027
chrX	20484455	20485306	RunxA	4.963
chrX	20579735	20579983	run	7.371
chrX	20579883	20580091	run	10.453
chrX	20579975	20580238	run	9.259
chrX	20585112	20585314	run	4.63
chrX	20601090	20601490	CG1324	6.237
chrX	20601698	20602062	CG1324	6.173
chrX	20613398	20613953	CG15452	5.396
chrX	20664649	20665170	shakB	9.174
chrX	20665107	20665786	shakB	7.396
chrX	20690628	20691217	CG15450	5.618
chrX	20702805	20703272	CG15450	7.895
chrX	20716127	20716427	CG15450	8.31
chrX	20716127	20716607	CG15450	5.025
chrX	20721449	20722409	CG1314	4.723
chrX	20732323	20732979	CG1314	7.859
chrX	21107853	21107985	CG32521	27.027
chrX	21227676	21228417	sol	4.065
chrX	21303993	21304232	CG42343	5.54
chrX	21350034	21350588	Ir20a	4.261
chrX	21939610	21939833	CG17600	5.146
chrX	22200275	22201278	CG12446	4.386

Table S2.4. Predicted clusters for the *Drosophila melanogaster* genome (Dm3). Clusters with a cluster coefficient ≥4 annotated to the nearest transcription start site.

Annotation	**Genomic coordinates (dm3)**
dpp +35	chr2L:2464301-2465300
wg -3.7	chr2L:7303415-7303860
wg +4.2	chr2L:7311428-7312755
Sema-1a	chr2L:8639890-8640550
ptc -6.4	chr2R:4530660-4531850
ptc -4.8	chr2R:4532251-4533000
PKA-R2	chr2R:5906490-5907830
kn +11	chr2R:10674125-10674700
kn -13	chr2R:10699301-10700165
Hs3st-A +4.3	chr2R:14609939-14611000
Hs3st-A +21	chr2R:14627251-14628100
dve -6.8	chr2R:18124601-18125550
dve +21	chr2R:18152960-18154300
dve +25	chr2R:18157301-18158200
dally	chr3L:8818181-8820095
PKA-C3	chr3L:15913901-15915270
boi	chrX:2350251-2351550
sgg	chrX:2538250-2539000

S5 Table. Clusters containing ci/GLI sites of low MSS tested in the chicken neural tube assay.

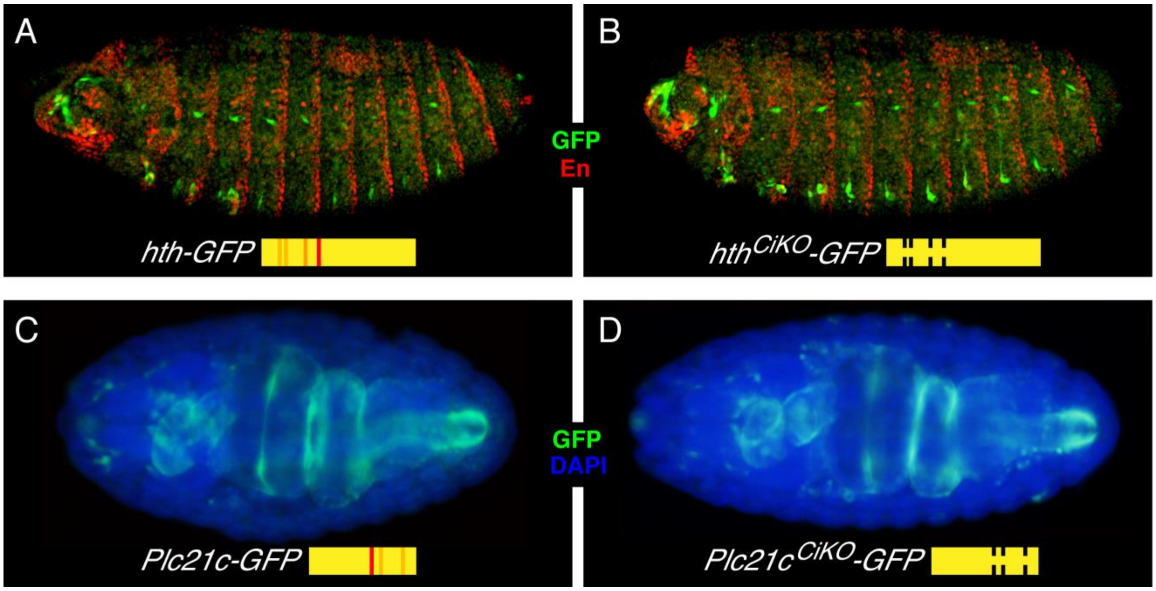


Figure S2.3. Expression of *hth* and *Plc21C* regions in the fly are not ci/GLI-dependent. Both *hth* and *Plc21C* drive GFP expression in the fly embryo. *Hth* exhibits expression in the brain as well as a punctate segmental pattern parallel but outside of En expression (shown in red) which marks cells that produce and secrete Hh ligand **(AB)**. *Plc21C* expresses throughout the gut **(C)**. Expression for both constructs is not Hh dependent since it persists after mutation of ci/GLI binding sites **(BD)**.

DamID locations from Biehs et al. (Build dm3)

Chromosome	Start	End	Cluster Start	Cluster End	Symbol	Gene
chr2L	1455284	1456528	1455873	1456140	snRNA:U3:22A	NR_001600
chr2L	1927769	1928140	1927228	1928142	CG7337	NM_001103581
chr2L	7538466	7543325	7538294	7539165	Rapgap1	NM_001103644
chr2L	9111843	9113084	9111745	9112729	Or30a	NM_078796
chr2L	15937296	15944819	15937185	15937383	beat-Ib	NM_078855
chr2L	17431677	17434112	17433182	17433529	CG5043	NM_135994
chr2R	2655624	2656580	2656051	2656477	Epac	NM_001103732
chr2R	6418206	6419765	6418353	6418759	lola*	NM_080027
chr2R	6462021	6462381	6461408	6462025	psq	NM_165790
chr2R	11004693	11007129	11004180	11005090	chn	NM_206119
chr2R	11336766	11337435	11336714	11337271	CG34365	NM_001103852
chr2R	12283866	12284542	12284061	12284394	CG33960	NM_001038863
chr2R	12412600	12412659	12412235	12412734	Sema-2a	NM_166178
chr2R	12414984	12419228	12416993	12417312	Sema-2a	NM_166178
chr2R	12498703	12500537	12498903	12499084	CG5065	NM_137299
chr2R	12658866	12659557	12659107	12659386	unc-104	NM_166192
chr2R	12677166	12679045	12676636	12677619	CG5522	NM_166193
chr2R	13045282	13055248	13051217	13051370	CG10953	NM_137355
chr2R	13073470	13078925	13073362	13073564	CG10950	NM_137356
chr2R	13166767	13167736	13166630	13167109	mbl	NM_176211
chr2R	13391488	13396940	13394739	13395102	CG4844	NM_001032265
chr2R	15209157	15212514	15211205	15211546	Rgk1	NM_137567
chr2R	15681071	15682013	15680992	15681678	Obp56g	NM_137603
chr2R	15742583	15743824	15743081	15743609	Obp56i	NM_166376
chr2R	18226254	18226613	18226458	18226970	CG11206	NM_001103944
chr2R	18259854	18261720	18260459	18261287	Rtf1	NM_137821
chr2R	18431154	18433651	18432448	18432907	px*	NM_001103947
chr2R	20272172	20272571	20272357	20273224	mAcR-60C	NM_079120
chr3L	8052940	8054760	8052894	8053443	bip1	NM_139912
chr3L	11862617	11864769	11864451	11864952	CG5906	NM_140261
chr3L	12458113	12459080	12457913	12458121	eyg	NM_079318
chr3L	13940701	13941699	13941029	13941736	CG32137	NM_168564
chr3L	17339408	17344264	17341139	17341588	Mip	NM_140714
chr3L	20692805	20697982	20692956	20693766	kni*	NM_079463
chr3R	2329935	2332092	2329972	2330257	CG15186	NM_169145
chr3R	3976809	3982873	3978441	3978655	grn	NM_001144554

chr3R	4101609	4106766	4102638	4102804	ato*	NM_169213
chr3R	4401007	4404074	4403133	4403663	Cenp-C	NM_169228
chr3R	5682908	5683267	5682873	5683534	Teh1	NM_141702
chr3R	9669658	9672691	9670696	9671137	CG31495	NM_169559
chr3R	17217597	17220086	17219899	17220257	CG6475	NM_001104389
chr3R	17227813	17229687	17227902	17228674	CG6475	NM_001104389
chr3R	20530764	20536210	20530430	20531229	slo	NM_001170241
chr3R	20549088	20550942	20549943	20550067	tok	NM_170168
chr3R	21180551	21181210	21180942	21181629	Fur1	NM_170654
chrX	3720410	3720469	3719976	3720491	ec	NM_130722
chrX	4249010	4249973	4249936	4250271	norpA	NM_001169190
chrX	4256130	4258561	4256588	4257103	norpA	NM_080330
chrX	4537017	4537076	4537020	4537166	CG3062	NM_131949
chrX	5540520	5540876	5539974	5540628	CG42492	NM_001169205
chrX	6202614	6205080	6202296	6202630	CG3823	NM_132085
chrX	6297612	6298259	6296956	6297618	CG33669	NM_001031872
chrX	7309802	7314072	7309556	7310205	CG34337	NM_001103431
chrX	7400950	7404588	7400758	7401576	CG32719	NM_167128
chrX	15536311	15537530	15537132	15537533	CG8117	NM_132821

Table S2.6. Overlap between clusters predicted in this study and DamID protected sites. Asterisks indicate four sites that map to one of the 52 probable ci target genes identified by Biehs *et al*. (Biehs et al., 2010).

Chapter III

Computational prediction and experimental validation of novel Hedgehog-responsive enhancers linked to genes of the Hedgehog pathway

3.1 Abstract

The Hedgehog (Hh) signaling pathway, acting through three homologous transcription factors (GLI1, GLI2, GLI3) in vertebrates, plays multiple roles in embryonic organ development and adult tissue homeostasis. At the level of the genome, GLI factors bind to specific motifs in enhancers, some of which are hundreds of kilobases removed from the gene promoter. These enhancers integrate the Hh signal in a context-specific manner to control the spatiotemporal pattern of target gene expression. Importantly, a number of genes that encode Hh pathway molecules are themselves targets of Hh signaling, allowing pathway regulation by an intricate balance of feed-back activation and inhibition. However, surprisingly few of the critical enhancer elements that control these pathway target genes have been identified despite the fact that such elements are central determinants of Hh signaling activity. Recently, ChIP studies have been carried out in multiple tissue contexts using mouse models carrying FLAG-tagged GLI proteins (GLI^{FLAG}). Using these datasets, we tested whether a meta-analysis of GLI binding sites, coupled with a machine learning approach, could reveal genomic features that could be used to

Gurdziel K, Vogt KR, Scheider GK, Richards N, Gumucio DL. *Compuational prediction and experimental validation of novel Hedgehog-responsive enhancers linked to genes of the Hedgehog pathway*. BMC Developmental Biology.

empirically identify Hh-regulated enhancers linked to loci of the Hh signaling pathway.

A meta-analysis of four existing GLI^{FLAG} datasets revealed a library of GLI binding motifs that was substantially more restricted than the potential sites predicted by previous *in vitro* binding studies. A machine learning method (kmer-SVM) was then applied to these datasets and enriched k-mers were identified that, when applied to the mouse genome, predicted as many as 37,000 potential Hh enhancers. For functional analysis, we selected nine regions which were annotated to putative Hh pathway molecules and found that seven exhibited GLI-dependent activity, indicating that they are directly regulated by Hh signaling (78% success rate).

The results suggest that Hh enhancer regions share common sequence features. The kmer-SVM machine learning approach identifies those features and can successfully predict functional Hh regulatory regions in genomic DNA surrounding Hh pathway molecules and likely, other Hh targets. Additionally, the library of enriched GLI binding motifs that we have identified may allow improved identification of functional GLI binding sites.

Keywords: Hedgehog signaling; enhancers; machine learning; GLI

3.2 Background

The Hedgehog (Hh) signaling pathway is critical for embryonic organ development and adult tissue homeostasis across animal phyla (McMahon et al., 2003; Jiang and Hui, 2008; Briscoe and Thérond, 2013; Petrova and Joyner, 2014). In multiple tissue-specific settings, Hh signaling directs specific cell fate choices, controls tissue patterning and governs cell proliferation. In mammals, Hh signaling originates with any of three ligands (Sonic hedgehog

(*Shh*), Indian hedgehog (*Ihh*) or Desert hedgehog (*Dhh*)) (for Review see (Varjosalo and Taipale, 2008)). Release of the lipid modified HH ligand has been shown to be facilitated by SCUBE in conjunction with the transmembrane protein Dispatched (Burke et al., 1999; Jeong and McMahon, 2002; Creanga et al., 2012; Jakobs et al., 2014). Once discharged, HH ligands interact with the Patched (PTCH1 or PTCH2) receptor protein and with Hh-binding proteins BOC, CDO and GAS1 on target cells to relieve PTCH-dependent inhibition of the Smoothened (SMO) transmembrane protein (Allen et al., 2011; Izzi et al., 2011). HH ligands can also be sequestered by the Hedgehog-interacting protein (HHIP), which dampens signaling (Chuang and McMahon, 1999).

Hh-mediated signal transduction culminates in the nucleus, with the binding of zinc-finger transcription factors (GLI1, GLI2, GLI3) to target gene sequences (Kim et al., 2009; Goetz and Anderson, 2010). However, proteolytic processing determines whether the GLI proteins act as repressors or activators. GLI1, which is not processed, functions exclusively as a transcriptional activator and may act to amplify Hh signals (Dai et al., 1999). GLI2 and GLI3 can be converted to a repressor form in the absence of Hh ligand. In the presence of the Hh ligand, this processing is inhibited, allowing full-length GLI proteins to traffic to the nucleus and activate gene expression (Dai et al., 1999; Sasaki et al., 1999; Shin et al., 1999). Processing of GLI proteins requires passage through the cilia (Kim et al., 2009; Beachy et al., 2010); the kinesin KIF7 helps to properly construct the cilium and is enriched at the cilium tip, along with GLI and SUFU (Suppressor of Fused) (Liem et al., 2009).

The Hh signaling pathway is regulated by both positive and negative feedback. Indeed, a number of Hh pathway components, including *Boc*, *Cdo*, *Gas1*, *Gli1*, *Hhip*, *Ptch1* and *Ptch2* are thought to be direct transcriptional targets of Hh signaling in multiple tissue contexts (Chuang and McMahon, 1999; Dai et al., 1999; Agren et al., 2004; Rahnama et al., 2004; Tenzen et al., 2006; Aglyamova and Agarwala, 2007; Martinelli and Fan, 2007; Vokes et al., 2007; Vokes et al., 2008; Lee et al., 2010; Peterson et al., 2012; Holtz et al., 2013). Thus, an important aspect of Hh pathway self-regulation is integrated at the level of the enhancers that control response of the pathway target genes to local Hh signaling levels. However, despite the high functional conservation of this pathway, surprisingly little is known about the enhancer elements that control self-regulation in any organism.

One way to identify Hh target enhancers is to perform chromatin immunoprecipitation (ChIP). Genetically modified mouse models carrying inducible FLAG-tagged GLI proteins have allowed analysis of GLI binding sites *in vivo* in several different tissue contexts. Four *in vivo* GLI binding studies, including three ChIP-chip analyses (Vokes et al., 2007; Vokes et al., 2008; Lee et al., 2010) and one ChIP-seq study (Peterson et al., 2012), have been carried out using these models. Interestingly, examination of all four datasets for common GLI binding sites that are annotated to Hh pathway molecules reveals only three such sites (in *Gli1*, *Ptch1*, and *Ptch2* loci (Dai et al., 1999; Agren et al., 2004; Holtz et al., 2013)) that are uniformly detectable. Several other established Hh pathway genes, including *Boc*, *Hhip*, *Gli2*, and *Hipk2*, appear to exhibit different GLI-bound genomic locations, depending on context, suggesting that each of these pathway components is regulated by multiple distinct genomic enhancers that have context-specific features.

Using ChIP studies on diverse tissues, it may be possible to eventually identify all of the multiple enhancers that control each target gene in every context. While a valuable goal, such analyses are expensive and time consuming. We therefore asked whether analysis of all existing GLI ChIP data could reveal common sequence features that might be used to empirically and globally predict functional enhancers *de novo*. A publicly available machine learning approach, kmer-SVM (Fletez-Brant et al., 2013), was used to predict novel Hh enhancer regions. This tool uses a support vector machine (SVM) to determine sequence features (k-mer frequencies) that identify positive genomic regulatory regions (Lee et al., 2011). SVMs are classifier algorithms that define a boundary between members of two different groups. Kmer-SVM calculates weights for sequence features that determine the effectiveness of that feature to distinguish between positive and negative regulatory regions. Once the features are determined, they can be used to identify novel enhancer regions not present in the original positive set. The strength of this approach is that it relies exclusively on short regions of DNA sequence (length 3-10 bp) which are in the size range of transcription factor binding sites (TFBS). Additionally, the organization of the k-mers within a sequence does not impact the score; this feature is consistent with the variable arrangement of TFBS in enhancers (Spitz and Furlong, 2012; Slattery et al., 2014).

Using the kmer-SVM tool (Fletez-Brant et al., 2013), analysis of the four existing GLI binding datasets identified a set of k-mers that appeared to successfully predict potential GLI-regulated enhancers. Application of this set of k-mers to the mouse genome pinpointed over 37,000 potential enhancers. Several putative enhancers that were annotated to Hh pathway components were then tested for their ability to drive Hh-dependent activity in transfected cells. The functional significance of the GLI binding motifs (GBM) was also tested within each active enhancer by mutation. Of the nine predicted regulatory regions tested, seven (78%) drove reporter expression in a GLI-dependent fashion. These findings substantially increase the number of functionally verified Hh enhancers found in Hh pathway molecules and validate the use of machine learning on ChIP data as a valuable tool to empirically predict likely Hh-dependent regulatory regions.

3.3 Results and discussion

3.3.1 Analysis of GLI^{FLAG} datasets to identify likely *in vivo* GLI transcription factor binding motifs

A previous *in vitro* analysis of GLI transcription factor binding resulted in the identification of a set of likely binding sites for this factor (Hallikas et al., 2006). However, this spectrum of sites may not accurately represent GLI binding site preferences *in vivo*. To begin to examine this, we performed a meta-analysis of four existing GLI-ChIP datasets. All of these datasets utilize transgenic mice carrying FLAG tagged GLI1 (GLI1^{FLAG}) or GLI3 (GLI3^{FLAG}) in the ROSA26 locus, activated by Cre recombination, in four different tissue contexts: limb bud development (LD) (Vokes et al., 2008), cerebellum development (CD), medulloblastoma (MB) resulting from Hh signaling overexpression (Lee et al., 2010), and neural progenitor cells (NP) (Peterson et al., 2012). An additional study of neural progenitors (Vokes et al., 2007) was excluded from analysis since it contained a low number of significant peaks and mirrors the same experimental conditions as the NP dataset (Peterson et al., 2012). For each of the datasets, the reported percentage of ChIP peak sequences with GLI binding motifs (GBM) was as follows: LD 55%, CD 26%, MB 46%, and NP 91%. However, the definition of GBM was not the same across all datasets: one study allowed only two mismatches from the consensus (Vokes et al.,

2008) and others generated a GLI motif *de novo* based on the sequences of recovered peaks (Lee et al., 2010; Peterson et al., 2012).

To collate the spectrum of GBM observed in all four datasets, we applied a *de novo* motif enrichment analysis to each dataset individually (Heinz et al., 2010). Sequences that contained at least one site that matched the *de novo* motifs were removed from the dataset. The remaining sequences were analyzed for residual motifs that resembled a GBM using DREME (Bailey, 2011) and TOMTOM (Gupta et al., 2007) (see Methods). This resulted in 548 putative GBM (12-mers) (Table S3.1), encompassing the range of GBM that are present in existing ChIP data. This set therefore represents a collection of likely genomic GLI binding sites, although some functional GLI binding sites *in vivo* could be absent from this set and some false positive sites may be included. Each 12-mer was classified as high confidence (HC), medium confidence (MC), or low confidence (LC) if it was found within sequences from all four datasets, two to three datasets, or one dataset, respectively. The sequence logos (Crooks et al., 2004) for each classification, provided in Figure 3.1A, show a nearly absolute representation of CCxC in positions 4-7 for all sites. Indeed, concordant (C and C or G and G) nucleotides at the 5th and 7th position were previously found to be required for GLI binding (Winklmayr et al., 2010). Interestingly, for high confidence sites, there is no variation at 5 of the 12 positions, including the 5th and 7th positions (xGxCCxCxCxxx).

Using the recommended matrix similarity score cutoff of 81% overall matrix similarity to the optimal consensus GLI site as defined by the *in vitro* DNA binding assay (Hallikas et al., 2006) results in 1,432,161 putative GLI TFBS across the mouse genome. This is substantially more than the 191,745 found using the new GLI library defined by the *in vivo* ChIP studies.

However, several of the sites predicted by the *in vitro* binding studies do not contain the concordant (C and C or G and G) nucleotides at the 5th and 7th position. Thus, the newly generated GLI library (Figure 3.1A) may more accurately represent functional GBM. According to this new library of 548 GBM, 41% of LD, 27% of CD, 32% of MB, and 80% of NP peaks contain putative GLI binding sites. For those sequences that contain a GBM, the vast majority contain only a single site (85.5% LD, 90.7% CD, 88.0% MB, 89.8% NP) (Figure 1B). The overlap of genomic binding regions among datasets is shown in Figure 3.1C; only 26 genomic coordinates are shared among all datasets (Table S3.2). Since pathway components must respond to the Hh signal in all tissues, it might be expected that this common response would be integrated by a single enhancer. However, only three of the 26 shared regions are annotated to known Hh pathway components (*Gli1*, *Ptch1*, *Ptch2*). Indeed, for *Boc* and *Hhip*, distinct genomic GLI binding regions are found in different datasets. This result suggests that some of these genes may have multiple enhancers that work to transduce the Hh signal in different tissue contexts.

Given this apparent complexity in regulatory regions, we next asked whether the existing datasets of ChIP peaks might contain additional sequence information that could be used to predict the location of other Hh-responsive enhancers in the mouse genome. A machine learning approach was employed to test this question.

3.3.2 Assessment of kmer-SVM performance and prediction

3.3.2.1 Kmer-SVM assessment of classification using GLI^{FLAG} datasets

For each GLI^{FLAG} dataset, only sequences with at least one GBM (wGBM, meaning *with GBM*) were used. This was done since a high proportion of the ChIP-chip datasets did not contain a putative GLI binding site as defined in the original papers (LD 55%, CD 26%, MB 46%, and NP 91%) or by our assessment (41% of LD, 27% of CD, 32% of MB, and 80% of NP peaks). Each individual dataset was submitted to kmer-SVM and the ability of each classifier to correctly label a candidate sequence as positive was assessed. Background sequences were randomly selected from the genome, but matched for GC content with the positive set.

Kmer-SVM randomly divides the data as follows: 80% of the sequences are used as a training set and 20% are used as a testing set. The ability of the classifier built with the training set to accurately identify the members of the remaining 20% testing set is then assessed. This is repeated five times, each with a different random division of the data. Receiver operating characteristic (ROC) curves and precision recall curves (PRC) are used to assess the success of the classifier to correctly label regions in the testing set as positive (see Methods).

ROC curves display the cumulative distribution of the true positive rate compared to the false positive rate. This characteristic assesses how well the classifier is able to label the positive sequences from the test set. The area under the curve was 0.898 for LDwGBM (Figure 3.2A), 0.856 for CDwGBM (Figure 3.2B), 0.862 for MBwGBM (Figure 3.2C) and 0.976 for NPwGBM (Figure 3.2D). Thus, the classifier performs best in LD and NP datasets.

PRC displays the predictive value against the true positive rate and represents the accuracy of the labeling. The PRC plots indicated high values for LDwGBM (AUC=0.753) and NPwGBM (AUC=0.880) but low values for CDwGBM (AUC=0.490) (Figure 3.2F) and

MBwGBM (AUC=0.546) (Figure 3.2E-H). The ROC and PRC plots for LDwGBM and NPwGBM datasets suggested that the classifier sequence features used were able to distinguish between positive and negative groups with a low level of false labeling.

3.3.2.2 Predictions

The classifiers for LDwGBM and NPwGBM were then individually run on 600 bp of sequence centered on every GBM in the mouse genome (191,745, as determined using the new GBM from in vivo data, described above). Use of both the LDwGBM and NPwGBM datasets for prediction incorporated data from the $\mathrm{GLI1}^{\mathrm{FLAG}}$ (predominately activator) and $\mathrm{GLI3}^{\mathrm{FLAG}}$ (predominantly repressor) transcription factors in two diverse contexts (neuronal precursor and limb development).

The length of 600 bp was selected based on motif enrichment analysis of the LD and NP datasets using MEME-ChIP (Machanick and Bailey, 2011) and Centrimo (Bailey and Machanick, 2012). This analysis showed that, within the ChIP-chip LD dataset, enrichment for the location of GLI motifs (green line) has a broad profile that spans 200 bp to either side of the midpoint (Figure S3.1A). The GLI motif has a narrower profile in the NP data, a feature that is expected for ChIP-seq (Figure S3.1B). The profile for the Sox motif (blue line), an established tissue specific GLI cofactor (Peterson et al., 2012), shows an enrichment peak that is centered around 200 bp on either side of the midpoint (Figure S3.1B) and suggests that cofactors for Hh may reside outside of the immediate vicinity of a GLI binding site. We therefore used 600 bp to capture both common Hh features as well as potential context specific sequence.

For the LDwGBM classifier, scores ranged from -4.33 to 12.00 with 18.4% of the 191,745 analyzed genomic regions scoring as positive (Score > 0). The NPwGBM results ranged from -2.54 to 5.48 with 5.7% positive (Figure 3.3A; Table S3.3). The categorization of a sequence is dependent on the sign of the score and the weight of the value is less important than the ranking. Overall, the correlation between scores for individual genomic regions calculated by the LDwGBM and NPwGBM classifiers is poor (0.68 Pearson) (Figure 3.3B). However, if only sequences with positive scores are considered, the correlation improves (0.85 Pearson). If scores are restricted to values indicating only the high confidence scores (calculated posterior probabilities = 1.0, Figure S3.2), the values are very well correlated (0.96 Pearson). In total, 8627 genomic regions were predicted as Hh enhancers by both classifiers. Of those, 1198 regions (14%) overlapped at least one peak in the four GLI^{FLAG} datasets. Among high confidence scores (LDwGBM: 5951 ≥ 1, NPwGM: 547 ≥ 1) 528 genomic regions were shared between the two datasets and 187 of these (35%) overlapped with peaks from at least one of the four GLI^{FLAG} datasets. All of the scored regions are listed in Table S3.3.

3.3.2.3 Evaluation of predictions

To assess whether kmer-SVM predictions were likely to represent Hh enhancers, we examined whether the predicted genomic regions overlapped publically available open chromatin and enhancer histone marks in tissues that were likely to be transducing Hh signals. We first examined the DNase I hypersensitive profile collected from mouse mesoderm at E11.5 at genomic regions that were predicted with high confidence as positive (1 ≤ score; posterior probability = 1) or negative (-1 ≥ score; posterior probability = 0) (Figure S3.2). A significantly higher proportion of overlap was found with the predicted positive regions than with predicted negative regions (Z-Score = 2.8332; p-value < 0.05) (Table S3.4). We also examined publically available H3K4me1, H3K4me3, and H3K27ac ENCODE data collected from heart and liver at E14.5. Monomethylated H3K4 (H3K4me1) and histone H3 acetyl Lys27 H3K27ac (Creyghton et al., 2010) were used as enhancer markers while trimethylated H3K4 (H3K4me3) was expected to be depleted in enhancer regions (Heintzman et al., 2007). Although Hh signaling is active during early development of both tissues, available *in situ* analysis for GLI1 (GenePaint: EN1215) (Visel et al., 2004; Diez-Roux et al., 2011) shows GLI1 expression in liver but not heart at E14.5 (Figure S3.3). Thus, we expected signals for both H3K4me1 (poised enhancer) and H3K27ac (active enhancer) to be enriched in the predicted positive regions in liver but not heart at this time point. Indeed this was the case: H3K4me1 (Z-Score=2.5511; p-value < 0.01) and H3K27ac (Z-Score=8.076; p-value <0.01), with no significant difference in H3K4me3 when predicted positive regions were compared to predicted negative regions. As expected, the heart data did not show enrichment for H3K4me1 or H3K27ac. Together, the results (summarized in Table S3.4) are consistent with the conclusion that the kmer-SVM classification correctly identifies Hh enhancer regions.

Next, we evaluated the sequence features, or k-mers, that kmer-SVM identified as primary components of Hh enhancer regions. The weights of k-mers are calculated during the SVM training and reflect the contribution of the k-mer to categorization of a sequence. Weights can be positive or negative and the sum of the weights of iterative k-mers across a sequence comprise the overall score of that sequence. Not surprisingly, alignment of k-mers with high scoring weights shared between both datasets returned a motif that strongly resembles the GBM (Figure 3.3C). Unique high weighted k-mers that occurred in each individual dataset represented potential context specific features. An E-box motif was identified for the LDwGBM dataset while a Sox motif was returned for NPwGBM (Figure 3.3D). Negative weights that occurred in both datasets include AC and ACC repeats as well as other C rich sequences.

3.3.3 Functional verification of GLI-dependent enhancer activity

Predicted genomic regions were annotated to the two nearest genes using GREAT (McLean et al., 2010). Because our goal was to identify enhancers for Hh pathway components, we selected a subset of predictions that were positive in both the LDwGBM and NPwGBM datasets and that were annotated to members of the GO:0007224 Smoothened signaling pathway gene set. These regions were functionally tested for enhancer activity. The test set consisted of genomic regions annotated to *Boc*, *Gli3*, *Hhip*, *Hipk2*, *Ptch1*, *Scube1*, *Shh*, and *Tgfbr2*. An additional region, annotated to *Dpp6* (near *Shh*) was also tested (Table 3.1).

The nine genomic regions were screened for Hh responsiveness in a cell culture assay that has been previously used to validate Hh enhancers (Zhao et al., 2006; Gerber et al., 2007). In this assay, C2C12 cells are transiently transfected with constructs containing the putative Hh regulatory region cloned upstream of a minimal promoter that drives luciferase expression (see Methods). To induce a Hh response, enhancer reporter constructs were co-transfected with a plasmid that drives constitutive expression of GLI1 in mammalian cells (Vokes et al., 2007). For those candidate enhancers that demonstrated apparent Hh activation, GLI-dependent activity was confirmed by retesting after mutagenesis of the GLI binding sites (GKO). Either complete loss of enhancer activity or attenuation of response in GKO sequence was considered GLI-dependent. An established Hh enhancer region for Ptch2 was used as a positive control (Holtz et al., 2013).

For the 9 regulatory regions annotated to Hh pathway component genes, 7 exhibited Hh activation that was directly dependent on a GLI binding site (Figure 3.4). The Ptch2 positive control region showed a complete loss of Hh response after mutation of the GLI site (Figure 3.4) as did the regulatory regions annotated to *Hhip*, *Hipk2*, *Ptch1*, and *Scube1*. Regions annotated to *Boc*, *Dpp6*, and *Tgfbr2* showed a significant decrease in Hh activation upon GLI TFBS mutation, but not a complete loss of response. This suggests that additional regulatory inputs influence the activity of these enhancers. Neither the *Gli3* nor *Shh* region exhibited Hh dependent enhancer activity. However, we cannot rule out the possibility that these regions might be positive if examined in a different cellular context (Vokes et al., 2007).

Two previous *in silico* methods have been described for the identification of Hh-regulated enhancers in vertebrates: Enhancer Element Locator (EEL) and Module Cluster Analysis (MCA). EEL analyzes the estimated energy of a single transcription factor binding event, as well as the possible interaction between adjacent, highly conserved transcription factor binding sites, to detect potential enhancers (Hallikas et al., 2006). In contrast, MCA utilizes Poisson modeling to determine the relative enrichment of binding sites in highly conserved, non-coding sequence and, thereby, identify putative enhancers (Vokes et al., 2007). While both of these methods have had some success (~25%) in detecting putative Hh-regulated enhancers, a disadvantage to these approaches is that the search is limited to regions of high sequence conservation and to regions close to promoters. In contrast, kmer-SVM approach used here employs a genome-wide empirical analysis to locate regions that contain sequence features predictive of Hh enhancer function. The high success rate (78%) of the kmer-SVM predictions far exceed the previous prediction rates for EEL or MCA.

To examine the impact of k-mers that contribute to predictions of the positive regions, weights were plotted across each of the sequences. The Ptch2 sequence (Figure 3.5A), a known enhancer region (Holtz et al., 2013), contained matching profiles for 8-mers predicted from LDwGBM (red) and NPwGBM (yellow) that are GC rich and similar to the GBM k-mers However, mutation of the single GLI TFBS (Figure 3.5B, green box) ablates the Hh response, indicating that the presence of this GBM is required to transduce Hh signaling. Mutation of the GBMs annotated by the green boxes for Hhip, Hipk2, Ptch1, and Scube1 (Figure 3.5EFGH) is also sufficient to abrogate Hh signal transduction. For Boc, Dpp6, and Tgfbr2, which show enhancer activity that remains after ablation of the GBM (Figure 3.5BCJ), there were no sequence characteristics that were indicative of a shared feature responsible for this remaining response to induction by GLI1. The Boc profile was the only one that contained a high weighted k-mer (annotated with an asterisk) that was unique to the LDwGBM (red) profile. This k-mer was similar to a Krox motif (TOMTOM p-value < 0.004) (Gupta et al., 2007) and may be enriched in the LDwGBM dataset as a context specific transcription factor, since it has roles in limb development (Levi et al., 1996; Nonchev et al., 1996). In general, most of the tested regions contain distributed high weighted 8-mers in addition to the central GBM and had profiles that contained consistent peaks in both LDwGM and NPwGBM datasets (Figure 3.5).

3.4 Conclusions

Facilitated by a new GBS library generated from a meta-analysis of genomic regions identified in *in vivo* binding studies (Vokes et al., 2007; Vokes et al., 2008; Lee et al., 2010; Peterson et al., 2012), we utilized the kmer-SVM machine learning approach to examine four existing GLI ChIP databases and to generate classifiers that can empirically predict functional Hh enhancers from genomic DNA. Of nine predicted Hh target regulatory regions tested, seven were functionally verified as GLI-dependent. All of the tested regions were annotated to genes believed to be components of the Hh pathway and important determinants of the Hh response. Given the high success rate of Hh enhancer prediction in this small scale screen (78%), it is quite possible that a large number of the other predicted regions (Score > 0 in Table S3.3) may harbor Hh enhancer activity.

3.5 Methods

3.5.1 Computing resources

Except where otherwise indicated, all computational steps were performed using custom Perl and R scripts.

3.5.2 Publically available datasets

Genomic analysis was conducted on chromosomes 1 to 19, X and Y of mouse build mm9. Mouse ENCODE data (Gerstein et al., 2012) comprising open chromatin DNase I data that was collected at embryonic day 11.5 in the mesoderm and histone (H3K4me1, H3K4me3, and H3K27ac) data collected from embryonic day 14.5 for heart and liver were downloaded from the UCSC genome repository (goldenPath).

3.5.3 Definition of putative GLI binding motifs

The library of putative GLI binding motifs (GBM) was compiled using *de novo* motif analysis (Heinz et al., 2010) on each of the individual GLI^{FLAG} datasets iteratively. Sequences that contained a GBM were removed from the dataset and the remaining sequences were analyzed for enriched motifs using DREME (Bailey, 2011). If TOMTOM (Gupta et al., 2007) returned a GLI motif, the dataset was reanalyzed using Homer. The process continued until no residual GBM remained enriched in the dataset. Confidence in the GBM was classified as high (HC) if it was shared across sequences from all four GLI^{FLAG} datasets, medium (MC) if it was found in two or three datasets, and low (LC) if it only occurred in one.

3.5.4 kmer-SVM parameters and evaluation of classifiers

Training was run on the Beer lab webserver (http://kmersvm.beerlab.org/), using a k-mer of length of 8.

Performance of the classifier built by kmer-SVM's training algorithm was assessed using Receiver Operating Characteristic (ROC) and Precision-Recall curves (PRC) generated within the kmer-SVM program. True positive, true negative, false positive and false negative counts were generated by segregating the sets of positive and negative sequences into a training set (80% of the sequences) and a testing set (the remaining 20% of the sequences). Each member (individual sequence) of the testing set that is correctly annotated as positive increases the true positive count while an incorrect prediction of a positive sequence as negative increases the false negative count. ROC curves asses the sensitivity and specificity of the classifier output. A steep curve with a high area under the curve (AUC) indicates a high true positive rate and a low false positive rate. PRC evaluate the accuracy and relevance of the classifier output. A high AUC indicates that the results have a low false positive rate (high precision) and a low false negative rate. The trained SVM is evaluated by assessing its ability to classify the testing set correctly. The classifier was assessed five times by resetting members in the training set and testing set.

3.5.5 Cloning of putative enhancer regions

Putative enhancers were amplified from C57BL/6 genomic DNA (supplied by Jackson Laboratory) using template-specific PCR primers (Table S3.4). A CACC extension was added to the end of one primer to facilitate directional cloning. PCR fragments were cloned into the pENTR/D-TOPO vector using the standard kit (Invitrogen) and then shuttled into the pGL3-Promoter luciferase vector (Promega) using the Gateway® cloning system (Invitrogen). QuikChange mutagenesis (Stratagene) was used to mutate putative GLI binding sites by replacing the C in the 6th position to a G.

3.5.6 Luciferase assay

C2C12 cells (35,000) were plated per well on 12-well plates (10% fetal bovine serum treated with penicillin, streptomycin and glutamate). After 24 hours, cells were transfected, using lipofectamine, with 400 ng of the construct containing the putative enhancer region plus either a control vector or GLI1 (in equal molecular weight). *Renilla* (Promega pRL-CMV) was also included to normalize transfection efficiency. After an additional 24 hours, cell media was changed to no serum to promote ciliogenesis (Santos and Reiter, 2008). Cell lysate was collected after 48 hours and measured for luciferase activity using the Dual-Luciferase® Reporter Assay System (Promega) on a Perkin Elmer Wallac Victor3 1420 Multilabel Counter. Three experimental replicates were collected for each condition.

3.6 Abbreviations

Hh: Hedgehog

HPC: Hedgehog pathway component

GBM: GLI binding motif

TFBS: transcription factor binding sites

SVM: support vector machine

E14.5: embryonic day 14.5 (mouse)

3.7 Competing interests

The authors have no competing interests to declare.

3.8 Authors' contributions

KG and DG conceived and designed the experiments. KG, GS, and KV performed the experiments. KG, KV, GS, and NR cloned and mutagenized constructs. KG analyzed the data. KG and DG wrote the manuscript. All authors reviewed the final manuscript.

3.9 Acknowledgements

KG was supported by University of Michigan NIH Training Program in Basic and Translational Digestive Science (T32 DK094775). DG acknowledges support from P01 DK062041.

3.10 Author details

[1]Department of Cell and Developmental Biology and [2]Department of Computational Medicine and Bioinformatics, University of Michigan, Ann Arbor, MI 48109

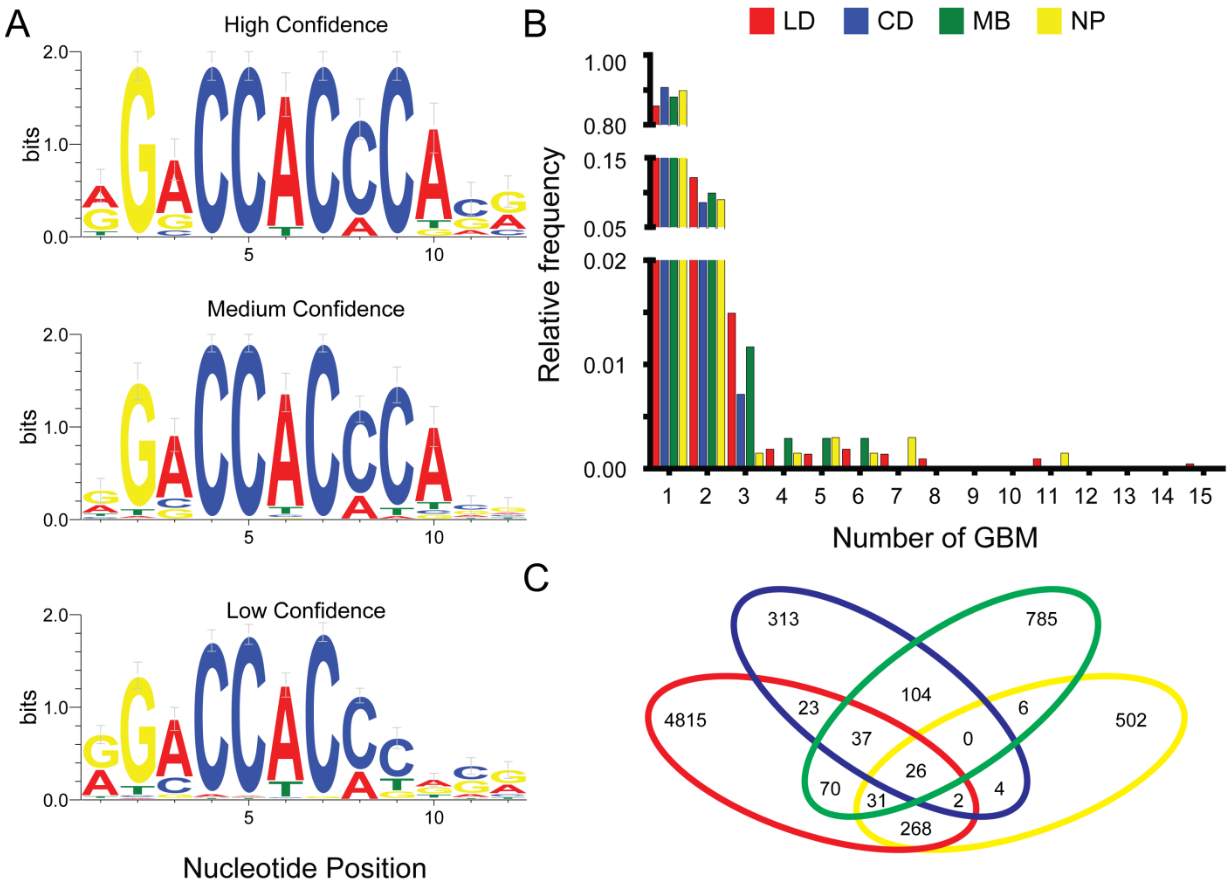


Figure 3.1. Definition of GLI binding motifs (GBM) and characterization of GLI^{FLAG} datasets. (A) Sequence logos (Weblogo) of 12-mer GBM. High confidence (HC), medium confidence (MC), and low confidence (LC) GBM are found in all four (HC), three or two (MC) or one (LC) datasets. Error bars represent twice the small sample correction. **(B)** Relative frequency of peaks containing one or more GBM in the GLI^{FLAG} ChIP-chip LD (red), CD (blue), MB (green), and GLI^{FLAG} ChIP-seq NP (yellow) datasets. A high proportion of sequences contain only one GBM. **(C)** Overlap of sequences identified by all four GLI^{FLAG} datasets; only 26 individual peaks are found in all contexts.

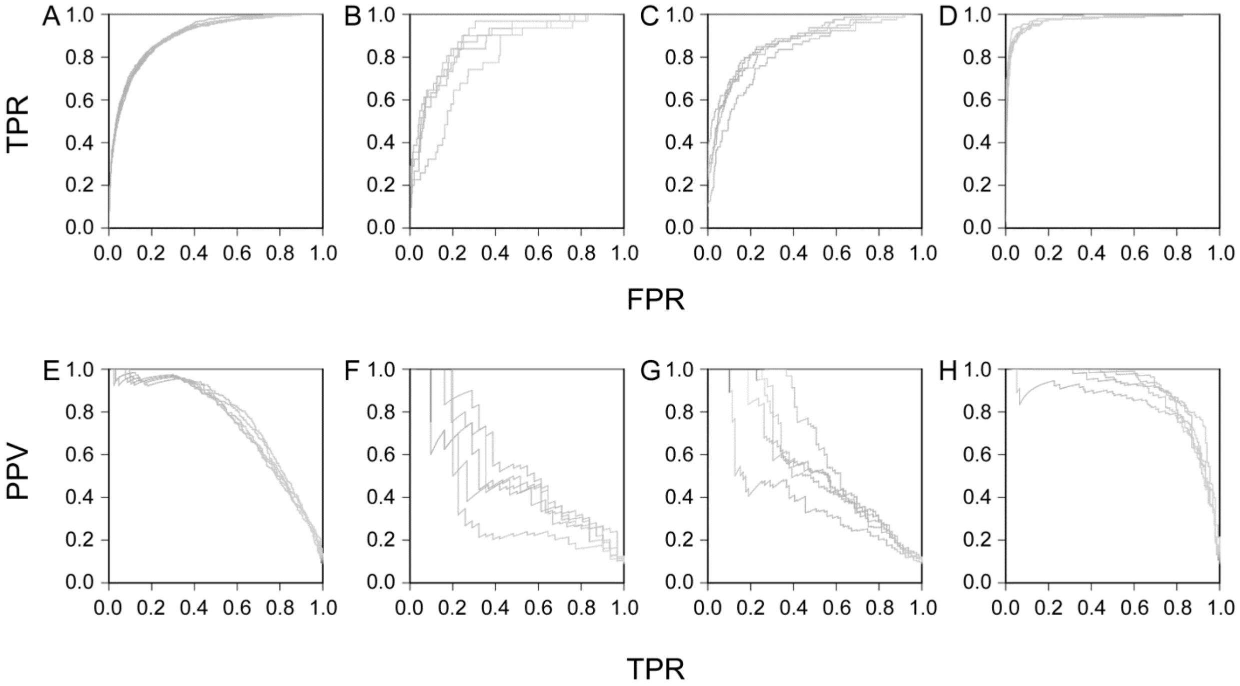


Figure 3.2. Assessment of classification capability of kmer-SVM trained GLI^{FLAG} datasets containing sequences with at least one GBM. For all curves, each dataset is randomly split into 80% for training and 20% for prediction and the prediction is repeated five times (represented by individual lines). Plots assess the likelihood that the specified classifier can successfully predict sequences that have at least one GBM as positive or negative. **(A-D)** ROC plots depicting true positive rates (TPR) and false positive rates (FPR). Area under the curve (AUC) scores as calculated by kmer-SVM are: 0.89 for LDwGBM (A), 0.85 for CDwGBM (B), 0.86 for MBwGBM (C) and 0.97 for NPwGBM (D) datasets. **(E-H)** Precision recall curves depicting the positive predictive value (PPV), calculated as true positive / (true positive + false positive), versus the TPR. AUC of 0.75 for LDwGBM (E) and 0.88 for NPwGBM (H) indicate reasonable confidence in the classification while AUC of 0.49 for CDwGBM (F) and 0.55 for MBwGBM (G) indicate a low probability that the region is correctly labeled when the sequence is classified as positive.

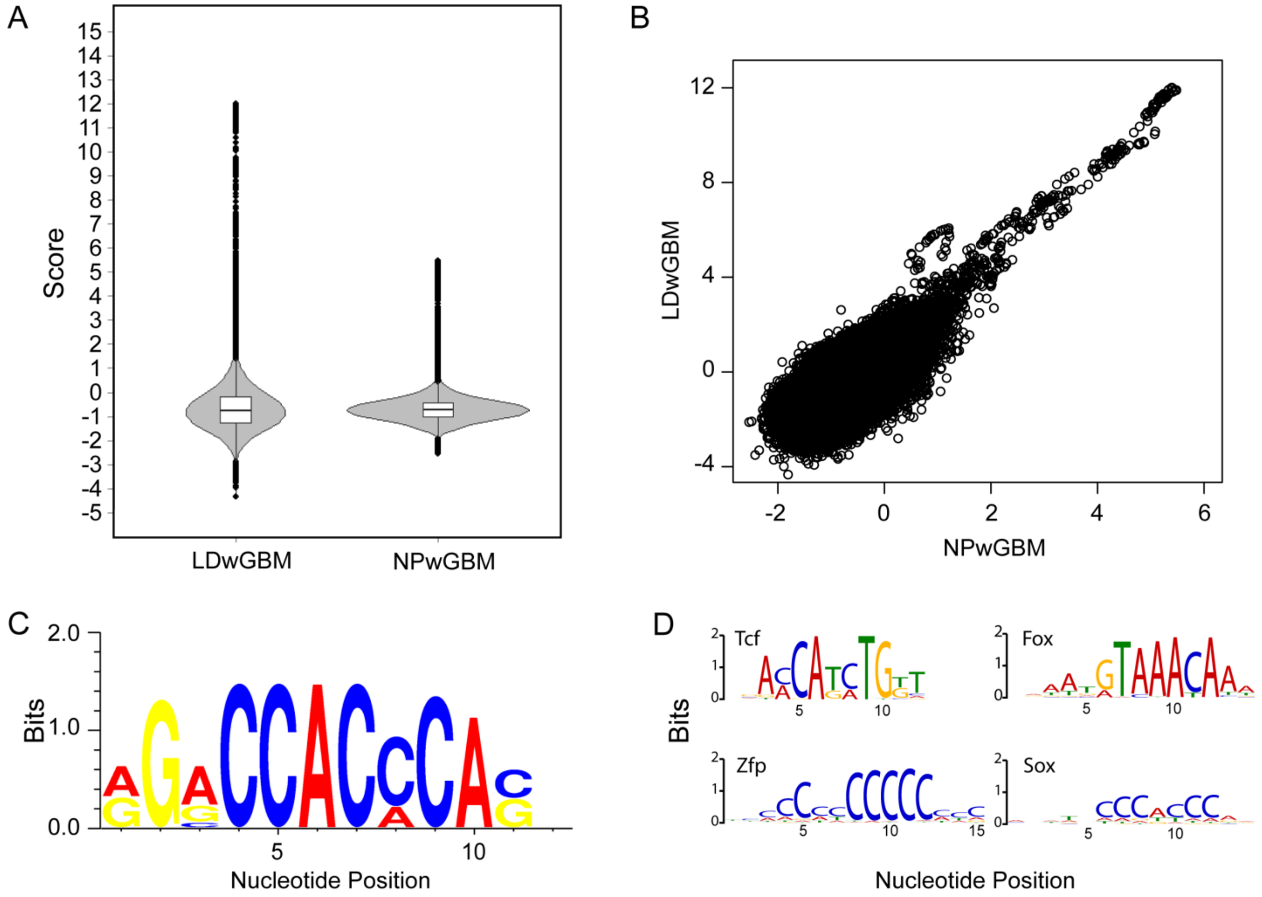


Figure 3.3. Assessment of genomic kmer-SVM predictions using classifiers trained on LDwGBM and NPwGBM datasets. (A) All genomic sequences matching the restricted 548 GBM 12-mers (wGMB) were identified and the 600bp surrounding each GBM were assessed and scored using the kmer-SVM classifier that was trained on each of the two datasets. **(B)** Correlation plot depicting the relationship between LDwGBM and NPwGBM scores; scores >1 are highly correlated in the two datasets. **(C)** GLI motif generated from overlapping high weighted k-mers shared between LDwGBM and NPwGBM classifiers. **(D)** High weighted k-mers (identified by TOMTOM) represented in either LDwGBM (Tcf and Zfp) or NPwGBM (Fox and Sox).

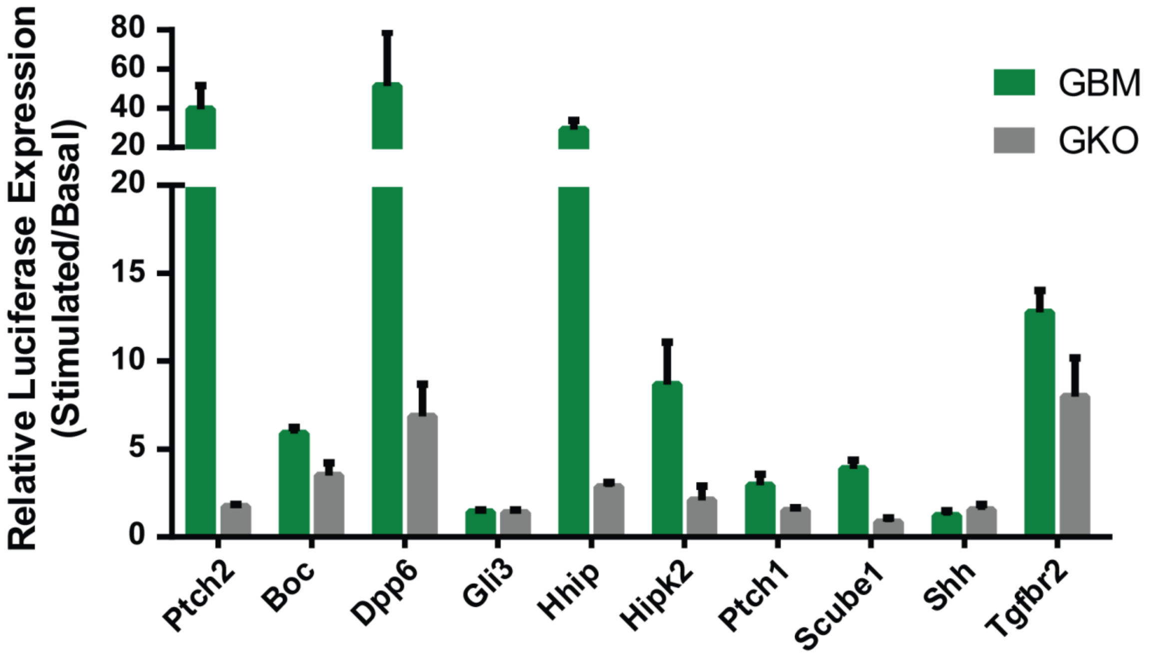


Figure 3.4. Functional verification of GLI-dependent enhancer activity. Putative regulatory regions were cloned upstream of a minimal promoter co-transfected into C2C12 cells, along with a GLI1 expression vector. Relative activity is plotted (stimulated/basal). The Ptch2 region is used as a positive control. Novel regions annotated to the *Boc*, *Dpp6*, *Hhip*, *Hipk2*, *Ptch1*, *Scube1*, and *Tgfbr2* loci exhibit upregulation in response to GLI1 co-transfection (green). Dependence on GLI was assessed by mutating all putative GLI TFBS (GKO) within the sequence and retesting in the assay (gray). Error bars represent the standard deviation of three experimental replicates.

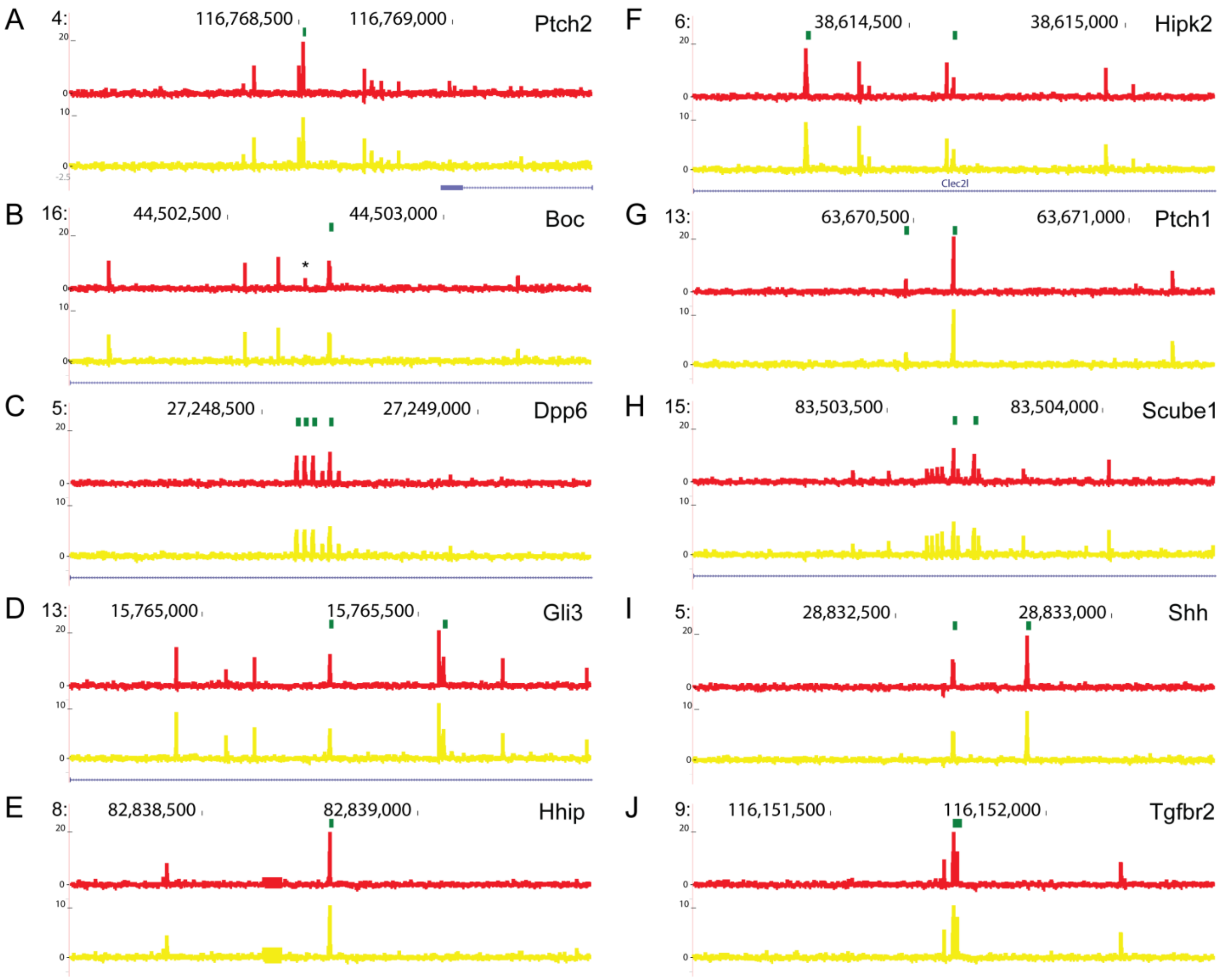


Figure 3.5. K-mer weights plotted across sequences that show enhancer activity. Diagrams were generated in UCSC Genome browser and show coordinate information. Green boxes represent GBM. Weights for LDwGBM and NPwGBM are represented by the red and yellow lines, respectively. Refseq gene annotations are represented in blue. A putative Krox-20 TFBS (*) that has a high weight in the LDwGBM classifier but not the NPwGBM classifier occurs in the sequence annotated to *Boc*. Note that most sequences show weighted k-mers located several hundred bp from the central GBM, suggesting that sequence motifs that predict Hh enhancer activity may be distributed.

Annotated Gene	**Genomic Coordinates (mm9)**	**Hh Responsive**	**LD**	**CD**	**MB**	**NP**
Ptch2	chr4:116,767,757-116,769,455	+	+	+	+	+
Boc	chr16:44,502,136-44,503,346	+	-	+	+	-
Dpp6	chr5:27,248,056-27,249,266	+	+	-	-	-
Gli3	chr13:15,764,694-15,765,904	-	-	-	-	-
Hhip	chr8:82,838,195-82,839,405	+	+	-	-	+
Hipk2	chr6:38,614,001-38,615,211	+	-	-	-	-
Ptch1	chr13:63669992-63671202	+	+	-	+	+
Scube1	chr15:83503053-83504263	+	-	-	-	-
Shh	chr5:28832033-28833243	-	-	-	-	-
Tgfbr2	chr9:116,151,184-116,152,394	+	-	-	-	-

Table 3.1. Assessment of predicted Hh enhancer regions. Seven of the nine regions predicted to be GLI-driven enhancers were indeed determined to be Hh responsive and GLI binding site dependent in a cell culture assay. Overlap of the predicted regions with peaks from the GLI^{FLAG} ChIP datasets (LD, CD, MB, NP) is indicated by the plus sign. Boc, Hipk2, Scube1 and Tgfbr2 were predicted by kmer-SVM and found to be positive, even though those regions do not overlap any of the peaks identified in the LD or NP datasets used to generate the kmer-SVM classifier.

Gli binding motifs (12mer)	**Confidence**
AGCCCACCCAGG	HC
AGCCCACCCACG	HC
AGCCCACCCACA	HC
AGACCTCCCAGG	HC
AGACCTCCCACG	HC
AGACCTCCCACA	HC
AGACCACCCTGG	HC
AGACCACCCTCG	HC
AGACCACCCTCA	HC
AGACCACCCGGG	HC
AGACCACCCGCG	HC
AGACCACCCGCA	HC
AGACCACCCATG	HC
AGACCACCCAGG	HC
AGACCACCCAGC	HC
AGACCACCCAGA	HC
AGACCACCCACT	HC
AGACCACCCACG	HC
AGACCACCCACC	HC
AGACCACCCACA	HC
AGACCACCCAAG	HC
AGACCACCCAAC	HC
AGACCACCCAAA	HC
AGACCACACAGG	HC
AGACCACACAGA	HC
AGACCACACACG	HC
AGACCACACACC	HC
AGACCACACACA	HC
AGACCACACAAG	HC
AGGCCACCCAGG	HC
AGGCCACCCAGC	HC
AGGCCACCCAGA	HC
AGGCCACCCACG	HC
AGGCCACCCACC	HC
AGGCCACCCACA	HC
AGGCCACCCAAG	HC
AGGCCACCCAAA	HC

Gli binding motifs (12mer)	**Confidence**
AGGCCACACACG	HC
CGACCACCCACG	HC
GGGCCACCCAGG	HC
GGGCCACCCAGA	HC
GGGCCACCCACG	HC
GGGCCACCCACC	HC
GGGCCACCCACA	HC
GGGCCACCCAAG	HC
GGGCCACACACG	HC
GGCCCACCCAGG	HC
GGCCCACCCAGA	HC
GGCCCACCCACG	HC
GGCCCACCCACA	HC
GGACCTCCCAGG	HC
GGACCTCCCACG	HC
GGACCTCCCACA	HC
GGACCACCCTGG	HC
GGACCACCCTGA	HC
GGACCACCCTCG	HC
GGACCACCCTCA	HC
GGACCACCCGGG	HC
GGACCACCCGCG	HC
GGACCACCCGCA	HC
GGACCACCCATG	HC
GGACCACCCATA	HC
GGACCACCCAGG	HC
GGACCACCCAGC	HC
GGACCACCCAGA	HC
GGACCACCCACG	HC
GGACCACCCACC	HC
GGACCACCCACA	HC
GGACCACCCAAG	HC
GGACCACCCAAC	HC
GGACCACCCAAA	HC
GGACCACACAGG	HC
GGACCACACAGA	HC
GGACCACACACG	HC

Gli binding motifs (12mer)	**Confidence**
GGACCACACACC	HC
GGACCACACACA	HC
GGACCACACAAG	HC
TGACCACCCAGG	HC
TGACCACCCAGA	HC
TGACCACCCACG	HC
TGACCACCCACC	HC
TGACCACCCACA	HC
TGACCACCCAAG	HC
TGGCCACCCACG	HC
TGGCCACCCACA	HC
AGCCCACCCAGA	MC
AGCCCACCCACT	MC
AGCCCACCCACC	MC
AGCCCACCCAAG	MC
AGACCTCCCACC	MC
AGACCTCCCAAG	MC
AGACCCCCCACG	MC
AGACCACCTAGG	MC
AGACCACCTACG	MC
AGACCACCTACA	MC
AGACCACCCTCC	MC
AGACCACCCCGG	MC
AGACCACCCCCG	MC
AGACCACCCATT	MC
AGACCACCCATC	MC
AGACCACCCATA	MC
AGACCACCCAGT	MC
AGACCACCCAAT	MC
AGACCACCAAGG	MC
AGACCACCAACG	MC
AGACCACACATG	MC
AGACCACACAGT	MC
AGACCACACAGC	MC
AGACCACACACT	MC
AGACCACACAAA	MC
ACACCACCCACG	MC

AAACCACCCACG	MC
ATACCACCCAGG	MC
ATACCACCCACG	MC
AGGCCACCCATG	MC
AGGCCACCCACT	MC
CGGCCACCCACG	MC
CGCCCACCCACG	MC
CGACCACCCATG	MC
CGACCACCCAGT	MC
CGACCACCCAGG	MC
CGACCACCCAGC	MC
CGACCACCCAGA	MC
CGACCACCCACT	MC
CGACCACCCACC	MC
CGACCACCCACA	MC
CGACCACCCAAG	MC
CGACCACCCAAA	MC
CGACCACACACG	MC
CGACCACACACA	MC
GAACCACCCAGG	MC
GAACCACCCACG	MC
GTACCACCCAGG	MC
GTACCACCCAGA	MC
GTACCACCCACG	MC
GTACCACCCACC	MC
GTACCACCCACA	MC
GTACCACCCAAG	MC
GGGCCTCCCACG	MC
GGGCCACCCATG	MC
GGGCCACCCATA	MC
GGGCCACCCAGT	MC
GGGCCACCCAGC	MC
GGGCCACCCACT	MC
GGGCCACCCAAT	MC
GGGCCACCCAAC	MC
GGGCCACCCAAA	MC
GGGCCACACAGG	MC
GGGCCACACACA	MC
GGCCCACCCATG	MC

GGCCCACCCAGT	MC
GGCCCACCCAGC	MC
GGCCCACCCACT	MC
GGCCCACCCACC	MC
GGCCCACCCAAG	MC
GGCCCACCCAAA	MC
GGCCCACACACG	MC
GGACCTCCCAGC	MC
GGACCTCCCAGA	MC
GGACCTCCCACT	MC
GGACCTCCCACC	MC
GGACCTCCCAAG	MC
GGACCGCCCAGG	MC
GGACCGCCCACG	MC
GGACCCCCCAGG	MC
GGACCCCCCACG	MC
GGACCCCCCACA	MC
GGACCACCTAGG	MC
GGACCACCTAGA	MC
GGACCACCTACT	MC
GGACCACCTACG	MC
GGACCACCTACC	MC
GGACCACCTACA	MC
GGACCACCTAAG	MC
GGACCACCCTTG	MC
GGACCACCCTGC	MC
GGACCACCCTCT	MC
GGACCACCCTCC	MC
GGACCACCCTAG	MC
GGACCACCCGGC	MC
GGACCACCCGGA	MC
GGACCACCCGCT	MC
GGACCACCCGCC	MC
GGACCACCCGAG	MC
GGACCACCCCGG	MC
GGACCACCCCGA	MC
GGACCACCCCCG	MC
GGACCACCCCCC	MC
GGACCACCCCCA	MC

GGACCACCCCAG	MC
GGACCACCCATT	MC
GGACCACCCATC	MC
GGACCACCCAGT	MC
GGACCACCCACT	MC
GGACCACCCAAT	MC
GGACCACCAAGG	MC
GGACCACCAACG	MC
GGACCACACTCG	MC
GGACCACACGCG	MC
GGACCACACATG	MC
GGACCACACATC	MC
GGACCACACATA	MC
GGACCACACAGT	MC
GGACCACACAGC	MC
GGACCACACACT	MC
GGACCACACAAT	MC
GGACCACACAAC	MC
GGACCACACAAA	MC
TGACCTCCCACG	MC
TGACCACCCTCG	MC
TGACCACCCATG	MC
TGACCACCCATC	MC
TGACCACCCATA	MC
TGACCACCCAGT	MC
TGACCACCCAGC	MC
TGACCACCCACT	MC
TGACCACCCAAT	MC
TGACCACCCAAC	MC
TGACCACCCAAA	MC
TGACCACACAGG	MC
TGACCACACACG	MC
TGACCACACACC	MC
TGACCACACACA	MC
TGACCACACAAG	MC
TGGCCACCCAGG	MC
TGCCCACCCAGG	MC
TGCCCACCCACG	MC
AGCCCACCCATG	MC

AGCCCACCCAGC	MC
AGCCCACCCAAA	MC
AGCCCACACAGG	MC
AGCCCACACACG	MC
AGACCTCCCAGA	MC
AGACCACACAAC	MC
AGGCCACACACA	MC
AGACCACCCTGA	MC
AGGCCACCCTCG	MC
AGGCCACCCAGT	MC
AGGCCACACAGG	MC
GGGCCACCCTCG	MC
AGACCACCCGGA	MC
AGACCACACTGG	MC
AGACCACACTCG	MC
AGACCACACGCG	MC
GGACCACACTGG	MC
AGATCACCCACG	LC
AGACTACCCACG	LC
AGACCAGCCACG	LC
AGAACACCCAGG	LC
AGAACACCCACG	LC
ACACCACCCAGG	LC
CGGCCACCCAGG	LC
CGACCACCCATA	LC
CGACCACCCAAC	LC
CGACCACACAGG	LC
GCACCACCCAGG	LC
GCACCACCCAGA	LC
GCACCACCCACG	LC
GCACCACCCACC	LC
GCACCACCCACA	LC
GCACCACCCAAG	LC
GAACCACCCACC	LC
GAACCACCCACA	LC
GAACCACCCAAG	LC
GGTCCACCCAGG	LC
GGTCCACCCACG	LC
GGATCACCCAGG	LC

GGATCACCCACG	LC
GGATCACCCACA	LC
GGACTACCCAGG	LC
GGACTACCCACG	LC
GGACTACCCACA	LC
GGACCTCCCATG	LC
GGACCTCCCAGT	LC
GGACCTCCCAAA	LC
GGACCTCACACG	LC
GGACCCCCCACC	LC
GGACCATCCACG	LC
GGACCAGCCAGG	LC
GGACCAGCCACG	LC
GGACCAGCCACC	LC
GGACCAGCCACA	LC
GGACCAGCCAAG	LC
GGACCACCTATG	LC
GGACCACCGACG	LC
GGACCACCCGTG	LC
GGACCACCAAGA	LC
GGACCACCAACC	LC
GGACCACCAACA	LC
GGACCACCAAAG	LC
GGAACACCCAGG	LC
GGAACACCCAGA	LC
GGAACACCCACG	LC
GGAACACCCACC	LC
GGAACACCCACA	LC
GGAACACCCAAG	LC
TGACCACCCGCG	LC
AGCCCACACACA	LC
AGACCTCACACG	LC
CGCCCACCCACA	LC
TGCCCACCCACA	LC
AGGCCTCCCACG	LC
AGCCCACCTGGG	LC
AGCCCACCTGGA	LC
AGCCCACCTGCG	LC
AGCCCACCTGCA	LC

AGCCCACCGGGG	LC
AGCCCACCGGCG	LC
AGCCCACCCTGG	LC
AGCCCACCCTGA	LC
AGCCCACCCTCG	LC
AGCCCACCCGGG	LC
AGCCCACCCGGA	LC
AGCCCACCCGCG	LC
AGCCCACCCGCA	LC
AGCCCACATGGG	LC
AGCCCACATGCG	LC
AGCCCACACGGG	LC
AGCCCACACGGA	LC
AGCCCACACGCG	LC
AGCCCACACGCA	LC
AGACCTCCTGGG	LC
AGACCTCCTGCG	LC
AGACCTCCCGGG	LC
AGACCTCCCGGA	LC
AGACCTCCCGCG	LC
AGACCTCCCGCA	LC
AGACCACCTTGG	LC
AGACCACCTTGA	LC
AGACCACCTTCG	LC
AGACCACCTTCA	LC
AGACCACCTGGG	LC
AGACCACCTGGA	LC
AGACCACCTGCG	LC
AGACCACCTGCA	LC
AGACCACCGTGG	LC
AGACCACCGTCG	LC
AGACCACCGGGG	LC
AGACCACCGGGA	LC
AGACCACCGGCG	LC
AGACCACCGGCA	LC
AGACCACATTGG	LC
AGACCACATTCG	LC
AGACCACATGGG	LC
AGACCACATGGA	LC

AGACCACATGCG	LC
AGACCACATGCA	LC
AGACCACAGGGG	LC
AGACCACAGGGA	LC
AGACCACAGGCG	LC
AGACCACAGGCA	LC
AGACCACACTGA	LC
AGACCACACTCA	LC
AGACCACACGGG	LC
AGACCACACGGA	LC
AGACCACACGCA	LC
GGTCCACCCGGG	LC
GGTCCACCCGCG	LC
GGCCCTCCTGGG	LC
GGCCCTCCTGCG	LC
GGCCCTCCCGGG	LC
GGCCCTCCCGGA	LC
GGCCCTCCCGCG	LC
GGCCCTCCCGCA	LC
GGCCCACCTTGG	LC
GGCCCACCTTGA	LC
GGCCCACCTTCG	LC
GGCCCACCTTCA	LC
GGCCCACCTGGG	LC
GGCCCACCTGGA	LC
GGCCCACCTGCG	LC
GGCCCACCTGCA	LC
GGCCCACCGTGG	LC
GGCCCACCGTCG	LC
GGCCCACCGGGG	LC
GGCCCACCGGGA	LC
GGCCCACCGGCG	LC
GGCCCACCGGCA	LC
GGCCCACCCTGG	LC
GGCCCACCCTGA	LC
GGCCCACCCTCG	LC
GGCCCACCCTCA	LC
GGCCCACCCGGG	LC
GGCCCACCCGGA	LC

GGCCCACCCGCG	LC
GGCCCACCCGCA	LC
GGCCCACATTGG	LC
GGCCCACATTCG	LC
GGCCCACATGGG	LC
GGCCCACATGGA	LC
GGCCCACATGCG	LC
GGCCCACATGCA	LC
GGCCCACAGGGG	LC
GGCCCACAGGGA	LC
GGCCCACAGGCG	LC
GGCCCACAGGCA	LC
GGCCCACACTGG	LC
GGCCCACACTGA	LC
GGCCCACACTCG	LC
GGCCCACACTCA	LC
GGCCCACACGGG	LC
GGCCCACACGGA	LC
GGCCCACACGCG	LC
GGCCCACACGCA	LC
GGACCTCCTTGG	LC
GGACCTCCTTCG	LC
GGACCTCCTGGG	LC
GGACCTCCTGGA	LC
GGACCTCCTGCG	LC
GGACCTCCTGCA	LC
GGACCTCCGGGG	LC
GGACCTCCGGGA	LC
GGACCTCCGGCG	LC
GGACCTCCGGCA	LC
GGACCTCCCTGG	LC
GGACCTCCCTGA	LC
GGACCTCCCTCG	LC
GGACCTCCCTCA	LC
GGACCTCCCGGG	LC
GGACCTCCCGGA	LC
GGACCTCCCGCG	LC
GGACCTCCCGCA	LC
GGACCTCATGGG	LC

GGACCTCATGGA	LC
GGACCTCATGCG	LC
GGACCTCATGCA	LC
GGACCTCACGGG	LC
GGACCTCACGGA	LC
GGACCTCACGCG	LC
GGACCTCACGCA	LC
GGACCACCTTGG	LC
GGACCACCTTGA	LC
GGACCACCTTCG	LC
GGACCACCTTCA	LC
GGACCACCTGGG	LC
GGACCACCTGGA	LC
GGACCACCTGCG	LC
GGACCACCTGCA	LC
GGACCACCGTGG	LC
GGACCACCGTGA	LC
GGACCACCGTCG	LC
GGACCACCGTCA	LC
GGACCACCGGGG	LC
GGACCACCGGGA	LC
GGACCACCGGCG	LC
GGACCACCGGCA	LC
GGACCACATTGG	LC
GGACCACATTGA	LC
GGACCACATTCG	LC
GGACCACATTCA	LC
GGACCACATGGG	LC
GGACCACATGGA	LC
GGACCACATGCG	LC
GGACCACATGCA	LC
GGACCACAGTGG	LC
GGACCACAGTGA	LC
GGACCACAGTCG	LC
GGACCACAGTCA	LC
GGACCACAGGGG	LC
GGACCACAGGGA	LC
GGACCACAGGCG	LC
GGACCACAGGCA	LC

GGACCACACTGA	LC
GGACCACACTCA	LC
GGACCACACGGG	LC
GGACCACACGGA	LC
GGACCACACGCA	LC
AGCCCACCCAGT	LC
AGCCCACCCAAC	LC
AGACCTCCCAGT	LC
AGACCTCCCAGC	LC
AGACCTCCCACT	LC
AGACCTCCCAAA	LC
AGACCGCCCAGG	LC
AGACCGCCCACG	LC
AGACCCCCCAGG	LC
AGACCCCCCACC	LC
AGACCCCCCACA	LC
AGACCCCCCAAG	LC
AGACCACCTAGC	LC
AGACCACCTAGA	LC
AGACCACCTACT	LC
AGACCACCTACC	LC
AGACCACCTAAG	LC
AGACCACCCTTG	LC
AGACCACCCTGT	LC
AGACCACCCTGC	LC
AGACCACCCTCT	LC
AGACCACCCTAT	LC
AGACCACCCTAG	LC
AGACCACCCTAC	LC
AGACCACCCTAA	LC
AGACCACCCGTG	LC
AGACCACCCGGT	LC
AGACCACCCGGC	LC
AGACCACCCGCT	LC
AGACCACCCGCC	LC
AGACCACCCGAG	LC
AGACCACCCGAA	LC
AGACCACCCCTG	LC
AGACCACCCCGT	LC

AGACCACCCCGC	LC
AGACCACCCCGA	LC
AGACCACCCCCT	LC
AGACCACCCCCC	LC
AGACCACCCCCA	LC
AGACCACCCCAG	LC
AGACCACCCCAC	LC
AGACCACCCCAA	LC
AGACCACACCGG	LC
AGACCACACCCG	LC
AGACCACACATT	LC
AGACCACACATC	LC
AGACCACACATA	LC
AGACCACACAAT	LC
AGACAACCCAGG	LC
AGACAACCCACG	LC
AAACCACCCAGG	LC
AAACCACCCACA	LC
ATGCCACCCACG	LC
ATACCACCCATG	LC
ATACCACCCAGT	LC
ATACCACCCAGC	LC
ATACCACCCAGA	LC
ATACCACCCACT	LC
ATACCACCCACC	LC
ATACCACCCACA	LC
ATACCACCCAAT	LC
ATACCACCCAAG	LC
ATACCACCCAAC	LC
ATACCACCCAAA	LC
ATACCACACAGG	LC
ATACCACACACG	LC
AGGCCACCCTGG	LC
AGGCCACCCCCG	LC
AGGCCACCCATC	LC
AGGCCACCCATA	LC
AGGCCACCCAAT	LC
AGGCCACCCAAC	LC
AGGCCACACAGA	LC

AGGCCACACACC	LC
AGGCCACACAAG	LC
GTGCCACCCACG	LC
GTACCACCCATG	LC
GTACCACCCAGT	LC
GTACCACCCAGC	LC
GTACCACCCACT	LC
GTACCACCCAAT	LC
GTACCACCCAAC	LC
GTACCACCCAAA	LC
GTACCACACAGG	LC
GTACCACACACG	LC
GGGCCACCCATC	LC
GGGCCACACACC	LC
GGGCCACACAAG	LC
GGCCCACCCAAC	LC
GGACCACCTAGC	LC
GGACCACCCTGT	LC
GGACCACCCTAT	LC
GGACCACCCTAC	LC
GGACCACCCTAA	LC
GGACCACCCCTG	LC
GGACCACCCCGT	LC
GGACCACCCCGC	LC
GGACCACCCCCT	LC
GGACCACCCCAC	LC
GGACCACCCCAA	LC
GGACCACACCGG	LC
GGACCACACCCG	LC
GGACCACACATT	LC
GGACAACCCAGG	LC
GGACAACCCACG	LC
TGACCACCCTGG	LC
TGACCACCCCGG	LC
TGACCACCCCCG	LC
TGACCACCCATT	LC
TGACCACACAGC	LC
TGACCACACAGA	LC
TGACCACACACT	LC

TTACCACCCAGG	LC			TGGCCACCCACC	LC
TTACCACCCACG	LC	TGGCCACCCAGA	LC	TGGCCACCCAAG	LC

Table S3.1. GLI binding motif 12-mers. Library of 12-mers enriched in GLI^{FLAG} datasets. Motifs were considered high confidence (HC) if the 12-mer occurred in all four GLI^{FLAG} datasets, medium confidence (MC) if it occurred in 2 or 3, or low confidence (LC) if it only occurred in one dataset.

Annotated Gene	**Genomic location Build mm9**
Hdlbp	chr1:95374177-95376523
Slc35f5	chr1:127456701-127457719
Tpd52l1	chr10:31165049-31165879
Gli1	chr10:126775842-126779541
Blmh	chr11:76758416-76760372
Rab34	chr11:78001796-78004008
Mycn	chr12:12944525-12950747
Ptch1	chr13:63663502-63669743
Anks3	chr16:4963972-4964875
Fgf12	chr16:28841169-28841598
Stx5a	chr19:8814998-8816581
Prrg4	chr2:104689887-104690204
Stk35	chr2:129625777-129627521
4933425O20Rik	chr2:130233798-130234557
Ogfr	chr2:180323999-180325004
Zfp704	chr3:9607477-9609137
Ensa	chr3:95428396-95429195
Foxd2	chr4:114493666-114494927
Ptch2	chr4:116767756-116769455
1700041C02Rik	chr4:119087804-119088396
Thrap3	chr4:125878668-125880997
Park7	chr4:150287600-150289290
BC037393	chr5:151467448-151468648
D6Wsu116e	chr6:116157254-116158578
Scap	chr9:110207158-110208277
Eda2r	chrX:94571449-94572464

Table S3.2. Peak coordinates that overlap between all four GLI^{FLAG} datasets. The 26 regions that have shared peaks across all GLI^{FLAG} datasets. Peaks are annotated to nearest genes.

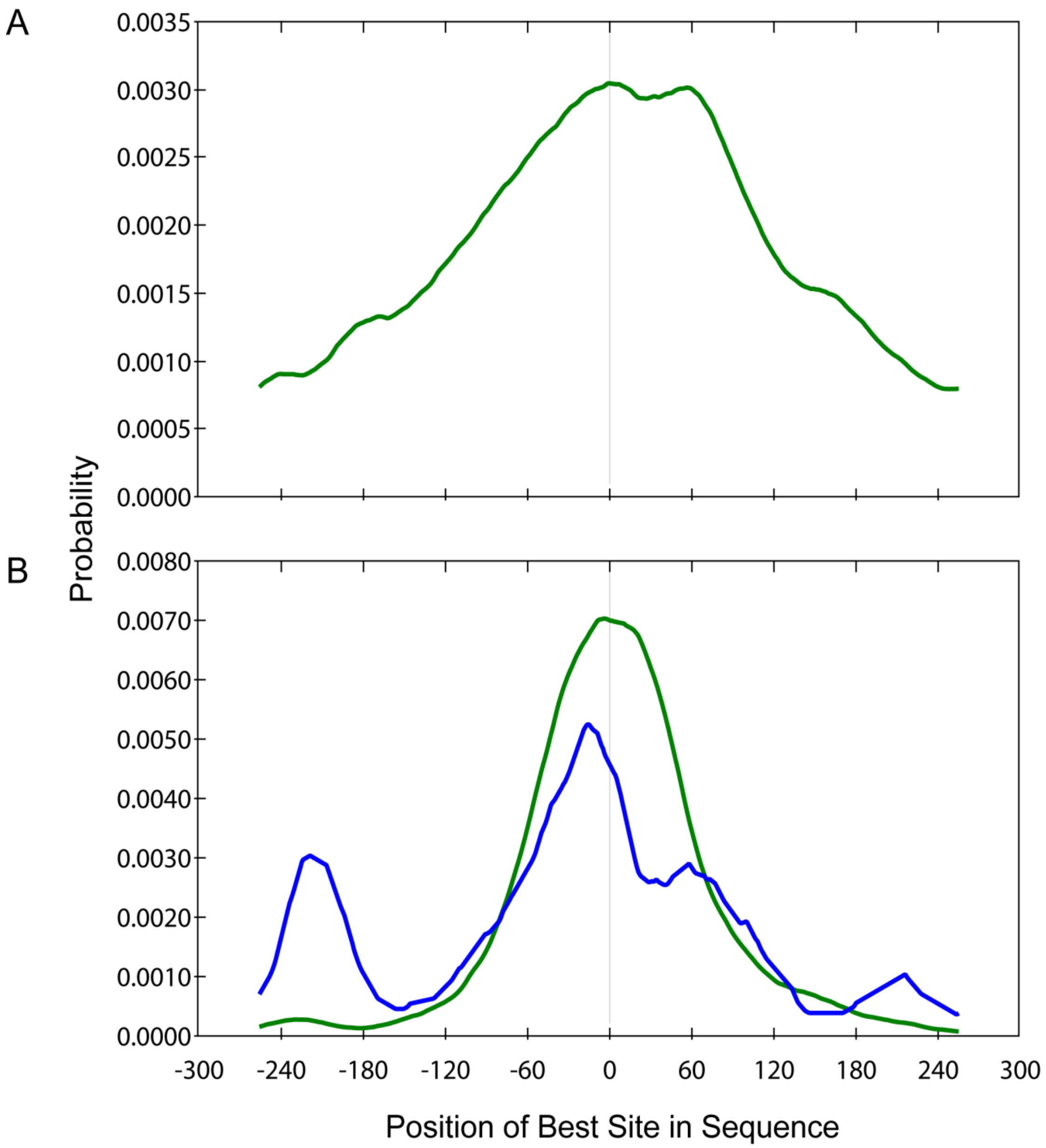


Figure S3.1. Determination of sequence length buffer surrounding the GBM. Plots depicting the positional distribution of the best GLI motif (green) were generated by submitting 300 bp of sequence surrounding the center of each peak to Centrimo. **(A)** LDwGBM shows a broad profile for the best GBM, consistent with ChIP-chip data. **(B)** The profile for the ChIP-seq sequences from NPwGBM is more narrow and suggests that most of the GBM fall within 240 bp around the center of the peak. In neural precursor cells, the motif for the GLI cofactor, Sox, has a profile that contains a central apex plus two additional summits at a distance of 240 bp on either side of the peak. This suggests that context-specific TF binding may occur outside the central peak region.

chromosome	start	end	LDw GBM score	NPw GBM score
chr1	3587497	3588097	0.7	0.3
chr1	3587588	3588188	1.2	0.8
chr1	3587846	3588446	0.4	0.4
chr1	4888793	4889393	0.3	0.2
chr1	5061403	5062003	2.1	0.5
chr1	5723207	5723807	0.7	0.0
chr1	6005639	6006239	0.8	0.6
chr1	6304149	6304749	0.8	0.2
chr1	7026800	7027400	1.0	0.1
chr1	8845727	8846327	0.1	0.2
chr1	8846863	8847463	0.7	0.2
chr1	8903718	8904318	0.7	0.1
chr1	8903766	8904366	0.9	0.1
chr1	9472063	9472663	0.6	0.0
chr1	9547480	9548080	1.3	0.3
chr1	9878331	9878931	0.4	0.1
chr1	10123157	10123757	1.3	0.1
chr1	10159934	10160534	0.4	0.1
chr1	10255539	10256139	1.0	0.0
chr1	10407014	10407614	1.1	0.4
chr1	10476343	10476943	0.3	0.2
chr1	10542821	10543421	1.6	0.2
chr1	10676492	10677092	0.5	0.2
chr1	11556647	11557247	0.6	0.0
chr1	11556678	11557278	0.6	0.2
chr1	11967664	11968264	1.9	0.2
chr1	12059564	12060164	0.3	0.3
chr1	12773280	12773880	0.7	0.1
chr1	12951731	12952331	0.4	0.2
chr1	13504749	13505349	0.2	0.1
chr1	13552845	13553445	2.6	0.7
chr1	13553140	13553740	2.8	0.3
chr1	13963660	13964260	0.5	0.1
chr1	14223396	14223996	0.6	0.1
chr1	15294431	15295031	2.0	0.2
chr1	15417776	15418376	0.9	0.2
chr1	15965121	15965721	0.7	0.1
chr1	15999414	16000014	1.1	0.2
chr1	16036197	16036797	0.0	0.3
chr1	16126714	16127314	1.4	0.9
chr1	17479394	17479994	0.5	0.0
chr1	17504340	17504940	0.3	0.2
chr1	17731913	17732513	3.0	0.8
chr1	17732042	17732642	3.0	0.6
chr1	19228039	19228639	0.1	0.1
chr1	20839991	20840591	0.8	0.1
chr1	21390250	21390850	0.3	0.1
chr1	21770730	21771330	0.1	0.2
chr1	21808362	21808962	0.3	0.0
chr1	22861086	22861686	1.4	0.2
chr1	23722805	23723405	1.0	0.2
chr1	23722862	23723462	1.2	0.2
chr1	24237238	24237838	0.9	0.0
chr1	24823606	24824206	0.5	0.0
chr1	25077359	25077959	0.2	0.1
chr1	25123198	25123798	1.5	0.2
chr1	25406397	25406997	1.8	0.1
chr1	25406432	25407032	1.8	0.3
chr1	25594072	25594672	1.1	0.1
chr1	26325256	26325856	0.3	0.0
chr1	26864740	26865340	0.3	0.1
chr1	27339458	27340058	1.1	0.2
chr1	27351080	27351680	0.7	0.1
chr1	29105779	29106379	1.3	0.0
chr1	29105799	29106399	1.2	0.0
chr1	29626691	29627291	1.0	0.1
chr1	30035432	30036032	0.4	0.2
chr1	30376569	30377169	0.6	0.2
chr1	31085911	31086511	0.4	0.0
chr1	31088854	31089454	0.0	0.0
chr1	31450635	31451235	0.2	0.0
chr1	31596355	31596955	0.3	0.1

chr1	31742046	31742646	1.1	0.4
chr1	33018590	33019190	0.7	0.1
chr1	33117174	33117774	1.8	0.2
chr1	33518563	33519163	1.5	0.1
chr1	33518617	33519217	1.6	0.1
chr1	33797481	33798081	2.0	0.5
chr1	33797720	33798320	1.2	0.1
chr1	33820583	33821183	0.5	0.6
chr1	34109352	34109952	0.4	0.1
chr1	34593375	34593975	1.4	0.4
chr1	34983602	34984202	1.9	0.4
chr1	34983809	34984409	2.3	0.5
chr1	35984923	35985523	0.0	0.4
chr1	36127397	36127997	2.0	0.4
chr1	36533380	36533980	1.1	0.6
chr1	36576831	36577431	2.6	1.1
chr1	37120191	37120791	0.1	0.2
chr1	37251438	37252038	0.8	0.0
chr1	37310144	37310744	0.8	0.3
chr1	37355221	37355821	0.5	0.1
chr1	37463376	37463976	0.9	0.0
chr1	37463581	37464181	1.1	0.2
chr1	37590466	37591066	1.3	0.3
chr1	37590492	37591092	1.4	0.2
chr1	37590518	37591118	1.5	0.2
chr1	37590544	37591144	1.4	0.3
chr1	37623397	37623997	0.7	0.1
chr1	37928508	37929108	0.0	0.0
chr1	37993942	37994542	1.1	0.4
chr1	37994044	37994644	0.0	0.0
chr1	38316421	38317021	1.2	0.6
chr1	38316480	38317080	1.0	0.6
chr1	38534769	38535369	1.5	0.6
chr1	38721537	38722137	0.4	0.0
chr1	38923902	38924502	0.1	0.5
chr1	38924136	38924736	1.2	0.9
chr1	38924175	38924775	1.5	1.1
chr1	38924292	38924892	1.5	1.2

chr1	38924331	38924931	1.7	1.3
chr1	38924409	38925009	1.9	1.4
chr1	38924448	38925048	1.6	1.2
chr1	39668786	39669386	0.4	0.2
chr1	39705638	39706238	0.5	0.1
chr1	39711932	39712532	0.9	0.1
chr1	39713365	39713965	1.6	0.4
chr1	40067917	40068517	1.6	0.1
chr1	40067981	40068581	1.6	0.2
chr1	40287515	40288115	0.1	0.3
chr1	40287613	40288213	0.6	0.6
chr1	40718882	40719482	0.0	0.4
chr1	40830222	40830822	0.8	0.4
chr1	40935328	40935928	1.1	0.2
chr1	41346635	41347235	0.3	0.2
chr1	41768973	41769573	0.2	0.3
chr1	42164674	42165274	0.8	0.3
chr1	43502070	43502670	1.7	0.1
chr1	44846756	44847356	0.3	0.2
chr1	48043163	48043763	0.8	0.1
chr1	48757381	48757981	1.9	0.7
chr1	48931916	48932516	2.7	0.5
chr1	49335477	49336077	0.2	0.4
chr1	49335721	49336321	1.2	0.6
chr1	49908767	49909367	0.2	0.3
chr1	50956466	50957066	0.1	0.1
chr1	53345598	53346198	0.1	0.3
chr1	53799247	53799847	0.4	0.1
chr1	54047502	54048102	0.5	0.0
chr1	54072278	54072878	1.6	0.3
chr1	54176567	54177167	0.6	0.0
chr1	54288808	54289408	0.7	0.2
chr1	54383175	54383775	1.9	0.5
chr1	54387025	54387625	1.5	0.4
chr1	54387299	54387899	1.6	0.6
chr1	54517139	54517739	1.0	0.3
chr1	54530947	54531547	1.8	0.3
chr1	54567172	54567772	0.7	0.1

chr1	54782868	54783468	0.7	0.6
chr1	54782935	54783535	0.5	0.4
chr1	55016357	55016957	1.0	0.6
chr1	56073425	56074025	1.5	0.8
chr1	56073683	56074283	1.9	1.2
chr1	56205110	56205710	0.4	0.0
chr1	56343351	56343951	0.4	0.3
chr1	56499537	56500137	0.5	0.4
chr1	56661064	56661664	0.4	0.2
chr1	56661089	56661689	0.5	0.2
chr1	57961107	57961707	2.0	0.5
chr1	57961140	57961740	1.9	0.4
chr1	58008076	58008676	2.9	1.5
chr1	58008095	58008695	2.8	1.5
chr1	58107997	58108597	1.3	0.0
chr1	58108152	58108752	1.5	0.2
chr1	58360626	58361226	1.0	0.3
chr1	58431250	58431850	0.9	0.5
chr1	58528396	58528996	0.3	0.1
chr1	58656726	58657326	1.1	0.3
chr1	58723003	58723603	0.3	0.1
chr1	59133074	59133674	0.8	0.2
chr1	59432710	59433310	1.2	0.2
chr1	59954114	59954714	1.0	0.1
chr1	60176447	60177047	0.8	0.1
chr1	61573959	61574559	0.9	0.2
chr1	62108284	62108884	1.0	0.1
chr1	62109784	62110384	1.1	0.2
chr1	62114633	62115233	0.5	0.8
chr1	62458899	62459499	1.2	0.6
chr1	62477593	62478193	1.3	0.4
chr1	62683344	62683944	0.8	0.2
chr1	63100532	63101132	1.2	0.4
chr1	63700824	63701424	0.3	0.2
chr1	63700928	63701528	0.3	0.0
chr1	63929166	63929766	0.8	0.2
chr1	64138421	64139021	0.8	0.5
chr1	64384475	64385075	1.3	0.2

chr1	64695128	64695728	0.0	0.3
chr1	64943282	64943882	1.3	0.7
chr1	65251132	65251732	0.2	0.3
chr1	65612857	65613457	2.0	0.9
chr1	65612867	65613467	1.9	0.9
chr1	65842421	65843021	1.1	0.2
chr1	67106933	67107533	0.5	0.1
chr1	67619759	67620359	0.5	0.0
chr1	68029348	68029948	0.8	0.2
chr1	68587471	68588071	0.0	0.2
chr1	69641000	69641600	0.6	0.1
chr1	70114225	70114825	0.5	0.0
chr1	70453531	70454131	0.4	0.3
chr1	70750830	70751430	0.2	0.1
chr1	71887505	71888105	1.0	0.2
chr1	72026765	72027365	0.2	0.0
chr1	72254058	72254658	1.2	0.4
chr1	72751159	72751759	0.9	0.1
chr1	73223612	73224212	1.7	0.2
chr1	73731980	73732580	1.2	0.1
chr1	75359007	75359607	0.7	0.1
chr1	75491418	75492018	0.1	0.1
chr1	75517680	75518280	1.3	0.3
chr1	75525034	75525634	0.4	0.0
chr1	75664087	75664687	0.9	0.6
chr1	76243575	76244175	1.4	0.2
chr1	76546995	76547595	0.1	0.1
chr1	77201537	77202137	0.8	0.5
chr1	77304468	77305068	1.8	0.0
chr1	77798374	77798974	0.9	0.1
chr1	78422306	78422906	0.8	0.1
chr1	79090147	79090747	0.0	0.1
chr1	79932530	79933130	1.4	0.4
chr1	79932820	79933420	0.9	0.4
chr1	80236449	80237049	2.2	0.7
chr1	80264794	80265394	2.4	0.5
chr1	81043211	81043811	0.4	0.1
chr1	81861035	81861635	0.5	0.3

chr1	81861106	81861706	0.1	0.0
chr1	82033827	82034427	0.8	0.7
chr1	82033854	82034454	0.8	0.7
chr1	82258491	82259091	3.4	1.3
chr1	82258781	82259381	4.2	1.2
chr1	82823462	82824062	0.2	0.0
chr1	84036917	84037517	0.7	0.1
chr1	84267874	84268474	0.6	0.0
chr1	84268523	84269123	0.3	0.1
chr1	84321261	84321861	0.5	0.0
chr1	84368458	84369058	0.8	0.3
chr1	84443514	84444114	0.5	0.0
chr1	84579102	84579702	1.2	0.2
chr1	84870201	84870801	0.7	0.1
chr1	87602425	87603025	1.2	0.4
chr1	87813558	87814158	3.1	1.9
chr1	87813802	87814402	2.5	1.8
chr1	87865926	87866526	0.4	0.1
chr1	88038640	88039240	1.8	0.3
chr1	88371531	88372131	0.9	0.3
chr1	89271564	89272164	0.0	0.3
chr1	89532378	89532978	0.3	0.0
chr1	89751849	89752449	0.7	0.0
chr1	90285339	90285939	0.1	0.0
chr1	90616098	90616698	1.1	0.2
chr1	90637623	90638223	0.6	0.3
chr1	90665449	90666049	1.3	0.2
chr1	90665468	90666068	1.3	0.1
chr1	90762002	90762602	0.9	0.3
chr1	90978194	90978794	1.1	0.1
chr1	91090882	91091482	2.0	0.2
chr1	91396066	91396666	1.0	0.3
chr1	91660947	91661547	0.8	0.0
chr1	91711063	91711663	1.4	0.3
chr1	92232131	92232731	1.0	0.6
chr1	92301760	92302360	0.3	0.2
chr1	92301801	92302401	0.4	0.3
chr1	92369536	92370136	0.8	0.0

chr1	92378845	92379445	0.4	0.1
chr1	92379002	92379602	0.2	0.1
chr1	92622432	92623032	1.4	0.4
chr1	92690829	92691429	1.4	0.9
chr1	92952085	92952685	0.1	0.1
chr1	93073516	93074116	0.9	0.6
chr1	93167832	93168432	1.0	0.3
chr1	93180693	93181293	0.2	0.2
chr1	93265187	93265787	0.5	0.2
chr1	93265359	93265959	0.8	0.5
chr1	93563128	93563728	0.3	0.0
chr1	93694993	93695593	0.9	0.1
chr1	93808568	93809168	1.9	0.4
chr1	93808751	93809351	1.7	0.3
chr1	94061751	94062351	0.9	0.3
chr1	94193930	94194530	0.1	0.1
chr1	94507566	94508166	0.8	0.2
chr1	94723808	94724408	0.5	0.2
chr1	94735502	94736102	0.8	0.3
chr1	94811814	94812414	0.1	0.3
chr1	94832832	94833432	0.1	0.3
chr1	94879251	94879851	0.3	0.2
chr1	94879476	94880076	0.8	0.0
chr1	94879488	94880088	0.8	0.0
chr1	94944629	94945229	0.0	0.2
chr1	94989485	94990085	1.7	0.2
chr1	95073408	95074008	1.3	0.5
chr1	95073529	95074129	1.6	0.2
chr1	95073574	95074174	1.5	0.1
chr1	95226272	95226872	0.5	0.0
chr1	95374431	95375031	0.2	0.2
chr1	95374615	95375215	0.0	0.5
chr1	95461016	95461616	1.4	0.5
chr1	95542751	95543351	1.1	0.8
chr1	95595255	95595855	1.3	0.4
chr1	96429589	96430189	0.7	0.5
chr1	96460205	96460805	0.9	0.3
chr1	96554281	96554881	0.4	0.1

chr1	96685689	96686289	0.7	0.1
chr1	97320574	97321174	0.8	0.2
chr1	99947459	99948059	2.1	0.3
chr1	100155930	100156530	0.0	0.2
chr1	100679858	100680458	0.8	0.3
chr1	100680011	100680611	1.2	0.4
chr1	101537290	101537890	0.2	0.2
chr1	102555674	102556274	0.2	0.1
chr1	102616625	102617225	0.9	0.1
chr1	104317551	104318151	1.5	0.1
chr1	107273156	107273756	0.2	0.1
chr1	107451799	107452399	0.6	0.4
chr1	107690411	107691011	0.8	0.4
chr1	107716235	107716835	0.3	0.3
chr1	107766663	107767263	1.8	0.6
chr1	107782299	107782899	0.1	0.2
chr1	108087176	108087776	0.6	0.0
chr1	108268892	108269492	0.7	0.4
chr1	109717474	109718074	0.5	0.2
chr1	110459102	110459702	1.0	0.2
chr1	110955073	110955673	0.4	0.0
chr1	110997170	110997770	0.1	0.1
chr1	112111586	112112186	0.3	0.1
chr1	112971026	112971626	1.7	0.0
chr1	113406467	113407067	0.8	0.6
chr1	113710670	113711270	1.5	0.0
chr1	113998336	113998936	0.1	0.0
chr1	115400418	115401018	0.8	0.1
chr1	116508023	116508623	0.2	0.3
chr1	117078348	117078948	0.5	0.3
chr1	117244322	117244922	0.3	0.3
chr1	118311346	118311946	0.7	0.2
chr1	120544640	120545240	0.1	0.7
chr1	120767868	120768468	0.9	0.0
chr1	120942827	120943427	1.5	0.4
chr1	120943037	120943637	1.6	0.6
chr1	121043940	121044540	0.3	0.3
chr1	121576346	121576946	0.5	0.1
chr1	121965855	121966455	0.4	0.1
chr1	122055225	122055825	0.7	0.2
chr1	122203865	122204465	0.0	0.1
chr1	122771283	122771883	0.8	0.0
chr1	123073168	123073768	0.0	0.7
chr1	123769927	123770527	0.5	0.0
chr1	124021917	124022517	0.1	0.0
chr1	124127903	124128503	1.6	0.3
chr1	124128093	124128693	1.5	0.7
chr1	124352337	124352937	1.0	0.4
chr1	124352519	124353119	0.6	0.2
chr1	125138573	125139173	0.5	0.4
chr1	126130535	126131135	0.9	0.1
chr1	126130629	126131229	0.5	0.1
chr1	126935121	126935721	0.6	0.3
chr1	127456890	127457490	1.1	0.7
chr1	127542776	127543376	1.1	0.2
chr1	127587623	127588223	1.3	0.0
chr1	127611885	127612485	0.8	0.0
chr1	127810549	127811149	0.0	0.4
chr1	129520754	129521354	0.8	0.2
chr1	130146291	130146891	0.2	0.4
chr1	130588519	130589119	1.1	0.0
chr1	130814015	130814615	0.3	0.4
chr1	131264285	131264885	0.1	0.1
chr1	131683795	131684395	2.4	0.7
chr1	131683875	131684475	2.4	0.3
chr1	132491151	132491751	1.2	0.4
chr1	133730886	133731486	0.5	0.2
chr1	133974327	133974927	1.6	0.3
chr1	134070192	134070792	0.9	0.1
chr1	134088495	134089095	0.3	0.4
chr1	134214304	134214904	1.2	0.1
chr1	134935066	134935666	1.2	0.6
chr1	135246492	135247092	0.7	0.2
chr1	135277536	135278136	0.1	0.1
chr1	135328831	135329431	0.4	0.3
chr1	136014721	136015321	0.4	0.1

chr1	136340711	136341311	0.4	0.4
chr1	136547886	136548486	1.4	0.0
chr1	137204467	137205067	0.1	0.1
chr1	137565459	137566059	0.5	0.6
chr1	137776826	137777426	0.5	0.1
chr1	137786132	137786732	0.2	0.1
chr1	137834537	137835137	0.5	0.5
chr1	137991408	137992008	2.0	0.4
chr1	138113880	138114480	0.1	0.2
chr1	138113962	138114562	0.5	0.4
chr1	138114057	138114657	0.1	0.3
chr1	138254303	138254903	0.2	0.1
chr1	139183288	139183888	0.9	0.2
chr1	139789215	139789815	1.6	0.6
chr1	139791383	139791983	1.3	0.0
chr1	140152141	140152741	1.3	0.4
chr1	140313669	140314269	0.5	0.1
chr1	140426693	140427293	0.9	0.1
chr1	140583083	140583683	0.1	0.1
chr1	143940556	143941156	0.3	0.1
chr1	145418005	145418605	0.9	0.0
chr1	145566866	145567466	0.8	0.2
chr1	145761689	145762289	0.6	0.2
chr1	147106914	147107514	0.6	0.2
chr1	148165241	148165841	0.1	0.1
chr1	148944566	148945166	0.9	0.4
chr1	149163350	149163950	0.3	0.0
chr1	149461361	149461961	1.7	0.2
chr1	149461511	149462111	2.6	0.9
chr1	149890370	149890970	0.2	0.0
chr1	151010474	151011074	0.4	0.0
chr1	151425058	151425658	2.2	1.0
chr1	151425303	151425903	2.3	0.6
chr1	151577627	151578227	0.3	0.2
chr1	152984625	152985225	0.8	0.1
chr1	153874090	153874690	0.7	0.2
chr1	154252755	154253355	0.1	0.1
chr1	154423595	154424195	0.1	0.1
chr1	155019301	155019901	0.6	0.1
chr1	155270926	155271526	0.5	0.4
chr1	155288071	155288671	0.2	0.2
chr1	155552065	155552665	0.4	0.8
chr1	155747284	155747884	2.3	0.6
chr1	156486803	156487403	0.1	0.0
chr1	156930807	156931407	0.9	0.5
chr1	156996429	156997029	0.4	0.2
chr1	157076184	157076784	1.1	0.2
chr1	157076223	157076823	0.9	0.1
chr1	157900999	157901599	0.1	0.1
chr1	158354281	158354881	0.2	0.1
chr1	158615859	158616459	0.2	0.2
chr1	158736226	158736826	2.5	0.3
chr1	158953487	158954087	0.2	0.0
chr1	159572338	159572938	0.5	0.3
chr1	159572353	159572953	0.6	0.4
chr1	159601822	159602422	0.3	0.1
chr1	159827331	159827931	1.4	0.7
chr1	159827381	159827981	1.4	0.7
chr1	160669129	160669729	1.0	0.0
chr1	160682132	160682732	0.2	0.2
chr1	161125465	161126065	0.4	0.0
chr1	161277574	161278174	0.8	0.1
chr1	161492874	161493474	0.7	0.0
chr1	162209983	162210583	4.3	0.6
chr1	162210015	162210615	4.4	0.6
chr1	162210047	162210647	4.4	0.7
chr1	162210079	162210679	4.5	0.6
chr1	162210111	162210711	4.6	0.7
chr1	162210143	162210743	4.7	0.6
chr1	162578450	162579050	0.2	0.4
chr1	163200019	163200619	0.7	0.2
chr1	163524927	163525527	0.5	0.0
chr1	163787101	163787701	1.7	0.3
chr1	164391836	164392436	0.5	0.2
chr1	164454371	164454971	1.1	0.1
chr1	164906862	164907462	1.3	0.9

chr1	165100413	165101013	0.2	0.0
chr1	165204497	165205097	0.0	0.1
chr1	165369332	165369932	1.4	0.7
chr1	165539936	165540536	1.5	0.1
chr1	165599948	165600548	2.5	0.7
chr1	165710392	165710992	0.6	0.3
chr1	165774540	165775140	0.0	0.3
chr1	166051435	166052035	0.1	0.2
chr1	166664635	166665235	0.9	0.8
chr1	166664673	166665273	0.8	0.8
chr1	166664711	166665311	0.8	0.9
chr1	166664749	166665349	0.9	0.9
chr1	166717329	166717929	1.0	0.0
chr1	166846362	166846962	0.6	0.4
chr1	167618712	167619312	1.5	1.1
chr1	167618960	167619560	0.6	0.7
chr1	168132037	168132637	0.4	0.1
chr1	168341568	168342168	2.0	0.6
chr1	168673166	168673766	0.6	0.2
chr1	169094282	169094882	0.8	0.4
chr1	170117484	170118084	1.8	0.3
chr1	170117658	170118258	1.6	0.4
chr1	170647234	170647834	0.3	0.2
chr1	170662941	170663541	0.5	0.1
chr1	170896101	170896701	0.2	0.0
chr1	171090336	171090936	2.2	0.6
chr1	171090362	171090962	2.2	0.5
chr1	171090388	171090988	1.8	0.3
chr1	171292616	171293216	1.3	0.2
chr1	171489268	171489868	0.4	0.1
chr1	171768846	171769446	0.8	0.3
chr1	171768899	171769499	0.6	0.2
chr1	171832242	171832842	1.0	0.1
chr1	172231177	172231777	0.9	0.4
chr1	172231393	172231993	0.6	0.1
chr1	172739356	172739956	0.3	0.0
chr1	172784390	172784990	1.9	0.6
chr1	173303828	173304428	2.8	0.6
chr1	173303847	173304447	2.8	0.6
chr1	173304087	173304687	2.0	0.5
chr1	173357684	173358284	1.2	0.2
chr1	173357704	173358304	1.3	0.2
chr1	173664687	173665287	0.1	0.2
chr1	174273899	174274499	0.9	0.3
chr1	174274068	174274668	1.6	0.2
chr1	174384497	174385097	0.7	0.1
chr1	174417674	174418274	1.6	0.3
chr1	174417910	174418510	1.0	0.2
chr1	175913856	175914456	0.2	0.1
chr1	176437383	176437983	0.8	0.0
chr1	176682686	176683286	0.3	0.0
chr1	176959988	176960588	0.1	0.5
chr1	177908196	177908796	1.0	0.4
chr1	177908279	177908879	1.4	0.3
chr1	178135443	178136043	0.7	0.0
chr1	178831220	178831820	0.1	0.1
chr1	179492329	179492929	1.3	0.3
chr1	179703461	179704061	0.1	0.2
chr1	180130001	180130601	0.6	0.1
chr1	180537108	180537708	0.0	0.3
chr1	180826922	180827522	0.7	0.6
chr1	181302599	181303199	0.1	0.0
chr1	181760838	181761438	0.1	0.2
chr1	181952472	181953072	1.1	0.1
chr1	181952729	181953329	2.3	0.8
chr1	182104198	182104798	1.6	0.2
chr1	182705877	182706477	1.1	0.5
chr1	182706139	182706739	0.3	0.7
chr1	182806918	182807518	0.7	0.1
chr1	182806948	182807548	0.5	0.2
chr1	182896797	182897397	0.0	0.2
chr1	182905786	182906386	0.4	0.0
chr1	183948492	183949092	0.7	0.0
chr1	184541791	184542391	0.4	0.0
chr1	184590128	184590728	0.6	0.1
chr1	184603322	184603922	1.2	0.4

chr1	184697170	184697770	1.2	0.4
chr1	184785677	184786277	0.6	0.1
chr1	186174874	186175474	0.6	0.3
chr1	186850665	186851265	0.3	0.1
chr1	187551713	187552313	0.2	0.2
chr1	187961838	187962438	0.7	0.0
chr1	188744377	188744977	0.3	0.2
chr1	189176720	189177320	2.8	1.1
chr1	189176782	189177382	2.9	1.2
chr1	189176844	189177444	2.5	1.0
chr1	189176906	189177506	2.5	1.1
chr1	189176968	189177568	2.7	1.2
chr1	189177030	189177630	2.3	1.0
chr1	189177154	189177754	2.3	1.0
chr1	189177216	189177816	2.2	1.0
chr1	189177340	189177940	2.2	0.9
chr1	189177402	189178002	2.5	1.1
chr1	189177464	189178064	2.5	1.1
chr1	189177526	189178126	2.4	1.1
chr1	189177588	189178188	2.7	1.1
chr1	189177650	189178250	2.6	1.1
chr1	189177712	189178312	2.6	1.1
chr1	189177774	189178374	2.6	1.0
chr1	189177836	189178436	2.6	1.0
chr1	189177898	189178498	2.6	1.0
chr1	189177960	189178560	2.7	1.1
chr1	189178022	189178622	2.9	1.2
chr1	189178084	189178684	2.9	1.3
chr1	189178146	189178746	2.9	1.2
chr1	189178208	189178808	2.6	1.1
chr1	189178270	189178870	2.6	1.1
chr1	189178332	189178932	2.6	1.1
chr1	189178394	189178994	2.1	0.9
chr1	189178518	189179118	2.3	1.1
chr1	189178580	189179180	2.3	1.1
chr1	189178704	189179304	2.4	1.1
chr1	189178766	189179366	2.8	1.4
chr1	189178828	189179428	2.8	1.4
chr1	189178890	189179490	2.8	1.3
chr1	189178952	189179552	3.3	1.5
chr1	189179014	189179614	3.2	1.5
chr1	189179076	189179676	3.1	1.4
chr1	189179138	189179738	3.0	1.3
chr1	189179200	189179800	3.1	1.4
chr1	189179262	189179862	3.0	1.4
chr1	189179324	189179924	2.8	1.3
chr1	189179386	189179986	2.7	1.1
chr1	189179448	189180048	2.4	1.0
chr1	189458845	189459445	1.2	0.5
chr1	190332957	190333557	0.0	0.1
chr1	190583972	190584572	1.2	0.6
chr1	190612282	190612882	0.5	0.2
chr1	190861312	190861912	0.0	0.0
chr1	191239425	191240025	0.2	0.0
chr1	191391759	191392359	1.2	0.0
chr1	191440470	191441070	0.8	0.1
chr1	191474914	191475514	0.8	0.3
chr1	191546773	191547373	1.1	0.6
chr1	192131933	192132533	0.2	0.1
chr1	192921730	192922330	0.4	0.0
chr1	192960294	192960894	1.0	0.1
chr1	193040011	193040611	0.1	0.0
chr1	193743204	193743804	1.1	0.3
chr1	193896581	193897181	0.4	0.2
chr1	194337349	194337949	1.8	0.0
chr1	194408492	194409092	0.3	0.1
chr1	194661047	194661647	1.4	0.2
chr1	194710632	194711232	1.5	0.5
chr1	194939474	194940074	0.7	0.6
chr1	194939530	194940130	0.3	0.4
chr1	195491658	195492258	0.8	0.0
chr1	195491743	195492343	0.7	0.1
chr1	195508969	195509569	0.7	0.0
chr1	195807492	195808092	0.5	0.2
chr1	196071121	196071721	0.4	0.2
chr1	196468092	196468692	1.4	0.2

chr1	196468151	196468751	1.4	0.3
chr10	3819540	3820140	0.2	0.1
chr10	3880926	3881526	4.3	1.5
chr10	3881167	3881767	4.4	1.5
chr10	3902545	3903145	0.2	0.3
chr10	4195772	4196372	1.9	0.4
chr10	4330631	4331231	0.9	0.1
chr10	4581449	4582049	0.4	0.1
chr10	4648493	4649093	6.8	3.4
chr10	4648510	4649110	6.7	3.3
chr10	4648545	4649145	6.9	3.3
chr10	4648579	4649179	7.0	3.3
chr10	4648614	4649214	6.8	3.3
chr10	4648631	4649231	6.9	3.4
chr10	5571905	5572505	1.5	0.9
chr10	5805606	5806206	0.3	0.2
chr10	6142049	6142649	1.3	0.1
chr10	6291429	6292029	2.0	0.1
chr10	6345239	6345839	1.4	0.3
chr10	6345292	6345892	1.5	0.4
chr10	6345345	6345945	1.5	0.5
chr10	6345398	6345998	1.1	0.5
chr10	6702631	6703231	0.8	0.6
chr10	7168531	7169131	0.8	0.1
chr10	7840178	7840778	0.0	0.0
chr10	7980825	7981425	0.4	0.1
chr10	8170051	8170651	1.5	0.4
chr10	9002171	9002771	1.4	0.1
chr10	9392712	9393312	0.2	0.3
chr10	9540471	9541071	0.6	0.3
chr10	9716105	9716705	1.0	0.2
chr10	10049905	10050505	1.9	0.5
chr10	10480507	10481107	0.6	0.1
chr10	10501500	10502100	0.0	0.1
chr10	10501665	10502265	0.3	0.4
chr10	11883730	11884330	0.5	0.4
chr10	12835056	12835656	1.5	0.8
chr10	12960003	12960603	0.7	0.2
chr10	13564860	13565460	2.4	0.7
chr10	16455943	16456543	2.5	1.4
chr10	16456200	16456800	0.9	0.3
chr10	16668707	16669307	0.1	0.3
chr10	17402159	17402759	0.3	0.2
chr10	18006167	18006767	2.0	0.3
chr10	18302245	18302845	0.8	0.3
chr10	18909951	18910551	1.2	0.2
chr10	18910027	18910627	1.1	0.2
chr10	19551118	19551718	0.9	0.4
chr10	19551178	19551778	0.9	0.5
chr10	20403983	20404583	0.8	0.3
chr10	20638928	20639528	0.4	0.0
chr10	20916905	20917505	0.8	0.3
chr10	20918427	20919027	0.3	0.2
chr10	21164103	21164703	1.2	0.7
chr10	21548841	21549441	1.2	0.7
chr10	21854706	21855306	0.2	0.3
chr10	21977114	21977714	1.3	0.3
chr10	22167335	22167935	1.2	0.2
chr10	22242099	22242699	1.0	0.4
chr10	22364663	22365263	0.8	0.2
chr10	22590001	22590601	1.6	1.0
chr10	23434859	23435459	1.1	0.1
chr10	24759591	24760191	0.9	0.8
chr10	24851607	24852207	0.7	0.3
chr10	24951116	24951716	1.3	0.2
chr10	25131506	25132106	1.0	0.4
chr10	25316999	25317599	0.3	0.3
chr10	25372197	25372797	1.6	0.4
chr10	25882009	25882609	0.5	0.2
chr10	26629169	26629769	1.1	0.4
chr10	26629260	26629860	1.5	0.6
chr10	27219280	27219880	1.3	0.2
chr10	27794699	27795299	1.0	0.3
chr10	28322204	28322804	1.9	0.8
chr10	28322274	28322874	2.1	0.8
chr10	29995354	29995954	1.9	0.0

chr10	30171634	30172234	0.0	0.2
chr10	30171697	30172297	0.3	0.4
chr10	30782815	30783415	0.9	0.7
chr10	31098017	31098617	0.6	0.3
chr10	31135992	31136592	0.2	0.0
chr10	31165213	31165813	1.1	0.1
chr10	31303417	31304017	0.6	0.0
chr10	31621815	31622415	0.8	0.2
chr10	31698805	31699405	1.4	0.1
chr10	32993880	32994480	0.3	0.3
chr10	34673236	34673836	0.8	0.0
chr10	34991946	34992546	0.2	0.2
chr10	35219556	35220156	0.4	0.2
chr10	35408616	35409216	0.5	0.4
chr10	36950777	36951377	0.9	1.0
chr10	37201693	37202293	0.5	0.2
chr10	38033828	38034428	0.8	0.1
chr10	38273716	38274316	1.3	0.4
chr10	39360418	39361018	0.8	0.5
chr10	39693785	39694385	0.5	0.3
chr10	39693969	39694569	1.1	0.0
chr10	39717159	39717759	1.0	0.2
chr10	39837048	39837648	0.5	0.2
chr10	40107635	40108235	0.5	0.1
chr10	40349245	40349845	1.0	0.3
chr10	40644851	40645451	1.8	0.9
chr10	41757279	41757879	0.2	0.1
chr10	41896681	41897281	1.1	0.3
chr10	42031925	42032525	1.0	0.1
chr10	42392822	42393422	2.0	0.4
chr10	42392960	42393560	1.4	0.3
chr10	43178252	43178852	0.6	0.3
chr10	43226789	43227389	1.1	0.1
chr10	43392901	43393501	1.4	0.3
chr10	43567966	43568566	1.4	0.4
chr10	43568038	43568638	1.6	0.5
chr10	44577706	44578306	1.2	1.0
chr10	44577732	44578332	1.3	1.1

chr10	44644096	44644696	2.6	1.1
chr10	44644128	44644728	2.7	1.2
chr10	45269165	45269765	0.8	0.2
chr10	45952166	45952766	0.5	0.1
chr10	46060546	46061146	0.9	0.2
chr10	46772077	46772677	0.0	0.3
chr10	48277945	48278545	0.6	0.3
chr10	48496883	48497483	1.0	0.5
chr10	49194286	49194886	0.8	0.0
chr10	49360263	49360863	0.8	0.0
chr10	49530995	49531595	0.8	0.9
chr10	49531254	49531854	1.6	0.4
chr10	49876444	49877044	2.5	0.5
chr10	50301433	50302033	0.7	0.6
chr10	50779359	50779959	0.3	0.1
chr10	51820219	51820819	1.3	0.2
chr10	52418193	52418793	0.7	0.2
chr10	52493304	52493904	1.0	0.2
chr10	52493334	52493934	0.8	0.3
chr10	52508953	52509553	1.0	0.2
chr10	53886344	53886944	0.9	0.3
chr10	54677858	54678458	0.5	0.0
chr10	54754972	54755572	0.2	0.6
chr10	55422722	55423322	0.3	0.1
chr10	55422812	55423412	0.7	0.2
chr10	56054851	56055451	0.6	0.0
chr10	56604158	56604758	1.1	0.0
chr10	56604234	56604834	1.1	0.2
chr10	56729715	56730315	0.6	0.1
chr10	57570532	57571132	1.3	0.2
chr10	57688018	57688618	1.1	0.2
chr10	57688244	57688844	2.0	0.1
chr10	57695697	57696297	1.5	0.5
chr10	57695923	57696523	2.3	0.4
chr10	59027504	59028104	0.1	0.2
chr10	59561073	59561673	2.0	0.3
chr10	59801363	59801963	0.5	0.1
chr10	59875916	59876516	1.9	0.6

chr10	59876071	59876671	3.0	1.0
chr10	59903784	59904384	1.4	0.1
chr10	59903800	59904400	1.3	0.1
chr10	60162128	60162728	0.8	0.1
chr10	60162141	60162741	0.9	0.2
chr10	60570731	60571331	0.9	0.1
chr10	60670047	60670647	1.1	0.3
chr10	60689323	60689923	0.8	0.4
chr10	60699789	60700389	0.6	0.2
chr10	60709505	60710105	1.1	0.0
chr10	60759353	60759953	0.9	0.3
chr10	60878483	60879083	0.2	0.5
chr10	60944250	60944850	0.5	0.4
chr10	60994188	60994788	0.6	0.1
chr10	61007892	61008492	2.2	0.7
chr10	61008154	61008754	1.0	0.6
chr10	61079299	61079899	0.6	0.0
chr10	61220897	61221497	0.2	0.3
chr10	61289445	61290045	1.5	0.0
chr10	61485427	61486027	0.2	0.3
chr10	61563328	61563928	0.5	0.0
chr10	61598076	61598676	0.2	0.3
chr10	61725507	61726107	0.1	0.1
chr10	62015409	62016009	2.5	0.8
chr10	62015597	62016197	2.2	0.6
chr10	62154073	62154673	0.7	0.1
chr10	62520035	62520635	0.5	0.1
chr10	62641798	62642398	0.5	0.2
chr10	62883872	62884472	0.4	0.1
chr10	63035782	63036382	1.5	0.8
chr10	64101514	64102114	0.8	0.4
chr10	64820359	64820959	0.2	0.4
chr10	65311977	65312577	0.5	0.1
chr10	65715734	65716334	0.0	0.1
chr10	65883443	65884043	0.6	0.0
chr10	65965146	65965746	0.8	0.6
chr10	66301637	66302237	0.9	0.6
chr10	66504481	66505081	0.3	0.0

chr10	66510155	66510755	1.2	0.2
chr10	67099574	67100174	0.1	0.3
chr10	67135518	67136118	2.6	1.0
chr10	68804695	68805295	0.2	0.0
chr10	68804800	68805400	0.1	0.1
chr10	69082254	69082854	1.9	0.5
chr10	69239081	69239681	0.8	0.5
chr10	69239270	69239870	0.8	0.8
chr10	69564379	69564979	2.2	0.2
chr10	70444319	70444919	1.3	0.5
chr10	70947152	70947752	0.9	0.2
chr10	71834076	71834676	1.0	0.1
chr10	72914085	72914685	0.3	0.1
chr10	72949498	72950098	0.9	0.3
chr10	74407859	74408459	0.7	0.2
chr10	74588813	74589413	0.3	0.4
chr10	74873710	74874310	0.4	0.1
chr10	74928128	74928728	0.7	0.0
chr10	75257235	75257835	0.2	0.1
chr10	75287204	75287804	1.5	0.1
chr10	75348268	75348868	0.8	0.1
chr10	75747227	75747827	2.0	0.6
chr10	75793043	75793643	4.9	1.1
chr10	75793073	75793673	5.0	1.1
chr10	75793103	75793703	5.1	1.2
chr10	75793133	75793733	5.2	1.1
chr10	75793163	75793763	5.5	1.2
chr10	75793194	75793794	5.7	1.2
chr10	75793224	75793824	5.9	1.2
chr10	75793284	75793884	6.0	1.2
chr10	75793314	75793914	6.1	1.2
chr10	75793344	75793944	6.0	1.1
chr10	75793374	75793974	6.0	1.1
chr10	75793404	75794004	6.0	1.1
chr10	75793434	75794034	5.8	0.9
chr10	75793464	75794064	5.6	0.8
chr10	75793494	75794094	5.8	0.9
chr10	75793524	75794124	5.8	0.9

chr10	75793554	75794154	5.7	0.9
chr10	75793584	75794184	5.7	0.9
chr10	75793614	75794214	5.6	0.8
chr10	75793644	75794244	5.5	0.8
chr10	75793674	75794274	5.3	0.7
chr10	75793704	75794304	5.0	0.5
chr10	75793734	75794334	4.9	0.5
chr10	75793764	75794364	4.6	0.5
chr10	76526437	76527037	0.2	0.1
chr10	76584507	76585107	1.3	0.4
chr10	76584656	76585256	1.7	0.2
chr10	76605485	76606085	0.8	0.1
chr10	76641706	76642306	1.4	0.9
chr10	76715343	76715943	0.7	1.1
chr10	76715392	76715992	0.9	1.2
chr10	76740036	76740636	0.9	0.6
chr10	77068206	77068806	0.7	0.1
chr10	77110376	77110976	0.1	0.0
chr10	77231984	77232584	0.2	0.0
chr10	77629700	77630300	0.6	0.1
chr10	77830458	77831058	1.0	0.3
chr10	77860136	77860736	0.9	0.8
chr10	77860361	77860961	1.1	0.5
chr10	77917672	77918272	1.1	0.1
chr10	78052411	78053011	0.9	0.2
chr10	78052603	78053203	1.1	0.4
chr10	78052685	78053285	0.9	0.6
chr10	79171441	79172041	0.9	0.1
chr10	79239882	79240482	2.5	1.0
chr10	79251909	79252509	1.1	0.1
chr10	79257965	79258565	0.5	0.1
chr10	79419186	79419786	0.7	1.0
chr10	79419303	79419903	0.3	0.7
chr10	79479205	79479805	1.4	0.1
chr10	79615072	79615672	0.4	0.2
chr10	79854623	79855223	0.7	0.0
chr10	79901909	79902509	1.0	0.6
chr10	79906958	79907558	0.7	0.0

chr10	79911406	79912006	0.2	0.1
chr10	80009968	80010568	0.9	0.7
chr10	80300184	80300784	0.7	0.5
chr10	80330905	80331505	0.4	0.1
chr10	80622526	80623126	0.6	0.1
chr10	80863145	80863745	0.5	0.4
chr10	80994052	80994652	1.7	0.8
chr10	80994297	80994897	1.5	0.6
chr10	81078162	81078762	3.0	0.4
chr10	81078192	81078792	2.8	0.3
chr10	81647665	81648265	0.5	0.1
chr10	81647825	81648425	0.7	0.3
chr10	81932130	81932730	0.5	0.1
chr10	82233216	82233816	1.2	0.1
chr10	82233391	82233991	1.8	0.2
chr10	82235926	82236526	0.1	0.1
chr10	82336661	82337261	0.7	0.2
chr10	82421126	82421726	0.0	0.2
chr10	82646358	82646958	2.0	0.2
chr10	83194872	83195472	1.2	0.4
chr10	83229520	83230120	1.1	0.1
chr10	84049043	84049643	0.2	0.2
chr10	84378724	84379324	0.2	0.4
chr10	84407993	84408593	1.0	0.3
chr10	84658743	84659343	0.1	0.3
chr10	84726919	84727519	1.6	1.0
chr10	84727128	84727728	0.8	0.3
chr10	84727214	84727814	1.0	0.3
chr10	84916402	84917002	0.7	0.1
chr10	85002437	85003037	0.0	0.4
chr10	85237605	85238205	3.0	0.4
chr10	85308661	85309261	2.6	0.5
chr10	85308816	85309416	3.8	1.0
chr10	85309015	85309615	0.9	0.1
chr10	85507817	85508417	1.4	0.2
chr10	85741879	85742479	0.1	0.0
chr10	86029432	86030032	2.3	0.2
chr10	86029586	86030186	3.5	0.7

chr10	86089229	86089829	2.0	0.1
chr10	86089384	86089984	1.8	0.1
chr10	86453251	86453851	0.6	0.3
chr10	86755875	86756475	0.7	0.3
chr10	86756136	86756736	0.4	0.2
chr10	86975727	86976327	0.7	0.5
chr10	86975929	86976529	1.1	0.2
chr10	87126034	87126634	0.5	1.2
chr10	87308052	87308652	1.1	0.3
chr10	87308142	87308742	1.1	0.4
chr10	87308172	87308772	1.1	0.4
chr10	88165132	88165732	0.8	0.4
chr10	88318335	88318935	0.8	0.1
chr10	88318360	88318960	0.8	0.2
chr10	88927326	88927926	0.3	0.2
chr10	89598599	89599199	1.4	0.4
chr10	90235543	90236143	1.1	0.2
chr10	90366704	90367304	3.0	0.3
chr10	90703658	90704258	1.1	0.3
chr10	90712873	90713473	0.5	0.1
chr10	90781638	90782238	1.1	0.1
chr10	91751820	91752420	0.7	0.0
chr10	91901331	91901931	1.7	0.3
chr10	92286973	92287573	0.6	0.1
chr10	92819153	92819753	1.1	0.1
chr10	92865427	92866027	1.8	0.6
chr10	93004904	93005504	0.9	0.0
chr10	93592157	93592757	0.1	0.2
chr10	94412582	94413182	1.1	0.2
chr10	95851185	95851785	1.2	0.0
chr10	95890511	95891111	1.0	0.7
chr10	95890565	95891165	0.7	0.7
chr10	96465651	96466251	0.3	0.1
chr10	98049719	98050319	0.5	0.5
chr10	98384486	98385086	0.4	0.1
chr10	98634713	98635313	1.4	0.2
chr10	98703141	98703741	1.0	0.2
chr10	98703351	98703951	1.0	0.2
chr10	98714431	98715031	0.8	0.1
chr10	99015248	99015848	0.4	0.1
chr10	99409998	99410598	0.1	0.1
chr10	100155812	100156412	0.9	0.2
chr10	102242085	102242685	0.5	0.2
chr10	102242096	102242696	0.4	0.2
chr10	103236016	103236616	0.7	0.1
chr10	104034713	104035313	1.0	0.3
chr10	104034757	104035357	0.8	0.2
chr10	104034846	104035446	1.4	0.3
chr10	105119274	105119874	0.9	0.2
chr10	105775477	105776077	0.2	0.4
chr10	106740165	106740765	0.7	0.2
chr10	106966265	106966865	0.8	0.2
chr10	106979248	106979848	1.0	0.5
chr10	107917092	107917692	0.6	0.5
chr10	108091900	108092500	0.4	0.2
chr10	109376178	109376778	0.7	0.3
chr10	110316762	110317362	1.1	0.3
chr10	111283687	111284287	0.3	0.1
chr10	112181379	112181979	0.2	0.0
chr10	114398102	114398702	0.6	0.1
chr10	115209987	115210587	1.8	0.8
chr10	115494449	115495049	0.8	0.0
chr10	115494503	115495103	0.8	0.1
chr10	115494530	115495130	1.0	0.1
chr10	115494584	115495184	0.9	0.1
chr10	115848025	115848625	0.2	0.2
chr10	115866720	115867320	0.9	0.3
chr10	116183016	116183616	0.2	0.4
chr10	116243669	116244269	1.2	0.1
chr10	116387893	116388493	0.6	0.2
chr10	116506735	116507335	0.7	0.1
chr10	116604010	116604610	0.7	0.8
chr10	117263339	117263939	0.7	0.1
chr10	118164861	118165461	0.9	0.2
chr10	118164914	118165514	2.0	0.5
chr10	118289735	118290335	1.0	0.5

chr10	118523199	118523799	0.7	0.0
chr10	118691991	118692591	0.1	0.0
chr10	119060457	119061057	1.1	0.4
chr10	119076572	119077172	0.9	0.2
chr10	119262800	119263400	0.6	0.3
chr10	119677405	119678005	1.4	0.3
chr10	119776163	119776763	1.2	0.6
chr10	119975455	119976055	1.4	0.5
chr10	120268453	120269053	1.6	0.0
chr10	120597070	120597670	0.4	0.4
chr10	120664318	120664918	0.4	0.1
chr10	120860722	120861322	0.3	0.1
chr10	120873550	120874150	1.0	0.3
chr10	121163502	121164102	1.7	0.4
chr10	121163522	121164122	1.7	0.4
chr10	121224810	121225410	0.7	0.2
chr10	121224830	121225430	0.7	0.1
chr10	121224840	121225440	0.9	0.1
chr10	121470141	121470741	0.9	0.4
chr10	121510830	121511430	0.0	0.4
chr10	121818832	121819432	0.8	0.5
chr10	121818935	121819535	1.3	0.4
chr10	122065359	122065959	1.0	0.0
chr10	122114534	122115134	0.1	0.3
chr10	122494769	122495369	1.6	0.0
chr10	122510007	122510607	0.8	0.3
chr10	122874032	122874632	1.2	0.6
chr10	123008092	123008692	0.1	0.0
chr10	123736661	123737261	0.8	0.8
chr10	123854620	123855220	1.1	0.2
chr10	124241632	124242232	1.4	0.0
chr10	124303992	124304592	0.7	0.4
chr10	124304049	124304649	0.4	0.3
chr10	124365943	124366543	1.0	0.1
chr10	124810881	124811481	0.9	0.4
chr10	124810959	124811559	0.7	0.3
chr10	125508362	125508962	0.4	0.0
chr10	125547207	125547807	0.2	0.1

chr10	125577977	125578577	1.2	0.3
chr10	126255092	126255692	1.0	0.5
chr10	126323914	126324514	1.3	0.3
chr10	126683133	126683733	1.1	0.1
chr10	126683228	126683828	1.2	0.3
chr10	126704357	126704957	1.1	0.0
chr10	126777465	126778065	1.4	0.0
chr10	126778289	126778889	0.6	0.3
chr10	126778503	126779103	1.3	0.1
chr10	127735802	127736402	1.3	0.0
chr10	127897566	127898166	0.8	0.1
chr10	128465185	128465785	0.5	0.0
chr10	128595534	128596134	0.6	0.1
chr11	3235724	3236324	0.8	0.0
chr11	3685880	3686480	0.5	0.7
chr11	3751159	3751759	1.2	0.1
chr11	3872531	3873131	0.1	0.1
chr11	3888487	3889087	0.3	0.2
chr11	4614204	4614804	0.6	0.1
chr11	4614390	4614990	1.4	0.3
chr11	4660299	4660899	0.7	0.1
chr11	4706309	4706909	0.1	0.6
chr11	4993389	4993989	0.7	0.1
chr11	5345724	5346324	0.2	0.2
chr11	5485492	5486092	0.4	0.0
chr11	5590447	5591047	0.9	0.6
chr11	5686103	5686703	2.0	0.4
chr11	5686224	5686824	1.4	0.3
chr11	5703385	5703985	0.9	0.1
chr11	5751692	5752292	1.5	0.2
chr11	5882692	5883292	1.2	0.4
chr11	5882731	5883331	1.2	0.4
chr11	5882770	5883370	1.0	0.3
chr11	6386856	6387456	1.1	0.2
chr11	6763535	6764135	2.1	0.3
chr11	6795001	6795601	0.3	0.5
chr11	7014415	7015015	0.4	0.2
chr11	7098206	7098806	0.7	0.2

chr11	7548134	7548734	0.2	0.3
chr11	7548164	7548764	0.1	0.2
chr11	7668575	7669175	0.9	0.3
chr11	8057339	8057939	0.3	0.2
chr11	8445499	8446099	1.4	0.1
chr11	8580887	8581487	0.1	0.2
chr11	8581103	8581703	0.6	0.1
chr11	8622904	8623504	0.4	0.3
chr11	8965205	8965805	0.2	0.2
chr11	8965461	8966061	0.8	0.3
chr11	9111342	9111942	1.1	0.3
chr11	10057652	10058252	0.5	0.0
chr11	11752607	11753207	0.6	0.1
chr11	12426229	12426829	0.6	0.1
chr11	12471499	12472099	0.9	0.8
chr11	12471647	12472247	1.3	0.5
chr11	13036181	13036781	0.4	0.7
chr11	13036359	13036959	0.4	0.5
chr11	13985838	13986438	0.3	0.1
chr11	14037730	14038330	1.1	0.3
chr11	14037821	14038421	1.2	0.4
chr11	14635860	14636460	0.2	0.2
chr11	16605397	16605997	0.7	0.8
chr11	18546177	18546777	0.0	0.6
chr11	18623702	18624302	1.1	0.2
chr11	19440198	19440798	1.3	0.3
chr11	19628607	19629207	1.5	0.1
chr11	19735702	19736302	2.4	0.8
chr11	19735891	19736491	2.6	0.4
chr11	19960605	19961205	0.0	0.3
chr11	21907685	21908285	1.2	0.3
chr11	22017782	22018382	1.5	0.6
chr11	22586634	22587234	1.1	0.1
chr11	24282066	24282666	0.2	0.0
chr11	24673646	24674246	0.8	0.2
chr11	25823863	25824463	1.6	0.4
chr11	25823873	25824473	2.2	0.7
chr11	25982695	25983295	2.0	0.1
chr11	27771942	27772542	0.4	0.0
chr11	27810572	27811172	0.4	0.0
chr11	27961386	27961986	0.9	0.1
chr11	27968203	27968803	0.4	0.0
chr11	29667928	29668528	0.4	0.0
chr11	29758750	29759350	0.9	0.0
chr11	31096130	31096730	1.0	0.5
chr11	31655743	31656343	0.4	0.4
chr11	31692944	31693544	1.3	0.1
chr11	31936867	31937467	1.8	0.3
chr11	33043611	33044211	0.1	0.0
chr11	33044944	33045544	1.5	0.3
chr11	33045051	33045651	1.3	0.2
chr11	33112358	33112958	0.4	0.1
chr11	33152111	33152711	0.2	0.2
chr11	33818489	33819089	0.3	0.1
chr11	34128539	34129139	0.1	0.1
chr11	34203131	34203731	0.6	0.0
chr11	35055131	35055731	1.1	0.3
chr11	35315363	35315963	1.4	1.3
chr11	35315634	35316234	1.2	1.2
chr11	35321182	35321782	1.7	0.2
chr11	35953032	35953632	1.1	0.1
chr11	36039054	36039654	1.4	0.6
chr11	36116355	36116955	1.5	0.9
chr11	36116443	36117043	1.6	0.7
chr11	36116536	36117136	1.6	0.8
chr11	37545880	37546480	1.4	0.1
chr11	37645748	37646348	1.5	0.5
chr11	37645828	37646428	1.5	0.4
chr11	38852134	38852734	0.5	0.2
chr11	41083260	41083860	0.7	0.3
chr11	41083466	41084066	0.8	0.4
chr11	41813073	41813673	1.2	0.3
chr11	41813350	41813950	0.8	0.0
chr11	42618360	42618960	1.0	0.2
chr11	42711486	42712086	0.6	0.1
chr11	43130338	43130938	0.2	0.2

chr11	43799980	43800580	0.6	0.1
chr11	44155495	44156095	0.4	0.2
chr11	44252338	44252938	0.2	0.1
chr11	44307802	44308402	0.6	0.1
chr11	44631370	44631970	0.3	0.2
chr11	44788792	44789392	1.5	0.2
chr11	45547887	45548487	0.8	0.3
chr11	45742234	45742834	0.8	0.0
chr11	46460576	46461176	2.0	0.1
chr11	46548518	46549118	0.3	0.2
chr11	46740663	46741263	0.4	0.1
chr11	46931885	46932485	0.8	0.2
chr11	47164497	47165097	2.0	0.6
chr11	47164522	47165122	2.0	0.6
chr11	48296090	48296690	0.3	0.2
chr11	48514652	48515252	0.1	0.0
chr11	48813987	48814587	1.8	0.1
chr11	48814277	48814877	1.1	0.1
chr11	49785930	49786530	2.1	0.1
chr11	49785951	49786551	2.1	0.0
chr11	49903428	49904028	0.7	0.5
chr11	50029518	50030118	0.5	0.0
chr11	50029857	50030457	0.5	0.1
chr11	50376527	50377127	0.5	0.1
chr11	50476622	50477222	0.6	0.2
chr11	50506893	50507493	1.5	0.7
chr11	50507002	50507602	1.7	0.6
chr11	50751919	50752519	0.6	0.1
chr11	51451348	51451948	0.9	0.3
chr11	52154650	52155250	0.3	0.1
chr11	52154732	52155332	1.1	0.0
chr11	52194403	52195003	0.3	0.0
chr11	52248464	52249064	0.7	0.2
chr11	52408945	52409545	0.7	0.7
chr11	52675604	52676204	0.8	0.1
chr11	53044085	53044685	1.2	0.2
chr11	53044111	53044711	1.4	0.2
chr11	53044188	53044788	1.9	0.4
chr11	53044262	53044862	2.2	0.5
chr11	53044288	53044888	2.3	0.6
chr11	53044349	53044949	2.8	0.8
chr11	53044392	53044992	2.5	0.6
chr11	53044424	53045024	2.4	0.5
chr11	53044450	53045050	2.4	0.6
chr11	53044490	53045090	2.2	0.5
chr11	53044545	53045145	3.2	0.9
chr11	53044571	53045171	2.9	0.9
chr11	53044605	53045205	2.8	0.8
chr11	53044631	53045231	3.3	1.0
chr11	54579147	54579747	0.5	0.2
chr11	54674077	54674677	1.0	0.6
chr11	54714250	54714850	0.5	0.1
chr11	54924196	54924796	0.9	0.1
chr11	55135901	55136501	3.1	1.8
chr11	55136048	55136648	3.0	1.4
chr11	55137105	55137705	0.5	0.1
chr11	55137357	55137957	0.3	0.5
chr11	55755275	55755875	1.2	0.0
chr11	55774043	55774643	0.3	0.2
chr11	55788684	55789284	0.0	0.2
chr11	56119863	56120463	0.7	0.5
chr11	56948089	56948689	1.1	0.1
chr11	56955732	56956332	0.0	0.1
chr11	57510088	57510688	0.7	0.6
chr11	57600609	57601209	1.6	0.6
chr11	57811695	57812295	0.4	0.4
chr11	57830540	57831140	1.2	0.0
chr11	58007060	58007660	2.0	1.3
chr11	58007309	58007909	2.0	1.3
chr11	58078876	58079476	0.6	0.3
chr11	58094484	58095084	0.3	0.4
chr11	58415812	58416412	1.3	0.0
chr11	58615425	58616025	1.5	1.1
chr11	58946676	58947276	1.8	0.8
chr11	58946920	58947520	0.6	0.4
chr11	58970556	58971156	0.9	0.4

chr11	59076253	59076853	0.1	0.0
chr11	59118741	59119341	1.1	0.2
chr11	59178622	59179222	0.6	0.3
chr11	59601955	59602555	0.4	0.2
chr11	59709158	59709758	0.2	0.2
chr11	59725585	59726185	0.5	0.9
chr11	59725731	59726331	1.1	1.2
chr11	59926531	59927131	0.9	0.6
chr11	60076537	60077137	1.2	0.2
chr11	60771381	60771981	0.7	0.0
chr11	60876911	60877511	1.3	0.6
chr11	61121574	61122174	2.2	1.2
chr11	61121604	61122204	2.2	1.2
chr11	61140302	61140902	0.5	0.0
chr11	61228750	61229350	0.1	0.0
chr11	61286687	61287287	0.3	0.0
chr11	61433598	61434198	0.0	0.4
chr11	61623127	61623727	1.0	0.0
chr11	62193426	62194026	1.2	0.4
chr11	62837491	62838091	1.3	0.7
chr11	63002244	63002844	1.3	0.4
chr11	63002395	63002995	0.9	0.0
chr11	63635244	63635844	1.0	0.1
chr11	64453369	64453969	1.2	0.1
chr11	64557380	64557980	0.4	0.2
chr11	64557426	64558026	0.4	0.1
chr11	64745674	64746274	2.6	0.6
chr11	65018331	65018931	0.8	0.1
chr11	65283270	65283870	0.7	0.3
chr11	65346216	65346816	0.6	0.0
chr11	65359878	65360478	0.4	0.5
chr11	65438223	65438823	0.6	0.1
chr11	66465625	66466225	0.6	0.1
chr11	66503425	66504025	0.0	0.1
chr11	66710518	66711118	1.3	0.3
chr11	66710538	66711138	1.4	0.3
chr11	66710564	66711164	1.4	0.4
chr11	66801807	66802407	0.4	0.2
chr11	66819487	66820087	1.2	0.0
chr11	67162642	67163242	1.0	0.4
chr11	67469062	67469662	1.4	0.1
chr11	67627299	67627899	2.4	0.1
chr11	67627323	67627923	2.3	0.2
chr11	67627452	67628052	2.3	0.2
chr11	68119339	68119939	2.2	0.4
chr11	68119418	68120018	2.4	0.7
chr11	68606034	68606634	0.6	0.0
chr11	69080930	69081530	0.3	0.3
chr11	69181180	69181780	1.9	0.3
chr11	69181354	69181954	2.2	0.5
chr11	69332402	69333002	1.9	0.1
chr11	69332445	69333045	1.7	0.2
chr11	69332486	69333086	1.6	0.2
chr11	69332536	69333136	1.8	0.3
chr11	69332583	69333183	2.0	0.4
chr11	69651725	69652325	2.1	1.0
chr11	69651758	69652358	1.6	0.9
chr11	69721858	69722458	0.1	0.1
chr11	69955626	69956226	0.2	0.1
chr11	70032011	70032611	0.3	0.4
chr11	70032274	70032874	0.6	0.4
chr11	70367053	70367653	0.7	0.4
chr11	70597068	70597668	0.5	0.2
chr11	70609162	70609762	0.6	0.2
chr11	71292220	71292820	1.1	0.1
chr11	71685160	71685760	1.5	0.4
chr11	71879192	71879792	1.9	0.1
chr11	71916960	71917560	0.3	0.1
chr11	72760562	72761162	0.9	0.4
chr11	73715143	73715743	2.1	0.8
chr11	73715234	73715834	2.3	0.6
chr11	74066521	74067121	0.6	0.3
chr11	74249796	74250396	0.6	0.2
chr11	74252578	74253178	1.0	0.2
chr11	74860001	74860601	1.1	0.3
chr11	74943671	74944271	0.3	0.2

chr11	74969858	74970458	0.5	0.0
chr11	75698358	75698958	0.2	0.2
chr11	75892558	75893158	0.2	0.0
chr11	76253385	76253985	1.1	0.3
chr11	76296686	76297286	0.6	0.4
chr11	76759528	76760128	1.0	1.1
chr11	77573697	77574297	0.7	0.2
chr11	77656879	77657479	0.4	0.1
chr11	77982569	77983169	0.6	0.0
chr11	78002692	78003292	0.9	0.5
chr11	78024959	78025559	0.1	0.3
chr11	78059400	78060000	0.5	0.2
chr11	78690083	78690683	0.3	0.4
chr11	78786892	78787492	0.2	0.0
chr11	79002845	79003445	1.7	0.3
chr11	79002965	79003565	1.3	0.1
chr11	79003136	79003736	1.1	0.0
chr11	79013938	79014538	0.9	0.1
chr11	79424694	79425294	1.4	0.1
chr11	79424749	79425349	1.3	0.2
chr11	79576852	79577452	4.6	2.1
chr11	79576862	79577462	4.6	2.1
chr11	79576872	79577472	4.7	2.1
chr11	79576882	79577482	4.8	2.1
chr11	79576892	79577492	4.8	2.1
chr11	79576902	79577502	4.8	2.1
chr11	80128184	80128784	0.6	0.1
chr11	80128313	80128913	0.4	0.0
chr11	80128322	80128922	0.3	0.0
chr11	80241725	80242325	1.2	0.1
chr11	80800663	80801263	0.1	0.2
chr11	81764619	81765219	0.2	0.1
chr11	82072898	82073498	0.4	0.3
chr11	82383322	82383922	0.6	0.6
chr11	83261185	83261785	0.6	0.2
chr11	83699385	83699985	0.2	0.1
chr11	85115807	85116407	0.0	0.6
chr11	85728010	85728610	0.9	0.2

chr11	86768004	86768604	1.3	0.6
chr11	87259698	87260298	1.0	0.1
chr11	87906334	87906934	0.1	0.0
chr11	87969933	87970533	1.6	0.8
chr11	87970042	87970642	1.7	0.7
chr11	88534964	88535564	0.4	0.0
chr11	88674884	88675484	0.5	0.0
chr11	88682925	88683525	0.1	0.2
chr11	88966262	88966862	2.5	0.6
chr11	89045032	89045632	0.8	0.0
chr11	89468451	89469051	1.3	0.1
chr11	89474618	89475218	0.8	0.7
chr11	89926704	89927304	0.3	0.1
chr11	89978557	89979157	2.9	1.0
chr11	89978831	89979431	2.1	0.6
chr11	89981092	89981692	0.8	0.1
chr11	90135225	90135825	0.1	0.2
chr11	90161664	90162264	1.0	0.2
chr11	90207038	90207638	0.3	0.3
chr11	91278350	91278950	1.7	0.6
chr11	91278455	91279055	1.4	0.6
chr11	91931199	91931799	1.3	0.2
chr11	92073357	92073957	0.3	0.2
chr11	93394684	93395284	0.7	0.2
chr11	93985699	93986299	0.2	0.2
chr11	94299357	94299957	0.2	0.3
chr11	94386779	94387379	1.6	0.4
chr11	94387070	94387670	0.9	0.4
chr11	94455209	94455809	0.4	0.2
chr11	94565644	94566244	1.4	0.2
chr11	94642898	94643498	0.8	0.2
chr11	95066659	95067259	0.4	0.7
chr11	95066687	95067287	0.6	0.8
chr11	95073863	95074463	0.7	0.2
chr11	95521289	95521889	1.4	0.2
chr11	96302997	96303597	1.2	0.4
chr11	96566006	96566606	2.1	0.0
chr11	97285696	97286296	0.6	0.0

chr11	97354896	97355496	0.9	0.2
chr11	97354931	97355531	0.7	0.1
chr11	97420621	97421221	0.1	0.1
chr11	97420690	97421290	0.2	0.3
chr11	97767307	97767907	0.8	0.1
chr11	98329036	98329636	0.2	0.1
chr11	98329076	98329676	0.3	0.3
chr11	98512076	98512676	1.5	0.1
chr11	98917238	98917838	1.0	0.3
chr11	99964180	99964780	1.9	0.7
chr11	100023951	100024551	1.1	0.5
chr11	100024062	100024662	1.6	0.6
chr11	100136215	100136815	0.6	0.1
chr11	100380906	100381506	0.7	0.1
chr11	100381029	100381629	0.8	0.0
chr11	100512644	100513244	0.8	0.0
chr11	100666949	100667549	0.7	0.5
chr11	100755430	100756030	0.5	0.4
chr11	100966215	100966815	0.4	0.2
chr11	101037427	101038027	0.5	0.3
chr11	101401401	101402001	1.2	0.3
chr11	101654950	101655550	0.2	0.1
chr11	101740055	101740655	1.2	0.3
chr11	101804082	101804682	0.5	0.1
chr11	101935157	101935757	0.7	0.2
chr11	101953109	101953709	0.9	0.7
chr11	101996327	101996927	1.3	0.1
chr11	102417068	102417668	1.2	0.3
chr11	102498257	102498857	1.1	0.4
chr11	103556172	103556772	0.0	0.1
chr11	103594408	103595008	0.1	0.1
chr11	103744563	103745163	0.0	0.2
chr11	104112477	104113077	0.2	0.0
chr11	104181604	104182204	1.1	0.4
chr11	104585907	104586507	1.0	0.2
chr11	104586075	104586675	1.9	0.2
chr11	104876082	104876682	1.1	0.6
chr11	104876322	104876922	0.7	0.8
chr11	104983955	104984555	1.2	0.1
chr11	105400003	105400603	1.1	0.2
chr11	105991180	105991780	0.7	0.2
chr11	106129287	106129887	1.7	0.7
chr11	106473724	106474324	1.1	0.2
chr11	106473819	106474419	1.2	0.1
chr11	106566303	106566903	0.8	0.1
chr11	106566402	106567002	0.9	0.1
chr11	106979361	106979961	1.0	0.2
chr11	107065887	107066487	1.3	0.0
chr11	107830795	107831395	0.7	0.1
chr11	107899176	107899776	0.8	0.5
chr11	107899443	107900043	1.1	0.2
chr11	108447959	108448559	1.1	0.5
chr11	108898765	108899365	0.3	0.1
chr11	109783148	109783748	0.3	0.2
chr11	109848240	109848840	2.0	0.1
chr11	110054835	110055435	0.1	0.0
chr11	110718601	110719201	0.4	0.2
chr11	110889756	110890356	0.8	0.1
chr11	110909194	110909794	1.3	0.7
chr11	110953955	110954555	0.4	0.1
chr11	111293838	111294438	0.3	0.4
chr11	111357129	111357729	0.8	0.1
chr11	111603432	111604032	0.7	0.1
chr11	112645909	112646509	1.2	0.4
chr11	112645926	112646526	1.4	0.4
chr11	112750905	112751505	1.6	0.1
chr11	112751114	112751714	2.1	0.3
chr11	112887675	112888275	2.6	0.4
chr11	112917279	112917879	0.1	0.8
chr11	112921028	112921628	1.3	0.1
chr11	112921199	112921799	1.4	0.2
chr11	113195124	113195724	1.5	0.3
chr11	113195181	113195781	1.6	0.2
chr11	113204928	113205528	2.8	1.1
chr11	113204954	113205554	2.6	1.2
chr11	113204967	113205567	2.6	1.3

chr11	113226892	113227492	0.7	0.0
chr11	113413800	113414400	1.2	0.0
chr11	113447662	113448262	1.3	0.1
chr11	113684038	113684638	1.3	0.1
chr11	113684068	113684668	2.5	0.9
chr11	113720730	113721330	0.3	0.0
chr11	113906149	113906749	1.0	0.2
chr11	114372280	114372880	0.5	0.0
chr11	114428099	114428699	1.9	0.7
chr11	114428215	114428815	2.2	0.8
chr11	115042827	115043427	0.2	0.3
chr11	115105065	115105665	0.1	0.0
chr11	115105602	115106202	0.2	0.4
chr11	115105881	115106481	0.5	0.5
chr11	115243045	115243645	0.9	0.0
chr11	115243055	115243655	0.9	0.1
chr11	115323666	115324266	1.1	0.5
chr11	115690000	115690600	0.4	0.0
chr11	117157737	117158337	0.8	0.1
chr11	117271453	117272053	0.8	0.5
chr11	117427598	117428198	1.3	0.1
chr11	117427697	117428297	0.7	0.2
chr11	117637459	117638059	1.5	0.9
chr11	117717867	117718467	0.4	0.0
chr11	117774128	117774728	0.2	0.0
chr11	117870313	117870913	0.5	0.2
chr11	117885066	117885666	1.0	0.1
chr11	117885186	117885786	1.0	0.0
chr11	117937670	117938270	1.7	0.8
chr11	118018784	118019384	0.4	0.1
chr11	118344875	118345475	1.4	0.5
chr11	118373788	118374388	1.1	0.2
chr11	118373799	118374399	1.0	0.1
chr11	118769286	118769886	0.1	0.0
chr11	118783007	118783607	0.0	0.1
chr11	118939111	118939711	1.0	0.2
chr11	118990085	118990685	1.7	0.7
chr11	118990348	118990948	1.1	0.7

chr11	119263698	119264298	0.4	0.1
chr11	119377301	119377901	0.6	0.2
chr11	119618331	119618931	1.2	0.3
chr11	119618557	119619157	1.5	0.6
chr11	119891333	119891933	0.0	0.2
chr11	119891662	119892262	0.3	0.1
chr11	119931947	119932547	2.5	0.7
chr11	119932233	119932833	2.4	0.9
chr11	120121453	120122053	0.4	0.4
chr11	120123406	120124006	0.9	0.5
chr11	120126828	120127428	0.3	0.1
chr11	120127048	120127648	0.9	0.7
chr11	120377466	120378066	0.5	0.2
chr11	120377510	120378110	0.3	0.2
chr11	120474838	120475438	0.6	0.1
chr11	121418576	121419176	0.6	0.4
chr11	121488555	121489155	0.6	0.3
chr11	121570266	121570866	0.4	0.0
chr11	121699621	121700221	0.2	0.1
chr12	3352910	3353510	0.7	0.4
chr12	4178741	4179341	1.6	0.2
chr12	4494741	4495341	0.5	0.1
chr12	5095914	5096514	0.7	0.7
chr12	5102574	5103174	0.6	0.4
chr12	5102662	5103262	0.2	0.6
chr12	5137621	5138221	1.0	0.2
chr12	6006109	6006709	1.0	0.3
chr12	6006188	6006788	1.3	0.5
chr12	6068236	6068836	0.2	0.1
chr12	6075083	6075683	0.6	0.2
chr12	6825538	6826138	0.0	0.1
chr12	7377761	7378361	0.2	0.9
chr12	7505927	7506527	0.5	0.4
chr12	7514039	7514639	0.5	0.0
chr12	7514243	7514843	0.3	0.0
chr12	7544083	7544683	1.1	0.0
chr12	8535846	8536446	1.2	0.4
chr12	8601811	8602411	0.8	0.1

chr12	8604332	8604932	0.9	0.3
chr12	8604450	8605050	0.6	0.3
chr12	9036736	9037336	0.7	0.8
chr12	9053345	9053945	1.0	0.2
chr12	10445890	10446490	0.7	0.1
chr12	10698516	10699116	1.6	0.1
chr12	11511376	11511976	0.5	0.2
chr12	12203256	12203856	0.3	0.4
chr12	12203418	12204018	0.5	0.1
chr12	12333460	12334060	1.3	0.3
chr12	12910700	12911300	1.0	0.2
chr12	12910714	12911314	1.2	0.3
chr12	14618698	14619298	0.9	0.3
chr12	15569531	15570131	1.1	0.4
chr12	15756420	15757020	1.7	0.1
chr12	15897294	15897894	1.3	0.9
chr12	15951372	15951972	0.2	0.2
chr12	16434778	16435378	0.4	0.2
chr12	16546344	16546944	1.7	0.1
chr12	16555607	16556207	1.1	0.7
chr12	16708274	16708874	0.8	0.1
chr12	16739133	16739733	0.1	0.1
chr12	16841491	16842091	1.4	0.4
chr12	17277258	17277858	0.9	0.3
chr12	17277424	17278024	1.3	0.1
chr12	17580452	17581052	0.4	0.1
chr12	17960103	17960703	0.5	0.0
chr12	18480303	18480903	0.3	0.1
chr12	18833161	18833761	0.5	0.4
chr12	20257049	20257649	0.2	0.1
chr12	20532533	20533133	0.2	0.2
chr12	21330919	21331519	0.6	0.1
chr12	21671313	21671913	0.5	0.1
chr12	22041821	22042421	0.5	0.3
chr12	23139036	23139636	0.4	0.3
chr12	23422886	23423486	0.5	0.3
chr12	24458775	24459375	0.5	0.2
chr12	24606574	24607174	0.6	0.3
chr12	24892085	24892685	0.4	0.3
chr12	25183516	25184116	1.0	0.1
chr12	25407113	25407713	0.6	0.0
chr12	25471112	25471712	0.3	0.3
chr12	25568557	25569157	1.8	0.2
chr12	25642211	25642811	2.3	0.5
chr12	25642217	25642817	2.3	0.5
chr12	25916962	25917562	0.8	0.8
chr12	25917199	25917799	1.2	0.5
chr12	26080294	26080894	1.5	0.0
chr12	26080386	26080986	0.4	0.1
chr12	26139457	26140057	0.5	0.0
chr12	26238049	26238649	0.8	0.2
chr12	26508995	26509595	0.1	0.3
chr12	26820078	26820678	0.4	0.4
chr12	27067886	27068486	0.5	0.3
chr12	27068160	27068760	1.4	0.5
chr12	27074422	27075022	1.3	0.1
chr12	27302126	27302726	0.3	0.2
chr12	27400749	27401349	1.8	0.3
chr12	27400774	27401374	1.7	0.3
chr12	27400799	27401399	1.8	0.5
chr12	27859132	27859732	0.6	0.0
chr12	28301576	28302176	1.0	0.1
chr12	29076999	29077599	1.6	0.0
chr12	29591790	29592390	1.4	0.3
chr12	29822561	29823161	0.6	0.5
chr12	29822690	29823290	0.4	0.0
chr12	30267501	30268101	0.1	0.1
chr12	30311529	30312129	0.2	0.0
chr12	30810235	30810835	1.2	0.1
chr12	30810359	30810959	1.3	0.1
chr12	31030095	31030695	0.4	0.1
chr12	31502586	31503186	1.3	0.4
chr12	31627402	31628002	0.6	0.1
chr12	31684813	31685413	0.4	0.2
chr12	32145638	32146238	1.1	0.3
chr12	32179275	32179875	0.2	0.1

chr12	32707976	32708576	1.0	0.1
chr12	33416920	33417520	0.5	0.1
chr12	33560582	33561182	1.1	0.2
chr12	33883748	33884348	2.2	0.2
chr12	33934135	33934735	0.9	0.1
chr12	34074474	34075074	1.7	0.7
chr12	35002023	35002623	0.4	0.4
chr12	36322356	36322956	1.1	0.3
chr12	36922715	36923315	0.1	0.2
chr12	37000105	37000705	1.1	0.0
chr12	37265232	37265832	0.9	0.2
chr12	37390745	37391345	0.8	0.4
chr12	37390761	37391361	0.9	0.4
chr12	37391200	37391800	0.0	0.1
chr12	37468527	37469127	3.0	1.3
chr12	37468609	37469209	2.8	1.3
chr12	38681101	38681701	0.4	0.3
chr12	38702410	38703010	0.5	0.7
chr12	38702511	38703111	0.6	0.9
chr12	40107342	40107942	0.4	0.0
chr12	40430814	40431414	0.8	0.3
chr12	41212438	41213038	0.3	0.8
chr12	41454576	41455176	1.0	0.3
chr12	41498959	41499559	0.7	0.4
chr12	41696779	41697379	1.0	0.4
chr12	42016492	42017092	1.2	0.1
chr12	42994148	42994748	0.0	0.1
chr12	43090114	43090714	0.0	0.3
chr12	43468740	43469340	1.3	0.3
chr12	43984599	43985199	0.0	0.0
chr12	44234888	44235488	2.4	0.7
chr12	44234972	44235572	2.6	0.6
chr12	44485025	44485625	1.0	0.3
chr12	44807221	44807821	2.0	0.5
chr12	44941959	44942559	0.2	0.1
chr12	45008481	45009081	0.3	0.2
chr12	45429381	45429981	0.2	0.1
chr12	45476121	45476721	1.0	0.2

chr12	45964954	45965554	0.4	0.0
chr12	46204144	46204744	1.7	0.1
chr12	49536737	49537337	1.8	0.1
chr12	49887480	49888080	1.9	0.7
chr12	49887737	49888337	1.9	0.7
chr12	50267308	50267908	3.0	1.3
chr12	51278084	51278684	2.0	1.3
chr12	51278176	51278776	1.9	1.0
chr12	51278238	51278838	2.3	1.2
chr12	51832716	51833316	1.6	0.0
chr12	52039038	52039638	0.0	0.0
chr12	52068289	52068889	1.6	0.7
chr12	52684950	52685550	0.4	0.2
chr12	53177993	53178593	0.4	0.1
chr12	53865781	53866381	0.7	0.5
chr12	54115778	54116378	1.1	0.2
chr12	54429158	54429758	0.7	0.2
chr12	54844042	54844642	0.9	0.4
chr12	55080446	55081046	0.9	0.4
chr12	55080467	55081067	1.0	0.4
chr12	55334997	55335597	0.8	0.1
chr12	55455234	55455834	0.3	0.2
chr12	56191483	56192083	1.6	0.2
chr12	56266543	56267143	1.5	0.2
chr12	56341607	56342207	1.5	0.2
chr12	56933943	56934543	0.6	0.0
chr12	57190564	57191164	1.1	0.2
chr12	57621255	57621855	1.0	0.3
chr12	57715332	57715932	1.1	1.0
chr12	57722074	57722674	2.2	1.2
chr12	58166665	58167265	1.0	0.1
chr12	58209703	58210303	0.2	0.2
chr12	58650201	58650801	1.0	0.4
chr12	58650359	58650959	1.1	0.1
chr12	59235702	59236302	0.9	0.0
chr12	59814025	59814625	2.8	0.8
chr12	59814036	59814636	2.8	0.8
chr12	59814127	59814727	2.4	1.0

chr12	60617712	60618312	0.9	0.2
chr12	60676528	60677128	0.8	0.2
chr12	61617252	61617852	0.1	0.1
chr12	62556248	62556848	0.2	0.2
chr12	66268684	66269284	0.9	0.3
chr12	66268837	66269437	0.9	0.6
chr12	67940513	67941113	1.2	0.3
chr12	68432407	68433007	0.2	0.1
chr12	68921867	68922467	0.5	0.3
chr12	69917849	69918449	1.5	0.4
chr12	71096545	71097145	1.4	0.5
chr12	71122324	71122924	0.3	0.1
chr12	71211881	71212481	1.3	0.4
chr12	71594194	71594794	0.2	0.2
chr12	72480640	72481240	0.9	0.1
chr12	72480660	72481260	0.9	0.1
chr12	72583070	72583670	0.5	0.7
chr12	72720563	72721163	0.4	0.1
chr12	72844651	72845251	0.2	0.1
chr12	72885855	72886455	0.3	0.4
chr12	73379468	73380068	1.1	0.0
chr12	73665817	73666417	0.7	0.8
chr12	73946926	73947526	2.2	0.9
chr12	74139914	74140514	0.8	0.3
chr12	74139989	74140589	0.8	0.5
chr12	74653922	74654522	1.0	0.0
chr12	75577773	75578373	1.2	0.1
chr12	75821292	75821892	0.9	0.3
chr12	75999050	75999650	0.2	0.1
chr12	76188590	76189190	0.9	0.4
chr12	76383165	76383765	0.7	0.0
chr12	76425665	76426265	0.3	0.1
chr12	76437263	76437863	1.0	0.1
chr12	76620577	76621177	1.4	0.3
chr12	76620795	76621395	1.6	0.4
chr12	76780743	76781343	0.9	0.0
chr12	77344487	77345087	0.6	0.2
chr12	77356092	77356692	0.5	0.1
chr12	77654776	77655376	1.3	0.1
chr12	77871807	77872407	0.2	0.1
chr12	78131938	78132538	0.5	0.1
chr12	79577377	79577977	0.5	0.0
chr12	80041334	80041934	0.6	0.2
chr12	80197831	80198431	1.2	0.5
chr12	80197946	80198546	1.5	0.8
chr12	80198052	80198652	1.1	0.6
chr12	80940378	80940978	1.3	0.0
chr12	81135685	81136285	0.6	0.2
chr12	81207147	81207747	0.7	0.3
chr12	81324018	81324618	0.5	0.0
chr12	81994754	81995354	0.3	0.1
chr12	82110763	82111363	1.9	0.2
chr12	82231682	82232282	0.9	0.2
chr12	82316651	82317251	0.3	0.2
chr12	82432139	82432739	1.2	0.2
chr12	82839911	82840511	0.1	0.0
chr12	83510848	83511448	0.1	0.2
chr12	83558321	83558921	0.4	0.3
chr12	83578761	83579361	0.4	0.4
chr12	83579757	83580357	0.9	0.2
chr12	83977469	83978069	0.9	0.1
chr12	84259120	84259720	0.5	0.3
chr12	84528192	84528792	0.5	0.3
chr12	84726055	84726655	0.2	0.3
chr12	85399547	85400147	1.8	0.0
chr12	85502386	85502986	0.3	0.7
chr12	85518775	85519375	1.2	0.0
chr12	85778940	85779540	0.6	0.2
chr12	85887446	85888046	1.8	0.4
chr12	85887709	85888309	1.0	0.1
chr12	85928581	85929181	1.7	0.1
chr12	86391792	86392392	1.0	0.2
chr12	86541437	86542037	0.8	0.1
chr12	86827140	86827740	1.3	0.5
chr12	87022309	87022909	0.4	0.1
chr12	87154275	87154875	1.1	0.4

chr12	87154565	87155165	1.0	0.2
chr12	87512944	87513544	0.2	0.6
chr12	87517858	87518458	0.5	0.3
chr12	88156230	88156830	0.1	0.0
chr12	88245496	88246096	0.8	0.1
chr12	88281306	88281906	0.5	0.1
chr12	89231359	89231959	0.0	0.1
chr12	89329044	89329644	0.2	0.0
chr12	89330136	89330736	0.7	0.2
chr12	89330423	89331023	0.8	0.4
chr12	89335178	89335778	1.1	0.1
chr12	89357771	89358371	0.6	0.0
chr12	89599011	89599611	0.7	0.2
chr12	89697531	89698131	0.8	0.1
chr12	90419778	90420378	1.1	0.3
chr12	90422907	90423507	1.5	0.2
chr12	90680688	90681288	0.4	0.1
chr12	90807350	90807950	0.3	0.6
chr12	91467539	91468139	0.4	0.5
chr12	92050356	92050956	0.7	0.3
chr12	92162559	92163159	1.0	0.1
chr12	92768728	92769328	0.7	0.4
chr12	92768748	92769348	0.8	0.5
chr12	93547140	93547740	0.6	0.4
chr12	95636549	95637149	1.9	0.1
chr12	95770500	95771100	1.2	0.2
chr12	95976806	95977406	1.5	0.8
chr12	95976849	95977449	1.6	0.7
chr12	96026750	96027350	0.2	0.0
chr12	96224173	96224773	0.6	0.0
chr12	96762352	96762952	0.5	0.1
chr12	98295022	98295622	0.6	0.0
chr12	98804354	98804954	0.8	0.1
chr12	98804370	98804970	0.9	0.2
chr12	98804640	98805240	1.4	0.5
chr12	99174127	99174727	0.3	0.5
chr12	100348295	100348895	0.5	0.0
chr12	101301296	101301896	1.2	0.2

chr12	101728460	101729060	0.5	0.4
chr12	101728740	101729340	0.7	0.4
chr12	101729202	101729802	0.6	0.4
chr12	101729268	101729868	0.6	0.4
chr12	101729499	101730099	0.5	0.4
chr12	101729598	101730198	0.5	0.3
chr12	101747718	101748318	0.2	0.2
chr12	102181589	102182189	0.4	0.5
chr12	103016247	103016847	0.4	0.2
chr12	103066571	103067171	0.5	0.2
chr12	103330877	103331477	0.8	0.2
chr12	103745808	103746408	0.7	0.5
chr12	103806895	103807495	1.6	1.6
chr12	103807064	103807664	1.2	1.4
chr12	104061561	104062161	0.8	0.0
chr12	104137347	104137947	1.4	0.6
chr12	104543013	104543613	0.7	0.1
chr12	104626973	104627573	2.2	0.5
chr12	104627161	104627761	1.9	0.1
chr12	105011631	105012231	0.2	0.2
chr12	105357944	105358544	6.2	2.6
chr12	105358022	105358622	6.2	2.6
chr12	105358066	105358666	6.3	2.5
chr12	105358088	105358688	6.3	2.5
chr12	105358132	105358732	6.3	2.4
chr12	105358154	105358754	6.3	2.4
chr12	105358176	105358776	6.1	2.5
chr12	105358242	105358842	5.7	2.5
chr12	106248222	106248822	1.2	0.3
chr12	106609804	106610404	1.0	0.1
chr12	106659900	106660500	0.8	0.0
chr12	106659944	106660544	0.8	0.1
chr12	106784081	106784681	1.2	0.7
chr12	106837443	106838043	0.5	0.2
chr12	107103321	107103921	1.7	0.2
chr12	107103388	107103988	1.8	0.2
chr12	107106793	107107393	2.1	0.6
chr12	107106931	107107531	1.8	0.6

chr12	107121851	107122451	1.0	0.1
chr12	107398309	107398909	0.3	0.3
chr12	107422389	107422989	0.0	0.1
chr12	107606637	107607237	0.8	0.6
chr12	107992651	107993251	0.2	0.0
chr12	108111343	108111943	2.4	0.5
chr12	108321000	108321600	0.4	0.0
chr12	108577955	108578555	0.9	0.4
chr12	108949778	108950378	0.1	0.2
chr12	108982043	108982643	1.2	0.2
chr12	109001281	109001881	1.2	0.2
chr12	109127893	109128493	1.6	0.1
chr12	109128061	109128661	1.4	0.3
chr12	109192636	109193236	1.3	0.4
chr12	109700765	109701365	0.7	0.2
chr12	109700925	109701525	0.6	0.2
chr12	109926642	109927242	1.0	0.5
chr12	109926773	109927373	1.0	0.5
chr12	109997496	109998096	1.1	0.4
chr12	111070099	111070699	0.7	0.8
chr12	111426707	111427307	1.3	0.8
chr12	112075127	112075727	1.1	0.1
chr12	112182380	112182980	1.5	0.4
chr12	112182435	112183035	1.6	0.5
chr12	112312181	112312781	0.5	0.0
chr12	112418837	112419437	1.4	0.5
chr12	112531751	112532351	1.5	0.4
chr12	113191621	113192221	1.1	0.0
chr12	113316436	113317036	0.2	0.1
chr12	113389323	113389923	1.1	0.2
chr12	113420241	113420841	1.0	0.2
chr12	113420375	113420975	0.3	0.3
chr12	113565435	113566035	1.5	0.0
chr12	113783302	113783902	0.4	0.7
chr12	113817037	113817637	0.4	0.0
chr12	113939649	113940249	1.5	0.1
chr12	114325695	114326295	0.9	0.2
chr12	114335683	114336283	1.2	0.2
chr12	114335776	114336376	1.1	0.3
chr12	114422429	114423029	0.7	0.5
chr12	114464799	114465399	0.3	0.0
chr12	114464816	114465416	0.3	0.0
chr12	116349676	116350276	1.5	0.2
chr12	116568054	116568654	1.4	0.3
chr12	116765580	116766180	0.0	0.2
chr12	117677673	117678273	0.3	0.1
chr12	118015846	118016446	0.8	0.6
chr12	118024115	118024715	0.7	1.0
chr12	118024388	118024988	0.9	0.5
chr12	118031955	118032555	0.5	0.2
chr12	118490417	118491017	1.1	0.6
chr12	118740024	118740624	0.6	0.0
chr12	119442044	119442644	1.5	0.1
chr12	119649865	119650465	0.2	0.1
chr12	119650100	119650700	0.1	0.1
chr13	3141417	3142017	0.2	0.3
chr13	3145877	3146477	1.9	0.2
chr13	3700652	3701252	1.0	0.1
chr13	4013524	4014124	1.0	0.2
chr13	4533432	4534032	1.9	0.2
chr13	6239839	6240439	0.5	0.1
chr13	7351236	7351836	0.3	0.1
chr13	8342681	8343281	1.2	0.2
chr13	8966439	8967039	2.0	0.0
chr13	9145278	9145878	0.1	0.1
chr13	9173506	9174106	1.2	0.4
chr13	9177787	9178387	1.5	0.4
chr13	9178032	9178632	0.9	0.6
chr13	9414543	9415143	0.1	0.0
chr13	9764397	9764997	0.5	0.3
chr13	10530001	10530601	0.7	0.1
chr13	10709824	10710424	0.4	0.2
chr13	11731806	11732406	0.3	0.0
chr13	11853501	11854101	0.9	0.2
chr13	11853622	11854222	0.4	0.1
chr13	12148067	12148667	1.3	0.9

chr13	12156627	12157227	0.6	0.2
chr13	12384075	12384675	0.9	0.7
chr13	12589553	12590153	1.1	0.6
chr13	12604090	12604690	0.0	0.6
chr13	12604357	12604957	0.4	0.7
chr13	14570318	14570918	1.1	0.2
chr13	14570420	14571020	1.3	0.2
chr13	14742670	14743270	0.7	0.1
chr13	14939445	14940045	1.1	0.2
chr13	15737059	15737659	1.2	0.9
chr13	15764999	15765599	1.9	0.4
chr13	15765263	15765863	2.5	1.0
chr13	16049133	16049733	0.4	0.2
chr13	16170278	16170878	0.5	0.3
chr13	16231909	16232509	0.9	0.7
chr13	16232078	16232678	0.5	0.4
chr13	16602078	16602678	0.9	0.0
chr13	16870430	16871030	0.2	0.1
chr13	17472412	17473012	0.4	0.0
chr13	17675785	17676385	1.1	0.4
chr13	18318840	18319440	0.7	0.5
chr13	18319346	18319946	0.1	0.0
chr13	18667204	18667804	0.0	0.3
chr13	19159543	19160143	1.8	0.2
chr13	20146914	20147514	1.9	0.9
chr13	20146943	20147543	1.9	1.0
chr13	20390404	20391004	2.3	0.6
chr13	20390417	20391017	2.6	0.6
chr13	20478901	20479501	1.4	0.1
chr13	20571486	20572086	0.9	0.0
chr13	20730387	20730987	1.1	0.2
chr13	22568631	22569231	0.4	0.0
chr13	23629303	23629903	0.9	0.1
chr13	23988713	23989313	1.7	0.6
chr13	24011449	24012049	1.0	0.3
chr13	24267776	24268376	0.4	0.1
chr13	24686126	24686726	1.0	0.0
chr13	24709161	24709761	0.7	0.7

chr13	24726205	24726805	0.6	0.0
chr13	25037360	25037960	0.8	0.4
chr13	25519378	25519978	0.0	0.0
chr13	25890580	25891180	0.3	0.0
chr13	26440922	26441522	0.1	0.1
chr13	28169774	28170374	0.2	0.0
chr13	28646529	28647129	0.9	1.4
chr13	28646614	28647214	0.9	1.3
chr13	28646670	28647270	1.2	1.3
chr13	28867023	28867623	1.9	0.0
chr13	28900682	28901282	0.8	0.5
chr13	29097075	29097675	0.7	0.1
chr13	29172897	29173497	1.0	0.1
chr13	29297879	29298479	0.7	0.0
chr13	29307262	29307862	0.4	0.3
chr13	29448748	29449348	0.3	0.0
chr13	29671695	29672295	0.8	0.4
chr13	30329249	30329849	2.0	1.0
chr13	30329450	30330050	1.2	0.4
chr13	30329511	30330111	1.3	0.3
chr13	30999261	30999861	0.4	0.1
chr13	31058354	31058954	1.0	0.1
chr13	31058367	31058967	1.2	0.1
chr13	31119017	31119617	0.2	0.6
chr13	31367668	31368268	0.7	0.0
chr13	31915409	31916009	1.2	0.5
chr13	32093658	32094258	0.8	0.1
chr13	32545735	32546335	0.5	0.3
chr13	33765040	33765640	0.7	0.0
chr13	33765188	33765788	1.4	0.2
chr13	33780175	33780775	0.0	0.0
chr13	33790276	33790876	2.1	0.9
chr13	33790522	33791122	1.6	0.6
chr13	33840568	33841168	0.9	0.0
chr13	33999627	34000227	0.3	0.1
chr13	34080313	34080913	1.5	0.2
chr13	34235172	34235772	0.5	0.1
chr13	34852698	34853298	1.7	0.2

chr13	34870451	34871051	0.9	0.3
chr13	35243623	35244223	0.3	0.8
chr13	35586756	35587356	0.1	0.2
chr13	35836476	35837076	0.6	0.1
chr13	36022536	36023136	0.6	0.1
chr13	36245593	36246193	0.3	0.2
chr13	36254782	36255382	0.9	0.0
chr13	36524507	36525107	0.6	0.1
chr13	36769748	36770348	0.4	0.1
chr13	36777405	36778005	0.5	0.6
chr13	38246851	38247451	0.2	0.2
chr13	38288435	38289035	0.6	0.0
chr13	38492627	38493227	0.7	0.2
chr13	38518158	38518758	0.5	0.4
chr13	39629855	39630455	1.7	0.4
chr13	40418650	40419250	1.3	0.2
chr13	40599173	40599773	0.7	0.3
chr13	40915499	40916099	2.2	0.6
chr13	41473052	41473652	0.6	0.0
chr13	41593125	41593725	1.5	0.9
chr13	41654438	41655038	0.0	0.2
chr13	41724313	41724913	0.6	0.1
chr13	41724345	41724945	0.6	0.2
chr13	41724377	41724977	0.5	0.1
chr13	42156022	42156622	0.1	0.0
chr13	42961706	42962306	0.9	0.0
chr13	43072201	43072801	0.5	0.1
chr13	43200337	43200937	0.2	0.2
chr13	43295260	43295860	2.6	0.7
chr13	43295313	43295913	2.6	0.6
chr13	43467824	43468424	1.7	0.0
chr13	43529700	43530300	0.1	0.1
chr13	43588511	43589111	0.8	0.1
chr13	43753379	43753979	0.1	0.1
chr13	43987158	43987758	0.9	0.2
chr13	44115868	44116468	1.7	0.1
chr13	44503808	44504408	1.1	0.4
chr13	44598891	44599491	0.7	0.0

chr13	44995987	44996587	1.3	0.1
chr13	45325176	45325776	0.2	0.2
chr13	45781105	45781705	0.8	0.1
chr13	45855685	45856285	0.3	0.0
chr13	45947135	45947735	1.7	0.3
chr13	45947169	45947769	1.6	0.2
chr13	45958061	45958661	0.3	0.1
chr13	46002474	46003074	0.5	0.1
chr13	46054224	46054824	1.1	0.2
chr13	46571013	46571613	0.7	0.3
chr13	47261469	47262069	1.3	0.2
chr13	47802884	47803484	1.0	0.1
chr13	47901745	47902345	0.7	0.4
chr13	47902005	47902605	1.9	1.0
chr13	47902106	47902706	0.7	0.5
chr13	48107131	48107731	1.0	0.4
chr13	48339796	48340396	1.0	0.2
chr13	49165744	49166344	0.0	0.1
chr13	49208762	49209362	0.7	0.1
chr13	49304498	49305098	2.0	0.6
chr13	49304653	49305253	0.7	0.0
chr13	49315210	49315810	0.9	0.0
chr13	49415246	49415846	0.1	0.1
chr13	49557089	49557689	2.5	0.2
chr13	49557312	49557912	2.3	0.4
chr13	49835977	49836577	0.4	0.2
chr13	49964900	49965500	0.2	0.0
chr13	50574627	50575227	0.6	0.2
chr13	50975265	50975865	0.1	0.3
chr13	51543751	51544351	0.3	0.2
chr13	52122931	52123531	1.3	0.8
chr13	52123185	52123785	0.3	0.2
chr13	52170448	52171048	2.3	0.8
chr13	52170493	52171093	2.2	0.8
chr13	52672118	52672718	0.9	0.4
chr13	52672155	52672755	1.7	0.5
chr13	52857087	52857687	0.5	0.0
chr13	53155491	53156091	0.4	0.0

chr13	53756011	53756611	0.9	0.0
chr13	54071787	54072387	0.7	0.1
chr13	54678303	54678903	1.4	0.3
chr13	54709693	54710293	1.9	0.6
chr13	54710129	54710729	0.2	0.5
chr13	54783090	54783690	0.7	0.4
chr13	54846575	54847175	0.3	0.0
chr13	54860863	54861463	0.7	0.1
chr13	55104510	55105110	1.0	0.3
chr13	55104588	55105188	1.0	0.3
chr13	55566068	55566668	0.6	0.2
chr13	55614160	55614760	1.2	0.2
chr13	55614348	55614948	1.6	0.7
chr13	55762257	55762857	0.1	0.0
chr13	55810616	55811216	1.7	0.8
chr13	56552448	56553048	0.3	0.0
chr13	56555884	56556484	1.1	0.2
chr13	56555900	56556500	1.1	0.2
chr13	56891455	56892055	0.9	0.6
chr13	57408115	57408715	0.4	0.1
chr13	57518474	57519074	0.4	0.1
chr13	58108160	58108760	2.3	0.1
chr13	58108200	58108800	2.3	0.1
chr13	58108241	58108841	2.3	0.1
chr13	58108282	58108882	2.1	0.0
chr13	58108323	58108923	2.1	0.1
chr13	58108364	58108964	2.2	0.2
chr13	58108405	58109005	2.2	0.2
chr13	58521122	58521722	0.5	0.2
chr13	59083367	59083967	0.4	0.0
chr13	59215386	59215986	0.6	0.1
chr13	59498322	59498922	0.8	0.1
chr13	60029076	60029676	1.1	0.4
chr13	60067507	60068107	0.2	0.4
chr13	60067567	60068167	0.4	0.5
chr13	61332179	61332779	0.5	0.6
chr13	62044928	62045528	0.9	0.3
chr13	63134502	63135102	1.0	0.2

chr13	63272690	63273290	1.3	0.7
chr13	63272898	63273498	0.9	1.0
chr13	63431416	63432016	1.2	0.8
chr13	63444130	63444730	0.8	0.2
chr13	63622518	63623118	0.8	0.2
chr13	63629787	63630387	0.8	1.2
chr13	63657573	63658173	0.5	0.0
chr13	63664092	63664692	2.4	1.6
chr13	63664341	63664941	2.7	2.1
chr13	63667448	63668048	1.4	0.2
chr13	63670185	63670785	1.2	0.8
chr13	63670297	63670897	1.2	0.7
chr13	63674477	63675077	2.4	0.7
chr13	63686558	63687158	1.4	0.8
chr13	63718233	63718833	1.3	0.1
chr13	63820750	63821350	1.2	0.1
chr13	63999983	64000583	0.3	0.1
chr13	64052387	64052987	1.6	0.3
chr13	64081604	64082204	1.2	0.5
chr13	64081639	64082239	0.8	0.3
chr13	64089547	64090147	1.1	0.8
chr13	64104324	64104924	2.3	0.7
chr13	64122220	64122820	0.1	0.2
chr13	64209757	64210357	2.0	0.9
chr13	64210028	64210628	1.6	0.2
chr13	64222147	64222747	0.2	0.2
chr13	64243197	64243797	0.6	0.3
chr13	64263573	64264173	1.4	1.0
chr13	65163135	65163735	0.7	0.4
chr13	65592758	65593358	0.9	0.4
chr13	65706449	65707049	0.4	0.0
chr13	65728378	65728978	0.8	0.5
chr13	65931406	65932006	1.1	0.2
chr13	65948659	65949259	0.0	0.2
chr13	66179122	66179722	0.0	0.2
chr13	66196389	66196989	1.0	0.2
chr13	66551712	66552312	0.8	0.5
chr13	67035823	67036423	0.4	0.0

chr13	67035854	67036454	0.5	0.1
chr13	67035885	67036485	0.7	0.1
chr13	67605302	67605902	0.8	0.4
chr13	67713869	67714469	0.1	0.3
chr13	69305893	69306493	0.8	0.3
chr13	69354805	69355405	0.9	0.1
chr13	69362819	69363419	1.8	0.6
chr13	69362879	69363479	1.6	0.6
chr13	69362908	69363508	2.8	1.2
chr13	69378449	69379049	1.2	0.2
chr13	69479823	69480423	1.2	0.2
chr13	69479836	69480436	1.2	0.2
chr13	69479849	69480449	1.1	0.3
chr13	69490153	69490753	1.1	0.1
chr13	69596925	69597525	0.4	0.8
chr13	69632913	69633513	1.8	0.8
chr13	69710370	69710970	3.4	1.2
chr13	69710418	69711018	3.4	1.1
chr13	69710463	69711063	3.7	1.2
chr13	69710511	69711111	3.7	1.1
chr13	69710559	69711159	3.7	1.1
chr13	69836788	69837388	1.4	0.3
chr13	71493410	71494010	0.8	0.1
chr13	71751292	71751892	0.1	0.0
chr13	72246016	72246616	1.2	0.2
chr13	72319441	72320041	1.6	0.6
chr13	72319461	72320061	1.4	0.6
chr13	72319501	72320101	1.4	0.6
chr13	73509554	73510154	0.4	0.0
chr13	73570816	73571416	0.2	0.3
chr13	73681120	73681720	0.9	0.3
chr13	73854673	73855273	0.3	0.1
chr13	73954001	73954601	1.2	0.5
chr13	73954018	73954618	1.1	0.5
chr13	74564807	74565407	0.5	0.4
chr13	74838665	74839265	1.6	0.2
chr13	75353634	75354234	1.0	0.2
chr13	75365880	75366480	0.5	0.0

chr13	75487613	75488213	0.4	0.1
chr13	75551808	75552408	1.8	0.1
chr13	75552100	75552700	2.2	0.2
chr13	76056347	76056947	0.6	0.7
chr13	76291450	76292050	0.3	0.4
chr13	76864828	76865428	0.2	0.3
chr13	77053501	77054101	1.2	0.2
chr13	77263136	77263736	0.3	0.1
chr13	77417428	77418028	0.0	0.0
chr13	77607226	77607826	1.3	0.1
chr13	77805515	77806115	0.7	0.1
chr13	78233842	78234442	0.6	0.0
chr13	78856327	78856927	0.5	0.3
chr13	79513599	79514199	0.8	0.0
chr13	79664160	79664760	1.0	0.1
chr13	79844688	79845288	0.9	0.4
chr13	81131637	81132237	1.2	0.2
chr13	81173625	81174225	0.1	0.0
chr13	82233388	82233988	0.9	0.3
chr13	84385413	84386013	0.1	0.2
chr13	84385593	84386193	0.7	0.4
chr13	84540494	84541094	1.2	0.2
chr13	86207028	86207628	0.7	0.0
chr13	86207176	86207776	0.8	0.1
chr13	86215620	86216220	0.3	0.1
chr13	89243979	89244579	1.1	0.2
chr13	89244237	89244837	1.9	0.5
chr13	89568290	89568890	1.1	0.0
chr13	89694197	89694797	1.0	0.0
chr13	89699088	89699688	1.4	0.2
chr13	89880893	89881493	0.6	0.5
chr13	90179103	90179703	1.1	0.4
chr13	90404487	90405087	0.4	0.1
chr13	90594152	90594752	1.2	0.0
chr13	93319847	93320447	0.6	0.0
chr13	93362784	93363384	1.3	0.5
chr13	94013964	94014564	0.5	0.1
chr13	94154550	94155150	0.2	0.1

chr13	94736151	94736751	0.4	0.3
chr13	95472480	95473080	0.9	0.1
chr13	96196013	96196613	0.5	0.3
chr13	96196042	96196642	0.5	0.5
chr13	97250770	97251370	0.2	0.2
chr13	98387347	98387947	0.6	0.5
chr13	98579600	98580200	1.3	0.1
chr13	98758964	98759564	5.3	2.0
chr13	98758984	98759584	5.2	2.1
chr13	98758994	98759594	5.3	2.2
chr13	98759032	98759632	5.5	2.2
chr13	98759052	98759652	5.5	2.4
chr13	98974941	98975541	3.7	1.2
chr13	98975038	98975638	3.8	1.0
chr13	99343020	99343620	0.8	0.0
chr13	99343424	99344024	1.4	0.6
chr13	99343442	99344042	1.5	0.6
chr13	99921027	99921627	1.4	0.2
chr13	100252932	100253532	0.4	0.1
chr13	100411572	100412172	0.3	0.3
chr13	101052825	101053425	0.8	0.1
chr13	101052864	101053464	0.7	0.1
chr13	101132010	101132610	0.1	0.2
chr13	101132049	101132649	0.1	0.4
chr13	101203095	101203695	0.8	0.1
chr13	101203134	101203734	1.0	0.3
chr13	101203213	101203813	1.0	0.3
chr13	101203226	101203826	1.0	0.3
chr13	101269491	101270091	0.0	0.1
chr13	101269533	101270133	0.1	0.1
chr13	101616486	101617086	0.7	0.1
chr13	101951998	101952598	0.3	0.0
chr13	102367530	102368130	0.1	0.3
chr13	102500492	102501092	1.0	0.2
chr13	102953892	102954492	0.9	0.2
chr13	103749862	103750462	0.1	0.1
chr13	105616989	105617589	0.3	0.0
chr13	105634490	105635090	0.5	0.0

chr13	105634573	105635173	0.2	0.0
chr13	106083293	106083893	0.8	0.0
chr13	106175286	106175886	0.4	0.1
chr13	107366904	107367504	0.0	0.3
chr13	108155870	108156470	0.1	0.1
chr13	108571696	108572296	1.0	0.2
chr13	109207743	109208343	0.9	0.1
chr13	109939587	109940187	0.3	0.1
chr13	110289760	110290360	0.3	0.0
chr13	110327480	110328080	0.5	0.4
chr13	110690889	110691489	1.3	0.2
chr13	110738767	110739367	0.5	0.1
chr13	112089848	112090448	1.2	0.0
chr13	112788377	112788977	0.2	0.2
chr13	112788550	112789150	2.4	0.9
chr13	112788801	112789401	2.0	0.4
chr13	112893151	112893751	1.8	0.1
chr13	112893369	112893969	2.3	0.5
chr13	112893390	112893990	2.3	0.4
chr13	113128084	113128684	0.2	0.3
chr13	114124283	114124883	1.8	0.5
chr13	114124577	114125177	1.2	0.3
chr13	114349598	114350198	1.0	0.1
chr13	114473255	114473855	0.9	0.2
chr13	114950991	114951591	0.8	0.3
chr13	114951202	114951802	0.7	0.3
chr13	114977721	114978321	0.4	0.0
chr13	115251873	115252473	1.0	0.2
chr13	115251963	115252563	0.7	0.5
chr13	115421349	115421949	0.1	0.0
chr13	115421377	115421977	0.0	0.0
chr13	115500608	115501208	0.6	0.0
chr13	116313386	116313986	0.3	0.3
chr13	116450085	116450685	1.3	0.4
chr13	116864989	116865589	0.9	0.0
chr13	117071687	117072287	0.4	0.6
chr13	117109602	117110202	0.1	0.0
chr13	117206687	117207287	1.3	0.9

chr13	117206732	117207332	1.0	0.9
chr13	117310080	117310680	1.4	0.7
chr13	117310091	117310691	1.5	0.8
chr13	117962635	117963235	0.8	0.8
chr13	117962730	117963330	1.4	0.8
chr13	117999085	117999685	0.8	0.2
chr13	117999156	117999756	0.9	0.6
chr13	117999176	117999776	1.0	0.7
chr13	118006115	118006715	1.3	0.3
chr13	118006307	118006907	0.8	0.1
chr13	118423565	118424165	0.6	0.1
chr13	119065165	119065765	0.9	0.3
chr13	119257171	119257771	0.1	0.1
chr13	119260796	119261396	0.8	0.1
chr13	119325650	119326250	0.8	0.1
chr13	119325805	119326405	0.9	0.2
chr13	119563488	119564088	1.3	0.1
chr13	119580007	119580607	0.6	0.2
chr13	119590766	119591366	0.5	0.1
chr14	8672531	8673131	1.6	0.1
chr14	8863146	8863746	0.9	0.5
chr14	9165334	9165934	0.5	0.0
chr14	10227160	10227760	1.0	0.1
chr14	10789266	10789866	0.0	0.1
chr14	10912479	10913079	1.1	0.3
chr14	11400486	11401086	1.2	0.1
chr14	11400529	11401129	1.3	0.2
chr14	12176856	12177456	0.1	0.0
chr14	12888835	12889435	0.2	0.1
chr14	13271373	13271973	0.9	0.1
chr14	13909715	13910315	0.4	0.1
chr14	14176961	14177561	2.0	0.1
chr14	14738547	14739147	0.9	0.4
chr14	14738745	14739345	0.8	0.5
chr14	15199243	15199843	0.7	0.1
chr14	15522727	15523327	0.5	0.3
chr14	15522755	15523355	0.4	0.2
chr14	15720649	15721249	0.8	0.1

chr14	16713977	16714577	1.3	0.2
chr14	16768675	16769275	0.9	0.3
chr14	17934505	17935105	0.4	0.1
chr14	18021225	18021825	0.3	0.1
chr14	18391203	18391803	0.8	0.2
chr14	18651273	18651873	0.5	0.1
chr14	19953727	19954327	0.2	0.1
chr14	20919764	20920364	1.6	0.0
chr14	20919930	20920530	1.7	0.0
chr14	20964983	20965583	0.7	0.5
chr14	20985859	20986459	0.7	0.4
chr14	21015511	21016111	1.2	0.5
chr14	21518432	21519032	0.6	0.4
chr14	21552737	21553337	0.3	0.1
chr14	22017692	22018292	0.1	0.0
chr14	22758673	22759273	0.7	0.2
chr14	23277672	23278272	0.2	0.5
chr14	23487562	23488162	1.8	0.6
chr14	24610113	24610713	1.6	0.1
chr14	24705128	24705728	0.3	0.0
chr14	25416521	25417121	0.4	0.1
chr14	25738820	25739420	0.1	0.1
chr14	25786216	25786816	0.4	0.0
chr14	25805068	25805668	1.5	0.1
chr14	25839899	25840499	0.7	0.3
chr14	25937644	25938244	0.8	0.0
chr14	25940121	25940721	0.4	0.0
chr14	25942879	25943479	0.6	0.2
chr14	26027401	26028001	0.7	0.2
chr14	26168447	26169047	0.1	0.5
chr14	26380204	26380804	0.8	0.1
chr14	26380302	26380902	0.8	0.2
chr14	26437499	26438099	0.6	0.1
chr14	26736495	26737095	1.4	0.5
chr14	26876257	26876857	1.4	0.5
chr14	27015871	27016471	1.4	0.5
chr14	27440832	27441432	0.7	0.1
chr14	27570118	27570718	0.5	0.0

chr14	27880968	27881568	0.9	0.5
chr14	28382973	28383573	1.6	0.4
chr14	29228511	29229111	1.0	0.2
chr14	29228765	29229365	1.6	0.2
chr14	29646422	29647022	0.7	0.2
chr14	29728620	29729220	2.1	0.5
chr14	29981281	29981881	0.6	0.2
chr14	30114126	30114726	1.4	0.6
chr14	30114279	30114879	2.4	0.5
chr14	30898405	30899005	0.6	0.3
chr14	30898776	30899376	0.2	0.2
chr14	30955801	30956401	0.3	0.2
chr14	31034024	31034624	0.0	0.5
chr14	31140596	31141196	0.1	0.1
chr14	32127935	32128535	0.8	0.2
chr14	32237115	32237715	1.1	0.2
chr14	32331105	32331705	0.8	0.5
chr14	32880779	32881379	0.9	0.4
chr14	32964429	32965029	0.8	0.3
chr14	33247821	33248421	0.2	0.0
chr14	33508490	33509090	1.1	0.2
chr14	33836695	33837295	1.2	0.9
chr14	33836733	33837333	1.2	0.9
chr14	33912251	33912851	2.7	0.3
chr14	33997833	33998433	0.3	0.3
chr14	34592618	34593218	0.6	0.0
chr14	34775097	34775697	0.7	0.1
chr14	34905225	34905825	0.2	0.0
chr14	35356251	35356851	1.1	0.1
chr14	35409632	35410232	1.8	0.6
chr14	35409802	35410402	1.7	0.5
chr14	35428474	35429074	0.4	0.4
chr14	35477109	35477709	1.2	0.0
chr14	35735670	35736270	0.1	0.4
chr14	35735807	35736407	0.8	0.5
chr14	35807479	35808079	0.3	0.1
chr14	36005002	36005602	0.3	0.6
chr14	36840799	36841399	0.2	0.1

chr14	37544444	37545044	1.9	0.1
chr14	40491698	40492298	0.8	0.1
chr14	41229499	41230099	0.9	0.2
chr14	41491866	41492466	0.0	0.1
chr14	41767739	41768339	0.7	0.0
chr14	45473847	45474447	0.1	0.0
chr14	46205392	46205992	0.5	0.1
chr14	46764724	46765324	1.5	0.3
chr14	47090069	47090669	0.5	0.1
chr14	47615824	47616424	0.8	0.4
chr14	47808914	47809514	0.4	0.2
chr14	48800568	48801168	0.7	0.0
chr14	48975326	48975926	1.0	0.2
chr14	49682008	49682608	0.2	0.1
chr14	50398477	50399077	0.9	0.0
chr14	50840951	50841551	0.5	0.0
chr14	51308707	51309307	0.1	0.1
chr14	51723922	51724522	0.2	0.2
chr14	52100729	52101329	1.3	0.0
chr14	53187163	53187763	0.7	0.2
chr14	54394249	54394849	0.2	0.1
chr14	54454884	54455484	0.9	0.1
chr14	54790744	54791344	0.7	0.2
chr14	55162753	55163353	2.7	0.9
chr14	55163027	55163627	0.9	0.2
chr14	55386318	55386918	1.9	1.1
chr14	55386548	55387148	2.4	1.0
chr14	55850054	55850654	0.8	0.5
chr14	56179170	56179770	0.6	0.2
chr14	56370654	56371254	1.4	0.5
chr14	56677515	56678115	0.3	0.2
chr14	57109618	57110218	1.2	0.4
chr14	57203937	57204537	0.2	0.0
chr14	57644182	57644782	0.6	0.1
chr14	57644379	57644979	0.7	0.2
chr14	57788786	57789386	2.1	1.0
chr14	57788795	57789395	2.0	1.0
chr14	57788804	57789404	2.0	1.0

chr14	57788813	57789413	2.0	0.9
chr14	57788822	57789422	2.1	0.9
chr14	57788831	57789431	2.2	0.9
chr14	58033363	58033963	0.3	0.1
chr14	58157001	58157601	0.3	0.0
chr14	58436774	58437374	0.0	0.1
chr14	58540104	58540704	0.4	0.4
chr14	58540297	58540897	0.6	0.4
chr14	59486860	59487460	2.3	0.5
chr14	59487037	59487637	2.6	0.4
chr14	59660190	59660790	1.1	0.2
chr14	59727646	59728246	0.6	0.3
chr14	59727656	59728256	0.8	0.3
chr14	59727676	59728276	0.8	0.2
chr14	59840829	59841429	0.8	0.2
chr14	59879513	59880113	0.2	0.1
chr14	60944530	60945130	0.6	0.3
chr14	61173204	61173804	0.3	0.4
chr14	61383869	61384469	0.7	0.7
chr14	61405725	61406325	0.1	0.1
chr14	61586469	61587069	1.0	0.5
chr14	61784562	61785162	0.1	0.0
chr14	62352990	62353590	1.4	0.4
chr14	62453051	62453651	2.1	0.1
chr14	62459762	62460362	0.0	0.0
chr14	62911604	62912204	0.8	0.2
chr14	62998379	62998979	0.4	0.2
chr14	63237470	63238070	0.8	0.0
chr14	63237499	63238099	0.9	0.2
chr14	63460854	63461454	1.0	0.3
chr14	63993050	63993650	0.9	0.1
chr14	64519889	64520489	1.3	0.3
chr14	64583040	64583640	1.6	0.6
chr14	65216635	65217235	0.4	0.2
chr14	65242123	65242723	0.5	0.4
chr14	65621231	65621831	0.6	0.0
chr14	65670824	65671424	1.2	0.4
chr14	66487791	66488391	1.3	0.2
chr14	66488077	66488677	2.4	0.5
chr14	66535206	66535806	0.7	0.0
chr14	66614774	66615374	9.6	4.8
chr14	66614790	66615390	9.6	4.8
chr14	66614809	66615409	9.6	4.8
chr14	66614825	66615425	9.6	4.8
chr14	66614841	66615441	9.6	4.8
chr14	66614860	66615460	9.7	4.8
chr14	66614876	66615476	9.7	4.8
chr14	66614959	66615559	9.7	4.9
chr14	66614991	66615591	9.7	4.9
chr14	66615015	66615615	10.0	5.1
chr14	66615031	66615631	10.2	5.1
chr14	66671070	66671670	0.9	0.4
chr14	66691474	66692074	0.3	0.3
chr14	66976253	66976853	1.4	0.2
chr14	67623278	67623878	0.8	0.0
chr14	67758592	67759192	0.3	0.2
chr14	67813244	67813844	1.6	0.5
chr14	69514567	69515167	0.2	0.2
chr14	70259531	70260131	0.9	0.1
chr14	70401697	70402297	2.8	1.4
chr14	70401711	70402311	2.7	1.4
chr14	70849211	70849811	0.4	0.2
chr14	70908403	70909003	0.0	0.1
chr14	70934078	70934678	0.3	0.0
chr14	71005346	71005946	0.9	0.3
chr14	71005412	71006012	0.9	0.2
chr14	71287248	71287848	1.0	0.1
chr14	71328853	71329453	0.1	0.0
chr14	71429423	71430023	0.0	0.7
chr14	72501559	72502159	0.3	0.0
chr14	74002659	74003259	0.6	0.2
chr14	74055574	74056174	2.6	1.0
chr14	74055666	74056266	2.7	1.1
chr14	74055712	74056312	2.8	1.2
chr14	75088515	75089115	1.4	0.5
chr14	75088521	75089121	1.3	0.4

chr14	75235247	75235847	0.4	0.5
chr14	75558436	75559036	1.2	0.8
chr14	75558453	75559053	1.2	0.9
chr14	75558470	75559070	1.3	0.8
chr14	75793115	75793715	0.0	0.6
chr14	76263177	76263777	0.8	0.1
chr14	76267397	76267997	1.1	0.6
chr14	76573682	76574282	1.0	0.1
chr14	76574740	76575340	0.0	0.1
chr14	76719743	76720343	1.0	0.3
chr14	76974785	76975385	1.4	0.3
chr14	78065321	78065921	0.7	0.0
chr14	78518902	78519502	2.2	0.4
chr14	78568143	78568743	1.9	0.2
chr14	78665152	78665752	1.2	0.1
chr14	79086589	79087189	3.1	0.2
chr14	79086847	79087447	1.6	0.3
chr14	79255233	79255833	1.5	0.2
chr14	79628997	79629597	1.3	0.4
chr14	79819976	79820576	0.4	0.5
chr14	79954568	79955168	0.4	0.3
chr14	80141514	80142114	0.4	0.2
chr14	80311980	80312580	0.0	0.2
chr14	81705322	81705922	0.1	0.4
chr14	83175705	83176305	0.7	0.1
chr14	85703672	85704272	0.6	0.8
chr14	86784008	86784608	0.5	0.4
chr14	87067690	87068290	0.9	0.2
chr14	90149228	90149828	0.8	0.2
chr14	90476409	90477009	0.5	0.1
chr14	90921879	90922479	0.1	0.0
chr14	91289411	91290011	0.3	0.0
chr14	91362105	91362705	0.9	0.0
chr14	91927752	91928352	1.1	0.5
chr14	92163633	92164233	0.2	0.2
chr14	93119166	93119766	1.2	0.5
chr14	93119308	93119908	1.3	0.8
chr14	94116635	94117235	2.0	0.2
chr14	94116833	94117433	2.2	0.3
chr14	94304026	94304626	0.2	0.2
chr14	94304171	94304771	0.9	0.1
chr14	95377939	95378539	0.1	0.1
chr14	96840539	96841139	0.2	0.0
chr14	98075767	98076367	0.0	0.1
chr14	98342020	98342620	1.1	0.1
chr14	98342225	98342825	0.5	0.1
chr14	99611122	99611722	1.0	0.2
chr14	99611205	99611805	0.8	0.2
chr14	100802062	100802662	0.2	0.1
chr14	101406089	101406689	0.2	0.3
chr14	101628595	101629195	0.4	0.0
chr14	102319498	102320098	0.8	0.1
chr14	103487088	103487688	1.4	0.8
chr14	103758527	103759127	1.2	0.5
chr14	103977848	103978448	0.7	0.3
chr14	104353278	104353878	0.1	0.3
chr14	104576801	104577401	0.2	0.2
chr14	105006849	105007449	0.4	0.1
chr14	105383242	105383842	0.6	0.2
chr14	105383425	105384025	0.8	0.4
chr14	105540957	105541557	1.4	0.4
chr14	106053561	106054161	0.5	0.2
chr14	106772741	106773341	1.7	0.2
chr14	108376606	108377206	0.5	0.1
chr14	108458750	108459350	1.5	0.2
chr14	108458851	108459451	1.9	0.3
chr14	108791774	108792374	0.1	0.4
chr14	109813865	109814465	1.2	0.0
chr14	113182583	113183183	0.6	0.0
chr14	113248813	113249413	0.4	0.4
chr14	113426187	113426787	0.0	0.1
chr14	116018392	116018992	0.1	0.0
chr14	116177509	116178109	0.5	0.2
chr14	116410768	116411368	0.3	0.2
chr14	116454998	116455598	0.8	0.2
chr14	116541666	116542266	0.1	0.0

chr14	116541690	116542290	0.1	0.0
chr14	116611381	116611981	0.7	0.1
chr14	117027944	117028544	0.3	0.1
chr14	117028034	117028634	2.0	0.8
chr14	117028045	117028645	2.2	0.8
chr14	117028295	117028895	1.0	0.0
chr14	118747263	118747863	0.8	0.5
chr14	118836927	118837527	1.4	0.2
chr14	119184001	119184601	0.7	0.2
chr14	119245025	119245625	0.1	0.2
chr14	119325602	119326202	0.4	0.1
chr14	119652012	119652612	0.9	0.0
chr14	119744524	119745124	0.3	0.5
chr14	119754093	119754693	1.1	0.2
chr14	119882703	119883303	1.2	0.7
chr14	120591020	120591620	0.4	0.1
chr14	120933850	120934450	0.8	0.3
chr14	120934077	120934677	1.2	0.6
chr14	121255754	121256354	1.0	0.1
chr14	121266996	121267596	0.6	0.0
chr14	122075685	122076285	0.5	0.7
chr14	122118189	122118789	0.7	0.2
chr14	122426580	122427180	0.6	0.4
chr14	122426646	122427246	0.7	0.5
chr14	122506493	122507093	1.1	0.1
chr14	123093787	123094387	1.5	0.1
chr14	123521954	123522554	0.8	0.1
chr14	124318206	124318806	0.9	0.0
chr15	3219092	3219692	0.0	0.0
chr15	3439889	3440489	1.2	0.2
chr15	3534694	3535294	1.0	0.3
chr15	3534892	3535492	0.9	0.2
chr15	4281436	4282036	0.7	0.2
chr15	4283320	4283920	0.9	0.7
chr15	4389496	4390096	1.4	0.0
chr15	5302436	5303036	0.9	0.6
chr15	5302524	5303124	1.1	0.2
chr15	5384782	5385382	0.7	0.3

chr15	5384826	5385426	0.6	0.4
chr15	5863398	5863998	0.5	0.2
chr15	5863501	5864101	0.3	0.0
chr15	6530701	6531301	1.6	0.1
chr15	6564334	6564934	0.7	0.0
chr15	6578629	6579229	0.2	0.4
chr15	6799131	6799731	1.0	0.6
chr15	7147618	7148218	1.1	0.1
chr15	7157185	7157785	0.9	0.4
chr15	7161490	7162090	0.3	0.2
chr15	7367589	7368189	1.0	0.3
chr15	7481189	7481789	0.1	0.3
chr15	7523923	7524523	1.5	0.3
chr15	8435089	8435689	1.4	0.3
chr15	8579317	8579917	2.3	0.6
chr15	8582203	8582803	1.4	0.6
chr15	8582240	8582840	1.0	0.4
chr15	9963548	9964148	1.2	0.9
chr15	10217637	10218237	0.9	0.5
chr15	10395327	10395927	4.0	1.9
chr15	10395364	10395964	4.0	1.9
chr15	10395401	10396001	4.1	2.0
chr15	10395438	10396038	4.4	2.3
chr15	10395476	10396076	4.6	2.3
chr15	10395513	10396113	4.5	2.3
chr15	10395589	10396189	4.7	2.4
chr15	10395626	10396226	4.4	2.2
chr15	10395663	10396263	4.3	2.1
chr15	10395700	10396300	4.2	2.1
chr15	10395738	10396338	3.7	1.8
chr15	10462928	10463528	3.8	0.7
chr15	10462963	10463563	3.8	0.7
chr15	10462998	10463598	3.7	0.6
chr15	10463033	10463633	3.7	0.7
chr15	10463068	10463668	3.8	0.7
chr15	10616940	10617540	0.6	0.2
chr15	10672217	10672817	1.4	0.1
chr15	10824497	10825097	0.9	0.5

chr15	11005650	11006250	1.5	0.1
chr15	11127058	11127658	0.0	0.1
chr15	11633594	11634194	0.2	0.0
chr15	11766170	11766770	1.2	0.5
chr15	11954786	11955386	1.5	0.8
chr15	11954807	11955407	1.3	0.8
chr15	12241718	12242318	2.0	0.6
chr15	12241735	12242335	1.9	0.5
chr15	12317048	12317648	0.0	0.1
chr15	12821397	12821997	0.3	0.2
chr15	12949802	12950402	1.3	0.1
chr15	14550439	14551039	0.1	0.2
chr15	16443922	16444522	0.7	0.1
chr15	16924119	16924719	0.1	0.1
chr15	17130125	17130725	0.6	0.2
chr15	17982030	17982630	1.0	0.4
chr15	20141486	20142086	1.3	0.5
chr15	21127222	21127822	0.8	0.1
chr15	21530727	21531327	1.1	0.1
chr15	21918457	21919057	1.0	0.4
chr15	22562365	22562965	0.5	0.1
chr15	22562560	22563160	0.6	0.0
chr15	22758186	22758786	0.6	0.0
chr15	23015527	23016127	0.4	0.1
chr15	23015630	23016230	0.7	0.1
chr15	23870791	23871391	0.7	0.1
chr15	24979395	24979995	0.2	0.2
chr15	25191082	25191682	0.7	0.4
chr15	25566265	25566865	0.1	0.0
chr15	26733810	26734410	0.6	0.4
chr15	26856420	26857020	0.9	0.0
chr15	27103144	27103744	1.4	0.1
chr15	27170438	27171038	0.1	0.1
chr15	27249413	27250013	0.1	0.2
chr15	27446248	27446848	0.2	0.9
chr15	27508449	27509049	1.5	0.3
chr15	27562842	27563442	0.9	0.5
chr15	27563049	27563649	0.9	0.5

chr15	27651527	27652127	0.7	0.2
chr15	27795776	27796376	1.3	0.4
chr15	27927711	27928311	0.2	0.1
chr15	28765701	28766301	0.8	0.1
chr15	31020807	31021407	0.1	0.2
chr15	31174935	31175535	0.5	0.0
chr15	31862280	31862880	0.6	0.0
chr15	32076688	32077288	0.5	0.0
chr15	32129164	32129764	0.1	0.3
chr15	32580119	32580719	0.6	0.1
chr15	33805617	33806217	0.8	0.0
chr15	34261684	34262284	0.2	0.1
chr15	34461916	34462516	0.8	0.5
chr15	34677543	34678143	0.1	0.2
chr15	35090191	35090791	1.3	0.4
chr15	35853651	35854251	0.4	0.0
chr15	36042283	36042883	1.5	0.4
chr15	36417193	36417793	1.2	0.3
chr15	36417394	36417994	1.1	0.5
chr15	37288466	37289066	1.3	0.4
chr15	37528603	37529203	0.6	0.3
chr15	37546489	37547089	0.3	0.1
chr15	37764531	37765131	0.5	0.3
chr15	37857266	37857866	0.6	0.2
chr15	37942348	37942948	0.4	0.3
chr15	38116379	38116979	0.8	0.2
chr15	38211882	38212482	1.3	0.6
chr15	38979593	38980193	0.2	0.2
chr15	38979613	38980213	0.2	0.3
chr15	41815333	41815933	1.1	0.2
chr15	42255213	42255813	0.7	0.2
chr15	42255247	42255847	0.3	0.1
chr15	42454124	42454724	0.0	0.0
chr15	42745662	42746262	0.9	0.3
chr15	42745805	42746405	1.1	0.1
chr15	43554816	43555416	0.7	0.2
chr15	43964330	43964930	0.0	0.4
chr15	44384931	44385531	1.3	0.2

chr15	44384949	44385549	1.5	0.2
chr15	46377114	46377714	1.3	0.8
chr15	46377206	46377806	1.5	0.7
chr15	46514941	46515541	1.7	0.4
chr15	46768642	46769242	0.8	0.0
chr15	46975748	46976348	0.4	0.0
chr15	50419545	50420145	0.0	0.2
chr15	50651907	50652507	0.6	0.1
chr15	50726702	50727302	0.5	0.1
chr15	51772034	51772634	6.1	2.7
chr15	51772059	51772659	6.0	2.7
chr15	51772084	51772684	6.1	2.7
chr15	51772109	51772709	6.1	2.7
chr15	51772134	51772734	6.4	2.8
chr15	51772159	51772759	6.6	2.8
chr15	51772284	51772884	6.3	2.6
chr15	51988450	51989050	0.9	0.2
chr15	52044553	52045153	1.3	0.1
chr15	52044752	52045352	3.1	1.1
chr15	52045025	52045625	2.2	0.9
chr15	52405302	52405902	0.0	0.2
chr15	53056691	53057291	0.3	0.2
chr15	53402788	53403388	0.2	0.1
chr15	53915085	53915685	1.0	0.4
chr15	54407345	54407945	0.2	0.4
chr15	54407436	54408036	0.3	0.4
chr15	54932110	54932710	0.6	0.4
chr15	54969158	54969758	0.9	0.3
chr15	55299217	55299817	0.3	0.1
chr15	55448058	55448658	0.6	0.1
chr15	56257413	56258013	0.8	0.3
chr15	56639118	56639718	1.3	0.1
chr15	57072308	57072908	0.6	0.2
chr15	57170310	57170910	0.7	0.2
chr15	57340934	57341534	0.9	0.4
chr15	59022670	59023270	1.3	0.7
chr15	59802212	59802812	0.9	0.2
chr15	59802313	59802913	3.8	1.6
chr15	59802517	59803117	2.3	1.2
chr15	60039124	60039724	0.7	0.1
chr15	60214309	60214909	0.4	0.0
chr15	61056602	61057202	1.2	0.3
chr15	61487041	61487641	0.3	0.4
chr15	61487100	61487700	0.5	0.4
chr15	61900062	61900662	1.8	0.3
chr15	63368091	63368691	1.0	0.4
chr15	63548840	63549440	1.3	0.0
chr15	63838890	63839490	1.4	0.2
chr15	63867239	63867839	0.7	0.6
chr15	64343324	64343924	2.5	0.2
chr15	64343403	64344003	2.5	0.4
chr15	64403941	64404541	0.5	0.1
chr15	64410440	64411040	3.0	0.8
chr15	65332729	65333329	0.8	0.2
chr15	65759788	65760388	1.6	0.1
chr15	65759824	65760424	1.4	0.1
chr15	66087989	66088589	0.3	0.1
chr15	66098649	66099249	1.2	0.4
chr15	66138116	66138716	0.5	0.1
chr15	66942621	66943221	0.4	0.1
chr15	68088586	68089186	1.1	0.5
chr15	69200728	69201328	0.1	0.3
chr15	70977538	70978138	1.4	0.3
chr15	71750848	71751448	0.4	0.3
chr15	71750893	71751493	0.0	0.5
chr15	71770587	71771187	0.2	0.1
chr15	72063496	72064096	0.2	0.5
chr15	73009193	73009793	1.4	0.1
chr15	73562659	73563259	0.8	0.1
chr15	73701031	73701631	1.0	0.1
chr15	73701057	73701657	1.1	0.1
chr15	73817957	73818557	2.6	0.4
chr15	73818201	73818801	1.6	0.1
chr15	74366054	74366654	0.6	0.6
chr15	74424066	74424666	0.3	0.0
chr15	75210756	75211356	0.3	0.4

chr15	75472311	75472911	1.2	0.1
chr15	75799155	75799755	1.9	0.3
chr15	75830322	75830922	1.7	0.1
chr15	75903462	75904062	0.1	0.1
chr15	76075976	76076576	0.0	0.0
chr15	76990622	76991222	1.2	0.1
chr15	77030508	77031108	0.6	0.2
chr15	77064083	77064683	1.1	0.2
chr15	77252946	77253546	0.5	0.2
chr15	77393200	77393800	0.6	0.1
chr15	77548812	77549412	0.5	0.2
chr15	77575345	77575945	0.5	0.1
chr15	77575545	77576145	1.1	0.9
chr15	77936381	77936981	1.2	0.3
chr15	77936425	77937025	1.2	0.4
chr15	78320236	78320836	0.6	0.1
chr15	78453903	78454503	0.6	0.2
chr15	78475246	78475846	0.4	0.1
chr15	78656993	78657593	0.6	0.1
chr15	78724402	78725002	0.4	0.1
chr15	78950550	78951150	0.4	0.2
chr15	79181421	79182021	0.2	0.1
chr15	79191708	79192308	2.1	0.1
chr15	79199918	79200518	1.2	0.3
chr15	79199933	79200533	1.4	0.2
chr15	79336375	79336975	1.7	0.5
chr15	79336551	79337151	1.8	0.7
chr15	79506375	79506975	0.6	0.1
chr15	79793862	79794462	1.3	0.1
chr15	80137481	80138081	0.0	0.0
chr15	80456932	80457532	0.4	0.1
chr15	81475480	81476080	0.2	0.1
chr15	81824864	81825464	2.8	0.7
chr15	81825067	81825667	2.9	0.7
chr15	81937252	81937852	0.1	0.5
chr15	81945721	81946321	1.9	0.1
chr15	81945870	81946470	2.4	0.5
chr15	82741552	82742152	0.6	0.3

chr15	82830895	82831495	1.6	0.2
chr15	82976064	82976664	1.4	0.2
chr15	83139127	83139727	2.8	1.1
chr15	83139188	83139788	3.2	1.3
chr15	83139249	83139849	3.3	1.3
chr15	83139305	83139905	3.4	1.4
chr15	83139356	83139956	3.6	1.5
chr15	83139420	83140020	3.7	1.6
chr15	83139480	83140080	3.6	1.4
chr15	83139540	83140140	3.6	1.4
chr15	83139596	83140196	3.7	1.5
chr15	83139652	83140252	2.9	1.0
chr15	83139712	83140312	3.3	1.1
chr15	83139832	83140432	2.8	0.8
chr15	83139892	83140492	2.4	0.6
chr15	83139952	83140552	2.0	0.3
chr15	83140012	83140612	1.6	0.1
chr15	83312298	83312898	1.2	0.1
chr15	83404443	83405043	0.4	0.0
chr15	83503358	83503958	2.5	0.4
chr15	83503406	83504006	2.5	0.4
chr15	83687187	83687787	0.3	0.2
chr15	83804728	83805328	0.2	0.0
chr15	83972897	83973497	1.4	0.8
chr15	84257542	84258142	0.6	0.0
chr15	84355734	84356334	0.3	0.6
chr15	84421153	84421753	0.6	0.2
chr15	84492140	84492740	0.5	0.1
chr15	84551239	84551839	1.7	0.8
chr15	84560039	84560639	0.0	0.5
chr15	84635263	84635863	1.0	0.1
chr15	85014430	85015030	1.5	0.2
chr15	85014691	85015291	1.6	0.7
chr15	85516477	85517077	0.1	0.1
chr15	85957824	85958424	2.4	1.4
chr15	85957882	85958482	2.2	1.4
chr15	86426317	86426917	1.2	0.8
chr15	86573788	86574388	1.2	0.0

chr15	87831179	87831779	1.1	0.7
chr15	87831274	87831874	1.0	0.2
chr15	87922516	87923116	1.1	0.1
chr15	87922552	87923152	0.9	0.1
chr15	88123503	88124103	0.3	0.5
chr15	88734319	88734919	0.7	0.4
chr15	88747074	88747674	0.1	0.1
chr15	88793204	88793804	1.4	0.5
chr15	88793443	88794043	1.0	0.3
chr15	88805168	88805768	1.4	0.3
chr15	88805336	88805936	1.9	0.5
chr15	88805378	88805978	2.0	0.6
chr15	88805420	88806020	2.1	0.7
chr15	88805504	88806104	2.4	0.8
chr15	88805546	88806146	2.6	0.9
chr15	88805588	88806188	2.8	1.0
chr15	88805672	88806272	2.7	1.0
chr15	88805714	88806314	2.7	1.0
chr15	88805756	88806356	2.8	1.0
chr15	88805798	88806398	2.8	1.0
chr15	88805840	88806440	2.6	0.9
chr15	88805882	88806482	2.5	0.9
chr15	88805924	88806524	2.4	0.8
chr15	88806008	88806608	2.6	0.9
chr15	88806050	88806650	2.3	0.8
chr15	88806176	88806776	1.7	0.6
chr15	88806260	88806860	1.6	0.6
chr15	88806302	88806902	1.6	0.6
chr15	88936394	88936994	0.6	0.3
chr15	88985736	88986336	1.4	0.0
chr15	88985917	88986517	1.2	0.1
chr15	89234263	89234863	1.4	0.4
chr15	89234283	89234883	1.2	0.3
chr15	89234303	89234903	1.3	0.3
chr15	89365704	89366304	1.1	0.1
chr15	89996286	89996886	0.8	0.1
chr15	90577598	90578198	0.3	0.2
chr15	90861136	90861736	0.3	0.0

chr15	90908332	90908932	1.0	0.0
chr15	90969774	90970374	0.6	0.2
chr15	91271457	91272057	0.7	0.2
chr15	91416212	91416812	0.8	0.2
chr15	91798236	91798836	0.3	0.1
chr15	92257625	92258225	1.9	0.4
chr15	92831159	92831759	1.6	0.5
chr15	93600821	93601421	0.9	0.2
chr15	94139465	94140065	1.4	0.1
chr15	94176746	94177346	0.5	0.2
chr15	94233186	94233786	0.3	0.2
chr15	94233245	94233845	0.0	0.4
chr15	94234061	94234661	2.2	1.2
chr15	94431114	94431714	0.8	0.0
chr15	94694487	94695087	1.0	0.3
chr15	94963726	94964326	1.8	0.7
chr15	94963751	94964351	2.1	0.8
chr15	95358657	95359257	0.3	0.1
chr15	95780024	95780624	1.8	0.5
chr15	95780104	95780704	1.8	0.3
chr15	95780141	95780741	1.7	0.3
chr15	95792443	95793043	0.3	0.0
chr15	96010493	96011093	0.9	0.5
chr15	96141081	96141681	0.6	0.3
chr15	96508232	96508832	0.2	0.0
chr15	97135916	97136516	0.4	0.0
chr15	97280723	97281323	1.6	0.5
chr15	97751200	97751800	0.9	0.1
chr15	97751261	97751861	0.8	0.0
chr15	97786536	97787136	1.2	0.3
chr15	97786800	97787400	1.3	0.6
chr15	98213444	98214044	0.1	0.0
chr15	98240538	98241138	0.6	0.2
chr15	98240794	98241394	1.5	0.3
chr15	98481333	98481933	0.6	0.2
chr15	99261786	99262386	0.9	0.2
chr15	99433320	99433920	0.7	0.6
chr15	99733878	99734478	0.2	0.1

chr15	99733907	99734507	0.0	0.2
chr15	101393929	101394529	1.3	0.5
chr15	101394191	101394791	0.3	0.4
chr15	101576337	101576937	0.7	0.0
chr15	101669360	101669960	0.5	0.2
chr15	101769613	101770213	2.6	0.7
chr15	101769818	101770418	1.9	0.1
chr15	101855730	101856330	0.2	0.1
chr15	101917754	101918354	0.2	0.3
chr15	102229715	102230315	1.8	0.1
chr15	102781366	102781966	1.9	0.7
chr15	103057252	103057852	1.7	0.4
chr16	3006414	3007014	1.6	0.1
chr16	4576851	4577451	0.4	0.1
chr16	4613827	4614427	1.1	0.9
chr16	4673258	4673858	0.1	0.4
chr16	4710938	4711538	0.6	0.1
chr16	4964159	4964759	0.9	0.6
chr16	5256112	5256712	0.7	0.4
chr16	5318887	5319487	0.2	0.1
chr16	5318936	5319536	0.3	0.2
chr16	5334844	5335444	0.9	0.1
chr16	5585062	5585662	0.7	0.2
chr16	5676951	5677551	0.7	0.2
chr16	6471281	6471881	0.6	0.2
chr16	7400731	7401331	0.4	0.6
chr16	8198873	8199473	0.6	0.0
chr16	8628282	8628882	0.1	0.4
chr16	8708186	8708786	0.3	0.0
chr16	8833487	8834087	0.1	0.1
chr16	9081873	9082473	0.9	0.3
chr16	9188999	9189599	1.1	0.7
chr16	9355219	9355819	1.4	0.0
chr16	9355256	9355856	1.3	0.0
chr16	9355293	9355893	1.2	0.1
chr16	9384031	9384631	0.4	0.5
chr16	9508651	9509251	1.2	0.1
chr16	9561756	9562356	0.6	0.4

chr16	10118728	10119328	1.1	0.3
chr16	10411813	10412413	1.3	0.0
chr16	10487033	10487633	1.0	0.7
chr16	10506832	10507432	2.0	0.6
chr16	10506956	10507556	1.8	0.7
chr16	10506987	10507587	1.8	0.6
chr16	10987154	10987754	0.9	0.3
chr16	10987306	10987906	1.2	0.5
chr16	11497686	11498286	0.2	0.3
chr16	11542675	11543275	0.2	0.1
chr16	11924159	11924759	3.9	1.6
chr16	11924263	11924863	4.1	1.6
chr16	11924416	11925016	4.4	1.3
chr16	12003869	12004469	2.1	0.2
chr16	12788741	12789341	0.1	0.2
chr16	13107460	13108060	0.5	0.2
chr16	13233404	13234004	0.6	0.3
chr16	13233657	13234257	0.9	0.2
chr16	13597340	13597940	0.5	0.2
chr16	14508108	14508708	0.4	0.0
chr16	15181978	15182578	1.7	0.0
chr16	15182123	15182723	1.6	0.2
chr16	15473155	15473755	0.4	0.1
chr16	15783249	15783849	0.1	0.2
chr16	15874856	15875456	0.7	0.1
chr16	16783878	16784478	0.3	0.1
chr16	17919771	17920371	0.0	0.1
chr16	17927729	17928329	1.0	0.1
chr16	18017354	18017954	0.3	0.3
chr16	18469975	18470575	0.5	0.0
chr16	18498449	18499049	1.5	0.3
chr16	18714864	18715464	1.9	0.6
chr16	18715024	18715624	1.6	0.3
chr16	18856834	18857434	0.6	0.1
chr16	19564920	19565520	0.1	0.1
chr16	19884413	19885013	0.6	0.0
chr16	20425807	20426407	1.4	0.1
chr16	20460666	20461266	1.2	0.2

chr16	20460839	20461439	0.8	0.1
chr16	21074395	21074995	0.8	0.4
chr16	21322053	21322653	2.3	0.5
chr16	21322159	21322759	2.1	0.5
chr16	22218589	22219189	0.4	0.1
chr16	22336818	22337418	0.8	0.3
chr16	22336886	22337486	0.6	0.5
chr16	23506296	23506896	0.4	0.4
chr16	23589365	23589965	0.0	0.0
chr16	23708572	23709172	0.0	0.0
chr16	23792487	23793087	0.8	0.2
chr16	24066716	24067316	0.1	0.3
chr16	24607987	24608587	0.8	0.2
chr16	24746237	24746837	1.7	0.2
chr16	25906047	25906647	1.5	0.2
chr16	25912375	25912975	0.6	0.4
chr16	25996258	25996858	1.9	0.9
chr16	25996457	25997057	1.8	0.8
chr16	26078972	26079572	0.9	0.2
chr16	26282444	26283044	0.7	0.1
chr16	28360042	28360642	0.2	0.1
chr16	28379128	28379728	0.5	0.1
chr16	28714267	28714867	1.2	0.3
chr16	28841117	28841717	0.8	0.2
chr16	29215685	29216285	0.8	0.5
chr16	29579309	29579909	0.3	0.1
chr16	29703832	29704432	1.3	0.1
chr16	29759088	29759688	0.3	0.1
chr16	29796796	29797396	1.4	0.3
chr16	29895928	29896528	0.1	0.2
chr16	30054265	30054865	0.5	0.4
chr16	30123709	30124309	0.2	0.6
chr16	30143013	30143613	0.6	0.6
chr16	30190659	30191259	2.4	0.1
chr16	30522587	30523187	0.8	0.1
chr16	30773721	30774321	1.4	0.4
chr16	30773946	30774546	1.2	0.4
chr16	31314282	31314882	0.6	0.2

chr16	31800458	31801058	0.7	0.2
chr16	32139399	32139999	1.2	0.1
chr16	32140655	32141255	0.3	0.1
chr16	32332869	32333469	0.7	0.0
chr16	32444660	32445260	0.5	0.5
chr16	32795798	32796398	1.4	0.1
chr16	33310587	33311187	0.4	0.1
chr16	33607408	33608008	0.2	0.0
chr16	33860791	33861391	0.1	0.0
chr16	34196258	34196858	1.7	0.2
chr16	34364794	34365394	1.1	0.1
chr16	34364847	34365447	0.9	0.1
chr16	34676985	34677585	1.2	0.1
chr16	34711336	34711936	0.9	0.2
chr16	35177989	35178589	1.0	0.1
chr16	35644819	35645419	3.5	1.3
chr16	35644978	35645578	3.0	1.1
chr16	35871606	35872206	0.4	1.0
chr16	38213340	38213940	0.2	0.1
chr16	38429321	38429921	0.2	0.1
chr16	38998529	38999129	0.7	0.1
chr16	39043417	39044017	0.7	0.6
chr16	39143262	39143862	0.4	0.2
chr16	39143275	39143875	0.4	0.1
chr16	39383097	39383697	0.6	0.2
chr16	40210862	40211462	0.6	0.2
chr16	40211121	40211721	0.6	0.1
chr16	43185506	43186106	1.2	0.2
chr16	43591511	43592111	0.2	0.1
chr16	43963819	43964419	1.5	0.1
chr16	43985588	43986188	0.6	0.7
chr16	44285051	44285651	1.5	0.1
chr16	44502441	44503041	0.9	0.1
chr16	44551974	44552574	0.7	0.4
chr16	45716596	45717196	0.3	0.1
chr16	46320290	46320890	0.3	0.0
chr16	46617505	46618105	0.3	0.2
chr16	47046936	47047536	1.0	0.4

chr16	47047091	47047691	0.6	0.2
chr16	47398301	47398901	0.4	0.2
chr16	47668853	47669453	0.7	0.2
chr16	48519846	48520446	0.8	0.3
chr16	48519955	48520555	0.8	0.2
chr16	49300317	49300917	1.6	0.5
chr16	49300426	49301026	1.6	0.5
chr16	51453244	51453844	1.6	0.1
chr16	51764811	51765411	2.6	0.4
chr16	51804043	51804643	0.5	0.5
chr16	52008058	52008658	1.0	0.0
chr16	52434377	52434977	1.1	0.6
chr16	53037697	53038297	0.6	0.0
chr16	53686621	53687221	1.4	0.4
chr16	53686632	53687232	1.3	0.4
chr16	53732408	53733008	0.9	0.3
chr16	54105206	54105806	1.6	0.3
chr16	54442136	54442736	0.4	0.1
chr16	55112504	55113104	1.5	0.3
chr16	55112632	55113232	1.1	0.4
chr16	55253486	55254086	0.8	0.8
chr16	55549058	55549658	1.0	0.2
chr16	56030087	56030687	0.7	0.1
chr16	56363629	56364229	0.5	0.0
chr16	56697405	56698005	1.0	0.2
chr16	56697415	56698015	1.0	0.2
chr16	57112982	57113582	1.2	0.3
chr16	57347073	57347673	0.1	0.2
chr16	57419310	57419910	0.5	0.2
chr16	58017749	58018349	0.3	0.2
chr16	58348729	58349329	0.4	0.2
chr16	58824175	58824775	0.7	0.4
chr16	58872616	58873216	0.2	0.2
chr16	60301491	60302091	0.7	0.5
chr16	60618239	60618839	0.5	0.0
chr16	60838269	60838869	0.5	0.2
chr16	61528503	61529103	0.9	0.2
chr16	61528604	61529204	0.8	0.2
chr16	62249242	62249842	1.6	0.7
chr16	62249341	62249941	2.0	0.7
chr16	63274435	63275035	0.7	0.1
chr16	63497207	63497807	0.7	0.1
chr16	63717894	63718494	0.7	0.1
chr16	63979762	63980362	0.2	0.1
chr16	63979974	63980574	0.0	0.1
chr16	64635959	64636559	0.1	0.1
chr16	65826635	65827235	0.4	0.1
chr16	68199224	68199824	1.6	0.0
chr16	68199354	68199954	1.9	0.5
chr16	71683777	71684377	0.4	0.0
chr16	71878717	71879317	1.3	0.1
chr16	72164244	72164844	0.5	0.0
chr16	72769302	72769902	0.7	0.7
chr16	74129999	74130599	1.4	0.1
chr16	74426988	74427588	2.3	0.9
chr16	74427168	74427768	1.5	1.1
chr16	75292910	75293510	0.3	0.1
chr16	76566434	76567034	1.4	0.2
chr16	77472675	77473275	0.7	0.1
chr16	77495470	77496070	0.5	0.1
chr16	77606280	77606880	0.6	0.5
chr16	77857370	77857970	1.1	0.1
chr16	78101825	78102425	0.7	0.4
chr16	78183827	78184427	0.5	0.1
chr16	78725581	78726181	1.3	0.1
chr16	79321371	79321971	2.1	0.1
chr16	80702087	80702687	0.1	0.2
chr16	82975888	82976488	1.6	0.7
chr16	83722652	83723252	0.7	0.1
chr16	83742679	83743279	0.9	0.3
chr16	84557065	84557665	1.0	0.3
chr16	84557083	84557683	1.0	0.3
chr16	84557094	84557694	0.9	0.3
chr16	84618615	84619215	0.6	0.1
chr16	85012233	85012833	1.2	0.0
chr16	85116036	85116636	0.1	0.1

chr16	85195626	85196226	0.3	0.3
chr16	85380613	85381213	1.5	0.1
chr16	85380654	85381254	1.6	0.1
chr16	85556784	85557384	0.4	0.1
chr16	85680611	85681211	0.7	0.0
chr16	85800948	85801548	0.9	0.3
chr16	86442104	86442704	0.0	0.2
chr16	86950771	86951371	0.5	0.2
chr16	87093052	87093652	0.4	0.1
chr16	87901243	87901843	1.3	0.6
chr16	88098873	88099473	0.7	0.3
chr16	89680043	89680643	0.7	0.5
chr16	89770502	89771102	0.2	0.1
chr16	89861541	89862141	0.4	0.2
chr16	90122175	90122775	1.1	0.6
chr16	90122368	90122968	1.7	0.4
chr16	90599696	90600296	1.7	0.1
chr16	90706565	90707165	1.6	0.1
chr16	90727010	90727610	0.9	0.0
chr16	90950363	90950963	1.7	0.1
chr16	91011456	91012056	1.0	0.2
chr16	91258170	91258770	0.6	0.1
chr16	91752097	91752697	1.3	0.1
chr16	91922429	91923029	0.0	0.4
chr16	91922654	91923254	0.7	0.4
chr16	91997932	91998532	1.9	0.1
chr16	92531028	92531628	1.1	0.0
chr16	92539257	92539857	0.5	0.2
chr16	92578845	92579445	0.4	0.0
chr16	92605286	92605886	1.2	0.4
chr16	92777966	92778566	1.1	0.0
chr16	93140222	93140822	0.1	0.4
chr16	93309352	93309952	1.5	0.8
chr16	93398565	93399165	0.6	0.0
chr16	93576408	93577008	2.3	0.5
chr16	93688287	93688887	1.8	0.6
chr16	93688394	93688994	2.0	0.9
chr16	94429848	94430448	0.7	0.1

chr16	94745086	94745686	1.0	0.2
chr16	94842564	94843164	0.5	0.2
chr16	94974911	94975511	0.1	0.1
chr16	95404758	95405358	0.8	0.2
chr16	95580823	95581423	0.1	0.1
chr16	95988800	95989400	1.0	0.5
chr16	96184340	96184940	0.5	0.3
chr16	96184384	96184984	0.6	0.2
chr16	96422682	96423282	0.8	0.2
chr16	96470365	96470965	0.4	0.2
chr16	96485466	96486066	0.4	0.0
chr16	96548967	96549567	1.3	0.1
chr16	96606839	96607439	0.3	0.1
chr16	96740351	96740951	0.2	0.1
chr16	96766997	96767597	0.0	0.1
chr16	96876546	96877146	1.9	0.5
chr16	97334875	97335475	0.8	0.2
chr16	97367845	97368445	1.3	0.4
chr16	97576582	97577182	1.7	0.2
chr16	97875708	97876308	0.5	0.1
chr16	97919579	97920179	0.3	0.4
chr16	97919728	97920328	0.9	0.1
chr17	3778356	3778956	1.0	0.4
chr17	4442565	4443165	1.5	0.3
chr17	4442584	4443184	1.9	0.4
chr17	4442641	4443241	2.2	0.7
chr17	4442736	4443336	2.8	0.9
chr17	4442793	4443393	2.5	0.7
chr17	4442812	4443412	2.5	0.7
chr17	4442869	4443469	2.3	0.7
chr17	4442907	4443507	2.1	0.5
chr17	4442926	4443526	2.1	0.5
chr17	4442945	4443545	1.7	0.4
chr17	4442964	4443564	1.7	0.3
chr17	4443021	4443621	2.3	0.7
chr17	4443135	4443735	2.0	0.5
chr17	4474143	4474743	0.2	0.3
chr17	4562618	4563218	0.2	0.1

chr17	4617265	4617865	0.6	0.1
chr17	4617307	4617907	0.4	0.1
chr17	4743980	4744580	0.3	0.1
chr17	4861203	4861803	2.2	0.2
chr17	4861225	4861825	2.2	0.2
chr17	4861271	4861871	2.2	0.2
chr17	4861293	4861893	2.1	0.1
chr17	4861317	4861917	1.8	0.0
chr17	5058270	5058870	1.2	0.7
chr17	5431574	5432174	0.3	0.1
chr17	5431661	5432261	0.3	0.2
chr17	5711379	5711979	1.2	0.5
chr17	5967813	5968413	0.6	0.1
chr17	6374166	6374766	0.7	0.5
chr17	6540189	6540789	0.7	0.5
chr17	6914177	6914777	0.5	0.6
chr17	7078321	7078921	1.4	0.5
chr17	7136754	7137354	0.2	0.2
chr17	7136828	7137428	0.2	0.1
chr17	7139026	7139626	0.1	0.1
chr17	7142024	7142624	0.3	0.3
chr17	7142098	7142698	0.5	0.2
chr17	7159303	7159903	0.6	0.1
chr17	7313683	7314283	1.6	0.3
chr17	7313692	7314292	1.7	0.2
chr17	7398489	7399089	0.6	0.1
chr17	7547022	7547622	3.6	1.6
chr17	7547048	7547648	3.6	1.5
chr17	7547074	7547674	3.8	1.6
chr17	7547192	7547792	3.9	1.5
chr17	7924638	7925238	0.3	0.0
chr17	7997580	7998180	0.4	0.3
chr17	7997801	7998401	0.7	0.5
chr17	8208967	8209567	1.7	0.3
chr17	8208976	8209576	1.6	0.3
chr17	9034575	9035175	0.2	0.2
chr17	9523891	9524491	1.2	0.1
chr17	9752015	9752615	0.1	0.0

chr17	10008537	10009137	0.0	0.2
chr17	10129505	10130105	0.4	0.2
chr17	10129590	10130190	0.6	0.2
chr17	10642335	10642935	0.2	0.2
chr17	10646894	10647494	0.9	0.0
chr17	10705733	10706333	1.1	0.1
chr17	10763751	10764351	2.8	0.4
chr17	10763802	10764402	2.7	0.3
chr17	10763836	10764436	2.5	0.2
chr17	10834780	10835380	0.7	0.3
chr17	11259878	11260478	1.2	0.3
chr17	11443703	11444303	0.1	0.0
chr17	12009926	12010526	0.4	0.1
chr17	12384309	12384909	0.5	0.3
chr17	12401021	12401621	0.5	0.1
chr17	12691729	12692329	0.8	0.0
chr17	12691989	12692589	1.1	0.4
chr17	12898156	12898756	1.5	0.4
chr17	12904460	12905060	1.5	0.3
chr17	13061045	13061645	1.3	0.4
chr17	13272138	13272738	3.7	1.6
chr17	13272190	13272790	3.8	1.6
chr17	13272216	13272816	3.6	1.5
chr17	13272334	13272934	4.0	1.5
chr17	13566714	13567314	4.6	2.2
chr17	13566766	13567366	4.3	1.9
chr17	13566818	13567418	4.1	1.7
chr17	13566844	13567444	4.0	1.6
chr17	13566962	13567562	4.5	1.7
chr17	13662177	13662777	0.3	0.5
chr17	13667132	13667732	0.5	0.6
chr17	14100096	14100696	0.9	0.6
chr17	14180646	14181246	1.0	0.6
chr17	14296634	14297234	0.6	0.0
chr17	14405693	14406293	1.8	0.4
chr17	14405714	14406314	1.9	0.4
chr17	14405735	14406335	1.9	0.4
chr17	14405840	14406440	1.9	0.3

chr17	14405898	14406498	2.0	0.3
chr17	15339567	15340167	0.3	0.1
chr17	15418259	15418859	0.3	0.2
chr17	15840845	15841445	1.0	0.5
chr17	15841137	15841737	1.5	0.6
chr17	16004096	16004696	0.2	0.0
chr17	16055180	16055780	0.5	0.1
chr17	16288362	16288962	0.9	0.2
chr17	16355365	16355965	2.1	0.9
chr17	16355383	16355983	2.3	1.0
chr17	16731538	16732138	0.2	0.3
chr17	16874439	16875039	1.6	0.1
chr17	16906863	16907463	0.2	0.1
chr17	17166768	17167368	1.0	0.2
chr17	17169875	17170475	0.6	0.2
chr17	17172712	17173312	0.9	0.1
chr17	17172916	17173516	1.7	0.3
chr17	17173074	17173674	1.1	0.1
chr17	17218109	17218709	1.0	0.0
chr17	17221177	17221777	1.3	0.1
chr17	17275307	17275907	1.0	0.0
chr17	17278392	17278992	1.3	0.1
chr17	17394820	17395420	1.1	0.1
chr17	17451728	17452328	0.9	0.2
chr17	18702853	18703453	0.4	0.1
chr17	19093264	19093864	0.5	0.4
chr17	20242100	20242700	0.4	0.4
chr17	21121502	21122102	0.6	0.0
chr17	21470372	21470972	0.5	0.3
chr17	21608784	21609384	1.1	0.3
chr17	22566779	22567379	0.2	0.3
chr17	23570405	23571005	0.5	0.0
chr17	23736040	23736640	1.0	0.3
chr17	23960390	23960990	1.0	0.0
chr17	24070721	24071321	0.9	0.4
chr17	24273035	24273635	0.2	0.2
chr17	24582055	24582655	1.2	0.1
chr17	24633241	24633841	2.1	0.5
chr17	24633265	24633865	2.1	0.4
chr17	24633485	24634085	2.1	0.5
chr17	24633510	24634110	2.5	0.6
chr17	24898696	24899296	1.9	0.4
chr17	24898895	24899495	0.9	0.4
chr17	25113173	25113773	2.1	0.2
chr17	25568446	25569046	1.0	0.1
chr17	25580403	25581003	0.3	0.1
chr17	25611107	25611707	1.0	0.5
chr17	25705631	25706231	2.2	0.3
chr17	25707933	25708533	0.9	0.5
chr17	25860260	25860860	1.7	0.3
chr17	25921410	25922010	1.6	0.1
chr17	25921417	25922017	1.5	0.0
chr17	26051593	26052193	1.1	0.4
chr17	26278987	26279587	0.4	0.2
chr17	26448445	26449045	0.9	0.5
chr17	26449484	26450084	1.4	0.1
chr17	26500179	26500779	0.8	0.3
chr17	26515497	26516097	0.4	0.2
chr17	27092235	27092835	1.4	0.0
chr17	27109171	27109771	0.4	0.1
chr17	27177785	27178385	0.9	0.1
chr17	27281721	27282321	0.3	0.2
chr17	27326346	27326946	1.3	0.0
chr17	27590876	27591476	0.7	0.1
chr17	27636304	27636904	0.6	0.0
chr17	27779433	27780033	0.4	0.4
chr17	28904040	28904640	0.1	0.2
chr17	29322461	29323061	2.1	0.7
chr17	29534647	29535247	0.7	0.6
chr17	29539748	29540348	0.3	0.6
chr17	29587807	29588407	1.4	0.7
chr17	29626788	29627388	1.7	0.2
chr17	29940742	29941342	0.5	0.1
chr17	30168477	30169077	1.6	0.0
chr17	30846676	30847276	0.5	0.2
chr17	30986454	30987054	0.1	0.1

chr17	31596889	31597489	1.7	0.7
chr17	31615859	31616459	0.6	0.2
chr17	31758984	31759584	2.4	0.8
chr17	31759021	31759621	2.2	0.8
chr17	31759053	31759653	2.2	0.8
chr17	32113485	32114085	0.6	0.1
chr17	32177437	32178037	1.1	0.1
chr17	32284148	32284748	1.5	0.2
chr17	32476581	32477181	0.6	0.1
chr17	32682966	32683566	0.3	0.3
chr17	32840077	32840677	0.8	0.2
chr17	33061283	33061883	1.3	0.3
chr17	33638920	33639520	0.8	0.1
chr17	33894313	33894913	0.9	0.1
chr17	34197724	34198324	0.4	0.1
chr17	34501781	34502381	0.0	0.0
chr17	34753348	34753948	0.9	0.2
chr17	35160876	35161476	1.0	0.1
chr17	35378738	35379338	0.2	0.2
chr17	35841029	35841629	0.7	0.2
chr17	36001274	36001874	0.7	0.2
chr17	36155835	36156435	1.0	0.5
chr17	37183765	37184365	1.3	0.1
chr17	37460558	37461158	1.0	0.0
chr17	37843431	37844031	0.9	0.0
chr17	38161567	38162167	0.4	0.2
chr17	38228676	38229276	1.0	0.1
chr17	41389526	41390126	0.4	0.0
chr17	42096293	42096893	0.9	0.2
chr17	42715051	42715651	1.3	0.6
chr17	42715076	42715676	1.4	0.7
chr17	42715101	42715701	1.4	0.7
chr17	42715126	42715726	1.5	0.7
chr17	42715151	42715751	1.5	0.7
chr17	42715176	42715776	1.5	0.7
chr17	42715201	42715801	1.5	0.7
chr17	42715226	42715826	1.5	0.7
chr17	42715251	42715851	1.4	0.7

chr17	42715276	42715876	1.5	0.7
chr17	42715301	42715901	1.4	0.7
chr17	42715326	42715926	1.5	0.7
chr17	42715351	42715951	1.5	0.7
chr17	42715376	42715976	1.5	0.7
chr17	42715401	42716001	1.5	0.7
chr17	42715426	42716026	1.5	0.7
chr17	42715451	42716051	1.5	0.7
chr17	42715476	42716076	1.5	0.7
chr17	42715501	42716101	1.5	0.7
chr17	42715526	42716126	1.5	0.8
chr17	42715551	42716151	1.6	0.8
chr17	42715576	42716176	1.6	0.8
chr17	42715601	42716201	1.6	0.8
chr17	42715626	42716226	1.6	0.8
chr17	42715651	42716251	1.6	0.8
chr17	42715676	42716276	1.5	0.8
chr17	42715701	42716301	1.5	0.7
chr17	42715726	42716326	1.5	0.8
chr17	42715751	42716351	1.6	0.8
chr17	42715776	42716376	1.6	0.8
chr17	42715801	42716401	1.7	0.9
chr17	42715826	42716426	1.7	0.9
chr17	42715851	42716451	1.7	0.9
chr17	42715876	42716476	1.7	0.9
chr17	42715901	42716501	1.7	0.9
chr17	42715926	42716526	1.7	0.8
chr17	42715951	42716551	1.7	0.9
chr17	42715976	42716576	1.6	0.8
chr17	42716001	42716601	1.6	0.8
chr17	42716026	42716626	1.6	0.8
chr17	42716051	42716651	1.7	0.8
chr17	42716076	42716676	1.7	0.8
chr17	42993696	42994296	1.3	0.1
chr17	43296456	43297056	1.6	0.3
chr17	43350381	43350981	1.3	0.2
chr17	43350389	43350989	1.2	0.1
chr17	43507432	43508032	0.1	0.1

chr17	43671831	43672431	2.0	0.4
chr17	43752941	43753541	1.4	0.2
chr17	43850065	43850665	0.3	0.1
chr17	43953230	43953830	2.0	0.4
chr17	43953267	43953867	2.0	0.3
chr17	43953305	43953905	1.9	0.3
chr17	43953325	43953925	1.9	0.3
chr17	43953462	43954062	1.6	0.3
chr17	44211934	44212534	0.7	0.1
chr17	44394793	44395393	0.9	0.2
chr17	44394856	44395456	1.1	0.3
chr17	44437696	44438296	0.8	0.4
chr17	44603997	44604597	0.6	0.3
chr17	44965666	44966266	0.3	0.1
chr17	44995781	44996381	1.4	0.3
chr17	45209288	45209888	2.0	0.5
chr17	45399987	45400587	0.4	0.3
chr17	45654098	45654698	1.3	0.6
chr17	45657109	45657709	1.1	0.2
chr17	46000250	46000850	0.3	0.3
chr17	46000337	46000937	0.8	0.6
chr17	46003967	46004567	0.9	0.2
chr17	46012284	46012884	1.1	0.0
chr17	46013745	46014345	1.2	0.4
chr17	46093419	46094019	1.3	0.1
chr17	46119009	46119609	0.8	0.4
chr17	46701304	46701904	0.9	0.2
chr17	46813269	46813869	0.3	0.1
chr17	46936578	46937178	0.9	0.5
chr17	46971282	46971882	0.4	0.1
chr17	46980566	46981166	0.1	0.2
chr17	47503963	47504563	0.7	0.1
chr17	47650877	47651477	0.9	0.2
chr17	47823229	47823829	0.3	0.0
chr17	48630855	48631455	0.5	0.3
chr17	48751879	48752479	0.5	0.3
chr17	49134505	49135105	0.6	0.4
chr17	49376199	49376799	0.2	0.3
chr17	49416070	49416670	0.4	0.4
chr17	49513947	49514547	1.3	0.4
chr17	49549371	49549971	1.3	0.8
chr17	49549571	49550171	1.1	0.9
chr17	49549602	49550202	1.1	1.0
chr17	49612603	49613203	2.0	0.2
chr17	49665298	49665898	0.4	0.1
chr17	49983457	49984057	0.7	0.9
chr17	50165648	50166248	1.6	0.1
chr17	50335508	50336108	1.1	0.1
chr17	50340427	50341027	1.2	0.6
chr17	50340705	50341305	0.9	0.5
chr17	50564542	50565142	0.6	0.2
chr17	51402239	51402839	0.4	0.1
chr17	51457515	51458115	0.9	0.6
chr17	51899852	51900452	0.6	0.4
chr17	51917453	51918053	1.8	0.6
chr17	51917674	51918274	0.9	0.7
chr17	52123898	52124498	0.0	0.0
chr17	52941131	52941731	0.9	0.1
chr17	53736570	53737170	0.8	0.0
chr17	53851275	53851875	0.8	0.3
chr17	53895760	53896360	0.5	0.1
chr17	54177192	54177792	1.7	0.2
chr17	54177218	54177818	2.1	0.5
chr17	54769609	54770209	0.1	0.2
chr17	55017984	55018584	0.1	0.0
chr17	56274326	56274926	0.6	0.2
chr17	56274386	56274986	0.4	0.4
chr17	56289323	56289923	1.0	0.4
chr17	56376958	56377558	0.4	0.1
chr17	56521471	56522071	1.9	0.3
chr17	56538110	56538710	1.7	0.6
chr17	56538152	56538752	1.5	0.5
chr17	56730283	56730883	0.3	0.3
chr17	56878494	56879094	0.4	0.1
chr17	56885273	56885873	0.6	0.4
chr17	56885347	56885947	1.0	0.5

chr17	56889809	56890409	0.9	0.0
chr17	56889967	56890567	1.3	0.2
chr17	56994937	56995537	1.2	0.1
chr17	56995149	56995749	1.4	0.2
chr17	57033310	57033910	0.6	0.1
chr17	57033425	57034025	0.3	0.1
chr17	57039929	57040529	0.8	0.3
chr17	57202550	57203150	1.9	0.7
chr17	57202620	57203220	1.9	0.8
chr17	58128515	58129115	1.6	0.2
chr17	58382457	58383057	0.7	0.1
chr17	60561079	60561679	0.3	0.0
chr17	61801212	61801812	0.3	0.0
chr17	62860674	62861274	0.7	0.2
chr17	62898695	62899295	1.1	0.3
chr17	62898780	62899380	1.1	0.1
chr17	63108362	63108962	0.1	0.4
chr17	64034320	64034920	0.3	0.3
chr17	64177786	64178386	0.2	0.2
chr17	64673754	64674354	0.2	0.1
chr17	64987728	64988328	1.0	0.4
chr17	65492776	65493376	0.2	0.3
chr17	66324124	66324724	0.7	0.1
chr17	66489873	66490473	0.5	0.3
chr17	66951071	66951671	1.4	0.2
chr17	67717338	67717938	0.1	0.1
chr17	68046960	68047560	0.3	0.7
chr17	68243823	68244423	0.9	0.1
chr17	68244041	68244641	0.4	0.0
chr17	68346117	68346717	0.3	0.4
chr17	68389267	68389867	1.2	0.2
chr17	68779824	68780424	0.1	0.2
chr17	68861011	68861611	1.1	0.0
chr17	69260417	69261017	0.2	0.1
chr17	69369443	69370043	1.1	0.2
chr17	69369468	69370068	1.0	0.2
chr17	69369485	69370085	1.0	0.2
chr17	69369538	69370138	1.0	0.2

chr17	69850714	69851314	0.2	0.2
chr17	70817977	70818577	1.1	0.2
chr17	71481835	71482435	2.5	0.6
chr17	71604989	71605589	1.4	0.0
chr17	71939964	71940564	0.6	0.1
chr17	72319236	72319836	0.3	0.1
chr17	72820710	72821310	0.8	0.2
chr17	73207973	73208573	1.0	0.4
chr17	73372808	73373408	0.6	0.0
chr17	73885071	73885671	1.6	0.5
chr17	73885302	73885902	1.3	0.2
chr17	74321516	74322116	0.6	0.3
chr17	74321875	74322475	0.1	0.1
chr17	74351711	74352311	0.9	0.0
chr17	74357814	74358414	2.1	0.1
chr17	74389983	74390583	0.5	0.0
chr17	74577703	74578303	1.9	0.4
chr17	74577714	74578314	1.9	0.3
chr17	74611509	74612109	0.2	0.1
chr17	75784374	75784974	0.2	0.1
chr17	75784636	75785236	0.5	0.4
chr17	75839875	75840475	0.6	0.1
chr17	75982191	75982791	0.4	0.2
chr17	75982211	75982811	0.5	0.1
chr17	76282476	76283076	1.3	0.9
chr17	77826137	77826737	0.0	0.1
chr17	78803365	78803965	0.2	0.1
chr17	78803394	78803994	0.2	0.2
chr17	78884332	78884932	0.9	0.1
chr17	78962073	78962673	0.7	0.2
chr17	79011483	79012083	0.7	0.2
chr17	79230889	79231489	0.9	0.0
chr17	79975967	79976567	1.8	0.2
chr17	79976174	79976774	1.5	0.2
chr17	80743059	80743659	1.3	0.1
chr17	80754167	80754767	1.2	0.0
chr17	80782141	80782741	1.1	0.8
chr17	81109402	81110002	0.9	0.2

chr17	81763281	81763881	0.9	0.6
chr17	81792297	81792897	1.5	0.0
chr17	82784622	82785222	0.3	0.0
chr17	83374212	83374812	0.7	0.3
chr17	83626341	83626941	0.3	0.3
chr17	83626451	83627051	0.9	0.5
chr17	84770824	84771424	0.6	0.1
chr17	85160869	85161469	1.3	0.3
chr17	85962562	85963162	1.0	0.4
chr17	85979113	85979713	0.5	0.2
chr17	85982749	85983349	0.4	0.0
chr17	86302984	86303584	4.1	1.3
chr17	86303050	86303650	4.0	1.3
chr17	86303072	86303672	3.9	1.3
chr17	86303094	86303694	3.9	1.3
chr17	86303116	86303716	3.7	1.3
chr17	86303138	86303738	3.7	1.4
chr17	86303160	86303760	3.8	1.3
chr17	86303182	86303782	3.6	1.3
chr17	86801069	86801669	0.2	0.3
chr17	87011828	87012428	2.2	0.2
chr17	87012090	87012690	1.9	0.3
chr17	87041882	87042482	1.0	0.3
chr17	87157470	87158070	0.6	0.0
chr17	87201328	87201928	1.7	0.6
chr17	87212013	87212613	0.0	0.1
chr17	88133429	88134029	1.6	0.0
chr17	88133444	88134044	1.9	0.2
chr17	88141323	88141923	0.8	0.1
chr17	88240650	88241250	2.7	0.5
chr17	88620820	88621420	0.3	0.0
chr17	89208403	89209003	1.8	0.0
chr17	90800734	90801334	1.7	0.0
chr17	93357502	93358102	1.4	0.3
chr17	93357569	93358169	1.4	0.3
chr17	93489381	93489981	1.3	0.1
chr17	93912914	93913514	0.8	0.1
chr17	94307634	94308234	0.0	0.1

chr17	95070917	95071517	1.1	0.1
chr17	95075975	95076575	0.8	0.7
chr17	95076016	95076616	0.8	0.7
chr18	3609246	3609846	1.2	0.0
chr18	5641317	5641917	1.0	0.2
chr18	6282155	6282755	0.2	0.2
chr18	6328221	6328821	1.4	0.1
chr18	6562806	6563406	1.0	0.5
chr18	6636335	6636935	1.2	0.0
chr18	7079103	7079703	1.8	0.1
chr18	7556032	7556632	2.0	0.9
chr18	7556083	7556683	2.3	1.0
chr18	7556134	7556734	2.5	1.1
chr18	7556185	7556785	2.8	1.3
chr18	7556236	7556836	2.9	1.4
chr18	7556287	7556887	2.9	1.4
chr18	7556338	7556938	2.5	1.2
chr18	7556389	7556989	2.4	1.2
chr18	7556440	7557040	2.2	1.2
chr18	8161837	8162437	2.0	1.0
chr18	8162060	8162660	2.7	0.5
chr18	9454450	9455050	0.4	0.0
chr18	10316749	10317349	0.6	0.3
chr18	10316771	10317371	0.8	0.2
chr18	11415513	11416113	0.3	0.1
chr18	11898104	11898704	0.5	0.0
chr18	12180593	12181193	2.4	0.2
chr18	12398623	12399223	0.6	0.1
chr18	12644281	12644881	0.7	0.1
chr18	12653827	12654427	0.7	0.1
chr18	13040678	13041278	1.1	0.2
chr18	13523205	13523805	0.2	0.1
chr18	14154917	14155517	0.3	0.0
chr18	14291263	14291863	2.1	0.6
chr18	14291327	14291927	2.1	0.6
chr18	14291359	14291959	2.0	0.5
chr18	14291455	14292055	1.7	0.6
chr18	14291487	14292087	1.9	0.6

chr18	14291519	14292119	2.0	0.7
chr18	14374360	14374960	0.6	0.0
chr18	14506404	14507004	1.4	0.2
chr18	15008814	15009414	0.6	0.3
chr18	15320933	15321533	1.2	0.2
chr18	15321015	15321615	1.3	0.2
chr18	15682803	15683403	1.0	0.0
chr18	16914606	16915206	0.3	0.2
chr18	17093435	17094035	0.7	0.1
chr18	17093653	17094253	1.2	0.6
chr18	17312852	17313452	0.4	0.4
chr18	17425277	17425877	0.4	0.3
chr18	17611203	17611803	0.1	0.0
chr18	17683908	17684508	1.2	0.1
chr18	18763056	18763656	0.5	0.0
chr18	18906440	18907040	0.1	0.1
chr18	18906531	18907131	0.1	0.1
chr18	19184740	19185340	0.6	0.1
chr18	19872225	19872825	0.9	0.1
chr18	20369360	20369960	0.8	0.3
chr18	20485095	20485695	0.1	0.3
chr18	20866096	20866696	0.7	0.0
chr18	21414500	21415100	0.6	0.3
chr18	22017524	22018124	0.1	0.3
chr18	22171214	22171814	0.2	0.2
chr18	23202768	23203368	0.2	0.1
chr18	23651553	23652153	1.0	0.3
chr18	23651830	23652430	1.3	0.6
chr18	24015837	24016437	0.4	0.1
chr18	24049971	24050571	0.3	0.1
chr18	24050188	24050788	0.4	0.1
chr18	24210803	24211403	0.3	0.2
chr18	24427103	24427703	0.1	0.0
chr18	24476737	24477337	1.7	0.1
chr18	24909069	24909669	0.9	0.4
chr18	25720145	25720745	0.4	0.4
chr18	25720366	25720966	0.6	0.1
chr18	25994962	25995562	0.4	0.1

chr18	26347004	26347604	0.9	0.4
chr18	26513172	26513772	0.6	0.5
chr18	27007734	27008334	0.1	0.2
chr18	27155896	27156496	0.6	0.3
chr18	27156056	27156656	1.1	0.4
chr18	27164719	27165319	0.4	0.1
chr18	27811922	27812522	0.9	0.3
chr18	27947486	27948086	0.8	0.2
chr18	28367155	28367755	0.0	0.0
chr18	28371835	28372435	0.3	0.0
chr18	28530029	28530629	1.6	0.1
chr18	28960749	28961349	0.4	0.2
chr18	29213688	29214288	0.9	0.1
chr18	29507231	29507831	0.2	0.1
chr18	29637794	29638394	1.4	0.5
chr18	30638988	30639588	1.6	0.3
chr18	30781765	30782365	1.6	0.2
chr18	30781919	30782519	1.1	0.3
chr18	30825642	30826242	0.1	0.1
chr18	30925750	30926350	1.1	0.3
chr18	31357887	31358487	4.2	1.2
chr18	31358000	31358600	3.3	1.0
chr18	31358072	31358672	2.7	0.5
chr18	31358153	31358753	2.8	0.5
chr18	32048149	32048749	1.2	0.2
chr18	32089236	32089836	0.6	0.1
chr18	32089406	32090006	1.2	0.6
chr18	32525884	32526484	0.5	0.3
chr18	33055462	33056062	0.2	0.0
chr18	33893074	33893674	0.6	0.1
chr18	33957798	33958398	0.2	0.1
chr18	34340630	34341230	1.7	0.3
chr18	34768204	34768804	0.5	0.3
chr18	34768478	34769078	0.2	0.3
chr18	34927626	34928226	1.6	0.1
chr18	35137409	35138009	0.7	0.1
chr18	35642099	35642699	1.2	0.4
chr18	35821465	35822065	0.7	0.0

chr18	35990987	35991587	1.4	0.6
chr18	36033458	36034058	0.4	0.0
chr18	36033574	36034174	1.2	0.1
chr18	36055522	36056122	0.2	0.3
chr18	36132777	36133377	1.9	0.4
chr18	36132788	36133388	1.9	0.4
chr18	36434096	36434696	1.9	0.2
chr18	36434115	36434715	1.8	0.2
chr18	36434160	36434760	1.9	0.1
chr18	36434250	36434850	2.1	0.1
chr18	36434295	36434895	2.1	0.1
chr18	36447629	36448229	0.5	0.1
chr18	36547999	36548599	1.3	0.2
chr18	37507927	37508527	1.7	0.0
chr18	38003446	38004046	1.7	0.9
chr18	38003590	38004190	1.8	0.6
chr18	38302388	38302988	0.9	0.2
chr18	38485769	38486369	0.4	0.0
chr18	39098955	39099555	0.1	0.3
chr18	39148471	39149071	0.2	0.1
chr18	40789230	40789830	1.2	0.5
chr18	40948563	40949163	0.2	0.2
chr18	41470725	41471325	0.0	0.2
chr18	41641372	41641972	1.0	0.0
chr18	42208083	42208683	1.7	0.6
chr18	42362849	42363449	1.5	0.5
chr18	43478598	43479198	0.7	0.4
chr18	43532378	43532978	1.1	0.5
chr18	43660743	43661343	1.3	0.2
chr18	44290183	44290783	0.2	0.4
chr18	44525348	44525948	0.6	0.1
chr18	44535932	44536532	0.4	0.3
chr18	44601528	44602128	0.2	0.1
chr18	45915803	45916403	1.0	0.1
chr18	45952313	45952913	0.6	0.1
chr18	47027153	47027753	0.1	0.2
chr18	47718473	47719073	0.2	0.1
chr18	48023046	48023646	0.9	0.6
chr18	48023075	48023675	1.0	0.6
chr18	48118802	48119402	0.9	0.4
chr18	48282779	48283379	1.3	0.2
chr18	48353016	48353616	0.6	0.1
chr18	49930388	49930988	0.7	0.5
chr18	49939236	49939836	1.0	0.1
chr18	50349316	50349916	1.3	0.5
chr18	50388623	50389223	1.0	0.3
chr18	50630452	50631052	1.3	0.1
chr18	51703611	51704211	0.3	0.4
chr18	52289434	52290034	0.2	0.3
chr18	52569375	52569975	1.0	0.2
chr18	52970496	52971096	0.3	0.0
chr18	53176317	53176917	0.6	0.0
chr18	53468991	53469591	0.5	0.9
chr18	53822538	53823138	0.4	0.1
chr18	54933806	54934406	0.5	0.1
chr18	55108947	55109547	0.7	0.2
chr18	55833803	55834403	1.3	0.4
chr18	55900216	55900816	0.7	0.0
chr18	56413178	56413778	0.3	0.6
chr18	56544253	56544853	1.5	0.2
chr18	56544329	56544929	1.6	0.2
chr18	56544395	56544995	1.5	0.3
chr18	56548898	56549498	1.7	0.8
chr18	56549152	56549752	2.7	1.2
chr18	57838350	57838950	0.9	0.3
chr18	58172484	58173084	0.5	0.2
chr18	58172492	58173092	0.5	0.2
chr18	58383283	58383883	0.8	0.1
chr18	58624639	58625239	0.1	0.5
chr18	58816656	58817256	0.6	0.4
chr18	58885967	58886567	0.6	0.4
chr18	58898039	58898639	0.4	0.4
chr18	59120699	59121299	1.3	0.5
chr18	59419439	59420039	1.3	0.2
chr18	59765320	59765920	0.9	0.1
chr18	60117725	60118325	1.2	0.0

chr18	60457886	60458486	0.8	0.5
chr18	60458171	60458771	1.5	1.0
chr18	60731188	60731788	1.6	0.5
chr18	60731212	60731812	1.3	0.5
chr18	60864615	60865215	0.4	0.2
chr18	61483170	61483770	0.3	0.5
chr18	61491460	61492060	1.2	0.4
chr18	61491486	61492086	1.3	0.4
chr18	61710599	61711199	0.4	0.2
chr18	61817378	61817978	0.7	0.4
chr18	61820420	61821020	1.5	0.0
chr18	61831340	61831940	2.2	0.1
chr18	61954314	61954914	1.5	0.3
chr18	61954366	61954966	1.5	0.4
chr18	61954442	61955042	1.3	0.2
chr18	62110592	62111192	1.2	0.1
chr18	62160891	62161491	0.8	0.4
chr18	63560248	63560848	0.5	0.2
chr18	64558732	64559332	0.7	0.3
chr18	64829559	64830159	0.5	0.2
chr18	64844496	64845096	0.7	0.1
chr18	65045719	65046319	0.1	0.5
chr18	65157103	65157703	1.3	0.4
chr18	65187227	65187827	0.3	0.2
chr18	65523417	65524017	1.5	0.7
chr18	65523663	65524263	2.0	0.3
chr18	65683738	65684338	1.6	0.1
chr18	65963651	65964251	1.0	0.0
chr18	65963661	65964261	1.1	0.0
chr18	66188085	66188685	0.1	0.1
chr18	66339422	66340022	0.5	0.0
chr18	66643559	66644159	0.6	0.2
chr18	66643640	66644240	0.5	0.3
chr18	66712249	66712849	2.3	0.6
chr18	66712515	66713115	0.8	0.3
chr18	66796979	66797579	0.6	0.3
chr18	67221523	67222123	0.6	0.0
chr18	67457737	67458337	1.5	0.3
chr18	67803259	67803859	0.1	0.2
chr18	67959829	67960429	0.9	0.3
chr18	68090308	68090908	0.8	0.0
chr18	68786633	68787233	1.6	0.2
chr18	69992507	69993107	0.5	0.1
chr18	70131498	70132098	1.6	1.1
chr18	70581644	70582244	1.0	0.3
chr18	70581742	70582342	1.0	0.4
chr18	70581751	70582351	0.9	0.3
chr18	70581867	70582467	0.8	0.3
chr18	71805414	71806014	0.4	0.5
chr18	71805497	71806097	0.3	0.5
chr18	71955927	71956527	0.2	0.1
chr18	72080140	72080740	0.3	0.1
chr18	72493113	72493713	0.4	0.2
chr18	73031614	73032214	0.2	0.0
chr18	73733355	73733955	0.9	0.1
chr18	74026830	74027430	1.4	0.5
chr18	74445661	74446261	0.4	0.1
chr18	74899556	74900156	0.9	0.2
chr18	75286317	75286917	0.3	0.0
chr18	75535128	75535728	0.9	0.3
chr18	75707212	75707812	1.5	0.7
chr18	75707258	75707858	1.6	0.7
chr18	75736134	75736734	0.6	0.3
chr18	76000038	76000638	1.5	0.7
chr18	76059129	76059729	0.9	0.1
chr18	76061130	76061730	1.2	0.0
chr18	76305371	76305971	0.8	0.5
chr18	76502304	76502904	0.8	0.5
chr18	76580064	76580664	0.6	0.1
chr18	77250828	77251428	1.7	0.5
chr18	77738393	77738993	0.9	0.0
chr18	77971286	77971886	1.5	0.0
chr18	77971561	77972161	2.1	0.4
chr18	78211620	78212220	1.1	0.2
chr18	78258337	78258937	0.7	0.1
chr18	78361963	78362563	0.9	0.8

chr18	78362055	78362655	0.8	0.7
chr18	78637513	78638113	1.0	0.0
chr18	78637606	78638206	1.1	0.2
chr18	79180432	79181032	1.2	0.3
chr18	79198255	79198855	1.0	0.4
chr18	79828490	79829090	0.7	0.3
chr18	80157546	80158146	1.5	0.1
chr18	80476385	80476985	0.8	0.4
chr18	80499673	80500273	0.3	0.3
chr18	80750488	80751088	0.7	0.4
chr18	80802300	80802900	0.9	0.3
chr18	81383013	81383613	0.5	0.1
chr18	82428374	82428974	1.2	0.2
chr18	82560183	82560783	0.8	0.6
chr18	82577978	82578578	2.5	0.3
chr18	82577994	82578594	2.4	0.3
chr18	82757388	82757988	0.9	0.3
chr18	83067554	83068154	0.3	0.1
chr18	83630785	83631385	0.4	0.2
chr18	83912329	83912929	0.2	0.5
chr18	83912618	83913218	0.7	0.2
chr18	83964770	83965370	0.1	0.0
chr18	84036044	84036644	2.0	0.2
chr18	84084252	84084852	1.2	0.1
chr18	84933981	84934581	1.3	0.1
chr18	84938270	84938870	0.6	0.2
chr18	84947937	84948537	0.8	0.1
chr18	86526664	86527264	0.4	0.0
chr18	86659425	86660025	1.2	0.2
chr18	88750649	88751249	0.2	0.1
chr18	89923931	89924531	1.0	0.5
chr18	90478448	90479048	0.9	0.2
chr18	90478461	90479061	0.9	0.3
chr19	3071623	3072223	1.5	0.2
chr19	3551623	3552223	0.2	0.8
chr19	3840286	3840886	0.3	0.5
chr19	3912405	3913005	1.2	0.3
chr19	4297469	4298069	2.8	0.7

chr19	4297591	4298191	2.8	0.8
chr19	4397426	4398026	0.6	0.0
chr19	4456543	4457143	1.2	0.5
chr19	4688160	4688760	0.6	0.1
chr19	5056640	5057240	1.4	0.1
chr19	5134385	5134985	0.3	0.3
chr19	5659295	5659895	0.3	0.0
chr19	5659492	5660092	1.4	0.1
chr19	5745767	5746367	0.7	0.2
chr19	5766258	5766858	0.5	0.1
chr19	5943110	5943710	3.1	0.5
chr19	5943120	5943720	3.1	0.5
chr19	5943128	5943728	3.1	0.5
chr19	6261020	6261620	0.8	0.3
chr19	8374973	8375573	0.1	0.1
chr19	8521652	8522252	0.2	0.5
chr19	8640359	8640959	0.9	0.2
chr19	8815455	8816055	0.9	0.2
chr19	8832951	8833551	1.3	0.4
chr19	8833055	8833655	1.3	0.3
chr19	8877091	8877691	0.7	0.0
chr19	9008229	9008829	0.8	0.1
chr19	9149900	9150500	0.4	0.0
chr19	9339438	9340038	0.2	0.4
chr19	9746311	9746911	0.2	0.2
chr19	9923156	9923756	0.5	0.2
chr19	10026881	10027481	1.1	0.1
chr19	10073575	10074175	1.3	0.2
chr19	10412788	10413388	0.4	0.1
chr19	10456097	10456697	0.5	0.3
chr19	10606893	10607493	0.7	0.0
chr19	10864058	10864658	0.3	0.3
chr19	11069521	11070121	0.7	0.3
chr19	11071977	11072577	0.5	0.0
chr19	11328338	11328938	1.1	0.3
chr19	11400623	11401223	0.2	0.3
chr19	11923431	11924031	0.3	0.2
chr19	11951414	11952014	0.5	0.0

chr19	12243874	12244474	0.9	0.0
chr19	12306333	12306933	1.0	0.1
chr19	12888784	12889384	2.0	0.8
chr19	12889038	12889638	1.8	0.6
chr19	12985733	12986333	1.0	0.3
chr19	13225962	13226562	0.9	0.0
chr19	14183370	14183970	0.0	0.1
chr19	15522868	15523468	1.5	0.0
chr19	16128604	16129204	0.2	0.1
chr19	16132433	16133033	1.3	0.5
chr19	16347796	16348396	2.4	0.7
chr19	16347824	16348424	2.6	0.8
chr19	16347852	16348452	2.8	0.7
chr19	16347880	16348480	3.1	0.8
chr19	17849506	17850106	0.2	0.4
chr19	18472251	18472851	2.4	0.4
chr19	18472519	18473119	2.1	0.5
chr19	19015579	19016179	2.0	0.6
chr19	19015603	19016203	2.0	0.6
chr19	19083757	19084357	0.7	0.2
chr19	20072690	20073290	0.9	0.2
chr19	20451316	20451916	0.0	0.1
chr19	21704281	21704881	1.6	0.1
chr19	21899782	21900382	0.7	0.1
chr19	21914401	21915001	1.0	0.1
chr19	22035093	22035693	0.5	0.2
chr19	22349003	22349603	0.8	0.2
chr19	22423081	22423681	0.4	0.3
chr19	22543785	22544385	0.2	0.4
chr19	22746140	22746740	1.5	0.4
chr19	22937295	22937895	1.0	0.2
chr19	22994179	22994779	0.2	0.4
chr19	23097932	23098532	0.1	0.0
chr19	23690325	23690925	1.5	0.1
chr19	23690403	23691003	1.9	0.3
chr19	24370546	24371146	0.5	0.1
chr19	24463654	24464254	0.6	0.9
chr19	24463759	24464359	0.9	0.7
chr19	25019385	25019985	1.0	0.3
chr19	25368942	25369542	0.3	0.1
chr19	25579617	25580217	0.6	0.0
chr19	25774440	25775040	1.0	0.7
chr19	26542357	26542957	1.1	0.3
chr19	27004908	27005508	0.7	0.3
chr19	27005002	27005602	0.8	0.2
chr19	27013390	27013990	0.9	0.1
chr19	27376027	27376627	1.0	0.1
chr19	27541984	27542584	0.9	0.2
chr19	27586568	27587168	0.9	0.7
chr19	28144211	28144811	0.4	0.3
chr19	28982571	28983171	2.4	0.3
chr19	28982636	28983236	2.1	0.3
chr19	29657870	29658470	1.0	0.2
chr19	30369263	30369863	0.6	0.9
chr19	32184783	32185383	1.0	0.6
chr19	32297980	32298580	0.1	0.5
chr19	32391816	32392416	0.8	0.3
chr19	32417230	32417830	0.7	0.0
chr19	32542720	32543320	0.4	0.2
chr19	33230658	33231258	0.5	0.4
chr19	34079233	34079833	0.6	0.2
chr19	34079417	34080017	0.4	0.1
chr19	34329676	34330276	0.9	0.3
chr19	34512739	34513339	1.3	0.4
chr19	34512887	34513487	1.1	0.3
chr19	34852569	34853169	0.0	0.1
chr19	36258985	36259585	2.8	1.3
chr19	36259011	36259611	3.0	1.3
chr19	36259064	36259664	3.0	1.2
chr19	36344219	36344819	1.4	0.4
chr19	36344318	36344918	1.0	0.3
chr19	36350988	36351588	0.2	0.4
chr19	36608778	36609378	0.9	0.2
chr19	36781656	36782256	0.9	0.2
chr19	37462083	37462683	0.0	0.0
chr19	38102297	38102897	0.6	0.2

chr19	38158940	38159540	0.3	0.0
chr19	38199311	38199911	1.2	0.2
chr19	38423358	38423958	1.1	0.3
chr19	38493593	38494193	1.2	0.2
chr19	38545948	38546548	1.0	0.2
chr19	38546121	38546721	1.2	0.5
chr19	39582690	39583290	1.0	0.3
chr19	40197119	40197719	0.7	0.1
chr19	40623222	40623822	1.4	0.1
chr19	41181581	41182181	0.5	0.2
chr19	42225694	42226294	0.2	0.0
chr19	42264476	42265076	1.6	0.6
chr19	42315302	42315902	0.9	0.1
chr19	42909158	42909758	0.7	0.2
chr19	43123804	43124404	0.7	0.3
chr19	43173536	43174136	1.1	0.8
chr19	43173627	43174227	1.1	0.5
chr19	43593061	43593661	1.1	0.1
chr19	43637574	43638174	0.1	0.3
chr19	44547213	44547813	0.9	0.3
chr19	44624028	44624628	0.3	0.1
chr19	44793981	44794581	1.3	0.9
chr19	44875677	44876277	0.9	0.4
chr19	44890671	44891271	0.8	0.1
chr19	44959623	44960223	0.4	0.1
chr19	45385539	45386139	0.2	0.1
chr19	45528808	45529408	1.6	0.4
chr19	46407303	46407903	1.1	0.4
chr19	47402458	47403058	1.3	0.3
chr19	47402471	47403071	1.3	0.3
chr19	47418788	47419388	0.3	0.1
chr19	47486524	47487124	1.3	0.6
chr19	47486586	47487186	1.4	0.5
chr19	47602197	47602797	0.5	0.1
chr19	47787474	47788074	0.8	0.1
chr19	47979730	47980330	0.0	0.4
chr19	48075910	48076510	1.2	0.1
chr19	48213963	48214563	2.1	0.2

chr19	48821723	48822323	0.7	0.1
chr19	48955859	48956459	0.0	0.1
chr19	49212272	49212872	0.5	0.5
chr19	49441293	49441893	1.4	0.1
chr19	49755803	49756403	0.8	0.2
chr19	49858039	49858639	2.0	0.3
chr19	49957735	49958335	0.9	0.2
chr19	50219204	50219804	1.4	0.3
chr19	51434063	51434663	0.7	0.1
chr19	51701780	51702380	0.8	0.3
chr19	53497705	53498305	1.7	0.6
chr19	53567361	53567961	0.7	0.0
chr19	53576319	53576919	0.2	0.7
chr19	53611484	53612084	1.3	0.1
chr19	54765745	54766345	1.2	0.0
chr19	55490452	55491052	0.4	0.2
chr19	55524167	55524767	1.8	0.4
chr19	55590759	55591359	1.4	0.4
chr19	55778633	55779233	0.3	0.0
chr19	56257158	56257758	0.4	0.3
chr19	56438980	56439580	0.8	0.3
chr19	56830732	56831332	1.2	0.6
chr19	56954683	56955283	0.6	0.3
chr19	56965499	56966099	1.6	0.0
chr19	57060405	57061005	0.7	0.8
chr19	57205719	57206319	0.2	0.3
chr19	57475020	57475620	0.7	0.1
chr19	57475142	57475742	0.5	0.3
chr19	57581238	57581838	0.1	0.3
chr19	57859732	57860332	0.0	0.1
chr19	58277368	58277968	1.8	0.1
chr19	58482516	58483116	0.6	0.3
chr19	58946274	58946874	0.9	0.4
chr19	59341758	59342358	1.5	0.4
chr19	61305607	61306207	0.2	0.2
chr2	3290023	3290623	1.5	0.5
chr2	3290051	3290651	1.5	0.5
chr2	3902999	3903599	0.1	0.3

chr2	4015467	4016067	0.4	0.1
chr2	4076394	4076994	0.5	0.3
chr2	4503486	4504086	0.4	0.1
chr2	4640476	4641076	1.5	0.7
chr2	4640526	4641126	1.1	0.7
chr2	4838035	4838635	0.0	0.1
chr2	4838068	4838668	0.0	0.0
chr2	4909488	4910088	0.3	0.2
chr2	5445175	5445775	0.8	0.4
chr2	6803262	6803862	1.5	0.0
chr2	7279856	7280456	0.5	0.2
chr2	8431236	8431836	1.6	0.6
chr2	8431378	8431978	2.1	0.7
chr2	8944769	8945369	1.7	0.0
chr2	10094725	10095325	0.8	0.1
chr2	10105791	10106391	0.9	0.2
chr2	10295760	10296360	0.8	0.2
chr2	10528307	10528907	0.6	0.5
chr2	11205232	11205832	0.4	0.1
chr2	12203748	12204348	1.6	0.1
chr2	13056224	13056824	0.7	0.0
chr2	13600704	13601304	1.1	0.1
chr2	13609784	13610384	0.8	0.1
chr2	13909073	13909673	1.0	0.1
chr2	14387018	14387618	0.8	0.2
chr2	14803380	14803980	0.2	0.0
chr2	14986137	14986737	0.9	0.2
chr2	15268690	15269290	1.6	1.0
chr2	15291662	15292262	0.3	0.3
chr2	15548832	15549432	0.5	0.2
chr2	16291109	16291709	0.4	0.0
chr2	18752206	18752806	2.0	0.2
chr2	18817785	18818385	0.0	0.4
chr2	18946159	18946759	0.7	0.5
chr2	19017452	19018052	1.5	0.1
chr2	20021294	20021894	0.5	0.0
chr2	20156313	20156913	0.5	0.1
chr2	20994376	20994976	1.3	0.1

chr2	21113331	21113931	1.4	0.3
chr2	21113544	21114144	1.5	0.3
chr2	21329330	21329930	1.2	0.2
chr2	21471982	21472582	1.5	0.9
chr2	21472228	21472828	1.9	0.8
chr2	23149418	23150018	0.7	0.1
chr2	24125664	24126264	0.1	0.2
chr2	24150733	24151333	1.4	0.1
chr2	24487501	24488101	1.2	0.2
chr2	24561439	24562039	0.2	0.0
chr2	24561622	24562222	0.8	0.5
chr2	24960496	24961096	0.9	0.2
chr2	24960587	24961187	0.9	0.1
chr2	25008881	25009481	1.1	0.3
chr2	25438881	25439481	1.1	0.6
chr2	25438923	25439523	0.6	0.4
chr2	25693856	25694456	4.0	2.0
chr2	25693889	25694489	4.1	2.0
chr2	25693922	25694522	4.1	2.0
chr2	25693955	25694555	4.0	2.0
chr2	25693988	25694588	3.6	2.0
chr2	25694021	25694621	3.8	2.0
chr2	25694054	25694654	3.7	2.0
chr2	25941474	25942074	1.1	0.0
chr2	25960210	25960810	0.1	0.5
chr2	26031426	26032026	2.4	0.1
chr2	26031467	26032067	2.3	0.1
chr2	26187836	26188436	0.7	0.3
chr2	26197302	26197902	0.5	0.0
chr2	26271374	26271974	0.2	0.1
chr2	26582014	26582614	0.9	0.1
chr2	26582116	26582716	1.0	0.2
chr2	26916272	26916872	1.5	0.2
chr2	26991730	26992330	0.9	0.2
chr2	27266260	27266860	1.4	0.9
chr2	27266272	27266872	1.5	0.8
chr2	27266340	27266940	1.4	0.6
chr2	27550603	27551203	1.1	0.3

chr2	27919783	27920383	0.7	0.0
chr2	27947043	27947643	1.1	0.1
chr2	27954327	27954927	0.4	0.0
chr2	28042351	28042951	0.5	0.2
chr2	29459481	29460081	1.5	0.4
chr2	29889010	29889610	0.3	0.3
chr2	30423799	30424399	0.2	0.1
chr2	30562956	30563556	0.6	0.7
chr2	30656711	30657311	0.1	0.1
chr2	31032161	31032761	1.0	0.1
chr2	31032256	31032856	1.2	0.3
chr2	31063866	31064466	0.0	0.0
chr2	31699827	31700427	0.9	0.5
chr2	32183219	32183819	1.4	0.5
chr2	32850463	32851063	0.2	0.1
chr2	33033780	33034380	2.0	1.1
chr2	33033918	33034518	2.0	0.8
chr2	33126537	33127137	0.7	0.1
chr2	33437945	33438545	0.3	0.5
chr2	33808231	33808831	0.5	0.1
chr2	33867008	33867608	1.0	0.2
chr2	34458445	34459045	0.3	0.5
chr2	34726335	34726935	0.2	0.3
chr2	34783202	34783802	1.3	0.5
chr2	34903707	34904307	0.1	0.1
chr2	35036144	35036744	1.2	0.0
chr2	35364121	35364721	0.6	0.3
chr2	35469137	35469737	1.0	0.2
chr2	35948115	35948715	1.1	0.1
chr2	36753676	36754276	2.0	0.1
chr2	37610973	37611573	2.1	0.2
chr2	37610999	37611599	2.3	0.2
chr2	38145586	38146186	1.2	0.4
chr2	38834955	38835555	1.3	0.2
chr2	38902528	38903128	1.2	0.3
chr2	38902757	38903357	1.2	0.1
chr2	40189115	40189715	0.4	0.0
chr2	40309284	40309884	0.5	0.0

chr2	40851691	40852291	0.1	0.2
chr2	41393065	41393665	1.1	0.3
chr2	41429089	41429689	0.7	0.4
chr2	42101568	42102168	0.2	0.1
chr2	42365703	42366303	1.2	0.1
chr2	43462062	43462662	0.1	0.3
chr2	43580559	43581159	1.2	0.1
chr2	44196868	44197468	1.0	0.1
chr2	44317309	44317909	0.2	0.0
chr2	44419276	44419876	1.2	0.1
chr2	45051143	45051743	1.1	0.4
chr2	45051153	45051753	1.1	0.4
chr2	45085940	45086540	0.0	0.1
chr2	46099889	46100489	0.4	0.2
chr2	46885828	46886428	0.4	0.1
chr2	47865946	47866546	0.7	0.4
chr2	48312882	48313482	1.3	0.6
chr2	48313125	48313725	2.0	0.7
chr2	48679836	48680436	0.4	0.2
chr2	49876239	49876839	1.0	0.2
chr2	49922207	49922807	1.2	0.1
chr2	50003317	50003917	0.1	0.2
chr2	50084392	50084992	0.8	0.2
chr2	50642047	50642647	0.0	0.3
chr2	50642065	50642665	0.1	0.3
chr2	50726328	50726928	0.5	0.2
chr2	52040782	52041382	1.1	0.5
chr2	52081184	52081784	0.7	0.1
chr2	53550942	53551542	0.3	0.1
chr2	54045076	54045676	0.0	0.0
chr2	55037782	55038382	1.9	0.0
chr2	55570738	55571338	0.2	0.1
chr2	56431435	56432035	0.9	0.3
chr2	56761030	56761630	1.3	0.1
chr2	56761133	56761733	1.1	0.0
chr2	57815262	57815862	0.5	0.1
chr2	57815363	57815963	0.3	0.1
chr2	58636875	58637475	1.2	0.4

chr2	60114713	60115313	0.4	0.2
chr2	60180427	60181027	0.3	0.1
chr2	60235288	60235888	1.4	0.1
chr2	60335597	60336197	0.7	0.2
chr2	60335624	60336224	0.7	0.3
chr2	60422431	60423031	2.4	0.5
chr2	61014904	61015504	1.8	0.6
chr2	61196844	61197444	0.1	0.0
chr2	61291652	61292252	1.2	0.2
chr2	62845675	62846275	0.4	0.1
chr2	62867262	62867862	0.0	0.3
chr2	64043624	64044224	1.7	0.2
chr2	64043714	64044314	0.8	0.1
chr2	65404473	65405073	1.4	0.2
chr2	66001905	66002505	0.6	0.3
chr2	66202907	66203507	0.3	0.0
chr2	66581386	66581986	1.4	0.1
chr2	67000648	67001248	0.7	0.6
chr2	67081654	67082254	0.9	0.1
chr2	67482347	67482947	1.7	0.6
chr2	67482377	67482977	1.6	0.7
chr2	67482407	67483007	1.6	0.7
chr2	67482437	67483037	1.6	0.7
chr2	67482467	67483067	1.5	0.8
chr2	67482497	67483097	1.5	0.8
chr2	68369476	68370076	1.2	0.2
chr2	68369582	68370182	0.7	0.2
chr2	69217184	69217784	1.4	0.1
chr2	69940273	69940873	0.9	0.1
chr2	70054826	70055426	1.3	0.0
chr2	70399359	70399959	0.9	0.5
chr2	70467897	70468497	0.9	0.2
chr2	70892027	70892627	0.7	0.1
chr2	71376305	71376905	0.0	0.0
chr2	71508483	71509083	0.4	0.3
chr2	72826707	72827307	0.9	0.3
chr2	72826714	72827314	0.9	0.3
chr2	73355713	73356313	0.5	0.4
chr2	73789772	73790372	1.6	0.1
chr2	73967367	73967967	0.9	0.3
chr2	74103151	74103751	2.2	0.7
chr2	74201705	74202305	0.1	0.3
chr2	74487638	74488238	2.3	0.5
chr2	74487771	74488371	2.6	0.4
chr2	74487916	74488516	2.7	0.2
chr2	74622490	74623090	0.8	0.3
chr2	75164134	75164734	0.3	0.1
chr2	75553023	75553623	1.6	0.2
chr2	75652899	75653499	1.3	0.7
chr2	75928471	75929071	0.3	0.0
chr2	76391029	76391629	0.5	0.1
chr2	76702445	76703045	1.0	0.4
chr2	76762840	76763440	0.5	0.0
chr2	77240869	77241469	0.1	0.1
chr2	77893911	77894511	0.5	0.2
chr2	78598031	78598631	0.9	0.3
chr2	78736385	78736985	1.2	0.1
chr2	78844677	78845277	1.9	0.7
chr2	79161601	79162201	0.6	0.0
chr2	79388338	79388938	1.2	0.0
chr2	81211316	81211916	1.0	0.2
chr2	83244114	83244714	2.2	0.9
chr2	83244205	83244805	2.3	0.9
chr2	83561321	83561921	0.2	0.5
chr2	84068519	84069119	0.7	0.4
chr2	84526743	84527343	0.9	0.4
chr2	84735292	84735892	1.4	0.3
chr2	84859024	84859624	0.4	0.2
chr2	85003512	85004112	0.4	0.2
chr2	85869679	85870279	0.1	0.1
chr2	85869704	85870304	0.0	0.1
chr2	85979133	85979733	0.5	0.0
chr2	85980169	85980769	1.7	0.4
chr2	86390825	86391425	0.2	0.0
chr2	86803330	86803930	0.1	0.1
chr2	87196768	87197368	1.2	0.1

chr2	87433390	87433990	0.7	0.3
chr2	88096016	88096616	0.2	0.2
chr2	88538794	88539394	1.7	0.2
chr2	90469661	90470261	0.0	0.4
chr2	90736624	90737224	1.1	0.2
chr2	90736754	90737354	1.5	0.0
chr2	90914889	90915489	1.2	0.1
chr2	91079046	91079646	0.6	0.2
chr2	91628644	91629244	0.5	0.1
chr2	92274104	92274704	1.1	0.8
chr2	92776985	92777585	0.5	0.2
chr2	92831173	92831773	1.2	0.6
chr2	92872052	92872652	0.9	0.6
chr2	93016906	93017506	1.2	0.5
chr2	93059949	93060549	0.7	0.1
chr2	93203326	93203926	1.3	0.2
chr2	93203500	93204100	0.7	0.7
chr2	93308493	93309093	1.5	0.1
chr2	93815477	93816077	0.4	0.2
chr2	94626398	94626998	1.5	0.0
chr2	95049960	95050560	1.3	0.5
chr2	95576159	95576759	0.6	0.5
chr2	96285454	96286054	1.4	0.6
chr2	96738770	96739370	0.6	0.2
chr2	98916698	98917298	0.1	0.1
chr2	100254900	100255500	0.5	0.5
chr2	100254912	100255512	0.7	0.4
chr2	101121720	101122320	0.9	0.3
chr2	101121738	101122338	1.0	0.4
chr2	101315909	101316509	0.7	0.4
chr2	101805544	101806144	0.8	0.0
chr2	102386877	102387477	0.2	0.2
chr2	102429995	102430595	0.8	0.1
chr2	102642814	102643414	1.1	0.1
chr2	102983379	102983979	0.3	0.1
chr2	103905602	103906202	0.1	0.1
chr2	104414869	104415469	1.8	0.8
chr2	104414976	104415576	1.9	0.7

chr2	104656303	104656903	2.1	0.7
chr2	104689790	104690390	0.4	0.8
chr2	105562753	105563353	0.7	0.0
chr2	105933429	105934029	1.6	0.3
chr2	106490188	106490788	0.9	0.2
chr2	107710010	107710610	0.9	0.2
chr2	107801008	107801608	1.2	0.2
chr2	107801278	107801878	0.9	0.2
chr2	109513239	109513839	0.4	0.0
chr2	109517190	109517790	1.1	0.9
chr2	109517349	109517949	0.8	1.2
chr2	109876338	109876938	0.0	0.0
chr2	110088339	110088939	0.1	0.3
chr2	110249903	110250503	1.0	0.4
chr2	111900323	111900923	1.3	0.9
chr2	111900571	111901171	1.6	0.7
chr2	112610227	112610827	0.4	0.0
chr2	112840088	112840688	0.7	0.2
chr2	113093272	113093872	1.5	0.3
chr2	113832863	113833463	0.0	0.0
chr2	113983923	113984523	0.4	0.1
chr2	114061167	114061767	4.3	2.0
chr2	114061225	114061825	4.1	1.7
chr2	114061254	114061854	4.1	1.7
chr2	114061312	114061912	4.3	1.8
chr2	116723105	116723705	0.1	0.3
chr2	116805509	116806109	0.2	0.2
chr2	117369388	117369988	0.2	0.2
chr2	118055860	118056460	1.9	0.4
chr2	118056070	118056670	1.6	0.2
chr2	118395383	118395983	0.6	0.5
chr2	119370035	119370635	0.7	0.2
chr2	119500218	119500818	0.2	0.7
chr2	119739649	119740249	0.1	0.1
chr2	119870945	119871545	2.3	0.4
chr2	121051849	121052449	1.0	0.7
chr2	121367830	121368430	1.1	0.1
chr2	121636296	121636896	0.8	0.5

chr2	123104784	123105384	1.3	0.1
chr2	123137494	123138094	0.9	0.0
chr2	123533025	123533625	0.2	0.2
chr2	123533107	123533707	0.3	0.4
chr2	123920822	123921422	0.4	0.4
chr2	124643051	124643651	1.7	0.4
chr2	124643247	124643847	1.6	0.6
chr2	124838512	124839112	1.3	0.3
chr2	125061707	125062307	0.7	0.3
chr2	125261840	125262440	0.8	0.2
chr2	126378343	126378943	0.3	0.3
chr2	126598337	126598937	1.3	0.2
chr2	126998613	126999213	0.7	0.0
chr2	127333912	127334512	1.5	0.1
chr2	128104574	128105174	0.9	0.1
chr2	128172861	128173461	1.4	0.2
chr2	128219033	128219633	0.4	0.4
chr2	128690591	128691191	0.8	0.7
chr2	128690867	128691467	0.0	0.3
chr2	128946960	128947560	0.4	0.0
chr2	129570803	129571403	0.2	0.0
chr2	129625614	129626214	0.7	0.5
chr2	129771061	129771661	1.0	0.2
chr2	129771256	129771856	0.9	0.4
chr2	130233854	130234454	1.4	0.5
chr2	131004649	131005249	1.2	0.0
chr2	131013178	131013778	1.4	0.0
chr2	131327062	131327662	0.3	0.4
chr2	131330650	131331250	1.5	0.2
chr2	131330670	131331270	1.7	0.2
chr2	131523377	131523977	0.9	0.2
chr2	132819209	132819809	1.1	0.4
chr2	133252236	133252836	0.7	0.5
chr2	133385341	133385941	0.3	0.1
chr2	133398162	133398762	1.1	0.1
chr2	133701914	133702514	0.4	0.7
chr2	134130559	134131159	1.1	0.6
chr2	134673931	134674531	1.0	0.1

chr2	136358333	136358933	0.4	0.2
chr2	137068980	137069580	0.4	0.4
chr2	137369519	137370119	0.4	0.3
chr2	137607847	137608447	0.5	0.2
chr2	137790865	137791465	0.7	0.2
chr2	137843293	137843893	0.4	0.4
chr2	137846910	137847510	0.1	0.2
chr2	138191005	138191605	0.1	0.3
chr2	138191156	138191756	0.6	0.5
chr2	139339896	139340496	0.6	0.2
chr2	139731712	139732312	0.1	0.1
chr2	139843437	139844037	1.0	0.3
chr2	140545207	140545807	0.2	0.1
chr2	141418764	141419364	1.0	0.1
chr2	141855672	141856272	0.2	0.3
chr2	143599930	143600530	1.0	0.0
chr2	143638771	143639371	0.3	0.4
chr2	143639000	143639600	0.1	0.4
chr2	143681602	143682202	0.7	0.1
chr2	143921574	143922174	2.5	0.7
chr2	143921721	143922321	2.6	0.0
chr2	144733353	144733953	1.4	0.8
chr2	145132545	145133145	0.6	0.0
chr2	145373304	145373904	1.1	0.0
chr2	145373382	145373982	1.3	0.2
chr2	146346761	146347361	0.9	0.2
chr2	146746321	146746921	1.3	0.3
chr2	146784809	146785409	0.7	0.5
chr2	146784838	146785438	0.4	0.4
chr2	146938937	146939537	0.8	0.1
chr2	147012666	147013266	1.4	1.0
chr2	147013691	147014291	0.9	0.6
chr2	147112530	147113130	0.1	0.2
chr2	147847683	147848283	0.8	0.1
chr2	147974331	147974931	0.1	0.0
chr2	148008153	148008753	2.7	0.7
chr2	148008431	148009031	2.1	0.3
chr2	148595502	148596102	0.9	0.2

chr2	148700347	148700947	0.5	0.1
chr2	149966813	149967413	1.6	0.1
chr2	149966904	149967504	0.9	0.1
chr2	150401033	150401633	0.3	0.4
chr2	150401057	150401657	0.2	0.5
chr2	150544505	150545105	1.5	0.0
chr2	150565952	150566552	0.3	0.1
chr2	150609593	150610193	0.1	0.3
chr2	152444655	152445255	0.0	0.1
chr2	152543564	152544164	0.2	0.1
chr2	152845894	152846494	0.9	0.4
chr2	152988050	152988650	1.6	0.6
chr2	153311910	153312510	0.8	0.3
chr2	153811918	153812518	0.8	0.4
chr2	154026062	154026662	0.6	0.4
chr2	154499792	154500392	0.2	0.4
chr2	154549222	154549822	0.3	0.8
chr2	155544553	155545153	1.9	0.2
chr2	155544578	155545178	2.0	0.3
chr2	155544628	155545228	1.8	0.3
chr2	155544655	155545255	1.7	0.3
chr2	155544836	155545436	1.7	0.3
chr2	155544863	155545463	1.5	0.2
chr2	156212722	156213322	1.8	0.3
chr2	156580178	156580778	0.5	0.1
chr2	156580374	156580974	0.3	0.3
chr2	156665625	156666225	2.1	0.1
chr2	156863126	156863726	0.3	0.2
chr2	157166185	157166785	0.9	0.2
chr2	157183116	157183716	0.4	0.3
chr2	157383124	157383724	0.6	0.4
chr2	157427073	157427673	1.1	0.1
chr2	157500863	157501463	0.6	0.7
chr2	157657650	157658250	1.3	0.2
chr2	158484397	158484997	0.8	0.1
chr2	158738518	158739118	1.1	0.5
chr2	158738604	158739204	0.9	0.8
chr2	158838366	158838966	3.9	2.0

chr2	158838390	158838990	3.7	2.0
chr2	158838414	158839014	3.6	1.8
chr2	158838438	158839038	3.6	1.6
chr2	158958987	158959587	1.6	0.1
chr2	158959111	158959711	1.3	0.0
chr2	159107580	159108180	1.4	0.2
chr2	159256585	159257185	0.3	0.1
chr2	159553416	159554016	0.4	0.3
chr2	159586975	159587575	0.9	0.1
chr2	160670477	160671077	1.5	0.1
chr2	160750723	160751323	0.5	0.2
chr2	160778383	160778983	0.6	0.2
chr2	160778674	160779274	0.3	0.4
chr2	162082327	162082927	0.3	0.2
chr2	162156396	162156996	0.4	0.2
chr2	162355590	162356190	0.6	0.0
chr2	162546865	162547465	0.8	0.2
chr2	163043849	163044449	1.4	0.0
chr2	163126991	163127591	0.3	0.0
chr2	163170860	163171460	0.8	0.2
chr2	163318318	163318918	0.2	0.1
chr2	163579774	163580374	0.3	0.1
chr2	163647716	163648316	0.3	0.5
chr2	163709003	163709603	1.6	0.1
chr2	163732256	163732856	0.0	0.1
chr2	164381862	164382462	1.8	0.8
chr2	164381913	164382513	1.7	0.8
chr2	164381964	164382564	1.1	0.4
chr2	164560241	164560841	0.6	0.7
chr2	164680363	164680963	0.7	0.1
chr2	164704420	164705020	1.1	0.2
chr2	164928085	164928685	0.2	0.0
chr2	164970227	164970827	1.1	0.2
chr2	165074320	165074920	1.3	0.3
chr2	165182203	165182803	2.1	1.1
chr2	165182265	165182865	2.2	1.1
chr2	165182296	165182896	2.3	1.1
chr2	165182389	165182989	2.2	1.0

chr2	165182420	165183020	2.2	1.0
chr2	165226522	165227122	0.1	0.2
chr2	165307605	165308205	2.9	0.4
chr2	165359474	165360074	0.4	0.1
chr2	165521220	165521820	1.5	0.1
chr2	165521240	165521840	1.5	0.1
chr2	165521313	165521913	1.5	0.1
chr2	165618794	165619394	0.6	0.0
chr2	165622546	165623146	0.8	0.8
chr2	166230424	166231024	1.4	0.4
chr2	167412293	167412893	1.8	0.6
chr2	167412398	167412998	1.9	0.7
chr2	167421151	167421751	0.8	0.3
chr2	167484946	167485546	0.2	0.2
chr2	167487650	167488250	0.8	0.6
chr2	167530270	167530870	0.3	0.1
chr2	168093964	168094564	0.6	0.4
chr2	168094205	168094805	1.0	0.1
chr2	168094234	168094834	1.0	0.1
chr2	168472034	168472634	1.1	0.5
chr2	168636385	168636985	0.7	0.1
chr2	168784081	168784681	0.3	0.5
chr2	168964971	168965571	0.3	0.0
chr2	169456116	169456716	0.3	0.0
chr2	169725809	169726409	0.0	0.5
chr2	169839700	169840300	0.1	0.4
chr2	169869469	169870069	1.0	0.3
chr2	169904020	169904620	0.5	0.2
chr2	170167131	170167731	0.8	0.4
chr2	170389355	170389955	0.3	0.2
chr2	170804022	170804622	1.8	0.5
chr2	170804042	170804642	1.9	0.6
chr2	171688162	171688762	6.8	2.5
chr2	171688190	171688790	6.2	2.2
chr2	171688204	171688804	6.5	2.3
chr2	171688218	171688818	6.7	2.5
chr2	171688246	171688846	6.3	2.3
chr2	171688260	171688860	6.0	2.1
chr2	171688274	171688874	5.8	2.0
chr2	171688288	171688888	5.6	1.9
chr2	171688316	171688916	5.5	1.9
chr2	171688344	171688944	5.6	1.9
chr2	171688358	171688958	5.4	1.8
chr2	171688386	171688986	5.4	1.8
chr2	171688400	171689000	5.6	1.9
chr2	171688414	171689014	5.4	1.8
chr2	171688498	171689098	6.3	2.3
chr2	171688512	171689112	6.2	2.2
chr2	171688610	171689210	6.6	2.4
chr2	171688624	171689224	6.6	2.5
chr2	171688680	171689280	7.3	2.9
chr2	171688694	171689294	7.4	2.9
chr2	171688722	171689322	7.3	2.9
chr2	171688736	171689336	7.4	2.9
chr2	171688753	171689353	7.9	3.2
chr2	171688784	171689384	8.3	3.5
chr2	171688815	171689415	8.1	3.4
chr2	171688829	171689429	8.4	3.6
chr2	171688877	171689477	9.3	4.2
chr2	171688891	171689491	9.3	4.2
chr2	171688908	171689508	9.2	4.2
chr2	171688922	171689522	8.8	3.9
chr2	171688939	171689539	9.4	4.3
chr2	171688956	171689556	9.5	4.4
chr2	171688987	171689587	9.4	4.4
chr2	171689018	171689618	9.1	4.2
chr2	171689049	171689649	8.8	4.0
chr2	171689063	171689663	9.0	4.1
chr2	171689111	171689711	9.0	4.2
chr2	171689125	171689725	9.2	4.3
chr2	171689142	171689742	9.1	4.2
chr2	171689156	171689756	9.4	4.4
chr2	171689173	171689773	9.5	4.4
chr2	171689190	171689790	9.4	4.4
chr2	171689221	171689821	9.2	4.3
chr2	171689235	171689835	9.1	4.2

chr2	171689252	171689852	9.1	4.2
chr2	171689269	171689869	9.2	4.3
chr2	171689300	171689900	9.3	4.4
chr2	171689331	171689931	9.3	4.5
chr2	171689348	171689948	9.1	4.4
chr2	171689365	171689965	9.2	4.3
chr2	171689393	171689993	9.6	4.6
chr2	171689421	171690021	9.4	4.5
chr2	171689449	171690049	9.4	4.5
chr2	171689466	171690066	9.2	4.4
chr2	171689483	171690083	9.0	4.3
chr2	171689500	171690100	8.8	4.2
chr2	171689545	171690145	8.6	4.1
chr2	171867177	171867777	0.9	0.2
chr2	172500396	172500996	1.0	0.1
chr2	172560037	172560637	0.4	0.0
chr2	172713520	172714120	1.9	1.0
chr2	172720673	172721273	1.1	0.1
chr2	172947507	172948107	0.4	0.0
chr2	172947549	172948149	0.2	0.0
chr2	173323378	173323978	0.7	0.4
chr2	173323420	173324020	0.8	0.6
chr2	173404132	173404732	0.7	0.2
chr2	173743176	173743776	0.8	0.4
chr2	173801392	173801992	0.8	0.0
chr2	173801542	173802142	1.2	0.3
chr2	173849817	173850417	1.2	0.5
chr2	173884845	173885445	0.4	0.0
chr2	173926444	173927044	0.2	0.0
chr2	173955137	173955737	0.9	0.4
chr2	174121753	174122353	1.0	0.5
chr2	174212668	174213268	1.3	0.2
chr2	174297230	174297830	1.7	0.1
chr2	174651843	174652443	1.5	0.8
chr2	175438141	175438741	1.9	0.5
chr2	175438373	175438973	1.8	0.5
chr2	176682487	176683087	1.9	0.5
chr2	176682719	176683319	1.8	0.5
chr2	177840076	177840676	1.8	0.1
chr2	178289755	178290355	0.3	0.0
chr2	178350950	178351550	1.0	0.0
chr2	178350967	178351567	1.1	0.0
chr2	178600708	178601308	0.3	0.2
chr2	179373613	179374213	1.1	0.1
chr2	179553930	179554530	0.5	0.4
chr2	179553973	179554573	0.2	0.1
chr2	179851059	179851659	0.2	0.2
chr2	179891466	179892066	0.6	0.3
chr2	179930151	179930751	2.3	1.0
chr2	179930243	179930843	1.7	0.8
chr2	180051669	180052269	0.7	0.1
chr2	180089626	180090226	0.0	0.0
chr2	180492264	180492864	1.7	0.7
chr2	180492418	180493018	1.8	0.7
chr2	180971153	180971753	0.4	0.1
chr2	180971226	180971826	0.6	0.0
chr2	181008354	181008954	1.8	0.7
chr2	181008620	181009220	2.6	0.9
chr2	181171484	181172084	1.6	0.6
chr2	181254466	181255066	1.1	0.2
chr2	181309088	181309688	1.2	0.5
chr2	181409670	181410270	0.5	0.1
chr2	181427468	181428068	1.8	0.8
chr2	181664839	181665439	0.5	0.2
chr3	3134043	3134643	2.0	0.3
chr3	3734292	3734892	0.5	0.1
chr3	4831042	4831642	0.2	1.1
chr3	4831053	4831653	0.1	1.1
chr3	6443709	6444309	0.7	0.2
chr3	7464560	7465160	1.2	0.6
chr3	7464650	7465250	1.1	0.5
chr3	7464661	7465261	1.2	0.6
chr3	8379569	8380169	1.6	0.3
chr3	8469512	8470112	0.2	0.4
chr3	9200994	9201594	0.4	0.4
chr3	9607710	9608310	0.4	0.3

chr3	9851593	9852193	1.9	0.2
chr3	9851715	9852315	1.4	0.1
chr3	10086650	10087250	0.1	0.3
chr3	10118665	10119265	0.3	0.0
chr3	11508053	11508653	0.9	0.4
chr3	11508250	11508850	1.4	0.6
chr3	11635014	11635614	0.4	0.2
chr3	12049127	12049727	0.2	0.1
chr3	12803431	12804031	0.8	0.4
chr3	12803533	12804133	0.4	0.5
chr3	12947296	12947896	0.2	0.3
chr3	12947385	12947985	0.3	0.3
chr3	13666813	13667413	0.8	0.2
chr3	14507448	14508048	2.7	0.1
chr3	14663453	14664053	0.8	0.1
chr3	14668676	14669276	0.5	0.1
chr3	16193224	16193824	0.9	0.1
chr3	17687616	17688216	0.7	0.1
chr3	17967808	17968408	0.1	0.2
chr3	18037298	18037898	0.8	0.3
chr3	20172639	20173239	1.8	0.3
chr3	20331692	20332292	0.5	0.4
chr3	21840652	21841252	0.6	0.3
chr3	22580455	22581055	0.7	0.3
chr3	24855077	24855677	0.9	0.3
chr3	25722906	25723506	1.1	0.4
chr3	25756822	25757422	1.0	0.1
chr3	25757075	25757675	2.3	1.0
chr3	27915552	27916152	2.8	0.9
chr3	27915566	27916166	2.8	0.9
chr3	27915573	27916173	2.8	0.8
chr3	28330818	28331418	0.8	0.0
chr3	28579965	28580565	0.3	0.1
chr3	28902293	28902893	0.0	0.0
chr3	29041523	29042123	1.0	0.5
chr3	29103052	29103652	1.7	0.0
chr3	29103314	29103914	1.9	0.3
chr3	29114186	29114786	0.4	0.1

chr3	29605853	29606453	1.1	0.1
chr3	30716156	30716756	1.1	0.1
chr3	30959896	30960496	1.4	0.6
chr3	30964874	30965474	2.1	0.3
chr3	30965156	30965756	1.0	0.1
chr3	31120886	31121486	0.3	0.1
chr3	31656281	31656881	0.1	0.2
chr3	31967258	31967858	0.1	0.5
chr3	32835589	32836189	1.5	0.1
chr3	32919487	32920087	0.6	0.1
chr3	33026733	33027333	2.0	0.6
chr3	33026926	33027526	3.1	0.7
chr3	33317862	33318462	1.5	0.5
chr3	33650475	33651075	1.3	0.1
chr3	33650742	33651342	1.4	0.4
chr3	34340140	34340740	1.1	0.0
chr3	34796908	34797508	0.2	0.2
chr3	35012880	35013480	0.1	0.1
chr3	35234644	35235244	1.5	0.4
chr3	35397753	35398353	0.2	0.1
chr3	35953448	35954048	0.3	0.9
chr3	36262083	36262683	0.0	0.1
chr3	36288153	36288753	1.1	0.7
chr3	36386130	36386730	0.3	0.1
chr3	37890946	37891546	0.4	0.2
chr3	37986438	37987038	1.4	0.0
chr3	38247484	38248084	1.7	0.8
chr3	38445864	38446464	0.1	0.3
chr3	38618576	38619176	0.6	0.2
chr3	39096551	39097151	1.7	0.2
chr3	39096613	39097213	1.1	0.2
chr3	39133713	39134313	1.1	0.0
chr3	39221080	39221680	1.4	0.3
chr3	39861125	39861725	0.7	0.9
chr3	40321630	40322230	0.8	0.5
chr3	40602699	40603299	0.7	0.1
chr3	40855079	40855679	0.6	0.2
chr3	40877254	40877854	0.6	0.1

chr3	41005966	41006566	0.1	0.1
chr3	41026817	41027417	0.1	0.0
chr3	41026918	41027518	0.3	0.2
chr3	41151298	41151898	0.1	0.3
chr3	41245980	41246580	1.3	0.4
chr3	41864625	41865225	1.9	0.4
chr3	41864871	41865471	1.6	0.4
chr3	42166303	42166903	0.8	0.0
chr3	44441748	44442348	0.7	0.0
chr3	46334486	46335086	0.4	0.3
chr3	46421193	46421793	0.1	0.2
chr3	46618183	46618783	1.3	0.2
chr3	46625323	46625923	2.7	0.8
chr3	46625334	46625934	2.9	0.8
chr3	46625467	46626067	2.6	0.7
chr3	46763996	46764596	0.6	0.0
chr3	48349302	48349902	0.2	0.2
chr3	49523309	49523909	0.7	0.0
chr3	50144876	50145476	0.3	0.0
chr3	50491530	50492130	2.2	0.4
chr3	50491583	50492183	2.1	0.5
chr3	50720596	50721196	1.1	0.0
chr3	50840731	50841331	0.5	0.1
chr3	50875982	50876582	2.2	0.6
chr3	51312520	51313120	0.6	0.2
chr3	51576102	51576702	1.0	0.3
chr3	51625236	51625836	0.8	0.2
chr3	51625301	51625901	0.9	0.2
chr3	51767411	51768011	0.9	0.1
chr3	52059665	52060265	0.1	0.0
chr3	52081413	52082013	0.9	0.1
chr3	52169571	52170171	0.3	0.0
chr3	52201066	52201666	0.6	0.3
chr3	52343999	52344599	0.1	0.2
chr3	52584823	52585423	0.8	0.4
chr3	52835027	52835627	0.5	0.1
chr3	53215825	53216425	0.9	0.3
chr3	53414778	53415378	0.9	0.1
chr3	53618804	53619404	0.6	0.3
chr3	54323482	54324082	0.7	0.7
chr3	54820747	54821347	0.4	0.0
chr3	54864928	54865528	3.7	1.0
chr3	54864966	54865566	3.5	1.0
chr3	54865004	54865604	3.3	0.8
chr3	54865042	54865642	3.6	0.8
chr3	54865080	54865680	3.7	0.9
chr3	54865118	54865718	3.8	0.9
chr3	54865924	54866524	0.4	0.1
chr3	54899994	54900594	1.0	0.2
chr3	55027889	55028489	0.1	0.3
chr3	55030738	55031338	0.1	0.2
chr3	55703309	55703909	0.5	0.3
chr3	56553671	56554271	0.0	0.0
chr3	56608075	56608675	0.3	0.1
chr3	56940766	56941366	0.2	0.3
chr3	57057001	57057601	1.2	0.0
chr3	57826049	57826649	1.0	0.0
chr3	58367326	58367926	1.0	0.0
chr3	58777488	58778088	1.5	0.1
chr3	60368097	60368697	0.6	0.1
chr3	61732140	61732740	0.9	0.4
chr3	61732280	61732880	0.9	0.3
chr3	61763027	61763627	0.5	0.1
chr3	61975129	61975729	1.3	0.5
chr3	62184711	62185311	1.2	0.4
chr3	62196423	62197023	0.4	0.2
chr3	63215568	63216168	0.5	0.3
chr3	63215652	63216252	0.6	0.3
chr3	63381666	63382266	0.6	0.3
chr3	63418285	63418885	0.3	0.0
chr3	64023117	64023717	1.5	0.1
chr3	65075607	65076207	0.4	0.0
chr3	65390221	65390821	0.6	0.2
chr3	65462478	65463078	1.4	0.0
chr3	65974520	65975120	0.6	0.2
chr3	65974565	65975165	0.8	0.2

chr3	66012953	66013553	1.2	0.0
chr3	67307740	67308340	1.0	0.1
chr3	67471822	67472422	0.3	0.1
chr3	68841356	68841956	0.4	0.1
chr3	69012589	69013189	2.5	0.3
chr3	69012622	69013222	2.1	0.3
chr3	69142935	69143535	0.6	0.3
chr3	69626492	69627092	0.1	0.2
chr3	69626583	69627183	0.4	0.2
chr3	69646169	69646769	0.7	0.2
chr3	69892268	69892868	0.7	0.1
chr3	71727670	71728270	1.4	0.3
chr3	71727761	71728361	0.6	0.1
chr3	71767529	71768129	0.9	0.0
chr3	72728160	72728760	1.0	0.1
chr3	73929174	73929774	1.6	0.5
chr3	73929402	73930002	1.4	0.3
chr3	74933159	74933759	0.1	0.0
chr3	75306969	75307569	0.5	0.3
chr3	75313712	75314312	0.1	0.1
chr3	75379498	75380098	1.6	0.2
chr3	76515278	76515878	1.8	1.1
chr3	76515542	76516142	0.9	0.3
chr3	76593518	76594118	0.5	0.3
chr3	77796384	77796984	0.2	0.1
chr3	78541198	78541798	1.1	0.3
chr3	79015214	79015814	0.0	0.1
chr3	79198026	79198626	1.6	0.3
chr3	79490507	79491107	1.3	0.2
chr3	80412324	80412924	1.2	0.5
chr3	80901377	80901977	0.5	0.0
chr3	82252920	82253520	0.8	0.1
chr3	82503760	82504360	0.0	0.2
chr3	82578100	82578700	0.4	0.2
chr3	83635570	83636170	0.4	0.2
chr3	83731873	83732473	0.9	0.0
chr3	83757124	83757724	1.2	0.1
chr3	84055261	84055861	0.8	0.4

chr3	84215789	84216389	0.6	1.0
chr3	84295262	84295862	0.1	0.1
chr3	84316919	84317519	0.8	0.8
chr3	84800541	84801141	0.5	0.1
chr3	85103910	85104510	0.3	0.0
chr3	85453198	85453798	1.3	0.5
chr3	85453322	85453922	1.4	0.6
chr3	85626912	85627512	0.5	0.1
chr3	85901192	85901792	1.0	0.1
chr3	86925584	86926184	2.4	0.6
chr3	87156585	87157185	0.6	0.1
chr3	87216259	87216859	5.3	2.2
chr3	87216313	87216913	5.2	2.1
chr3	87216367	87216967	5.1	2.2
chr3	87216421	87217021	4.6	1.9
chr3	87216475	87217075	4.6	1.9
chr3	87216529	87217129	4.5	1.9
chr3	87787202	87787802	0.8	0.1
chr3	87937441	87938041	0.1	0.1
chr3	88945663	88946263	0.9	0.3
chr3	88983049	88983649	0.1	0.0
chr3	89468867	89469467	0.3	0.3
chr3	89473188	89473788	0.7	0.2
chr3	89881774	89882374	1.0	0.1
chr3	91606520	91607120	0.7	0.0
chr3	91673888	91674488	0.4	0.1
chr3	91855332	91855932	1.2	0.5
chr3	92338013	92338613	1.1	0.0
chr3	93222810	93223410	0.7	0.1
chr3	93222901	93223501	0.4	0.2
chr3	93396328	93396928	0.3	0.3
chr3	94402604	94403204	0.2	0.2
chr3	94504221	94504821	0.0	0.2
chr3	94962865	94963465	0.9	0.5
chr3	94963008	94963608	0.3	0.4
chr3	95231581	95232181	0.2	0.6
chr3	96155532	96156132	1.2	0.4
chr3	96185863	96186463	1.2	0.4

chr3	96435175	96435775	1.1	0.3
chr3	96435378	96435978	0.4	0.2
chr3	97028522	97029122	0.7	0.0
chr3	97382401	97383001	2.2	0.6
chr3	97382505	97383105	1.9	0.5
chr3	97382530	97383130	2.0	0.5
chr3	97382547	97383147	1.9	0.5
chr3	97382566	97383166	1.9	0.5
chr3	97382638	97383238	1.9	0.4
chr3	97382692	97383292	2.6	0.8
chr3	97382711	97383311	2.2	0.6
chr3	97411802	97412402	0.0	0.2
chr3	97442700	97443300	1.9	0.2
chr3	97687075	97687675	0.3	0.0
chr3	98228782	98229382	0.9	0.1
chr3	98903263	98903863	0.6	0.7
chr3	98903357	98903957	1.1	0.7
chr3	99467462	99468062	0.7	0.1
chr3	99565327	99565927	1.0	0.0
chr3	99633397	99633997	0.1	0.0
chr3	99955342	99955942	0.5	0.1
chr3	100279414	100280014	0.4	0.1
chr3	100900121	100900721	0.8	0.0
chr3	101119397	101119997	0.4	0.2
chr3	101119425	101120025	0.2	0.2
chr3	101258803	101259403	0.8	0.6
chr3	101471516	101472116	0.3	0.2
chr3	101601582	101602182	0.6	0.0
chr3	101929817	101930417	0.9	0.7
chr3	101993805	101994405	1.8	0.1
chr3	102322262	102322862	1.0	0.3
chr3	102426091	102426691	0.2	0.3
chr3	102432370	102432970	1.0	0.4
chr3	102459899	102460499	2.6	0.5
chr3	102742994	102743594	0.9	0.6
chr3	102937519	102938119	1.2	0.7
chr3	102937553	102938153	1.1	0.6
chr3	102937587	102938187	1.4	0.7

chr3	103025594	103026194	0.1	0.2
chr3	103500466	103501066	0.7	0.5
chr3	104024207	104024807	0.8	0.2
chr3	104701035	104701635	1.2	0.6
chr3	104944356	104944956	1.5	0.1
chr3	105018747	105019347	0.1	0.2
chr3	105075015	105075615	2.2	0.7
chr3	105075248	105075848	2.0	0.5
chr3	105303884	105304484	0.7	0.0
chr3	105455250	105455850	1.2	0.1
chr3	105455271	105455871	1.1	0.2
chr3	106235300	106235900	0.4	0.4
chr3	106486172	106486772	2.1	0.7
chr3	106486184	106486784	1.9	0.6
chr3	107708308	107708908	1.0	0.2
chr3	107820127	107820727	1.0	0.0
chr3	107909548	107910148	0.9	0.0
chr3	108194871	108195471	0.1	0.6
chr3	108350907	108351507	2.5	1.1
chr3	108468877	108469477	0.6	0.4
chr3	108694757	108695357	0.6	0.3
chr3	108709281	108709881	0.6	0.1
chr3	109704130	109704730	0.8	0.1
chr3	109934916	109935516	1.4	0.0
chr3	109946595	109947195	1.4	0.4
chr3	109946746	109947346	1.7	0.5
chr3	110235918	110236518	0.5	0.0
chr3	110859421	110860021	0.6	0.4
chr3	111678936	111679536	0.3	0.1
chr3	112660711	112661311	1.2	0.2
chr3	112660978	112661578	0.7	0.2
chr3	113054449	113055049	0.8	0.1
chr3	113087061	113087661	0.7	0.1
chr3	113119666	113120266	0.8	0.1
chr3	113152271	113152871	0.7	0.1
chr3	113246145	113246745	1.3	0.5
chr3	113415053	113415653	0.4	0.3
chr3	114773513	114774113	1.0	0.3

chr3	114960609	114961209	1.0	0.3
chr3	114986604	114987204	0.0	0.2
chr3	115731383	115731983	1.2	0.0
chr3	115969880	115970480	0.4	0.0
chr3	117129066	117129666	0.5	0.2
chr3	117141504	117142104	0.7	0.1
chr3	117608998	117609598	2.1	0.6
chr3	117847433	117848033	0.6	0.4
chr3	119457064	119457664	0.4	0.2
chr3	119594417	119595017	0.8	0.5
chr3	119609713	119610313	1.7	0.7
chr3	119609924	119610524	1.6	0.8
chr3	120685379	120685979	1.5	0.7
chr3	120728459	120729059	1.2	0.3
chr3	120871675	120872275	1.3	0.1
chr3	121159092	121159692	0.6	0.1
chr3	121185573	121186173	0.5	0.0
chr3	121239335	121239935	0.6	0.1
chr3	121316029	121316629	0.7	0.5
chr3	121316102	121316702	0.3	0.3
chr3	121778528	121779128	0.2	0.3
chr3	121814643	121815243	1.7	0.2
chr3	121981418	121982018	0.8	0.0
chr3	122107816	122108416	2.7	1.5
chr3	122108002	122108602	2.0	0.6
chr3	122607729	122608329	1.1	0.2
chr3	122607760	122608360	1.1	0.2
chr3	122607789	122608389	1.1	0.2
chr3	122607882	122608482	1.1	0.2
chr3	122649987	122650587	0.8	0.5
chr3	122808011	122808611	0.3	0.1
chr3	122866158	122866758	0.1	0.3
chr3	122894460	122895060	1.3	0.4
chr3	124230742	124231342	1.1	0.0
chr3	124391028	124391628	0.8	0.1
chr3	124391124	124391724	0.7	0.2
chr3	124947415	124948015	0.4	0.1
chr3	125151356	125151956	0.4	0.0
chr3	125381058	125381658	1.8	0.3
chr3	125804641	125805241	0.1	0.1
chr3	127194115	127194715	0.6	0.0
chr3	127599905	127600505	0.5	0.2
chr3	128349460	128350060	0.7	0.4
chr3	128349493	128350093	0.7	0.5
chr3	128373222	128373822	1.3	0.3
chr3	128941698	128942298	1.3	0.2
chr3	129060934	129061534	1.8	0.5
chr3	129061070	129061670	0.9	0.1
chr3	129425814	129426414	1.4	0.5
chr3	129663770	129664370	0.6	0.4
chr3	129727010	129727610	0.3	0.1
chr3	130069681	130070281	0.8	0.1
chr3	130720340	130720940	0.2	0.0
chr3	131421617	131422217	0.7	0.1
chr3	131782718	131783318	1.2	0.2
chr3	132269054	132269654	0.7	0.2
chr3	132314904	132315504	1.5	0.0
chr3	132392767	132393367	1.0	0.3
chr3	132393016	132393616	1.8	0.5
chr3	132677106	132677706	0.6	0.1
chr3	133133781	133134381	0.0	0.1
chr3	133437079	133437679	1.0	0.4
chr3	134688150	134688750	0.0	0.2
chr3	134715440	134716040	0.2	0.2
chr3	135270514	135271114	0.9	0.2
chr3	135274737	135275337	0.5	0.6
chr3	135517881	135518481	0.1	0.0
chr3	135680985	135681585	1.2	0.5
chr3	135778685	135779285	0.3	0.2
chr3	135834505	135835105	0.1	0.1
chr3	135873077	135873677	0.7	0.1
chr3	135988529	135989129	0.7	0.0
chr3	136029847	136030447	0.2	0.3
chr3	137215077	137215677	0.9	0.1
chr3	138276212	138276812	0.6	0.3
chr3	138349803	138350403	0.4	0.2

chr3	138724161	138724761	0.8	0.0
chr3	139637654	139638254	0.1	0.2
chr3	139793853	139794453	0.6	0.2
chr3	140839974	140840574	1.8	0.6
chr3	140839984	140840584	1.7	0.6
chr3	141381104	141381704	1.2	0.0
chr3	141418770	141419370	0.4	0.2
chr3	141885706	141886306	1.3	0.0
chr3	143140822	143141422	0.9	0.0
chr3	143247512	143248112	0.4	0.1
chr3	143425011	143425611	1.7	0.2
chr3	143529341	143529941	1.0	0.5
chr3	143529429	143530029	0.8	0.4
chr3	144087767	144088367	1.5	0.6
chr3	144088006	144088606	0.5	0.1
chr3	144295269	144295869	1.5	0.3
chr3	144333647	144334247	0.6	0.0
chr3	145172552	145173152	0.7	0.2
chr3	145433383	145433983	0.4	0.5
chr3	145499714	145500314	0.6	0.2
chr3	145580187	145580787	0.5	0.4
chr3	145621161	145621761	0.1	0.1
chr3	145706537	145707137	0.8	0.1
chr3	145895871	145896471	0.0	0.0
chr3	146433532	146434132	0.1	0.4
chr3	147194351	147194951	0.9	0.1
chr3	147226798	147227398	0.9	0.1
chr3	147803200	147803800	0.7	0.1
chr3	148344379	148344979	1.7	0.3
chr3	149070160	149070760	0.1	0.1
chr3	149427248	149427848	1.2	0.3
chr3	149501413	149502013	1.1	0.1
chr3	151080554	151081154	0.3	0.1
chr3	151098694	151099294	1.9	0.9
chr3	151098947	151099547	0.8	0.6
chr3	152240816	152241416	0.5	0.8
chr3	152680490	152681090	1.5	0.0
chr3	153083290	153083890	1.1	0.0

chr3	153279338	153279938	1.1	0.5
chr3	153375067	153375667	1.8	0.4
chr3	153670298	153670898	0.0	0.1
chr3	153904244	153904844	0.0	0.0
chr3	154035049	154035649	0.4	0.1
chr3	154064338	154064938	1.2	0.3
chr3	154210839	154211439	1.2	0.1
chr3	154660332	154660932	0.4	0.2
chr3	154704408	154705008	0.3	0.1
chr3	155103760	155104360	1.1	0.1
chr3	156642749	156643349	1.2	0.0
chr3	156658221	156658821	1.0	0.2
chr3	156827428	156828028	0.7	0.0
chr3	157413993	157414593	1.3	0.5
chr3	157414155	157414755	1.0	0.2
chr3	157575572	157576172	1.1	0.1
chr3	157575848	157576448	2.3	0.3
chr3	157575868	157576468	1.5	0.0
chr3	158018575	158019175	0.0	0.0
chr3	158318512	158319112	1.3	0.1
chr4	3149202	3149802	0.7	0.0
chr4	4672072	4672672	1.0	0.7
chr4	6380223	6380823	1.0	0.2
chr4	6616924	6617524	1.0	0.1
chr4	6995969	6996569	0.3	0.0
chr4	7069800	7070400	0.2	0.0
chr4	7129012	7129612	1.0	0.1
chr4	7315871	7316471	0.6	0.1
chr4	7365292	7365892	1.4	0.1
chr4	7922579	7923179	1.4	0.2
chr4	7922606	7923206	1.6	0.2
chr4	8989400	8990000	0.7	0.0
chr4	10071122	10071722	0.6	0.0
chr4	10970957	10971557	0.7	0.0
chr4	11253533	11254133	0.5	0.4
chr4	11723744	11724344	0.0	0.0
chr4	11814684	11815284	0.4	0.1
chr4	11835128	11835728	1.6	0.1

chr4	12574713	12575313	0.4	0.1
chr4	13034293	13034893	0.2	0.2
chr4	13096242	13096842	0.8	0.3
chr4	13096332	13096932	0.8	0.3
chr4	13196976	13197576	1.0	0.5
chr4	13197013	13197613	0.9	0.6
chr4	13643674	13644274	0.9	0.1
chr4	13988450	13989050	0.2	0.2
chr4	14584848	14585448	1.8	0.3
chr4	15192545	15193145	0.4	0.1
chr4	15608665	15609265	0.0	0.1
chr4	16214649	16215249	0.1	0.0
chr4	17699147	17699747	0.3	0.0
chr4	19217961	19218561	0.5	0.1
chr4	19262648	19263248	1.0	0.3
chr4	19719225	19719825	0.6	0.3
chr4	20180099	20180699	0.1	0.3
chr4	21716175	21716775	0.1	0.2
chr4	22882558	22883158	1.0	0.2
chr4	22971009	22971609	0.3	0.0
chr4	23857180	23857780	0.9	0.2
chr4	25261221	25261821	1.0	0.3
chr4	25482903	25483503	0.6	0.2
chr4	26989873	26990473	0.2	0.1
chr4	27579137	27579737	1.3	0.1
chr4	28081658	28082258	0.8	0.1
chr4	29474092	29474692	0.9	0.1
chr4	29666322	29666922	1.2	0.3
chr4	31820419	31821019	1.5	0.1
chr4	31820428	31821028	1.4	0.1
chr4	31839915	31840515	0.2	0.0
chr4	32134304	32134904	0.8	0.0
chr4	32270657	32271257	1.2	0.0
chr4	32622901	32623501	0.7	0.1
chr4	32747137	32747737	0.8	0.0
chr4	32931688	32932288	2.3	0.1
chr4	33781557	33782157	0.4	0.3
chr4	34244143	34244743	1.3	0.0
chr4	35366642	35367242	2.5	0.9
chr4	35366748	35367348	2.9	1.0
chr4	38446175	38446775	0.4	0.3
chr4	38446319	38446919	0.7	0.3
chr4	38725432	38726032	0.7	0.1
chr4	39302163	39302763	0.2	0.1
chr4	39381294	39381894	1.0	0.2
chr4	40091543	40092143	1.1	0.1
chr4	40362477	40363077	0.5	0.3
chr4	40859073	40859673	1.1	0.1
chr4	40977817	40978417	0.1	0.1
chr4	41130738	41131338	2.1	0.6
chr4	42184500	42185100	1.0	0.1
chr4	42832801	42833401	0.9	0.1
chr4	43144239	43144839	0.7	0.2
chr4	43298045	43298645	0.9	0.1
chr4	44484523	44485123	0.8	0.0
chr4	45059884	45060484	0.4	0.1
chr4	45514326	45514926	0.1	0.1
chr4	45638604	45639204	0.1	0.6
chr4	46158574	46159174	1.1	0.1
chr4	46184392	46184992	0.8	0.1
chr4	46215480	46216080	1.4	0.7
chr4	46224316	46224916	0.7	0.1
chr4	46366244	46366844	0.4	0.3
chr4	46622166	46622766	0.5	0.0
chr4	47298951	47299551	0.9	0.4
chr4	47304122	47304722	0.4	0.0
chr4	47755418	47756018	0.4	0.3
chr4	47839285	47839885	0.4	0.1
chr4	48060827	48061427	0.6	0.2
chr4	49465523	49466123	1.5	0.4
chr4	50031989	50032589	0.1	0.2
chr4	50846863	50847463	0.0	0.2
chr4	52089007	52089607	1.7	0.2
chr4	52337766	52338366	0.0	0.0
chr4	52954070	52954670	0.7	0.1
chr4	53123614	53124214	0.9	0.3

chr4	53696549	53697149	0.6	0.2
chr4	55219073	55219673	0.2	0.5
chr4	55233336	55233936	1.5	0.5
chr4	55319672	55320272	0.0	0.0
chr4	55858950	55859550	0.9	0.1
chr4	56150475	56151075	2.5	0.8
chr4	56150721	56151321	2.3	0.6
chr4	56150751	56151351	2.4	0.6
chr4	56267515	56268115	1.4	0.2
chr4	56396910	56397510	0.8	0.2
chr4	56764638	56765238	0.7	0.0
chr4	56902660	56903260	0.0	0.1
chr4	57262046	57262646	1.0	0.4
chr4	57703574	57704174	0.7	0.4
chr4	57784272	57784872	1.1	0.6
chr4	57784449	57785049	1.6	0.5
chr4	57784492	57785092	1.8	0.6
chr4	57784570	57785170	1.6	0.4
chr4	57784613	57785213	1.8	0.5
chr4	57784704	57785304	2.0	0.6
chr4	57839785	57840385	0.8	0.0
chr4	58128150	58128750	0.6	0.0
chr4	58469843	58470443	0.1	0.1
chr4	58741970	58742570	1.2	0.2
chr4	59007497	59008097	0.9	0.3
chr4	59280893	59281493	0.0	0.1
chr4	59280955	59281555	0.0	0.1
chr4	59297078	59297678	0.5	0.1
chr4	59297229	59297829	0.9	0.1
chr4	59854010	59854610	0.1	0.5
chr4	60206128	60206728	0.5	0.0
chr4	60646006	60646606	1.3	0.2
chr4	61233310	61233910	0.9	0.0
chr4	61939711	61940311	0.4	0.1
chr4	62666048	62666648	0.2	0.2
chr4	62765217	62765817	1.4	0.6
chr4	62765243	62765843	1.7	0.7
chr4	62824329	62824929	0.9	0.4
chr4	62887220	62887820	0.2	0.4
chr4	62960447	62961047	0.9	0.6
chr4	63031496	63032096	0.1	0.0
chr4	63031834	63032434	0.7	0.6
chr4	63080194	63080794	1.3	0.5
chr4	63120147	63120747	2.7	0.6
chr4	63226875	63227475	0.1	0.0
chr4	64408035	64408635	0.7	0.3
chr4	64408281	64408881	0.8	0.5
chr4	64790074	64790674	0.1	0.2
chr4	67004715	67005315	1.2	0.4
chr4	67207598	67208198	0.6	0.4
chr4	67361292	67361892	0.7	0.3
chr4	68077700	68078300	0.2	0.3
chr4	69275957	69276557	1.5	0.0
chr4	70718038	70718638	0.3	0.0
chr4	71146192	71146792	1.1	0.6
chr4	71392497	71393097	0.7	0.1
chr4	71507790	71508390	1.4	0.5
chr4	73854496	73855096	1.2	0.4
chr4	73872452	73873052	0.4	0.2
chr4	73931110	73931710	1.7	0.3
chr4	74354619	74355219	0.8	0.4
chr4	75290269	75290869	1.1	0.3
chr4	75846956	75847556	1.1	0.2
chr4	76577810	76578410	0.5	0.0
chr4	77188584	77189184	0.2	0.2
chr4	77527747	77528347	0.6	0.2
chr4	77718083	77718683	3.0	0.5
chr4	77718163	77718763	2.7	0.6
chr4	78117424	78118024	0.6	0.1
chr4	78132343	78132943	0.8	0.1
chr4	79919995	79920595	1.1	0.3
chr4	81482601	81483201	0.8	0.0
chr4	81724042	81724642	0.9	0.5
chr4	82047609	82048209	1.3	0.1
chr4	82575248	82575848	0.4	0.0
chr4	82666941	82667541	1.0	0.2

chr4	82697121	82697721	0.5	0.1
chr4	82904092	82904692	0.4	0.2
chr4	83435297	83435897	1.0	0.0
chr4	83547390	83547990	0.9	0.1
chr4	83621857	83622457	1.9	0.2
chr4	83735561	83736161	2.4	0.3
chr4	83764112	83764712	1.0	0.0
chr4	83764305	83764905	1.8	0.5
chr4	83764332	83764932	1.9	0.5
chr4	83764464	83765064	1.3	0.1
chr4	83764514	83765114	1.4	0.2
chr4	83940689	83941289	1.1	0.5
chr4	84001236	84001836	0.6	0.2
chr4	84584205	84584805	0.1	0.1
chr4	84704538	84705138	0.5	0.1
chr4	84929883	84930483	1.2	0.8
chr4	84930021	84930621	1.3	0.6
chr4	85339807	85340407	0.1	0.2
chr4	85627155	85627755	1.6	0.4
chr4	85764810	85765410	0.9	0.2
chr4	86294054	86294654	1.7	0.3
chr4	86294091	86294691	1.5	0.3
chr4	86349900	86350500	0.7	0.3
chr4	86797886	86798486	0.5	0.1
chr4	87126401	87127001	1.1	0.2
chr4	87413790	87414390	1.7	1.0
chr4	87489980	87490580	1.5	0.2
chr4	88365718	88366318	0.9	0.1
chr4	89049770	89050370	0.7	0.3
chr4	89049875	89050475	1.1	0.4
chr4	89570124	89570724	0.7	0.4
chr4	90250851	90251451	0.6	0.5
chr4	90250894	90251494	0.3	0.4
chr4	90563100	90563700	0.6	0.2
chr4	90696819	90697419	1.0	0.2
chr4	90696910	90697510	0.5	0.2
chr4	92209328	92209928	0.8	0.1
chr4	92440224	92440824	0.7	0.1

chr4	93887442	93888042	0.3	0.0
chr4	93899332	93899932	0.9	0.0
chr4	94412854	94413454	0.3	0.2
chr4	94412930	94413530	0.5	0.5
chr4	94470389	94470989	0.0	0.2
chr4	94476031	94476631	0.2	0.1
chr4	94486734	94487334	0.2	0.4
chr4	94693844	94694444	0.2	0.2
chr4	94791797	94792397	1.7	1.5
chr4	94791948	94792548	2.0	1.1
chr4	94852699	94853299	1.0	0.1
chr4	95300262	95300862	1.1	0.2
chr4	95496066	95496666	0.1	0.1
chr4	95500258	95500858	0.4	0.1
chr4	95500508	95501108	0.8	0.3
chr4	95773574	95774174	0.2	0.0
chr4	96455148	96455748	0.4	0.4
chr4	97374487	97375087	1.0	0.2
chr4	97506443	97507043	1.2	0.1
chr4	98360594	98361194	1.6	0.4
chr4	98360647	98361247	1.4	0.3
chr4	98490779	98491379	0.8	0.1
chr4	98963409	98964009	0.3	0.6
chr4	99679005	99679605	1.0	0.8
chr4	99679112	99679712	1.4	0.8
chr4	99849125	99849725	0.7	0.2
chr4	99849159	99849759	0.7	0.3
chr4	100519094	100519694	0.6	0.5
chr4	100519158	100519758	1.2	0.6
chr4	101974691	101975291	0.3	0.3
chr4	102111041	102111641	1.2	0.2
chr4	103225551	103226151	0.9	0.0
chr4	103282507	103283107	0.1	0.1
chr4	103301500	103302100	1.0	0.1
chr4	103335002	103335602	0.3	0.1
chr4	103981631	103982231	0.4	0.0
chr4	104151024	104151624	1.0	0.1
chr4	104395764	104396364	1.1	0.3

chr4	104395870	104396470	1.2	0.2
chr4	104553936	104554536	1.3	0.1
chr4	104839622	104840222	0.5	0.1
chr4	104999480	105000080	1.0	0.2
chr4	105745313	105745913	0.4	0.1
chr4	106175181	106175781	0.6	0.0
chr4	106233085	106233685	0.5	0.3
chr4	106233105	106233705	0.5	0.3
chr4	106389449	106390049	0.5	0.3
chr4	106642566	106643166	0.8	0.5
chr4	106882230	106882830	1.9	0.3
chr4	106967380	106967980	1.2	0.3
chr4	106967645	106968245	1.6	0.5
chr4	107178173	107178773	1.7	0.4
chr4	107178195	107178795	1.9	0.5
chr4	108035286	108035886	0.4	0.4
chr4	108035430	108036030	0.5	0.2
chr4	108661949	108662549	5.7	2.3
chr4	108661969	108662569	6.5	2.7
chr4	108661989	108662589	6.8	2.9
chr4	108662009	108662609	7.0	2.9
chr4	108662029	108662629	7.2	2.9
chr4	108722977	108723577	0.7	0.2
chr4	109267089	109267689	0.4	0.0
chr4	109314376	109314976	0.3	0.1
chr4	110038217	110038817	0.1	0.1
chr4	110367175	110367775	1.0	0.3
chr4	111811001	111811601	1.9	0.0
chr4	112625555	112626155	0.1	0.2
chr4	113059581	113060181	0.6	0.4
chr4	113791462	113792062	0.5	0.0
chr4	114439910	114440510	0.6	0.0
chr4	114457068	114457668	0.9	0.1
chr4	114472030	114472630	0.1	0.0
chr4	114494336	114494936	0.6	0.9
chr4	115610255	115610855	0.9	0.1
chr4	115691481	115692081	0.8	0.1
chr4	116260583	116261183	0.9	0.4
chr4	116768218	116768818	2.7	1.3
chr4	116770946	116771546	1.4	0.6
chr4	116976945	116977545	0.1	0.1
chr4	117197335	117197935	2.8	0.9
chr4	117528365	117528965	2.4	0.8
chr4	117528384	117528984	2.7	0.8
chr4	117528502	117529102	1.6	0.2
chr4	117547283	117547883	0.2	0.2
chr4	117547374	117547974	0.2	0.5
chr4	117637123	117637723	1.1	0.2
chr4	117723144	117723744	0.7	0.2
chr4	117826880	117827480	0.8	0.1
chr4	117898843	117899443	0.8	0.5
chr4	118746244	118746844	2.0	0.8
chr4	118958407	118959007	1.0	0.2
chr4	118969264	118969864	0.6	0.6
chr4	118976067	118976667	0.3	0.2
chr4	119376482	119377082	1.1	0.2
chr4	119637752	119638352	1.0	0.5
chr4	119637864	119638464	0.4	0.1
chr4	119694874	119695474	1.1	0.3
chr4	119704980	119705580	0.5	0.3
chr4	119744471	119745071	0.5	0.2
chr4	119763891	119764491	0.3	0.1
chr4	119829746	119830346	0.0	0.5
chr4	119871483	119872083	1.6	1.0
chr4	119871648	119872248	0.7	0.0
chr4	119995985	119996585	0.1	0.2
chr4	120313791	120314391	1.1	0.6
chr4	120321946	120322546	0.8	0.2
chr4	120432033	120432633	1.5	0.5
chr4	120558379	120558979	1.1	0.4
chr4	121172877	121173477	0.1	0.2
chr4	122673972	122674572	1.9	1.0
chr4	122674007	122674607	2.2	0.9
chr4	122843435	122844035	2.3	1.0
chr4	122843617	122844217	2.3	1.2
chr4	122910545	122911145	0.8	0.0

chr4	122924570	122925170	0.9	0.3
chr4	123266151	123266751	0.1	0.0
chr4	123731248	123731848	0.5	0.1
chr4	123825823	123826423	0.7	0.1
chr4	123845369	123845969	0.6	0.0
chr4	124532387	124532987	0.3	0.0
chr4	124854068	124854668	1.2	0.2
chr4	125189929	125190529	1.7	1.0
chr4	125190111	125190711	2.0	1.1
chr4	125221890	125222490	1.0	0.2
chr4	125250309	125250909	0.4	0.4
chr4	125396354	125396954	1.9	0.2
chr4	125437442	125438042	1.5	0.5
chr4	125879826	125880426	1.8	1.0
chr4	127032634	127033234	0.2	0.2
chr4	127072818	127073418	0.2	0.6
chr4	127087650	127088250	0.4	0.2
chr4	127521878	127522478	1.4	0.0
chr4	127671910	127672510	0.3	0.3
chr4	127907047	127907647	0.4	0.1
chr4	128520518	128521118	0.4	0.2
chr4	128789024	128789624	1.2	0.2
chr4	128916913	128917513	0.3	0.0
chr4	129051835	129052435	1.4	0.3
chr4	129052084	129052684	1.0	0.2
chr4	129611639	129612239	1.2	1.0
chr4	130125069	130125669	0.0	0.1
chr4	130384745	130385345	1.4	0.1
chr4	130421682	130422282	1.0	0.1
chr4	130421777	130422377	0.8	0.5
chr4	130839918	130840518	2.1	0.5
chr4	130840099	130840699	2.1	0.6
chr4	130840209	130840809	1.9	0.5
chr4	130936340	130936940	1.0	0.2
chr4	131026004	131026604	2.9	1.5
chr4	131074638	131075238	0.6	0.2
chr4	131236930	131237530	0.2	0.0
chr4	131986849	131987449	0.2	0.0

chr4	132076476	132077076	0.5	0.4
chr4	133165731	133166331	1.5	0.7
chr4	133165924	133166524	1.3	0.2
chr4	133243995	133244595	0.3	0.1
chr4	133606192	133606792	1.7	0.5
chr4	133606429	133607029	1.5	0.6
chr4	133715533	133716133	1.0	0.1
chr4	133808895	133809495	1.0	0.6
chr4	134489703	134490303	0.9	0.3
chr4	134489843	134490443	0.6	0.5
chr4	134534841	134535441	2.0	0.5
chr4	134535096	134535696	2.1	0.4
chr4	134643358	134643958	1.0	0.2
chr4	134655160	134655760	1.7	0.1
chr4	135202236	135202836	0.8	0.1
chr4	135455957	135456557	0.5	0.4
chr4	135607695	135608295	1.2	0.1
chr4	135632973	135633573	0.1	0.3
chr4	135700328	135700928	0.0	0.3
chr4	135700668	135701268	0.1	0.1
chr4	135758353	135758953	2.1	0.3
chr4	135824650	135825250	2.4	0.9
chr4	135824668	135825268	2.4	0.9
chr4	135987032	135987632	0.7	0.4
chr4	136338701	136339301	0.2	0.3
chr4	136408874	136409474	0.3	0.3
chr4	136446011	136446611	0.8	0.5
chr4	136510018	136510618	0.8	0.1
chr4	136809849	136810449	1.1	0.1
chr4	136818487	136819087	0.9	0.1
chr4	136849825	136850425	0.3	0.2
chr4	137156400	137157000	0.6	0.1
chr4	137292094	137292694	1.0	0.4
chr4	137630056	137630656	1.5	0.5
chr4	138249221	138249821	0.1	0.6
chr4	138458391	138458991	0.7	0.3
chr4	139161234	139161834	0.5	0.0
chr4	139239760	139240360	0.7	0.7

chr4	139239794	139240394	0.7	0.6
chr4	139586118	139586718	0.8	0.2
chr4	139586200	139586800	0.9	0.3
chr4	139625217	139625817	1.4	0.3
chr4	139813620	139814220	0.2	0.0
chr4	139945439	139946039	1.2	0.1
chr4	140053758	140054358	1.4	0.6
chr4	140053874	140054474	1.5	0.6
chr4	140097172	140097772	0.4	0.0
chr4	140349413	140350013	1.7	0.2
chr4	140349511	140350111	0.9	0.3
chr4	140488713	140489313	1.5	0.4
chr4	140515210	140515810	2.2	0.9
chr4	140515357	140515957	2.0	0.8
chr4	140702213	140702813	0.9	0.1
chr4	140744376	140744976	0.8	0.2
chr4	141451175	141451775	0.0	0.4
chr4	141473579	141474179	0.8	1.1
chr4	141473598	141474198	1.0	1.1
chr4	141619504	141620104	0.2	0.2
chr4	142022019	142022619	1.1	0.5
chr4	142212396	142212996	1.3	0.0
chr4	142750093	142750693	0.5	0.1
chr4	142943749	142944349	0.6	0.2
chr4	143004235	143004835	0.6	0.1
chr4	143981428	143982028	0.8	0.0
chr4	144737329	144737929	1.0	0.1
chr4	144740087	144740687	0.1	0.3
chr4	144922753	144923353	0.9	0.4
chr4	144922840	144923440	0.8	0.2
chr4	145825690	145826290	1.2	0.0
chr4	146099490	146100090	1.2	0.0
chr4	146371046	146371646	1.2	0.0
chr4	147222129	147222729	2.7	0.2
chr4	147321195	147321795	0.8	0.3
chr4	147340476	147341076	0.0	0.2
chr4	147633755	147634355	0.4	0.1
chr4	147651981	147652581	0.3	0.1

chr4	148051345	148051945	1.7	0.0
chr4	148819832	148820432	1.7	0.7
chr4	148981584	148982184	1.4	1.5
chr4	148981621	148982221	1.5	1.4
chr4	149230678	149231278	0.7	0.0
chr4	149237107	149237707	0.6	0.0
chr4	149254514	149255114	0.5	0.1
chr4	149254533	149255133	0.3	0.0
chr4	149338672	149339272	1.7	0.1
chr4	149565703	149566303	1.9	0.1
chr4	149944788	149945388	1.2	0.2
chr4	149954904	149955504	0.9	0.4
chr4	149954928	149955528	0.7	0.3
chr4	149954952	149955552	1.4	0.7
chr4	149955048	149955648	0.7	0.3
chr4	150031016	150031616	1.1	0.0
chr4	150288239	150288839	1.3	0.5
chr4	150504886	150505486	0.6	0.6
chr4	150504978	150505578	0.6	0.5
chr4	150650615	150651215	0.9	0.2
chr4	150699410	150700010	3.7	0.9
chr4	150699500	150700100	4.0	1.0
chr4	150699575	150700175	4.0	0.9
chr4	151488347	151488947	0.3	0.2
chr4	151635488	151636088	1.6	0.5
chr4	151809297	151809897	0.3	0.6
chr4	152113607	152114207	0.6	0.2
chr4	152136719	152137319	1.8	0.5
chr4	152267362	152267962	10.9	4.9
chr4	152267400	152268000	11.0	4.9
chr4	152267414	152268014	11.2	5.1
chr4	152267442	152268042	11.3	5.0
chr4	152267470	152268070	11.3	5.1
chr4	152267484	152268084	11.5	5.2
chr4	152267498	152268098	11.6	5.3
chr4	152267512	152268112	11.5	5.2
chr4	152267526	152268126	11.8	5.4
chr4	152267540	152268140	11.9	5.5

chr4	152267554	152268154	11.6	5.3
chr4	152267568	152268168	11.5	5.2
chr4	152267582	152268182	11.7	5.3
chr4	152267596	152268196	11.8	5.4
chr4	152267610	152268210	11.7	5.3
chr4	152267638	152268238	11.9	5.4
chr4	152267652	152268252	11.6	5.3
chr4	152267680	152268280	11.3	5.1
chr4	152267694	152268294	11.6	5.3
chr4	152267708	152268308	11.6	5.3
chr4	152267722	152268322	11.5	5.1
chr4	152267736	152268336	12.0	5.4
chr4	152267750	152268350	12.0	5.4
chr4	152267764	152268364	12.0	5.4
chr4	152267778	152268378	11.7	5.2
chr4	152267792	152268392	11.9	5.3
chr4	152267820	152268420	11.6	5.2
chr4	152267834	152268434	11.7	5.2
chr4	152267862	152268462	11.5	5.2
chr4	152267876	152268476	11.4	5.1
chr4	152267890	152268490	11.4	5.2
chr4	152267904	152268504	11.3	5.1
chr4	152267918	152268518	11.2	5.0
chr4	152267932	152268532	11.0	5.0
chr4	152267960	152268560	10.8	4.9
chr4	152267974	152268574	11.2	5.0
chr4	152267988	152268588	11.1	5.1
chr4	152268002	152268602	11.0	5.0
chr4	152268030	152268630	11.0	5.0
chr4	152268044	152268644	10.8	4.9
chr4	152268072	152268672	10.6	4.9
chr4	152268086	152268686	10.4	4.8
chr4	152268100	152268700	10.1	4.7
chr4	152268128	152268728	9.7	4.5
chr4	152271544	152272144	7.2	3.4
chr4	152271586	152272186	7.7	3.7
chr4	152271614	152272214	8.8	4.1
chr4	152271628	152272228	8.6	3.9
chr4	152271642	152272242	8.6	3.9
chr4	152271656	152272256	8.6	4.0
chr4	152271726	152272326	8.5	3.9
chr4	152271828	152272428	9.0	4.3
chr4	152271856	152272456	8.8	4.3
chr4	152271884	152272484	7.9	3.8
chr4	152271898	152272498	8.2	4.0
chr4	152718232	152718832	1.2	0.1
chr4	153256905	153257505	0.1	0.2
chr4	153261184	153261784	1.4	0.2
chr4	153261213	153261813	1.8	0.3
chr4	153261242	153261842	1.8	0.3
chr4	153288505	153289105	1.1	0.4
chr4	153288697	153289297	1.0	0.2
chr4	153307912	153308512	0.0	0.1
chr4	153406617	153407217	1.2	0.5
chr4	153495347	153495947	0.3	0.2
chr4	153524402	153525002	0.6	0.1
chr4	153542541	153543141	0.7	0.0
chr4	153636055	153636655	0.8	0.0
chr4	153713590	153714190	1.1	0.6
chr4	153713840	153714440	1.3	0.7
chr4	153896612	153897212	1.1	0.5
chr4	154328832	154329432	0.0	0.4
chr4	155015864	155016464	0.6	0.0
chr4	155015942	155016542	1.0	0.1
chr4	155016108	155016708	2.1	0.1
chr4	155231902	155232502	1.2	0.2
chr4	155232052	155232652	1.4	0.4
chr4	155252901	155253501	0.9	0.1
chr4	155405172	155405772	1.5	0.3
chr4	155405404	155406004	2.7	0.3
chr5	3305969	3306569	0.6	0.0
chr5	3381202	3381802	0.2	0.0
chr5	3381302	3381902	0.3	0.0
chr5	3857592	3858192	2.0	0.2
chr5	3857611	3858211	2.3	0.4
chr5	3857630	3858230	2.3	0.4

chr5	4636033	4636633	0.2	0.1
chr5	7196044	7196644	1.2	0.4
chr5	7196299	7196899	1.0	0.3
chr5	7987249	7987849	1.1	0.1
chr5	8231745	8232345	1.3	0.3
chr5	8231809	8232409	1.3	0.4
chr5	9575774	9576374	0.0	0.1
chr5	9575813	9576413	0.1	0.1
chr5	9575852	9576452	0.0	0.2
chr5	9575891	9576491	0.1	0.2
chr5	9575930	9576530	0.1	0.2
chr5	9575969	9576569	0.2	0.3
chr5	9576008	9576608	0.1	0.3
chr5	9730822	9731422	1.4	0.6
chr5	9730841	9731441	1.3	0.6
chr5	9770375	9770975	0.7	0.1
chr5	10923768	10924368	0.0	0.0
chr5	11019509	11020109	0.3	0.2
chr5	11107025	11107625	0.0	0.2
chr5	11474347	11474947	0.1	0.1
chr5	11574358	11574958	0.3	0.2
chr5	11661400	11662000	0.0	0.2
chr5	12767204	12767804	2.9	0.9
chr5	12767476	12768076	2.2	0.5
chr5	13114059	13114659	0.3	0.2
chr5	13619250	13619850	0.6	0.0
chr5	14373837	14374437	0.1	0.1
chr5	14373928	14374528	0.7	0.2
chr5	14540139	14540739	0.9	0.1
chr5	15010490	15011090	0.8	0.6
chr5	15010521	15011121	0.8	0.5
chr5	15440088	15440688	0.5	0.2
chr5	15477167	15477767	0.0	0.0
chr5	15629218	15629818	0.2	0.1
chr5	15984980	15985580	1.0	0.1
chr5	17027539	17028139	0.9	0.1
chr5	17255393	17255993	0.1	0.0
chr5	17865259	17865859	0.4	0.0

chr5	18763137	18763737	0.0	0.2
chr5	19128558	19129158	2.2	1.0
chr5	19128600	19129200	2.3	1.0
chr5	19128642	19129242	2.3	1.0
chr5	19128684	19129284	2.2	0.9
chr5	19128726	19129326	2.1	0.9
chr5	19128768	19129368	2.0	0.9
chr5	19128810	19129410	1.9	1.0
chr5	19128852	19129452	1.9	1.0
chr5	19128894	19129494	1.7	1.0
chr5	19128936	19129536	1.6	1.0
chr5	19385645	19386245	0.3	0.0
chr5	19574217	19574817	1.1	0.4
chr5	20621233	20621833	0.8	0.2
chr5	21056506	21057106	0.4	0.1
chr5	21265503	21266103	0.6	0.0
chr5	21394041	21394641	0.8	0.0
chr5	21476252	21476852	1.5	0.0
chr5	22082016	22082616	0.5	0.5
chr5	22082099	22082699	0.4	0.5
chr5	22148195	22148795	0.1	0.5
chr5	22550052	22550652	1.4	0.2
chr5	22957324	22957924	0.2	0.3
chr5	23039667	23040267	0.6	0.2
chr5	23138767	23139367	0.5	0.1
chr5	23420452	23421052	0.7	0.7
chr5	23432931	23433531	0.1	0.2
chr5	23468491	23469091	0.3	0.0
chr5	23603653	23604253	0.6	1.0
chr5	23603671	23604271	0.7	0.9
chr5	23764481	23765081	0.5	0.0
chr5	24141439	24142039	1.6	0.3
chr5	24141714	24142314	1.7	0.5
chr5	24494706	24495306	3.9	1.1
chr5	24494732	24495332	3.5	0.9
chr5	24494758	24495358	3.3	0.9
chr5	24516017	24516617	0.7	0.5
chr5	26601961	26602561	2.4	0.3

chr5	26932717	26933317	0.9	0.0
chr5	27248284	27248884	2.4	1.1
chr5	27248303	27248903	2.1	1.1
chr5	27248322	27248922	2.2	1.2
chr5	27248361	27248961	2.2	1.0
chr5	28832338	28832938	1.5	0.2
chr5	28832509	28833109	1.5	0.2
chr5	28898798	28899398	0.3	0.1
chr5	28898881	28899481	0.5	0.2
chr5	29856712	29857312	0.4	0.3
chr5	30222058	30222658	1.6	0.3
chr5	30222090	30222690	1.5	0.3
chr5	30359992	30360592	1.3	0.3
chr5	30465552	30466152	1.0	0.1
chr5	30611950	30612550	0.7	0.2
chr5	30685079	30685679	0.5	0.2
chr5	30685190	30685790	0.9	0.7
chr5	30772759	30773359	1.1	0.1
chr5	30910482	30911082	0.3	0.1
chr5	31643437	31644037	0.3	0.4
chr5	32626697	32627297	0.2	0.4
chr5	32635840	32636440	1.2	0.0
chr5	33088488	33089088	1.8	0.2
chr5	33145522	33146122	1.5	0.5
chr5	33678559	33679159	0.6	0.2
chr5	33797916	33798516	0.1	0.1
chr5	34049609	34050209	0.6	0.0
chr5	34068683	34069283	0.3	0.2
chr5	34075368	34075968	0.3	0.2
chr5	34354345	34354945	1.4	0.5
chr5	34882877	34883477	1.1	0.0
chr5	35330276	35330876	0.1	0.0
chr5	35818230	35818830	0.1	0.0
chr5	35907133	35907733	1.7	0.8
chr5	35907362	35907962	1.3	0.6
chr5	35937375	35937975	0.3	0.0
chr5	36361727	36362327	1.0	0.1
chr5	36361794	36362394	0.9	0.0
chr5	36365165	36365765	1.2	0.3
chr5	36457726	36458326	0.9	0.1
chr5	36892953	36893553	0.4	0.0
chr5	36968668	36969268	1.2	0.5
chr5	37079766	37080366	0.7	0.3
chr5	38529448	38530048	0.6	0.3
chr5	38541571	38542171	1.5	0.5
chr5	38541797	38542397	0.7	0.7
chr5	38681930	38682530	1.7	0.5
chr5	38856323	38856923	1.1	0.5
chr5	38888282	38888882	0.5	0.2
chr5	38978122	38978722	0.5	0.1
chr5	39154387	39154987	0.2	0.2
chr5	41530638	41531238	0.6	0.2
chr5	43312876	43313476	1.5	0.4
chr5	43386285	43386885	0.5	0.1
chr5	43673917	43674517	0.0	0.1
chr5	44235829	44236429	1.0	0.1
chr5	44361187	44361787	0.8	0.2
chr5	44664408	44665008	0.6	0.1
chr5	44932210	44932810	1.4	0.0
chr5	45907087	45907687	0.3	0.7
chr5	45907324	45907924	1.1	0.4
chr5	46359886	46360486	0.6	0.1
chr5	46597286	46597886	1.7	0.3
chr5	46738406	46739006	0.5	0.0
chr5	47163100	47163700	0.4	0.2
chr5	48638370	48638970	0.6	0.2
chr5	50514058	50514658	1.4	0.5
chr5	52983300	52983900	0.8	0.0
chr5	52983410	52984010	1.2	0.2
chr5	52983464	52984064	1.1	0.3
chr5	52983519	52984119	1.2	0.3
chr5	52983546	52984146	1.3	0.4
chr5	52983574	52984174	1.4	0.4
chr5	52983629	52984229	1.3	0.4
chr5	52983656	52984256	1.6	0.5
chr5	52983683	52984283	1.8	0.6

chr5	52983711	52984311	1.9	0.6
chr5	52983739	52984339	2.0	0.7
chr5	52983767	52984367	2.1	0.8
chr5	52983794	52984394	2.2	0.8
chr5	52983821	52984421	2.3	0.9
chr5	52983849	52984449	2.2	0.8
chr5	52983876	52984476	2.2	0.8
chr5	52983903	52984503	2.3	0.8
chr5	52983931	52984531	2.2	0.8
chr5	52983958	52984558	2.3	0.8
chr5	52983985	52984585	2.3	0.8
chr5	52984013	52984613	2.4	0.8
chr5	52984040	52984640	2.4	0.9
chr5	52984068	52984668	2.3	0.8
chr5	52984095	52984695	2.3	0.9
chr5	52984122	52984722	2.6	1.0
chr5	52984178	52984778	3.0	1.2
chr5	52984206	52984806	3.0	1.1
chr5	52984233	52984833	3.1	1.2
chr5	52984261	52984861	2.9	1.1
chr5	52984288	52984888	2.9	1.2
chr5	52984316	52984916	2.7	1.1
chr5	53329225	53329825	0.8	0.1
chr5	53429601	53430201	0.5	0.0
chr5	54099228	54099828	0.6	0.3
chr5	54152072	54152672	0.6	0.2
chr5	54834890	54835490	0.9	0.0
chr5	56066222	56066822	1.2	0.8
chr5	56066474	56067074	2.4	0.8
chr5	56476728	56477328	0.5	0.1
chr5	58635866	58636466	0.4	0.2
chr5	58849808	58850408	0.4	0.2
chr5	59784836	59785436	0.5	0.1
chr5	59910844	59911444	0.3	0.2
chr5	60236684	60237284	0.3	0.2
chr5	60296474	60297074	0.7	0.0
chr5	60296576	60297176	0.8	0.2
chr5	62587337	62587937	0.9	0.2
chr5	62656092	62656692	0.3	0.1
chr5	63056813	63057413	0.8	0.2
chr5	64032832	64033432	0.2	0.1
chr5	64255660	64256260	0.1	0.1
chr5	64601956	64602556	0.3	0.2
chr5	64852685	64853285	2.6	0.6
chr5	64852717	64853317	2.7	0.5
chr5	64855010	64855610	1.0	0.1
chr5	64855217	64855817	0.6	0.2
chr5	65058784	65059384	0.0	0.2
chr5	65787368	65787968	0.4	0.0
chr5	65812924	65813524	0.1	0.1
chr5	65855780	65856380	2.1	0.5
chr5	66032754	66033354	0.6	0.2
chr5	66032818	66033418	0.3	0.1
chr5	66458089	66458689	1.6	0.5
chr5	66463038	66463638	1.8	0.3
chr5	66531899	66532499	0.0	0.0
chr5	66600703	66601303	0.1	0.1
chr5	67343753	67344353	0.1	0.0
chr5	67380633	67381233	0.1	0.0
chr5	67576024	67576624	0.4	0.1
chr5	67576170	67576770	0.8	0.0
chr5	67889418	67890018	0.4	0.4
chr5	70159753	70160353	0.8	0.3
chr5	70664126	70664726	0.3	0.3
chr5	71722252	71722852	0.2	0.1
chr5	71843733	71844333	0.2	0.0
chr5	71956355	71956955	0.7	0.1
chr5	72122818	72123418	0.4	0.0
chr5	72432845	72433445	0.5	0.0
chr5	72647982	72648582	0.3	0.0
chr5	72653910	72654510	2.1	0.4
chr5	72654178	72654778	1.8	0.4
chr5	72657555	72658155	0.7	0.2
chr5	72813029	72813629	0.1	0.0
chr5	72973168	72973768	1.7	0.0
chr5	73020074	73020674	0.0	0.1

chr5	73055644	73056244	0.5	0.3
chr5	73055655	73056255	0.4	0.2
chr5	73403270	73403870	1.5	0.1
chr5	73715840	73716440	0.5	0.1
chr5	73916716	73917316	1.9	0.1
chr5	73916987	73917587	1.1	0.4
chr5	73954597	73955197	0.5	0.2
chr5	74153523	74154123	0.9	0.1
chr5	74670011	74670611	2.3	0.2
chr5	75102600	75103200	0.4	0.3
chr5	75394852	75395452	1.0	0.4
chr5	75818402	75819002	1.1	0.0
chr5	75818415	75819015	1.2	0.1
chr5	75836850	75837450	1.5	0.1
chr5	76065501	76066101	0.1	0.0
chr5	76105702	76106302	1.1	0.3
chr5	76563299	76563899	0.3	0.1
chr5	76841094	76841694	0.8	0.5
chr5	77110681	77111281	1.5	0.7
chr5	77339699	77340299	1.0	0.1
chr5	77780598	77781198	0.4	0.0
chr5	77798254	77798854	1.4	0.1
chr5	77798469	77799069	1.4	0.1
chr5	78675000	78675600	1.7	0.0
chr5	79064894	79065494	0.6	0.4
chr5	79064925	79065525	0.8	0.3
chr5	81348777	81349377	0.5	0.1
chr5	81584126	81584726	0.1	0.1
chr5	82484773	82485373	0.4	0.0
chr5	83769685	83770285	1.9	0.7
chr5	83769943	83770543	1.3	0.2
chr5	85313253	85313853	0.9	0.0
chr5	85417331	85417931	0.6	0.0
chr5	88436883	88437483	1.8	0.0
chr5	89521396	89521996	1.6	0.5
chr5	89521447	89522047	1.4	0.5
chr5	90312883	90313483	1.2	0.1
chr5	90429056	90429656	0.4	0.2
chr5	91127829	91128429	1.2	0.5
chr5	91670801	91671401	0.5	0.2
chr5	92002452	92003052	0.1	0.1
chr5	92273653	92274253	0.6	0.3
chr5	93522374	93522974	0.5	0.1
chr5	93890812	93891412	0.3	0.4
chr5	96848391	96848991	0.6	0.5
chr5	96888010	96888610	0.2	0.1
chr5	97575997	97576597	0.1	0.2
chr5	97625384	97625984	1.2	0.5
chr5	97625413	97626013	1.4	0.4
chr5	97625442	97626042	1.8	0.4
chr5	97645211	97645811	0.9	0.2
chr5	97808873	97809473	0.8	0.1
chr5	98596350	98596950	0.5	0.6
chr5	98654094	98654694	0.6	0.0
chr5	99080139	99080739	0.8	0.2
chr5	99286414	99287014	2.1	0.6
chr5	99735057	99735657	1.1	0.0
chr5	100011497	100012097	0.5	0.1
chr5	100158544	100159144	1.1	0.1
chr5	100229075	100229675	0.8	0.1
chr5	100372652	100373252	1.6	0.1
chr5	100372750	100373350	1.6	0.1
chr5	100668930	100669530	1.0	0.2
chr5	101107014	101107614	0.1	0.0
chr5	101345345	101345945	0.3	0.1
chr5	101701244	101701844	1.0	0.1
chr5	101950347	101950947	0.9	0.1
chr5	102495984	102496584	0.6	0.1
chr5	102615732	102616332	0.0	0.1
chr5	102808095	102808695	0.1	0.1
chr5	102810100	102810700	0.9	0.7
chr5	102810137	102810737	0.8	0.6
chr5	102810211	102810811	0.7	0.7
chr5	102951494	102952094	1.1	0.1
chr5	103068984	103069584	1.1	0.3
chr5	103716303	103716903	2.0	0.4

chr5	104281922	104282522	0.2	0.1
chr5	104300875	104301475	1.3	0.2
chr5	104490796	104491396	0.8	0.4
chr5	104690738	104691338	1.0	0.6
chr5	105218612	105219212	0.7	0.1
chr5	105218818	105219418	0.8	0.2
chr5	105523597	105524197	0.0	0.1
chr5	106013440	106014040	1.3	0.0
chr5	106511653	106512253	1.4	0.1
chr5	106648505	106649105	0.7	0.4
chr5	106814636	106815236	0.4	0.0
chr5	107506101	107506701	0.4	0.1
chr5	107606043	107606643	0.9	0.1
chr5	107976651	107977251	0.1	0.0
chr5	108732214	108732814	0.6	0.1
chr5	108860647	108861247	0.5	0.3
chr5	109108920	109109520	2.0	0.7
chr5	109108956	109109556	2.3	0.7
chr5	109109081	109109681	1.7	0.7
chr5	109484881	109485481	0.1	0.8
chr5	109719406	109720006	0.4	0.2
chr5	109956522	109957122	0.5	0.2
chr5	110771035	110771635	0.3	0.2
chr5	110804881	110805481	0.4	0.1
chr5	110804892	110805492	0.5	0.1
chr5	111039980	111040580	1.1	0.4
chr5	111040117	111040717	1.1	0.7
chr5	111213612	111214212	0.5	0.1
chr5	111355151	111355751	0.9	0.1
chr5	111476074	111476674	0.6	0.6
chr5	111624836	111625436	0.6	0.3
chr5	111848383	111848983	0.7	0.1
chr5	111856746	111857346	1.6	0.5
chr5	112009740	112010340	0.4	0.1
chr5	112037672	112038272	0.7	0.0
chr5	112060689	112061289	0.3	0.0
chr5	112069067	112069667	0.8	0.0
chr5	112097972	112098572	0.8	0.3
chr5	112098052	112098652	0.8	0.3
chr5	112186331	112186931	1.5	0.2
chr5	112186636	112187236	0.5	0.1
chr5	112289350	112289950	3.4	0.3
chr5	112691271	112691871	0.4	0.2
chr5	112934574	112935174	0.2	0.5
chr5	113170836	113171436	0.5	0.2
chr5	113416142	113416742	0.1	0.0
chr5	113426671	113427271	0.1	0.2
chr5	113878219	113878819	0.0	0.0
chr5	113987236	113987836	1.9	0.1
chr5	113992519	113993119	0.3	0.1
chr5	114091732	114092332	1.3	0.3
chr5	114187517	114188117	0.3	0.4
chr5	114521223	114521823	0.4	0.2
chr5	114521367	114521967	0.8	0.1
chr5	114904077	114904677	0.7	0.0
chr5	114918760	114919360	1.0	0.6
chr5	114918958	114919558	0.3	0.3
chr5	115153220	115153820	0.8	0.1
chr5	115358697	115359297	0.5	0.2
chr5	115611183	115611783	1.3	0.1
chr5	115618391	115618991	1.5	0.2
chr5	115618536	115619136	1.4	0.1
chr5	115750924	115751524	2.6	0.8
chr5	115974894	115975494	0.3	0.1
chr5	116115936	116116536	0.4	0.2
chr5	116246874	116247474	0.1	0.2
chr5	116485188	116485788	1.7	0.2
chr5	116703735	116704335	0.5	0.0
chr5	117109877	117110477	1.1	0.1
chr5	117109897	117110497	1.5	0.1
chr5	117260380	117260980	0.9	0.1
chr5	117260486	117261086	1.0	0.2
chr5	117511149	117511749	0.6	0.1
chr5	118089502	118090102	0.5	0.1
chr5	118350504	118351104	0.5	0.1
chr5	118548186	118548786	0.1	0.4

chr5	118607068	118607668	0.3	0.0
chr5	118607193	118607793	0.4	0.0
chr5	118609369	118609969	0.8	0.0
chr5	118689445	118690045	0.3	0.1
chr5	119106771	119107371	3.2	1.0
chr5	119352286	119352886	0.3	0.2
chr5	119443571	119444171	2.2	0.5
chr5	119443580	119444180	2.2	0.5
chr5	119443589	119444189	2.1	0.5
chr5	119443598	119444198	2.1	0.5
chr5	119443607	119444207	2.1	0.5
chr5	119628525	119629125	0.5	0.1
chr5	119638346	119638946	0.7	0.6
chr5	119717628	119718228	0.4	0.0
chr5	119874518	119875118	1.0	0.1
chr5	119922254	119922854	0.9	0.1
chr5	120010765	120011365	1.2	0.2
chr5	120270882	120271482	0.2	0.3
chr5	120945091	120945691	1.4	0.1
chr5	121020931	121021531	1.7	0.1
chr5	121665153	121665753	0.7	0.2
chr5	121980604	121981204	0.6	0.2
chr5	122534218	122534818	0.5	0.3
chr5	122636567	122637167	1.0	0.2
chr5	122636577	122637177	1.0	0.2
chr5	122707649	122708249	0.7	0.3
chr5	122707661	122708261	0.7	0.3
chr5	122708836	122709436	1.6	0.3
chr5	122708898	122709498	1.7	0.2
chr5	123150731	123151331	0.3	0.0
chr5	123321023	123321623	0.9	0.1
chr5	123581246	123581846	0.6	0.1
chr5	124177870	124178470	0.3	0.0
chr5	124515282	124515882	1.6	1.0
chr5	124626668	124627268	0.4	0.2
chr5	124642799	124643399	0.2	0.2
chr5	125073140	125073740	0.6	0.1
chr5	125657564	125658164	1.5	0.9
chr5	125659570	125660170	1.2	0.8
chr5	125659577	125660177	1.2	0.8
chr5	125674351	125674951	2.0	0.2
chr5	125760416	125761016	0.1	0.1
chr5	126295594	126296194	0.3	0.3
chr5	126508154	126508754	0.8	0.4
chr5	126783378	126783978	0.9	0.5
chr5	127322652	127323252	1.3	0.1
chr5	127322689	127323289	1.4	0.2
chr5	127666364	127666964	0.3	0.0
chr5	127840843	127841443	0.6	0.0
chr5	127852749	127853349	1.4	0.8
chr5	127852845	127853445	1.8	0.7
chr5	128259319	128259919	0.3	0.1
chr5	128364192	128364792	0.7	0.0
chr5	128603442	128604042	1.2	0.3
chr5	128603535	128604135	1.6	0.5
chr5	128603751	128604351	1.5	0.2
chr5	128848349	128848949	1.6	0.2
chr5	128848457	128849057	1.8	0.2
chr5	128962831	128963431	0.0	0.0
chr5	129003694	129004294	1.6	0.2
chr5	129003802	129004402	1.8	0.2
chr5	129047305	129047905	0.5	0.4
chr5	129087215	129087815	1.7	0.5
chr5	129490425	129491025	0.3	0.1
chr5	129627146	129627746	1.1	0.3
chr5	129666471	129667071	0.5	0.1
chr5	129675211	129675811	1.2	0.3
chr5	129709714	129710314	0.0	0.2
chr5	129836937	129837537	0.7	0.1
chr5	129854431	129855031	0.5	0.5
chr5	130408791	130409391	1.2	0.2
chr5	131591359	131591959	0.3	0.2
chr5	132833354	132833954	0.9	0.1
chr5	132976414	132977014	0.3	0.5
chr5	133203928	133204528	0.8	0.1
chr5	133412343	133412943	1.5	0.2

chr5	133526480	133527080	0.8	0.4
chr5	134731017	134731617	0.5	0.0
chr5	134759698	134760298	0.9	0.2
chr5	134921551	134922151	0.8	0.5
chr5	134921698	134922298	0.8	0.7
chr5	134931383	134931983	0.7	0.9
chr5	135262552	135263152	1.3	0.3
chr5	135262763	135263363	1.5	0.1
chr5	135372901	135373501	0.2	0.0
chr5	135392494	135393094	0.3	0.1
chr5	135514921	135515521	1.7	0.4
chr5	136003203	136003803	1.8	0.8
chr5	136136242	136136842	1.6	0.2
chr5	136511097	136511697	0.8	0.2
chr5	136721971	136722571	0.1	0.0
chr5	136858124	136858724	0.5	0.2
chr5	136858189	136858789	1.2	0.3
chr5	137904310	137904910	0.1	0.2
chr5	138416041	138416641	0.2	0.1
chr5	139076441	139077041	0.7	0.0
chr5	139170349	139170949	1.1	0.4
chr5	139639323	139639923	0.6	0.6
chr5	139737378	139737978	0.6	0.1
chr5	140200455	140201055	0.6	0.1
chr5	140345757	140346357	0.4	0.1
chr5	140449475	140450075	0.2	0.1
chr5	140608361	140608961	0.1	0.3
chr5	140608625	140609225	0.9	0.3
chr5	140891664	140892264	1.8	0.4
chr5	141105251	141105851	0.7	0.1
chr5	141133441	141134041	1.4	0.4
chr5	141209347	141209947	1.2	0.5
chr5	141209600	141210200	0.7	0.1
chr5	142888732	142889332	0.6	0.0
chr5	143111112	143111712	0.9	0.1
chr5	143535600	143536200	0.5	0.7
chr5	143970353	143970953	0.5	0.3
chr5	143970430	143971030	0.4	0.0
chr5	144073334	144073934	1.0	0.1
chr5	144119088	144119688	1.7	0.1
chr5	144119175	144119775	1.9	0.2
chr5	144141622	144142222	0.7	0.1
chr5	144510920	144511520	0.6	0.6
chr5	144755014	144755614	0.4	0.4
chr5	144885623	144886223	0.3	0.1
chr5	144885912	144886512	0.6	0.4
chr5	144982057	144982657	0.1	0.0
chr5	145149601	145150201	0.3	0.2
chr5	145266879	145267479	0.2	0.1
chr5	145546372	145546972	0.6	0.1
chr5	146021231	146021831	0.7	0.0
chr5	146103504	146104104	0.5	0.6
chr5	146181923	146182523	0.1	0.1
chr5	146891727	146892327	0.2	0.0
chr5	147024396	147024996	0.1	0.0
chr5	147689587	147690187	0.0	0.6
chr5	148116490	148117090	0.3	0.2
chr5	148367557	148368157	0.4	0.0
chr5	148445305	148445905	1.8	0.6
chr5	148445406	148446006	1.3	0.3
chr5	148467748	148468348	1.1	0.1
chr5	148672085	148672685	0.1	0.2
chr5	149043693	149044293	0.6	0.2
chr5	149265424	149266024	0.2	0.5
chr5	149401462	149402062	0.9	0.1
chr5	149402722	149403322	0.9	0.2
chr5	149442851	149443451	1.5	0.2
chr5	149443835	149444435	1.5	0.4
chr5	149501634	149502234	0.6	0.3
chr5	149725285	149725885	3.7	1.7
chr5	149826076	149826676	0.1	0.0
chr5	150040059	150040659	2.0	0.6
chr5	150040287	150040887	1.8	0.6
chr5	150169621	150170221	0.2	0.0
chr5	150397015	150397615	0.4	0.6
chr5	150397143	150397743	0.5	1.0

chr5	150471540	150472140	1.3	0.9
chr5	150471777	150472377	1.0	0.6
chr5	150620224	150620824	1.8	0.5
chr5	150968318	150968918	1.5	0.5
chr5	151792542	151793142	0.5	0.0
chr5	151802840	151803440	0.9	0.3
chr5	151938329	151938929	1.3	0.1
chr5	152336905	152337505	0.8	0.4
chr5	152410337	152410937	0.3	0.1
chr6	3128179	3128779	0.7	0.0
chr6	3384851	3385451	0.2	0.1
chr6	3611688	3612288	0.3	0.1
chr6	3858412	3859012	0.2	0.3
chr6	4372222	4372822	1.6	0.7
chr6	4372472	4373072	0.5	0.2
chr6	4775420	4776020	1.7	0.5
chr6	5395533	5396133	1.0	0.1
chr6	5623949	5624549	1.0	0.2
chr6	5660580	5661180	0.3	0.0
chr6	5866681	5867281	0.7	0.5
chr6	6729240	6729840	0.1	0.2
chr6	6971871	6972471	1.6	0.2
chr6	7186588	7187188	0.5	0.0
chr6	8068880	8069480	1.3	0.4
chr6	8381936	8382536	1.2	0.4
chr6	8447090	8447690	0.2	0.3
chr6	8763888	8764488	0.7	0.0
chr6	8952544	8953144	0.9	0.4
chr6	10812691	10813291	1.2	0.1
chr6	11803556	11804156	0.2	0.5
chr6	11829769	11830369	0.2	0.5
chr6	13071764	13072364	0.6	0.2
chr6	14433413	14434013	0.9	0.0
chr6	14614993	14615593	0.0	0.1
chr6	14960338	14960938	0.4	0.1
chr6	15810202	15810802	0.9	0.1
chr6	16814261	16814861	0.2	0.0
chr6	16827770	16828370	2.0	0.5

chr6	16828028	16828628	1.0	0.5
chr6	17525320	17525920	1.3	0.6
chr6	17525360	17525960	1.5	0.5
chr6	17632836	17633436	0.0	0.1
chr6	18698872	18699472	0.8	0.3
chr6	19317353	19317953	1.1	0.1
chr6	20591800	20592400	1.0	0.1
chr6	21163582	21164182	0.6	0.3
chr6	21164654	21165254	0.8	0.8
chr6	22092727	22093327	0.1	0.1
chr6	22329136	22329736	1.1	0.0
chr6	23831893	23832493	0.9	0.5
chr6	24107155	24107755	0.5	0.5
chr6	24925893	24926493	0.3	0.2
chr6	24928421	24929021	0.5	0.3
chr6	24928564	24929164	1.3	0.5
chr6	25627038	25627638	1.5	0.2
chr6	27991113	27991713	0.4	0.0
chr6	27991216	27991816	0.2	0.1
chr6	28267798	28268398	0.4	0.1
chr6	28372961	28373561	0.2	0.1
chr6	28678476	28679076	1.5	0.7
chr6	28836711	28837311	0.1	0.0
chr6	28906647	28907247	0.1	0.1
chr6	28993762	28994362	0.7	0.2
chr6	29343645	29344245	1.4	0.2
chr6	29495883	29496483	0.5	0.1
chr6	29668777	29669377	1.0	0.6
chr6	29738612	29739212	0.1	0.1
chr6	30107018	30107618	1.0	0.2
chr6	30539727	30540327	0.6	0.2
chr6	30980656	30981256	1.2	0.2
chr6	31096667	31097267	1.4	0.3
chr6	31102482	31103082	1.3	0.1
chr6	31102732	31103332	1.0	0.3
chr6	31988599	31989199	0.9	0.2
chr6	32089966	32090566	0.7	0.4
chr6	32359220	32359820	0.7	0.1

chr6	32660255	32660855	0.2	0.0
chr6	33144930	33145530	0.3	0.2
chr6	33805371	33805971	0.7	0.2
chr6	34570246	34570846	0.8	0.2
chr6	34700870	34701470	2.3	1.0
chr6	34701140	34701740	2.1	0.8
chr6	35577175	35577775	0.3	0.1
chr6	37077060	37077660	0.9	0.3
chr6	37342155	37342755	1.1	0.1
chr6	37471660	37472260	0.2	0.1
chr6	37540546	37541146	1.0	0.3
chr6	37626081	37626681	0.4	0.3
chr6	37626097	37626697	0.4	0.2
chr6	37723519	37724119	0.9	0.1
chr6	37910713	37911313	1.3	0.4
chr6	38484731	38485331	0.5	0.1
chr6	38590135	38590735	0.8	0.0
chr6	38602442	38603042	1.3	0.3
chr6	38602463	38603063	1.2	0.2
chr6	38613966	38614566	0.3	0.4
chr6	38758521	38759121	0.0	0.2
chr6	39347744	39348344	0.4	0.2
chr6	40267019	40267619	0.0	0.1
chr6	40332250	40332850	0.1	0.0
chr6	40375842	40376442	0.6	0.1
chr6	40430293	40430893	0.3	0.2
chr6	40795540	40796140	0.6	0.3
chr6	40990996	40991596	0.4	0.0
chr6	41048161	41048761	0.8	0.0
chr6	41275843	41276443	1.7	0.5
chr6	41276069	41276669	0.0	0.2
chr6	41609218	41609818	0.4	0.3
chr6	41900444	41901044	0.6	0.1
chr6	42146699	42147299	1.5	0.0
chr6	42307707	42308307	0.5	0.0
chr6	43317731	43318331	1.0	0.0
chr6	43339070	43339670	0.1	0.1
chr6	43877874	43878474	0.4	0.2
chr6	43877935	43878535	0.5	0.2
chr6	44727360	44727960	0.9	0.0
chr6	45181341	45181941	0.2	0.0
chr6	47600702	47601302	0.7	0.5
chr6	47600952	47601552	0.9	0.7
chr6	48538491	48539091	1.6	0.4
chr6	48671382	48671982	0.4	0.1
chr6	48916329	48916929	0.4	0.2
chr6	49032349	49032949	0.7	0.4
chr6	49239289	49239889	1.7	0.4
chr6	49719198	49719798	1.6	0.6
chr6	49719493	49720093	0.1	0.4
chr6	50179696	50180296	0.2	0.7
chr6	50209897	50210497	1.5	0.1
chr6	50209927	50210527	1.5	0.1
chr6	50741590	50742190	1.4	0.2
chr6	50741674	50742274	1.4	0.3
chr6	50741698	50742298	1.4	0.4
chr6	50741722	50742322	1.4	0.3
chr6	50741770	50742370	1.3	0.3
chr6	50741818	50742418	1.1	0.3
chr6	50741842	50742442	1.0	0.2
chr6	50936358	50936958	0.7	0.2
chr6	51010343	51010943	1.4	0.7
chr6	51569410	51570010	0.2	0.2
chr6	51961726	51962326	1.1	0.2
chr6	52168240	52168840	0.8	0.3
chr6	52168319	52168919	1.4	0.4
chr6	53828610	53829210	0.5	0.3
chr6	53923585	53924185	0.4	0.0
chr6	53923650	53924250	0.3	0.0
chr6	54818269	54818869	0.4	0.1
chr6	55116144	55116744	1.5	0.3
chr6	55234058	55234658	0.4	0.0
chr6	55324004	55324604	0.4	0.1
chr6	55324024	55324624	0.2	0.0
chr6	55774113	55774713	0.8	0.2
chr6	56076413	56077013	1.1	0.1

chr6	56217626	56218226	0.9	0.2
chr6	56514703	56515303	1.1	0.1
chr6	56839416	56840016	0.6	0.0
chr6	57134890	57135490	0.3	0.0
chr6	57914123	57914723	1.3	0.0
chr6	58364093	58364693	1.2	0.1
chr6	58862058	58862658	0.1	0.3
chr6	58966131	58966731	2.2	1.2
chr6	58966215	58966815	1.7	1.0
chr6	58966243	58966843	1.6	0.9
chr6	58966355	58966955	1.7	1.0
chr6	58966411	58967011	1.8	1.1
chr6	59135730	59136330	1.4	0.2
chr6	59135775	59136375	1.0	0.3
chr6	62292629	62293229	1.6	0.2
chr6	62557419	62558019	1.2	0.3
chr6	63314857	63315457	1.3	0.3
chr6	63879161	63879761	0.6	0.1
chr6	64801711	64802311	0.6	0.4
chr6	65078233	65078833	0.8	0.1
chr6	65622400	65623000	2.6	0.7
chr6	66477976	66478576	2.1	0.2
chr6	66478030	66478630	2.6	0.5
chr6	66986261	66986861	1.0	0.9
chr6	67155790	67156390	1.0	0.0
chr6	67832444	67833044	0.6	0.2
chr6	67832593	67833193	0.3	0.3
chr6	67981943	67982543	2.3	0.2
chr6	67981986	67982586	1.9	0.2
chr6	68874795	68875395	0.6	0.5
chr6	70045165	70045765	1.0	0.1
chr6	70994018	70994618	2.0	0.7
chr6	70994027	70994627	1.9	0.7
chr6	70994036	70994636	2.0	0.7
chr6	71032063	71032663	0.9	0.6
chr6	71032109	71032709	0.9	0.4
chr6	71861485	71862085	0.2	0.1
chr6	72168330	72168930	2.0	0.5

chr6	72184039	72184639	1.3	0.1
chr6	72198525	72199125	0.9	0.6
chr6	72504895	72505495	0.7	0.3
chr6	73105496	73106096	1.1	0.1
chr6	73494294	73494894	0.2	0.5
chr6	73847147	73847747	0.7	0.1
chr6	75191540	75192140	0.4	0.1
chr6	76448504	76449104	0.9	0.4
chr6	76448760	76449360	0.7	0.2
chr6	77138387	77138987	0.2	0.4
chr6	78015669	78016269	1.0	0.1
chr6	78442455	78443055	0.4	0.5
chr6	78662763	78663363	0.0	0.2
chr6	78663010	78663610	0.1	0.1
chr6	79456901	79457501	0.2	0.0
chr6	81293406	81294006	0.8	0.2
chr6	82062336	82062936	1.0	0.3
chr6	82683521	82684121	0.2	0.0
chr6	82687112	82687712	1.0	0.8
chr6	82688288	82688888	1.4	0.3
chr6	82792502	82793102	1.7	0.2
chr6	82993409	82994009	1.3	0.3
chr6	83717628	83718228	1.4	0.1
chr6	83754173	83754773	1.0	0.1
chr6	83754201	83754801	1.3	0.3
chr6	84149644	84150244	0.8	0.2
chr6	84565109	84565709	0.4	0.6
chr6	84565368	84565968	0.9	0.4
chr6	85146722	85147322	0.3	0.0
chr6	85916463	85917063	0.6	0.0
chr6	86119625	86120225	1.2	0.1
chr6	86530166	86530766	1.3	0.7
chr6	86530327	86530927	0.9	0.7
chr6	86530385	86530985	1.2	0.6
chr6	86611475	86612075	0.8	0.2
chr6	86638522	86639122	0.7	0.1
chr6	86779373	86779973	0.2	0.0
chr6	87233748	87234348	0.0	0.6

chr6	87294879	87295479	0.6	0.2
chr6	87295156	87295756	0.6	0.2
chr6	88073576	88074176	1.6	0.1
chr6	88073646	88074246	1.1	0.0
chr6	88150499	88151099	0.4	0.3
chr6	88185062	88185662	0.8	0.6
chr6	88430583	88431183	0.9	0.8
chr6	88771451	88772051	1.2	0.2
chr6	88776373	88776973	0.4	0.5
chr6	88823166	88823766	1.5	0.0
chr6	90049492	90050092	1.7	0.6
chr6	90049583	90050183	1.3	0.6
chr6	90157817	90158417	2.8	0.5
chr6	90687215	90687815	0.7	0.1
chr6	90736938	90737538	0.4	0.0
chr6	91284568	91285168	0.3	0.2
chr6	91685346	91685946	0.1	0.3
chr6	92502311	92502911	1.5	0.1
chr6	92546538	92547138	1.0	0.0
chr6	92671084	92671684	2.3	0.5
chr6	92852946	92853546	0.0	0.3
chr6	92890877	92891477	1.2	0.0
chr6	92942427	92943027	0.2	0.4
chr6	93026435	93027035	1.3	0.3
chr6	93109128	93109728	1.0	0.2
chr6	93124539	93125139	0.9	0.1
chr6	93891381	93891981	0.5	0.1
chr6	94000065	94000665	1.7	0.9
chr6	94000125	94000725	1.9	0.9
chr6	94000245	94000845	2.2	0.8
chr6	94113177	94113777	0.7	0.2
chr6	94196906	94197506	0.1	0.1
chr6	94419825	94420425	0.3	0.2
chr6	94567327	94567927	0.4	0.4
chr6	94838882	94839482	2.3	0.5
chr6	94838928	94839528	1.8	0.4
chr6	95886961	95887561	0.8	0.0
chr6	95993290	95993890	0.6	0.1
chr6	96189923	96190523	0.6	0.1
chr6	96231264	96231864	0.8	0.0
chr6	97415174	97415774	1.0	1.1
chr6	97415344	97415944	1.1	1.1
chr6	97471202	97471802	2.4	0.6
chr6	97471307	97471907	2.6	0.6
chr6	97616675	97617275	1.6	0.6
chr6	97674098	97674698	0.4	0.2
chr6	98245002	98245602	0.6	0.2
chr6	98292407	98293007	0.0	0.0
chr6	98326400	98327000	0.8	0.2
chr6	98851534	98852134	0.7	0.1
chr6	99402060	99402660	0.5	0.1
chr6	99437393	99437993	0.1	0.2
chr6	99581833	99582433	2.0	0.2
chr6	99581858	99582458	1.8	0.2
chr6	99841295	99841895	1.0	0.2
chr6	100159216	100159816	0.9	0.0
chr6	100205422	100206022	1.4	0.5
chr6	100205615	100206215	1.4	0.9
chr6	101234253	101234853	1.7	0.4
chr6	101458141	101458741	0.7	0.2
chr6	101798733	101799333	4.0	1.4
chr6	101798755	101799355	4.2	1.5
chr6	101798777	101799377	4.1	1.5
chr6	102049855	102050455	1.1	0.4
chr6	102050058	102050658	1.5	0.4
chr6	102058315	102058915	0.8	0.2
chr6	103542462	103543062	2.2	0.5
chr6	103784583	103785183	0.2	0.1
chr6	103996069	103996669	1.3	0.3
chr6	104048822	104049422	0.4	0.0
chr6	104386955	104387555	1.6	0.6
chr6	104387223	104387823	1.5	0.4
chr6	104809973	104810573	0.2	0.0
chr6	104830227	104830827	0.4	0.3
chr6	105437253	105437853	0.9	0.2
chr6	105599132	105599732	1.7	0.7

chr6	105599388	105599988	1.3	0.5
chr6	106294695	106295295	0.6	0.4
chr6	106380339	106380939	0.5	0.4
chr6	106549414	106550014	0.9	0.1
chr6	106566182	106566782	0.1	0.1
chr6	106663946	106664546	0.4	0.2
chr6	106914533	106915133	0.7	0.1
chr6	107173937	107174537	0.1	0.2
chr6	108238956	108239556	0.8	0.0
chr6	108263276	108263876	0.8	0.1
chr6	108412679	108413279	1.6	0.2
chr6	108640955	108641555	1.0	0.1
chr6	108659717	108660317	1.5	1.0
chr6	108953222	108953822	1.9	0.7
chr6	109208286	109208886	0.9	0.2
chr6	111090786	111091386	0.2	0.1
chr6	112460084	112460684	0.9	0.2
chr6	112463013	112463613	0.1	0.2
chr6	112492484	112493084	0.9	0.3
chr6	112728565	112729165	0.4	0.1
chr6	112906001	112906601	0.2	0.2
chr6	113207630	113208230	0.7	0.2
chr6	113481131	113481731	0.7	0.5
chr6	113550605	113551205	0.1	0.3
chr6	113957642	113958242	0.5	0.1
chr6	114107248	114107848	0.4	0.3
chr6	114107258	114107858	0.4	0.4
chr6	114382403	114383003	1.8	0.4
chr6	114382433	114383033	2.0	0.5
chr6	114382537	114383137	2.5	0.8
chr6	115069831	115070431	0.5	0.1
chr6	116190801	116191401	1.7	0.4
chr6	116190950	116191550	2.2	0.9
chr6	116496938	116497538	0.2	0.5
chr6	116556640	116557240	0.9	0.3
chr6	116556795	116557395	1.1	0.1
chr6	116625867	116626467	0.5	0.3
chr6	116935203	116935803	1.3	0.2

chr6	117153529	117154129	1.2	0.1
chr6	117360938	117361538	0.5	0.0
chr6	117421085	117421685	0.9	0.3
chr6	117775255	117775855	0.5	0.1
chr6	118117928	118118528	1.6	0.2
chr6	118136745	118137345	1.4	0.6
chr6	118526760	118527360	0.7	0.1
chr6	118906672	118907272	0.5	0.2
chr6	118962086	118962686	0.1	0.0
chr6	119044526	119045126	0.4	0.0
chr6	119139253	119139853	0.7	0.1
chr6	119323096	119323696	0.6	0.0
chr6	119439680	119440280	1.2	0.2
chr6	120137127	120137727	2.4	0.2
chr6	120137215	120137815	2.5	0.1
chr6	120144488	120145088	0.3	0.2
chr6	120343094	120343694	1.0	0.0
chr6	120772423	120773023	0.6	0.1
chr6	121127573	121128173	2.1	0.5
chr6	121296553	121297153	0.4	0.0
chr6	121911845	121912445	1.3	0.0
chr6	122850886	122851486	0.7	0.3
chr6	123923266	123923866	0.4	0.0
chr6	124184044	124184644	0.0	0.3
chr6	124288495	124289095	0.0	0.2
chr6	124445495	124446095	0.8	0.0
chr6	124687391	124687991	1.2	0.1
chr6	125169250	125169850	0.1	0.3
chr6	125244920	125245520	0.9	0.2
chr6	125383209	125383809	0.8	0.3
chr6	126080455	126081055	1.0	0.1
chr6	127298986	127299586	0.8	0.6
chr6	127299111	127299711	1.3	0.6
chr6	127822885	127823485	1.3	0.3
chr6	127860501	127861101	1.0	0.3
chr6	127860748	127861348	0.7	0.2
chr6	127937134	127937734	0.2	0.3
chr6	129021350	129021950	0.2	0.0

chr6	129542676	129543276	0.6	0.3
chr6	129709069	129709669	0.3	0.5
chr6	129709131	129709731	0.5	0.2
chr6	131206864	131207464	0.0	0.1
chr6	131358365	131358965	0.5	0.2
chr6	131820457	131821057	0.4	0.5
chr6	131943577	131944177	0.2	0.2
chr6	132005625	132006225	2.1	0.2
chr6	132064879	132065479	1.7	0.2
chr6	132064897	132065497	1.8	0.2
chr6	132261849	132262449	3.3	0.8
chr6	132262053	132262653	2.6	0.5
chr6	132262071	132262671	2.5	0.5
chr6	132262107	132262707	2.7	0.5
chr6	132311429	132312029	1.5	0.1
chr6	132311447	132312047	1.8	0.3
chr6	132388384	132388984	1.1	0.1
chr6	132729247	132729847	0.7	0.2
chr6	133231351	133231951	1.1	0.0
chr6	134844555	134845155	0.6	0.3
chr6	135718343	135718943	1.6	0.0
chr6	135762167	135762767	0.7	0.1
chr6	135923315	135923915	0.4	0.2
chr6	136088057	136088657	0.9	0.2
chr6	136207876	136208476	1.0	0.0
chr6	136408095	136408695	0.5	0.0
chr6	136441917	136442517	0.8	0.2
chr6	136442056	136442656	0.9	0.0
chr6	137292074	137292674	1.5	0.3
chr6	137604438	137605038	1.2	0.3
chr6	138023801	138024401	1.3	0.2
chr6	140091125	140091725	0.0	0.0
chr6	140145975	140146575	2.9	0.1
chr6	140146019	140146619	3.0	0.2
chr6	140146063	140146663	2.9	0.2
chr6	140146107	140146707	3.0	0.2
chr6	140146151	140146751	3.1	0.2
chr6	140146195	140146795	3.0	0.1
chr6	140298654	140299254	0.3	0.2
chr6	140505532	140506132	0.2	0.3
chr6	140984164	140984764	0.7	0.2
chr6	141176394	141176994	0.5	0.2
chr6	141797615	141798215	1.4	0.1
chr6	141823790	141824390	1.2	0.5
chr6	142123102	142123702	0.1	0.3
chr6	142682230	142682830	1.5	0.4
chr6	142682262	142682862	1.5	0.3
chr6	142682446	142683046	1.9	0.7
chr6	143352949	143353549	1.1	0.5
chr6	143373630	143374230	0.7	0.8
chr6	143435867	143436467	1.5	0.4
chr6	143561604	143562204	1.8	0.2
chr6	143561623	143562223	1.9	0.1
chr6	143746827	143747427	0.6	0.0
chr6	144098220	144098820	0.8	0.1
chr6	144483523	144484123	7.5	3.4
chr6	144483539	144484139	7.7	3.5
chr6	144483571	144484171	7.6	3.4
chr6	144483615	144484215	7.6	3.5
chr6	144483631	144484231	7.4	3.3
chr6	144483754	144484354	7.5	3.3
chr6	144483879	144484479	6.0	2.6
chr6	145081153	145081753	1.4	0.6
chr6	145081204	145081804	1.4	0.6
chr6	145081255	145081855	1.3	0.6
chr6	145081306	145081906	1.5	0.6
chr6	145081357	145081957	1.4	0.6
chr6	145081408	145082008	1.7	0.7
chr6	145124940	145125540	1.0	0.3
chr6	145258985	145259585	0.5	0.5
chr6	145900081	145900681	0.6	0.7
chr6	145946713	145947313	1.3	0.0
chr6	146206245	146206845	0.3	0.2
chr6	146229252	146229852	0.9	0.1
chr6	146459948	146460548	1.0	0.1
chr6	146753205	146753805	0.8	0.3

chr6	147401960	147402560	0.1	0.1
chr6	147523392	147523992	1.1	0.6
chr6	147606015	147606615	0.5	0.0
chr6	147746788	147747388	0.9	0.1
chr6	147954852	147955452	0.2	0.2
chr6	148310538	148311138	1.5	0.3
chr6	148336417	148337017	1.5	0.2
chr6	148919963	148920563	0.2	0.3
chr7	3120923	3121523	0.4	0.4
chr7	3240357	3240957	0.9	0.0
chr7	3425923	3426523	0.8	0.2
chr7	3672823	3673423	0.0	0.1
chr7	3724445	3725045	0.2	0.3
chr7	3778138	3778738	0.0	0.1
chr7	4433933	4434533	0.6	0.0
chr7	4729658	4730258	1.1	0.1
chr7	4966910	4967510	0.5	0.1
chr7	5104385	5104985	0.6	0.1
chr7	5940962	5941562	0.0	0.0
chr7	6494268	6494868	0.5	0.1
chr7	6537017	6537617	1.1	0.0
chr7	6537856	6538456	1.6	0.4
chr7	6538116	6538716	2.0	0.3
chr7	6600732	6601332	0.5	0.3
chr7	6652970	6653570	3.5	1.0
chr7	6653106	6653706	2.2	0.2
chr7	6778387	6778987	0.2	0.2
chr7	6878687	6879287	1.0	0.6
chr7	7048615	7049215	1.0	0.1
chr7	7048764	7049364	0.8	0.1
chr7	7166660	7167260	0.0	0.0
chr7	7188651	7189251	0.1	0.2
chr7	7341341	7341941	0.7	0.3
chr7	7341432	7342032	0.9	0.3
chr7	7498274	7498874	1.0	0.2
chr7	7498284	7498884	1.1	0.1
chr7	7508329	7508929	0.5	0.6
chr7	7508420	7509020	0.9	0.6
chr7	7800227	7800827	0.6	0.4
chr7	7800318	7800918	0.9	0.5
chr7	8034229	8034829	0.6	0.5
chr7	8034320	8034920	0.8	0.5
chr7	8611529	8612129	0.8	0.5
chr7	8611620	8612220	0.6	0.3
chr7	8799052	8799652	0.7	0.5
chr7	8799143	8799743	0.5	0.3
chr7	8995673	8996273	0.5	0.4
chr7	8995764	8996364	0.2	0.5
chr7	9090541	9091141	1.0	0.6
chr7	9090632	9091232	0.7	0.6
chr7	9107797	9108397	1.1	0.1
chr7	9107807	9108407	1.1	0.2
chr7	9754520	9755120	1.0	0.5
chr7	9754611	9755211	0.7	0.4
chr7	9764678	9765278	0.6	0.1
chr7	9817755	9818355	0.4	0.3
chr7	9817846	9818446	0.4	0.3
chr7	9833367	9833967	0.4	0.1
chr7	10232589	10233189	0.5	0.3
chr7	10232680	10233280	0.8	0.5
chr7	10869452	10870052	0.1	0.3
chr7	11365671	11366271	1.0	0.5
chr7	11470208	11470808	0.2	0.0
chr7	11605475	11606075	0.4	0.3
chr7	11632797	11633397	0.5	0.3
chr7	11997679	11998279	0.4	0.2
chr7	12114052	12114652	0.4	0.2
chr7	12997130	12997730	0.7	0.2
chr7	13193823	13194423	0.6	0.3
chr7	13793065	13793665	1.1	0.3
chr7	14459509	14460109	0.3	0.5
chr7	14620177	14620777	1.2	0.2
chr7	14941700	14942300	0.7	0.3
chr7	17266513	17267113	0.1	0.4
chr7	17326474	17327074	1.3	0.4
chr7	17326499	17327099	1.4	0.4

chr7	17438393	17438993	4.0	1.2
chr7	17438504	17439104	3.7	1.2
chr7	17438569	17439169	3.3	1.1
chr7	17785736	17786336	0.8	0.5
chr7	19720256	19720856	0.2	0.1
chr7	19826134	19826734	1.2	0.1
chr7	19930710	19931310	1.3	0.5
chr7	19993312	19993912	0.5	0.2
chr7	20160237	20160837	0.1	0.0
chr7	20249423	20250023	1.2	0.3
chr7	20283560	20284160	1.0	0.4
chr7	20286670	20287270	0.2	0.2
chr7	24095206	24095806	1.2	0.5
chr7	24429118	24429718	0.3	0.3
chr7	24462539	24463139	0.8	0.1
chr7	24511628	24512228	0.3	0.1
chr7	24792991	24793591	0.1	0.1
chr7	25022873	25023473	0.1	0.0
chr7	25247869	25248469	1.4	0.2
chr7	25631570	25632170	1.1	0.3
chr7	25864974	25865574	0.6	0.0
chr7	25865199	25865799	1.2	0.4
chr7	25999340	25999940	0.8	0.2
chr7	26082655	26083255	0.8	0.2
chr7	26115600	26116200	0.2	0.1
chr7	26115658	26116258	0.3	0.1
chr7	26183084	26183684	1.0	0.1
chr7	26464092	26464692	1.7	0.5
chr7	26473265	26473865	1.3	0.3
chr7	26492426	26493026	1.6	0.1
chr7	26492707	26493307	1.2	0.2
chr7	26624000	26624600	0.4	0.3
chr7	27959342	27959942	0.2	0.5
chr7	27987197	27987797	0.7	0.3
chr7	28067270	28067870	0.3	0.1
chr7	28360398	28360998	1.3	0.0
chr7	28880674	28881274	1.5	0.6
chr7	28880708	28881308	1.5	0.6
chr7	28880742	28881342	1.7	0.6
chr7	28880776	28881376	1.8	0.7
chr7	28880810	28881410	1.9	0.7
chr7	28880844	28881444	1.9	0.7
chr7	28880878	28881478	1.9	0.7
chr7	28880912	28881512	1.9	0.7
chr7	28880946	28881546	2.0	0.7
chr7	28880980	28881580	2.0	0.7
chr7	28881014	28881614	1.8	0.6
chr7	28881048	28881648	1.8	0.6
chr7	28881082	28881682	1.8	0.6
chr7	28881116	28881716	1.9	0.6
chr7	28881150	28881750	1.9	0.6
chr7	28881184	28881784	2.0	0.6
chr7	28881218	28881818	2.0	0.6
chr7	28881252	28881852	2.0	0.6
chr7	28881320	28881920	2.0	0.6
chr7	28881354	28881954	2.0	0.6
chr7	28881388	28881988	1.8	0.6
chr7	28881422	28882022	1.8	0.6
chr7	28881456	28882056	1.8	0.6
chr7	28881490	28882090	1.8	0.6
chr7	28881524	28882124	1.8	0.6
chr7	28881558	28882158	1.8	0.6
chr7	28881592	28882192	2.0	0.7
chr7	28881626	28882226	2.0	0.6
chr7	28881657	28882257	2.0	0.6
chr7	28881691	28882291	2.0	0.6
chr7	28881725	28882325	1.9	0.6
chr7	28881759	28882359	1.9	0.6
chr7	28881793	28882393	1.8	0.6
chr7	28881827	28882427	1.8	0.6
chr7	28881861	28882461	1.8	0.6
chr7	28881895	28882495	1.8	0.6
chr7	28881933	28882533	1.9	0.6
chr7	28881967	28882567	1.9	0.6
chr7	28882001	28882601	1.9	0.6
chr7	28882039	28882639	1.9	0.6

chr7	28882073	28882673	1.9	0.6
chr7	28882107	28882707	1.9	0.6
chr7	28882138	28882738	2.0	0.6
chr7	28882172	28882772	2.0	0.7
chr7	28882206	28882806	2.0	0.7
chr7	28882240	28882840	1.9	0.7
chr7	28882274	28882874	1.9	0.7
chr7	28882308	28882908	1.9	0.7
chr7	28882342	28882942	1.9	0.7
chr7	28882376	28882976	2.0	0.7
chr7	28882410	28883010	1.9	0.7
chr7	28882444	28883044	2.0	0.7
chr7	28882478	28883078	2.0	0.7
chr7	28882512	28883112	2.0	0.7
chr7	28882546	28883146	2.0	0.7
chr7	28882580	28883180	2.0	0.7
chr7	28882614	28883214	2.0	0.7
chr7	28882644	28883244	2.0	0.7
chr7	28882678	28883278	2.0	0.7
chr7	28882712	28883312	2.0	0.7
chr7	28882746	28883346	1.9	0.7
chr7	28882780	28883380	1.9	0.7
chr7	28882814	28883414	1.9	0.7
chr7	28882848	28883448	1.9	0.6
chr7	28882882	28883482	1.9	0.7
chr7	28882916	28883516	1.9	0.7
chr7	28882950	28883550	1.9	0.7
chr7	28882984	28883584	1.9	0.7
chr7	28883018	28883618	1.9	0.7
chr7	28883052	28883652	1.8	0.7
chr7	28883086	28883686	1.8	0.6
chr7	28883120	28883720	1.7	0.6
chr7	28883154	28883754	1.8	0.7
chr7	28883188	28883788	1.8	0.7
chr7	28883222	28883822	1.7	0.5
chr7	28883256	28883856	1.6	0.4
chr7	28883290	28883890	1.6	0.4
chr7	28883324	28883924	1.6	0.4

chr7	28933049	28933649	2.2	0.9
chr7	28933173	28933773	1.5	0.6
chr7	28981690	28982290	1.8	0.6
chr7	28981699	28982299	1.7	0.7
chr7	29349551	29350151	0.6	0.1
chr7	30105566	30106166	0.3	0.2
chr7	30132482	30133082	0.6	0.2
chr7	30185249	30185849	0.3	0.1
chr7	30195705	30196305	0.5	0.1
chr7	30196166	30196766	0.2	0.2
chr7	30425221	30425821	0.5	0.0
chr7	31185086	31185686	0.5	0.2
chr7	31311957	31312557	1.4	0.0
chr7	31317933	31318533	0.5	0.5
chr7	31407982	31408582	0.7	0.0
chr7	31408106	31408706	0.6	0.2
chr7	31430422	31431022	2.8	0.5
chr7	31430461	31431061	2.9	0.4
chr7	31989253	31989853	0.4	0.0
chr7	32291160	32291760	0.7	0.0
chr7	32884598	32885198	0.7	0.1
chr7	32887176	32887776	0.3	0.3
chr7	32938677	32939277	1.0	0.2
chr7	33117907	33118507	0.2	0.2
chr7	33620299	33620899	0.7	0.1
chr7	33622877	33623477	0.4	0.4
chr7	33847194	33847794	0.7	0.1
chr7	33849772	33850372	0.4	0.4
chr7	33904109	33904709	1.2	0.3
chr7	34313688	34314288	1.2	0.1
chr7	34678718	34679318	1.2	0.1
chr7	35216048	35216648	6.2	3.1
chr7	35216064	35216664	6.3	3.1
chr7	35216080	35216680	6.5	3.2
chr7	35216096	35216696	6.5	3.2
chr7	35216128	35216728	6.5	3.0
chr7	35623108	35623708	0.3	0.6
chr7	35907948	35908548	1.3	0.1

chr7	35914757	35915357	0.5	0.4
chr7	35977340	35977940	1.1	0.4
chr7	36116493	36117093	0.1	0.3
chr7	36164309	36164909	1.1	0.4
chr7	36164531	36165131	1.1	0.3
chr7	36288396	36288996	0.1	0.1
chr7	36300942	36301542	0.5	0.2
chr7	36825640	36826240	0.8	0.1
chr7	37155124	37155724	1.3	0.5
chr7	37209449	37210049	0.2	0.0
chr7	37555442	37556042	1.8	0.3
chr7	37798906	37799506	0.7	0.1
chr7	38118429	38119029	1.5	0.2
chr7	38281176	38281776	0.7	0.8
chr7	38281272	38281872	1.0	0.7
chr7	38281357	38281957	1.2	0.8
chr7	39023219	39023819	1.4	0.2
chr7	39039036	39039636	1.5	0.5
chr7	46467711	46468311	1.8	0.1
chr7	46467721	46468321	1.9	0.1
chr7	46655158	46655758	1.8	0.1
chr7	46655168	46655768	2.0	0.1
chr7	47169981	47170581	1.1	0.4
chr7	47828441	47829041	0.4	0.1
chr7	47914987	47915587	0.3	0.2
chr7	49406634	49407234	0.5	0.1
chr7	51606264	51606864	1.3	0.4
chr7	51859634	51860234	1.8	0.7
chr7	51859710	51860310	2.1	0.7
chr7	52059248	52059848	0.7	0.2
chr7	52159276	52159876	0.6	0.1
chr7	52367215	52367815	0.6	0.3
chr7	52404688	52405288	1.2	0.1
chr7	52404694	52405294	1.1	0.0
chr7	52593162	52593762	1.0	0.4
chr7	52716157	52716757	0.2	0.3
chr7	52928482	52929082	0.1	0.6
chr7	53187505	53188105	0.4	0.2

chr7	53187569	53188169	0.2	0.2
chr7	53317960	53318560	0.5	0.1
chr7	53341084	53341684	0.3	0.5
chr7	53383056	53383656	0.3	0.1
chr7	54483974	54484574	2.2	1.0
chr7	54755216	54755816	0.9	0.3
chr7	54838673	54839273	0.3	0.5
chr7	54953689	54954289	0.6	0.2
chr7	54982324	54982924	0.6	0.1
chr7	55027780	55028380	0.8	0.5
chr7	55072514	55073114	0.6	0.1
chr7	55157505	55158105	1.1	0.2
chr7	55157561	55158161	1.4	0.1
chr7	55229986	55230586	1.1	0.1
chr7	55286206	55286806	1.7	0.3
chr7	55286296	55286896	0.8	0.1
chr7	56113452	56114052	0.9	0.1
chr7	56561219	56561819	0.9	0.5
chr7	56643324	56643924	0.9	0.3
chr7	56657762	56658362	0.1	0.0
chr7	57120855	57121455	0.3	0.3
chr7	57192086	57192686	1.1	0.0
chr7	57612475	57613075	0.4	0.0
chr7	57802880	57803480	1.2	0.3
chr7	58438342	58438942	0.3	0.0
chr7	58558429	58559029	0.5	0.2
chr7	58834589	58835189	0.6	0.1
chr7	58947438	58948038	0.9	0.2
chr7	59963961	59964561	0.2	0.1
chr7	60287648	60288248	0.3	0.2
chr7	60803299	60803899	1.0	0.3
chr7	60862656	60863256	0.7	0.2
chr7	60862832	60863432	0.9	0.2
chr7	61073313	61073913	0.7	0.2
chr7	62131615	62132215	1.1	0.2
chr7	62366796	62367396	0.3	0.1
chr7	62564826	62565426	1.8	0.3
chr7	62565019	62565619	1.3	0.2

chr7	62783536	62784136	0.7	0.1
chr7	62984413	62985013	1.1	0.3
chr7	65707850	65708450	1.1	0.5
chr7	65741595	65742195	1.3	0.6
chr7	65790270	65790870	0.3	0.0
chr7	67148895	67149495	0.6	0.1
chr7	67458988	67459588	0.7	0.1
chr7	67833063	67833663	0.2	0.1
chr7	67946405	67947005	0.6	0.1
chr7	68402074	68402674	0.7	0.1
chr7	68417230	68417830	1.3	0.1
chr7	68417427	68418027	1.6	0.1
chr7	68452119	68452719	1.3	0.2
chr7	68484987	68485587	0.1	0.0
chr7	69531926	69532526	1.7	0.8
chr7	69532015	69532615	1.9	0.7
chr7	69600542	69601142	0.2	0.2
chr7	69709274	69709874	0.7	0.2
chr7	70244099	70244699	1.0	0.2
chr7	70598488	70599088	0.4	0.2
chr7	70941102	70941702	0.9	0.2
chr7	71056823	71057423	0.4	0.3
chr7	71137198	71137798	0.8	0.2
chr7	71170971	71171571	1.0	0.4
chr7	71765603	71766203	1.2	0.1
chr7	72087239	72087839	1.5	0.5
chr7	72087324	72087924	2.3	0.8
chr7	73096918	73097518	0.8	0.0
chr7	73276632	73277232	0.8	0.1
chr7	73307189	73307789	1.0	0.1
chr7	73328077	73328677	2.5	0.4
chr7	73328288	73328888	1.5	0.1
chr7	73517794	73518394	0.5	0.3
chr7	73601909	73602509	0.9	0.1
chr7	73645010	73645610	0.6	0.1
chr7	74110317	74110917	0.1	0.2
chr7	74762940	74763540	0.4	0.0
chr7	75055763	75056363	0.5	0.2
chr7	75352117	75352717	2.0	0.4
chr7	75352386	75352986	1.2	0.3
chr7	77620306	77620906	1.1	0.9
chr7	77620355	77620955	1.1	0.7
chr7	78513571	78514171	1.6	0.5
chr7	78513740	78514340	1.5	0.2
chr7	78513849	78514449	1.5	0.2
chr7	78757256	78757856	1.2	0.4
chr7	79054472	79055072	1.4	0.0
chr7	79645921	79646521	0.1	0.4
chr7	80559118	80559718	1.5	0.3
chr7	80559183	80559783	1.9	0.6
chr7	80723821	80724421	1.4	0.1
chr7	81123590	81124190	0.6	0.6
chr7	81706123	81706723	4.4	1.5
chr7	81706151	81706751	4.1	1.3
chr7	81706207	81706807	4.7	1.7
chr7	81706235	81706835	4.6	1.6
chr7	81706291	81706891	4.4	1.6
chr7	81706319	81706919	4.4	1.6
chr7	81706347	81706947	4.4	1.5
chr7	81706459	81707059	3.4	1.0
chr7	81719376	81719976	1.8	0.5
chr7	81719485	81720085	1.8	0.6
chr7	82108351	82108951	0.9	0.3
chr7	82519557	82520157	0.4	0.1
chr7	82683199	82683799	0.0	0.1
chr7	82766300	82766900	1.5	0.1
chr7	83383267	83383867	0.6	0.1
chr7	84025388	84025988	1.8	0.3
chr7	84828618	84829218	0.2	0.1
chr7	85635981	85636581	0.8	0.6
chr7	85675033	85675633	1.8	0.1
chr7	85697007	85697607	0.2	0.5
chr7	85876813	85877413	0.5	0.2
chr7	86147220	86147820	0.1	0.3
chr7	86147289	86147889	0.1	0.2
chr7	86637017	86637617	2.4	0.8

chr7	86637037	86637637	2.3	1.0
chr7	86930855	86931455	0.8	0.0
chr7	86951723	86952323	0.1	0.1
chr7	87026880	87027480	2.5	0.8
chr7	87026890	87027490	2.5	0.9
chr7	87026927	87027527	2.5	0.9
chr7	87026937	87027537	2.6	0.8
chr7	87026957	87027557	2.7	0.9
chr7	87026975	87027575	2.5	0.9
chr7	87378076	87378676	0.7	0.2
chr7	87562620	87563220	0.2	0.4
chr7	87587572	87588172	2.6	0.8
chr7	87587816	87588416	1.9	0.6
chr7	87700665	87701265	0.8	0.1
chr7	87954014	87954614	0.0	0.4
chr7	88004857	88005457	0.5	0.3
chr7	88070723	88071323	0.5	0.1
chr7	88202257	88202857	0.3	0.6
chr7	88430015	88430615	0.8	0.1
chr7	88625528	88626128	1.3	0.7
chr7	89208203	89208803	0.9	0.1
chr7	89823743	89824343	1.5	0.0
chr7	89823859	89824459	1.8	0.1
chr7	89968741	89969341	0.9	0.2
chr7	90246367	90246967	0.5	0.2
chr7	90249977	90250577	1.7	0.0
chr7	90307884	90308484	0.5	0.2
chr7	90698282	90698882	1.0	0.2
chr7	91068820	91069420	1.3	0.5
chr7	91481472	91482072	0.8	0.0
chr7	91915250	91915850	0.8	0.1
chr7	92025503	92026103	0.6	0.2
chr7	93839800	93840400	0.3	0.3
chr7	93919095	93919695	0.1	0.5
chr7	94394606	94395206	0.1	0.0
chr7	96426284	96426884	1.2	0.7
chr7	96561741	96562341	0.3	0.1
chr7	96561927	96562527	0.2	0.3

chr7	97029521	97030121	1.1	0.2
chr7	97263996	97264596	0.5	0.2
chr7	98162025	98162625	1.1	0.2
chr7	98162228	98162828	1.3	0.3
chr7	98644293	98644893	1.1	0.1
chr7	98862357	98862957	1.1	0.6
chr7	99771107	99771707	0.1	0.2
chr7	99771197	99771797	0.3	0.2
chr7	99806487	99807087	1.7	0.3
chr7	99806509	99807109	1.6	0.3
chr7	99806548	99807148	1.5	0.3
chr7	100035943	100036543	1.1	0.1
chr7	100113181	100113781	0.3	0.1
chr7	100241834	100242434	0.8	0.2
chr7	100331895	100332495	0.3	0.0
chr7	100452025	100452625	0.6	0.2
chr7	100825476	100826076	0.6	0.3
chr7	100840047	100840647	1.4	0.5
chr7	101553690	101554290	0.0	0.0
chr7	101690456	101691056	0.4	0.1
chr7	102249535	102250135	0.1	0.7
chr7	102534530	102535130	0.1	0.3
chr7	102947858	102948458	0.5	0.0
chr7	102958465	102959065	1.1	0.7
chr7	103305816	103306416	0.5	0.1
chr7	103329519	103330119	1.2	0.3
chr7	103629270	103629870	0.5	0.5
chr7	104323322	104323922	0.6	0.8
chr7	104562607	104563207	1.2	0.4
chr7	104562783	104563383	1.1	0.3
chr7	105242757	105243357	1.3	0.1
chr7	105275140	105275740	1.4	0.5
chr7	105468184	105468784	0.9	0.1
chr7	105645444	105646044	1.7	0.5
chr7	105645527	105646127	2.6	0.8
chr7	106003505	106004105	0.2	0.1
chr7	106079297	106079897	1.2	0.3
chr7	106311915	106312515	0.7	0.0

chr7	106417167	106417767	1.0	0.0
chr7	106590220	106590820	0.2	0.1
chr7	106596862	106597462	0.9	0.1
chr7	106857188	106857788	0.4	0.1
chr7	107178346	107178946	0.6	0.2
chr7	107228104	107228704	1.4	0.2
chr7	107228118	107228718	1.6	0.3
chr7	107324467	107325067	1.1	0.9
chr7	107324527	107325127	1.3	0.8
chr7	108379087	108379687	1.7	0.3
chr7	108432911	108433511	0.5	0.1
chr7	108439594	108440194	1.0	0.2
chr7	108533285	108533885	0.7	0.1
chr7	108543829	108544429	1.3	0.1
chr7	108549314	108549914	0.1	0.1
chr7	110101559	110102159	1.0	0.3
chr7	110130103	110130703	1.2	0.1
chr7	110206360	110206960	0.9	0.1
chr7	110405710	110406310	0.7	0.0
chr7	110498826	110499426	1.7	0.2
chr7	111616893	111617493	0.0	0.1
chr7	112356686	112357286	0.5	0.2
chr7	112685292	112685892	0.5	0.5
chr7	112800917	112801517	2.1	0.6
chr7	112817581	112818181	0.3	0.0
chr7	112953641	112954241	0.0	0.0
chr7	113395682	113396282	1.0	0.3
chr7	114203734	114204334	0.1	0.0
chr7	116010608	116011208	1.3	0.3
chr7	116493993	116494593	0.7	0.2
chr7	116880800	116881400	0.2	0.3
chr7	117163118	117163718	1.7	0.2
chr7	119874210	119874810	0.1	0.0
chr7	119914242	119914842	0.2	0.0
chr7	119959887	119960487	1.9	0.3
chr7	120375483	120376083	0.5	0.0
chr7	120604136	120604736	1.9	0.5
chr7	120939306	120939906	1.1	0.3

chr7	120940002	120940602	0.1	0.1
chr7	121209892	121210492	0.9	1.4
chr7	121406383	121406983	1.6	0.2
chr7	122018330	122018930	0.1	0.0
chr7	122288064	122288664	0.5	0.3
chr7	123004169	123004769	0.8	0.2
chr7	123095219	123095819	0.9	0.4
chr7	123809593	123810193	0.8	0.2
chr7	123809690	123810290	1.4	0.1
chr7	123939075	123939675	0.6	0.0
chr7	124176121	124176721	0.4	0.2
chr7	124274183	124274783	0.9	0.0
chr7	124325365	124325965	0.8	0.2
chr7	124859950	124860550	1.4	0.1
chr7	125445154	125445754	0.6	0.2
chr7	125458854	125459454	0.8	0.4
chr7	125459016	125459616	0.7	0.2
chr7	125632739	125633339	1.7	0.0
chr7	125721723	125722323	0.1	0.3
chr7	127556784	127557384	1.7	0.4
chr7	127737271	127737871	1.5	1.2
chr7	127737338	127737938	1.9	1.2
chr7	128173385	128173985	1.6	0.4
chr7	129006880	129007480	1.0	0.2
chr7	129017566	129018166	0.8	0.0
chr7	129159484	129160084	0.0	0.1
chr7	129159735	129160335	0.9	0.3
chr7	130483033	130483633	4.8	1.7
chr7	130483064	130483664	4.6	1.6
chr7	130483095	130483695	4.5	1.6
chr7	130483157	130483757	4.4	1.8
chr7	130483188	130483788	4.4	1.8
chr7	130483250	130483850	4.5	1.9
chr7	130483281	130483881	4.6	1.9
chr7	130655615	130656215	0.1	0.2
chr7	132353722	132354322	0.0	0.0
chr7	132354855	132355455	0.7	0.5
chr7	132541756	132542356	2.7	0.6

chr7	132541795	132542395	2.6	0.6
chr7	132541831	132542431	2.8	0.6
chr7	132541855	132542455	2.8	0.7
chr7	132541949	132542549	2.9	0.8
chr7	132757949	132758549	0.2	0.0
chr7	133108681	133109281	0.7	0.6
chr7	133108832	133109432	0.1	0.2
chr7	134867709	134868309	1.1	0.6
chr7	135185117	135185717	0.0	0.0
chr7	135371087	135371687	0.6	0.1
chr7	135516536	135517136	1.1	0.2
chr7	135728826	135729426	0.7	0.4
chr7	135729055	135729655	0.9	0.3
chr7	135800679	135801279	0.5	0.1
chr7	136532866	136533466	0.6	0.1
chr7	136953608	136954208	0.7	0.0
chr7	137285439	137286039	0.4	0.5
chr7	137317793	137318393	0.6	0.3
chr7	137456415	137457015	0.5	0.4
chr7	137578487	137579087	0.5	0.0
chr7	137578720	137579320	0.6	0.0
chr7	137818008	137818608	0.3	0.1
chr7	138280465	138281065	0.1	0.2
chr7	138393972	138394572	0.8	0.1
chr7	138752491	138753091	0.5	0.2
chr7	138841784	138842384	1.0	0.4
chr7	138928387	138928987	1.0	0.2
chr7	139092186	139092786	1.5	0.0
chr7	139284794	139285394	0.0	0.1
chr7	139560443	139561043	0.6	0.3
chr7	139605350	139605950	0.0	0.2
chr7	139753044	139753644	0.8	0.0
chr7	139912270	139912870	0.1	0.1
chr7	140029938	140030538	0.5	0.0
chr7	140049026	140049626	1.6	0.7
chr7	140988958	140989558	1.8	0.1
chr7	141466478	141467078	1.1	0.3
chr7	141807688	141808288	1.3	0.2

chr7	141810732	141811332	1.5	0.3
chr7	141887988	141888588	0.2	0.1
chr7	141899694	141900294	1.7	0.5
chr7	141899792	141900392	1.3	0.6
chr7	142459946	142460546	0.6	0.2
chr7	143401031	143401631	0.9	0.1
chr7	143639372	143639972	0.7	0.2
chr7	143799331	143799931	1.6	0.0
chr7	144241913	144242513	0.9	0.2
chr7	144650461	144651061	0.4	0.2
chr7	146320803	146321403	0.6	0.5
chr7	147301835	147302435	1.1	0.5
chr7	147834646	147835246	0.6	0.1
chr7	147904565	147905165	0.3	0.4
chr7	147904582	147905182	0.3	0.4
chr7	148139260	148139860	0.9	0.1
chr7	148240411	148241011	1.0	0.4
chr7	148240590	148241190	1.2	0.5
chr7	148268556	148269156	0.6	0.0
chr7	148296507	148297107	4.1	1.6
chr7	148296545	148297145	4.0	1.5
chr7	148296564	148297164	3.9	1.5
chr7	148296583	148297183	3.9	1.6
chr7	148296602	148297202	3.9	1.5
chr7	148296621	148297221	3.7	1.4
chr7	148296640	148297240	3.8	1.5
chr7	148296663	148297263	3.8	1.5
chr7	148296686	148297286	3.8	1.6
chr7	148296705	148297305	3.8	1.6
chr7	148296736	148297336	3.7	1.6
chr7	148481871	148482471	0.8	0.0
chr7	148993726	148994326	2.3	0.6
chr7	148993834	148994434	2.4	0.9
chr7	148995835	148996435	2.3	0.6
chr7	148995943	148996543	2.4	0.8
chr7	149056628	149057228	0.5	0.0
chr7	149231610	149232210	0.2	0.1
chr7	149312345	149312945	0.1	0.5

chr7	149557719	149558319	0.1	0.1
chr7	149629061	149629661	0.7	0.4
chr7	149629152	149629752	0.6	0.1
chr7	149629171	149629771	0.8	0.2
chr7	149660502	149661102	1.2	0.2
chr7	149660654	149661254	1.2	0.3
chr7	150197011	150197611	0.7	0.2
chr7	150447928	150448528	1.2	0.0
chr7	150448001	150448601	1.4	0.2
chr7	150665227	150665827	1.0	0.1
chr7	150754119	150754719	0.8	0.0
chr7	150790559	150791159	0.5	0.5
chr7	150826738	150827338	0.5	0.1
chr7	150912613	150913213	0.8	0.2
chr7	151175635	151176235	0.1	0.0
chr7	151195127	151195727	0.4	0.1
chr7	151593305	151593905	0.6	0.3
chr7	151593556	151594156	0.6	0.2
chr7	151593563	151594163	0.8	0.2
chr7	151839659	151840259	0.7	0.1
chr7	151967202	151967802	0.9	0.5
chr7	151967235	151967835	1.0	0.4
chr7	152196485	152197085	1.0	0.3
chr7	152402676	152403276	0.4	0.0
chr8	4341918	4342518	0.2	0.3
chr8	4341933	4342533	0.1	0.3
chr8	4653571	4654171	0.7	0.2
chr8	5686176	5686776	0.4	0.2
chr8	6309687	6310287	0.9	0.7
chr8	6597991	6598591	0.2	0.0
chr8	6701775	6702375	0.9	0.0
chr8	6701872	6702472	1.1	0.2
chr8	6960156	6960756	2.9	0.0
chr8	8210664	8211264	2.2	0.5
chr8	8210865	8211465	2.6	0.6
chr8	8440815	8441415	0.7	0.2
chr8	8524859	8525459	0.2	0.2
chr8	8633351	8633951	1.0	0.0
chr8	8633433	8634033	0.6	0.2
chr8	8663291	8663891	1.6	0.3
chr8	8663588	8664188	1.2	0.6
chr8	8929988	8930588	0.3	0.3
chr8	8930008	8930608	0.2	0.3
chr8	8984288	8984888	0.9	0.1
chr8	9154077	9154677	0.6	0.1
chr8	9154282	9154882	0.5	0.5
chr8	9388436	9389036	1.2	0.4
chr8	9824580	9825180	1.7	0.1
chr8	9824614	9825214	2.1	0.2
chr8	9960457	9961057	0.1	0.4
chr8	9960546	9961146	0.4	0.0
chr8	10264218	10264818	1.1	0.5
chr8	10264411	10265011	1.1	0.3
chr8	10467259	10467859	1.9	1.1
chr8	10467330	10467930	1.5	1.3
chr8	10507472	10508072	1.0	0.2
chr8	11002509	11003109	1.4	0.1
chr8	11393099	11393699	0.2	0.0
chr8	11914714	11915314	1.0	0.1
chr8	12244895	12245495	0.2	0.0
chr8	12698550	12699150	1.7	0.2
chr8	12976724	12977324	0.2	0.3
chr8	13169354	13169954	0.1	0.1
chr8	13274204	13274804	0.1	0.1
chr8	13275915	13276515	1.1	0.1
chr8	13477603	13478203	0.1	0.0
chr8	13479552	13480152	0.2	0.2
chr8	13571333	13571933	0.6	0.0
chr8	13757136	13757736	0.9	0.1
chr8	14377192	14377792	1.0	0.2
chr8	14452924	14453524	0.5	0.1
chr8	14887240	14887840	0.6	0.3
chr8	15132206	15132806	0.2	0.1
chr8	15192284	15192884	1.2	0.1
chr8	15192378	15192978	1.2	0.1
chr8	16011472	16012072	0.2	0.1

chr8	16011501	16012101	0.3	0.2
chr8	16148446	16149046	1.5	0.5
chr8	17277799	17278399	0.2	0.1
chr8	18464525	18465125	2.6	0.8
chr8	18464767	18465367	1.5	0.1
chr8	18565677	18566277	1.2	0.1
chr8	19788055	19788655	1.3	0.1
chr8	19889097	19889697	1.4	0.1
chr8	20016374	20016974	1.2	0.1
chr8	23092205	23092805	0.1	0.1
chr8	23100914	23101514	1.3	0.5
chr8	23100997	23101597	1.9	0.4
chr8	23279744	23280344	0.7	0.0
chr8	23851451	23852051	1.3	0.1
chr8	24141881	24142481	0.1	0.1
chr8	24164923	24165523	0.7	0.0
chr8	24185193	24185793	0.5	0.1
chr8	24241797	24242397	0.2	0.1
chr8	24472185	24472785	0.2	0.3
chr8	24520747	24521347	0.3	0.0
chr8	24704643	24705243	1.2	0.4
chr8	24740658	24741258	1.7	0.4
chr8	24810321	24810921	0.8	0.1
chr8	24979226	24979826	0.7	0.2
chr8	25651840	25652440	1.1	0.1
chr8	25654741	25655341	0.3	0.4
chr8	25875080	25875680	1.1	0.5
chr8	25923740	25924340	0.4	0.1
chr8	26111987	26112587	0.8	0.4
chr8	26112520	26113120	1.2	0.7
chr8	26112754	26113354	1.5	0.9
chr8	26112944	26113544	1.3	0.7
chr8	26113210	26113810	0.8	0.5
chr8	26149201	26149801	2.1	0.4
chr8	26149271	26149871	2.4	0.4
chr8	26635362	26635962	1.1	0.0
chr8	26869078	26869678	0.3	0.0
chr8	27027404	27028004	0.9	0.2
chr8	27779763	27780363	0.4	0.3
chr8	29632329	29632929	1.0	0.3
chr8	31070989	31071589	0.3	0.2
chr8	31220104	31220704	0.3	0.0
chr8	31714356	31714956	0.2	0.1
chr8	31968630	31969230	1.2	0.4
chr8	32191415	32192015	1.8	0.4
chr8	32377766	32378366	0.5	0.4
chr8	32377786	32378386	0.5	0.4
chr8	32686650	32687250	0.7	0.4
chr8	33264180	33264780	0.9	0.1
chr8	33264397	33264997	0.6	0.3
chr8	33740162	33740762	1.1	0.7
chr8	34028049	34028649	1.1	0.1
chr8	34785616	34786216	0.1	0.0
chr8	35143464	35144064	1.5	0.5
chr8	35209817	35210417	1.4	0.2
chr8	35209860	35210460	1.2	0.3
chr8	35485354	35485954	0.7	0.1
chr8	36617848	36618448	0.7	0.2
chr8	36780685	36781285	0.4	0.8
chr8	36780828	36781428	1.0	0.7
chr8	36993396	36993996	0.6	0.2
chr8	37043913	37044513	0.4	0.2
chr8	37058760	37059360	1.2	0.2
chr8	37058770	37059370	1.1	0.3
chr8	37168338	37168938	0.2	0.1
chr8	37582500	37583100	0.7	0.6
chr8	37589619	37590219	1.2	0.1
chr8	37610912	37611512	0.9	0.2
chr8	38000358	38000958	0.5	0.1
chr8	40621026	40621626	0.6	0.1
chr8	41137651	41138251	2.2	0.3
chr8	41137738	41138338	2.1	0.6
chr8	41435688	41436288	0.7	0.0
chr8	41829253	41829853	0.3	0.4
chr8	42126792	42127392	1.9	0.5
chr8	42127016	42127616	2.1	0.6

chr8	42290964	42291564	0.7	0.2
chr8	42406544	42407144	1.0	0.2
chr8	43487917	43488517	0.2	0.0
chr8	43616477	43617077	0.8	0.1
chr8	43672299	43672899	0.9	0.5
chr8	44600757	44601357	0.5	0.2
chr8	45194034	45194634	0.2	0.1
chr8	45596205	45596805	0.8	0.5
chr8	45596241	45596841	0.8	0.5
chr8	46081756	46082356	1.8	0.8
chr8	46809156	46809756	0.3	0.4
chr8	46961340	46961940	2.4	0.2
chr8	46961354	46961954	2.2	0.1
chr8	47947470	47948070	2.5	0.8
chr8	48829828	48830428	0.7	0.3
chr8	49449992	49450592	0.9	0.5
chr8	49706600	49707200	0.4	0.1
chr8	49766960	49767560	1.0	0.2
chr8	50154733	50155333	0.5	0.1
chr8	51490730	51491330	1.2	0.3
chr8	53016535	53017135	1.0	0.1
chr8	53207765	53208365	1.2	0.2
chr8	53675876	53676476	2.9	1.2
chr8	53676124	53676724	2.2	1.2
chr8	54192347	54192947	0.9	0.0
chr8	54322597	54323197	0.3	0.0
chr8	54697286	54697886	0.5	0.1
chr8	54767754	54768354	0.5	0.1
chr8	54892193	54892793	0.1	0.2
chr8	54963971	54964571	0.2	0.2
chr8	55205738	55206338	0.8	0.1
chr8	55916149	55916749	0.9	0.4
chr8	58840377	58840977	0.6	0.0
chr8	58840393	58840993	0.8	0.1
chr8	58840433	58841033	1.0	0.1
chr8	59461765	59462365	1.9	0.0
chr8	59492843	59493443	0.7	0.2
chr8	59883958	59884558	1.5	0.6
chr8	59920119	59920719	0.2	0.1
chr8	61092259	61092859	0.8	0.1
chr8	61623439	61624039	0.1	0.2
chr8	62748996	62749596	5.7	2.0
chr8	62749013	62749613	5.8	2.1
chr8	62749030	62749630	5.8	1.9
chr8	62749047	62749647	5.2	1.6
chr8	62749064	62749664	5.1	1.6
chr8	62749081	62749681	5.0	1.7
chr8	62749098	62749698	4.9	1.6
chr8	63092589	63093189	1.9	0.8
chr8	63092680	63093280	1.3	0.6
chr8	63175356	63175956	0.2	0.2
chr8	63310518	63311118	2.7	0.5
chr8	63671778	63672378	1.3	0.5
chr8	63671945	63672545	0.9	0.4
chr8	63807179	63807779	1.4	0.1
chr8	63819997	63820597	1.3	0.3
chr8	64305095	64305695	0.4	0.0
chr8	64917618	64918218	0.1	0.4
chr8	65125302	65125902	2.2	1.0
chr8	65125552	65126152	2.2	0.8
chr8	66194858	66195458	0.0	0.0
chr8	66556056	66556656	0.4	0.2
chr8	67066875	67067475	0.8	0.2
chr8	67185872	67186472	1.2	0.2
chr8	67623726	67624326	0.2	0.0
chr8	69430897	69431497	1.6	0.4
chr8	70141629	70142229	1.2	0.0
chr8	70365281	70365881	2.9	0.3
chr8	70365509	70366109	2.6	0.1
chr8	71050888	71051488	1.6	0.1
chr8	71279464	71280064	1.6	0.2
chr8	72631297	72631897	0.6	0.2
chr8	72875088	72875688	0.6	0.1
chr8	73219412	73220012	0.2	0.1
chr8	73310527	73311127	0.9	0.0
chr8	73417331	73417931	0.5	0.2

chr8	73447837	73448437	0.3	0.0
chr8	73899919	73900519	0.9	0.1
chr8	73994466	73995066	1.2	0.1
chr8	74006719	74007319	1.2	0.2
chr8	74006808	74007408	0.4	0.1
chr8	74217325	74217925	0.2	0.0
chr8	74251011	74251611	0.9	0.0
chr8	74293322	74293922	0.9	0.4
chr8	74525822	74526422	1.4	0.1
chr8	74907653	74908253	0.5	0.2
chr8	74907673	74908273	0.4	0.1
chr8	75000801	75001401	0.7	0.1
chr8	75000945	75001545	0.9	0.0
chr8	75734737	75735337	0.2	0.0
chr8	77257472	77258072	1.4	0.6
chr8	77375681	77376281	0.8	0.3
chr8	77375933	77376533	0.9	0.0
chr8	78499616	78500216	0.2	0.2
chr8	79548501	79549101	0.9	0.2
chr8	80257583	80258183	0.6	0.4
chr8	80552566	80553166	1.4	0.3
chr8	81401152	81401752	2.1	0.3
chr8	81423228	81423828	1.8	0.6
chr8	81651122	81651722	0.4	0.1
chr8	81847679	81848279	1.9	0.3
chr8	81847713	81848313	2.0	0.3
chr8	81847755	81848355	1.8	0.3
chr8	81847797	81848397	1.9	0.4
chr8	81847818	81848418	1.9	0.3
chr8	81986733	81987333	2.0	0.4
chr8	82361806	82362406	1.5	0.1
chr8	82784508	82785108	0.6	0.1
chr8	82838500	82839100	0.9	0.4
chr8	83074079	83074679	0.1	0.2
chr8	83210965	83211565	0.5	0.2
chr8	83211002	83211602	0.6	0.2
chr8	83280867	83281467	0.3	0.1
chr8	83483389	83483989	0.4	0.3

chr8	85449298	85449898	0.0	0.1
chr8	85486307	85486907	0.7	0.2
chr8	86186041	86186641	1.2	0.3
chr8	86243838	86244438	1.4	0.7
chr8	86243941	86244541	0.8	0.4
chr8	86304054	86304654	0.7	0.4
chr8	86439326	86439926	0.5	0.0
chr8	86782392	86782992	0.8	0.1
chr8	86917694	86918294	0.4	0.7
chr8	87179776	87180376	2.5	0.5
chr8	87179793	87180393	2.4	0.3
chr8	87285282	87285882	0.4	0.1
chr8	87361863	87362463	1.2	0.2
chr8	87640612	87641212	1.2	0.3
chr8	88049265	88049865	0.7	0.5
chr8	88076554	88077154	0.5	0.1
chr8	88407829	88408429	0.7	0.1
chr8	88519658	88520258	1.1	0.2
chr8	89833189	89833789	0.7	0.2
chr8	89833378	89833978	0.1	0.0
chr8	90095439	90096039	0.0	0.1
chr8	90231273	90231873	0.4	0.2
chr8	90279923	90280523	0.7	0.1
chr8	90552237	90552837	1.2	0.3
chr8	90811644	90812244	0.1	0.1
chr8	90840222	90840822	1.4	0.1
chr8	90975664	90976264	2.1	0.1
chr8	91138357	91138957	0.6	0.3
chr8	91138448	91139048	1.2	0.4
chr8	91587950	91588550	0.9	0.1
chr8	91644801	91645401	1.1	0.4
chr8	91693687	91694287	0.4	0.2
chr8	92401412	92402012	1.5	0.5
chr8	92402399	92402999	1.7	0.6
chr8	92758461	92759061	0.1	0.1
chr8	92819679	92820279	0.5	0.4
chr8	93580682	93581282	1.7	0.4
chr8	93849587	93850187	0.4	0.4

chr8	94390771	94391371	0.5	0.1
chr8	94821000	94821600	0.3	0.5
chr8	94884315	94884915	0.2	0.2
chr8	94997357	94997957	1.6	0.1
chr8	94997384	94997984	1.4	0.1
chr8	95443397	95443997	0.5	0.0
chr8	95484730	95485330	2.0	0.4
chr8	95893166	95893766	1.4	0.3
chr8	95977529	95978129	0.6	0.5
chr8	96013569	96014169	0.2	0.3
chr8	96333088	96333688	0.1	0.1
chr8	96356338	96356938	0.9	0.1
chr8	96400587	96401187	1.4	0.5
chr8	97031118	97031718	0.6	0.0
chr8	97176564	97177164	0.9	0.1
chr8	97290034	97290634	1.7	0.8
chr8	97387604	97388204	0.7	0.1
chr8	97497608	97498208	0.8	0.2
chr8	97711137	97711737	1.0	0.1
chr8	98415572	98416172	2.1	0.3
chr8	98415794	98416394	2.0	0.4
chr8	98703957	98704557	0.2	0.0
chr8	98851110	98851710	1.2	0.3
chr8	98851149	98851749	1.0	0.2
chr8	100058842	100059442	1.0	0.2
chr8	101024405	101025005	0.6	0.5
chr8	102201275	102201875	0.0	0.3
chr8	102507130	102507730	1.9	0.2
chr8	103825154	103825754	1.2	0.1
chr8	104444921	104445521	1.8	0.1
chr8	104828044	104828644	0.6	0.1
chr8	106022037	106022637	0.2	0.2
chr8	106308487	106309087	1.3	0.1
chr8	106355422	106356022	0.4	0.0
chr8	106432456	106433056	2.6	0.6
chr8	106432466	106433066	2.7	0.5
chr8	106546761	106547361	1.4	0.0
chr8	107730614	107731214	2.2	0.8

chr8	107730672	107731272	2.3	0.9
chr8	107735856	107736456	1.1	0.1
chr8	107736464	107737064	0.9	0.1
chr8	107832263	107832863	1.4	0.2
chr8	107897802	107898402	0.4	0.3
chr8	108041433	108042033	1.1	0.2
chr8	108041530	108042130	0.5	0.1
chr8	108043568	108044168	1.1	0.1
chr8	108379361	108379961	0.6	0.1
chr8	108384619	108385219	0.6	0.2
chr8	108490727	108491327	0.5	0.3
chr8	108490748	108491348	0.5	0.4
chr8	108924169	108924769	1.1	0.0
chr8	108924355	108924955	1.3	0.1
chr8	108924551	108925151	1.1	0.1
chr8	108924641	108925241	1.4	0.2
chr8	109089947	109090547	0.6	0.2
chr8	109089967	109090567	0.4	0.1
chr8	109474095	109474695	0.2	0.2
chr8	109829120	109829720	0.4	0.1
chr8	109829223	109829823	1.1	0.4
chr8	110155355	110155955	0.3	0.1
chr8	110504281	110504881	0.8	0.1
chr8	111461184	111461784	1.5	0.9
chr8	112625205	112625805	0.5	0.4
chr8	114159289	114159889	1.0	0.1
chr8	114651130	114651730	0.8	0.7
chr8	114651172	114651772	0.9	0.8
chr8	114927890	114928490	1.1	0.7
chr8	114928124	114928724	1.0	0.4
chr8	115349698	115350298	0.7	0.0
chr8	116106301	116106901	0.9	0.5
chr8	116191233	116191833	1.5	0.4
chr8	116355467	116356067	0.3	0.2
chr8	116487009	116487609	0.4	0.7
chr8	117467194	117467794	0.9	0.4
chr8	117546146	117546746	2.1	0.8
chr8	117546440	117547040	1.8	0.3

chr8	117801576	117802176	1.8	0.5
chr8	117801856	117802456	0.5	0.4
chr8	118179074	118179674	0.7	0.1
chr8	118500913	118501513	1.0	0.2
chr8	119037465	119038065	0.8	0.1
chr8	119122972	119123572	0.9	0.7
chr8	119123067	119123667	1.1	0.7
chr8	119814852	119815452	0.9	0.6
chr8	119925785	119926385	0.6	0.0
chr8	120309560	120310160	1.0	0.4
chr8	120513612	120514212	0.6	0.2
chr8	120891550	120892150	1.3	0.3
chr8	121655168	121655768	1.7	0.2
chr8	121655404	121656004	1.5	0.3
chr8	121877193	121877793	0.4	0.2
chr8	121886692	121887292	0.5	0.1
chr8	122023390	122023990	0.8	0.2
chr8	122377778	122378378	0.2	0.7
chr8	122382545	122383145	1.1	0.0
chr8	122493190	122493790	1.0	0.1
chr8	122687593	122688193	0.2	0.2
chr8	122854855	122855455	2.0	0.5
chr8	122855032	122855632	1.9	0.8
chr8	122949036	122949636	0.2	0.1
chr8	123008639	123009239	2.0	0.5
chr8	123093618	123094218	0.4	0.2
chr8	123264123	123264723	1.5	1.0
chr8	123270211	123270811	1.4	0.6
chr8	123270305	123270905	1.6	0.7
chr8	123375181	123375781	1.4	0.1
chr8	123384534	123385134	0.8	0.2
chr8	123398699	123399299	1.3	0.4
chr8	123398756	123399356	1.8	0.5
chr8	123422849	123423449	1.4	0.3
chr8	123436283	123436883	1.6	0.1
chr8	123436323	123436923	1.3	0.1
chr8	123527365	123527965	1.3	0.2
chr8	123527425	123528025	1.3	0.2

chr8	123567037	123567637	1.8	0.5
chr8	123567097	123567697	1.6	0.5
chr8	123567116	123567716	1.5	0.5
chr8	123567135	123567735	1.5	0.4
chr8	123567178	123567778	1.8	0.4
chr8	123651319	123651919	0.2	0.3
chr8	123746618	123747218	1.2	0.5
chr8	123804028	123804628	1.6	0.5
chr8	124539916	124540516	0.5	0.0
chr8	124598497	124599097	1.4	0.2
chr8	124598543	124599143	1.3	0.0
chr8	124716923	124717523	0.8	0.2
chr8	124783785	124784385	1.6	0.1
chr8	124856011	124856611	1.6	0.8
chr8	124856060	124856660	2.1	0.9
chr8	124856105	124856705	2.1	0.9
chr8	124856330	124856930	1.6	0.7
chr8	125061088	125061688	1.6	1.1
chr8	125061310	125061910	1.8	0.6
chr8	125140039	125140639	0.7	0.1
chr8	125224537	125225137	0.8	0.3
chr8	125709238	125709838	2.1	0.3
chr8	125957342	125957942	0.7	0.0
chr8	126415356	126415956	1.2	0.4
chr8	126802497	126803097	0.1	0.0
chr8	126819861	126820461	0.7	0.5
chr8	126820105	126820705	0.2	0.2
chr8	126854421	126855021	1.6	0.2
chr8	126854459	126855059	1.6	0.2
chr8	127325885	127326485	4.5	1.7
chr8	127325927	127326527	4.7	1.9
chr8	127325969	127326569	4.8	1.8
chr8	127326011	127326611	4.9	1.7
chr8	127326053	127326653	4.9	1.7
chr8	127358644	127359244	0.2	0.0
chr8	127582724	127583324	0.0	0.0
chr8	127963832	127964432	0.9	0.4
chr8	127963934	127964534	0.6	0.4

chr8	128446026	128446626	0.3	0.0
chr8	128547828	128548428	0.1	0.0
chr8	128550545	128551145	0.9	0.1
chr8	129080307	129080907	0.6	0.8
chr8	129080321	129080921	0.5	0.8
chr8	129135087	129135687	0.6	0.1
chr8	129457656	129458256	0.2	0.0
chr8	129562062	129562662	0.1	0.3
chr8	130241704	130242304	0.2	0.0
chr8	130503312	130503912	1.9	0.8
chr8	130503433	130504033	2.4	0.8
chr8	130709522	130710122	0.1	0.1
chr8	130812059	130812659	1.4	0.2
chr8	131208897	131209497	0.9	0.1
chr8	131584648	131585248	0.7	0.1
chr9	3098462	3099062	0.3	0.2
chr9	3423568	3424168	1.4	0.5
chr9	4258122	4258722	0.6	0.1
chr9	6426537	6427137	0.5	0.3
chr9	7150289	7150889	0.7	0.2
chr9	7221952	7222552	0.5	0.3
chr9	8704726	8705326	0.4	0.4
chr9	8704861	8705461	0.7	0.3
chr9	9100484	9101084	0.5	0.0
chr9	9166111	9166711	2.4	0.5
chr9	9191718	9192318	0.3	0.2
chr9	9421590	9422190	1.5	0.0
chr9	9779066	9779666	0.6	0.4
chr9	10621842	10622442	0.1	0.1
chr9	12132053	12132653	1.8	0.3
chr9	13084092	13084692	0.4	0.0
chr9	13271501	13272101	0.5	0.2
chr9	13379741	13380341	0.8	0.4
chr9	13379805	13380405	0.8	0.5
chr9	14417333	14417933	0.8	0.3
chr9	14444368	14444968	0.5	0.0
chr9	14488429	14489029	0.9	0.0
chr9	14544142	14544742	0.0	0.0

chr9	14544213	14544813	0.1	0.2
chr9	14774806	14775406	0.7	0.5
chr9	15315295	15315895	0.6	0.1
chr9	15743993	15744593	1.0	0.3
chr9	16118583	16119183	1.7	0.5
chr9	18056205	18056805	0.4	0.1
chr9	18526262	18526862	0.6	0.7
chr9	18763337	18763937	0.7	0.7
chr9	19796348	19796948	1.9	0.2
chr9	21420021	21420621	1.7	0.3
chr9	21634296	21634896	0.6	0.1
chr9	21651149	21651749	1.7	0.6
chr9	21651182	21651782	1.7	0.6
chr9	21766202	21766802	1.1	0.0
chr9	22283356	22283956	0.7	0.2
chr9	22298258	22298858	1.0	0.3
chr9	22298472	22299072	1.1	0.1
chr9	22467988	22468588	0.0	0.2
chr9	22834004	22834604	1.2	0.3
chr9	23345731	23346331	0.9	0.4
chr9	23570871	23571471	0.5	0.3
chr9	23571054	23571654	0.6	0.4
chr9	23625116	23625716	1.9	0.0
chr9	25253445	25254045	1.2	0.0
chr9	25253700	25254300	1.2	0.0
chr9	25987110	25987710	1.7	0.6
chr9	25987335	25987935	2.3	0.6
chr9	26302863	26303463	0.4	0.2
chr9	26824167	26824767	0.0	0.0
chr9	26938742	26939342	1.7	0.5
chr9	26938907	26939507	0.8	0.1
chr9	27058266	27058866	0.9	0.4
chr9	27978798	27979398	1.2	0.2
chr9	28177945	28178545	0.1	0.1
chr9	28688726	28689326	0.9	0.1
chr9	29458455	29459055	0.9	0.4
chr9	29662869	29663469	0.1	0.0
chr9	30693651	30694251	0.9	0.2

chr9	30693733	30694333	1.0	0.2
chr9	31286944	31287544	0.9	0.1
chr9	31287018	31287618	1.3	0.3
chr9	31299306	31299906	1.3	0.4
chr9	31299398	31299998	1.3	0.6
chr9	31707867	31708467	1.0	0.6
chr9	32217177	32217777	1.3	0.5
chr9	32528895	32529495	0.9	0.1
chr9	32565868	32566468	0.5	0.1
chr9	32572223	32572823	1.7	0.4
chr9	32753175	32753775	1.4	0.1
chr9	32753302	32753902	1.6	0.3
chr9	33168037	33168637	0.2	0.2
chr9	33655993	33656593	0.2	0.2
chr9	34564016	34564616	0.5	0.2
chr9	34565537	34566137	0.3	0.2
chr9	34681538	34682138	0.9	0.0
chr9	34758763	34759363	1.0	0.9
chr9	34758775	34759375	0.9	0.9
chr9	35098985	35099585	0.1	0.2
chr9	35272362	35272962	0.8	0.5
chr9	35272418	35273018	0.7	0.3
chr9	36521611	36522211	1.1	0.1
chr9	36521618	36522218	1.2	0.2
chr9	36524894	36525494	0.1	0.6
chr9	36837794	36838394	0.4	0.5
chr9	36860626	36861226	2.2	0.4
chr9	37062062	37062662	0.1	0.1
chr9	37206644	37207244	0.7	0.1
chr9	37277785	37278385	0.7	0.4
chr9	37292661	37293261	1.0	0.0
chr9	38680372	38680972	1.1	0.2
chr9	39352822	39353422	0.7	0.5
chr9	40263828	40264428	1.8	0.9
chr9	40264120	40264720	0.5	0.3
chr9	40409374	40409974	1.2	0.7
chr9	40409670	40410270	0.4	0.1
chr9	40494885	40495485	1.6	0.1

chr9	41418464	41419064	0.4	0.2
chr9	41777688	41778288	1.0	0.3
chr9	41925603	41926203	0.2	0.2
chr9	42078521	42079121	1.3	0.5
chr9	42078626	42079226	0.3	0.0
chr9	42085531	42086131	1.7	0.3
chr9	42085558	42086158	1.7	0.2
chr9	42198126	42198726	1.2	0.1
chr9	42468945	42469545	0.8	0.0
chr9	42688183	42688783	1.0	0.6
chr9	43063418	43064018	0.8	0.3
chr9	44254914	44255514	2.5	0.9
chr9	44707388	44707988	1.1	0.4
chr9	44794936	44795536	0.9	0.1
chr9	45157883	45158483	0.5	0.7
chr9	45240414	45241014	1.2	0.3
chr9	45310430	45311030	0.7	0.5
chr9	45480068	45480668	3.4	1.5
chr9	45480110	45480710	3.3	1.5
chr9	45480152	45480752	3.0	1.2
chr9	45480194	45480794	2.9	1.2
chr9	45480345	45480945	3.0	0.9
chr9	46517058	46517658	0.2	0.4
chr9	46771502	46772102	0.3	0.2
chr9	46899757	46900357	0.4	0.2
chr9	46953461	46954061	0.2	0.2
chr9	47674197	47674797	0.9	0.0
chr9	47985319	47985919	0.4	0.1
chr9	48716302	48716902	1.0	0.3
chr9	49764520	49765120	0.7	0.0
chr9	50109037	50109637	0.8	0.1
chr9	50246320	50246920	1.1	0.1
chr9	50535150	50535750	1.6	0.2
chr9	50640593	50641193	6.8	2.8
chr9	50640617	50641217	7.1	3.0
chr9	50640641	50641241	7.2	3.1
chr9	50640689	50641289	7.1	3.0
chr9	50640713	50641313	7.2	3.1

chr9	50640737	50641337	7.2	3.1
chr9	50640761	50641361	7.2	3.0
chr9	50640785	50641385	7.2	3.0
chr9	50640809	50641409	6.9	2.8
chr9	50640833	50641433	6.9	2.8
chr9	50640857	50641457	7.0	2.9
chr9	50640881	50641481	7.1	2.9
chr9	50640905	50641505	7.2	3.0
chr9	50640929	50641529	7.2	3.0
chr9	50640953	50641553	7.3	3.1
chr9	50640977	50641577	7.4	3.1
chr9	50641001	50641601	7.5	3.2
chr9	50641025	50641625	7.2	3.1
chr9	50641049	50641649	7.4	3.2
chr9	50641073	50641673	7.2	3.1
chr9	50641121	50641721	7.0	3.0
chr9	50641145	50641745	6.7	2.8
chr9	50641169	50641769	6.7	2.8
chr9	50641193	50641793	6.8	2.9
chr9	50755284	50755884	1.2	0.3
chr9	52335330	52335930	0.1	0.3
chr9	52529624	52530224	0.3	0.3
chr9	53668322	53668922	0.9	0.0
chr9	53955285	53955885	0.8	0.1
chr9	54063437	54064037	2.0	0.4
chr9	54063666	54064266	1.6	0.2
chr9	55210156	55210756	0.7	0.6
chr9	55210200	55210800	0.5	0.7
chr9	55777612	55778212	3.1	1.1
chr9	55777880	55778480	1.8	0.9
chr9	55782139	55782739	0.8	0.7
chr9	56139998	56140598	0.5	0.1
chr9	56360966	56361566	0.4	0.2
chr9	56395134	56395734	0.4	0.1
chr9	57098342	57098942	0.5	0.5
chr9	57099597	57100197	0.7	0.1
chr9	57251959	57252559	0.9	0.1
chr9	57413524	57414124	0.8	0.1

chr9	57490539	57491139	1.4	0.0
chr9	57982178	57982778	0.8	0.4
chr9	58032205	58032805	0.7	0.1
chr9	58373712	58374312	2.2	0.2
chr9	58669860	58670460	0.0	0.0
chr9	58871938	58872538	0.9	0.3
chr9	59116164	59116764	0.9	0.4
chr9	59235205	59235805	1.4	0.4
chr9	59739667	59740267	1.4	0.8
chr9	59787859	59788459	1.6	0.3
chr9	59849134	59849734	1.7	0.1
chr9	60641753	60642353	1.3	0.4
chr9	60885716	60886316	1.4	0.1
chr9	60918722	60919322	1.1	0.4
chr9	60984017	60984617	1.1	0.9
chr9	61000044	61000644	2.1	0.6
chr9	61478087	61478687	0.1	0.4
chr9	61604807	61605407	1.1	0.1
chr9	62286295	62286895	0.1	0.1
chr9	62327355	62327955	0.2	0.1
chr9	62335425	62336025	2.0	0.5
chr9	62335434	62336034	2.0	0.5
chr9	62335471	62336071	2.0	0.4
chr9	62335480	62336080	1.9	0.4
chr9	62335525	62336125	1.9	0.4
chr9	62335566	62336166	1.9	0.4
chr9	62335615	62336215	1.7	0.3
chr9	62335651	62336251	1.3	0.3
chr9	62438712	62439312	1.0	0.0
chr9	62660222	62660822	0.9	0.1
chr9	62911783	62912383	1.0	0.5
chr9	63043192	63043792	1.4	0.3
chr9	63150519	63151119	1.2	0.8
chr9	63150565	63151165	1.3	0.9
chr9	63211301	63211901	0.2	0.1
chr9	63560483	63561083	0.9	0.2
chr9	63560547	63561147	0.7	0.2
chr9	63560643	63561243	0.8	0.1

chr9	63582632	63583232	1.7	0.7
chr9	63582733	63583333	2.1	0.7
chr9	63619456	63620056	1.6	0.9
chr9	63641187	63641787	1.8	0.5
chr9	63753655	63754255	1.0	0.0
chr9	63753676	63754276	1.3	0.1
chr9	63798083	63798683	0.7	0.1
chr9	63825424	63826024	1.0	0.1
chr9	64378282	64378882	0.4	0.2
chr9	64701760	64702360	0.8	0.5
chr9	64702005	64702605	1.2	0.8
chr9	65117675	65118275	0.7	0.2
chr9	65394459	65395059	0.2	0.3
chr9	65478723	65479323	0.4	0.1
chr9	66829100	66829700	0.1	0.2
chr9	66886925	66887525	0.4	0.1
chr9	66918876	66919476	0.9	0.0
chr9	66946614	66947214	0.6	0.0
chr9	67123750	67124350	0.5	0.1
chr9	67166768	67167368	0.4	0.0
chr9	67209739	67210339	0.1	0.6
chr9	67306686	67307286	0.5	0.2
chr9	67369841	67370441	0.4	0.2
chr9	67449507	67450107	0.9	0.1
chr9	67845171	67845771	0.6	0.2
chr9	68846966	68847566	0.7	0.4
chr9	69554973	69555573	1.4	0.0
chr9	69555111	69555711	0.3	0.1
chr9	69611616	69612216	1.2	0.2
chr9	70224194	70224794	0.7	0.8
chr9	70224203	70224803	0.7	0.9
chr9	70224293	70224893	1.3	0.6
chr9	70665088	70665688	0.4	0.5
chr9	70698803	70699403	0.2	0.4
chr9	71118079	71118679	1.3	0.3
chr9	71337460	71338060	0.0	0.1
chr9	72605492	72606092	1.6	0.2
chr9	72611990	72612590	0.6	0.0
chr9	72612174	72612774	0.5	0.3
chr9	72950909	72951509	1.4	0.3
chr9	72950990	72951590	2.3	0.7
chr9	72951197	72951797	2.2	0.9
chr9	73588992	73589592	0.8	0.1
chr9	74151711	74152311	0.8	0.0
chr9	74336612	74337212	0.7	0.2
chr9	75684789	75685389	0.8	0.7
chr9	75684799	75685399	0.8	0.6
chr9	75684819	75685419	1.0	0.7
chr9	76488643	76489243	1.0	0.3
chr9	77470537	77471137	0.1	0.0
chr9	78312582	78313182	0.2	0.1
chr9	78532817	78533417	1.1	0.5
chr9	78688949	78689549	0.6	0.3
chr9	78813596	78814196	1.6	0.2
chr9	79143694	79144294	1.3	0.1
chr9	79179831	79180431	1.0	0.3
chr9	79791231	79791831	0.3	0.2
chr9	79799337	79799937	0.9	0.1
chr9	79799611	79800211	0.4	0.0
chr9	79931929	79932529	1.1	0.6
chr9	80670073	80670673	0.4	0.1
chr9	82001387	82001987	0.1	0.1
chr9	82044078	82044678	0.5	0.3
chr9	82325816	82326416	0.9	0.1
chr9	82373740	82374340	0.4	0.5
chr9	82875248	82875848	0.4	0.0
chr9	83024117	83024717	1.0	0.3
chr9	83143600	83144200	0.5	0.0
chr9	83531969	83532569	0.3	0.1
chr9	83532267	83532867	1.0	0.3
chr9	83675994	83676594	0.4	0.2
chr9	83935981	83936581	0.1	0.2
chr9	85529552	85530152	0.8	0.5
chr9	85529771	85530371	1.2	0.3
chr9	85700533	85701133	1.1	0.1
chr9	85768979	85769579	0.3	0.0

chr9	85778911	85779511	1.0	0.0
chr9	86068365	86068965	0.6	0.7
chr9	86615836	86616436	0.8	0.0
chr9	87656722	87657322	0.9	0.2
chr9	88598488	88599088	0.6	0.2
chr9	88859245	88859845	0.6	0.1
chr9	89523600	89524200	1.0	0.2
chr9	89605626	89606226	0.1	0.1
chr9	89653755	89654355	0.3	0.1
chr9	89653978	89654578	1.2	0.2
chr9	89687718	89688318	1.3	0.2
chr9	90072780	90073380	0.1	0.1
chr9	90257876	90258476	0.8	0.1
chr9	90602781	90603381	1.8	0.1
chr9	90865010	90865610	0.1	0.1
chr9	91214227	91214827	2.7	1.1
chr9	91214263	91214863	3.0	0.9
chr9	91446919	91447519	0.9	0.0
chr9	92860266	92860866	0.3	0.0
chr9	92860353	92860953	0.1	0.0
chr9	92994648	92995248	1.6	0.8
chr9	93433129	93433729	0.3	0.0
chr9	94104917	94105517	0.1	0.1
chr9	94244362	94244962	0.5	0.0
chr9	94341375	94341975	0.2	0.0
chr9	94475791	94476391	0.2	0.0
chr9	95224105	95224705	0.2	0.2
chr9	95433810	95434410	0.4	0.1
chr9	95477866	95478466	1.2	0.0
chr9	95669830	95670430	0.6	0.0
chr9	95674972	95675572	2.5	1.2
chr9	95675016	95675616	2.4	1.3
chr9	95675236	95675836	2.5	0.9
chr9	96298292	96298892	2.3	0.8
chr9	96629766	96630366	0.2	0.3
chr9	96862734	96863334	0.1	0.1
chr9	96996816	96997416	0.2	0.0
chr9	97518153	97518753	0.8	0.3

chr9	97518173	97518773	1.1	0.4
chr9	97572423	97573023	0.3	0.8
chr9	97672379	97672979	1.1	0.8
chr9	97672421	97673021	1.3	0.6
chr9	97679835	97680435	0.8	0.2
chr9	97819983	97820583	0.3	0.5
chr9	97838710	97839310	0.7	0.3
chr9	98104702	98105302	0.2	0.5
chr9	98104974	98105574	0.5	0.0
chr9	98299047	98299647	0.3	0.2
chr9	98509155	98509755	1.6	0.3
chr9	98753825	98754425	0.1	0.2
chr9	98890551	98891151	1.7	0.1
chr9	99142271	99142871	1.1	0.3
chr9	99206347	99206947	1.3	0.7
chr9	99206571	99207171	1.2	0.1
chr9	100009174	100009774	0.8	0.5
chr9	100009204	100009804	0.7	0.4
chr9	100350975	100351575	0.0	0.2
chr9	100497874	100498474	0.9	0.1
chr9	100497886	100498486	0.8	0.1
chr9	100816147	100816747	0.6	0.3
chr9	100957291	100957891	0.7	0.3
chr9	101257441	101258041	0.8	0.4
chr9	101770811	101771411	0.8	0.3
chr9	102169261	102169861	0.7	0.0
chr9	102537580	102538180	0.2	0.2
chr9	102625750	102626350	0.6	0.1
chr9	103037847	103038447	0.4	0.3
chr9	103074206	103074806	1.3	0.4
chr9	103288755	103289355	1.3	0.4
chr9	103842136	103842736	0.1	0.1
chr9	104108803	104109403	0.1	0.1
chr9	104898446	104899046	0.7	0.3
chr9	105047015	105047615	0.3	0.3
chr9	105873567	105874167	1.0	0.1
chr9	106041837	106042437	0.5	0.1
chr9	106102395	106102995	0.9	0.6

chr9	106109332	106109932	1.1	0.3
chr9	106359257	106359857	0.6	0.4
chr9	106394715	106395315	1.3	0.4
chr9	106496428	106497028	1.6	0.5
chr9	106496450	106497050	1.6	0.5
chr9	106590335	106590935	1.0	0.2
chr9	106787575	106788175	3.5	1.1
chr9	106787743	106788343	2.9	1.1
chr9	107203498	107204098	0.5	0.4
chr9	107251843	107252443	0.2	0.2
chr9	107393034	107393634	2.1	0.3
chr9	107478827	107479427	1.2	0.1
chr9	107669875	107670475	1.2	0.3
chr9	107669993	107670593	1.7	0.5
chr9	107948863	107949463	0.9	0.0
chr9	108439814	108440414	1.3	0.3
chr9	108439948	108440548	1.7	0.3
chr9	108480468	108481068	1.0	0.5
chr9	109567718	109568318	0.2	0.4
chr9	110206936	110207536	0.2	0.6
chr9	110526187	110526787	0.2	0.0
chr9	110526259	110526859	0.3	0.2
chr9	110647902	110648502	0.5	0.4
chr9	110647912	110648512	0.5	0.5
chr9	111162673	111163273	0.9	0.2
chr9	111401478	111402078	0.8	0.4
chr9	112811659	112812259	2.5	0.6
chr9	112811774	112812374	2.1	0.6
chr9	113395486	113396086	1.9	0.6
chr9	114457243	114457843	0.5	0.3
chr9	114493350	114493950	1.2	0.9
chr9	114493520	114494120	0.8	0.8
chr9	114907828	114908428	1.4	0.2
chr9	114916459	114917059	0.6	0.2
chr9	115090237	115090837	1.0	0.6
chr9	115348538	115349138	1.3	0.1
chr9	115348557	115349157	1.1	0.1
chr9	115735300	115735900	1.3	0.7
chr9	115764068	115764668	1.1	0.1
chr9	115963356	115963956	0.6	0.1
chr9	115999419	116000019	0.1	0.1
chr9	116107746	116108346	0.8	0.0
chr9	116151489	116152089	2.8	0.8
chr9	116151499	116152099	3.0	0.7
chr9	116706479	116707079	1.4	0.2
chr9	116983359	116983959	0.9	0.2
chr9	116983388	116983988	0.8	0.3
chr9	117668358	117668958	1.8	0.2
chr9	117668454	117669054	1.6	0.0
chr9	119043646	119044246	0.8	0.2
chr9	119043837	119044437	0.9	0.3
chr9	119860526	119861126	0.9	0.1
chr9	119913024	119913624	0.2	0.4
chr9	119913865	119914465	0.7	0.1
chr9	119920352	119920952	0.7	0.0
chr9	120061652	120062252	1.1	0.4
chr9	120482098	120482698	0.2	0.1
chr9	120722083	120722683	0.6	0.4
chr9	120722173	120722773	0.4	0.2
chr9	120776600	120777200	2.9	1.3
chr9	120776897	120777497	1.4	0.2
chr9	121176012	121176612	1.0	0.3
chr9	121176026	121176626	0.8	0.3
chr9	121252681	121253281	1.7	0.2
chr9	121252724	121253324	1.7	0.3
chr9	121704849	121705449	1.0	0.1
chr9	122010185	122010785	1.4	0.1
chr9	122087182	122087782	0.3	0.2
chr9	122306760	122307360	0.6	0.2
chr9	122333170	122333770	0.9	0.5
chr9	122518807	122519407	0.7	0.3
chr9	122566970	122567570	0.5	0.5
chr9	122591615	122592215	0.4	0.2
chr9	122878534	122879134	0.7	0.3
chr9	123294992	123295592	0.1	0.1
chr9	124062401	124063001	2.2	0.5

chr9	124062559	124063159	1.3	0.1
chrX	4272062	4272662	0.4	0.2
chrX	5643332	5643932	2.1	0.4
chrX	5643397	5643997	2.0	0.4
chrX	5647206	5647806	0.4	0.2
chrX	5700950	5701550	1.1	0.1
chrX	5963446	5964046	2.0	0.5
chrX	6123797	6124397	1.8	0.3
chrX	7071710	7072310	0.6	0.2
chrX	7094621	7095221	0.1	0.3
chrX	7105041	7105641	1.9	0.7
chrX	7105314	7105914	2.3	0.8
chrX	7356380	7356980	0.7	0.1
chrX	7635129	7635729	0.2	0.3
chrX	8746588	8747188	0.9	0.2
chrX	9051500	9052100	1.0	0.1
chrX	9853987	9854587	0.8	0.2
chrX	10617809	10618409	0.8	0.0
chrX	10652805	10653405	0.4	0.4
chrX	10811214	10811814	3.4	1.1
chrX	10811240	10811840	3.2	1.1
chrX	10811258	10811858	3.2	1.2
chrX	10933903	10934503	1.3	0.7
chrX	10934020	10934620	0.3	0.2
chrX	11005533	11006133	1.2	0.6
chrX	11129288	11129888	0.4	0.2
chrX	11221855	11222455	1.0	0.0
chrX	11623780	11624380	2.4	1.0
chrX	11623816	11624416	2.3	0.9
chrX	11623825	11624425	2.5	0.8
chrX	12081422	12082022	1.3	0.1
chrX	12081432	12082032	1.3	0.1
chrX	12102491	12103091	0.6	0.1
chrX	12145728	12146328	0.0	0.1
chrX	12906686	12907286	0.4	0.7
chrX	13105630	13106230	0.2	0.0
chrX	13162516	13163116	0.8	0.2
chrX	13420066	13420666	0.4	0.0
chrX	13711964	13712564	0.5	0.0
chrX	13879000	13879600	0.9	0.1
chrX	13880889	13881489	0.8	0.2
chrX	15141831	15142431	1.1	0.5
chrX	15141922	15142522	1.5	0.5
chrX	16470272	16470872	3.9	1.7
chrX	16470297	16470897	3.8	1.7
chrX	16470494	16471094	3.1	1.5
chrX	16515623	16516223	1.3	0.1
chrX	16515714	16516314	1.4	0.1
chrX	16817307	16817907	0.6	0.0
chrX	16845896	16846496	1.9	0.2
chrX	17030280	17030880	0.7	0.6
chrX	17030539	17031139	0.8	0.5
chrX	17128454	17129054	0.6	0.0
chrX	17267808	17268408	0.1	0.0
chrX	17910140	17910740	0.7	0.1
chrX	18012246	18012846	0.6	1.2
chrX	18154935	18155535	0.4	0.4
chrX	19595875	19596475	1.1	0.1
chrX	20515512	20516112	0.8	0.3
chrX	20690967	20691567	0.3	0.0
chrX	21175976	21176576	0.1	0.1
chrX	21762433	21763033	0.5	0.2
chrX	22271013	22271613	1.0	0.0
chrX	22271202	22271802	0.4	0.3
chrX	23793072	23793672	0.5	0.0
chrX	33410358	33410958	0.5	0.0
chrX	33548024	33548624	0.9	0.1
chrX	34345486	34346086	0.1	0.1
chrX	35361487	35362087	1.6	0.1
chrX	35437172	35437772	0.1	0.1
chrX	35450381	35450981	0.4	0.0
chrX	35450483	35451083	0.3	0.1
chrX	36150159	36150759	1.8	0.6
chrX	38035395	38035995	0.7	0.3
chrX	38093616	38094216	1.6	0.2
chrX	38665966	38666566	0.6	0.0

chrX	38666122	38666722	1.6	0.5
chrX	39311624	39312224	1.3	0.8
chrX	39311715	39312315	1.6	0.9
chrX	39488506	39489106	0.3	0.0
chrX	40187706	40188306	0.5	0.2
chrX	40908209	40908809	0.9	0.1
chrX	43805009	43805609	1.4	0.3
chrX	44622559	44623159	1.3	0.1
chrX	45266300	45266900	0.6	0.1
chrX	45369913	45370513	0.2	0.5
chrX	46736856	46737456	1.6	0.3
chrX	46737037	46737637	1.9	0.5
chrX	47467954	47468554	0.3	0.1
chrX	47629312	47629912	1.0	0.4
chrX	48604297	48604897	0.6	0.2
chrX	49258754	49259354	0.8	0.0
chrX	49846310	49846910	0.3	0.1
chrX	49893185	49893785	0.4	0.3
chrX	49918438	49919038	0.4	0.1
chrX	50514475	50515075	2.2	0.6
chrX	50731056	50731656	0.3	0.0
chrX	51711711	51712311	0.5	0.3
chrX	51802797	51803397	0.5	0.3
chrX	51893777	51894377	0.5	0.3
chrX	51984780	51985380	0.5	0.3
chrX	52082441	52083041	0.6	0.4
chrX	52331883	52332483	0.5	0.3
chrX	52539715	52540315	0.5	0.3
chrX	53018289	53018889	0.6	0.4
chrX	54497343	54497943	0.5	0.2
chrX	54929014	54929614	1.3	0.3
chrX	55167666	55168266	0.3	0.1
chrX	55418457	55419057	0.7	0.3
chrX	55815277	55815877	1.3	0.1
chrX	58733879	58734479	0.1	0.2
chrX	59705482	59706082	0.2	0.3
chrX	60317871	60318471	0.3	0.2
chrX	61057172	61057772	0.3	0.1
chrX	62301456	62302056	0.7	0.2
chrX	62822198	62822798	0.7	0.3
chrX	62822389	62822989	0.8	0.7
chrX	63344980	63345580	1.4	0.0
chrX	65824271	65824871	0.1	0.0
chrX	66039169	66039769	1.1	0.2
chrX	66146082	66146682	0.2	0.1
chrX	66351900	66352500	0.5	0.0
chrX	66833289	66833889	0.4	0.1
chrX	68904266	68904866	0.2	0.4
chrX	69247106	69247706	0.3	0.1
chrX	69267644	69268244	0.3	0.4
chrX	69513215	69513815	1.2	0.5
chrX	69807857	69808457	0.5	0.1
chrX	69945298	69945898	0.8	0.0
chrX	70018228	70018828	1.3	0.2
chrX	70476951	70477551	0.9	0.0
chrX	70566788	70567388	1.4	0.3
chrX	70591858	70592458	0.3	0.0
chrX	71336329	71336929	2.4	0.8
chrX	71336583	71337183	1.6	0.3
chrX	71585325	71585925	1.2	0.5
chrX	72028025	72028625	0.3	0.0
chrX	72199465	72200065	0.2	0.0
chrX	72664017	72664617	0.9	0.1
chrX	73097387	73097987	0.3	0.4
chrX	73177703	73178303	1.0	0.1
chrX	73399335	73399935	2.3	0.4
chrX	73399408	73400008	2.0	0.4
chrX	75354138	75354738	0.0	0.1
chrX	75576983	75577583	0.6	0.1
chrX	75586843	75587443	0.5	0.0
chrX	75594051	75594651	0.5	0.0
chrX	76334763	76335363	0.4	0.4
chrX	76403639	76404239	0.8	0.1
chrX	76505308	76505908	0.6	0.3
chrX	77419494	77420094	0.2	0.1
chrX	77425035	77425635	0.8	0.1

chrX	78346782	78347382	0.8	0.1
chrX	78531719	78532319	1.2	0.0
chrX	78531876	78532476	0.8	0.0
chrX	79398787	79399387	0.7	0.4
chrX	81247429	81248029	0.1	0.1
chrX	81425937	81426537	1.4	0.0
chrX	82682213	82682813	0.5	0.3
chrX	82682232	82682832	0.5	0.3
chrX	83495134	83495734	1.1	0.2
chrX	83766695	83767295	1.3	0.3
chrX	84009636	84010236	0.3	0.3
chrX	84847752	84848352	0.0	0.3
chrX	85713870	85714470	1.8	0.6
chrX	85904595	85905195	0.6	0.0
chrX	86070807	86071407	0.8	0.2
chrX	86096379	86096979	0.7	0.2
chrX	86615750	86616350	1.5	0.2
chrX	88270576	88271176	0.4	0.2
chrX	88270673	88271273	0.3	0.3
chrX	88432647	88433247	1.3	0.3
chrX	88622833	88623433	1.5	0.2
chrX	88622926	88623526	1.3	0.3
chrX	88623106	88623706	1.1	0.4
chrX	88707001	88707601	0.8	0.2
chrX	88707094	88707694	0.7	0.3
chrX	88933247	88933847	0.5	0.5
chrX	89196090	89196690	0.7	0.2
chrX	89196183	89196783	0.7	0.1
chrX	89606352	89606952	0.0	0.5
chrX	89725894	89726494	3.4	1.3
chrX	89726004	89726604	3.6	1.4
chrX	89726015	89726615	3.6	1.5
chrX	90120001	90120601	2.4	0.5
chrX	90120242	90120842	2.0	0.5
chrX	90351676	90352276	0.2	0.2
chrX	91264395	91264995	0.8	0.7
chrX	91658946	91659546	0.2	0.0
chrX	92705331	92705931	0.3	0.2

chrX	94571607	94572207	1.3	0.6
chrX	94624163	94624763	0.0	0.0
chrX	94807087	94807687	0.4	0.2
chrX	95127626	95128226	0.2	0.1
chrX	95812346	95812946	0.4	0.4
chrX	96197618	96198218	0.3	0.1
chrX	96212930	96213530	0.4	0.0
chrX	96473806	96474406	0.2	0.2
chrX	96614245	96614845	0.4	0.7
chrX	97241905	97242505	0.3	0.3
chrX	97380206	97380806	0.6	0.0
chrX	97866565	97867165	1.2	0.2
chrX	98183043	98183643	1.1	0.1
chrX	98943384	98943984	1.9	0.9
chrX	98943446	98944046	2.1	1.0
chrX	98943580	98944180	3.6	1.5
chrX	98943778	98944378	0.5	0.3
chrX	99375437	99376037	0.0	0.2
chrX	100175778	100176378	0.4	0.2
chrX	100175869	100176469	0.4	0.1
chrX	100513396	100513996	0.6	0.4
chrX	101851945	101852545	0.4	0.1
chrX	101900098	101900698	1.2	0.6
chrX	103417558	103418158	0.5	0.1
chrX	103980577	103981177	2.4	0.0
chrX	103980846	103981446	2.0	0.3
chrX	104508166	104508766	2.7	1.0
chrX	105045932	105046532	0.1	0.1
chrX	105605730	105606330	1.9	0.2
chrX	106538065	106538665	0.4	0.3
chrX	107470367	107470967	1.2	0.2
chrX	107470436	107471036	1.3	0.4
chrX	107515410	107516010	1.2	0.7
chrX	107684568	107685168	1.5	0.8
chrX	107684818	107685418	1.5	0.2
chrX	109025139	109025739	0.3	0.1
chrX	109519437	109520037	1.0	0.5
chrX	110556029	110556629	1.6	0.6

chrX	112715125	112715725	0.4	0.4
chrX	112769264	112769864	0.1	0.3
chrX	113178324	113178924	1.1	0.4
chrX	113235014	113235614	1.7	0.2
chrX	113235104	113235704	1.9	0.2
chrX	113657251	113657851	0.1	0.0
chrX	113733249	113733849	1.4	0.1
chrX	114407155	114407755	1.9	0.1
chrX	114549089	114549689	0.7	0.1
chrX	114549190	114549790	1.0	0.1
chrX	114712096	114712696	0.7	0.6
chrX	115752005	115752605	0.1	0.2
chrX	115797910	115798510	1.0	0.4
chrX	115797989	115798589	1.1	0.3
chrX	117485369	117485969	0.5	0.1
chrX	117611945	117612545	0.2	0.0
chrX	118838623	118839223	0.4	0.3
chrX	119521144	119521744	0.4	0.8
chrX	119521245	119521845	0.3	0.7
chrX	121404169	121404769	0.7	0.4
chrX	122058060	122058660	0.7	0.4
chrX	122830774	122831374	1.2	0.1
chrX	122999039	122999639	0.4	0.2
chrX	124186820	124187420	0.7	0.3
chrX	124622891	124623491	1.8	0.2
chrX	125947393	125947993	1.2	0.7
chrX	127000540	127001140	1.2	0.0
chrX	127172924	127173524	0.9	0.3
chrX	127703399	127703999	0.6	0.4
chrX	129379897	129380497	0.5	0.1
chrX	129427233	129427833	0.3	0.2
chrX	129627676	129628276	0.7	0.0
chrX	130017058	130017658	0.5	0.5
chrX	131202379	131202979	0.9	0.4
chrX	131293320	131293920	0.1	0.1
chrX	132619204	132619804	0.9	0.3
chrX	132619391	132619991	1.4	0.5
chrX	132792437	132793037	0.8	0.3

chrX	132902002	132902602	0.4	0.1
chrX	132936149	132936749	0.4	0.1
chrX	133250817	133251417	1.3	0.5
chrX	133250970	133251570	1.4	0.6
chrX	133531367	133531967	0.2	0.1
chrX	133572588	133573188	2.4	0.8
chrX	133698727	133699327	0.3	0.1
chrX	134120898	134121498	1.3	0.3
chrX	134251649	134252249	1.0	0.1
chrX	135219553	135220153	0.2	0.2
chrX	135888928	135889528	0.2	0.0
chrX	136442945	136443545	1.6	0.1
chrX	136442971	136443571	1.9	0.1
chrX	136873226	136873826	0.9	0.7
chrX	136873366	136873966	0.8	0.6
chrX	137388746	137389346	0.4	0.0
chrX	137491259	137491859	0.6	0.2
chrX	137673919	137674519	0.4	0.0
chrX	137897967	137898567	3.7	1.2
chrX	137898236	137898836	2.6	1.0
chrX	138199435	138200035	0.5	0.3
chrX	138411515	138412115	1.7	0.5
chrX	138443280	138443880	1.1	0.5
chrX	139928123	139928723	0.1	0.1
chrX	140004105	140004705	0.6	0.0
chrX	140191708	140192308	1.4	0.8
chrX	140191754	140192354	1.4	0.7
chrX	142209172	142209772	0.1	0.2
chrX	143212241	143212841	0.8	0.3
chrX	143212504	143213104	0.8	0.3
chrX	144080578	144081178	0.0	0.2
chrX	144120978	144121578	1.3	0.4
chrX	144571373	144571973	0.8	0.0
chrX	144890742	144891342	0.8	0.0
chrX	145063857	145064457	0.8	0.0
chrX	145674152	145674752	0.8	0.0
chrX	145843186	145843786	0.8	0.1
chrX	145956632	145957232	0.8	0.0

chrX	145990147	145990747	0.7	0.1
chrX	147102679	147103279	1.5	0.5
chrX	147240025	147240625	1.2	0.2
chrX	147733228	147733828	0.4	0.1
chrX	148726016	148726616	2.0	0.7
chrX	152087385	152087985	1.4	0.3
chrX	152194045	152194645	0.3	0.2
chrX	153109221	153109821	0.0	0.1
chrX	153928051	153928651	1.7	1.1
chrX	153928221	153928821	1.5	0.8
chrX	153939813	153940413	1.5	0.1
chrX	154018749	154019349	0.5	0.3
chrX	154095817	154096417	1.8	0.3
chrX	154095881	154096481	1.5	0.1
chrX	154242950	154243550	0.3	0.0
chrX	156554318	156554918	0.1	0.1
chrX	157693189	157693789	0.6	0.1
chrX	158047878	158048478	0.7	0.0
chrX	158156223	158156823	0.4	0.1
chrX	158156275	158156875	0.6	0.3
chrX	158366447	158367047	1.3	0.3
chrX	158472601	158473201	0.7	0.2
chrX	158678799	158679399	1.2	0.4
chrX	159024164	159024764	0.3	0.1
chrX	159394422	159395022	0.9	0.4
chrX	159475703	159476303	0.6	0.0
chrX	161433803	161434403	1.1	0.1
chrX	162214490	162215090	1.9	0.3
chrX	162214515	162215115	1.9	0.2
chrX	162862448	162863048	0.8	0.3
chrX	163129181	163129781	1.2	0.2
chrX	163129329	163129929	1.5	0.3
chrX	163500366	163500966	0.4	0.0
chrX	163598635	163599235	0.1	0.0
chrX	163973351	163973951	0.3	0.0
chrX	166116121	166116721	0.4	0.9
chrX	166517629	166518229	2.1	0.5
chrX	166517848	166518448	2.2	0.7
chrX	166640384	166640984	2.1	0.5
chrX	166640603	166641203	2.2	0.7
chrY	789610	790210	0.7	0.0
chrY	1041707	1042307	2.0	0.1
chrY	2877772	2878372	0.7	0.3

Table S3.3 GLI^{FLAG} dataset kmer-SVM scores. kmer-SVM scores for LDwGBM and NPwGBM datasets.

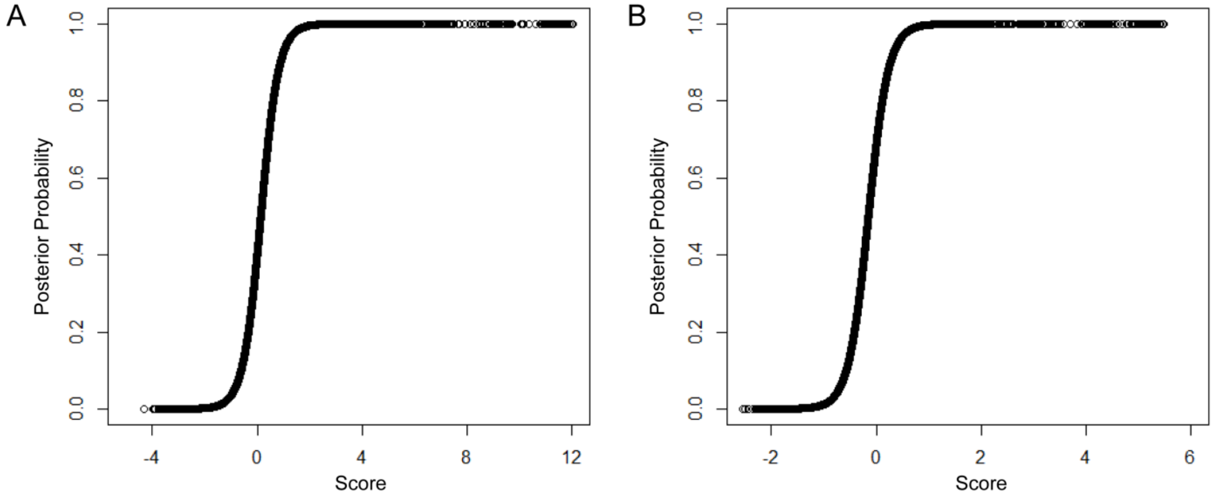


Figure S3.2. Posterior probability of kmer-SVM scores. Plots depicting the posterior probabilities assigned to scores for both (A) LDwGBM and (B) NPwGBM datasets. The graphs indicate that scores above 1 have a high confidence of being Hh regulatory regions.

	Positive (kmer-SVM score >= 1; posterior probability = 1)		**Negative (kmer-SVM score <= -1; posterior probability = 0)**			
Open Chromatin Markers	**Number that overlap with markers**	**Number with no overlap**	**Number that overlap with markers**	**Number with no overlap**	**Z-Test**	**two-tailed p-value**
DNase I Mesoderm E11.5	112	416	5970	30023	2.8332	p < 0.05
H3K4me1 Heart	37	491	5011	30982		
H3K4me3 Heart	7	521	541	35452		
H3K27ac Heart	8	520	1064	34929		
H3K4me1 Liver	75	453	3864	32129	2.5511	p < 0.01
H3K4me3 Liver	9	519	494	35499		
H3K27ac Liver	43	485	905	35088	8.076	p < 0.0

Table S3.4. Overlap of predicted high confidence positive and negative regions with embryonic open chromatin. Tabulation of the number of genomic regions predicted by both LDwGBM and NPwGBM that are classified with high confidence as Hh enhancer regions or as nonregulatory regions that overlap with mesoderm DNase I (E 11.5) or enhancer markers (E14.5).

Figure S3.3. Expression of GLI1 within E14.5 mouse embryo. *In situ* hybridization of GLI1 (image from genepaint.org, EN1215) showing active Hh signaling at E14.5 in liver but not heart.

Annotated Hedgehog Pathway Gene	Forward Primer	Reverse Primer
Boc	GGTAGAGAGGATGCAGGGC	GGTAGAGAGGATGCAGGGC
Dpp6	CTCATTTCAAGATGAGGCTAG	GACCAGAGAGCCATTCAATCG
Gli3	TAATGCTGATGAATTCTCCG	TAATGCTGATGAATTCTCCG
Hhip	GCAAGACCTTCCTCCCAGTC	CAGCCTGCCTCTCTTACTTTC
Hipk2	GTACTTCTCACGCTTCTACC	TGAATGGAGGTAGGGCACC
Ptch1	GTATGGCATCGCTCTATAGACG	TGTCATCCTAGCACTTGGAC
Scube1	AGGCTCTAAGCACAGCCTTG	CTGGCCTGAGGCTAATGGAT
Shh	CATCACAGGCAGAAAGCTCA	CTCAGCTTCTCCTGCACCAT
Tgfbr2	GGCAATGCTTTGACATGAGAC	ACATACGTGTCCTAGCCAGG
Hhat	CAGCTGTGAGAGGAACCAC	CTGTGTATGGCTGCTGGGC

Table S3.5. PCR primers for amplification of mouse genomic regions. Mouse genomic coordinates (mm9) for primer sequence used to amplify candidate regions. **Format: xls**

Chapter IV

Transcriptome of the inner circular smooth muscle of the developing mouse intestine: evidence for regulation of visceral smooth muscle genes by the Hedgehog target gene, *cJun*

4.1 Abstract

Two layers of visceral smooth muscle comprise the intestinal muscularis externa: the inner circular muscle (ICM) and outer longitudinal muscle (OLM). Coordinated contraction of these layers facilitates digestion. During development, the ICM forms two days earlier than the OLM. Exploiting this developmental timing difference, we performed transcriptome analysis of intestinal mesenchyme tissue at E14.5, when the ICM, but not the OLM is present, to investigate the transcriptional program of the ICM.

We identified 3967 genes enriched in E14.5 intestinal mesenchyme. The gene expression profiles were clustered and annotated to known muscle genes identifying a muscle-enriched subcluster. Using publically available *in situ* data, 127 were verified as expressed in ICM. Examination of the promoter and regulatory regions for these co-expressed genes revealed enrichment for cJUN transcription factor binding sites and cJUN protein was also enriched in ICM. cJUN ChIP-seq was then performed at E14.5, revealing that cJUN regulatory regions contain characteristics of muscle enhancers. Additional analysis established that cJUN is a target of Hedgehog signaling.

Gurdziel K, Vogt KR, Walton KD, Scheider GK, Gumucio DL. *Transcriptome of the inner circular smooth muscle of the developing intestine: evidence for regulation of visceral smooth muscle genes by Hedgehog target gene,* cJun. Developmental Dynamics.

This work provides the first transcriptional catalog for the developing ICM and suggests that cJUN is an important regulator of gene expression in the ICM.

4.2 Introduction

Smooth muscle (SM) is a critical component for the function of many organs, including respiratory (Tollet et al., 2001; Goyal and Chaudhury, 2008), urogenital (Baker and Gomez, 1998; DiSandro et al., 1998) and gastrointestinal tissues. The adult intestine contains several populations of visceral smooth muscle (ISM), located in different regions of the tube. A thin muscularis mucosa lies just beneath the epithelium, while the muscularis externa (ME) forms the outside of the tube, surrounding the mucosa and submucosa. The bi-layered ME contains an inner circular (ICM) and outer longitudinal muscle (OLM), with enteric nerves nestled between these layers (Gabella, 1985; Thomason et al., 2012).

The smooth muscle populations of the ME are of particular clinical interest because of their critical role in gut motility (Bitar, 2003). Alterations to muscle contractility are seen in irritable bowel syndrome (Whorwell et al., 1986; Van der Vliet et al., 1992; Abrams et al., 2012) and during gut inflammation (Ohama et al., 2007a). Some forms of chronic intestinal pseudoobstruction are also rooted in ISM pathology (visceral myopathy) (Antonucci et al., 2008). Both familial (Anuras et al., 1981; Sipponen et al., 2009) and sporadic cases (Montalvo et al., 2004) of visceral myopathy have been reported and a few susceptibility loci have been identified, including DNA POLG (Ch. 21) (Vissing et al., 2002; Van Goethem et al., 2003; Giordano et al., 2009) and ACTG2 (Ch. 2) (Lehtonen et al., 2012; Holla et al., 2014; Thorson et al., 2014; Wangler et al., 2014). Interestingly, the various ISM layers can be differently affected.

Pathological changes specific to the muscularis mucosae (Alstead et al., 1988) or to the OLM (Anuras et al., 1983) have been reported and loss of alpha-smooth muscle actin expression has been noted specifically in the ICM (Smith et al., 1992; Donnell et al., 2008).

In addition to their distinct patterns of pathology, the layers of ISM develop in different time windows. The ICM is the first layer to appear; it is well developed by embryonic day 14 (E14). The OLM becomes clearly organized by E16 (Kedinger et al., 1990; Thomason et al., 2012). Development of villus smooth muscle occurs at approximately E18, while the sub-epithelial muscularis mucosa matures after birth (Kolterud et al., 2009; Zacharias et al., 2011).

Despite their critical importance to gut homeostasis, little is known about the molecular characteristics or gene regulatory programs of any of the ISM layers. In this study, we report the first transcriptome profile for the embryonic ISM. The early development of the ICM allowed us the opportunity to restrict the analysis to that layer. Using clustering analysis of RNA-seq data in combination with publically available *in situ* expression data for the E14.5 mouse (Visel et al., 2004; Diez-Roux et al., 2011), we identified a subcluster of over 100 genes with confirmed expression in the ICM and analyzed the promoters of co-clustered genes to identify transcription factors that might be involved in the regulation of these ISM genes. Among these enriched transcription factors was cJUN; antibody staining of intestinal sections confirmed that cJUN protein is strongly expressed in ICM. Further ChIP-seq studies identified 2741 potential cJUN regulatory regions that are also expressed in ICM. Our data suggest a previously undocumented role for cJUN in the regulation of the ICM transcriptional program.

We also further explored the regulatory relationship between cJUN and Hedgehog (Hh) signaling with respect to ICM gene regulation. Hh has been previously shown to be important in activating gene expression in smooth muscle of several tissues, including the bladder (Shiroyanagi et al., 2007; Liu et al., 2010; Tasian et al., 2010), intestine (Sukegawa et al., 2000; Kolterud et al., 2009; Zacharias et al., 2011; Huang et al., 2013) and ureter (Yu et al., 2002; Caubit et al., 2008). Here, we document that cJUN is a Hh target and identify an enhancer that mediates Hh-dependent cJUN induction.

4.3 Results and Discussion

4.3.1 Identification of intestinal visceral smooth muscle genes

We began this analysis by identifying genes that are enriched in the mesenchymal layer of the E14.5 intestine. To do this, we separated epithelial and mesenchymal tissue populations from WT mouse intestines at E14.5 and collected RNA from each layer for high-throughput sequencing (see Methods). The two transcriptomes were compared to identify genes that were differentially expressed between the intestinal mesenchyme (which contains muscle) and the intestinal epithelial tissue (which is devoid of muscle) (n = 3). This analysis identified 3967 (adjusted p-value ≤ 0.05) genes that were at least 2 fold enriched in the mesenchyme tissue (Supplemental Table 1).

To begin to identify potential smooth muscle genes within this enriched set, we used Gene Set Enrichment Analysis (GSEA) (Subramanian et al., 2005). Although its Molecular Signatures Database contained no sets of enriched muscle genes derived from SM tissue, we reasoned that due to its contractile nature, some smooth muscle genes might overlap with genes identified in vascular, cardiac and skeletal muscle. Indeed, overlap between gene expression and regulatory programs in muscle subtypes has been observed (Li et al., 1996). Comparing those muscle gene sets to our 3967 mesenchymally enriched genes identified 253 putative ISM genes (enriched muscle gene sets, p-value ≤ 0.05, are listed in Table 1). Using publically available *in situ* images (Visel et al., 2004; Diez-Roux et al., 2011), we next examined the expression pattern of each of these 253 genes in E14.5 mouse intestine. This analysis confirmed 33 genes that exhibited clear expression in the area of the ICM (Figure 4.1A).

To further expand this ISM dataset, we hierarchically clustered genes upregulated in the mesenchyme compared to epithelial tissue (Eisen et al., 1998). Since many of the 33 identified genes were structural genes that are associated with contractility, we expected that they might be expressed at similar levels within the mesenchyme and that other, similarly expressed genes might also cluster with these genes. Indeed, Figure 4.1B shows that when the expression profiles of 9490 mesenchymally expressed genes are clustered, all 33 genes with verified expression in the ICM domain (annotated with black tick marks) cluster together. Other genes within this same subcluster, with an average expression value >500 were then examined for localized expression within the ICM (Visel et al., 2004; Diez-Roux et al., 2011). This comparison identified an additional 94 genes that are expressed in the ICM (Figure 4.1C).

Among the genes that are express in the ICM, several (e.g., *Actc1*, *Lmod1*, *Myom1*, *Tnnt2*) were associated with other muscle types (Gunning et al., 1984; Vinkemeier et al., 1993; Townsend et al., 1994; Zhang et al., 1996). Others are apparently unique to smooth muscle (e.g., *Cav1, Cnn1, Myl9, Smtn, Tagln*) (Lees-Miller et al., 1987; Kumar et al., 1989; Strasser et al., 1993; van der Loop et al., 1996; Austin et al., 2012). Several expected muscle regulatory factors (e.g., *Mef2C*, *Myocd*, and *SRF*) are present in the expression profile and are expressed in the ICM according to the *in situ* analysis (Miano, 2003; Wang et al., 2003; Creemers et al., 2006). Additionally, several components or known targets of the Hh signaling pathway (e.g., Boc, Gli1, Gli3, Hhip, Mef2C, Myocd) several of which are known to be enriched in ISM (Kolterud et al., 2009), are present in the list.

These 127 genes are clearly not a comprehensive catalog of ICM gene expression. The analysis is based on one developmental time period (E14.5) and the study was purposefully initiated using genes that are mesenchymally enriched at this time and expressed at medium to high levels. For example, *Arid5b*, a regulator of smooth muscle differentiation (Watanabe et al., 2002), is not differentially expressed between epithelial and mesenchyme tissue (Teillet et al., 1998) and the SM-associated genes, *Il1b* and *Mitf* are both expressed in the mesenchyme but at low levels (Chen et al., 2006; Chi et al., 2007). We also excluded genes that are not expressed in the ICM at E14.5. For example, *Pbx1*, a transcription factor associated with myogenic programs (Berkes et al., 2004), is mesenchymally enriched in our dataset but is not present in the ICM at this time point (Genepaint ID: ES1284).

4.3.2 Identification of transcriptional regulators of intestinal visceral smooth muscle genes

To begin to identify transcription factors that might be responsible for coordinating smooth muscle gene expression, we next analyzed the promoter regions of the subcluster containing the 127 muscle genes with verified ICM expression using DiRE (Gotea and Ovcharenko, 2008). The top ten transcription factors enriched in these gene promoters included several known to be involved in regulatory programs in skeletal muscle or in vascular smooth muscle, including RP58, NF1, TAL1, NOTCH1, PAX4, cJUN, HOXA9, and MEIS1 (Figure 4.2A) (Kami et al., 1995; Tao et al., 1998; Knoepfler et al., 1999; Daury et al., 2001; Ema et al., 2003; Di Padova et al., 2007; Yokoyama et al., 2009; Kossler et al., 2011; Raines et al., 2013; Mourikis and Tajbakhsh, 2014; Summers et al., 2015). To narrow this putative regulator list to those potentially relevant to ICM regulation, we again turned to the *in situ* patterns. Of the top 10 enriched transcription factors, cJUN is unique in that it is expressed robustly in the inner circular muscle region at E14.5 (Figure 4.2K). Thus, we further examined the role of cJUN in intestinal ISM expression.

To confirm cJUN expression in ICM, we examined whether this protein co-localizes with the smooth muscle marker, alpha smooth muscle actin (αSMA) and with GLI1, a target of Hedgehog signaling that is required for intestinal smooth muscle development and maintenance (Ramalho-Santos et al., 2000; Sukegawa et al., 2000; Madison et al., 2005; Kolterud et al., 2009; Zacharias et al., 2011). Intestines from *Gli1*$^{eGFP/+}$ mice were immunostained with anti-cJUN, anti-αSMA and anti-eGFP (*Gli1*) at key time points during ISM development (E12.5, E14.5, E16.5 and E18.5). At E12.5, prior to formation of the ICM, αSMA staining marks subepithelial mesenchymal cells. Neither GLI1 nor cJUN localize with cells staining positive for αSMA at this stage (Figure 4.3A-D). However, GLI1 and cJUN co-localize in a different subset of mesenchymal cells of unknown type (Figure 4.3RT). By E14.5, when the ICM is clearly formed, cJUN co-localizes entirely with αSMA (Figure 4.3GH). GLI1 (EGFP) expression is most robust in the inner boundary of the ICM (Figure 4.3F), as shown previously (Kolterud et al., 2009). At E16.5 cJUN and αSMA mark both the ICM and the newly established outer longitudinal muscle

(OLM) layer (Figure 4.3KL). GLI1 remains most strongly expressed in the ICM (Figure 4.3J). At E18.5, αSMA marks the cells in the inner circular, outer longitudinal and villus core muscle (Figure 4.3W). Neither GLI1 nor cJUN are expressed in the villus core muscle prior to birth; however, both are still expressed within the ICM (Figure 4.3NP). In addition, these two markers stain a population of vascular smooth muscle cells in the submucosal vascular plexus (Figure 4.3VX).

4.3.3 Identification of cJUN binding locations in E14.5 intestines

Taken together, these data suggest that cJUN may be a regulator of intestinal ISM genes; it is enriched in the promoters of mesenchymally enriched genes and it exclusively marks the ICM region at E14.5. To investigate this further, we used ChIP-seq to identify cJUN binding sites. Intestines from E14.5 C57BL/6J fetuses were harvested and grown in culture under conditions identical to the collection of the epithelial and mesenchyme profiles except that the tissue separation was not done. ChIP was performed on whole intestines with cJUN antibody and the resulting libraries were sequenced. In total, 21.1 million cJUN immunoprecipitated and 23.5 million input 50-bp short reads were generated. Using a p-value threshold of < 0.05, 2741 sequence peaks were identified by comparing read enrichment from cJUN immunoprecipitated DNA to input control.

The sequence peaks (Supplemental Table 2) were annotated to the nearest gene by measuring the distance between the coordinates of the center of the peak and the transcriptional start sites (TSS) of neighboring genes. Location of the peak was then categorized as 5’ distal, within 2Kbp of the promoter, within the gene, 3’ proximal, 3’ distal, or within a gene desert

(>100 Kbp from the TSS or TES). All peaks that mapped within genes were intronic. Since the majority of peaks were found in gene deserts outside of the immediate vicinity of a gene (Figure 4.4A), we examined the conservation of these regions (Figure 4.4B). This analysis demonstrated that conservation was highest in the central peak regions, suggesting that these regions are functionally important (Figure 4.4B).

Enhancers are expected to lie in open chromatin in the tissues in which they are expressed, a feature which makes them typically DNase I sensitive (Malin et al., 2013). Indeed, 37% of cJUN peaks overlap with DNase I hypersensitivity sites identified in the axial somatic and lateral plate mesoderm of headless and limbless E11.5 mice (expected to include tissue that will give rise to ICM one day later). We also examined the overlap between the set of cJUN peaks and publically available data for genomic regions containing enhancer histone marks. Approximately 40% of cJUN peaks overlap with genomic regions that contain at least one enhancer affiliated histone mark annotated in whole small intestines of adult mice. Additionally, we noticed that the number of cJUN peaks with a H3K27me3 mark, thought to represent a poised enhancer (Rada-Iglesias et al., 2011) was relatively high (27%). Interestingly, the ENCODE data reveals that adult small intestine has a significantly larger proportion of poised enhancers than does the adult cerebellum (Z-Score 8.03; p-value <0.01) (Figure 4.4C). The basis for this tissue specificity in poised enhancers is unknown.

Motif analysis of the cJUN peaks revealed enrichment of several muscle-associated transcription factors (Figure 4.4D). Of particular interest here is the enrichment for SRF, which, with its co-factor, Myocd, is a master regulator of smooth muscle gene expression (Wang et al., 2003; Wang et al., 2004). Enrichment of SRF sites with cJUN sites further supports the idea that these regulatory regions are active in ISM. Other enriched factors of the SOX, FOXO, HOX, TEAD and EGR families were also noted. Members of all of these families have been implicated in the regulation of cardiac muscle, skeletal muscle or vascular smooth muscle (Wang et al., 2001; Schmidt et al., 2003; Wada et al., 2003; Lee et al., 2004; Liu et al., 2005; Meeson et al., 2007; Papanicolaou et al., 2008; Qiu et al., 2011; Benhaddou et al., 2012; Fan et al., 2013; Wang et al., 2013; Liu et al., 2014; Sanchez et al., 2014), though none have been previously characterized in visceral smooth muscle.

To functionally verify enhancer activity, four cJUN peaks were screened for responsiveness in a muscle cell culture assay. The putative regulatory regions were cloned upstream of a minimal promoter that drives luciferase expression and transiently transfected into C2C12 cells along with either a plasmid encoding full length cJUN or a dominant negative version of cJUN (see Methods). For the four regulatory regions tested, all were up-regulated when co-expressed with cJUN. In all cases, co-transfection with the dominant negative cJUN construct diminished luciferase expression (Figure 4.5A).

4.3.4 Relationship between Hh signaling and cJUN transcription in intestinal ISM development

Previous studies suggested the possibility that cJUN and GLI1 might act together to co-regulate genes, since the two factors bind together at the human cJUN promoter (Laner-Plamberger et al., 2009; Amable et al., 2014). The Hh signaling pathway is an established regulator of the development of both the ME and the villus smooth muscle populations (Sukegawa et al., 2000; Yu et al., 2002; Shiroyanagi et al., 2007; Caubit et al., 2008; Kolterud et al., 2009; Liu et al., 2010; Tasian et al., 2010; Zacharias et al., 2011; Huang et al., 2013) and our studies here suggest that cJUN is a regulator of ME genes as well. However, we found no enrichment for predicted GLI TFBS within the cJUN peaks; only 54 predicted GLI TFBS were found within the 2741 cJUN peaks. Though it remains quite possible that these two regulatory factors bind separate enhancers for the same genes, it appears that the co-binding paradigm seen in the human cJUN promoter is not a prevalent regulatory pattern for ISM.

To further probe a possible regulatory relationship between cJUN and GLI in the control of ICM gene expression, we treated E14.5 intestines with the Hh inhibitor, cyclopamine, (Chen et al., 2002) and examined the response of the verified ICM genes (n = 3) (Figure 4.1AB). Of the 127 ICM genes, 33% were downregulated at least 2 fold by cyclopamine, confirming a substantial effect of Hh signaling on the maintenance of ICM gene expression. As expected, Hh pathway components were also robustly downregulated by cyclopamine treatment (fold change (FC): *Gli1*, -138.14; *Ptch2*, -51.27; *Hhip*, -29.86; *Ptch1*, -9.64; *Gli2*, -4.17) as were other intestinal Hh target genes (FC: *Foxl1*, -31.56; *Foxf2*, -7.41; *Foxf1*, -3.84; *Grem1*, -3.56; *Myocd*, -2.13) (Supplemental Table 3). Additionally, other downregulated genes suggest similar roles for Hh in ISM to those previously seen in skeletal muscle (Duprez et al., 1998; Borycki et al., 1999; Pownall et al., 2002; Singh et al., 2012). Several downregulated genes were modulators of Wnt signaling, affiliated with proliferation of muscle precursors or involved in promotion of differentiation into muscle cells (Table 2).

Surprisingly, however, *cJun* itself was not strongly downregulated by cyclopamine treatment (*cJun* FC: -1.21), despite the fact that *cJun* is a Hh target in other settings (Kudo et al., 2012). To further investigate this finding, we used qPCR in C2C12 myoblast cells to test whether endogenous *cJun* responds to upregulated Hh signaling induced by SAG treatment over an 8-hour period. These studies revealed that *cJun* transcription is upregulated by increased Hh signaling with similar kinetics to PTCH1 upregulation (Figure 4.5B), consistent with the idea that *cJun* is a transcriptional target of Hh signaling in C2C12 cells. Additionally, we separated E14.5 intestinal mesenchyme from epithelium and cultured the isolated mesenchyme in the presence or absence of the Hh agonist, SAG. Under these conditions, cJUN was again upregulated (FC: 2.30) at a comparable level to PTCH1 (FC: 2.01) (Figure 4.5C). Together, these data suggest that *cJun* is likely to be a direct Hh target in muscle cells, but that additional signals may maintain *cJun* levels (or the transcript may be very stable) in the context of the cyclopamine-treated whole intestine. In accord with the idea that acute reduction in Hh signaling by cyclopamine does not alter cJUN levels, only 7% of the genes associated with cJUN peaks (363/2741) were down-regulated by cyclopamine treatment.

Because *cJun* appears to be a direct target of Hh signaling in intestinal ISM, we looked for a Hh-responsive enhancer region that could be responsible for directing *cJun* transcription. In a previous study, we used kmer-SVM (Fletez-Brant et al., 2013), a machine learning method, to globally identify Hh regulatory regions. That analysis identified a putative Hh enhancer upstream of *cJun.* This genomic region was cloned into a luciferase reporter plasmid and co-transfected with a plasmid that drives constitutive expression of GLI1 in C2C12 cells (Vokes et al., 2007). As shown in Figure 4.5D, this *cJun* enhancer is indeed activated by GLI1; this activation depends on the GLI1 binding site since expression of luciferase is attenuated when the enhancer GLI binding site is mutated (GKO, Figure 4.5D). These data establish a mechanism by which Hh signaling can activate cJUN in the ICM.

4.4 Conclusions

Using transcriptome profiling paired with *in situ* datasets, we have identified a catalog of 127 ISM genes with confirmed expression in the E14.5 inner circular muscle. Subsequent promoter analysis of co-clustered genes implicated cJUN as a regulatory component in intestinal ISM formation. Using ChIP-seq on intestinal tissue, we identified 2741 potential cJUN binding locations and found enrichment of other muscle TFBS within these regions, indicating that they are likely enhancers for visceral muscle genes. Previously, cJUN has been linked to proliferation of skeletal muscle and vascular smooth muscle (Kami et al., 1995) (Daury et al., 2001) (Yasumoto et al., 2001; Chiba et al., 2014); this study further enlarges this regulatory landscape to include ISM.

Since Hh is an important regulator of ISM gene expression, we further explored the possible regulatory relationships between cJUN and GLI in the regulation of ISM genes. Our data show that co-binding of the two transcription factors at the same enhancer is rare. However, *cJun* is likely a direct target of Hh signaling in the ICM (Figure 4.5BC) and we have identified an enhancer element in the *cJun* gene that could control this regulation. Thus, in addition to its direct effect on ISM gene transcription, Hh signaling could further influence ISM gene expression through induction of *cJun*, which we establish as a regulator of ISM gene expression.

4.5 Experimental Procedures

4.5.1 Intestine collection

Intestines were collected from C57BL/6J mouse fetuses at E14.5. Fetal stages were determined by date of coitus and confirmed by Theiler staging. Isolated intestines were grown on transwell membranes with BGJb media supplemented with ascorbic acid (5mg/mL) and Penicillin-Streptomycin-Glutamine (50mg/mL). Conditions were no treatment epithelial, no treatment mesenchyme and whole intestines treated with cyclopamine (5 µM) as well as mesenchyme treated with or without SAG (1 µm) (Walton et al., 2012). After 24 hours of culture, the entire intestine from below the common bile duct to above the cecum was collected.

4.5.2 Epithelial-Mesenchymal Separation

Each intestine was treated for at least one hour with BD Biosciences Cell Recovery Solution on ice to facilitate the mechanical separation into two distinct epithelial and mesenchyme tissue populations as previously described (Li et al., 2009).

4.5.3 Immunohistochemistry

Intestines collected from Gli1$^{eGFP/+}$ mice at E12.5, E14.5, E16.5 and E18.5 were fixed overnight in 4% paraformaldehyde and then embedded in 7% agarose. Vibratome sections of 50 µm were permeabilized in 0.5% TritonX-100 for 25 minutes at room temperature and then blocked with 20% goat serum, 0.1% Tween20 for 30 minutes. Sections were sequentially stained with rabbit anti-cJUN (1:400; Santa Cruz sc-44) overnight at 4° followed by anti-rabbit secondary antibody for 45 minutes at room temperature (1:1000; Life Technologies A-21244) and then anti-GFP-488 (1:500; Life Technologies A-21311), anti-αSMA-CY3 (1:1000; Sigma C6198), and DAPI overnight at 4°. Stained sections were mounted on slides with Prolong gold and imaged on a Nikon A1 confocal microscope.

4.5.4 RNA collection and mRNA-seq

Total RNA was collected for each sample using the Life Technologies mirVana^{TM} miRNA Isolation Kit following the standard protocol. mRNA-seq on three biological replicates for each condition was performed by the University of Michigan DNA Sequencing Core following Illumina guidelines.

4.5.5 ChIP assay

ChIP was performed following a previously described protocol (Vokes et al., 2007). Prior to experimental collection, antibodies (16 uL of 0.05 ug/uL into 100uL) were coupled to magnetic beads (Dynabeads Protein G) at 4° C for 24 hours. Between six and eight pups harvested from the same litter were pooled for each ChIP experiment. Intestines were snap-frozen in liquid nitrogen and ground with a mortar and pestle to dissociate the tissue into single cells. DNA and protein were cross-linked with 1% formaldehyde for 10 minutes and then treated with 0.125 M glycine to halt the reaction. DNA was sonicated to an average fragment size of 500 bp. DNA fragments were incubated with cJUN (Polyclonal Rabbit; Santa Cruz sc-44 or sc-1694) or IgG (Polyclonal Rabbit; Santa Cruz sc-2027) bound beads overnight at 4°C. cJUN bound DNA was eluted from the beads overnight at 70° C and purified with phenol-chloroform DNA extraction after RNase and DNase treatment. Both cJUN immunoprecipitated and input DNA were submitted to the University of Michigan DNA Sequencing Core for sequencing.

4.5.6 Sequencing and data analysis

RNA and DNA were sequenced on an Illumina HiSeq machine generating 50 cycle single reads. Reads containing up to 1 mismatch were mapped to the mouse reference genome (Build mm9) using TopHat for RNA (Trapnell et al., 2009) and Bowtie for DNA (Langmead et al., 2009). Three replicates were collected for each of the three conditions (isolated epithelium, isolated mesenchyme, and cyclopamine treated whole intestine). Experiments were barcoded and run on three lanes with paired epithelial and mesenchyme samples within the same lane. Reads for each sample ranged from 29 million to 33 million. Differential expression of RNA samples was determined using DESeq (estimateSizeFactors and estimateDispersions functions) (Anders and Huber, 2010). ChIP peaks were identified using MACS (version 1.4) (Zhang et al., 2008). Raw and processed data files were deposited in GEO under accession number GSE74993**.**

4.5.7 qPCR

cDNA was reverse transcribed from 400 μg of RNA using the iScript kit. Three samples per condition were tested in triplicate with the following primer sets: (*18sRNA*: GTAACCCGTTGAACCCCATT, CCATCCAATCGGTAGTAGCG; *Rp113a*: GACCTCCTCCTTTCCCAGGC, GCCTCGGCCATCCAATACC; *Ptch1*: GGCTACTGGCCGGAAAGC, GAATGTAACAACCCAGTTTAAATAAGAGTCT; *cJun*: GTGTGGGACGACGATCAAAAG, TGACCACTAACAGGGAAGGAC). After adjusting for primer efficiency (E) expression values for *cJun* (E: 107.1%) and *Ptch1* (E: 90.4%) were normalized to *18sRNA* (E: 98.4%) and *Rp113a* (E: 90.4%).

4.5.8 Computing resources

Except where otherwise indicated, all computational steps were performed using custom Perl and R scripts.

4.5.9 Publically available datasets

Mouse ENCODE data (Bernstein et al., 2012) comprising: 1) open chromatin DNase I treated samples from E11.5 mesoderm (axial somatic and lateral plate mesoderm of headless and limbless bodies) and 2) histone (H3K4me1, H3K4me3, H3K27me3 and H3K27ac) marks from adult (8 week) mouse small intestine and cerebellum were downloaded from the UCSC genome repository (goldenPath). The refFlat file containing annotation information for mouse build mm9 was also downloaded from UCSC.

4.5.10 Cluster analysis

Hierarchical clustering analysis of transcript expression data was performed within Cluster 3.0 using uncentered correlation with average linkage (Eisen et al., 1998). Java Treeview was used to visualize the clustered data (Saldanha, 2004).

4.5.11 Conservation analysis

A total of 1250 bp of sequence from both sides of the center of each peak was uploaded to the UCSC genome browser. The PhastCons score (phastCons30way) for each nucleotide position was downloaded from the UCSC table browser. Scores were averaged across all peak positions and binned in 25 bp increments.

4.5.12 Motif analysis

To identify enriched motifs, 100 bp of sequence from the center of each peak was submitted to DREME (Bailey, 2011). Discovered motifs were annotated using the JASPAR vertebrate database in Tomtom (Gupta et al., 2007).

4.5.13 Gene Set Enrichment Analysis

A gene list comprising the upregulated mesenchyme genes was run using the GseaPreranked tool (1000 permutations) (Subramanian et al., 2005).

4.5.14 Cloning of putative enhancer regions

Putative enhancers were amplified from C57BL/6 genomic DNA (supplied by Jackson Laboratory) using template-specific PCR primers (*Gpr125*: GAGTGGAGTGGAAGGGGTTT, CTTTCTGCCACTCCTTCTGC; *Lmo4*: GGAGAAGTACAACAGACCCTTCA, ACAATCACAGCGAAGAAGCA; *Mef2C*: CCTAGCCAAAGTCATTGTGGA, GGCATCATCCTGAGTGAGGT; *Rnf182*: CCAGATTCAGTAGAGCACCCA, TACCTACATGCGAAGGCAAG; *cJun*: CTTAAGTGTTGAGGGCAGGCAG, CATGAGAAAATGCAGGGGATCT). A CACC extension was added to the end of one primer to facilitate directional cloning. PCR fragments were cloned into the pENTR/D-TOPO vector using the standard kit (Invitrogen) and then shuttled into the pGL3-Promoter luciferase vector (Promega) using the Gateway cloning system (Invitrogen). QuikChange mutagenesis (Stratagene) was used to mutate putative GLI binding sites in the *cJun* regulatory region by replacing the C in the 6th position to a G (GAAAAGACAAGAGACCAGCCATCCCAGCCTTTGAT, ATCAAAGGCTGGGATGGCTGGTCTCTTGTCTTTTC;

GAACTCCATGGGACCAGCCAGAAGAGGCTGATG,
CATCAGCCTCTTCTGGCTGGTCCCATGGAGTTC).

4.5.15 Luciferase assay

C2C12 cells (35,000 per well) were plated on 12-well plates and grown with DMEM media supplemented with 10% fetal bovine serum, 1x penicillin, streptomycin and glutamate. After 24 hours, cells were lipofectamine transfected with 400 ng of the construct containing the putative enhancer region plus either a control vector, GLI1 (pCIG) (Vokes et al., 2007), cJUN (pMIEG3-c-Jun; Addgene 40348) or dominant negative cJUN (pMIEG3-JunDN; Addgene 40350) (in equal molecular weight). *Renilla* (Promega pRL-CMV) was also included to normalize transfection efficiency. After an additional 24 hours, cells were changed to serum-free media to promote ciliogenesis required for Hh signaling (Santos and Reiter, 2008). Cell lysates were collected after 48 hours and measured for luciferase activity using the Dual-Luciferase Reporter Assay System (Promega) on a Perkin Elmer Wallac Victor3 1420 Multilabel Counter. Three experimental replicates were collected for each condition.

4.6 Acknowledgements

The authors would like to thank Dr. Will Zacharias for helpful comments and Dr. Steve Vokes and Dr. Lihong Shi for generously providing advice on ChIP-seq.

4.7 Authors’ contributions

KG and DG conceived and designed the experiments. KG, KV and GS performed the experiments. KW performed imaging. KG and DG wrote the manuscript.

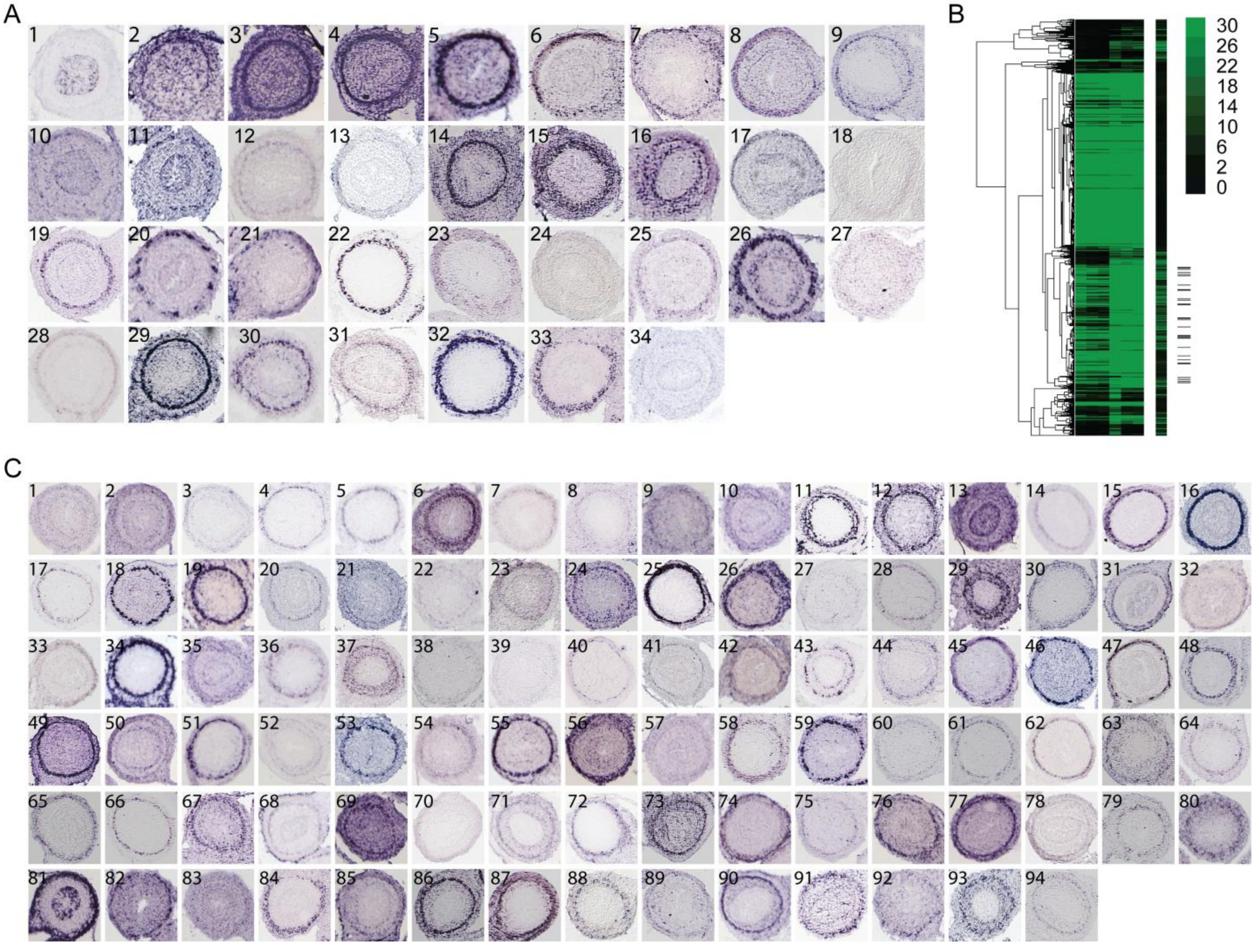


Figure 4.1. Identification of intestinal visceral smooth muscle genes. (A) RNA *in situ* localization images of (A1) epithelial marker Cdx1 [EH4673] and (A2-34) GSEA identified prospective intestinal smooth muscle genes with ICM localization at E14.5. Intestinal cross sections are from Genepaint.org (Set ID in brackets). Panels are (2) ACTC1 [DC37], (3) ACTA2 [EH2333], (4) ACTG2 [ES688], (5) ADCY5 [MH851], (6) ATP1A2 [EN427], (7) BOC [EB1453], (8) CACNA1H [ES1420], (9) CALD1 [EG423], (10) CCL2 [EH401], (11) CNP1 [EH672], (12) DDR2 [EH3223], (13) DES [EH1766], (14) FLNA [EN2546], (15) FN1 [EN386], (16) FOXF2 [MH3070], (17) FXYD2 [EH804], (18) GLI3 [MH1026], (19) LMOD1 [EH4061], (20) MAPT [EH1455], (21) MEF2C [MH765], (22) MYL9 [EB2526], (23) NCAM1 [ES2731], (24) PLAU [MH1483], (25) PLCB4 [EH4161], (26) RBP1 [EH1743], (27) SALL2 [EH4737], (28) SLC8A1 [MH1892], (29) SMTN [EH1228], (30) SORBS1 [EH2043], (31) SVIL [EN1436], (32) TAGLN [EB415], (33) TGFBR2 [EB1113] and (34) TNNT2 [EH505] **(B)** Hierarchically clustered expression data, three replicates of epithelial and mesenchyme read counts, for genes upregulated in mesenchyme. Fold change is depicted in the additional column. The location of the confirmed smooth muscle genes (A2-34) are denoted on the right with black tick marks. **(C)** RNA in situ analysis of 94 other genes within the subcluster of confirmed GSEA enriched genes showing ICM localization. (1) ABI2 [EH4750], (2) ACOT7 [EH3555], (3) ADAM19 [EB509],

(4) ADAMTS8 [EB1785], (5) ADCY5 [MH851], (6) AKAP2 [EH3708], (7) AKAP6 [EH3709], (8) AKAP12 [EB1789], (9) AKT3 [EH2186], (10) ATP2B4 [EG2318], (11) CAV1 [EG91], (12) CASQ1 [EN103], (13) CBX6 [EH1869], (14) CCKAR [EH3710], (15) CHRM2 [EH2853], (16) CNN1 [EH1511], (17) CRISPLD2 [ES1352], (18) CRMP1 [ES1162], (19) CTTNBP2 [EH1103], (20) EFS [EH2735], (21) CUEDC1 [EH1301], (22) DDR2 [EH3223], (23) DUSP10 [MH1605], (24) CSPR1 [HD13], (25) ENC1 [MH749], (26) FNBP1 [ES598], (27) FBXO32 [ES255], (28) FOXP2 [EG742], (29) EMILIN3 [EB1359], (30) FOXF1 [MH3518], (31) GDNF [EH574], (32) GAB2 [EN1340], (33) FREM2 [EN2329], (34) FZD3 [MH732], (35) GAS1 [MH360], (36) GEM [EH1664], (37) GNAQ [EN2590], (38) GPR20 [EH2873], (39) GLI1 [EN1215], (40) HAND1 [MH519], (41) GREM2 [EH1239], (42) GREM1 [EB63], (43) HOXB5 [EH612], (44) HHIP [EB1363], (45) HOXA5 [EN692], (46) HOXD3 [EN1290], (47) HOXB4 [MH3073], (48) ID4 [EN2437], (49) ITIH5 [EH3960], (50) ITGA9 [EH3560], (51) ITGA5 [EH3234], (52) KCNIP1 [EH1584], (53) LEBREL1 [EH4020], (54) IGFBP2 [ES388], (55) LRGI1 [MH431], (56) MYADM [EG746], (57) MTAP1B [ES1557], (58) MRVI1 [ES819], (59) LTBP1 [EH4243], (60) MAPK8IP1 [EH3404], (61) NEXN [ES414], (62) MYOCD [EN2445], (63) NCAM1 [ES2731], (64) MYOM1 [DC35], (65) NCALD [EG960], (66) NELL2 [EG1866], (67) NRBP2 [EH2160], (68) PSD [EB1667], (69) NPNT [MH2326], (70) PCDH7 [EB2060], (71) NKD1 [EB1514], (72) PKRG1 [EB1942], (73) PTN [EH3730], (74) PTMS [EG1747], (75) RGMA [EH2791], (76) RSPO3 [EN1484], (77) RARB [EH1089], (78) PYGL [MH3193], (79) SOX12 [MH3020], (80) SMOC2 [EH2269], (81) TGFB2 [EB1113], (82) SLC24A3 [MH3376], (83) SLC22A17 [MH2066], (84) SOX4 [MH3053], (85) TGFB1I1 [EG2803], (86) TGFB3 [EH2000], (87) TSPAN9 [EH2385], (88) THBS4 [MH1698], (89) THBS2 [ES844], (90) TMEM47 [EH2893], (91) TSHZ1 [EB2573], (92) TULP4 [MY240], (93) ZYX [EG1608], (94) WWTR1 [EH904)

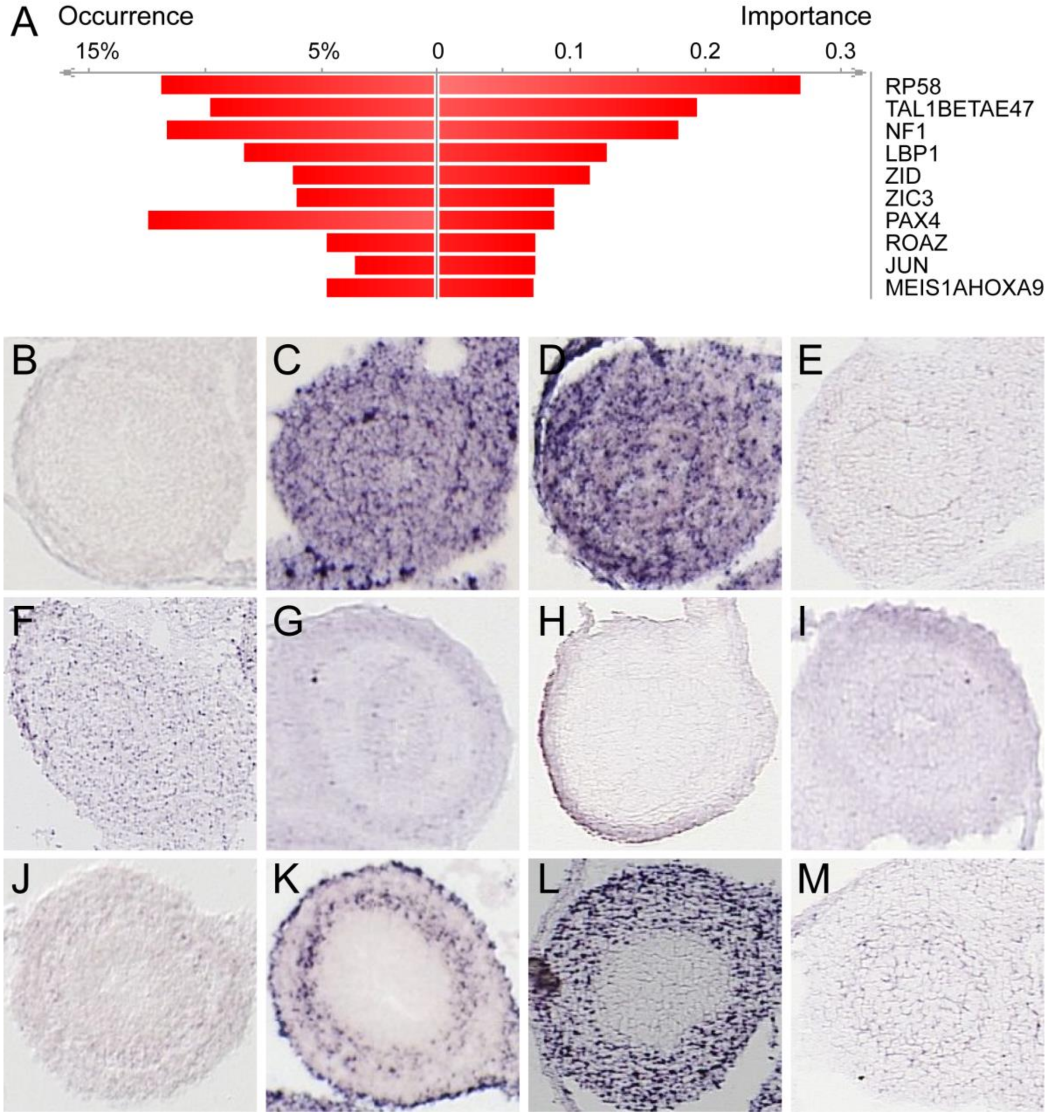


Figure 4.2. cJUN is enriched in the promoters of upregulated mesenchyme genes and is expressed in intestinal ICM at E14.5. (A) The top ten promoter enriched transcription factors include known muscle regulators RP58, NF1, ZIC3 and the MEIS1/HOXA9 complex. *In situ* images from Genepaint.org (Set ID in brackets) of E14.5 intestinal cross sections for (B) RP58 (ZFP238) [MH813], (C) TAL1 [EH2794], (D) E47 (TCF3) [MH770], (E) NF1 [ES1724], (F) LDP1 (UBP1) [EN293], (G) ZID (ZBTB6) [MH3098], (H) ZIC3 [EB2075], (I) PAX4 [MH3124], (J) ROAZ (ZFP423) [MH1157], (K) JUN [MH524], (L) MEIS1 [EG1701], and (M) HOXA9 [EB2525].

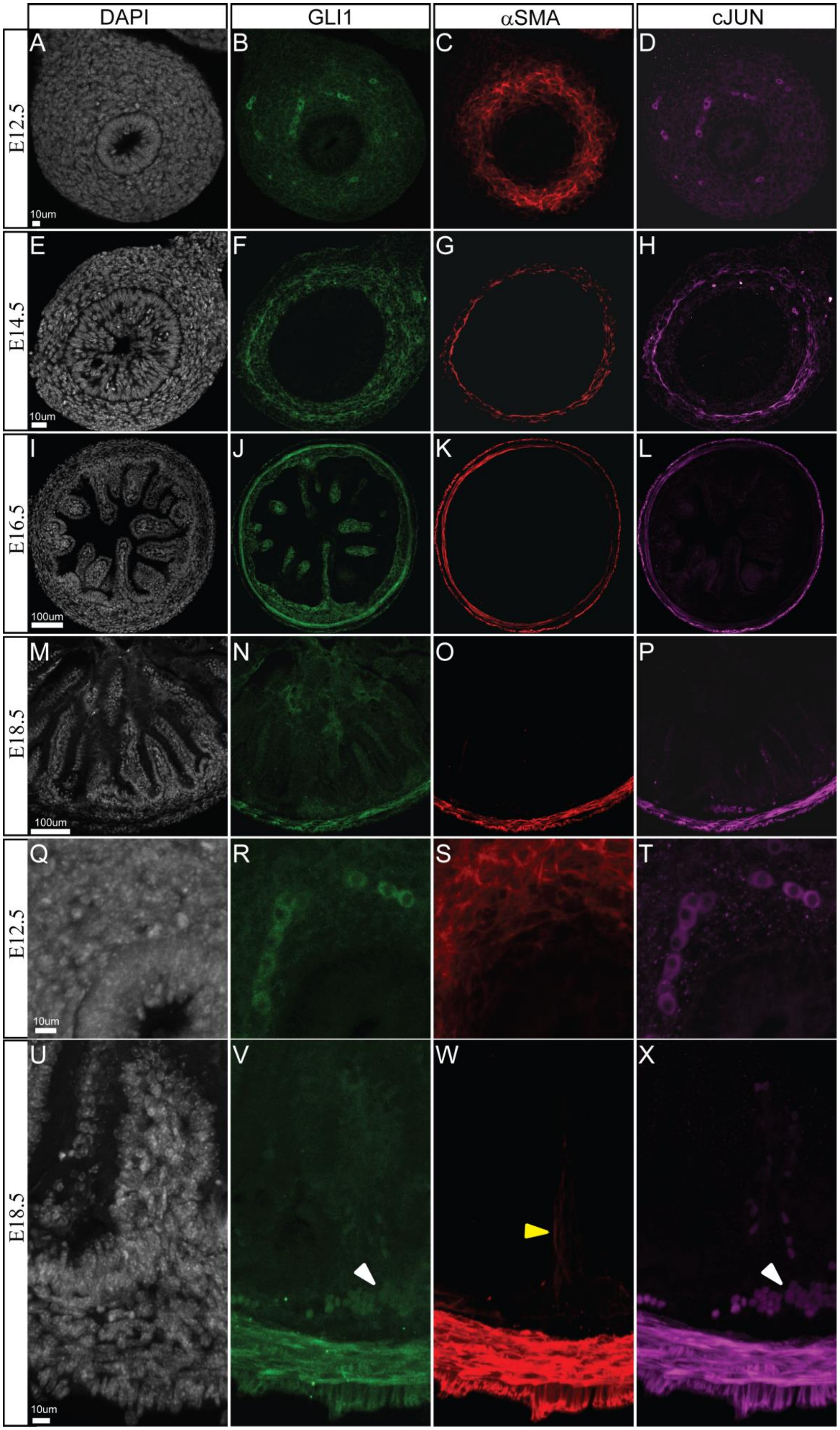

DAPI
GLI1
αSMA
cJUN
E12.5
E14.5
E16.5
E18.5
E12.5
E18.5
A
B
C
D
E
F
G
H
I
J
K
L
M
N
O
P
Q
R
S
T
U
V
W
X
10um
10um
100um
100um
10um
10um

Figure 4.3. GLI1 and cJUN co-localize with visceral smooth muscle during intestinal development. Intestines collected from *Gli1*$^{eGFP/+}$ mice were cross sectioned and stained for DAPI (gray), eGFP (green), the smooth muscle marker αSMA (red) and cJUN (purple) at E12.5 **(A-D; Q-T)**, E14.5 **(E-H)**, E16.5 **(I-L)** and E18.5 **(M-P; U-X)**. cJUN co-localizes with αSMA in the ICM and OLM within the GLI1 expression domain. GLI1 is also expressed in the mesenchymal cluster cells (Figure 3J) where an essential role for Hh signaling has been demonstrated for villus development (Walton et al., 2012). At E18.5 GLI1 and cJUN stain an additional cell population (VX white arrowheads) to the ISM. However, neither GLI1 or cJUN co-localizes with villus smooth muscle (W yellow arrowhead).

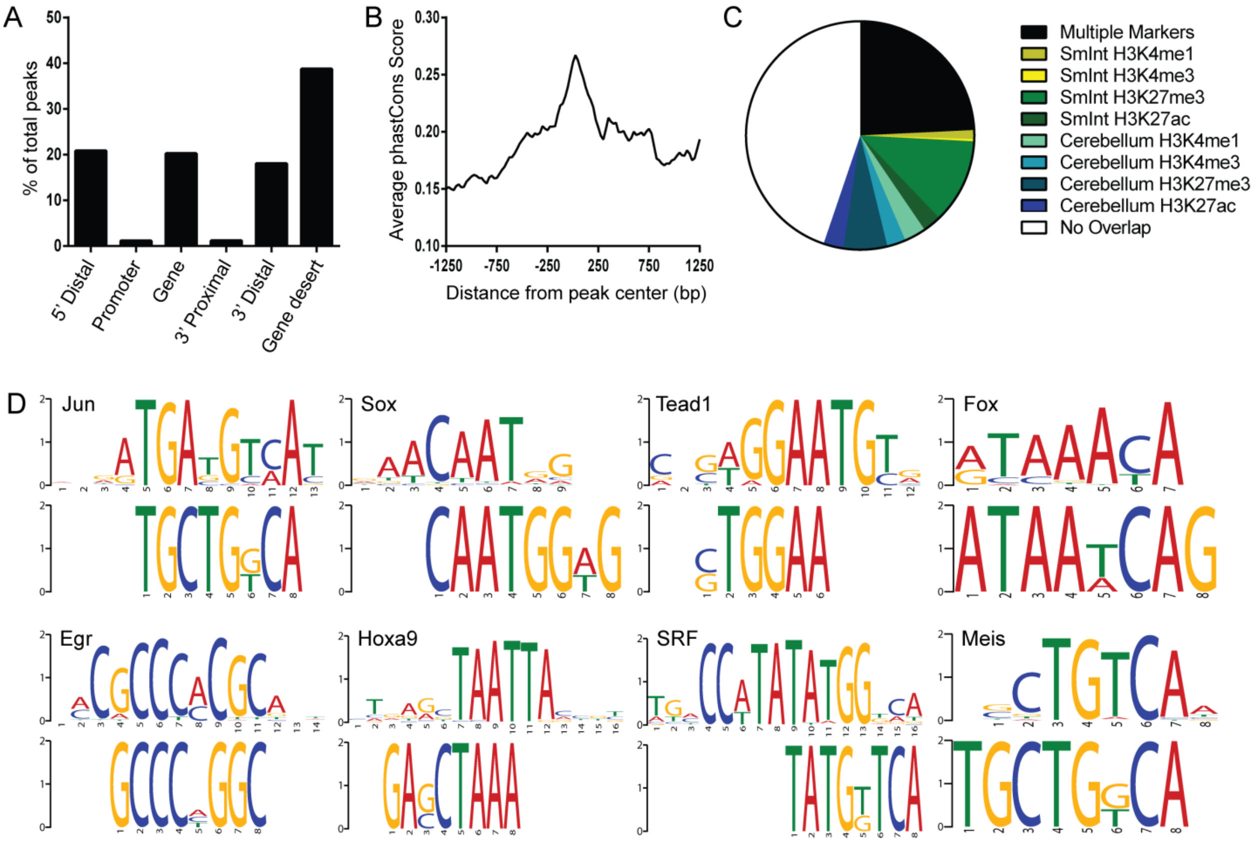


Figure 4.4. Characterization of genomic regions bound by cJUN in E14.5 intestine. (A) Distribution of peaks relative to the nearest transcription start site (TSS) or transcription end site (TES) of the closest gene. Location of the peak is categorized as within a gene if it is between the TSS and TES, gene desert if it is greater than 100 Kbp from the gene, 5’ distal if it is between 100 Kbp and 2 Kbp upstream of the TSS, promoter if it is ≤2 Kbp upstream of the TSS, 3’ proximal if it is ≤2 Kbp downstream of the TES or 3’ distal if it is between 2 Kbp and 100 Kbp from the TES. **(B)** Average vertebrate phastCons score for each nucleotide position mapped from the center of the peak. **(C)** Percentage of peaks that overlap with ENCODE enhancer histone markers. Regions categorized as multiple markers overlapped with more than one histone marker or overlapped within both tissues. **(D)** Motif enrichment analysis of the central 100 bps of the peaks identified several transcriptional factors involved in muscle development.

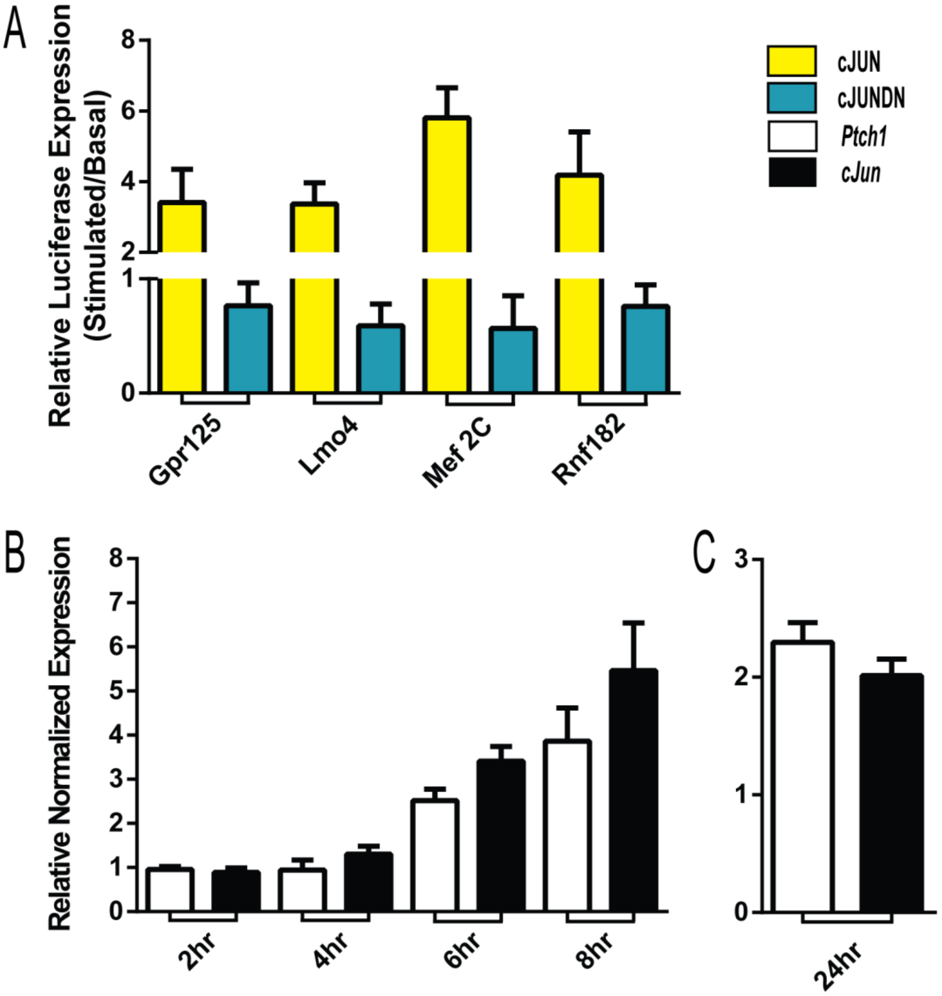


Figure 4.5. Response of ISM enhancers to *cJun* and response of *cJun* to Hh signaling.

(A) Putative regulatory regions from cJUN ChIP peaks, cloned upstream of a minimal luciferase promoter, were transfected into C2C12 cells with cJUN (yellow) or dominant negative cJUN (blue). Relative activity is plotted (stimulated/basal). cJUN responsive enhancer activity was confirmed for regions annotated to *Gpr125*, *Lmo4*, *Mef2C* and *Rnf182*. **(BC)** Relative transcript levels measured by qPCR. **(B)** Fold change of *Ptch1* (white) and *cJun* (black) comparing untreated and SAG treated C2C12 cells at two-hour intervals after stimulation. **(C)** Fold change of *Ptch1* and *cJun* 24 hours after SAG treatment of E14.5 isolated mesenchyme tissue. Error bars represent the standard deviation of three experimental replicates.

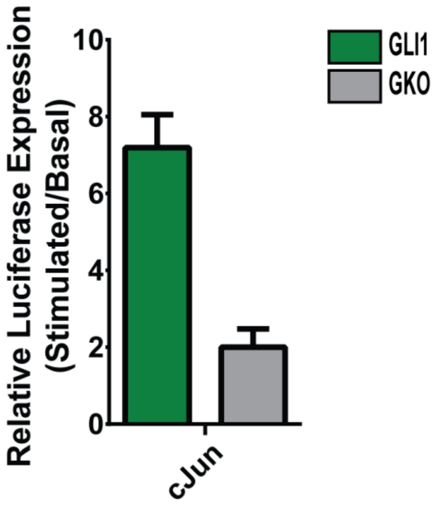


Figure 4.6. Functional verification of GLI-dependent enhancer upstream of cJun.

(A) A putative Hh regulatory region upstream of *cJun* cloned upstream of a minimal luciferase promoter then co-transfected into C2C12 cells with a GLI1 expression vector exhibits characteristic Hh responsiveness (green). Specificity of the response is confirmed to be GLI dependent by mutagenesis of the GLI TFBS (GKO) (gray). Error bars represent the standard deviation of three experimental replicates.

Gene Set	**Genes Found**	**Set Size**	**Enrichment Score**
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	37	115	0.378421
KEGG_CARDIAC_MUSCLE_CONTRACTION	25	81	0.374815
REACTOME_MUSCLE_CONTRACTION	18	48	0.321722
KAYO_CALORIE_RESTRICTION_MUSCLE_DN	15	89	0.297956
KAYO_AGING_MUSCLE_UP	59	206	0.249085
ROME_INSULIN_TARGETS_IN_MUSCLE_DN	34	246	0.204829
KAYO_CALORIE_RESTRICTION_MUSCLE_UP	30	95	0.201314
MUSCLE_DEVELOPMENT	35	93	0.149875

Table 4.1. GSEA muscle gene sets enriched in E14.5 intestinal mesenchyme tissue.

Gene	**Fold Change**	**Affiliation**	**Reference**
Dkk1	-84.45	Wnt modulator	He et al. 2013
Edar	-21.86	Wnt modulator	Wells et al. 2010
Sall1	-17.75	Wnt modulator	Kiefer et al. 2010
Mmp9	-16.22	Muscle Stem Cell	Zimowska et al. 2008
Epha8	-10.70	Muscle Stem Cell	Star et al. 2011
Il1b	-12.82	Muscle Stem Cell	Luo et al. 2003; Chen el al. 2006
Klhl14	-32.90	Muscle Differentiation	Abou-Elhamd et al. 2009
Mir24-1	-8.34	Muscle Differentiation	Sun et al. 2008

Table 4.2. Muscle affiliated genes downregulated by attenuation of Hh signaling.

Gene	Epi	Mes	FC	pval
Grik2	11.8	259.6	22.0	7.7E-32
Cacnb2	14.5	189.4	13.0	5.5E-20
Itgax	9.5	139.9	14.7	1.4E-04
Apod	0.8	7.6	9.8	2.8E-02
Ncam1	125.5	5006.5	39.9	6.9E-13
Ppfia2	2.9	103.7	35.2	1.5E-19
Abca4	5.7	64.9	11.5	1.2E-09
Fkbp14	143.2	894.4	6.2	8.7E-26
Sarm1	10.4	166.7	16.0	2.1E-12
Cd34	69.2	2018.4	29.2	1.3E-80
Pcdhb13	4.7	70.1	15.0	5.6E-10
Rgs9	40.2	904.7	22.5	5.4E-55
Spock1	12.3	153.4	12.5	2.8E-11
Cd84	6.0	48.7	8.1	1.5E-07
Pmepa1	283.5	2869.9	10.1	2.3E-45
Pxylp1	288.6	1237.1	4.3	8.4E-20
Icam2	10.7	503.4	47.0	5.5E-62
St8sia1	33.8	1149.9	34.1	8.5E-12
Nfic	280.5	3270.4	11.7	2.7E-04
Hoxb7	52.8	253.0	4.8	1.2E-12
Map6d1	5.9	55.0	9.3	1.3E-02
Rsad2	4.2	40.2	9.6	1.9E-08
Hsd11b2	5.8	64.8	11.1	1.8E-04
Emilin3	125.8	3571.5	28.4	5.2E-88
Gm21949	82.6	1183.4	14.3	4.2E-22
Gna14	35.1	554.3	15.8	1.5E-39
Nodal	0.2	16.1	67.1	4.3E-04
Tnni3	5.7	27.9	4.9	8.1E-03
Cysltr1	10.9	124.9	11.4	1.2E-14
Cpxm2	3.9	28.9	7.5	6.0E-04
Gstt1	15.5	72.3	4.7	3.7E-05
Ptgs2os2	0.2	9.2	38.6	6.9E-04
Fabp7	24.4	400.2	16.4	2.2E-09
Cldn11	6.2	138.1	22.3	7.4E-07
Lrrc4	7.9	162.6	20.5	1.0E-02
Tlr12	17.3	345.3	19.9	4.8E-24
Efcc1	2.7	35.7	13.1	6.8E-06
Apbb1	198.0	1130.4	5.7	4.0E-28
Il33	32.1	748.6	23.3	5.0E-56
Ifitm7	0.7	21.3	29.2	2.9E-05

Gene	Epi	Mes	FC	pval
Slc14a1	2.5	18.2	7.4	7.9E-03
Kcnj15	2.4	42.3	17.4	2.3E-05
Pcp4	11.7	274.7	23.4	7.4E-10
Kcnj10	3.8	89.0	23.4	2.4E-04
Glis1	3.2	37.3	11.7	2.4E-02
Fermt2	292.7	5320.9	18.2	4.3E-51
Ccl11	26.8	1060.4	39.6	1.1E-35
Hpcal4	9.6	273.9	28.6	6.1E-25
Pcdhac2	20.1	185.3	9.2	1.5E-20
Aldh1a2	76.9	2060.9	26.8	2.5E-34
Ticam2	3.9	17.5	4.5	7.1E-03
Ddah2	426.2	2509.5	5.9	2.1E-15
Myom1	133.2	1247.3	9.4	3.0E-38
Gprc5b	90.7	1385.0	15.3	2.4E-40
Cetn4	2.8	12.7	4.6	1.9E-02
Il7r	2.0	16.8	8.4	2.5E-03
Cyth3	491.1	2135.7	4.3	4.3E-22
Cyp26b1	18.4	324.5	17.6	6.3E-11
Hhatl	2.5	23.9	9.7	8.8E-04
C530044C16Rik	2.4	38.3	15.7	2.3E-05
Lrat	9.3	161.4	17.3	1.4E-13
Myo16	2.2	42.7	19.4	2.2E-04
Fnbp1	328.2	1906.9	5.8	7.0E-27
Cux2	133.6	827.1	6.2	2.3E-05
Gpr88	1.7	24.3	14.4	5.6E-04
Otor	0.3	9.2	34.3	6.0E-04
D430019H16Rik	78.8	1252.4	15.9	1.2E-24
Fam179a	0.7	9.1	12.7	2.1E-02
Tnfrsf26	1.7	21.6	12.6	4.8E-03
Rasgrp3	26.7	903.5	33.9	3.4E-71
Chat	2.0	43.6	21.5	8.5E-09
Arhgap20	3.2	116.7	36.3	2.8E-21
Pla2g4a	145.9	1795.4	12.3	1.2E-22
Sprn	0.8	23.5	29.1	2.8E-07
Csrp1	780.3	5049.9	6.5	1.2E-28
Pcsk2os2	2.4	48.7	20.1	1.8E-06
Nmur2	0.2	38.3	160.0	4.4E-09
Cacnb4	15.0	77.9	5.2	4.9E-07
Nid2	254.2	3554.4	14.0	3.3E-60
Fyb	9.0	119.2	13.2	5.5E-15

Pitpnc1	255.7	2289.7	9.0	5.7E-14
Gm20748	13.9	325.2	23.4	7.4E-08
Col22a1	9.3	237.8	25.5	1.5E-15
Clvs1	199.7	865.5	4.3	1.5E-16
Celf3	270.5	2108.6	7.8	2.7E-09
Sapcd1	10.1	61.0	6.0	4.0E-06
Ero1lb	24.3	104.3	4.3	3.3E-06
Gm5868	6.0	57.8	9.7	1.3E-07
Gfra1	134.7	2867.4	21.3	2.9E-62
3110007F17Rik	1.0	23.1	22.9	2.1E-05
Ushbp1	20.5	527.8	25.7	7.0E-28
Stmn4	14.9	240.4	16.1	3.2E-12
C920009B18Rik	0.3	8.2	30.4	1.8E-02
Bai3	5.1	141.6	27.7	5.4E-24
Ssc5d	66.1	1855.8	28.1	2.0E-21
F13a1	6.0	65.4	11.0	2.0E-06
Kcnmb1	9.4	190.7	20.4	1.3E-12
1810041L15Rik	18.6	217.7	11.7	3.8E-20
Fndc4	211.3	973.2	4.6	5.0E-20
Ank2	520.0	2251.0	4.3	3.6E-14
Gdap1l1	25.0	220.4	8.8	6.8E-21
Abca8a	1.7	34.9	20.5	1.6E-06
Mapk8ip2	40.3	407.0	10.1	8.3E-20
Apcdd1	28.6	123.6	4.3	1.9E-07
Lrig1	751.8	5849.8	7.8	2.2E-41
9930012K11Rik	21.5	91.6	4.3	2.5E-06
Pik3cg	15.3	432.4	28.2	5.3E-38
Sec14l1	536.4	4127.2	7.7	2.5E-21
Dock3	17.4	73.1	4.2	1.4E-04
Drp2	24.7	119.2	4.8	5.3E-07
Rbms3	129.4	2405.2	18.6	1.6E-23
Tll1	10.9	252.1	23.2	3.8E-28
Cadm3	18.9	499.6	26.5	4.4E-35
Pcdh20	6.4	155.7	24.5	9.7E-24
Dusp10	41.4	536.1	13.0	2.3E-35
Hapln3	1.7	42.3	24.5	3.3E-07
B3gat1	0.7	33.4	46.5	5.5E-08
Flnc	241.9	4762.9	19.7	1.2E-19
B3galt1	4.9	146.5	30.1	2.1E-23
Rfx2	66.4	303.8	4.6	2.0E-10
Slc2a12	3.9	42.9	11.1	4.6E-06

Rcsd1	136.2	1908.6	14.0	1.1E-56
Hand1	31.7	667.2	21.1	1.7E-51
2810468N07Rik	26.1	130.6	5.0	6.5E-08
Lrp1b	4.4	22.2	5.1	2.1E-02
H1fx	110.4	555.7	5.0	7.8E-13
Slc18a2	77.0	453.3	5.9	5.4E-19
Atp2b4	306.0	4112.2	13.4	4.6E-13
Fmo1	6.8	130.5	19.3	9.2E-16
Tmem158	46.3	769.6	16.6	4.2E-17
Fabp4	57.5	1610.7	28.0	3.3E-10
Sox10	60.8	1119.1	18.4	1.4E-32
Clec4a2	5.5	52.2	9.5	3.1E-07
Serpini1	50.8	818.0	16.1	2.2E-37
Apol7c	49.2	732.3	14.9	5.8E-06
Pcdha6-g	729.4	5876.7	8.1	1.6E-12
Rem1	11.2	275.4	24.6	5.2E-19
Gm10591	2.9	34.8	12.0	1.3E-05
Vipr2	16.7	126.1	7.5	2.8E-10
Snhg18	52.4	657.1	12.6	8.3E-38
Fry	77.2	608.1	7.9	1.6E-03
Rora	59.7	362.1	6.1	5.9E-05
Fhl3	124.3	523.3	4.2	9.1E-05
Dclk3	4.5	32.9	7.4	4.5E-04
Ppp2r2c	1.8	46.2	26.3	1.9E-11
Igf1	43.0	1361.9	31.7	5.7E-14
Actl6b	2.7	58.4	21.4	4.4E-11
Snai2	40.7	1538.4	37.8	4.1E-84
2700070H01Rik	0.3	8.1	32.5	2.4E-02
Cacna1b	34.9	444.1	12.7	7.5E-07
Ascl1	59.7	1053.2	17.6	6.5E-34
Tlr1	3.0	36.0	12.1	1.7E-07
Dmpk	246.9	2559.7	10.4	4.8E-34
2610307P16Rik	4.4	79.3	18.1	9.2E-07
Slc12a4	284.2	1606.1	5.7	3.5E-26
Arhgap30	11.4	153.1	13.5	2.8E-10
Esrrb	2.0	61.5	30.5	2.4E-05
Rbfox1	4.4	95.2	21.9	2.1E-14
Dmp1	29.1	208.5	7.2	7.3E-10
Pcdha11	19.3	172.5	9.0	5.2E-19
Zmat4	2.2	25.1	11.3	9.2E-04
Serpinf1	146.7	1535.8	10.5	5.1E-07

Prph	132.7	1606.8	12.1	8.5E-30
Arl5c	2.0	32.2	16.0	8.1E-06
Kirrel	158.1	2757.5	17.4	7.6E-10
Adamts7	97.5	2509.6	25.7	1.1E-47
Map7d1	544.2	3843.9	7.1	3.3E-38
Stmn2	65.4	1205.3	18.4	5.2E-32
Hdgfrp3	53.4	1490.0	27.9	1.5E-78
Sh3gl3	30.4	466.9	15.3	4.3E-36
Clec4a1	6.2	60.3	9.8	4.7E-08
Prex2	74.9	1140.8	15.2	2.2E-25
Tacr2	1.0	36.9	37.7	5.9E-07
Gnb4	44.7	1007.3	22.5	8.5E-62
Sostdc1	1.5	39.7	26.0	2.4E-07
Fam65c	5.2	133.7	25.8	1.0E-20
Lrrn4	26.4	250.5	9.5	2.4E-03
Eln	130.1	3077.9	23.7	1.0E-59
Antxr2	360.1	1643.9	4.6	1.4E-22
Klf14	7.8	71.0	9.1	6.2E-08
Fibin	50.4	1313.1	26.0	1.6E-43
Olfml3	132.5	3459.9	26.1	4.1E-84
AW549542	18.6	141.9	7.6	1.1E-10
Flt4	19.1	810.4	42.3	8.5E-21
Dcx	19.8	412.1	20.8	6.5E-25
Tmem130	9.0	74.6	8.2	9.4E-09
2810442N19Rik	0.5	11.2	23.4	1.5E-02
Mapkbp1	173.5	1009.4	5.8	4.1E-12
Lyz2	98.0	598.2	6.1	9.6E-26
Pcdhgc3	943.2	8857.7	9.4	1.5E-10
C2cd4a	10.2	56.2	5.5	3.6E-04
Rnf122	131.9	1027.2	7.8	3.9E-31
Ptpn5	3.2	67.0	20.9	1.1E-11
Tnfsf13	9.7	47.1	4.8	2.0E-04
Amotl2	261.4	1320.3	5.1	1.6E-20
6530402F18Rik	3.5	61.4	17.7	3.6E-08
Evi2a	6.2	81.7	13.1	7.0E-10
Ntf3	6.9	176.0	25.4	1.1E-23
Scn7a	3.3	55.6	17.0	7.9E-08
2610203C22Rik	2.5	25.3	10.1	4.1E-04
Pcnxl2	1.6	50.6	32.3	7.1E-03
Sh2b2	28.7	170.2	5.9	1.1E-10
Pcdha1	18.3	168.9	9.2	4.8E-19
Trib2	49.7	1001.3	20.1	1.1E-57
Calcrl	98.0	2465.7	25.2	2.1E-17
Mtss1l	400.9	3299.2	8.2	4.6E-08
Tnnt2	5.8	69.0	12.0	9.6E-07
9530026P05Rik	1.9	23.8	12.3	6.4E-03
4921511I17Rik	0.5	27.2	56.8	9.3E-06
Lyst	238.4	1020.0	4.3	5.2E-04
Srpx	6.2	186.1	29.9	3.7E-31
Nkain4	27.3	417.1	15.3	2.1E-32
Gm3893	0.2	21.8	91.0	1.6E-03
Laptm5	58.1	836.1	14.4	1.8E-08
D030025P21Rik	0.7	11.0	14.7	2.7E-02
Slc7a10	10.9	46.2	4.2	2.9E-03
Gdf5	1.7	15.9	9.3	1.1E-02
B230216N24Rik	1.5	34.8	23.2	3.2E-05
Ier5l	70.3	380.4	5.4	1.5E-15
Il2rb	0.5	11.9	25.0	5.9E-03
Acr	0.5	12.5	25.5	1.1E-02
Ndrg4	35.4	393.4	11.1	3.6E-30
Chrdl2	0.5	8.1	16.5	1.3E-02
Mtcl1	80.0	1782.6	22.3	3.5E-14
Pbx3	113.3	1043.5	9.2	4.5E-38
Sema4f	5.0	78.4	15.8	2.0E-13
Hlx	35.2	983.0	27.9	1.4E-47
Cabyr	4.5	31.7	7.0	4.7E-02
Synpr	3.0	77.3	25.9	6.7E-15
Lpl	92.3	530.4	5.7	1.1E-21
Elk3	159.5	2093.2	13.1	4.2E-21
Gprasp1	744.4	3578.5	4.8	1.3E-26
Rbpjl	0.7	31.0	41.9	2.4E-02
Tek	9.4	248.8	26.4	7.2E-30
Fam19a2	13.6	265.7	19.5	2.4E-34
Pcdhb9	3.8	104.9	27.9	8.4E-19
Clip4	22.9	249.5	10.9	1.3E-20
Thbd	207.8	5759.9	27.7	3.6E-91
Usp13	12.6	92.4	7.3	7.3E-09
Cnr1	30.4	306.6	10.1	2.7E-26
Zcchc12	30.8	414.4	13.5	7.1E-36
Gad1	1.0	12.4	12.2	3.3E-02
Klhdc8b	219.1	1685.9	7.7	1.2E-37
Wnt5a	125.6	2875.6	22.9	7.0E-21

Cckar	31.2	699.3	22.4	4.2E-50
Cap2	7.6	294.2	38.5	8.4E-39
H2-Ab1	9.3	50.4	5.4	4.4E-05
Cdyl2	72.3	292.8	4.0	3.0E-04
Rab13	76.5	317.9	4.2	8.7E-05
Doc2b	139.6	789.0	5.7	7.0E-19
Kif1a	491.1	2027.8	4.1	7.1E-10
Cd1d2	4.0	49.0	12.3	1.2E-08
Gpr137c	7.9	86.7	11.0	5.5E-10
Cyfip2	208.5	1297.4	6.2	4.5E-13
Scx	10.8	51.9	4.8	5.5E-06
Wisp1	169.5	3154.9	18.6	6.5E-13
Slc35f1	42.8	329.7	7.7	2.1E-20
Arap3	97.2	2420.2	24.9	5.4E-36
Tagln3	28.0	466.4	16.6	2.8E-40
C1ql1	18.0	424.3	23.6	8.1E-38
Fam219aos	10.9	95.6	8.8	1.3E-09
Jam2	5.7	128.6	22.6	1.1E-18
Dkk1	0.8	28.0	37.2	4.6E-05
Ptp4a3	875.2	3636.8	4.2	4.6E-21
Rgs4	16.0	356.9	22.4	3.7E-45
Synpo	87.3	2130.7	24.4	7.1E-07
4732416N19Rik	7.5	82.5	11.0	6.9E-06
Serping1	29.5	917.5	31.1	6.9E-68
Ssbp2	92.4	1040.8	11.3	9.6E-44
Sdk1	114.3	3145.6	27.5	2.9E-12
Akap5	22.7	236.3	10.4	2.7E-18
Lrrn3	29.1	499.7	17.2	4.6E-46
Vgll3	3.1	25.3	8.2	5.3E-05
Gm12429	0.5	24.1	47.5	2.2E-02
Agap2	36.3	825.5	22.7	8.3E-15
5730409E04Rik	29.8	301.1	10.1	3.1E-25
Rhoh	2.2	28.3	12.6	1.3E-04
Chrna3	27.8	672.1	24.2	1.1E-58
Dok7	1.5	15.2	10.1	4.2E-03
Ccdc65	0.7	10.8	15.1	1.5E-02
Nos3	20.9	449.9	21.5	1.7E-39
Irf2bpl	408.2	1782.7	4.4	9.4E-12
Pik3r5	6.5	74.1	11.4	1.0E-08
Oasl2	17.7	104.5	5.9	3.0E-09
Apba2	10.4	229.4	22.1	5.6E-29

Lats2	179.4	949.6	5.3	2.9E-22
Emcn	12.6	535.7	42.4	1.0E-14
Usp44	1.8	14.9	8.4	5.0E-03
AW011738	6.9	105.8	15.3	5.3E-13
Slc8a3	13.6	149.2	11.0	2.3E-13
A630019I02Rik	1.0	12.7	13.2	5.9E-03
Gfra4	3.2	68.7	21.6	8.6E-10
Fhl1	72.1	426.7	5.9	3.9E-21
Ccl21b	2.9	34.0	11.7	2.5E-05
Phox2b	96.8	2111.3	21.8	2.6E-70
Nxn	440.7	1866.5	4.2	2.4E-21
Atp1a4	1.0	13.1	13.5	2.7E-02
Shisa3	8.2	575.4	70.6	9.0E-75
C5ar2	1.1	9.6	9.1	4.0E-02
Arhgef6	12.4	194.9	15.8	3.1E-22
Angpt2	72.5	329.6	4.5	8.3E-06
Cpa2	22.2	397.1	17.9	2.1E-02
I830077J02Rik	1.0	23.7	23.4	3.3E-04
Nrros	40.9	682.2	16.7	2.1E-43
Insc	7.5	131.3	17.6	7.2E-18
Itga1	35.1	885.7	25.2	9.8E-46
1700018A04Rik	1.8	54.2	30.5	4.5E-08
AW551984	56.1	557.9	9.9	2.2E-17
Arhgef15	15.5	377.6	24.4	1.4E-36
Crispld2	57.9	1888.8	32.6	2.2E-82
Rai2	18.3	604.6	33.1	1.5E-31
Myo1f	16.2	136.9	8.4	2.0E-13
Stxbp1	164.1	1712.3	10.4	1.8E-16
Kcnq4	3.7	135.7	37.0	5.2E-19
Cyyr1	2.2	128.2	58.4	2.3E-05
Lepre1	287.6	1541.5	5.4	1.8E-17
Cnn1	60.4	1643.3	27.2	5.4E-34
Rbpms2	52.1	292.1	5.6	1.1E-09
Slit2	183.2	1644.6	9.0	2.1E-11
Cdk5r2	12.9	92.0	7.1	2.8E-05
Ptpdc1	49.8	555.4	11.1	6.1E-32
Epha8	10.4	108.9	10.5	6.9E-08
Mmp10	0.3	14.6	54.4	5.4E-04
Sema4c	501.4	2130.9	4.3	1.4E-20
Sema7a	11.0	186.5	16.9	6.4E-24
Oaz2	396.9	1989.3	5.0	9.1E-26

Tmem108	45.4	248.5	5.5	5.1E-06
Shisa4	19.6	262.6	13.4	7.8E-25
Soga3	9.9	358.1	36.1	3.7E-28
Klhl1	2.5	28.5	11.5	7.5E-07
Sv2b	4.7	106.7	22.8	2.3E-17
Draxin	1.7	33.1	19.5	5.3E-07
Nkd1	50.5	1145.6	22.7	8.2E-59
Kcnma1	18.1	506.1	28.0	1.5E-26
Scn1b	2.9	25.9	8.9	6.1E-04
Msc	1.0	30.4	31.4	3.6E-06
Krt17	9.0	50.3	5.6	4.9E-05
Gjd2	4.7	149.4	31.9	2.6E-28
Syt17	14.6	171.8	11.7	3.9E-19
Cryab	10.0	94.8	9.5	1.7E-10
Cthrc1	17.2	370.2	21.5	1.3E-37
Neurl1a	44.2	605.3	13.7	1.7E-15
Agtr1b	0.7	9.1	12.5	1.9E-02
Frmd6	144.0	648.9	4.5	1.6E-16
Elavl2	21.5	214.7	10.0	1.5E-24
Tcf4	1251.3	6513.0	5.2	1.5E-29
Arrdc3	198.2	2747.3	13.9	3.6E-61
Nell2	30.7	805.5	26.2	9.5E-26
Cacna1d	41.1	1114.7	27.1	9.1E-10
Nme5	1.0	8.5	8.4	4.0E-02
Slc44a5	3.9	75.3	19.4	7.4E-13
Lsamp	2.2	43.8	20.1	9.7E-08
Clec2l	2.0	29.1	14.3	1.9E-06
Sh3rf3	4.7	74.5	15.7	7.6E-06
Exoc3l	37.4	442.8	11.8	1.1E-20
Il18rap	3.0	18.9	6.2	1.7E-02
Aff3	47.8	1765.9	37.0	1.8E-12
Spats2l	180.8	1131.6	6.3	3.3E-29
Tmem178	3.2	59.5	18.8	1.4E-10
Tmem132d	2.6	14.1	5.4	2.0E-02
Arrb1	701.4	3160.8	4.5	2.4E-06
Frem1	159.7	4348.4	27.2	2.6E-16
Zcchc18	17.7	348.0	19.7	3.0E-38
Chrna4	2.0	62.9	32.0	1.4E-12
Card11	3.2	26.7	8.2	4.9E-04
Id4	36.5	637.3	17.5	3.4E-45
Icos	1.0	11.7	12.0	2.2E-02
5830444B04Rik	1.0	15.0	15.2	1.7E-02
Zmat1	12.0	81.0	6.8	4.4E-09
St18	34.8	217.3	6.3	6.2E-06
Fxyd2	14.6	135.7	9.3	2.5E-08
Adamts3	16.8	360.0	21.5	8.9E-09
Dagla	179.4	935.4	5.2	3.0E-03
Vcam1	6.6	152.3	23.1	3.1E-15
Pthlh	2.2	13.7	6.2	4.0E-02
Ptger2	3.1	71.0	22.6	1.0E-10
Sorcs2	191.6	2185.1	11.4	3.1E-28
Ermap	1.5	10.8	7.4	3.1E-02
Irx3	0.8	14.7	18.6	4.7E-03
Rftn2	43.3	1054.3	24.3	3.6E-63
Fcgr4	1.0	22.9	22.9	7.8E-06
A430090L17Rik	2.2	61.4	28.2	2.5E-03
Dram1	25.5	124.9	4.9	4.2E-08
6330403A02Rik	5.8	184.8	31.9	2.2E-07
Gper1	10.2	181.3	17.8	6.3E-19
Med12l	101.4	564.8	5.6	3.6E-18
Gm684	1.7	14.6	8.4	1.0E-02
E130310I04Rik	23.4	517.9	22.1	3.1E-17
Cox4i2	2.2	56.5	25.1	4.0E-10
Batf	2.5	33.9	13.5	2.0E-05
Ildr2	26.9	302.7	11.2	3.4E-09
Kank4	25.5	950.3	37.3	5.4E-16
Cartpt	6.6	152.4	23.1	2.9E-21
Ina	31.9	508.2	15.9	1.5E-32
Nfix	60.7	1898.7	31.3	3.1E-05
A330074K22Rik	7.9	201.1	25.5	2.8E-02
Adcy3	85.6	676.7	7.9	1.4E-27
Zap70	1.3	12.0	9.4	3.3E-02
Chd5	96.4	516.9	5.4	1.8E-11
Bank1	0.3	36.2	134.3	1.5E-08
Ryr3	25.8	260.1	10.1	6.8E-09
Col14a1	105.7	4431.5	41.9	1.6E-26
Lrrc4b	23.6	462.0	19.5	4.8E-26
Adam33	0.8	38.0	49.4	4.3E-07
Hoxc4	17.2	755.1	43.8	1.1E-16
Ntrk3	18.3	770.3	42.0	1.2E-40
Jph2	53.7	1410.6	26.3	1.4E-72
A530058N18Rik	1.0	12.2	12.6	2.1E-03

Clstn2	13.2	59.1	4.5	5.1E-04
Edar	5.4	189.0	34.9	7.0E-17
Bmp3	121.4	3662.3	30.2	1.1E-85
Ppp1r18	149.5	1784.1	11.9	7.1E-48
Hoxa2	34.7	459.0	13.2	4.4E-30
Mapk8ip1	230.0	1253.6	5.4	1.1E-25
Etv1	66.6	1624.6	24.4	2.7E-30
Ptprs	1969.6	12588.7	6.4	2.1E-35
Slc8a2	37.4	896.7	24.0	2.2E-24
Pitpnm3	24.5	651.1	26.6	1.7E-10
Alas2	4.5	52.5	11.6	1.2E-03
Dusp15	0.2	7.1	29.6	3.1E-02
S100a4	6.9	31.4	4.5	4.8E-03
Fnd3c2	0.5	46.7	91.7	3.1E-10
Kcnd3	55.8	2180.5	39.1	2.0E-12
Efemp2	194.6	1621.4	8.3	1.3E-38
Pkd2	569.9	3580.7	6.3	1.6E-34
Ltbp2	6.4	136.1	21.3	7.0E-13
Csmd2	5.3	90.8	17.0	1.0E-04
Gpr45	0.5	8.0	15.7	2.5E-02
Abca6	0.7	21.8	29.1	1.7E-05
Arhgef40	337.8	4616.3	13.7	5.2E-62
Efhb	0.7	16.7	22.4	9.2E-04
Id3	130.8	1618.4	12.4	5.3E-32
Slc2a4	43.6	1114.7	25.6	2.0E-63
Unc79	14.9	182.3	12.3	7.7E-11
Trp53inp2	280.0	2065.9	7.4	1.2E-28
Nbl1	256.6	1596.0	6.2	2.9E-29
Cpz	3.3	61.8	18.9	1.4E-09
Pnma3	2.5	34.1	13.8	4.1E-05
N28178	3.5	49.7	14.4	3.2E-03
Bgn	81.7	1932.3	23.6	2.0E-13
Dnm3os	182.8	3986.0	21.8	1.0E-75
Slc6a13	1.2	9.5	7.8	1.9E-02
Pcdhga8	786.1	6075.7	7.7	3.8E-11
Gpc4	128.9	554.9	4.3	3.4E-15
Siglec1	2.8	39.1	14.1	1.6E-02
Hcar1	15.8	85.0	5.4	4.1E-05
Tnf	4.0	33.0	8.3	3.1E-04
Apol7e	5.5	27.4	5.0	9.3E-03
Zfp580	91.0	489.9	5.4	1.5E-04

Matn4	6.1	164.0	26.9	1.2E-14
Gria2	14.7	244.8	16.6	2.7E-26
Il17rd	192.9	1030.8	5.3	4.5E-07
Chrm1	18.2	89.4	4.9	2.0E-02
Gpr114	9.1	92.0	10.1	7.3E-04
Fermt3	27.2	187.3	6.9	2.5E-08
Il1r1	39.7	546.1	13.7	3.5E-34
B3gnt8	5.8	132.0	22.7	1.7E-17
Thsd7a	59.3	320.9	5.4	2.7E-10
Actg2	289.1	6985.2	24.2	3.8E-63
Celf4	46.2	390.5	8.4	1.1E-23
Frmpd4	0.5	21.0	42.9	9.8E-07
Plekhg1	137.5	1284.2	9.3	7.6E-08
Prss35	4.7	59.4	12.8	2.8E-07
Plekha2	33.0	132.9	4.0	1.2E-06
Foxd2os	26.0	120.6	4.6	1.4E-03
Hoxb9	10.3	63.2	6.1	9.8E-06
Armcx2	367.5	3045.3	8.3	4.8E-42
Ffar3	2.2	18.7	8.3	2.7E-03
Eva1a	57.4	349.8	6.1	1.8E-13
Vstm2b	0.3	15.5	62.0	4.1E-04
Tmem121	12.5	172.9	13.8	1.0E-18
Hoxb6	56.8	639.9	11.3	5.5E-22
Necab1	1.5	44.1	29.0	7.7E-10
Abca1	97.0	1694.1	17.5	1.5E-14
Lag3	3.8	50.0	13.0	6.3E-07
6330403K07Rik	79.8	1323.7	16.6	6.2E-59
Ptms	1199.3	7092.9	5.9	1.5E-31
Pcdha10	18.6	177.1	9.5	1.4E-19
Unc13a	54.7	304.5	5.6	1.3E-13
Adam5	0.2	5.6	23.5	2.5E-02
Hhipl1	7.6	32.2	4.2	1.8E-02
Snap25	23.2	259.6	11.2	3.1E-24
1700023L04Rik	0.8	9.1	11.7	1.5E-02
Pdgfrl	7.7	67.7	8.8	2.5E-08
S1pr2	170.3	1067.8	6.3	5.3E-22
Zfp941	5.9	52.4	9.0	5.7E-08
Gjc2	2.8	35.2	12.7	1.2E-06
Cacna1c	37.5	903.6	24.1	4.9E-07
Lhx6	1.5	16.4	11.0	1.2E-02
Mir1903	1.9	16.1	8.3	2.0E-03

Cbln1	2.4	17.7	7.3	4.0E-03
Kcnab1	5.0	87.3	17.5	4.5E-11
Pcbp3	117.2	1088.2	9.3	5.2E-37
Acsl6	16.6	94.8	5.7	2.0E-07
Zfp449	86.4	383.6	4.4	6.0E-14
Myh11	617.3	17746.4	28.7	3.6E-53
Pcdhgb2	751.2	6059.9	8.1	5.7E-12
Cd93	127.2	4897.8	38.5	2.6E-17
Ttc12	15.5	77.2	5.0	9.8E-06
Dnase1l3	16.2	224.0	13.8	1.2E-09
Pik3r6	5.2	148.8	28.4	1.1E-21
Ikzf4	36.4	209.2	5.8	2.3E-02
Abcg1	52.3	304.7	5.8	6.5E-06
Snai1	15.6	517.0	33.2	6.9E-06
Ccdc69	3.2	15.6	4.8	2.2E-02
Tnfsf12Tnfsf13	17.9	152.5	8.5	4.2E-08
Bai2	16.5	544.1	32.9	3.8E-51
Thbs4	89.5	2771.5	31.0	3.1E-28
Dnah2	16.3	89.4	5.5	2.9E-04
Fgf10	5.0	203.4	40.5	1.4E-31
Dnaic1	1.5	42.4	28.5	1.2E-06
Tmem151b	38.6	640.8	16.6	4.8E-10
Pknox2	28.3	1066.1	37.7	1.6E-54
Bmp1	645.6	5654.3	8.8	6.6E-46
Alk	4.2	129.7	31.0	7.9E-14
Galnt14	3.6	16.9	4.7	4.1E-02
Maneal	6.4	115.3	18.0	6.6E-17
9930111J21Rik2	0.7	11.6	15.8	3.5E-03
Dsc3	5.6	30.9	5.5	7.6E-03
Olfr78	0.2	10.6	44.3	5.3E-03
Wnt5b	20.8	181.9	8.8	2.4E-17
Hpse2	30.7	770.6	25.1	8.0E-11
Fam196b	0.3	11.7	43.6	1.3E-03
Bmper	13.5	311.7	23.1	1.1E-18
Cacna1i	0.7	20.1	28.1	6.4E-04
2900011O08Rik	1.5	37.4	25.6	1.5E-09
Ulk2	384.9	1603.9	4.2	2.0E-20
Bcl6b	81.0	1305.1	16.1	3.6E-54
Nr2f1	13.1	296.9	22.6	2.4E-32
Trnp1	14.8	88.4	6.0	3.1E-07
Cyp2d9	0.2	11.4	47.8	1.4E-02
Pmp22	47.5	756.3	15.9	4.0E-50
Cdh12	0.7	36.9	51.4	1.4E-06
Prrx2	1.5	18.3	12.3	4.4E-04
Ebf3	21.4	218.8	10.2	6.5E-23
Adcyap1	1.9	34.2	17.5	1.7E-07
Gm15319	2.7	81.1	29.9	3.1E-03
Pcdh15	4.7	77.8	16.5	1.9E-08
Irs4	11.5	177.2	15.3	6.0E-06
A730056A06Rik	4.9	101.0	20.7	6.4E-18
Col4a1	1204.3	31774.2	26.4	5.8E-72
Prima1	1.7	35.9	20.6	1.9E-06
Tagln	194.5	3967.4	20.4	4.8E-24
Sema3a	26.5	772.5	29.1	5.4E-33
Maml2	25.9	409.5	15.8	2.1E-08
Bnc1	19.1	161.6	8.4	1.6E-05
Gprin1	52.0	238.1	4.6	2.4E-11
D630003M21Rik	14.1	349.2	24.8	5.2E-30
Fap	16.8	719.0	42.9	2.8E-13
Fgf11	38.6	212.1	5.5	7.6E-04
Gm5535	0.2	8.1	34.0	4.0E-02
Elfn1	2.2	16.0	7.2	1.6E-02
Sncg	13.0	161.3	12.4	3.8E-13
9930111J21Rik1	1.7	19.1	11.3	2.1E-03
Gpnmb	106.8	537.6	5.0	4.3E-03
Gm16702	2.5	41.8	16.7	8.4E-07
Csmd1	2.6	26.1	10.1	5.1E-03
Csf1r	128.0	1484.6	11.6	1.3E-46
Cdh2	90.6	1940.4	21.4	7.1E-61
Apoe	620.2	3527.2	5.7	1.1E-06
Fstl4	13.5	291.3	21.6	6.8E-08
Wnk3	62.6	352.4	5.6	5.9E-08
Col4a5	137.4	1916.3	13.9	2.5E-55
Ifitm3	112.4	1903.8	16.9	4.4E-17
Kcnh8	8.1	33.0	4.1	5.1E-03
Fndc9	4.1	71.6	17.3	1.2E-03
Sgcd	3.6	89.2	24.8	5.5E-12
A4galt	8.8	123.0	14.0	8.4E-15
Hs3st5	3.2	69.6	21.5	2.1E-11
Fbln2	146.7	1024.7	7.0	1.2E-09
Iqgap2	630.2	3898.0	6.2	3.1E-17
C430049B03Rik	23.1	380.2	16.5	1.0E-17

Tnc	37.0	703.4	19.0	2.4E-45
Ptchd2	13.4	83.2	6.2	2.1E-02
Ltbp1	114.3	2029.3	17.8	5.1E-38
Pcdh19	5.5	255.2	46.5	3.3E-15
Smoc2	439.3	4381.1	10.0	1.9E-49
Aoc3	19.3	577.6	29.9	2.6E-13
Colq	0.7	31.1	43.4	1.4E-07
Kcnn3	43.2	1016.2	23.5	6.7E-06
Kcnb1	27.3	749.5	27.5	1.6E-08
Lgi1	1.2	11.1	9.1	7.5E-03
Cerk	266.8	1386.2	5.2	8.6E-24
P2rx1	3.2	50.3	15.9	4.0E-04
Fzd4	148.8	721.3	4.8	1.2E-08
Gpr179	3.6	23.0	6.5	8.4E-03
Zcchc16	1.9	14.4	7.4	3.1E-03
Megf10	13.0	167.5	12.8	5.7E-18
Nrgn	3.0	38.6	12.9	2.7E-05
Camsap2	478.2	2040.2	4.3	1.8E-20
Ppap2b	107.3	2114.5	19.7	2.4E-67
Cpxm1	70.8	1129.8	16.0	8.0E-46
Olfr1372-ps1	6.0	37.2	6.2	2.1E-03
Gpr141	3.5	28.4	8.1	2.1E-03
Susd5	0.3	11.1	41.1	2.1E-03
Myt1l	4.2	98.8	23.4	2.3E-17
Gimap4	14.8	434.0	29.3	1.3E-31
Pnpla3	6.3	29.0	4.6	9.6E-04
Fam57b	9.0	149.3	16.6	3.6E-06
Ifi27	18.6	328.6	17.6	4.7E-33
Pcdhb6	1.7	45.0	26.4	4.1E-10
A230057D06Rik	2.4	41.7	17.1	3.2E-06
Lifr	27.8	727.5	26.1	1.0E-22
Plp1	91.1	365.3	4.0	2.5E-12
Hoxc8	36.1	481.0	13.3	1.4E-03
9030612E09Rik	0.7	11.0	15.1	9.9E-03
Fam124a	23.7	148.6	6.3	2.2E-11
Ggta1	105.1	1421.2	13.5	2.1E-49
Cplx1	7.3	35.4	4.9	5.0E-04
Loxl4	3.2	51.5	16.0	1.6E-06
Arhgap15	0.5	6.4	13.2	1.5E-02
Scnn1b	1.7	9.2	5.3	2.7E-02
St3gal5	65.4	343.3	5.3	9.4E-18
Mmp17	19.8	298.6	15.1	1.1E-27
Pcdhb20	12.8	219.6	17.2	3.6E-27
Asb4	23.2	949.3	41.0	4.7E-49
Gfra2	11.5	247.5	21.4	1.0E-30
Dlg2	37.1	774.6	20.9	1.4E-25
Snn	322.6	2420.2	7.5	1.4E-37
Lppr2	108.8	471.0	4.3	8.9E-11
Sh3bgr	17.1	139.1	8.1	3.1E-09
Atp2b2	6.0	130.4	21.9	3.1E-13
Slmo1	4.2	55.1	13.1	1.1E-07
Sh3bp5	137.1	1299.3	9.5	1.5E-29
Ccdc141	42.9	536.2	12.5	3.4E-23
Gdnf	21.9	745.2	34.1	3.0E-21
Bmp7	244.7	1049.6	4.3	1.3E-17
Flrt1	7.6	113.8	15.0	2.0E-02
Aspdh	0.8	10.3	13.5	2.3E-02
Fbxo32	72.9	517.2	7.1	3.8E-22
Tgfb2	51.3	814.8	15.9	8.0E-30
Gm11549	1.5	15.1	10.0	7.6E-03
Fhl4	2.0	14.2	7.2	1.9E-02
Plcl1	24.2	456.6	18.9	2.5E-34
Kcnh3	4.9	28.9	5.9	7.4E-03
Rasd2	51.3	232.8	4.5	2.3E-02
Mapk11	26.4	380.7	14.4	1.9E-29
Emilin2	6.8	64.3	9.4	1.5E-07
Xylt1	21.8	137.0	6.3	5.9E-03
Pygl	56.3	433.6	7.7	1.6E-26
Cd38	106.3	655.9	6.2	2.7E-25
Lrp12	252.6	1049.7	4.2	2.4E-18
Unc5c	95.4	2290.3	24.0	2.3E-32
Cspg5	13.1	125.7	9.6	2.9E-12
Btbd11	19.5	248.5	12.7	5.9E-05
Rab8b	275.1	1328.6	4.8	1.2E-23
Creg2	2.0	21.0	10.7	1.0E-04
Nlgn3	20.6	349.9	17.0	4.2E-08
Il1rap	83.2	355.1	4.3	5.7E-14
Myh3	5.3	75.3	14.3	4.2E-04
Ap1s2	68.2	599.7	8.8	1.0E-30
Cd300lb	2.0	14.2	6.9	2.2E-02
Ggt5	32.7	1078.5	33.0	2.1E-31
Foxl1	26.0	860.4	33.1	6.2E-23

Slc1a6	2.3	23.8	10.4	5.7E-04
Atp8b4	1.2	15.5	12.9	4.3E-03
Fmo2	1.7	16.5	9.8	7.4E-03
Ltc4s	11.1	72.6	6.6	7.5E-03
Tlr8	0.8	5.0	6.5	2.5E-02
Glyatl3	0.5	18.8	36.1	6.8E-05
Zeb2	137.6	4076.6	29.6	2.3E-51
Cntln	107.5	933.4	8.7	5.4E-21
Usp35	101.4	413.6	4.1	2.2E-08
Smad5	1084.6	4728.8	4.4	1.8E-12
Abcg3	6.7	69.8	10.4	8.9E-09
Evc	232.8	1439.9	6.2	4.0E-28
Serpinh1	5013.8	23480.5	4.7	7.8E-14
Heg1	164.2	2110.1	12.8	2.7E-03
Chl1	24.2	539.9	22.3	2.1E-50
Reep5	260.8	1807.7	6.9	1.8E-35
Tnn	33.1	907.7	27.5	1.6E-55
Fzd3	253.5	1209.2	4.8	2.9E-07
Gm15663	13.3	55.7	4.2	1.2E-06
Dio3	3.0	38.8	13.0	1.0E-05
Pamr1	104.0	1337.9	12.9	1.4E-49
Rassf8	30.5	347.3	11.4	8.8E-18
Tbkbp1	65.7	1103.2	16.8	1.8E-28
Ankrd45	1.4	30.2	20.9	3.9E-07
Serpina6	9.4	197.2	21.0	4.2E-03
Grid1	1.7	9.4	5.6	3.8E-02
Pltp	143.1	1290.1	9.0	4.4E-24
Il21r	1.0	10.0	9.8	7.6E-03
4931403E22Rik	1.7	17.8	10.4	2.2E-02
Caskin1	63.3	542.3	8.6	7.2E-13
Nkx3-2	4.8	118.4	24.5	8.9E-12
Gm1987	1.2	24.2	20.2	7.5E-05
Gmfg	4.0	21.8	5.5	3.3E-03
Ephb1	27.7	696.1	25.1	1.6E-55
Kcnt2	36.6	186.9	5.1	2.0E-11
Plxnb3	2.7	61.9	22.6	4.8E-09
Gbp9	11.7	155.2	13.2	2.8E-16
Hic1	254.8	5450.6	21.4	5.5E-25
Sall2	416.9	1971.0	4.7	3.5E-10
AI504432	9.2	228.5	24.8	7.1E-29
Mfrp	6.6	171.4	25.8	5.4E-21

Timp1	40.5	179.8	4.4	6.3E-09
Mmd2	1.8	33.3	18.9	8.7E-07
Dusp8	138.5	560.9	4.1	4.9E-05
Hck	6.9	95.9	14.0	1.1E-05
Pdlim2	7.3	54.3	7.4	1.3E-06
Ddr2	133.9	3916.8	29.3	6.2E-57
Rufy4	3.3	21.1	6.4	6.1E-03
Gpr50	9.1	146.1	16.1	5.8E-14
B230217C12Rik	4.7	87.3	18.7	8.2E-14
AF357359	6.9	53.4	7.7	1.2E-05
Eno2	93.8	401.6	4.3	7.7E-08
Madcam1	4.5	111.3	25.0	3.4E-21
Zfp9	52.2	691.9	13.3	1.8E-39
Hba-a1	386.5	3153.0	8.2	4.5E-28
Wwtr1	609.0	3702.2	6.1	1.7E-33
Sparc	731.3	15324.7	21.0	9.4E-68
LOC100505025	0.7	29.8	41.5	3.3E-07
Eya1	10.5	335.3	31.8	4.5E-18
Gpr176	1.3	17.9	13.9	4.8E-03
Dok5	0.5	12.5	26.1	2.3E-04
42067	11.8	54.7	4.6	1.9E-03
Postn	166.4	4176.8	25.1	1.6E-26
Serpinb9	26.1	346.1	13.2	5.6E-28
Smoc1	153.8	2276.3	14.8	1.2E-57
Chsy3	2.7	85.4	31.1	1.5E-15
Tubb6	198.9	1775.5	8.9	3.0E-20
Gm15217	0.5	29.6	58.2	2.1E-03
Dcdc2a	1.2	25.4	21.0	4.7E-02
Ntm	7.6	60.6	8.0	2.8E-06
Gabrb3	32.2	147.6	4.6	9.4E-11
Nrg3	1.0	42.0	42.0	1.8E-08
Pik3cd	30.6	375.1	12.2	1.0E-27
Pcdhb4	4.0	56.0	14.1	2.2E-09
Cacng8	0.8	33.5	43.1	6.9E-06
Tril	68.6	1926.5	28.1	1.7E-17
Apln	29.6	700.1	23.6	2.2E-49
Numbl	118.4	950.3	8.0	5.7E-27
Duxbl3	36.3	217.6	6.0	2.0E-13
Stab2	3.3	26.5	8.1	3.1E-02
Smarcd3	72.2	543.2	7.5	6.9E-20
8430408G22Rik	25.6	226.2	8.8	7.0E-18

Gpr22	19.3	445.1	23.1	2.9E-40
Arpp21	0.7	14.2	19.0	1.6E-03
Zkscan2	27.8	179.0	6.4	1.2E-11
Vim	1285.1	14949.3	11.6	4.6E-29
Abcc9	334.5	8870.1	26.5	3.5E-22
Zfp286	103.5	533.7	5.2	4.9E-17
Col5a1	1017.3	18936.5	18.6	1.7E-78
Nlrp3	1.3	17.4	13.7	2.8E-03
Sparcl1	351.8	7229.6	20.6	8.3E-32
Igtp	25.8	177.9	6.9	5.3E-08
Adarb2	2.5	11.5	4.7	1.7E-02
Eltd1	8.2	282.0	34.2	3.0E-38
Fendrr	63.0	2843.3	45.1	2.2E-03
Gja5	4.4	99.0	22.6	1.6E-05
Pcdhgc4	739.9	6058.5	8.2	1.7E-11
Ccl3	3.3	43.2	13.1	5.7E-07
Kcna2	1.3	46.7	36.9	3.3E-11
Pacsin1	12.1	50.1	4.1	5.7E-04
Hnmt	0.5	17.5	35.0	6.8E-06
Col2a1	3.0	88.0	29.2	4.6E-11
Rasip1	102.2	1197.8	11.7	6.1E-43
Trpa1	7.2	70.5	9.7	2.9E-06
Timp2	295.3	3393.5	11.5	5.9E-47
Syt1	25.0	658.3	26.3	1.1E-28
Pgbd5	16.6	254.8	15.3	1.0E-27
Prtn3	2.2	10.7	4.8	4.0E-02
Adam11	47.6	233.3	4.9	9.3E-06
Pcdha12	19.3	180.3	9.3	5.8E-20
Meis1	267.5	3016.7	11.3	2.2E-51
Cd33	9.3	136.3	14.6	5.6E-15
Epor	13.2	165.4	12.6	2.5E-15
Sv2c	4.4	66.6	15.0	8.7E-09
Obscn	27.9	115.4	4.1	1.1E-05
Fndc5	3.4	54.5	16.0	3.1E-08
Cd244	0.8	8.7	11.4	4.8E-02
Iigp1	7.3	181.8	25.0	2.5E-12
Trim62	56.3	458.8	8.1	2.1E-10
Olfml1	11.7	193.3	16.6	9.2E-27
Klhl8	35.3	230.3	6.5	2.6E-16
Mx2	6.0	26.2	4.4	1.5E-02
Dclk1	16.6	351.4	21.2	1.6E-39
Actc1	2.2	75.5	34.3	3.5E-18
Rims3	3.3	53.4	16.3	3.1E-09
Dzip1l	59.4	578.4	9.7	1.9E-28
Ccdc177	2.5	17.7	7.2	1.4E-03
Saa1	0.2	7.6	32.0	4.3E-02
Dnah7b	9.3	54.8	5.9	1.5E-05
Gbp10	4.0	26.2	6.6	6.6E-04
Acap1	21.8	342.8	15.7	7.2E-29
3425401B19Rik	0.3	21.5	79.7	1.9E-02
Nrxn3	3.1	127.0	40.5	2.2E-04
Mboat2	153.3	669.1	4.4	1.2E-17
Coro2b	37.1	848.3	22.8	2.5E-14
4930578C19Rik	0.3	17.6	70.2	1.1E-04
Dusp2	20.4	246.4	12.1	1.1E-22
Tenm2	9.8	184.5	18.9	4.2E-08
Mdga2	1.0	24.1	24.1	1.5E-04
Pcdhb2	1.7	23.4	13.8	9.8E-05
Tbxa2r	13.9	303.8	21.9	6.9E-25
Kcnmb2	5.2	67.4	12.9	4.7E-08
Lsp1	211.9	4151.0	19.6	1.9E-26
Gng3	47.3	222.4	4.7	3.2E-12
Map2	83.5	607.0	7.3	1.3E-28
D430041D05Rik	1.3	10.2	8.1	1.5E-02
A830082K12Rik	1.4	43.1	29.8	1.3E-08
Wnt11	2.7	34.7	12.8	7.2E-05
Fndc1	17.9	580.9	32.5	3.5E-07
Dync1i1	1.2	8.3	6.6	3.4E-02
42251	6.9	206.6	30.0	4.6E-15
Fam171b	16.7	495.8	29.6	2.3E-23
Entpd1	21.6	451.3	20.9	1.9E-40
C2cd4d	0.5	11.7	24.0	7.6E-03
Gpr63	9.2	37.8	4.1	1.1E-02
Lppr5	1.5	96.6	63.6	6.3E-23
Aard	2.2	26.7	11.9	2.8E-05
Zfp354c	246.8	2097.6	8.5	4.0E-41
Zfp287	32.1	333.7	10.4	1.1E-21
Gsg1l	6.3	150.5	23.9	1.9E-18
Golga7b	4.2	30.3	7.2	6.1E-06
Tmem119	114.7	2573.9	22.4	3.1E-54
Tmem8b	82.6	568.4	6.9	1.9E-12
4930429F24Rik	1.2	18.3	15.0	2.8E-04

Bdh2	10.7	84.0	7.9	1.6E-09
Mettl24	2.5	46.6	18.7	3.8E-07
A930011O12Rik	11.8	392.5	33.2	3.3E-10
Filip1l	188.8	1735.1	9.2	2.0E-42
Pcdhb14	6.3	94.1	14.9	1.2E-13
Gm5415	0.5	15.3	32.0	3.8E-03
Pou2f2	7.8	81.8	10.5	1.2E-06
Ccl21c	2.9	35.1	12.0	1.1E-05
Ccdc136	78.0	827.1	10.6	7.5E-36
Cxcr6	3.3	29.5	9.0	1.4E-03
Lynx1	2.8	31.7	11.3	2.6E-05
Gm13629	0.7	9.8	13.1	3.2E-02
Slc45a1	2.9	51.8	17.7	1.7E-09
Akap2	237.9	3685.1	15.5	8.6E-36
Adamts19	12.7	307.2	24.1	3.7E-35
Trpc6	3.2	54.3	16.8	1.0E-10
Has2os	1.7	39.3	23.0	4.4E-07
Soga1	434.9	6150.4	14.1	5.3E-03
Csf3r	2.8	27.9	10.1	8.0E-05
Slc2a3	58.3	757.7	13.0	3.4E-21
Glis3	9.9	125.7	12.8	3.2E-02
Leprel2	127.6	2096.2	16.4	1.0E-34
Nkain2	9.4	54.9	5.8	9.4E-07
Notch3	518.8	3165.8	6.1	1.9E-03
Msr1	12.9	181.9	14.1	7.3E-04
Sepn1	399.3	2030.2	5.1	1.4E-10
Cuedc1	122.7	1345.0	11.0	3.1E-44
Gpr137b-ps	67.2	288.8	4.3	4.0E-11
Pla2r1	2.7	43.3	16.3	2.0E-06
Sox2ot	4.7	52.8	11.3	6.4E-08
Mybph	4.2	56.5	13.5	2.7E-02
Rasgrp2	10.4	251.8	24.2	3.2E-28
Crispld1	6.7	89.1	13.3	2.9E-13
Gpihbp1	21.3	374.7	17.6	3.4E-28
Rtn2	58.4	409.3	7.0	7.7E-23
Ctnnd2	21.6	239.5	11.1	2.6E-20
Gpm6b	81.1	1346.9	16.6	3.1E-56
Mir6992	2.3	18.4	8.0	2.2E-02
Ccdc184	6.0	29.5	4.9	2.3E-04
6030408B16Rik	13.3	265.1	20.0	4.0E-25
Sdk2	13.5	439.6	32.6	1.8E-05
Pcdhga12	744.0	6055.1	8.1	4.7E-12
Agtr2	10.1	87.5	8.7	1.3E-06
Xkr4	8.7	52.3	6.0	2.6E-02
Tcp11l2	56.7	644.8	11.4	1.0E-35
Stmn3	22.3	349.1	15.7	7.5E-21
Fgf5	2.4	19.0	7.8	5.2E-03
Angptl1	91.7	2737.5	29.9	5.6E-19
Gm13889	16.6	441.4	26.6	2.9E-19
Klhl14	1.8	29.7	17.0	1.1E-04
Pgm5	140.5	4184.6	29.8	3.9E-92
Gm2115	3.0	49.8	16.6	2.1E-08
Tceal3	9.0	78.2	8.7	1.7E-11
Adamts5	4.2	91.3	21.8	4.2E-14
Ccdc60	3.9	39.2	9.9	1.2E-05
Fgf13	21.8	481.9	22.1	2.6E-36
Isl2	4.5	139.3	31.1	2.1E-14
Pxdn	1108.1	14285.4	12.9	1.5E-44
Hcls1	33.4	252.8	7.6	2.4E-05
Klhl4	8.9	372.0	41.8	1.0E-32
Grik3	18.5	498.4	26.9	1.1E-10
Trim30d	2.5	29.7	12.0	3.1E-05
Ror1	14.3	567.1	39.6	4.1E-11
Spock3	19.4	318.1	16.4	1.8E-20
Mos	0.7	9.0	12.4	1.3E-02
Amer3	2.2	69.1	30.9	6.6E-11
Sv2a	52.9	482.8	9.1	2.6E-26
Pcdhb8	4.4	52.2	11.7	3.5E-08
Mansc4	5.8	28.8	5.0	1.9E-04
Sat2	33.8	145.4	4.3	5.8E-07
Igfbp7	51.0	1154.0	22.6	6.2E-12
Scn9a	5.9	129.0	21.7	1.5E-22
Adam12	55.7	1038.1	18.7	1.4E-18
Xkr7	1.5	32.8	21.8	7.3E-07
Cybrd1	148.7	964.0	6.5	3.4E-09
Atp2b3	2.7	35.8	13.0	1.5E-06
Lhfpl3	0.3	4.1	16.4	2.2E-02
Fam150b	4.5	34.6	7.7	1.2E-05
Slitrk5	20.6	526.7	25.5	1.4E-15
Nsg2	38.2	695.4	18.2	2.7E-50
Cbr3	3.8	30.1	7.9	6.2E-05
Sema3g	23.7	343.4	14.5	1.1E-22

Cdh4	26.8	118.7	4.4	1.5E-06
Hey2	6.9	141.1	20.4	1.9E-21
Lgals1	353.7	5797.2	16.4	1.5E-07
Wnt4	33.2	333.9	10.0	6.8E-19
Cd40	9.3	168.9	18.2	6.7E-20
Cx3cr1	22.0	277.5	12.6	1.9E-26
Frzb	3.7	49.7	13.3	3.7E-07
Csf1	41.8	1070.0	25.6	1.3E-59
Mog	1.2	13.3	10.8	4.1E-02
Csmd3	4.7	104.3	22.1	1.5E-04
Mapk10	11.6	380.0	32.6	5.4E-50
9230102K24Rik	4.4	48.9	11.1	3.5E-06
AI607873	10.0	113.3	11.3	1.9E-12
Ap3b2	10.2	184.4	18.0	2.6E-27
Pde7b	8.9	161.9	18.2	6.2E-20
Duxbl1	21.2	129.0	6.1	3.9E-10
Ypel3	160.4	909.7	5.7	1.8E-23
Fam114a1	92.6	805.8	8.7	3.5E-35
Ppp1r9b	693.4	4028.7	5.8	1.3E-30
Fat4	131.1	8267.5	63.1	7.8E-09
Tlr9	3.1	46.4	15.2	2.3E-04
Thsd1	32.2	241.7	7.5	1.4E-16
Col6a4	511.9	16206.4	31.7	1.2E-22
Disc1	3.6	46.4	12.9	4.1E-02
42250	47.6	1035.0	21.8	1.3E-38
Pcdha5	20.3	176.7	8.7	1.0E-18
Pcdhga3	758.0	6103.7	8.1	2.9E-12
6330409D20Rik	1.2	34.9	29.2	3.5E-04
Plod1	205.4	2410.2	11.7	3.2E-46
Slc2a10	23.2	300.9	13.0	1.9E-23
Dnah7a	3.5	16.3	4.7	4.9E-02
F2rl3	12.8	402.2	31.4	4.0E-41
Hand2	96.7	1789.7	18.5	8.2E-67
Plac1	1.5	14.4	9.6	6.7E-04
Iqck	20.6	160.7	7.8	1.9E-14
Ccdc158	8.0	64.8	8.1	3.0E-06
Arl4d	39.3	173.1	4.4	4.2E-11
Dock2	9.9	123.0	12.4	6.6E-14
Tcf15	1.7	38.2	22.0	2.4E-08
Gjd3	1.5	24.0	16.1	1.4E-03
S1pr3	118.2	3028.4	25.6	2.0E-32

Dpp6	4.5	69.7	15.5	1.1E-12
Mamdc2	6.1	145.8	24.1	1.3E-22
Lrrc4c	9.8	245.7	25.1	1.9E-32
Ano1	169.8	1648.7	9.7	3.2E-19
Copg2	1490.4	6724.2	4.5	2.0E-24
Btnl9	9.6	295.1	30.7	6.8E-39
Prickle1	195.5	1280.1	6.5	2.0E-17
Colgalt2	7.8	127.4	16.3	1.3E-18
Fcgrt	192.4	1068.8	5.6	3.9E-25
Npy1r	1.6	19.4	12.2	1.7E-05
Tnfaip2	34.1	283.2	8.3	7.4E-04
Adarb1	39.6	173.4	4.4	1.7E-06
Nipal4	5.4	59.4	11.0	2.5E-10
Pdlim4	28.4	361.3	12.7	4.7E-31
Peli2	215.4	1141.1	5.3	4.5E-08
Rftn1	9.3	122.5	13.2	2.2E-15
Upp1	15.1	114.5	7.6	6.4E-10
Tgfb1i1	128.7	3898.0	30.3	1.9E-55
Oprl1	5.7	93.0	16.3	4.7E-14
Kcne4	23.2	377.1	16.3	4.3E-31
Itga11	61.8	1797.7	29.1	4.6E-44
Zfp300	10.2	83.1	8.1	1.1E-09
Coro1a	44.1	482.9	11.0	1.0E-08
Tgtp1	2.9	23.1	7.9	3.9E-03
Fam26e	0.5	28.2	56.4	3.9E-08
Rasl11b	141.3	973.7	6.9	2.0E-30
Srrm4os	0.7	44.8	60.0	3.5E-02
Klrb1c	1.9	53.8	27.9	1.2E-07
Adamts8	56.0	1318.7	23.5	8.3E-65
Cav2	13.4	298.5	22.3	4.9E-41
Fgf12	1.6	8.5	5.5	2.2E-02
Rab40b	9.9	61.8	6.3	1.9E-07
Syp	77.1	524.5	6.8	5.7E-24
Sema5b	15.2	236.0	15.5	1.6E-12
Adcy1	146.6	615.7	4.2	1.4E-04
Btk	5.5	43.3	7.8	1.8E-05
Rarb	36.2	470.5	13.0	1.2E-35
Gm11747	11.2	244.0	21.9	4.8E-10
Hivep2	245.3	1113.7	4.5	7.7E-04
Col9a2	59.4	1208.1	20.3	1.5E-11
Lrp1	5628.1	23258.5	4.1	1.1E-02

Ccdc106	43.0	277.5	6.5	1.5E-16
4933407L21Rik	0.2	10.8	45.1	3.9E-03
Gm14005	1.8	24.2	13.8	2.7E-03
Agt	4.3	60.7	14.2	4.8E-09
Ephb3	226.8	1398.5	6.2	5.0E-15
Pcdhgb6	770.1	6271.2	8.1	2.8E-12
Colec10	63.1	2468.5	39.1	3.2E-79
Foxp2	85.3	1529.2	17.9	5.1E-63
Sphk1	6.1	113.7	18.6	2.9E-13
Lrrc36	0.5	9.4	18.4	2.2E-02
Amdhd1	4.8	42.2	8.7	6.4E-05
Col9a3	8.4	48.8	5.8	1.3E-04
She	14.5	540.5	37.3	1.2E-56
Smad9	19.3	948.8	49.1	4.5E-37
Enpp2	24.8	599.0	24.2	3.2E-18
Parvg	6.0	73.0	12.1	1.1E-09
Mfng	52.6	623.0	11.8	1.1E-36
Arhgef3	98.5	709.0	7.2	9.5E-29
Ablim3	4.4	140.8	31.8	4.8E-22
9630013A20Rik	1.5	18.3	12.3	4.5E-03
Pcdhac1	18.1	168.8	9.3	1.8E-19
Sox18	21.4	826.5	38.6	3.2E-40
Cxcl14	2.5	82.5	33.1	4.1E-08
Bach2os	5.1	53.6	10.5	1.4E-02
Nap1l3	13.9	74.8	5.4	6.6E-10
Tead2	717.1	4549.7	6.3	2.3E-36
Zfp128	64.4	287.4	4.5	1.6E-11
Uchl1os	4.2	49.4	11.7	4.3E-08
Stard8	53.6	241.1	4.5	9.5E-11
Pcdha6	18.1	167.1	9.3	2.2E-19
Fcrls	6.7	113.6	17.0	4.2E-19
Podxl2	79.8	1530.7	19.2	2.3E-30
Lonrf2	40.4	264.1	6.5	2.0E-07
Sorcs1	12.4	332.5	26.9	1.1E-27
Tdo2	0.8	29.5	37.9	1.2E-05
Ddo	0.2	13.5	56.4	2.4E-03
Rgs2	71.9	513.0	7.1	1.7E-10
Lama4	224.8	6436.4	28.6	7.1E-72
Ecm2	6.0	69.8	11.7	1.7E-08
Dennd5a	1009.4	4857.7	4.8	7.9E-27
Ccdc109b	2.7	12.1	4.5	3.6E-02
Hoxa3	95.5	1101.7	11.5	1.2E-07
Egflam	66.2	2140.9	32.3	9.8E-79
Aplnr	31.3	675.5	21.6	9.5E-06
Col25a1	42.8	293.4	6.9	3.9E-12
5430435G22Rik	5.9	40.2	6.8	7.3E-06
Olfml2b	29.1	522.6	17.9	5.3E-21
Vamp5	9.0	84.9	9.4	9.8E-10
Mrc1	30.3	168.3	5.6	5.0E-14
Hmx2	2.3	44.9	19.7	8.7E-11
Nwd2	6.3	109.7	17.3	5.6E-09
Odf3l1	0.5	31.5	65.9	3.4E-07
Foxf2	100.6	3759.7	37.4	1.4E-58
Fcgr1	6.2	76.5	12.4	2.7E-10
Dgki	1.0	47.3	48.0	4.5E-09
A330076H08Rik	4.0	34.7	8.7	4.3E-04
Pcsk6	79.1	593.0	7.5	3.8E-26
Pcdhb5	6.9	96.0	13.9	3.4E-14
Cdk17	291.3	1602.9	5.5	4.3E-28
Gng2	98.3	2019.9	20.5	2.4E-73
Csn3	1.7	48.9	28.2	9.5E-09
Hspa12b	33.8	654.5	19.4	3.5E-46
Shc4	25.8	213.8	8.3	6.6E-19
Trim67	10.2	266.5	26.0	1.2E-08
Cdk5r1	49.5	233.1	4.7	1.3E-12
Rarres1	1.8	23.3	13.2	8.6E-05
Pcdhgc5	732.6	5969.9	8.1	1.9E-11
Chst3	40.3	922.6	22.9	3.9E-15
Pik3ip1	43.0	297.8	6.9	2.0E-19
Fam184b	20.6	324.8	15.8	4.4E-32
Dlc1	174.2	3923.2	22.5	2.3E-13
Gypc	39.8	859.5	21.6	1.3E-53
Msrb3	64.0	1448.9	22.6	1.5E-69
Rspo1	12.6	167.2	13.2	9.5E-19
Aph1c	26.3	144.3	5.5	2.0E-07
St6galnac4	59.8	533.1	8.9	1.0E-25
Nmnat2	5.9	103.9	17.6	8.5E-12
Rnf150	45.6	684.4	15.0	1.9E-21
Hspb6	120.0	677.9	5.7	1.6E-11
Brsk2	15.5	363.0	23.4	1.4E-23
Kcnn2	3.0	25.5	8.6	2.2E-04
Trpm5	17.1	362.4	21.2	6.3E-18

Kctd17	52.9	1093.9	20.7	5.9E-56
Prelp	6.6	228.1	34.4	1.7E-08
Thsd7b	0.2	28.6	119.5	4.6E-09
Dzip1	75.4	940.5	12.5	1.4E-44
Pcdhb17	23.6	341.5	14.5	8.0E-33
Nexn	36.0	644.9	17.9	6.8E-15
Angptl2	104.5	2110.7	20.2	1.5E-50
Tlr7	10.2	132.5	13.0	8.0E-17
Col5a2	614.6	11490.2	18.7	2.8E-24
Itpr1	581.6	2768.5	4.8	4.1E-13
Serp2	8.2	55.4	6.7	3.2E-07
Trps1	104.2	1732.6	16.6	2.1E-14
Kcng2	5.1	27.1	5.3	7.3E-03
D730005E14Rik	1.0	10.8	11.3	2.0E-02
Hvcn1	94.8	605.9	6.4	1.0E-22
Rab39b	29.5	152.4	5.2	2.6E-10
Mmp2	561.4	15966.8	28.4	2.0E-98
Pecam1	91.4	2216.1	24.2	2.5E-48
Pcdhgb5	748.0	6050.9	8.1	6.7E-12
Arhgap24	21.4	450.1	21.0	1.6E-27
Gpr153	52.0	1401.5	27.0	4.9E-69
Ccdc36	9.3	52.6	5.6	7.1E-05
Amotl1	767.8	4869.6	6.3	1.7E-05
Npr3	58.2	1227.7	21.1	6.5E-12
2810405F15Rik	0.5	38.7	80.9	1.8E-04
Scn1a	3.5	56.2	16.2	2.0E-07
Cdh13	11.7	144.3	12.3	8.3E-15
Pdpn	44.4	876.0	19.7	6.0E-54
Chst7	6.2	70.9	11.5	1.2E-08
Ppp1r14c	5.8	32.7	5.7	2.0E-03
Cnksr2	5.9	86.2	14.6	5.1E-05
Ogfrl1	41.9	281.5	6.7	4.1E-19
Boc	59.7	1143.0	19.1	1.4E-22
Mmrn1	5.1	133.8	26.2	9.3E-17
Dpysl3	367.3	8740.2	23.8	4.4E-74
Cdo1	11.5	82.6	7.2	4.4E-09
Hectd2	27.1	224.7	8.3	4.9E-16
Htra1	15.5	91.5	5.9	1.2E-07
Il1b	4.1	75.1	18.1	1.9E-09
Ccdc80	93.8	1646.5	17.5	1.3E-53
Clec1a	2.4	150.3	61.6	2.6E-31
Smtn	355.4	2814.0	7.9	1.2E-37
Fxyd6	59.0	897.4	15.2	2.9E-51
Mfhas1	90.6	619.6	6.8	3.1E-08
Metrn	212.1	1196.2	5.6	7.4E-26
Mcam	437.2	4106.1	9.4	2.1E-27
Syt6	3.6	90.3	24.9	4.0E-16
Adcy4	16.3	281.9	17.3	1.6E-25
Sox5	36.5	619.9	17.0	1.5E-10
Zfp30	67.4	273.0	4.0	3.0E-12
Stk33	0.2	6.0	25.0	1.5E-02
Cav1	45.8	1241.0	27.1	1.0E-76
DQ267102	0.7	9.4	12.9	3.8E-02
AB124611	4.6	34.8	7.6	5.7E-03
Bcl2a1d	2.5	14.8	5.9	3.0E-03
Tmtc1	57.6	1372.0	23.8	7.2E-15
Ptprv	3.9	21.5	5.5	2.8E-02
Efs	82.9	1738.0	21.0	5.8E-28
Pnma2	12.8	71.3	5.5	5.8E-08
Svop	5.2	94.8	18.2	8.6E-18
Oprk1	7.2	42.1	5.8	4.0E-02
Adamtsl2	2.4	102.8	42.0	2.6E-16
Fabp5	172.6	754.5	4.4	3.6E-10
Gpr37	0.7	31.1	41.6	4.8E-08
Leprel1	17.9	486.1	27.1	5.4E-35
Prrt1	1.0	13.5	13.9	1.5E-02
Rasa3	143.4	1257.1	8.8	4.6E-37
Prr33	14.3	518.6	36.4	1.5E-04
Dlk1	1010.1	14775.1	14.6	2.2E-26
Ntrk1	1.5	16.0	10.9	6.5E-03
Inpp5d	19.0	276.9	14.5	1.3E-23
Pkia	86.5	506.9	5.9	5.6E-14
Lbp	6.7	29.7	4.4	4.0E-02
Art3	1.7	17.5	10.4	1.8E-03
Mkx	20.2	98.7	4.9	3.4E-06
Ets1	349.3	4805.4	13.8	2.5E-27
Serpinb8	3.8	32.3	8.6	6.1E-05
Klhl32	6.2	57.2	9.3	6.9E-08
Cxx1b	159.2	1050.3	6.6	1.8E-26
Scn2b	53.0	222.7	4.2	1.1E-05
Kcnq5	11.1	135.9	12.3	1.8E-16
Azin2	21.1	213.5	10.1	4.0E-20

Slc10a4	21.2	464.7	21.9	1.4E-42
Pdlim3	51.4	1275.8	24.8	2.2E-29
Magel2	13.0	130.9	10.0	2.9E-12
Nfkbie	25.6	104.4	4.1	5.7E-07
Irf5	20.1	233.4	11.6	8.4E-18
Ltb	1.5	42.0	28.7	4.9E-07
Resp18	3.6	33.3	9.4	6.3E-06
B3gnt5	26.6	388.9	14.6	4.1E-38
Hdac7	307.8	1936.2	6.3	2.3E-08
Ms4a6d	15.3	146.3	9.6	2.2E-07
Fut8	166.3	682.6	4.1	6.7E-17
Hip1	698.1	4627.7	6.6	1.0E-08
Tnnt3	0.2	16.7	69.8	2.6E-04
Mir24-1	2.1	20.5	9.9	1.6E-02
Kcnk13	2.5	20.2	8.2	1.7E-03
Ptrf	449.2	4495.6	10.0	7.0E-53
Nos1	3.0	51.0	17.1	3.0E-03
Csrnp3	8.4	218.1	26.0	2.2E-20
Ms4a7	7.2	98.7	13.8	4.7E-15
Gm5084	1.4	21.2	14.6	1.3E-03
5330439B14Rik	4.3	228.8	52.8	1.9E-05
Anks1b	1.2	21.0	17.2	1.3E-03
Pcdh18	100.6	3251.7	32.3	5.0E-86
Paqr7	60.1	468.0	7.8	1.7E-14
Dact3	102.1	2003.8	19.6	1.7E-24
Ramp3	20.1	174.3	8.7	6.2E-15
Dlgap2	4.3	36.4	8.5	4.6E-05
Gabrb2	19.9	171.3	8.6	3.2E-15
Gm527	30.9	177.7	5.8	6.1E-12
Pln	0.7	35.9	49.3	1.4E-02
Ikbip	206.9	902.5	4.4	3.0E-19
Arhgap23	103.9	1409.6	13.6	5.4E-10
Gm21119	9.2	171.6	18.6	4.0E-04
Fam110b	154.8	842.8	5.4	2.1E-22
Aatk	23.4	803.4	34.4	1.2E-58
Npr2	35.7	955.5	26.7	4.2E-61
Fbll1	1.7	30.6	17.5	1.9E-06
1700001K19Rik	2.3	22.9	10.1	4.1E-03
Cd248	87.8	2233.8	25.4	9.6E-15
Stx11	2.2	31.8	14.3	2.2E-07
Gulp1	63.7	322.4	5.1	2.0E-17

Zfp41	230.3	1045.5	4.5	2.7E-13
Nhsl2	57.3	766.8	13.4	1.2E-03
Kcnc1	6.0	99.8	16.6	3.6E-04
Kcna5	15.3	419.5	27.4	3.3E-45
Shank3	66.3	1355.7	20.5	4.7E-03
Slco2b1	6.7	123.9	18.4	7.3E-17
Afap1	365.9	1547.7	4.2	3.0E-03
Htr3b	0.5	24.8	51.7	4.9E-08
Cadm1	282.7	2562.8	9.1	1.3E-34
Amy2a2	5.7	51.3	9.0	4.5E-02
Unc5a	19.1	118.3	6.2	4.3E-09
Wnt7b	1.8	17.0	9.4	3.9E-02
Sorcs3	2.8	34.4	12.4	2.0E-05
Tekt2	28.6	118.4	4.1	7.2E-06
Pabpc4l	18.0	338.4	18.8	4.6E-39
Emr1	17.9	173.6	9.7	1.6E-21
Vash1	196.4	4387.5	22.3	6.1E-20
Hmcn1	16.6	487.8	29.4	4.2E-06
Ctxn1	183.9	1352.9	7.4	1.8E-31
Gpsm1	307.4	1401.3	4.6	3.3E-19
Icam5	1.0	9.1	9.5	2.9E-02
Nkx2-3	78.3	2230.0	28.5	5.9E-67
Disp2	55.6	321.1	5.8	8.8E-06
H2-Aa	1.3	26.0	20.8	5.8E-04
Dusp1	52.3	398.8	7.6	2.3E-22
Epha4	208.1	1418.5	6.8	1.6E-30
Zc2hc1c	21.3	115.8	5.4	4.4E-08
Kcnd3os	0.5	18.5	38.7	6.8E-04
Ppef2	12.3	65.0	5.3	3.2E-03
Pcdh9	8.7	315.9	36.2	7.5E-43
Fosl1	20.7	84.6	4.1	1.7E-04
Alox12	2.3	21.1	9.2	3.2E-03
Slc22a17	208.6	2055.7	9.9	4.2E-43
Kit	422.1	2275.9	5.4	7.2E-16
Sacs	3.7	89.9	24.4	2.4E-03
Ehd2	177.9	2440.3	13.7	1.4E-56
Rims1	4.2	145.2	34.5	3.6E-24
Mef2c	24.4	597.7	24.5	6.4E-55
Slc10a6	0.3	14.0	52.0	1.8E-03
Slc25a45	6.9	103.4	14.9	2.4E-13
Prr18	10.3	66.0	6.4	3.7E-04

Ctsf	129.7	659.7	5.1	4.6E-13
Ncf1	42.3	379.2	9.0	2.3E-10
Pou6f1	73.1	874.2	12.0	5.0E-17
Il23a	2.0	18.0	8.8	4.4E-03
Tshz1	764.1	3153.4	4.1	6.0E-12
Kndc1	1.0	20.9	21.0	3.4E-04
Pirt	17.0	427.3	25.1	5.1E-36
Nrp2	889.9	4250.4	4.8	3.3E-17
Akap12	255.7	6878.0	26.9	7.4E-92
Gsn	328.5	2772.9	8.4	3.0E-11
Prrx1	1.2	17.6	14.1	4.3E-04
Akap6	29.3	1067.9	36.5	9.3E-15
Igfbp6	8.1	58.5	7.2	3.3E-06
Pcsk2	4.6	54.3	11.8	6.4E-09
Chrm2	21.1	654.7	31.0	3.6E-23
1810011H11Rik	5.2	48.9	9.4	1.7E-04
Mapt	71.7	816.5	11.4	9.5E-27
Parp12	73.8	311.1	4.2	1.4E-12
Gnaz	19.8	81.4	4.1	2.2E-05
Col4a2	683.7	18005.9	26.3	2.2E-94
Myzap	13.0	279.6	21.5	7.3E-32
Robo1	137.6	3635.1	26.4	3.4E-49
Fam49a	45.4	831.3	18.3	2.3E-52
Synpo2	179.6	7255.8	40.4	6.8E-23
Jam3	74.1	1201.0	16.2	2.4E-55
Serpina3g	3.8	34.2	9.1	1.5E-04
Nkain3	1.4	42.5	29.6	3.8E-09
Satb1	183.4	1143.8	6.2	9.2E-23
Rgs12	97.2	1366.8	14.1	4.2E-31
Lrrc49	97.5	436.8	4.5	1.9E-16
Lix1l	126.8	2557.3	20.2	1.3E-71
Scarf1	21.8	315.5	14.5	1.5E-29
Nr2f2	312.6	2283.7	7.3	6.5E-08
Nckap1l	42.6	321.7	7.5	6.5E-20
Brinp1	49.9	352.1	7.1	7.3E-22
Prnd	51.3	1777.4	34.6	5.9E-87
Zfp61	104.5	444.7	4.3	3.4E-15
F730043M19Rik	9.7	72.5	7.4	1.3E-06
4930503L19Rik	196.8	862.5	4.4	7.6E-15
D930028M14Rik	5.2	21.0	4.0	2.6E-02
Ttyh1	24.8	302.1	12.2	4.5E-27

Ltbp3	173.1	2680.5	15.5	5.8E-21
Spon1	58.1	720.3	12.4	1.1E-14
Atp1b2	18.5	651.0	35.2	1.2E-06
4933428G20Rik	6.7	59.5	8.9	6.5E-06
Fst	33.9	387.7	11.4	4.1E-06
Mgat5b	7.0	205.3	29.2	2.5E-08
Snph	16.9	321.8	19.0	4.0E-13
Syt4	11.1	361.6	32.4	1.6E-47
Casz1	194.2	1051.3	5.4	2.8E-03
Zfp462	566.1	2381.7	4.2	3.7E-02
Lamc3	2.8	34.0	12.1	5.2E-05
Aif1l	99.3	412.3	4.2	2.8E-14
Slc38a5	7.0	67.7	9.7	1.5E-05
Tmem35	7.6	135.4	17.7	8.4E-23
Zfp366	1.2	56.4	46.7	1.7E-10
Susd2	25.9	167.4	6.5	5.1E-12
Fam180a	2.8	23.5	8.4	5.5E-04
Kcnip2	3.5	30.7	8.8	5.7E-04
Palmd	0.5	19.5	39.0	5.0E-06
Bdnf	6.7	122.9	18.2	1.9E-20
Shank1	27.1	582.8	21.5	3.8E-02
Nlrp1a	1.3	15.6	12.2	9.6E-03
C1qc	49.5	554.5	11.2	4.3E-11
Vwf	8.1	127.4	15.7	2.5E-05
Tmem169	4.6	102.5	22.1	1.6E-21
Cacng1	0.5	8.5	16.6	1.2E-02
Cass4	4.3	46.7	10.8	6.2E-05
Mir351	1.2	12.3	10.1	3.4E-02
Fstl5	13.8	337.3	24.5	1.6E-25
Cacna2d3	1.7	47.5	27.6	1.4E-08
Bmp6	15.3	79.0	5.2	2.5E-07
Lingo2	1.3	14.5	11.5	2.9E-03
2810032G03Rik	0.5	23.2	48.4	3.8E-08
Kif5c	61.8	1685.6	27.3	3.8E-33
Mid2	65.2	480.9	7.4	1.1E-21
Tmeff2	18.9	531.9	28.1	5.8E-44
Nuak1	18.8	146.4	7.8	5.9E-10
Zim1	245.8	1078.6	4.4	3.4E-08
Spi1	14.1	205.0	14.6	2.5E-11
Cdkn1c	877.0	6155.6	7.0	1.4E-20
Epha3	21.7	228.9	10.6	5.3E-06

Timd4	4.0	50.0	12.6	2.7E-03
Mmp14	1358.8	6879.0	5.1	3.2E-29
Triqk	27.7	113.1	4.1	2.4E-08
Ppfia4	36.2	243.0	6.7	9.9E-11
Gm5577	10.7	126.2	11.8	5.3E-12
Fam167b	2.9	67.4	23.5	1.9E-08
B630019K06Rik	31.5	146.5	4.7	4.8E-09
Scube1	31.9	786.1	24.7	7.7E-41
Dkk3	42.6	992.5	23.3	1.9E-42
4930467E23Rik	6.7	98.0	14.6	4.3E-05
Sfrp2	46.2	871.8	18.9	6.9E-16
Chodl	14.8	345.8	23.3	4.2E-22
Hoxa6	2.2	93.1	42.0	3.1E-08
Ccr1	6.0	54.4	9.1	6.5E-09
Pcdh17	34.9	1088.6	31.2	4.4E-14
Basp1	167.8	2045.8	12.2	7.1E-47
Gbp3	6.5	71.7	11.1	2.2E-06
Gpc2	241.6	1030.6	4.3	4.1E-18
Ust	7.5	277.0	37.0	7.5E-38
Rbp1	375.3	1747.9	4.7	7.7E-07
Syt9	41.6	182.0	4.4	2.1E-11
Ccl2	5.7	114.9	20.2	3.9E-16
Foxc2	1.2	11.4	9.5	3.6E-02
Prtg	26.6	155.4	5.9	6.6E-04
Pde1a	20.8	717.9	34.4	9.4E-69
Gm14057	7.8	54.5	7.0	6.3E-04
Vstm4	23.2	980.9	42.2	2.8E-22
Cd52	7.3	56.7	7.8	2.0E-07
Mmp16	91.9	455.5	5.0	1.0E-10
Csf2rb2	4.2	53.3	12.7	3.5E-06
Pam	377.2	4299.3	11.4	1.5E-13
Gm16793	1.4	24.8	17.1	1.1E-04
Tmem200b	5.0	106.6	21.5	1.0E-17
Stab1	131.6	1314.2	10.0	5.7E-40
Steap4	1.8	27.6	15.6	4.8E-06
Syne3	5.1	21.9	4.3	9.0E-03
1700071M16Rik	8.2	119.8	14.6	5.0E-11
Tmem136	66.1	387.2	5.9	5.1E-16
2010111I01Rik	565.2	2498.1	4.4	1.1E-21
Casq2	1.3	21.8	17.3	1.2E-03
Kcna3	1.0	67.3	70.3	7.6E-05
Phyhipl	16.5	182.7	11.1	3.4E-20
Calhm2	12.7	178.0	14.0	1.8E-20
Tspan2	52.5	1061.7	20.2	7.5E-59
Irs1	63.7	1740.7	27.3	2.7E-04
Osr1	51.4	753.8	14.7	1.9E-43
Scn5a	18.3	155.1	8.5	1.1E-07
1500017E21Rik	9.4	99.2	10.5	1.7E-10
Syndig1	7.1	72.5	10.3	1.4E-10
Bend5	48.2	357.0	7.4	1.4E-19
Fbxo41	11.2	79.1	7.1	5.9E-05
Lhfpl4	8.8	196.5	22.2	1.5E-32
Lrrtm2	4.4	174.8	39.5	1.3E-19
Esm1	34.6	981.3	28.4	3.0E-27
Slc8a1	96.8	1083.0	11.2	5.2E-29
Pcdhga5	759.1	6033.3	7.9	1.5E-11
Slc13a5	0.5	23.4	46.0	1.2E-05
Elavl3	34.1	799.1	23.4	2.8E-57
Edn3	45.1	572.7	12.7	1.5E-27
Rtn1	38.6	813.8	21.1	8.5E-58
Cxcl5	0.7	35.1	48.1	2.2E-07
Mira	14.1	126.8	9.0	2.7E-07
Nrbp2	202.0	851.5	4.2	7.9E-08
Slc1a2	1.5	26.2	17.0	2.5E-05
Itgal	23.8	198.5	8.3	1.4E-14
Hs3st3b1	43.5	833.2	19.2	2.8E-14
Kank2	529.1	2361.2	4.5	5.7E-12
Syde1	268.7	1604.0	6.0	1.8E-17
Slc24a4	4.4	102.6	23.2	2.8E-13
Fam124b	2.5	44.1	17.8	6.4E-10
Rgma	55.6	1759.8	31.6	1.1E-06
Kcnj8	109.8	2141.8	19.5	6.4E-67
Slitrk1	2.9	89.1	30.7	6.0E-17
Cxcr4	112.7	2192.3	19.5	4.2E-67
C1qtnf1	69.0	1528.3	22.2	1.9E-07
Rasal3	9.5	66.6	7.0	4.3E-06
Fam155a	6.9	118.0	17.0	3.7E-18
Ptprb	63.0	642.3	10.2	1.8E-10
Hcn4	13.3	109.5	8.2	1.5E-05
Tlr6	0.5	20.8	43.6	1.3E-05
Rnf165	14.4	300.3	20.9	1.7E-04
B3galt5	21.4	195.4	9.1	4.2E-04

Dcn	195.4	4604.2	23.6	5.0E-33
Fbxl13	2.8	31.9	11.4	2.2E-04
Kcnk3	78.4	2605.8	33.2	8.7E-32
Slit3	54.8	1794.4	32.7	1.2E-12
Abcg4	13.6	225.3	16.5	2.7E-16
Tgtp2	5.4	44.4	8.2	8.2E-05
Il1rapl1	0.5	27.1	56.7	1.3E-06
Sipa1	360.7	1984.4	5.5	2.5E-25
Ifi47	6.5	70.7	10.9	3.0E-08
Runx2	7.7	164.2	21.4	4.5E-07
Rgs6	2.0	18.6	9.1	1.0E-02
Ncam2	12.2	119.8	9.8	4.0E-08
Adcy2	21.0	522.4	24.9	1.4E-44
Inhbb	8.5	182.2	21.4	1.8E-22
Gpr85	12.8	121.3	9.5	4.0E-14
Cmya5	2.9	76.6	26.4	9.5E-15
Abtb2	35.7	309.2	8.6	1.8E-23
Sgip1	19.2	466.5	24.3	1.5E-46
Gpr173	18.8	273.2	14.5	1.1E-11
Nap1l2	20.9	159.6	7.6	3.5E-11
Gm16617	10.7	155.4	14.6	2.8E-05
Il16	15.9	239.4	15.0	2.6E-23
Myo5a	366.1	1703.4	4.7	6.7E-18
Rhbdl3	10.4	107.7	10.3	7.0E-15
Ccdc88a	164.6	1619.4	9.8	1.3E-44
St8sia2	24.2	802.8	33.1	1.1E-13
Otx2	1.0	27.9	29.1	8.9E-05
Hpgd	61.3	345.8	5.6	5.7E-20
Fam102b	292.0	2081.1	7.1	1.1E-28
Aldh1a3	16.6	462.8	27.9	2.3E-30
Cldn1	10.4	58.0	5.6	3.4E-06
Slc18a3	7.0	256.9	36.5	2.3E-35
Fhod3	22.7	444.0	19.6	5.6E-40
Six4	12.6	99.7	7.9	3.8E-09
Slc6a17	23.6	106.6	4.5	7.6E-07
Ica1l	2.0	29.8	15.2	1.9E-05
Gm2002	75.1	437.8	5.8	3.2E-20
Cntn2	3.2	50.2	15.7	4.1E-08
Abca9	4.0	48.8	12.2	1.5E-08
Fbxl7	59.3	982.6	16.6	1.2E-23
Jph4	55.1	517.1	9.4	1.1E-05
Tcerg1l	0.3	8.4	33.5	1.8E-02
Sptssb	14.4	99.2	6.9	9.3E-13
Adamts18	3.0	82.4	27.8	8.3E-13
A430105I19Rik	20.1	312.6	15.5	2.1E-28
Cadps	71.6	519.1	7.2	2.2E-26
Hoxa4	46.8	842.1	18.0	1.2E-21
Reln	10.1	91.0	9.0	2.9E-02
Il10ra	8.0	108.7	13.6	2.2E-11
Iglon5	20.6	601.3	29.2	4.3E-46
F630028O10Rik	3.5	40.3	11.5	3.7E-05
Mest	758.1	14656.6	19.3	3.4E-80
Gm12709	2.3	42.3	18.7	2.0E-07
Scn2a1	13.3	127.8	9.6	1.1E-12
Hivep3	10.4	198.3	19.1	3.6E-02
Gng8	7.3	183.8	25.0	1.7E-16
Slc26a4	0.3	11.0	43.9	2.3E-03
Amy2b	1.3	12.6	9.9	4.0E-02
Ccdc3	55.7	223.7	4.0	6.4E-12
Cldn10	0.3	23.1	92.1	1.7E-02
Efna5	99.7	1868.1	18.7	5.8E-09
Cacng7	39.5	1056.5	26.7	4.5E-62
C5ar1	10.7	106.1	9.9	5.9E-12
Syn2	8.9	62.3	7.0	1.1E-08
Msx1os	2.0	11.2	5.6	4.7E-03
9630001P10Rik	1.6	12.1	7.7	8.3E-03
Scg3	49.6	263.5	5.3	9.0E-10
Chrdl1	4.5	250.4	55.6	1.5E-44
Ifitm1	69.2	1947.7	28.2	1.4E-75
Cxcl10	11.4	103.8	9.1	1.6E-09
Nckap5l	298.0	1654.5	5.6	7.4E-04
Nfatc1	44.4	325.0	7.3	3.6E-03
Begain	58.4	441.0	7.5	4.5E-05
Mchr1	0.8	8.1	10.6	8.1E-03
A330009N23Rik	6.2	58.6	9.4	1.6E-06
Gabrg2	2.0	42.5	21.1	6.5E-07
Gpm6a	15.3	84.0	5.5	1.9E-04
4930570G19Rik	0.3	17.3	64.1	1.4E-04
Pnck	16.1	218.1	13.5	2.2E-22
Ank1	6.6	35.8	5.4	3.1E-03
Chn1	74.3	540.6	7.3	2.9E-26
Klhl29	28.8	666.3	23.2	2.1E-19

Ncoa7	99.2	440.4	4.4	3.5E-15
Pde1b	24.4	327.7	13.4	1.6E-28
Esam	28.8	915.4	31.8	1.6E-68
Spns2	19.8	197.0	9.9	5.0E-07
Pth1r	73.8	680.5	9.2	1.1E-29
Mmrn2	30.0	1050.7	35.1	5.8E-69
AF251705	3.0	40.7	13.5	2.4E-06
Pdzd4	114.6	912.7	8.0	1.2E-30
Lingo1	7.6	119.3	15.6	3.5E-09
Ache	29.2	311.1	10.7	3.9E-18
Sgk1	35.0	524.7	15.0	1.6E-37
L1cam	105.3	1346.1	12.8	8.3E-27
Slc24a3	40.6	1325.3	32.7	2.2E-72
Lalba	0.3	7.4	27.4	4.3E-02
Adam22	48.8	407.1	8.3	6.1E-20
Lilrb4	9.3	86.8	9.3	4.8E-09
A730046J19Rik	1.2	12.1	9.9	1.1E-02
Ret	119.5	1524.0	12.8	5.2E-30
Cplx2	236.5	1240.6	5.2	4.3E-23
Gal3st3	5.5	80.5	14.6	6.5E-08
Sult5a1	3.7	51.9	14.1	2.1E-08
Unc13c	0.5	11.2	22.0	2.6E-03
Bcl2a1b	1.5	19.8	13.0	7.9E-05
Vip	10.1	246.1	24.4	1.7E-36
Cep85l	11.4	232.6	20.3	4.8E-15
Trim16	143.8	603.2	4.2	2.1E-14
Tceal6	6.0	34.0	5.7	2.4E-04
Gm11837	0.8	20.6	27.1	3.3E-06
Pcdhb7	10.3	128.6	12.5	4.8E-16
Gm10125	0.3	19.7	78.4	4.0E-03
Clec5a	2.7	48.3	17.7	9.0E-08
Cadm2	2.9	32.3	11.1	8.6E-05
Dpysl2	294.4	2060.4	7.0	3.0E-02
Lrrtm4	4.6	79.3	17.1	1.5E-06
Map1b	719.3	7417.2	10.3	2.9E-04
Mir214	6.6	101.6	15.4	1.9E-07
Trim47	19.0	223.9	11.8	5.6E-19
Sphkap	34.1	270.4	7.9	2.9E-16
Cybb	26.7	341.7	12.8	2.3E-28
Gpr65	2.5	14.4	5.7	8.2E-04
Cbln3	8.3	53.5	6.4	1.2E-04
Car5b	2.5	28.0	11.4	4.7E-04
Slc2a6	6.9	27.7	4.0	3.0E-02
Brdt	11.5	118.3	10.3	9.2E-13
St3gal2	149.6	1374.9	9.2	5.1E-29
E130307A14Rik	38.2	169.0	4.4	9.8E-09
Nap1l5	12.5	195.1	15.6	1.8E-13
Mxd4	180.3	739.3	4.1	1.5E-16
Tie1	54.9	1909.7	34.8	5.6E-39
Zc3h12b	14.3	84.9	5.9	2.3E-02
Des	67.8	1189.2	17.5	4.0E-50
Optc	1.5	41.3	27.8	1.6E-10
Adamts2	24.3	812.9	33.5	6.1E-16
Siglec5	0.3	12.0	44.7	7.1E-03
Celf6	5.2	63.2	12.1	7.4E-13
Tspan18	209.0	2978.0	14.2	2.8E-10
Irgm2	44.2	491.5	11.1	1.4E-30
Bdkrb2	6.7	114.4	17.2	1.4E-13
Cntnap4	4.1	115.0	27.8	4.2E-18
Slamf8	0.8	8.8	11.4	4.5E-02
Frmpd1	6.3	139.0	22.2	1.1E-18
Tspyl3	50.0	249.0	5.0	3.9E-12
Lum	294.0	7421.9	25.2	2.0E-37
Cdon	496.0	2918.7	5.9	2.6E-09
Gm10677	17.0	120.3	7.1	1.3E-08
Islr2	14.4	373.7	26.0	1.8E-46
Cd74	14.9	242.1	16.2	7.8E-17
Best1	0.5	10.5	21.9	3.8E-03
Rgs10	13.8	367.7	26.7	1.2E-34
Cend1	3.4	51.4	15.0	4.4E-12
Fam184a	16.1	162.9	10.1	2.6E-16
AA414768	11.1	51.6	4.6	1.6E-05
Hoxb8	36.9	843.0	22.8	1.1E-08
Rasgrp1	2.3	25.7	11.3	4.3E-04
Lrrtm1	11.7	129.9	11.1	6.5E-08
Gm13304	2.9	34.8	12.0	1.3E-05
Klrb1b	4.7	26.4	5.6	4.0E-03
Tub	58.4	1206.2	20.7	9.5E-61
Fam81a	2.5	22.5	9.1	1.4E-03
Pcdhb15	3.7	78.0	21.1	4.7E-03
Tg	1.4	29.3	20.2	2.0E-03
Tubb2a	518.8	2678.7	5.2	1.2E-29

Shd	19.1	286.5	15.0	1.9E-22
Stom	256.0	2300.7	9.0	1.6E-28
Ebf2	2.5	34.9	13.9	5.8E-05
Nefl	15.9	189.2	11.9	7.2E-25
Cd86	3.5	38.1	10.9	6.6E-06
Spon2	26.4	361.6	13.7	1.3E-32
Nnat	175.5	2643.5	15.1	2.5E-39
Dpp10	3.6	58.3	16.2	1.0E-12
Hes5	1.0	7.7	7.8	2.2E-02
Nkd2	9.2	156.0	16.9	2.8E-18
Brinp3	0.2	19.5	81.5	1.3E-05
Cd180	5.0	72.2	14.4	4.5E-12
Limch1	18.8	324.5	17.2	2.7E-23
Ifi27l2a	1.2	20.2	16.4	3.4E-05
Il2rg	9.5	117.3	12.3	1.8E-13
Asphd2	15.6	289.8	18.5	1.3E-31
Asic4	10.0	229.1	22.8	9.0E-30
Stac	6.6	72.5	11.0	4.4E-11
Cacna1h	254.2	5272.1	20.7	1.4E-12
Acss1	126.9	683.0	5.4	6.7E-21
Htr2b	4.2	69.1	16.4	9.2E-10
Pde10a	2.9	110.7	38.0	4.1E-20
Hbb-bt	150.6	1214.7	8.1	3.0E-15
Tacr1	7.3	284.0	39.1	1.4E-20
Tmem252	18.0	485.3	26.9	3.6E-46
Spry4	190.8	1534.1	8.0	3.3E-02
Gramd1a	352.2	3321.9	9.4	3.1E-45
Mafb	25.3	287.4	11.4	4.9E-23
Prokr2	0.3	3.6	13.4	4.7E-02
Ttc28	475.0	3433.0	7.2	1.4E-02
B230312C02Rik	0.8	8.8	10.8	1.7E-02
Rspo2	4.8	190.7	39.9	4.6E-40
Dzank1	17.2	70.2	4.1	2.4E-05
Fam131b	7.0	123.1	17.6	1.3E-18
6720468P15Rik	3.4	46.4	13.9	3.9E-07
Cdh11	352.5	8101.9	23.0	1.4E-24
Flt1	16.7	728.2	43.6	5.9E-27
Mamstr	12.8	116.1	9.0	4.4E-04
Cers1	44.1	305.1	6.9	2.3E-07
Fn1	2205.4	21584.8	9.8	3.1E-09
Cnih2	23.4	237.5	10.1	3.0E-19
Grpr	1.7	39.1	23.4	3.0E-03
Ncan	7.7	198.7	25.8	3.6E-08
Pak3	15.6	146.2	9.3	3.8E-17
Hoxc6	30.7	724.8	23.6	1.6E-07
Klf12	99.8	577.3	5.8	4.6E-04
Lrp3	206.6	943.3	4.6	8.0E-11
Adra1b	1.4	51.2	35.4	3.6E-05
Msantd3	139.1	563.3	4.1	9.0E-16
Dbn1	523.8	4665.3	8.9	5.0E-29
Ankrd50	346.0	2046.5	5.9	8.7E-10
Cpe	374.3	3709.6	9.9	7.6E-18
Col1a1	1413.6	39723.6	28.1	5.3E-23
Nrcam	9.5	138.4	14.6	1.4E-19
Grem2	15.3	830.0	54.1	5.4E-75
Rit2	1.0	14.5	14.8	8.1E-04
Tnr	1.5	109.9	74.4	4.8E-05
Shc3	0.8	8.5	11.0	4.6E-02
Grik1	3.7	50.6	13.8	6.7E-04
Phactr2	181.5	946.5	5.2	1.9E-06
Sdpr	65.4	2073.1	31.7	1.5E-37
Galnt18	28.8	434.9	15.1	1.2E-27
Kcnb2	11.2	134.2	11.9	3.1E-04
Fndc3c1	17.8	514.4	28.9	9.7E-50
Npy2r	2.7	108.5	40.7	4.9E-15
Nab2	101.1	884.9	8.8	6.1E-33
Myl9	278.4	6816.0	24.5	1.5E-28
Sobp	14.8	349.4	23.7	1.6E-05
Tmem63c	0.7	44.9	61.6	4.6E-10
Sptbn4	6.5	50.4	7.8	1.1E-06
Gm1564	2.3	37.4	16.6	1.2E-05
Jakmip3	1.5	20.0	13.4	2.4E-03
Adamtsl1	11.2	193.3	17.2	1.9E-13
Runx1	44.5	294.0	6.6	1.2E-03
Gsg1	0.8	11.2	14.5	1.0E-02
Peg13	161.4	939.9	5.8	8.0E-14
Zfp382	14.0	126.3	9.0	4.8E-12
Rhoj	66.1	1137.3	17.2	2.1E-55
Pdgfrb	449.6	8848.6	19.7	8.2E-12
Kcnj12	7.9	159.8	20.2	1.0E-22
Aldh3b1	4.2	24.5	5.8	2.4E-03
Mrc2	151.5	3422.6	22.6	4.3E-64

Coch	1.8	19.2	10.7	3.7E-02
F2r	152.3	2786.3	18.3	2.7E-69
Camk2a	12.3	83.0	6.8	1.4E-07
Slfn5	3.0	34.3	11.5	4.5E-03
Samd14	179.2	1892.1	10.6	1.7E-45
Olfm2	15.3	130.3	8.5	8.5E-12
Pcdha7-g	730.1	5878.4	8.1	1.8E-12
Sardh	23.5	522.4	22.2	1.5E-46
B3gnt9	81.6	484.4	5.9	2.1E-19
Gngt2	5.4	92.2	17.0	7.2E-06
Marveld1	280.2	1354.2	4.8	1.8E-21
Nxf2	1.7	16.0	9.5	4.2E-03
Tgfbr3	317.7	2570.5	8.1	3.0E-08
Gm14207	12.5	95.8	7.7	3.9E-09
A2m	0.5	10.2	20.0	2.5E-02
Fam105a	31.8	236.5	7.4	9.6E-17
Aldh1a7	60.0	374.3	6.2	2.2E-11
Tgfbi	350.2	6230.9	17.8	3.9E-68
42066	6.1	29.4	4.8	1.4E-02
Acvrl1	41.7	1088.0	26.1	3.2E-30
Pygo1	11.6	278.5	24.1	2.6E-16
Tgfb1	110.6	1158.8	10.5	2.8E-11
Mir1668	9.2	85.5	9.3	1.1E-06
Rgs16	14.6	215.5	14.7	1.9E-26
Slc6a11	9.5	100.6	10.6	2.6E-08
Fzd1	240.7	2767.0	11.5	5.7E-52
Zcchc24	156.3	3300.5	21.1	4.4E-44
Myo1b	516.8	3794.2	7.3	1.1E-40
Pianp	8.4	50.4	6.0	1.1E-04
Pde8a	45.3	193.6	4.3	8.9E-09
Prrg3	120.1	1051.1	8.8	3.5E-17
Chrnb4	13.8	527.4	38.3	7.8E-28
Itih3	2.0	39.5	19.9	2.3E-06
Alcam	160.5	873.8	5.4	1.3E-16
Pcdhb19	12.0	225.9	18.7	3.3E-27
Col6a6	1.3	62.2	49.5	5.6E-06
Ltbp4	416.4	8293.3	19.9	1.7E-28
Ralyl	2.2	38.1	17.1	1.5E-07
Nyap2	0.2	31.1	130.1	4.4E-05
4930511M06Rik	0.5	32.8	68.4	1.0E-03
C1qb	66.0	716.1	10.8	2.2E-08

Cdh6	5.9	122.1	20.8	3.0E-09
Adcyap1r1	75.5	1603.6	21.2	1.7E-20
Emp3	77.8	823.4	10.6	2.7E-30
Prkcq	12.4	194.3	15.7	1.7E-19
Stk32c	1.5	46.9	32.0	5.7E-10
Wscd1	21.0	129.4	6.2	2.7E-10
Hoxd9	1.0	13.1	13.4	7.9E-03
Chrd	24.3	413.4	17.0	6.0E-33
Rspo3	26.9	915.3	34.0	3.2E-62
Pcdhgb1	775.2	6001.9	7.7	1.9E-11
Fam227a	26.8	120.5	4.5	4.8E-06
Nhs	42.5	196.0	4.6	4.5E-05
Amy2a3	5.7	51.6	9.1	4.6E-02
Mpdz	265.4	2168.1	8.2	3.4E-40
Grk5	115.5	477.9	4.1	5.5E-15
Sh3pxd2a	1740.5	8690.3	5.0	1.5E-04
Zfpm2	6.6	215.5	32.8	2.3E-28
Eml1	78.5	1913.6	24.4	2.9E-31
Adamts12	23.5	530.4	22.6	9.9E-15
Cd200r1	2.2	29.1	13.1	9.8E-06
Ptx3	5.5	27.4	5.0	2.4E-03
Fgfr1	276.7	4058.0	14.7	2.2E-61
Ptpn7	7.1	54.9	7.7	1.9E-06
Pkd1	854.1	8472.3	9.9	8.5E-04
Prickle2	67.4	1798.6	26.7	2.9E-18
Fcer1g	31.6	344.1	10.9	3.1E-13
Arhgap6	98.3	597.7	6.1	1.8E-21
Map1a	94.4	1420.4	15.1	1.7E-07
Pdzrn4	7.1	159.4	22.4	2.5E-25
Syngr3	5.7	87.5	15.4	4.1E-16
Tac2	4.6	42.5	9.3	1.1E-04
Daam2	99.2	2057.7	20.7	1.6E-20
Bai1	4.2	50.7	12.2	4.3E-07
Prune2	42.5	201.1	4.7	1.7E-03
Qpct	10.6	72.1	6.8	4.3E-10
Cpa1	43.4	605.9	14.0	4.4E-02
Maf	122.6	1161.1	9.5	5.9E-40
Hoga1	8.1	40.5	5.0	1.5E-03
Gm16336	0.7	24.2	33.1	8.5E-06
Prkar2b	71.4	938.5	13.1	2.4E-36
Pcdhgb7	754.3	6160.1	8.2	1.5E-11

Tbx2	85.5	1564.8	18.3	2.1E-54
Hba-a2	380.8	3101.3	8.1	7.5E-28
Sox17	5.7	154.2	27.0	1.3E-25
Atp1a3	6.8	210.6	31.1	1.7E-22
Spred3	100.3	613.4	6.1	1.5E-03
Pcdha4	19.0	176.0	9.2	1.7E-19
Tmem178b	1.0	24.9	26.0	1.6E-04
Mpeg1	93.6	1346.6	14.4	4.7E-52
Dclk2	49.5	940.7	19.0	1.1E-21
Cnn2	676.1	3271.5	4.8	3.2E-27
2610305D13Rik	7.2	32.9	4.6	1.8E-04
Glipr2	234.7	1221.7	5.2	1.0E-25
Cd36	24.2	192.0	7.9	1.0E-05
Negr1	12.5	318.5	25.5	4.3E-29
Adora2a	15.8	230.4	14.6	8.9E-24
2900041M22Rik	0.5	9.8	19.2	4.3E-03
Ncf2	33.6	141.9	4.2	1.3E-06
Mapre3	128.2	610.5	4.8	8.4E-15
Bmp4	69.2	1579.8	22.8	3.2E-66
Myo1g	8.1	33.2	4.1	1.2E-03
Zyx	747.7	3300.5	4.4	5.6E-05
Mir143hg	21.3	806.0	37.9	5.6E-04
Mmd	286.0	1171.5	4.1	2.0E-17
Tnfrsf25	6.4	28.8	4.5	2.2E-02
Dlx1	25.8	432.6	16.8	1.3E-40
Lrrc32	34.3	1433.0	41.8	2.2E-12
Bcl2a1a	1.0	8.7	8.9	2.3E-02
Nfia	136.5	3065.2	22.5	1.8E-03
Gem	66.7	1028.6	15.4	1.3E-51
Armc2	1.3	13.5	10.6	1.5E-02
Rab31	315.5	1580.4	5.0	4.6E-24
Purg	83.0	378.9	4.6	2.7E-14
Hba-x	10.9	123.7	11.4	1.7E-07
Ebf1	15.5	280.4	18.1	1.9E-26
Lphn3	45.3	959.4	21.2	1.1E-09
Opcml	16.6	225.5	13.6	1.9E-13
Serpine2	244.1	2481.6	10.2	1.2E-50
Rassf2	67.6	819.0	12.1	2.5E-40
Trim9	5.7	48.6	8.5	2.5E-05
Fam19a1	3.5	165.8	48.0	1.5E-25
Vtn	2.8	20.9	7.5	3.5E-02
Gm2a	90.3	655.8	7.3	2.6E-27
Itga8	85.7	1938.1	22.6	4.5E-72
A430078G23Rik	1.7	37.5	21.6	8.2E-06
Nin	280.2	2322.9	8.3	2.5E-29
Iqsec3	1.3	49.0	38.9	1.9E-11
Magi2	11.0	137.2	12.5	3.5E-16
Clca5	9.7	353.1	36.2	6.7E-39
Tm6sf1	12.5	399.9	32.0	1.1E-49
Rimklb	22.5	360.7	16.0	9.0E-35
Fmnl3	564.2	2719.6	4.8	5.7E-25
Col6a1	1347.0	38396.4	28.5	4.3E-101
Zfp521	90.0	941.4	10.5	5.8E-22
Gpr162	30.2	449.9	14.9	3.7E-17
Ren1	0.7	9.2	12.6	4.0E-02
Mirg	72.9	490.4	6.7	3.0E-07
Amigo2	48.5	376.1	7.8	3.1E-19
Ifi205	0.5	6.7	13.8	3.9E-02
Filip1	7.6	238.0	31.3	7.7E-37
Plekho2	77.7	590.2	7.6	2.1E-26
Ms4a4d	0.5	18.9	37.7	1.7E-04
Pdgfra	330.4	10076.2	30.5	1.0E-46
Frmd4a	177.1	2971.0	16.8	4.4E-29
C230035I16Rik	9.5	66.2	7.0	3.1E-06
Pcdha4-g	730.3	5885.6	8.1	1.8E-12
Capn6	89.1	1672.8	18.8	1.4E-28
Adm	7.5	104.6	14.0	4.8E-13
9330158H04Rik	0.5	25.9	54.1	7.5E-08
Zfp488	1.7	78.4	46.2	4.4E-04
Enox1	12.8	293.8	22.9	1.1E-33
Nfam1	11.0	156.0	14.2	2.9E-16
Wt1os	1.3	7.3	5.7	2.9E-02
Col13a1	44.6	969.0	21.7	2.6E-06
Col6a5	5.7	106.6	18.8	2.4E-12
Radil	4.8	32.9	6.8	5.6E-04
Setbp1	237.3	2114.7	8.9	2.0E-06
Serpine1	4.0	30.8	7.6	2.1E-03
Kcnk10	1.0	6.6	6.5	2.3E-02
Anxa6	882.7	10869.0	12.3	7.7E-09
Nanos3	5.3	23.8	4.5	3.5E-02
Rian	1875.0	7685.8	4.1	2.5E-22
Pcdhb18	12.9	188.5	14.6	3.1E-10

Dgkb	6.2	142.3	22.9	3.7E-23
Vstm2l	2.0	21.4	10.6	1.6E-04
Klhl6	17.9	281.3	15.7	3.3E-26
Bmp5	21.8	538.9	24.7	1.1E-46
Tmem145	3.9	108.1	27.5	2.9E-06
Calb1	0.3	20.8	83.1	5.7E-07
Pdzrn3	280.8	2076.7	7.4	1.5E-37
Lyl1	7.8	61.5	7.9	5.5E-07
Nrsn1	3.4	60.1	17.6	6.7E-13
Sp110	1.2	10.7	8.7	2.0E-02
Nxph4	6.2	112.7	18.1	3.0E-15
5430427O19Rik	1.2	9.2	7.6	2.2E-02
Ptch2	24.8	743.6	30.0	1.3E-09
Podn	14.9	62.1	4.2	1.3E-02
Cped1	106.1	3140.2	29.6	2.7E-35
Ngfr	66.7	953.9	14.3	1.1E-34
Cald1	338.1	9118.2	27.0	1.3E-86
Arhgef25	231.9	3017.5	13.0	7.0E-27
Slc11a1	12.1	121.4	10.1	1.8E-14
Ppp1r3c	11.2	145.2	13.0	1.1E-19
Haglr	19.4	268.4	13.8	1.6E-25
Trpc3	9.8	80.2	8.2	4.0E-07
Ifi203	2.3	16.8	7.4	4.4E-03
Xlr	0.5	9.2	17.7	1.6E-02
C3ar1	17.0	186.6	11.0	6.8E-23
Skida1	61.4	395.3	6.4	9.1E-19
Csdc2	19.0	289.2	15.2	2.0E-08
Pros1	148.2	1180.3	8.0	6.4E-24
Pde4b	29.7	723.6	24.4	7.5E-41
Nfasc	70.4	889.7	12.6	2.2E-14
Ahnak	1046.1	10815.6	10.3	2.2E-02
A730036I17Rik	1.2	18.4	15.0	3.6E-03
Tyrobp	22.9	270.4	11.8	1.3E-05
Creb3l1	414.9	1703.3	4.1	1.3E-02
Dpysl5	82.4	909.8	11.0	1.3E-18
Tmem204	27.2	470.2	17.3	2.8E-38
A730017C20Rik	4.6	109.5	23.7	2.2E-21
Arsj	4.2	72.7	17.4	6.2E-09
Tex15	20.4	214.3	10.5	1.1E-17
Dnm3	23.1	311.7	13.5	3.0E-16
Arhgap33	92.2	728.6	7.9	1.8E-05

Adap2	4.8	39.9	8.3	3.9E-05
Itga9	80.7	2541.8	31.5	2.2E-36
Slc26a7	7.3	65.2	8.9	2.1E-04
Glp2r	9.2	251.1	27.4	7.4E-17
Sbspon	14.0	234.6	16.8	5.7E-26
Ctla2a	7.9	124.4	15.8	6.1E-17
Fam131a	42.9	275.7	6.4	3.8E-16
Nptx2	16.3	279.6	17.2	2.4E-21
Slc4a3	227.8	1122.1	4.9	4.7E-20
Gbp8	3.2	39.5	12.5	2.3E-05
Ncf4	5.6	37.4	6.7	2.6E-04
Fbln5	50.7	327.8	6.5	1.4E-17
Unc45b	2.5	74.0	30.1	1.3E-06
Anks6	22.4	178.1	8.0	2.8E-14
Epyc	0.7	12.7	16.9	1.0E-02
Fli1	28.0	528.0	18.8	1.3E-43
Camk1g	20.9	319.9	15.3	3.4E-27
Fsd1	34.5	320.8	9.3	3.7E-22
Tnfsf12	17.3	278.7	16.1	5.7E-27
Olfr1033	1.9	31.4	16.3	3.7E-06
Gm13305	64.7	400.4	6.2	6.2E-21
Hoxa5	80.2	1861.6	23.2	3.7E-74
Fam65b	6.6	65.8	9.9	2.8E-08
Notch4	58.9	1762.0	29.9	2.1E-28
Hsd11b1	0.2	6.1	25.4	4.3E-02
Tmcc2	52.8	904.4	17.1	3.4E-50
Kcnk2	35.9	823.9	23.0	7.2E-15
Cdh19	7.1	104.7	14.7	1.5E-14
Prmt8	0.5	9.5	18.7	1.5E-02
Klf2	5.5	70.1	12.7	2.1E-06
Cdkn2c	19.1	184.7	9.7	5.9E-10
Nov	4.4	21.9	4.9	1.4E-02
Adamts17	54.9	454.3	8.3	6.3E-09
Igfbp3	327.4	6115.3	18.7	2.7E-75
Carns1	18.0	86.9	4.8	3.1E-04
Cntn3	7.9	310.2	39.2	3.0E-46
Cd109	18.4	558.9	30.4	7.6E-23
Pcdhb11	4.7	61.3	13.0	1.5E-09
Fbn2	327.0	9433.5	28.8	1.7E-18
Cyp7b1	8.8	252.4	28.6	1.3E-35
Stat4	2.2	23.4	10.9	8.4E-06

Ramp1	13.8	163.5	11.8	2.1E-18
Lrrn2	13.0	244.6	18.9	1.6E-27
Samd5	30.7	574.2	18.7	2.0E-13
Lincenc1	2.0	14.9	7.4	5.4E-03
Ren2	0.7	8.7	12.0	4.9E-02
Ctsk	21.3	333.9	15.7	4.6E-14
Plau	52.8	1115.6	21.1	2.6E-58
Tlr4	7.3	109.5	15.1	1.4E-14
Ptgir	16.3	400.9	24.6	7.2E-17
Edaradd	1.2	26.6	21.3	6.5E-06
Mxra8	123.9	2338.8	18.9	3.1E-66
Eva1b	100.8	537.9	5.3	6.2E-18
Smyd1	1.5	20.7	13.6	5.2E-03
Fgfr2	1238.5	5474.3	4.4	1.8E-23
Qk	347.5	3312.1	9.5	3.6E-47
Fosb	6.0	26.4	4.4	2.4E-02
Chst2	59.0	1238.5	21.0	1.4E-27
C130030K03Rik	1.0	24.9	25.0	2.3E-05
Bean1	5.1	95.4	18.6	7.1E-16
Cdh5	108.7	3754.1	34.5	1.6E-77
Cdk14	206.4	924.4	4.5	5.2E-20
Tmem59l	2.9	35.1	11.9	9.2E-07
Cdh22	4.0	56.2	14.1	2.0E-02
Col18a1	354.7	4336.9	12.2	4.2E-15
A830082N09Rik	22.9	149.1	6.5	1.9E-07
Grk4	12.4	60.1	4.9	3.4E-04
H2-Eb1	5.5	23.2	4.2	2.5E-02
Chst15	120.4	3808.5	31.6	6.1E-41
Slc4a10	19.0	427.4	22.5	2.8E-06
Ifi44	0.8	9.4	12.2	1.7E-02
Npas4	1.7	54.3	32.0	2.9E-10
Mfap4	221.0	6618.7	30.0	2.7E-80
Thbs1	232.8	1993.3	8.6	7.5E-18
Gpr4	17.5	154.9	8.8	1.4E-05
Ly6h	22.9	289.2	12.6	3.9E-21
Myct1	3.4	223.2	64.8	8.1E-41
Tmem173	102.5	454.4	4.4	5.3E-14
Nsg1	53.9	778.2	14.5	4.9E-49
Adamdec1	424.5	12337.6	29.1	4.7E-16
H2-DMb2	0.5	7.9	16.5	4.7E-02
Nrxn2	11.6	254.0	21.8	5.9E-31

Ackr3	32.6	1120.9	34.3	4.2E-73
Tmem132c	2.7	42.5	15.6	9.3E-05
Khdrbs2	2.0	35.0	17.2	2.1E-07
Apc2	71.3	1644.2	23.1	4.3E-10
Slfn5os	0.5	11.0	22.9	2.8E-02
Hoxa7	7.1	84.1	11.8	1.9E-10
Fam43a	73.2	1031.5	14.1	3.4E-46
Nnmt	2.0	15.8	7.9	2.9E-02
Gm7457	1.0	36.9	38.6	3.3E-05
Syt5	9.8	68.4	7.0	3.8E-09
Kcnip1	19.7	448.8	22.8	1.1E-25
Pcdhga2	780.7	6111.3	7.8	1.7E-11
P2ry14	1.7	94.0	54.1	4.1E-19
Olfm1	146.6	1017.8	6.9	2.4E-28
Dlx5	5.5	77.5	14.1	3.4E-10
Tnfaip8l1	35.3	263.2	7.5	2.1E-20
Cdh10	9.3	159.2	17.0	3.4E-12
Pcdha8	18.3	165.3	9.0	6.6E-19
Ano2	0.7	6.1	8.3	4.0E-02
Adam23	7.0	159.3	22.9	4.7E-18
Hoxd8	17.3	263.2	15.2	2.2E-27
Ptgs1	35.2	526.4	14.9	6.9E-16
Map6	9.9	313.6	31.6	3.2E-22
Casq1	26.1	544.3	20.9	1.7E-46
Col8a1	3.4	28.6	8.3	3.6E-04
Ecel1	5.4	51.2	9.5	2.5E-04
Efemp1	13.9	86.0	6.2	1.4E-09
Astn2	5.6	177.4	31.6	7.7E-29
Lgi2	80.9	886.9	11.0	3.6E-37
Ccl7	0.7	15.5	21.6	1.3E-03
Lrrk2	28.5	268.8	9.4	4.1E-19
Igfbp5	4576.7	21820.8	4.8	1.9E-06
Bves	16.0	198.9	12.5	2.0E-18
Fez1	16.8	215.4	12.8	1.2E-10
Six5	309.2	1630.1	5.3	4.9E-12
Mturn	37.5	641.1	17.1	1.1E-48
Copz2	19.4	338.2	17.4	4.0E-11
Tspan9	412.3	4711.8	11.4	3.6E-54
Atl1	28.8	137.2	4.8	5.6E-10
Ntng1	6.6	128.4	19.5	3.5E-20
Smarca1	145.7	1096.5	7.5	3.9E-19

Tppp	13.6	138.8	10.2	3.9E-16
Fos	22.9	128.2	5.6	1.4E-08
Gm6377	2.0	19.6	9.6	7.6E-03
Chn1os3	15.2	87.6	5.8	2.5E-06
Fcgr3	23.2	220.5	9.5	3.3E-11
Snap91	14.8	364.6	24.6	2.5E-43
Apela	2.5	72.8	28.9	5.4E-13
Scarf2	77.3	1633.3	21.1	3.1E-60
Ramp2	47.9	926.7	19.3	1.8E-50
Akt3	135.3	1672.8	12.4	3.8E-29
Sema3d	19.9	215.8	10.9	9.4E-11
Pcdhb21	5.6	87.0	15.4	3.8E-11
Cmklr1	19.6	455.9	23.3	2.2E-05
Igfbp4	2618.5	14229.2	5.4	3.7E-31
Zfyve28	5.7	75.7	13.3	9.5E-09
Dixdc1	33.1	560.9	16.9	2.3E-43
Sema6c	57.6	803.5	13.9	4.7E-29
Ccm2l	3.7	119.1	32.3	5.2E-18
Fcgr2b	3.7	17.7	4.7	7.2E-03
Mn1	35.1	975.3	27.8	1.2E-03
Ptprm	38.6	1321.5	34.2	1.9E-42
Tcf21	111.0	2685.9	24.2	3.7E-66
Slc5a7	9.0	292.2	32.5	7.1E-43
Adamts6	28.8	575.6	20.0	4.5E-29
Ptgs2	13.2	198.5	15.1	1.8E-21
Col8a2	19.1	317.7	16.7	1.7E-22
Fkbp7	28.9	347.0	12.0	1.5E-19
Sfmbt2	21.3	248.5	11.7	2.4E-09
Cd300a	17.3	145.9	8.4	2.2E-10
Myl1	1.5	44.7	30.0	9.2E-10
Grem1	31.1	1406.1	45.2	4.0E-84
Pcdhga1	762.1	5987.6	7.9	2.0E-12
Elmod1	1.7	14.2	8.5	1.3E-02
Dach1	80.9	710.0	8.8	1.6E-21
Ccr5	1.2	20.8	17.0	4.2E-05
Slc7a2	150.3	661.2	4.4	3.2E-03
Zfp423	21.0	527.5	25.1	2.1E-05
Fat3	16.4	423.9	25.9	8.8E-04
Gbp2	10.9	111.3	10.2	1.1E-05
Phox2a	30.6	443.1	14.5	4.5E-23
Aldh1a1	229.4	3551.2	15.5	3.5E-10

Pcdhb16	10.1	194.6	19.3	2.5E-09
Dner	7.2	126.3	17.5	6.2E-18
Scimp	0.5	12.7	26.6	1.3E-02
Nrep	658.2	8582.4	13.0	1.2E-66
Sntg2	18.2	447.6	24.5	4.9E-34
Chst1	29.1	796.3	27.4	2.9E-16
Dock4	158.5	887.8	5.6	1.4E-12
Slitrk3	2.0	85.1	42.6	1.5E-17
Cyth4	16.2	152.0	9.4	1.7E-15
Sod3	1.0	8.8	8.8	3.3E-02
Sez6	1.5	36.8	25.3	5.5E-07
Syngap1	274.5	1652.1	6.0	8.2E-04
Gm21541	2.9	34.8	12.0	1.3E-05
Pnoc	2.8	41.9	15.1	2.5E-06
Kcnj2	102.3	1058.3	10.3	2.8E-21
Tmem196	0.5	23.6	47.1	1.4E-03
Notum	3.1	13.8	4.5	5.0E-02
Bach2	54.9	1015.9	18.5	1.1E-05
Celsr3	73.9	883.7	12.0	3.6E-10
Lmtk3	268.1	1090.3	4.1	7.8E-05
Rnf112	11.5	110.4	9.6	9.2E-12
Ism1	4.2	101.2	24.3	9.5E-11
Rab12	282.4	1420.0	5.0	1.7E-25
Cygb	49.4	1117.9	22.6	4.6E-61
Upk1b	17.8	71.6	4.0	7.7E-05
Scube3	23.5	204.3	8.7	1.3E-07
Rhov	6.4	26.6	4.1	3.3E-02
Sema3e	8.9	142.5	16.1	4.9E-10
Gja4	10.1	424.7	42.0	4.5E-47
Lrrc19	2.7	15.0	5.5	2.7E-02
E130114P18Rik	1.9	66.8	34.4	9.3E-14
Fam26f	2.3	19.5	8.5	2.3E-03
Dbh	0.5	7.8	15.9	1.2E-02
Nrk	68.5	612.3	8.9	2.8E-10
4833422C13Rik	6.6	122.3	18.5	1.2E-06
Wdr86	14.6	263.8	18.1	6.9E-30
Gucy1b3	142.3	3960.1	27.8	5.4E-64
Antxr1	110.4	2550.1	23.1	1.2E-51
Fam162b	2.9	67.1	23.4	2.3E-10
Dusp27	1.2	25.4	20.7	6.7E-09
Aebp1	123.3	1728.4	14.0	4.4E-52

Pcdhga9	740.9	6051.7	8.2	2.9E-11
C1ql3	16.1	82.7	5.1	1.2E-06
Rgs7bp	11.5	221.7	19.3	3.4E-24
Trpc1	27.9	233.5	8.4	1.1E-18
Riiad1	7.2	36.1	5.0	8.2E-04
Plvap	28.8	587.0	20.4	1.4E-12
2610316D01Rik	1.2	25.9	21.1	8.3E-06
Zfhx4	85.8	2648.6	30.9	1.4E-06
Cebpd	51.7	291.2	5.6	2.5E-16
AI593442	0.3	4.4	17.4	3.8E-02
Ppp1r14a	41.9	391.9	9.3	8.1E-10
Hbb-b1	218.0	1625.1	7.5	1.1E-13
Sall1	43.8	1267.9	29.0	5.1E-09
N4bp2l1	26.8	130.1	4.8	5.5E-07
Ehd3	23.5	455.0	19.4	1.3E-37
Glb1l2	5.8	31.1	5.4	1.2E-03
Meis2	136.1	2929.6	21.5	5.1E-74
Cpa4	0.7	25.8	35.9	3.4E-05
Lax1	2.2	18.5	8.3	1.9E-02
Maged1	2991.6	16121.2	5.4	3.8E-33
B3galnt1	21.2	420.0	19.8	1.5E-43
A830018L16Rik	4.2	110.2	26.2	1.7E-18
6030419C18Rik	18.3	276.6	15.1	2.0E-25
Ednrb	305.4	8780.2	28.8	1.9E-43
Lmo2	25.9	662.5	25.6	3.4E-36
Kcnh4	0.8	33.8	43.4	7.7E-07
Kcnip3	11.6	204.2	17.6	7.0E-26
Adora1	59.7	371.5	6.2	1.6E-03
Apba1	15.5	286.8	18.5	2.8E-22
Cdkl1	1.7	16.3	9.4	4.1E-03
Clec4n	8.3	129.1	15.6	2.6E-15
Themis2	4.5	79.6	17.7	1.9E-10
Ch25h	4.6	56.4	12.3	1.5E-06
Ly9	1.2	21.0	16.9	1.2E-04
Cd4	2.3	15.4	6.8	1.3E-02
Ppp1r16b	17.9	501.8	28.1	1.2E-20
Jakmip2	5.8	110.6	19.2	2.0E-12
A630075F10Rik	1.0	30.6	31.5	3.0E-02
Trem2	7.1	52.5	7.4	1.2E-07
Tmem179	2.2	48.0	21.3	1.9E-12
Add2	24.4	462.1	18.9	2.3E-26
Tcp11l1	79.3	361.0	4.6	2.7E-02
Kcnc2	4.2	86.9	20.6	6.2E-13
Fgd1	278.9	1233.4	4.4	7.4E-10
Gja1	684.9	3047.5	4.4	2.6E-24
Gm10638	8.4	70.8	8.4	2.4E-07
Hoxb4	85.1	1112.5	13.1	1.1E-43
Arc	11.1	112.3	10.1	6.0E-05
Myocd	37.0	1734.2	46.9	9.8E-09
Dact1	106.0	1975.7	18.6	1.0E-64
Cyp2j9	6.9	75.3	10.9	2.9E-09
Tmem47	95.5	1293.0	13.5	1.6E-53
Thbs3	99.2	1118.2	11.3	1.3E-10
Foxs1	2.9	13.9	4.9	1.8E-02
Ajap1	12.4	191.2	15.5	8.6E-20
Col4a6	32.2	508.3	15.8	9.8E-35
Sspn	14.2	320.8	22.5	1.2E-37
Grid2	0.8	19.3	25.4	2.5E-04
Slfn2	12.3	87.3	7.1	6.5E-09
Pdlim7	262.1	2645.2	10.1	2.0E-48
Csf2rb	13.3	172.2	12.9	1.9E-06
Msx1	2.5	16.4	6.6	2.8E-04
Hhex	11.7	68.2	5.8	1.6E-07
Bnc2	41.1	1445.5	35.1	1.8E-05
Loxl1	36.6	553.1	15.1	1.4E-39
Casp12	5.0	155.6	31.2	9.1E-25
Ankfn1	0.2	8.2	34.3	2.9E-02
Gm11627	2.2	37.9	17.3	1.1E-08
Adcy7	56.1	352.6	6.3	2.4E-15
Cxx1c	32.6	405.5	12.5	3.4E-30
Sstr2	2.5	19.6	7.8	7.8E-03
Gsap	4.8	72.8	15.3	1.3E-09
Nlgn1	4.6	91.7	19.9	1.5E-15
Pcyt1b	30.5	140.6	4.6	1.3E-10
Slc16a2	37.5	625.0	16.7	1.4E-10
Acta2	674.1	15717.6	23.3	1.0E-32
Col5a3	12.5	176.8	14.1	2.6E-17
Vegfc	41.9	217.5	5.2	7.5E-11
Bhlhe22	3.1	46.2	15.0	8.4E-08
Ptn	188.6	2899.8	15.4	3.2E-11
Parp3	33.3	213.2	6.4	6.2E-04
P2rx7	7.6	80.8	10.6	4.6E-11

Arhgap36	0.5	23.6	43.8	7.3E-06
Proca1	3.0	30.4	10.1	1.4E-02
Grrp1	5.9	112.3	18.9	8.6E-09
Nell1	4.7	86.6	18.3	5.7E-14
Lox	32.7	800.2	24.4	1.1E-55
Psd2	9.6	46.5	4.8	5.2E-04
Wscd2	6.6	242.4	36.9	5.9E-17
Trpv2	10.4	127.9	12.4	9.8E-16
Wasf3	9.1	258.0	28.3	5.4E-14
Palm2	10.9	447.1	41.0	5.4E-07
Gm16897	4.4	111.7	25.2	3.3E-12
Nrg1	13.4	479.1	35.7	7.3E-46
Atcay	11.1	184.7	16.6	2.0E-24
Plxnc1	15.1	302.6	20.1	1.7E-30
Evi2b	4.0	46.7	11.8	1.3E-02
Plag1	214.6	1174.7	5.5	7.3E-06
Mgp	29.3	548.9	18.7	3.8E-15
Cntfr	48.9	1437.5	29.4	2.2E-23
Cacna2d1	257.7	2289.4	8.9	1.8E-44
Sh3kbp1	124.3	1903.8	15.3	3.9E-57
Pcdha2	20.1	169.7	8.4	1.4E-18
Phldb1	387.6	1956.8	5.0	4.3E-23
Ccrl2	3.3	31.6	9.6	3.2E-05
Adamts10	513.1	2802.2	5.5	2.9E-28
Sgcb	74.5	581.5	7.8	4.4E-29
Tlr3	20.6	158.1	7.7	3.0E-13
Wnt2b	22.8	177.9	7.8	2.0E-04
Aif1	6.6	94.7	14.3	5.3E-04
Clec4a4	0.5	10.6	21.7	1.0E-02
Pcdhga7	809.8	6111.5	7.5	2.3E-11
Fmod	3.9	50.9	13.2	8.8E-04
Gli1	121.1	3807.6	31.4	3.2E-86
Kif26b	140.7	3042.6	21.6	2.6E-05
Kctd15	335.5	1358.4	4.0	1.4E-18
9330182L06Rik	21.1	152.7	7.2	6.0E-12
Itpripl2	598.1	2997.5	5.0	2.2E-19
Rgs1	1.0	10.4	10.6	2.6E-02
Gli3	173.1	2371.3	13.7	1.1E-10
Angpt1	34.9	455.2	13.1	7.2E-16
Islr	154.1	4515.1	29.3	7.3E-90
Nwd1	3.7	57.9	15.5	5.9E-04
Masp1	0.5	33.2	69.3	3.7E-08
Tmem132b	16.1	140.4	8.7	8.8E-04
Zfp641	17.0	74.6	4.4	3.5E-04
Chst10	11.2	84.7	7.5	8.2E-12
Lhfp	57.4	1196.6	20.9	2.2E-54
Stx1b	11.4	240.1	21.0	2.2E-24
Sncaip	27.7	618.4	22.3	4.8E-54
Pdp1	138.9	940.0	6.8	5.2E-30
Gp49a	3.0	33.7	11.0	6.5E-07
Adamts1	207.3	1629.8	7.9	2.0E-31
Ccdc151	3.8	21.1	5.5	6.2E-03
Slc38a4	508.1	3441.8	6.8	9.1E-24
Cfh	2.2	43.7	19.8	5.9E-10
Siglech	0.3	7.1	28.5	4.7E-02
Ctxn3	0.7	12.8	17.2	3.3E-03
Grm7	2.4	30.8	12.7	8.2E-05
Dock10	26.5	601.7	22.7	2.4E-21
Cabp1	11.1	53.9	4.9	4.2E-04
Fbln7	6.9	85.6	12.4	9.2E-11
Calcr	4.7	20.7	4.4	4.1E-02
Trpc4	5.2	99.3	19.0	1.8E-18
3830408C21Rik	16.6	84.6	5.1	1.5E-05
Slc9a3r2	116.2	1186.0	10.2	4.7E-41
Kcnmb4	8.6	117.0	13.6	5.2E-14
Sp7	2.0	57.1	28.9	8.4E-09
Twist1	16.5	266.5	16.2	2.4E-25
Lmo1	1.8	15.7	8.8	1.8E-02
Col28a1	1.5	47.6	31.6	3.0E-04
Stox1	2.5	12.3	4.9	4.3E-02
Pappa	43.9	1516.7	34.6	8.5E-08
Sh2d3c	110.8	1091.6	9.8	5.2E-37
Cpne2	20.0	142.4	7.1	2.2E-11
Tenc1	229.4	3165.3	13.8	1.2E-14
BC028528	8.4	96.4	11.5	3.4E-09
Camk4	42.5	202.3	4.8	2.5E-06
Tnxb	80.3	2103.9	26.2	3.8E-05
Ccdc88b	21.0	150.2	7.2	1.8E-08
2610203C20Rik	91.7	2369.4	25.8	2.0E-08
Ranbp3l	38.1	343.6	9.0	1.5E-18
Sez6l	34.2	700.3	20.5	5.0E-07
Cxcl12	120.8	2520.3	20.9	1.5E-19

Pcdhga4	753.2	6049.8	8.0	3.9E-12
C77370	6.3	56.7	9.0	7.6E-07
Acot7	158.0	750.2	4.7	3.0E-12
Lrrc15	1.0	32.2	33.2	4.9E-05
Cdc42ep3	43.8	502.2	11.5	3.7E-34
Ak5	4.5	26.7	6.0	1.1E-03
Rbfox3	6.1	53.8	8.9	7.4E-07
Axl	771.2	4042.4	5.2	6.0E-29
Ndufa4l2	31.6	205.0	6.5	6.5E-12
Cmtm5	1.2	19.4	16.2	1.4E-04
C1qtnf2	0.5	11.9	23.3	1.7E-04
Slc13a4	2.2	12.4	5.5	2.3E-02
Arsi	7.6	150.4	19.8	6.5E-21
Tmem229a	2.8	135.0	48.5	4.3E-28
Vcan	1309.3	13133.2	10.0	3.3E-15
Ptpro	10.0	119.7	11.9	2.3E-10
Ndst3	2.5	100.8	40.0	4.0E-16
Pcdhb12	4.4	47.3	10.7	6.6E-06
Sfxn4	26.3	106.6	4.1	3.0E-05
D930007P13Rik	1.0	18.3	18.6	1.5E-03
Samsn1	4.2	69.7	16.5	7.3E-11
Gli2	52.5	2065.1	39.3	6.0E-06
Mab21l1	26.4	496.6	18.8	1.2E-44
S1pr1	30.0	689.5	23.0	9.1E-56
Fn3k	6.3	46.1	7.3	6.7E-05
Th	1.7	13.1	7.7	1.3E-02
Plek	12.0	117.2	9.8	5.6E-18
Cacna1e	5.1	205.9	40.0	9.8E-09
Shisa9	1.0	25.7	26.9	6.6E-07
Ankrd6	64.5	286.7	4.4	7.8E-12
Adcy5	44.0	1154.5	26.2	5.3E-29
Cel	8.1	96.8	11.9	3.6E-02
Fut10	55.1	722.5	13.1	1.2E-40
Ms4a6b	12.1	157.0	13.0	1.1E-17
Unc93b1	83.8	379.7	4.5	4.7E-06
Fxyd7	6.0	154.2	25.9	3.8E-21
Ly86	7.3	80.0	11.0	8.3E-10
Cpne4	1.0	16.5	16.8	4.7E-03
Casp1	4.8	34.3	7.2	1.9E-04
9430020K01Rik	99.6	1948.2	19.6	1.2E-43
Dll4	115.5	1413.8	12.2	4.7E-48

Fxyd5	9.6	120.6	12.5	1.2E-05
Tmem132e	7.1	196.6	27.6	2.0E-26
Apbb1ip	4.8	41.8	8.7	1.0E-05
Elovl4	22.0	248.3	11.3	3.9E-25
Gnao1	129.2	1432.7	11.1	9.4E-07
Epha5	2.9	50.3	17.4	1.9E-09
Scrt1	7.0	110.0	15.7	7.8E-07
Ctgf	44.8	288.8	6.4	2.5E-18
Kctd1	48.6	229.0	4.7	1.5E-09
Adamts20	9.3	179.3	19.3	2.0E-11
Klhl38	6.9	118.9	17.4	2.0E-18
Rassf5	18.7	95.0	5.1	8.7E-06
Emilin1	465.6	11914.1	25.6	1.2E-93
Gm266	19.9	286.3	14.4	1.6E-29
Rab37	15.0	108.8	7.3	7.5E-05
Ogn	10.8	209.0	19.4	7.6E-31
Gm11149	6.6	237.9	36.3	2.0E-05
Syt2	3.6	48.4	13.3	8.8E-07
Arhgap28	337.5	2107.0	6.2	9.2E-16
Rbm24	8.0	305.2	38.0	4.7E-37
Gria1	2.0	38.5	19.2	4.9E-07
Ptprc	19.9	313.5	15.8	7.8E-07
Bicc1	75.7	975.8	12.9	1.6E-21
Zfp532	299.7	1837.4	6.1	6.1E-12
Nog	8.6	338.7	39.5	4.2E-33
Nptxr	41.6	384.6	9.2	1.2E-06
Ggt7	20.5	165.6	8.1	1.2E-13
Ndn	181.3	1546.2	8.5	1.4E-42
Clca1	9.0	127.6	14.1	1.7E-13
Lrrc18	1.4	13.3	9.3	1.3E-03
3010001F23Rik	3.5	21.9	6.2	2.9E-03
Svil	1415.2	6574.6	4.6	7.7E-23
Scara3	32.9	423.3	12.9	3.2E-33
Htr2a	0.5	8.3	17.4	2.2E-02
Erich2	0.7	14.8	19.9	1.4E-03
Gria4	14.7	439.9	30.0	6.8E-49
Cacng4	12.7	337.0	26.6	7.2E-24
Emp1	426.9	2989.2	7.0	8.3E-37
E030013I19Rik	4.3	74.3	17.3	5.5E-12
C1qtnf5	6.6	171.2	25.7	6.0E-21
Tmem154	3.9	72.3	18.4	5.4E-11

Pcdhga6	754.1	6052.5	8.0	2.7E-12
Uchl1	117.8	1287.3	10.9	1.8E-21
Cd28	5.3	60.6	11.4	1.2E-07
4930432J09Rik	1.0	14.9	14.9	5.7E-03
Luzp2	3.3	28.2	8.5	1.5E-04
Prdm8	1.2	33.7	27.3	3.2E-03
Car2	40.8	450.6	11.0	4.4E-12
Erg	12.9	492.1	38.2	7.2E-52
Adrb3	1.2	59.0	48.1	6.2E-12
Epas1	30.6	468.2	15.3	5.4E-08
Layn	7.6	47.2	6.2	3.6E-04
Pbx1	502.4	3959.9	7.9	1.8E-17
Meox2	0.5	7.6	15.8	1.3E-02
Rab3c	28.5	260.9	9.1	8.2E-22
Ptpn13	170.8	1109.4	6.5	8.2E-19
Eif4e3	71.3	510.5	7.2	6.0E-23
Hfm1	5.2	45.6	8.8	3.5E-06
Pcdh8	4.9	21.2	4.4	1.6E-02
Rasl12	5.2	24.9	4.8	1.1E-02
Lgi3	3.5	68.0	19.6	1.7E-12
Ccr7	0.8	11.0	14.5	9.1E-03
Dscam	1.6	38.9	24.8	2.6E-08
Il11ra2	74.6	434.0	5.8	3.8E-20
Fam171a2	71.8	1367.8	19.0	9.1E-60
Slitrk2	4.9	200.7	41.0	4.6E-29
Col6a3	816.6	22225.2	27.2	1.4E-09
Gm10584	3.3	111.2	33.9	1.3E-16
Pcdhga10	756.3	6075.6	8.0	1.0E-11
Tmem26	25.3	395.6	15.7	2.0E-18
Nlrx1	44.3	222.6	5.0	4.0E-06
Slco5a1	12.6	140.8	11.2	1.3E-13
Gpr123	0.3	5.0	20.1	4.3E-02
Agtr1a	2.5	94.5	38.0	4.1E-07
Grm8	1.7	82.1	47.5	5.6E-17
Parvb	25.5	738.8	28.9	1.3E-10
Gpx7	27.6	327.1	11.9	1.0E-27
Plxnd1	216.7	6108.4	28.2	2.3E-63
Mfap2	202.7	4496.3	22.2	1.5E-61
B930003M22Rik	2.7	30.0	11.2	1.2E-04
Myl4	3.5	26.1	7.4	1.0E-03
Ednra	89.8	2350.6	26.2	5.6E-62
Slc12a5	30.2	274.8	9.1	4.9E-07
Grap	8.1	191.6	23.6	7.0E-26
Cers4	183.9	832.4	4.5	2.9E-18
Tm4sf1	12.6	231.5	18.4	2.1E-25
Mir6244	1.2	17.5	14.1	2.4E-02
Pcsk2os1	0.3	5.4	20.1	4.0E-02
Arhgap31	73.2	1864.3	25.5	1.7E-08
St8sia5	1.2	19.7	16.3	7.7E-04
Stard13	349.8	1523.4	4.4	4.7E-17
Fam198a	7.9	131.7	16.7	4.3E-09
Adam19	131.8	3600.4	27.3	4.9E-28
St8sia6	2.3	17.7	7.7	2.2E-02
Scn3a	43.7	347.2	7.9	2.6E-22
Has2	37.6	1003.0	26.7	5.4E-61
Vps37d	41.4	260.0	6.3	6.2E-16
Efnb3	99.3	1166.6	11.8	1.5E-38
Lbh	499.5	2332.4	4.7	1.3E-22
B230119M05Rik	0.5	16.9	35.3	7.9E-04
Srrm4	24.6	549.8	22.3	8.3E-06
Kctd8	1.6	11.0	6.9	2.1E-02
Nos2	12.5	263.7	21.2	3.2E-27
Adamts15	68.4	1176.2	17.2	8.8E-16
Cpt1c	179.9	1092.6	6.1	8.9E-18
LOC102634401	0.7	7.9	11.0	1.5E-02
Gfod1	20.8	356.5	17.1	4.5E-29
Gm13298	3.5	57.1	16.5	3.4E-05
Sertm1	1.3	27.5	21.4	1.8E-05
Lix1	8.2	176.0	21.4	2.7E-30
Kdelr3	78.2	756.3	9.7	2.7E-33
Prnp	186.5	1594.9	8.6	5.7E-40
Mpped1	0.5	6.2	11.5	3.7E-02
Itm2a	323.3	5764.2	17.8	1.5E-33
LOC102633315	7.1	113.2	15.9	2.6E-04
Sertad4	98.7	1149.9	11.6	2.8E-17
Crb2	32.0	290.5	9.1	9.9E-04
A330033J07Rik	1.5	63.7	41.6	2.0E-10
Zfp811	21.9	271.5	12.4	1.1E-24
Fam20a	2.3	32.4	14.1	3.6E-05
Pcdha7	18.8	168.6	9.0	4.7E-19
Sdc3	218.1	4612.0	21.2	5.2E-20
Thbs2	99.5	4224.5	42.4	1.3E-104

Dio2	1.7	20.4	11.7	1.9E-04
Syt11	239.6	2084.7	8.7	1.0E-36
Rab3b	3.5	46.5	13.2	5.6E-09
Tceal1	36.7	270.0	7.4	2.1E-11
Dmc1	6.0	61.2	10.2	4.3E-07
Apobec3	11.9	139.8	11.7	2.9E-15
Arhgap25	6.4	171.4	26.7	1.5E-25
Kcna6	9.1	341.8	37.6	1.7E-15
Gdf10	22.9	472.6	20.6	8.4E-27
Tifab	10.2	175.2	17.3	6.0E-18
A930012L18Rik	2.5	86.4	34.5	3.8E-03
Batf3	14.5	129.6	8.9	4.0E-11
Dlx1as	15.7	230.6	14.7	5.2E-26
Col23a1	369.3	10733.3	29.1	9.8E-31
Adamts4	24.0	564.7	23.5	4.4E-29
Gm16596	11.4	186.2	16.4	3.6E-20
2210416O15Rik	2.0	37.5	18.8	2.5E-06
Dse	48.7	919.6	18.9	1.9E-55
Plagl1	2037.1	13048.7	6.4	1.2E-27
Aox3	0.2	7.6	32.0	4.4E-02
Dnajc6	6.3	145.7	23.0	2.3E-25
Nlrp5-ps	18.0	137.6	7.7	1.9E-03
Itgb2	3.8	69.4	18.4	1.5E-05
Ifi204	5.3	36.5	6.9	2.2E-05
Tro	114.3	2783.0	24.4	3.1E-31
Foxf1	212.9	7047.1	33.1	1.7E-97
Kcnab2	31.2	251.0	8.0	1.1E-17
Tal1	6.5	85.6	13.1	1.1E-13
Traf5	43.1	389.0	9.0	3.9E-25
Cyp46a1	4.7	62.1	13.1	1.3E-04
Pcdhgb4	761.3	6005.4	7.9	7.3E-12
Eng	109.3	2311.6	21.2	2.4E-12
Penk	39.8	534.8	13.5	1.9E-27
Cntn4	0.5	7.5	15.3	3.7E-02
Cpeb1	2.2	16.5	7.5	7.1E-03
Nrxn1	10.6	118.6	11.1	3.9E-14
Rgmb	320.3	2231.8	7.0	3.0E-19
Reck	89.7	1482.5	16.5	2.1E-41
Gria3	74.5	449.3	6.0	1.0E-17
Gdf6	5.5	146.8	26.9	7.3E-19
Miat	215.5	3756.2	17.4	2.3E-13
Lgr6	1.9	120.5	62.2	8.1E-20
Tmem215	2.2	40.7	18.3	2.2E-08
Hbb-y	58.4	705.2	12.1	1.4E-12
Lrrc7	5.4	198.7	36.5	2.5E-05
Tppp3	17.2	153.3	8.9	2.6E-14
Tslp	1.5	49.6	33.8	2.6E-10
Hgf	48.0	391.3	8.1	1.0E-20
Lzts1	1.8	20.7	11.8	2.2E-04
Dsel	152.8	624.7	4.1	4.1E-17
Lphn1	1801.4	7238.8	4.0	4.9E-03
Fbn1	234.1	7820.7	33.4	1.0E-95
Mrgprf	0.2	60.9	254.7	1.6E-14
Gpbar1	4.6	153.3	33.1	1.5E-05
Tnfrsf11b	78.0	361.4	4.6	2.3E-15
Kcng1	17.1	654.3	38.2	3.7E-09
Ttbk1	6.2	151.9	24.6	3.1E-10
Pcdh10	15.5	271.9	17.6	2.1E-30
Gas1	239.8	6135.4	25.6	2.7E-88
Ttc9b	1.2	36.9	30.1	2.6E-10
Exoc3l4	12.5	158.1	12.6	3.2E-15
Tns1	156.5	4251.5	27.2	4.0E-05
Kcnq3	1.2	71.4	58.2	2.6E-05
C030023E24Rik	0.3	12.8	47.5	2.7E-03
Prrt2	61.5	685.3	11.2	4.1E-05
Ngf	2.4	77.3	31.7	9.6E-13
Dlx3	2.3	19.1	8.2	4.3E-03
Clmp	63.8	1890.5	29.6	6.8E-82
9430041J12Rik	0.7	20.0	26.7	4.3E-04
Lrfn5	1.5	38.0	24.7	1.4E-10
Ntsr1	7.8	262.2	33.7	1.8E-23
Pf4	4.0	34.8	8.8	1.4E-06
Gm19461	5.2	87.2	16.8	1.3E-02
Fkbp10	347.8	2911.1	8.4	4.9E-42
Brinp2	2.1	57.0	27.5	1.4E-10
Pcdha9	20.8	180.8	8.7	3.3E-19
Loxl2	332.0	5700.5	17.2	6.7E-30
Chrna5	6.3	91.5	14.4	3.6E-16
Nrsn2	2.4	26.5	10.8	1.3E-05
Hmx3	5.2	95.0	18.3	7.6E-17
Il12rb1	2.8	15.1	5.4	2.1E-02
Atp10a	12.1	166.1	13.7	1.2E-17

Pcolce	81.8	1310.5	16.0	3.2E-31
Wt1	25.5	189.7	7.5	9.1E-14
Inpp4b	17.3	276.4	16.0	1.5E-25
Fam189a1	12.6	101.1	8.0	8.6E-04
Dpysl4	31.8	635.6	20.0	3.3E-49
Gpc6	521.3	3839.8	7.4	3.7E-08
Npr1	17.3	250.7	14.5	8.8E-24
Npnt	309.4	3663.5	11.8	1.3E-57
Pld4	18.7	231.6	12.4	2.2E-22
Kctd12b	19.5	686.6	35.3	1.8E-63
Rapgef3	44.6	323.9	7.3	6.1E-18
Ptch1	804.8	8255.6	10.3	7.3E-04
Zcchc5	6.6	78.7	11.9	1.9E-09
Cd48	3.3	40.4	12.4	3.5E-07
Egr3	5.8	98.6	17.1	3.3E-13
Cemip	9.2	52.0	5.7	1.4E-09
Ccr2	3.5	24.7	7.0	1.4E-03
Sh2d1b1	0.5	8.5	17.4	2.5E-02
Hoxc5	23.6	666.5	28.3	5.5E-35
Srgn	2.0	44.2	21.7	8.2E-09
Wdr54	12.5	74.2	6.0	1.3E-05
Efna2	112.3	656.0	5.8	3.7E-20
Ankrd63	1.7	87.3	50.8	2.0E-13
Psd3	237.5	1119.5	4.7	2.8E-09
Tmem255b	0.5	27.6	55.1	2.4E-06
Chst5	3.5	34.2	9.8	1.2E-05
Sctr	1.5	72.0	49.3	3.5E-06
Parp8	30.3	460.4	15.2	7.8E-35
Gata2	2.4	61.7	25.3	2.9E-10
Wnt9a	13.2	182.9	13.8	3.7E-19
Hspa12a	80.1	455.3	5.7	5.4E-18
Crmp1	113.5	1913.2	16.9	2.5E-61
Gfap	1.2	20.5	16.6	3.8E-04
Tunar	5.5	35.6	6.5	1.4E-03
Adamts9	54.6	1420.2	26.0	5.0E-58
Nav1	1139.5	6552.6	5.8	2.8E-02
42248	16.1	148.9	9.3	5.2E-14
Cd59a	16.2	92.9	5.7	1.8E-08
Gap43	59.8	703.2	11.8	2.6E-46
Gpr156	3.7	49.5	13.4	8.4E-07
2610028E06Rik	1.2	54.8	45.3	4.1E-11

Abca5	77.5	565.2	7.3	3.4E-26
Pld5	0.7	8.6	12.0	1.9E-02
Nrp1	276.9	4224.7	15.3	1.5E-52
Sla	8.3	74.8	9.1	1.8E-09
LOC102636514	26.4	432.2	16.4	9.0E-37
Gm9767	4.2	68.0	16.2	1.6E-10
Itgb8	7.7	130.0	16.9	1.1E-16
Tmem100	30.9	881.3	28.5	5.6E-60
Frem2	629.6	2754.3	4.4	6.3E-04
Ccna1	0.5	6.9	13.6	1.5E-02
Hecw2	5.6	242.2	43.1	3.6E-22
Atp2a3	444.6	2783.3	6.3	6.3E-16
Kdr	66.7	2396.2	35.9	3.1E-81
Lppr1	4.2	38.5	9.1	2.5E-07
Tnfsf11	0.7	9.5	13.0	2.2E-02
Slc9a9	7.4	62.4	8.4	3.5E-09
Gpc1	605.7	4629.3	7.6	5.8E-40
Tmem74	1.8	32.6	18.6	3.0E-08
Sdc2	324.0	1643.5	5.1	3.7E-27
1700026D08Rik	0.5	10.4	21.3	3.2E-02
Rin3	269.3	1179.3	4.4	5.5E-03
Sema3f	214.7	1883.0	8.8	9.9E-38
St8sia4	25.7	604.8	23.5	3.1E-53
Mical1	192.3	927.5	4.8	3.8E-21
Gpr17	43.1	940.1	21.8	4.1E-45
Il1rl2	14.8	336.3	22.7	9.7E-33
Aspn	13.2	497.9	37.7	9.0E-17
Plxdc2	91.7	935.6	10.2	5.3E-37
Mex3b	84.9	1305.6	15.4	9.0E-53
Mir3074-1	3.6	30.5	8.5	7.5E-03
Pcdh7	55.9	1172.8	21.0	3.8E-43
Galnt16	18.8	276.1	14.7	9.8E-17
Dnah8	3.3	24.2	7.4	1.7E-03
Il1r2	0.7	21.8	29.2	1.0E-05
Apol7b	7.3	41.8	5.7	5.8E-04
Dock9	974.5	6699.8	6.9	2.6E-38
Plcb4	87.8	478.9	5.5	1.1E-09
Robo2	75.5	1650.1	21.8	7.7E-44
Aoah	4.0	45.7	11.6	4.3E-07
Jph3	15.5	180.4	11.7	7.5E-21
Piezo2	50.0	1594.7	31.9	1.5E-18

Ipw	0.7	26.7	36.0	3.3E-05
Man2a2	1302.9	5680.0	4.4	4.8E-16
Lst1	1.7	18.3	10.6	8.6E-04
Mr1	12.1	371.5	30.6	9.5E-41
Igsf10	143.0	3444.7	24.1	2.4E-27
Tlx2	17.2	348.3	20.2	1.3E-38
Wdfy4	7.1	105.7	15.0	1.4E-07
Mcc	73.2	1502.4	20.5	4.4E-06
Klhl34	2.0	24.3	12.1	7.6E-03
Hecw1	2.5	106.5	43.0	1.6E-20
Mt3	1.1	8.7	8.2	1.6E-02
Kctd12	477.1	3208.5	6.7	5.9E-36
B430306N03Rik	1.6	17.0	10.8	1.9E-03
Dkk2	31.0	717.9	23.1	4.8E-40
Zfp583	24.4	121.8	5.0	2.3E-08
Dlgap1	9.8	119.6	12.2	2.1E-15
Maged2	721.5	5459.1	7.6	3.3E-14
Col6a2	1310.4	36168.8	27.6	6.7E-76
Cd1d1	25.6	302.0	11.8	8.3E-29
Col16a1	118.0	2171.6	18.4	4.0E-09
Myh1	0.3	9.2	36.8	9.4E-03
Clec7a	16.9	158.8	9.4	2.1E-10
Slc46a3	12.2	56.7	4.6	1.3E-04
Mtap7d3	3.9	22.7	5.9	1.1E-02
Palld	682.5	2814.3	4.1	1.0E-19
Havcr2	4.2	28.3	6.7	5.1E-03
Magee1	70.2	905.1	12.9	2.7E-42
Pcdhga11	747.7	6082.7	8.1	9.1E-12
Col12a1	178.6	3827.4	21.4	3.0E-28
Cd97	348.0	3858.7	11.1	5.2E-53
Dtx1	20.7	322.8	15.6	1.8E-29
Myt1	92.2	593.0	6.4	3.9E-18
Cadm4	99.2	482.4	4.9	7.1E-15
Sec24d	406.0	4409.6	10.9	5.1E-51
Amph	8.3	124.9	15.1	1.6E-17
Stc1	61.1	775.3	12.7	5.8E-20
P2ry13	4.0	46.6	11.7	2.7E-05
Gpr116	158.6	1636.7	10.3	1.5E-42
Peg10	225.2	8530.4	37.9	1.3E-16
Mmp9	93.1	1645.5	17.7	2.3E-13
Plxna2	393.1	2441.1	6.2	5.7E-06
Kcnd2	5.1	81.5	16.0	1.0E-14
Msn	223.9	4020.7	18.0	1.5E-71
Fbxl16	57.2	427.7	7.5	1.8E-22
3110035E14Rik	0.3	26.6	98.9	8.5E-03
Mir6935	6.6	35.0	5.3	7.7E-03
Ccbe1	7.3	217.6	29.9	8.3E-33
Dtx4	961.5	5010.8	5.2	2.3E-27
Dnaja4	48.4	237.4	4.9	2.2E-11
Creb5	5.0	131.5	26.3	3.4E-05
Mir199a-2	1.2	24.4	20.2	1.7E-04
Mc5r	0.2	16.8	70.3	2.6E-04
Lamb1	2327.3	14847.5	6.4	2.9E-38
Ikzf1	10.6	109.3	10.3	4.0E-11
Dpf1	36.1	254.5	7.0	1.7E-15
Medag	4.2	35.4	8.3	2.2E-06
Tmem44	73.8	388.3	5.3	4.9E-16
Cobl	139.2	1400.5	10.1	8.2E-07
Stac2	1.8	16.5	9.2	2.2E-02
Rbm46	18.7	490.4	26.2	3.9E-19
Egln3	386.7	1640.7	4.2	9.8E-20
Lrrc75b	4.4	81.5	18.5	2.7E-17
Ccl21a	1.2	24.4	20.4	6.5E-05
Tshz2	444.7	4610.0	10.4	7.5E-08
Scg5	45.1	229.2	5.1	4.0E-10
Chst14	114.4	778.0	6.8	6.3E-14
Hbb-b2	150.3	1218.5	8.1	1.9E-15
Art4	3.4	63.2	18.5	3.7E-11
Otogl	4.5	27.4	6.1	2.9E-02
Artn	10.2	147.7	14.5	1.3E-06
Gpr27	7.0	57.9	8.3	4.3E-07
Samd4	89.4	1104.0	12.4	7.9E-14
Sgtb	30.8	235.3	7.6	3.8E-17
Enho	7.6	198.9	26.3	1.4E-29
Vat1l	17.6	397.9	22.7	6.3E-43
Mir1906-1	44.0	255.0	5.8	1.7E-02
Itga7	11.5	95.5	8.3	2.8E-08
Slc7a14	12.0	354.6	29.6	8.8E-18
Col24a1	26.5	977.2	36.9	9.6E-70
9330159F19Rik	13.1	279.3	21.3	1.6E-33
Cdh18	1.3	11.3	9.0	1.1E-02
Igf1r	574.8	5472.3	9.5	5.1E-03

Snx32	37.6	178.2	4.7	2.5E-09
Adrb1	2.0	24.7	12.3	3.1E-04
Syt16	1.8	20.9	11.8	1.8E-04
Duxbl2	36.3	217.6	6.0	2.0E-13
Pyroxd2	14.2	87.8	6.2	1.4E-06
Pnliprp1	55.5	671.6	12.1	3.9E-02
Slc16a7	12.0	68.8	5.8	2.5E-06
Ptafr	3.0	36.0	11.9	1.8E-06
Cxx1a	155.2	924.7	6.0	3.2E-24
Gpr68	1.4	20.5	14.1	1.5E-03
Itga5	622.1	5579.9	9.0	2.6E-46
Vstm2a	5.2	58.7	11.2	2.9E-09
Ldlrad4	15.1	407.5	27.1	6.4E-37
Gas7	76.7	1444.5	18.8	1.0E-30
Vwa5b1	0.7	13.0	17.6	1.2E-02
Lrfn2	2.7	68.8	25.3	2.1E-11
Cxcl1	0.2	9.6	40.2	8.5E-03
Snx20	8.2	53.5	6.5	6.4E-06
Popdc2	11.7	278.3	23.7	2.9E-34
Gm11541	1.7	47.1	28.1	6.3E-07
Cacng5	0.3	9.4	37.5	1.4E-02
Ly6e	365.2	1521.7	4.2	2.1E-15
Armcx4	509.3	3869.3	7.6	9.7E-25
Sox8	17.2	334.8	19.4	7.4E-29
Vav1	6.7	95.7	14.2	6.7E-12
Slc16a9	1.5	77.1	50.4	3.1E-15
Evi2a-evi2b	4.7	62.7	13.3	4.9E-03
Zdhhc14	36.7	242.5	6.6	1.5E-13
Speg	157.3	1508.2	9.6	5.5E-08
Panx2	4.3	38.1	8.8	1.9E-04
Mmp25	2.2	90.0	40.8	2.6E-14
Elavl4	75.8	1407.7	18.6	3.0E-58
Zc3h12c	72.5	589.7	8.1	8.2E-17
Cacna1g	160.4	3892.2	24.3	2.3E-13
Ahrr	20.3	86.5	4.3	4.2E-03
Frrs1l	3.2	33.6	10.4	2.4E-05
Crtac1	8.8	189.0	21.5	1.4E-22
Zfp467	331.9	1648.1	5.0	2.7E-02
Itih5	53.0	1677.1	31.7	5.8E-54
Gm12295	0.5	15.9	32.4	2.4E-04
Clvs2	3.9	58.7	14.9	3.0E-13
Tmprss5	2.4	44.8	18.4	5.6E-07
Plxna4	30.2	799.2	26.4	1.3E-08
Mmp11	90.2	981.5	10.9	1.3E-40
2510009E07Rik	129.0	1979.8	15.4	1.5E-58
Rgs5	38.7	1528.4	39.5	9.5E-31
Spp1	54.3	368.1	6.8	2.2E-02
Hhip	55.2	1968.1	35.7	3.3E-14
Ccl6	3.9	20.4	5.3	2.1E-03
Rasl10b	12.5	170.6	13.7	9.9E-24
Cntn1	3.5	104.1	29.7	1.1E-20
Arhgdib	16.7	179.2	10.7	9.6E-21
Slit1	14.9	106.0	7.1	5.5E-09
Ptprz1	14.3	453.8	31.8	9.4E-49
Ackr1	2.2	53.3	23.8	7.4E-09
Srgap3	199.6	1136.0	5.7	9.5E-04
Zeb2os	3.5	108.5	31.0	1.7E-19
Dock6	694.6	4147.0	6.0	3.4E-04
Man1c1	36.4	475.6	13.1	8.2E-27
Hdac9	6.5	123.7	18.9	4.4E-11
Fes	24.2	262.9	10.9	9.5E-12
Stxbp6	76.0	345.7	4.5	1.1E-13
Gpr133	1.7	47.0	27.1	3.4E-08
Fgd5	23.9	746.1	31.3	5.5E-59
Col9a1	3.6	155.3	42.9	2.3E-13
Pi15	10.0	166.5	16.7	6.8E-10
Lrrn4cl	10.3	59.7	5.8	8.8E-06
Cyp2d22	24.1	549.1	22.8	1.4E-41
Rtn4rl2	9.9	143.6	14.6	1.6E-02
Ptges	10.0	223.5	22.3	2.1E-24
Inpp4a	191.7	818.6	4.3	7.1E-04
Foxo6	14.7	115.4	7.8	2.3E-07
Gm20597	0.5	8.9	18.5	1.3E-02
Tbxas1	2.5	19.5	7.7	4.5E-03
Fam13c	18.5	376.2	20.3	1.5E-37
Schip1	84.3	1193.3	14.2	2.3E-21
Tshz3	55.3	1618.0	29.2	2.7E-09
Was	4.7	45.3	9.6	2.6E-05
Mndal	0.5	9.6	19.2	9.3E-04
Robo4	28.1	1083.4	38.5	2.3E-71
Myh10	1814.1	8005.5	4.4	2.8E-16
Ptchd1	1.5	57.3	38.5	1.4E-16

Nrip3	7.8	34.5	4.4	5.7E-03
Kcnt1	5.3	52.5	9.9	1.9E-04
Tram1l1	27.8	248.7	8.9	3.4E-22
2700069I18Rik	1.0	13.8	13.4	5.1E-03
Fam212a	24.4	397.1	16.2	3.9E-35
Slc24a1	0.2	12.7	53.2	8.4E-03
Limd2	312.5	1550.0	5.0	1.1E-24
Col3a1	3826.6	82206.0	21.5	6.2E-18
Prdm6	7.8	104.3	13.4	1.6E-15
Gpr126	18.6	295.6	15.9	4.1E-30
Ccdc13	2.0	27.3	13.8	5.8E-04
Lrrc55	11.4	366.4	32.1	1.2E-35
Mgll	82.8	2904.4	35.1	1.5E-93
Slc6a12	5.9	54.1	9.2	1.5E-05
C1qtnf6	77.3	1108.4	14.3	2.8E-48
Il17b	1.0	14.6	15.3	6.9E-04
Gdf1	46.6	309.4	6.6	3.0E-07
Tgfb3	50.6	1317.4	26.0	8.6E-49
Htra3	78.2	2849.2	36.4	5.3E-91
Epha10	1.7	33.9	19.8	4.5E-06
Lama2	20.4	869.1	42.6	1.1E-14
Plcb2	5.7	165.2	29.1	5.4E-14
Rgag1	2.5	82.9	33.3	1.1E-14
Ms4a6c	8.7	101.2	11.6	6.7E-14
Prkd1	25.9	509.6	19.7	2.0E-41
Alox5ap	3.5	23.7	6.7	2.4E-03
Flna	5517.8	40785.7	7.4	4.2E-43
Rrad	5.2	45.1	8.6	9.4E-07
Eml5	482.0	2247.0	4.7	8.8E-23
Lpar4	16.9	482.3	28.5	8.0E-50
Ptgis	39.9	574.1	14.4	3.9E-37
Srpx2	10.5	630.0	60.0	1.4E-15
Tmem200a	43.3	854.3	19.7	7.9E-54
Slco3a1	41.7	410.0	9.8	8.3E-27
Eef1a2	2.9	87.7	29.9	6.9E-18
Smarca2	428.5	2825.8	6.6	1.8E-35
Rarres2	70.3	419.5	6.0	1.2E-05
Fscn1	782.2	4722.7	6.0	5.6E-20
Itpkb	341.1	2006.9	5.9	2.0E-05
C1qtnf7	4.9	81.8	16.8	3.1E-14
Tspan11	17.0	545.4	32.1	4.2E-42
Pou3f1	0.8	32.4	42.7	7.5E-07
Asap3	86.2	386.1	4.5	7.8E-13
Mill2	1.7	26.2	15.1	1.3E-04
Tet1	164.0	1341.6	8.2	2.9E-05
Nptx1	17.0	328.1	19.3	9.2E-07
Otof	5.7	296.0	51.7	3.7E-04
Sez6l2	68.1	499.1	7.3	1.7E-10
Nacad	34.1	430.9	12.6	1.5E-11
Ntng2	2.5	31.7	12.6	4.3E-04
Itgb3	20.9	760.1	36.3	2.0E-64
St6galnac3	56.9	775.4	13.6	3.1E-42
Lcat	4.8	33.9	7.1	9.4E-04
Gpr20	47.7	844.4	17.7	1.2E-49
Kcnmb4os1	3.0	40.9	13.8	2.5E-08
Fignl2	73.2	366.8	5.0	3.8E-02
Igsf6	22.2	134.5	6.1	2.8E-08
Dlg4	177.9	1515.8	8.5	2.8E-07
Astn1	11.3	347.7	30.7	3.9E-45
Avpr1a	1.9	71.0	36.9	4.0E-06
Sgce	44.9	750.8	16.7	8.1E-29
Cldn5	26.6	700.4	26.3	1.2E-42
Hey1	23.4	692.8	29.5	6.8E-61
Slc15a3	27.8	170.2	6.1	1.1E-10
Dpt	0.8	17.7	22.9	9.5E-05
Igfbp2	126.4	1372.6	10.9	1.6E-20
Scrn1	10.6	71.3	6.7	1.3E-10
Kcnv1	1.5	26.0	17.7	3.9E-07
Col1a2	1250.3	29205.8	23.4	1.7E-30
Palm	384.1	1768.7	4.6	2.0E-21
Sorbs1	169.9	1443.1	8.5	7.6E-29
Zfp804a	16.4	406.2	24.8	2.1E-27
Cd53	12.1	147.8	12.2	2.3E-07
4632428N05Rik	176.1	734.0	4.2	6.8E-17
Gprin2	0.7	14.9	20.1	4.6E-03
Gm12250	3.7	26.7	7.3	1.4E-03
Pilrb1	0.2	11.6	48.5	5.7E-03
Gucy1a3	111.6	4068.3	36.4	5.8E-99
BC024386	0.2	9.3	38.7	1.7E-02
Fam78b	11.8	309.1	26.3	2.8E-14
Abi3bp	15.2	487.8	32.0	7.6E-18
Gabra2	0.5	17.8	36.4	3.8E-04

Cttnbp2	100.8	787.5	7.8	1.0E-26
Pard6g	173.5	920.4	5.3	3.5E-22
Pnmal1	15.6	102.6	6.6	8.3E-10
Gbp5	1.8	17.1	9.6	8.6E-03
Bik	7.7	54.6	7.1	9.1E-07
Pde5a	1089.8	4684.5	4.3	2.8E-22
Iffo1	41.3	587.3	14.2	6.3E-36
Dusp26	16.1	321.8	20.0	3.6E-23
S100b	3.3	82.9	25.0	1.1E-13
Kalrn	121.2	1440.0	11.9	2.9E-12
Ecscr	20.5	345.1	16.8	3.1E-34
Flrt2	58.6	794.9	13.6	8.0E-17
Afap1l2	85.2	1837.6	21.6	5.6E-68
Dnaaf3	23.5	112.3	4.8	3.1E-06
Prkcdbp	42.8	686.8	16.0	4.3E-22
Crip2	51.8	855.1	16.5	2.2E-49
Dysf	16.7	556.3	33.3	2.9E-50
Sash3	8.3	59.2	7.2	2.0E-07
Pcdhb3	5.9	61.1	10.3	1.7E-08
Pea15a	487.7	2129.9	4.4	2.1E-23
Gm4980	8.1	87.8	10.8	1.3E-04
Slc6a15	29.3	284.1	9.7	6.1E-25
Ntn1	63.4	2815.6	44.4	4.2E-63
Atxn1	100.3	411.9	4.1	6.3E-03
Caly	2.0	20.7	10.2	7.8E-04
Hoxd3	117.4	1087.6	9.3	4.4E-36
Lmod1	18.6	579.4	31.2	1.6E-58
Celf5	21.9	193.4	8.8	1.6E-07
Nod2	2.8	27.0	9.5	7.5E-04
Car11	30.2	198.0	6.5	1.3E-11
Slc1a3	97.6	410.2	4.2	4.6E-11
Nol4	7.5	93.1	12.4	1.1E-12
Phactr1	10.8	279.2	25.9	1.0E-29
Nova2	31.2	695.8	22.3	2.8E-02
Pcdhb22	19.0	227.7	12.0	9.8E-23
5330434G04Rik	0.3	39.4	146.5	1.0E-02
Sox2	6.9	145.1	21.1	9.1E-16
Hk3	11.4	100.0	8.8	3.1E-03
Foxd3	13.2	191.1	14.5	4.8E-20
Mab21l2	257.5	7267.2	28.2	6.4E-94
Mdga1	11.4	150.7	13.3	5.7E-14
Ntn3	35.4	1157.5	32.7	1.5E-28
Ctla2b	2.7	50.4	19.0	8.1E-11
Cecr6	4.8	37.7	7.9	9.9E-06
Hlf	9.8	189.0	19.3	1.7E-13
Gal	4.0	45.1	11.2	8.6E-05
Fstl1	507.8	10566.3	20.8	2.1E-67
Rerg	61.0	673.3	11.0	1.3E-15
Ptger3	4.4	32.5	7.3	2.7E-04
3110099E03Rik	2.6	13.9	5.4	9.1E-03
Gm8221	22.6	383.4	17.0	1.6E-04
Gpr97	4.3	40.6	9.5	6.6E-05
Itga4	25.7	257.0	10.0	1.2E-19
P2ry12	2.2	45.6	20.5	1.3E-09
Pcp4l1	16.8	493.0	29.4	1.1E-45
Sned1	22.0	327.9	14.9	4.5E-04
Sox4	814.1	3972.4	4.9	6.2E-17
Gm10190	2.8	15.7	5.6	4.5E-02
Ryr2	31.3	367.5	11.7	1.8E-06
Sema6b	46.5	237.9	5.1	1.1E-11
Asb10	1.0	12.6	13.2	5.1E-03
B130024G19Rik	6.9	107.9	15.7	3.0E-12
Myo18b	1.2	33.7	27.9	1.1E-07
Prkg1	35.8	1127.4	31.5	2.2E-73
Apold1	11.6	243.8	21.0	2.5E-21
H2-DMb1	2.5	14.0	5.6	1.7E-02
Runx1t1	48.8	859.7	17.6	1.4E-17
Psd	211.4	2929.0	13.9	1.1E-37
Hoxb5	87.8	1926.0	21.9	4.3E-34
Tsku	82.7	952.3	11.5	5.5E-22
Nox4	41.8	170.5	4.1	9.6E-10
Cd83	12.0	125.9	10.5	2.2E-16
Edil3	16.3	598.0	36.7	9.1E-18
Igsf3	385.2	2750.4	7.1	1.5E-05
Gpsm3	21.6	306.2	14.2	5.7E-11
Nalcn	11.7	267.0	22.8	2.0E-23
Nrg2	1.7	72.4	41.5	4.5E-15
Kcnj3	2.1	10.6	5.2	4.4E-02
Cntnap5a	0.7	17.2	23.5	2.5E-04
Itgam	15.7	132.2	8.4	1.3E-12
Gm15612	31.8	678.2	21.3	4.9E-38
Sfrp1	265.7	12761.9	48.0	1.6E-121

Cep170	437.9	3470.7	7.9	1.4E-35
Colec12	97.8	1858.2	19.0	2.6E-68
Gbp4	5.7	58.9	10.3	6.7E-05
A630001G21Rik	4.5	24.8	5.4	5.4E-03
Nxph3	2.3	19.4	8.5	3.5E-04
Efna3	27.5	192.4	7.0	1.1E-14
Trim30a	5.5	71.9	13.0	6.5E-11
Tmem151a	10.6	113.4	10.7	4.0E-05
Fmn2	16.6	220.7	13.3	7.9E-14
Ube2ql1	1.0	13.7	13.7	7.7E-03
Cd302	40.4	211.8	5.2	1.2E-11
Ankrd34a	3.7	77.9	21.0	1.6E-10
Glt8d2	11.1	136.6	12.3	2.9E-07
Hrct1	1.0	10.8	10.8	2.4E-02
Cnrip1	27.1	421.6	15.6	2.3E-36
Gabra3	3.7	89.6	24.0	5.1E-16
Gm5607	5.7	109.2	19.3	9.0E-13
H2-Oa	0.5	10.0	19.7	1.9E-02
Cilp	3.7	193.6	53.0	1.7E-04
Abcd2	6.6	107.8	16.2	2.4E-18
Lcp2	11.6	179.9	15.6	6.4E-12
Ccdc30	8.5	35.4	4.2	3.6E-03
Il11ra1	118.0	688.9	5.8	1.0E-12
Pla2g7	77.0	936.2	12.2	3.6E-04
Ppp2r2b	9.8	132.1	13.5	3.3E-15
Hspb7	9.0	119.1	13.3	1.2E-20
Ypel4	7.9	126.8	16.0	1.4E-07
Lrrc25	5.6	52.9	9.5	5.5E-07
Fam19a5	16.3	264.6	16.3	1.6E-30
F930015N05Rik	2.7	77.4	28.8	4.4E-10
Syn1	23.1	215.1	9.3	4.9E-08
Phactr3	5.3	108.5	20.6	4.7E-18
Procr	35.9	1152.2	32.1	1.5E-16
Adamts14	5.2	137.0	26.6	1.5E-14
Pcdhb10	2.2	38.2	17.4	3.1E-08
Mylk	592.5	17998.1	30.4	1.7E-101
Tmem255a	29.0	1116.8	38.5	1.4E-29
Lppr4	0.7	12.8	17.8	6.8E-04
Apol10b	1.5	23.6	15.6	1.2E-04
Klhl30	1.2	9.5	7.8	2.8E-02
Cdh20	2.0	43.9	21.8	2.9E-09
Cspg4	144.9	3683.6	25.4	3.9E-03
Wbscr17	3.7	71.0	19.1	2.5E-11
Slitrk6	180.5	3225.4	17.9	9.0E-70
Plekho1	87.2	1335.2	15.3	3.1E-22
Lair1	5.2	56.5	10.9	9.2E-08
C920021L13Rik	13.7	112.1	8.2	2.5E-09
Garnl3	69.9	361.3	5.2	1.4E-14
Cpne5	8.8	345.1	39.1	8.0E-19
Bhlhe41	17.8	72.4	4.1	2.5E-04
Tecta	5.7	63.8	11.2	3.1E-08
4933409K07Rik	6.3	68.9	10.9	3.7E-03
Tubb3	140.6	2033.6	14.5	4.0E-62
AI662270	2.5	38.8	15.6	9.2E-07
Syne1	141.9	1839.4	13.0	3.4E-16
Hs3st3a1	6.4	162.8	25.3	8.7E-13
Lrrc17	32.7	1038.1	31.8	6.6E-39
Lrrn1	11.5	338.2	29.5	6.0E-43
Dnah1	17.5	267.9	15.3	6.5E-18
4930426D05Rik	1.5	13.1	8.6	3.4E-02
Kif26a	59.4	1510.6	25.4	7.1E-12
Twist2	5.9	111.1	18.9	2.4E-15
Zfp575	5.3	110.4	20.8	3.4E-10
2010015L04Rik	4.2	58.1	13.7	5.3E-07
Dio3os	1.2	23.3	19.0	2.3E-04
Rnf182	2.3	64.8	28.7	3.7E-11
Gnb3	0.2	13.0	54.5	6.5E-04
Ocstamp	2.8	81.0	29.2	2.1E-03
Gm9899	5.4	142.0	26.2	1.4E-21
C1qa	40.0	565.9	14.2	3.5E-08
Nfatc4	246.0	2894.6	11.8	1.3E-21
Lrrtm3	10.9	260.5	24.0	8.1E-28
Ube2l6	66.7	336.3	5.0	3.1E-15
Plce1	142.3	689.2	4.8	1.8E-15
Tlr13	4.2	53.3	12.6	8.1E-10
Dgkh	44.4	249.6	5.6	3.9E-02
C4b	4.7	44.5	9.5	2.1E-03
4930512B01Rik	18.9	79.8	4.2	1.5E-05
P4ha2	173.5	1049.2	6.0	2.0E-06
Tspyl4	54.7	796.7	14.6	2.2E-47
Dmrt3	0.3	9.0	36.0	5.0E-03
Mras	37.0	320.0	8.7	1.4E-22

Tspan5	144.8	763.3	5.3	2.1E-20
Rdx	294.9	4423.5	15.0	2.3E-43
Mctp1	3.6	24.0	6.7	8.9E-04
2810433D01Rik	0.3	11.7	43.6	2.5E-03
9530077C05Rik	15.9	88.5	5.6	2.8E-06
Anxa5	662.1	3114.3	4.7	6.4E-06
Pdzd2	266.0	1269.7	4.8	2.6E-02
Lrmp	1.5	36.2	24.0	3.9E-07
Dlx2	21.0	371.4	17.6	2.0E-12
Erp27	0.2	11.9	49.9	1.2E-03
Aplp1	266.4	1224.2	4.6	3.9E-22
Rab39	5.0	22.8	4.6	3.1E-03
Ptplad2	10.5	64.9	6.2	4.4E-07
Cyp1b1	13.9	316.5	22.7	2.5E-37
Pald1	429.5	2024.7	4.7	3.3E-23
Snx33	134.3	795.4	5.9	4.8E-06
Diras1	4.0	48.1	12.1	4.3E-07
Mrvi1	59.2	1556.7	26.3	1.8E-64
Asphd1	2.0	16.5	8.1	3.4E-02
Ptprn	48.0	435.9	9.1	2.3E-25
Gab2	266.3	1775.7	6.7	2.5E-09
B3galt2	1.0	47.8	49.9	1.3E-02
Tmem45a	18.4	550.6	29.9	1.6E-15
Ctnna2	31.2	669.7	21.5	1.7E-24
Scel	2.6	14.4	5.5	9.6E-03
Ctss	48.1	505.3	10.5	1.5E-05
Meox1	7.5	127.3	17.1	1.2E-15
Oaf	443.2	2529.4	5.7	5.6E-30
Ppp1r1a	5.0	85.9	17.1	2.8E-13
Ldb2	59.0	1377.0	23.3	3.5E-67
Tnni1	1.0	8.9	9.2	1.2E-02
Tnfaip6	1.2	13.8	11.5	2.9E-03
Sox7	27.7	1395.9	50.4	1.8E-15
Rab38	9.6	52.2	5.4	2.8E-05
Tpbg	95.8	620.2	6.5	1.4E-24
Pcdhgb8	734.7	5944.1	8.1	1.2E-11
Gbgt1	16.9	378.2	22.3	4.3E-12
Nav3	4.4	125.0	28.2	9.3E-11
Ldhb	78.3	721.6	9.2	2.2E-37
Aff2	5.6	114.8	20.4	2.1E-05
Rnf144a	185.4	2148.7	11.6	1.3E-37

Srrm3	6.6	106.3	16.0	4.9E-15
Naalad2	7.3	64.7	8.9	2.5E-08
Cntnap3	14.5	322.5	22.2	3.2E-20
Slc37a2	18.4	149.2	8.1	3.4E-11
Cacnb1	38.8	569.0	14.7	2.3E-36
Fam214b	68.5	332.9	4.9	2.0E-12
Fxyd1	7.1	144.0	20.3	2.2E-05
Mmp13	3.7	69.7	18.9	3.9E-10
Rorb	1.4	10.4	7.2	4.5E-02
Sstr4	1.0	48.6	49.6	6.2E-11
Gm4951	0.7	11.9	16.1	9.5E-03
Fgl2	21.8	222.5	10.2	4.0E-09
Pak7	1.5	41.3	27.2	1.1E-09
Sema5a	336.9	5750.7	17.1	3.8E-08
Trhde	1.2	11.7	9.6	1.1E-02
Ankrd34b	0.5	5.2	10.3	3.4E-02
Bag3	147.6	1436.2	9.7	1.3E-15
Fam210b	129.3	531.4	4.1	5.3E-15
Arl11	4.0	39.4	9.9	2.9E-06
St6galnac5	3.0	24.2	8.1	5.5E-04
Fam101a	2.8	60.4	21.8	1.1E-08
5830432E09Rik	2.3	33.6	14.4	9.5E-03
Col15a1	62.8	2286.7	36.4	2.6E-87
Insrr	2.4	33.4	13.8	1.3E-03
Gbp6	9.4	81.8	8.7	2.0E-07
Mamld1	21.1	110.0	5.2	4.8E-04
Kcnq2	3.6	145.3	39.9	4.5E-08
Gpr137b	36.6	197.8	5.4	3.6E-12
Nid1	392.3	9114.9	23.2	5.5E-85
Fam181b	4.8	61.3	12.8	1.1E-10
Galnt9	1.0	10.8	10.9	4.8E-03
St6gal1	170.0	1053.8	6.2	2.4E-17
Pappa2	0.2	19.4	81.2	8.2E-05
Plscr4	25.5	350.5	13.7	7.5E-30
3830403N18Rik	2.6	19.6	7.7	9.6E-04
Lrrc8c	16.6	389.6	23.5	2.0E-12
Htr3a	3.5	61.1	17.6	4.7E-07
Dpep2	1.2	18.4	14.9	6.6E-04
Fgf1	5.5	47.6	8.6	3.1E-03
Ppm1e	19.5	228.9	11.7	3.8E-23
Timp3	395.7	4973.1	12.6	1.0E-22

Rac2	21.3	243.8	11.5	2.6E-22
Clip3	143.5	3817.2	26.6	6.1E-08
Fzd2	275.5	2990.5	10.9	5.8E-21
Pcdh12	13.4	600.7	44.9	1.4E-65
Chrna7	2.0	29.0	14.7	3.0E-07
Amy2a4	5.7	51.3	9.0	4.5E-02
Svopl	1.3	19.7	14.9	4.8E-02
Pcsk1n	16.0	222.3	13.9	7.2E-26
Cxcr5	4.8	22.9	4.8	1.3E-02
Ahi1	104.8	694.4	6.6	8.3E-25
Gpx8	143.5	846.5	5.9	4.9E-15
Thy1	2.3	36.4	16.1	1.2E-05
Clec14a	5.2	199.3	38.4	1.0E-34
Creb3l2	161.5	1736.3	10.8	2.2E-04
Mir7025	0.7	36.4	49.9	3.7E-05
Tmod2	153.4	982.1	6.4	2.0E-09
Kcp	59.9	1154.7	19.3	1.8E-11
Tcte1	5.0	120.5	24.2	1.2E-11
Mmp19	122.3	591.4	4.8	1.2E-09
Hoxb2	101.2	930.6	9.2	2.2E-35
Synm	20.5	279.1	13.6	1.0E-24
Kirrel3	13.1	179.6	13.7	7.5E-04
Plekhh2	506.8	3744.9	7.4	2.5E-25
Fam163a	21.2	429.5	20.3	9.4E-17
Pde2a	107.6	1428.7	13.3	7.9E-51
Ckap4	562.4	3125.0	5.6	1.7E-29
4930474M22Rik	2.5	29.5	11.8	9.5E-05
Rcn3	234.6	4357.9	18.6	1.8E-14
Kcng4	1.7	40.3	23.6	6.4E-05
Gpr161	50.3	346.9	6.9	6.7E-05
4930447K03Rik	1.5	10.2	6.8	1.8E-02
Megf6	54.6	668.4	12.2	9.7E-16
Npas3	21.9	168.8	7.7	1.1E-05
Reep2	27.7	228.0	8.2	7.9E-18
Rab11fip5	161.8	768.5	4.8	4.9E-14
Vwa1	28.0	525.8	18.8	5.0E-44
C1s1	4.5	49.5	11.0	1.0E-08
Pcdha3	20.8	167.9	8.1	7.1E-18
Tmem200c	3.1	14.0	4.5	2.6E-02
Atp1a2	30.4	647.7	21.3	1.9E-36
Cxcl9	2.5	17.6	7.1	2.0E-02

Heyl	55.3	1390.2	25.1	2.1E-13
Syt15	2.0	12.7	6.4	3.5E-02
Vmn1r90	1.5	23.0	15.3	2.2E-02
Gm13446	4.0	57.7	14.5	2.0E-08
Zeb1	105.3	2554.1	24.2	2.6E-44
AU021063	2.7	20.4	7.5	1.4E-03
Grap2	0.5	9.9	20.2	3.3E-02
Gdap1	17.0	148.9	8.8	5.0E-17
Gpr124	282.0	6864.4	24.3	1.6E-36
Ago4	26.1	222.5	8.5	4.6E-17
Dchs1	335.0	11679.5	34.9	1.7E-05
Larp6	5.7	57.8	10.1	3.1E-09
Cytip	3.2	41.4	12.7	2.0E-05
Rinl	9.9	53.1	5.3	2.4E-05
Gpr183	3.3	95.6	29.1	6.7E-03
Gjc3	2.0	87.7	43.7	2.7E-15
Clec9a	0.7	26.2	36.5	1.8E-06
Ncald	55.7	784.7	14.1	1.5E-41
Gprasp2	77.6	1069.3	13.8	7.3E-50
Adamtsl3	2.4	129.0	52.8	1.8E-14
Ypel1	61.7	257.1	4.2	1.3E-11
Camta1	155.4	724.6	4.7	5.0E-20
Tnfaip8l2	6.5	67.9	10.4	7.8E-09
Ndst4	1.8	96.9	54.0	2.2E-19
Ssu2	0.5	15.0	30.5	1.6E-04
Pgf	29.3	637.4	21.8	1.6E-49
Sulf1	98.7	1752.9	17.8	4.5E-17
Dennd2a	197.5	2139.5	10.8	2.8E-37
Vasn	370.4	1961.4	5.3	4.3E-06
Gjc1	309.9	1718.3	5.5	2.8E-27
Rab9b	1.2	13.8	11.6	5.2E-04
Scube2	1.5	31.4	21.1	7.1E-07
Cnp	190.6	791.8	4.2	6.4E-18
Kif5a	50.2	1086.4	21.6	8.7E-43
1700025G04Rik	686.7	3235.1	4.7	2.2E-11
Stra6	22.5	414.4	18.4	1.2E-14
Prn	58.0	1818.0	31.4	3.4E-84
Asb2	22.9	598.7	26.2	1.8E-55
Svep1	21.3	1057.2	49.6	8.2E-09
Krt14	13.0	61.1	4.7	8.9E-05
Lepr	1.3	38.8	30.6	6.2E-08

Prex1	232.6	1302.2	5.6	1.5E-16
Hoxb3	126.8	1846.3	14.6	9.5E-55
Hmgn3	54.3	257.0	4.7	5.6E-06
Zfp536	8.8	311.0	35.5	4.9E-07
Pnmal2	77.6	1481.3	19.1	1.6E-59
Enc1	690.1	3096.1	4.5	3.2E-19
Scn3b	15.0	200.0	13.4	2.1E-20
Selplg	4.5	28.7	6.4	2.4E-04
Osmr	8.4	213.1	25.3	4.4E-13
Car3	2.5	44.9	17.8	6.1E-13
Lims2	6.6	150.0	22.6	4.2E-19
Crb1	1.3	14.3	10.9	1.1E-02
Tpm2	166.2	3484.3	21.0	5.6E-08
Hapln1	11.6	78.2	6.8	5.3E-13
Zbtb46	17.8	255.0	14.4	5.3E-13
Gimap6	26.1	651.0	25.0	2.1E-31
Col11a1	25.3	950.9	37.6	1.2E-28
Mir1906-2	43.5	253.3	5.8	1.9E-02
Lmo3	4.0	156.4	39.3	1.1E-23
Hbb-bs	218.0	1622.6	7.4	1.2E-13

Table S4.1. Genes expressed in E14.5 intestinal epithelial and mesenchyme tissues by mRNA-Seq. Average read counts for genes 2 fold (FC) upregulated in mesenchyme (Mes) when compared to epithelial (Epi) (p-value ≤ 0.05).

Chr	Peak Start	Peak End	Enrichment	LOG P
chr2	10618201	10618402	45.25	163.92
chr13	43791436	43791578	29.97	89.6
chr1	79734413	79734535	29.48	88.49
chr12	3061656	3061799	29.48	93.81
chr17	86824432	86824599	29.48	98.38
chr2	108779130	108779253	29.48	88.16
chr2	150938008	150938138	29.48	98.1
chr3	30640809	30641026	29.48	85.75
chr6	65157495	65157619	29.48	100.23
chr6	86524473	86524616	29.48	82.01
chrX	129100326	129100511	29.48	82.36
chrX	161662873	161662960	29.48	94.27
chr15	33416594	33416686	29.13	101.46
chr7	50575370	50575471	28.42	80.25
chr1	107959856	107959927	28.14	118.51
chr10	8915193	8915293	28.14	110.36
chr2	70619999	70620078	27.79	132.32
chr8	92745420	92745598	27.55	96.99
chr16	66384262	66384407	27.2	89.6
chr10	82514973	82515075	25.79	69.37
chr10	109801734	109801826	25.79	81.6
chr10	117040466	117040562	25.79	69.37
chr11	37571637	37571760	25.79	76.12
chr13	54058547	54058755	25.79	87.77
chr13	59206342	59206498	25.79	67.49
chr14	80450008	80450169	25.79	55.93
chr14	92830897	92831010	25.79	79.24
chr14	110259259	110259422	25.79	87.96
chr14	120757226	120757442	25.79	107.75
chr16	85239133	85239234	25.79	69.37
chr17	9684635	9684816	25.79	72.54
chr17	54210943	54211064	25.79	76.72
chr18	19446697	19446880	25.79	72.11
chr18	32921985	32922073	25.79	81.6
chr19	21294497	21294631	25.79	96.73
chr19	33361154	33361382	25.79	73.24
chr19	45168315	45168415	25.79	69.37
chr2	78201905	78202120	25.79	119.37
chr2	117256751	117256840	25.79	81.6
chr2	144170647	144170757	25.79	80.23
chr3	143585765	143585892	25.79	74.95
chr4	9421198	9421300	25.79	69.37
chr4	12247073	12247286	25.79	86.64
chr4	13854435	13854671	25.79	71.76
chr4	23066032	23066162	25.79	74.1
chr4	60991172	60991253	25.79	94.27
chr4	112600137	112600259	25.79	76.42
chr4	130779237	130779363	25.79	75.24
chr4	143601042	143601189	25.79	69.63
chr5	29205165	29205296	25.79	73.82
chr5	47548981	47549159	25.79	95.28
chr5	125071963	125072062	25.79	69.37
chr6	11698665	11698820	25.79	90.2
chr6	72756976	72757095	25.79	77.33
chr6	83729069	83729174	25.79	81.6
chr7	97840989	97841088	25.79	69.37
chr7	101458950	101459052	25.79	69.37
chr7	145456762	145456858	25.79	69.37
chr8	15680782	15680926	25.79	70.38
chr8	86383139	86383323	25.79	128.87
chr8	103984972	103985066	25.79	69.37
chr8	116126816	116126969	25.79	79.28
chr8	121371046	121371170	25.79	75.82
chr9	24706523	24706614	25.79	81.6
chrX	18087719	18087832	25.79	79.24
chrX	48789864	48789966	25.79	69.37
chrX	55918512	55918606	25.79	69.37
chrX	89101814	89101951	25.79	72.19
chrX	115524203	115524318	25.79	78.59
chrX	138269822	138269960	25.79	71.92
chrX	161195340	161195456	25.79	78.27
chr3	148461827	148461980	25.12	67.23
chr7	23770561	23770712	24.79	67.23
chr1	39148413	39148486	24.62	105.25
chr1	149928854	149929061	24.62	65.42
chr14	112248657	112248757	24.62	67.86
chr17	5864718	5864820	24.62	67.86
chr17	52613440	52613536	24.62	67.86

chr3	111494363	111494467	24.62	79.89
chr4	56448273	56448458	24.62	69.84
chr5	86981683	86981886	24.62	66.18
chr4	60094570	60094802	24.35	77.28
chr2	89114849	89114997	24.3	78.21
chr7	138638183	138638331	24.3	89.6
chr15	71420336	71420532	24.13	76.91
chr7	24477695	24477788	23.99	106.52
chr5	37353868	37354012	23.64	67.23
chr7	39350780	39351005	23.45	89.85
chr9	94727301	94727458	23.45	74.42
chr7	16007756	16007858	23.23	65.97
chr6	13721083	13721177	23.15	65.85
chr1	109957786	109957972	22.9	76.91
chr1	7985417	7985599	22.41	66.77
chr9	12025331	12025422	22.41	76.42
chr6	139775888	139775979	22.39	76.38
chrX	120870194	120870296	22.39	64.77
chr3	78576013	78576171	22.23	66.77
chr1	16729772	16729904	22.11	85.27
chr1	19678020	19678209	22.11	70.83
chr1	26529999	26530142	22.11	59.7
chr1	30760454	30760591	22.11	61.07
chr1	48796796	48796996	22.11	68.59
chr1	61555000	61555146	22.11	69.88
chr1	68520230	68520369	22.11	60.6
chr1	72173461	72173617	22.11	56.93
chr1	74290175	74290288	22.11	79.24
chr1	77479332	77479561	22.11	83.19
chr1	101083462	101083626	22.11	76.49
chr1	108745760	108745982	22.11	74.4
chr1	113528090	113528212	22.11	64.8
chr1	115700573	115700696	22.11	64.54
chr1	117512575	117512714	22.11	60.6
chr1	140730198	140730310	22.11	67.58
chr1	143929422	143929553	22.11	73.82
chr1	153309187	153309311	22.11	75.82
chr1	162569025	162569212	22.11	71.25
chr1	168400843	168401035	22.11	80.72
chr10	11513344	11513480	22.11	72.45

chr10	22138577	22138794	22.11	75.38
chr10	29940689	29940867	22.11	73.21
chr10	31204002	31204110	22.11	68.76
chr10	50083146	50083291	22.11	59.25
chr10	50263519	50263631	22.11	67.58
chr10	65404254	65404467	22.11	66.11
chr10	81437305	81437490	22.11	61.4
chr10	86144316	86144465	22.11	58.39
chr10	103978398	103978557	22.11	66.8
chr10	105408944	105409057	22.11	67.29
chr10	107443109	107443277	22.11	64.83
chr10	113012795	113013001	22.11	77.65
chr10	114301325	114301453	22.11	63.25
chr10	129407760	129407919	22.11	77.73
chr11	3634914	3635060	22.11	59.03
chr11	8225330	8225500	22.11	64.41
chr11	10571080	10571282	22.11	68.2
chr11	15186262	15186381	22.11	65.61
chr11	21809122	21809277	22.11	57.13
chr11	56027367	56027503	22.11	72.45
chr11	64386701	64386878	22.11	73.43
chr11	88775526	88775663	22.11	61.07
chr12	39616570	39616685	22.11	66.72
chr12	43639414	43639561	22.11	58.82
chr12	45160728	45160877	22.11	69.14
chr12	97999814	97999948	22.11	61.78
chr12	99104883	99105033	22.11	58.17
chr12	116924062	116924294	22.11	92.99
chr12	120989216	120989419	22.11	68
chr13	3111500	3111668	22.11	75.52
chr13	8470841	8471003	22.11	66.13
chr13	10700702	10700909	22.11	67.24
chr13	11337067	11337179	22.11	67.58
chr13	15362521	15362682	22.11	55.93
chr13	15980177	15980291	22.11	67
chr13	19086689	19086833	22.11	59.47
chr13	26144856	26144993	22.11	61.07
chr13	29562088	29562235	22.11	58.82
chr13	29978099	29978204	22.11	69.37
chr13	50175661	50175816	22.11	57.13

chr13	54926768	54926892	22.11	64.28
chr13	64684131	64684285	22.11	79.02
chr13	65098018	65098242	22.11	74.01
chr13	82628192	82628313	22.11	65.07
chr13	82711737	82711919	22.11	83.08
chr13	83581054	83581183	22.11	63
chr13	87282880	87283053	22.11	74.35
chr13	108149357	108149495	22.11	60.84
chr14	19029066	19029185	22.11	65.61
chr14	23552870	23553022	22.11	79.54
chr14	36637007	36637155	22.11	104.28
chr14	41599790	41599929	22.11	60.6
chr14	44254546	44254732	22.11	71.46
chr14	53205389	53205605	22.11	96.7
chr14	79066140	79066282	22.11	70.88
chr14	91817101	91817264	22.11	65.91
chr14	91988959	91989117	22.11	67.03
chr14	103155232	103155452	22.11	64.85
chr14	107363262	107363368	22.11	69.37
chr14	119201826	119201950	22.11	75.82
chr14	123582509	123582642	22.11	62.02
chr14	124828091	124828304	22.11	86.64
chr15	4674128	4674261	22.11	62.02
chr15	7877134	7877320	22.11	71.46
chr15	15849282	15849450	22.11	64.83
chr15	22954851	22954980	22.11	74.38
chr15	31873811	31873959	22.11	58.6
chr15	33345959	33346126	22.11	75.76
chr15	39698543	39698711	22.11	86.62
chr15	44078743	44078957	22.11	86.41
chr15	49086270	49086405	22.11	72.72
chr15	53703311	53703437	22.11	63.76
chr15	69401882	69402082	22.11	58.65
chr15	71097086	71097206	22.11	65.34
chr15	84578654	84578883	22.11	63.29
chr15	90285658	90285777	22.11	65.61
chr15	97881679	97881809	22.11	62.75
chr16	3386116	3386303	22.11	92.89
chr16	12343469	12343642	22.11	74.35
chr16	15945014	15945149	22.11	61.54
chr16	19588942	19589057	22.11	66.72
chr16	21354246	21354415	22.11	86.35
chr16	22923896	22924075	22.11	72.99
chr16	27218541	27218690	22.11	58.39
chr16	52246278	52246388	22.11	56.61
chr16	52557653	52557797	22.11	70.38
chr16	58117932	58118075	22.11	70.63
chr16	59124409	59124541	22.11	62.26
chr16	66588366	66588479	22.11	67.29
chr16	74553919	74554062	22.11	59.7
chr16	82636690	82636806	22.11	66.44
chr17	8413750	8413901	22.11	57.96
chr17	9801225	9801358	22.11	73.27
chr17	16399539	16399652	22.11	67.29
chr17	35508616	35508752	22.11	61.3
chr17	38372535	38372650	22.11	66.72
chr17	39599936	39600040	22.11	69.37
chr17	69873582	69873814	22.11	72.49
chr17	72981959	72982108	22.11	69.14
chr17	75306218	75306388	22.11	64.41
chr17	77727178	77727289	22.11	56.35
chr17	90182658	90182833	22.11	73.89
chr17	94184997	94185152	22.11	67.72
chr18	3231687	3231825	22.11	60.84
chr18	12872133	12872251	22.11	65.88
chr18	26992305	26992450	22.11	70.13
chr18	29176467	29176581	22.11	67
chr18	30988433	30988602	22.11	75.28
chr18	33556303	33556460	22.11	67.26
chr18	33860923	33861073	22.11	58.17
chr18	37735439	37735547	22.11	68.76
chr18	37775972	37776121	22.11	58.39
chr18	41712346	41712469	22.11	64.54
chr18	45271768	45271946	22.11	84.06
chr18	48699871	48700030	22.11	66.8
chr18	50536459	50536653	22.11	69.79
chr18	51817953	51818088	22.11	61.54
chr18	63607614	63607740	22.11	63.76
chr18	75412873	75412980	22.11	57.39
chr18	76818805	76818938	22.11	73.27

chr18	78695403	78695515	22.11	67.58
chr18	80576525	80576672	22.11	58.82
chr18	85489212	85489345	22.11	62.02
chr18	88184905	88185042	22.11	61.07
chr19	9903104	9903248	22.11	59.47
chr19	30704135	30704259	22.11	75.82
chr2	3767404	3767524	22.11	77.03
chr2	4604706	4604823	22.11	66.16
chr2	7508607	7508769	22.11	66.13
chr2	21993102	21993220	22.11	77.64
chr2	23277240	23277385	22.11	59.25
chr2	53618483	53618619	22.11	72.45
chr2	63682890	63683036	22.11	59.03
chr2	75065716	75065898	22.11	72.32
chr2	83773900	83774006	22.11	69.37
chr2	86824090	86824206	22.11	66.44
chr2	95097486	95097634	22.11	69.39
chr2	98568602	98568760	22.11	77.98
chr2	123348807	123348929	22.11	64.8
chr2	130075327	130075431	22.11	69.37
chr2	146823906	146824066	22.11	66.58
chr2	150893888	150894014	22.11	63.76
chr3	9955681	9955831	22.11	58.17
chr3	12410386	12410499	22.11	67.29
chr3	44264822	44264980	22.11	67.03
chr3	48783224	48783334	22.11	56.61
chr3	69446865	69447026	22.11	55.93
chr3	76824734	76824859	22.11	64.02
chr3	85951974	85952159	22.11	61.4
chr3	112641314	112641459	22.11	59.25
chr3	113165603	113165810	22.11	67.24
chr3	128509759	128509905	22.11	59.03
chr3	137331649	137331795	22.11	59.03
chr3	139346267	139346404	22.11	72.19
chr3	140391071	140391271	22.11	78.94
chr4	8842967	8843167	22.11	68.59
chr4	18916714	18916835	22.11	65.07
chr4	26226425	26226611	22.11	82.12
chr4	28267435	28267584	22.11	58.39
chr4	32884317	32884487	22.11	75.05

chr4	37868590	37868749	22.11	77.73
chr4	43059281	43059458	22.11	84.31
chr4	46027540	46027653	22.11	67.29
chr4	50755499	50755638	22.11	60.6
chr4	53827897	53828202	22.11	108.59
chr4	54165361	54165500	22.11	60.6
chr4	60319568	60319683	22.11	66.72
chr4	61231898	61232043	22.11	70.13
chr4	68333582	68333716	22.11	61.78
chr4	68626893	68627030	22.11	61.07
chr4	70663147	70663256	22.11	68.46
chr4	74574977	74575161	22.11	61.59
chr4	79500960	79501096	22.11	61.3
chr4	102420382	102420529	22.11	58.82
chr4	103405727	103405889	22.11	88.23
chr4	109774950	109775071	22.11	65.07
chr4	111246247	111246458	22.11	76.6
chr4	113938037	113938174	22.11	72.19
chr4	119936515	119936670	22.11	67.72
chr5	17808628	17808848	22.11	95.75
chr5	22666828	22666957	22.11	86.21
chr5	23601331	23601466	22.11	61.54
chr5	58890592	58890751	22.11	77.73
chr5	60548035	60548255	22.11	74.79
chr5	61928912	61929041	22.11	63
chr5	93807025	93807180	22.11	67.72
chr5	120176827	120176957	22.11	62.75
chr5	144536152	144536311	22.11	66.8
chr5	146247083	146247205	22.11	64.8
chr6	11632195	11632352	22.11	67.26
chr6	21825960	21826123	22.11	76.73
chr6	28876763	28876974	22.11	56.77
chr6	41043679	41043826	22.11	58.82
chr6	120916671	120916888	22.11	65.39
chr6	128631776	128631914	22.11	60.84
chr6	139296276	139296391	22.11	66.72
chr7	11495919	11496058	22.11	71.66
chr7	19460526	19460700	22.11	63.58
chr7	20743643	20743816	22.11	63.78
chr7	21036271	21036468	22.11	79.6

chr7	34830448	34830588	22.11	60.38
chr7	48967142	48967274	22.11	62.26
chr7	52224255	52224443	22.11	92.63
chr7	54762692	54762852	22.11	66.58
chr7	65296624	65296817	22.11	70
chr7	65361906	65362052	22.11	69.88
chr7	66466050	66466199	22.11	58.39
chr7	68394611	68394789	22.11	73.21
chr7	83099738	83099879	22.11	60.15
chr7	83852127	83852258	22.11	62.51
chr7	113246795	113246939	22.11	59.47
chr7	132129439	132129640	22.11	100.46
chr7	132248907	132249048	22.11	60.15
chr7	132444563	132444713	22.11	58.17
chr7	133472386	133472521	22.11	61.54
chr7	144059915	144060083	22.11	75.52
chr7	144060678	144060907	22.11	83.19
chr7	147610323	147610464	22.11	60.15
chr8	22552209	22552360	22.11	68.66
chr8	28807241	28807415	22.11	63.58
chr8	38621973	38622087	22.11	67
chr8	38681748	38681854	22.11	69.37
chr8	42535888	42536001	22.11	67.29
chr8	62537780	62537945	22.11	76.24
chr8	75496219	75496353	22.11	61.78
chr8	79375972	79376152	22.11	83.56
chr8	82873002	82873147	22.11	70.13
chr8	89148585	89148763	22.11	62.77
chr8	89473753	89473929	22.11	63.17
chr8	112885808	112885994	22.11	61.21
chr9	85957889	85958065	22.11	84.56
chr9	86443183	86443311	22.11	63.25
chr9	93369530	93369732	22.11	78.5
chr9	95293690	95293802	22.11	67.58
chr9	123525178	123525323	22.11	70.13
chrX	3983042	3983157	22.11	66.72
chrX	17809629	17809767	22.11	60.84
chrX	17914163	17914338	22.11	73.89
chrX	20165780	20165895	22.11	66.72
chrX	24122917	24123097	22.11	83.56

chrX	25885781	25885916	22.11	61.54
chrX	27290538	27290687	22.11	80.35
chrX	27293399	27293565	22.11	65.26
chrX	46653838	46653984	22.11	81.17
chrX	53336421	53336562	22.11	60.15
chrX	59361214	59361384	22.11	64.41
chrX	63228344	63228531	22.11	81.88
chrX	63393902	63394074	22.11	74.58
chrX	73952154	73952272	22.11	65.88
chrX	76184288	76184438	22.11	58.17
chrX	89068972	89069192	22.11	95.75
chrX	92763494	92763654	22.11	77.48
chrX	93601140	93601273	22.11	62.02
chrX	97370170	97370316	22.11	69.88
chrX	123147080	123147267	22.11	71.25
chrX	123252827	123252942	22.11	66.72
chrX	135918195	135918354	22.11	66.8
chrX	149332475	149332668	22.11	91.37
chr16	76137592	76137696	21.95	69.14
chrX	40039535	40039691	21.95	56.7
chr14	8388317	8388434	21.87	65.81
chr11	56286033	56286166	21.83	67.23
chr1	69094090	69094245	21.81	67.23
chr17	27752716	27752809	21.81	94.99
chr15	95294689	95294766	21.67	105.57
chr4	23124283	23124437	21.67	56.7
chr11	40831455	40831555	21.41	63.33
chr4	52507159	52507260	21.41	63.33
chrX	3548435	3548586	21.25	56.7
chr1	37012639	37012780	21.11	69.46
chr11	6433444	6433608	21.11	64.03
chr12	53833086	53833222	21.11	59.82
chr14	43629780	43629918	21.11	59.35
chr14	47763558	47763735	21.11	128.41
chr14	53378463	53378612	21.11	56.91
chr15	26214829	26215044	21.11	105.4
chr15	32762935	32763043	21.11	67.25
chr17	39625171	39625292	21.11	63.57
chr18	8847315	8847465	21.11	56.7
chr18	21423502	21423649	21.11	90.5

chr2	35375959	35376113	21.11	55.87
chr2	58739063	58739217	21.11	55.87
chr2	97024214	97024418	21.11	65.99
chr2	134335941	134336100	21.11	75.87
chr4	23818512	23818626	21.11	65.5
chr5	105421350	105421509	21.11	65.14
chr7	16288598	16288749	21.11	56.49
chr7	60393156	60393331	21.11	61.73
chr8	85038937	85039109	21.11	83.52
chr9	17865130	17865290	21.11	64.92
chr9	121863282	121863444	21.11	64.47
chrX	3132046	3132206	21.11	75.62
chrX	139905959	139906116	21.11	65.59
chr11	109183233	109183361	21.01	67.23
chr17	23917661	23917810	20.97	56.7
chr14	41874284	41874457	20.96	66.13
chr5	94408658	94408743	20.93	73.92
chr14	39351528	39351676	20.83	76.91
chr14	86993604	86993766	20.79	63.94
chr14	83287429	83287576	20.68	56.7
chr17	46148939	46149107	20.68	66.77
chr3	9048810	9049005	20.58	66.77
chr6	35753634	35753780	20.54	56.7
chr6	10661598	10661788	20.52	71.25
chr4	143638266	143638460	20.47	66.77
chr7	28708761	28708954	20.37	98.29
chr3	139051742	139051885	20.12	56.7
chr1	142716780	142716976	20.1	65.65
chr1	178476901	178477034	20.1	69.81
chr11	37571460	37571583	20.1	61.47
chr12	14458957	14459087	20.1	70.64
chr13	32397751	32397900	20.1	55.37
chr14	75828305	75828479	20.1	60.2
chr14	104140056	104140201	20.1	56.23
chr14	104987375	104987512	20.1	68.74
chr15	14412706	14412903	20.1	75.45
chr15	97566383	97566526	20.1	56.67
chr3	99167698	99167820	20.1	61.74
chr4	15790261	15790395	20.1	80.79
chr4	88131385	88131521	20.1	58.26

chr4	110362352	110362523	20.1	81.63
chr5	101483930	101484080	20.1	65.48
chr6	79082481	79082598	20.1	74.47
chr7	24582592	24582716	20.1	61.22
chr7	79787453	79787589	20.1	58.26
chr7	114232178	114232285	20.1	54.7
chr8	78493685	78493837	20.1	54.74
chr9	92911406	92911623	20.1	61.69
chrX	111412492	111412642	20.1	55.16
chrX	149277126	149277308	20.1	58.62
chr10	119948743	119948857	20.05	116.98
chr14	117333976	117334098	20.03	67.23
chr17	57954950	57955092	19.98	67.23
chr2	101409238	101409427	19.95	66.77
chr8	108320419	108320581	19.95	57.03
chr8	105472528	105472649	19.86	78.21
chr1	137542841	137542981	19.7	56.7
chr10	116043835	116043933	19.7	60.65
chr2	59591741	59591861	19.7	67.23
chr4	10148287	10148435	19.7	80.32
chr8	34825996	34826136	19.7	56.7
chr9	117999895	118000035	19.7	56.7
chr4	24387060	24387199	19.56	67.23
chr6	16968784	16968923	19.56	56.7
chrX	77611695	77611834	19.56	67.23
chr11	101201869	101201948	19.45	82.72
chr18	59889670	59889808	19.42	56.7
chrX	120863290	120863456	19.41	59.58
chr1	65996051	65996234	19.31	57.03
chr4	128031714	128031897	19.31	66.77
chr3	60903763	60903900	19.28	56.7
chr1	13545121	13545283	19.19	61.08
chr10	19105185	19105374	19.19	85.58
chr11	45465353	45465508	19.19	52.67
chr13	6722087	6722225	19.19	56.33
chr13	108846676	108846818	19.19	65.78
chr15	82436275	82436441	19.19	70.35
chr18	71004330	71004440	19.19	52.62
chr2	90023625	90023751	19.19	70.08
chr2	126794898	126795021	19.19	59.98

chr3	98441681	98441787	19.19	64.77
chr5	9292718	9292872	19.19	52.87
chr8	106282635	106282760	19.19	59.47
chr11	49178950	49179130	19	66.77
chr2	177336613	177336748	19	56.7
chr9	99606200	99606380	19	76.91
chr18	9423161	9423260	18.94	59.4
chr16	7738353	7738577	18.91	76.87
chr9	93220536	93220651	18.88	67.23
chr12	107751608	107751742	18.86	78.21
chr5	38867090	38867224	18.86	67.23
chrX	63143890	63144043	18.84	57.03
chr1	46114458	46114610	18.71	57.03
chr2	54238174	54238307	18.71	67.23
chr4	136267289	136267365	18.71	81.15
chr7	7397890	7398023	18.71	56.7
chr8	120114575	120114708	18.71	67.23
chr6	114465937	114466120	18.68	85.84
chr6	114522155	114522344	18.62	74.13
chr1	107733462	107733638	18.57	76.91
chr4	14657678	14657777	18.57	64.78
chr5	106280189	106280387	18.57	68.43
chr4	22999572	22999685	18.55	67.23
chr1	8180906	8181037	18.42	73.82
chr1	18805547	18805695	18.42	58.6
chr1	23734702	23734829	18.42	63.51
chr1	24866976	24867130	18.42	67.95
chr1	28418382	28418543	18.42	55.93
chr1	28563980	28564110	18.42	62.75
chr1	32318115	32318236	18.42	65.07
chr1	34916155	34916273	18.42	65.88
chr1	35226113	35226238	18.42	64.02
chr1	37845817	37845958	18.42	71.14
chr1	46237728	46237864	18.42	61.3
chr1	46642857	46643011	18.42	57.34
chr1	46757565	46757779	18.42	75.99
chr1	46827746	46827901	18.42	57.13
chr1	52641355	52641495	18.42	60.38
chr1	56441719	56441852	18.42	62.02
chr1	60012251	60012399	18.42	58.6
chr1	68518774	68518929	18.42	57.13
chr1	70287877	70288021	18.42	59.47
chr1	73519573	73519732	18.42	66.8
chr1	76309456	76309608	18.42	68.42
chr1	79337999	79338132	18.42	62.02
chr1	79381901	79382053	18.42	57.75
chr1	79958334	79958497	18.42	65.91
chr1	80879168	80879313	18.42	59.25
chr1	89358349	89358527	18.42	84.06
chr1	95854350	95854531	18.42	62.17
chr1	106465038	106465187	18.42	58.39
chr1	108015889	108016023	18.42	61.78
chr1	109782838	109782979	18.42	60.15
chr1	109822150	109822361	18.42	76.6
chr1	111622728	111622868	18.42	60.38
chr1	114258788	114258921	18.42	62.02
chr1	114495239	114495383	18.42	59.47
chr1	116124836	116124981	18.42	59.25
chr1	121839038	121839194	18.42	56.93
chr1	127031452	127031600	18.42	69.39
chr1	129776700	129776841	18.42	60.15
chr1	130430118	130430272	18.42	57.34
chr1	132501920	132502066	18.42	59.03
chr1	134596054	134596236	18.42	61.98
chr1	139185861	139186008	18.42	69.63
chr1	143927742	143927887	18.42	59.25
chr1	145917590	145917759	18.42	75.28
chr1	147870421	147870562	18.42	60.15
chr1	156780735	156780887	18.42	57.75
chr1	164947132	164947272	18.42	71.4
chr1	169056135	169056274	18.42	60.6
chr1	169131514	169131641	18.42	74.95
chr1	186623555	186623685	18.42	62.75
chr1	195072016	195072207	18.42	70.41
chr10	3895050	3895208	18.42	67.03
chr10	5088874	5088990	18.42	66.44
chr10	15143385	15143530	18.42	59.25
chr10	16468759	16468909	18.42	58.17
chr10	21364417	21364566	18.42	58.39
chr10	23194875	23195018	18.42	59.7

chr10	24825081	24825212	18.42	73.82
chr10	27544200	27544343	18.42	59.7
chr10	27577046	27577211	18.42	65.47
chr10	28188781	28188922	18.42	71.14
chr10	28731741	28731911	18.42	64.41
chr10	29683575	29683740	18.42	76.24
chr10	32618243	32618396	18.42	68.19
chr10	33542636	33542753	18.42	66.16
chr10	45255332	45255464	18.42	62.26
chr10	47403210	47403364	18.42	57.34
chr10	50923320	50923469	18.42	58.39
chr10	51511440	51511651	18.42	87.09
chr10	53294918	53295069	18.42	57.96
chr10	63239617	63239751	18.42	61.78
chr10	71648866	71649012	18.42	59.03
chr10	73428219	73428381	18.42	66.13
chr10	86262725	86262868	18.42	59.7
chr10	86901269	86901385	18.42	66.44
chr10	95991717	95991860	18.42	59.7
chr10	99199105	99199294	18.42	60.64
chr10	104202396	104202574	18.42	62.77
chr10	111865239	111865400	18.42	55.93
chr10	112903229	112903378	18.42	58.39
chr11	4566799	4566948	18.42	69.14
chr11	13248777	13248912	18.42	61.54
chr11	13658199	13658357	18.42	67.03
chr11	18202881	18203020	18.42	60.6
chr11	35757592	35757802	18.42	76.81
chr11	47495934	47496068	18.42	61.78
chr11	48446766	48446905	18.42	71.66
chr11	58492912	58493081	18.42	75.28
chr11	67685093	67685215	18.42	64.8
chr11	79398722	79398933	18.42	87.09
chr11	87371811	87371957	18.42	59.03
chr11	93403134	93403277	18.42	59.7
chr11	94489388	94489506	18.42	65.88
chr11	102909786	102909914	18.42	74.66
chr11	104100690	104100831	18.42	60.15
chr11	116624568	116624736	18.42	75.52
chr12	10926081	10926229	18.42	58.6

chr12	13227732	13227881	18.42	69.14
chr12	14969781	14969924	18.42	59.7
chr12	15033422	15033551	18.42	63
chr12	17131031	17131186	18.42	67.72
chr12	19325873	19326025	18.42	57.75
chr12	19999583	19999732	18.42	58.39
chr12	22796606	22796741	18.42	61.54
chr12	23228766	23228901	18.42	61.54
chr12	26739991	26740134	18.42	59.7
chr12	31199730	31199882	18.42	57.75
chr12	34252585	34252726	18.42	60.15
chr12	34753891	34754041	18.42	58.17
chr12	36533868	36534001	18.42	62.02
chr12	39815716	39815836	18.42	65.34
chr12	47724615	47724771	18.42	56.93
chr12	54101713	54101861	18.42	58.6
chr12	55470095	55470238	18.42	59.7
chr12	57087278	57087434	18.42	56.93
chr12	60136127	60136283	18.42	56.93
chr12	60139420	60139606	18.42	71.46
chr12	66129845	66129981	18.42	61.3
chr12	68853873	68854012	18.42	60.6
chr12	69849069	69849225	18.42	67.49
chr12	73067937	73068080	18.42	59.7
chr12	81524731	81524884	18.42	68.19
chr12	89212648	89212804	18.42	56.93
chr12	97258045	97258192	18.42	58.82
chr12	99595456	99595604	18.42	69.39
chr12	102038626	102038782	18.42	56.93
chr12	106543014	106543158	18.42	59.47
chr12	121228301	121228451	18.42	68.9
chr13	3233949	3234099	18.42	68.9
chr13	14031075	14031210	18.42	61.54
chr13	17370591	17370713	18.42	64.8
chr13	20973599	20973753	18.42	57.34
chr13	22590568	22590724	18.42	67.49
chr13	22999438	22999644	18.42	88.24
chr13	24633482	24633612	18.42	62.75
chr13	25321841	25321991	18.42	58.17
chr13	27882192	27882337	18.42	70.13

chr13	29343565	29343752	18.42	71.25
chr13	32981434	32981619	18.42	71.67
chr13	33815951	33816089	18.42	60.84
chr13	34563031	34563167	18.42	61.3
chr13	37359188	37359348	18.42	66.58
chr13	46676600	46676788	18.42	60.83
chr13	50965513	50965641	18.42	63.25
chr13	54876372	54876524	18.42	79.54
chr13	68207375	68207516	18.42	60.15
chr13	71564747	71564910	18.42	65.91
chr13	74848790	74848944	18.42	57.34
chr13	75310828	75310959	18.42	62.51
chr13	78191576	78191720	18.42	59.47
chr13	79089564	79089733	18.42	64.62
chr13	81861155	81861309	18.42	67.95
chr13	83367002	83367194	18.42	60.09
chr13	86770980	86771146	18.42	76
chr13	87201485	87201640	18.42	67.72
chr13	91313337	91313513	18.42	63.17
chr13	103191548	103191689	18.42	60.15
chr13	107176390	107176541	18.42	57.96
chr13	111105795	111105964	18.42	64.62
chr13	116683501	116683648	18.42	58.82
chr14	3018916	3019042	18.42	63.76
chr14	3374563	3374694	18.42	62.51
chr14	3699829	3699963	18.42	61.78
chr14	4195482	4195640	18.42	67.03
chr14	24231095	24231243	18.42	58.6
chr14	29432853	29433008	18.42	57.13
chr14	36247846	36247959	18.42	67.29
chr14	36683989	36684113	18.42	64.28
chr14	36710761	36710903	18.42	70.88
chr14	40916127	40916274	18.42	69.63
chr14	42054819	42054992	18.42	63.78
chr14	42097727	42097872	18.42	59.25
chr14	42351681	42351830	18.42	58.39
chr14	42640050	42640187	18.42	61.07
chr14	43126514	43126665	18.42	57.96
chr14	51533594	51533761	18.42	75.76
chr14	62669101	62669237	18.42	61.3
chr14	68875482	68875617	18.42	61.54
chr14	69372590	69372738	18.42	58.6
chr14	70150730	70150877	18.42	58.82
chr14	79187903	79188051	18.42	58.6
chr14	80260998	80261146	18.42	58.6
chr14	81357623	81357778	18.42	57.13
chr14	82765027	82765183	18.42	67.49
chr14	83907247	83907396	18.42	58.39
chr14	84831982	84832134	18.42	68.42
chr14	91818448	91818659	18.42	87.09
chr14	92433703	92433843	18.42	60.38
chr14	95964490	95964640	18.42	58.17
chr14	100053057	100053201	18.42	59.47
chr14	106513777	106513930	18.42	68.19
chr14	108872346	108872510	18.42	65.69
chr14	109798817	109798939	18.42	64.8
chr14	110143989	110144132	18.42	59.7
chr14	110314584	110314707	18.42	64.54
chr14	112965638	112965782	18.42	59.47
chr14	114196547	114196673	18.42	63.76
chr14	114911861	114912017	18.42	56.92
chr14	117040583	117040707	18.42	64.28
chr14	117657728	117657877	18.42	58.39
chr14	124204260	124204412	18.42	57.75
chr15	4793290	4793427	18.42	61.07
chr15	13976108	13976232	18.42	64.28
chr15	17854328	17854471	18.42	59.7
chr15	18989362	18989502	18.42	60.38
chr15	21875550	21875712	18.42	66.13
chr15	23170311	23170446	18.42	61.54
chr15	23660607	23660779	18.42	74.58
chr15	33925290	33925433	18.42	59.7
chr15	41537156	41537369	18.42	76.19
chr15	42192210	42192340	18.42	62.75
chr15	43352026	43352209	18.42	61.78
chr15	52303038	52303185	18.42	58.82
chr15	52568284	52568495	18.42	66.48
chr15	59265951	59266073	18.42	64.8
chr15	59891164	59891312	18.42	58.6
chr15	66488199	66488326	18.42	74.95

chr15	68976613	68976761	18.42	58.6
chr15	73704217	73704356	18.42	60.6
chr15	85241902	85242063	18.42	55.93
chr15	90567216	90567393	18.42	73.43
chr15	96812293	96812426	18.42	62.02
chr16	21603332	21603504	18.42	63.99
chr16	21982955	21983101	18.42	59.03
chr16	26808858	26809002	18.42	59.47
chr16	39180015	39180146	18.42	73.82
chr16	39385243	39385408	18.42	65.47
chr16	41576034	41576163	18.42	63
chr16	45054863	45054999	18.42	61.3
chr16	47121706	47121855	18.42	58.39
chr16	58867219	58867368	18.42	58.39
chr16	61655318	61655462	18.42	59.47
chr16	66754579	66754748	18.42	64.62
chr16	74552837	74552978	18.42	60.15
chr16	74555940	74556085	18.42	59.25
chr16	76058196	76058352	18.42	67.49
chr16	76062739	76062881	18.42	70.88
chr16	77939875	77940014	18.42	71.66
chr16	78863842	78863988	18.42	59.03
chr16	79786002	79786145	18.42	59.7
chr16	80289322	80289454	18.42	62.26
chr16	80766975	80767129	18.42	57.34
chr16	81078689	81078883	18.42	69.79
chr16	82545182	82545338	18.42	56.93
chr16	82589087	82589224	18.42	61.07
chr16	84282328	84282478	18.42	58.17
chr16	88065208	88065323	18.42	66.72
chr17	9978053	9978204	18.42	68.66
chr17	18881703	18881859	18.42	56.93
chr17	27299163	27299364	18.42	58.47
chr17	27402486	27402611	18.42	64.02
chr17	33302620	33302777	18.42	67.26
chr17	37432208	37432363	18.42	57.13
chr17	38097718	38097861	18.42	70.63
chr17	39814451	39814584	18.42	62.02
chr17	41187899	41188042	18.42	59.7
chr17	42055932	42056091	18.42	66.8

chr17	52009819	52009966	18.42	58.82
chr17	55521332	55521513	18.42	62.17
chr17	59431750	59431884	18.42	72.99
chr17	67041041	67041182	18.42	60.15
chr17	69685651	69685794	18.42	70.63
chr17	82863959	82864125	18.42	76
chr17	83376162	83376331	18.42	86.35
chr17	90987087	90987219	18.42	62.26
chr17	92040840	92040985	18.42	59.25
chr17	94393422	94393573	18.42	57.96
chr18	4661894	4662045	18.42	57.96
chr18	9682459	9682596	18.42	61.07
chr18	16139871	16140075	18.42	88.7
chr18	22459090	22459242	18.42	57.75
chr18	22727472	22727621	18.42	91.97
chr18	27461912	27462068	18.42	56.93
chr18	29656162	29656306	18.42	59.47
chr18	33171699	33171844	18.42	59.25
chr18	39762037	39762202	18.42	65.47
chr18	41495612	41495762	18.42	58.17
chr18	44529126	44529283	18.42	67.26
chr18	46856168	46856294	18.42	63.76
chr18	50944464	50944607	18.42	59.7
chr18	52613731	52613879	18.42	58.6
chr18	54603734	54603878	18.42	59.47
chr18	55475468	55475634	18.42	76
chr18	73445018	73445146	18.42	63.25
chr18	76046764	76046910	18.42	59.03
chr18	83494496	83494642	18.42	59.03
chr18	84778518	84778652	18.42	61.78
chr19	15788407	15788528	18.42	76.72
chr19	34105584	34105736	18.42	57.75
chr19	57746718	57746870	18.42	57.75
chr2	9427889	9428045	18.42	56.93
chr2	9435612	9435763	18.42	57.96
chr2	12862986	12863124	18.42	60.84
chr2	13079400	13079575	18.42	63.37
chr2	13585860	13586036	18.42	73.66
chr2	15501984	15502139	18.42	57.13
chr2	16028078	16028218	18.42	60.38

chr2	19212287	19212416	18.42	63
chr2	26554145	26554261	18.42	66.44
chr2	46122817	46122974	18.42	67.26
chr2	50238965	50239117	18.42	57.75
chr2	55904105	55904257	18.42	68.42
chr2	58195017	58195137	18.42	65.34
chr2	64465003	64465151	18.42	69.39
chr2	75339928	75340074	18.42	59.03
chr2	80802734	80802882	18.42	58.6
chr2	89732527	89732663	18.42	61.3
chr2	95938159	95938354	18.42	69.59
chr2	96811794	96811946	18.42	68.42
chr2	98035191	98035335	18.42	59.47
chr2	99093014	99093159	18.42	59.25
chr2	99789805	99789921	18.42	66.44
chr2	100483852	100483967	18.42	66.72
chr2	105690768	105690912	18.42	59.47
chr2	110082791	110082962	18.42	74.81
chr2	111191353	111191507	18.42	67.95
chr2	112936025	112936173	18.42	58.6
chr2	114720817	114720971	18.42	57.34
chr2	125839109	125839242	18.42	62.02
chr2	135423055	135423176	18.42	65.07
chr2	138252355	138252496	18.42	60.15
chr2	138405892	138406026	18.42	61.78
chr2	146828524	146828644	18.42	65.34
chr2	148288397	148288540	18.42	59.7
chr2	148951583	148951718	18.42	61.54
chr2	150943483	150943619	18.42	61.3
chr2	156686798	156686924	18.42	63.76
chr2	165653281	165653430	18.42	58.39
chr2	174926597	174926732	18.42	61.54
chr2	176723217	176723370	18.42	68.19
chr2	181619869	181619998	18.42	63
chr3	3455192	3455301	18.42	68.46
chr3	7220792	7220929	18.42	61.07
chr3	8654683	8654819	18.42	61.3
chr3	12918470	12918598	18.42	63.25
chr3	14835666	14835809	18.42	59.7
chr3	16298188	16298313	18.42	64.02

chr3	21094972	21095122	18.42	58.17
chr3	22216730	22216866	18.42	61.3
chr3	22358723	22358859	18.42	61.3
chr3	23481670	23481843	18.42	74.35
chr3	31086043	31086192	18.42	58.39
chr3	43684799	43684942	18.42	59.7
chr3	43884298	43884446	18.42	58.6
chr3	44824625	44824746	18.42	65.07
chr3	48805622	48805774	18.42	68.42
chr3	50471375	50471582	18.42	77.43
chr3	51425662	51425834	18.42	63.99
chr3	52417078	52417229	18.42	57.96
chr3	52938366	52938574	18.42	67.05
chr3	53849161	53849270	18.42	68.46
chr3	61525400	61525547	18.42	58.82
chr3	61659870	61660015	18.42	59.25
chr3	62092940	62093104	18.42	76.49
chr3	62163733	62163860	18.42	63.51
chr3	66661299	66661414	18.42	66.72
chr3	71830411	71830580	18.42	75.28
chr3	75467240	75467423	18.42	61.78
chr3	77040627	77040773	18.42	59.03
chr3	79574328	79574463	18.42	61.54
chr3	81426302	81426454	18.42	57.75
chr3	85429208	85429359	18.42	68.66
chr3	85429872	85430016	18.42	59.47
chr3	86042712	86042842	18.42	74.1
chr3	90853881	90854025	18.42	59.47
chr3	90899819	90899973	18.42	57.34
chr3	98284871	98285016	18.42	70.13
chr3	102245961	102246120	18.42	66.8
chr3	108386147	108386290	18.42	82.01
chr3	108841726	108841858	18.42	62.26
chr3	110954299	110954448	18.42	58.39
chr3	111600792	111600949	18.42	67.26
chr3	111607371	111607489	18.42	65.88
chr3	111637432	111637600	18.42	86.62
chr3	111869250	111869422	18.42	74.58
chr3	113046405	113046559	18.42	57.34
chr3	113551137	113551281	18.42	59.47

chr3	113667463	113667627	18.42	76.49
chr3	113972425	113972576	18.42	57.96
chr3	114684808	114684958	18.42	68.9
chr3	115886247	115886437	18.42	60.46
chr3	117634972	117635160	18.42	71.04
chr3	118274996	118275149	18.42	68.19
chr3	118915481	118915602	18.42	65.07
chr3	131209087	131209231	18.42	59.47
chr3	132789841	132789972	18.42	62.51
chr3	133229059	133229196	18.42	61.07
chr3	150405411	150405600	18.42	70.83
chr3	159491445	159491594	18.42	58.39
chr4	10037839	10038002	18.42	65.91
chr4	10601698	10601841	18.42	59.7
chr4	13862516	13862653	18.42	61.07
chr4	24127436	24127588	18.42	68.42
chr4	24230502	24230674	18.42	63.99
chr4	26675788	26675939	18.42	68.66
chr4	26837872	26838012	18.42	60.38
chr4	29638929	29639077	18.42	69.39
chr4	30161829	30162041	18.42	86.86
chr4	31498616	31498766	18.42	58.17
chr4	34489287	34489443	18.42	56.93
chr4	35816986	35817122	18.42	61.3
chr4	36220494	36220639	18.42	59.25
chr4	39001318	39001447	18.42	63
chr4	39797279	39797435	18.42	56.93
chr4	40541879	40542033	18.42	57.34
chr4	46998116	46998250	18.42	61.78
chr4	49475948	49476157	18.42	77.02
chr4	58237651	58237833	18.42	83.08
chr4	60293344	60293533	18.42	70.83
chr4	64074313	64074446	18.42	62.02
chr4	65086913	65087032	18.42	65.61
chr4	66242057	66242208	18.42	57.96
chr4	67776452	67776598	18.42	59.03
chr4	73291476	73291613	18.42	61.07
chr4	73323116	73323246	18.42	62.75
chr4	86119925	86120065	18.42	60.38
chr4	88028643	88028812	18.42	64.62
chr4	94560822	94560977	18.42	57.13
chr4	109277045	109277193	18.42	58.6
chr4	112880228	112880395	18.42	65.04
chr4	118344412	118344566	18.42	57.34
chr4	127500144	127500299	18.42	57.13
chr4	134923349	134923514	18.42	76.24
chr4	143238847	143239036	18.42	81.42
chr4	143569930	143570066	18.42	61.3
chr4	144407358	144407542	18.42	71.89
chr4	147209741	147209886	18.42	59.25
chr4	150906241	150906433	18.42	70.2
chr4	150906712	150906862	18.42	58.17
chr5	15341021	15341166	18.42	59.25
chr5	19767441	19767585	18.42	59.47
chr5	45961408	45961567	18.42	66.8
chr5	47520101	47520246	18.42	59.25
chr5	50708316	50708448	18.42	62.26
chr5	57676590	57676727	18.42	61.07
chr5	62310971	62311095	18.42	64.28
chr5	67665256	67665428	18.42	74.58
chr5	69866991	69867138	18.42	58.82
chr5	69923101	69923273	18.42	63.99
chr5	78630720	78630870	18.42	68.9
chr5	79764173	79764328	18.42	57.13
chr5	80711457	80711619	18.42	66.13
chr5	83989662	83989824	18.42	66.13
chr5	84223923	84224089	18.42	65.26
chr5	85403980	85404124	18.42	59.47
chr5	95910509	95910663	18.42	57.34
chr5	109495880	109496075	18.42	69.59
chr5	109502973	109503133	18.42	66.58
chr5	116599713	116599846	18.42	62.02
chr5	121277282	121277433	18.42	57.96
chr5	131532206	131532362	18.42	56.93
chr5	133206872	133207013	18.42	71.14
chr5	144191090	144191278	18.42	71.04
chr5	146301241	146301366	18.42	64.02
chr6	3594595	3594709	18.42	67
chr6	3741508	3741656	18.42	69.39
chr6	6655607	6655746	18.42	60.6

chr6	9530932	9531088	18.42	56.93
chr6	10664565	10664694	18.42	63
chr6	11198120	11198253	18.42	62.02
chr6	12625242	12625393	18.42	57.96
chr6	19892431	19892585	18.42	67.95
chr6	23462995	23463126	18.42	62.51
chr6	25568537	25568713	18.42	63.17
chr6	29183472	29183627	18.42	57.13
chr6	31802920	31803067	18.42	69.63
chr6	32693037	32693205	18.42	64.83
chr6	33442815	33443005	18.42	70.62
chr6	33615176	33615311	18.42	61.54
chr6	36035039	36035213	18.42	63.58
chr6	37924642	37924803	18.42	55.93
chr6	42041655	42041782	18.42	63.51
chr6	42804914	42805064	18.42	58.17
chr6	44642600	44642769	18.42	64.62
chr6	55467239	55467393	18.42	67.95
chr6	56197640	56197789	18.42	58.39
chr6	61582729	61582880	18.42	57.96
chr6	65209046	65209191	18.42	59.25
chr6	67457564	67457716	18.42	57.75
chr6	67457982	67458147	18.42	76.24
chr6	82300814	82300996	18.42	61.98
chr6	87356822	87356989	18.42	65.04
chr6	97323819	97323958	18.42	60.6
chr6	98177178	98177314	18.42	61.3
chr6	102638976	102639127	18.42	57.96
chr6	108429025	108429184	18.42	66.8
chr6	116430841	116430977	18.42	61.3
chr6	118165596	118165746	18.42	68.9
chr6	133963639	133963769	18.42	62.75
chr6	139565535	139565665	18.42	62.75
chr6	143455183	143455335	18.42	57.75
chr6	147851262	147851402	18.42	71.4
chr7	3716949	3717081	18.42	62.26
chr7	5954860	5955084	18.42	74.01
chr7	11642212	11642346	18.42	61.78
chr7	12875123	12875297	18.42	63.58
chr7	16146589	16146741	18.42	79.54

chr7	23970149	23970339	18.42	60.46
chr7	32749816	32749964	18.42	69.39
chr7	34256569	34256704	18.42	61.54
chr7	34826519	34826681	18.42	76.98
chr7	49047902	49048046	18.42	59.47
chr7	59540979	59541146	18.42	65.04
chr7	64510754	64510879	18.42	64.02
chr7	79667046	79667237	18.42	80.95
chr7	80820896	80821055	18.42	66.8
chr7	83393130	83393277	18.42	58.82
chr7	84618956	84619097	18.42	60.15
chr7	93719628	93719817	18.42	81.42
chr7	95139819	95139989	18.42	64.41
chr7	100305658	100305853	18.42	69.59
chr7	104380540	104380700	18.42	66.58
chr7	120458921	120459043	18.42	76.42
chr7	126574022	126574165	18.42	59.7
chr7	149962534	149962688	18.42	57.34
chr7	151039176	151039316	18.42	60.38
chr8	4892698	4892834	18.42	61.3
chr8	5223170	5223323	18.42	68.19
chr8	6494957	6495103	18.42	69.88
chr8	14296677	14296801	18.42	64.28
chr8	15696265	15696416	18.42	57.96
chr8	19055201	19055351	18.42	68.9
chr8	27076508	27076652	18.42	59.47
chr8	31278335	31278489	18.42	57.34
chr8	31881392	31881552	18.42	66.58
chr8	33827515	33827652	18.42	72.19
chr8	35633015	35633140	18.42	64.02
chr8	39496664	39496824	18.42	66.58
chr8	39886049	39886207	18.42	67.03
chr8	42747971	42748107	18.42	61.3
chr8	43420886	43421020	18.42	61.78
chr8	43948660	43948811	18.42	57.96
chr8	47101942	47102184	18.42	80.58
chr8	50073010	50073148	18.42	60.83
chr8	55597869	55598021	18.42	57.75
chr8	58368423	58368580	18.42	67.26
chr8	59426426	59426573	18.42	58.82

chr8	59427520	59427699	18.42	72.99
chr8	60775050	60775194	18.42	59.47
chr8	66218374	66218513	18.42	60.6
chr8	68453516	68453672	18.42	56.93
chr8	69988035	69988176	18.42	60.15
chr8	70318991	70319141	18.42	58.17
chr8	71096079	71096234	18.42	57.13
chr8	74930802	74930931	18.42	63
chr8	75772697	75772841	18.42	81.73
chr8	76340913	76341047	18.42	61.78
chr8	76874462	76874609	18.42	58.82
chr8	78224205	78224352	18.42	69.63
chr8	79995057	79995207	18.42	58.17
chr8	82934008	82934149	18.42	60.15
chr8	88773932	88774145	18.42	76.19
chr8	96007881	96008000	18.42	65.61
chr8	96780350	96780481	18.42	62.51
chr8	100988390	100988521	18.42	62.51
chr8	102598562	102598699	18.42	61.07
chr8	102640215	102640377	18.42	66.13
chr8	104490575	104490697	18.42	64.8
chr8	121861480	121861621	18.42	60.15
chr8	123934922	123935083	18.42	77.23
chr8	126701428	126701585	18.42	67.26
chr8	131337415	131337578	18.42	65.91
chr9	3144055	3144166	18.42	56.35
chr9	4950852	4950996	18.42	59.47
chr9	6447084	6447236	18.42	57.75
chr9	8282761	8282918	18.42	78.24
chr9	8784065	8784204	18.42	60.6
chr9	17559931	17560069	18.42	60.84
chr9	18306222	18306377	18.42	57.13
chr9	19285481	19285673	18.42	60.09
chr9	20686316	20686440	18.42	64.28
chr9	23083932	23084070	18.42	71.92
chr9	23952209	23952459	18.42	99.56
chr9	24075108	24075252	18.42	59.47
chr9	25968511	25968629	18.42	65.88
chr9	26016791	26016941	18.42	58.17
chr9	33200551	33200698	18.42	58.82

chr9	47306287	47306412	18.42	64.02
chr9	56123950	56124076	18.42	63.76
chr9	70313388	70313533	18.42	59.25
chr9	71813826	71813989	18.42	76.73
chr9	75771697	75771846	18.42	58.39
chr9	76584976	76585118	18.42	70.88
chr9	76978862	76979009	18.42	58.82
chr9	83993462	83993627	18.42	65.47
chr9	85797545	85797707	18.42	66.13
chr9	90756160	90756314	18.42	57.34
chr9	91159273	91159418	18.42	70.13
chr9	109313285	109313397	18.42	67.58
chr9	117998080	117998234	18.42	57.34
chr9	122618464	122618601	18.42	72.19
chrX	3115191	3115382	18.42	70.41
chrX	4213042	4213186	18.42	59.47
chrX	4411655	4411793	18.42	60.84
chrX	8096870	8097014	18.42	59.47
chrX	9983664	9983804	18.42	60.38
chrX	14066503	14066648	18.42	59.25
chrX	15874320	15874463	18.42	82.01
chrX	18512674	18512877	18.42	99.94
chrX	19899919	19900055	18.42	61.3
chrX	22908203	22908345	18.42	70.88
chrX	25222896	25223037	18.42	60.15
chrX	26941104	26941254	18.42	58.17
chrX	29017063	29017200	18.42	61.07
chrX	36688516	36688671	18.42	57.13
chrX	37537409	37537565	18.42	56.93
chrX	40258358	40258497	18.42	60.6
chrX	42072328	42072465	18.42	61.07
chrX	51922518	51922674	18.42	56.93
chrX	52472418	52472565	18.42	58.82
chrX	53374147	53374295	18.42	58.6
chrX	54796764	54796913	18.42	69.14
chrX	55585209	55585365	18.42	56.93
chrX	56896785	56896928	18.42	59.7
chrX	59194377	59194503	18.42	63.76
chrX	69389648	69389794	18.42	59.03
chrX	71222431	71222556	18.42	64.02

chrX	71864017	71864163	18.42	59.03
chrX	77100612	77100748	18.42	61.3
chrX	77869610	77869762	18.42	57.75
chrX	78211273	78211455	18.42	61.98
chrX	78400537	78400669	18.42	62.26
chrX	80218298	80218447	18.42	69.14
chrX	84471401	84471549	18.42	58.6
chrX	87954077	87954215	18.42	60.84
chrX	88296671	88296823	18.42	57.75
chrX	90337687	90337826	18.42	60.6
chrX	94784535	94784700	18.42	76.24
chrX	95421096	95421242	18.42	59.03
chrX	95428719	95428874	18.42	57.13
chrX	95557957	95558096	18.42	60.6
chrX	95696643	95696772	18.42	63
chrX	99981739	99981894	18.42	67.72
chrX	105266490	105266631	18.42	60.15
chrX	110313719	110313863	18.42	59.47
chrX	116014037	116014173	18.42	61.3
chrX	118870716	118870839	18.42	64.54
chrX	122277117	122277269	18.42	68.42
chrX	123665135	123665291	18.42	78.5
chrX	130410523	130410681	18.42	67.03
chrX	130947206	130947352	18.42	59.03
chrX	133117276	133117422	18.42	59.03
chrX	133304686	133304847	18.42	55.93
chrX	134223901	134224061	18.42	66.58
chrX	135205304	135205452	18.42	58.6
chrX	139577797	139577947	18.42	58.17
chrX	140125083	140125216	18.42	62.02
chrX	140973434	140973569	18.42	61.54
chrX	143134912	143135042	18.42	62.75
chrX	146949150	146949355	18.42	77.86
chrX	156738878	156739045	18.42	65.04
chrX	163265753	163265898	18.42	59.25
chrX	163425764	163425908	18.42	59.47
chr13	30462944	30463101	18.41	67.23
chr16	92572747	92572904	18.41	78.21
chr1	15487619	15487765	18.35	63.2
chr10	32688939	32689110	18.35	67.43

chr10	56743568	56743683	18.35	60.71
chr11	9644984	9645205	18.35	76.1
chr11	42593163	42593303	18.35	64.69
chr13	23132994	23133137	18.35	53.8
chr18	74421011	74421165	18.35	51.49
chr3	11125292	11125439	18.35	52.94
chr3	33680986	33681150	18.35	59.08
chr3	88437738	88437882	18.35	53.59
chr4	146072534	146072659	18.35	68.76
chr7	77338495	77338638	18.35	53.8
chr9	24377099	24377236	18.35	55.15
chr9	77820631	77820759	18.35	67.91
chr9	80849759	80849988	18.35	65.11
chr16	93702364	93702498	18.32	72.79
chrX	144867477	144867663	18.32	58.12
chr10	51466170	51466326	18.29	56.7
chr11	16562383	16562513	18.29	56.7
chr15	44839824	44839980	18.29	56.7
chr16	5562919	5563075	18.29	56.7
chr2	106974695	106974851	18.29	56.7
chr5	86794120	86794276	18.29	56.7
chr8	44747450	44747606	18.29	67.23
chr2	52555869	52555992	18.24	74.13
chr3	22629474	22629625	18.24	66.02
chr1	78237751	78237906	18.18	56.7
chr17	70223379	70223534	18.18	67.23
chr19	36435308	36435463	18.18	67.23
chr8	8315566	8315721	18.18	56.7
chr14	112734997	112735126	18.15	67.23
chr8	69562916	69563130	18.07	67.31
chr14	23944203	23944357	18.06	56.7
chr16	66431189	66431343	18.06	56.7
chr6	62136515	62136643	18.01	67.23
chrX	42736515	42736643	18.01	56.7
chr12	33591082	33591235	17.94	67.23
chr6	21100236	21100406	17.94	57.03
chr1	34975277	34975422	17.85	66.77
chr15	40327562	40327707	17.85	57.03
chr2	114983015	114983167	17.82	56.7
chr5	53426567	53426719	17.82	56.7

chr6	65170573	65170725	17.82	56.7
chr17	52138526	52138652	17.73	107.5
chr1	47141835	47141986	17.71	56.7
chr1	164268940	164269091	17.71	78.21
chr11	22436579	22436730	17.71	56.7
chr4	17709515	17709666	17.71	56.7
chr4	114837302	114837453	17.71	56.7
chr1	90228040	90228323	17.7	126.7
chr8	67964277	67964444	17.62	57.03
chr1	13545592	13545719	17.59	56.2
chr1	26326880	26327038	17.59	58.9
chr1	74705320	74705468	17.59	57.13
chr10	51606854	51606997	17.59	58.22
chr10	52220892	52221059	17.59	63.39
chr10	68526278	68526434	17.59	65.82
chr10	82931856	82932001	17.59	57.78
chr10	103634301	103634451	17.59	56.7
chr12	6616009	6616172	17.59	64.25
chr12	11515214	11515360	17.59	57.56
chr13	18024592	18024743	17.59	56.49
chr13	31329214	31329357	17.59	58.22
chr13	49221043	49221196	17.59	66.52
chr13	67749263	67749399	17.59	59.82
chr13	95507700	95507850	17.59	60.73
chr13	101432409	101432597	17.59	90.4
chr14	42858062	42858254	17.59	58.46
chr14	46832276	46832432	17.59	55.46
chr14	74078524	74078670	17.59	57.56
chr14	87787047	87787203	17.59	65.82
chr15	21800331	21800483	17.59	56.28
chr15	26103280	26103499	17.59	74.54
chr15	39923949	39924101	17.59	66.76
chr15	44813709	44813853	17.59	58
chr15	62519607	62519751	17.59	68.7
chr16	21940219	21940349	17.59	61.26
chr16	36326489	36326639	17.59	56.7
chr16	48545402	48545533	17.59	61.02
chr16	51325493	51325648	17.59	66.05
chr16	97424515	97424658	17.59	58.22
chr17	14898702	14898856	17.59	55.87

chr18	17147855	17147983	17.59	61.76
chr18	21699385	21699540	17.59	55.67
chr18	50663848	50663973	17.59	67.23
chr18	52553903	52554038	17.59	71.04
chr2	71615806	71615956	17.59	56.7
chr2	80924351	80924501	17.59	56.7
chr2	87612392	87612559	17.59	63.39
chr2	114307162	114307343	17.59	60.53
chr2	122469739	122469889	17.59	67.23
chr2	138219154	138219304	17.59	56.7
chr2	160462852	160463002	17.59	67.23
chr3	9735112	9735257	17.59	57.78
chr3	14467147	14467315	17.59	73.67
chr3	24302945	24303081	17.59	59.82
chr3	113109411	113109561	17.59	56.7
chr3	126730247	126730380	17.59	71.58
chr4	3970307	3970446	17.59	59.12
chr4	28345995	28346143	17.59	57.13
chr4	53960194	53960321	17.59	62.01
chr4	60900151	60900292	17.59	58.67
chr4	61156526	61156655	17.59	61.51
chr4	69035329	69035482	17.59	66.52
chr4	69370324	69370474	17.59	67.23
chr4	90646930	90647096	17.59	63.6
chr4	116867202	116867343	17.59	58.67
chr5	58713538	58713657	17.59	64.11
chr5	96720168	96720307	17.59	81.29
chr5	122834311	122834461	17.59	67.23
chr5	152271088	152271221	17.59	60.53
chr6	33220860	33220992	17.59	60.78
chr6	117480367	117480541	17.59	61.93
chr7	23898963	23899107	17.59	58
chr8	22401499	22401662	17.59	64.25
chr8	39816826	39817026	17.59	59.69
chr8	45511860	45511989	17.59	61.51
chr8	52084464	52084608	17.59	58
chr8	83714342	83714464	17.59	74.72
chr9	17211911	17212058	17.59	57.34
chr9	18140966	18141149	17.59	60.14
chr9	22523516	22523652	17.59	59.82

chr9	30451380	30451506	17.59	62.27
chr9	32966071	32966215	17.59	58
chr9	93220003	93220160	17.59	59.12
chr9	94208864	94208986	17.59	63.31
chr9	119777512	119777640	17.59	72.97
chrX	86138017	86138181	17.59	74.63
chrX	89370496	89370646	17.59	56.7
chrX	114323749	114323889	17.59	69.72
chrX	116621989	116622126	17.59	74.53
chr4	73493584	73493745	17.5	75.17
chr15	35944980	35945122	17.48	57.03
chr1	114298993	114299142	17.47	56.7
chr1	157666146	157666295	17.47	56.7
chr1	169196936	169197085	17.47	56.7
chr10	50143048	50143197	17.47	56.7
chr11	40799203	40799352	17.47	56.7
chr12	119375662	119375811	17.47	56.7
chr14	52786811	52786960	17.47	56.7
chr16	57589368	57589517	17.47	56.7
chrX	32115713	32115859	17.46	86.05
chr17	14152162	14152286	17.45	56.7
chr4	129635216	129635340	17.45	56.7
chr11	60396987	60397159	17.44	55.64
chr7	20946293	20946458	17.41	57.03
chr6	114552335	114552456	17.37	67.95
chr11	73283210	73283351	17.36	57.03
chr1	10970716	10970864	17.35	56.7
chr3	26395318	26395466	17.35	56.7
chr4	84681940	84682088	17.35	56.7
chr13	114069375	114069556	17.33	60.01
chr9	70506224	70506435	17.32	51.25
chr8	126122845	126123028	17.28	65.52
chr6	56190525	56190634	17.25	76.91
chr2	146315013	146315160	17.24	56.7
chr7	142141711	142141858	17.24	67.23
chr4	145887525	145887695	17.16	74.98
chr5	95660820	95660972	17.16	55.5
chr7	120841691	120841900	17.16	51.25
chr1	152190229	152190403	17.14	58.12
chr4	24121235	24121381	17.12	56.7
chr6	61404344	61404490	17.12	56.7
chr13	74667304	74667680	17.1	210.19
chr12	78986024	78986145	17.03	67.23
chr15	40269432	40269553	17.03	56.7
chr6	110646719	110646840	17.03	67.23
chr4	107823238	107823478	16.99	87.1
chr15	58271773	58272024	16.98	133.82
chr8	19853401	19853573	16.94	67.31
chr8	30627832	30627981	16.91	55.67
chr14	34482345	34482534	16.89	60.29
chr19	58021724	58021844	16.89	56.7
chr5	7529094	7529238	16.89	56.7
chr5	95008241	95008475	16.89	88.36
chr8	13275334	13275478	16.89	56.7
chrX	64627524	64627697	16.89	63.71
chr1	146657688	146657831	16.77	56.7
chr18	44211807	44211950	16.77	56.7
chr2	51855310	51855453	16.77	67.23
chr2	138785478	138785621	16.77	56.7
chr8	67681234	67681377	16.77	56.7
chr1	128566013	128566178	16.75	72.44
chr10	20931481	20931633	16.75	54.74
chr10	111493372	111493520	16.75	65.96
chr10	128581313	128581490	16.75	59.6
chr11	14291426	14291588	16.75	62.73
chr11	22482416	22482551	16.75	58.5
chr11	98475569	98475751	16.75	58.62
chr12	28090112	28090268	16.75	53.93
chr12	40265641	40265795	16.75	54.33
chr12	66134111	66134271	16.75	63.18
chr12	101698842	101698967	16.75	60.96
chr13	11347610	11347760	16.75	55.16
chr14	3069447	3069587	16.75	67.96
chr14	7139438	7139607	16.75	71.49
chr14	27653439	27653554	16.75	63.64
chr14	65900090	65900238	16.75	55.59
chr14	106345979	106346137	16.75	74.17
chr15	50459974	50460136	16.75	62.73
chr15	62352026	62352194	16.75	71.72
chr15	69221136	69221256	16.75	62.27

chr17	48314956	48315106	16.75	55.16
chr2	12185735	12185886	16.75	54.95
chr3	22865933	22866082	16.75	55.37
chr3	140726853	140726995	16.75	67.45
chr4	11369186	11369402	16.75	81.45
chr4	52142346	52142498	16.75	54.74
chr5	95280155	95280307	16.75	54.74
chr6	62939290	62939445	16.75	54.13
chr6	130588578	130588706	16.75	60.2
chr7	19072373	19072509	16.75	58.26
chr7	27871462	27871606	16.75	56.45
chr7	49426556	49426708	16.75	54.74
chr7	57558707	57558880	16.75	60.41
chr8	52083236	52083407	16.75	60.82
chrX	118669555	118669705	16.75	65.48
chrX	121616298	121616453	16.75	54.13
chr10	121150203	121150322	16.74	56.7
chr8	37367674	37367872	16.72	58.12
chr4	150897982	150898551	16.68	195.31
chr11	20828799	20828941	16.65	67.23
chr7	92868168	92868365	16.63	58.12
chr1	149928854	149929061	16.62	63.45
chr17	82400274	82400392	16.6	56.7
chr2	44227431	44227549	16.6	56.7
chr7	71619661	71619850	16.6	65.45
chr10	54164689	54164830	16.53	56.7
chr13	119379602	119379743	16.53	56.7
chr16	21107595	21107736	16.53	56.7
chrX	120674719	120674860	16.53	56.7
chrX	122985728	122985869	16.53	56.7
chr12	8584165	8584321	16.46	66.77
chr3	80343193	80343333	16.42	56.7
chr2	123580529	123580715	16.36	76.91
chr3	74397817	74397972	16.36	57.03
chr5	116260405	116260591	16.36	66.77
chr6	7235982	7236137	16.36	66.77
chr14	112734163	112734302	16.3	56.7
chr2	40644707	40644892	16.27	66.77
chr4	112246463	112246648	16.27	66.77
chr1	58875111	58875265	16.25	57.03
chr10	16156209	16156341	16.25	57.03
chrX	113155610	113155764	16.25	66.77
chr3	109914654	109914772	16.24	55.99
chr5	89942330	89942459	16.24	63.24
chr7	70949585	70949718	16.24	62.15
chr15	4365348	4365486	16.18	56.7
chr17	13435224	13435383	16.11	55.61
chr17	88151239	88151422	16.09	76.91
chr5	100565275	100565471	16.09	51.25
chr9	123194180	123194363	16.09	57.03
chr16	23142146	23142283	16.06	56.7
chr4	60543456	60543601	16.06	54.91
chr7	104495524	104495638	16.04	56.7
chr14	19383057	19383122	16.01	97.28
chr1	29465246	29465409	15.99	71.08
chr1	70014806	70014968	15.99	61.08
chr1	96290069	96290204	15.99	57.02
chr1	99071002	99071174	15.99	58.97
chr1	151303168	151303328	15.99	71.81
chr11	82864804	82864961	15.99	62.2
chr11	98479214	98479408	15.99	64.23
chr12	59766190	59766330	15.99	66.29
chr13	21859303	21859506	15.99	62.47
chr13	23133631	23133972	15.99	152.06
chr13	47837274	47837437	15.99	60.87
chr13	65080322	65080530	15.99	71.1
chr14	15171087	15171233	15.99	54.55
chr16	13137567	13137725	15.99	72.31
chr16	70543918	70544069	15.99	53.49
chr16	88027116	88027274	15.99	61.97
chr17	76918748	76918891	15.99	55.2
chr18	72736575	72736713	15.99	56.33
chr19	3037478	3037618	15.99	55.87
chr2	24054001	24054156	15.99	52.67
chr2	87959043	87959213	15.99	59.38
chr3	98338344	98338495	15.99	63.58
chr3	155924304	155924459	15.99	52.67
chr4	20868259	20868386	15.99	58.96
chr4	42406327	42406454	15.99	58.96
chr4	56054766	56054912	15.99	54.55

chr4	155298231	155298417	15.99	56.23
chr5	30552151	30552321	15.99	59.38
chr5	71647192	71647353	15.99	71.57
chr5	82626309	82626433	15.99	59.73
chr5	83451313	83451460	15.99	54.33
chr5	107349833	107349989	15.99	52.47
chr6	44061510	44061648	15.99	56.33
chr6	64108128	64108269	15.99	76.86
chr8	16045798	16045961	15.99	60.87
chr8	67037610	67037766	15.99	52.47
chr9	38124389	38124545	15.99	52.47
chr9	88841405	88841565	15.99	61.52
chr9	92544188	92544344	15.99	52.47
chrX	89375358	89375508	15.99	63.82
chrX	124759299	124759455	15.99	52.47
chr19	40583029	40583256	15.97	78.69
chr5	100564417	100564553	15.95	56.7
chr19	24989670	24989871	15.92	53.39
chr15	34109823	34109936	15.9	56.7
chr17	84861249	84861460	15.89	82.32
chr5	106280845	106281101	15.89	72.07
chr8	124346866	124346974	15.87	58.08
chr17	35511091	35511252	15.86	76.87
chr14	17871650	17871785	15.83	56.7
chr2	57072385	57072565	15.83	57.03
chr4	19687154	19687289	15.83	56.7
chr7	130840469	130840604	15.83	56.7
chr8	77011050	77011185	15.83	67.23
chr1	87371065	87371238	15.77	68.19
chr1	11534926	11535054	15.76	57.03
chrX	121017753	121017859	15.75	74.17
chr19	24991283	24991462	15.74	66.77
chr3	3430891	3431070	15.74	57.03
chr6	64876943	64877077	15.71	67.23
chr5	148422964	148423187	15.69	76.87
chr19	24989987	24990296	15.63	95.2
chr2	129347015	129347140	15.63	53
chr4	123400651	123400822	15.63	52.06
chr14	67394605	67394753	15.62	57.03
chr6	9554063	9554196	15.6	56.7

chr7	14347161	14347294	15.6	56.7
chr8	98039371	98039466	15.6	53.25
chr9	83452763	83452935	15.56	61.46
chr11	86517932	86518079	15.51	57.03
chr7	90936719	90936851	15.48	56.7
chr9	36479901	36480033	15.48	56.7
chrX	5288880	5289026	15.41	66.77
chr3	50906269	50906390	15.39	58.16
chr19	24988468	24988599	15.36	56.7
chr3	66713139	66713270	15.36	56.7
chr7	62552071	62552202	15.36	56.7
chr1	59403271	59403419	15.29	52.73
chr1	150310444	150310589	15.29	53.37
chr10	101926056	101926196	15.29	54.47
chr11	66287457	66287598	15.29	64.44
chr12	115877624	115877818	15.29	62.5
chr13	14476549	14476684	15.29	55.62
chr13	45107308	45107463	15.29	61.07
chr13	98855110	98855254	15.29	53.59
chr15	46394634	46394779	15.29	53.37
chr15	102431060	102431200	15.29	64.69
chr16	28500814	28500955	15.29	54.25
chr16	63442307	63442453	15.29	63.2
chr17	33186069	33186221	15.29	61.77
chr18	42034078	42034252	15.29	57.01
chr2	5608239	5608388	15.29	52.52
chr4	23215909	23216088	15.29	65.64
chr5	8658433	8658553	15.29	59.35
chr5	84019314	84019498	15.29	64.56
chr5	116252015	116252180	15.29	58.87
chr7	9101327	9101463	15.29	55.38
chr8	11781564	11781719	15.29	51.29
chr8	41501628	41501773	15.29	53.37
chr8	51686780	51686932	15.29	51.9
chr8	59300432	59300604	15.29	67.2
chr8	87703408	87703547	15.29	54.7
chr8	107305642	107305813	15.29	57.62
chrX	36514615	36514761	15.29	53.15
chrX	121109192	121109333	15.29	54.25
chr17	46151187	46151317	15.24	56.7

chr9	78676916	78677089	15.21	57.03
chr4	13358329	13358437	15.2	56.7
chr10	3776789	3776918	15.13	56.7
chr10	108334680	108334809	15.13	56.7
chr9	14492213	14492385	15.13	57.03
chrX	4759741	4759815	15.11	83.33
chr2	165754428	165754552	15.08	52.11
chr8	126102325	126102463	15.08	58.24
chr1	127219204	127219375	15.04	57.03
chr12	66133537	66133708	15.04	57.03
chr9	94725530	94725701	15.04	66.77
chrX	58179127	58179269	14.99	68.43
chr6	114573827	114573977	14.97	51.64
chr5	63263280	63263450	14.95	57.03
chr14	44705928	44706110	14.94	68.43
chr16	39052769	39052962	14.94	60.23
chr3	155950535	155950747	14.92	67.31
chr6	146663058	146663270	14.92	59.66
chr8	71959907	71960046	14.92	61.44
chr18	77994777	77994904	14.89	56.7
chr2	58086805	58086946	14.88	66.77
chr6	114509651	114509819	14.84	57.19
chr12	76343548	76343701	14.8	71.65
chr14	37355681	37355807	14.77	56.7
chr4	15167433	15167538	14.77	56.4
chr1	10884432	10884566	14.74	61.78
chr1	23978359	23978513	14.74	67.95
chr1	26647313	26647460	14.74	58.82
chr1	31402725	31402882	14.74	67.26
chr1	37662079	37662234	14.74	57.13
chr1	48771900	48772039	14.74	60.6
chr1	52012535	52012686	14.74	57.96
chr1	64846186	64846324	14.74	60.84
chr1	65013457	65013613	14.74	56.93
chr1	67588346	67588491	14.74	59.25
chr1	74706591	74706745	14.74	57.34
chr1	83511859	83511992	14.74	62.02
chr1	89360638	89360798	14.74	66.58
chr1	92631350	92631500	14.74	58.17
chr1	96126244	96126389	14.74	59.25

chr1	102895665	102895848	14.74	72.11
chr1	105102407	105102539	14.74	62.26
chr1	108010294	108010449	14.74	57.13
chr1	110305596	110305746	14.74	58.17
chr1	119601787	119601941	14.74	57.34
chr1	128836068	128836233	14.74	65.47
chr1	136234702	136234852	14.74	58.17
chr1	144483342	144483489	14.74	58.82
chr1	146309792	146309940	14.74	58.6
chr1	156303430	156303561	14.74	62.51
chr1	156954766	156954922	14.74	56.93
chr1	167460404	167460543	14.74	60.6
chr1	168670098	168670234	14.74	61.3
chr1	177900217	177900360	14.74	59.7
chr1	183425941	183426087	14.74	59.03
chr1	195911569	195911721	14.74	57.75
chr1	196887050	196887194	14.74	59.47
chr10	22475132	22475279	14.74	58.82
chr10	24568213	24568372	14.74	66.8
chr10	25138738	25138888	14.74	58.17
chr10	33559339	33559483	14.74	59.47
chr10	35587900	35588055	14.74	57.13
chr10	36542071	36542227	14.74	56.93
chr10	41423678	41423829	14.74	57.96
chr10	46791491	46791649	14.74	67.03
chr10	52302879	52303030	14.74	57.96
chr10	56446781	56446937	14.74	56.93
chr10	71473214	71473370	14.74	56.93
chr10	71598701	71598857	14.74	56.93
chr10	82034944	82035096	14.74	57.75
chr10	86594976	86595132	14.74	56.93
chr10	111210365	111210521	14.74	56.93
chr10	113220073	113220224	14.74	57.96
chr10	116048249	116048387	14.74	60.84
chr10	121146593	121146721	14.74	63.25
chr10	129025967	129026115	14.74	58.6
chr11	4472885	4473031	14.74	59.03
chr11	12467558	12467702	14.74	59.47
chr11	15844843	15845012	14.74	64.62
chr11	21811471	21811610	14.74	60.6

chr11	32479772	32480001	14.74	115.55
chr11	39019273	39019409	14.74	61.3
chr11	40770843	40770992	14.74	58.39
chr11	47661769	47661920	14.74	57.96
chr11	51251359	51251513	14.74	57.34
chr11	56405067	56405225	14.74	67.03
chr11	57160606	57160761	14.74	57.13
chr11	64188682	64188822	14.74	60.38
chr11	66678970	66679115	14.74	59.25
chr11	104185844	104185976	14.74	62.26
chr11	113774233	113774401	14.74	64.83
chr12	3003009	3003163	14.74	57.34
chr12	6524987	6525146	14.74	66.8
chr12	13430438	13430586	14.74	58.6
chr12	16630340	16630468	14.74	63.25
chr12	19636850	19637014	14.74	65.69
chr12	21643970	21644125	14.74	57.13
chr12	21646592	21646747	14.74	57.13
chr12	21791709	21791843	14.74	61.78
chr12	43418368	43418524	14.74	56.93
chr12	43543214	43543343	14.74	63
chr12	44605217	44605369	14.74	57.75
chr12	44691815	44691985	14.74	64.41
chr12	44991832	44991997	14.74	65.47
chr12	45359213	45359369	14.74	56.93
chr12	48382818	48382974	14.74	56.93
chr12	60530697	60530843	14.74	69.88
chr12	68366065	68366202	14.74	61.07
chr12	70160789	70160930	14.74	60.15
chr12	92519435	92519582	14.74	58.82
chr12	93985026	93985175	14.74	58.39
chr12	95331349	95331494	14.74	59.25
chr12	119626185	119626330	14.74	59.25
chr13	6437240	6437395	14.74	57.13
chr13	11358144	11358300	14.74	56.93
chr13	20623125	20623262	14.74	61.07
chr13	27355485	27355619	14.74	61.78
chr13	39598358	39598504	14.74	59.03
chr13	61049774	61049921	14.74	58.82
chr13	63263732	63263881	14.74	58.39
chr13	64748305	64748460	14.74	57.13
chr13	70599493	70599643	14.74	58.17
chr13	76073022	76073158	14.74	61.3
chr13	81859321	81859487	14.74	65.26
chr13	82323475	82323624	14.74	58.39
chr13	86308953	86309114	14.74	55.93
chr13	107421546	107421697	14.74	68.66
chr13	110881615	110881766	14.74	57.96
chr13	112484490	112484633	14.74	59.7
chr13	116758167	116758316	14.74	58.39
chr14	3465363	3465519	14.74	56.93
chr14	3793583	3793732	14.74	58.39
chr14	7251606	7251760	14.74	67.95
chr14	15475086	15475227	14.74	60.15
chr14	36308392	36308531	14.74	60.6
chr14	38987152	38987306	14.74	57.34
chr14	43787110	43787283	14.74	63.78
chr14	59210779	59210933	14.74	57.34
chr14	69092171	69092326	14.74	57.13
chr14	73373481	73373633	14.74	57.75
chr14	75839820	75839976	14.74	56.93
chr14	79400751	79400915	14.74	65.69
chr14	88317459	88317613	14.74	57.34
chr14	89690532	89690686	14.74	67.95
chr14	95549920	95550071	14.74	57.96
chr14	104420096	104420252	14.74	56.93
chr14	110804916	110805059	14.74	59.7
chr14	111780902	111781057	14.74	57.13
chr14	113027467	113027630	14.74	65.91
chr14	113684781	113684928	14.74	58.82
chr14	125180570	125180748	14.74	62.77
chr15	14039328	14039468	14.74	60.38
chr15	32763548	32763704	14.74	56.93
chr15	35518860	35519019	14.74	66.8
chr15	50269917	50270068	14.74	57.96
chr15	65549363	65549511	14.74	58.6
chr15	89490327	89490472	14.74	59.25
chr15	90473467	90473619	14.74	57.75
chr16	3765508	3765670	14.74	66.13
chr16	11978150	11978280	14.74	62.75

chr16	14688009	14688166	14.74	67.26
chr16	40614326	40614477	14.74	57.96
chr16	40666302	40666456	14.74	57.34
chr16	47137688	47137832	14.74	59.47
chr16	58654351	58654499	14.74	58.6
chr16	69393540	69393687	14.74	58.82
chr16	75953467	75953616	14.74	58.39
chr16	86952042	86952209	14.74	65.04
chr16	86976912	86977066	14.74	57.34
chr16	87888508	87888660	14.74	57.75
chr17	21477837	21477991	14.74	67.95
chr17	22316787	22316932	14.74	59.25
chr17	30220631	30220781	14.74	58.17
chr17	36150450	36150577	14.74	63.51
chr17	39033786	39033938	14.74	57.75
chr17	54267087	54267234	14.74	58.82
chr17	54669145	54669293	14.74	58.6
chr17	57528941	57529091	14.74	58.17
chr17	58685002	58685145	14.74	59.7
chr17	58987205	58987345	14.74	60.38
chr17	64567734	64567885	14.74	57.96
chr17	69036905	69037054	14.74	58.39
chr17	70099403	70099557	14.74	67.95
chr17	75158875	75159024	14.74	58.39
chr17	80041068	80041222	14.74	57.34
chr17	82117112	82117268	14.74	56.93
chr18	5850345	5850495	14.74	58.17
chr18	6373209	6373384	14.74	63.37
chr18	9684476	9684628	14.74	57.75
chr18	11187825	11187970	14.74	59.25
chr18	17819988	17820155	14.74	65.04
chr18	23127749	23127899	14.74	58.17
chr18	27157913	27158062	14.74	58.39
chr18	28788268	28788424	14.74	56.93
chr18	29178186	29178338	14.74	57.75
chr18	33406197	33406344	14.74	58.82
chr18	37524781	37524946	14.74	76.24
chr18	39915070	39915235	14.74	65.47
chr18	45669828	45669967	14.74	60.6
chr18	48871419	48871577	14.74	67.03

chr18	50698417	50698568	14.74	57.96
chr18	59152875	59153031	14.74	56.93
chr18	60611077	60611240	14.74	65.91
chr18	70354108	70354275	14.74	65.04
chr18	74773394	74773598	14.74	67.81
chr18	88470174	88470318	14.74	59.47
chr18	90084485	90084629	14.74	59.47
chr19	4471504	4471648	14.74	59.47
chr19	20032801	20032921	14.74	65.34
chr19	26031298	26031434	14.74	61.3
chr19	32952438	32952578	14.74	60.38
chr19	34431566	34431709	14.74	59.7
chr19	39459802	39459957	14.74	57.13
chr2	11738411	11738560	14.74	58.39
chr2	18401499	18401655	14.74	56.93
chr2	19050740	19050874	14.74	61.78
chr2	25016789	25016941	14.74	57.75
chr2	28179945	28180085	14.74	60.38
chr2	36820152	36820290	14.74	60.84
chr2	37106242	37106399	14.74	67.26
chr2	47929680	47929818	14.74	60.84
chr2	53314027	53314181	14.74	57.34
chr2	54022001	54022161	14.74	66.58
chr2	54741023	54741190	14.74	65.04
chr2	64157142	64157308	14.74	65.26
chr2	69912632	69912786	14.74	57.34
chr2	77442344	77442490	14.74	59.03
chr2	80663383	80663522	14.74	60.6
chr2	88083732	88083886	14.74	57.34
chr2	88272628	88272765	14.74	61.07
chr2	94446658	94446829	14.74	64.2
chr2	97601281	97601456	14.74	73.89
chr2	99390534	99390681	14.74	58.82
chr2	120463404	120463560	14.74	56.93
chr2	123347546	123347690	14.74	59.47
chr2	124874819	124874967	14.74	58.6
chr2	138892289	138892424	14.74	61.54
chr2	147744921	147745065	14.74	59.47
chr2	150891507	150891648	14.74	60.15
chr2	151162255	151162425	14.74	64.41

chr2	163434701	163434848	14.74	58.82
chr2	167576730	167576884	14.74	57.34
chr2	176827992	176828144	14.74	57.75
chr3	5436228	5436384	14.74	56.93
chr3	5650965	5651119	14.74	57.34
chr3	6946180	6946324	14.74	59.47
chr3	12003217	12003363	14.74	59.03
chr3	16133952	16134108	14.74	56.93
chr3	18449781	18449931	14.74	58.17
chr3	21091016	21091167	14.74	57.96
chr3	22651802	22651942	14.74	60.38
chr3	23210505	23210690	14.74	71.67
chr3	39060999	39061150	14.74	57.96
chr3	39083823	39083978	14.74	57.13
chr3	41923615	41923764	14.74	58.39
chr3	48477686	48477848	14.74	66.13
chr3	53644251	53644406	14.74	57.13
chr3	56871013	56871153	14.74	60.38
chr3	59220420	59220569	14.74	58.39
chr3	60981298	60981453	14.74	57.13
chr3	61779965	61780114	14.74	58.39
chr3	64378427	64378566	14.74	60.6
chr3	68530959	68531093	14.74	61.78
chr3	68541919	68542074	14.74	67.72
chr3	72079911	72080067	14.74	56.93
chr3	72829965	72830117	14.74	68.42
chr3	75895679	75895835	14.74	56.93
chr3	81104419	81104569	14.74	58.17
chr3	83946876	83947025	14.74	58.39
chr3	86748988	86749129	14.74	60.15
chr3	90900423	90900563	14.74	60.38
chr3	90900882	90901029	14.74	58.82
chr3	92975928	92976083	14.74	57.13
chr3	93799651	93799798	14.74	58.82
chr3	94358247	94358409	14.74	66.13
chr3	96920553	96920674	14.74	76.72
chr3	105144482	105144626	14.74	59.47
chr3	108741315	108741470	14.74	67.72
chr3	111324730	111324886	14.74	56.93
chr3	112087052	112087197	14.74	59.25

chr3	114569261	114569406	14.74	59.25
chr3	128396391	128396542	14.74	57.96
chr3	134821440	134821579	14.74	60.6
chr3	135783335	135783496	14.74	55.93
chr3	140817235	140817390	14.74	57.13
chr3	144406343	144406494	14.74	57.96
chr3	148415374	148415524	14.74	58.17
chr4	10794754	10794905	14.74	57.96
chr4	11324444	11324589	14.74	59.25
chr4	16361948	16362103	14.74	57.13
chr4	16362166	16362317	14.74	57.96
chr4	28549176	28549330	14.74	57.34
chr4	31980465	31980621	14.74	56.93
chr4	35565847	35565997	14.74	58.17
chr4	38457960	38458112	14.74	57.75
chr4	40005343	40005489	14.74	59.03
chr4	44153946	44154100	14.74	57.34
chr4	53829531	53829672	14.74	60.15
chr4	60628819	60628964	14.74	59.25
chr4	62238370	62238525	14.74	57.13
chr4	62592413	62592549	14.74	61.3
chr4	65741218	65741367	14.74	58.39
chr4	79210883	79211032	14.74	58.39
chr4	81651595	81651740	14.74	59.25
chr4	81752306	81752487	14.74	62.17
chr4	109305562	109305734	14.74	63.99
chr4	112128594	112128750	14.74	56.93
chr4	124617941	124618096	14.74	57.13
chr4	134504585	134504724	14.74	60.6
chr5	6151981	6152117	14.74	61.3
chr5	12518402	12518557	14.74	57.13
chr5	19870192	19870346	14.74	57.34
chr5	20578075	20578218	14.74	59.7
chr5	21711921	21712075	14.74	57.34
chr5	26732938	26733084	14.74	59.03
chr5	45800159	45800348	14.74	70.83
chr5	46854374	46854552	14.74	73.21
chr5	54020361	54020508	14.74	58.82
chr5	56045727	56045872	14.74	59.25
chr5	58040219	58040401	14.74	61.98

chr5	59985567	59985700	14.74	62.02
chr5	60040616	60040770	14.74	57.34
chr5	72510015	72510162	14.74	58.82
chr5	83451795	83451945	14.74	58.17
chr5	94579585	94579725	14.74	71.4
chr5	98180418	98180573	14.74	57.13
chr5	133484931	133485082	14.74	57.96
chr5	146096539	146096694	14.74	67.72
chr5	146264362	146264502	14.74	60.38
chr6	9093255	9093411	14.74	56.93
chr6	9470130	9470262	14.74	62.26
chr6	10219726	10219882	14.74	56.93
chr6	13915820	13915967	14.74	58.82
chr6	23465145	23465272	14.74	63.51
chr6	25478243	25478398	14.74	57.13
chr6	25569439	25569568	14.74	63
chr6	35383655	35383811	14.74	56.93
chr6	40367070	40367217	14.74	58.82
chr6	41193892	41194046	14.74	57.34
chr6	42078107	42078263	14.74	56.93
chr6	45632777	45632918	14.74	60.15
chr6	46095021	46095178	14.74	67.26
chr6	60450102	60450256	14.74	57.34
chr6	64877453	64877617	14.74	76.49
chr6	67458471	67458612	14.74	60.15
chr6	71909387	71909541	14.74	57.34
chr6	74652415	74652556	14.74	60.15
chr6	81044385	81044551	14.74	65.26
chr6	82115838	82115983	14.74	59.25
chr6	89477686	89477870	14.74	71.89
chr6	95361142	95361280	14.74	60.84
chr6	97322633	97322782	14.74	58.39
chr6	105617442	105617589	14.74	58.82
chr6	106353398	106353541	14.74	59.7
chr6	108967374	108967522	14.74	58.6
chr6	110966824	110966967	14.74	59.7
chr6	114714041	114714188	14.74	69.63
chr6	120751361	120751535	14.74	63.58
chr6	123023110	123023260	14.74	58.17
chr6	128725837	128725973	14.74	61.3

chr6	131214531	131214679	14.74	58.6
chr6	132790915	132791059	14.74	59.47
chr6	133212107	133212240	14.74	62.02
chr6	147969273	147969418	14.74	59.25
chr7	3720530	3720659	14.74	63
chr7	3785665	3785815	14.74	68.9
chr7	9396464	9396619	14.74	57.13
chr7	9681856	9682011	14.74	57.13
chr7	20257407	20257556	14.74	58.39
chr7	22263477	22263625	14.74	58.6
chr7	62196578	62196732	14.74	57.34
chr7	63333357	63333490	14.74	62.02
chr7	66139282	66139427	14.74	59.25
chr7	66460355	66460506	14.74	57.96
chr7	66464168	66464331	14.74	65.91
chr7	66759773	66759916	14.74	59.7
chr7	67054725	67054876	14.74	57.96
chr7	70540944	70541082	14.74	60.84
chr7	104318378	104318517	14.74	60.6
chr7	109775188	109775320	14.74	62.26
chr7	115371940	115372078	14.74	60.84
chr7	115690200	115690355	14.74	57.13
chr7	122915068	122915212	14.74	59.47
chr7	138635252	138635408	14.74	56.93
chr7	145211716	145211854	14.74	60.84
chr7	146587608	146587749	14.74	60.15
chr8	7261654	7261810	14.74	56.93
chr8	9691814	9691963	14.74	58.39
chr8	13710889	13711051	14.74	66.13
chr8	15095284	15095429	14.74	59.25
chr8	17191719	17191875	14.74	56.93
chr8	24985267	24985386	14.74	65.61
chr8	26986495	26986643	14.74	58.6
chr8	38129408	38129556	14.74	58.6
chr8	41955162	41955339	14.74	62.97
chr8	43287601	43287730	14.74	63
chr8	43445166	43445321	14.74	57.13
chr8	43666863	43666990	14.74	63.51
chr8	51148230	51148369	14.74	60.6
chr8	51685581	51685735	14.74	57.34

chr8	53681167	53681315	14.74	58.6
chr8	53925026	53925167	14.74	60.15
chr8	59662491	59662632	14.74	60.15
chr8	66726139	66726302	14.74	76.73
chr8	72168866	72169030	14.74	65.69
chr8	84439246	84439382	14.74	61.3
chr8	88312033	88312176	14.74	59.7
chr8	89208175	89208331	14.74	56.93
chr8	93165212	93165347	14.74	61.54
chr8	98861229	98861386	14.74	67.26
chr8	101599503	101599666	14.74	65.91
chr8	111851679	111851833	14.74	57.34
chr8	112325558	112325696	14.74	60.84
chr8	116128503	116128651	14.74	58.6
chr8	120735225	120735376	14.74	57.96
chr8	127370677	127370829	14.74	57.75
chr9	7609981	7610136	14.74	67.72
chr9	20424087	20424241	14.74	57.34
chr9	38282508	38282645	14.74	61.07
chr9	42175445	42175596	14.74	57.96
chr9	44026331	44026478	14.74	58.82
chr9	67825571	67825731	14.74	66.58
chr9	68070296	68070434	14.74	60.84
chr9	82595539	82595675	14.74	61.3
chr9	83887419	83887595	14.74	63.17
chr9	86276836	86277003	14.74	65.04
chrX	5142843	5142989	14.74	59.03
chrX	9472662	9472816	14.74	57.34
chrX	13534224	13534369	14.74	59.25
chrX	19376294	19376443	14.74	58.39
chrX	50769292	50769436	14.74	59.47
chrX	52513035	52513188	14.74	68.19
chrX	56976296	56976425	14.74	63
chrX	60161289	60161444	14.74	57.13
chrX	62921579	62921726	14.74	58.82
chrX	75849037	75849173	14.74	61.3
chrX	77455336	77455503	14.74	65.04
chrX	78063599	78063743	14.74	59.47
chrX	79634821	79634971	14.74	58.17
chrX	81637532	81637687	14.74	57.13
chrX	82755572	82755723	14.74	57.96
chrX	85408840	85408998	14.74	67.03
chrX	87952590	87952745	14.74	57.13
chrX	90487079	90487215	14.74	61.3
chrX	94646873	94647014	14.74	60.15
chrX	101942408	101942600	14.74	70.2
chrX	102063960	102064120	14.74	66.58
chrX	105213181	105213332	14.74	57.96
chrX	106458350	106458487	14.74	61.07
chrX	108833726	108833871	14.74	59.25
chrX	108896149	108896304	14.74	57.13
chrX	111258420	111258559	14.74	60.6
chrX	114993875	114994009	14.74	61.78
chrX	118096409	118096565	14.74	56.93
chrX	118702613	118702764	14.74	57.96
chrX	120932150	120932299	14.74	58.39
chrX	130951207	130951344	14.74	61.07
chrX	133433895	133434030	14.74	61.54
chrX	133449583	133449719	14.74	61.3
chrX	142062585	142062723	14.74	60.84
chrX	142596658	142596812	14.74	57.34
chrX	146760939	146761094	14.74	57.13
chrX	159557803	159557968	14.74	65.47
chr15	23663452	23663609	14.73	67.23
chr15	46337071	46337228	14.73	67.23
chr3	3315995	3316152	14.73	67.23
chrX	92139057	92139322	14.73	83.26
chr7	18443969	18444108	14.67	57.03
chr10	71470969	71471121	14.66	50.57
chr10	126735753	126735903	14.66	50.98
chr12	69159858	69160006	14.66	51.4
chr13	82666835	82666980	14.66	52.04
chr14	109845891	109846016	14.66	56.7
chr15	40327418	40327543	14.66	56.7
chr16	82089814	82089931	14.66	58.8
chr18	35395519	35395644	14.66	56.7
chr18	53222370	53222547	14.66	54.93
chr3	23256890	23257007	14.66	58.8
chr5	12481687	12481827	14.66	53.13
chr5	95021584	95021727	14.66	62.42

chr6	101770210	101770348	14.66	53.59
chr7	23247653	23247803	14.66	50.98
chr7	64211045	64211195	14.66	50.98
chr8	59300887	59301037	14.66	50.98
chrX	38303774	38303950	14.66	55.13
chrX	42401187	42401318	14.66	55.22
chrX	64719862	64720008	14.66	51.82
chr12	120256495	120256614	14.65	57.03
chr1	147829363	147829519	14.63	56.7
chr11	86697850	86698006	14.63	56.7
chr12	91927162	91927318	14.63	56.7
chr2	151867203	151867359	14.63	56.7
chr3	48658738	48658842	14.63	56.1
chr4	77772251	77772407	14.63	56.7
chr7	15819225	15819384	14.56	61.23
chr3	80326580	80326735	14.54	56.7
chr3	154919362	154919486	14.54	56.7
chr3	158898848	158899003	14.54	56.7
chr4	68092298	68092453	14.54	56.7
chr7	10333281	10333436	14.54	56.7
chr8	62629614	62629769	14.54	56.7
chrX	32437741	32437896	14.54	56.7
chr13	6715211	6715384	14.51	63.22
chr8	126080483	126080626	14.46	55.53
chr12	110512602	110512756	14.45	56.7
chr16	17955729	17955883	14.45	56.7
chr18	49547607	49547761	14.45	56.7
chr7	83137191	83137345	14.45	56.7
chr14	105110135	105110283	14.43	57.93
chr12	12166472	12166595	14.42	56.7
chr7	71626917	71627132	14.4	67.52
chr8	126143787	126143914	14.3	55.42
chr3	17880645	17880848	14.28	66.77
chr7	3844274	3844477	14.28	67.31
chrX	43845906	43845993	14.28	60.19
chr1	182565143	182565312	14.27	58.12
chr10	120580001	120580153	14.26	56.7
chr15	92302285	92302437	14.26	56.7
chr17	60922827	60922979	14.26	56.7
chr8	30370380	30370582	14.21	58.12

chr6	50795694	50795815	14.19	56.7
chr3	84168111	84168262	14.17	56.7
chr4	86264875	86265026	14.17	56.7
chr4	90222422	90222573	14.17	56.7
chr7	146607314	146607465	14.17	56.7
chrX	58470592	58470743	14.17	67.23
chr15	16048627	16048788	14.16	66.77
chr17	28405157	28405358	14.14	58.12
chrX	120975830	120975916	14.12	59.78
chrX	139917454	139917684	14.09	262.56
chr1	39138115	39138277	14.07	56.59
chr1	99677847	99677991	14.07	58
chr1	116108066	116108228	14.07	66.28
chr1	165641082	165641219	14.07	52.54
chr10	19713464	19713615	14.07	56.49
chr10	51468556	51468685	14.07	61.51
chr11	40905012	40905158	14.07	57.56
chr11	43052154	43052300	14.07	57.56
chr13	28715247	28715402	14.07	55.67
chr16	76866367	76866501	14.07	60.29
chr17	35504292	35504459	14.07	63.39
chr17	39012814	39012951	14.07	59.59
chr17	41446646	41446794	14.07	57.13
chr18	45700095	45700250	14.07	55.67
chr19	30682664	30682816	14.07	56.28
chr2	39384230	39384422	14.07	68.37
chr2	68672905	68673061	14.07	55.46
chr2	80085373	80085520	14.07	57.34
chr2	86834925	86835087	14.07	56.59
chr2	93582662	93582812	14.07	56.7
chr2	181212029	181212184	14.07	55.67
chr3	23478793	23478937	14.07	58
chr3	78854879	78855033	14.07	55.87
chr3	81515052	81515204	14.07	56.28
chr3	135784636	135784783	14.07	57.34
chr4	3968110	3968283	14.07	62.13
chr4	35378283	35378438	14.07	55.67
chr4	41833429	41833558	14.07	54.42
chr5	9818983	9819150	14.07	63.39
chr5	63346579	63346729	14.07	56.7

chr5	95684371	95684508	14.07	52.54
chr6	122146220	122146369	14.07	56.91
chr6	122910391	122910546	14.07	55.67
chr6	137972998	137973153	14.07	55.67
chr7	144061549	144061711	14.07	56.59
chr8	7262239	7262388	14.07	56.91
chr8	52085166	52085318	14.07	56.28
chr8	63170275	63170446	14.07	62.55
chr8	85599806	85599970	14.07	64.03
chr9	8051989	8052171	14.07	70.48
chr9	12373588	12373751	14.07	64.25
chrX	22457123	22457284	14.07	54.47
chrX	43109213	43109413	14.07	70.01
chrX	78209618	78209780	14.07	64.47
chrX	137431070	137431207	14.07	62.49
chr13	65772993	65773226	14.05	53.35
chr8	126141580	126141743	14.02	56.24
chr13	35139415	35139647	13.99	53.35
chr1	41736565	41736724	13.98	57.03
chr10	95656822	95656971	13.98	56.7
chr15	100394326	100394475	13.98	56.7
chr5	132595944	132596103	13.98	66.77
chr8	123769766	123769915	13.98	56.7
chrX	138958697	138958846	13.98	56.7
chr5	95782437	95782615	13.93	60.77
chr9	13560304	13560436	13.93	76.91
chr9	22648176	22648334	13.9	66.77
chr2	77853010	77853158	13.88	56.7
chr17	24540558	24540727	13.87	51.25
chr16	47560731	47560849	13.84	56.7
chr16	7957215	7957346	13.82	57.03
chr1	146311318	146311465	13.79	56.7
chr3	81516067	81516214	13.79	56.7
chr3	99222430	99222577	13.79	56.7
chr4	66159143	66159290	13.79	56.7
chr7	18227956	18228103	13.79	56.7
chr14	46432476	46432635	13.77	74.71
chr5	96103334	96103471	13.73	58.8
chr2	65616559	65616705	13.7	56.7
chr5	14551101	14551247	13.7	56.7
chr6	131915442	131915588	13.7	56.7
chr6	114454844	114455038	13.65	59.66
chr14	40575634	40575789	13.63	57.03
chr7	15771271	15771399	13.63	63.79
chrX	122531567	122531707	13.62	63.58
chr12	44830905	44831050	13.6	56.7
chr4	13976004	13976149	13.6	56.7
chr9	71777901	71778046	13.6	56.7
chr17	67354215	67354408	13.58	58.12
chr5	41862742	41862852	13.54	57.03
chr5	68805467	68805621	13.54	66.77
chr1	170574262	170574394	13.53	52.47
chr10	24824163	24824394	13.53	68.39
chr12	77861431	77861547	13.53	56.53
chr13	107168636	107168796	13.53	55.66
chr16	80308151	80308289	13.53	51.09
chr18	50490477	50490615	13.53	51.09
chr18	55478898	55479036	13.53	51.09
chr4	7763651	7763778	13.53	53.68
chr5	63372326	63372502	13.53	61.53
chr8	57976784	57977000	13.53	68.83
chr9	121142887	121143018	13.53	52.71
chrX	120313683	120313803	13.51	67.31
chrX	121434101	121434229	13.51	68.43
chr7	67050164	67050383	13.48	68.27
chr1	91308094	91308176	13.46	67.98
chr5	94505760	94505919	13.42	58.12
chr14	31775990	31776133	13.41	56.7
chr14	104039882	104040025	13.41	56.7
chr3	29889342	29889485	13.41	56.7
chr5	82733024	82733167	13.41	56.7
chr1	131293185	131293358	13.4	60.41
chr1	141437234	141437390	13.4	53.93
chr1	150607568	150607748	13.4	59.01
chr1	190750154	190750305	13.4	54.95
chr11	9614412	9614563	13.4	54.95
chr12	111141452	111141620	13.4	61.44
chr13	90578131	90578286	13.4	54.13
chr14	16849514	16849659	13.4	56.23
chr14	28500019	28500171	13.4	54.74

chr14	58671433	58671585	13.4	54.74
chr15	7498204	7498360	13.4	53.93
chr15	24691177	24691323	13.4	56.01
chr15	31131846	31132002	13.4	64.08
chr15	103246256	103246402	13.4	56.01
chr16	76519516	76519686	13.4	61.02
chr19	57593518	57593665	13.4	55.8
chr2	152036592	152036743	13.4	54.95
chr4	136195301	136195445	13.4	56.45
chr4	142569267	142569421	13.4	54.33
chr5	19467311	19467452	13.4	57.12
chr5	30553639	30553795	13.4	53.93
chr6	21793532	21793676	13.4	56.45
chr6	79232022	79232159	13.4	58.03
chr6	139779560	139779715	13.4	54.13
chr7	4181527	4181678	13.4	54.95
chr7	22256266	22256421	13.4	54.13
chr7	24664086	24664234	13.4	65.96
chr8	101465140	101465291	13.4	54.95
chr8	116089360	116089515	13.4	54.13
chr9	76585137	76585287	13.4	55.16
chr9	93276339	93276486	13.4	55.8
chr1	113604068	113604182	13.37	56.7
chr14	33212184	33212336	13.37	57.03
chrX	93544669	93544783	13.37	56.7
chrX	121652766	121652918	13.37	57.03
chr8	126068487	126068606	13.32	55.25
chr10	36762490	36762679	13.3	67.31
chr14	112825562	112825643	13.3	67.5
chr5	67666089	67666240	13.28	57.03
chr10	13121843	13121988	13.26	67.76
chr13	6943291	6943432	13.23	56.7
chr2	29121733	29121874	13.23	51.25
chr6	68237634	68237822	13.23	58.12
chr15	47064888	47065022	13.2	58.12
chr5	95145860	95146036	13.19	53.62
chr6	45788730	45788880	13.19	57.03
chr1	164742035	164742120	13.16	84.9
chr18	3456540	3456758	13.15	53.35
chr5	94491457	94491612	13.15	53.54

chr11	97586415	97586498	13.14	75.87
chr4	42420050	42420210	13.13	64.05
chr6	17486890	17487030	13.13	56.7
chr6	104334522	104334671	13.1	57.03
chr8	87771478	87771627	13.1	57.03
chr3	48802335	48802521	13.09	55.57
chr11	23824736	23824875	13.04	56.7
chr12	115831674	115831813	13.04	56.7
chr13	103620011	103620150	13.04	56.7
chr1	48423620	48423753	13.03	51.06
chr1	143039234	143039359	13.03	53
chr10	8321315	8321476	13.03	63.52
chr19	24992192	24992384	13.03	56.75
chr3	51044389	51044551	13.03	53.92
chr5	7616820	7616951	13.03	51.53
chr8	7683503	7683628	13.03	53
chr13	74665902	74666389	13	135.69
chr7	33188950	33189029	12.97	66.52
chrX	57011367	57011505	12.95	56.7
chr3	120853334	120853471	12.85	56.7
chr4	37631334	37631471	12.85	56.7
chr12	93632595	93632767	12.81	77.52
chr2	29472845	29472923	12.8	66.02
chr3	41989187	41989369	12.8	68.43
chr1	34477911	34478067	12.79	52.47
chr1	177270039	177270195	12.79	52.47
chr1	187387830	187387980	12.79	53.7
chr1	197180859	197181021	12.79	71.32
chr10	21823811	21823979	12.79	59.8
chr11	29025740	29025889	12.79	53.91
chr12	120835644	120835789	12.79	65.03
chr14	65126531	65126691	12.79	61.52
chr14	93911047	93911198	12.79	53.49
chr14	116050563	116050713	12.79	53.7
chr17	91806868	91807024	12.79	52.47
chr18	85991572	85991724	12.79	53.28
chr3	11737387	11737537	12.79	53.7
chr3	12583913	12584060	12.79	54.33
chr3	23587896	23588041	12.79	54.76
chr4	17704508	17704660	12.79	53.28

chr4	27815795	27815929	12.79	57.26
chr5	41886298	41886454	12.79	52.47
chr5	49933794	49933948	12.79	52.87
chr6	129020423	129020569	12.79	54.55
chr6	146662014	146662169	12.79	66.35
chr7	22357587	22357726	12.79	56.1
chr7	65377679	65377814	12.79	57.02
chr7	111111061	111111205	12.79	54.98
chr7	124979554	124979702	12.79	54.12
chr8	130614235	130614389	12.79	62.88
chr9	60574164	60574307	12.79	55.2
chrX	121640724	121640828	12.79	51.88
chr12	82612412	82612575	12.74	50.49
chr5	96025194	96025347	12.7	55.01
chr7	23562658	23562817	12.68	61.43
chr11	16594334	16594469	12.66	56.7
chr11	56407037	56407217	12.66	80.05
chrX	28107038	28107182	12.66	57.03
chrX	122336785	122336908	12.6	55.99
chr17	13365009	13365147	12.56	55.76
chr4	68622908	68623108	12.56	53.83
chr5	113817860	113818047	12.56	56.37
chr8	72047745	72047898	12.56	59.66
chr5	32836820	32836929	12.51	58.86
chr7	113399071	113399233	12.51	70.43
chrX	92130878	92131110	12.51	73.05
chr2	85124332	85124465	12.48	51.25
chr7	6573354	6573459	12.42	50.95
chr14	74465630	74465825	12.41	111.63
chr8	23554189	23554394	12.36	87.75
chr8	126122554	126122714	12.34	52.48
chr3	11724393	11724495	12.3	68.04
chr7	67049408	67049517	12.27	58.12
chr7	95502520	95502629	12.27	58.12
chr10	73620612	73620764	12.24	51.9
chr10	83139102	83139247	12.24	53.37
chr12	24196552	24196682	12.24	56.81
chr13	94989757	94989905	12.24	52.73
chr14	113424151	113424301	12.24	52.31
chr16	78350970	78351121	12.24	52.1

chr2	16546762	16546914	12.24	51.9
chr5	20661421	20661573	12.24	51.9
chr6	10662752	10662908	12.24	51.09
chr6	22599509	22599660	12.24	52.1
chr7	27438645	27438795	12.24	52.31
chr7	65844231	65844379	12.24	52.73
chr7	67471012	67471164	12.24	51.9
chr7	94531097	94531241	12.24	53.59
chr8	60154715	60154859	12.24	53.59
chr8	76769243	76769397	12.24	51.49
chrX	43896943	43897092	12.24	52.52
chrX	148015962	148016107	12.24	53.37
chr8	86280650	86280887	12.17	143.53
chr11	40788646	40788720	12.15	73.8
chr14	107552799	107552921	12.13	51.52
chr15	85024657	85024801	12.13	55.53
chr17	61153853	61154056	12.13	60.45
chr16	27597331	27597460	12.1	56.7
chr3	128722632	128722761	12.1	56.7
chr6	117589622	117589751	12.1	56.7
chr8	48657943	48658072	12.1	67.23
chr9	121136042	121136223	12.06	57.42
chr8	126077789	126077913	12.05	50.8
chr8	126080861	126081001	12.05	56.27
chr18	65263660	65263824	12	91.45
chrX	121526774	121526916	11.99	67.31
chr3	90769562	90769732	11.96	58.12
chr18	17010511	17010709	11.94	53.35
chr15	87798415	87798625	11.93	64.4
chr3	15409963	15410132	11.89	58.12
chrX	106248228	106248396	11.82	57.03
chr14	68910841	68910990	11.79	55.57
chr5	89942532	89942699	11.75	58.12
chr1	21987013	21987162	11.73	51.19
chr1	22562639	22562814	11.73	68.62
chr1	24862386	24862529	11.73	54.59
chr1	104932356	104932506	11.73	50.98
chr1	168511686	168511834	11.73	51.4
chr10	104277311	104277462	11.73	50.78
chr11	61235100	61235245	11.73	61.93

chr13	14660795	14660963	11.73	56.75
chr13	99760938	99761090	11.73	50.57
chr14	52325145	52325294	11.73	51.19
chr16	17129057	17129196	11.73	63.43
chr3	26663425	26663576	11.73	50.78
chr4	61429418	61429568	11.73	50.98
chr5	141337804	141337952	11.73	51.4
chr7	24339084	24339230	11.73	51.82
chr7	62221821	62221946	11.73	56.7
chr8	8744909	8745083	11.73	56.48
chr8	22400301	22400437	11.73	54.04
chr8	76277774	76277915	11.73	62.92
chr8	85168710	85168907	11.73	69.7
chrX	121768155	121768282	11.73	52.39
chr2	177035630	177035796	11.68	57.03
chr4	77816218	77816417	11.67	51.25
chr8	71979732	71979864	11.61	57.03
chr9	27020665	27020861	11.6	100.15
chr4	146396508	146396649	11.58	52.52
chrX	121643135	121643320	11.57	50.49
chr15	43163313	43163436	11.54	56.7
chr2	91933827	91933997	11.53	92.98
chr8	57991007	57991191	11.53	61.56
chr12	10700703	10700875	11.52	68.62
chr8	126089493	126089639	11.44	51.06
chr13	74667940	74668154	11.41	187.76
chrX	122521453	122521571	11.41	53.98
chr19	34206693	34206855	11.4	57.03
chrX	59215578	59215659	11.4	65.37
chr4	146164662	146164827	11.35	57.26
chr5	63368559	63368702	11.35	53.46
chr15	91552871	91553032	11.33	51.25
chr17	84859532	84859693	11.33	58.12
chrX	92145247	92145482	11.3	59.01
chr10	32536348	32536508	11.26	56.52
chr2	52553207	52553387	11.26	52.94
chr9	87484194	87484330	11.26	52.76
chrX	88749030	88749176	11.26	50.56
chr7	66934086	66934484	11.22	76.92
chr11	56019442	56019601	11.19	57.03

chr13	5280301	5280459	11.12	57.03
chr14	105250337	105250495	11.12	57.03
chr12	116525055	116525212	11.05	57.03
chr10	11211918	11211985	11	79.31
chr3	50908224	50908408	10.99	69.3
chr7	124268486	124268829	10.97	93.71
chr3	127912957	127913137	10.95	87.51
chrX	121007135	121007224	10.94	50.94
chr4	146581691	146581829	10.91	51.33
chr13	6609241	6609400	10.87	56.01
chr13	101359066	101359225	10.82	55.88
chr16	93700726	93700865	10.82	50.86
chr3	101558971	101559138	10.82	54.17
chr4	145857158	145857343	10.82	59.57
chr7	23575573	23575708	10.82	51.77
chr7	76246827	76246991	10.82	55.45
chr8	126145453	126145639	10.82	59.4
chr9	74487978	74488128	10.82	57.91
chrX	120999268	120999442	10.82	71.15
chr13	6609697	6609819	10.78	54.82
chr3	87229045	87229226	10.78	87.27
chr18	7033641	7033799	10.77	97.33
chr8	57988533	57988801	10.77	68.62
chr7	67049226	67049340	10.73	63.25
chrX	121267544	121267722	10.7	56.02
chr4	146432880	146433032	10.69	51.25
chr8	73837744	73837820	10.69	71.78
chr16	20573657	20573789	10.66	54.06
chr8	126138308	126138495	10.66	50.21
chr5	14996958	14997181	10.55	50.87
chr4	99048062	99048243	10.52	56.54
chrX	116018006	116018169	10.51	76.48
chr6	148116560	148116746	10.47	58.12
chr5	16212029	16212207	10.44	51.25
chr14	22183684	22183838	10.42	55.68
chr6	114578814	114578977	10.42	63.04
chr7	15768041	15768213	10.42	51.86
chr12	106762878	106763040	10.38	113.74
chr15	88422808	88423103	10.38	67.76
chr7	39196407	39196543	10.35	50.14

chr8	126092675	126092892	10.35	51.23
chr4	94533314	94533431	10.29	55.57
chr13	4258111	4258286	10.26	51.25
chr8	126072008	126072134	10.16	51.95
chr10	86308156	86308462	10.13	113.75
chr2	3885469	3885613	10.13	59.66
chr12	42241700	42241863	10.12	85.25
chr6	47604236	47604625	10.1	113.82
chr1	194277870	194278010	10.06	145.52
chr6	61541703	61541846	10.06	57.03
chr8	71945650	71945976	10.06	83.12
chr16	59127242	59127374	10.05	50.17
chrX	166438482	166438754	9.98	89.35
chr6	39952640	39952750	9.95	53.35
chr4	145292166	145292472	9.94	82.12
chr6	47718202	47718708	9.93	143.93
chrX	122338691	122338812	9.93	51.25
chr1	139878001	139878170	9.91	51.25
chr1	172994407	172994630	9.85	54.84
chr14	122968194	122968326	9.83	84.41
chr8	124349322	124349512	9.77	54.29
chrX	119285493	119285572	9.73	55.43
chrX	131582079	131582365	9.72	89.61
chr1	189178306	189178474	9.7	50.22
chr13	6607052	6607217	9.7	50.83
chrX	166439777	166440590	9.69	120.24
chrX	92123524	92123822	9.68	53.9
chr4	63263280	63263417	9.64	51.25
chrX	166427551	166427800	9.58	95.62
chr3	21597296	21597455	9.55	92.43
chr16	93789432	93789583	9.54	138.72
chr5	71085219	71085327	9.5	55.57
chrX	21257685	21257760	9.5	69.46
chrX	121015175	121015391	9.47	61.52
chrX	166440666	166441619	9.41	80.41
chr18	14897485	14897655	9.4	56.52
chr16	10975168	10975344	9.33	112.43
chrX	122343233	122343573	9.3	54.71
chr8	126134837	126135126	9.24	70.03
chr5	32932809	32932973	9.23	58.12

chr1	97978201	97978273	9.12	76.02
chrX	122211928	122212204	9.09	64.2
chr8	124348031	124348203	9.08	55.68
chr5	93718590	93718742	9.07	77.15
chr8	57983660	57983742	9.07	52.8
chr3	59849583	59849752	9.06	62.64
chr6	47726666	47726850	9.06	52.99
chr10	23708417	23708555	8.96	60.59
chrX	166441675	166441915	8.96	59.44
chrX	121004248	121004327	8.95	52.32
chrX	166432617	166432994	8.93	79.14
chrX	166424028	166424200	8.9	64.06
chr13	27082106	27082169	8.86	94.66
chr14	8838544	8838716	8.8	56.6
chr7	67028898	67029420	8.79	84.42
chr9	121838729	121838953	8.76	65.56
chrX	121002662	121002964	8.75	52.06
chr4	64158852	64159100	8.72	135.22
chr7	101995966	101996121	8.59	71.79
chr7	46516464	46516648	8.58	50.35
chr14	112918039	112918184	8.57	61.78
chr6	47722205	47722497	8.56	66.56
chrX	121941121	121941296	8.52	53.9
chr18	48170067	48170208	8.5	131.02
chr17	63086892	63086987	8.47	85.61
chrX	166443917	166444375	8.47	69.49
chr16	3747734	3747804	8.44	96.33
chr3	29396844	29396910	8.36	79.92
chr16	63312358	63312491	8.35	75.24
chr10	129172480	129172604	8.34	73.87
chr8	57994356	57994540	8.32	50.15
chr7	67035856	67036208	8.27	77.3
chrX	83790932	83790999	8.25	66.01
chrX	166441976	166442142	8.24	73.06
chr2	51482221	51482299	8.23	62.54
chr7	67044915	67045110	8.23	52.8
chr17	7809090	7809213	8.22	66
chrX	166437772	166438151	8.2	90.52
chr13	25142264	25142601	8.18	51.35
chr17	13498831	13499176	8.14	152.97

chr10	66140909	66140986	8.13	61.92
chr6	133119979	133120056	8.13	93.21
chr10	22168074	22168264	8.11	92.92
chr7	111576510	111576657	8.09	51.14
chr1	197105357	197105480	8.08	52.8
chr6	47614276	47614982	8.07	181.6
chrX	166444766	166445449	8.06	141.48
chr1	79746742	79746990	8.05	60.59
chr17	13743482	13744624	8.03	729.68
chr1	69503315	69503445	8	64.76
chr6	47722552	47723261	7.88	171.37
chr7	67014444	67015006	7.88	102.34
chrX	121707393	121707631	7.88	58.09
chr4	152527171	152527424	7.83	66.16
chr7	66935816	66936088	7.78	63.55
chr1	173010776	173010964	7.75	59.01
chr12	15260345	15260455	7.74	61.75
chr6	47709043	47709421	7.72	74.47
chr17	13744631	13746064	7.71	1303.37
chrX	92151362	92151663	7.7	68.61
chr2	41751683	41751796	7.67	86.92
chr10	21977853	21978027	7.65	82.08
chr15	91737289	91737670	7.54	91.44
chr1	173001870	173002241	7.5	75.2
chr8	30622624	30622695	7.49	65.8
chr4	70039150	70039359	7.45	145.3
chr5	103286288	103286354	7.43	63.27
chr10	94334764	94334869	7.39	94.61
chr6	47604629	47604702	7.38	65.03
chr14	59277517	59277625	7.37	99.92
chrY	2652207	2652331	7.36	135.38
chrX	166445558	166445701	7.34	66.7
chr13	24818086	24818174	7.32	59.53
chr14	86598789	86599005	7.31	237.42
chr10	105467934	105468008	7.29	52.43
chr12	41620283	41620357	7.29	52.43
chr7	67037232	67037501	7.28	53.71
chr6	47609169	47609633	7.27	91.15
chr1	147581414	147581489	7.26	68.45
chr13	53365268	53365364	7.24	150.28
chr6	47706684	47707365	7.24	83.23
chr12	74719547	74719631	7.22	53.95
chr6	29697880	29698655	7.22	367.93
chr6	47617124	47617661	7.22	105.44
chr6	47703466	47704009	7.2	87.23
chr3	159494853	159494921	7.18	71.42
chr1	159529595	159529707	7.16	88.28
chr10	52248389	52248971	7.15	84.1
chr9	90197137	90197235	7.15	94.86
chr6	47635840	47636720	7.09	165.2
chr1	19166310	19166423	7.07	54.71
chr15	6266895	6266972	7.04	71.07
chr5	63370483	63370712	7.04	53.55
chr3	148715715	148715944	7.01	62.13
chr7	67028222	67028782	6.99	77.33
chr12	75904868	75905022	6.97	51.4
chr14	8703417	8704140	6.97	103.75
chrX	166443466	166443758	6.92	134.24
chr14	13370175	13370266	6.86	60.59
chr1	63676438	63676712	6.84	86.24
chr10	94055178	94055272	6.84	100.93
chr13	74667006	74667177	6.84	55.76
chr14	105114985	105115293	6.84	57.4
chr1	149524793	149524861	6.83	70.49
chr18	43073568	43073665	6.82	107.5
chr2	57481806	57482159	6.79	189.63
chr16	49584479	49584596	6.78	52.06
chr6	47631527	47632280	6.76	144.26
chr7	67045117	67045261	6.75	51.29
chr6	47601605	47602084	6.74	64.55
chr14	69780402	69780503	6.73	54.4
chr14	69780049	69780155	6.71	132.31
chr2	98503828	98504259	6.71	844.69
chr7	67034848	67035506	6.7	103.02
chr7	67012022	67012449	6.68	89.84
chr8	57981044	57981332	6.66	61.64
chr8	103670007	103670093	6.66	50.01
chr10	52249630	52249885	6.64	51.19
chr5	110503495	110503581	6.64	130.36
chr11	18231979	18232288	6.62	73.87

chrX	131577633	131577934	6.62	61.75
chr17	68090701	68090875	6.61	89.6
chr9	115259944	115260045	6.61	141.81
chr19	53118296	53118363	6.6	56.06
chr1	143223048	143223120	6.59	80.83
chr6	47726867	47727195	6.59	62.64
chr8	19759407	19760421	6.5	155.17
chr6	47634520	47634959	6.46	86.96
chr12	16754622	16754720	6.45	121.8
chr6	47612004	47612333	6.45	80.71
chr7	67024633	67025282	6.44	65.56
chr1	78570908	78571223	6.43	71.96
chr3	128639637	128639732	6.42	75.56
chr8	20036846	20037256	6.4	60.02
chr6	47630215	47630651	6.39	65.78
chr6	103264591	103264774	6.38	122.31
chr1	102635460	102635564	6.37	75.71
chr6	47694075	47694668	6.35	91.93
chr1	195054005	195054153	6.34	103.22
chr4	31281334	31281416	6.31	143.69
chr10	79222514	79222581	6.29	55.39
chr6	47627992	47628757	6.28	113.23
chr9	121840342	121840638	6.28	53.46
chr13	74666399	74666512	6.26	119.89
chr10	37540255	37540341	6.24	119.94
chr3	23742074	23742176	6.24	54.02
chr13	77578163	77578318	6.21	390.24
chr15	86025419	86025750	6.21	72.24
chr16	5403565	5403628	6.21	53.38
chr16	93686947	93687010	6.21	53.38
chr9	95326320	95326451	6.21	153
chr11	88943134	88943364	6.19	128.64
chr6	47635025	47635629	6.19	82.92
chr8	19908630	19909040	6.19	56.43
chr2	98505030	98505379	6.18	771.06
chr7	67009366	67010147	6.18	110.93
chr16	18533224	18533412	6.17	54.24
chrX	122653116	122653573	6.17	62.15
chr6	47617729	47618117	6.15	59.95
chr11	110283562	110283649	6.12	90.59

chr9	3027377	3038415	6.12	3189.25
chrX	92159702	92159983	6.12	54.19
chr6	47715105	47716510	6.1	183.44
chr8	36197953	36198052	6.08	104.04
chr12	94815426	94815664	6.06	85.57
chr19	50385106	50385189	6.06	106.86
chr9	3000000	3019519	6.06	291.66
chr1	135492186	135492664	6.05	110.2
chr13	116983103	116983198	6.04	130.66
chr3	120925931	120925992	6.01	59.52
chr10	121200273	121200343	5.98	93.49
chr8	19926127	19927227	5.96	490.21
chr6	47699092	47699832	5.95	105.25
chr8	54520443	54520503	5.91	58.75
chr7	97590474	97590543	5.89	98.95
chr2	110133772	110133860	5.88	120.94
chr7	67020447	67020892	5.87	94.62
chr16	5709256	5709348	5.83	105.06
chr19	61275596	61275823	5.83	51.6
chr6	47608487	47608998	5.78	76.16
chr7	67027126	67027396	5.78	58.15
chr7	117203057	117203131	5.78	54.33
chr6	47704037	47704526	5.77	62
chr5	46827004	46827079	5.74	113.87
chr6	47688387	47688720	5.74	52.65
chr14	91310973	91311062	5.71	121.6
chr15	64272335	64272393	5.71	57.16
chr7	67004241	67004883	5.7	65.05
chr6	47633753	47634232	5.69	66.97
chr13	113368372	113368530	5.67	59.44
chr4	93511096	93511194	5.66	58.17
chr6	47689898	47690279	5.64	54.96
chr4	29547479	29547549	5.63	50.34
chr1	44258101	44258187	5.62	51.23
chr14	119686162	119686236	5.62	120.47
chr8	56198977	56199637	5.62	106.84
chr8	71998730	71999012	5.61	143.95
chr10	7232165	7232404	5.59	62.71
chr6	47622869	47623654	5.59	119.76
chrX	166427209	166427527	5.59	79.59

chr17	93445774	93445844	5.58	87.39
chr4	118219804	118221346	5.58	1241.44
chr16	30829613	30829716	5.57	64.24
chr6	47708267	47709019	5.57	140.02
chr18	3005174	3005552	5.54	74.18
chr6	47610692	47611414	5.54	89.33
chr6	47627523	47627982	5.54	98.22
chr6	47700302	47701484	5.51	148.56
chr6	103599040	103599289	5.5	474.75
chr1	64463470	64463542	5.49	68.23
chr10	7232499	7235308	5.49	1433.76
chr6	47618721	47619101	5.49	66.87
chr8	19924002	19926114	5.45	609.47
chr8	57997900	57998210	5.45	54.08
chr9	3019522	3027346	5.44	3100
chr18	68851719	68851968	5.41	79.89
chr6	47629458	47630207	5.41	69.49
chr6	47702050	47702534	5.41	71.18
chr1	183673115	183673899	5.39	106.4
chr6	47633164	47633730	5.37	76.71
chr10	7231149	7231722	5.36	272.18
chr17	53291811	53291955	5.35	50.08
chr7	66930199	66930491	5.33	56.49
chr12	75905129	75905494	5.31	117.39
chrX	106468144	106468224	5.28	56.25
chr2	109211944	109212012	5.26	63.34
chr12	34758613	34758683	5.23	81.78
chr2	143210313	143210378	5.23	53.7
chr6	47603579	47604112	5.23	81.87
chr5	80929912	80929991	5.22	110.32
chr6	47625554	47626312	5.2	111.91
chr6	47609898	47610583	5.18	63.72
chr7	67029542	67029777	5.17	58.97
chr9	24346455	24346605	5.17	87.2
chr6	47605382	47606315	5.16	161.39
chr6	47689039	47689596	5.16	75.51
chr16	57391230	57391792	5.15	107.71
chrX	166527166	166527506	5.15	506.51
chr6	56183651	56183743	5.12	85.78
chr10	7236727	7237128	5.1	176.53
chr6	47696239	47697173	5.07	98.27
chr6	47698225	47698968	5.04	72.72
chr10	7231816	7232083	5.03	136.01
chr17	3379790	3379866	5.03	65.65
chr10	7229298	7230583	5.02	592.5
chr6	47622100	47622842	5.01	82.02
chr1	111472754	111472818	5	59.49
chr10	102131266	102131337	5	101.4
chr5	106605800	106605878	4.99	103.17
chrX	39993112	39993182	4.92	52.3
chr1	135491289	135492174	4.91	80.44
chr16	34743083	34743171	4.9	51.56
chr2	92008268	92008344	4.88	79.81
chr3	59724068	59724132	4.88	72.65
chr10	7236089	7236668	4.83	304.03
chr11	57116135	57116203	4.78	73.35
chr12	3109866	3110124	4.78	922.22
chr1	71125913	71125989	4.77	87.13
chr2	20821474	20821836	4.75	90.82
chr6	47713805	47714278	4.73	89.36
chr16	93598171	93598238	4.71	64.07
chr2	19430946	19431023	4.7	86.31
chr6	47693231	47694054	4.69	95.34
chr15	63458454	63458512	4.66	54.72
chr10	114174434	114174503	4.61	83.92
chr8	15519757	15520122	4.61	73.16
chr2	98502384	98503147	4.58	2821.78
chr6	47623866	47624974	4.56	90.72
chr8	73956987	73957069	4.52	54.53
chr2	98506392	98507492	4.51	3100
chr6	3150763	3151669	4.48	141.76
chr6	47615376	47615963	4.47	53.51
chr5	147072568	147072899	4.37	54.42
chr9	47766423	47766492	4.37	72.74
chr12	104131172	104131234	4.36	70.47
chr6	47687049	47688336	4.36	82.35
chr8	40240697	40241218	4.34	57.65
chr14	123850840	123850906	4.33	64.48
chr10	29690764	29690845	4.32	66.87
chr6	47702567	47703443	4.32	107.22

chr7	93955096	93955157	4.29	50.59
chr19	23431914	23431989	4.27	59.69
chr9	35112795	35113178	4.27	1638.31
chr10	57690558	57691224	4.26	82.91
chr3	100120375	100120452	4.26	67.91
chr10	57685673	57686316	4.15	61.67
chr6	47606796	47607994	4.14	82.9
chr8	56203858	56205488	4.14	101.08
chr6	4874136	4874199	4.06	53.64
chr15	74916669	74917478	4.04	252
chr1	78570272	78570692	4.01	57.96
chr6	50997469	50997534	4	58.71
chr4	25399420	25399489	3.97	64.56
chr6	47615997	47616708	3.96	51.68
chr10	51864279	51864343	3.94	62.96
chr8	56201204	56201912	3.93	60.87
chr9	123782210	123782296	3.83	59.55
chr6	47694705	47695522	3.77	74.36
chr8	56205500	56209057	3.75	266.86
chr8	56201933	56202418	3.49	64.56
chr16	86821030	86821490	3.42	75.22
chr17	39979941	39985862	3.04	748.7
chr1	24618373	24623102	2.4	68.9

Table S4.2. Prospective cJUN target genes identified from cJUN ChIP-seq peaks. Statistically enriched cJUN peak regions. Enrichment (Fold Enrichment) LOG P (-10*LOG10(pvalue)).

Gene	Cyc	FC	pval	Up in Mes
Baz2b	1402.8	0.465	5.97E-07	
Tmem204	233.7	0.497	1.66E-04	+
Chpf	1197.6	0.468	3.11E-06	+
Nckap5l	547.6	0.331	3.62E-02	+
Pi4ka	981.2	0.475	6.68E-07	
Tro	1261.8	0.453	2.99E-03	+
Masp2	324.1	0.351	1.83E-04	
Adamts7	767.0	0.306	2.43E-09	+
Arhgef11	856.0	0.496	5.78E-05	
Brsk1	374.1	0.422	2.97E-07	+
Scube3	71.7	0.351	8.97E-03	+
Ypel4	34.6	0.273	1.15E-02	+
Gm11541	0.3	0.007	3.62E-09	+
Daam2	576.2	0.280	2.85E-05	+
Whrn	187.2	0.247	7.90E-06	
Ppp1r13l	143.6	0.484	2.62E-03	
Adcy5	500.5	0.434	1.57E-03	+
Ttll4	567.1	0.476	2.13E-04	
Fam189b	428.9	0.500	3.21E-02	
Zfyve28	20.8	0.275	1.82E-03	+
Zscan18	162.9	0.478	9.36E-05	+
Snx32	83.3	0.467	2.00E-03	+
Lrrc16b	179.7	0.327	2.40E-10	+
Apol7b	12.1	0.291	1.04E-02	+
Ankrd34a	25.5	0.328	1.05E-02	+
Vegfa	1280.0	0.308	3.71E-09	
Gpr17	298.3	0.317	1.44E-08	+
Ccdc141	257.6	0.480	3.54E-03	+
Ikzf1	52.2	0.477	2.79E-02	+
Pknox2	308.4	0.289	1.28E-09	+
Unc13a	133.0	0.437	3.02E-04	+
Safb2	754.1	0.482	3.64E-08	
Kcp	317.3	0.275	2.52E-03	+
Mettl17	227.4	0.453	2.81E-07	
1700029J07Rik	46.8	0.478	9.16E-03	
Prickle1	602.3	0.471	8.06E-04	+
Itga1	426.6	0.482	3.19E-04	+
Ccdc114	50.5	0.435	8.32E-03	+
Sec31b	8.6	0.233	9.56E-03	
Lrrc55	22.3	0.061	1.87E-26	+
Bank1	10.6	0.293	3.63E-02	+
Lgr6	15.2	0.126	9.79E-09	+
Il20rb	39.2	0.441	3.84E-02	
Dnaaf3	47.3	0.421	9.75E-03	+
Acsl6	41.2	0.434	6.85E-03	+
Dnah1	103.7	0.387	1.67E-03	+
I830077J02Rik	3.2	0.135	1.19E-02	+
Piezo1	1229.7	0.366	4.26E-05	
Adam15	624.0	0.475	3.09E-06	
Csf1r	472.7	0.318	2.97E-13	+
Gm6377	3.3	0.170	2.99E-02	+
Dyrk1b	337.7	0.439	3.39E-03	+
Clec5a	13.4	0.278	4.10E-03	+
Gngt2	31.9	0.346	4.02E-02	+
Emc1	683.2	0.419	3.33E-04	
Gm14137	10.4	0.184	1.50E-02	
Kcnd3	225.9	0.104	2.48E-06	+
Slc22a15	164.2	0.480	1.01E-03	+
Piezo2	414.6	0.260	2.34E-04	+
4930467E23Rik	19.0	0.193	1.34E-02	+
Mroh8	50.7	0.488	1.93E-04	
Evi5l	154.4	0.498	6.02E-04	+
Iffo1	228.3	0.389	1.56E-06	+
Tmem120b	87.7	0.444	2.04E-04	
Peg10	2872.8	0.337	9.70E-03	+
Cd74	46.5	0.192	5.33E-08	+
Smad7	258.8	0.369	1.21E-02	+
Eml1	617.8	0.323	1.26E-06	+
Timp1	83.9	0.467	2.08E-03	+
Akna	310.0	0.397	8.76E-03	
Scimp	0.9	0.072	3.07E-02	+
Mink1	657.5	0.370	6.25E-10	
Dysf	192.1	0.345	1.55E-07	+
Syne1	845.2	0.460	1.45E-02	+
Fgfr1	1346.2	0.332	4.87E-13	+
Vamp1	82.2	0.309	1.35E-05	
Prdm10	137.2	0.452	1.92E-02	
Cass4	4.1	0.087	5.42E-05	+

Parp8	210.4	0.457	5.83E-05	+
Srgap2	878.3	0.461	1.15E-02	+
Adamts6	210.6	0.366	3.36E-05	+
Dock9	1973.0	0.294	2.15E-17	+
Ptpn23	1036.1	0.377	2.83E-02	
Adamts14	14.5	0.106	1.02E-08	+
Kcng1	16.0	0.024	1.66E-09	+
Kcnq4	30.1	0.222	8.99E-06	+
Lama5	1684.0	0.194	1.29E-12	
Frmpd1	58.1	0.418	3.83E-03	+
Kif13b	333.4	0.370	4.34E-04	
Gpr116	705.4	0.431	3.08E-07	+
Flnc	2084.9	0.438	1.16E-02	+
Fam65a	648.0	0.400	3.52E-02	+
Vcan	4562.1	0.347	2.65E-04	+
Uggt2	355.9	0.361	3.68E-09	+
Hpse2	240.3	0.312	9.95E-03	+
Ccdc142	166.2	0.431	4.89E-06	
Ccdc88b	63.1	0.420	6.10E-03	+
Trio	1728.2	0.407	1.68E-04	
Ppp1r12b	129.5	0.435	4.88E-04	+
Slc9a5	113.2	0.142	3.66E-16	+
Plekhg4	7.9	0.145	1.36E-04	
Sipa1l2	804.3	0.498	8.37E-03	+
Cped1	1270.5	0.405	8.24E-05	+
Trrap	2415.1	0.384	1.49E-02	
Adamts3	103.3	0.287	1.53E-02	+
Klhl14	0.9	0.030	2.00E-05	+
Fndc1	59.5	0.102	4.19E-04	+
Rbm24	103.8	0.340	5.48E-06	+
Gtf2ird1	1221.7	0.492	9.36E-07	
Pik3r6	51.4	0.345	1.33E-04	+
Sap25	49.0	0.285	1.25E-04	
Mkl1	601.0	0.396	1.92E-03	
Itgam	63.8	0.482	3.87E-03	+
Ubp1	1890.3	0.498	3.39E-06	
Cacna1d	273.4	0.245	6.39E-03	+
Gria2	109.0	0.445	1.82E-04	+
Pth1r	336.0	0.494	3.15E-05	+
Ndufa4l2	81.6	0.398	4.49E-04	+

Ajap1	46.0	0.241	9.22E-08	+
Zkscan16	68.7	0.357	1.83E-02	+
Myof	411.2	0.449	2.23E-07	
Pnmal2	633.7	0.428	3.62E-07	+
Adat3	82.9	0.417	1.42E-04	
Cyp4f17	60.5	0.400	1.05E-02	+
Gsg1l	33.4	0.222	1.63E-06	+
Prrt2	155.7	0.227	1.19E-02	+
Col6a6	12.1	0.195	3.39E-02	+
Rai2	245.7	0.406	7.34E-04	+
Gas7	532.4	0.369	4.34E-05	+
Phf21a	999.8	0.433	7.43E-03	+
Cbfa2t3	119.1	0.350	1.51E-03	
Trpc2	91.7	0.428	6.22E-04	
Ebf4	327.6	0.315	3.77E-05	+
Cd33	45.9	0.337	4.76E-04	+
Atg16l2	149.2	0.370	5.82E-06	
Wdfy1	189.0	0.319	4.99E-10	
Ptprc	111.6	0.356	2.58E-02	+
Ifitm1	768.9	0.395	2.85E-09	+
Ncam1	1562.1	0.312	1.66E-02	+
Lrrc32	347.2	0.242	4.58E-03	+
Ltbp4	2755.4	0.332	1.88E-05	+
Stxbp1	696.7	0.407	1.75E-03	+
Pdlim7	1044.6	0.395	1.05E-10	+
Smarcc2	2133.9	0.434	3.39E-09	
Pnpla6	523.2	0.367	8.90E-11	
Upf1	1321.3	0.495	1.16E-06	
Il1r1	250.7	0.459	1.55E-04	+
Sema4c	1043.4	0.490	3.45E-06	+
Acrbp	44.3	0.325	1.47E-03	
Gm1564	11.3	0.302	3.88E-02	+
Arhgef1	1050.6	0.462	2.71E-08	
Prickle2	854.2	0.475	4.22E-02	+
Ccdc62	39.3	0.445	9.28E-03	
Cntfr	654.9	0.456	2.13E-02	+
Cyp1a1	21.6	0.044	6.47E-14	
Ptger4	63.6	0.395	5.72E-04	+
Atat1	294.6	0.451	1.76E-04	+
Vwa5b2	109.3	0.465	4.58E-02	

Gm13889	108.4	0.245	6.02E-06	+
Runx2	25.7	0.156	1.21E-03	+
Lgals3	229.4	0.391	2.73E-02	+
Gpr114	7.3	0.080	2.38E-04	+
Parp4	196.4	0.357	3.32E-02	
Hk1	840.1	0.445	1.27E-07	+
Smoc1	780.0	0.343	2.50E-12	+
Eng	431.4	0.187	4.97E-05	+
Smtn	974.9	0.346	1.61E-11	+
Upp1	47.0	0.410	2.98E-03	+
Igfbp7	120.0	0.104	8.90E-08	+
Adcy3	295.3	0.436	4.57E-06	+
Klrb1c	16.4	0.306	3.67E-02	+
Ubr4	2550.6	0.299	6.43E-03	
Megf8	1560.7	0.472	9.17E-03	+
Kif26b	648.6	0.213	3.24E-02	+
Mthfr	1047.2	0.491	3.96E-05	
T2	3.0	0.170	4.15E-02	
Stra6	113.5	0.274	3.25E-04	+
Igsf10	862.2	0.250	4.33E-07	+
2410089E03Rik	557.9	0.464	2.16E-02	+
Eme2	143.8	0.479	1.34E-03	
C2cd4a	19.4	0.344	2.69E-02	+
Col4a5	717.4	0.374	8.76E-11	+
Begain	148.1	0.336	3.35E-02	+
Cmip	1448.7	0.419	1.05E-03	
Tubgcp6	820.4	0.481	3.06E-04	
Clk2	522.7	0.458	4.24E-07	
Rhpn1	35.1	0.431	8.03E-03	+
Hectd2	110.8	0.493	5.55E-03	+
Cyp2d22	119.8	0.218	1.95E-13	+
Stard13	689.7	0.453	5.28E-06	+
Emcn	213.9	0.399	1.47E-02	+
Osbpl3	343.1	0.392	1.62E-08	+
Wdr90	351.1	0.416	1.33E-07	
Taok2	1207.0	0.491	1.10E-05	
Ntf3	68.0	0.386	2.12E-04	+
Rerg	159.7	0.237	2.68E-07	+
Efemp2	632.4	0.390	3.93E-10	+
Sipa1	637.0	0.321	1.96E-12	+

Iglon5	272.2	0.453	2.14E-04	+
Znf512b	1393.3	0.335	2.14E-12	+
Adamts20	47.3	0.264	9.08E-04	+
Rgs9	290.8	0.321	1.55E-10	+
Pias3	465.0	0.409	2.37E-07	+
2010015L04Rik	11.6	0.200	9.02E-04	+
Fam129c	22.6	0.415	9.60E-03	
Mgll	1398.6	0.482	3.05E-07	+
Sec14l1	1388.8	0.336	3.38E-07	+
Rhbdf2	325.3	0.429	5.20E-06	
Sirt4	110.3	0.351	1.01E-06	
Tcirg1	382.7	0.281	3.88E-12	
Col6a5	8.5	0.080	6.83E-10	+
Sugp2	434.9	0.413	2.52E-07	
Nfatc4	1197.9	0.414	6.78E-04	+
Pla2g4c	16.7	0.328	4.98E-03	
Tsku	470.3	0.494	6.83E-03	+
Tifab	72.6	0.414	3.13E-03	+
Sbf1	1024.5	0.421	2.72E-08	
Trim66	37.6	0.060	1.99E-03	
Pcdha4-g	2841.0	0.483	2.12E-02	+
Dbn1	2278.1	0.488	3.76E-05	+
Ubr2	1546.8	0.434	3.03E-07	
Usp35	158.3	0.383	1.28E-04	+
Slc25a22	311.9	0.483	2.16E-04	
Gm2897	35.7	0.472	4.75E-02	
Rapgef3	111.3	0.344	6.04E-07	+
Adamtsl3	42.4	0.328	9.78E-03	+
Camta2	433.2	0.309	2.51E-04	
Kcnip1	30.4	0.068	9.55E-21	+
Kirrel3	39.2	0.218	3.11E-02	+
Dlc1	1550.4	0.395	2.93E-02	+
Tgfbr3l	20.2	0.335	2.04E-02	
Dclk2	280.0	0.298	3.25E-05	+
Prr22	18.1	0.453	2.25E-02	
Frem1	1807.7	0.416	3.03E-02	+
Arhgef2	1527.0	0.343	1.62E-12	
Prrc2a	6514.0	0.416	2.91E-02	
Macf1	4201.9	0.472	1.58E-02	+
Slc44a2	910.2	0.437	3.04E-07	+

Fbxl13	6.6	0.208	9.93E-03	+
Hdac7	723.2	0.374	3.71E-03	+
Trim47	77.8	0.347	3.26E-05	+
Cyb5r2	14.3	0.199	1.10E-04	
Arap3	624.5	0.258	1.32E-08	+
Ano1	285.7	0.173	1.59E-12	+
Col6a3	4256.9	0.192	1.23E-03	+
Fam193a	936.5	0.461	4.43E-03	
Pde2a	613.7	0.430	3.67E-08	+
Tle2	102.3	0.234	8.49E-12	+
Cpt1c	289.9	0.265	1.06E-10	+
Ecm1	94.4	0.467	2.56E-03	+
Kcnma1	224.5	0.444	5.20E-03	+
Slc12a4	429.4	0.267	2.21E-16	+
Irx3	2.4	0.163	4.94E-02	+
Itgal	51.2	0.258	2.51E-07	+
Gbp4	14.2	0.241	1.03E-02	+
Myo7a	251.8	0.442	8.04E-06	
Eif4g3	2227.4	0.384	1.19E-10	
Arrb2	337.2	0.465	1.32E-06	
Sorbs3	568.1	0.439	4.26E-03	+
Nfam1	66.8	0.428	5.38E-03	+
4930426D05Rik	1.1	0.086	2.49E-02	
Ampd3	47.9	0.457	1.30E-02	+
Nxf1	1673.6	0.335	1.87E-14	
Chrd	110.1	0.266	4.85E-10	+
Syngap1	334.8	0.203	2.97E-03	+
Cacnb1	263.3	0.463	1.33E-04	+
42251	50.2	0.243	1.11E-04	+
Tead2	2172.7	0.478	7.24E-08	+
Paqr7	172.2	0.368	1.19E-04	+
Trim3	390.0	0.473	5.42E-06	+
Ncf1	132.5	0.349	7.83E-04	+
Lepre1	609.0	0.395	6.20E-07	+
Otx2	4.5	0.161	1.45E-02	+
Tsc2	1117.5	0.441	2.82E-06	
Hgf	67.5	0.173	1.08E-15	+
Pitpnm2	522.3	0.441	3.84E-02	
Exoc3l4	63.8	0.403	2.63E-03	+
Egflam	827.7	0.387	1.62E-09	+

Tgfb1i1	1482.2	0.380	1.43E-06	+
Celf3	834.9	0.396	6.27E-03	+
Kctd17	422.5	0.386	2.67E-08	+
2010111I01Rik	1190.4	0.477	1.18E-06	+
Col12a1	1350.9	0.353	4.52E-05	+
Vsig10l	87.2	0.453	4.29E-02	
Snapc4	379.8	0.450	6.79E-06	
Flna	17960.0	0.440	4.77E-09	+
Kmt2b	1313.9	0.390	1.42E-02	
Ppp1r3f	133.2	0.266	9.42E-09	+
Cd302	84.8	0.401	7.93E-05	+
Ebf1	114.6	0.409	4.02E-04	+
Aff3	480.0	0.272	6.55E-03	+
Lmtk3	217.7	0.200	3.32E-06	+
Sema6d	908.5	0.497	3.86E-02	+
Mapk7	848.7	0.495	9.18E-04	
Adam8	24.4	0.260	1.70E-04	
Polr2a	3198.0	0.278	3.12E-02	
Pcsk6	224.8	0.379	6.89E-08	+
Slit2	775.4	0.472	2.37E-02	+
Aebp1	597.1	0.345	6.17E-11	+
Apela	34.1	0.469	4.15E-02	+
Inpp4b	87.8	0.318	2.73E-06	+
Agap2	251.8	0.305	2.11E-03	+
Edc4	948.0	0.483	1.80E-06	
Pcdha6-g	2840.2	0.483	2.12E-02	+
Pcdha7-g	2845.3	0.484	2.17E-02	+
Fst	71.0	0.183	5.43E-04	+
Aatk	193.2	0.241	7.09E-14	+
Adcy7	91.2	0.259	2.74E-09	+
Angpt2	87.0	0.264	7.12E-05	+
Agtr2	34.2	0.391	2.78E-02	+
Speg	517.6	0.343	1.21E-02	+
Bcat1	199.0	0.271	1.68E-12	+
Bmp4	407.6	0.258	2.85E-17	+
Bmp5	228.9	0.425	7.13E-06	+
Cd28	20.1	0.331	8.11E-03	+
Ovgp1	15.7	0.200	2.03E-06	
Cit	168.4	0.444	1.74E-02	
Clk4	1094.6	0.401	1.92E-06	

Col11a1	299.0	0.314	1.52E-05	+
Col13a1	192.1	0.198	4.99E-03	+
Col5a2	5402.2	0.470	1.63E-03	+
Col7a1	15.5	0.239	8.95E-05	
Col9a2	462.6	0.383	8.48E-03	+
Col1a1	10200.4	0.257	1.51E-05	+
Col1a2	9259.1	0.317	1.30E-06	+
Csf1	351.6	0.329	4.69E-10	+
Csf2rb2	17.6	0.330	4.11E-02	+
Csn3	17.4	0.356	2.62E-02	+
Ctsk	151.6	0.454	8.25E-03	+
Cybb	159.7	0.467	1.45E-04	+
Gadd45a	151.9	0.220	4.96E-04	
Dlg4	530.2	0.350	1.45E-02	+
Dll1	456.0	0.262	1.03E-08	+
Dnase1l3	7.7	0.034	1.98E-13	+
Ednrb	3785.3	0.431	3.91E-05	+
Eln	1481.8	0.481	6.38E-06	+
Enc1	1160.5	0.375	5.77E-09	+
Enpep	1196.0	0.224	5.94E-14	
Epha4	700.4	0.494	2.04E-05	+
Epha8	10.2	0.093	8.39E-08	+
Eps15l1	729.8	0.485	1.29E-06	
F2rl3	110.8	0.275	3.69E-09	+
Fap	188.6	0.262	1.38E-03	+
Fbn1	3421.3	0.437	2.19E-08	+
Foxl1	27.3	0.032	2.15E-22	+
Flt4	258.0	0.318	1.84E-03	+
Gapdhs	25.1	0.355	4.28E-03	
Slc6a9	557.4	0.220	9.06E-19	
Gna14	270.0	0.487	5.93E-05	+
Grik5	998.9	0.433	3.86E-04	+
Mr1	145.3	0.391	1.27E-05	+
Has2	256.1	0.255	3.30E-15	+
Hcls1	103.9	0.411	3.16E-02	+
Map4k1	61.2	0.422	1.62E-04	
Hspg2	4157.3	0.241	2.25E-02	
Igfbp2	660.1	0.481	1.03E-03	+
Igfbp6	26.7	0.457	4.71E-02	+
Il10ra	48.1	0.443	2.92E-02	+
Il1b	5.8	0.078	3.50E-08	+
Lrig1	2799.9	0.479	5.80E-07	+
Itga2	222.5	0.445	7.00E-04	
Itga7	22.2	0.232	5.46E-05	+
Itih3	6.4	0.161	1.00E-03	+
Lama1	332.4	0.394	1.37E-03	+
Lama2	397.3	0.457	4.39E-02	+
Lamb1	5494.1	0.370	4.23E-13	+
Lamb2	1185.2	0.406	1.20E-09	
Lcat	8.7	0.256	1.61E-02	+
Lrp1	4222.5	0.182	1.79E-03	+
Lrp5	1508.4	0.485	1.32E-03	
Ltbp3	1173.3	0.438	4.51E-03	+
Ltc4s	9.2	0.126	3.74E-03	+
Tm4sf1	87.6	0.378	4.48E-05	+
Mfap2	1884.5	0.419	3.66E-08	+
Mcpt1	0.9	0.050	8.38E-03	
Mdm4	729.9	0.460	6.93E-04	
Cxcl9	1.9	0.107	9.89E-03	+
Mmp13	14.6	0.209	8.71E-05	+
Mmp14	3179.8	0.462	2.45E-08	+
Mmp2	4578.9	0.287	2.07E-19	+
Mpp1	685.8	0.483	1.34E-05	
Mrc2	1137.8	0.332	4.19E-11	+
Msi1	174.9	0.427	7.65E-03	
Nbl1	617.6	0.387	1.05E-09	+
Ncoa3	953.9	0.355	3.62E-04	
Nid2	1655.5	0.466	5.68E-07	+
Nkx2-3	947.1	0.425	7.44E-08	+
Nog	148.6	0.439	4.23E-04	+
Nos3	198.7	0.442	7.98E-05	+
Notch3	949.1	0.300	4.45E-02	+
Npc1	714.2	0.376	2.82E-05	
Npr1	102.8	0.410	1.33E-04	+
Ntn1	1383.0	0.491	3.76E-04	+
Cldn11	25.6	0.185	2.45E-03	+
Pcolce	627.8	0.479	2.14E-04	+
Pde8a	92.0	0.475	2.42E-03	+
Pde9a	502.6	0.473	1.38E-04	+
Pdgfrb	2075.2	0.235	5.14E-04	+

Peg3	5454.7	0.477	1.44E-02	
Pim1	180.2	0.434	5.65E-05	
Prkd1	153.3	0.301	2.71E-10	+
Prkcq	44.7	0.230	7.50E-08	+
Plau	415.7	0.373	2.34E-09	+
Plxna1	1933.8	0.443	1.98E-02	
Plxna2	746.3	0.306	3.13E-03	+
Plxna3	567.8	0.382	2.89E-05	+
Ppox	327.6	0.420	9.70E-08	
Ptch1	854.7	0.104	9.82E-04	+
Ptch2	14.5	0.020	1.09E-11	+
Ptger2	25.3	0.356	1.06E-02	+
Ptgir	161.9	0.404	1.67E-02	+
Ptgis	281.1	0.490	1.47E-04	+
Ptgs1	258.9	0.492	1.52E-02	+
Ptprm	527.3	0.399	3.65E-05	+
Ptprn	210.0	0.482	1.69E-04	+
Rem1	81.6	0.296	1.78E-04	+
Rfng	412.7	0.491	4.57E-03	
Rfx1	350.0	0.386	9.43E-08	
Rfx2	97.7	0.322	2.50E-06	+
Slc50a1	357.6	0.483	3.30E-04	
Rgl2	739.6	0.424	2.91E-08	
S100b	33.7	0.407	8.77E-03	+
Atxn2	801.8	0.308	2.83E-03	
Scn7a	19.8	0.356	3.60E-02	+
Sh3bp1	215.2	0.272	4.57E-13	+
Slc2a4	504.0	0.452	1.47E-06	+
Slc4a3	365.6	0.326	7.08E-11	+
Stc1	284.8	0.367	2.55E-04	+
Tbx2	751.8	0.480	2.55E-05	+
Tbxa2r	147.9	0.487	1.30E-02	+
Tcea2	82.4	0.315	5.05E-07	+
Phf1	219.6	0.288	2.38E-12	+
Tert	110.3	0.381	6.33E-04	
Tgfb3	514.9	0.391	3.25E-06	+
Tgm2	1305.6	0.333	1.01E-14	+
Tg	4.7	0.162	3.93E-02	+
Thbd	1395.1	0.242	1.63E-22	+
Thy1	9.5	0.260	1.63E-02	+

Tiam1	615.8	0.497	6.99E-03	
Tll1	103.2	0.409	5.53E-04	+
Tnfaip2	67.2	0.237	2.24E-02	+
Ulk1	981.0	0.455	6.13E-03	+
Vegfc	105.3	0.484	3.99E-03	+
Wnt4	111.1	0.333	5.02E-06	+
Wnt5a	1398.7	0.486	2.18E-02	+
Pcgf2	629.3	0.432	8.42E-05	
Abcg1	72.6	0.238	2.96E-04	+
Chrnb1	66.9	0.421	1.05E-03	
Acvrl1	427.5	0.393	2.89E-04	+
Adam19	1613.5	0.448	6.92E-03	+
Adm	47.5	0.454	1.27E-02	+
Ahrr	24.1	0.279	1.10E-02	+
Anxa5	1539.3	0.494	2.07E-02	+
Aoc3	125.4	0.217	4.26E-04	+
Nr2f2	893.4	0.391	1.46E-02	+
Atp10a	47.3	0.285	3.21E-06	+
Bdkrb2	25.2	0.221	1.20E-05	+
C4b	7.4	0.165	9.93E-03	+
Cacna1g	960.7	0.247	7.62E-04	+
Car11	76.4	0.386	4.14E-04	+
Car2	123.1	0.273	9.78E-05	+
Casp1	14.2	0.414	4.28E-02	+
Cckar	229.5	0.328	1.86E-10	+
Cdc7	624.7	0.401	1.75E-05	
Cdh10	67.5	0.424	8.99E-03	+
Cdh11	3810.7	0.470	2.58E-03	+
Cdh4	48.1	0.405	2.43E-03	+
Ch25h	8.2	0.145	1.01E-04	+
Clcn2	265.4	0.427	1.03E-06	
Cln3	197.9	0.453	2.81E-06	
Col11a2	52.0	0.488	5.89E-04	
Col15a1	754.2	0.330	8.79E-13	+
Col18a1	1805.2	0.416	3.30E-03	+
Col3a1	33354.4	0.406	2.17E-03	+
Col4a1	7181.6	0.226	4.49E-20	+
Col4a2	3763.4	0.209	7.95E-28	+
Col6a1	7260.8	0.189	1.93E-32	+
Cpt1b	28.5	0.315	1.65E-04	

Csf2ra	267.2	0.488	9.80E-03	
Clip2	1275.1	0.409	9.12E-09	+
Cyp2d9	0.6	0.050	3.57E-02	+
Cyp46a1	15.5	0.250	3.59E-02	+
Dkk1	0.3	0.012	1.17E-05	+
Dlk1	6954.3	0.471	2.79E-03	+
Dmc1	21.0	0.343	1.10E-02	+
Dnm1	878.2	0.451	1.89E-02	
Edar	8.6	0.046	4.02E-14	+
Efnb1	961.3	0.350	1.88E-12	+
Efs	864.8	0.498	1.32E-02	+
Rhbdf1	630.1	0.478	2.85E-06	
Pou6f1	424.2	0.485	2.09E-02	+
Ephb3	660.3	0.472	1.77E-03	+
Epor	43.0	0.260	4.74E-06	+
Fbln1	2687.0	0.496	9.87E-07	+
Fbn2	2658.1	0.282	3.29E-04	+
Fbrs	633.4	0.392	1.58E-02	
Fes	118.3	0.450	7.36E-03	+
Il4i1	42.9	0.397	2.48E-03	+
Fkbp10	1215.4	0.418	2.96E-09	+
Foxf2	506.3	0.135	6.81E-23	+
Flt1	231.8	0.318	2.15E-04	+
Fmo1	45.6	0.350	4.48E-04	+
Fn1	4775.7	0.221	8.50E-05	+
Fosl1	35.1	0.415	2.13E-02	+
Ggta1	663.6	0.467	3.68E-06	+
Gli1	27.6	0.007	1.18E-136	+
Gng8	51.9	0.282	3.99E-04	+
Pdpn	358.7	0.409	4.08E-08	+
H2-DMa	43.4	0.431	5.16E-03	
Herc2	1829.4	0.436	3.85E-03	
Foxf1	1835.4	0.260	1.45E-19	+
Hoxa3	419.4	0.381	4.78E-02	+
Hoxa7	35.8	0.426	8.08E-03	+
Hoxb4	431.8	0.388	7.66E-08	+
Hoxb8	255.5	0.303	2.66E-02	+
Hoxc6	189.2	0.261	1.88E-02	+
Hsd17b1	0.9	0.059	8.39E-03	

Igfbp5	9447.2	0.433	1.70E-02	+
Il18bp	21.0	0.214	3.28E-02	
Inpp5d	110.8	0.400	3.35E-04	+
Inppl1	1485.8	0.394	2.18E-10	
Irs4	35.4	0.200	5.65E-03	+
Itga5	2263.9	0.406	6.49E-10	+
Itpr1	1147.8	0.415	5.71E-05	+
Jup	1950.4	0.433	1.15E-07	
Kcnk2	302.5	0.367	8.01E-03	+
Kcnk3	940.4	0.361	1.67E-04	+
Kifc2	131.6	0.300	8.92E-04	+
Lama4	1881.0	0.292	4.31E-14	+
Lamc1	5614.3	0.388	8.46E-08	+
Lcp2	68.0	0.378	3.46E-03	+
Lipe	185.9	0.442	1.15E-03	+
Myom1	406.3	0.326	4.68E-12	+
Ncoa1	760.0	0.469	1.97E-03	
Nid1	2909.0	0.319	6.85E-15	+
Nnmt	1.8	0.112	2.39E-02	
Nos2	95.1	0.361	6.10E-05	+
Notch4	681.4	0.387	1.20E-03	+
Pnoc	14.2	0.339	3.25E-02	+
Ntn3	321.6	0.278	6.19E-06	+
P4ha1	1131.2	0.431	1.68E-03	+
P4ha2	271.4	0.259	2.32E-04	+
Furin	1172.5	0.496	1.85E-03	
Per1	342.2	0.424	3.45E-02	
Per2	198.0	0.439	7.28E-05	
Prkcg	10.4	0.292	1.71E-02	
Plaur	129.8	0.329	1.63E-06	
Plod1	808.1	0.335	3.12E-12	+
Pltp	111.5	0.086	1.07E-28	+
Ppard	448.5	0.448	4.10E-02	
Ppef2	17.0	0.261	1.58E-02	+
Mapk11	182.7	0.480	8.98E-04	+
Procr	51.9	0.045	3.65E-14	+
Lgmn	1140.1	0.431	1.43E-03	
Ptgs2	80.5	0.406	1.63E-04	+
Ptpre	91.5	0.406	3.48E-04	+
Ptprs	4778.7	0.380	7.35E-11	+

Rasgrp2	53.5	0.213	4.44E-10	+
S100a4	9.5	0.301	2.12E-02	+
Ccl11	94.1	0.089	8.70E-20	+
Ccl2	42.2	0.367	6.79E-04	+
Serpinf1	397.4	0.259	2.24E-03	+
Sema3f	451.6	0.240	4.12E-18	+
Spi1	71.4	0.348	2.70E-03	+
Slc7a5	1663.7	0.423	5.36E-05	
Slit3	486.7	0.271	4.23E-03	+
C4a	7.8	0.297	3.57E-02	
Ncor2	1745.4	0.271	4.62E-02	
Snai1	72.8	0.141	7.91E-03	+
Sox5	214.7	0.346	1.57E-02	+
Tead3	734.6	0.475	3.27E-06	+
Tgfb1	276.6	0.239	3.95E-05	+
Tgfbr3	863.3	0.336	4.14E-03	+
Thbs1	868.6	0.436	5.97E-04	+
Thbs2	1276.0	0.302	1.26E-16	+
Thbs4	937.9	0.338	2.71E-05	+
Tia1	1986.3	0.481	2.68E-07	+
Tie1	911.4	0.477	6.66E-04	+
Tln1	3111.9	0.348	8.42E-13	+
Fmnl3	1082.2	0.398	6.19E-10	+
Zim1	360.7	0.334	9.42E-05	+
Aplnr	175.6	0.260	3.75E-02	+
C1ql1	124.4	0.293	1.66E-08	+
Gdf15	77.1	0.495	8.84E-04	
Ggt5	385.3	0.357	1.46E-04	+
Grem1	395.7	0.281	2.21E-15	+
Esyt1	780.4	0.416	6.86E-10	+
Nt5e	105.5	0.318	2.01E-06	+
Spry2	695.6	0.478	1.19E-04	+
Tekt2	35.8	0.302	1.29E-04	+
Angptl2	1039.0	0.492	2.06E-04	+
Cd97	891.2	0.231	3.82E-23	+
Clcn6	222.8	0.442	1.34E-05	
Clcn7	518.8	0.379	1.12E-09	
Mapkbp1	452.0	0.448	2.49E-03	+
Map3k3	755.1	0.483	4.28E-06	
Creb3l1	407.8	0.239	1.02E-02	+

Plod3	963.6	0.420	6.48E-10	
Spag1	47.8	0.254	5.83E-08	
Abca1	790.1	0.466	3.74E-02	+
Anxa6	3958.6	0.364	7.02E-03	+
Eno2	158.3	0.394	7.68E-04	+
Stom	963.8	0.419	3.66E-06	+
Flt3l	11.4	0.343	2.97E-02	
Gfpt2	81.3	0.498	9.56E-03	+
Gpr162	173.3	0.385	2.50E-03	+
Leprel2	785.8	0.375	9.49E-07	+
Hoxc4	288.7	0.382	2.77E-02	+
Kcnh2	795.7	0.497	6.10E-04	+
Ksr1	249.0	0.463	2.43E-03	
Loxl3	346.0	0.472	3.40E-06	+
Ltbp2	38.2	0.281	8.32E-04	+
Matn4	30.0	0.183	5.62E-06	+
Mc5r	3.3	0.194	4.50E-02	+
Mmp9	101.7	0.062	5.29E-13	+
Ngf	20.9	0.271	7.58E-04	+
Pam	1977.4	0.460	5.94E-03	+
Sema4b	425.9	0.465	2.57E-05	
Sema5b	67.2	0.285	7.30E-04	+
Sema6b	108.2	0.455	5.68E-04	+
Thbs3	307.2	0.275	1.83E-04	+
Itgb1bp2	3.6	0.154	1.56E-02	
Pla2g7	196.1	0.209	1.61E-02	+
Dok3	27.9	0.362	2.41E-03	
Pald1	849.4	0.420	1.57E-08	+
Magel2	62.4	0.477	1.74E-02	+
Abcc5	971.6	0.456	2.38E-07	
Plk3	52.1	0.321	2.03E-06	
Jag1	421.6	0.419	1.48E-05	+
Abca7	468.7	0.337	8.04E-12	
Bag3	535.5	0.373	5.49E-04	+
Ndrg2	477.2	0.426	5.69E-06	+
Zfp385a	305.8	0.433	3.40E-02	
Mapk12	106.6	0.454	2.26E-03	+
Dpf1	79.2	0.311	6.20E-07	+
Heyl	299.7	0.216	2.40E-04	+
Adamts8	467.2	0.354	4.59E-11	+

Apln	267.8	0.383	4.68E-07	+
Usp21	562.1	0.460	6.26E-07	
Mapk8ip3	1135.1	0.342	4.54E-12	
Ddx25	69.9	0.437	3.76E-03	+
Col5a1	5032.5	0.266	3.17E-20	+
Slit1	48.7	0.459	1.37E-02	+
Sufu	899.0	0.486	1.03E-02	+
Dkk3	462.5	0.466	7.83E-05	+
Capn15	292.3	0.403	3.47E-05	
Syt3	25.1	0.194	1.21E-06	+
Clasrp	236.9	0.243	1.56E-11	
Atp2a3	1158.0	0.416	1.46E-04	+
Dmp1	60.5	0.290	2.42E-05	+
Cntnap1	67.2	0.239	3.12E-02	
Nptx2	99.4	0.356	7.29E-05	+
Srrm1	2152.5	0.452	1.71E-04	
Chst3	310.3	0.336	4.01E-03	+
Vamp5	33.9	0.399	3.15E-03	+
Col5a3	52.3	0.296	1.59E-05	+
Krt14	24.7	0.404	1.60E-02	+
Stag3	56.1	0.359	2.61E-05	
Akap8l	397.1	0.414	3.71E-09	
Cd244	0.5	0.061	4.41E-02	
Scn1a	16.3	0.290	1.18E-02	+
Rassf5	40.7	0.428	2.48E-02	+
Calcrl	1051.7	0.427	7.37E-03	+
Prpf40b	443.2	0.390	1.10E-09	
Arc	17.2	0.153	7.55E-04	+
Plxnc1	91.6	0.303	1.75E-07	+
Hs3st3b1	198.6	0.238	6.94E-05	+
Sh2b2	81.3	0.478	6.29E-03	+
Wisp1	564.3	0.179	6.37E-06	+
Cpxm2	8.1	0.279	1.86E-02	+
Tmem131	2168.2	0.451	1.06E-02	
Avpr2	0.3	0.024	4.88E-02	
Cacng4	160.4	0.476	9.41E-03	+
Gabbr1	841.4	0.444	8.89E-07	+
Irgm2	234.2	0.477	1.02E-04	+
Ramp2	347.6	0.375	7.04E-08	+
Grk4	23.8	0.396	3.91E-02	+

Trpc3	34.5	0.431	4.26E-02	+
Grasp	179.9	0.486	5.60E-05	
Htra1	39.7	0.434	4.90E-03	+
Cxcl14	27.7	0.336	3.96E-02	+
Plxnb3	16.1	0.260	4.58E-03	+
Tmem45a	259.2	0.471	3.06E-02	+
Wsb1	3704.0	0.475	8.92E-08	+
Ddx39b	3671.4	0.494	1.04E-07	
Cpxm1	516.9	0.458	1.74E-06	+
Cdh13	62.5	0.434	4.10E-03	+
Runx3	9.5	0.210	2.28E-03	
Ggcx	288.2	0.343	3.46E-08	+
Git2	731.0	0.478	5.43E-06	
Copz2	118.5	0.350	3.50E-03	+
Tdo2	2.5	0.083	9.73E-04	+
Clcf1	67.5	0.423	2.60E-02	
Supt20	420.0	0.404	8.60E-09	
Clec4n	52.8	0.409	2.00E-03	+
Mtor	975.8	0.475	3.07E-05	
Fgf21	3.5	0.189	4.15E-02	
Slc37a2	71.1	0.476	2.44E-02	+
Hhip	66.1	0.034	2.16E-13	+
Ank	685.0	0.407	7.88E-09	
Ehd3	203.3	0.447	1.30E-04	+
Cramp1l	817.2	0.471	3.41E-02	
Nrip3	9.8	0.283	1.81E-02	+
Abcc9	2733.5	0.308	2.69E-04	+
Cxcl10	50.2	0.483	4.42E-02	+
Plcg1	1360.7	0.331	1.12E-14	+
Evc	486.0	0.338	1.61E-11	+
Itgax	8.3	0.059	6.91E-05	+
Kcne4	101.6	0.270	4.47E-10	+
Neurl1a	281.9	0.466	2.29E-02	+
Pappa	109.6	0.072	3.70E-05	+
Sall1	71.2	0.056	2.90E-07	+
Rab37	25.2	0.232	2.51E-03	+
Mmp19	294.1	0.497	1.02E-02	+
Cacna1h	838.2	0.159	6.91E-06	+
Adamdec1	5736.4	0.465	1.81E-02	+
Rps6kb2	150.9	0.311	3.93E-11	

Med12	910.3	0.307	1.36E-13	
Huwe1	6213.6	0.481	6.49E-03	
Slc22a17	834.3	0.406	1.17E-08	+
Agrn	4870.8	0.480	5.30E-06	
Doc2g	34.3	0.353	8.68E-05	
Fxyd7	66.4	0.431	3.90E-03	+
Parvg	32.3	0.442	1.78E-02	+
Herpud1	905.2	0.485	5.10E-07	
Ptges	104.7	0.469	5.74E-03	+
Fndc4	459.0	0.472	3.56E-06	+
Ddr2	1563.2	0.399	3.01E-06	+
Nisch	7609.3	0.479	3.46E-04	
Svep1	309.3	0.293	4.43E-02	+
Pmepa1	776.1	0.270	8.80E-17	+
Slc9a3r2	547.5	0.462	7.27E-07	+
Pkmyt1	408.5	0.479	9.28E-04	
Jam3	598.4	0.498	3.08E-06	+
Tmem132e	93.2	0.474	4.89E-03	+
Isyna1	1266.6	0.434	4.13E-09	
Tnfrsf22	58.6	0.248	6.64E-03	
Lime1	306.1	0.364	4.80E-09	
Wdr54	31.6	0.426	3.86E-02	+
Gdpd3	17.1	0.260	1.56E-03	
Fbln7	42.1	0.492	3.60E-02	+
Mxra8	1065.4	0.456	2.92E-07	+
Ipo4	846.0	0.444	3.17E-08	
Bves	70.0	0.352	5.53E-05	+
Tnfrsf23	28.1	0.120	1.80E-05	+
Stx1b	60.9	0.254	3.43E-07	+
Sharpin	313.5	0.493	2.08E-05	
Pcp4l1	126.7	0.257	1.08E-11	+
Exoc2	744.0	0.364	4.14E-12	+
Abi3	77.4	0.380	1.47E-03	+
Pnisr	1850.0	0.455	9.68E-09	
Col27a1	1004.8	0.266	2.69E-05	+
Aspn	231.6	0.465	1.93E-02	+
Dnase1l2	21.1	0.304	1.62E-03	
Kcng4	6.1	0.151	1.06E-02	+
Plbd1	26.1	0.320	1.77E-03	
Smarcd3	211.1	0.389	3.54E-06	+

Cap2	115.2	0.391	1.85E-05	+
Plxdc2	425.1	0.454	4.52E-06	+
Plxnd1	2192.7	0.359	1.90E-08	+
Tmem100	192.8	0.219	1.04E-17	+
Ppm1m	304.7	0.429	8.68E-08	+
Murc	26.2	0.310	2.80E-02	
Rcn3	1755.7	0.403	4.10E-03	+
Sdccag3	778.3	0.483	2.19E-06	
Col6a4	614.7	0.038	5.06E-21	+
Cthrc1	163.6	0.442	2.11E-05	+
Srpx2	129.6	0.206	1.42E-04	+
Cdan1	479.1	0.435	7.90E-07	
Sec31a	2343.7	0.451	1.20E-07	
Kmt2e	2449.1	0.442	3.33E-03	+
Sat2	67.8	0.466	7.90E-03	+
Dennd6b	124.5	0.345	6.36E-09	
Clic3	7.9	0.237	2.00E-02	
Sec24d	1272.9	0.289	3.18E-16	+
Col22a1	39.8	0.167	5.78E-07	+
Zmynd8	1617.4	0.410	7.74E-07	
Nkd1	435.4	0.380	3.46E-08	+
Chp2	2.9	0.098	1.51E-02	
Mier2	414.1	0.448	3.57E-06	
Ddo	0.6	0.042	8.47E-03	+
Sik3	828.8	0.480	1.25E-02	
Spef1	194.6	0.489	1.93E-04	
4933413G19Rik	31.2	0.458	4.23E-02	
Col24a1	334.5	0.342	2.02E-10	+
Izumo4	47.5	0.477	7.91E-03	
Rarres2	202.6	0.483	3.61E-02	+
Syde1	540.0	0.337	2.02E-07	+
Gramd1a	751.2	0.226	1.25E-22	+
Amdhd1	8.7	0.207	2.23E-03	+
Caskin1	161.9	0.299	4.54E-05	+
Osgin1	31.3	0.353	8.91E-05	
Zswim8	1694.4	0.354	5.64E-12	
Arhgef25	974.5	0.323	1.39E-07	+
Cda	44.4	0.463	9.52E-03	
Nkd2	45.2	0.290	1.12E-05	+
Fryl	880.3	0.443	1.20E-02	

Vps9d1	296.9	0.405	4.29E-07	+
Shmt2	1953.2	0.426	5.08E-09	
Rbm33	1279.9	0.463	3.11E-02	
Dzip1l	204.0	0.353	1.34E-07	+
Col16a1	833.3	0.384	1.76E-02	+
Anks3	437.8	0.473	6.06E-07	
Hspa12b	280.7	0.429	2.56E-06	+
Angptl1	1313.1	0.480	1.25E-02	+
Neil1	76.5	0.483	1.17E-03	
Fam101a	6.4	0.107	7.93E-06	+
Pear1	442.3	0.302	2.04E-04	
Bmper	113.6	0.364	7.99E-04	+
Col20a1	9.6	0.227	6.44E-03	
Rasip1	561.6	0.469	9.28E-06	+
1700094D03Rik	88.8	0.426	1.16E-03	
Btbd11	60.3	0.243	2.52E-02	+
Slc25a27	170.5	0.457	1.03E-03	+
Rftn2	495.9	0.470	1.79E-06	+
Syvn1	598.2	0.439	1.26E-03	
Ampd2	1032.8	0.326	4.59E-14	
Robo4	332.2	0.307	6.39E-12	+
Crtc2	398.8	0.386	7.45E-08	
Mau2	1353.5	0.488	1.83E-05	
Glb1l	293.2	0.444	4.66E-06	+
Ocstamp	3.9	0.049	4.69E-03	+
Atp13a2	924.5	0.452	1.17E-07	+
Lmbr1l	169.9	0.469	6.50E-05	
Hspb9	4.0	0.175	2.31E-02	
Ep400	2119.6	0.461	4.62E-02	
Fam227a	44.6	0.370	2.26E-03	+
Bcor	1202.7	0.493	2.04E-02	
Abcc3	71.6	0.498	3.53E-02	+
Gper1	48.2	0.266	4.68E-06	+
2310014L17Rik	12.7	0.135	7.82E-05	
Ppp1r12c	972.9	0.336	3.58E-07	+
Rgs7bp	90.2	0.407	6.40E-04	+
Fam162b	14.2	0.211	1.91E-04	+
Ptprb	299.2	0.466	4.38E-02	+
Chst15	1696.4	0.445	6.97E-04	+
Nup210l	15.5	0.274	1.28E-04	

Adamtsl2	17.3	0.169	2.05E-06	+
Batf3	19.1	0.147	3.03E-09	+
Htra3	1233.9	0.433	9.32E-08	+
Clip4	86.9	0.348	4.56E-06	+
Usp54	544.9	0.474	2.35E-03	+
Sfi1	266.0	0.494	4.66E-05	
Dync1h1	5270.8	0.388	2.82E-05	
Igsf6	50.4	0.375	2.47E-03	+
Tmprss5	15.9	0.356	4.10E-02	+
Dtx3	1351.7	0.278	8.51E-06	+
Sorcs2	916.8	0.420	5.38E-05	+
Id4	259.8	0.408	1.78E-07	+
Ift122	368.6	0.500	2.49E-05	
Tex15	99.5	0.464	3.70E-03	+
Fstl3	31.1	0.428	1.11E-02	+
Cnnm1	14.8	0.186	4.66E-06	
Bicc1	436.6	0.447	1.20E-03	+
Srrt	1673.4	0.439	3.04E-10	
Gigyf1	733.7	0.232	1.21E-20	
Dpp7	253.5	0.463	7.56E-05	
Otof	19.0	0.064	7.26E-03	+
Wasf1	389.5	0.408	1.48E-03	+
Plvap	96.8	0.165	7.02E-06	+
Dmpk	1093.5	0.427	3.79E-06	+
Rnf123	409.6	0.465	9.92E-07	
Tnfrsf25	6.3	0.219	2.54E-02	+
42255	1461.1	0.471	2.60E-04	+
B3galt5	10.3	0.053	7.64E-06	+
Loxl2	2832.8	0.497	2.43E-03	+
Rab34	630.8	0.384	3.65E-11	+
Slc4a10	45.7	0.107	3.21E-04	+
Pcdhgb1	2880.3	0.480	2.47E-02	+
Pcdhgb2	2907.9	0.480	2.34E-02	+
Pcdhgb4	2904.8	0.484	2.48E-02	+
Pcdhgb5	2903.4	0.480	2.41E-02	+
Pcdhgb6	3030.8	0.483	2.38E-02	+
Pcdhgb7	2971.2	0.482	2.92E-02	+
Pcdhgb8	2856.3	0.481	2.67E-02	+
Pcdhgc3	4061.6	0.459	3.76E-02	+
Pcdhgc4	2882.8	0.476	2.64E-02	+

Pcdhgc5	2842.8	0.476	2.66E-02	+
Pcdhga1	2896.2	0.484	2.03E-02	+
Pcdhga2	2942.0	0.481	2.59E-02	+
Pcdhga3	2949.4	0.483	2.29E-02	+
Pcdhga4	2914.1	0.482	2.29E-02	+
Pcdhga5	2906.6	0.482	2.67E-02	+
Pcdhga6	2929.5	0.484	2.27E-02	+
Pcdhga7	2995.2	0.490	2.88E-02	+
Pcdhga8	2893.2	0.476	2.51E-02	+
Pcdhga9	2890.5	0.478	2.93E-02	+
Pcdhga10	2932.0	0.483	2.66E-02	+
Pcdhga11	2935.5	0.483	2.73E-02	+
Pcdhga12	2922.9	0.483	2.49E-02	+
Adam33	8.4	0.221	1.77E-02	+
Fxyd2	8.0	0.059	5.81E-11	+
Fgd6	397.3	0.307	2.10E-02	+
Loxl4	12.3	0.240	8.72E-03	+
Cox4i2	21.9	0.387	1.95E-02	+
Trim8	692.6	0.495	7.68E-03	
Col4a6	158.5	0.312	2.21E-08	+
Slc24a3	465.3	0.351	3.73E-10	+
Antxr1	1144.0	0.449	2.52E-05	+
Gpr124	3078.0	0.448	9.14E-04	+
Gpr98	16.0	0.347	3.23E-02	
Mta1	1266.1	0.473	2.30E-06	
Necab2	33.2	0.430	1.32E-02	+
Bag6	2526.9	0.458	8.09E-08	
Cttnbp2	175.4	0.223	1.16E-15	+
Adcy4	81.8	0.290	5.99E-07	+
Celsr3	357.8	0.405	2.58E-02	+
Gjc3	29.4	0.335	4.16E-03	+
Synpo2	3349.5	0.462	3.90E-02	+
Ppap2b	999.8	0.473	1.06E-06	+
Emid1	410.4	0.468	9.94E-07	
Caskin2	671.8	0.387	1.52E-05	
Zcchc14	2251.0	0.478	4.74E-02	
Slc2a10	102.7	0.341	7.47E-06	+
Sp7	9.6	0.169	4.08E-04	+
Baiap2	189.8	0.362	1.88E-08	
Cacng7	343.9	0.325	1.05E-10	+

Il1rl2	101.7	0.302	1.92E-07	+
Znrf1	1035.3	0.473	1.35E-04	+
Slc8b1	159.5	0.310	2.10E-09	+
Atp13a1	915.2	0.443	1.11E-07	
Mapre3	213.1	0.349	1.73E-07	+
Erg	222.9	0.453	5.40E-05	+
Slc6a12	0.6	0.011	1.72E-10	+
Ier3	108.7	0.434	6.32E-04	+
Antxr2	794.0	0.483	9.40E-07	+
Ssbp4	456.7	0.499	1.11E-04	
Olfml3	1521.5	0.440	8.14E-09	+
Chpf2	685.0	0.482	2.41E-05	+
Krba1	665.0	0.489	2.69E-02	
Unc45a	612.9	0.484	5.29E-07	
Farp1	1052.4	0.490	7.10E-05	
Kdelr3	286.3	0.379	2.86E-08	+
Sgsm3	272.0	0.325	1.10E-12	
Gpsm3	76.7	0.251	3.16E-04	+
Actn1	3032.0	0.418	2.21E-10	
Havcr2	5.0	0.178	1.02E-02	+
Slc26a6	120.4	0.485	1.99E-04	
Mical1	388.0	0.418	3.04E-08	+
Arhgap4	50.1	0.458	8.13E-03	
Prpf8	4724.5	0.491	1.62E-06	
Abcg4	106.8	0.474	3.27E-02	+
Gbgt1	108.7	0.287	3.15E-03	+
Cytip	9.6	0.231	8.97E-03	+
Vasn	677.2	0.345	3.97E-03	+
Otoa	2.1	0.128	3.31E-02	
Prdm15	374.8	0.451	1.91E-06	
Tmem63a	387.6	0.434	1.53E-06	
Camk1g	108.6	0.340	2.06E-06	+
Nrbp2	367.6	0.432	2.02E-03	+
Dus3l	562.0	0.465	2.06E-08	
Lims2	50.3	0.335	2.41E-04	+
Pcnxl3	1434.6	0.459	8.73E-03	
Eml3	500.1	0.354	7.54E-11	
Rad9b	70.7	0.418	7.15E-04	
Tmem150a	191.0	0.439	1.53E-05	
Tnrc6a	2027.9	0.483	4.45E-04	

Sez6l2	233.3	0.467	1.82E-02	+
Map7d1	1604.3	0.417	7.98E-10	+
Lgi2	262.9	0.296	8.68E-12	+
Crtac1	72.2	0.382	4.03E-04	+
Mgat5	207.8	0.292	8.21E-03	
Gtpbp6	286.9	0.454	3.31E-07	
Angptl6	285.8	0.318	4.05E-09	
Pla2g4b	113.7	0.475	5.02E-04	
Fam193b	739.5	0.486	9.79E-04	
Pxk	319.5	0.383	1.78E-09	
Cerk	637.1	0.460	8.28E-07	+
P2rx3	57.5	0.412	1.16E-03	
Ccm2l	51.5	0.432	1.71E-02	+
Mypop	119.3	0.346	1.99E-03	+
Igflr1	41.8	0.303	5.61E-06	
Prr14	577.4	0.495	1.35E-05	
C1qtnf5	30.3	0.177	6.35E-09	+
Gdf10	133.7	0.283	1.65E-06	+
Pitpnc1	925.8	0.404	2.06E-03	+
Ranbp10	816.8	0.496	1.18E-03	
Xylt2	591.2	0.448	4.65E-07	+
Tpcn1	758.2	0.317	2.35E-04	
Cc2d1a	358.9	0.421	9.98E-09	
Hip1	1623.8	0.351	1.97E-03	+
Col6a2	5761.6	0.159	1.57E-29	+
Arhgap9	29.4	0.319	1.47E-04	+
Chd3	5860.9	0.287	1.13E-12	+
Plekhh3	361.3	0.458	7.21E-06	
Atf7	114.6	0.431	2.22E-04	
Zdhhc14	94.8	0.391	1.59E-04	+
Fam13b	796.7	0.466	9.13E-08	
Apbb3	231.2	0.356	5.48E-09	
Afap1l2	766.8	0.417	1.01E-08	+
Tesk2	212.2	0.432	2.07E-06	+
Tmem119	1187.6	0.461	3.20E-06	+
Lrch4	466.2	0.434	9.61E-07	
Cnot3	803.9	0.464	4.36E-06	
Ccdc106	123.4	0.445	8.02E-05	+
B3gnt8	55.5	0.420	9.41E-03	+
Wdr62	165.3	0.472	1.48E-04	

Tpcn2	148.4	0.490	4.53E-04	
Mfrp	30.6	0.178	7.09E-09	+
Rbm5	1791.6	0.435	6.86E-10	
Slco4a1	30.9	0.064	4.38E-31	+
Slc1a3	144.3	0.352	3.03E-06	+
Slc8a2	447.7	0.499	3.01E-02	+
Plcd3	55.6	0.469	1.58E-02	
Nmur2	11.0	0.287	2.56E-02	+
Sec16a	1684.7	0.483	2.27E-02	
Mmrn2	435.9	0.415	6.05E-07	+
Svil	3244.5	0.493	1.08E-05	+
BC037034	305.1	0.391	2.38E-08	
Cpne5	106.5	0.309	1.09E-03	+
Csrnp1	115.4	0.490	1.29E-02	+
Col23a1	3801.8	0.354	6.04E-05	+
Gpr156	19.4	0.391	4.15E-02	+
Gpsm1	674.4	0.481	2.43E-05	+
Nphp4	73.2	0.341	5.45E-05	+
Ankrd23	69.0	0.323	1.19E-05	
Cpne2	70.3	0.494	7.86E-03	+
Tenc1	917.7	0.290	1.99E-04	+
Adcy2	120.2	0.230	7.53E-14	+
Phldb1	837.4	0.428	3.10E-07	+
Aldh1l2	531.4	0.280	7.50E-16	
Strip1	1047.1	0.490	1.86E-07	
Mill2	8.0	0.304	4.14E-02	+
Acap1	94.2	0.275	3.20E-09	+
Scarf2	572.0	0.350	6.23E-10	+
Cpne7	13.0	0.169	1.50E-05	+
Adam1b	11.1	0.271	1.22E-02	
Adam1a	57.5	0.228	1.60E-07	+
Zdhhc8	862.0	0.461	1.55E-02	
Slc24a4	15.1	0.147	8.16E-07	+
Mark4	331.9	0.413	5.50E-07	
2210018M11Rik	565.4	0.496	1.29E-04	
Plcg2	71.9	0.466	2.40E-04	
Slc36a4	195.2	0.471	2.01E-02	+
Gpc2	509.5	0.494	1.52E-05	+
Ccdc134	131.5	0.414	8.06E-06	+
Cfap69	31.4	0.372	5.48E-03	

Adamts18	22.2	0.269	6.75E-04	+
Dennd2a	1022.4	0.478	4.65E-05	+
Cobl	387.2	0.276	4.50E-03	+
Dcaf15	536.5	0.479	1.59E-06	
Boc	529.1	0.463	1.03E-02	+
Polrmt	406.8	0.433	2.36E-08	
Hlf	74.4	0.394	1.70E-02	+
Unk	672.2	0.465	7.58E-06	
Lhfpl2	535.6	0.350	1.25E-07	+
Ldlrad4	158.6	0.389	3.52E-05	+
Pogz	1426.2	0.474	4.78E-04	
Gcn1l1	1694.2	0.477	5.84E-06	
Fgd5	371.3	0.498	1.39E-04	+
Leng8	1327.8	0.252	4.17E-09	
Gramd1b	59.2	0.260	2.54E-09	
Gbp9	69.6	0.448	5.05E-03	+
Dock4	382.1	0.430	7.00E-04	+
Adamts4	242.2	0.429	1.55E-03	+
Kank4	163.0	0.171	1.18E-05	+
Slc6a11	2.4	0.024	1.96E-14	+
Man2a2	2304.0	0.406	1.11E-06	+
Nlgn3	95.7	0.274	9.82E-03	+
Ankrd13b	597.4	0.471	4.00E-06	
Mtcl1	420.7	0.236	1.28E-04	+
Sap130	827.0	0.487	3.21E-02	
4930503L19Rik	349.1	0.405	1.23E-06	+
Pank4	499.8	0.353	1.16E-12	
Ssc5d	735.7	0.396	6.78E-03	+
Gpr97	11.3	0.278	1.51E-02	+
Gga3	476.1	0.430	2.42E-04	
Bai2	268.3	0.493	6.21E-04	+
Chd6	2064.5	0.450	1.35E-03	+
Leprel1	141.9	0.292	4.93E-08	+
Bmp3	518.0	0.141	1.02E-34	+
Arsj	7.9	0.108	1.96E-06	+
Ube2o	715.2	0.476	6.88E-06	
Zfp641	31.0	0.415	4.41E-02	+
Npr2	402.0	0.421	3.69E-07	+
Slc41a1	591.6	0.490	5.12E-05	+
Phf12	1189.0	0.446	2.34E-03	

Impg2	38.5	0.361	1.31E-03	
Gpbar1	7.1	0.046	8.57E-05	+
Slc38a2	6147.4	0.458	6.03E-08	
Dnaic1	7.1	0.167	3.36E-03	+
Zdhhc1	159.9	0.319	1.17E-07	+
Atxn7l2	297.9	0.359	2.10E-08	
Kif27	39.1	0.460	2.51E-02	+
Dock10	240.8	0.400	9.47E-04	+
Chdh	41.7	0.362	7.28E-04	+
2700081O15Rik	2824.0	0.484	3.87E-06	+
Apol7c	50.8	0.069	6.46E-06	+
Gsap	30.6	0.420	3.48E-02	+
Slitrk6	1578.4	0.489	8.80E-07	+
Hcar1	37.6	0.443	4.94E-02	+
Zfp384	955.5	0.466	1.21E-04	
Adamts2	318.6	0.392	1.13E-02	+
Tnfrsf26	4.0	0.184	4.43E-02	+
Gpr4	39.1	0.252	5.54E-03	+
Glp2r	37.1	0.148	6.20E-08	+
A230050P20Rik	167.2	0.281	9.40E-10	
Snhg11	98.7	0.311	1.74E-03	
Hoxc5	259.7	0.390	1.60E-04	+
Leprel4	746.3	0.498	4.11E-04	+
Bptf	2663.7	0.476	1.19E-02	
Itga11	209.2	0.116	7.65E-22	+
Fbxl7	387.6	0.395	5.29E-04	+
Dock6	791.8	0.191	7.94E-04	+
Fstl4	50.9	0.175	1.25E-03	+
Fndc9	11.2	0.157	2.94E-02	+
Adrbk2	748.6	0.459	8.12E-03	+
Casc1	3.6	0.166	1.08E-02	
Ankrd16	230.6	0.438	1.93E-06	
Itgb8	49.8	0.383	1.04E-03	+
Zfp653	169.8	0.431	2.12E-06	
Ust	131.1	0.473	5.23E-04	+
Micall1	1231.7	0.497	4.12E-02	+
Slx4	499.9	0.500	1.06E-04	
Arhgef15	168.8	0.447	4.06E-04	+
Plcb2	56.5	0.342	1.01E-02	+
Mkx	39.5	0.400	6.64E-03	+

Plekhh2	980.6	0.262	1.12E-12	+
Ryr3	95.1	0.366	1.48E-02	+
D630003M21Rik	45.6	0.131	1.61E-15	+
Fhod1	267.6	0.253	2.09E-14	
4933408B17Rik	21.8	0.199	8.71E-06	
Trpa1	17.0	0.241	1.50E-03	+
Prex1	528.5	0.406	1.91E-05	+
Exoc3l	165.7	0.374	3.31E-05	+
Mettl24	14.6	0.312	2.07E-02	+
Sh2d4b	2.1	0.134	4.15E-02	
Med12l	236.5	0.419	1.14E-05	+
Sdk1	1099.1	0.349	1.89E-02	+
Tmem150b	135.5	0.381	8.79E-06	+
Mapk15	6.4	0.237	1.10E-02	
Lrrtm2	67.9	0.388	9.19E-03	+
Setd1a	1304.9	0.370	3.54E-04	
Trim62	158.0	0.344	1.38E-03	+
Amigo2	98.4	0.262	1.13E-09	+
Arrb1	1341.8	0.425	9.43E-03	+
Hapln3	8.5	0.201	2.12E-03	+
Sorbs1	605.1	0.419	4.49E-06	+
Gpr153	633.3	0.452	2.00E-06	+
Nrg1	110.7	0.231	1.85E-11	+
Rcsd1	937.7	0.491	8.73E-07	+
Gjd3	2.5	0.105	5.66E-03	+
Uvrag	783.7	0.452	1.55E-07	
Oaf	990.4	0.392	1.52E-10	+
Tigd5	125.9	0.452	1.90E-02	+
Lrrtm3	63.9	0.245	2.99E-08	+
Clca5	68.2	0.193	1.12E-12	+
Dpy19l3	378.2	0.443	3.82E-03	+
Zfp592	1128.4	0.467	3.89E-02	
Plscr4	172.2	0.492	4.36E-04	+
Slc26a11	134.9	0.477	1.07E-03	
Pced1a	319.0	0.428	1.46E-06	
Rasal3	22.8	0.342	6.91E-03	+
Vstm4	222.3	0.227	4.00E-06	+
Hs3st3a1	56.2	0.345	4.27E-03	+
Dcun1d4	923.3	0.425	2.39E-08	+
Prkd2	342.1	0.374	5.64E-03	+

Pld4	113.5	0.490	1.04E-03	+
Gbf1	1163.1	0.475	3.70E-06	
Aoc2	51.1	0.346	1.32E-02	
Slc25a29	55.6	0.491	3.79E-02	+
Pxdn	6052.4	0.424	9.43E-07	+
Ushbp1	211.1	0.400	2.22E-04	+
Gpr141	6.6	0.231	2.46E-02	+
Fam167b	26.9	0.398	2.42E-02	+
Ntrk3	306.0	0.397	2.70E-04	+
Zfp692	249.9	0.353	1.53E-10	
Atxn2l	1615.2	0.335	7.94E-07	
Helz2	407.5	0.447	1.74E-02	
Fsd1	115.0	0.359	6.96E-07	+
Fat4	1508.3	0.182	9.86E-03	+
Proser3	206.5	0.448	1.03E-02	
Klhl6	103.3	0.367	1.16E-05	+
Gbp6	32.3	0.395	2.42E-02	+
Rnf31	284.6	0.485	1.34E-04	
Atg2a	500.6	0.343	6.64E-06	
1700025G04Rik	1592.3	0.492	3.16E-03	+
Cuedc1	506.0	0.376	3.81E-10	+
Ranbp3l	9.3	0.027	1.38E-35	+
Tbkbp1	445.6	0.404	2.23E-04	+
Tmem63b	730.7	0.481	1.12E-06	
Szt2	688.0	0.315	3.73E-04	
Arhgef40	1532.4	0.332	2.29E-14	+
Tanc1	1009.6	0.440	1.01E-04	
Klhl17	327.3	0.447	8.63E-06	
Ablim3	53.3	0.379	3.59E-04	+
Tmtc1	267.8	0.195	1.55E-05	+
Dgkq	361.0	0.460	1.02E-05	
Zfp335	549.7	0.382	7.76E-09	
Jade2	206.4	0.384	1.24E-02	
Ece1	2183.8	0.487	2.36E-06	+
Dot1l	988.1	0.439	1.06E-06	
Cdh24	254.0	0.438	1.09E-05	+
Ccdc84	86.1	0.318	1.57E-08	
Tlr12	21.1	0.061	4.12E-22	+
Mycbp2	2430.4	0.489	2.23E-03	
Gpr137	213.0	0.452	5.04E-05	+

Lmo3	57.4	0.367	2.43E-04	+
Acap3	460.0	0.438	2.04E-06	
Gtf3c1	1836.2	0.440	4.51E-08	
Plcxd1	228.5	0.461	1.22E-06	
Egfr	587.4	0.435	2.58E-04	+
Ccnl2	1575.6	0.462	2.00E-08	
Dnm3os	1104.1	0.277	5.13E-17	+
Has2os	11.1	0.283	1.38E-02	+
Snhg1	282.6	0.399	5.85E-09	
Pvt1	73.6	0.492	2.65E-03	
Neat1	498.5	0.368	9.62E-04	
Pisd-ps1	526.1	0.388	2.38E-04	
Pisd-ps3	526.7	0.389	2.37E-04	
ChkbCpt1b	339.0	0.413	7.22E-09	
3830408C21Rik	36.6	0.433	2.94E-02	+
2610203C20Rik	614.9	0.260	1.75E-02	+
C230035I16Rik	24.0	0.362	8.87E-03	+
A230057D06Rik	13.9	0.333	3.99E-02	+
Rab10os	85.8	0.488	2.61E-03	
4933439C10Rik	121.5	0.466	2.31E-04	
4732416N19Rik	16.3	0.198	1.53E-03	+
Peg3os	889.8	0.491	7.91E-03	+
Gm5577	41.5	0.329	9.29E-04	+
Clk1	4273.8	0.464	1.73E-05	
Ppp4r1l-ps	140.1	0.404	5.67E-05	+
D930048N14Rik	103.9	0.468	3.70E-03	
Gm5607	44.7	0.409	2.62E-02	+
Mirg	157.9	0.322	2.16E-03	+
AI450353	25.3	0.250	3.49E-02	
4930404I05Rik	5.2	0.193	3.33E-02	
Ftx	236.4	0.414	7.83E-07	
4930528A17Rik	23.8	0.413	2.22E-02	
9230102K24Rik	19.3	0.395	4.43E-02	+
F930015N05Rik	25.5	0.329	9.65E-03	+
Snord88c	0.9	0.074	4.29E-02	
Snord37	1.4	0.098	1.72E-02	
Snora17	0.9	0.059	5.21E-03	
Gm14005	0.5	0.022	2.24E-04	+
1700018A04Rik	3.6	0.066	3.58E-06	+
6530402F18Rik	13.1	0.213	1.01E-03	+

Gm11149	46.4	0.195	4.11E-02	+
Ppp1r3fos	18.6	0.418	4.42E-02	
Mir24-1	2.5	0.119	2.35E-02	+
Mir214	30.1	0.296	1.64E-02	+
Mir199a-2	6.2	0.254	4.13E-02	+
Mir671	16.8	0.360	4.29E-02	+
Mir761	0.6	0.108	4.44E-02	
Mir702	4.5	0.221	1.26E-02	
Gm4532	19.6	0.348	3.20E-03	
2810410L24Rik	88.6	0.388	1.01E-04	+
Mir22hg	48.2	0.492	1.56E-02	
F630028O10Rik	13.7	0.339	4.79E-02	+
Foxd2os	21.4	0.177	2.28E-04	+
Zfp57	549.3	0.427	8.93E-08	+
Gm20605	531.9	0.414	1.79E-07	
Bmp1	1719.2	0.304	2.31E-16	+
Prr33	67.8	0.131	2.50E-02	+
BC065397	43.0	0.451	1.44E-02	
Npff	16.5	0.295	2.96E-02	
AI504432	93.3	0.408	8.75E-05	+
Gm8221	27.4	0.072	3.40E-04	+
Miat	1474.4	0.393	1.56E-02	+
6030408B16Rik	19.1	0.072	5.46E-21	+
Gm5084	1.5	0.073	1.61E-03	+
Chkb	332.6	0.435	9.74E-08	
Mir3064	89.8	0.404	1.72E-04	+
Mir3074-1	4.1	0.133	9.95E-03	+
Adamts10	582.6	0.208	6.29E-25	+
1600020E01Rik	101.0	0.430	3.97E-05	
4930579G18Rik	78.1	0.340	2.71E-03	
4931403G20Rik	3.7	0.085	2.80E-02	
E230016M11Rik	45.4	0.250	2.75E-04	
Gm19434	5.2	0.194	2.78E-02	
Gm19897	39.2	0.281	9.56E-07	
Gm16796	3.4	0.380	4.09E-02	
Gm10785	21.0	0.295	4.39E-02	
Gm9899	70.0	0.493	8.07E-03	+
C920021L13Rik	38.4	0.342	1.38E-03	+
Pcsk2os2	5.7	0.116	2.26E-04	+
E130102H24Rik	34.8	0.474	1.32E-02	

A930011O12Rik	80.1	0.204	2.07E-03	+
Kcnd3os	2.5	0.134	2.19E-02	+
2700038G22Rik	36.9	0.378	3.25E-03	
Slc2a4rg-ps	100.8	0.315	2.97E-05	
2900076A07Rik	53.9	0.481	1.62E-02	
Gm20748	78.0	0.240	1.11E-02	+
1700071M16Rik	22.6	0.188	1.41E-05	+
Fendrr	259.8	0.091	4.49E-02	+
2210416O15Rik	9.0	0.240	6.41E-03	+
Klc2	408.6	0.477	1.62E-06	
AW549542	63.8	0.450	9.95E-03	+
E130310I04Rik	167.9	0.324	2.91E-04	+
Gm16617	39.1	0.252	2.56E-02	+
Gm16596	55.0	0.296	4.27E-06	+
A430090L17Rik	7.8	0.127	4.42E-02	+
B130024G19Rik	24.1	0.223	3.51E-05	+
Gm15612	318.6	0.470	7.62E-05	+
Gm11747	79.7	0.327	2.06E-02	+
Frs3os	10.8	0.259	8.78E-03	
9530052E02Rik	13.8	0.282	5.94E-03	
4732471J01Rik	24.6	0.373	1.80E-02	
Milr1	17.0	0.336	2.60E-02	+
Ager	31.7	0.242	6.11E-06	+
Phc1	982.1	0.454	4.36E-06	
Sema6c	324.7	0.404	7.64E-05	+
Pitpnm1	252.1	0.493	1.51E-04	
A330033J07Rik	5.5	0.087	2.35E-06	+
Cd22	5.7	0.282	4.27E-02	
Plekhg5	343.8	0.429	4.05E-06	+
Xntrpc	314.3	0.498	1.31E-04	
Mir6418	50.0	0.338	3.70E-07	
Mir6935	9.4	0.269	3.85E-02	+
Mir6991	1.8	0.109	6.92E-03	
Mir6992	2.3	0.128	2.58E-02	+
Mir7077	0.3	0.054	2.80E-02	
Mir8093	3.2	0.178	4.75E-03	
Mir8094	215.3	0.405	1.79E-08	
Mir1668	15.1	0.177	6.31E-05	+
Tmem67	181.4	0.498	2.04E-04	+
Map4k2	312.1	0.262	3.72E-15	+
Ndst3	42.4	0.420	1.82E-02	+
Trim46	121.0	0.257	1.09E-04	
Mb21d1	78.1	0.398	2.91E-04	+

Table S4.3. Genes downregulated by loss of Hh signaling. Average read counts for genes in whole intestine downregulated 2 fold (FC) by cyclopamine (Cyc) treatment (p-value ≤0.05)

Chapter V

Conclusions

In multiple tissue-specific settings, Hh signaling directs specific cell fate choices, controls tissue patterning and governs cell proliferation. While it is well established that Hh signaling is critical to the formation of several cell types in the developing intestine as well as influencing at least seven cell types in the adult intestine, almost nothing is known about *how* it does so. The critical questions are: What specific genes are activated? Which genomic enhancers activate those genes? How is context (cell-type) specificity of response established? This work has made several advances towards understanding characteristics of Hh enhancers as well as expanding on the role of Hh signaling in one context, the developing intestinal inner circular muscle (ICM), a component of the ISM. Computational methods, described in Chapter II and III, have made advances towards understanding characteristics of Hh enhancers. Results presented in Chapter II reveal that although some *Drosophila* Hh enhancer regions contain homotypic clustering of ci/GLI sites, homotypic clustering alone is insufficient information to predict Hh enhancers. Chapter III validates machine learning as a prediction method that has a high success rate for the identification of mammalian Hh enhancers and also establishes a new *in vitro* GLI library containing higher confidence binding sites for this factor. Finally, biological data presented in Chapter IV demonstrate a previously unknown role for the Hh target gene *cJun* in development of the ICM. Additionally, the work in Chapter IV suggests that Hh signaling may play similar roles in SM and skeletal muscle. Together, these results make important advances to understanding methods for identifying Hh signaling targets and suggest additional areas that require further study.

5.1 Computational Prediction

5.1.1 Effectiveness of Using Highly Conserved Sequence and Clustering for Hh Enhancer Prediction

Prior to the computational prediction methods presented in Chapters II and III, two computational tools had been developed to globally predict Hh enhancer regions: Enhancer Element Locator (EEL) and Module Cluster Analysis (MCA) (Hallikas et al., 2006; Vokes et al., 2007). EEL relies on the presence of clusters of TFBS within orthologous sequences from two species to predict active enhancer regions. Using human to mouse conservation and the presence of at least two predicted GLI TFBS, the authors identified only 42 elements as putative Hh enhancers in the mouse genome. Two of these 42 were previously known Hh enhancers for *Gli1* and *Ptch1* (Dai et al., 1999; Agren et al., 2004; Ikram et al., 2004), but none of the other 40 have ever been tested for Hh-responsiveness in functional assays. Therefore, the rate of false positive selection using this method is not clear. However, the false negative rate is very high. The set of 42 missed the other known Hh enhancer at the time *FoxA2* (Sasaki et al., 1997) and does not contain any of twelve additional Hh enhancer regions (Table 1.1) or regulatory regions confirmed as GLI dependent within this dissertation (*Boc, cJun, Dpp6, Hhip, Hipk2, Ptch1, Scube1*, *Tgfbr2*).

MCA predicts Hh enhancer regions by searching for enrichment of GLI TFBS against a background Markov model within highly conserved (across mouse, rat, human, dog and zebrafish) sequences. Using qPCR of GLI1^{FLAG} ChIP peaks from SHH treated embryoid bodies, the authors confirmed that 11/28 predicted regions, six previously identified, were bound by GLI1. The total number of MCA predicted enhancers was not reported. While almost 50% of predicted regions appear to be bound, none of these were actually tested for Hh responsiveness or for loss of responsiveness upon mutation of the GLI binding sites.

Both of these methods rely on the presence of more than one GLI TFBS and on the presence of highly conserved surrounding sequence. These approaches are most similar to the homotypic ci/GLI clustering method outlined in Chapter II, which searches for enrichment of ci/GLI binding sites against background chromosomes containing the same GC/AT landscape and have the same number and type of ci/GLI binding sites as the native genome. This method which identified 8/22 enhancers, one previously known, includes a conservation component, although it is far less restrictive than the ones used in EEL and MCA, only requiring a minimal overlap between enriched clusters in *D. melanogaster* and *D. pseudoobscura*. Comparing the success rate for MCA (22%, excluding previously known enhancers), to the method in Chapter II (33%), suggests that conservation might not be an important factor for predicting Hh enhancer regions. The low yields for these results also suggest that while some Hh enhancers may contain multiple ci/GLI sites, not all clusters function as enhancers. Indeed, the machine learning method implemented in Chapter III, using only sequence information from GLI^{FLAG} ChIP peaks, predicts Hh enhancers with a much higher accuracy 77% (Fletez-Brant et al., 2013).

The strength of these types of machine learning approaches is that no prior knowledge of enhancer characteristics is required for prediction. The kmer-SVM method implemented in Chapter III has no prior constraints regarding clustering of TFBS, conservation, or other parameters. However, it does rely on high quality biological data to use for training and such data might not be readily available in all cases. In fact, evaluation of the five publically available GLI^{FLAG} datasets (Vokes et al., 2007; Vokes et al., 2008; Lee et al., 2010; Peterson et al., 2012) resulted in only two (Vokes et al., 2008; Peterson et al., 2012) that were useful for prediction (Figure 3.2). One data set contained too few data points for training (Vokes et al., 2007) while the other two datasets (Lee et al., 2010) contained too much variability across its sequences for the classifier to effectively distinguish true from false positives within the training set (Figure 3.2FG).

The approach in Chapter III was designed to remove context specific characteristics by overlapping predictions generated in two different contexts and focusing on Hh pathway components, which should hypothetically be shared across any tissue with Hh activity. The results suggest that when Hh regulates its own pathway components in different tissues, multiple Hh enhancers may exist for regulation in each tissue context. The identification of additional Hh enhancers for *Hhip* and *Ptch1* is consistent with the analysis of the GLI1^{FLAG} and GLI3^{FLAG} datasets, which collect multiple peaks for *Boc*, *Hhip*, *Gli2*, *Hhipk2*, and *Ptch1*. It remains unclear whether these enhancers are active in different contexts or if they function together as secondary enhancers in an enhancer complex to drive gene expression. It would be interesting to link these enhancers to reporters and test their tissue and temporal specificity in transgenic mice. Evidence currently suggests that *Boc*, *Hhip*, *Gli2*, and *Hipk2* (Figure 3.4), as well as the *Drosophila ptc* enhancers (Table 2.1), have different enhancer regions that are active in different contexts. This is in line with work in other enhancer settings that suggests that the totality of the gene expression domain for a given gene might be determined by a large number of individual enhancers that are expressed in different spatial and temporal contexts (Goto et al., 1989). On the other hand, *Ptch1* appears to have multiple enhancers that are active at the same place and time (Vokes et al., 2007; Vokes et al., 2008; Lee et al., 2010; Peterson et al., 2012). The origin of these enhancers has not been studied. It is possible that they arose from duplication, or they may have independently evolved similar expression patterns, though the driving force for the latter is difficult to imagine.

5.1.2 Context Specific Predictions

The machine learning approach implemented in Chapter III might also work for predicting context specific features. In fact, the analysis of the neural progenitor dataset detected a SOX motif, likely representing the binding site for the neural specific GLI1 cofactor *Sox2* (Peterson et al., 2012). In addition, a TFBS for KROX-20, a putative limb factor was also detected in the GLI3^{FLAG} limb data. However, the successful use of machine learning to detect context specific features relies on the availability of high quality biological data.

5.1.3 Control of Regulatory Regions

The temporal and spatial specific activation of genes results from a complex regulatory circuitry, involving transcription factors as well as higher order regulatory elements (histone modifications) within chromatin that are modified to affect access to DNA (Calo and Wysocka, 2013). In order for transcription to initiate (RNA polymerase binding to a promoter) the DNA needs to be open and the transcription factors that complex into the enhancer need to be present. The ENCODE project is helping to strengthen predictions of putative enhancer regions (on a tissue specific level) by assaying multiple types of chromatin modifications across multiple cell types on a global scale. In particular, DNase I sensitive regions, P300 binding and histone marker combinations such as H3K4me1 and H3K4ac have been shown to correlate with enhancer activity and can be used to both uncover new enhancers as well as indicate the contexts in which a known enhancer is active (Heintzman et al., 2009; Rada-Iglesias et al., 2012). The approaches used in this dissertation focused on only on sequence features of transcription factor binding sites. Thus, while these genomic features predict the possibility of gene expression, it is likely that each Hh enhancer will only be active in a subset of contexts because of chromatin access (Figure 5.1). Newer machine learning methods have now been successfully implemented that incorporate chromatin accessibility with sequence information (Tsai et al., 2015). However, these methods require robust biological datasets that pair markers of open chromatin with GLI binding information. These currently do not exist.

5.1.4 Null Model Selection

Intrinsic properties of the native sequence are critical to genomic function but still poorly understood (Parker et al., 2009). For this reason, determining what to use as a background for sequence comparisons still remains an unresolved issue in enhancer prediction although the importance of maintaining the original properties of the native sequence when generating a background comparison has been discussed previously (Fitch, 1983). Distribution of GC content has been strongly correlated with gene density and regulatory features (Lander et al., 2001; Wang et al., 2012b). Therefore, when establishing background genomes for comparison of ci/GLI density, in Chapter II, we used a strategy that randomly flips each base to its complimentary partner. This approach maintains the GC/AT landscape of the native *Drosophila* chromosomes. This is particularly important because of the disparity between the average GC content of the *D. melanogaster* genome (43%) and the GC rich ci/GLI binding site (67%) (Hallikas et al., 2006; Keightley et al., 2009). However, generation of background sequence in this way ignores the relationship between sequential nucleotide sequences, such as those captured in dinucleotide frequencies. One way to incorporate intrinsic properties of the native sequence is to select background regions from the native genome. kmer-SVM randomly selects sequences with matching GC content from the native genome to compare the positive sequences against. The disadvantage to this approach is that it may include functional enhancers within the background sequence, which may train the classifier to miss some components of functional enhancers.

5.1.5 Evaluation of Prediction Methods

One of the issues in enhancer prediction is inconsistency in the methods used to verify predictions. While the gold standard is to test enhancer activity and to show that enhancer activity relies on transcription factor binding, this is very seldom done. For example, Biehs et al. used a DAM methylase protection assay to define Hh enhancers for *Drosophila*. They identified 52 supposed target genes that had protected regions and that were modulated when Hh signaling was increased or decreased, but none of these were actually functionally tested in enhancer assays (Biehs et al., 2010). A more appropriate and meaningful validation focuses on actually testing the proportion of true positives within a predicted positive set and this was the level of assessment that we performed in Chapter II and Chapter III. Of critical importance, we also verified positives as directly dependent on GLI binding. This is particularly important for evaluating Hh signaling, since it is an upstream regulator of many other transcription factors. Without the mutagenesis of GLI TFBS, it would be impossible to distinguish if enhancer activity in response to Hh signaling is direct or indirect. An additional strength would be to include predicted negatives in evaluations. Since only a small proportion of the hundreds of predictions can be biologically validated, including predicted negatives would help determine effectiveness of the method. If the prediction method correctly identifies 50% of putative positives but only 10% of the putative negatives are true negatives, it should not be considered successful. Of course, testing can be done on several levels. One approach is the use of transfected cell lines. However, while these generally reveal the potential for regulation, they do not always correctly reflect context specificity *in vivo*. A major challenge for functional testing is establishment of an assay system that can actually detect specific spatiotemporal activity. Perhaps the best assessment tool is the transgenic animal (e.g., transgenic *Drosophila* or mice), but these models require a significant amount of time and expense to generate and evaluate, especially in the case of mice. In addition, if the objective is to functionally test enhancers that were found by computational means and the spatiotemporal expression pattern is unknown (as was the case for our study in Chapter II), the requirement to analyze a large number of tissues and time points to find the specific site of expression can greatly complicate the analysis.

5.1.6 Annotation of Enhancers to Target Genes

A critical component to understanding gene regulation is linking enhancer regions to their target genes. Computationally, this still remains a large challenge since enhancers can target genes from great distances. Currently, most enhancer regions are annotated to the nearest neighboring genes; this is the annotation method we employed in Chapters II and III. Additionally, in Chapter II the other genes within the CCCTC-binding factor (CTCF) boundaries were also reported, since it is expected that enhancers would most likely target genes within the same boundaries (Chen et al., 2012). Without proper annotation, initial assessment of predictions using GO or GSEA may be misleading. Annotation is also of critical importance to understanding the underlying biology of the system. As high throughput chromatin interaction techniques including ChIA-PET, 3C, 5C, and Hi-C continue to advance and become more prominent, data that links enhancers to target genes will become increasing available.

5.2 Biological Conclusions and Future Directions

5.2.1 Regulators of ISM

Chapters II and III of this thesis start with computational strategies to predict features of biological systems that can be further tested in order to understand biological function. In Chapter IV, the analysis was run in the other direction: biological data was generated and then analyzed computationally to uncover how one of the visceral smooth muscle layers of the intestine, the ICM, is formed. Although ISM is of critical importance to the function of the intestine, surprisingly little is known about what genes are transcribed in this tissue or what molecular pathways control its development. One signaling pathway that had previously been linked to the development and homeostasis of ISM is Hedgehog. Acting downstream of Hh signaling, BMP is known to regulate smooth muscle progenitor populations (Kedinger et al., 1998a; Torihashi et al., 2009), while MYOCD, a master regulator of smooth muscle, is likely involved in maintenance of ISM in the adult (Zacharias et al., 2011).

Although these anecdotal studies have pinpointed some aspects of ISM transcriptional control, I reasoned that a more comprehensive analysis of gene expression in ISM might reveal important upstream regulators of ISM development. Therefore, I performed transcriptome profiling during early muscle development to identify genes that are enriched in intestinal mesenchyme tissue. Using gene set enrichment and clustering analysis followed by examination of *in situ* data at E14.5, I identified over 100 genes that are expressed in the ICM. The promoters of these genes were then analyzed to identify transcription factors that might be involved in the regulation of ISM genes. This analysis identified *cJun* as a regulator of ISM, expanding its previously suggested role as a regulator of both vascular and skeletal muscle cell homeostasis (Kami et al., 1995; Daury et al., 2001; Yasumoto et al., 2001; Chiba et al., 2014).

Since Hh signaling had been shown to be a regulator of *cJun* in some contexts (Laner-Plamberger et al., 2009; Amable et al., 2014), we confirmed that the same is true in muscle (Figure 4.5C). To identify a possible Hh enhancer, we examined the results presented in Chapter III and identified a predicted Hh-controlled regulatory region 60 kb upstream of *cJun*. This genomic region was found to drive gene activation in response to Hh and GLI-dependent activity was confirmed by retesting after mutagenesis of the GLI binding site (GKO). Attenuated response of the GKO sequence confirmed GLI-dependent activity (Figure 5.6).

This is the first study to recognize a potential role for *cJun* in the regulation of ISM. Analysis of the regions bound by cJUN in our ChIP-seq analysis revealed that many of these regions are also bound by factors known to be important for muscle development, including SRF and MYOCD. This finding implicates *cJun* as a participant in a transcriptional cascade that directs smooth muscle identity. Previous studies of cJUN primarily emphasize its role in the stimulation of gene expression in adult tissues that is medicated cellular stressors, such as inflammation or UV light. In this context, it works as a heterodimer with cFOS, which, like cJUN, is a cellular oncogene. It has also been established that in some cases, cells require cJUN for progression through the cell cycle and *cJun* null cells are arrested in G1 (Wisdom et al., 1999). In fact, previous analyses had demonstrated that *cJun* is required for proliferation of vascular smooth muscle (Yasumoto et al., 2001). We speculate that this proliferation function could be important in the context of the developing ISM as well. It will be important to functionally test the degree to which *cJun* actually participates in smooth muscle proliferation and differentiation by conditionally removing this factor from ISM. This could be accomplished with a conditional deletion of *cJun* using the Twist2-Cre line that expresses Cre recombinase throughout the mesenchymal compartment at E14.5 (Šošić et al., 2003).

The fact that *cJun* appears to be a Hh target, coupled with the potential role of cJUN as an important regulator of ISM genes suggests that Hh might function as a master regulator in this tissue. To examine other muscle regulatory factors downstream of Hh signaling, I next examined the transcriptome of the ICM after downregulating the Hh pathway using cyclopamine. In addition to the previously known Hh target *Myocd* (fold change with adj. p-values < 0.05 (FC): -2.13), several genes implicated in stem cell regulation or shown to regulate differentiation in other muscle types were also downregulated (Table 4.2). These data suggest dual roles for Hh in proliferation of smooth muscle precursors and promotion of differentiation into ISM. This is similar to skeletal muscle where Hh regulates both *MyoD* and *Myf5* (Borycki et al., 1999) (Chiang et al., 1996) (Gustafsson, 2002; Borello et al., 2006; Voronova et al., 2013), to control the establishment and maintenance of muscle progenitor cells (Pownall et al., 2002), as well as

Pax-3, to initiate differentiation (Borycki et al., 1998; Duprez et al., 1998; Pownall et al., 2002; Hammond et al., 2007). Additionally in skeletal muscle, Wnt acts downstream of Hh to coordinate the progenitor cell population (Braun and Gautel, 2011; Singh et al., 2012). The downregulation of several modulators of Wnt signaling by cyclopamine in our analysis (FC: *Dkk1*, -84.45; *Edar*, -21.86; *Sall1*, -17.75) suggests that a similar phenomenon might also occur in SM (He et al., 2013) (Kiefer et al., 2010; Wells et al., 2010) . This would be of interest to directly test, by carrying out a ChIP-seq for Hh targets in the ISM. Though no ChIP grade GLI antibody is available, a mouse line has been described that carries a FLAG-tagged version of GLI1. This line has been used successfully in several other studies, as described in Chapter III. Use of the Twist2-Cre driver to activate GLI1^{FLAG} at E14.5, in combination with the cyclopamine data already obtained, would provide an excellent approach to the elucidation of the Hh transcriptome in ISM. Hh signaling is likely to be very important in ISM, since overexpression of Hh has been shown to greatly amplify the SM population in the intestinal mesenchyme (Zacharias et al., 2011).

Surprisingly, *cJun* (fold change with adj. p-values > 0.05 (FCNS): -1.21) was not downregulated in this dataset. Since we showed that *cJun* was a direct target of Hh in muscle (Figure 4.5B) and had seen upregulation of *cJun* (Figure 4.5C) when intestinal mesenchyme (without epithelial tissue) was treated with the Hh agonist, SAG, it is likely that either the transcript is very stable or that additional signals maintain *cJun* levels in the context of the cyclopamine-treated whole intestine. One obvious possibility is *Mef2C*, which has been shown to modulate *cJun* through promoter interaction (Han et al., 1992; Han and Prywes, 1995) and was also not downregulated (FCNS: -1.03) in this dataset. The ERK pathway, which stimulates critical muscle factors, including *Caldesmon* and *IL-1β* (Hedges et al., 2000a; Hedges et al., 2000b) in airway smooth muscle, has been shown to act upstream of *Mef2C* to upregulate *cJun* (Fanger et al., 1997). However, imaging of *cJun* and *Mef2C* at this time point indicates that *Mef2C* expression occurs outside the ICM (Figure 5.2). Interestingly, muscle fibers stained with *Mef2C* appear to run in the longitudinal direction and overlap with the *Gli2* expression domain where the OLM will develop (Figure 5.2) (Kolterud et al., 2009). Since MEF2C and GLI2 have been previously shown to both regulate each other's expression and to form a cofactor complex in both cardiac and skeletal muscle (Voronova et al., 2012; Voronova et al., 2013), it would be interesting to test whether a similar phenomenon is occurring in the OLM of developing intestine.

5.2.2 Regulation and Timing of Hh Components (Coordination of Gene Targets)

Hh signaling was previously known to target muscle transcription factors *FoxF1, Mef2C* and *Myocd* with the data presented in Chapter IV expanding this list to include *cJun.* The next challenge is to determine how the downstream targets of Hh are coordinated. Many of the Hh muscle targets regulate each other; feedback and feedforward regulation is likely. A protein interaction between cJUN and MYOCD has been described in vascular smooth muscle that indicates that over expression of *cJun* represses *Myocd* function (Gordon et al., 2009b). Additionally, FOXF2 interacts with promoters of *Myocd* and *FoxF1* to modulate SRF signaling (Bolte et al., 2015). Determining the organization of these feedback loops would require functional experiments in genetic mouse models, coupled with gene expression analyses.

However, given recent successes in the use of embryonic stem cells to generate specific tissues *in vitro*, it is also interesting to imagine the development of an *in vitro* assay system for smooth muscle development and differentiation. Given the current paucity of good cell lines for the study of smooth muscle biology, this would provide a much needed and valuable tool.

Another important consideration regarding Hh signaling in the context of the intact tissue is the possibility that a morphogen gradient of Hh is important in smooth muscle specification. Experiments done over a decade ago by Sukegawa et al. suggested that a high concentration of Hh ligand is actually inhibitory to smooth muscle development. These authors concluded that this requirement for lower concentrations of Hh ligand accounts for the fact that the muscularis externa develops so far away from the epithelium, the source of the ligand. In fact, they made intestinal sandwich cultures in which the epithelium was placed on the outside of the intestinal tube and found that this shifted the location of smooth muscle development (Sukegawa et al., 2000). Though later experiments showed that this may be an over-simplification (i.e., overexpression of Hh in the epithelium causes ectopic muscle to develop in mesenchyme directly adjacent to the epithelium) (Zacharias et al., 2011), it is nevertheless true that Hh does act as a morphogen in several settings (Vokes et al., 2007; Vokes et al., 2008; Peterson et al., 2012) and it is interesting to consider how this could play out at the level of the enhancers. It is likely that these complex questions about spatial patterning might be best tackled by developing simple systems such as the *in vitro* models discussed above, in which both Hh concentration and tissue patterning could be engineered.

5.3 Outcomes

In conclusion, the results of this dissertation emphasize the importance of integrating computational methods with biological data. By using both in parallel, advances have been made in understanding characteristics of Hh enhancers and critical findings, determining gene targets as well as regulatory regions, within the context of inner circular muscle development were uncovered. These findings further implicate Hh signaling as a master regulator of intestinal smooth muscle development and identify a new role for *cJun* within this cascade. Together these results may lead to a greater understanding of disorders of the intestine.

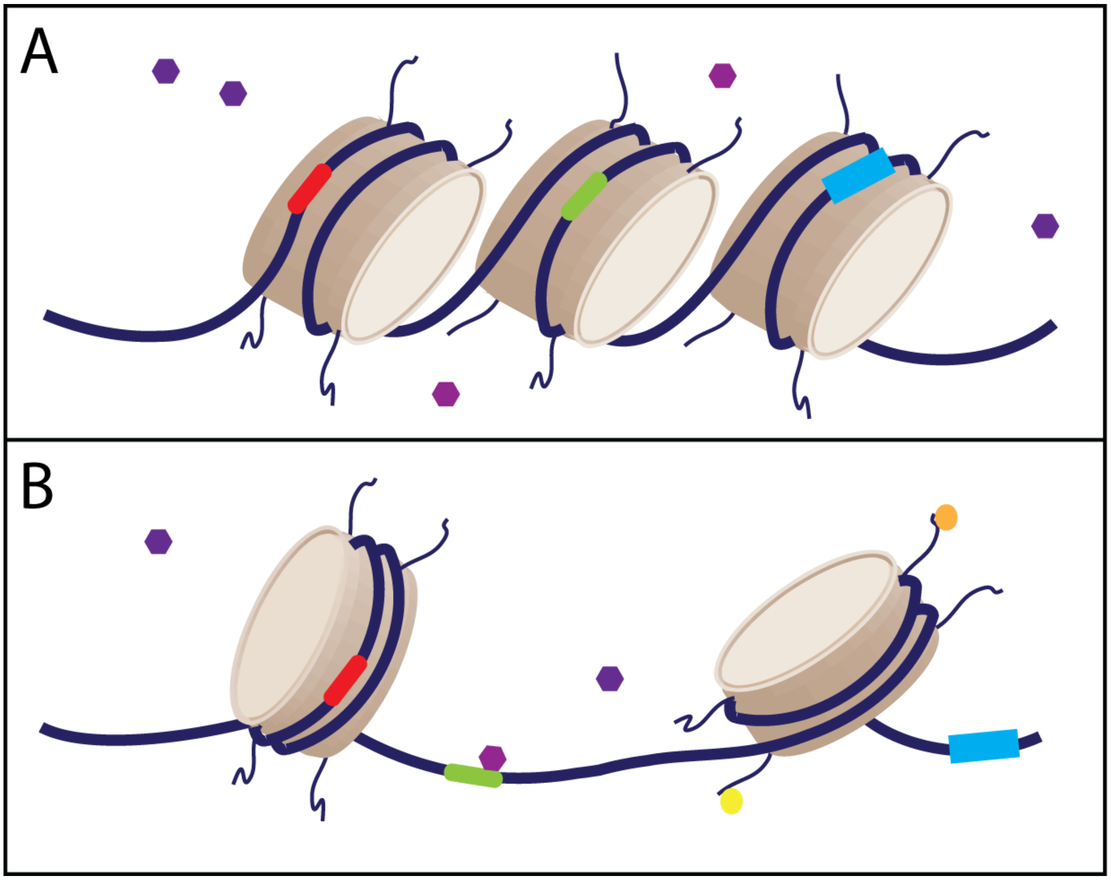


Figure 5.1. Effect of chromatin accessibility on enhancer function. (A) Nucleosomes limiting access of regulatory regions (red and green) and gene (blue) to transcriptional machinery. **(B)** Histone modifications (yellow circles) exposing an enhancer (green) region to transcription factors (purple).

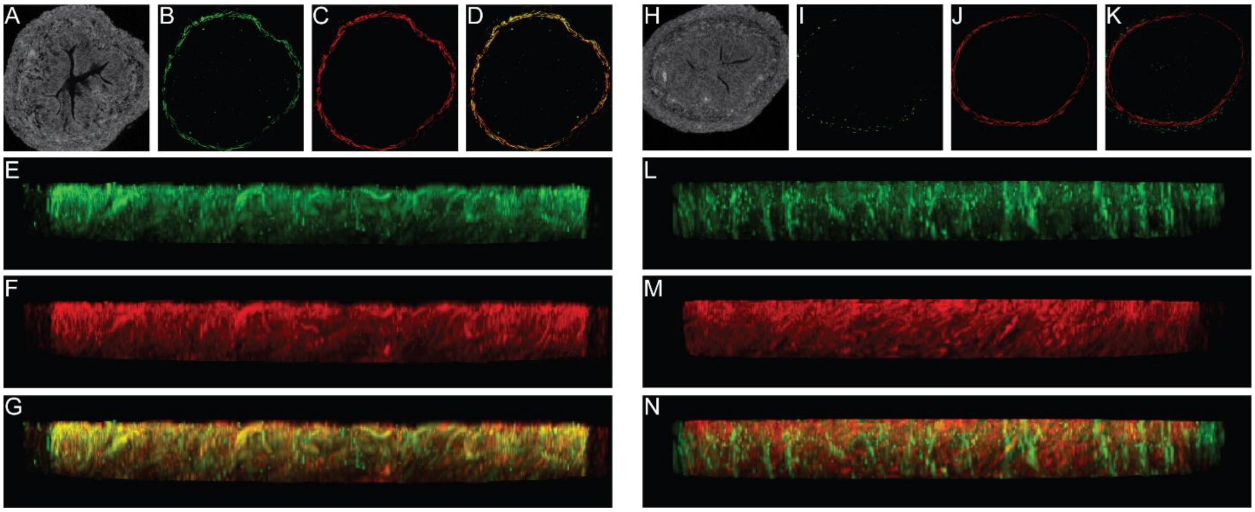


Figure 5.2. cJUN and MEF2C localize to different populations in E14.5 intestines. Intestines collected from BL6 mice were cross sectioned and stained for DAPI (grey) **(AH)**, the smooth muscle marker αSMA (red) **(CFGJMN)**, cJUN (green) **(BEG)** or MEF2C (green) **(ILN)**. Images for cross sectioned intestines **(ABCDHIJK)** and the side profile of the intestine **(EFGLMN)** are shown. At E14.5, αSMA exclusively stains the ICM. cJUN co-localizes with αSMA **(DG)**. MEF2C staining occurs outside of the ICM in the region where the OLM will develop **(KN)**.

References

Abrams J, Davuluri G, Seiler C, Pack M. 2012. Smooth muscle caldesmon modulates peristalsis in the wild type and non-innervated zebrafish intestine. Neurogastroenterol Motil 24:288-299.

Aglyamova GV, Agarwala S. 2007. Gene expression analysis of the hedgehog signaling cascade in the chick midbrain and spinal cord. Dev Dyn 236:1363-1373.

Agren M, Kogerman P, Kleman MI, Wessling M, Toftgard R. 2004. Expression of the PTCH1 tumor suppressor gene is regulated by alternative promoters and a single functional Gli-binding site. Gene 330:101-114.

Ahmad SM, Busser BW, Huang, Cozart EJ, Michaud S, Zhu X, Jeffries N, Aboukhalil A, Bulyk ML, Ovcharenko I, Michelson AM. 2014. Machine learning classification of cell-specific cardiac enhancers uncovers developmental subnetworks regulating progenitor cell division and cell fate specification. Development (Cambridge, England) 141:878-888.

Alexandre C, Jacinto A, Ingham PW. 1996. Transcriptional activation of hedgehog target genes in Drosophila is mediated directly by the cubitus interruptus protein, a member of the GLI family of zinc finger DNA-binding proteins. Genes & Development 10:1-12.

Alkema WB, Johansson O, Lagergren J, Wasserman WW. 2004. MSCAN: identification of functional clusters of transcription factor binding sites. Nucleic Acids Research 32:W195-198.

Allen BL, Song JY, Izzi L, Althaus IW, Kang JS, Charron F, Krauss RS, McMahon AP. 2011. Overlapping roles and collective requirement for the coreceptors GAS1, CDO, and BOC in SHH pathway function. Dev Cell 20:775-787.

Alstead EM, Murphy MN, Flanagan AM, Bishop AE, Hodgson HJ. 1988. Familial autonomic visceral myopathy with degeneration of muscularis mucosae. J Clin Pathol 41:424-429.

Amable L, Gavin E, Kudo K, Meng E, Rocconi RP, Shevde LA, Reed E. 2014. GLI1 upregulates C-JUN through a specific 130-kDa isoform. Int J Oncol 44:655-661.

Anders S, Huber W. 2010. Differential expression analysis for sequence count data. Genome Biol 11:R106.

Antonucci A, Fronzoni L, Cogliandro L, Cogliandro RF, Caputo C, De Giorgio R, Pallotti F, Barbara G, Corinaldesi R, Stanghellini V. 2008. Chronic intestinal pseudo-obstruction. World J Gastroenterol 14:2953-2961.

Anuras S, Mitros FA, Nowak TV, Ionasescu VV, Gurll NJ, Christensen J, Green JB. 1983. A familial visceral myopathy with external ophthalmoplegia and autosomal recessive transmission. Gastroenterology 84:346-353.

Anuras S, Shaw A, Christensen J. 1981. The familial syndromes of intestinal pseudoobstruction. Am J Hum Genet 33:584-591.

Austin ED, Ma L, LeDuc C, Berman Rosenzweig E, Borczuk A, Phillips JA, 3rd, Palomero T, Sumazin P, Kim HR, Talati MH, West J, Loyd JE, Chung WK. 2012. Whole exome sequencing to identify a novel gene (caveolin-1) associated with human pulmonary arterial hypertension. Circ Cardiovasc Genet 5:336-343.

Bailey TL. 2011. DREME: motif discovery in transcription factor ChIP-seq data. Bioinformatics 27:1653-1659.

Bailey TL, Machanick P. 2012. Inferring direct DNA binding from ChIP-seq. Nucleic Acids Res 40:e128.

Baker LA, Gomez RA. 1998. Embryonic development of the ureter and bladder: acquisition of smooth muscle. J Urol 160:545-550.

Barakat MT, Humke EW, Scott MP. 2010. Learning from Jekyll to control Hyde: Hedgehog signaling in development and cancer. Trends Mol Med 16:337-348.

Barolo S, Posakony JW. 2002. Three habits of highly effective signaling pathways: principles of transcriptional control by developmental cell signaling. Genes Dev 16:1167-1181.

Beachy PA, Hymowitz SG, Lazarus RA, Leahy DJ, Siebold C. 2010. Interactions between Hedgehog proteins and their binding partners come into view. Genes & Development 24:2001-2012.

Bejerano G, Pheasant M, Makunin I, Stephen S, Kent WJ, Mattick JS, Haussler D. 2004. Ultraconserved elements in the human genome. Science (New York, N.Y.) 304:1321-1325.

Benhaddou A, Keime C, Ye T, Morlon A, Michel I, Jost B, Mengus G, Davidson I. 2012. Transcription factor TEAD4 regulates expression of myogenin and the unfolded protein response genes during C2C12 cell differentiation. Cell Death Differ 19:220-231.

Berkes CA, Bergstrom DA, Penn BH, Seaver KJ, Knoepfler PS, Tapscott SJ. 2004. Pbx marks genes for activation by MyoD indicating a role for a homeodomain protein in establishing myogenic potential. Mol Cell 14:465-477.

Berman BP, Nibu Y, Pfeiffer BD, Tomancak P, Celniker SE, Levine M, Rubin GM, Eisen MB. 2002. Exploiting transcription factor binding site clustering to identify cis-regulatory modules involved in pattern formation in the Drosophila genome. Proceedings of the National Academy of Sciences of the United States of America 99:757-762.

Berman BP, Pfeiffer BD, Laverty TR, Salzberg SL, Rubin GM, Eisen MB, Celniker SE. 2004. Computational identification of developmental enhancers: conservation and function of transcription factor binding-site clusters in Drosophila melanogaster and Drosophila pseudoobscura. In: Genome Biology. pp R61-24.

Bernstein BE, Birney E, Dunham I, Green ED, Gunter C, Snyder M. 2012. An integrated encyclopedia of DNA elements in the human genome. Nature 489:57-74.

Bery A, Bery i, Martynoga, Guillemot F, Joly J, Rétaux S. 2013. Characterization of Enhancers Active in the Mouse Embryonic Cerebral Cortex Suggests Sox/Pou cis-Regulatory Logics and Heterogeneity of Cortical Progenitors. Cerebral cortex (New York, N.Y. : 1991):1-13.

Biehs B, Kechris K, Liu S, Kornberg TB. 2010. Hedgehog targets in the Drosophila embryo and the mechanisms that generate tissue-specific outputs of Hedgehog signaling. Development (Cambridge, England) 137:1-12.

Birnbaum RY, Clowney EJ, Agamy O, Kim MJ, Zhao J, Yamanaka T, Pappalardo Z, Clarke SL, Wenger AM, Nguyen L, Gurrieri F, Everman DB, Schwartz CE, Birk OS, Bejerano G, Lomvardas S, Ahituv N. 2012. Coding exons function as tissue-specific enhancers of nearby genes. Genome Research 22:1059-1068.

Bischof J, Maeda RK, Hediger M, Karch F, Basler K. 2007. An optimized transgenesis system for Drosophila using germ-line-specific phiC31 integrases. Proc Natl Acad Sci U S A 104:3312-3317.

Bitar KN. 2003. Function of gastrointestinal smooth muscle: from signaling to contractile proteins. Am J Med 115 Suppl 3A:15S-23S.

Blanchette M, Kent WJ, Riemer C, Elnitski L, Smit AF, Roskin KM, Baertsch R, Rosenbloom K, Clawson H, Green ED, Haussler D, Miller W. 2004. Aligning multiple genomic sequences with the threaded blockset aligner. Genome Res 14:708-715.

Blanco J, Seimiya M, Pauli T, Reichert H, Gehring WJ. 2009. Wingless and Hedgehog signaling pathways regulate orthodenticle and eyes absent during ocelli development in Drosophila. Dev Biol 329:104-115.

Bolte C, Ren X, Tomley T, Ustiyan V, Pradhan A, Hoggatt A, Kalin TV, Herring BP, Kalinichenko VV. 2015. Forkhead box F2 regulation of platelet-derived growth factor and myocardin/serum response factor signaling is essential for intestinal development. J Biol Chem 290:7563-7575.

Borello U, Berarducci B, Murphy P, Bajard L, Buffa V, Piccolo S, Buckingham M, Cossu G. 2006. The Wnt/beta-catenin pathway regulates Gli-mediated Myf5 expression during somitogenesis. Development 133:3723-3732.

Borycki AG, Brunk B, Tajbakhsh S, Buckingham M, Chiang C, Emerson CP, Jr. 1999. Sonic hedgehog controls epaxial muscle determination through Myf5 activation. Development 126:4053-4063.

Borycki AG, Mendham L, Emerson CP, Jr. 1998. Control of somite patterning by Sonic hedgehog and its downstream signal response genes. Development 125:777-790.

Bouchard M, St-Amand J, Cote S. 2000. Combinatorial activity of pair-rule proteins on the Drosophila gooseberry early enhancer. Dev Biol 222:135-146.

Boy AL, Zhai Z, Habring-Muller A, Kussler-Schneider Y, Kaspar P, Lohmann I. 2010. Vectors for efficient and high-throughput construction of fluorescent drosophila reporters using the PhiC31 site-specific integration system. Genesis 48:452-456.

Braun T, Gautel M. 2011. Transcriptional mechanisms regulating skeletal muscle differentiation, growth and homeostasis. Nature reviews. Molecular cell biology 12:349-361.

Braun T, Rudnicki MA, Arnold HH, Jaenisch R. 1992. Targeted inactivation of the muscle regulatory gene Myf-5 results in abnormal rib development and perinatal death. Cell 71:369-382.

Bren-Mattison Y, Hausburg M, Olwin BB. 2011. Growth of limb muscle is dependent on skeletal-derived Indian hedgehog. Dev Biol 356:486-495.

Briscoe J, Thérond PP. 2013. The mechanisms of Hedgehog signalling and its roles in development and disease. Nature reviews. Molecular cell biology 14:416-429.

Bulyk ML. 2003. Computational prediction of transcription-factor binding site locations. Genome Biology 5:201.

Burke R, Nellen D, Bellotto M, Hafen E, Senti KA, Dickson BJ, Basler K. 1999. Dispatched, a novel sterol-sensing domain protein dedicated to the release of cholesterol-modified hedgehog from signaling cells. Cell 99:803-815.

Burzynski GM, Reed X, Taher L, Stine ZE, Matsui T, Ovcharenko I, McCallion AS. 2012. Systematic elucidation and in vivo validation of sequences enriched in hindbrain transcriptional control. Genome Research 22:2278-2289.

Byrd N, Grabel L. 2004. Hedgehog signaling in murine vasculogenesis and angiogenesis. Trends Cardiovasc Med 14:308-313.

Calo E, Wysocka J. 2013. Modification of enhancer chromatin: what, how, and why? Mol Cell 49:825-837.

Caubit X, Lye CM, Martin E, Core N, Long DA, Vola C, Jenkins D, Garratt AN, Skaer H, Woolf AS, Fasano L. 2008. Teashirt 3 is necessary for ureteral smooth muscle differentiation downstream of SHH and BMP4. Development 135:3301-3310.

Celniker SE, Wheeler DA, Kronmiller B, Carlson JW, Halpern A, Patel S, Adams M, Champe M, Dugan SP, Frise E, Hodgson A, George RA, Hoskins RA, Laverty T, Muzny DM, Nelson CR, Pacleb JM, Park S, Pfeiffer BD, Richards S, Sodergren EJ, Svirskas R, Tabor PE, Wan K, Stapleton M, Sutton GG, Venter C, Weinstock G, Scherer SE, Myers EW, Gibbs RA, Rubin GM. 2002. Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence. Genome Biol 3:RESEARCH0079.

Chen CN, Li YS, Yeh YT, Lee PL, Usami S, Chien S, Chiu JJ. 2006. Synergistic roles of platelet-derived growth factor-BB and interleukin-1beta in phenotypic modulation of human aortic smooth muscle cells. Proc Natl Acad Sci U S A 103:2665-2670.

Chen H, Tian Y, Shu W, Bo X, Wang S. 2012. Comprehensive identification and annotation of cell type-specific and ubiquitous CTCF-binding sites in the human genome. PLoS One 7:e41374.

Chen JK, Taipale J, Cooper MK, Beachy PA. 2002. Inhibition of Hedgehog signaling by direct binding of cyclopamine to Smoothened. Genes Dev 16:2743-2748.

Chi J, Rodriguez EH, Wang Z, Nuyten DS, Mukherjee S, Rijn M, Vijver MJ, Hastie T, Brown PO. 2007. Gene expression programs of human smooth muscle cells: tissue-specific differentiation and prognostic significance in breast cancers. PLoS genetics 3:1770-1784.

Chiang C, Litingtung Y, Lee E, Young KE, Corden JL, Westphal H, Beachy PA. 1996. Cyclopia and defective axial patterning in mice lacking Sonic hedgehog gene function. Nature 383:407-413.

Chiba S, Sumi Y, Okayasu K, Okamoto T, Tateishi T, Furusawa H, Tsuchiya K, Fujie T, Tamaoka M, Sakashita H, Miyazaki Y, Inase N. 2014. The c-jun N-terminal kinase signaling pathway regulates airway smooth muscle cell proliferation. European Respiratory Journal 44.

Christ B, Ordahl CP. 1995. Early stages of chick somite development. Anat Embryol (Berl) 191:381-396.

Chuang PT, McMahon AP. 1999. Vertebrate Hedgehog signalling modulated by induction of a Hedgehog-binding protein. Nature 397:617-621.

Cooper AF, Yu KP, Brueckner M, Brailey LL, Johnson L, McGrath JM, Bale AE. 2005. Cardiac and CNS defects in a mouse with targeted disruption of suppressor of fused. Development 132:4407-4417.

Coward E. 1999. Shufflet: shuffling sequences while conserving the k-let counts. Bioinformatics 15:1058-1059.

Creanga A, Glenn TD, Mann RK, Saunders AM, Talbot WS, Beachy PA. 2012. Scube/You activity mediates release of dually lipid-modified Hedgehog signal in soluble form. Genes Dev 26:1312-1325.

Creemers EE, Sutherland LB, Oh J, Barbosa AC, Olson EN. 2006. Coactivation of MEF2 by the SAP domain proteins myocardin and MASTR. Molecular cell 23:83-96.

Creyghton MP, Cheng AW, Welstead GG, Kooistra T, Carey BW, Steine EJ, Hanna J, Lodato MA, Frampton GM, Sharp PA, Boyer LA, Young RA, Jaenisch R. 2010. Histone H3K27ac separates active from poised enhancers and predicts developmental state. Proceedings of the National Academy of Sciences of the United States of America 107:21931-21936.

Crooks GE, Hon G, Chandonia JM, Brenner SE. 2004. WebLogo: a sequence logo generator. Genome Res 14:1188-1190.

Cusanovich DA, Pavlovic B, Pritchard JK, Gilad Y. 2014. The functional consequences of variation in transcription factor binding. PLoS genetics 10:e1004226.

Dai P, Akimaru H, Tanaka Y, Maekawa T, Nakafuku M, Ishii S. 1999. Sonic Hedgehog-induced activation of the Gli1 promoter is mediated by GLI3. The Journal of biological chemistry 274:8143-8152.

Daury L, Busson M, Tourkine N, Casas F, Cassar-Malek I, Wrutniak-Cabello C, Castellazzi M, Cabello G. 2001. Opposing functions of ATF2 and Fos-like transcription factors in c-Jun-mediated myogenin expression and terminal differentiation of avian myoblasts. Oncogene 20:7998-8008.

De Santa Barbara P, Williams J, Goldstein AM, Doyle AM, Nielsen C, Winfield S, Faure S, Roberts DJ. 2005. Bone morphogenetic protein signaling pathway plays multiple roles during gastrointestinal tract development. Dev Dyn 234:312-322.

de Sauvage F. 2007. The Hh signaling pathway in cancer. Bull Mem Acad R Med Belg 162:219-223.

Dean A. 2011. In the loop: long range chromatin interactions and gene regulation. Briefings in functional genomics 10:3-10.

Dermitzakis ET, Clark AG. 2002. Evolution of transcription factor binding sites in Mammalian gene regulatory regions: conservation and turnover. Mol Biol Evol 19:1114-1121.

DeRouen MC, Oro AE. 2009. The primary cilium: a small yet mighty organelle. J Invest Dermatol 129:264-265.

Dessaud E, McMahon AP, Briscoe J. 2008. Pattern formation in the vertebrate neural tube: a sonic hedgehog morphogen-regulated transcriptional network. Development 135:2489-2503.

Di Padova M, Caretti G, Zhao P, Hoffman EP, Sartorelli V. 2007. MyoD acetylation influences temporal patterns of skeletal muscle gene expression. J Biol Chem 282:37650-37659.

Diez-Roux G, Banfi S, Sultan M, Geffers L, Anand S, Rozado D, Magen A, Canidio E, Pagani M, Peluso I, Lin-Marq N, Koch M, Bilio M, Cantiello I, Verde R, De Masi C, Bianchi SA, Cicchini J, Perroud E, Mehmeti S, Dagand E, Schrinner S, Nurnberger A, Schmidt K, Metz K, Zwingmann C, Brieske N, Springer C, Hernandez AM, Herzog S, Grabbe F, Sieverding C, Fischer B, Schrader K, Brockmeyer M, Dettmer S, Helbig C, Alunni V, Battaini MA, Mura C, Henrichsen CN, Garcia-Lopez R, Echevarria D, Puelles E, Garcia-Calero E, Kruse S, Uhr M, Kauck C, Feng G, Milyaev N, Ong CK, Kumar L, Lam M, Semple CA, Gyenesei A, Mundlos S, Radelof U, Lehrach H, Sarmientos P, Reymond A, Davidson DR, Dolle P, Antonarakis SE, Yaspo ML, Martinez S, Baldock RA, Eichele G, Ballabio A. 2011. A high-resolution anatomical atlas of the transcriptome in the mouse embryo. PLoS Biol 9:e1000582.

DiSandro MJ, Li Y, Baskin LS, Hayward S, Cunha G. 1998. Mesenchymal-epithelial interactions in bladder smooth muscle development: epithelial specificity. J Urol 160:1040-1046; discussion 1079.

Domené S, Bumaschny VF, Souza FS, Franchini LF, Nasif S, Low MJ, Rubinstein M. 2013. Enhancer turnover and conserved regulatory function in vertebrate evolution. Philosophical transactions of the Royal Society of London. Series B, Biological sciences 368:20130027.

Dong X, Navratilova P, Fredman D, Drivenes Ø, Becker TS, Lenhard B. 2010. Exonic remnants of whole-genome duplication reveal cis-regulatory function of coding exons. Nucleic Acids Research 38:1071-1085.

Donnell AM, Doi T, Hollwarth M, Kalicinski P, Czauderna P, Puri P. 2008. Deficient alpha-smooth muscle actin as a cause of functional intestinal obstruction in childhood. Pediatr Surg Int 24:1191-1195.

Duprez D, Fournier-Thibault C, Le Douarin N. 1998. Sonic Hedgehog induces proliferation of committed skeletal muscle cells in the chick limb. Development 125:495-505.

Eichenlaub MP, Ettwiller L. 2011. De novo genesis of enhancers in vertebrates. PLoS biology 9:e1001188.

Eisen MB, Spellman PT, Brown PO, Botstein D. 1998. Cluster analysis and display of genome-wide expression patterns. Proc Natl Acad Sci U S A 95:14863-14868.

El-Kasti MM, Wells T, Carter DA. 2012. A novel long-range enhancer regulates postnatal expression of Zeb2: implications for Mowat-Wilson syndrome phenotypes. Human Molecular Genetics 21:5429-5442.

Ema M, Faloon P, Zhang WJ, Hirashima M, Reid T, Stanford WL, Orkin S, Choi K, Rossant J. 2003. Combinatorial effects of Flk1 and Tal1 on vascular and hematopoietic development in the mouse. Genes Dev 17:380-393.

Etchevers HC, Vincent C, Le Douarin NM, Couly GF. 2001. The cephalic neural crest provides pericytes and smooth muscle cells to all blood vessels of the face and forebrain. Development 128:1059-1068.

Evans NC, Swanson CI, Barolo S. 2012. Sparkling insights into enhancer structure, function, and evolution. Curr Top Dev Biol 98:97-120.

Fan YY, Ye GH, Lin KZ, Yu LS, Wu SZ, Dong MW, Han JG, Feng XP, Li XB. 2013. Time-dependent expression and distribution of Egr-1 during skeletal muscle wound healing in rats. J Mol Histol 44:75-81.

Fanger GR, Gerwins P, Widmann C, Jarpe MB, Johnson GL. 1997. MEKKs, GCKs, MLKs, PAKs, TAKs, and tpls: upstream regulators of the c-Jun amino-terminal kinases? Curr Opin Genet Dev 7:67-74.

Fitch WM. 1983. Random sequences. J Mol Biol 163:171-176.

Fletez-Brant C, Lee D, McCallion AS, Beer MA. 2013. kmer-SVM: a web server for identifying predictive regulatory sequence features in genomic data sets. Nucleic Acids Research 41:W544-556.

Fujita PA, Rhead B, Zweig AS, Hinrichs AS, Karolchik D, Cline MS, Goldman M, Barber GP, Clawson H, Coelho A, Diekhans M, Dreszer TR, Giardine BM, Harte RA, Hillman-Jackson J, Hsu F, Kirkup V, Kuhn RM, Learned K, Li CH, Meyer LR, Pohl A, Raney BJ, Rosenbloom KR, Smith KE, Haussler D, Kent WJ. 2011. The UCSC Genome Browser database: update 2011. Nucleic Acids Res 39:D876-882.

Gabella G. 1985. Structure of the musculature of the chicken small intestine. Anat Embryol (Berl) 171:139-149.

Gerber AN, Wilson CW, Li YJ, Chuang PT. 2007. The hedgehog regulated oncogenes Gli1 and Gli2 block myoblast differentiation by inhibiting MyoD-mediated transcriptional activation. Oncogene 26:1122-1136.

Gerstein MB, Kundaje A, Hariharan M, L SG, Landt SG, t, Yan K, Cheng C, Mu XJ, Khurana E, Rozowsky J, Alexander R, Alex R, Min R, er, Alves P, Abyzov A, Addleman N, Bhardwaj N, Boyle AP, Cayting P, Charos A, Chen DZ, Alex, Cheng Y, Charos r, Clarke D, Eastman C, Euskirchen G, Frietze S, Fu Y, Gertz J, Grubert F, Harmanci A, Jain P, Kasowski M, Lacroute P, Leng J, Lian J, Monahan H, O'Geen H, Ouyang Z, Partridge EC, Patacsil D, Pauli F, Raha D, Ramirez L, Reddy TE, Reed B, Shi M, Slifer T, Wang J, Wu L, Yang X, Yip KY, Zilberman-Schapira G, Batzoglou S, Sidow A, Farnham PJ, Myers RM, Weissman SM, Snyder M. 2012. Architecture of the human regulatory network derived from ENCODE data. Nature 489:91-100.

Gianakopoulos PJ, Skerjanc IS. 2005. Hedgehog signaling induces cardiomyogenesis in P19 cells. The Journal of biological chemistry 280:21022-21028.

Giordano C, Powell H, Leopizzi M, De Curtis M, Travaglini C, Sebastiani M, Gallo P, Taylor RW, d'Amati G. 2009. Fatal congenital myopathy and gastrointestinal pseudo-obstruction due to POLG1 mutations. Neurology 72:1103-1105.

Giresi PG, Kim J, McDaniell RM, Iyer VR, Lieb JD. 2007. FAIRE (Formaldehyde-Assisted Isolation of Regulatory Elements) isolates active regulatory elements from human chromatin. Genome Res 17:877-885.

Goetz SC, Anderson KV. 2010. The primary cilium: a signalling centre during vertebrate development. Nat Rev Genet 11:331-344.

Gordon CT, Tan TY, Benko S, Fitzpatrick D, Lyonnet S, Farlie PG. 2009a. Long-range regulation at the SOX9 locus in development and disease. Journal of medical genetics 46:649-656.

Gordon JW, Pagiatakis C, Salma J, Min, Andreucci JJ, Zhao J, Hou G, Perry RL, Dan Q, Courtman D, Bendeck MP, McDermott JC. 2009b. Protein kinase A-regulated assembly of a MEF2{middle dot}HDAC4 repressor complex controls c-Jun expression in vascular smooth muscle cells. The Journal of biological chemistry 284:19027-19042.

Gotea V, Ovcharenko I. 2008. DiRE: identifying distant regulatory elements of co-expressed genes. Nucleic Acids Research 36:1-7.

Gotea V, Visel A, Westlund JM, Nobrega MA, Pennacchio LA, Ovcharenko I. 2010. Homotypic clusters of transcription factor binding sites are a key component of human promoters and enhancers. Genome Research 20:565-577.

Goto T, Macdonald P, Maniatis T. 1989. Early and late periodic patterns of even skipped expression are controlled by distinct regulatory elements that respond to different spatial cues. Cell 57:413-422.

Göttgens B, Ferreira R, Sanchez M, Ishibashi S, Li J, Spensberger D, Lefevre P, Ottersbach K, Chapman M, Kinston S, Knezevic K, Hoogenkamp M, Follows GA, Bonifer C, Amaya E, Green AR. 2010. cis-Regulatory remodeling of the SCL locus during vertebrate evolution. Molecular and Cellular Biology 30:5741-5751.

Goyal RK, Chaudhury A. 2008. Physiology of normal esophageal motility. J Clin Gastroenterol 42:610-619.

Gruel J, LeBorgne M, LeMeur N, Théret N. 2011. Simple Shared Motifs (SSM) in conserved region of promoters: a new approach to identify co-regulation patterns. BMC bioinformatics 12:365.

Guerrero L, Marco-Ferreres R, Serrano AL, Arredondo JJ, Cervera M. 2010. Secondary enhancers synergise with primary enhancers to guarantee fine-tuned muscle gene expression. Developmental Biology 337:16-28.

Gunning P, Ponte P, Kedes L, Eddy R, Shows T. 1984. Chromosomal location of the co-expressed human skeletal and cardiac actin genes. Proc Natl Acad Sci U S A 81:1813-1817.

Guo Y, Mahony S, Gifford DK. 2012. High resolution genome wide binding event finding and motif discovery reveals transcription factor spatial binding constraints. PLoS computational biology 8:e1002638-1002614.

Gupta S, Stamatoyannopoulos JA, Bailey TL, Noble WS. 2007. Quantifying similarity between motifs. Genome Biol 8:R24.

Gustafsson MK. 2002. Myf5 is a direct target of long-range Shh signaling and Gli regulation for muscle specification. Genes & Development 16:114-126.

Halfon MS, Zhu Q, Brennan ER, Zhou Y. 2011. Erroneous attribution of relevant transcription factor binding sites despite successful prediction of cis-regulatory modules. BMC Genomics 12:578.

Hallikas O, Palin K, Sinjushina N, Rautiainen R, Partanen J, Ukkonen E, Taipale J. 2006. Genome-wide prediction of mammalian enhancers based on analysis of transcription-factor binding affinity. Cell 124:1-13.

Hammond CL, Hinits Y, Osborn DP, Minchin JE, Tettamanti G, Hughes SM. 2007. Signals and myogenic regulatory factors restrict pax3 and pax7 expression to dermomyotome-like tissue in zebrafish. Dev Biol 302:504-521.

Hammonds AS, Bristow CA, Fisher WW, Weiszmann R, Wu S, Hartenstein V, Kellis M, Yu B, Frise E, Celniker SE. 2013. Spatial expression of transcription factors in Drosophila embryonic organ development. Genome Biol 14:R140.

Han TH, Lamph WW, Prywes R. 1992. Mapping of epidermal growth factor-, serum-, and phorbol ester-responsive sequence elements in the c-jun promoter. Molecular and Cellular Biology 12:4472-4477.

Han TH, Prywes R. 1995. Regulatory role of MEF2D in serum induction of the c-jun promoter. Mol Cell Biol 15:2907-2915.

Hansen L, Mariño-Ramírez L, Landsman D. 2012. Differences in local genomic context of bound and unbound motifs. Gene 506:125-134.

Harmston N, Lenhard B. 2013. Chromatin and epigenetic features of long-range gene regulation. Nucleic Acids Research 41:7185-7199.

Hasty P, Bradley A, Morris JH, Edmondson DG, Venuti JM, Olson EN, Klein WH. 1993. Muscle deficiency and neonatal death in mice with a targeted mutation in the myogenin gene. Nature 364:501-506.

He Y, Chen Y, Zhao Q, Tan Z. 2013. Roles of brain and muscle ARNT-like 1 and Wnt antagonist Dkk1 during osteogenesis of bone marrow stromal cells. Cell Prolif 46:644-653.

Hedges JC, Oxhorn BC, Carty M, Adam LP, Yamboliev IA, Gerthoffer WT. 2000a. Phosphorylation of caldesmon by ERK MAP kinases in smooth muscle. Am J Physiol Cell Physiol 278:C718-726.

Hedges JC, Singer CA, Gerthoffer WT. 2000b. Mitogen-activated protein kinases regulate cytokine gene expression in human airway myocytes. Am J Respir Cell Mol Biol 23:86-94.

Heintzman ND, Hon GC, Hawkins RD, Kheradpour P, Stark A, Harp LF, Ye Z, Lee LK, Stuart RK, Ching CW, Ching KA, Antosiewicz-Bourget JE, Liu H, Zhang X, Green RD, Lobanenkov VV, Stewart R, Thomson JA, Crawford GE, Kellis M, Ren B. 2009. Histone modifications at human enhancers reflect global cell-type-specific gene expression. Nature 459:108-112.

Heintzman ND, Stuart RK, Hon G, Fu Y, Ching CW, Hawkins RD, Barrera LO, Calcar S, Qu C, Ching KA, Wang W, Weng Z, Green RD, Crawford GE, Ren B. 2007. Distinct and predictive chromatin signatures of transcriptional promoters and enhancers in the human genome. Nature genetics 39:311-318.

Heinz S, Benner C, Spann N, Bertolino E, Lin YC, Laslo P, Cheng JX, Murre C, Singh H, Glass CK. 2010. Simple combinations of lineage-determining transcription factors prime cis-regulatory elements required for macrophage and B cell identities. Mol Cell 38:576-589.

Hersh BM, Carroll SB. 2005. Direct regulation of knot gene expression by Ultrabithorax and the evolution of cis-regulatory elements in Drosophila. Development (Cambridge, England) 132:1567-1577.

Hill RE, Lettice LA. 2013. Alterations to the remote control of Shh gene expression cause congenital abnormalities. Philosophical transactions of the Royal Society of London. Series B, Biological sciences 368:20120357.

Holla OL, Bock G, Busk OL, Isfoss BL. 2014. Familial visceral myopathy diagnosed by exome sequencing of a patient with chronic intestinal pseudo-obstruction. Endoscopy 46:533-537.

Holohan EE, Kwong C, Adryan B, Bartkuhn M, Herold M, Renkawitz R, Russell S, White R. 2007. CTCF genomic binding sites in Drosophila and the organisation of the bithorax complex. PLoS Genet 3:e112.

Holtz AM, Peterson KA, Nishi Y, Morin S, Song JY, Charron F, McMahon AP, Allen BL. 2013. Essential role for ligand-dependent feedback antagonism of vertebrate hedgehog signaling by PTCH1, PTCH2 and HHIP1 during neural patterning. Development 140:3423-3434.

Hong J, Hendrix DA, Levine MS. 2008. Shadow enhancers as a source of evolutionary novelty. Science (New York, N.Y.) 321:1314.

Hosseinpour B, Bakhtiarizadeh MR, Khosravi P, Ebrahimie E. 2013. Predicting distinct organization of transcription factor binding sites on the promoter regions: a new genome-based approach to expand human embryonic stem cell regulatory network. Gene:1-8.

Huang H, Cotton JL, Wang Y, Rajurkar M, Zhu LJ, Lewis BC, Mao J. 2013. Specific Requirement of Gli Transcription Factors in Hedgehog-mediated Intestinal Development. The Journal of biological chemistry 288:17589-17596.

Huang J, Min Lu M, Cheng L, Yuan LJ, Zhu X, Stout AL, Chen M, Li J, Parmacek MS. 2009a. Myocardin is required for cardiomyocyte survival and maintenance of heart function. Proc Natl Acad Sci U S A 106:18734-18739.

Huang W, Sherman BT, Lempicki RA. 2009b. Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources. Nature protocols 4:44-57.

Ikram MS, Neill GW, Regl G, Eichberger T, Frischauf A, Aberger F, Quinn A, Philpott M. 2004. GLI2 is expressed in normal human epidermis and BCC and induces GLI1 expression by binding to its promoter. The Journal of investigative dermatology 122:1503-1509.

Izzi L, Levesque M, Morin S, Laniel D, Wilkes BC, Mille F, Krauss RS, McMahon AP, Allen BL, Charron F. 2011. Boc and Gas1 each form distinct Shh receptor complexes with Ptch1 and are required for Shh-mediated cell proliferation. Dev Cell 20:788-801.

Jakobs P, Exner S, Schurmann S, Pickhinke U, Bandari S, Ortmann C, Kupich S, Schulz P, Hansen U, Seidler DG, Grobe K. 2014. Scube2 enhances proteolytic Shh processing from the surface of Shh-producing cells. J Cell Sci 127:1726-1737.

Jeong J, McMahon AP. 2002. Cholesterol modification of Hedgehog family proteins. J Clin Invest 110:591-596.

Jeong J, McMahon AP. 2005. Growth and pattern of the mammalian neural tube are governed by partially overlapping feedback activities of the hedgehog antagonists patched 1 and Hhip1. Development 132:143-154.

Jiang J, Hui CC. 2008. Hedgehog signaling in development and cancer. Dev Cell 15:801-812.

Jin F, Li Y, Ren B, Natarajan R. 2011. Enhancers: Multi-dimensional signal integrators. Transcription 2:226-230.

Jory A, Estella C, Giorgianni MW, Slattery M, Laverty TR, Rubin GM, Mann RS. 2012. A Survey of 6,300 Genomic Fragments for cis-Regulatory Activity in the Imaginal Discs of Drosophila melanogaster. Cell reports 2:1014-1024.

Kami K, Noguchi K, Senba E. 1995. Localization of myogenin, c-fos, c-jun, and muscle-specific gene mRNAs in regenerating rat skeletal muscle. Cell Tissue Res 280:11-19.

Karlsson L, Lindahl P, Heath JK, Betsholtz C. 2000. Abnormal gastrointestinal development in PDGF-A and PDGFR-(alpha) deficient mice implicates a novel mesenchymal structure with putative instructive properties in villus morphogenesis. Development 127:3457-3466.

Kassar-Duchossoy L, Gayraud-Morel B, Gomes D, Rocancourt D, Buckingham M, Shinin V, Tajbakhsh S. 2004. Mrf4 determines skeletal muscle identity in Myf5:Myod double-mutant mice. Nature 431:466-471.

Katzman S, Kern AD, Bejerano G, Fewell G, Fulton L, Wilson RK, Salama SR, Haussler D. 2007. Human genome ultraconserved elements are ultraselected. Science (New York, N.Y.) 317:915.

Kedinger M, Duluc I, Fritsch C, Lorentz O, Plateroti M, Freund JN. 1998a. Intestinal epithelial-mesenchymal cell interactions. Ann N Y Acad Sci 859:1-17.

Kedinger M, Lefebvre O, Duluc I, Freund JN, Simon-Assmann P. 1998b. Cellular and molecular partners involved in gut morphogenesis and differentiation. Philos Trans R Soc Lond B Biol Sci 353:847-856.

Kedinger M, Simon-Assmann P, Bouziges F, Arnold C, Alexandre E, Haffen K. 1990. Smooth muscle actin expression during rat gut development and induction in fetal skin fibroblastic cells associated with intestinal embryonic epithelium. Differentiation 43:87-97.

Keightley PD, Trivedi U, Thomson M, Oliver F, Kumar S, Blaxter ML. 2009. Analysis of the genome sequences of three Drosophila melanogaster spontaneous mutation accumulation lines. Genome Res 19:1195-1201.

Kent D, Bush EW, Hooper JE. 2006. Roadkill attenuates Hedgehog responses through degradation of Cubitus interruptus. Development 133:2001-2010.

Khan AH, Lin A, Smith DJ. 2012. Discovery and characterization of human exonic transcriptional regulatory elements. PloS one 7:e46098.

Kiefer SM, Robbins L, Stumpff KM, Lin C, Ma L, Rauchman M. 2010. Sall1-dependent signals affect Wnt signaling and ureter tip fate to initiate kidney development. Development 137:3099-3106.

Kikuta H, Fredman D, Rinkwitz S, Lenhard B, Becker TS. 2007. Retroviral enhancer detection insertions in zebrafish combined with comparative genomics reveal genomic regulatory blocks - a fundamental feature of vertebrate genomes. Genome Biology 8 Suppl 1:S4.

Kim BM, Mao J, Taketo MM, Shivdasani RA. 2007. Phases of canonical Wnt signaling during the development of mouse intestinal epithelium. Gastroenterology 133:529-538.

Kim J, Kato M, Beachy PA. 2009. Gli2 trafficking links Hedgehog-dependent activation of Smoothened in the primary cilium to transcriptional activation in the nucleus. Proc Natl Acad Sci U S A 106:21666-21671.

Kim T, Hemberg M, Gray JM, Costa AM, Bear DM, Wu J, Harmin DA, Laptewicz M, Barbara-Haley K, Kuersten S, Markenscoff-Papadimitriou E, Kuhl D, Bito H, Worley PF, Kreiman G, Greenberg ME. 2010. Widespread transcription at neuronal activity-regulated enhancers. Nature 465:182-187.

Knoepfler PS, Bergstrom DA, Uetsuki T, Dac-Korytko I, Sun YH, Wright WE, Tapscott SJ, Kamps MP. 1999. A conserved motif N-terminal to the DNA-binding domains of myogenic bHLH transcription factors mediates cooperative DNA binding with pbx-Meis1/Prep1. Nucleic Acids Res 27:3752-3761.

Kolterud A, Grosse AS, Zacharias WJ, Walton KD, Kretovich KE, Madison BB, Waghray M, Ferris JE, Hu C, Merchant JL, Dlugosz AA, Kottmann AH, Gumucio DL. 2009. Paracrine Hedgehog signaling in stomach and intestine: new roles for hedgehog in gastrointestinal patterning. Gastroenterology 137:618-628.

Kossler N, Stricker S, Rodelsperger C, Robinson PN, Kim J, Dietrich C, Osswald M, Kuhnisch J, Stevenson DA, Braun T, Mundlos S, Kolanczyk M. 2011. Neurofibromin (Nf1) is required for skeletal muscle development. Hum Mol Genet 20:2697-2709.

Kudo K, Gavin E, Das S, Amable L, Shevde LA, Reed E. 2012. Inhibition of Gli1 results in altered c-Jun activation, inhibition of cisplatin-induced upregulation of ERCC1, XPD and XRCC1, and inhibition of platinum-DNA adduct repair. Oncogene 31:4718-4724.

Kumar CC, Mohan SR, Zavodny PJ, Narula SK, Leibowitz PJ. 1989. Characterization and differential expression of human vascular smooth muscle myosin light chain 2 isoform in nonmuscle cells. Biochemistry 28:4027-4035.

Kwon C, Hays R, Fetting J, Orenic TV. 2004. Opposing inputs by Hedgehog and Brinker define a stripe of hairy expression in the Drosophila leg imaginal disc. Development 131:2681-2692.

Lander ES, Linton LM, Birren B, Nusbaum C, Zody MC, Baldwin J, Devon K, Dewar K, Doyle M, FitzHugh W, Funke R, Gage D, Harris K, Heaford A, Howland J, Kann L, Lehoczky J, LeVine R, McEwan P, McKernan K, Meldrim J, Mesirov JP, Miranda C, Morris W, Naylor J, Raymond C, Rosetti M, Santos R, Sheridan A, Sougnez C, Stange-Thomann Y, Stojanovic N, Subramanian A, Wyman D, Rogers J, Sulston J, Ainscough R, Beck S, Bentley D, Burton J, Clee C, Carter N, Coulson A, Deadman R, Deloukas P, Dunham A, Dunham I, Durbin R, French L, Grafham D, Gregory S, Hubbard T, Humphray S, Hunt A, Jones M, Lloyd C, McMurray A, Matthews L, Mercer S, Milne S, Mullikin JC, Mungall A, Plumb R, Ross M, Shownkeen R, Sims S, Waterston RH, Wilson RK, Hillier LW, McPherson JD, Marra MA, Mardis ER, Fulton LA, Chinwalla AT, Pepin KH, Gish WR, Chissoe SL, Wendl MC, Delehaunty KD, Miner TL, Delehaunty A, Kramer JB, Cook LL, Fulton RS, Johnson DL, Minx PJ, Clifton SW, Hawkins T, Branscomb E, Predki P, Richardson P, Wenning S, Slezak T, Doggett N, Cheng JF, Olsen A, Lucas S, Elkin C, Uberbacher E, Frazier M, Gibbs RA, Muzny DM, Scherer SE, Bouck JB, Sodergren EJ, Worley KC, Rives CM, Gorrell JH, Metzker ML, Naylor SL, Kucherlapati RS, Nelson DL, Weinstock GM, Sakaki Y, Fujiyama A, Hattori M, Yada T, Toyoda A, Itoh T, Kawagoe C, Watanabe H, Totoki Y, Taylor T, Weissenbach J, Heilig R, Saurin W, Artiguenave F, Brottier P, Bruls T, Pelletier E, Robert C, Wincker P, Smith DR, Doucette-Stamm L, Rubenfield M, Weinstock K, Lee HM, Dubois J, Rosenthal A, Platzer M, Nyakatura G, Taudien S, Rump A, Yang H, Yu J, Wang J, Huang G, Gu J, Hood L, Rowen L, Madan A, Qin S, Davis RW, Federspiel NA, Abola AP, Proctor MJ, Myers RM, Schmutz J, Dickson M, Grimwood J, Cox DR, Olson MV, Kaul R, Shimizu N, Kawasaki K, Minoshima S, Evans GA, Athanasiou M, Schultz R, Roe BA, Chen F, Pan H, Ramser J, Lehrach H, Reinhardt R, McCombie WR, de la Bastide M, Dedhia N, Blocker H, Hornischer K, Nordsiek G, Agarwala R, Aravind L, Bailey JA, Bateman A, Batzoglou S, Birney E, Bork P, Brown DG, Burge CB, Cerutti L, Chen HC, Church D, Clamp M, Copley RR, Doerks T, Eddy SR, Eichler EE, Furey TS, Galagan J, Gilbert JG, Harmon C, Hayashizaki Y, Haussler D, Hermjakob H, Hokamp K, Jang W, Johnson LS, Jones TA, Kasif S, Kaspryzk A, Kennedy S, Kent WJ, Kitts P, Koonin EV, Korf I, Kulp D, Lancet D, Lowe TM, McLysaght A, Mikkelsen T, Moran JV, Mulder N, Pollara VJ, Ponting CP, Schuler G, Schultz J, Slater G, Smit AF, Stupka E, Szustakowki J, Thierry-Mieg D, Thierry-Mieg J, Wagner L, Wallis J, Wheeler R, Williams A, Wolf YI, Wolfe KH, Yang SP, Yeh RF, Collins F, Guyer MS, Peterson J, Felsenfeld A, Wetterstrand KA, Patrinos A, Morgan MJ, de Jong P, Catanese JJ, Osoegawa K, Shizuya H, Choi S, Chen YJ. 2001. Initial sequencing and analysis of the human genome. Nature 409:860-921.

Laner-Plamberger S, Kaser A, Paulischta M, Hauser-Kronberger C, Eichberger T, Frischauf AM. 2009. Cooperation between GLI and JUN enhances transcription of JUN and selected GLI target genes. Oncogene 28:1639-1651.

Lang M, Hadzhiev Y, Siegel N, Amemiya CT, Parada C, Strahle U, Becker MB, Muller F, Meyer A. 2010. Conservation of shh cis-regulatory architecture of the coelacanth is consistent with its ancestral phylogenetic position. Evodevo 1:11.

Langmead, Trapnell C, Pop M, Salzberg SL. 2009. Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. Genome Biology 10:R25-10.

Le Lievre CS, Le Douarin NM. 1975. Mesenchymal derivatives of the neural crest: analysis of chimaeric quail and chick embryos. J Embryol Exp Morphol 34:125-154.

Lee C, Huang C. 2012. Searching for transcription factor binding sites in vector spaces. BMC bioinformatics 13:215.

Lee D, Karchin R, Beer MA. 2011. Discriminative prediction of mammalian enhancers from DNA sequence. Genome Research 21:2167-2180.

Lee EY, Ji H, Ouyang Z, Zhou B, Ma W, Vokes SA, McMahon AP, Wong WH, Scott MP. 2010. Hedgehog pathway-regulated gene networks in cerebellum development and tumorigenesis. Proceedings of the National Academy of Sciences of the United States of America 107:9736-9741.

Lee HJ, Goring W, Ochs M, Muhlfeld C, Steding G, Paprotta I, Engel W, Adham IM. 2004. Sox15 is required for skeletal muscle regeneration. Mol Cell Biol 24:8428-8436.

Lees-Miller JP, Heeley DH, Smillie LB, Kay CM. 1987. Isolation and characterization of an abundant and novel 22-kDa protein (SM22) from chicken gizzard smooth muscle. J Biol Chem 262:2988-2993.

Lefterova MI, Zhang Y, Steger DJ, Schupp M, Schug J, Cristancho A, Feng D, Zhuo D, Stoeckert CJ, Liu XS, Lazar MA. 2008. PPAR and C/EBP factors orchestrate adipocyte biology via adjacent binding on a genome-wide scale. Genes & Development 22:2941-2952.

Lehtonen HJ, Sipponen T, Tojkander S, Karikoski R, Jarvinen H, Laing NG, Lappalainen P, Aaltonen LA, Tuupanen S. 2012. Segregation of a missense variant in enteric smooth muscle actin gamma-2 with autosomal dominant familial visceral myopathy. Gastroenterology 143:1482-1491 e1483.

Lei Q, Jeong Y, Misra K, Li S, Zelman AK, Epstein DJ, Matise MP. 2006. Wnt signaling inhibitors regulate the transcriptional response to morphogenetic Shh-Gli signaling in the neural tube. Developmental Cell 11:325-337.

Lettice LA, Heaney SJ, Purdie LA, Li L, Beer P, Oostra A, Goode D, Elgar G, Hill RE, Graaff E. 2003. A long-range Shh enhancer regulates expression in the developing limb and fin and is associated with preaxial polydactyly. Human Molecular Genetics 12:1725-1735.

Levi G, Topilko P, Schneider-Maunoury S, Lasagna M, Mantero S, Cancedda R, Charnay P. 1996. Defective bone formation in Krox-20 mutant mice. Development 122:113-120.

Li L, Miano JM, Cserjesi P, Olson EN. 1996. SM22 alpha, a marker of adult smooth muscle, is expressed in multiple myogenic lineages during embryogenesis. Circulation research 78:188-195.

Li X, Noll M. 1993. Role of the gooseberry gene in Drosophila embryos: maintenance of wingless expression by a wingless--gooseberry autoregulatory loop. EMBO J 12:4499-4509.

Li X, Udager AM, Hu C, Qiao XT, Richards N, Gumucio DL. 2009. Dynamic patterning at the pylorus: Formation of an epithelial intestineâ"stomach boundary in late fetal life. Developmental Dynamics 238:3205-3217.

Liem KF, Jr., He M, Ocbina PJ, Anderson KV. 2009. Mouse Kif7/Costal2 is a cilia-associated protein that regulates Sonic hedgehog signaling. Proc Natl Acad Sci U S A 106:13377-13382.

Lifanov AP. 2003. Homotypic Regulatory Clusters in Drosophila. Genome Research 13:579-588.

Lipinski RJ, Song C, Sulik KK, Everson JL, Gipp JJ, Yan D, Bushman W, Rowland IJ. 2010. Cleft lip and palate results from Hedgehog signaling antagonism in the mouse: Phenotypic characterization and clinical implications. Birth Defects Res A Clin Mol Teratol 88:232-240.

Liu B, Feng D, Lin G, Cao M, Kan YW, Cunha GR, Baskin LS. 2010. Signalling molecules involved in mouse bladder smooth muscle cellular differentiation. Int J Dev Biol 54:175-180.

Liu F, Wang X, Hu G, Wang Y, Zhou J. 2014. The transcription factor TEAD1 represses smooth muscle-specific gene expression by abolishing myocardin function. J Biol Chem 289:3308-3316.

Liu J, Li Q, Kuehn MR, Litingtung Y, Vokes SA, Chiang C. 2013. Sonic hedgehog signaling directly targets Hyaluronic Acid Synthase 2, an essential regulator of phalangeal joint patterning. Dev Biol 375:160-171.

Liu Z, Wang Z, Yanagisawa H, Olson EN. 2005. Phenotypic modulation of smooth muscle cells through interaction of Foxo4 and myocardin. Developmental Cell 9:261-270.

Lomvardas S, Barnea G, Pisapia DJ, Mendelsohn M, Kirkl J, Kirkland J, Axel R. 2006. Interchromosomal interactions and olfactory receptor choice. Cell 126:403-413.

Lowe CB, Bejerano G, Haussler D. 2007. Thousands of human mobile element fragments undergo strong purifying selection near developmental genes. Proceedings of the National Academy of Sciences of the United States of America 104:8005-8010.

Machanick P, Bailey TL. 2011. MEME-ChIP: motif analysis of large DNA datasets. Bioinformatics 27:1696-1697.

Madison BB, Braunstein K, Kuizon E, Portman K, Qiao XT, Gumucio DL. 2005. Epithelial hedgehog signals pattern the intestinal crypt-villus axis. Development 132:279-289.

Madison BB, McKenna LB, Dolson D, Epstein DJ, Kaestner KH. 2009. FoxF1 and FoxL1 link hedgehog signaling and the control of epithelial proliferation in the developing stomach and intestine. The Journal of biological chemistry 284:5936-5944.

Malin J, Aniba MR, Hannenhalli S. 2013. Enhancer networks revealed by correlated DNAse hypersensitivity states of enhancers. Nucleic Acids Research 41:6828-6838.

Markstein M. 2001. Genome-wide analysis of clustered Dorsal binding sites identifies putative target genes in the Drosophila embryo. Proceedings of the National Academy of Sciences 99:763-768.

Martinelli DC, Fan CM. 2007. Gas1 extends the range of Hedgehog action by facilitating its signaling. Genes Dev 21:1231-1243.

Martinez-Salas E, Cupo DY, DePamphilis ML. 1988. The need for enhancers is acquired upon formation of a diploid nucleus during early mouse development. Genes Dev 2:1115-1126.

Maston GA, Landt SG, Snyder M, Green MR. 2012. Characterization of Enhancer Function from Genome-Wide Analyses. Annual Review of Genomics and Human Genetics 13:29-57.

McBride DJ, Buckle A, Heyningen V, Kleinjan DA. 2011. DNaseI hypersensitivity and ultraconservation reveal novel, interdependent long-range enhancers at the complex Pax6 cis-regulatory region. PloS one 6:e28616.

McHugh KM. 1995. Molecular analysis of smooth muscle development in the mouse. Dev Dyn 204:278-290.

McKay DJ, Lieb JD. 2013. A common set of DNA regulatory elements shapes Drosophila appendages. Dev Cell 27:306-318.

McLean C, Bejerano G. 2008. Dispensability of mammalian DNA. Genome Research 18:1743-1751.

McLean CY, Bristor D, Hiller M, Clarke SL, Schaar BT, Lowe CB, Wenger AM, Bejerano G. 2010. GREAT improves functional interpretation of cis-regulatory regions. Nature biotechnology 28:495-501.

McLin VA, Henning SJ, Jamrich M. 2009. The role of the visceral mesoderm in the development of the gastrointestinal tract. Gastroenterology 136:2074-2091.

McMahon AP, Ingham PW, Tabin CJ. 2003. Developmental roles and clinical significance of hedgehog signaling. Curr Top Dev Biol 53:1-114.

McQuilton P, St Pierre SE, Thurmond J, FlyBase C. 2012. FlyBase 101--the basics of navigating FlyBase. Nucleic Acids Res 40:D706-714.

Meeson AP, Shi X, Alexander MS, Williams RS, Allen RE, Jiang N, Adham IM, Goetsch SC, Hammer RE, Garry DJ. 2007. Sox15 and Fhl3 transcriptionally coactivate Foxk1 and regulate myogenic progenitor cells. EMBO J 26:1902-1912.

Megason SG, McMahon AP. 2002. A mitogen gradient of dorsal midline Wnts organizes growth in the CNS. Development 129:2087-2098.

Melo CA, Drost J, Wijchers PJ, Werken H, Wit E, Vrielink JA, Elkon R, Melo SA, Léveillé N, Kalluri R, Laat W, Agami R. 2013. eRNAs are required for p53-dependent enhancer activity and gene transcription. Molecular cell 49:524-535.

Miano JM. 2003. Serum response factor: toggling between disparate programs of gene expression. Journal of molecular and cellular cardiology 35:577-593.

Michel M, Kupinski AP, Raabe I, Bokel C. 2012. Hh signalling is essential for somatic stem cell maintenance in the Drosophila testis niche. Development 139:2663-2669.

Miller JC, Brown BD, Shay T, Gautier EL, Jojic V, Cohain A, Pandey G, Leboeuf M, Elpek KG, Helft J, Hashimoto D, Chow A, Price J, Greter M, Bogunovic M, Bellemare-Pelletier A, Frenette PS, Randolph GJ, Turley SJ, Merad M. 2012. Deciphering the transcriptional network of the dendritic cell lineage. Nature immunology 13:888-899.

Moltó E, Fernández A, Montoliu L. 2009. Boundaries in vertebrate genomes: different solutions to adequately insulate gene expression domains. Briefings in functional genomics & proteomics 8:283-296.

Montalvo P, Paz L, Chiappa E, Aronne S, Novelli M, Biain ME. 2004. [Intestinal pseudo-obstruction due to sporadic visceral myopathy]. Medicina (B Aires) 64:525-528.

Morgan XC, Ni S, Miranker DP, Iyer VR. 2007. Predicting combinatorial binding of transcription factors to regulatory elements in the human genome by association rule mining. BMC bioinformatics 8:445.

Mourikis P, Tajbakhsh S. 2014. Distinct contextual roles for Notch signalling in skeletal muscle stem cells. BMC Dev Biol 14:2.

Mousavi K, Zare H, Dell'orso S, Grontved L, Gutierrez-Cruz G, Derfoul A, Hager GL, Sartorelli V. 2013. eRNAs Promote Transcription by Establishing Chromatin Accessibility at Defined Genomic Loci. Molecular cell 51:606-617.

Müller B, Basler K. 2000. The repressor and activator forms of Cubitus interruptus control Hedgehog target genes through common generic gli-binding sites. Development (Cambridge, England) 127:1-9.

Murdoch JN, Copp AJ. 2010. The relationship between sonic Hedgehog signaling, cilia, and neural tube defects. Birth Defects Res A Clin Mol Teratol 88:633-652.

Narayanan A, Lekven AC. 2012. Biphasic wnt8a expression is achieved through interactions of multiple regulatory inputs. Developmental dynamics : an official publication of the American Association of Anatomists 241:1062-1075.

Narlikar L, Sakabe NJ, Blanski AA, Arimura FE, Westlund JM, Nobrega MA, Ovcharenko I. 2010. Genome-wide discovery of human heart enhancers. Genome Research 20:381-392.

Nathan E, Monovich A, Tirosh-Finkel L, Harrelson Z, Rousso T, Rinon A, Harel I, Evans SM, Tzahor E. 2008. The contribution of Islet1-expressing splanchnic mesoderm cells to distinct branchiomeric muscles reveals significant heterogeneity in head muscle development. Development 135:647-657.

Neph S, Vierstra J, Stergachis AB, Reynolds AP, Haugen E, Vernot B, Thurman RE, John S, Sandstrom R, Johnson AK, Maurano MT, Humbert R, Rynes E, Wang H, Vong S, Lee K, Bates D, Diegel M, Roach V, Dunn D, Neri J, Schafer A, Hansen RS, Kutyavin T, Giste E, Weaver M, Canfield T, Sabo P, Zhang M, Balasundaram G, Byron R, MacCoss MJ, Akey JM, Bender MA, Groudine M, Kaul R, Stamatoyannopoulos JA. 2012. An expansive human regulatory lexicon encoded in transcription factor footprints. Nature 489:83-90.

Ngan ES, Kim KH, Hui CC. 2013. Sonic Hedgehog Signaling and VACTERL Association. Mol Syndromol 4:32-45.

Nishi Y, Zhang X, Jeong J, Peterson KA, Vedenko A, Bulyk ML, Hide WA, McMahon AP. 2015. A direct fate exclusion mechanism by Sonic hedgehog-regulated transcriptional repressors. Development 142:3286-3293.

Noah TK, Donahue B, Shroyer NF. 2011. Intestinal development and differentiation. Exp Cell Res 317:2702-2710.

Nolis IK, McKay DJ, Mantouvalou E, Lomvardas S, Merika M, Thanos D. 2009. Transcription factors mediate long-range enhancer-promoter interactions. Proceedings of the National Academy of Sciences of the United States of America 106:20222-20227.

Nolte C, Jinks T, Wang X, Pastor MT, Krumlauf R. 2013. Shadow enhancers flanking the HoxB cluster direct dynamic Hox expression in early heart and endoderm development. Developmental Biology 383:158-173.

Nonchev S, Maconochie M, Vesque C, Aparicio S, Ariza-McNaughton L, Manzanares M, Maruthainar K, Kuroiwa A, Brenner S, Charnay P, Krumlauf R. 1996. The conserved role of Krox-20 in directing Hox gene expression during vertebrate hindbrain segmentation. Proc Natl Acad Sci U S A 93:9339-9345.

Nusslein-Volhard C, Wieschaus E. 1980. Mutations affecting segment number and polarity in Drosophila. Nature 287:795-801.

Occhipinti K, Smith JW. 2012. Irritable bowel syndrome: a review and update. Clin Colon Rectal Surg 25:46-52.

Odom DT, Dowell RD, Jacobsen ES, Gordon W, Danford TW, MacIsaac KD, Rolfe PA, Conboy CM, Gifford DK, Fraenkel E. 2007. Tissue-specific transcriptional regulation has diverged significantly between human and mouse. Nature genetics 39:730-732.

Ohama T, Hori M, Momotani E, Iwakura Y, Guo F, Kishi H, Kobayashi S, Ozaki H. 2007a. Intestinal inflammation downregulates smooth muscle CPI-17 through induction of TNF-alpha and causes motility disorders. Am J Physiol Gastrointest Liver Physiol 292:G1429-1438.

Ohama T, Hori M, Ozaki H. 2007b. Mechanism of abnormal intestinal motility in inflammatory bowel disease: how smooth muscle contraction is reduced? J Smooth Muscle Res 43:43-54.

Ohlen T, Hooper JE. 1997. Hedgehog signaling regulates transcription through Gli/Ci binding sites in the wingless enhancer. Mechanisms of Development 68:1-8.

Oosterveen T, Kurdija S, Alekseenko Z, Uhde CW, Bergsland M, Sandberg M, Andersson E, Dias JM, Muhr J, Ericson J. 2012. Mechanistic differences in the transcriptional interpretation of local and long-range shh morphogen signaling. Developmental Cell 23:1006-1019.

Ormestad M, Astorga J, Landgren H, Wang T, Johansson BR, Miura N, Carlsson P. 2006. Foxf1 and Foxf2 control murine gut development by limiting mesenchymal Wnt signaling and promoting extracellular matrix production. Development (Cambridge, England) 133:833-843.

Pan Y, Bai CB, Joyner AL, Wang B. 2006. Sonic hedgehog signaling regulates Gli2 transcriptional activity by suppressing its processing and degradation. Mol Cell Biol 26:3365-3377.

Papanicolaou KN, Izumiya Y, Walsh K. 2008. Forkhead transcription factors and cardiovascular biology. Circ Res 102:16-31.

Parker SC, Hansen L, Abaan HO, Tullius TD, Margulies EH. 2009. Local DNA topography correlates with functional noncoding regions of the human genome. Science 324:389-392.

Pepicelli CV, Lewis PM, McMahon AP. 1998. Sonic hedgehog regulates branching morphogenesis in the mammalian lung. Curr Biol 8:1083-1086.

Peterson KA, Nishi Y, Ma W, Vedenko A, Shokri L, Zhang X, McFarlane M, Baizabal J, Junker JP, Oudenaarden A, Mikkelsen T, Bernstein BE, Bailey TL, Bulyk ML, Wong WH, McMahon AP. 2012. Neural-specific Sox2 input and differential Gli-binding affinity provide context and positional information in Shh-directed neural patterning. Genes & Development 26:2802-2816.

Petropoulos H, Gianakopoulos PJ, Ridgeway AG, Skerjanc IS. 2004. Disruption of Meox or Gli activity ablates skeletal myogenesis in P19 cells. J Biol Chem 279:23874-23881.

Petrova R, Joyner AL. 2014. Roles for Hedgehog signaling in adult organ homeostasis and repair. Development 141:3445-3457.

Piepenburg O, Vorbrüggen G, Jäckle H. 2000. Drosophila segment borders result from unilateral repression of hedgehog activity by wingless signaling. Molecular cell 6:203-209.

Pownall ME, Gustafsson MK, Emerson CP. 2002. Myogenic regulatory factors and the specification of muscle progenitors in vertebrate embryos. Annual Review of Cell and Developmental Biology 18:747-783.

Qiu H, Wang F, Liu C, Xu X, Liu B. 2011. TEAD1-dependent expression of the FoxO3a gene in mouse skeletal muscle. BMC Mol Biol 12:1.

Quandt K, Frech K, Karas H, Wingender E, Werner T. 1995. MatInd and MatInspector: new fast and versatile tools for detection of consensus matches in nucleotide sequence data. Nucleic Acids Res 23:4878-4884.

Rada-Iglesias A, Bajpai R, Prescott S, Brugmann SA, Swigut T, Wysocka J. 2012. Epigenomic annotation of enhancers predicts transcriptional regulators of human neural crest. Cell stem cell 11:633-648.

Rada-Iglesias A, Bajpai R, Swigut T, Brugmann SA, Flynn RA, Wysocka J. 2011. A unique chromatin signature uncovers early developmental enhancers in humans. Nature 470:279-283.

Rahnama F, Toftgard R, Zaphiropoulos PG. 2004. Distinct roles of PTCH2 splice variants in Hedgehog signalling. Biochem J 378:325-334.

Raines AM, Adam M, Magella B, Meyer SE, Grimes HL, Dey SK, Potter SS. 2013. Recombineering-based dissection of flanking and paralogous Hox gene functions in mouse reproductive tracts. Development 140:2942-2952.

Ramalho-Santos M, Melton DA, McMahon AP. 2000. Hedgehog signals regulate multiple aspects of gastrointestinal development. Development 127:2763-2772.

Ramos AI, Barolo S. 2013. Low-affinity transcription factor binding sites shape morphogen responses and enhancer evolution. Philosophical transactions of the Royal Society of London. Series B, Biological sciences 368:20130018.

Raney BJ, Cline MS, Rosenbloom KR, Dreszer TR, Learned K, Barber GP, Meyer LR, Sloan CA, Malladi VS, Roskin KM, Suh BB, Hinrichs AS, Clawson H, Zweig AS, Kirkup V, Fujita PA, Rhead B, Smith KE, Pohl A, Kuhn RM, Karolchik D, Haussler D, Kent WJ. 2011. ENCODE whole-genome data in the UCSC genome browser (2011 update). Nucleic Acids Res 39:D871-875.

Rebeiz M, Reeves N, Posakony JW. 2002. SCORE: A computational approach to the identification of cis-regulatory modules and target genes in whole-genome sequence data. Site clustering over random expectation. Proc Natl Acad Sci U S A 99:9888-9893.

Richards S, Liu Y, Bettencourt BR, Hradecky P, Letovsky S, Nielsen R, Thornton K, Hubisz MJ, Chen R, Meisel RP, Couronne O, Hua S, Smith MA, Zhang P, Liu J, Bussemaker HJ, van Batenburg MF, Howells SL, Scherer SE, Sodergren E, Matthews BB, Crosby MA, Schroeder AJ, Ortiz-Barrientos D, Rives CM, Metzker ML, Muzny DM, Scott G, Steffen D, Wheeler DA, Worley KC, Havlak P, Durbin KJ, Egan A, Gill R, Hume J, Morgan MB, Miner G, Hamilton C, Huang Y, Waldron L, Verduzco D, Clerc-Blankenburg KP, Dubchak I, Noor MA, Anderson W, White KP, Clark AG, Schaeffer SW, Gelbart W, Weinstock GM, Gibbs RA. 2005. Comparative genome sequencing of Drosophila pseudoobscura: chromosomal, gene, and cis-element evolution. Genome Res 15:1-18.

Ritter DI, Dong Z, Guo S, Chuang JH. 2012. Transcriptional enhancers in protein-coding exons of vertebrate developmental genes. PloS one 7:e35202.

Robbins DJ, Fei DL, Riobo NA. 2012. The Hedgehog signal transduction network. Sci Signal 5:re6.

Roberts DJ, Johnson RL, Burke AC, Nelson CE, Morgan BA, Tabin C. 1995. Sonic hedgehog is an endodermal signal inducing Bmp-4 and Hox genes during induction and regionalization of the chick hindgut. Development 121:3163-3174.

Rubin GM, Spradling AC. 1982. Genetic transformation of Drosophila with transposable element vectors. Science 218:348-353.

Rubinstein M, Souza FS. 2013. Evolution of transcriptional enhancers and animal diversity. Philosophical transactions of the Royal Society of London. Series B, Biological sciences 368:20130017.

Rudnicki MA, Braun T, Hinuma S, Jaenisch R. 1992. Inactivation of MyoD in mice leads to up-regulation of the myogenic HLH gene Myf-5 and results in apparently normal muscle development. Cell 71:383-390.

Ruzicka DL, Schwartz RJ. 1988. Sequential activation of alpha-actin genes during avian cardiogenesis: vascular smooth muscle alpha-actin gene transcripts mark the onset of cardiomyocyte differentiation. J Cell Biol 107:2575-2586.

Sakabe NJ, Chicago U, Savic D, Nobrega MA, Sakabe N. 2012. Transcriptional enhancers in development and disease. Genome Biology 13:238.

Saldanha AJ. 2004. Java Treeview--extensible visualization of microarray data. Bioinformatics 20:3246-3248.

Sanchez AM, Candau RB, Bernardi H. 2014. FoxO transcription factors: their roles in the maintenance of skeletal muscle homeostasis. Cell Mol Life Sci 71:1657-1671.

Sanges R, Kalmar E, Claudiani P, D'Amato M, Muller F, Stupka E. 2006. Shuffling of cis-regulatory elements is a pervasive feature of the vertebrate lineage. Genome Biology 7:R56.

Santagati F, Abe K, Schmidt V, Schmitt-John T, Suzuki M, Yamamura K, Imai K. 2003. Identification of Cis-regulatory elements in the mouse Pax9/Nkx2-9 genomic region: implication for evolutionary conserved synteny. Genetics 165:235-242.

Santos N, Reiter JF. 2008. Building it up and taking it down: the regulation of vertebrate ciliogenesis. Dev Dyn 237:1972-1981.

Sasaki H, Hui C, Nakafuku M. 1997. A binding site for Gli proteins is essential for HNF-3beta floor plate enhancer activity in transgenics and can respond to Shh in vitro. Development.

Sasaki H, Nishizaki Y, Hui C, Nakafuku M, Kondoh H. 1999. Regulation of Gli2 and Gli3 activities by an amino-terminal repression domain: implication of Gli2 and Gli3 as primary mediators of Shh signaling. Development 126:3915-3924.

Sawaya S, Bagshaw A, Buschiazzo E, Kumar P, Chowdhury S, Black MA, Gemmell N. 2013. Microsatellite tandem repeats are abundant in human promoters and are associated with regulatory elements. PLoS One 8:e54710.

Scales SJ, de Sauvage FJ. 2009. Mechanisms of Hedgehog pathway activation in cancer and implications for therapy. Trends Pharmacol Sci 30:303-312.

Schachter KA, Krauss RS. 2008. Murine models of holoprosencephaly. Curr Top Dev Biol 84:139-170.

Schmidt K, Glaser G, Wernig A, Wegner M, Rosorius O. 2003. Sox8 is a specific marker for muscle satellite cells and inhibits myogenesis. J Biol Chem 278:29769-29775.

Sekulic A, Migden MR, Oro AE, Dirix L, Lewis KD, Hainsworth JD, Solomon JA, Yoo S, Arron ST, Friedlander PA, Marmur E, Rudin CM, Chang AL, Low JA, Mackey HM, Yauch RL, Graham RA, Reddy JC, Hauschild A. 2012. Efficacy and safety of vismodegib in advanced basal-cell carcinoma. N Engl J Med 366:2171-2179.

Shin SH, Kogerman P, Lindstrom E, Toftgard R, Biesecker LG. 1999. GLI3 mutations in human disorders mimic Drosophila cubitus interruptus protein functions and localization. Proc Natl Acad Sci U S A 96:2880-2884.

Shiroyanagi Y, Liu B, Cao M, Agras K, Li J, Hsieh MH, Willingham EJ, Baskin LS. 2007. Urothelial sonic hedgehog signaling plays an important role in bladder smooth muscle formation. Differentiation; research in biological diversity 75:968-977.

Singh BN, Doyle MJ, Weaver CV, Koyano-Nakagawa N, Garry DJ. 2012. Hedgehog and Wnt coordinate signaling in myogenic progenitors and regulate limb regeneration. Dev Biol 371:23-34.

Sipponen T, Karikoski R, Nuutinen H, Markkola A, Kaitila I. 2009. Three-generation familial visceral myopathy with alpha-actin-positive inclusion bodies in intestinal smooth muscle. J Clin Gastroenterol 43:437-443.

Slattery M, Zhou T, Yang L, Dantas Machado AC, Gordan R, Rohs R. 2014. Absence of a simple code: how transcription factors read the genome. Trends Biochem Sci 39:381-399.

Smith JD, McManus KF, Fraser HB. 2013. A novel test for selection on cis-regulatory elements reveals positive and negative selection acting on mammalian transcriptional enhancers. Molecular biology and evolution 30:2509-2518.

Smith VV, Lake BD, Kamm MA, Nicholls RJ. 1992. Intestinal pseudo-obstruction with deficient smooth muscle alpha-actin. Histopathology 21:535-542.

Song L, Zhang Z, Grasfeder LL, Boyle AP, Giresi PG, Lee B, Sheffield NC, Gräf S, Huss M, Keefe D, Liu Z, London D, McDaniell RM, Shibata Y, Showers KA, Simon JM, Vales T, Wang T, Winter D, Zhang Z, Clarke ND, Birney E, Iyer VR, Crawford GE, Lieb JD, Furey TS. 2011. Open chromatin defined by DNaseI and FAIRE identifies regulatory elements that shape cell-type identity. Genome Research 21:1757-1767.

Šošić D, Richardson JA, Yu K, Ornitz DM, Olson EN. 2003. Twist regulates cytokine gene expression through a negative feedback loop that represses NF-kappaB activity. Cell 112:169-180.

Spence JR, Lauf R, Shroyer NF. 2011. Vertebrate intestinal endoderm development. Dev Dyn 240:501-520.

Spilianakis CG, Lalioti MD, Town T, Lee GR, Flavell RA. 2005. Interchromosomal associations between alternatively expressed loci. Nature 435:637-645.

Spitz F, Furlong EE. 2012. Transcription factors: from enhancer binding to developmental control. Nature reviews. Genetics 13:613-626.

Strasser P, Gimona M, Moessler H, Herzog M, Small JV. 1993. Mammalian calponin. Identification and expression of genetic variants. FEBS Lett 330:13-18.

Subramanian A, Tamayo P, Mootha VK, Mukherjee S, Ebert BL, Gillette MA, Paulovich A, Pomeroy SL, Golub TR, Lander ES, Mesirov JP. 2005. Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. Proc Natl Acad Sci U S A 102:15545-15550.

Sukegawa A, Narita T, Kameda T, Saitoh K, Nohno T, Iba H, Yasugi S, Fukuda K. 2000. The concentric structure of the developing gut is regulated by Sonic hedgehog derived from endodermal epithelium. Development 127:1971-1980.

Summers MA, Quinlan KG, Payne JM, Little DG, North KN, Schindeler A. 2015. Skeletal muscle and motor deficits in Neurofibromatosis Type 1. J Musculoskelet Neuronal Interact 15:161-170.

Suryamohan K, Halfon MS. 2014. Identifying transcriptional cis-regulatory modules in animal genomes. Wiley Interdisciplinary Reviews: Developmental Biology:n/a-n/a.

Swanson CI, Evans NC, Barolo S. 2010. Structural rules and complex regulatory circuitry constrain expression of a Notch- and EGFR-regulated eye enhancer. Dev Cell 18:359-370.

Swanson CI, Hinrichs T, Johnson LA, Zhao Y, Barolo S. 2008. A directional recombination cloning system for restriction- and ligation-free construction of GFP, DsRed, and lacZ transgenic Drosophila reporters. Gene 408:180-186.

Taher L, McGaughey DM, Maragh S, Aneas I, Bessling SL, Miller W, Nobrega MA, McCallion AS, Ovcharenko I. 2011. Genome-wide identification of conserved regulatory function in diverged sequences. Genome Research 21:1139-1149.

Taher L, Narlikar L, Ovcharenko I. 2015. Identification and computational analysis of gene regulatory elements. Cold Spring Harb Protoc 2015:pdb top083642.

Tang JY, Mackay-Wiggan JM, Aszterbaum M, Yauch RL, Lindgren J, Chang K, Coppola C, Chanana AM, Marji J, Bickers DR, Epstein EH, Jr. 2012. Inhibiting the hedgehog pathway in patients with the basal-cell nevus syndrome. N Engl J Med 366:2180-2188.

Tao T, Wasson J, Bernal-Mizrachi E, Behn PS, Chayen S, Duprat L, Meyer J, Glaser B, Permutt MA. 1998. Isolation and characterization of the human PAX4 gene. Diabetes 47:1650-1653.

Tasian G, Cunha G, Baskin L. 2010. Smooth muscle differentiation and patterning in the urinary bladder. Differentiation 80:106-117.

Teglund S, Toftgard R. 2010. Hedgehog beyond medulloblastoma and basal cell carcinoma. Biochim Biophys Acta 1805:181-208.

Teillet M, Watanabe Y, Jeffs P, Duprez D, Lapointe F, Le Douarin NM. 1998. Sonic hedgehog is required for survival of both myogenic and chondrogenic somitic lineages. Development 125:2019-2030.

Tenzen T, Allen BL, Cole F, Kang JS, Krauss RS, McMahon AP. 2006. The cell surface membrane proteins Cdo and Boc are components and targets of the Hedgehog signaling pathway and feedback network in mice. Dev Cell 10:647-656.

Thomas NA, Koudijs M, van Eeden FJ, Joyner AL, Yelon D. 2008. Hedgehog signaling plays a cell-autonomous role in maximizing cardiac developmental potential. Development 135:3789-3799.

Thomason RT, Bader DM, Winters NI. 2012. Comprehensive timeline of mesodermal development in the quail small intestine. Dev Dyn 241:1678-1694.

Thorson W, Diaz-Horta O, Foster J, 2nd, Spiliopoulos M, Quintero R, Farooq A, Blanton S, Tekin M. 2014. De novo ACTG2 mutations cause congenital distended bladder, microcolon, and intestinal hypoperistalsis. Hum Genet 133:737-742.

Timmer J, Johnson J, Niswander L. 2001. The use of in ovo electroporation for the rapid analysis of neural-specific murine enhancers. Genesis 29:123-132.

Tollet J, Everett AW, Sparrow MP. 2001. Spatial and temporal distribution of nerves, ganglia, and smooth muscle during the early pseudoglandular stage of fetal mouse lung development. Dev Dyn 221:48-60.

Tomancak P, Beaton A, Weiszmann R, Kwan E, Shu S, Lewis SE, Richards S, Ashburner M, Hartenstein V, Celniker SE, Rubin GM. 2002. Systematic determination of patterns of gene expression during Drosophila embryogenesis. Genome Biol 3:RESEARCH0088.

Tomancak P, Berman BP, Beaton A, Weiszmann R, Kwan E, Hartenstein V, Celniker SE, Rubin GM. 2007. Global analysis of patterns of gene expression during Drosophila embryogenesis. Genome Biol 8:R145.

Torihashi S, Hattori T, Hasegawa H, Kurahashi M, Ogaeri T, Fujimoto T. 2009. The expression and crucial roles of BMP signaling in development of smooth muscle progenitor cells in the mouse embryonic gut. Differentiation 77:277-289.

Townsend PJ, Farza H, MacGeoch C, Spurr NK, Wade R, Gahlmann R, Yacoub MH, Barton PJ. 1994. Human cardiac troponin T: identification of fetal isoforms and assignment of the TNNT2 locus to chromosome 1q. Genomics 21:311-316.

Trapnell C, Pachter L, Salzberg SL. 2009. TopHat: discovering splice junctions with RNA-Seq. Bioinformatics (Oxford, England) 25:1105-1111.

Tsai ZT, Shiu SH, Tsai HK. 2015. Contribution of Sequence Motif, Chromatin State, and DNA Structure Features to Predictive Models of Transcription Factor Binding in Yeast. PLoS Comput Biol 11:e1004418.

Tsukui T, Capdevila J, Tamura K, Ruiz-Lozano P, Rodriguez-Esteban C, Yonei-Tamura S, Magallon J, Chandraratna RA, Chien K, Blumberg B, Evans RM, Belmonte JC. 1999. Multiple left-right asymmetry defects in Shh(-/-) mutant mice unveil a convergence of the shh and retinoic acid pathways in the control of Lefty-1. Proc Natl Acad Sci U S A 96:11376-11381.

Uchikawa M, Ishida Y, Takemoto T, Kamachi Y, Kondoh H. 2003. Functional analysis of chicken Sox2 enhancers highlights an array of diverse regulatory elements that are conserved in mammals. Developmental Cell 4:509-519.

Vadasz S, Marquez J, Tulloch M, Shylo NA, Garcia-Castro MI. 2013. Pax7 is regulated by cMyb during early neural crest development through a novel enhancer. Development 140:3691-3702.

van den Brink GR, Rubin DC. 2013. Foxf2: a mesenchymal regulator of intestinal adenoma development. Gastroenterology 144:873-876.

van der Loop FT, Schaart G, Timmer ED, Ramaekers FC, van Eys GJ. 1996. Smoothelin, a novel cytoskeletal protein specific for smooth muscle cells. J Cell Biol 134:401-411.

Van der Vliet A, Tuinstra TJ, Rademaker B, Bast A. 1992. Role of the epithelium in the control of intestinal motility: implications for intestinal damage after anoxia and reoxygenation. Agents Actions 36:159-167.

Van Goethem G, Schwartz M, Lofgren A, Dermaut B, Van Broeckhoven C, Vissing J. 2003. Novel POLG mutations in progressive external ophthalmoplegia mimicking mitochondrial neurogastrointestinal encephalomyopathy. Eur J Hum Genet 11:547-549.

Varjosalo M, Taipale J. 2008. Hedgehog: functions and mechanisms. Genes & Development 22:2454-2472.

Villar D, Berthelot C, Aldridge S, Rayner TF, Lukk M, Pignatelli M, Park TJ, Deaville R, Erichsen JT, Jasinska AJ, Turner JM, Bertelsen MF, Murchison EP, Flicek P, Odom DT. 2015. Enhancer evolution across 20 mammalian species. Cell 160:554-566.

Vinkemeier U, Obermann W, Weber K, Furst DO. 1993. The globular head domain of titin extends into the center of the sarcomeric M band. cDNA cloning, epitope mapping and immunoelectron microscopy of two titin-associated proteins. J Cell Sci 106 (Pt 1):319-330.

Visel A, Blow MJ, Li Z, Zhang T, Akiyama JA, Holt A, Plajzer-Frick I, Shoukry M, Wright C, Chen F, Afzal V, Ren B, Rubin EM, Pennacchio LA. 2009. ChIP-seq accurately predicts tissue-specific activity of enhancers. Nature 457:854-858.

Visel A, Thaller C, Eichele G. 2004. GenePaint.org: an atlas of gene expression patterns in the mouse embryo. Nucleic Acids Res 32:D552-556.

Vissing J, Ravn K, Danielsen ER, Duno M, Wibrand F, Wevers RA, Schwartz M. 2002. Multiple mtDNA deletions with features of MNGIE. Neurology 59:926-929.

Vokes SA, Ji H, McCuine S, Tenzen T, Giles S, Zhong S, Longabaugh WJ, Davidson EH, Wong WH, McMahon AP. 2007. Genomic characterization of Gli-activator targets in sonic hedgehog-mediated neural patterning. Development (Cambridge, England) 134:1977-1989.

Vokes SA, Ji H, Wong WH, McMahon AP. 2008. A genome-scale analysis of the cis-regulatory circuitry underlying sonic hedgehog-mediated patterning of the mammalian limb. Genes & Development 22:2651-2663.

Von Ohlen T, Lessing D, Nusse R, Hooper JE. 1997. Hedgehog signaling regulates transcription through cubitus interruptus, a sequence-specific DNA binding protein. Proc Natl Acad Sci U S A 94:2404-2409.

Voronova A, Coyne E, Madhoun A, Fair JV, Bosiljcic N, St-Louis C, Li G, Thurig S, Wallace VA, Wiper-Bergeron N, Skerjanc IS. 2013. Hedgehog signaling regulates MyoD expression and activity. The Journal of biological chemistry 288:4389-4404.

Voronova A, Madhoun A, Fischer A, Shelton M, Karamboulas C, Skerjanc IS. 2012. Gli2 and MEF2C activate each other's expression and function synergistically during cardiomyogenesis in vitro. Nucleic Acids Research 40:3329-3347.

Wada Y, Fujimori M, Suzuki J, Tsukioka K, Ito K, Sawa Y, Morishita R, Kaneda Y, Isobe M, Amano J. 2003. Egr-1 in vascular smooth muscle cell proliferation in response to allo-antigen. J Surg Res 115:294-302.

Wahlbuhl M, Reiprich S, Vogl MR, Bösl MR, Wegner M. 2012. Transcription factor Sox10 orchestrates activity of a neural crest-specific enhancer in the vicinity of its gene. Nucleic Acids Research 40:88-101.

Walton KD, Kolterud A, Czerwinski MJ, Bell MJ, Prakash A, Kushwaha J, Grosse AS, Schnell S, Gumucio DL. 2012. Hedgehog-responsive mesenchymal clusters direct patterning and emergence of intestinal villi. Proc Natl Acad Sci U S A 109:15817-15822.

Wang B, Fallon JF, Beachy PA. 2000. Hedgehog-regulated processing of Gli3 produces an anterior/posterior repressor gradient in the developing vertebrate limb. Cell 100:423-434.

Wang D, Chang PS, Wang Z, Sutherland L, Richardson JA, Small E, Krieg PA, Olson EN. 2001. Activation of cardiac gene expression by myocardin, a transcriptional cofactor for serum response factor. Cell 105:851-862.

Wang D, Rendon A, Ouwehand W, Wernisch L. 2012a. Transcription factor co-localization patterns affect human cell type-specific gene expression. BMC genomics 13:263.

Wang F, Wang H, Wu H, Qiu H, Zeng C, Sun L, Liu B. 2013. TEAD1 controls C2C12 cell proliferation and differentiation and regulates three novel target genes. Cell Signal 25:674-681.

Wang H, Lei Q, Oosterveen T, Ericson J, Matise MP. 2011. Tcf/Lef repressors differentially regulate Shh-Gli target gene activation thresholds to generate progenitor patterning in the developing CNS. Development 138:3711-3721.

Wang J, Zhuang J, Iyer S, Lin X, Whitfield TW, Greven MC, Pierce BG, Dong X, Kundaje A, Cheng Y, Rando OJ, Birney E, Myers RM, Noble WS, Snyder M, Weng Z. 2012b. Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. Genome Research 22:1798-1812.

Wang Z, Wang D, Hockemeyer D, McAnally J. 2004. Myocardin and ternary complex factors compete for SRF to control smooth muscle gene expression. Nature:185-189.

Wang Z, Wang Z, Wang D, Pipes G. 2003. Myocardin is a master regulator of smooth muscle gene expression. In: Proceedings of the National Academy of Sciences. pp 7129-7134.

Wangler MF, Gonzaga-Jauregui C, Gambin T, Penney S, Moss T, Chopra A, Probst FJ, Xia F, Yang Y, Werlin S, Eglite I, Kornejeva L, Bacino CA, Baldridge D, Neul J, Lehman EL, Larson A, Beuten J, Muzny DM, Jhangiani S, Gibbs RA, Lupski JR, Beaudet A. 2014. Heterozygous de novo and inherited mutations in the smooth muscle actin (ACTG2) gene underlie megacystis-microcolon-intestinal hypoperistalsis syndrome. PLoS Genet 10:e1004258.

Washington Smoak I, Byrd NA, Abu-Issa R, Goddeeris MM, Anderson R, Morris J, Yamamura K, Klingensmith J, Meyers EN. 2005. Sonic hedgehog is required for cardiac outflow tract and neural crest cell development. Dev Biol 283:357-372.

Watanabe M, Layne MD, Hsieh C, Maemura K, Gray S, Lee M, Jain MK. 2002. Regulation of smooth muscle cell differentiation by AT-rich interaction domain transcription factors Mrf2alpha and Mrf2beta. Circulation research 91:382-389.

Wells KL, Mou C, Headon DJ, Tucker AS. 2010. Recombinant EDA or Sonic Hedgehog rescue the branching defect in Ectodysplasin A pathway mutant salivary glands in vitro. Dev Dyn 239:2674-2684.

Wen X, Lai CK, Evangelista M, Hongo JA, de Sauvage FJ, Scales SJ. 2010. Kinetics of hedgehog-dependent full-length Gli3 accumulation in primary cilia and subsequent degradation. Mol Cell Biol 30:1910-1922.

Whitfield TW, Wang J, Collins PJ, Partridge EC, Aldred SF, Trinklein ND, Myers RM, Weng Z. 2012. Functional analysis of transcription factor binding sites in human promoters. Genome Biology 13:R50.

Whorwell PJ, McCallum M, Creed FH, Roberts CT. 1986. Non-colonic features of irritable bowel syndrome. Gut 27:37-40.

Winklmayr M, Schmid C, Laner-Plamberger S, Kaser A, Aberger F, Eichberger T, Frischauf AM. 2010. Non-consensus GLI binding sites in Hedgehog target gene regulation. BMC Mol Biol 11:2.

Wisdom R, Johnson RS, Moore C. 1999. c-Jun regulates cell cycle progression and apoptosis by distinct mechanisms. EMBO J 18:188-197.

Xie J, Murone M, Luoh SM, Ryan A, Gu Q, Zhang C, Bonifas JM, Lam CW, Hynes M, Goddard A, Rosenthal A, Epstein EH, Jr., de Sauvage FJ. 1998. Activating Smoothened mutations in sporadic basal-cell carcinoma. Nature 391:90-92.

Yaragatti M, Sandler T, Ungar L. 2009. A predictive model for identifying mini-regulatory modules in the mouse genome. Bioinformatics (Oxford, England) 25:353-357.

Yasumoto H, Kim S, Zhan Y, Miyazaki H, Hoshiga M, Kaneda Y, Morishita R, Iwao H. 2001. Dominant negative c-jun gene transfer inhibits vascular smooth muscle cell proliferation and neointimal hyperplasia in rats. Gene Ther 8:1682-1689.

Yokoyama S, Ito Y, Ueno-Kudoh H, Shimizu H, Uchibe K, Albini S, Mitsuoka K, Miyaki S, Kiso M, Nagai A, Hikata T, Osada T, Fukuda N, Yamashita S, Harada D, Mezzano V, Kasai M, Puri PL, Hayashizaki Y, Okado H, Hashimoto M, Asahara H. 2009. A systems approach reveals that the myogenesis genome network is regulated by the transcriptional repressor RP58. Dev Cell 17:836-848.

Yoon JK, Wold B. 2000. The bHLH regulator pMesogenin1 is required for maturation and segmentation of paraxial mesoderm. Genes Dev 14:3204-3214.

Yu J, Carroll TJ, McMahon AP. 2002. Sonic hedgehog regulates proliferation and differentiation of mesenchymal cells in the mouse metanephric kidney. Development (Cambridge, England) 129:5301-5312.

Zacharias WJ, Madison BB, Kretovich KE, Walton KD, Richards N, Udager AM, Li X, Gumucio DL. 2011. Hedgehog signaling controls homeostasis of adult intestinal smooth muscle. Developmental Biology 355:152-162.

Zhang XM, Ramalho-Santos M, McMahon AP. 2001. Smoothened mutants reveal redundant roles for Shh and Ihh signaling including regulation of L/R symmetry by the mouse node. Cell 106:781-792.

Zhang Y, Liu T, Meyer CA, Eeckhoute J, Johnson DS, Bernstein BE, Nusbaum C, Myers RM, Brown M, Li W, Liu XS. 2008. Model-based analysis of ChIP-Seq (MACS). Genome Biol 9:R137.

Zhang ZG, Wall JR, Bernard NF. 1996. Tissue distribution and quantitation of a gene expressing a 64-kDa antigen associated with thyroid-associated ophthalmopathy. Clin Immunol Immunopathol 80:236-244.

Zhao M, Qiao M, Harris SE, Chen D, Oyajobi BO, Mundy GR. 2006. The zinc finger transcription factor Gli2 mediates bone morphogenetic protein 2 expression in osteoblasts in response to hedgehog signaling. Mol Cell Biol 26:6197-6208.

Zorn AM, Wells JM. 2009. Vertebrate endoderm development and organ formation. Annu Rev Cell Dev Biol 25:221-251.