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To the most incredible women in my life:

Alana, Darlene, and Yvonne

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CONTRIBUTIONS

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Chapters 2 and 4 are taken from a manuscript that is currently in submission*:* "The Genetics of Splicing in Neuroblastoma" by Justin Chen, Christopher S. Hackett, Shile Zhang, Young K. Song, Robert J.A. Bell, Annette Molinaro, David A. Quigley, Allan Balmain, Jun S. Song, Joseph F. Costello, W. Clay Gustafson, Terry Van Dyke, Pui-Yan Kwok, Javed Khan, and William A. Weiss. Chapter 3 is modified from this same manuscript:

Christopher Hackett set up the initial backcrossed modifier screen and harvested the SCG and CB. He also genotyped the mice with the help of Pui-Yan Kwok's lab and ran exon arrays on the SCG with the assistance of Young Song in Javed Khan's lab with arrays provided by Terry Van Dyke. David Quigley in Allan Balmain's lab provided the eQTL software used in this analysis. Shile Zhang provided RNA-Seq data on human neuroblastoma patients. Rob Bell in Jun Song's lab provided somatic mutation calls from TCGA GBM samples and ran my scripts on the germline variants. Annette Molinaro provided statistical support. Clay Gustafson provided helpful experimental insights and William Weiss oversaw the project. I have performed all other experiments and wrote the manuscript.

ABSTRACT

Alternative splicing plays critical roles in normal development and can promote growth and survival in cancer. Genes that have canonical splice variants that function antagonistically can be ectopically expressed to drive malignant progression. Additionally, aberrant splicing, the production of noncanonical and cancer-specific mRNA transcripts, can lead to loss-of-function in tumor suppressors or activation of oncogenes and cancer pathways. Emerging data suggests that aberrant splicing products and loss of canonically spliced variants correlate with stage and progression in malignancy. Not only do these data illuminate roles for alternative splicing in cancer and intersections between alternative splicing pathways and therapy, but they illustrate the importance of understanding the genetic basis of splicing.

Using a transgenic model of neuroblastoma, we set up a backcrossed genetic system to derive distinct virtual genomes of over 100 individual mice in which we have profiled exon expression in two different neural tissues. We identified splicing quantitative trait loci (sQTL) which map genetic control of splicing and define key splicing motifs. We identify these motifs as sites of recurrent somatic mutations in cancer. We also use this analysis to identify novel effector splicing events. Among these, we show that a triplet splicing event within *FUBP1* modulates levels of the MYC oncoprotein in human neuroblastoma-derived cell line, and correlates with outcome in neuroblastoma.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

CHAPTER 1: INTRODUCTION

Alternative splicing generates multiple different mRNAs and downstream proteins from a single gene through the inclusion or exclusion of specific exons. This process occurs in 95% of all multi-exonic genes[1] and is catalyzed by the spliceosome, a complex comprised from a core of five small nuclear ribonucleoproteins (snRNPs) (U1, U2, U4, U5 and U6) (reviewed in [2]). The spliceosome is aided by over 200 *trans*-acting factors that recognize *cis*-regulatory sequences within the pre-mRNA and direct the spliceosome to include or exclude specific exons (reviewed in [3,4]). Splice variants can thus arise from mechanisms including alternative promoters, preferential usage of exons or splice sites, scrambling of exon order, and alternative polyadenylation (Figure 1.1).

Alternative splicing affords a significant evolutionary advantage by providing a large source of proteomic diversity.[5] Alternative splicing is often regulated at the tissue level, and tissue-specific variants cooperate to modulate protein-protein interaction networks.[6] Stem cells express specific splice variants at each stage of differentiation, with undifferentiated stem cells maintaining the highest levels of diversity for splice isoforms.[7] Alternative splicing is also critical in development and can be responsive to normal external stimuli (reviewed in [8,9]). As with other developmentally related pathways, alternative splicing can be aberrantly regulated by cancer cells to their advantage. Genome-wide studies have long revealed the existence of cancer-specific splicing patterns.[10–12] The ability to commandeer alternative splicing could be beneficial to cancer cells if early developmental-stage isoforms critical for proliferation are also ectopically expressed, driving uncontrolled growth. This switch in splicing preference can be critical since numerous genes possess splice variants that are mutually antagonistic.

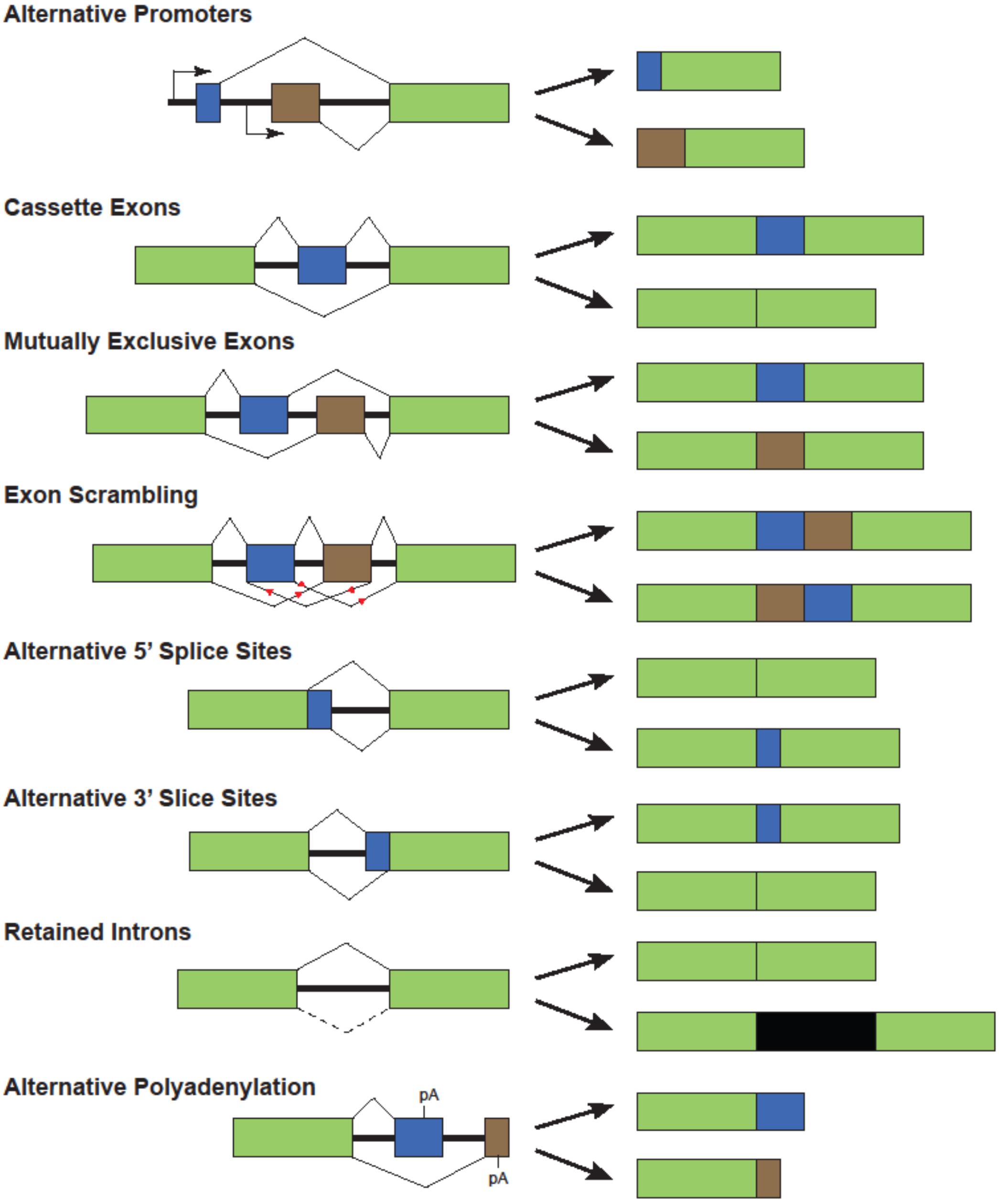


Figure 1.1: Common Mechanisms of Alternative Splicing

Alternative splicing can occur though a number of different processes and give rise to different mature transcripts (right). Exons and final transcripts are illustrated as boxes while lines represent introns. Constitutively expressed exons are depicted in green, and alternatively spliced exons are depicted in blue or brown. Retained introns occur with the absence of splicing, with the intervening intron (black) included in the final transcript.

Escape from cell death is critical for tumorigenesis and some alternatively spliced genes in cancer modulate apoptosis. For example, *BCL2L1* possesses an alternative 5' splice site after exon 2 that produces long and short isoforms that are translated into the BCL-X_L and BCL-X_S proteins, respectively (Figure 1.2A). BCL-X_S promotes apoptosis whereas BCL-X_L has anti-apoptotic effects[13]. Cancers show predominant expression of the BCL-X_L isoform.[14,15] Similarly, the FAS receptor (*TNR6*) is a cell surface receptor that can initiate cell death when bound to TNFS6, the FAS ligand.[16] *TNR6* is subject to alternative splicing (Fig 1-2B); in particular, a splice variant lacking the transmembrane domain results from exon skipping at exon six.[17] This shorter product is soluble and inhibits FAS-mediated cell death, presumably by binding competition for FAS ligand.[18] Soluble FAS is detectable in serum, with higher concentrations found in cancer patients compared to healthy individuals.[19–21]

Metabolic pathways are also frequently altered in cancer. The Warburg effect, a shift from oxidative phosphorylation to aerobic glycolysis, enables synthetic pathways at the expense of ATP production in cancer cells[22] and is partly driven by alternative splicing of the pyruvate kinase M gene (*PKM*). Exons 9 and 10 are mutually exclusive (Fig 1-2C), giving rise to *PKM1* (Exon 9), the adult isoform, or *PKM2* (Exon 10), the embryonic or tumor isoform.[23] PKM2 is expressed widely in cancer (reviewed in [24]), and replacement of PKM2 with PKM1 reverses the Warburg effect and increases oxidative phosphorylation.[25]

The regulation between antagonistic splice variants of the same gene can also be disrupted to affect proliferative pathways, interactions with proto-oncogenes and tumor suppressors, and the epithelial to mesenchymal transition, a pathway that promotes invasion and metastasis. While the switch between antagonistic gene isoforms in cancer illustrates

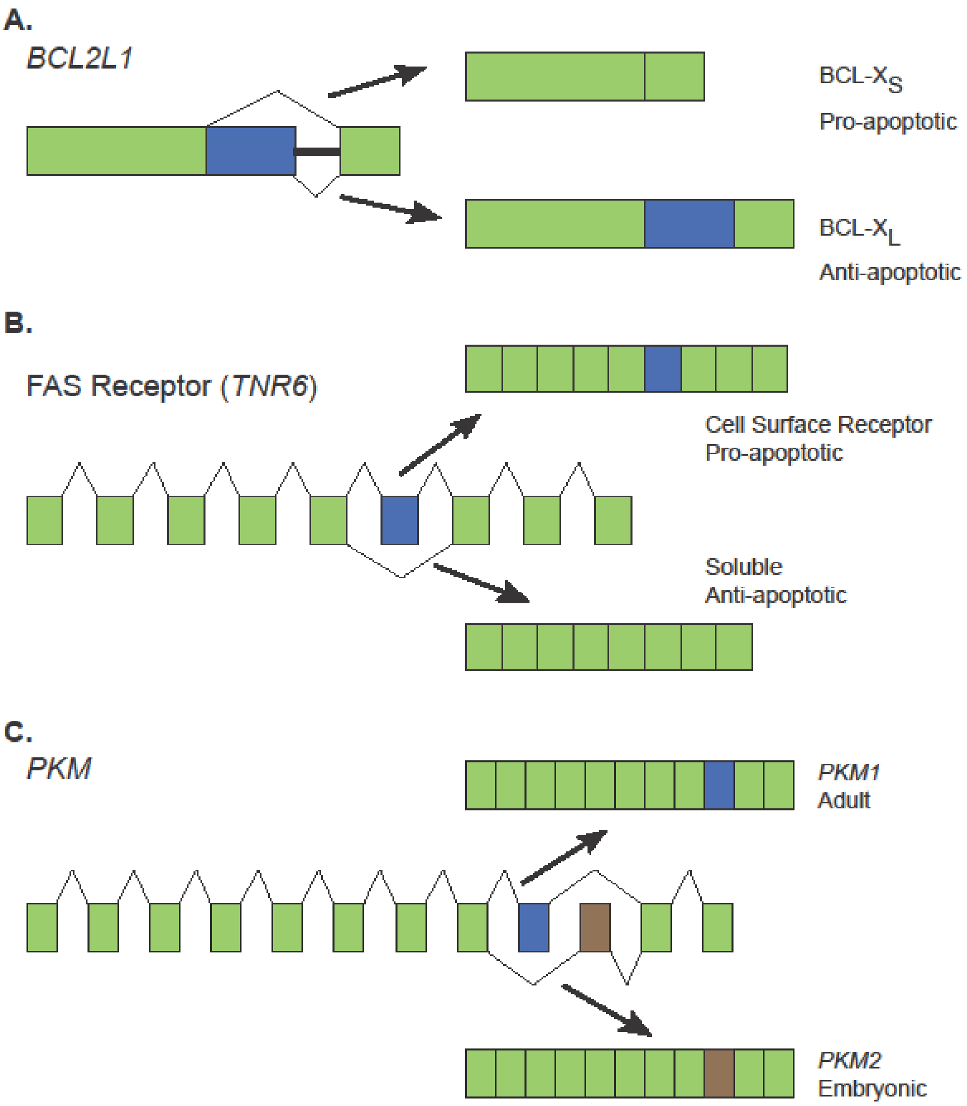


Figure 1.2: Alternative Splicing Leads to Antagonistic Variants

A) BCL2L1 is spliced into two variants based on an alternative 5' splice site (blue). Expression of the two canonical exons (green) results in the pro-apoptotic BCL-XS short isoform, whereas the long isoform, BCL-XL, arises from the splice site downstream of exon 1 and is anti-apoptotic. Exon sizes are relative to actual length, but the intron is not drawn to scale.

B) Exon 6 (blue) of TNR6 is a cassette exon. Inclusion in the mature mRNA leads to expression of the FAS Receptor on the cell surface where it mediates cell death. Exclusion of exon 6 results in a soluble FAS isoform which has anti-apoptotic effects by competing for ligand. Exons and introns are not drawn to scale.

C) PKM exons 9 (blue) and 10 (brown) are mutually exclusive exons. The embryonic variant PKM2 arises with incorporation of exon 10. Upon maturation to adulthood, this variant is typically switched to PKM1 by the alternative incorporation of exon 9. PKM2 promotes aerobic glycolysis whereas PKM1 promotes oxidative phosphorylation. Exons and introns are not drawn to scale.

critical roles for alternative splicing, this subject has been covered recently[26] and will not be reviewed here.

These splice variants are considered canonical products of alternative splicing because they are expressed in somatic tissue as part of normal development or to facilitate cell-specific functions. While the definition of canonical splicing patterns will continue to evolve as transcript isoforms are dissected in more detail, alternative splicing does not need to follow these patterns to provide a tumorigenic advantage. This process may be harnessed to produce novel exon combinations and transcripts that are rarely, if ever seen in normal somatic cells. We focus here on examples of this *aberrant* splicing and its association with outcome as well as the therapeutic impact of the alternative splicing pathway. Aberrant splicing can arise through a couple of mechanistic models: alterations in core spliceosomal components can lead to global splicing deregulation and result in a large number of aberrant products. Similarly, alterations in an accessory splicing factor can lead to deregulation of splicing for the limited set of transcripts where the factor is required for accurate splicing. Alternatively, genomic mutations in a critical splicing motif of a single gene will change the splicing pattern of just that transcript.

Regardless of the mechanism, aberrant splicing of proto-oncogenes can produce constitutively active or even gain-of-function variants that confer new survival or proliferative abilities. In contrast, a tumor suppressor with aberrant splicing could result in an altered reading frame and a premature stop codon; subsequent destruction by the nonsense-mediated decay (NMD) process would ultimately lower the total protein level and its tumor suppressive capacity. Still, some transcripts may manage to avoid NMD, and if the truncated protein gains dominant-negative regulatory functions, tumor suppression would be lowered even further.

Until recently, technical reasons have led researchers to focus primarily on nonsynonymous coding mutations with easily predictable consequences. By doing so, the single largest source of protein diversity has been woefully neglected. This is best exemplified by the fact that there is perhaps no tumor suppressor as prominent as p53, yet its splicing has only recently gained significant appreciation.

p53

P53 is encoded by the gene *TP53* and is one of the most well-known and well-studied tumor suppressors since its discovery over 30 years ago.[27,28] Although it was originally considered an oncogene for nearly a decade,[29–31] p53 is a transcription factor[32,33] that enacts tumor suppression by mediating cellular functions including, but not limited to, apoptosis,[34,35] cellular senescence,[36,37] and DNA repair[38] (reviewed in [31,39]). P53 activity is largely governed through a negative feedback loop with MDM2,[40–42] an E3 ubiquitin-protein ligase that mediates proteasomal degradation of p53. Mutations in p53 that disrupt either of the tandem transactivating domains often contribute to tumorigeneisis (reviewed in [43]).

Alternative splicing of *TP53* was originally identified over twenty years ago in both mouse and humans,[44,45] however investigation into the functional roles of these splice variants is still ongoing. *TP53* contains 11 exons which encode major functional domains including: the two tandem transactivation domains (TAD), the first of which also serves as the binding domain for MDM2, the DNA-binding domain (DBD), and the oligomerization domain (OD) (Figure 1.3A). Due to intron inclusion, normal human lymphocytes express an alternatively spliced variant of *TP53* with a truncated C-terminal domain. This isoform is found in significant amounts only in quiescent cells and provided the first observation that *TP53* splicing could have functional consequences; presumably due to the truncation of the OD,[46] it fails to bind DNA and possesses a transcriptional defect. Subsequently, an N-terminal truncated isoform, Δ40-p53, was discovered in the breast cancer cell line 21PT, arising from an internal transcriptional start site in the first exon.[47] Additional splice variants carrying N-terminal deletions arise from an internal promoter prior to exon 5 to produce Δ133-p53 and Δ160-p53 isoforms that utilize start methionines at amino acid positions 133 and 160, respectively[48] (Figure 1.3B). Interestingly, local internal ribosomal entry sequences (IRES) have been shown to produce N-terminal truncated isoforms, indicating the need for further study into how these isoforms are generated.[49,50] All three of these N-terminal variants can theoretically combine with three different C-terminal variants that arise from alternative splicing downstream of exon 9 (α, β, and γ).[48,51] Canonical splicing of the transcript after exon 9 leads to the α-isoform with a complete OD and the inclusion of exons 10 and 11. The β- and γ-isoforms are formed due to intron retention and stop codons which follow after translation of 10 or 15 new amino acids, respectively (Figure 1.3C). Coexpression of full-length p53 and p53β enhances transcriptional activity on the *p21* promoter but not the *BAX* promoter, and the two isoforms cooperate to promote senescence.[52]

Additional C-terminal variants were described recently. P53δ and p53ζ arise due to splice site point mutations and result in intron retention. p53δ, similar to the β- and γ-isoforms, truncates the OD after exon 9 and 27 new amino acids. Intron retention in p53ζ results in a frame-shift and a premature termination codon in the middle of exon seven.[53]

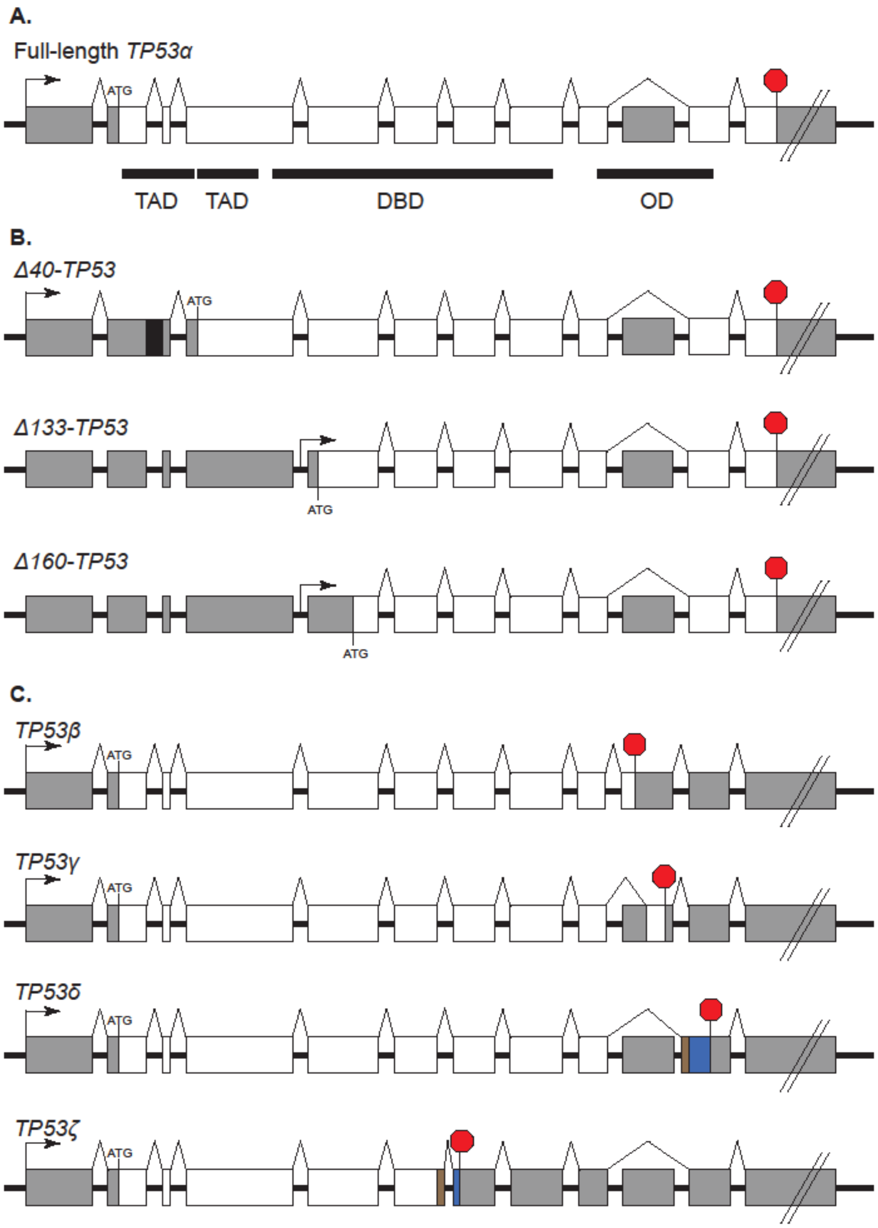


Figure 1.3: Splicing Schematic of TP53

A) Exon structure of full-length TP53 with relative locations encoding the transactivation domains (TAD), DNA binding domain (DBD) and oligomerization domain (OD) indicated (as described in UniProt). Exon sizes are relative to actual length, but introns are not drawn to scale. Start and stop codons are located at the indicated positions. Coding sequences are indicated as white-filled boxes, and untranslated regions are indicated as gray-filled boxes. Splice variants containing combinations between B and C have also been identified.

B) N-terminal TP53 splice variants. An alternative promoter between exons 4 and 5 leads to variants that utilize different start codons. Intron retention is indicated by the black-filled box.

C) C-terminal TP53 splice variants. Alternative 5' or 3' splice sites are indicated by brown-filled boxes, and alternative reading frames are indicated by blue-filled boxes.

In omitting the first 39-159 amino acids and truncating the transactivating domain, N-terminal variants of p53 likely act as dominant-negative regulators. Δ133-p53 inhibits full-length p53 activity as shown by *in vitro* reporter assays.[48,54] Additional *in vitro* studies indicate that Δ133-p53α does not bind p53 response elements (p53REs) and inhibits full-length p53 from binding p53Res.[55] Δ133-p53 is expressed in a p53-dependent fashion,[56] raising the possibility that this isoform participates in a negative feedback loop to modulate full-length p53 activity. However, by encoding for an earlier translational start site, Δ40-p53 still retains the second transactivation domain, and in a study analyzing p53 mutations within the TADs, activity of just the second TAD allowed for minimal transactivation of most p53 target genes.[57] Indeed, the Δ40-p53 has impaired transcriptional activation and impairs growth suppression by oligomerizing with full-length p53.[47,58] In p53-null cell lines, transfection of Δ40-p53 alone was insufficient to initiate transcriptional activity of a p53RE reporter, whereas cotransfection with full-length p53 decreased total p53 transcriptional activity in a dose-dependent manner. Interestingly, in Saos-2 cells, a lower ratio of Δ40-p53/full-length p53 increased transcriptional activity over full-length p53 alone, suggesting that this interaction varies upon cellular context. In these studies, full-length p53 was also protected from degradation by MDM2 when cotransfected with Δ40-p53[59]. Although splice variants in p53 which alter the C-terminal domain require more investigation, p53β has been shown to display promoter-specific binding capabilities.[48]

Given functional differences among p53 splice variants, deregulation of these variants in cancer has come under scrutiny. Mutations affecting *TP53* splicing are found in many different cancers, with some of these splice variants previously considered to be “neutral” since they do not change amino acid composition.[60] In an RT-PCR analysis of pooled RNA from normal breast tissue, all three C-terminal splice variants could be detected, but Δ133-p53 variants were absent. In the same analysis on RNA extracted from a panel of 30 breast tumors, only 5 of which were identified to harbor p53 mutations, p53γ was not observed, while Δ133-p53α was found in 24 samples.[48] In a separate cohort of 127 breast tumors, only 19% expressed both p53β and p53γ. By comparing tumors with p53 mutations, patients with concomitant loss of p53γ showed poor survival, while those who co-expressed p53γ had lower rates of recurrence, with survival similar to patients with functional wild-type p53.[61] Both Δ40-p53 and p53β are expressed in a majority of melanoma cell lines and primary isolates of metastatic melanoma, but are absent or expressed at low levels in fibroblasts and melanocytes. Δ133-p53β is the only other splice variant expressed in melanoma cell lines, but at very low levels.[62]

In addition to the previously described N-terminal and C-terminal splice variants, a panel of 34 ovarian cancer cell lines revealed that internal exon skipping of *TP53* can also occur. This was validated in a cohort of 245 primary ovarian cancers, with expression of the splice variants lower than observed in the cell lines. P53δ associated with decreased recurrence-free and overall survival, supporting the idea that splice-site variants and nonsynonymous mutations can be similarly detrimental. Concomitant expression of p53β and functional wild-type p53 also correlated with decreased survival.[53] In a separate study, Δ133-p53 and Δ40-p53 isoforms were identified in both stage I and stage III (n=83 and 86, respectively) ovarian cancers. Neither was associated with malignant progression, although the authors could not rule out a role in tumor initiation.[63]

Overall, it appears that the N-terminal and C-terminal splice variants of *TP53* have distinct effects in cancer. The absent TAD in N-terminal variants provides an apparent mechanism to inactivate p53, and perhaps unsurprisingly, has been identified repeatedly in cancer. C-terminal variants require further investigation, however some of these isoforms appear to be functional, given that expression of p53γ alongside mutant p53 phenocopies the survival of patients with wild-type p53.[61]

***BRCA1*-associated ring domain 1 (*BARD1*)**

A majority of women who inherit mutations in the *BRCA1* breast cancer susceptibility gene will develop breast cancer[64] and 39% will develop ovarian cancer.[65] The search for potential binding partners of this tumor suppressor led to identification of *BARD1,*[66] a gene that spans 11 exons and encompasses nearly 85 kb on chromosome 2. Both BRCA1 and BARD1 have similar protein structures and form a heterodimer by binding through their RING finger domains (Figure 1.4A). This domain contains critical residues which are mutated in *BRCA1* in association with breast and ovarian tumors. These data suggest that interactions between BRCA1 and BARD1 are required for tumor suppression.

Given this critical interaction, it is surprising that *BRCA1* shows frequent mutations (1653 as surveyed by the HGMD[67]), while *BARD1* mutations in both familial and sporadic breast cancer are relatively rare.[67–70] *BARD1* is more than just an accessory protein for *BRCA1;* the two genes are not co-expressed universally in all tissues,[71] and in response to genotoxic stress, *BARD1* functions in a *BRCA1*-independent manner to induce p53-dependent apoptosis.[72] Additionally, homozygous loss of *BARD1* in mice results in an embryonic lethal phenotype, similar to *BRCA1*-null mice.[73] Indeed, *BARD1* itself has come to be recognized as a potent tumor suppressor.[74]

The relative paucity of *BARD1* mutations is especially puzzling in light of several GWAS studies that identified *BARD1* as a susceptibility gene for neuroblastoma.[75–77] Among the first clues to this puzzle was the observation of aberrant *BARD1* splicing in NuTu-19 cells, a rat ovarian cancer cell line[78] that does not express full-length *BARD1.* Reintroduction of the full-length protein induced apoptosis, suggesting that this splice variant is defective in tumor-suppression. Lacking the RING domain, this variant (*BARD1δ,* Figure 1.4B) is also expressed in several breast cancer lines, and co-immunoprecipitation experiments have shown that it is unable to interact with *BRCA1.*[79]

Could aberrant *BARD1* splicing also confer dominant-negative regulation or other oncogenic properties? This scenario is suggested by the finding that BARD1 overexpression is associated with poor survival in breast and ovarian tumors.[80] That BARD1 expression is inversely associated with outcome contrasts its purported role as a tumor suppressor. Additionally, while the protein had been described as nuclear,[66,81] non-apoptotic cells exhibit cytoplasmic localization. Analysis at the RNA level revealed that many of these transcripts have N-terminal truncations and lead to decreased protein stability.[82]

An additional survey of cervical, breast, ovarian, and endometrial cancer cell lines, along with ovarian tumor tissue arrays revealed that *BARD1* spliced isoforms are often more abundant than the full-length product.[83] This survey also identified and enumerated splice isoforms *BARD1α-η* (Figure 1.4B), as well as alternative transcriptional start sites in exon 4 (Ω1, Ω2, Ψ) (Figure 1.4C). RNA interference experiments directed only towards the full-length transcript did not affect cell growth, whereas siRNAs targeting both full-length and *BARD1* splice isoforms reduced proliferation, suggesting that *BARD1* splice variants play functional roles.[83,84] Indeed,

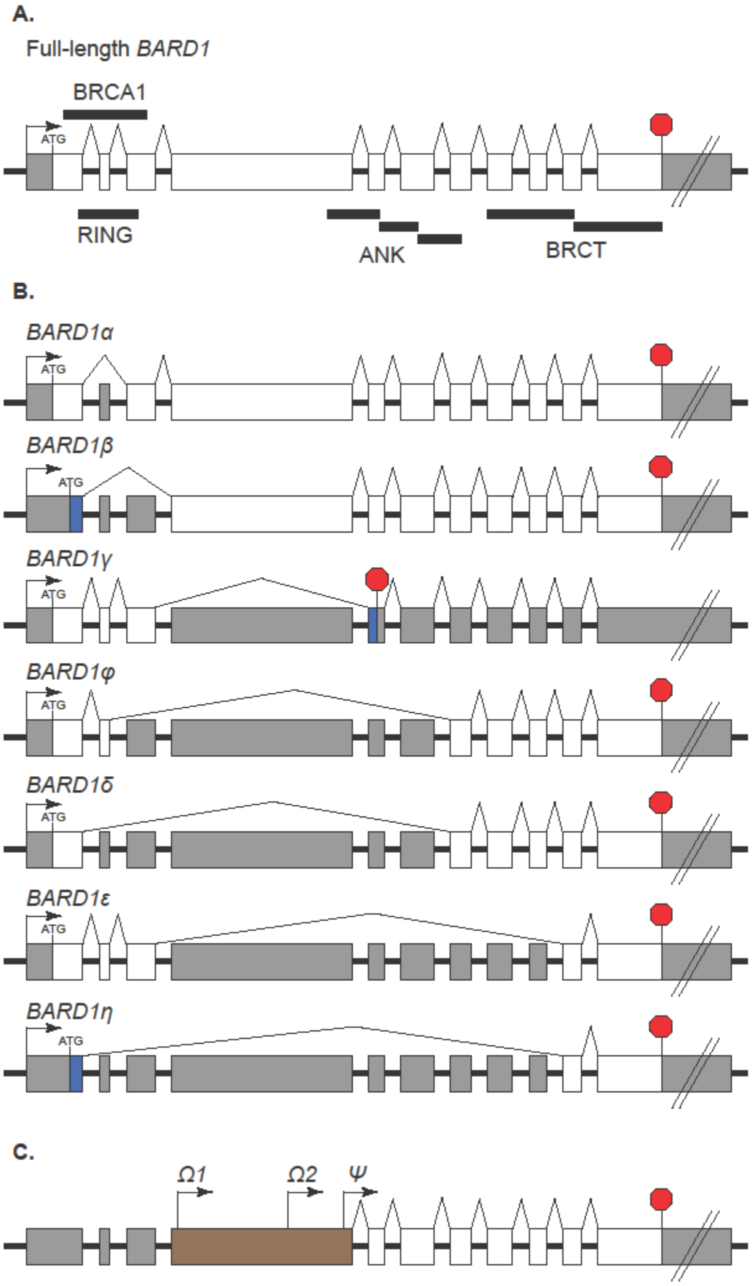


Figure 1.4: Splicing Schematic of BARD1

A) Exon structure of full-length BARD1 with relative locations encoding the RING domain, ANK repeats, and BRCT domains (as described in UniProt). BRCA1 and BARD1 interact through their respective ring domains. Exon sizes are relative to actual length, but introns are not drawn to scale. Start and stop codons are located at the indicated positions. Coding sequences are indicated as white-filled boxes, and untranslated regions are indicated as gray-filled boxes.

B) BARD1 splice variants exhibit various combinations of alternative polyadenylation and exon skipping. Alternative reading frames are depicted in blue.

C) Alternative promoters were found in exon 4 (brown) and encode for varying translational start methionines.

while full-length BARD1 normally promotes Aurora B degradation, BARD1β opposes this and promotes proliferation by scaffolding Aurora B and BRCA2 in late-stage mitosis in a BRCA1-independent manner.[84] BARD1δ also has antagonistic functions relative to full-length BARD1. In MCF7 cells, the BRCA1-BARD1 complex leads to estrogen receptor alpha (ERα) ubiquitination and degradation, but overexpression of BARD1δ instead enhances ERα stability and transcriptional activity.[85]

Up to 19 different splice isoforms of *BARD1* have been identified in colon cancer[86] with a concomitant lack of full length BARD1 expression.[87] Furthermore, in analyses of human tumor biopsies with BARD1 epitope-specific immunohistochemistry, patients with expression of BARD1κ and BARD1π, both presumed to be internal deletion mutants, as well as expression of BARD1β showed poor outcome in non-small cell lung cancers.[88] Since aberrant splicing of *BARD1* is not limited to hormonally regulated tumors, could the susceptibility locus in neuroblastoma demonstrate aberrant splicing as well? Analysis of *BARD1* isoforms cloned from neuroblastoma cell lines and fetal sympathetic ganglia characterized a total of 15 unique splice variants in addition to the full-length transcript.[89] In particular, expression of *BARD1β* was associated with the homozygous GG neuroblastoma risk allele at rs6435862. Similar to observations in ovarian cancer, knockdown and overexpression experiments in neuroblastoma cell lines reiterated the oncogenic characteristics of *BARD1β.*[89]

It remains unclear why *BARD1* loss-of-function in cancer proceeds predominantly through alternative splicing as opposed to mutation. *BARD1* has functions outside of the *BRCA1* signaling axis, and mutations within *BARD1* may be too deleterious for cancerous cells to overcome. In this case, alternative splicing could provide a mechanism in which activity is finely modulated, rather than abolished. The distinction between the loss of a tumor suppressor and the activation of oncogenic properties can be difficult. It is also possible that these splice variants gain oncogenic BRCA1-independent functions. The effects of *BARD1* alternative splicing in neuroblastoma also demonstrate the importance of evaluating alternative splicing in conjunction with mutational surveys when considering loci and genes identified through GWAS or QTL methodologies.

Androgen Receptor

Signaling through the androgen receptor (*AR*), a steroid hormone receptor transcription factor,[90] is critical for prostate cancer development.[91,92] Ligand binding triggers receptor homodimerization and nuclear translocation, which in turn executes a transcriptional growth program through binding specific androgen receptor element (ARE) sequences.[93] *AR* spans approximately 200 kb on Xq11-12 and has 8 exons that encode the full length 110 kDa protein.[94] Exons 2 and 3 encode most of the DNA binding domain (DBD)[95] and exons 4-8 encode the ligand binding domain (LBD)[96] (Figure 1.5A). A naturally-occurring splice variant of *AR* exists and consists of an alternative first exon. This transcript is found in various tissues, with robust expression in the heart.[97] While the canonical first exon constitutes over 50% of the full-length transcript, this alternative N-terminal domain (NTD) contains only seven amino acids and was shown to inhibit proliferation when overexpressed in LNCaP cells (Figure 1.5B). Dubbed AR45 due its calculated 45 kDa molecular weight, this isoform forms heterodimers with full-length AR in a ligand-dependent fashion and inhibits AR activity, presumably due an inability of the alternative NTD to recruit a full set of transcriptional coactivators.[97–99]

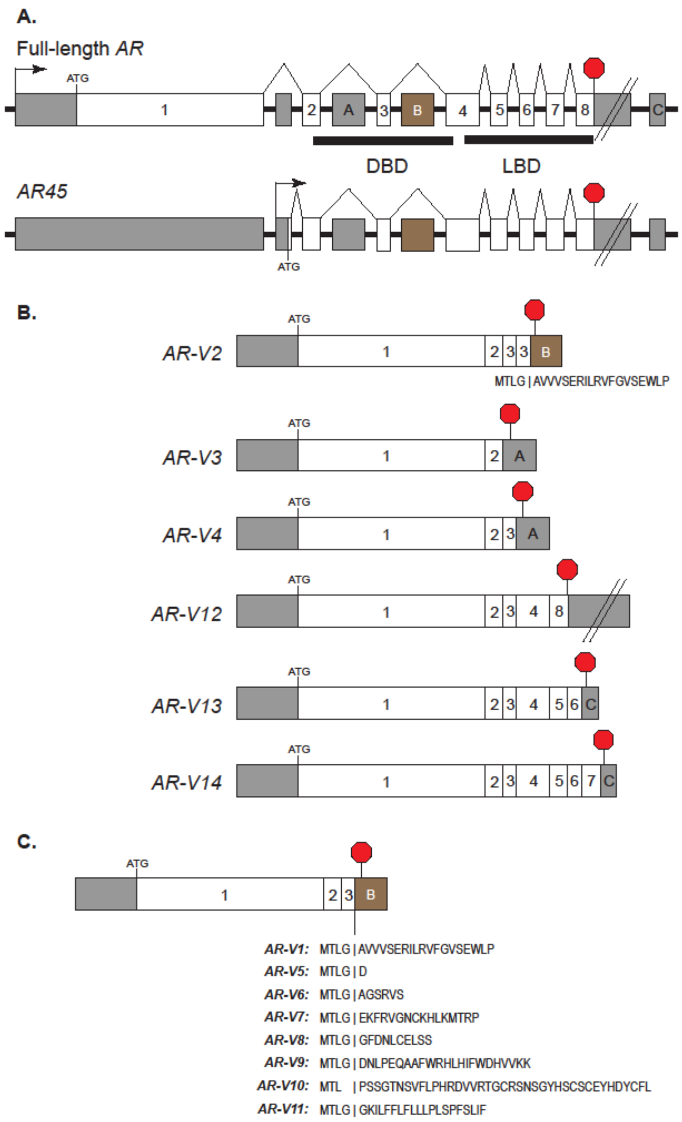


Figure 1.5: Splicing Schematic of AR

A) Exon structures of full-length AR and the canonically spliced AR45 variant. Relative locations encoding the DNA binding domain (DBD) and ligand binding domain (LBD) are indicated (as described in UniProt). Exon sizes are relative to actual length, but introns are not drawn to scale. Start and stop codons are located at the indicated positions. Coding sequences are indicated as white-filled boxes, and untranslated regions are indicated as gray-filled boxes. Exons are numbered as they appear in full-length AR. Exon A has been previously described as Cryptic Exon 4 (CE-4), and exon C has been previously described as exon 9. Region B (brown) includes the previously described CE-2, CE-3, CE-4, CE-5 and various cases of intron retention.

B) Aberrant splicing of AR can include exon scrambling (AR-V2 and AR-V4) as well as exon skipping (AR-V12 - AR-V14). The translated amino acid sequence for the truncated C-terminus in region B is given for AR-V2 starting with the end of exon 3.

C) AR splice variants often include intron retention or the splicing of cryptic exons and subsequent truncation after exon 3. The translated amino acid sequence for the truncated C-terminus in region B is given for the splice variants starting with the end of exon 3.

Androgen deprivation therapy has formed the backbone of prostate cancer therapy for over 70 years,[100] achieved through surgical castration or drugs that block androgen biosynthesis.[101,102] Recurrent disease arises when the tumor loses androgen sensitivity, termed castration-resistant prostate cancer (CRPC). Comparative genomic hybridization revealed that amplification of *AR* may be utilized by CRPC to promote growth in low androgen conditions.[103] The fact that normal *AR* isoforms show functional differences based on alternative splicing suggests another mechanism that could be exploited by CRPC. In fact, androgen insensitivity syndrome, a developmental disorder resulting in the impaired development of internal and external male phenotypes, is due to compromised androgen signaling.[104] Interestingly, aberrant splicing of *AR* has been found in both partial and complete androgen insensitivity syndrome, resulting in receptors unable to bind ligand, as well as receptors that have no transcriptional activity even after ligand binding.[105–109]

All of these previously described alternatively spliced variants result in loss of function in AR. Might gain of function in AR isoforms be advantageous in CRPC? An AR isoform lacking the LBD was first identified in the prostate cancer cell line 22Rv1[110] and subsequently detected in prostate cancer tumor tissue.[111] This isoform could act independently of ligand and was more efficient than full-length AR in activating transcription. While this isoform was originally thought to result from proteolytic cleavage, knockdown experiments indicated that the truncated isoform arises due to alternative splicing. RNA interference targeting an exon partly encoding the LBD only eliminated full-length AR, whereas siRNAs targeting exon 1 knocked down all AR isoforms. In fact, the truncated isoform was found to use an alternative exon 2,[112] which excluded post-translational modifications as a mechanism to generate this isoform. Further analysis of the 22Rv1 line has since revealed several other *AR* splice variants.[113]

Computational methods have identified three cryptic exons located between exons 3 and 4 and led to discovery of one of the best-characterized splice variants, *AR-V7* (Figure 1.5B). Also cloned from 22Rv1 cells, this transcript contains a cryptic exon adjoined to exon 3 that harbors a stop codon after 17 amino acids.[114,115] Expression of this transcript was increased by ~20-fold when comparing CRPC to hormone naïve prostate cancer. A subset of the hormone naïve samples with high expression levels indicated that high *AR-V7* expression was a strongly associated with recurrence following surgical treatment.[114] Expression of AR-V7 was examined by immunohistochemical analysis of 429 human prostate tissue samples, where it was also found to be upregulated in CRPC as compared to hormone naïve samples. A higher cytoplasmic staining score also correlated with increased risk of recurrence after surgery.[115] AR-V7 was constitutively active, with isoform-specific knockdown resulting in reduced proliferation *in vitro* and *in vivo.*[114,115]

An additional novel *AR* splice variant, identified from a human bone metastasis, contains a partially retained intron between exons 2 and 3 that disrupts the DNA binding domain.[116] The LuCaP xenografts, 25 prostate cancers mostly derived from CRPC metastases, identified another splice variant lacking exons 5-7.[117] Other cryptic exons, including one downstream of exon 8, were discovered in two CRPC samples using a custom tiling microarray that spanned 200 kb and encompassed the *AR* locus.[118] Furthermore, a separate immunohistochemical tissue microarray analysis of 50 primary prostate cancers and 162 metastatic CRPC samples, using AR antibodies specific either for the N- or C-terminus, noted an increase of AR variants in CRPC but not primary prostate cancer.[119]

Additional *AR* splice variants have also been profiled in the VCaP (human) and Myc-CaP (murine) cell lines using deep sequencing methods.[120] Interestingly, these variants were expressed at very low levels relative to full-length *AR* (~0.1-2.5%) and gain of function was dependent on expression of full-length *AR*. Although these data suggest that *AR* splicing is inconsequential in these models, subsequent RNAi experiments targeting full-length *AR* while measuring the activity of AR-V7 in the presence or absence of the AR agonist R1881 showed no difference.[118] Since constitutively active splice variants can be expressed in the absence of full-length *AR,*[117] it appears that cellular context is critical to modulate the activity of conditionally active splice variants. Further functional analysis of truncated AR variants showed that C-terminal variation leads to differences in nuclear localization. However, regardless of the specific C-terminus, AR isoforms possess a basal level of nuclear localization and ligand-independent, constitutive transcriptional activity. Indeed, the transcriptional ability of each individual variant is promoter-dependent and is not affected by mutations that alter nuclear localization.[121]

Ultimately, the complex interplay between AR and its splice variants requires further investigation, but the abundance of aberrant splicing after exon 3 also adds to the intrigue of *AR* splicing. Transcripts involving out of order sequences (*AR-V3* and *AR-V4*, Figure 1.5B) have been identified, but are these splice variants examples of exon scrambling,[122,123] or are there underlying genomic structural variations? This region remains a prime candidate to examine genetic control of splicing given the abundance of cryptic exons and diverse examples of intron retention (Figure 1.5C).

The Splicing Pathway

The serine/arginine rich (SR) family of proteins and heterogeneous nuclear ribonucleoproteins (hnRNPs) were among the first to be identified to regulate alternative splicing[124,125] and remain the best studied *trans*-acting splicing factors. SR proteins typically facilitate splice site recognition and promote inclusion of alternatively spliced exons by binding to regulatory sequences present in the pre-mRNA, intronic and exonic splicing enhancers (ISEs and ESEs) (Figure 1.6A and B). Upon binding, they can interact with other splicing co-activators or directly recruit spliceosomal snRNPs to the splice site and activate splicing.[126,127] HnRNPs can oppose this action by binding to intronic and exonic splicing silencers (ISSs and ESSs) on the pre-mRNA and inhibit recognition of the splice site (Figure 1.6A and C).[3,128] These splicing inhibitors are generally thought to sterically hinder spliceosomal snRNPs or other splicing enhancers from binding, although additional mechanisms have been proposed to contribute to exclusion of alternatively spliced exons (reviewed in [3]). Ultimately, whether an exon is included or excluded from the final mRNA transcript is determined by the relative concentrations of the activators and repressors at the splice site.[129,130]

While the cause of most aberrant splicing events remains unknown, an understanding of known splicing factors serves as a starting point for understanding mechanism. SF2/ASF, encoded by the gene *SFRS1*, is an SR protein that is also essential for genomic stability.[131] Overexpression of this gene in a large panel of lung, colon, and breast tumors identified *SFRS1* as a proto-oncogene,[132] and its transforming abilities have been shown to act through the mTORC1 signaling axis.[133] Downregulation of another SR family member, *SRSF3*, promotes alternative splicing of p53, resulting in an increase of p53β and downstream cellular senescence.[134]

The transcription of several hnRNP proteins, including the polypyrimidine tract binding protein, is activated by the MYC oncogene. In cancer, these splicing factors bind to and inhibit inclusion of exon 9 for *PKM*, promoting the embryonic PKM2 isoform and aerobic glycolysis.[135] Similarly, transcriptional upregulation of hnRNPA1 is downstream of EGFRvIII in glioma, and it affects alternative splicing of *MAX* to produce ΔMax and promote glycolytic gene expression and proliferation in glioma cells.[136] HnRNPA1 deregulation is also prominent in lung, colon, and renal cancers.[137–139] Another hnRNP family member, hnRNPH, is overexpressed in glioblastoma where it may promote malignant progression by switching the splicing preferences of *RON* and *MADD*. *RON* encodes a receptor tyrosine kinase and is spliced into a ligand-independent, constitutively active form that promotes invasion and metastasis. *MADD* encodes a death domain containing adaptor protein that mediates apoptotic TNFα signaling, and it is spliced into an antagonistic anti-apoptotic variant.[140]

While these two protein families are perhaps the most ubiquitously expressed and well-studied splicing factors, others have also been found to contribute to tumorigenesis. For example, *CD44* is known to undergo complex alternative splicing involving 10 variant exons,[141] and in particular, exon v5 is critical for promoting metastasis.[142] The transcriptional co-activator SND1 is also an effector of alternative splicing, as it interacts with the splicing factor SAM68 to promote *CD44* exon v5 inclusion. Both SND1 and SAM68 are upregulated in prostate cancer, and knockdown of SND1 or SAM68 reduces proliferation and migration of prostate cancer cells.[143]

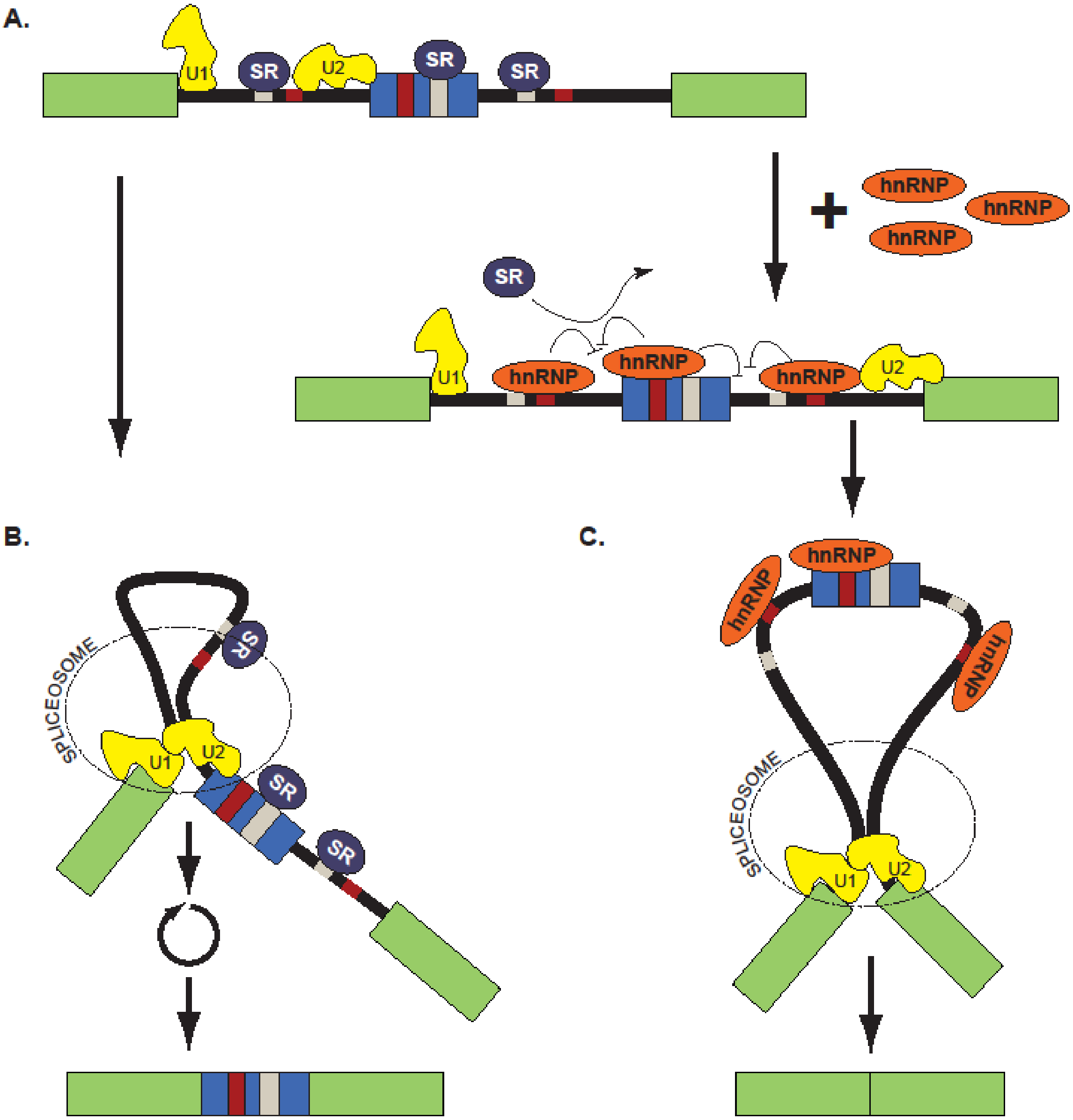


Figure 1.6: Genomic Regulation of Splicing

The decision to splice an alternative exon (blue) with constitutively expressed exons (green) is largely governed by the concentration of accessory splicing factors that recognize and bind splicing motifs. A) SR proteins promote exon inclusion by binding Intronic Splicing Enhancers (ISEs) or Exonic Splicing Enhancers (ESEs) (gray) on the pre-mRNA and recruit spliceosomal small nuclear ribonucleoproteins (snRNPs - yellow) to the splice site. Other spliceosomal snRNPs are also recruited to splice the alternative exon, with successive rounds of splicing at downstream exons as in B. This can be opposed by heterogeneous nuclear ribonucleoproteins (hnRNPs) that recognize Intronic Splicing Silencers (ISSs) or Exonic Splicing Silencers (ESSs) (red) on the pre-mRNA and inhibit SR protein binding or spliceosomal snRNPs from recognizing the splice site. The downstream splice site is recognized instead, and the alternative exon is excised with the rest of the intron as in C.

The splicing landscape as a whole has also come under recent scrutiny in cancer. Exon array analysis of a cohort of 47 neuroblastoma patients revealed numerous splicing differences separating stage 1 and high-risk stage 4 disease, including *PKM*, *KIF1B*, and *MAP2.*[144] Similarly, exon arrays have been used to examine alternative splicing in 102 normal and cancer tissue samples from colon, urinary bladder, and prostate cancer. Over 2000 candidate alternative splicing events distinguished tumor and normal tissues, with a few genes (*ACTN1*, *CALD1*, *VCL*) found in all three tumor tissues.[145] Additionally, whole-exome sequencing of 29 myelodysplasia specimens, a frequent precursor of acute myeloid leukemia, identified frequent mutations in the splicing pathway.[146]

Alternative Splicing and Cancer Therapy

The tumorigenic advantages provided by alternative splicing are not limited to proliferation or apoptotic blockade. Aberrant splicing can also provide a means for therapeutic evasion by gain of function. As we improve our understanding of the molecular basis of different cancers, the development of highly specific small molecule inhibitors has yielded tremendous success.[147] Once cancer is detected in the clinic and treatment commences, selective pressures within a tumor typically promote therapy resistance. Almost 80% of patients enrolled in a phase I clinical trial for metastatic melanoma observed partial or complete response to vemurafenib, an inhibitor of BRAF(V600E).[148] Invariably, patients relapse, developing resistance through a number of mechanisms.[149–151] Interestingly, in an *in vitro* model of inhibitor resistance, a novel splice variant lacking exons 4-8 has promoted BRAF dimerization and vemurafenib-resistant ERK signaling. Six of nineteen patients with acquired resistance to vemurafenib also displayed BRAF(V600E) splice variants, indicating that therapy resistance could also be achieved through aberrant splicing.[152]

With emerging data associating splice variants with survival, can this information be used to improve therapy? If aberrant splicing leads to functional consequences, would correcting the splicing, perhaps in conjunction with conventional therapy, improve survival in cancer? A mouse model of spinal muscular atrophy (SMA) provides clues in this regard. SMA is a genetic disease where loss of the SMN protein causes death of motor neurons in the anterior horn of the spinal cord, resulting in progressive and debilitating weakness. Although caused by loss of function mutations in *SMN1,*[153] disease severity is modulated by the paralog *SMN2,* which is able to produce varying levels of functional protein. The variability in expression of functional *SMN2* stems from the fact that exon 7 is predominantly skipped, resulting in a nonfunctional SMN.[154] Anti-sense oligonucleotides (ASO) targeting an intronic splicing silencer have been used to correct *SMN2* splicing and restore SMN expression, providing effective long-term rescue of SMA in mice.[155] If pharmacologic ASOs can be developed to achieve specific knockdown *in vivo*, this approach could be directed to tumor-specific splice variants for cancer therapy.

As the pharmacologic development of ASOs continues, conventional therapy remains driven by small-molecule inhibitors and derivatives of naturally-occurring compounds with anti-tumor effects. Herboxidiene,[156] FR901464,[157] and the pladienolides[158] are natural products that modulate spliceosomal components. These were of particular interest due to their low nanomolar IC_{50} and cytotoxic effects in cancer cell lines and animal models. They have led directly to the development of synthetic derivatives: E7107 from pladienolide B, spliceostatin A and meayamycin from FR901464, and the sudemycins, a set of molecules designed using a consensus pharmacophore gleaned from known structure-activity relationships (reviewed in

[159,160]). SF3B, a subunit of the U2 snRNP that facilitates splice site recognition (Figure 1.6), is the main target of these compounds,[161,162] and they modulate not only alternative splicing, but also expression of genes critical to cancer progression.[163–165]

By effecting intron retention or exon skipping, these drugs ultimately lead to activation of the NMD pathway or the production of inactive cell cycle genes, resulting in cellular arrest.[161,162,166] Interestingly, these drugs show tumor-specific effects with little toxicity, despite theoretical deleterious effects on normal cells. One plausible explanation is that drug dosage is critical to avoid complete inhibition of splicing, which would be universally toxic. At an appropriate dose, these drugs may still be effective at eliminating aberrant splicing or minimizing the splice isoforms that are critical for cancer progression. In this setting, cancers that have acquired deregulation of global splicing patterns may be best suited for spliceosome-inhibitory therapy. It is also possible that tumors driven in-part through functionally aberrant splicing may be exquisitely sensitive to these spliceosomal modulators, as the drugs reverse the splicing dependency. Future studies analyzing the molecular underpinnings of these drugs may reveal more about the functional roles of alternative splicing in cancer.

Conclusions and Perspectives

The overexpression experiments in p53-null cells that revealed the dose-dependent dominant-negative regulatory effects of Δ40-p53[59] also serve to highlight the importance of the ratio between splice variants. Is there an absolute threshold for expression of any particular splice isoform to produce a biological effect? The answer is certainly transcript-specific, as the normal function of the full-length product is just as critical as the distinction of the novel splice isoforms as gain-of-function or dominant-negative regulators. All three genes discussed here suggest that cellular context is also an important factor, and as evidenced by the inconsistent data between splice isoform ratios in *AR*, the answer is not always clear. Furthermore, minor amounts of aberrant splice isoforms may be indicative of global splicing deregulation with combinatorial effects in cancer. These issues may be better addressed as technology continues to improve in detecting splice isoforms and quantitating their expression.

Despite the uncertainty in this regard, the influence and impact that alternative splicing has in cancer is evident in the association of splice variants with outcome and the profound effects that splicing can have on therapy. Although interest in cancer-associated splicing continues to increase, the specific regulatory mechanisms harnessed to confer tumorigenic advantages are still poorly understood. This is true regardless of whether these events occur through aberrant splicing or modulation of existing alternative splicing.

Large-scale, unbiased proteomic approaches have been used to identify additional splicing factors.[167] However, given the tissue- and cellular-specificity of splicing programs, can these methods be truly comprehensive? Along these same lines, splicing motifs have been so far defined by various methods. SELEX (systematic evolution of ligands by exponential enrichment) has identified ESEs *in vitro*[168,169] and *in vivo,*[170] but this method necessitates a known splicing factor to begin. Computational methods have also identified ESEs[171,172] and ISEs[173,174] utilizing several approaches including motif comparisons between introns and exons, exons with weak splice sites and exons with strong splice sites, and evolutionary conservation. An unbiased approach using a splicing reporter assay to analyze all possible decamer motif combinations identified 109 ISEs.[175] The fact that some of these motifs overlapped with previously identified ESSs indicates the importance of positional effects on motif function. This assay utilized a reporter system in which random decamers were cloned into a specific position, but since human introns extend an average of 3.7 kb,[176] a truly unbiased approach including positional effects remains to be examined.

The importance of defining and understanding these motifs should not be understated. The genetics of splicing clearly play crucial roles in cancer, as exemplified by the common variation associated with *BARD1* splicing and the splice site mutations demonstrated in both *TP53* and *AR*. Current technologies provide a wealth of sequencing data that has revolutionized the way we analyze mutations in cancer. However, mutational effects on splicing are typically ignored when distinguishing synonymous from nonsynonymous mutations. Similarly, a mutation that ultimately results in a premature stop codon often leads the resulting transcript and protein to be automatically classified as non-functional, without regard to additional splice variants. For example, some of the *TP53* splicing experiments were performed in K562 cells, which have been categorized as a "p53-null" line due to a premature stop codon at residue 148. These cells still expressed the Δ160-p53 isoform, indicating that functional splice variants are still be produced from transcripts carrying frameshift or nonsense mutations.[177]

Additionally, high throughput sequencing in cancer primarily focuses on the exome, mostly due to the benefits of the accompanying increase in coverage depth. While these studies clearly yield insights into the genetics of disease, changes in splicing can easily be missed by failing to capture regulatory regions within the introns. It could be argued that since we do not have a definition for precise motifs at specific intronic positions to look for, there is no justification for whole-genome sequencing. Yet is there a better way to understand the genetic regulation of splicing without these data?

Next generation precision medicine therapies are on the horizon and promise highly-specific, perhaps even isoform-specific, targeting abilities. In-depth genomic studies of splicing will be critical for defining splicing mutations that occur away from intron-exon boundaries. These data, coupled with biochemical and molecular analyses using splicing-modulating drugs, promise to uncover new targets in cancer and to enable novel approaches to block canonical cancer targets and pathways.

CHAPTER 2: THE GENETICS OF SPLICING IN NEUROBLASTOMA

Alternative splicing of mRNA is a conserved process that provides the main source of proteomic diversity in eukaryotes. Splicing proceeds through a canonical process involving the spliceosome, a complex of conserved small nuclear ribonucleoprotein particles (snRNPs), and is subject to both genetic regulation and heritability.[178,179] Some of these regulatory systems act in *cis* within the primary sequence of the pre-mRNA transcript, defined as intronic splicing enhancers (ISEs), intronic splicing silencers (ISSs), and their exonic counterparts, ESEs/ESSs. Splicing regulatory systems can also act in *trans,* through genetically distant factors recruited to the splice site, to modulate exon inclusion or exclusion.[180,181]

Splicing programs often go awry in disease. Consequently, it has become important to consider possible alternative splicing products when investigating the function of a gene. Initial analyses of genetic complexity of splicing in disease utilized human cell lines, which confirmed a genetic component to alternative splicing.[182–184] However, by focusing on unrelated human samples, these studies were limited by a GWAS approach to form associations with specific SNPs and splicing events, many of which were localized to immediate intron-exon boundaries. Thus, the genetic complexity of this process, *in vivo*, remains poorly described.

Alternative splicing may be particularly important to cancer,[185] as the unique cancer environment can select for novel splice isoforms that promote tumor growth, metastasis, or response to treatment.[83,89,132,152,186,187] Alternative splicing products have therefore become increasingly important as targets for therapy in cancer.[188–190] Neuroblastoma, the most common cancer of infancy and the most common extracranial solid tumor of childhood, represents an enigmatic disease in which differential splicing has the potential to be a major contributor to progression. Despite extensive whole-genome and whole exome studies, including sequencing analyses of over 300 tumors, point mutations in genetic drivers of neuroblastoma (*MYCN*, *ALK*[191], *PHOX2B*[192,193], *ARID1A/B*[194], and *ATRX*[195,196]) account for a minority of patients.[197] In the absence of recurrent exonic mutations, what drives neuroblastoma tumorigenesis and/or progression? Interestingly in this regard, one of the most robust GWAS signals in high-risk neuroblastoma is located at the *BARD1* locus.[75] Although *BARD1* itself shows a relative paucity of mutations in cancer,[74] a recent report identified functional effects of *BARD1* splicing associated with the neuroblastoma risk allele.[89] Coupled with the identification of several genes as alternatively spliced in neuroblastoma cells,[198–200] and exon level analysis of neuroblastoma patients that indicate numerous differences in splicing between stage 1 and stage 4 disease,[144] alternative splicing may be critical to pathogenesis.

We used an integrative genomics approach to survey the splicing landscape in neuroblastoma, combining both genome and transcriptome data into a single analysis. This type of approach, when used to query expression quantitative trait loci (eQTL), represents a powerful tool to discover genetic mechanisms governing gene expression.[201] We extended this concept to a splicing quantitative trait locus (sQTL) analysis, using exon-level expression as a proxy for splicing. To establish a more comprehensive overview of splicing genetics, we harnessed the power of linkage mapping in a defined backcrossed mouse system. Our analysis uncovered a complex genome-wide splicing landscape and revealed splicing motifs.

We report here a genome-wide analysis of splicing in a genetically engineered mouse model of neuroblastoma driven by mis-expression of *MYCN* in the developing neural crest.[202] By comparing two somatic neural tissues, our sQTL analysis identifies novel candidate *trans*-acting splicing factors. Coupled with available whole-genome sequencing data, our mouse genotypes presented a map for navigating over a hundred virtual genomes and identified novel candidate intronic splicing motifs. To establish further relevance to human disease, we utilize these splicing motifs to identify additional genes with recurrent mutations in cancer. We also examine a strain-specific triplet splicing preference within *FUBP1* that leads to deregulation of MYC, with functional correlations in human neuroblastoma.

Results

sQTL Analysis

Superior cervical ganglia (SCG) and cerebellum (CB), representing peripheral neural crest- and brain-derived tissues respectively, were harvested from the N1 generation of FVB/NJ mice transgenic for *TH-MYCN,* backcrossed to wild-type 129/SvJ mice (n=102, Figure 4.1) and profiled on Affymetrix Exon Arrays. Mice were genotyped at 349 SNP and microsatellite markers, with an average genome-wide spacing of 8 Mb (Table 4.1). To control for variation in expression levels of a gene across samples, we first generated values for normalized exon expression (NE) by taking the ratio of exon expression as compared to transcript expression. To identify unique differential splicing events between strains, we then examined NE as a quantitative trait and used linear regression to look for genomic loci that could influence the regulation of splicing in CB and SCG.

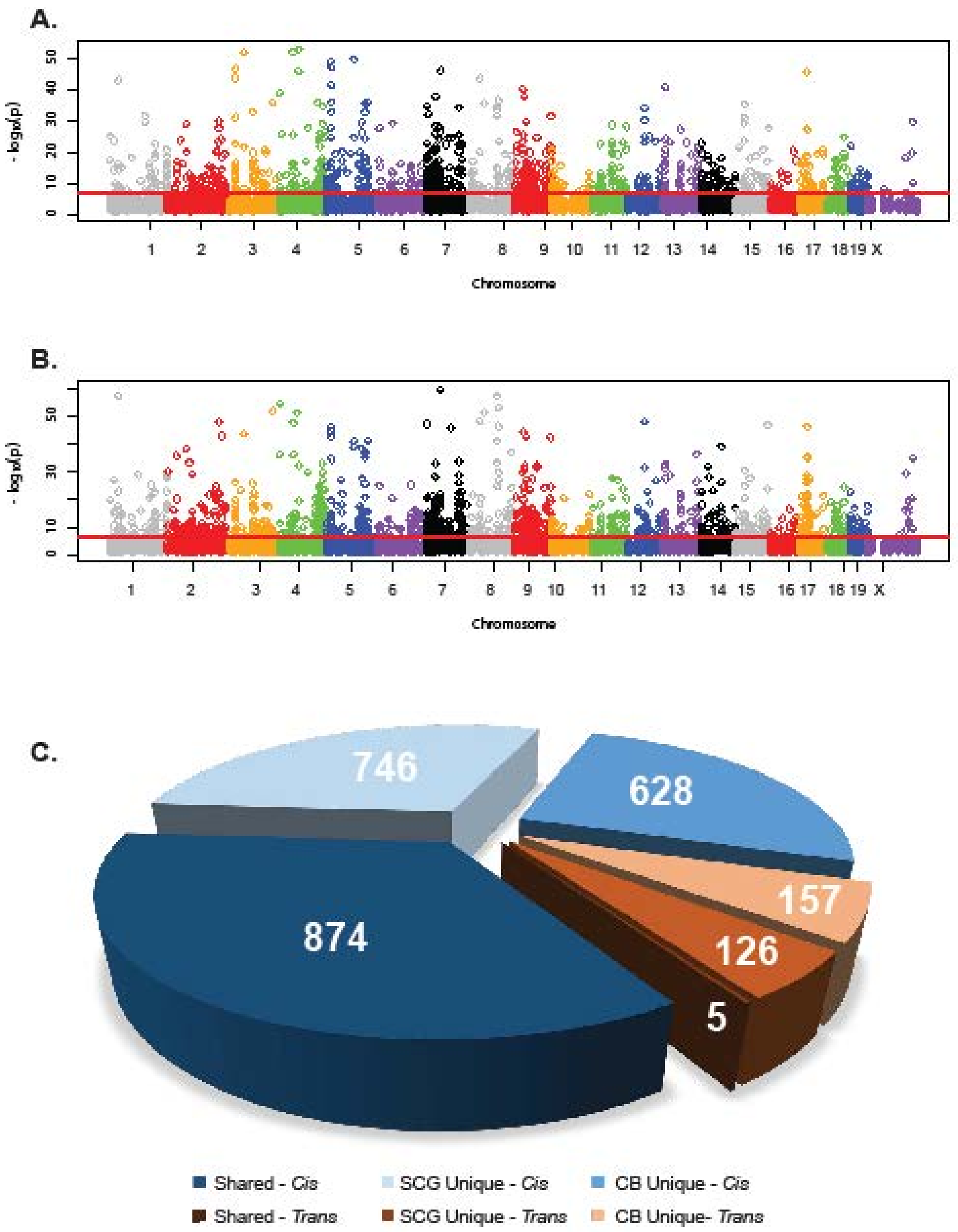


Figure 2.1 Genomic Distribution of sQTL

sQTL are distributed throughout the genome similarly in CB (A) and SCG (B). The x-axis indicates the location of each SNP, and the y-axis indicates the level of significance of an associated sQTL. The horizontal red line is drawn to mark an estimation of genome-wide significance at an FDR < 0.05.

C) Cis-sQTL were more abundant than trans-sQTL, and a majority were shared between both tissues. In contrast, trans-sQTL were largely tissue specific.

We identified 1664 and 1751 sQTL in CB and SCG (defined here as pairs of alternatively spliced exons associated with a marker), respectively (Figures 2.1 A and B, 5% false detection rate). The majority of the sQTL was within 50 Mb of the spliced transcript and thus defined to be *cis* (90.3% in CB and 92.5% in SCG, Appendices A and B). 874 of these *cis*-sQTL reflected similar splicing events in both CB and SCG whereas *trans*-sQTL (mapping at least 50 Mb away from the spliced transcript or to a different chromosome) showed little overlap between tissues (Figure 2.1C, Appendix C). *Trans*-sQTL likely represent polymorphisms within splicing factor genes, which can then affect the splicing of multiple unlinked transcripts. Conversely, *cis*-sQTL represent polymorphisms at or near the gene being spliced which alter the splice site itself, create novel cryptic splice sites or polyadenylation signals, or alter the ability of ISSs/ISEs/ESSs/ESEs to recruit additional splicing factors.

***Trans*-sQTL Identify Novel Candidate Splicing Factors**

Trans-eQTL have become a powerful tool to identify transcription factors, as these proteins work in *trans* to promote transcription of other genes. We therefore looked at candidate *trans*-sQTL to identify novel splicing factors and potential regulators that could affect splicing in a number of unlinked genes. *Trans*-sQTL were identified throughout the genome (Figure 2.2A), however only a few co-localized at "hotspots," where a single locus was linked to several splicing events (Figure 2.2B). We observed 5 *trans*-sQTL linked to the marker rs29347557 on chromosome 10 in SCG and 8 *trans*-sQTL linked to the marker rs33477935 on the X chromosome in CB.

Candidate splicing factors in these regions were identified by examining differential transcript expression between SCG and CB (Figures 2.2B and 2.3). Given the overwhelming tissue-specific nature of the *trans*-sQTL, we hypothesized their origin to be from tissue-specific regulation of putative splicing factor genes in these regions. The minimal overlapping 95% confidence interval for sQTL mapping to rs29347557 in SCG encompassed the range between markers rs13480474 and rs38621064 on chromosome 10. This region spans over 13 Mb and contains 66 known genes, of which 30 were differentially expressed between CB and SCG (Appendix D). Almost all of these genes had known functions. Among these, *SF3B5* encodes a splicing factor subunit and was the only gene known to function within the splicing pathway, suggesting a proof of principle for this methodology (Figure 2.2B). The sQTL mapping to rs33477935 in CB possessed 95% confidence intervals that minimally overlapped from rs33478059 to rs13483805 on the X chromosome. This region spans over 77 Mb and contains 489 known genes, 123 of were differentially expressed (Appendix E). Similar to our analysis in SCG, only one of these genes is a known splicing factor, *HNRNPA3*. However, several other genes have no known function but have domains that suggest that they interact with RNA. We derived candidate splicing factors from these transcripts: 3 relatively uncharacterized genes that encode RNA-binding motifs (*RBMX, RBM10, RBM2*) and *DDX26B*, a gene that encodes a DEAD-box peptide (Figure 2.2B).

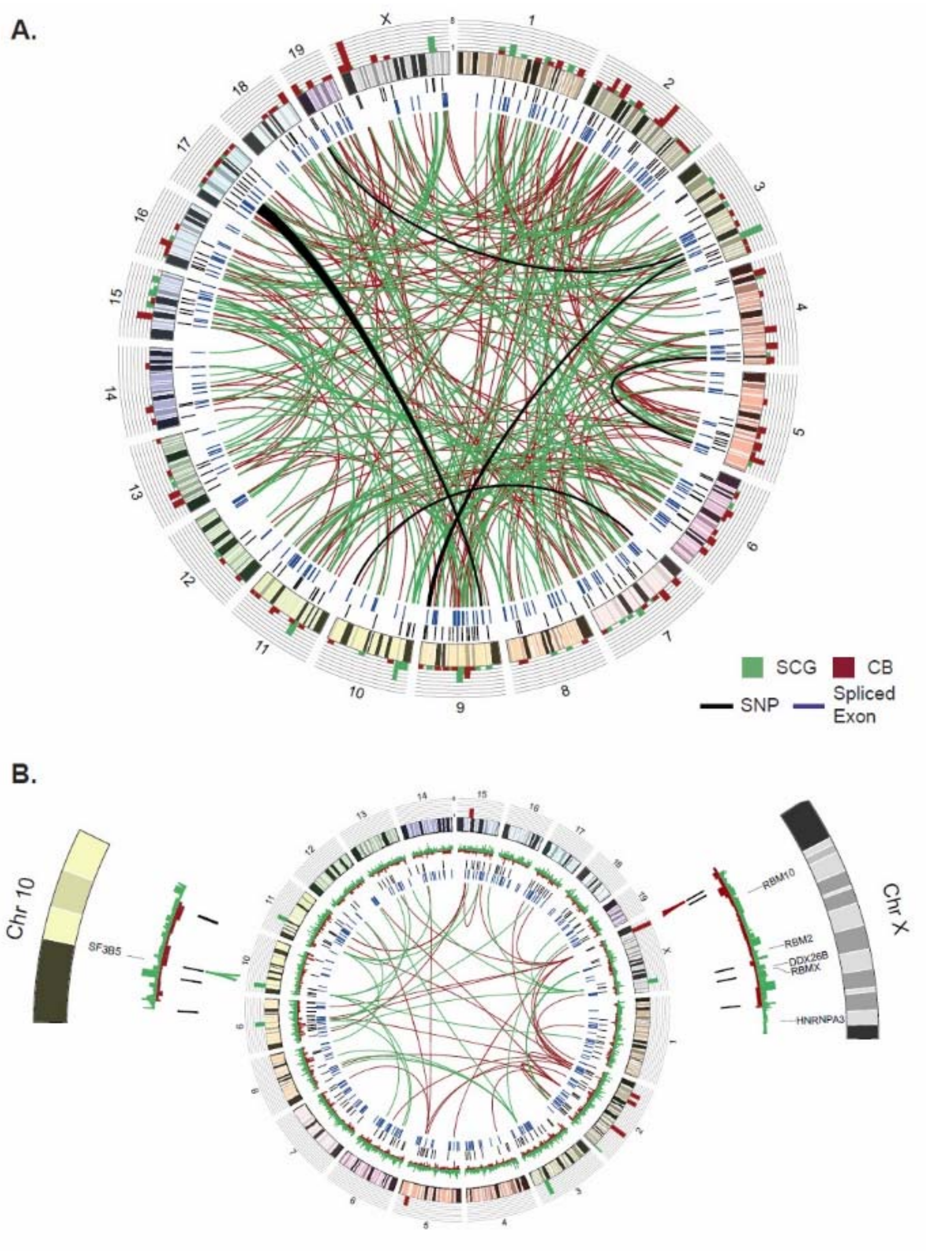


Figure 2.2 Trans-sQTL in the Cerebellum and SCG

A. Circos plot of 162 cerebella and 131 SCG trans-sQTL identified at an FDR < 0.05.

Mouse chromosomes are plotted on the outer ring, with locations of SNPs with sQTL indicated in black on the first inner ring. Locations of spliced exons are defined in blue on the second inner ring. sQTL are drawn linking SNPs to exons from cerebellum (red), and SCG (green), with shared sQTL drawn in black. The histogram outside of the chromosomes indicates the number of sQTL (on a scale of 1-8) that map to a particular locus.

B. Circos plot of sQTL hotspots, where 4 or more co-localized. An additional data track between the chromosome ideograms and SNP loci indicates differentially expressed genes at the transcript level (red = higher expression in CB, green = higher expression in SCG). Five SCG-specific trans-sQTL mapped to rs29347557 on chromosome 10. This region included differential expression of *SF3B5*, encoding a splicing factor subunit. Eight CB-specific trans-sQTL mapped to rs33477935 on the X chromosome. Shown are the locations of the candidate splicing factors that are differentially expressed at this locus.

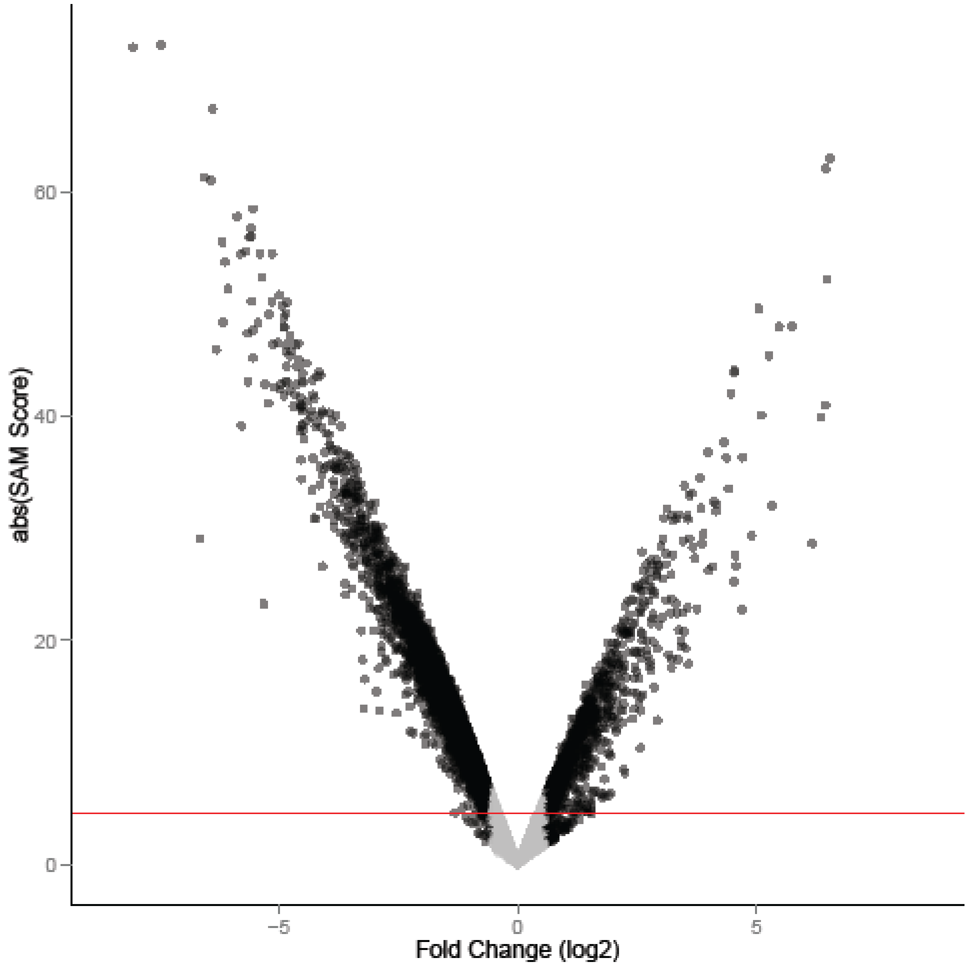


Figure 2.3 Differential Whole-Transcript Expression Between SCG and CB

Volcano plot from SAM analysis showing differences in transcript-level expression between CB and SCG. The x-axis indicates the log2 fold change between CB and SCG and the y-axis is the absolute value of the SAM score. A red horizontal line is drawn to estimate statistical significance at a delta of 2 (FDR < 0.0006). Genes with a fold change greater than 1.5 are indicated in black.

***Cis*-sQTL Reveal Novel Candidate Splicing Motifs**

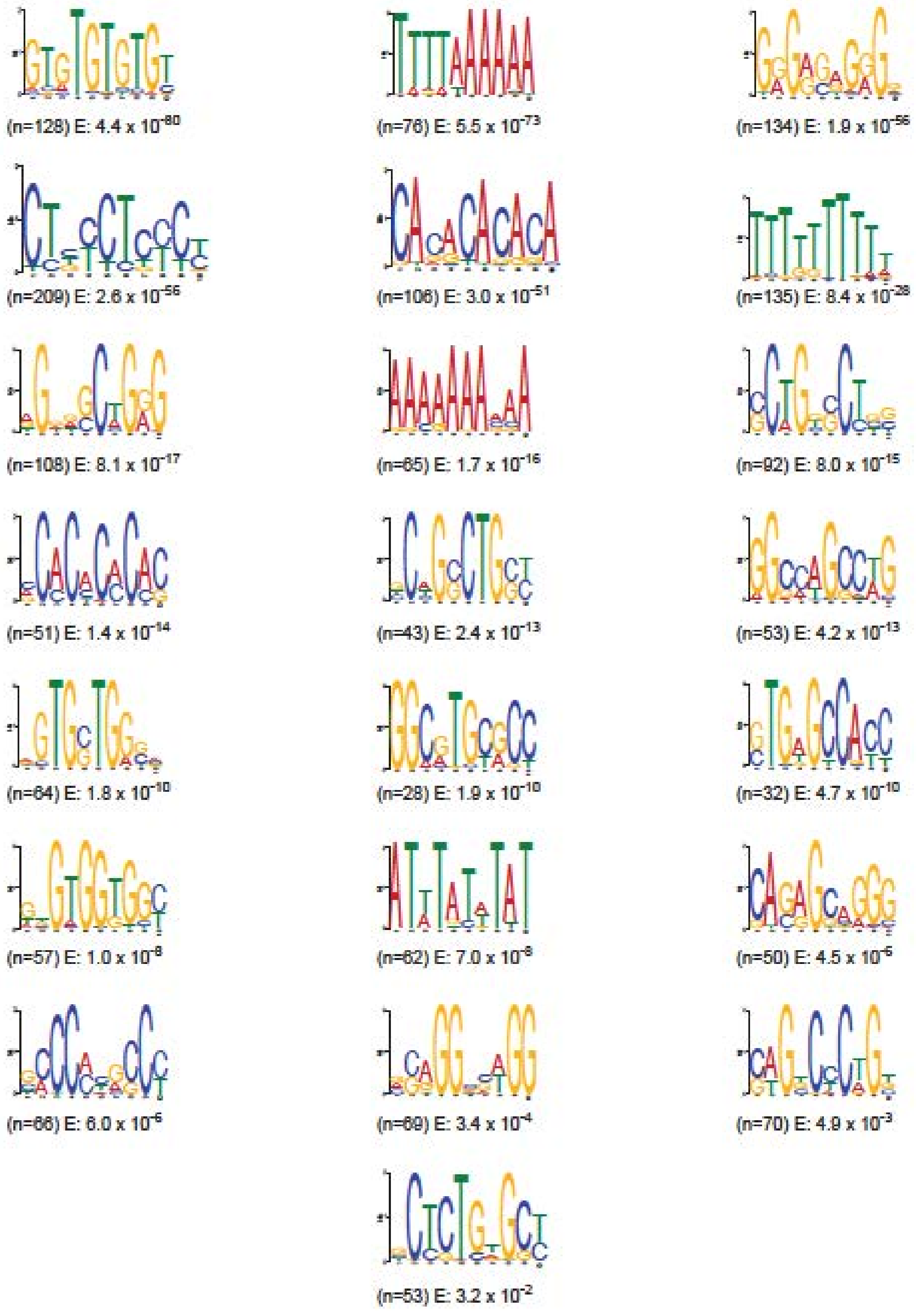
Our genotyping marker set was not designed to identify functional polymorphisms. Rather, markers were selected to map chromosomal regions to either parental strain. Using available whole-genome sequencing (WGS) for laboratory inbred mouse strains[203,204], we were able to compare sequence information for FVB/NJ[205] and 129/SvJ[206], provided at 53x and 28.9x coverage, respectively. When compared to the reference C57BL/6 genome, 5,453,320 and 2,643,008 SNPs were identified in FVB/NJ and 129/SvJ, respectively, with 1,233,556 of these shared between both strains. Together with our genotyping set, the WGS data provided us with local nucleotide-level sequences of our individual backcrossed mice.

As *cis*-sQTL represent differences in splicing driven by polymorphisms in regulatory sequence elements, we hypothesized that these sequence elements would be common sites for polymorphisms between the two parental strains. Thus to identify recurrent splicing motifs, we compared genomic sequences between strains surrounding alternatively spliced exons possessing *cis*-sQTL in both tissues. In contrast to previous efforts that have focused heavily on identifying ESEs/ESSs, we looked for recurrent intronic decamer motifs that spanned the SNP by extracting 19-mer sequences centered on strain-specific intronic polymorphisms.

Enrichment analysis in these sequences, using MEME,[207,208] identified 22 unique motifs [after removing redundant results that shared a high degree of similarity with each other (Figure 2.4, correlation coefficient > 0.60)]. A TOMTOM[209] search in a database of known RNA binding motifs[210] revealed that seven had been described previously. Of these, six were highly similar to motifs known to bind splicing factors (Figure 2.5, FDR < 0.05), confirming that our approach could define bona fide splicing motifs. Thus, the remaining 15 sequence motifs represent previously undescribed motifs critical for proper regulation of alternative splicing.

To see if these splicing motifs could represent functional sites commonly mutated in cancer, we queried the TCGA cancer database, analyzing whole genome sequencing of 42 high-risk glioblastoma (GBM) tumors,[211,212] each with a paired normal sample. MAST[213] was used to examine the sequence immediately surrounding both intronic germline variants (GVs) and intronic somatic mutations (SMs) for a match to any of the 22 splicing motifs (sequence-level match $p < 0.0001$). 21 out of 22 of the splicing motifs were found to match either GVs and/or SMs.

Candidate genes with splicing mutations were identified by enrichment of somatic mutations compared to germline variation in intronic splicing motifs. Three GBM samples (7.1%) had a recurrent C>T mutation at position 117618623 on chromosome 5 in a splicing motif within the intron of the uncharacterized lncRNA *LOC100505811* (Figure 2.6A). Another three samples had a recurrent T>G mutation at chr6:52445058, in a splicing motif within an intron of the antisense RNA *TRAM2-AS1* (Figure 2.6B). Furthermore, five samples possessed intronic somatic splicing motif mutations within the Nuclear Pore Complex Interacting Protein Family, Member A1 gene, *NPIPA1.* One of these was a G>C mutation at chr16:15031765 and the remaining four were recurrent G>A mutations at chr16:15040359. It should be noted that a separate germline sample was also heterozygous for the A allele at the recurrent chr16: 15040359 position (Figure 2.6C).



(n=128) E: 4.4 x 10^{-80}

(n=76) E: 5.5 x 10^{-73}

(n=134) E: 1.9 x 10^{-56}

(n=209) E: 2.6 x 10^{-56}

(n=106) E: 3.0 x 10^{-51}

(n=135) E: 8.4 x 10^{-28}

(n=108) E: 8.1 x 10^{-17}

(n=65) E: 1.7 x 10^{-16}

(n=92) E: 8.0 x 10^{-15}

(n=51) E: 1.4 x 10^{-14}

(n=43) E: 2.4 x 10^{-13}

(n=53) E: 4.2 x 10^{-13}

(n=64) E: 1.8 x 10^{-10}

(n=28) E: 1.9 x 10^{-10}

(n=32) E: 4.7 x 10^{-10}

(n=57) E: 1.0 x 10^{-8}

(n=62) E: 7.0 x 10^{-8}

(n=50) E: 4.5 x 10^{-6}

(n=66) E: 6.0 x 10^{-6}

(n=69) E: 3.4 x 10^{-4}

(n=70) E: 4.9 x 10^{-3}

(n=53) E: 3.2 x 10^{-2}

Figure 2.4 Total set of identified unique splicing motifs

RBM38, **ARET**, **SM**, **HNRPLL**, **BRUNOL5**, PAPI, **HNRNPL**

SAMD4A, VTS1P

SRSF10

PP_0228, TV_0236, PABPC4, **SXL**,
HUR, OT_0262, LM_0255

SXL, PABPC4, PP_0228, TV_0236, HUR,
OT_0262, LM_0255, TB_0253, SART3, PABPC1

Figure 2.5 Motifs with matches to an RNA Binding database

Known protein binding relationships are indicated below the indicated motifs. Those in bold are known to have roles as splicing factors.

Each of these mutations occurred at highly conserved positions within the splicing motif and either substituted a nucleotide that was not normally observed at that position (*LOC100505811* and *NPIPA1*), or replaced a nucleotide with the conserved nucleotide (*TRAM2-AS1*), creating a match to the splicing motif. RNA-seq data were available for 25 of the 42 GBM samples. To see if these mutations led to changes in splicing of these genes, we profiled NE for the exons immediately proximal to the introns with splicing motif mutations. While the trend in differences of NE between the two exons in *LOC100505811* was not statistically significant, the splicing motif mutations in *TRAM2-AS1* and *NPIPA1* were associated with a significant decrease in NE for the exons downstream of the intron. Thus, these mutations are located in sites with functional changes in alternative splicing (Figure 2.6).

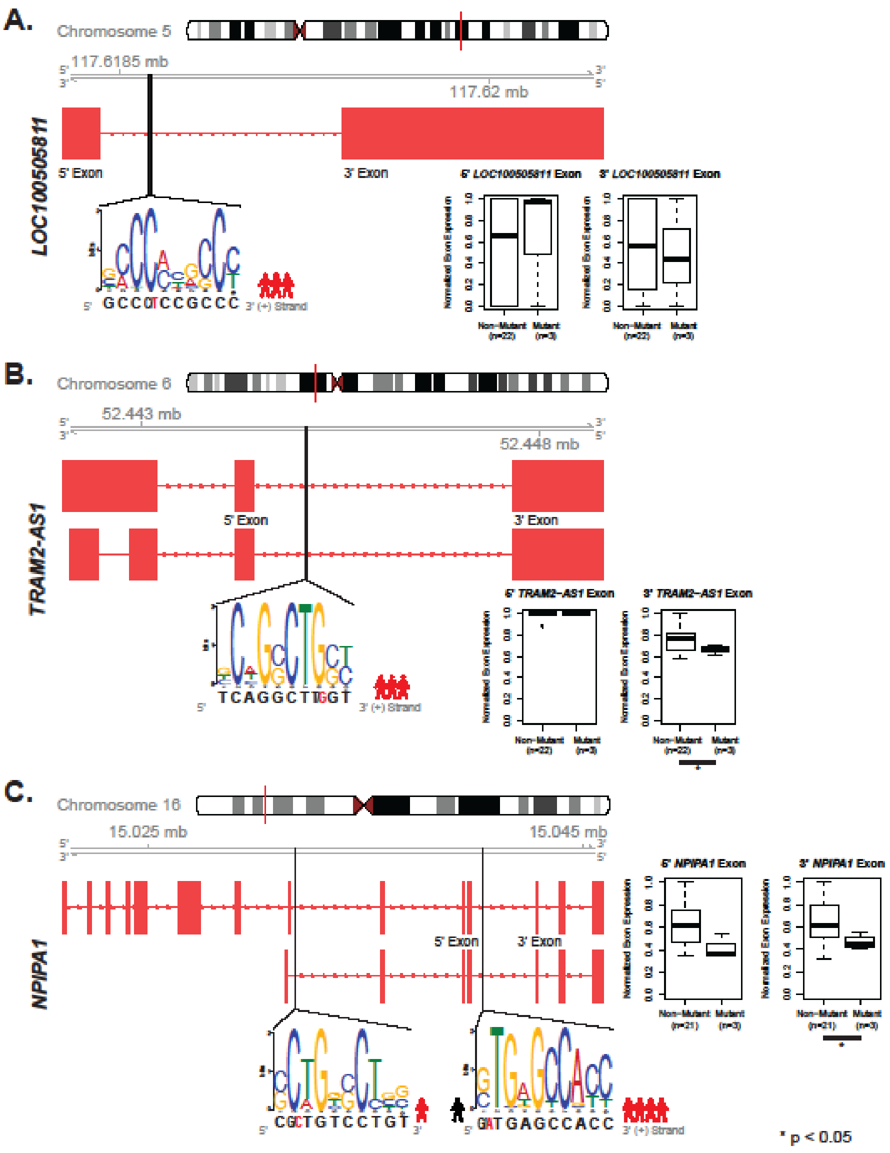


Figure 2.6 Recurrent Somatic Mutations Occur in Intronic Splicing Motifs in GBM

Recurrent mutations in *LOC100505811* (A), *TRAM2-AS1* (B), and *NPIPA1* (C) occur in separate splicing motifs. The sequence logo of the splicing motif is drawn linked to the genomic location of the somatic mutation. The total height of each nucleotide position is the information content in bits and represents the level of conservation for that position. The height of each nucleotide letter represents the ratio that they are found to occupy that position. The reference sequence (black) is given directly beneath the sequence logo with the position and nucleotide of the mutant allele shown in red. Red silhouettes indicate the number of tumor samples with that particular mutation. A black silhouette indicates the allele was found in a normal sample. Boxplots indicate the normalized exon expression of the 5’ exon and 3’ exon immediately proximal to the intron with recurrent splicing mutations. Significance was assessed by Student’s t-test. Data are based on 42 total paired samples with WGS and 25 overlapping samples with RNA-seq.

Ten genes in total were found to have enriched somatic splicing motif mutations in multiple GBM samples (Table 2.1). The recurrence of these mutations span across 18 distinct samples (42.9%), indicating that these splicing motifs represent potential sites for recurrent mutations in cancer and provide an alternative means for the mutation of known genes.

Table 2.1: Recurrent Genes with Splicing Motif Mutations

Recurrent genes were identified by taking the ratio of samples with somatic mutations (SMs) within splicing motifs to samples with germline variants (GVs) within splicing motifs.

Gene Name	Splicing Motif GVs	Splicing Motif SMs
LOC100505811	0	3
TRAM2-AS1	0	3
NPIPA1	1	5
PRDM12	0	2
PSG11	0	2
TIGD7	0	2
AIMP1	0	2
FBXO45	0	2
CST2	0	2
SLC4A1	0	2

Cis-sQTL Identify Alternative Isoforms Due to Structural Variation

The gene with the highest LOD score in CB belonged to *ASTN2.* A *cis*-sQTL identified the fifth exon of *ASTN2* was skipped in 129/SvJ and retained in FVB/NJ, and showed a LOD score of 65.1 at rs13477756 (Figures 2.7A and B). *ASTN2* may function in neuronal migration, and exonic deletions have been identified in patients with schizophrenia.[214] Interestingly, a comparison of 13 inbred mouse strains found that while 129/SvJ mice did not exhibit a lack of prepulse inhibition (a hallmark of schizophrenia), they displayed the poorest startle response.[215]

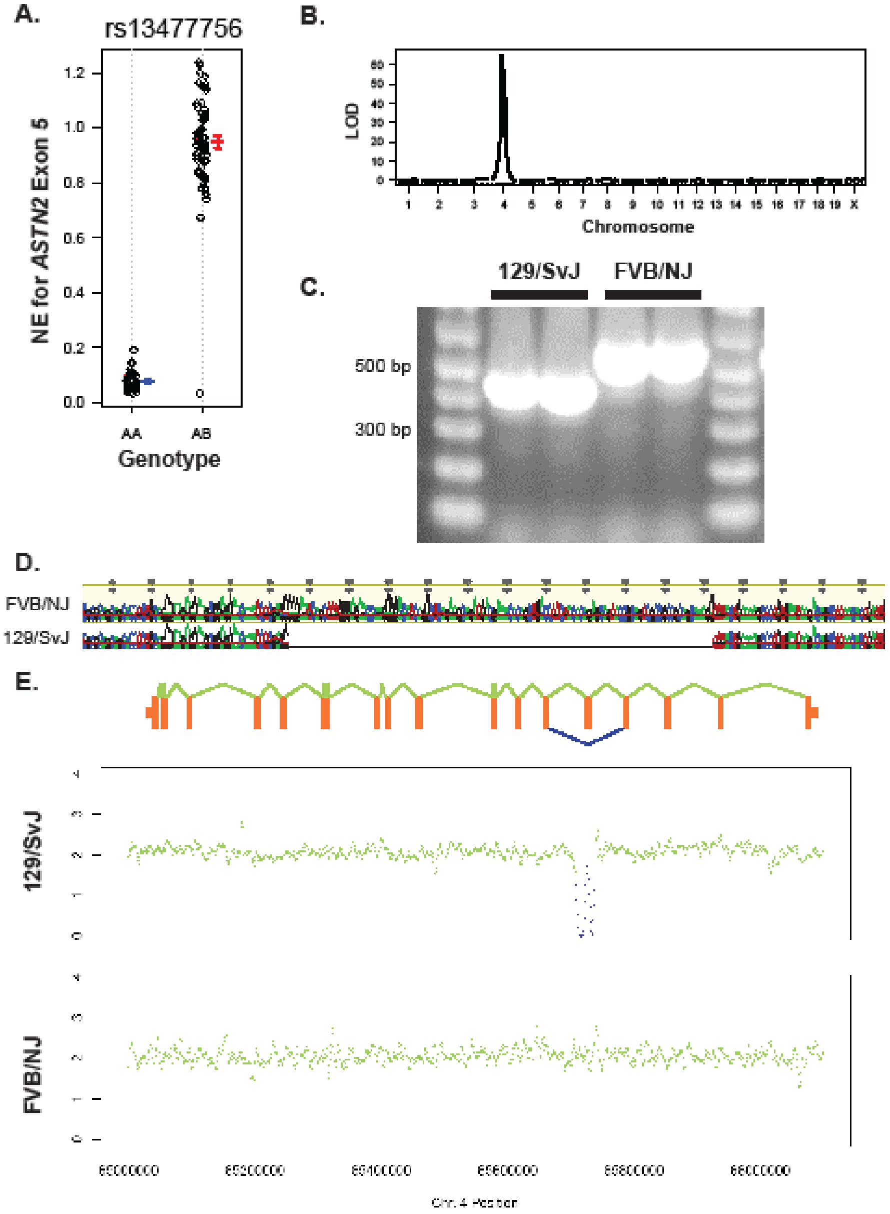


Figure 2.7 *ASTN2* possesses a cis-sQTL

A. Normalized Exon Expression (NE) levels for exon 5 of *ASTN2* show loss of expression in the homozygotes (129/SvJ)

B. The sQTL for *ASTN2* has a LOD score of 65.1 on chromosome 4 where the gene is located, indicating a *cis* effect.

C. RT-PCR of the parental 129/SvJ and FVB/NJ strains indicate that 129/SvJ expresses an alternative isoform.

D. Chromatogram from Sanger sequencing of the bands extracted in C indicating loss of Exon 5.

E. Exon 5 of *ASTN2* resides in a SCNV that is lost in 129/SvJ. *ASTN2* exons (orange) are overlayed on plot depicting copy number at this locus in 129/SvJ (top) and FVB/NJ (bottom). The blue line indicates exon skipping of exon 5 that corresponds with copy number loss in 129/SvJ. *ASTN2* resides on the (-) strand.

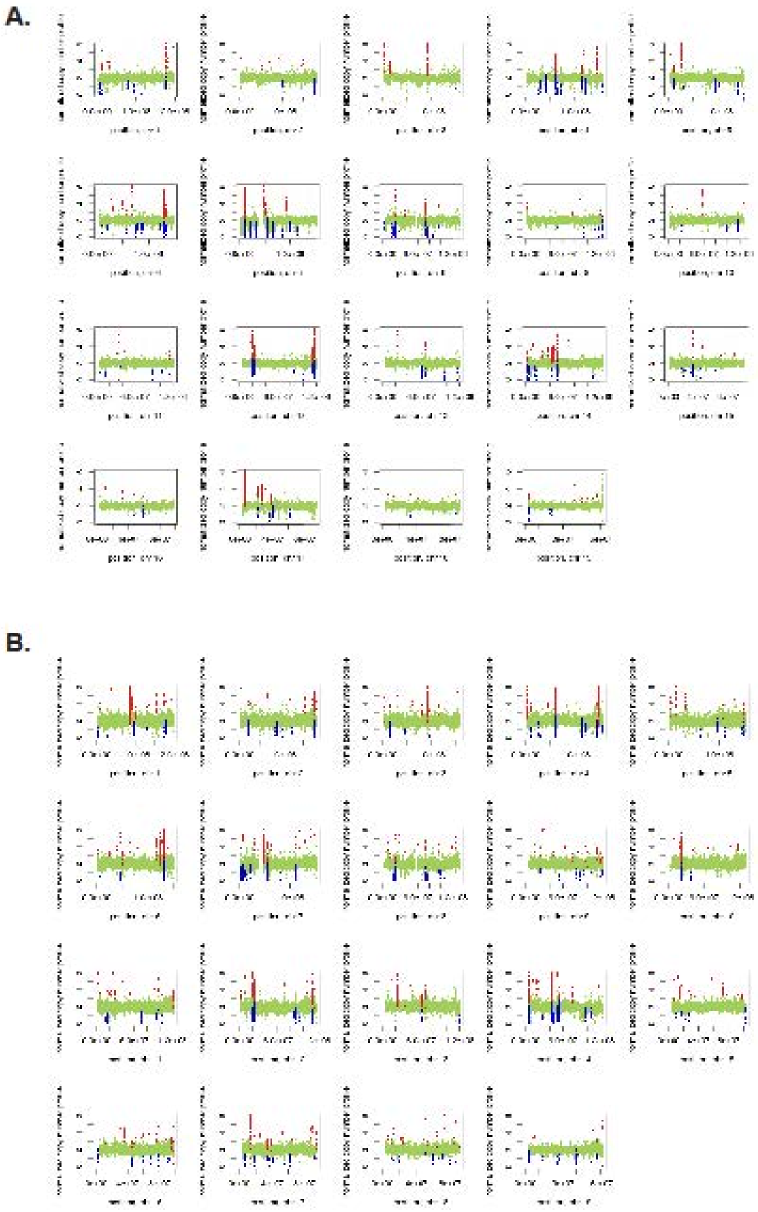


Figure 2.8 SCNVs Identified by WGS

A) SCNVs in 129/SvJ

B) SCNVs in FVB/NJ

RT-PCR on cDNA derived from CB in both parental strains confirmed that 129/SvJ mice specifically expressed a transcript omitting an exon in this region (Figures 2.7C and D). Whole genome sequencing data revealed a lack of coverage throughout exon 5 in 129/SvJ,

leading us to examine the WGS data for structural variation across both strains. After excluding the X chromosome due to the mixed source for the 129/SvJ WGS, we identified 1,324 somatic copy number variations (SCNVs) in 129/SvJ mice and 1,802 SCNVs in FVB/NJ (Figures 2.8A and B). Fifty-five of these co-localized with *cis*-sQTL-identified spliced exons in 129/SvJ and fifty-eight co-localized in FVB/NJ, with 38 shared between strains (Appendix F). Importantly, a ~30 kb deletion present in 129/SvJ, but not in FVB/NJ, co-localized with *ASTN2* and encompassed the entirety of exon 5 (Figure 2.7E). Expression of the alternative isoform in 129/SvJ is thus likely caused by genomic structural variation. Despite this alternative mechanism, the sensitive detection of strain-specific exon usage in *ASTN2* is a clear proof of principle for our sQTL method.

A *cis*-sQTL Within *FUBP1* Identifies a Triplet Splicing Event with Functional Consequences in NB

The highest LOD score observed in SCG belonged to the *FUSE*-Binding Protein 1 (*FUBP1*) gene. Normalized intensity in SCG for the fifth exon showed linkage disequilibrium with a LOD score of 73.9 (Figure 2.9A) to a polymorphism at the STS marker D3MIT147, located within 4 Mb of the gene. This was also one of the highest LOD scores observed in CB, and no structural variation was found at this locus. *FUBP1* is a transcription factor that binds the Far Upstream Element (*FUSE*), thereby regulating transcription of *MYC.*[216–218] Given the known importance of MYC proteins in neuroblastoma,[219,220] we further explored *FUBP1*, hypothesizing that an alternative splicing event could regulate FUBP1 activity and affect tumor progression.

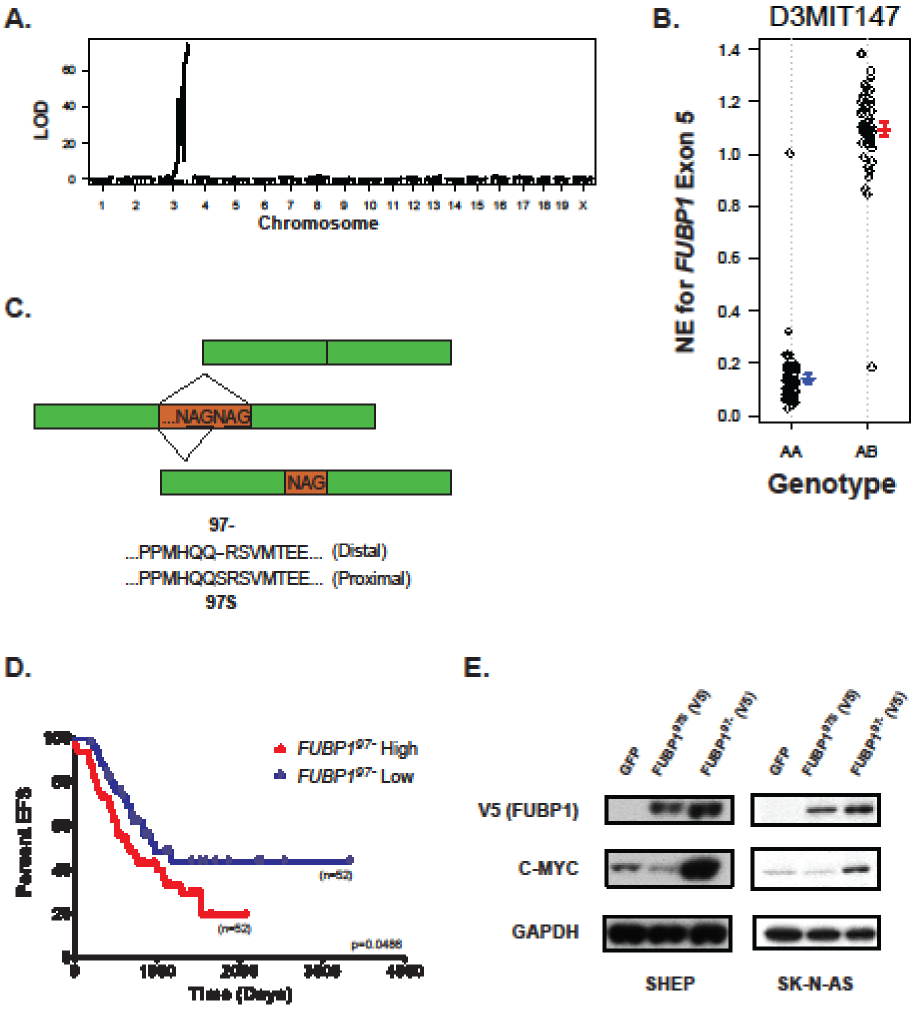


Figure 2.9 ***FUBP1*** **possesses a** ***cis*****-sQTL**

A. The sQTL for *FUBP1* has a LOD score of 73.9 on chromosome 3 where the gene is located, indicating a *cis* effect.

B. Normalized Exon Expression (NE) levels for *FUBP1* Exon 5 show loss of expression associated with the homozygous 129/SvJ allele.

C. Exon 5 of *FUBP1* is a site of triplet splicing. The distal isoform leads to incorporation of a serine at position 97 (*FUBP1*^{97S}) whereas the proximal isoform lacks the serine (*FUBP1*$^{97-}$).

D. MYCN non-amplified neuroblastoma patients with high levels of FUBP1^{97-} (red, n=52) had a reduced event free survival when compared to those with low FUBP197- levels (blue, n=52, Log-rank p = 0.0486).

E. Western Blot of human neuroblastoma cell lines transduced with *GFP* control, *FUBP1*^{97S}, or *FUBP1*$^{97-}$ lentivirus tagged with V5. MYC is upregulated in both SHEP and SK-N-AS lines in the presence of high FUBP1^{97-} levels.

Array data indicated that mice homozygous for the 129/SvJ allele exhibited a loss of expression for this exon compared to heterozygotes (Figure 2.9B) in both CB and SCG. Complete skipping of exon 5, which would ultimately lead to a frameshift for the remaining transcript, was not detected using RT-PCR using primers flanking the exon (Figure 2.10). We therefore explored other models through which aberrant splicing could modulate *FUBP1* activity. Exon 5 within *FUBP1* is a known site of triplet NAGNAG splicing,[221] which occurs at 3' splice sites. Bioinformatic studies indicate this process is conserved from plants to mammals and is subject to tissue-specific regulation.[222–224] In the case of *FUBP1*, this splicing event results in the incorporation of a serine at position 97 in the proximal isoform (*FUBP1*^{97S}) and its omission in the distal (*FUBP1*$^{97-}$) (Figure 2.9C). Given that our sQTL were based on exon array technology, we reasoned that differences in triplet splicing ratios between strains may have affected RNA secondary structure sufficiently to result in detection by our analysis.

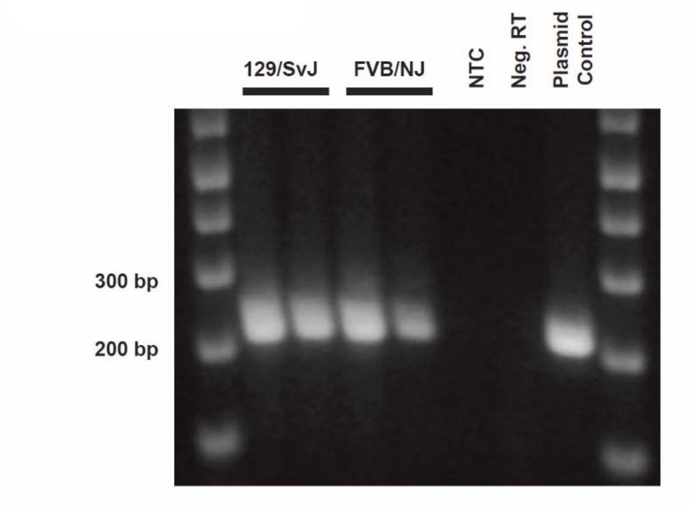


Figure 2.90 *FUBP1* RT-PCR From Parental Mouse Strains

RT-PCR of *FUBP1* in parental 129/SvJ and FVB/NJ strains did not indicate complete exon skipping of exon 5.

Whole transcript expression arrays supported the tumor suppressive effects of *FUBP1* in neuroblastoma, as patients with higher expression had better survival (p = 4.647 x 10^{-3}, Figure 2.11). Because these data do not have sufficient resolution to evaluate triplet splicing of exon 5, we analyzed RNA-seq data in stage 3, 4, and 4S neuroblastoma patients to quantify *FUBP1*^{97S}: *FUBP1*$^{97-}$ ratios. Given the inverse relationship between MYC and MYCN,[225] the poor survival of neuroblastoma patients expressing MYC,[226] and the known interaction between *MYC* and *FUBP1*, we looked specifically at *MYCN* non-amplified patients. Kaplan-Meier analysis revealed a median event-free survival of 669 days in patients who expressed high ratios of *FUBP1*$^{97-}$ as compared to 966 days for those with low ratios (p = 0.0486, Figure 2.9D). This indicated that a high *FUBP1*$^{97-}$ ratio was correlated with poor event-free survival in *MYCN* non-amplified disease, consistent with recent evidence that tissue-specific proximal:distal isoform ratios is subject to regulation and has functional consequences.[221]

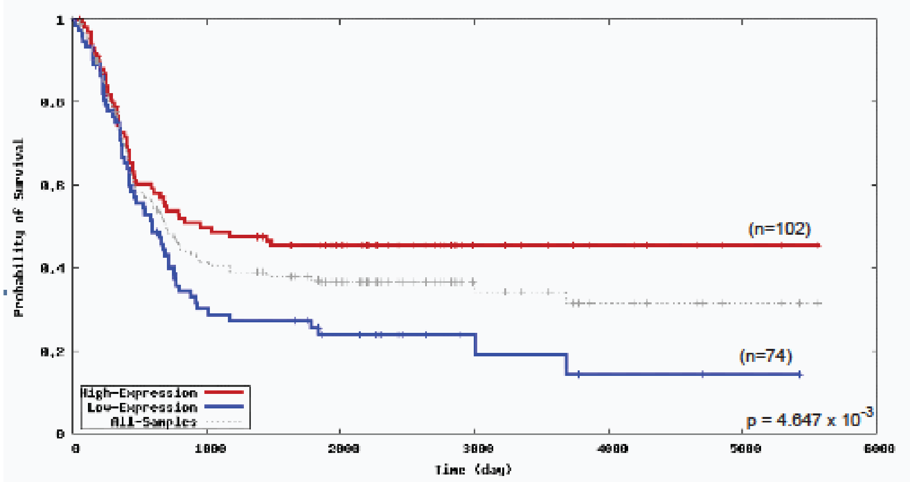


Figure 2.101 Whole-Transcript *FUBP1* Expression Suggests a Tumor Suppressive Function

Kaplan-Meier survival analysis indicates that patients with lower levels of total FUBP1 expression (blue n=74) have a reduced probability of survival compared to patients with higher levels of total FUBP1 (red n=102, p=4.647 x 10^{-3}).

To assess differential cellular function between isoforms, we expressed V5-tagged constructs of both *FUBP1*^{97S} and *FUBP1*$^{97-}$. Since *MYC* is a known target for *FUBP1*, we examined the effects of isoform-specific overexpression in MYC-expressing neuroblastoma cell lines by transducing *FUBP1*^{97S} and *FUBP1*$^{97-}$ viruses separately into SHEP and SK-N-AS cell lines. Overexpression of *FUBP1*$^{97-}$ but not *FUBP1*^{97S} led to higher MYC levels (Figure 2.9E), consistent with deregulation of triplet splicing within exon 5 of *FUBP1* having a functional effect in our model.

CHAPTER 3: DISCUSSION AND CONCLUSIONS

In this study we have leveraged a mouse genetic system to analyze and map genetic control of splicing. Previous genomic studies of splicing have identified only a modest number of sQTL (<200),[182–184] likely due to a GWAS approach dependent on the association of individual SNPs. Here we identify over 2500 putative sQTL, describing a far more complex landscape than has been reported previously.

The CB- and SCG-specific nature of our *trans*-sQTL suggest that the inclusion or exclusion an exon is governed by the relative concentrations of splicing activators and silencers at the splice site. Thus, CB or SCG-specific splicing factors residing at *trans*-sQTL can direct tissue-specific splicing programs by adding to the composition of splicing factors. However, that the overwhelming majority of sQTL were found to be *cis* suggests even tissue-specific alternative splicing programs are heavily influenced by genetic effects. Ultimately, CB- and SCG-specific *cis*-sQTL emphasize a difference in perspective - that alternative splicing decisions are regulated by the ability of the transcript to recruit splicing activators or silencers.

With the growing appreciation that alternative splicing can play functional roles in cancer, splicing factors have garnered considerable interest as potential targets for cancer therapy.[159] In this regard, we analyzed two neural tissues, with transcript-level differential gene expression between tissues enabling us to zero in on only a few genes in each region. Using this approach, we were able to identify critical loci harboring candidate novel splicing factors. It was surprising that we did not find loci containing a greater degree of *trans*-sQTL co-localization, as these might be indicative of master regulators. This could reflect a rarity of such *trans*-sQTL overall, or might alternatively be attributed to a limitation within our backcross system, as polymorphisms in such a critical component of the splicing process might not be tolerated in either strain.

The power of our backcross model is highlighted by WGS efforts to profile inbred mouse strains. With our backcross model we have created a cohort of animals which are genetically very similar, but individually heterogeneous. Using a combination of SNP analysis and known genome sequences of mouse strains, we were able to define each individual's genome at the local nucleotide level. This enabled us to identify novel splicing motifs that we established relevance for by analyzing WGS and RNA-seq data from GBM tumors. In the process, we identified novel candidate genes with functional implications. Previous splicing analyses have focused on exonic splicing motifs, using methods such as analyzing evolutionary conservation or systematic evolution of ligands by exponential enrichment (SELEX) on known and purified splicing factors. Until now, the most definitive analysis of intronic splicing enhancers utilized a splicing reporter construct to test the effects of random decamers inserted into the intron.[175] Our unbiased analysis is the first of which we are aware to identify recurrent intronic splicing motifs *in vivo*.

While lacking in whole-exome sequencing analyses, intronic mutations in key regulatory motifs are potentially just as disruptive as mutations in coding region. Even with whole-genome sequencing, the recurrent somatic mutations identified in GBM might be easily dismissed due to their intronic nature and the fact that *LOC100505811, TRAM2-AS1* and *NPIPA1* all have relatively unknown functions. However, their presence in novel splicing motifs argues for potential functional effects. Thus, the splicing motifs identified here enhance our understanding of the cancer genome by identifying potential sites for these recurrent intronic mutations.

Mutations in oligodendroglioma have implicated *FUBP1* as a tumor suppressor,[227–229] while other studies report that *FUBP1* overexpression can function as an oncogene.[230–232] *FUBP1* has been shown to both activate and repress *MYC* transcription,[217,233,234] further obfuscating its role in cancer. Our data suggest distinct functions for alternatively spliced *FUBP1* isoforms. Of the two triplet splicing products, *FUBP1*$^{97-}$ leads to deregulation of MYC whereas *FUBP1*^{97S} maintained the ability to reduce MYC levels. These data raise the possibility that mutations observed in oligodendroglioma are not strictly loss of function, but may act in a dominant negative fashion akin to the *FUBP1*$^{97-}$ isoform.

Despite the relationship between MYC and FUBP1 and the critical importance of MYC proteins in neuroblastoma tumorigenesis,[235,236] extensive genomic sequence analysis in neuroblastoma tumors has yet to show recurrent mutations in *FUBP1* or *MYC*. In the absence of recurrent mutation, our analysis reveals splicing differences in *FUBP1*, not detectable by conventional expression analysis, which associate with risk. MYC is an ideal therapeutic target in many cancers, yet it has long been thought to be “undruggable.” Most recently, attempts to target MYC have done so successfully by focusing on protein stability and downstream ubiquitination,[237] or through accessory proteins required for MYC-promoted transcription.[238] By identifying *FUBP1*$^{97-}$ as the specific isoform that leads to MYC deregulation, we present a new therapeutic target which may hold the key to restoring normal MYC function.

Further experiments are needed to identify the mechanism whereby *FUBP1* triplet splicing is regulated. The intron upstream of the splice acceptor and the fifth exon both contain several SNPs that are polymorphic between 129/SvJ and FVB/NJ, with a few of these residing in the splicing motifs we define here. Does one or a combination of these lend a preference to the proximal form or the distal form? Since *FUBP1* has been recently identified to function as a splicing factor,[239] could it affect its own splicing? ASOs that target these motifs could be used to modulate the signal of any splicing silencers or splicing enhancers *in vivo* or *in vitro*. However, a better experimental assay for *FUBP1* triplet splicing is critical to pursue this further. Due to the repetitive nature around the triplet region, we have been unsuccessful in our attempts to achieve quantitative results using standard allele-specific PCR methods or qPCR with SYBR or TaqMan techniques, including digital-droplet PCR. Molecular inversion probes have similarly been unsuccessful, leading us to pursue RNA-Seq. Low-cost and minimally procedure-intense assays will enable efficient hypothesis testing in this regard.

Furthermore, what is the mechanism that leads to the upregulation of MYC? Could the serine at position 97 be a key residue for phosphorylation? Or does omission of this single amino acid destroy a site required for interaction with other proteins such as the FUBP1-Interacting Repressor (FIR)? Co-immunoprecipitation experiments could be used to identify differential protein binding partners between the two splice isoforms. Similarly, ChIP-Seq or CLIP-Seq would be valuable experiments to identify differences in DNA or RNA binding preferences between the two variants.

Ultimately, our sQTL analysis in a mouse genetic system provided an unbiased method in which to analyze splicing. Not only do sQTL identify critical and functionally important alternative splicing events in neuroblastoma, but this system also define *de novo* splicing motifs that serve as sites for recurrent mutations in cancer. These mutations lead to functional changes in exon expression and enhance our understanding of the cancer genome.

CHAPTER 4: MATERIALS AND METHODS

Generation of a heterogeneous cohort backcrossed mice

Mice were obtained from the Jackson Labs (Bar Harbor, ME) and were housed and treated following UCSF IACUC guidelines. FVB/NJ mice transgenic for *TH-MYCN* were bred to wild-type 129/SvJ mice. Transgenic animals from the resulting F1 generation were identical genetically, possessing an allele for each gene from both parental strains. F1 mice were then backcrossed to 129/SvJ mice to generate the N1 generation used in this analysis (Figure 4.1). Superior cervical ganglia (SCG) and cerebellum (CB) were surgically isolated and snap-frozen in liquid nitrogen (n=102).

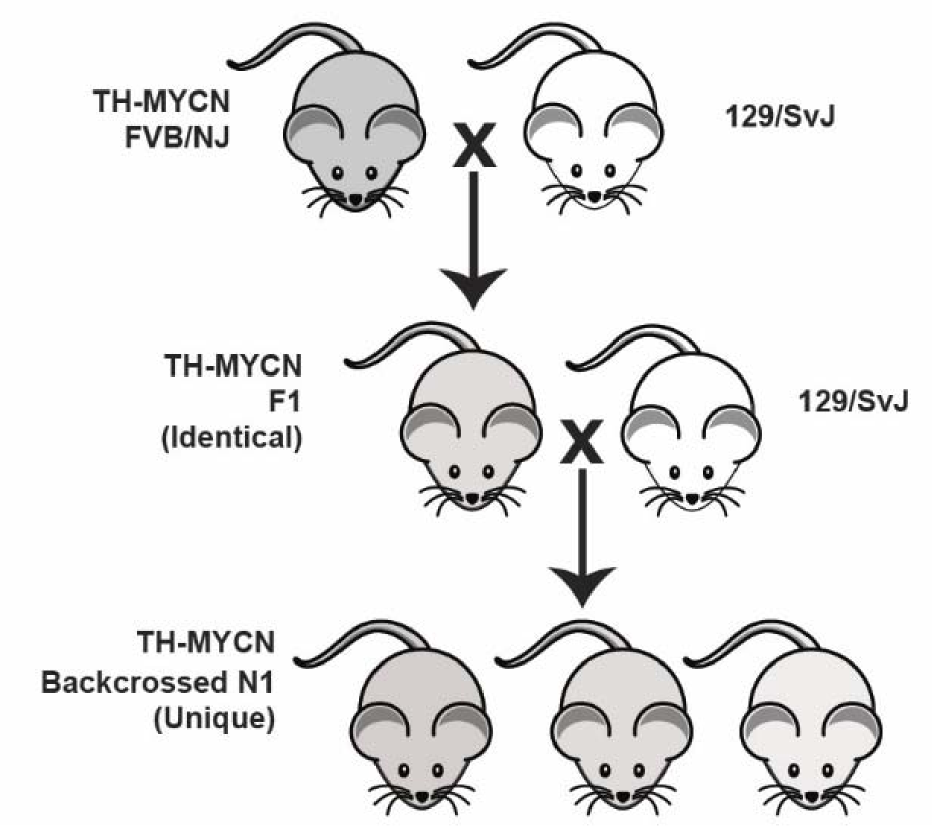


Figure 4.1 Schematic for Backcross Cohort Generation
The N1 generation is highly similar, yet genetically distinct from each other. This cohort was used as the basis for sQTL analysis.

Genotyping

DNA was isolated from spleen tissue using a proteinase K lysis followed by phenol chloroform extraction. Microsatellite marker genotyping was carried out by the Marshfield Clinic (Marshfield, WI), and CIDR (Baltimore, MD). SNP genotyping was performed using template-directed primer extension with fluorescence polarization detection (FP-TDI, Acycloprime II, Perkin Elmer, Waltham, MA) and SNPStream 48-plex (Beckman Coulter, Brea, CA). Markers and map positions are shown in Table 4.1. The marker set had an average spacing of 8 MB genome-wide (excluding the high density of markers on chromosome 10).

RNA Isolation

RNA was isolated from SCG using the RNeasy kit (QIAGEN, Valencia, CA). All other RNA isolations utilized Trizol (Invitrogen/Life Technologies, Grand Island, NY) for phase-separation prior to purification with the RNeasy kit.

Expression Arrays

1 µg of RNA was used as a starting template for RiboMinus rRNA subtraction (Invitrogen/Life Technologies) followed by the ST labeling protocol (Affymetrix, Santa Clara, CA). Labeled samples were hybridized to Affymetrix Mouse Exon 1.0 arrays. Arrays were normalized using RMA in the XPS Bioconductor package within R at both the exon level and the transcript level using core probes. Differential expression between tissue types was examined using Significance Analysis of Microarrays (SAM).[240]

QTL Analysis

Exon expression was normalized to gene expression by calculating Normalized Exon Expression (NE), a ratio of exon expression to gene expression (both values determined using the XPS Bioconductor package). sQTL were calculated using NE as a quantitative trait in eQTL software as previously described[241]. Briefly, linkage between NE and loci was assessed by linear regression with genome-wide significance determined using an $FDR < 0.05$. Due to the ability of exonic polymorphisms to function as ESEs or ESSs, we did not exclude exons that harbored SNPs between the two strains. *Trans*-sQTL were drawn using Circos.[242] LOD scores were calculated and drawn using the R-QTL Bioconductor package within R.

Mouse WGS Analysis

FVB/NJ and 129/SvJ whole-genome sequencing data were downloaded from the ENA (Accession: ERP000687) and SRA (Accession: SRX205921), respectively, as raw FASTQ files. Reads were mapped to the reference genome (mm9) using Bowtie2 (v. 2.1.0) using the "—fast-local" preset. Genotypes were called using the GATK UnifiedGenotyper package (v. 2.4-9). SNPs were compared using the VCFtools package (v. 1.10). Copy number was assessed using FREEC (v. 6.3)[243] with a 5kb window at 1 kb intervals and a breakpoint threshold of 0.4. Results from the X chromosome in 129/SvJ were discarded as WGS was performed on a mixed pool of 6 mice. Consensus sequences for both strains were generated using the samtools mpileup function.

Splicing Motifs

Spliced exons were identified as possessing a *cis*-sQTL in both tissues, and the direction of splicing in each strain was noted. 19-mer sequences surrounding polymorphic nucleotides and their positions relative to the spliced exon were acquired in the direction of transcription from consensus FASTA sequences generated from strain-specific WGS. Sequences were trimmed to exclude exonic bases, and regions where either strain returned a poly(N) motif indicative of a lack of sequencing coverage were discarded.

Extracted sequences were binned based on the direction of the associated splicing and their origin (5' intron or 3' intron). MEME was used to identify recurrent motifs with a width of at least 10 bases in these bins using a background GC content of 42%. Motifs with an E-Value < 0.05 and derived from at least 20 sequences were reported as significant.

Motif Analysis of GBM Whole-Genome Sequencing

Primary GBM and patient matched normal DNA WGS data for 42 patients were downloaded from The Cancer Genome Atlas project's Cancer Genomics Hub (www.cghub.ucsc.edu, dbGAP Study Accession number: phs000178).[211,212] Single-nucleotide variants (SNVs) were detected with MuTect, a Bayesian framework for the detection of somatic mutations.[244] Somatic and germline SNVs were filtered according to MuTect defaults (germline variants were kept at a LOD(N) threshold of 2.3). SNVs for samples aligned to HG18 were converted to HG19 coordinates using the UCSC liftover tool (http://genome.ucsc.edu/cgi-bin/hgLiftOver). For technical reasons, one sample only had SNV calls from chromosomes 1-7, and another sample only had SNV calls from chromosomes 1-12.

Intronic sequences were extracted from the hg19 reference genome encompassing 9 bp upstream and downstream of the identified in the 5'-3' direction of transcription. Reference sequences in addition to sequences containing the alternative allele were analyzed for splicing motif occurrences using MAST at a sequence p-value threshold of 0.0001, recording the best motif match to either the reference or alternative sequence as determined by the lowest sequence p-value.

GBM RNA-Seq Analysis

Level 3 RNA-Seq data for 25 samples that overlapped with the 42 WGS GBM samples were downloaded through the TCGA Data Portal (https://tcga-data.nci.nih.gov/tcga/). In the absence of transcript expression levels, normalized exon expression was calculated by taking the ratio of individual exon expression (RPKM) to the maximally expressed exon within the gene. Significance was determined by Student's t-Test.

Neuroblastoma RNA-Seq

Total RNA was extracted from the fresh frozen tumor samples by the Trizol/RNeasy kit protocol described previously.[245] Whole transcriptome libraries for Illumina HiSeq 2000 were prepared according to the TruSeq RNA protocol, in which poly-A mRNA is purified from total RNA at the initial step. Two indexed samples were pooled and sequenced on an Illumina HiSeq 2000 with 100-bp paired end. Quality of RNA and library was assessed by an Agilent BioAnalyzer. 100-bp paired end reads were first aligned to the reference human genome (hg19) using spliced read mapper Tophat 2.0.8.[246] We then used Cufflinks 2.1.1[247] for gene abundance estimation. Abundances in fragments per kilobase of exon per million fragments mapped (FPKM) were calculated for each annotated RefSeq gene. Kaplan-Meier analysis was performed using GraphPad Prism. Significance was determined by the Log-rank test.

Tissue Culture

SHEP cells were obtained from the UCSF Cell Culture Facility and grown in RPMI-1640 supplemented with 10% FBS. SK-N-AS cells were obtained from the UCSF Cell Culture Facility and grown in DMEM supplemented with 10% FBS, non-essential amino acids, and sodium pyruvate. All cell lines were maintained at 37 Degrees with 5% CO2 and tested for mycoplasma contamination.

Lentiviral Transduction

Human *FUBP1*$^{97-}$ cDNA was obtained from the IMAGE consortium (Accession: BC017247) and PCR-cloned into the pENTR-D/TOPO gateway vector (Invitrogen/Life Technologies) using the FUBP1 Cloning Forward (CAC CAT GGC AGA CTA TTC AAC AGT GCC) and FUBP1 Cloning Reverse primers (TTG GCC CTG AGG TGC TGG AGG ATG CTG T, Integrated DNA Technologies, Coralville, Iowa) to add the directional TOPO motif and exclude a stop codon. This entry clone was used as a substrate to create an *FUBP1*^{97S} entry vector using the Quickchange II XL Site-Directed Mutagenesis Kit (Stratagene/Agilent Technologies, Santa Clara, CA) and Site-Directed Mutagenesis Primers (CGA TGC ATC AGC AGC AAA GCA GAT CTG TAA TGA CAG AAG AA and TTC TTC TGT CAT TAC AGA TCT GCT TTG CTG CTG ATG CAT CG, Integrated DNA Technologies). Lentiviral constructs were made by LR recombination (Invitrogen/Life Technologies) with the pLenti 6.3 destination vector (Invitrogen/Life Technologies). Virus was packaged in 293FT cells using the ViraPower lentiviral packaging plasmid mix and Lipofectamine 2000 (Invitrogen/Life Technologies) over the course of 72 hours. Viral supernatant was harvested and filtered through a 0.45 μM syringe filter and used to directly transduce neuroblastoma cells for 24 hours. Stably transduced cells were selected with 10 μg/ml blasticidin (Invitrogen/Life Technologies).

Western Blotting

Cell lysate was harvested using Cell Lysis Buffer (Cell Signaling Technology, Danvers, MA) supplemented with protease inhibitor (Roche, Basel, Switzerland) and 1% SDS. Protein was quantitated with the BCA assay kit (Pierce Biotechnology, Rockford, IL). Equal amounts of total protein were loaded and run on 4%-12% SDS-polyacrylamide gels (Invitrogen/Life Technologies) and transferred to PVDF membranes using the iBlot (Invitrogen/Life Technologies). After blocking (1 hour @ RT, 5% non-fat milk in TBS-T), membranes were incubated overnight (4 degrees, 5% BSA in TBS-T) with V5-specific antibody (1:5000, Invitrogen/Life Technologies), GAPDH-specific antibody (1:10000, Millipore, Billerica, MA), or C-MYC-specific antibody (XP, 1:1000, Cell Signaling Technology). Antibodies were detected with HRP-linked mouse or rabbit (Calbiochem/Millipore) secondary antibodies followed by enhanced chemilluminescence (Amersham/GE, Piscataway, NJ).

cDNA Synthesis and RT-PCR

cDNA synthesis was performed using SuperScript VILO MasterMix (Invitrogen/Life Technologies) according to the manufacturer's instructions with a 120 minute incubation at 42 degrees C. 1 µg of total RNA was used as starting material.

RT-PCR to determine retention of *FUBP1* Exon 5 and validate the alternative *ASTN2* isoform was performed using GoTaq Green MasterMix (Promega, Madison, WI) in 25 ul reactions according to the manufacturer's instructions using 1 µL of cDNA and FUBP1-1F (AAC GAC GCT TTC AAA GAT GC)/FUBP1-7R (TTG GAC AGA TTC AGG TGT TCC) or ASTN2-F (TCA AGG AGA GTT TCC GTG CT)/ASTN2-R (CTG GGT CAC AGA GCT GTT CA) primers, respectively (Integrated DNA Technologies). PCR products were run on a 1.5% agarose gel.

Table 4.1: Genotyping Markers

Marker	Chr	cM	Marker	Chr	cM
RS32728630	1	6.020495	02.168.990	2	151.4053
01.021.731	1	16.19758	D2MIT113	2	164.0409
D1MIT169	1	18.85175	D2MIT148	2	167.7799
D1Mit374	1	27.02859	03.016.637	3	10.4
D1MIT236	1	37.41892	D3MIT304	3	14.40811
01.061.101	1	45.46082	D3Mit151	3	18.63179
D1MIT24	1	52.91828	03.033.871	3	22.08075
D1MIT132	1	55.20877	D3MIT6	3	28.26274
D1MIT215	1	55.6573	D3MIT67	3	34.10534
D1MIT134	1	59.85405	03.060.525	3	40.51916
01.102.953	1	66.3874	RS37321647	3	42.80783
RS30388122	1	66.3874	RS38010777	3	42.80783
RS50560599	1	67.50483	D3MIT98	3	51.73848
D1MIT1001	1	72.84145	RS31036560	3	62.868
01.136.071	1	77.74879	D3MIT49	3	73.77602
D1Mit102	1	80.03925	03.106.773	3	82.33049
D1MIT507	1	89.46999	D3MIT57	3	88.53548
01.183.109	1	96.11848	D3MIT315	3	89.68246
D2MIT1	2	2.4	D3MIT256	3	103.276
02.021.696	2	18.06443	D3MIT351	3	107.4657
D2MIT81	2	18.06443	03.141.220	3	108.244
D2MIT296	2	21.50213	RS30160288	3	119.3825
D2Mit297	2	25.96707	D3MIT147	3	137.3239
RS27953638	2	27.96753	D3Mit19	3	140.7312
D2MIT61	2	35.12792	04.013.290	4	8.3
RS28322831	2	43.67748	RS28262872	4	8.826905
D2MIT75	2	46.41465	D4mit94	4	20.99338
D2MIT100	2	54.19426	D4MIT196	4	27.14186
02.109.360	2	59.82539	D4MIT238	4	33.23278
D2Mit274	2	62.95823	04.053.650	4	40.48019
RS27416022	2	74.76293	D4MIT164	4	42.38961
D2MIT395	2	91.61399	04.063.977	4	50.52425
D2MIT423	2	107.8075	D4MIT132	4	51.3319
D2MIT285	2	110.6372	D4MIT348	4	56.03665
D2MIT411	2	112.9735	D4Mit166	4	66.23295
02.161.464	2	113.5093	04.098.998	4	75.01299
RS27258455	2	126.7319	RS27499066	4	79.43714
RS27267095	2	129.5613	RS27499062	4	79.43714
RS27267029	2	129.5613	D4MIT308	4	84.36025
RS27265584	2	129.5613	D4Mit203	4	89.73231

Marker	Chr	cM	Marker	Chr	cM
04.133.005	4	97.64222	07.013.915	7	8.7
D4MIT170	4	99.94085	07.017.531	7	12.92437
D4MIT232	4	109.1183	D7MIT294	7	15.72036
D4MIT42	4	117.1013	D7MIT267	7	18.29809
D5MIT123	5	4.1	D7MIT228	7	28.11811
05.018.430	5	14.15919	D7Mit232	7	35.20811
D5MIT294	5	15.58331	07.056.455	7	36.40088
D5MIT348	5	18.20559	D7MIT248	7	39.99047
D5MIT388	5	29.38073	D7MIT350	7	57.28732
D5MIT352	5	30.68587	07.088.976	7	61.08266
05.038.809	5	37.9822	RS32210051	7	61.08266
05.049.898	5	44.23678	RS36353338	7	66.26522
d5mit233	5	46.33401	RS32012407	7	66.26522
D5MIT183	5	47.99434	RS32021248	7	66.26522
RS33623243	5	52.83465	07.122.234	7	82.95546
D5MIT309	5	58.78964	d7mit109	7	91.14939
D5MIT10	5	65.80535	D7MIT223	7	99.51497
D5MIT239	5	66.11023	D7Mit259	7	100.7427
d5mit158	5	69.85959	D8MIT155	8	3.1
RS33085156	5	79.13497	08.010.585	8	4.520052
D5MIT425	5	93.27848	D8MIT94	8	19.42422
D5MIT95	5	98.81753	D8MIT292	8	21.90455
05.132.979	5	112.2658	D8Mit191	8	23.02066
D5MIT169	5	118.4503	08.046.718	8	30.74653
D5MIT143	5	120.9755	D8MIT68	8	37.44853
06.016.672	6	10.4	08.076.189	8	47.38677
RS50690369	6	10.78458	D8MIT346	8	54.67316
RS51272439	6	10.78458	D8MIT45	8	58.44006
RS49937148	6	13.13583	D8MIT242	8	71.21855
06.036.921	6	24.99854	D8MIT211	8	73.00564
D6Mit272	6	27.2529	D8MIT47	8	79.10975
D6MIT274	6	30.88472	D8MIT215	8	87.84173
d6mit123	6	39.56321	D8MIT42	8	102.8893
06.057.998	6	39.56321	D9MIT250	9	5.2
06.095.876	6	52.18486	09.014.560	9	12.99047
D6MIT67	6	52.18486	D9mit90	9	20.19926
RS30909511	6	57.9854	D9MIT247	9	25.36975
D6MIT328	6	75.24789	D9MIT2	9	25.36976
d6mit366	6	77.49561	D9MIT285	9	25.81754
D6MIT194	6	87.57626	09.046.588	9	34.49446
D6Mit14	6	101.6085	D9MIT71	9	37.69738
06.149.619	6	105.5067	D9MIT248	9	44.87553

Marker	Chr	cM	Marker	Chr	cM
D9MIT336	9	49.6331	D10MIT184	10	40.05957
D9MIT107	9	53.50038	RS37251794	10	40.05957
D9MIT123	9	55.0405	RS39284379	10	40.05957
09.079.053	9	64.60162	RS33837056	10	41.00292
D9MIT198	9	66.50428	RS29330419	10	41.00292
D9MIT24	9	73.18313	RS29363236	10	41.00292
D9MIT347	9	74.99181	RS29325964	10	41.00292
09.105.291	9	79.88305	RS33849981	10	41.94466
D9MIT212	9	79.88305	RS36294294	10	57.88258
D9MIT201	9	91.42427	D10MIT20	10	60.50708
D9Mit18	9	96.97845	D10MIT31	10	64.29048
D9MIT151	9	100.1162	RS46745265	10	65.86958
10.002.877	10	1.8	D10MIT117	10	70.67248
D10Mit123	10	3.021254	d10Mit96	10	80.83316
RS38343005	10	4.536629	10.113.678	10	88.29052
RS33543047	10	4.53663	D10Mit14	10	93.10254
RS29347557	10	5.696346	D11MIT2	11	6.596892
RS29316898	10	9.384466	RS26845852	11	14.21077
RS38621064	10	13.6511	D11MIT186	11	20.92052
RS29354311	10	13.6511	D11MIT51	11	21.64485
RS29366730	10	13.6511	rs29438202	11	24.71992
RS33635595	10	13.6511	RS26969123	11	32.41898
RS29365246	10	15.91284	D11Mit4	11	41.81419
RS29320979	10	15.91284	D11MIT320	11	43.28293
RS29322393	10	16.95714	11.072.405	11	44.30764
RS29367295	10	20.72734	D11MIT285	11	55.1716
RS33702022	10	21.75786	D11MIT289	11	58.27459
RS29351336	10	22.94397	11.104.430	11	64.37343
RS29316281	10	22.94397	D11MIT214	11	70.96276
RS29380418	10	27.66974	12.007.977	12	5
RS36323433	10	29.16132	D12MIT182	12	5.454624
RS37076985	10	29.16132	D12MIT60	12	21.02542
RS33755224	10	29.63866	12.039.760	12	26.67403
RS36274062	10	31.86503	D12Mit2	12	26.67403
RS36679837	10	31.86503	D12MIT285	12	30.22146
RS37117129	10	31.86503	12.065.348	12	37.44045
RS13480581	10	35.95662	D12MIT91	12	43.26798
RS29317824	10	38.21559	D12MIT143	12	49.40885
RS29313239	10	39.49873	D12MIT194	12	54.38605
RS29316185	10	39.49873	D12MIT7	12	66.69663
RS29376554	10	39.49873	13.013.314	13	8.3
RS29329200	10	39.49873	D13Mit207	13	8.688726

Marker	Chr	cM	Marker	Chr	cM
RS29514367	13	20.53923	RS4164914	16	9.413247
13.043.962	13	29.58329	RS4165334	16	14.91941
D13MIT250	13	36.46819	D16MIT60	16	28.75614
D13MIT13	13	37.01753	RS4187006	16	43.57925
13.061.624	13	39.87979	16.039.061	16	48.3587
RS30012306	13	43.69714	D16Mit125	16	48.35871
D13MIT125	13	47.51637	D16MIT185	16	54.3944
13.096.920	13	58.79686	D16MIT139	16	56.62781
D13MIT288	13	67.56495	16.065.697	16	59.66376
D13MIT213	13	69.65924	D16MIT188	16	69.33209
D13MIT53	13	72.69389	D16MIT189	16	73.83226
d13mit151	13	74.51442	16.083.701	16	79.82369
D13MIT78	13	76.84217	17.013.500	17	8.4
14.008.937	14	5.6	D17Mit213	17	12.20714
D14MIT98	14	6.470372	17.021.019	17	14.36839
14.027.409	14	32.01969	D17MIT231	17	38.54838
D14MIT174	14	33.32711	17.034.150	17	51.1372
14.042.462	14	41.89415	D17MIT51	17	53.34361
D14Mit183	14	42.79497	D17MIT180	17	63.0586
14.067.129	14	52.82241	D17MIT20	17	69.42766
D14MIT39	14	54.52991	17.059.041	17	71.70333
RS31380922	14	61.61076	D17Mit152	17	74.19469
D14MIT263	14	64.79535	D17Mit93	17	83.28793
D14Mit194	14	66.46956	D17MIT76	17	95.2661
14.095.016	14	67.37082	17.086.091	17	96.07344
RS31252045	14	77.8316	D18MIT222	18	9.2
D15MIT13	15	2.1	D18Mit68	18	14.5139
15.010.846	15	8.803289	18.038.678	18	24.45192
D15MIT252	15	9.706826	D18MIT202	18	28.05292
15.028.723	15	14.88113	D18MIT194	18	30.70688
15.046.034	15	20.5546	D18Mit123	18	38.31055
D15MIT143	15	21.45854	D18MIT208	18	45.2796
D15MIT103	15	31.66028	D18MIT152	18	47.63475
D15MIT67	15	36.95768	18.063.800	18	48.99442
D15Mit107	15	49.40097	D18MIT186	18	54.44325
D15MIT262	15	57.21236	RS30267686	18	60.34946
15.088.295	15	61.33407	19.000.325	19	0.2
15.090.122	15	63.15586	D19Mit68	19	0.200001
D15MIT44	15	76.94503	19.009.231	19	7.749799
D15MIT15	15	83.15474	19.013.429	19	11.12922
D16Mit131	16	4.5	D19MIT96	19	21.38792
16.010.089	16	7.349459	D19MIT13	19	37.09408

Marker	Chr	cM
D19MIT46	19	37.54307
D19MIT88	19	44.41135
19.046.444	19	55.55111
D19MIT103	19	59.41115
RS33457262	X	5.766691
RS33477935	X	5.766692
RS33478059	X	5.766693
RS33625666	X	9.993891
DXMIT68	X	20.02251
X.054.837	X	31.43357
DXMit119	X	34.98622
DXMIT172	X	47.92461
DXMit79	X	50.81363
DXMIT132	X	55.8167
DXMit216	X	58.90613
RS29086361	X	71.76246
RS29300656	X	89.33472

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APPENDIX A: CB CIS-SQTL

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Astn2	606487	4	65719549	D4MIT132	4	51.3319	70333587	0.07599	0.94394	0	2.16E-53	0	0	Shared
unassigned	604618	4	56789435	04.053.650	4	40.48019	53641772	0.40457	1.03306	0	1.37E-52	0	0	Shared
Dhx36	551036	3	62288882	03.060.525	3	40.51916	60240993	0.04402	0.5447	0	2.10E-52	0	0	Shared
unassigned	667701	5	86445069	RS33085156	5	79.13497	90112330	0.15767	1.02609	0	3.97E-50	0	0	Shared
Nub1	630339	5	24213621	05.018.430	5	14.15919	18423994	0.49676	1.02092	0	3.45E-49	0	0	Shared
Pmpcb	629687	5	21262242	D5MIT294	5	15.58331	20863135	0.10571	0.61505	0	1.68E-47	0	0	Shared
Bbs7	547502	3	36509494	03.033.871	3	22.08075	33578373	0.2192	0.85408	0	3.31E-47	0	0	Shared
Luzp2	741243	7	62313420	07.056.455	7	36.40088	63842351	0.25972	1.30672	0	1.26E-46	0	0	Shared
Ptprd	607395	4	75627986	D4MIT132	4	51.3319	70333587	0.82525	1.80418	0	2.70E-46	0	0	Shared
H2-D1	358652	17	35400786	17.034.150	17	51.1372	34678889	3.25237	1.76635	0	3.83E-46	0	0	Shared
unassigned	547520	3	36550409	03.033.871	3	22.08075	33578373	0.24632	0.66983	0	3.72E-44	0	0	CB
Tnks	816022	8	35952750	D8MIT94	8	19.42422	32452130	0.15009	0.77541	0	4.40E-44	0	0	Shared
Dst	3735	1	34301287	D1Mit374	1	27.02859	34816928	0.17265	1.05974	0	1.87E-43	0	0	Shared
Srpk2	657646	5	23046202	D5MIT294	5	15.58331	20863135	0.83132	1.38929	0	7.22E-42	0	0	Shared
Gpr137b-ps	222308	13	12708077	D13Mit207	13	8.688726	16526195	0.30048	1.2085	0	2.92E-41	0	0	Shared
Dlat	865416	9	50446044	D9MIT247	9	25.36975	36940492	0.86643	1.80071	0	1.25E-40	0	0	Shared
Decr1	598925	4	15846376	04.013.290	4	8.3	13290000	0.52407	1.24858	0	2.77E-39	0	0	Shared
unassigned	765273	7	52378646	D7MIT228	7	28.11811	47279833	0.21715	0.64494	0	3.06E-38	0	0	Shared
Arhgef12	863418	9	42786290	D9MIT285	9	25.81754	40462577	0.35387	0.7267	0	4.29E-38	0	0	Shared
Phkb	801157	8	88446043	D8MIT45	8	58.44006	89829274	0.33384	1.14781	0	3.48E-37	0	0	Shared
Tmem222	618465	4	132822037	D4Mit203	4	89.73231	1.29E+08	0.48302	0.91141	0	1.43E-36	0	0	Shared
Pion	629533	5	20733848	D5MIT294	5	15.58331	20863135	0.28267	1.17334	0	1.51E-36	0	0	Shared
Fubp1	541883	3	151880818	D3MIT147	3	137.3239	1.48E+08	0.07386	1.01581	0	2.48E-36	0	0	Shared
Fam20c	652127	5	139271009	05.132.979	5	112.2658	1.33E+08	1.10147	2.67846	0	4.29E-36	0	0	Shared
unassigned	650242	5	130252343	D5MIT95	5	98.81753	1.25E+08	0.20707	0.48381	0	5.02E-36	0	0	Shared
Acsl1	794594	8	47603622	08.046.718	8	30.74653	46304537	0.05554	0.2622	0	5.22E-36	0	0	Shared
Ctnnd2	285463	15	30816886	15.028.723	15	14.88113	28708166	0.78967	1.65495	0	8.12E-36	0	0	Shared
Elmod2	823265	8	85846596	D8MIT346	8	54.67316	85454038	0.19163	0.89825	0	2.59E-35	0	0	Shared
Tardbp	622399	4	147996089	D4MIT232	4	109.1183	1.45E+08	0.17398	0.44392	0	2.84E-35	0	0	Shared
Calm3	759889	7	17504984	07.013.915	7	8.7	15600169	0.48093	0.89032	0	5.45E-35	0	0	Shared
unassigned	776895	7	120476410	RS36353338	7	66.26522	1.13E+08	0.41695	1.00683	0	1.19E-34	0	0	Shared
Scfd1	169466	12	52516530	D12MIT285	12	30.22146	55750112	0.77426	1.80123	0	1.91E-34	0	0	Shared
unassigned	800309	8	85745155	D8MIT346	8	54.67316	85454038	0.75426	1.37697	0	3.55E-34	0	0	Shared
unassigned	657341	5	21545301	D5MIT294	5	15.58331	20863135	0.64183	1.01733	0	2.22E-33	0	0	Shared
Dclk2	554419	3	86640246	D3MIT98	3	51.73848	85985423	0.25735	0.84163	0	2.31E-33	0	0	Shared
unassigned	675710	5	123241783	D5MIT95	5	98.81753	1.25E+08	0.1715	0.58367	0	2.71E-33	0	0	Shared
unassigned	736718	7	30076450	07.017.531	7	12.92437	18957827	0.70877	1.17342	0	1.68E-32	0	0	CB
Sacm1l	856973	9	123457980	D9MIT151	9	100.1162	1.21E+08	0.04855	0.38925	0	4.68E-32	0	0	Shared
Rbbp5	19840	1	134390633	RS50560599	1	67.50483	1.17E+08	0.266	1.06594	0	4.70E-32	0	0	Shared
Scoc	823281	8	85961971	D8MIT346	8	54.67316	85454038	0.10817	0.74839	0	7.09E-32	0	0	Shared
Mccc1	547329	3	35877847	03.033.871	3	22.08075	33578373	2.0995	1.30352	0	1.22E-31	0	0	Shared
Rims2	287232	15	39342832	15.028.723	15	14.88113	28708166	0.51224	0.90861	0	1.80E-31	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Akap6	169755	12	54038131	D12MIT285	12	30.22146	55750112	0.14492	0.33109	0	7.89E-31	0	0	Shared
Epb4.1l1	473393	2	156325323	02.161.464	2	113.5093	1.62E+08	0.48531	1.06405	0	1.53E-30	0	0	Shared
Tspyl2	935130	X	148773303	DXMit216	X	58.90613	1.4E+08	1.33283	2.70491	4.07096	2.66E-30	0	0	Shared
unassigned	841413	9	51875677	09.046.588	9	34.49446	46645088	1.16145	1.62318	0	5.46E-30	0	0	Shared
Dpp10	49431	1	125582798	RS50560599	1	67.50483	1.17E+08	0.15016	0.54752	0	5.69E-30	0	0	CB
unassigned	646512	5	116011014	d5mit158	5	69.85959	1.15E+08	1.24594	1.75294	0	6.89E-30	0	0	Shared
Sema5a	285804	15	32404140	15.028.723	15	14.88113	28708166	0.23018	0.79379	0	9.41E-30	0	0	Shared
Pde1c	717042	6	56108966	06.057.998	6	39.56321	58018416	0.71417	1.26476	0	1.22E-29	0	0	CB
Mtor	594480	4	147924231	D4MIT232	4	109.1183	1.45E+08	0.47443	0.8427	0	1.40E-29	0	0	Shared
Rbms1	489847	2	60594523	D2MIT61	2	35.12792	60528325	0.70753	1.19985	0	2.61E-29	0	0	Shared
Rpain	121282	11	70787304	D11MIT320	11	39.87138	70766870	0.08051	0.52252	0	3.61E-29	0	0	Shared
unassigned	739972	7	53309586	D7MIT228	7	28.11811	47279833	0.4475	0.73521	0	5.74E-29	0	0	Shared
Srp68	160621	11	116124551	D11MIT214	11	79.65651	1.15E+08	1.56876	1.06928	0	1.13E-28	0	0	Shared
Mef2a	768572	7	74438480	D7Mit232	7	35.20811	59868792	0.55601	1.07748	0	1.49E-28	0	0	Shared
unassigned	582778	4	99634261	04.098.998	4	75.01299	99172673	0.58099	1.39079	0	2.06E-28	0	0	Shared
Faim2	317186	15	99341014	D15MIT15	15	83.15474	1.03E+08	0.90684	1.51685	0	2.56E-28	0	0	Shared
Ndrg3	508846	2	156795838	02.161.464	2	113.5093	1.62E+08	0.01949	0.20767	0	3.05E-28	0	0	Shared
Lsm8	685312	6	18798736	06.016.672	6	10.4	16672000	0.22279	0.61708	0	3.21E-28	0	0	Shared
Dpp6	630649	5	27144599	05.018.430	5	14.15919	18423994	0.05432	0.15882	0	4.70E-28	0	0	CB
unassigned	375344	17	33960076	17.034.150	17	51.1372	34678889	0.82724	0.50466	0	6.20E-28	0	0	Shared
unassigned	232581	13	67001532	13.061.624	13	39.87979	61715738	0.03182	0.13155	0	6.81E-28	0	0	Shared
Ddr1	376093	17	35826947	17.034.150	17	51.1372	34678889	0.83222	1.44173	0	1.04E-27	0	0	Shared
Nipa1	767081	7	63252886	07.056.455	7	36.40088	63842351	0.06848	0.18329	0	3.71E-27	0	0	Shared
Ilf3	835195	9	21193014	09.014.560	9	12.99047	14614051	0.97269	0.71046	0	4.11E-27	0	0	Shared
Kcnab2	623479	4	151781248	D4MIT42	4	117.1013	1.51E+08	1.50294	1.94688	0	9.84E-27	0	0	Shared
Svop	673598	5	114513056	d5mit158	5	69.85959	1.15E+08	0.59883	0.95923	0	1.17E-26	0	0	Shared
Ddost	592343	4	137865266	D4MIT170	4	99.94085	1.38E+08	1.39105	0.90195	0	1.78E-26	0	0	Shared
Gtf2h1	740165	7	54052803	D7MIT228	7	28.11811	47279833	0.08232	0.29377	0	2.36E-26	0	0	Shared
Otud6b	598773	4	14749848	RS28262872	4	8.826905	18026684	0.43759	0.80271	0	2.84E-26	0	0	Shared
Arntl	751303	7	120418187	RS36353338	7	66.26522	1.13E+08	0.6496	1.41232	0	3.79E-26	0	0	Shared
Dixdc1	865456	9	50495466	D9MIT247	9	25.36975	36940492	0.17738	0.76876	0	5.00E-26	0	0	Shared
unassigned	604763	4	57084092	04.053.650	4	40.48019	53641772	0.08303	0.18108	0	5.05E-26	0	0	Shared
Pik3c2a	777663	7	123520029	RS36353338	7	66.26522	1.13E+08	0.23285	0.64569	0	6.04E-26	0	0	Shared
Arntl	751325	7	120449550	RS36353338	7	66.26522	1.13E+08	0.12108	0.49774	0	6.22E-26	0	0	Shared
3110035E14Rik	704	1	9591269	RS32728630	1	6.020495	9632792	0.04048	0.12935	0	7.74E-26	0	0	CB
Psma3	172158	12	72094004	D12MIT91	12	43.26798	72843829	0.33348	0.98558	0	1.53E-25	0	0	Shared
Ap4s1	169560	12	52831896	D12MIT285	12	30.22146	55750112	0.11988	0.44942	0	1.95E-25	0	0	Shared
Folh1	772323	7	93905470	D7MIT350	7	57.28732	90734599	0.25605	0.53029	0	2.73E-25	0	0	Shared
A730017C20Rik	397289	18	59235505	D18MIT152	18	47.63475	62096421	0.91495	1.27507	0	2.88E-25	0	0	Shared
Slc4a4	640797	5	89608686	RS33085156	5	79.13497	90112330	1.09062	1.56163	0	3.71E-25	0	0	Shared
Dlg2	747244	7	99535430	07.088.976	7	61.08266	96249318	1.12835	1.79026	0	3.72E-25	0	0	Shared
Pion	629536	5	20752769	D5MIT294	5	15.58331	20863135	0.84642	1.44522	0	4.25E-25	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Elovl4	872585	9	83676795	09.079.053	9	64.60162	79115123	0.37233	0.59654	0	4.27E-25	0	0	Shared
Acap3	596643	4	155274225	D4MIT42	4	117.1013	1.51E+08	0.33226	0.7758	0	4.98E-25	0	0	Shared
Hmgcl	591417	4	135509782	04.133.005	4	97.64222	1.33E+08	1.09419	1.69839	0	7.08E-25	0	0	Shared
Amph	203688	13	19186642	D13Mit207	13	8.688726	16526195	0.17433	0.4176	0	9.56E-25	0	0	Shared
unassigned	475893	2	166765925	02.168.990	2	151.4053	1.69E+08	0.31535	0.74082	0	9.71E-25	0	0	Shared
unassigned	649422	5	125989147	D5MIT95	5	98.81753	1.25E+08	0.61436	0.92585	0	1.02E-24	0	0	Shared
Herc2	741488	7	63411776	D7Mit232	7	35.20811	59868792	0.15958	0.29319	0	1.23E-24	0	0	Shared
Stxbp1	484928	2	32667544	D2Mit297	2	25.96707	42461006	1.30112	0.96701	0	2.80E-24	0	0	Shared
Usp48	591923	4	137161672	04.133.005	4	97.64222	1.33E+08	2.4038	1.63667	0	3.32E-24	0	0	Shared
Nipal2	303735	15	34512479	15.028.723	15	14.88113	28708166	1.89277	3.04096	0	3.35E-24	0	0	Shared
Fam135a	34512	1	24064051	rs13475769	1	16.19758	24958696	0.83587	0.44156	0	3.88E-24	0	0	Shared
Gtf2a1	195507	12	92808207	D12MIT194	12	54.38605	92525886	1.21049	0.7281	0	5.14E-24	0	0	Shared
unassigned	841168	9	50608199	D9MIT247	9	25.36975	36940492	0.76732	1.5614	0	5.96E-24	0	0	Shared
unassigned	823691	8	87366940	D8MIT45	8	58.44006	89829274	0.71227	1.72647	0	8.48E-24	0	0	Shared
Cdkal1	225033	13	29417906	RS29514367	13	20.53923	29499372	0.35901	0.59852	0	8.64E-24	0	0	Shared
Scfd1	169470	12	52523937	D12MIT285	12	30.22146	55750112	0.08296	0.25741	0	1.09E-23	0	0	Shared
unassigned	129549	11	102053200	11.104.430	11	62.15042	1.04E+08	0.59278	1.06603	0	1.09E-23	0	0	Shared
Pafah1b1	149108	11	74491023	D11MIT320	11	39.87138	70766870	0.59145	1.01989	0	1.20E-23	0	0	Shared
Ift52	474783	2	162858999	D2MIT411	2	112.9735	1.59E+08	0.24765	0.56238	0	1.26E-23	0	0	Shared
unassigned	214141	13	77064888	D13MIT125	13	47.51637	80862016	0.15489	0.32695	0	1.45E-23	0	0	Shared
Synpr	243574	14	14326035	14.008.937	14	5.6	10975728	0.759	1.41611	0	1.71E-23	0	0	CB
Anxa5	547434	3	36356389	03.033.871	3	22.08075	33578373	1.7463	1.22421	0	2.57E-23	0	0	Shared
Snrpd2	734804	7	19738036	07.013.915	7	8.7	15600169	0.03728	0.11615	0	3.30E-23	0	0	Shared
unassigned	780345	7	135856114	07.122.234	7	82.95546	1.3E+08	0.7427	1.11664	0	4.12E-23	0	0	Shared
Psme4	112806	11	30718107	D11MIT186	11	23.608	35049231	0.89513	0.59986	0	5.38E-23	0	0	Shared
Dars2	56178	1	162986599	D1Mit102	1	80.03925	1.49E+08	0.4345	0.77795	0	5.86E-23	0	0	Shared
Tarsl2	742622	7	72797146	D7MIT248	7	39.99047	80656343	1.94817	2.63602	0	6.24E-23	0	0	Shared
Gde1	778086	7	125838582	RS36353338	7	66.26522	1.13E+08	0.38507	0.65747	0	6.43E-23	0	0	Shared
unassigned	755904	7	140172642	07.122.234	7	82.95546	1.3E+08	0.18923	0.3291	0	6.56E-23	0	0	Shared
Ndufs8	431235	19	3911183	D19Mit68	19	0.200001	3645155	1.18534	0.91656	0	1.36E-22	0	0	Shared
Gas7	120090	11	67466361	D11MIT320	11	39.87138	70766870	0.18297	0.35995	0	1.38E-22	0	0	CB
unassigned	835884	9	23902448	09.014.560	9	12.99047	14614051	10.83134	4.80896	0	1.42E-22	0	0	CB
Fyco1	880707	9	123749696	D9MIT151	9	100.1162	1.21E+08	0.48108	1.01912	0	1.74E-22	0	0	Shared
Rap1gap	592009	4	137277743	D4MIT170	4	99.94085	1.38E+08	1.67236	1.20995	0	2.57E-22	0	0	Shared
Slc6a5	740687	7	57191575	D7MIT228	7	28.11811	47279833	0.44265	0.81642	0	3.02E-22	0	0	CB
Cog6	549553	3	52804404	03.060.525	3	40.51916	60240993	1.25724	1.83638	0	3.51E-22	0	0	Shared
unassigned	219878	13	113749070	d13mit151	13	74.51442	1.16E+08	0.99655	0.61438	0	3.75E-22	0	0	Shared
Bxdc2	300710	15	10409364	15.010.846	15	8.803289	10831030	1.02804	0.61251	0	5.43E-22	0	0	Shared
Lztfl1	880650	9	123607904	D9Mit18	9	96.97845	1.2E+08	0.32362	0.47309	0	1.22E-21	0	0	Shared
unassigned	29374	1	187096046	01.183.109	1	96.11848	1.83E+08	0.39177	1.22107	0	1.54E-21	0	0	Shared
Fn3krp	134526	11	121286280	D11MIT214	11	79.65651	1.15E+08	0.29448	0.50111	0	1.57E-21	0	0	Shared
Cerk	313939	15	85981968	D15MIT262	15	57.21236	87111041	0.49897	0.71724	0	1.65E-21	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Ap2a1	765109	7	52161064	D7MIT228	7	28.11811	47279833	1.02872	1.47747	0	1.77E-21	0	0	Shared
Syne1	63589	10	5003042	rs13480474	10	1.8	4403267	0.3898	0.23969	0	1.88E-21	0	0	CB
Il10ra	864212	9	45073575	D9MIT247	9	25.36975	36940492	0.47087	0.77887	0	2.46E-21	0	0	Shared
unassigned	561727	3	122650175	RS30160288	3	119.3825	1.26E+08	0.27104	0.54317	0	3.04E-21	0	0	Shared
Psmc4	761456	7	28827675	D7MIT267	7	18.29809	30331965	2.04727	1.4849	0	3.29E-21	0	0	Shared
4833420G17Rik	220876	13	120260946	D13MIT78	13	76.84217	1.2E+08	0.67965	0.97715	0	3.43E-21	0	0	Shared
5033411D12Rik	222833	13	17067999	D13Mit207	13	8.688726	16526195	0.30034	0.61365	0	3.56E-21	0	0	Shared
unassigned	385958	17	87834568	D17MIT76	17	95.2661	86033231	0.54232	0.75363	0	4.32E-21	0	0	Shared
Nrip1	347072	16	76351884	D16MIT188	16	69.33209	76817838	0.05134	0.27891	0	4.97E-21	0	0	Shared
unassigned	506063	2	144078324	D2MIT285	2	110.6372	1.53E+08	0.8352	1.38114	0	5.10E-21	0	0	Shared
unassigned	508606	2	155950180	D2MIT285	2	110.6372	1.53E+08	0.982	1.27344	0	5.84E-21	0	0	Shared
Zfp426	859124	9	20280854	09.014.560	9	12.99047	14614051	1.92871	1.27856	0	6.90E-21	0	0	Shared
Fuz	739446	7	52154407	D7MIT228	7	28.11811	47279833	0.18218	0.4326	0	6.94E-21	0	0	Shared
Gm447	663240	5	52766784	d5mit233	5	46.33401	53088465	1.04885	0.93454	0	7.40E-21	0	0	Shared
Tanc1	454967	2	59484857	D2MIT61	2	35.12792	60528325	0.10634	0.26208	0	8.70E-21	0	0	Shared
unassigned	752306	7	125916634	RS36353338	7	66.26522	1.13E+08	0.54127	1.10161	0	1.15E-20	0	0	Shared
Gsr	792625	8	34790752	D8MIT94	8	19.42422	32452130	0.12739	0.21856	0	1.27E-20	0	0	Shared
Mtf2	644701	5	108533293	D5MIT239	5	66.11023	1.08E+08	0.0348	0.08716	0	1.27E-20	0	0	CB
Ap2b1	124727	11	83156223	D11MIT320	11	39.87138	70766870	0.57903	0.93353	0	1.43E-20	0	0	Shared
Ank2	562258	3	126661929	RS30160288	3	119.3825	1.26E+08	0.33834	0.50403	0	1.67E-20	0	0	Shared
unassigned	915598	X	131253383	DXMIT132	X	55.8167	1.38E+08	0.86942	1.06475	1.24112	1.75E-20	0	0	Shared
3830406C13Rik	243434	14	13133662	14.008.937	14	5.6	10975728	1.74461	2.32542	0	1.87E-20	0	0	Shared
unassigned	529269	3	87535632	D3MIT98	3	51.73848	85985423	0.04267	0.11067	0	1.97E-20	0	0	Shared
Sema7a	842781	9	57802349	D9MIT248	9	44.87553	58210366	0.71947	1.459	0	2.06E-20	0	0	Shared
Mlh1	878103	9	111158604	09.105.291	9	79.88305	1.05E+08	1.05571	2.13832	0	2.12E-20	0	0	Shared
Sacm1l	856985	9	123488074	D9MIT151	9	100.1162	1.21E+08	0.2612	0.43369	0	3.06E-20	0	0	Shared
Alg9	841161	9	50587075	D9MIT247	9	25.36975	36940492	0.71381	1.19701	0	3.08E-20	0	0	Shared
Htt	632825	5	35248195	D5MIT388	5	29.38073	33660748	1.28835	1.00625	0	3.14E-20	0	0	Shared
Tor1aip1	55128	1	157870282	D1Mit102	1	80.03925	1.49E+08	0.91337	0.53358	0	3.28E-20	0	0	Shared
Ddx19a	828651	8	113507507	D8MIT47	8	79.10975	1.09E+08	0.64359	0.8855	0	3.82E-20	0	0	Shared
Th1l	477441	2	174245837	D2MIT148	2	167.7799	1.79E+08	0.56902	0.87717	0	4.10E-20	0	0	Shared
Clip4	365100	17	72177038	D17Mit152	17	74.19469	65689824	0.58477	0.99787	0	4.12E-20	0	0	Shared
Txnl1	413359	18	63823769	D18MIT152	18	47.63475	62096421	0.04529	0.18686	0	4.75E-20	0	0	Shared
4933427D14Rik	148661	11	71990189	D11MIT320	11	39.87138	70766870	0.21423	0.43095	0	5.00E-20	0	0	CB
Exoc1	639258	5	76989369	D5MIT309	5	58.78964	79931746	1.44478	1.13169	0	5.12E-20	0	0	Shared
Tom1l1	153305	11	90532425	D11MIT285	11	55.01615	89789103	0.1554	0.30043	0	6.78E-20	0	0	Shared
Klraq1	368437	17	88961521	D17MIT76	17	95.2661	86033231	0.44564	0.59338	0	7.66E-20	0	0	Shared
unassigned	237074	13	97266798	13.096.920	13	58.79686	96589256	0.32483	0.47143	0	8.46E-20	0	0	CB
2810047C21Rik1	759130	7	9319827	07.013.915	7	8.7	15600169	1.24171	2.41498	0	1.18E-19	0	0	CB
Gm8909	376294	17	36304417	17.034.150	17	51.1372	34678889	12.32745	20.97596	0	1.18E-19	0	0	Shared
Enpp2	306578	15	54732908	D15MIT103	15	31.66028	63605769	0.34999	0.2242	0	1.44E-19	0	0	CB
Atp1a2	58692	1	174209444	01.183.109	1	96.11848	1.83E+08	2.5292	1.99389	0	1.48E-19	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Lyst	202916	13	13801795	D13Mit207	13	8.688726	16526195	0.07486	0.22891	0	1.96E-19	0	0	Shared
unassigned	376248	17	36255677	17.034.150	17	51.1372	34678889	0.72672	1.51764	0	2.04E-19	0	0	Shared
Capn7	247295	14	32176692	14.027.409	14	32.01969	29395320	1.83408	2.55168	0	2.21E-19	0	0	Shared
unassigned	831306	8	125767123	D8MIT42	8	102.8893	1.29E+08	0.30343	0.70767	0	2.76E-19	0	0	Shared
H2-Aa	375490	17	34420135	17.034.150	17	51.1372	34678889	1.24743	1.99782	0	3.48E-19	0	0	Shared
Cse1l	475884	2	166756084	02.168.990	2	151.4053	1.69E+08	0.81538	1.16999	0	3.54E-19	0	0	Shared
unassigned	42583	1	74488176	D1MIT24	1	52.91828	74458254	0.77756	1.30989	0	4.72E-19	0	0	Shared
Fam5c	22055	1	148678772	D1Mit102	1	80.03925	1.49E+08	0.58477	0.95935	0	5.52E-19	0	0	CB
Ddx55	649093	5	125018058	D5MIT95	5	98.81753	1.25E+08	0.77509	1.5575	0	6.13E-19	0	0	Shared
Zfp180	735114	7	24886474	07.017.531	7	12.92437	18957827	0.04681	0.1029	0	6.82E-19	0	0	Shared
Cep192	399044	18	68040964	18.063.800	18	48.99442	63834285	0.18542	0.55666	0	7.25E-19	0	0	Shared
Gla	932986	X	131125565	DXMIT172	X	47.92461	1.19E+08	0.77432	0.99578	1.29578	7.91E-19	0	0	Shared
Epb4.9	273543	14	71015069	D14MIT39	14	54.52991	69166099	0.28041	0.97183	0	8.51E-19	0	0	Shared
Ttc35	287826	15	43343302	15.046.034	15	20.5546	46035472	2.41222	1.7426	0	1.72E-18	0	0	Shared
Ube4b	622672	4	148711539	D4MIT232	4	109.1183	1.45E+08	0.42367	0.33678	0	1.73E-18	0	0	Shared
Bin1	392032	18	32536723	18.038.678	18	24.45192	38711680	0.66877	0.9084	0	2.03E-18	0	0	Shared
Bmpr1a	266534	14	35260958	14.027.409	14	32.01969	29395320	0.47243	0.71924	0	2.67E-18	0	0	Shared
unassigned	220871	13	120253164	D13MIT78	13	76.84217	1.2E+08	4.51305	3.09258	0	3.34E-18	0	0	Shared
unassigned	755075	7	136757508	07.122.234	7	82.95546	1.3E+08	0.32764	0.5172	0	3.58E-18	0	0	Shared
Adhfe1	682	1	9543733	RS32728630	1	6.020495	9632792	0.71569	1.05538	0	4.71E-18	0	0	Shared
Atp10a	741888	7	66082443	D7Mit232	7	35.20811	59868792	0.61075	1.08754	0	4.79E-18	0	0	CB
unassigned	569106	3	88716553	D3MIT49	3	73.77602	89036582	0.95122	0.72254	0	5.33E-18	0	0	Shared
Mios	683981	6	8174559	06.016.672	6	10.4	16672000	1.61363	2.32881	0	5.48E-18	0	0	Shared
Rgs17	63473	10	4505049	rs13480474	10	1.8	4403267	0.24461	0.35952	0	5.93E-18	0	0	Shared
Wdr36	392132	18	33007270	18.038.678	18	24.45192	38711680	0.54776	0.92623	0	6.33E-18	0	0	Shared
unassigned	349345	16	91714848	16.083.701	16	79.82369	83818653	0.45451	0.67024	0	6.58E-18	0	0	Shared
Lgi2	663261	5	52955222	d5mit233	5	46.33401	53088465	2.71413	1.75821	0	6.96E-18	0	0	Shared
Pcdhgb5	393358	18	37891248	D18MIT194	18	30.70688	43820481	0.70973	1.22652	0	7.59E-18	0	0	Shared
Sacm1l	856989	9	123494413	D9Mit18	9	96.97845	1.2E+08	1.41431	1.78822	0	7.79E-18	0	0	Shared
Arhgef10l	620398	4	140133004	D4MIT170	4	99.94085	1.38E+08	1.30442	0.87682	0	8.22E-18	0	0	Shared
Atm	866080	9	53264615	09.046.588	9	34.49446	46645088	0.29556	0.50037	0	1.02E-17	0	0	Shared
Faim2	317197	15	99351141	D15MIT44	15	76.94503	98951714	0.41025	0.56764	0	1.02E-17	0	0	Shared
unassigned	630144	5	23683772	D5MIT294	5	15.58331	20863135	0.2579	0.49766	0	1.07E-17	0	0	Shared
Gpr137b	222333	13	13459856	D13Mit207	13	8.688726	16526195	1.73214	1.24754	0	1.23E-17	0	0	Shared
Ift74	581659	4	94321532	D4Mit166	4	66.23295	93616234	0.20281	0.50669	0	1.29E-17	0	0	Shared
Cul4a	789102	8	13136337	08.010.585	8	4.520052	10585028	0.09282	0.19208	0	1.35E-17	0	0	Shared
Acad10	675311	5	122077401	D5MIT95	5	98.81753	1.25E+08	0.14024	0.33682	0	1.47E-17	0	0	Shared
Park2	352684	17	11749519	17.021.019	17	14.36839	21451267	0.5708	0.93832	0	1.58E-17	0	0	Shared
Fam163b	483546	2	26969083	D2MIT296	2	21.50213	31180075	0.94502	1.71124	0	1.61E-17	0	0	Shared
Oxsr1	879650	9	119193668	D9MIT151	9	100.1162	1.21E+08	1.48135	1.17707	0	1.67E-17	0	0	Shared
Fh1	59276	1	177539772	01.183.109	1	96.11848	1.83E+08	1.53208	1.2446	0	1.76E-17	0	0	Shared
Gpr137b-ps	222307	13	12707467	D13Mit207	13	8.688726	16526195	0.22887	0.43607	0	2.22E-17	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	835919	9	24117578	09.014.560	9	12.99047	14614051	0.74785	1.2442	0	2.35E-17	0	0	CB
Vrk3	739352	7	52007489	D7MIT228	7	28.11811	47279833	1.03938	1.61193	0	2.61E-17	0	0	Shared
Trpc3	547516	3	36537305	03.033.871	3	22.08075	33578373	1.53335	1.92337	0	2.69E-17	0	0	CB
Mfn2	622163	4	147259790	D4MIT232	4	109.1183	1.45E+08	1.50861	1.99826	0	2.99E-17	0	0	Shared
unassigned	869287	9	66368535	D9MIT107	9	53.50038	73315075	0.49794	0.30685	0	3.24E-17	0	0	Shared
unassigned	554317	3	85942677	D3MIT98	3	51.73848	85985423	0.57404	0.70569	0	3.30E-17	0	0	Shared
Ikbkap	604617	4	56788312	04.053.650	4	40.48019	53641772	0.66624	0.96076	0	4.31E-17	0	0	Shared
unassigned	672389	5	109084229	D5MIT239	5	66.11023	1.08E+08	0.88674	1.41164	0	5.59E-17	0	0	Shared
Efcab2	27991	1	180413478	01.183.109	1	96.11848	1.83E+08	0.50091	0.81989	0	5.70E-17	0	0	CB
unassigned	3715	1	34269037	D1Mit374	1	27.02859	34816928	0.92487	1.20124	0	5.80E-17	0	0	Shared
Gtf2h1	740173	7	54068059	D7MIT228	7	28.11811	47279833	1.05177	1.46135	0	5.86E-17	0	0	Shared
Wbp1	720029	6	83069169	RS30909511	6	57.9854	83140362	0.42734	0.65087	0	6.31E-17	0	0	CB
Rpl13a	765280	7	52381560	D7MIT228	7	28.11811	47279833	1.53565	1.90149	0	6.41E-17	0	0	Shared
Habp4	212220	13	64287025	13.061.624	13	39.87979	61715738	0.97061	1.2791	0	6.43E-17	0	0	Shared
Timm17a	51812	1	137205726	D1MIT1001	1	72.84145	1.31E+08	0.89324	1.32786	0	6.64E-17	0	0	Shared
Thbs2	371126	17	14824854	17.013.500	17	8.4	13900467	0.32144	0.60921	0	7.71E-17	0	0	Shared
Snx14	873324	9	88276609	d9mit198	9	66.50428	91176808	0.49442	0.81262	0	7.76E-17	0	0	Shared
Rif1	453902	2	51962475	RS27953638	2	27.96753	50041657	1.00701	0.67261	0	8.00E-17	0	0	CB
H2-K1	375394	17	34133422	17.034.150	17	51.1372	34678889	0.91136	1.18882	0	8.65E-17	0	0	Shared
Ikbkap	604611	4	56785906	04.053.650	4	40.48019	53641772	0.76252	1.63112	0	1.09E-16	0	0	Shared
Hiatl1	232467	13	65173381	13.061.624	13	39.87979	61715738	0.49559	0.76412	0	1.21E-16	0	0	Shared
Slco1a4	731431	6	141766260	D6Mit14	6	101.6085	1.46E+08	1.49456	1.1284	0	1.49E-16	0	0	CB
Gmfb	267956	14	47435274	14.042.462	14	41.89415	44159798	2.22434	1.77265	0	1.55E-16	0	0	Shared
unassigned	831688	8	127207013	D8MIT42	8	102.8893	1.29E+08	0.52806	0.75565	0	1.69E-16	0	0	Shared
Cdc40	91987	10	40570761	RS36274062	10	31.86503	31045127	1.85326	2.46673	0	2.07E-16	0	0	Shared
Golga3	645148	5	110638893	D5MIT239	5	66.11023	1.08E+08	1.32621	1.74929	0	2.13E-16	0	0	Shared
1600012F09Rik	223010	13	18081424	13.013.314	13	8.3	13614141	2.08981	1.68905	0	2.22E-16	0	0	Shared
Erc1	727148	6	119672197	d6mit366	6	77.49561	1.15E+08	0.05128	0.22656	0	2.70E-16	0	0	Shared
Iars2	61137	1	187118637	01.183.109	1	96.11848	1.83E+08	0.11743	0.32262	0	2.70E-16	0	0	Shared
Tmem25	864012	9	44601875	09.046.588	9	34.49446	46645088	0.41533	0.55356	0	2.71E-16	0	0	Shared
Strn4	734376	7	17407878	07.013.915	7	8.7	15600169	0.34136	0.49792	0	2.91E-16	0	0	Shared
Ppap2a	219830	13	113649852	d13mit151	13	74.51442	1.16E+08	2.39482	1.67395	0	2.97E-16	0	0	Shared
Tln2	869533	9	67202255	D9MIT336	9	49.6331	65425671	0.59911	0.88166	0	3.07E-16	0	0	Shared
Smarcc1	853798	9	110106736	09.105.291	9	79.88305	1.05E+08	0.66119	0.33945	0	3.32E-16	0	0	Shared
Sergef	765859	7	53698559	D7MIT228	7	28.11811	47279833	0.87955	0.67464	0	3.53E-16	0	0	Shared
unassigned	375399	17	34136077	D17MIT51	17	53.34361	43641790	1.37352	0.94804	0	3.71E-16	0	0	Shared
Myo1c	122621	11	75482705	D11MIT320	11	39.87138	70766870	0.86285	1.33714	0	3.83E-16	0	0	Shared
Sergef	765906	7	53889153	D7MIT228	7	28.11811	47279833	0.85885	1.20977	0	3.94E-16	0	0	Shared
Rit2	407422	18	31372324	18.038.678	18	24.45192	38711680	0.67088	0.83907	0	4.00E-16	0	0	Shared
Abcf2	657978	5	24073003	05.018.430	5	14.15919	18423994	0.80163	1.03195	0	4.90E-16	0	0	Shared
Lsm14a	763129	7	35132948	D7MIT267	7	18.29809	30331965	0.23257	0.40175	0	4.93E-16	0	0	Shared
unassigned	555088	3	88716546	D3MIT49	3	73.77602	89036582	0.98837	0.74694	0	5.03E-16	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Capza2	685120	6	17600003	RS51272439	6	10.78458	19888102	0.00429	0.01791	0	5.56E-16	0	0	Shared
unassigned	241139	13	115178267	d13mit151	13	74.51442	1.16E+08	1.31017	1.00452	0	5.56E-16	0	0	Shared
unassigned	465177	2	119853447	RS27258455	2	126.7319	1.3E+08	2.22152	1.66188	0	5.62E-16	0	0	Shared
Fbxo38	413154	18	62686883	D18MIT152	18	47.63475	62096421	1.23207	0.83747	0	7.04E-16	0	0	Shared
9330182L06Rik	628180	5	9421506	D5MIT123	5	4.1	6556176	0.71291	0.90873	0	7.57E-16	0	0	Shared
unassigned	51861	1	137327051	D1MIT1001	1	72.84145	1.31E+08	0.21343	0.32253	0	7.63E-16	0	0	Shared
Bivm	5816	1	44184516	D1MIT236	1	37.41892	45435458	0.48401	0.78109	0	8.64E-16	0	0	Shared
Mllt11	556275	3	95024337	D3MIT49	3	73.77602	89036582	0.27431	0.39782	0	8.68E-16	0	0	Shared
unassigned	843756	9	62225180	D9MIT336	9	49.6331	65425671	0.78044	1.15679	0	9.10E-16	0	0	Shared
Acad9	521873	3	35975650	03.033.871	3	22.08075	33578373	3.30747	2.72414	0	9.58E-16	0	0	Shared
Arhgef2	529684	3	88447268	D3MIT49	3	73.77602	89036582	0.77164	0.52625	0	9.82E-16	0	0	Shared
unassigned	651913	5	138538808	05.132.979	5	112.2658	1.33E+08	0.66335	0.90425	0	1.13E-15	0	0	Shared
Ivd	464751	2	118703407	RS27267095	2	129.5613	1.37E+08	0.42985	0.63779	0	1.17E-15	0	0	Shared
Gm447	663239	5	52765915	d5mit233	5	46.33401	53088465	0.99147	1.78475	0	1.21E-15	0	0	Shared
unassigned	726859	6	118556333	d6mit366	6	77.49561	1.15E+08	0.80014	0.62536	0	1.25E-15	0	0	CB
Msi1	646455	5	115890496	d5mit158	5	69.85959	1.15E+08	0.75762	1.17426	0	1.26E-15	0	0	Shared
Folh1	772325	7	93911456	D7MIT350	7	57.28732	90734599	0.36545	0.61804	0	1.27E-15	0	0	Shared
unassigned	156561	11	101886469	D11MIT289	11	59.90287	94741466	0.08428	0.26444	0	1.28E-15	0	0	CB
Arl6ip1	777905	7	125270649	RS36353338	7	66.26522	1.13E+08	0.58467	0.77867	0	1.34E-15	0	0	Shared
C230096C10Rik	592584	4	138933390	04.133.005	4	97.64222	1.33E+08	0.18956	0.28179	0	1.54E-15	0	0	CB
Pcdhga12	393376	18	37925404	18.038.678	18	24.45192	38711680	0.39641	0.73447	0	1.56E-15	0	0	CB
Exosc10	594496	4	147936424	D4MIT232	4	109.1183	1.45E+08	1.61862	2.21964	0	1.74E-15	0	0	Shared
Pkn1	823332	8	86201446	D8MIT346	8	54.67316	85454038	0.31379	0.47334	0	1.83E-15	0	0	Shared
Nomo1	739974	7	53312044	D7MIT228	7	28.11811	47279833	1.16326	1.55409	0	1.85E-15	0	0	Shared
Rad23b	576747	4	55383302	04.053.650	4	40.48019	53641772	0.5621	0.7041	0	1.96E-15	0	0	Shared
Ralgps1	485087	2	33023702	D2MIT296	2	21.50213	31180075	1.70561	1.32824	0	2.05E-15	0	0	Shared
unassigned	876293	9	105333716	D9MIT24	9	73.18313	1.03E+08	0.7707	0.93607	0	2.31E-15	0	0	Shared
Tln2	869509	9	67156692	D9MIT336	9	49.6331	65425671	0.85819	0.58769	0	2.41E-15	0	0	Shared
Rnf14	393609	18	38472871	18.038.678	18	24.45192	38711680	0.23162	0.13633	0	2.44E-15	0	0	Shared
unassigned	775344	7	112715704	RS36353338	7	66.26522	1.13E+08	0.64463	0.47858	0	2.56E-15	0	0	Shared
unassigned	800081	8	84414255	D8MIT346	8	54.67316	85454038	0.67851	0.95113	0	2.80E-15	0	0	CB
Epb4.9	273542	14	71014723	D14MIT39	14	54.52991	69166099	0.57928	0.8558	0	2.89E-15	0	0	Shared
Elmo2	510635	2	165120757	02.168.990	2	151.4053	1.69E+08	0.55588	0.73219	0	3.20E-15	0	0	Shared
Fus	754680	7	135115409	07.122.234	7	82.95546	1.3E+08	0.4552	0.68159	0	3.66E-15	0	0	Shared
Otud7a	742267	7	70880685	07.056.455	7	36.40088	63842351	0.40796	0.54425	0	3.95E-15	0	0	Shared
Wdtc1	618506	4	132879743	D4Mit203	4	89.73231	1.29E+08	0.36154	0.53318	0	4.39E-15	0	0	Shared
unassigned	232337	13	64470306	13.061.624	13	39.87979	61715738	0.43712	0.62786	0	4.39E-15	0	0	Shared
Nt5c2	440867	19	46973114	D19MIT46	19	37.54307	33009697	1.22935	0.88827	0	4.63E-15	0	0	Shared
unassigned	735243	7	25205344	07.017.531	7	12.92437	18957827	0.53308	0.76944	0	4.95E-15	0	0	Shared
Tbc1d9	800329	8	85788784	D8MIT346	8	54.67316	85454038	0.36924	0.60237	0	4.99E-15	0	0	Shared
Fxyd6	839871	9	45204063	D9MIT285	9	25.81754	40462577	0.42779	0.55225	0	5.71E-15	0	0	Shared
unassigned	179284	12	107294336	D12MIT7	12	66.69663	1.05E+08	1.66616	1.18497	0	5.89E-15	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Hps5	766002	7	54038537	07.056.455	7	36.40088	63842351	0.68983	1.10519	0	5.92E-15	0	0	Shared
unassigned	393364	18	37901141	18.038.678	18	24.45192	38711680	1.40566	1.9028	0	6.13E-15	0	0	CB
Setdb1	556340	3	95130084	D3MIT49	3	73.77602	89036582	0.28144	0.41419	0	6.47E-15	0	0	Shared
unassigned	806840	8	115377846	D8MIT215	8	87.84173	1.18E+08	0.36045	0.50314	0	6.48E-15	0	0	CB
unassigned	778044	7	125669307	RS36353338	7	66.26522	1.13E+08	0.85959	1.24645	0	7.07E-15	0	0	Shared
Dst	3676	1	34221942	D1Mit374	1	27.02859	34816928	1.29614	1.07031	0	7.49E-15	0	0	Shared
Terf1	1673	1	15809070	rs13475769	1	16.19758	24958696	0.33012	0.5442	0	7.59E-15	0	0	Shared
Ubash3b	862971	9	40836137	D9MIT285	9	25.81754	40462577	2.6462	2.21161	0	7.61E-15	0	0	Shared
Sidt2	864411	9	45755922	D9MIT247	9	25.36975	36940492	0.64574	0.85442	0	7.71E-15	0	0	Shared
unassigned	646513	5	116011269	d5mit158	5	69.85959	1.15E+08	1.22297	1.46251	0	8.28E-15	0	0	Shared
Poli	414835	18	70688356	D18MIT186	18	54.44325	72180072	0.17541	0.30143	0	9.62E-15	0	0	Shared
unassigned	646510	5	116009652	d5mit158	5	69.85959	1.15E+08	0.58958	0.43581	0	1.01E-14	0	0	Shared
unassigned	235672	13	90201563	13.096.920	13	58.79686	96589256	0.97849	0.69646	0	1.06E-14	0	0	Shared
Zfp39	144906	11	58714106	D11Mit4	11	39.42453	68422759	6.74921	4.93288	0	1.09E-14	0	0	CB
unassigned	26870	1	174105882	01.183.109	1	96.11848	1.83E+08	1.30987	1.6041	0	1.10E-14	0	0	Shared
Slc7a5	830908	8	124420344	D8MIT42	8	102.8893	1.29E+08	0.57717	0.82901	0	1.20E-14	0	0	Shared
Polr2k	286531	15	36106692	15.046.034	15	20.5546	46035472	0.1934	0.35458	0	1.22E-14	0	0	CB
Sox2ot	521499	3	34537376	03.033.871	3	22.08075	33578373	1.57491	0.92167	0	1.76E-14	0	0	CB
Cep164	864309	9	45583964	D9MIT247	9	25.36975	36940492	0.21799	0.43003	0	1.79E-14	0	0	Shared
Mcf2l	788991	8	13009502	08.010.585	8	4.520052	10585028	0.26373	0.38815	0	1.88E-14	0	0	Shared
unassigned	717034	6	56076747	d6mit123	6	39.56321	56801586	0.59932	0.38939	0	1.98E-14	0	0	CB
Hydin	806310	8	113063670	D8MIT215	8	87.84173	1.18E+08	3.69129	7.21288	0	2.04E-14	0	0	CB
Gpr137b-ps	222313	13	12712036	13.013.314	13	8.3	13614141	0.55639	0.78473	0	2.29E-14	0	0	Shared
Rmnd1	63860	10	5935618	D10Mit123	10	3.021254	9952319	0.03763	0.07022	0	2.31E-14	0	0	Shared
Abcg4	863761	9	44085552	D9MIT2	9	25.36976	37202486	0.59057	0.84223	0	2.34E-14	0	0	Shared
Npsr1	835918	9	24114454	09.014.560	9	12.99047	14614051	0.40234	0.72896	0	2.41E-14	0	0	CB
unassigned	761788	7	29756636	D7MIT267	7	18.29809	30331965	0.46376	0.65511	0	2.41E-14	0	0	Shared
Polr3f	469989	2	144364923	D2MIT285	2	110.6372	1.53E+08	0.25228	0.38116	0	2.55E-14	0	0	Shared
Zfp52	354363	17	21675584	17.021.019	17	14.36839	21451267	4.19243	2.87072	0	2.65E-14	0	0	Shared
Spg21	844575	9	65323695	09.046.588	9	34.49446	46645088	1.81962	1.50925	0	2.68E-14	0	0	Shared
unassigned	872972	9	86489867	d9mit198	9	66.50428	91176808	0.87187	1.106	0	3.09E-14	0	0	Shared
unassigned	329753	16	58456005	16.039.061	16	48.3587	39141781	2.36243	1.7721	0	3.13E-14	0	0	Shared
unassigned	622178	4	147287501	D4MIT232	4	109.1183	1.45E+08	0.91052	1.24994	0	3.20E-14	0	0	Shared
Slco1a4	731442	6	141803734	D6Mit14	6	101.6085	1.46E+08	1.91019	1.39186	0	3.30E-14	0	0	CB
unassigned	835885	9	23902553	09.014.560	9	12.99047	14614051	1.50381	0.70626	0	3.53E-14	0	0	CB
unassigned	144915	11	58747963	D11MIT320	11	39.87138	70766870	1.33661	1.77861	0	3.85E-14	0	0	Shared
unassigned	24431	1	162967784	D1Mit102	1	80.03925	1.49E+08	1.09989	1.36328	0	4.00E-14	0	0	Shared
unassigned	735172	7	25039807	07.013.915	7	8.7	15600169	0.42173	0.72126	0	4.04E-14	0	0	Shared
Papss1	538000	3	131230522	D3MIT256	3	103.276	1.36E+08	0.41834	0.27983	0	4.18E-14	0	0	Shared
Chd4	704122	6	125051268	D6MIT328	6	75.24789	1.13E+08	1.77183	1.38024	0	4.56E-14	0	0	Shared
Dnttip2	536280	3	121979309	D3MIT57	3	88.53548	1.16E+08	2.69174	3.30512	0	4.62E-14	0	0	Shared
Uevld	766070	7	54193327	D7MIT228	7	28.11811	47279833	0.71431	1.04073	0	4.77E-14	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Mfn2	622152	4	147252845	D4MIT232	4	109.1183	1.45E+08	0.97216	1.17045	0	5.05E-14	0	0	Shared
Uchl1	637596	5	67073860	RS33623243	5	52.83465	70546596	0.18738	0.25882	0	5.16E-14	0	0	Shared
unassigned	631847	5	32000542	D5MIT352	5	30.68587	35957616	2.83974	3.53346	0	5.31E-14	0	0	Shared
unassigned	856968	9	123438205	D9Mit18	9	96.97845	1.2E+08	0.21397	0.31636	0	5.31E-14	0	0	CB
unassigned	245170	14	22650891	14.008.937	14	5.6	10975728	0.08115	0.05121	0	5.75E-14	0	0	Shared
Hydin	806311	8	113065442	D8MIT215	8	87.84173	1.18E+08	1.24681	2.88712	0	6.74E-14	0	0	CB
unassigned	141633	11	43238162	D11MIT51	11	25.39412	36205252	1.42561	2.29185	0	7.05E-14	0	0	Shared
unassigned	679647	5	140247217	05.132.979	5	112.2658	1.33E+08	2.46373	1.94582	0	7.05E-14	0	0	Shared
unassigned	765271	7	52377978	D7MIT228	7	28.11811	47279833	1.5115	1.18946	0	7.31E-14	0	0	Shared
Psg16	734480	7	17678998	07.013.915	7	8.7	15600169	1.22846	1.55406	0	7.49E-14	0	0	Shared
unassigned	775342	7	112715220	RS36353338	7	66.26522	1.13E+08	1.25206	0.96053	0	7.81E-14	0	0	Shared
unassigned	240771	13	113704754	d13mit151	13	74.51442	1.16E+08	2.65307	2.09985	0	7.96E-14	0	0	Shared
Agt	831655	8	127081668	D8MIT42	8	102.8893	1.29E+08	0.62961	0.93738	0	8.23E-14	0	0	CB
Gmfb	267954	14	47434596	14.042.462	14	41.89415	44159798	0.0935	0.17458	0	8.50E-14	0	0	Shared
unassigned	607116	4	71787476	rs13477756	4	50.52425	68030949	0.34432	0.58984	0	8.69E-14	0	0	Shared
Gm13251	594080	4	146539461	D4MIT232	4	109.1183	1.45E+08	0.90985	0.62886	0	9.27E-14	0	0	Shared
Lrp1	107191	10	126978320	D10Mit14	10	93.10254	1.18E+08	1.49109	1.12684	0	1.01E-13	0	0	Shared
Sdk1	652818	5	142474695	05.132.979	5	112.2658	1.33E+08	0.42417	0.56368	0	1.12E-13	0	0	Shared
Timm17a	51813	1	137206393	01.136.071	1	77.74879	1.36E+08	0.52596	0.39515	0	1.30E-13	0	0	Shared
unassigned	717204	6	57463755	06.057.998	6	39.56321	58018416	0.98928	1.25783	0	1.32E-13	0	0	Shared
unassigned	269114	14	52704074	D14Mit183	14	42.79497	52629891	0.63784	0.85858	0	1.41E-13	0	0	Shared
Dapk1	211792	13	60824384	13.061.624	13	39.87979	61715738	0.50892	0.75888	0	1.45E-13	0	0	Shared
Mrps10	360839	17	47515589	17.034.150	17	51.1372	34678889	0.67948	0.50505	0	1.51E-13	0	0	Shared
Sumf1	725019	6	108058485	d6mit366	6	77.49561	1.15E+08	0.51599	0.61077	0	1.54E-13	0	0	Shared
Syne1	63585	10	4997835	rs13480474	10	1.8	4403267	0.61336	0.48634	0	1.55E-13	0	0	CB
Etfb	738842	7	50708210	D7Mit232	7	35.20811	59868792	0.36604	0.54904	0	1.59E-13	0	0	Shared
Sema6d	466108	2	124483738	RS27258455	2	126.7319	1.3E+08	2.0852	1.74159	0	1.64E-13	0	0	Shared
Freq	450213	2	31142807	D2MIT296	2	21.50213	31180075	1.18081	0.87531	0	1.72E-13	0	0	Shared
unassigned	812884	8	16358266	08.010.585	8	4.520052	10585028	0.21926	0.39326	0	1.74E-13	0	0	Shared
Map2k7	787523	8	4245981	D8MIT155	8	3.1	4976602	0.77516	0.63548	0	1.75E-13	0	0	CB
Herc2	741469	7	63389966	D7Mit232	7	35.20811	59868792	0.13204	0.17397	0	1.80E-13	0	0	Shared
Npsr1	835886	9	23902676	09.014.560	9	12.99047	14614051	0.75694	0.5213	0	1.80E-13	0	0	CB
Sacm1l	856988	9	123494205	D9Mit18	9	96.97845	1.2E+08	0.8715	1.08308	0	1.87E-13	0	0	Shared
Zfp459	232747	13	67509198	13.061.624	13	39.87979	61715738	0.5281	0.8268	0	1.88E-13	0	0	Shared
Ints1	679635	5	140238827	05.132.979	5	112.2658	1.33E+08	1.79726	1.24432	0	1.90E-13	0	0	Shared
Ablim1	442644	19	57114983	D19MIT103	19	59.41115	53838656	0.58938	0.4287	0	1.92E-13	0	0	Shared
Ncor1	146141	11	62148003	D11Mit4	11	39.42453	68422759	0.69069	0.84973	0	1.95E-13	0	0	Shared
unassigned	457361	2	71693712	RS28322831	2	43.67748	71063776	0.74036	1.3143	0	1.96E-13	0	0	Shared
Cntfr	601963	4	41633829	D4mit94	4	20.99338	33951862	2.85676	1.92755	0	2.12E-13	0	0	Shared
Galntl2	247414	14	32861255	14.027.409	14	32.01969	29395320	1.0856	1.61581	0	2.12E-13	0	0	CB
Gas5	24432	1	162968596	01.183.109	1	96.11848	1.83E+08	0.59535	0.3406	0	2.14E-13	0	0	Shared
Sacs	252572	14	61792211	D14Mit183	14	42.79497	52629891	0.33107	0.48276	0	2.22E-13	0	0	CB

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	376245	17	36254575	17.034.150	17	51.1372	34678889	0.08113	0.12561	0	2.36E-13	0	0	Shared
Inpp5f	754921	7	135820249	07.122.234	7	82.95546	1.3E+08	0.27662	0.38082	0	2.45E-13	0	0	Shared
Bai1	292166	15	74403244	D15MIT67	15	36.95768	70032295	0.80655	1.10102	0	2.52E-13	0	0	CB
Gm13157	593795	4	146633636	D4MIT232	4	109.1183	1.45E+08	10.82007	7.80613	0	2.52E-13	0	0	Shared
1500035H01Rik	839707	9	44592044	D9MIT285	9	25.81754	40462577	2.79057	2.42266	0	2.63E-13	0	0	Shared
unassigned	870307	9	71499011	D9MIT107	9	53.50038	73315075	2.13461	1.76909	0	2.74E-13	0	0	Shared
unassigned	521522	3	34576916	03.033.871	3	22.08075	33578373	0.94614	1.02578	0	2.78E-13	0	0	CB
unassigned	531138	3	94681317	03.106.773	3	82.33049	1.06E+08	1.29959	1.05426	0	2.93E-13	0	0	Shared
Epha3	345626	16	63603357	D16MIT185	16	54.3944	60434381	0.89884	1.27631	0	3.15E-13	0	0	CB
Ghitm	266910	14	37939147	D14MIT174	14	33.32711	32460166	1.08587	1.29705	0	3.32E-13	0	0	Shared
Abcc12	824109	8	89048594	D8MIT45	8	58.44006	89829274	1.46777	2.26412	0	3.40E-13	0	0	CB
Ddr1	376085	17	35821120	17.034.150	17	51.1372	34678889	1.05318	0.86737	0	4.42E-13	0	0	CB
unassigned	529915	3	89052885	D3MIT49	3	73.77602	89036582	1.901	1.6071	0	4.56E-13	0	0	Shared
Aars	806520	8	113574284	D8MIT215	8	87.84173	1.18E+08	0.87397	1.05805	0	4.85E-13	0	0	Shared
Rpap1	500606	2	119601081	D2MIT395	2	91.61399	1.19E+08	0.94453	0.696	0	5.58E-13	0	0	Shared
unassigned	377546	17	45706082	17.034.150	17	51.1372	34678889	2.34431	1.97269	0	5.91E-13	0	0	Shared
1700054N08Rik	831475	8	126365946	D8MIT42	8	102.8893	1.29E+08	2.48121	1.93378	0	5.98E-13	0	0	Shared
Dlat	865423	9	50457743	09.046.588	9	34.49446	46645088	0.5218	0.79462	0	5.99E-13	0	0	Shared
unassigned	740179	7	54078161	D7Mit232	7	35.20811	59868792	0.69976	0.90658	0	6.34E-13	0	0	Shared
Fam135b	309460	15	71359606	D15MIT103	15	31.66028	63605769	1.16309	1.39997	0	6.87E-13	0	0	CB
unassigned	166584	12	31273293	D12Mit2	12	26.67403	42747379	2.6645	2.33727	0	6.95E-13	0	0	Shared
Dzip1	279645	14	119285724	RS31252045	14	77.8316	1.11E+08	0.69087	1.07988	0	7.04E-13	0	0	Shared
Sfxn4	443435	19	60934587	D19MIT103	19	59.41115	53838656	0.41618	0.79103	0	7.35E-13	0	0	Shared
unassigned	598928	4	15851373	04.013.290	4	8.3	13290000	1.17148	1.54101	0	7.61E-13	0	0	Shared
Add1	632697	5	34953204	D5MIT388	5	29.38073	33660748	0.63747	0.54244	0	8.01E-13	0	0	Shared
unassigned	342923	16	44273546	D16Mit125	16	48.35871	42377567	0.38893	0.22163	0	8.03E-13	0	0	CB
Prkag2	658077	5	24386513	D5MIT348	5	18.20559	24424937	0.63768	0.80819	0	8.98E-13	0	0	Shared
Slc11a2	317413	15	100242622	D15MIT44	15	76.94503	98951714	0.08545	0.17083	0	9.54E-13	0	0	Shared
unassigned	831476	8	126368906	D8MIT42	8	102.8893	1.29E+08	0.24501	0.32561	0	9.56E-13	0	0	CB
Psg16	734473	7	17659482	07.013.915	7	8.7	15600169	1.87075	1.36089	0	9.74E-13	0	0	Shared
Pld5	59361	1	178020031	01.183.109	1	96.11848	1.83E+08	1.49447	1.17382	0	9.75E-13	0	0	CB
Vldlr	423643	19	27318692	D19MIT96	19	21.38792	21916083	1.304	0.96186	0	9.96E-13	0	0	Shared
Serinc3	510096	2	163449472	D2MIT411	2	112.9735	1.59E+08	0.13237	0.18191	0	1.04E-12	0	0	Shared
Rbks	659522	5	31962321	D5MIT388	5	29.38073	33660748	1.02143	1.31225	0	1.08E-12	0	0	Shared
Slc6a5	740692	7	57200890	D7MIT228	7	28.11811	47279833	0.70358	1.03144	0	1.09E-12	0	0	CB
C4a	375623	17	34866361	17.034.150	17	51.1372	34678889	0.45698	0.60582	0	1.10E-12	0	0	Shared
Rnaseh2a	823762	8	87483931	D8MIT346	8	54.67316	85454038	1.17623	0.9236	0	1.10E-12	0	0	Shared
Tnpo2	800970	8	87568935	D8MIT45	8	58.44006	89829274	1.95333	2.5329	0	1.11E-12	0	0	Shared
unassigned	402517	18	85047414	RS30267686	18	60.34946	81658329	0.13637	0.2836	0	1.11E-12	0	0	CB
Kif21b	20911	1	138058306	D1MIT1001	1	72.84145	1.31E+08	0.58909	0.82066	0	1.12E-12	0	0	CB
Zkscan1	651908	5	138534156	05.132.979	5	112.2658	1.33E+08	0.64179	0.45278	0	1.15E-12	0	0	CB
4933407N01Rik	139641	11	30848307	D11MIT186	11	23.608	35049231	0.74442	0.58883	0	1.22E-12	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	286529	15	36105232	15.028.723	15	14.88113	28708166	3.1966	2.24795	0	1.26E-12	0	0	Shared
Fam179b	171338	12	66107317	12.065.348	12	37.44045	65530382	1.46196	1.12817	0	1.31E-12	0	0	Shared
Mcam	839493	9	43950250	D9MIT2	9	25.36976	37202486	0.58858	0.7927	0	1.41E-12	0	0	Shared
Il6st	219731	13	113284790	D13MIT213	13	69.65924	1.09E+08	1.48384	1.23559	0	1.47E-12	0	0	Shared
Abhd12	507345	2	150668248	D2MIT285	2	110.6372	1.53E+08	0.08765	0.14094	0	1.48E-12	0	0	CB
Cpne7	808974	8	125649469	D8MIT42	8	102.8893	1.29E+08	1.03735	1.51547	0	1.65E-12	0	0	CB
H2-T22	893539	17	36177176	17.034.150	17	51.1372	34678889	0.50221	0.28319	0	1.66E-12	0	0	Shared
Myo6	847891	9	80113942	D9MIT107	9	53.50038	73315075	0.44355	0.74053	0	1.66E-12	0	0	Shared
Exoc6	425761	19	37668201	D19MIT88	19	44.41135	37331405	0.50837	0.34004	0	1.77E-12	0	0	Shared
unassigned	497867	2	104857073	D2MIT100	2	54.19426	1.06E+08	0.13094	0.22291	0	1.82E-12	0	0	Shared
Elac2	119494	11	64801562	11.041.143	11	25.39412	41113079	0.43119	0.68059	0	1.84E-12	0	0	Shared
Ece1	592069	4	137492631	D4MIT170	4	99.94085	1.38E+08	2.52559	2.05898	0	1.86E-12	0	0	Shared
unassigned	863827	9	44161870	D9MIT248	9	44.87553	58210366	0.47658	0.61296	0	1.94E-12	0	0	Shared
Rapgef5	182005	12	118982673	D12MIT7	12	66.69663	1.05E+08	0.1755	0.34484	0	1.98E-12	0	0	Shared
Ddost	592346	4	137866539	04.133.005	4	97.64222	1.33E+08	0.92486	1.08475	0	2.01E-12	0	0	Shared
Lars	409649	18	42410483	D18MIT202	18	28.05292	43551589	1.30537	1.03551	0	2.04E-12	0	0	Shared
Svop	673596	5	114504532	d5mit158	5	69.85959	1.15E+08	1.49287	1.25525	0	2.05E-12	0	0	Shared
unassigned	489533	2	59740077	D2MIT61	2	35.12792	60528325	0.35448	0.45269	0	2.26E-12	0	0	CB
Ssfa2	458864	2	79500390	D2MIT75	2	46.41465	80424883	0.81625	1.30001	0	2.31E-12	0	0	Shared
Etfdh	553208	3	79426692	D3MIT98	3	51.73848	85985423	0.38127	0.50355	0	2.39E-12	0	0	Shared
Pcdhga3	393331	18	37834017	18.038.678	18	24.45192	38711680	0.98793	1.33443	0	2.41E-12	0	0	CB
Kif1b	622609	4	148587756	D4MIT42	4	117.1013	1.51E+08	1.09811	1.32338	0	2.44E-12	0	0	Shared
Fyco1	880706	9	123747997	D9MIT151	9	100.1162	1.21E+08	0.94886	1.31481	0	2.48E-12	0	0	Shared
unassigned	762815	7	31917885	D7MIT267	7	18.29809	30331965	0.3855	0.52761	0	2.59E-12	0	0	Shared
Fbxo44	622301	4	147532721	D4MIT232	4	109.1183	1.45E+08	2.36454	2.00984	0	2.60E-12	0	0	Shared
unassigned	287222	15	39294174	15.028.723	15	14.88113	28708166	1.32556	1.67038	0	2.67E-12	0	0	Shared
Fxyd6	839870	9	45200759	D9MIT2	9	25.36976	37202486	1.14604	0.98957	0	3.01E-12	0	0	Shared
Acad9	521871	3	35974171	03.033.871	3	22.08075	33578373	0.95541	0.76465	0	3.18E-12	0	0	Shared
Ankrd54	311859	15	78891594	D15Mit107	15	49.40097	84216927	1.36186	1.97519	0	3.20E-12	0	0	Shared
Scg3	871227	9	75531463	D9MIT107	9	53.50038	73315075	1.27639	1.80187	0	3.24E-12	0	0	Shared
Arnt2	772007	7	91434288	D7MIT350	7	57.28732	90734599	0.7951	0.60945	0	3.40E-12	0	0	CB
Ptov1	765050	7	52118446	D7MIT228	7	28.11811	47279833	0.26522	0.38081	0	3.51E-12	0	0	Shared
Heatr5a	188685	12	53040809	D12MIT285	12	30.22146	55750112	0.81791	1.08604	0	3.53E-12	0	0	Shared
Mtf2	644689	5	108516968	D5MIT10	5	65.80535	1.05E+08	1.58464	1.25621	0	3.78E-12	0	0	Shared
Psmd6	262351	14	14944830	14.008.937	14	5.6	10975728	0.26987	0.4474	0	3.80E-12	0	0	Shared
Ptplad1	868994	9	64838800	D9MIT336	9	49.6331	65425671	1.88103	1.57671	0	3.94E-12	0	0	Shared
Mcam	839488	9	43948488	D9MIT285	9	25.81754	40462577	0.93409	1.20083	0	3.99E-12	0	0	Shared
Adam22	655791	5	8095048	D5MIT123	5	4.1	6556176	0.55267	0.7006	0	4.05E-12	0	0	CB
unassigned	810432	8	131229275	D8MIT42	8	102.8893	1.29E+08	0.12845	0.23689	0	4.51E-12	0	0	Shared
Ppil4	64162	10	7540825	RS29347557	10	5.696346	12661713	1.22558	0.9167	0	4.58E-12	0	0	Shared
Snrpa1	742748	7	73219273	D7Mit232	7	35.20811	59868792	0.33396	0.43099	0	4.70E-12	0	0	CB
Sap130	391774	18	31795648	D18Mit68	18	14.5139	21594126	1.39272	1.05446	0	4.76E-12	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	459334	2	83697846	D2MIT75	2	46.41465	80424883	0.80251	0.64442	0	4.85E-12	0	0	Shared
Herc2	741514	7	63440235	07.056.455	7	36.40088	63842351	1.7387	2.10306	0	5.39E-12	0	0	Shared
unassigned	273474	14	70892080	D14MIT39	14	54.52991	69166099	0.71754	0.91394	0	5.56E-12	0	0	Shared
Mmd	126542	11	90121218	D11MIT285	11	55.01615	89789103	0.63341	0.79087	0	5.82E-12	0	0	Shared
Miip	622126	4	147236360	D4MIT232	4	109.1183	1.45E+08	0.65016	0.90472	0	5.88E-12	0	0	CB
Dpp8	844348	9	64901585	D9MIT107	9	53.50038	73315075	0.62396	0.44689	0	6.44E-12	0	0	Shared
Sorbs1	438962	19	40427019	19.046.444	19	55.55111	46465179	1.10256	0.88273	0	7.13E-12	0	0	Shared
Pick1	293333	15	79060253	D15MIT67	15	36.95768	70032295	0.8614	0.49838	0	7.37E-12	0	0	Shared
Qpctl	760136	7	19728579	07.013.915	7	8.7	15600169	0.31775	0.47383	0	8.12E-12	0	0	CB
unassigned	541962	3	152042584	D3Mit19	3	140.7312	1.57E+08	1.0255	1.29186	0	8.20E-12	0	0	Shared
Ubtf	156804	11	102175475	11.104.430	11	62.15042	1.04E+08	1.10535	1.42068	0	8.28E-12	0	0	CB
Lphn1	800495	8	86442832	D8MIT45	8	58.44006	89829274	2.09819	2.55748	0	8.59E-12	0	0	Shared
Sept3	294402	15	82114133	D15Mit107	15	49.40097	84216927	2.46358	1.9384	0	8.71E-12	0	0	Shared
Fam116b	314595	15	89017206	15.090.122	15	63.15586	90124664	0.36662	0.43752	0	9.49E-12	0	0	CB
Cst3	506956	2	148697653	D2MIT285	2	110.6372	1.53E+08	0.92961	0.81502	0	9.94E-12	0	0	Shared
Clpx	844485	9	65149668	D9MIT336	9	49.6331	65425671	1.48483	1.12944	0	1.08E-11	0	0	Shared
Nomo1	739977	7	53316253	D7MIT228	7	28.11811	47279833	0.54047	0.67519	0	1.08E-11	0	0	Shared
Entpd4	254060	14	69965580	D14MIT39	14	54.52991	69166099	0.9289	1.19484	0	1.09E-11	0	0	Shared
1700029I01Rik	594083	4	146553783	D4MIT232	4	109.1183	1.45E+08	0.75822	0.92697	0	1.10E-11	0	0	Shared
unassigned	622226	4	147391898	D4MIT232	4	109.1183	1.45E+08	1.21656	1.36385	0	1.13E-11	0	0	Shared
unassigned	277936	14	103540213	RS31252045	14	77.8316	1.11E+08	0.1137	0.22576	0	1.14E-11	0	0	Shared
4933428G20Rik	128090	11	97351568	D11MIT289	11	59.90287	94741466	1.07949	0.77908	0	1.21E-11	0	0	Shared
unassigned	186939	12	36748507	12.039.760	12	26.67403	39976164	1.44024	1.30594	0	1.23E-11	0	0	Shared
Chd1	353553	17	15843920	17.013.500	17	8.4	13900467	0.13192	0.24064	0	1.29E-11	0	0	Shared
Crnkl1	506361	2	145745686	D2MIT285	2	110.6372	1.53E+08	1.42288	0.95349	0	1.32E-11	0	0	Shared
Tardbp	622400	4	147999326	D4MIT232	4	109.1183	1.45E+08	0.47393	0.69903	0	1.36E-11	0	0	Shared
Gtf2h1	740167	7	54057165	D7MIT228	7	28.11811	47279833	1.15617	0.96286	0	1.39E-11	0	0	Shared
Nckipsd	853302	9	108717005	09.105.291	9	79.88305	1.05E+08	1.58765	1.29738	0	1.39E-11	0	0	Shared
Dpp10	49428	1	125546865	01.136.071	1	77.74879	1.36E+08	2.01707	2.53379	0	1.41E-11	0	0	CB
Dpy19l3	763462	7	36493568	07.017.531	7	12.92437	18957827	1.57613	1.28026	0	1.61E-11	0	0	Shared
Eif3k	761793	7	29762226	D7MIT294	7	15.72036	28074461	0.57527	0.44005	0	1.74E-11	0	0	Shared
Vps13a	434575	19	16800063	19.013.429	19	11.12922	13436471	0.63257	0.44877	0	1.78E-11	0	0	Shared
Bat5	358549	17	35235845	17.034.150	17	51.1372	34678889	2.29611	2.61811	0	1.83E-11	0	0	Shared
Cadps2	711023	6	23213183	RS49937148	6	13.13583	22510745	0.36896	0.50664	0	1.86E-11	0	0	CB
Trf	875807	9	103118181	D9MIT24	9	73.18313	1.03E+08	1.33453	1.53438	0	1.92E-11	0	0	Shared
Zfp93	735169	7	25061561	07.013.915	7	8.7	15600169	0.63438	0.74883	0	1.93E-11	0	0	Shared
Ankrd52	85298	10	127820414	D10Mit14	10	93.10254	1.18E+08	1.26565	1.68373	0	2.03E-11	0	0	Shared
unassigned	237837	13	100277771	13.096.920	13	58.79686	96589256	0.83486	1.03313	0	2.05E-11	0	0	Shared
unassigned	521872	3	35974829	03.033.871	3	22.08075	33578373	0.80308	0.63515	0	2.07E-11	0	0	Shared
unassigned	295027	15	84884297	D15MIT262	15	57.21236	87111041	2.64754	2.27226	0	2.10E-11	0	0	CB
Gtf2h1	740168	7	54059232	D7Mit232	7	35.20811	59868792	1.49254	1.25491	0	2.14E-11	0	0	Shared
Pex16	460768	2	92217852	D2MIT75	2	46.41465	80424883	2.19519	1.85621	0	2.14E-11	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	496286	2	93681877	D2MIT75	2	46.41465	80424883	1.02282	0.75867	0	2.15E-11	0	0	CB
unassigned	139631	11	30834760	D11MIT51	11	25.39412	36205252	2.28325	1.62147	0	2.17E-11	0	0	Shared
Bsdc1	589586	4	129151327	D4Mit203	4	89.73231	1.29E+08	0.41066	0.49297	0	2.26E-11	0	0	CB
Jarid2	208641	13	44980322	D13MIT250	13	36.46819	56424004	1.31199	1.05816	0	2.29E-11	0	0	CB
Bxdc2	300702	15	10406201	D15MIT252	15	9.706826	22550163	0.48991	0.63362	0	2.46E-11	0	0	Shared
Svep1	605004	4	58097388	04.053.650	4	40.48019	53641772	1.39089	1.68335	0	2.47E-11	0	0	Shared
Kif1a	46477	1	94970408	01.102.953	1	66.3874	1.03E+08	0.91216	1.25563	0	2.48E-11	0	0	Shared
Patl1	420928	19	12006649	19.013.429	19	11.12922	13436471	1.16552	0.87111	0	2.48E-11	0	0	Shared
Sema3d	628370	5	12524251	D5MIT294	5	15.58331	20863135	0.30422	0.45078	0	2.49E-11	0	0	Shared
Gucy1a3	553582	3	81909729	D3MIT98	3	51.73848	85985423	1.02092	1.24976	0	2.50E-11	0	0	Shared
unassigned	730500	6	136766415	D6MIT194	6	87.57626	1.28E+08	0.44452	0.61098	0	2.54E-11	0	0	Shared
5033411D12Rik	222908	13	17786568	D13Mit207	13	8.688726	16526195	9.63635	6.22885	0	2.63E-11	0	0	Shared
Dctn1	695797	6	83140488	RS30909511	6	57.9854	83140362	1.12735	0.91742	0	2.64E-11	0	0	Shared
Ece1	592081	4	137512379	D4Mit203	4	89.73231	1.29E+08	1.37669	1.11831	0	2.73E-11	0	0	Shared
unassigned	219862	13	113721021	D13MIT53	13	72.69389	1.13E+08	1.38533	1.0698	0	2.76E-11	0	0	Shared
unassigned	148368	11	70775198	D11MIT320	11	39.87138	70766870	0.1375	0.07059	0	2.81E-11	0	0	Shared
Tdrd3	256896	14	87905782	D14MIT263	14	64.79535	89360701	0.79767	0.65811	0	2.89E-11	0	0	CB
Soat1	55261	1	158388096	D1Mit102	1	80.03925	1.49E+08	0.2137	0.12239	0	2.92E-11	0	0	Shared
unassigned	462217	2	103921273	D2MIT100	2	54.19426	1.06E+08	0.71724	0.46515	0	3.01E-11	0	0	CB
Sidt1	342914	16	44262149	D16MIT185	16	54.3944	60434381	1.58804	1.33576	0	3.10E-11	0	0	CB
Gm14288	513504	2	176712426	D2MIT113	2	164.0409	1.73E+08	19.2527	24.25896	0	3.12E-11	0	0	Shared
Trmt6	504267	2	132635833	RS27267095	2	129.5613	1.37E+08	0.32536	0.55267	0	3.28E-11	0	0	Shared
unassigned	582362	4	98104182	D4Mit166	4	66.23295	93616234	0.99146	0.76065	0	3.35E-11	0	0	CB
Hydin	806312	8	113065696	D8MIT215	8	87.84173	1.18E+08	1.12696	1.82046	0	3.45E-11	0	0	CB
Phldb1	863979	9	44534109	D9MIT247	9	25.36975	36940492	0.70697	0.94235	0	3.47E-11	0	0	Shared
C2	375764	17	35001010	D17MIT51	17	53.34361	43641790	1.13814	1.59347	0	3.52E-11	0	0	CB
Zfp239	702492	6	117813095	d6mit366	6	77.49561	1.15E+08	0.82623	0.59518	0	3.61E-11	0	0	Shared
Pclo	628664	5	14770297	D5MIT123	5	4.1	6556176	1.7545	1.5086	0	3.67E-11	0	0	CB
Galntl2	247409	14	32853543	14.027.409	14	32.01969	29395320	1.97477	1.56507	0	3.90E-11	0	0	CB
unassigned	735168	7	25058334	07.013.915	7	8.7	15600169	6.42194	5.00673	0	3.94E-11	0	0	CB
Aldh4a1	592746	4	139205042	04.133.005	4	97.64222	1.33E+08	0.68769	0.99632	0	4.56E-11	0	0	Shared
unassigned	806314	8	113075097	D8MIT215	8	87.84173	1.18E+08	0.75472	1.71437	0	4.72E-11	0	0	CB
unassigned	167097	12	33652322	D12MIT60	12	21.02542	35474805	1.17552	1.38612	0	4.77E-11	0	0	Shared
Npsr1	835916	9	24104847	09.014.560	9	12.99047	14614051	0.77112	1.22662	0	4.93E-11	0	0	CB
unassigned	358724	17	35534330	17.034.150	17	51.1372	34678889	4.22769	3.09897	0	5.27E-11	0	0	Shared
Supt16h	269183	14	52802746	D14Mit183	14	42.79497	52629891	0.44269	0.59738	0	5.48E-11	0	0	Shared
Pde1c	717037	6	56092131	d6mit123	6	39.56321	56801586	5.16871	3.2305	0	5.83E-11	0	0	CB
unassigned	251099	14	55642237	D14Mit183	14	42.79497	52629891	0.03456	0.0605	0	6.43E-11	0	0	CB
Mdm4	51181	1	134905714	D1Mit102	1	80.03925	1.49E+08	0.0919	0.05298	0	6.52E-11	0	0	Shared
unassigned	486988	2	42508058	D2MIT296	2	21.50213	31180075	1.08549	1.47354	0	6.69E-11	0	0	CB
2810002N01Rik	180917	12	112962572	D12MIT7	12	66.69663	1.05E+08	1.42113	1.02964	0	6.84E-11	0	0	CB
Cyp2d10	312843	15	82234629	D15Mit107	15	49.40097	84216927	10.78645	16.47678	0	6.88E-11	0	0	CB

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
1110059E24Rik	435348	19	21672742	D19MIT96	19	21.38792	21916083	1.47733	1.85192	0	7.11E-11	0	0	Shared
unassigned	863830	9	44163015	D9MIT285	9	25.81754	40462577	0.88871	1.02108	0	7.37E-11	0	0	Shared
Spon1	751498	7	121183600	RS32210051	7	61.08266	99669474	0.83286	1.01264	0	7.58E-11	0	0	CB
Fmn2	27306	1	176625733	01.183.109	1	96.11848	1.83E+08	1.42207	1.20723	0	7.72E-11	0	0	CB
Ercc2	734928	7	19975598	07.013.915	7	8.7	15600169	1.00955	1.30086	0	7.84E-11	0	0	CB
Akap9	627332	5	3976133	D5MIT123	5	4.1	6556176	2.05688	2.47417	0	8.28E-11	0	0	CB
unassigned	367296	17	84175111	D17MIT76	17	95.2661	86033231	0.80523	0.91431	0	8.28E-11	0	0	Shared
unassigned	810598	8	3613957	08.010.585	8	4.520052	10585028	0.63649	0.71841	0	8.29E-11	0	0	CB
Arntl2	708003	6	146761756	D6Mit14	6	101.6085	1.46E+08	3.96458	3.08312	0	8.52E-11	0	0	Shared
Cyfip1	741385	7	63150354	D7Mit232	7	35.20811	59868792	1.00231	0.83911	0	8.55E-11	0	0	CB
unassigned	262359	14	14952399	14.008.937	14	5.6	10975728	1.19827	0.97192	0	8.59E-11	0	0	CB
unassigned	285907	15	32947010	15.028.723	15	14.88113	28708166	0.06686	0.13775	0	8.90E-11	0	0	Shared
Tada3l	725760	6	113325843	d6mit366	6	77.49561	1.15E+08	3.01138	2.51241	0	8.97E-11	0	0	Shared
Sacm1l	856987	9	123491426	D9MIT151	9	100.1162	1.21E+08	0.49216	0.40688	0	9.41E-11	0	0	Shared
unassigned	562274	3	126684689	D3MIT315	3	89.68246	1.16E+08	0.85099	1.03244	0	9.89E-11	0	0	Shared
Gm13152	594120	4	146884878	D4MIT232	4	109.1183	1.45E+08	11.2654	15.17	0	1.00E-10	0	0	CB
Rnf146	90512	10	29066645	RS36274062	10	31.86503	31045127	1.91263	2.09493	0	1.06E-10	0	0	CB
Pak3	916971	X	140167695	DXMit216	X	58.90613	1.4E+08	0.82473	0.96175	1.1308	1.13E-10	0	0	Shared
Stx12	618383	4	132424107	D4Mit203	4	89.73231	1.29E+08	0.80805	0.66006	0	1.14E-10	0	0	Shared
Ube2e2	262921	14	19406830	14.008.937	14	5.6	10975728	0.38305	0.48658	0	1.14E-10	0	0	CB
Skiv2l2	240767	13	113697200	d13mit151	13	74.51442	1.16E+08	0.85177	0.56911	0	1.17E-10	0	0	Shared
Oca2	741562	7	63539961	D7Mit232	7	35.20811	59868792	0.39543	0.89105	0	1.29E-10	0	0	CB
Gm5665	231895	13	62807064	D13MIT250	13	36.46819	56424004	1.66879	1.0903	0	1.31E-10	0	0	Shared
Soat1	55244	1	158360465	D1Mit102	1	80.03925	1.49E+08	0.69466	0.88177	0	1.33E-10	0	0	Shared
unassigned	86491	10	7359981	RS38343005	10	4.536629	11465792	1.66822	1.46264	0	1.33E-10	0	0	CB
Lamc1	54407	1	155087455	D1Mit102	1	80.03925	1.49E+08	0.43787	0.64846	0	1.46E-10	0	0	Shared
unassigned	254228	14	70534696	D14MIT39	14	54.52991	69166099	0.82108	1.14505	0	1.47E-10	0	0	Shared
Pus7	657725	5	23268230	D5MIT294	5	15.58331	20863135	0.17847	0.2986	0	1.51E-10	0	0	CB
unassigned	171152	12	62951485	D12MIT285	12	30.22146	55750112	0.73343	1.02149	0	1.52E-10	0	0	CB
Ppp5c	759922	7	17613047	07.013.915	7	8.7	15600169	0.26622	0.32537	0	1.61E-10	0	0	Shared
Larp7	562436	3	127249488	RS30160288	3	119.3825	1.26E+08	0.15427	0.12224	0	1.63E-10	0	0	Shared
Sik2	865534	9	50704772	09.046.588	9	34.49446	46645088	0.47779	0.68163	0	1.73E-10	0	0	Shared
unassigned	440768	19	46626029	D19MIT88	19	44.41135	37331405	0.86657	0.66757	0	1.77E-10	0	0	Shared
unassigned	121283	11	70787647	D11MIT320	11	39.87138	70766870	0.58933	0.47942	0	1.79E-10	0	0	CB
unassigned	34626	1	24514978	D1MIT169	1	18.85175	24071806	2.31049	1.45853	0	1.84E-10	0	0	CB
unassigned	594520	4	147954357	D4MIT232	4	109.1183	1.45E+08	0.11843	0.17899	0	1.89E-10	0	0	Shared
unassigned	156257	11	100956700	11.104.430	11	62.15042	1.04E+08	1.52399	1.1851	0	1.91E-10	0	0	Shared
Rpl13a	765281	7	52381937	D7MIT228	7	28.11811	47279833	0.94687	1.08144	0	1.98E-10	0	0	Shared
Rps14	397531	18	60938103	D18MIT152	18	47.63475	62096421	0.29154	0.39344	0	1.99E-10	0	0	CB
Pias3	531793	3	96504153	03.106.773	3	82.33049	1.06E+08	0.16285	0.28059	0	2.04E-10	0	0	Shared
unassigned	808961	8	125626630	D8MIT42	8	102.8893	1.29E+08	0.70349	0.8958	0	2.11E-10	0	0	CB
Svep1	605001	4	58085551	04.053.650	4	40.48019	53641772	0.41303	0.56609	0	2.15E-10	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Alg1	319314	16	5241408	D16Mit131	16	4.5	7319135	0.91189	0.75174	0	2.16E-10	0	0	Shared
Gfap	157079	11	102748866	11.104.430	11	62.15042	1.04E+08	1.31936	1.66447	0	2.20E-10	0	0	CB
Pkig	474986	2	163551198	02.168.990	2	151.4053	1.69E+08	0.49176	0.64215	0	2.23E-10	0	0	CB
unassigned	787388	8	3636127	08.010.585	8	4.520052	10585028	0.44757	0.56731	0	2.23E-10	0	0	CB
unassigned	190391	12	66169963	12.065.348	12	37.44045	65530382	2.29941	1.84916	0	2.24E-10	0	0	CB
Lasp1	128206	11	97677036	D11MIT289	11	59.90287	94741466	2.57591	2.17035	0	2.25E-10	0	0	Shared
2210418O10Rik	513495	2	176687483	D2MIT148	2	167.7799	1.79E+08	1.51128	1.17653	0	2.27E-10	0	0	Shared
unassigned	734923	7	19972243	07.013.915	7	8.7	15600169	0.7819	0.87579	0	2.29E-10	0	0	CB
Nipal2	303747	15	34554734	15.046.034	15	20.5546	46035472	0.33957	0.19182	0	2.37E-10	0	0	CB
Zfp109	760462	7	25019398	07.013.915	7	8.7	15600169	9.10332	7.13592	0	2.57E-10	0	0	Shared
Psmc3ip	156253	11	100954239	11.104.430	11	62.15042	1.04E+08	0.77719	1.25964	0	2.62E-10	0	0	Shared
Amacr	283070	15	10924705	15.010.846	15	8.803289	10831030	0.6155	0.80753	0	2.64E-10	0	0	Shared
Eef1a1	871803	9	78328468	D9MIT24	9	73.18313	1.03E+08	0.48667	0.37971	0	2.65E-10	0	0	Shared
unassigned	69269	10	40351609	D10MIT184	10	40.05957	42088505	6.11305	4.81106	0	2.80E-10	0	0	CB
Efcab2	27990	1	180411470	D1MIT507	1	89.46999	1.67E+08	1.45251	1.88994	0	2.97E-10	0	0	Shared
Pik3c2a	777686	7	123561523	RS36353338	7	66.26522	1.13E+08	0.52261	0.67316	0	3.11E-10	0	0	CB
Bmpr1a	266536	14	35273696	14.027.409	14	32.01969	29395320	0.99491	0.81028	0	3.15E-10	0	0	Shared
Twf1	315779	15	94416927	D15MIT44	15	76.94503	98951714	0.4557	0.59488	0	3.21E-10	0	0	Shared
Ust	86697	10	8049877	rs13480474	10	1.8	4403267	1.88613	1.50331	0	3.25E-10	0	0	CB
Pcdhga4	393337	18	37844872	D18Mit123	18	38.31055	56130259	1.87719	1.46042	0	3.28E-10	0	0	Shared
unassigned	141630	11	43236216	11.041.143	11	25.39412	41113079	0.44719	0.88324	0	3.34E-10	0	0	CB
Scoc	823279	8	85961110	D8MIT45	8	58.44006	89829274	0.69562	0.51053	0	3.40E-10	0	0	Shared
Ssfa2	458868	2	79502467	D2MIT75	2	46.41465	80424883	0.55709	0.7781	0	3.40E-10	0	0	Shared
Dst	3661	1	34211384	D1Mit374	1	27.02859	34816928	1.76115	1.42793	0	3.50E-10	0	0	Shared
Fkbp9	692579	6	56801357	d6mit123	6	39.56321	56801586	0.87235	1.08247	0	3.66E-10	0	0	Shared
Fam19a5	295696	15	87587772	D15Mit107	15	49.40097	84216927	0.94138	1.04933	0	3.69E-10	0	0	CB
Notch2	532092	3	97921128	03.106.773	3	82.33049	1.06E+08	1.20959	0.97853	0	3.88E-10	0	0	Shared
Herc2	741461	7	63376940	07.056.455	7	36.40088	63842351	0.70158	0.83999	0	3.92E-10	0	0	Shared
unassigned	604597	4	56771213	D4MIT164	4	42.38961	59415112	0.62581	0.83263	0	4.22E-10	0	0	Shared
Snx7	560865	3	117535907	D3MIT315	3	89.68246	1.16E+08	0.27507	0.17547	0	4.24E-10	0	0	Shared
Med20	360923	17	47756084	D17MIT180	17	63.0586	51571276	0.68847	0.46439	0	4.26E-10	0	0	CB
Pkd2	643814	5	104895923	D5MIT239	5	66.11023	1.08E+08	1.64719	1.27539	0	4.28E-10	0	0	Shared
BC037034	679279	5	138704114	05.132.979	5	112.2658	1.33E+08	1.29834	1.09378	0	4.39E-10	0	0	Shared
A2m	703295	6	121592009	D6MIT328	6	75.24789	1.13E+08	1.17192	0.81767	0	4.45E-10	0	0	CB
H2-T10	376254	17	36258239	17.034.150	17	51.1372	34678889	1.07137	0.79622	0	4.54E-10	0	0	CB
Syne1	63591	10	5007205	rs13480474	10	1.8	4403267	0.8227	0.7161	0	4.57E-10	0	0	CB
Abcc9	731677	6	142641334	D6MIT194	6	87.57626	1.28E+08	1.82691	1.3642	0	4.81E-10	0	0	Shared
Mysm1	610147	4	94635694	D4Mit166	4	66.23295	93616234	0.43247	0.61063	0	4.83E-10	0	0	CB
unassigned	864014	9	44603820	D9MIT247	9	25.36975	36940492	1.42401	1.25452	0	5.20E-10	0	0	Shared
unassigned	749893	7	112705838	07.088.976	7	61.08266	96249318	1.00305	0.85549	0	5.25E-10	0	0	Shared
unassigned	324781	16	31829459	D16MIT60	16	28.75614	32704177	0.88543	1.03789	0	5.36E-10	0	0	Shared
Gsr	792626	8	34791965	D8MIT94	8	19.42422	32452130	0.48956	0.61277	0	5.41E-10	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	113216	11	32512823	D11MIT51	11	25.39412	36205252	0.37972	0.27376	0	5.73E-10	0	0	CB
Dgkz	495766	2	91781136	D2MIT75	2	46.41465	80424883	1.57136	1.38645	0	5.78E-10	0	0	CB
unassigned	409645	18	42403316	D18MIT202	18	28.05292	43551589	2.03301	1.65983	0	5.80E-10	0	0	Shared
2010005J08Rik	135463	11	5622442	D11MIT2	11	7.6	12218640	3.72244	2.83999	0	6.01E-10	0	0	Shared
unassigned	468067	2	132122912	RS27267095	2	129.5613	1.37E+08	0.5437	0.6625	0	6.05E-10	0	0	CB
unassigned	833257	9	6168431	D9MIT250	9	5.2	8393623	0.98869	1.27043	0	6.11E-10	0	0	Shared
unassigned	232098	13	63615658	13.061.624	13	39.87979	61715738	1.03166	1.18992	0	6.20E-10	0	0	CB
Gm13152	594122	4	146887640	D4MIT232	4	109.1183	1.45E+08	0.92165	1.12343	0	6.28E-10	0	0	Shared
unassigned	562260	3	126665356	RS30160288	3	119.3825	1.26E+08	1.39148	1.18722	0	6.46E-10	0	0	CB
Gpr180	259873	14	118559260	14.095.016	14	67.37082	96532085	0.79597	1.01582	0	6.72E-10	0	0	Shared
Dst	3747	1	34317012	D1Mit374	1	27.02859	34816928	0.7492	0.95892	0	6.73E-10	0	0	Shared
Igf1r	743190	7	75340056	D7MIT248	7	39.99047	80656343	0.97937	0.84025	0	7.06E-10	0	0	Shared
Bcat1	732273	6	144956244	D6MIT194	6	87.57626	1.28E+08	0.41016	0.34602	0	7.53E-10	0	0	Shared
Tbc1d9	800326	8	85782896	D8MIT45	8	58.44006	89829274	2.28145	2.0107	0	7.74E-10	0	0	Shared
Clstn1	594819	4	149017703	D4MIT232	4	109.1183	1.45E+08	0.70706	0.8692	0	7.96E-10	0	0	Shared
Cntnap2	690188	6	45870805	D6MIT274	6	30.88472	48676564	1.31907	1.06437	0	8.50E-10	0	0	Shared
Paip1	220864	13	120246129	D13MIT78	13	76.84217	1.2E+08	1.05501	0.90264	0	8.72E-10	0	0	Shared
Myo1e	845766	9	70224336	D9MIT107	9	53.50038	73315075	0.13661	0.19508	0	8.73E-10	0	0	Shared
AI314180	605138	4	58822331	04.053.650	4	40.48019	53641772	0.74886	0.63868	0	8.78E-10	0	0	CB
Agap3	630212	5	23982476	D5MIT348	5	18.20559	24424937	1.03814	1.4229	0	8.80E-10	0	0	Shared
Slco1a4	731428	6	141758971	D6Mit14	6	101.6085	1.46E+08	1.11323	0.77339	0	8.95E-10	0	0	CB
Rps11	765272	7	52378220	D7MIT228	7	28.11811	47279833	0.64009	0.53366	0	9.27E-10	0	0	Shared
Arhgap5	169678	12	53660990	D12MIT285	12	30.22146	55750112	0.89789	1.27922	0	1.01E-09	0	0	Shared
Stip1	432707	19	7103158	19.000.325	19	0.2	325000	0.62693	0.43651	0	1.01E-09	0	0	Shared
Ank2	562245	3	126639540	RS30160288	3	119.3825	1.26E+08	0.44366	0.56438	0	1.04E-09	0	0	Shared
Bpnt1	29411	1	187177853	01.183.109	1	96.11848	1.83E+08	0.38928	0.27437	0	1.08E-09	0	0	Shared
Degs1	60652	1	184209788	01.183.109	1	96.11848	1.83E+08	0.99172	0.77835	0	1.10E-09	0	0	Shared
Syne2	173463	12	77188751	D12MIT91	12	43.26798	72843829	0.34012	0.47689	0	1.12E-09	0	0	Shared
unassigned	831507	8	126441285	D8MIT42	8	102.8893	1.29E+08	0.93967	0.74645	0	1.13E-09	0	0	CB
unassigned	262855	14	19102221	14.008.937	14	5.6	10975728	2.32787	2.07674	0	1.16E-09	0	0	Shared
unassigned	433762	19	11851079	19.009.231	19	7.749799	9238445	1.85075	1.32832	0	1.22E-09	0	0	Shared
Tmem179	199424	12	113741463	D12MIT7	12	66.69663	1.05E+08	1.06576	0.80242	0	1.27E-09	0	0	Shared
unassigned	602848	4	46133203	d4mit238	4	33.23278	45243003	0.59827	0.78842	0	1.27E-09	0	0	Shared
Prrg2	765229	7	52315342	D7MIT228	7	28.11811	47279833	0.40201	0.64135	0	1.28E-09	0	0	CB
unassigned	607123	4	71802352	rs13477756	4	50.52425	68030949	0.73018	0.96924	0	1.29E-09	0	0	Shared
Hps5	765983	7	54016777	D7MIT228	7	28.11811	47279833	1.106	0.83705	0	1.32E-09	0	0	CB
C230096C10Rik	592583	4	138933208	D4MIT170	4	99.94085	1.38E+08	0.76686	0.97386	0	1.37E-09	0	0	CB
Pam	47051	1	99718478	01.136.071	1	77.74879	1.36E+08	0.3621	0.44942	0	1.45E-09	0	0	Shared
Nup85	132719	11	115445138	D11MIT214	11	79.65651	1.15E+08	0.07848	0.13654	0	1.47E-09	0	0	CB
4932438A13Rik	522104	3	36928844	03.033.871	3	22.08075	33578373	0.17987	0.2607	0	1.51E-09	0	0	Shared
unassigned	880618	9	123549341	D9MIT151	9	100.1162	1.21E+08	0.94381	1.16623	0	1.51E-09	0	0	CB
unassigned	787377	8	3630834	08.010.585	8	4.520052	10585028	1.84731	1.40231	0	1.52E-09	0	0	CB

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Tmem117	297223	15	94709813	15.090.122	15	63.15586	90124664	1.53769	1.27649	0	1.54E-09	0	0	CB
Gnas	477431	2	174171508	D2MIT148	2	167.7799	1.79E+08	16.63809	19.3879	0	1.55E-09	0	0	CB
Heatr1	202750	13	12514330	D13Mit207	13	8.688726	16526195	0.22283	0.30798	0	1.56E-09	0	0	Shared
Calm3	759883	7	17502179	07.013.915	7	8.7	15600169	1.09631	1.00898	0	1.58E-09	0	0	Shared
Rps28	375345	17	33960181	17.034.150	17	51.1372	34678889	0.70273	0.81812	0	1.59E-09	0	0	Shared
Strap	706340	6	137699099	D6MIT194	6	87.57626	1.28E+08	1.11082	1.30634	0	1.61E-09	0	0	Shared
Cacna1b	482605	2	24504011	D2MIT81	2	18.06443	24644623	0.90553	0.62838	0	1.63E-09	0	0	CB
unassigned	594742	4	148859232	D4MIT232	4	109.1183	1.45E+08	1.32697	1.09287	0	1.68E-09	0	0	Shared
Tbc1d17	765041	7	52100446	D7MIT228	7	28.11811	47279833	0.67387	0.81444	0	1.70E-09	0	0	CB
unassigned	840036	9	45734656	09.046.588	9	34.49446	46645088	0.54335	0.7477	0	1.71E-09	0	0	Shared
unassigned	358706	17	35517183	17.034.150	17	51.1372	34678889	0.30742	0.39877	0	1.72E-09	0	0	CB
Cdc5l	377498	17	45545311	D17MIT180	17	63.0586	51571276	2.07651	1.20679	0	1.76E-09	0	0	Shared
Atpbd4	499475	2	114347405	D2MIT100	2	54.19426	1.06E+08	0.81527	0.63938	0	1.78E-09	0	0	Shared
unassigned	678149	5	134762698	05.132.979	5	112.2658	1.33E+08	1.21895	0.94701	0	1.79E-09	0	0	Shared
Ank	284949	15	27521196	15.046.034	15	20.5546	46035472	0.33629	0.27615	0	1.81E-09	0	0	CB
Abcc12	824107	8	89041225	D8MIT45	8	58.44006	89829274	1.75319	2.46266	0	1.84E-09	0	0	CB
Slc7a8	269591	14	55348184	D14Mit183	14	42.79497	52629891	0.67718	0.94489	0	1.85E-09	0	0	Shared
Ust	86674	10	7967931	rs13480474	10	1.8	4403267	0.70032	0.81631	0	1.86E-09	0	0	CB
4833420G17Rik	220873	13	120255682	D13MIT78	13	76.84217	1.2E+08	1.18537	1.53727	0	1.94E-09	0	0	Shared
Akap9	627331	5	3975612	D5MIT388	5	29.38073	33660748	1.93539	2.27397	0	1.96E-09	0	0	CB
Slit2	634979	5	48379084	05.038.809	5	37.9822	38911990	1.17351	0.80309	0	2.01E-09	0	0	CB
Fam45a	430885	19	60890817	D19MIT103	19	59.41115	53838656	1.34398	1.13134	0	2.05E-09	0	0	Shared
unassigned	646396	5	115740829	d5mit158	5	69.85959	1.15E+08	1.11141	1.25967	0	2.10E-09	0	0	Shared
1110037F02Rik	570465	4	11469257	04.013.290	4	8.3	13290000	2.82612	2.45286	0	2.12E-09	0	0	CB
Nnt	241801	13	120193365	D13MIT53	13	72.69389	1.13E+08	0.46272	0.5628	0	2.17E-09	0	0	CB
unassigned	765191	7	52268669	D7MIT228	7	28.11811	47279833	0.29075	0.42217	0	2.17E-09	0	0	Shared
Tmem18	166585	12	31275393	D12MIT60	12	21.02542	35474805	0.86536	0.97478	0	2.25E-09	0	0	Shared
Aph1b	869366	9	66670054	D9MIT107	9	53.50038	73315075	3.22235	2.80364	0	2.31E-09	0	0	Shared
Wdr17	818993	8	55775543	D8MIT68	8	37.44853	59469763	1.18	1.00412	0	2.36E-09	0	0	Shared
Gsr	792635	8	34807822	D8Mit191	8	23.02066	36243839	0.89118	1.10318	0	2.44E-09	0	0	Shared
Gtf2h3	649118	5	125034163	D5MIT95	5	98.81753	1.25E+08	1.0106	1.31869	0	2.46E-09	0	0	Shared
Pi4k2a	426757	19	42175154	D19MIT46	19	37.54307	33009697	0.4135	0.32316	0	2.47E-09	0	0	Shared
Zfp790	736871	7	30608011	D7MIT267	7	18.29809	30331965	1.02243	1.17204	0	2.59E-09	0	0	CB
unassigned	715766	6	50272811	d6mit123	6	39.56321	56801586	0.37662	0.50109	0	2.60E-09	0	0	Shared
unassigned	870300	9	71489091	D9MIT107	9	53.50038	73315075	0.38629	0.50399	0	2.65E-09	0	0	Shared
Pttg1	141634	11	43239103	D11MIT51	11	25.39412	36205252	0.87007	0.61011	0	2.67E-09	0	0	Shared
unassigned	260011	14	119357215	14.095.016	14	67.37082	96532085	0.93514	1.24558	0	2.72E-09	0	0	Shared
unassigned	63848	10	5917528	RS29316898	10	9.384466	15819840	0.52216	0.68887	0	2.75E-09	0	0	Shared
unassigned	112448	11	29096572	RS26845852	11	16.78021	24370394	1.31085	1.04512	0	2.83E-09	0	0	CB
Vipr2	181623	12	117331118	D12MIT7	12	66.69663	1.05E+08	1.37259	1.05644	0	2.84E-09	0	0	CB
Ppp1r14a	736721	7	30078209	07.017.531	7	12.92437	18957827	0.7153	0.61155	0	2.88E-09	0	0	CB
Arg1	89833	10	24636589	RS13480581	10	35.95662	38685357	0.39948	0.63265	0	2.91E-09	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Cyp4f14	375105	17	33048387	17.034.150	17	51.1372	34678889	1.72213	1.28572	0	2.96E-09	0	0	CB
unassigned	741494	7	63419348	D7Mit232	7	35.20811	59868792	0.60384	0.74485	0	3.24E-09	0	0	Shared
Zfp94	760491	7	25088809	07.013.915	7	8.7	15600169	0.61774	0.78037	0	3.28E-09	0	0	Shared
unassigned	256891	14	87885889	14.095.016	14	67.37082	96532085	2.21668	1.90834	0	3.37E-09	0	0	Shared
Aaas	318184	15	102170195	D15MIT15	15	83.15474	1.03E+08	0.67354	0.54803	0	3.50E-09	0	0	CB
unassigned	409134	18	39078374	18.038.678	18	24.45192	38711680	0.19572	0.27999	0	3.53E-09	0	0	CB
Trim3	775382	7	112761446	RS36353338	7	66.26522	1.13E+08	0.98737	1.09433	0	3.75E-09	0	0	Shared
Tesk2	586638	4	116474836	RS27499066	4	79.43714	1.15E+08	1.51388	1.15888	0	3.76E-09	0	0	CB
Herc2	741457	7	63368415	07.017.531	7	12.92437	18957827	0.73705	0.90296	0	3.79E-09	0	0	Shared
Ptprg	243384	14	13053106	14.008.937	14	5.6	10975728	1.0636	1.39139	0	3.90E-09	0	0	Shared
unassigned	274726	14	76130283	D14Mit194	14	66.46956	94235479	2.96005	3.58284	0	3.92E-09	0	0	Shared
Usp48	591925	4	137163991	D4MIT170	4	99.94085	1.38E+08	1.3007	1.15562	0	3.93E-09	0	0	CB
unassigned	741351	7	63084523	D7Mit232	7	35.20811	59868792	0.13071	0.1924	0	3.93E-09	0	0	CB
Rpl31	4795	1	39428239	D1MIT236	1	37.41892	45435458	0.13197	0.19215	0	3.96E-09	0	0	CB
Mcam	839481	9	43945317	09.046.588	9	34.49446	46645088	0.66023	0.91194	0	4.03E-09	0	0	Shared
Cd59b	462211	2	103911179	D2MIT100	2	54.19426	1.06E+08	0.10136	0.06561	0	4.15E-09	0	0	Shared
Stxbp4	153228	11	90396804	D11MIT289	11	59.90287	94741466	1.43111	1.73456	0	4.16E-09	0	0	CB
H2-K1	375403	17	34136863	D17MIT51	17	53.34361	43641790	1.36504	0.97851	0	4.22E-09	0	0	Shared
AI314180	605167	4	58855449	D4MIT164	4	42.38961	59415112	1.04691	0.84019	0	4.25E-09	0	0	Shared
unassigned	497697	2	104271232	RS27416022	2	74.76293	93628229	1.83796	1.60736	0	4.36E-09	0	0	Shared
unassigned	740327	7	56072045	D7Mit232	7	35.20811	59868792	1.0141	1.18133	0	4.40E-09	0	0	Shared
unassigned	630766	5	28035954	05.018.430	5	14.15919	18423994	0.44858	0.54394	0	4.41E-09	0	0	CB
Pbrm1	247165	14	31867368	14.027.409	14	32.01969	29395320	0.34054	0.43392	0	4.42E-09	0	0	Shared
unassigned	740905	7	58876878	07.056.455	7	36.40088	63842351	0.20031	0.24704	0	4.49E-09	0.0005	0.041856	CB
Akap9	627358	5	4039240	D5MIT123	5	4.1	6556176	1.14707	0.84992	0	4.50E-09	0	0	Shared
Plcb3	432622	19	7039798	19.000.325	19	0.2	325000	2.53036	1.98617	0	4.50E-09	0	0	Shared
Pqlc2	620160	4	138862375	04.133.005	4	97.64222	1.33E+08	1.12052	0.94106	0	4.67E-09	0	0	CB
Plxnb2	314568	15	88992416	15.090.122	15	63.15586	90124664	0.5254	0.67778	0	4.74E-09	0	0	CB
unassigned	250954	14	55095333	14.042.462	14	41.89415	44159798	1.70853	1.40458	0	4.86E-09	0	0	CB
Sergef	765878	7	53771038	D7Mit232	7	35.20811	59868792	2.23954	2.69621	0	5.04E-09	0	0	Shared
unassigned	856984	9	123486180	D9Mit18	9	96.97845	1.2E+08	1.62581	1.42491	0	5.19E-09	0	0	CB
H2-Q2	358666	17	35482399	D17MIT51	17	53.34361	43641790	0.02099	0.01476	0	5.24E-09	0	0	CB
Stat2	85210	10	127721166	D10Mit14	10	93.10254	1.18E+08	0.66116	0.84269	0	5.26E-09	0	0	Shared
Zfp385c	156035	11	100490889	11.104.430	11	62.15042	1.04E+08	1.04496	1.40235	0	5.43E-09	0	0	CB
unassigned	643541	5	104011797	D5MIT239	5	66.11023	1.08E+08	0.60512	0.8874	0	5.57E-09	0	0	Shared
Zdhhc13	740320	7	56059724	D7MIT248	7	39.99047	80656343	0.48825	0.58852	0	5.72E-09	0	0	Shared
unassigned	865451	9	50490342	D9MIT247	9	25.36975	36940492	0.68482	0.80963	0	5.77E-09	0	0	Shared
unassigned	114671	11	43249397	11.041.143	11	25.39412	41113079	0.96245	1.20903	0	5.80E-09	0	0	Shared
unassigned	736841	7	30556312	07.017.531	7	12.92437	18957827	1.22547	1.52271	0	5.89E-09	0	0	CB
1700029I01Rik	594082	4	146550940	D4MIT232	4	109.1183	1.45E+08	4.81409	4.10327	0	6.14E-09	0	0	Shared
unassigned	367896	17	86887648	D17MIT76	17	95.2661	86033231	1.27815	1.44388	0	6.30E-09	0	0	Shared
Med13l	647293	5	119181363	D5MIT95	5	98.81753	1.25E+08	0.51541	0.64615	0	6.41E-09	0	0	CB

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	320444	16	11631681	16.010.089	16	7.349459	10175515	1.00922	1.25401	0	6.51E-09	0	0	CB
Med23	67109	10	24629609	RS29351336	10	22.94397	24605158	0.7944	1.10724	0	6.71E-09	0	0	Shared
Commd2	550399	3	57450637	03.060.525	3	40.51916	60240993	0.65199	0.47968	0	6.92E-09	0	0	Shared
Dtd1	470028	2	144442977	D2MIT285	2	110.6372	1.53E+08	2.00101	2.43216	0	7.26E-09	0	0	Shared
Gabra5	767267	7	64763435	D7Mit232	7	35.20811	59868792	0.5202	0.346	0	7.53E-09	0	0	CB
Gdi1	910345	X	71552184	DXMIT68	X	20.02251	50676500	0.45831	0.41424	0.30501	7.67E-09	0	0	Shared
Stx2	677108	5	129493661	D5MIT95	5	98.81753	1.25E+08	0.99242	0.80373	0	7.83E-09	0	0	Shared
Lamc1	54421	1	155102355	01.136.071	1	77.74879	1.36E+08	0.84699	0.6991	0	7.96E-09	0	0	Shared
Echdc1	67891	10	29051632	RS37076985	10	29.16132	28876470	0.96397	1.22058	0	8.06E-09	0	0	Shared
Speer4b	658555	5	27824498	05.018.430	5	14.15919	18423994	0.33473	0.47542	0	8.10E-09	0	0	CB
Rab11fip3	373333	17	26127950	17.021.019	17	14.36839	21451267	0.95688	0.78603	0	8.27E-09	0	0	CB
unassigned	428304	19	47937973	D19MIT88	19	44.41135	37331405	1.29531	1.44056	0	8.39E-09	0	0	CB
Psmc3ip	156256	11	100956261	11.104.430	11	62.15042	1.04E+08	0.7041	1.0369	0	8.55E-09	0	0	CB
Trak1	856349	9	121340599	D9Mit18	9	96.97845	1.2E+08	2.53088	2.10299	0	8.66E-09	0	0	Shared
2210418O10Rik	513494	2	176681807	D2MIT148	2	167.7799	1.79E+08	0.72221	0.51778	0	8.89E-09	0	0	Shared
unassigned	630175	5	23876525	05.018.430	5	14.15919	18423994	0.71021	0.96402	0	9.35E-09	0	0	Shared
Wdr45l	162210	11	121188959	D11MIT214	11	79.65651	1.15E+08	0.56111	0.69361	0	9.44E-09	0	0	CB
Jmjd7	465180	2	119857856	RS27258455	2	126.7319	1.3E+08	0.56596	0.70972	0	9.56E-09	0	0	CB
unassigned	491930	2	71114948	D2MIT61	2	35.12792	60528325	0.44268	0.53363	0	9.56E-09	0	0	Shared
Heatr3	801576	8	90663797	D8MIT346	8	54.67316	85454038	1.74688	2.01137	0	9.68E-09	0	0	CB
unassigned	765283	7	52382980	D7MIT228	7	28.11811	47279833	1.31109	1.13914	0	9.74E-09	0	0	Shared
Rps3a	554315	3	85941922	D3MIT98	3	51.73848	85985423	0.61583	0.42758	0	9.80E-09	0	0	Shared
Lrrk2	296487	15	91564430	15.090.122	15	63.15586	90124664	1.42732	1.22123	0	1.00E-08	0	0	CB
Mrpl46	770533	7	85920100	D7MIT350	7	57.28732	90734599	0.80899	0.92966	0	1.01E-08	0	0	Shared
Stxbp2	787386	8	3635618	D8MIT155	8	3.1	4976602	0.45577	0.59337	0	1.03E-08	0	0	CB
Aagab	844000	9	63487400	D9MIT107	9	53.50038	73315075	0.63849	0.48863	0	1.05E-08	0	0	Shared
Ppp5c	759912	7	17592463	07.013.915	7	8.7	15600169	0.78729	0.95315	0	1.07E-08	0	0	Shared
unassigned	63563	10	4926162	rs13480474	10	1.8	4403267	1.16789	1.31139	0	1.07E-08	0	0	CB
Pigy	717222	6	57641927	d6mit123	6	39.56321	56801586	1.46963	1.24592	0	1.08E-08	0	0	CB
Prdx6	56229	1	163170634	01.136.071	1	77.74879	1.36E+08	0.1073	0.1552	0	1.08E-08	0	0	Shared
Trappc6b	190013	12	60145283	D12Mit2	12	26.67403	42747379	0.73657	0.64867	0	1.08E-08	0	0	CB
unassigned	354214	17	21162171	17.021.019	17	14.36839	21451267	1.1734	1.31328	0	1.08E-08	0	0	Shared
unassigned	102134	10	95012355	d10Mit96	10	80.83316	99019575	1.05418	0.85702	0	1.10E-08	0	0	Shared
Serinc3	510098	2	163450630	02.168.990	2	151.4053	1.69E+08	0.16368	0.25515	0	1.12E-08	0	0	Shared
Trpc3	547522	3	36561684	D3Mit151	3	18.63179	31137265	0.97308	0.78191	0	1.12E-08	0	0	CB
Slc4a8	298630	15	100621363	D15MIT15	15	83.15474	1.03E+08	1.08315	1.25983	0	1.14E-08	0	0	CB
unassigned	219732	13	113285582	d13mit151	13	74.51442	1.16E+08	1.43083	1.19972	0	1.14E-08	0	0	Shared
Lancl1	41409	1	67085080	rs13475894	1	45.46082	63625006	2.20699	2.74068	0	1.17E-08	0	0	Shared
Macrod1	419763	19	7272022	19.000.325	19	0.2	325000	1.05609	1.42219	0	1.18E-08	0	0	Shared
Mrps5	466871	2	127416436	D2Mit274	2	62.95823	1.14E+08	1.07776	0.76784	0	1.18E-08	0	0	Shared
Smek2	112444	11	29088313	11.041.143	11	25.39412	41113079	1.63944	1.45515	0	1.19E-08	0	0	CB
unassigned	358656	17	35403088	17.034.150	17	51.1372	34678889	2.6836	3.14692	0	1.20E-08	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Syt17	778023	7	125577420	07.122.234	7	82.95546	1.3E+08	0.68979	0.87229	0	1.23E-08	0	0	Shared
Ppp2r5e	192270	12	76594414	D12MIT91	12	43.26798	72843829	1.57279	1.32526	0	1.26E-08	0	0	Shared
Smap2	615672	4	120647977	RS27499066	4	79.43714	1.15E+08	0.59883	0.72997	0	1.26E-08	0	0	Shared
Dcun1d1	547278	3	35791949	03.033.871	3	22.08075	33578373	0.83894	0.62392	0	1.27E-08	0	0	Shared
Creb3	574639	4	43578349	d4mit238	4	33.23278	45243003	1.0998	0.94063	0	1.29E-08	0	0	Shared
Ece1	592082	4	137513050	D4MIT232	4	109.1183	1.45E+08	1.27648	1.49203	0	1.34E-08	0	0	Shared
Pnpla6	787336	8	3538213	D8MIT155	8	3.1	4976602	0.70661	0.84406	0	1.35E-08	0	0	Shared
Slc45a3	19667	1	133878076	RS50560599	1	67.50483	1.17E+08	1.02974	1.16084	0	1.39E-08	0	0	CB
R3hdm2	84796	10	126934219	D10Mit14	10	93.10254	1.18E+08	0.65265	0.52648	0	1.40E-08	0	0	CB
Tjp1	768212	7	72457221	07.056.455	7	36.40088	63842351	0.44414	0.70096	0	1.41E-08	0	0	Shared
Zfp426	859121	9	20276149	09.014.560	9	12.99047	14614051	0.86804	0.64218	0	1.43E-08	0	0	Shared
Galntl2	247420	14	32869471	14.027.409	14	32.01969	29395320	1.06183	0.83366	0	1.44E-08	0	0	CB
unassigned	806684	8	114477711	D8MIT215	8	87.84173	1.18E+08	0.03855	0.05837	0	1.44E-08	0	0	Shared
Utrn	87498	10	12410534	RS29347557	10	5.696346	12661713	1.35806	1.10802	0	1.49E-08	0	0	Shared
Aph1b	869344	9	66632338	D9MIT336	9	49.6331	65425671	2.33141	2.10409	0	1.50E-08	0	0	CB
Mrpl46	770536	7	85926295	D7MIT350	7	57.28732	90734599	1.9273	1.64945	0	1.51E-08	0	0	Shared
unassigned	737027	7	31097761	07.017.531	7	12.92437	18957827	2.25413	2.51082	0	1.55E-08	0	0	Shared
unassigned	739477	7	52255454	D7MIT228	7	28.11811	47279833	1.93681	2.4207	0	1.55E-08	0	0	Shared
Aldh4a1	592740	4	139200028	04.133.005	4	97.64222	1.33E+08	1.575	1.30747	0	1.58E-08	0	0	Shared
Hmgcs1	894205	13_random	116310	d13mit151	13	74.51442	1.16E+08	1.07486	1.2293	0	1.58E-08	0	0	Shared
Supt3h	360195	17	45175029	17.059.041	17	71.70333	59495092	0.8204	0.6452	0	1.60E-08	0	0	Shared
Pik3ca	521105	3	32341679	D3Mit151	3	18.63179	31137265	0.86334	0.74362	0	1.68E-08	0	0	CB
Cntn6	700084	6	104796084	D6MIT328	6	75.24789	1.13E+08	0.44969	0.55401	0	1.70E-08	0	0	CB
Xab2	810592	8	3610882	D8MIT155	8	3.1	4976602	1.50634	1.76138	0	1.70E-08	0	0	CB
Asb3	112889	11	31001049	D11MIT51	11	25.39412	36205252	1.08928	0.94107	0	1.72E-08	0	0	Shared
Txnl4a	401595	18	80415452	RS30267686	18	60.34946	81658329	0.02624	0.19645	0	1.76E-08	0	0	CB
unassigned	54163	1	154378758	D1Mit102	1	80.03925	1.49E+08	0.74976	0.90775	0	1.76E-08	0	0	Shared
Cluap1	318998	16	3929844	D16Mit131	16	4.5	7319135	0.92516	0.74833	0	1.83E-08	0	0	CB
Lrrfip2	854152	9	111043777	09.105.291	9	79.88305	1.05E+08	0.30255	0.40645	0	1.88E-08	0	0	CB
Iars2	61164	1	187151504	01.183.109	1	96.11848	1.83E+08	0.4739	0.69199	0	1.90E-08	0	0	Shared
Dctn6	815836	8	35153817	D8MIT94	8	19.42422	32452130	0.87048	1.02999	0	1.92E-08	0	0	Shared
H13	471809	2	152514364	D2MIT285	2	110.6372	1.53E+08	1.06619	1.443	0	1.95E-08	0	0	Shared
Zc3h15	459253	2	83502401	D2MIT75	2	46.41465	80424883	2.43712	1.90293	0	1.95E-08	0	0	Shared
Vps52	357882	17	34094794	17.034.150	17	51.1372	34678889	0.62286	0.83254	0	1.96E-08	0	0	Shared
unassigned	474972	2	163444750	02.168.990	2	151.4053	1.69E+08	0.86273	1.05515	0	1.99E-08	0	0	Shared
Cst3	506963	2	148700902	D2MIT285	2	110.6372	1.53E+08	0.99601	1.18365	0	2.01E-08	0	0	Shared
unassigned	504273	2	132641370	RS27267095	2	129.5613	1.37E+08	2.81598	2.29046	0	2.01E-08	0	0	CB
Limk1	678177	5	135137587	D5MIT95	5	98.81753	1.25E+08	0.62513	0.53348	0	2.04E-08	0	0	Shared
unassigned	812749	8	15900807	D8MIT94	8	19.42422	32452130	0.33238	0.51251	0	2.12E-08	0	0	Shared
3830406C13Rik	243436	14	13134119	14.008.937	14	5.6	10975728	1.90402	1.59767	0	2.15E-08	0	0	Shared
Noc3l	438750	19	38888596	D19MIT88	19	44.41135	37331405	1.06445	0.8213	0	2.19E-08	0	0	Shared
Ctnnbip1	594776	4	148920516	D4MIT232	4	109.1183	1.45E+08	2.1026	1.76149	0	2.20E-08	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Mios	683980	6	8172486	RS49937148	6	13.13583	22510745	1.49468	1.85729	0	2.29E-08	0	0	Shared
H2-t9	376264	17	36263614	17.034.150	17	51.1372	34678889	10.37886	8.51246	0	2.40E-08	0	0	CB
Dzip1	279643	14	119282599	RS31252045	14	77.8316	1.11E+08	0.34646	0.44363	0	2.41E-08	0	0	CB
Cacna1d	265411	14	30892541	14.008.937	14	5.6	10975728	1.32791	1.02347	0	2.44E-08	0	0	CB
2010321M09Rik	844325	9	64829849	D9MIT248	9	44.87553	58210366	0.72009	0.55763	0	2.47E-08	0	0	Shared
Kif1b	622630	4	148620454	D4MIT42	4	117.1013	1.51E+08	0.88285	0.69452	0	2.51E-08	0	0	Shared
Ncald	304369	15	37514219	15.028.723	15	14.88113	28708166	0.76087	0.92529	0	2.63E-08	0	0	CB
Flt3	681271	5	148146396	D5MIT95	5	98.81753	1.25E+08	0.53413	0.40066	0	2.65E-08	0	0	CB
unassigned	244677	14	21170720	14.008.937	14	5.6	10975728	1.01929	0.84259	0	2.69E-08	0	0	CB
Zfp748	232829	13	67646274	13.061.624	13	39.87979	61715738	0.34411	0.4636	0	2.70E-08	0	0	Shared
Kif21a	314992	15	90822148	15.090.122	15	63.15586	90124664	0.47273	0.39395	0	2.72E-08	0	0	Shared
2810408P10Rik	622112	4	147202550	D4MIT232	4	109.1183	1.45E+08	0.78416	0.95691	0	2.73E-08	0	0	CB
Ctnnal1	604666	4	56851843	04.053.650	4	40.48019	53641772	0.99208	1.17914	0	2.75E-08	0	0	Shared
Hydin	806337	8	113111568	D8MIT47	8	79.10975	1.09E+08	1.74534	2.68546	0	2.75E-08	0	0	CB
Imp4	3813	1	34501860	D1Mit374	1	27.02859	34816928	0.23574	0.34197	0	2.75E-08	0	0	Shared
Asb7	768482	7	73833753	D7MIT228	7	28.11811	47279833	0.91675	1.30972	0	2.77E-08	0	0	CB
unassigned	547715	3	37614076	03.033.871	3	22.08075	33578373	0.71153	0.8264	0	2.80E-08	0	0	CB
unassigned	761798	7	29766601	D7MIT267	7	18.29809	30331965	0.92647	0.84022	0	2.83E-08	0	0	Shared
Aebp2	706804	6	140595332	D6MIT194	6	87.57626	1.28E+08	4.34321	3.68032	0	2.86E-08	0	0	Shared
unassigned	393346	18	37869333	D18MIT202	18	28.05292	43551589	1.56675	1.34251	0	2.86E-08	0	0	CB
Ncstn	58619	1	174012732	01.183.109	1	96.11848	1.83E+08	0.2999	0.39411	0	2.93E-08	0	0	Shared
unassigned	538702	3	135185912	D3MIT57	3	88.53548	1.16E+08	1.81179	1.4663	0	2.94E-08	0	0	Shared
unassigned	67243	10	25215410	RS37076985	10	29.16132	28876470	0.42557	0.55781	0	2.97E-08	0	0	CB
Fpr3	353907	17	18108505	17.021.019	17	14.36839	21451267	0.14861	0.18447	0	3.03E-08	0	0	CB
Lars2	856941	9	123365035	D9Mit18	9	96.97845	1.2E+08	0.28946	0.38751	0	3.03E-08	0	0	CB
Hps5	766003	7	54038878	D7MIT228	7	28.11811	47279833	3.27083	2.72685	0	3.15E-08	0	0	CB
Car12	844966	9	66611063	09.046.588	9	34.49446	46645088	1.38737	1.75924	0	3.22E-08	0	0	CB
Mtfmt	844559	9	65295034	D9MIT248	9	44.87553	58210366	0.57169	0.43266	0	3.29E-08	0.0005	0.041856	CB
Sult2b1	765603	7	53014772	D7MIT228	7	28.11811	47279833	1.30222	1.04892	0	3.32E-08	0	0	CB
unassigned	772006	7	91432455	D7MIT350	7	57.28732	90734599	0.46231	0.55508	0	3.32E-08	0	0	CB
Fzd6	287099	15	38838009	D15MIT143	15	21.45854	51985414	5.24616	3.98363	0	3.38E-08	0	0	CB
Pde1c	717071	6	56311911	d6mit123	6	39.56321	56801586	1.3435	0.99349	0	3.47E-08	0	0	CB
unassigned	23903	1	160594327	D1Mit102	1	80.03925	1.49E+08	1.18211	1.4619	0	3.49E-08	0	0	Shared
Hydin	806319	8	113081543	D8MIT215	8	87.84173	1.18E+08	0.64054	1.15172	0	3.60E-08	0	0	CB
Pkd2	643836	5	104932577	D5MIT239	5	66.11023	1.08E+08	0.80793	1.01019	0	3.62E-08	0	0	Shared
Cc2d2a	634384	5	44103483	05.038.809	5	37.9822	38911990	1.65332	1.39721	0	3.67E-08	0	0	CB
Pde1c	717038	6	56100606	d6mit123	6	39.56321	56801586	0.76736	0.51162	0	3.70E-08	0	0	CB
Psmb3	128178	11	97574758	D11MIT289	11	59.90287	94741466	0.42823	0.52261	0	3.72E-08	0	0	Shared
unassigned	562425	3	127244065	RS30160288	3	119.3825	1.26E+08	0.93954	1.24025	0	3.75E-08	0	0	Shared
Spata5	522274	3	37427108	03.033.871	3	22.08075	33578373	0.68492	0.81582	0	3.76E-08	0	0	Shared
Ddx55	649084	5	125006971	d5mit158	5	69.85959	1.15E+08	2.5669	2.25537	0	3.77E-08	0	0	CB
unassigned	139491	11	30059486	D11MIT186	11	23.608	35049231	1.18991	0.95383	0	3.77E-08	0	0	CB

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Lrrc28	768631	7	74786158	D7Mit232	7	35.20811	59868792	0.14932	0.20431	0	3.79E-08	0	0	CB
Cenpq	376821	17	41068604	D17MIT51	17	53.34361	43641790	0.18229	0.22722	0	3.84E-08	0	0	CB
Siva1	181212	12	113885080	D12MIT7	12	66.69663	1.05E+08	1.67751	1.14932	0	3.86E-08	0	0	Shared
AW146020	695517	6	81875766	RS30909511	6	57.9854	83140362	0.7995	0.62082	0	3.89E-08	0	0	CB
unassigned	762757	7	31836842	07.017.531	7	12.92437	18957827	0.11052	0.07661	0	3.89E-08	0	0	Shared
1500032L24Rik	294430	15	82178344	D15Mit107	15	49.40097	84216927	1.60585	1.71392	0	3.98E-08	0	0	Shared
Rbbp9	506145	2	144369170	D2Mit274	2	62.95823	1.14E+08	0.92783	1.02446	0	4.03E-08	0	0	CB
Nup133	831497	8	126428481	D8MIT42	8	102.8893	1.29E+08	2.29919	3.20462	0	4.05E-08	0	0	CB
Tekt2	616782	4	125999380	D4MIT308	4	84.36025	1.24E+08	0.3731	0.28193	0	4.06E-08	0	0	Shared
Mfn2	622171	4	147277047	D4MIT232	4	109.1183	1.45E+08	0.38698	0.30621	0	4.09E-08	0	0	CB
Mfn2	622173	4	147277542	D4MIT232	4	109.1183	1.45E+08	0.68145	0.5504	0	4.10E-08	0	0	CB
Rplp0	646514	5	116012467	d5mit158	5	69.85959	1.15E+08	2.27173	1.9101	0	4.18E-08	0	0	Shared
Zdhhc13	740318	7	56056701	D7MIT248	7	39.99047	80656343	1.69776	1.507	0	4.19E-08	0	0	CB
Arl5a	488456	2	52271604	RS28322831	2	43.67748	71063776	1.79004	1.46799	0	4.22E-08	0	0	CB
Apba2	742506	7	71878415	D7Mit232	7	35.20811	59868792	0.65808	0.78195	0	4.27E-08	0	0	CB
unassigned	703088	6	120812981	d6mit366	6	77.49561	1.15E+08	0.45997	0.59013	0	4.27E-08	0	0	CB
Prom1	661947	5	44392020	05.038.809	5	37.9822	38911990	0.47752	0.35164	0	4.29E-08	0	0	Shared
Rps2	355013	17	24858090	17.021.019	17	14.36839	21451267	1.38397	1.49086	0	4.32E-08	0	0	CB
Ube4b	622693	4	148746962	D4MIT42	4	117.1013	1.51E+08	0.86289	0.7638	0	4.39E-08	0	0	Shared
Zfpm1	808688	8	124856042	D8MIT42	8	102.8893	1.29E+08	1.62417	1.26069	0	4.48E-08	0	0	Shared
Akirin2	573389	4	34513583	D4mit94	4	20.99338	33951862	0.94882	1.14484	0	4.49E-08	0	0	Shared
unassigned	801056	8	87825524	D8MIT346	8	54.67316	85454038	0.8254	0.95762	0	4.62E-08	0	0	CB
5033411D12Rik	222870	13	17415049	D13Mit207	13	8.688726	16526195	0.22146	0.31338	0	4.75E-08	0	0	Shared
Rapgef4	457415	2	71872272	D2MIT75	2	46.41465	80424883	1.72082	1.47232	0	4.83E-08	0	0	CB
unassigned	361530	17	50745578	D17MIT180	17	63.0586	51571276	1.65177	1.38187	0	4.84E-08	0	0	CB
Ptchd2	622338	4	147635200	D4MIT232	4	109.1183	1.45E+08	0.64379	0.85664	0	4.85E-08	0	0	CB
Tmem131	36086	1	36869033	D1Mit374	1	27.02859	34816928	1.1603	0.96027	0	4.87E-08	0	0	Shared
Prkag2	658064	5	24368792	D5MIT348	5	18.20559	24424937	1.88313	2.36955	0	4.96E-08	0	0	Shared
Vwa5a	838533	9	38550716	D9MIT247	9	25.36975	36940492	0.48582	0.32698	0	4.99E-08	0	0	Shared
Fyco1	880708	9	123752641	D9Mit18	9	96.97845	1.2E+08	0.90344	0.73161	0	5.02E-08	0	0	CB
Wrn	815656	8	34395609	D8MIT292	8	21.90455	35848067	0.3629	0.53919	0	5.04E-08	0	0	Shared
unassigned	265758	14	32000456	D14MIT174	14	33.32711	32460166	0.88234	0.99721	0	5.11E-08	0	0	Shared
Cog2	809483	8	127057185	D8MIT42	8	102.8893	1.29E+08	0.91217	1.12829	0	5.15E-08	0	0	Shared
Spg21	844578	9	65329675	D9MIT336	9	49.6331	65425671	1.16669	1.28029	0	5.15E-08	0	0	CB
Pde1c	717016	6	56030735	06.057.998	6	39.56321	58018416	0.1273	0.09122	0	5.41E-08	0	0	CB
1200011I18Rik	274825	14	76507173	D14MIT39	14	54.52991	69166099	0.96682	0.77486	0	5.45E-08	0	0	Shared
Runx1t1	570844	4	13762810	04.013.290	4	8.3	13290000	0.78227	0.97937	0	5.48E-08	0	0	CB
Ptchd2	622336	4	147633941	D4MIT232	4	109.1183	1.45E+08	0.29368	0.3742	0	5.53E-08	0	0	CB
Prkd1	188362	12	51495861	D12Mit2	12	26.67403	42747379	0.65349	0.85515	0	5.59E-08	0	0	CB
Galntl2	247407	14	32842804	14.027.409	14	32.01969	29395320	0.64768	0.51989	0	5.69E-08	0	0	CB
Mlh1	878108	9	111164008	09.105.291	9	79.88305	1.05E+08	1.14435	1.47293	0	5.80E-08	0	0	Shared
Vmn2r42	759098	7	9371789	07.013.915	7	8.7	15600169	2.33748	3.27283	0	5.80E-08	0	0	CB

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Mocs2	220316	13	115611058	d13mit151	13	74.51442	1.16E+08	1.12973	1.00653	0	5.83E-08	0	0	CB
unassigned	880662	9	123624120	D9Mit18	9	96.97845	1.2E+08	1.89673	1.53643	0	5.85E-08	0	0	CB
BC056474	801017	8	87606000	D8MIT45	8	58.44006	89829274	0.19514	0.15682	0	5.87E-08	0	0	CB
unassigned	839812	9	44954599	D9MIT285	9	25.81754	40462577	2.01527	2.3299	0	5.87E-08	0	0	CB
Ldb3	266555	14	35355650	D14MIT174	14	33.32711	32460166	0.56471	0.73618	0	5.89E-08	0	0	CB
Cryab	841139	9	50560921	D9MIT247	9	25.36975	36940492	0.05646	0.03903	0	5.93E-08	0	0	CB
Mrpl3	852187	9	104956778	D9MIT24	9	73.18313	1.03E+08	1.13619	1.32074	0	5.95E-08	0	0	Shared
unassigned	123531	11	78331723	D11MIT320	11	39.87138	70766870	0.57818	0.50931	0	5.99E-08	0	0	CB
unassigned	262147	14	13321466	14.008.937	14	5.6	10975728	0.06884	0.09283	0	6.05E-08	0	0	CB
9030625A04Rik	275011	14	77429355	RS31380922	14	61.61076	78742431	0.61054	0.83332	0	6.13E-08	0	0	Shared
Dst	3706	1	34252702	D1Mit374	1	27.02859	34816928	0.15823	0.19929	0	6.24E-08	0	0	CB
Cdk5rap2	606924	4	69963158	rs13477756	4	50.52425	68030949	1.04078	1.21934	0	6.27E-08	0	0	CB
Cmpk1	613725	4	114637490	RS27499066	4	79.43714	1.15E+08	0.57997	0.49298	0	6.32E-08	0	0	Shared
Gas5	24429	1	162966680	D1Mit102	1	80.03925	1.49E+08	1.24774	1.10257	0	6.37E-08	0	0	CB
Qtrt1	835219	9	21221509	D9mit90	9	20.19926	32308040	1.15028	1.40993	0	6.37E-08	0	0	Shared
Zfp111	760466	7	24983171	D7MIT228	7	28.11811	47279833	0.89841	1.00751	0	6.42E-08	0	0	Shared
Tle3	843576	9	61262591	D9MIT285	9	25.81754	40462577	1.0656	1.30945	0	6.56E-08	0	0	CB
Pclo	628644	5	14668995	D5MIT294	5	15.58331	20863135	1.6788	1.06575	0	6.63E-08	0	0	Shared
Dpp10	49398	1	125295098	D1MIT1001	1	72.84145	1.31E+08	0.3433	0.42754	0	6.71E-08	0	0	CB
Rbm45	458346	2	76218439	D2MIT75	2	46.41465	80424883	1.40986	1.75817	0	6.74E-08	0	0	Shared
Nup37	78241	10	87610937	D10MIT117	10	70.67248	87027855	1.07093	1.28031	0	6.79E-08	0	0	Shared
Gns	83722	10	120827712	D10Mit14	10	93.10254	1.18E+08	0.93492	1.07713	0	6.81E-08	0	0	Shared
unassigned	567033	3	151998480	D3MIT147	3	137.3239	1.48E+08	0.4665	0.57166	0	7.03E-08	0	0	Shared
Scg5	499314	2	113669156	RS27267095	2	129.5613	1.37E+08	0.35779	0.2877	0	7.05E-08	0	0	Shared
unassigned	147459	11	69010190	D11Mit4	11	39.42453	68422759	1.59657	1.27716	0	7.06E-08	0	0	CB
unassigned	459299	2	83632017	RS27416022	2	74.76293	93628229	0.90715	0.77954	0	7.27E-08	0	0	Shared
Slc24a3	470178	2	145428264	D2MIT285	2	110.6372	1.53E+08	2.29962	2.05815	0	7.42E-08	0.0005	0.041856	Shared
unassigned	191615	12	73185521	D12MIT91	12	43.26798	72843829	1.38419	1.15094	0	7.42E-08	0	0	Shared
Ptpn5	766149	7	54343863	07.056.455	7	36.40088	63842351	2.57431	2.22303	0	7.44E-08	0	0	Shared
Ptprd	607429	4	75730250	D4MIT164	4	42.38961	59415112	1.26691	1.41056	0	7.47E-08	0	0	CB
Sass6	535263	3	116331438	D3MIT315	3	89.68246	1.16E+08	0.16247	0.24286	0	7.53E-08	0	0	Shared
Pftk1	655312	5	4804943	D5MIT123	5	4.1	6556176	1.49986	1.79514	0	7.55E-08	0	0	CB
unassigned	222323	13	13453358	13.013.314	13	8.3	13614141	0.52532	0.42099	0	7.82E-08	0	0	CB
Acap3	596639	4	155270685	D4MIT42	4	117.1013	1.51E+08	1.09337	0.93182	0	7.84E-08	0	0	Shared
Alpl	619837	4	137305494	D4MIT170	4	99.94085	1.38E+08	0.98656	0.77884	0	7.86E-08	0	0	Shared
unassigned	363621	17	65060210	D17Mit152	17	74.19469	65689824	0.76037	0.97321	0	7.92E-08	0	0	CB
Nbn	571116	4	15903185	04.013.290	4	8.3	13290000	2.12098	2.43877	0	7.96E-08	0	0	Shared
Pde1c	717051	6	56130081	06.057.998	6	39.56321	58018416	2.65057	2.22386	0	8.05E-08	0	0	CB
Ptprd	607444	4	75753207	D4MIT348	4	56.03665	82826651	1.6297	1.4779	0	8.05E-08	0	0	CB
Pigz	324915	16	31942143	16.039.061	16	48.3587	39141781	1.61261	1.44753	0	8.09E-08	0	0	CB
Tkt	246939	14	31372951	D14MIT174	14	33.32711	32460166	1.38754	1.10518	0	8.13E-08	0	0	Shared
unassigned	354864	17	24559249	D17Mit213	17	12.20714	16752157	0.5746	0.47792	0	8.14E-08	0	0	CB

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Lamc1	54398	1	155073525	01.136.071	1	77.74879	1.36E+08	0.88502	1.1265	0	8.19E-08	0	0	Shared
Rfx1	800596	8	86618668	D8MIT45	8	58.44006	89829274	0.33994	0.46184	0	8.27E-08	0	0	CB
unassigned	469930	2	144201486	D2MIT423	2	107.8075	1.49E+08	0.68599	0.52581	0	8.42E-08	0	0	CB
4933407N01Rik	139647	11	30852615	D11MIT186	11	23.608	35049231	0.42955	0.57641	0	8.47E-08	0	0	CB
Mms19	439566	19	42040762	D19MIT88	19	44.41135	37331405	0.87926	0.70733	0	8.87E-08	0	0	Shared
Pde1c	717070	6	56311747	d6mit123	6	39.56321	56801586	1.41416	1.10069	0	8.93E-08	0	0	CB
Gm13152	594123	4	146888643	D4MIT232	4	109.1183	1.45E+08	0.76985	0.68992	0	9.04E-08	0	0	Shared
Cnot10	878746	9	114535528	D9MIT201	9	91.42427	1.17E+08	0.51859	0.41556	0	9.07E-08	0	0	Shared
Terf1	1676	1	15823485	rs13475769	1	16.19758	24958696	0.49045	0.66379	0	9.25E-08	0	0	Shared
Slc11a2	317392	15	100218459	D15MIT44	15	76.94503	98951714	0.67896	0.55666	0	9.50E-08	0	0	Shared
Rnf213	133893	11	119344999	D11MIT214	11	79.65651	1.15E+08	0.55699	0.43102	0	9.59E-08	0	0	CB
unassigned	806517	8	113571733	D8MIT47	8	79.10975	1.09E+08	1.86233	2.26673	0	9.79E-08	0	0	Shared
Trmt2b	932892	X	130757515	DXMIT172	X	47.92461	1.19E+08	0.36232	0.53825	0.68012	9.82E-08	0	0	Shared
Alox8	147455	11	69002156	RS26969123	11	30.52371	53430698	0.81779	1.12078	0	9.92E-08	0.0005	0.041856	CB
Atxn7l1	167208	12	33934807	D12MIT285	12	30.22146	55750112	0.34429	0.44976	0	1.00E-07	0	0	CB
unassigned	1684	1	15833606	rs13475769	1	16.19758	24958696	0.60906	0.79455	0	1.01E-07	0	0	CB
Clpx	844490	9	65157969	D9MIT336	9	49.6331	65425671	2.01935	2.2867	0	1.02E-07	0	0	Shared
Slc5a2	780256	7	135415323	d7mit109	7	91.14939	1.44E+08	1.21881	1.53479	0	1.02E-07	0	0	Shared
Clstn1	594822	4	149019440	D4MIT232	4	109.1183	1.45E+08	1.57853	1.42066	0	1.05E-07	0	0	Shared
Hydin	806341	8	113119136	D8MIT211	8	73.00564	1.05E+08	0.87838	1.15718	0	1.06E-07	0	0	CB
Leprotl1	815865	8	35200401	D8Mit191	8	23.02066	36243839	0.62971	0.81448	0	1.10E-07	0	0	CB
Mphosph10	768045	7	71521483	07.056.455	7	36.40088	63842351	0.158	0.30975	0	1.10E-07	0	0	Shared
Uggt1	35852	1	36249256	D1Mit374	1	27.02859	34816928	0.90747	0.75438	0	1.11E-07	0	0	Shared
Cntnap2	690223	6	46120194	D6MIT274	6	30.88472	48676564	1.04228	0.87082	0	1.12E-07	0	0	Shared
Fundc2	910588	X	72639941	DXMit119	X	34.98622	69655585	0.639	0.69579	0.73451	1.12E-07	0	0	Shared
Gsk3b	326516	16	38170767	16.039.061	16	48.3587	39141781	0.63777	0.72914	0	1.13E-07	0	0	Shared
Ulk4	880048	9	121012677	D9MIT151	9	100.1162	1.21E+08	1.69001	1.31188	0	1.14E-07	0.0005	0.041856	CB
unassigned	340765	16	32836103	D16MIT60	16	28.75614	32704177	0.70804	0.82727	0	1.16E-07	0	0	CB
Bbs7	547495	3	36501753	03.033.871	3	22.08075	33578373	3.34652	2.8784	0	1.22E-07	0	0	Shared
Lama1	364205	17	68123027	D17Mit93	17	83.28793	74149996	0.30433	0.38377	0	1.22E-07	0	0	CB
unassigned	785919	7	20219334	07.017.531	7	12.92437	18957827	0.65762	0.72443	0	1.22E-07	0	0	Shared
Nfs1	508608	2	155952064	D2MIT285	2	110.6372	1.53E+08	0.75147	0.94971	0	1.25E-07	0	0	Shared
Dpp10	49447	1	125750743	RS50560599	1	67.50483	1.17E+08	0.75295	0.90543	0	1.29E-07	0	0	CB
Rap1gap	591986	4	137260013	04.133.005	4	97.64222	1.33E+08	0.44278	0.34234	0	1.33E-07	0	0	CB
Armc8	875088	9	99420083	D9MIT24	9	73.18313	1.03E+08	0.91246	1.03292	0	1.34E-07	0	0	CB
Golt1b	707081	6	142344714	D6MIT194	6	87.57626	1.28E+08	1.29847	1.11356	0	1.35E-07	0	0	Shared
Ncapd2	728272	6	125118666	d6mit366	6	77.49561	1.15E+08	2.44742	2.026	0	1.35E-07	0	0	CB
Ecsit	859833	9	21888514	09.014.560	9	12.99047	14614051	1.2193	0.87068	0	1.36E-07	0.0005	0.041856	Shared
Ppih	615265	4	118984137	D4MIT308	4	84.36025	1.24E+08	1.70966	1.93401	0	1.36E-07	0	0	CB
unassigned	829297	8	116290687	D8MIT47	8	79.10975	1.09E+08	0.69294	0.81901	0	1.38E-07	0	0	CB
unassigned	865426	9	50459055	09.046.588	9	34.49446	46645088	1.71333	1.50541	0	1.39E-07	0	0	CB
Rint1	630039	5	23317590	D5MIT294	5	15.58331	20863135	0.77228	0.95066	0	1.43E-07	0	0	Shared

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Abcb10	831529	8	126476634	D8MIT42	8	102.8893	1.29E+08	1.04026	1.38581	0	1.47E-07	0	0	Shared
Ccnd2	728699	6	127089124	D6MIT194	6	87.57626	1.28E+08	1.26678	1.08374	0	1.48E-07	0	0	Shared
Aldh4a1	592744	4	139204320	D4MIT170	4	99.94085	1.38E+08	1.52544	1.28093	0	1.52E-07	0	0	CB
Smarca2	423470	19	26753595	D19MIT96	19	21.38792	21916083	0.64089	0.77929	0	1.53E-07	0	0	CB
Vmn2r42	759202	7	9939695	07.013.915	7	8.7	15600169	3.83259	5.47319	0	1.55E-07	0	0	CB
unassigned	550403	3	57453910	03.060.525	3	40.51916	60240993	1.00647	1.23498	0	1.57E-07	0	0	Shared
Mmadhc	487944	2	50143383	D2MIT296	2	21.50213	31180075	0.78962	0.61448	0	1.60E-07	0	0	CB
unassigned	504034	2	131818545	D2Mit274	2	62.95823	1.14E+08	1.30254	1.05263	0	1.62E-07	0	0	Shared
Dennd4a	844269	9	64690300	09.046.588	9	34.49446	46645088	0.86722	0.97126	0	1.63E-07	0	0	CB
Mettl8	491863	2	70805110	RS28322831	2	43.67748	71063776	1.95122	1.62424	0	1.65E-07	0.0005	0.041856	CB
unassigned	765910	7	53895143	D7Mit232	7	35.20811	59868792	0.78042	0.6287	0	1.65E-07	0	0	CB
Snap91	873061	9	86719691	09.079.053	9	64.60162	79115123	1.15813	1.44542	0	1.66E-07	0	0	Shared
Spag1	286547	15	36125156	15.028.723	15	14.88113	28708166	0.31638	0.42473	0	1.66E-07	0	0	CB
Iars2	61145	1	187127235	01.183.109	1	96.11848	1.83E+08	0.60979	0.48747	0	1.67E-07	0.0005	0.041856	Shared
Lnx2	681212	5	147854017	D5MIT169	5	118.4503	1.5E+08	0.66419	0.54168	0	1.68E-07	0	0	CB
Calm3	759882	7	17500734	07.013.915	7	8.7	15600169	1.42391	1.24302	0	1.69E-07	0	0	CB
Hps5	765998	7	54032283	D7MIT294	7	15.72036	28074461	0.59822	0.78563	0	1.73E-07	0	0	CB
Arhgap4	927544	X	71142902	DXMit119	X	34.98622	69655585	1.51825	1.68211	2.03242	1.74E-07	0	0	CB
Lrrk2	296486	15	91561910	15.090.122	15	63.15586	90124664	1.4628	1.23532	0	1.74E-07	0	0	Shared
Parp8	241515	13	117656934	D13MIT78	13	76.84217	1.2E+08	0.91312	1.06701	0	1.77E-07	0	0	Shared
Entpd4	254072	14	69982125	14.095.016	14	67.37082	96532085	0.89263	1.10222	0	1.80E-07	0.0005	0.041856	Shared
Pigt	475193	2	164326774	02.168.990	2	151.4053	1.69E+08	0.83477	0.72182	0	1.81E-07	0	0	Shared
unassigned	219865	13	113725809	D13MIT53	13	72.69389	1.13E+08	0.5058	0.38885	0	1.83E-07	0	0	CB
Cyp4f13	375120	17	33069426	17.034.150	17	51.1372	34678889	2.77014	3.30214	0	1.87E-07	0	0	CB
Hydin	806318	8	113080943	D8MIT211	8	73.00564	1.05E+08	0.85738	1.12826	0	1.87E-07	0	0	CB
unassigned	739533	7	52415005	07.056.455	7	36.40088	63842351	0.65242	0.86712	0	1.89E-07	0	0	Shared
unassigned	3690	1	34231645	D1Mit374	1	27.02859	34816928	1.37326	1.55754	0	1.91E-07	0.0005	0.041856	Shared
unassigned	764678	7	50784453	D7MIT228	7	28.11811	47279833	0.34612	0.39028	0	1.91E-07	0	0	CB
Anxa2	845572	9	69330783	D9MIT336	9	49.6331	65425671	1.17789	0.94515	0	1.92E-07	0	0	Shared
Bbs7	547493	3	36497249	D3Mit151	3	18.63179	31137265	1.43692	1.77465	0	1.92E-07	0	0	CB
A730017C20Rik	397288	18	59232216	D18MIT152	18	47.63475	62096421	1.06081	0.88677	0	1.99E-07	0	0	Shared
Cog6	549550	3	52797398	D3MIT6	3	28.26274	48687327	0.73718	0.93416	0	2.00E-07	0	0	CB
Bmpr1a	266533	14	35257135	14.027.409	14	32.01969	29395320	0.58303	0.69007	0	2.01E-07	0	0	Shared
Ncoa7	90695	10	30368253	RS29380418	10	27.66974	27331665	3.06643	2.67395	0	2.01E-07	0	0	CB
Skiv2l	375725	17	34978948	17.034.150	17	51.1372	34678889	0.99398	0.85845	0	2.02E-07	0	0	Shared
Cela1	317539	15	100504883	D15MIT15	15	83.15474	1.03E+08	0.20338	0.26876	0	2.04E-07	0	0	Shared
Rasa1	235351	13	85395990	13.096.920	13	58.79686	96589256	1.85141	1.55283	0	2.04E-07	0	0	Shared
4833420G17Rik	220886	13	120274541	D13MIT78	13	76.84217	1.2E+08	0.31283	0.25543	0	2.06E-07	0	0	CB
Mllt11	556274	3	95024110	D3MIT315	3	89.68246	1.16E+08	1.66879	1.59228	0	2.07E-07	0	0	Shared
Aebp2	706810	6	140602358	D6Mit14	6	101.6085	1.46E+08	0.86651	0.72489	0	2.12E-07	0	0	CB
unassigned	302658	15	27666174	15.028.723	15	14.88113	28708166	0.69315	0.88083	0	2.17E-07	0	0	Shared
Tbc1d9	800325	8	85779750	D8MIT346	8	54.67316	85454038	1.68604	1.51874	0	2.18E-07	0	0	CB

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Col19a1	34630	1	24517682	D1MIT169	1	18.85175	24071806	0.73196	0.45065	0	2.19E-07	0	0	CB
Csmd1	812814	8	16081653	D8MIT94	8	19.42422	32452130	1.1505	0.93155	0	2.20E-07	0	0	Shared
Cpne4	852172	9	104909879	D9MIT24	9	73.18313	1.03E+08	0.58342	0.75426	0	2.22E-07	0	0	CB
Tctn2	649136	5	125048997	D5MIT95	5	98.81753	1.25E+08	0.76978	0.89721	0	2.28E-07	0	0	CB
Polr3d	273444	14	70838782	RS31380922	14	61.61076	78742431	0.71367	0.86921	0	2.34E-07	0	0	CB
Uevld	766074	7	54200602	D7Mit232	7	35.20811	59868792	1.34182	1.15652	0	2.34E-07	0	0	CB
unassigned	806300	8	113049528	D8MIT215	8	87.84173	1.18E+08	3.60771	3.01566	0	2.35E-07	0	0	CB
Pigy	717221	6	57639051	d6mit123	6	39.56321	56801586	0.81474	0.9412	0	2.37E-07	0	0	CB
unassigned	432672	19	7069281	19.013.429	19	11.12922	13436471	2.07186	1.65578	0	2.37E-07	0	0	Shared
Nop14	660203	5	35000559	D5MIT352	5	30.68587	35957616	2.01001	1.56565	0	2.38E-07	0	0	Shared
Ssrp1	459561	2	84886471	RS28322831	2	43.67748	71063776	1.29784	1.5947	0	2.38E-07	0	0	CB
unassigned	738320	7	46789950	07.056.455	7	36.40088	63842351	1.43088	1.22681	0	2.40E-07	0	0	Shared
Dhx29	219868	13	113731889	D13MIT288	13	67.56495	1.08E+08	0.79998	0.64321	0	2.41E-07	0	0	CB
Pip5k1b	435905	19	24420728	D19MIT96	19	21.38792	21916083	3.15107	2.84968	0	2.41E-07	0.0005	0.041856	CB
Hydin	806307	8	113059145	D8MIT211	8	73.00564	1.05E+08	1.91575	2.68485	0	2.42E-07	0	0	CB
unassigned	462223	2	103955794	02.109.360	2	59.82539	1.09E+08	1.31177	1.59445	0	2.43E-07	0	0	CB
Otof	659037	5	30672568	D5MIT294	5	15.58331	20863135	1.28275	0.91147	0	2.46E-07	0	0	CB
Tm2d3	742647	7	72840031	D7MIT248	7	39.99047	80656343	2.17548	1.80936	0	2.46E-07	0	0	CB
Sntg2	185877	12	30961576	D12MIT60	12	21.02542	35474805	0.81971	1.21194	0	2.50E-07	0.0005	0.041856	CB
H2-Bl	376271	17	36272893	17.034.150	17	51.1372	34678889	3.26562	2.10452	0	2.51E-07	0	0	CB
Pcdhgb8	393374	18	37923645	18.038.678	18	24.45192	38711680	1.48753	1.68235	0	2.51E-07	0	0	Shared
Ephb2	619536	4	136216624	04.098.998	4	75.01299	99172673	0.95943	1.14185	0	2.52E-07	0	0	CB
Sqrdl	465950	2	122613194	D2MIT395	2	91.61399	1.19E+08	0.94378	1.25642	0	2.52E-07	0	0	Shared
Mcam	839479	9	43944980	09.046.588	9	34.49446	46645088	0.85503	0.73953	0	2.55E-07	0	0	Shared
Dst	3749	1	34320148	D1Mit374	1	27.02859	34816928	0.86619	1.01718	0	2.58E-07	0	0	Shared
unassigned	130150	11	104151167	11.104.430	11	62.15042	1.04E+08	0.64693	0.77748	0	2.60E-07	0	0	CB
Pla2g7	359888	17	43736032	17.034.150	17	51.1372	34678889	2.39987	2.16987	0	2.62E-07	0	0	Shared
Ankrd27	737787	7	36392142	D7MIT267	7	18.29809	30331965	1.58632	1.32374	0	2.63E-07	0	0	Shared
Ncoa7	90686	10	30349131	RS29380418	10	27.66974	27331665	0.04866	0.06262	0	2.65E-07	0.0005	0.041856	CB
Tdrd3	256892	14	87886982	14.095.016	14	67.37082	96532085	1.36304	1.14286	0	2.66E-07	0	0	CB
Ppargc1a	662982	5	51854446	05.038.809	5	37.9822	38911990	0.87436	1.0168	0	2.73E-07	0	0	CB
Cpne9	701315	6	113251651	06.095.876	6	52.18486	95860531	3.00204	2.58635	0	2.74E-07	0	0	CB
unassigned	869261	9	65953299	D9MIT107	9	53.50038	73315075	2.60889	2.9594	0	2.76E-07	0.0005	0.041856	Shared
unassigned	317398	15	100228046	D15MIT44	15	76.94503	98951714	1.84363	1.6746	0	2.77E-07	0.0005	0.041856	Shared
unassigned	114669	11	43247475	D11MIT51	11	25.39412	36205252	0.34232	0.25583	0	2.79E-07	0	0	CB
Bmpr1b	565039	3	141645053	03.141.220	3	108.244	1.41E+08	0.57921	0.71082	0	2.82E-07	0.0005	0.041856	CB
Ttc13	831685	8	127202904	D8MIT42	8	102.8893	1.29E+08	0.11549	0.16112	0	2.83E-07	0	0	CB
Ppih	615273	4	118992132	D4MIT308	4	84.36025	1.24E+08	0.2726	0.18698	0	2.91E-07	0	0	Shared
Lrrfip2	854197	9	111126595	D9Mit18	9	96.97845	1.2E+08	2.7956	3.69117	0	2.96E-07	0	0	Shared
unassigned	844764	9	65981296	D9MIT107	9	53.50038	73315075	0.97618	0.83201	0	2.96E-07	0	0	Shared
Lamb1-1	166753	12	31983709	D12MIT60	12	21.02542	35474805	0.6852	0.8405	0	3.02E-07	0.0005	0.041856	CB
Idua	644934	5	109110693	D5MIT239	5	66.11023	1.08E+08	0.39679	0.3187	0	3.03E-07	0	0	CB

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Ncor2	676436	5	125536257	D5MIT95	5	98.81753	1.25E+08	0.85282	1.02299	0	3.03E-07	0	0	CB
Nipal3	619242	4	135022771	D4MIT170	4	99.94085	1.38E+08	0.93214	1.07327	0	3.06E-07	0	0	Shared
Rcan3	619222	4	134974322	D4Mit203	4	89.73231	1.29E+08	0.61728	0.74188	0	3.14E-07	0	0	Shared
Rad51l3	151223	11	82695306	D11MIT285	11	55.01615	89789103	0.98876	1.18067	0	3.18E-07	0.0005	0.041856	Shared
Map3k5	66007	10	19796288	RS29365246	10	15.91284	19378741	0.6072	0.47112	0	3.20E-07	0	0	Shared
unassigned	255589	14	77981950	D14MIT263	14	64.79535	89360701	0.62923	0.76623	0	3.24E-07	0	0	Shared
6330439K17Rik	506129	2	144335128	D2MIT411	2	112.9735	1.59E+08	0.05139	0.07402	0	3.27E-07	0	0	CB
Lba1	854255	9	111291671	09.105.291	9	79.88305	1.05E+08	1.8298	1.53152	0	3.28E-07	0	0	CB
Mical3	727538	6	120988505	d6mit366	6	77.49561	1.15E+08	0.5321	0.6502	0	3.32E-07	0	0	CB
Dixdc1	865440	9	50471403	D9MIT285	9	25.81754	40462577	2.77412	3.4493	0	3.42E-07	0	0	Shared
Hydin	806331	8	113104679	D8MIT215	8	87.84173	1.18E+08	0.9722	1.37441	0	3.43E-07	0	0	CB
Rims2	287284	15	39513226	D15MIT143	15	21.45854	51985414	1.1476	1.0043	0	3.43E-07	0	0	CB
unassigned	871198	9	75458689	D9MIT107	9	53.50038	73315075	0.85267	0.71298	0	3.43E-07	0	0	CB
unassigned	393375	18	37924112	D18MIT194	18	30.70688	43820481	0.92688	1.15006	0	3.45E-07	0	0	Shared
Scg5	499290	2	113616547	RS27416022	2	74.76293	93628229	0.50752	0.70372	0	3.48E-07	0	0	Shared
Mlh1	878089	9	111133423	D9MIT212	9	79.88305	1.09E+08	0.28848	0.41232	0	3.49E-07	0.0005	0.041856	CB
unassigned	156563	11	101887542	D11MIT289	11	59.90287	94741466	0.24094	0.30658	0	3.52E-07	0	0	CB
Dvl2	120878	11	69819647	D11MIT285	11	55.01615	89789103	1.4979	1.19734	0	3.60E-07	0	0	Shared
unassigned	80521	10	99551335	d10Mit96	10	80.83316	99019575	1.12986	0.93123	0	3.60E-07	0	0	CB
Pde1c	717036	6	56089415	06.057.998	6	39.56321	58018416	0.65478	0.8181	0	3.61E-07	0	0	CB
Tbc1d23	344797	16	57199012	D16MIT185	16	54.3944	60434381	0.90278	1.05152	0	3.62E-07	0	0	Shared
unassigned	388918	18	12047358	D18MIT222	18	9.2	14746018	1.91376	1.48258	0	3.65E-07	0	0	CB
Herc2	741540	7	63475116	D7Mit232	7	35.20811	59868792	0.57524	0.67182	0	3.69E-07	0	0	CB
Eya3	590543	4	132213493	D4Mit203	4	89.73231	1.29E+08	0.35437	0.25922	0	3.76E-07	0	0	CB
Abcc12	824110	8	89051171	D8MIT45	8	58.44006	89829274	1.82884	2.34487	0	3.78E-07	0	0	CB
Tnks	816009	8	35914689	D8MIT292	8	21.90455	35848067	0.6719	0.78971	0	3.80E-07	0	0	Shared
Akap9	627320	5	3948705	D5MIT123	5	4.1	6556176	0.57345	0.71147	0	3.83E-07	0	0	CB
Hydin	806309	8	113062629	D8MIT215	8	87.84173	1.18E+08	1.25688	1.74405	0	3.83E-07	0.0005	0.041856	CB
unassigned	730525	6	136824074	06.095.876	6	52.18486	95860531	5.26542	4.51554	0	3.85E-07	0	0	CB
1700065I17Rik	396710	18	56748024	D18MIT222	18	9.2	14746018	1.65461	2.17186	0	3.89E-07	0	0	CB
Tecr	823299	8	86095674	D8MIT346	8	54.67316	85454038	0.56882	0.75444	0	3.90E-07	0	0	CB
Ikbkap	604625	4	56800652	04.053.650	4	40.48019	53641772	2.87254	2.52336	0	3.91E-07	0	0	CB
Tbc1d5	378985	17	50921606	D17Mit152	17	74.19469	65689824	0.7244	0.62014	0	3.93E-07	0.0005	0.041856	CB
Xrcc6	294265	15	81859552	D15MIT262	15	57.21236	87111041	1.44305	1.21241	0	3.95E-07	0	0	Shared
Gramd1b	862790	9	40111912	D9MIT2	9	25.36976	37202486	0.43866	0.3842	0	3.97E-07	0.0005	0.041856	CB
Cdc14b	232285	13	64316811	13.061.624	13	39.87979	61715738	1.80066	2.11697	0	3.98E-07	0	0	CB
Tmem2	422477	19	21904301	D19MIT96	19	21.38792	21916083	0.87656	1.06828	0	4.00E-07	0	0	Shared
Zfp9	726794	6	118417259	d6mit366	6	77.49561	1.15E+08	0.44575	0.61572	0	4.01E-07	0	0	CB
Slc38a6	172792	12	74389442	12.065.348	12	37.44045	65530382	1.07122	1.17468	0	4.03E-07	0	0	CB
Zfp160	354207	17	21148649	17.021.019	17	14.36839	21451267	0.11999	0.08438	0	4.11E-07	0	0	Shared
Cda	619928	4	137899422	D4Mit203	4	89.73231	1.29E+08	0.98347	0.80349	0	4.14E-07	0	0	CB
unassigned	622632	4	148621997	D4MIT42	4	117.1013	1.51E+08	0.62249	0.48435	0	4.21E-07	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Igf1r	743201	7	75359807	D7Mit232	7	35.20811	59868792	0.49129	0.62935	0	4.27E-07	0	0	Shared
Aasdh	666874	5	77331182	d5mit233	5	46.33401	53088465	1.52431	1.20688	0	4.28E-07	0	0	CB
Rps14	397529	18	60937510	D18Mit123	18	38.31055	56130259	2.1514	1.98989	0	4.30E-07	0	0	CB
Fkbp9	692583	6	56818839	06.057.998	6	39.56321	58018416	1.02155	1.20426	0	4.32E-07	0	0	Shared
Dst	3773	1	34352315	D1Mit374	1	27.02859	34816928	2.01803	2.42233	0	4.34E-07	0	0	Shared
Zfp109	760464	7	25022117	07.013.915	7	8.7	15600169	0.68016	0.85658	0	4.35E-07	0	0	Shared
Gcn1l1	646574	5	116064890	D5MIT425	5	93.27848	1.2E+08	1.00946	1.23183	0	4.36E-07	0	0	Shared
unassigned	355011	17	24857413	17.021.019	17	14.36839	21451267	1.25893	1.12567	0	4.36E-07	0	0	Shared
Scarb2	669179	5	92878900	D5MIT10	5	65.80535	1.05E+08	1.07526	0.88616	0	4.42E-07	0	0	CB
Dopey1	872952	9	86449309	d9mit198	9	66.50428	91176808	0.63256	0.55103	0	4.56E-07	0	0	CB
Kif1b	622660	4	148681538	D4MIT232	4	109.1183	1.45E+08	0.36651	0.29777	0	4.56E-07	0	0	CB
Gcnt1	434720	19	17447256	19.013.429	19	11.12922	13436471	0.17066	0.13575	0	4.59E-07	0.0005	0.041856	CB
Eif3m	497857	2	104846194	02.109.360	2	59.82539	1.09E+08	2.46752	2.26663	0	4.61E-07	0	0	CB
C030039L03Rik	736152	7	28478554	D7MIT228	7	28.11811	47279833	4.42635	4.97795	0	4.70E-07	0	0	CB
App	348011	16	85173545	D16MIT189	16	73.83226	82534333	0.79728	0.97021	0	4.84E-07	0	0	Shared
Gak	672358	5	109035418	D5MIT10	5	65.80535	1.05E+08	1.56233	1.73456	0	4.84E-07	0	0	CB
H2-D1	358662	17	35404155	17.034.150	17	51.1372	34678889	2.09663	2.54348	0	4.99E-07	0	0	Shared
Trim2	553921	3	84012103	D3MIT49	3	73.77602	89036582	0.94744	0.84589	0	5.01E-07	0	0	CB
unassigned	847019	9	75296917	D9MIT107	9	53.50038	73315075	2.2063	1.91983	0	5.12E-07	0	0	CB
unassigned	565110	3	142015850	D3MIT147	3	137.3239	1.48E+08	0.49761	0.40379	0	5.20E-07	0	0	CB
Gaa	133754	11	119138818	D11MIT214	11	79.65651	1.15E+08	1.5022	1.3478	0	5.21E-07	0	0	CB
Rgs8	23067	1	155500388	D1Mit102	1	80.03925	1.49E+08	0.92956	0.81925	0	5.37E-07	0	0	CB
unassigned	67107	10	24627631	RS29316281	10	22.94397	25167321	1.50976	1.33705	0	5.45E-07	0	0	CB
Rps13	777620	7	123475127	RS32210051	7	61.08266	99669474	0.79013	0.9558	0	5.49E-07	0.0005	0.041856	CB
Mms19	439541	19	42024473	19.046.444	19	55.55111	46465179	1.91224	1.69871	0	5.53E-07	0	0	Shared
unassigned	51822	1	137268575	01.136.071	1	77.74879	1.36E+08	0.72375	0.8386	0	5.58E-07	0	0	Shared
Cstf1	476931	2	172201155	D2MIT148	2	167.7799	1.79E+08	2.14297	1.90669	0	5.60E-07	0	0	CB
Cntnap2	690234	6	46184227	D6MIT274	6	30.88472	48676564	0.94384	0.77238	0	5.66E-07	0.0005	0.041856	Shared
Elk4	50892	1	133920214	01.136.071	1	77.74879	1.36E+08	0.48351	0.57154	0	5.75E-07	0	0	CB
Folh1	772324	7	93910211	D7MIT350	7	57.28732	90734599	1.50582	1.83358	0	5.81E-07	0.0005	0.041856	CB
unassigned	279680	14	119394123	RS31252045	14	77.8316	1.11E+08	0.79105	0.96781	0	5.89E-07	0.0005	0.041856	Shared
unassigned	232105	13	63624186	13.061.624	13	39.87979	61715738	1.16547	1.03119	0	5.97E-07	0.0005	0.041856	Shared
Tubgcp3	811943	8	12641102	08.010.585	8	4.520052	10585028	1.32063	1.58584	0	6.01E-07	0	0	Shared
unassigned	540439	3	144240729	D3MIT147	3	137.3239	1.48E+08	1.93423	1.70967	0	6.08E-07	0	0	CB
Gtf2i	678157	5	134771454	05.132.979	5	112.2658	1.33E+08	0.78885	0.59706	0	6.15E-07	0.0005	0.041856	CB
Cntnap5b	16073	1	102170975	D1MIT134	1	59.85405	80264451	0.23994	0.28667	0	6.16E-07	0	0	CB
Nomo1	739992	7	53336798	D7MIT294	7	15.72036	28074461	0.96848	0.84769	0	6.24E-07	0	0	Shared
Ank2	562259	3	126662572	RS30160288	3	119.3825	1.26E+08	1.41879	1.19672	0	6.27E-07	0	0	Shared
Tgds	279452	14	118511927	14.095.016	14	67.37082	96532085	0.33996	0.39131	0	6.35E-07	0	0	CB
Lrp1b	486936	2	41644500	D2Mit297	2	25.96707	42461006	2.26763	2.67962	0	6.50E-07	0	0	Shared
Brf1	199579	12	114221238	D12MIT7	12	66.69663	1.05E+08	2.24601	1.94477	0	6.51E-07	0	0	CB
Cux1	678627	5	136726414	05.132.979	5	112.2658	1.33E+08	0.08867	0.05448	0	6.58E-07	0.0005	0.041856	CB

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Acer2	580769	4	86563530	D4Mit166	4	66.23295	93616234	0.61651	0.77017	0	6.70E-07	0	0	Shared
Rassf2	504035	2	131822148	D2Mit274	2	62.95823	1.14E+08	1.57505	1.83297	0	6.74E-07	0	0	CB
6330439K17Rik	506115	2	144307422	02.161.464	2	113.5093	1.62E+08	0.28045	0.36913	0	6.88E-07	0	0	CB
Acrbp	704099	6	125011133	D6MIT194	6	87.57626	1.28E+08	2.10637	1.77407	0	7.03E-07	0	0	CB
Uevld	766058	7	54182791	D7MIT228	7	28.11811	47279833	0.2163	0.30886	0	7.04E-07	0	0	Shared
Rarb	262634	14	17341489	14.008.937	14	5.6	10975728	0.97277	1.1725	0	7.12E-07	0	0	CB
Atp11b	521818	3	35733226	03.033.871	3	22.08075	33578373	1.54004	1.24098	0	7.31E-07	0	0	Shared
Vps52	357890	17	34098093	17.034.150	17	51.1372	34678889	1.78375	2.01567	0	7.44E-07	0	0	Shared
Itpr2	732606	6	146363854	D6Mit14	6	101.6085	1.46E+08	1.24689	1.46238	0	7.50E-07	0	0	Shared
Hps5	765995	7	54030194	D7Mit232	7	35.20811	59868792	1.74279	2.03247	0	7.53E-07	0.0005	0.041856	Shared
Slc25a17	312487	15	81150063	D15MIT262	15	57.21236	87111041	0.9441	0.82958	0	7.61E-07	0	0	Shared
Wbscr17	677533	5	131382453	05.132.979	5	112.2658	1.33E+08	1.06631	1.24119	0	7.63E-07	0	0	CB
Gli1	107139	10	126778261	D10Mit14	10	93.10254	1.18E+08	1.06917	1.27218	0	7.81E-07	0	0	CB
Kcnab2	623496	4	151808908	D4MIT232	4	109.1183	1.45E+08	0.63223	0.87551	0	7.82E-07	0	0	Shared
Mtor	594482	4	147926824	D4MIT232	4	109.1183	1.45E+08	2.06415	1.81556	0	7.83E-07	0	0	CB
Polr3f	469981	2	144358090	RS27267029	2	129.5613	1.37E+08	0.99773	0.77027	0	7.83E-07	0.0005	0.041856	Shared
Adssl1	181196	12	113870921	D12MIT7	12	66.69663	1.05E+08	1.96793	1.71619	0	7.94E-07	0	0	CB
Nup188	449940	2	30177417	D2MIT81	2	18.06443	24644623	1.06617	1.26145	0	7.97E-07	0	0	Shared
Rif1	453889	2	51945093	D2MIT61	2	35.12792	60528325	1.26045	1.10741	0	7.98E-07	0	0	CB
unassigned	391651	18	30470805	D18MIT194	18	30.70688	43820481	0.67792	0.57093	0	8.08E-07	0	0	CB
Id4	209309	13	48356890	RS29514367	13	20.53923	29499372	0.66141	0.54161	0	8.12E-07	0	0	CB
Ablim1	442686	19	57193316	D19MIT103	19	59.41115	53838656	0.67959	0.81857	0	8.19E-07	0	0	CB
Slc6a5	740681	7	57172987	D7MIT294	7	15.72036	28074461	3.15757	2.72356	0	8.23E-07	0	0	CB
Ncald	304372	15	37590787	15.028.723	15	14.88113	28708166	1.40908	1.6039	0	8.28E-07	0.0005	0.041856	CB
6030458C11Rik	301308	15	12741692	15.010.846	15	8.803289	10831030	1.55845	1.78931	0	8.31E-07	0	0	CB
Tbc1d9	800315	8	85760456	D8MIT346	8	54.67316	85454038	1.49631	1.66151	0	8.32E-07	0	0	CB
Ndufs2	58398	1	173169421	01.183.109	1	96.11848	1.83E+08	0.49097	0.59835	0	8.37E-07	0	0	Shared
unassigned	353904	17	18025037	D17MIT51	17	53.34361	43641790	1.12851	0.82909	0	8.46E-07	0	0	CB
2810055F11Rik	191609	12	73174909	D12MIT143	12	49.40885	80981262	0.89702	1.10879	0	8.48E-07	0	0	CB
Mrps27	217247	13	100170217	D13MIT213	13	69.65924	1.09E+08	1.8256	2.09395	0	8.78E-07	0.0005	0.041856	CB
Phf2	228908	13	48918356	13.043.962	13	29.58329	44046397	1.45275	1.22739	0	8.84E-07	0	0	Shared
unassigned	448712	2	26874857	RS27953638	2	27.96753	50041657	0.73748	0.62645	0	8.89E-07	0	0	Shared
Thnsl1	447400	2	21127493	D2MIT81	2	18.06443	24644623	0.66138	0.88036	0	9.02E-07	0.0005	0.041856	CB
Slc6a5	740693	7	57201886	D7MIT248	7	39.99047	80656343	2.9331	2.50919	0	9.06E-07	0.0005	0.041856	CB
Gsbs	692442	6	55981473	06.057.998	6	39.56321	58018416	2.21448	2.52002	0	9.16E-07	0	0	CB
unassigned	222281	13	12552976	D13Mit207	13	8.688726	16526195	0.30463	0.36043	0	9.17E-07	0	0	CB
Crym	778438	7	127330149	RS36353338	7	66.26522	1.13E+08	0.83269	0.6825	0	9.20E-07	0	0	CB
Inadl	582386	4	98213461	04.098.998	4	75.01299	99172673	0.64258	0.76542	0	9.22E-07	0.0005	0.041856	CB
Aars	806527	8	113578428	D8MIT47	8	79.10975	1.09E+08	1.05072	1.2033	0	9.26E-07	0	0	Shared
Abi1	517414	2	22808995	D2MIT81	2	18.06443	24644623	1.33119	1.16561	0	9.34E-07	0.0005	0.041856	Shared
St3gal6	345031	16	58473537	D16MIT185	16	54.3944	60434381	1.233	1.04585	0	9.36E-07	0	0	Shared
Ryr1	761868	7	29859615	D7MIT267	7	18.29809	30331965	1.68094	1.99661	0	9.38E-07	0	0	CB

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	787397	8	3643673	08.010.585	8	4.520052	10585028	7.867	5.90194	0	9.38E-07	0	0	CB
Bmp5	847104	9	75746957	d9mit198	9	66.50428	91176808	1.42272	1.20721	0	9.42E-07	0	0	CB
Galntl2	247421	14	32871376	14.027.409	14	32.01969	29395320	0.54862	0.64726	0	9.43E-07	0	0	CB
Efhb	379402	17	53540104	D17MIT51	17	53.34361	43641790	0.50362	0.66048	0	9.50E-07	0	0	Shared
Slc6a5	740694	7	57203619	D7MIT248	7	39.99047	80656343	2.36537	1.90959	0	9.51E-07	0	0	CB
Psme4	112838	11	30753177	RS26845852	11	16.78021	24370394	2.24173	2.00603	0	9.63E-07	0	0	CB
Atm	866063	9	53248140	D9MIT71	9	37.69738	50007830	0.38052	0.49272	0	9.77E-07	0.0005	0.041856	CB
Mpdz	607901	4	80949524	D4MIT348	4	56.03665	82826651	0.57191	0.69267	0	9.81E-07	0	0	CB
Tmod1	575349	4	46096435	04.053.650	4	40.48019	53641772	1.45542	1.305	0	9.90E-07	0.0005	0.041856	Shared
Pqlc1	401609	18	80453565	RS30267686	18	60.34946	81658329	0.93453	1.06941	0	9.93E-07	0	0	CB
Sh3bp1	293194	15	78734898	D15MIT262	15	57.21236	87111041	1.77	1.98877	0	9.94E-07	0	0	CB
Gtpbp1	293522	15	79546282	D15MIT67	15	36.95768	70032295	0.57794	0.67996	0	9.99E-07	0	0	Shared
Dlat	865431	9	50466793	09.046.588	9	34.49446	46645088	1.4066	1.24406	0	1.01E-06	0	0	CB
unassigned	395935	18	52647056	D18Mit123	18	38.31055	56130259	0.97549	1.17611	0	1.01E-06	0	0	Shared
Cul3	43878	1	80273021	D1MIT134	1	59.85405	80264451	1.98249	1.78003	0	1.03E-06	0	0	Shared
Ikbkap	604603	4	56775136	d4mit238	4	33.23278	45243003	0.10339	0.15532	0	1.03E-06	0	0	CB
Pcx	418758	19	4602515	19.000.325	19	0.2	325000	1.40877	1.21611	0	1.03E-06	0	0	Shared
Bmp1	273462	14	70874950	14.067.129	14	52.82241	68793727	1.24843	1.44152	0	1.04E-06	0	0	CB
unassigned	223009	13	18078835	D13Mit207	13	8.688726	16526195	0.48256	0.52152	0	1.05E-06	0	0	Shared
Folh1	772327	7	93920268	D7MIT350	7	57.28732	90734599	2.2573	1.90287	0	1.06E-06	0	0	CB
Fau	419274	19	6058251	19.000.325	19	0.2	325000	0.50994	0.60662	0	1.08E-06	0	0	Shared
Stk11ip	11687	1	75521998	D1MIT24	1	52.91828	74458254	0.78915	0.94905	0	1.08E-06	0	0	Shared
6330439K17Rik	506121	2	144315874	D2MIT285	2	110.6372	1.53E+08	1.40033	1.57802	0	1.12E-06	0.0005	0.041856	CB
Kif17	592337	4	137857165	D4MIT232	4	109.1183	1.45E+08	0.74056	0.53277	0	1.12E-06	0	0	CB
Pcgf3	644864	5	108902838	D5MIT239	5	66.11023	1.08E+08	0.96265	0.8289	0	1.12E-06	0.0005	0.041856	CB
Actr10	172140	12	72063093	D12MIT91	12	43.26798	72843829	2.27287	1.51364	0	1.14E-06	0	0	Shared
unassigned	357887	17	34097069	17.034.150	17	51.1372	34678889	1.03254	0.89836	0	1.16E-06	0	0	CB
Dnajc3	260018	14	119369918	14.095.016	14	67.37082	96532085	2.41575	2.1222	0	1.17E-06	0	0	CB
Erc1	727177	6	119775709	d6mit366	6	77.49561	1.15E+08	1.01285	1.14826	0	1.18E-06	0.0005	0.041856	Shared
Npr2	574666	4	43646456	d4mit238	4	33.23278	45243003	0.52543	0.61269	0	1.18E-06	0	0	CB
Rnf213	133892	11	119344265	D11MIT214	11	79.65651	1.15E+08	0.99832	1.20294	0	1.19E-06	0	0	CB
Tnfrsf21	359724	17	43201976	D17MIT51	17	53.34361	43641790	0.98617	1.11583	0	1.20E-06	0	0	Shared
unassigned	856435	9	121574899	D9Mit18	9	96.97845	1.2E+08	1.75825	2.3459	0	1.21E-06	0.0005	0.041856	CB
Bdh2	538597	3	134953960	D3MIT57	3	88.53548	1.16E+08	0.76179	0.97129	0	1.23E-06	0	0	CB
Tardbp	622398	4	147994798	D4MIT232	4	109.1183	1.45E+08	3.18398	2.77797	0	1.23E-06	0	0	CB
Zfyve21	180973	12	113061454	D12MIT7	12	66.69663	1.05E+08	1.64593	1.3737	0	1.23E-06	0	0	Shared
unassigned	300705	15	10408157	15.010.846	15	8.803289	10831030	1.11021	1.27726	0	1.23E-06	0	0	CB
unassigned	86673	10	7965674	rs13480474	10	1.8	4403267	1.81434	2.00402	0	1.23E-06	0.0005	0.041856	CB
Atp11b	521820	3	35735881	03.033.871	3	22.08075	33578373	1.3583	1.51295	0	1.27E-06	0.0005	0.041856	CB
unassigned	262149	14	13324384	14.008.937	14	5.6	10975728	1.9573	1.77219	0	1.27E-06	0	0	CB
Per3	623148	4	150393069	D4MIT42	4	117.1013	1.51E+08	0.23751	0.20531	0	1.29E-06	0	0	CB
unassigned	157590	11	104211525	11.104.430	11	62.15042	1.04E+08	2.27611	2.4849	0	1.29E-06	0	0	CB

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	740171	7	54064404	D7MIT267	7	18.29809	30331965	1.01329	0.86196	0	1.29E-06	0	0	CB
Crispld1	1942	1	17743059	rs13475769	1	16.19758	24958696	0.32912	0.42022	0	1.30E-06	0	0	Shared
Vps13a	434578	19	16815265	19.013.429	19	11.12922	13436471	2.16398	1.89212	0	1.31E-06	0	0	CB
unassigned	808797	8	125135516	D8MIT42	8	102.8893	1.29E+08	0.79403	0.96002	0	1.32E-06	0	0	CB
Fpr2	353905	17	18030342	17.021.019	17	14.36839	21451267	2.06887	1.72413	0	1.34E-06	0.0005	0.041856	CB
Mios	683988	6	8185915	06.016.672	6	10.4	16672000	0.75633	0.92401	0	1.34E-06	0	0	CB
Grin2d	765655	7	53113824	D7MIT228	7	28.11811	47279833	0.98432	1.29143	0	1.35E-06	0	0	CB
Dtd1	470032	2	144461517	D2MIT411	2	112.9735	1.59E+08	1.71855	1.52458	0	1.39E-06	0	0	Shared
Tekt2	616786	4	126000374	D4MIT308	4	84.36025	1.24E+08	0.83006	1.14917	0	1.40E-06	0	0	Shared
Pik3c3	391645	18	30462574	D18Mit68	18	14.5139	21594126	0.61354	0.4584	0	1.41E-06	0	0	Shared
Mdm4	51176	1	134900380	D1MIT1001	1	72.84145	1.31E+08	2.22734	2.39521	0	1.43E-06	0	0	CB
Slc39a10	37846	1	46877377	D1MIT236	1	37.41892	45435458	1.11432	0.94796	0	1.47E-06	0	0	CB
Lrpprc	385412	17	85163801	D17MIT76	17	95.2661	86033231	0.71734	0.86463	0	1.48E-06	0.0005	0.041856	CB
Sclt1	548357	3	41451369	D3MIT6	3	28.26274	48687327	1.02489	1.33773	0	1.48E-06	0	0	CB
Arpc5	22876	1	154622291	D1Mit102	1	80.03925	1.49E+08	0.99639	1.06403	0	1.50E-06	0	0	Shared
Enox1	255595	14	77992652	RS31380922	14	61.61076	78742431	0.72633	0.86856	0	1.50E-06	0	0	Shared
Eltd1	541741	3	151155337	D3MIT147	3	137.3239	1.48E+08	4.54922	3.68222	0	1.51E-06	0	0	Shared
Hydin	806313	8	113073505	D8MIT215	8	87.84173	1.18E+08	2.7439	3.4963	0	1.51E-06	0.0005	0.041856	CB
Sacm1l	856979	9	123475511	D9Mit18	9	96.97845	1.2E+08	0.76204	0.66721	0	1.54E-06	0.0005	0.041856	CB
Zfp108	735175	7	25043484	07.013.915	7	8.7	15600169	8.31923	7.23829	0	1.55E-06	0.0005	0.041856	CB
Fam108b	422430	19	21755379	19.013.429	19	11.12922	13436471	0.11971	0.14022	0	1.56E-06	0	0	CB
BC020535	471967	2	152902140	D2MIT100	2	54.19426	1.06E+08	1.70231	1.44592	0	1.57E-06	0.0005	0.041856	CB
Lrrc68	785850	7	20116744	07.013.915	7	8.7	15600169	0.9143	1.36226	0	1.57E-06	0	0	Shared
Tmem67	598360	4	11980844	04.013.290	4	8.3	13290000	0.85878	0.64002	0	1.57E-06	0.0005	0.041856	CB
Rmnd1	63851	10	5918886	RS38343005	10	4.536629	11465792	1.29917	1.51037	0	1.58E-06	0	0	CB
Tmem143	739926	7	53164692	D7Mit232	7	35.20811	59868792	0.61138	0.73886	0	1.58E-06	0.0005	0.041856	CB
Coro2b	868346	9	62277042	D9MIT248	9	44.87553	58210366	1.55932	1.72617	0	1.59E-06	0	0	CB
Opn4	266590	14	35407969	D14MIT174	14	33.32711	32460166	2.37684	1.81899	0	1.59E-06	0.0005	0.041856	CB
OTTMUSG00000010657	594075	4	146508732	D4MIT232	4	109.1183	1.45E+08	0.7075	0.91956	0	1.60E-06	0	0	CB
unassigned	562428	3	127247045	D3MIT256	3	103.276	1.36E+08	0.06968	0.05748	0	1.61E-06	0.0005	0.041856	Shared
unassigned	866597	9	55075624	D9MIT336	9	49.6331	65425671	0.73816	1.01791	0	1.61E-06	0.0005	0.041856	CB
unassigned	690621	6	48355442	06.057.998	6	39.56321	58018416	1.67883	1.45349	0	1.63E-06	0	0	CB
Ccbl2	540051	3	142401206	D3MIT147	3	137.3239	1.48E+08	1.97265	1.69295	0	1.64E-06	0	0	Shared
Fam20b	55301	1	158611456	D1Mit102	1	80.03925	1.49E+08	0.83273	0.75213	0	1.65E-06	0	0	CB
Rab6b	851801	9	103064875	D9MIT24	9	73.18313	1.03E+08	1.13189	1.01848	0	1.66E-06	0.0005	0.041856	Shared
unassigned	298646	15	100644843	D15MIT44	15	76.94503	98951714	0.7451	1.12552	0	1.66E-06	0	0	Shared
unassigned	266825	14	37709413	14.008.937	14	5.6	10975728	0.4846	0.56713	0	1.66E-06	0.0005	0.041856	CB
unassigned	643835	5	104930760	D5MIT10	5	65.80535	1.05E+08	0.82991	0.7241	0	1.66E-06	0.0005	0.041856	CB
unassigned	734452	7	17547699	D7MIT267	7	18.29809	30331965	1.21616	1.05547	0	1.67E-06	0	0	CB
Tmem18	166581	12	31272074	D12MIT60	12	21.02542	35474805	2.78047	2.35264	0	1.71E-06	0.0005	0.041856	CB
Kif5c	453440	2	49550291	D2Mit297	2	25.96707	42461006	1.59835	1.77432	0	1.72E-06	0	0	Shared
Rnaseh2b	252777	14	62984109	D14MIT263	14	64.79535	89360701	1.7752	1.26694	0	1.72E-06	0	0	CB

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Plekhg5	595518	4	151482591	D4MIT42	4	117.1013	1.51E+08	0.61752	0.71254	0	1.74E-06	0	0	CB
Ifi204	58978	1	175685749	01.183.109	1	96.11848	1.83E+08	1.62962	1.13164	0	1.78E-06	0	0	CB
unassigned	708011	6	146773303	06.149.619	6	105.5067	1.49E+08	12.34422	15.26888	0	1.79E-06	0	0	CB
unassigned	787488	8	4206196	D8MIT155	8	3.1	4976602	0.85954	0.98474	0	1.80E-06	0	0	CB
Slc29a1	377576	17	45729215	D17MIT180	17	63.0586	51571276	0.51141	0.43365	0	1.83E-06	0.0005	0.041856	CB
Thnsl1	447406	2	21135331	D2MIT1	2	2.4	3803361	1.25147	1.16877	0	1.83E-06	0.0005	0.041856	CB
Aph1b	869349	9	66641945	D9MIT336	9	49.6331	65425671	1.31123	1.63688	0	1.84E-06	0.0005	0.041856	CB
unassigned	619631	4	136488774	D4MIT42	4	117.1013	1.51E+08	0.80623	0.60048	0	1.84E-06	0	0	CB
unassigned	53915	1	153254675	01.183.109	1	96.11848	1.83E+08	0.93895	0.78768	0	1.85E-06	0	0	CB
Bms1	726747	6	118339266	d6mit366	6	77.49561	1.15E+08	1.03855	1.20612	0	1.86E-06	0.0005	0.041856	CB
Park2	352675	17	11685572	17.021.019	17	14.36839	21451267	1.02903	0.85197	0	1.88E-06	0.0005	0.041856	CB
Snapc1	173030	12	75083468	12.065.348	12	37.44045	65530382	0.22763	0.16526	0	1.89E-06	0	0	CB
Rbm45	458349	2	76221526	D2MIT100	2	54.19426	1.06E+08	0.78664	0.67898	0	1.92E-06	0.0005	0.041856	Shared
unassigned	262355	14	14948155	14.008.937	14	5.6	10975728	1.67967	1.5579	0	1.93E-06	0	0	CB
Iars2	61140	1	187121376	D1MIT507	1	89.46999	1.67E+08	0.28269	0.38944	0	1.95E-06	0.0005	0.041856	Shared
unassigned	710962	6	23042599	06.016.672	6	10.4	16672000	0.86241	0.70232	0	1.99E-06	0	0	CB
Mgl1	120960	11	69949137	D11MIT320	11	39.87138	70766870	0.23471	0.28914	0	2.02E-06	0	0	CB
unassigned	809484	8	127059141	D8MIT42	8	102.8893	1.29E+08	1.13218	1.32333	0	2.03E-06	0	0	CB
Chm	931841	X	110226164	DXMit79	X	50.81363	1.27E+08	2.17526	2.06398	1.77399	2.04E-06	0	0	CB
Alox8	147453	11	69001169	RS26969123	11	30.52371	53430698	1.28706	1.58341	0	2.08E-06	0.0005	0.041856	CB
Nmt2	444205	2	3243533	D2MIT1	2	2.4	3803361	0.82347	0.9992	0	2.08E-06	0	0	Shared
Pld1	520182	3	27987572	RS37321647	3	42.80783	68043880	0.99991	1.24314	0	2.08E-06	0.0005	0.041856	Shared
Snrpa1	742746	7	73216166	D7MIT294	7	15.72036	28074461	0.57392	0.66928	0	2.11E-06	0.0005	0.041856	CB
unassigned	630230	5	24005856	D5MIT388	5	29.38073	33660748	0.4915	0.58637	0	2.11E-06	0	0	Shared
Gcnt1	434709	19	17409817	19.013.429	19	11.12922	13436471	0.44125	0.36079	0	2.12E-06	0	0	CB
Rapgef4	457502	2	72077139	RS28322831	2	43.67748	71063776	1.0468	1.2367	0	2.12E-06	0	0	CB
Zdhhc18	618582	4	133168843	04.133.005	4	97.64222	1.33E+08	1.36208	1.60461	0	2.12E-06	0	0	Shared
unassigned	602280	4	43546307	d4mit238	4	33.23278	45243003	0.20687	0.16362	0	2.18E-06	0.0005	0.041856	Shared
unassigned	880658	9	123620293	D9Mit18	9	96.97845	1.2E+08	0.76662	0.63222	0	2.20E-06	0	0	CB
Spnb1	192529	12	77729882	D12MIT91	12	43.26798	72843829	1.88593	1.49797	0	2.21E-06	0	0	CB
Ranbp10	827607	8	108310542	D8MIT215	8	87.84173	1.18E+08	1.04913	1.23265	0	2.22E-06	0.0005	0.041856	CB
unassigned	878086	9	111131179	09.105.291	9	79.88305	1.05E+08	1.02549	0.79629	0	2.22E-06	0.0005	0.041856	CB
Tmem2	422488	19	21922447	19.013.429	19	11.12922	13436471	0.54153	0.68681	0	2.24E-06	0	0	CB
unassigned	760265	7	20022251	07.013.915	7	8.7	15600169	1.62012	1.40077	0	2.24E-06	0.0005	0.041856	CB
Dis3l	868873	9	64173631	D9MIT248	9	44.87553	58210366	1.82768	1.57891	0	2.26E-06	0.0005	0.041856	CB
Snx29	320475	16	11738402	16.010.089	16	7.349459	10175515	1.46116	1.27489	0	2.26E-06	0	0	Shared
unassigned	414074	18	67573691	18.038.678	18	24.45192	38711680	0.39081	0.45253	0	2.31E-06	0	0	CB
unassigned	894212	13_random	121844	D13MIT53	13	72.69389	1.13E+08	2.00092	1.84204	0	2.32E-06	0.0005	0.041856	CB
Bxdc2	300703	15	10406587	15.010.846	15	8.803289	10831030	1.47765	1.69545	0	2.34E-06	0	0	CB
Arntl	751327	7	120452130	07.088.976	7	61.08266	96249318	1.51467	1.23988	0	2.38E-06	0.0005	0.041856	CB
unassigned	453482	2	49625892	RS27953638	2	27.96753	50041657	1.67901	1.51919	0	2.40E-06	0	0	CB
unassigned	582764	4	99601976	04.098.998	4	75.01299	99172673	0.91905	0.74142	0	2.43E-06	0	0	CB

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Ube4a	864110	9	44761098	09.046.588	9	34.49446	46645088	0.27021	0.35046	0	2.46E-06	0	0	CB
Cbfa2t3	831154	8	125166871	D8MIT42	8	102.8893	1.29E+08	0.58508	0.75517	0	2.47E-06	0.0005	0.041856	CB
Chd1	353565	17	15872740	D17Mit213	17	12.20714	16752157	2.42759	2.69476	0	2.47E-06	0	0	CB
Ccna2	547468	3	36463877	03.033.871	3	22.08075	33578373	1.43122	1.89175	0	2.49E-06	0.0005	0.041856	CB
unassigned	680240	5	143050670	D5MIT169	5	118.4503	1.5E+08	0.88981	1.01456	0	2.50E-06	0	0	CB
unassigned	63865	10	5942789	D10Mit123	10	3.021254	9952319	1.99325	1.77823	0	2.51E-06	0.0005	0.041856	Shared
Fh1	59275	1	177537970	01.183.109	1	96.11848	1.83E+08	0.76858	0.85819	0	2.57E-06	0	0	CB
Lsm8	685315	6	18803713	06.016.672	6	10.4	16672000	1.09622	0.96952	0	2.57E-06	0	0	Shared
Cse1l	475883	2	166755395	02.168.990	2	151.4053	1.69E+08	2.47841	2.23609	0	2.58E-06	0	0	CB
Dennd4a	844267	9	64683761	D9MIT247	9	25.36975	36940492	2.02236	1.72509	0	2.61E-06	0.0005	0.041856	Shared
unassigned	357203	17	31667864	17.034.150	17	51.1372	34678889	0.43861	0.37131	0	2.61E-06	0	0	Shared
Vars2	376050	17	35796752	17.034.150	17	51.1372	34678889	0.64523	0.76845	0	2.69E-06	0	0	CB
1700081L11Rik	157592	11	104217215	D11MIT214	11	79.65651	1.15E+08	0.35037	0.41867	0	2.70E-06	0	0	CB
Actr3b	630544	5	25356271	05.018.430	5	14.15919	18423994	0.80253	0.93806	0	2.71E-06	0	0	CB
Bmp1	273478	14	70894575	D14MIT39	14	54.52991	69166099	1.55148	1.35316	0	2.72E-06	0	0	Shared
Spire1	414135	18	67712404	18.063.800	18	48.99442	63834285	0.22462	0.2736	0	2.74E-06	0	0	CB
Mtor	594479	4	147923922	D4MIT232	4	109.1183	1.45E+08	0.44056	0.58625	0	2.77E-06	0.0005	0.041856	CB
unassigned	547527	3	36570596	D3Mit151	3	18.63179	31137265	0.51758	0.37943	0	2.77E-06	0	0	CB
Park2	352622	17	11430536	17.034.150	17	51.1372	34678889	2.05165	1.85235	0	2.79E-06	0.0005	0.041856	CB
Tmem63b	377647	17	45814880	17.059.041	17	71.70333	59495092	0.74051	0.89224	0	2.81E-06	0	0	Shared
Sacm1l	856974	9	123461814	D9MIT201	9	91.42427	1.17E+08	1.99585	1.83411	0	2.83E-06	0	0	CB
unassigned	500560	2	119482208	RS27267095	2	129.5613	1.37E+08	1.16431	1.01879	0	2.83E-06	0	0	CB
Zfp459	232749	13	67514854	13.061.624	13	39.87979	61715738	5.0602	4.46803	0	2.84E-06	0	0	Shared
unassigned	761796	7	29765417	D7MIT267	7	18.29809	30331965	2.1761	1.97966	0	2.87E-06	0.0005	0.041856	Shared
Gfap	157085	11	102754393	D11MIT214	11	79.65651	1.15E+08	1.09214	1.2784	0	2.88E-06	0.0005	0.041856	CB
Piwil2	273429	14	70801868	D14Mit194	14	66.46956	94235479	1.02671	1.29233	0	2.88E-06	0.0005	0.041856	CB
unassigned	169471	12	52527127	D12MIT285	12	30.22146	55750112	2.44763	2.05178	0	2.94E-06	0	0	Shared
Atpbd3	738912	7	50932608	D7MIT228	7	28.11811	47279833	0.82583	1.06464	0	2.97E-06	0.0005	0.041856	CB
unassigned	66125	10	19928169	RS29316898	10	9.384466	15819840	4.66723	4.28286	0	2.97E-06	0.0005	0.041856	CB
Stxbp2	787379	8	3632500	D8MIT155	8	3.1	4976602	1.26912	1.03367	0	2.99E-06	0	0	CB
unassigned	358650	17	35400148	17.034.150	17	51.1372	34678889	0.93833	0.82621	0	2.99E-06	0.0005	0.041856	Shared
Reck	574741	4	43943065	d4mit238	4	33.23278	45243003	0.74372	0.62428	0	3.00E-06	0.0005	0.041856	CB
unassigned	771615	7	89796637	D7MIT350	7	57.28732	90734599	3.73874	3.05059	0	3.00E-06	0	0	CB
Tra2a	715633	6	49194867	D6MIT274	6	30.88472	48676564	1.63647	1.41558	0	3.03E-06	0	0	CB
unassigned	474780	2	162853881	D2MIT411	2	112.9735	1.59E+08	1.49358	1.2703	0	3.05E-06	0	0	CB
Clk1	39691	1	58476967	D1MIT236	1	37.41892	45435458	2.11298	2.48594	0	3.09E-06	0	0	Shared
Hydin	806348	8	113131643	D8MIT47	8	79.10975	1.09E+08	1.68469	2.52906	0	3.10E-06	0	0	CB
Hydin	806298	8	113047006	D8MIT215	8	87.84173	1.18E+08	15.08164	13.33413	0	3.18E-06	0.0005	0.041856	CB
Elmo1	203869	13	20300006	13.013.314	13	8.3	13614141	0.40008	0.51254	0	3.22E-06	0	0	CB
H2-T10	893542	17	36178849	17.021.019	17	14.36839	21451267	1.9039	2.12298	0	3.23E-06	0	0	Shared
Prune	556303	3	95069388	RS30160288	3	119.3825	1.26E+08	0.90062	0.99463	0	3.26E-06	0	0	CB
Ldb3	266550	14	35342646	14.027.409	14	32.01969	29395320	1.25361	1.60915	0	3.33E-06	0.0005	0.041856	CB

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Dhx9	54490	1	155328300	01.136.071	1	77.74879	1.36E+08	0.90678	0.78437	0	3.34E-06	0	0	Shared
Zdhhc18	618585	4	133169735	D4Mit203	4	89.73231	1.29E+08	0.53805	0.46864	0	3.37E-06	0.0005	0.041856	CB
Paqr8	2257	1	20912348	D1Mit374	1	27.02859	34816928	0.02634	0.03883	0	3.42E-06	0	0	CB
Dzip1	279652	14	119299722	RS31252045	14	77.8316	1.11E+08	1.34468	1.17814	0	3.46E-06	0	0	CB
Stx3	420873	19	11849858	19.009.231	19	7.749799	9238445	0.83999	1.06568	0	3.52E-06	0	0	Shared
B230118H07Rik	497000	2	101425402	D2MIT100	2	54.19426	1.06E+08	2.04028	2.39211	0	3.53E-06	0	0	Shared
Pcdhga7	393349	18	37874617	D18Mit123	18	38.31055	56130259	1.89293	1.59297	0	3.53E-06	0	0	CB
Tmod1	575341	4	46073842	d4mit238	4	33.23278	45243003	0.56953	0.65245	0	3.59E-06	0.0005	0.041856	Shared
Tmod4	531251	3	94933033	D3MIT315	3	89.68246	1.16E+08	1.09373	0.78096	0	3.59E-06	0	0	CB
Pnpla6	787324	8	3530995	D8MIT155	8	3.1	4976602	1.05324	1.16657	0	3.61E-06	0.0005	0.041856	Shared
Mdc1	358844	17	35991379	17.034.150	17	51.1372	34678889	0.74197	0.61036	0	3.74E-06	0.0005	0.041856	CB
Mecr	590286	4	131410578	D4MIT308	4	84.36025	1.24E+08	2.16316	1.95217	0	3.75E-06	0.0005	0.041856	Shared
Reln	657339	5	21540390	D5MIT294	5	15.58331	20863135	1.03534	1.13713	0	3.78E-06	0.0005	0.041856	CB
unassigned	3809	1	34500786	D1Mit374	1	27.02859	34816928	1.81364	1.67395	0	3.79E-06	0	0	CB
unassigned	646569	5	116062023	D5MIT95	5	98.81753	1.25E+08	0.24857	0.30529	0	3.79E-06	0.0005	0.041856	CB
4930506M07Rik	443028	19	59048529	D19MIT103	19	59.41115	53838656	0.77439	0.90772	0	3.84E-06	0.0005	0.041856	CB
Baz2b	489531	2	59737467	D2MIT61	2	35.12792	60528325	1.12748	1.02755	0	3.89E-06	0.0005	0.041856	CB
D3Ertd751e	523111	3	41559974	D3MIT67	3	34.10534	52956484	5.60716	4.80431	0	3.93E-06	0.0005	0.041856	CB
Gucy1a3	553595	3	81949724	D3MIT98	3	51.73848	85985423	0.59579	0.43959	0	3.93E-06	0	0	CB
unassigned	734886	7	19935654	07.013.915	7	8.7	15600169	1.03152	1.17921	0	3.93E-06	0	0	CB
Pgcp	285938	15	33179837	15.028.723	15	14.88113	28708166	0.84368	0.75663	0	3.99E-06	0.0005	0.041856	CB
BC051070	558832	3	106192777	D3MIT256	3	103.276	1.36E+08	0.99962	0.80387	0	4.04E-06	0.0005	0.041856	CB
Ccdc53	78262	10	87678728	RS46745265	10	65.86958	69258223	1.80824	2.12292	0	4.05E-06	0	0	CB
Faim2	317192	15	99344842	D15MIT44	15	76.94503	98951714	1.95075	1.87517	0	4.06E-06	0.0005	0.041856	Shared
Snhg11	473909	2	158201454	D2Mit274	2	62.95823	1.14E+08	0.46855	0.53316	0	4.06E-06	0	0	CB
Tpsb2	355290	17	25504259	17.013.500	17	8.4	13900467	0.9866	1.23356	0	4.12E-06	0.0005	0.041856	CB
Nudcd3	135648	11	6093283	D11MIT2	11	7.6	12218640	1.09516	1.19344	0	4.21E-06	0.0005	0.041856	Shared
Chrna7	767863	7	70304423	D7Mit232	7	35.20811	59868792	0.05405	0.07906	0	4.26E-06	0	0	CB
unassigned	734868	7	19880754	07.013.915	7	8.7	15600169	2.00707	2.43556	0	4.29E-06	0	0	Shared
unassigned	24427	1	162965233	D1Mit102	1	80.03925	1.49E+08	0.94366	0.78989	0	4.32E-06	0	0	Shared
Cpne1	508588	2	155904340	D2MIT100	2	54.19426	1.06E+08	0.84642	0.7269	0	4.44E-06	0.0005	0.041856	CB
D17H6S56E-5	375820	17	35137166	17.034.150	17	51.1372	34678889	2.44684	2.13734	0	4.45E-06	0	0	CB
unassigned	202897	13	13756382	D13Mit207	13	8.688726	16526195	0.77058	0.92199	0	4.45E-06	0.0005	0.041856	CB
Slc35a5	343118	16	45158520	16.039.061	16	48.3587	39141781	1.17783	1.34729	0	4.72E-06	0	0	CB
Syngr2	133432	11	117671023	D11MIT214	11	79.65651	1.15E+08	1.58078	1.30043	0	4.73E-06	0.0005	0.041856	Shared
Nfs1	508617	2	155967893	D2Mit274	2	62.95823	1.14E+08	2.16302	1.90373	0	4.80E-06	0	0	Shared
Hnrnpa3	458254	2	75507078	RS28322831	2	43.67748	71063776	0.54675	0.48471	0	4.82E-06	0	0	CB
Klc4	378028	17	46767744	D17MIT51	17	53.34361	43641790	0.64864	0.75951	0	4.89E-06	0.0005	0.041856	CB
unassigned	765985	7	54019871	D7MIT294	7	15.72036	28074461	1.52366	1.29341	0	4.99E-06	0	0	CB
Zfp758	354507	17	22510630	D17MIT51	17	53.34361	43641790	27.67984	24.94355	0	5.05E-06	0.0005	0.041856	CB
Sfmbt1	247010	14	31587137	D14MIT174	14	33.32711	32460166	0.97388	0.85559	0	5.12E-06	0.0005	0.041856	CB
unassigned	614698	4	117558189	RS27499066	4	79.43714	1.15E+08	1.2231	1.34714	0	5.17E-06	0.0005	0.041856	CB

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Psme4	112831	11	30745188	D11MIT186	11	23.608	35049231	1.05777	0.91065	0	5.29E-06	0	0	CB
Med23	67108	10	24628440	RS29367295	10	20.72734	23573544	1.25667	1.10129	0	5.49E-06	0.0005	0.041856	Shared
D11Bwg0517e	161334	11	118672602	D11MIT214	11	79.65651	1.15E+08	1.3435	1.11154	0	5.52E-06	0.0005	0.041856	CB
Vps13a	434549	19	16761576	19.013.429	19	11.12922	13436471	1.79722	1.54765	0	5.62E-06	0	0	CB
Cul1	690457	6	47464981	06.057.998	6	39.56321	58018416	1.70029	1.51762	0	5.64E-06	0	0	CB
Tjp2	435834	19	24209340	D19MIT96	19	21.38792	21916083	0.70476	0.6136	0	5.69E-06	0	0	CB
Gsbs	692436	6	55972406	D6MIT274	6	30.88472	48676564	1.00576	0.87911	0	5.73E-06	0.0005	0.041856	CB
Leprel1	339546	16	25972375	D16MIT139	16	56.62781	65669762	0.82026	0.65672	0	5.73E-06	0.0005	0.041856	CB
Mccc1	547336	3	35892842	D3MIT6	3	28.26274	48687327	0.79725	0.9337	0	5.92E-06	0	0	CB
Herc2	741479	7	63401146	D7MIT248	7	39.99047	80656343	1.12633	0.99367	0	5.96E-06	0	0	CB
unassigned	173536	12	77402410	D12MIT285	12	30.22146	55750112	0.47854	0.64049	0	6.05E-06	0	0	Shared
Mlh1	878094	9	111143762	09.105.291	9	79.88305	1.05E+08	0.75892	0.58944	0	6.10E-06	0	0	CB
Trim9	191298	12	71391273	D12MIT91	12	43.26798	72843829	1.11242	0.96899	0	6.29E-06	0.0005	0.041856	CB
Gabarapl2	806682	8	114477273	D8MIT215	8	87.84173	1.18E+08	0.07746	0.09928	0	6.33E-06	0	0	CB
Cntn6	700045	6	104518953	d6mit366	6	77.49561	1.15E+08	1.92724	1.68467	0	6.46E-06	0.0005	0.041856	CB
Psg16	734486	7	17716086	07.013.915	7	8.7	15600169	0.08806	0.11783	0	6.46E-06	0	0	CB
H47	742752	7	73228298	07.056.455	7	36.40088	63842351	0.82356	1.09654	0	6.52E-06	0.0005	0.041856	Shared
Nup155	282448	15	8071499	D15MIT252	15	9.706826	22550163	1.30888	1.17038	0	6.78E-06	0.0005	0.041856	Shared
Zfp39	144903	11	58704506	11.072.405	11	39.87138	72402307	1.96701	2.21938	0	6.84E-06	0.0005	0.041856	CB
Bivm	5817	1	44185577	D1MIT236	1	37.41892	45435458	1.33998	1.17031	0	6.97E-06	0.0005	0.041856	CB
Klk6	738972	7	51080820	D7MIT228	7	28.11811	47279833	0.31029	0.36137	0	7.03E-06	0.0005	0.041856	CB
Heatr5a	188645	12	52977406	12.007.977	12	5	7957798	1.37058	1.70711	0	7.24E-06	0	0	CB
unassigned	809152	8	125984881	D8MIT42	8	102.8893	1.29E+08	1.31477	1.05822	0	7.29E-06	0.0005	0.041856	Shared
Pgbd5	831609	8	126908402	D8MIT42	8	102.8893	1.29E+08	0.65568	0.79559	0	7.30E-06	0.0005	0.041856	CB
unassigned	296039	15	88924532	D15Mit107	15	49.40097	84216927	1.61326	1.73366	0	7.33E-06	0.0005	0.041856	CB
Ift74	581667	4	94345894	04.098.998	4	75.01299	99172673	2.8479	2.37677	0	7.35E-06	0.0005	0.041856	CB
unassigned	851664	9	102532220	09.079.053	9	64.60162	79115123	0.78965	0.84711	0	7.50E-06	0.0005	0.041856	Shared
Smek2	112443	11	29082448	D11MIT51	11	25.39412	36205252	0.80229	0.94067	0	7.60E-06	0	0	CB
Slco1c1	706966	6	141513036	D6MIT194	6	87.57626	1.28E+08	1.12247	1.31782	0	7.61E-06	0	0	CB
unassigned	673934	5	115705450	d5mit158	5	69.85959	1.15E+08	1.07115	1.16457	0	7.62E-06	0.0005	0.041856	Shared
unassigned	871802	9	78328345	D9MIT24	9	73.18313	1.03E+08	0.65429	0.58977	0	7.70E-06	0.0005	0.041856	CB
Serinc3	510109	2	163460193	02.168.990	2	151.4053	1.69E+08	1.08328	0.96578	0	7.79E-06	0.0005	0.041856	CB
Zfp658	738871	7	50820086	D7Mit232	7	35.20811	59868792	0.9577	1.19414	0	7.90E-06	0.0005	0.041856	CB
unassigned	21832	1	145591997	D1Mit102	1	80.03925	1.49E+08	1.02703	0.97368	0	7.95E-06	0	0	CB
Cnksr3	63323	10	3217423	D10Mit123	10	3.021254	9952319	0.21515	0.16798	0	7.96E-06	0	0	CB
Atxn1	228176	13	45793191	RS30012306	13	43.69714	70428413	1.33425	1.4953	0	8.19E-06	0.0005	0.041856	CB
Slco1c1	706957	6	141490614	D6MIT194	6	87.57626	1.28E+08	1.30701	1.09523	0	8.24E-06	0	0	CB
Thy1	839424	9	43854974	D9MIT107	9	53.50038	73315075	1.1402	1.0719	0	8.25E-06	0.0005	0.041856	CB
Mfn2	622160	4	147257357	D4MIT232	4	109.1183	1.45E+08	1.20197	1.10529	0	8.34E-06	0.0005	0.041856	Shared
Abat	319854	16	8602388	RS4165334	16	14.91941	23467678	0.60565	0.67585	0	8.67E-06	0	0	CB
unassigned	731788	6	142980056	D6Mit14	6	101.6085	1.46E+08	0.48108	0.39051	0	8.82E-06	0.0005	0.041856	Shared
Ada	510143	2	163556054	02.168.990	2	151.4053	1.69E+08	0.36236	0.47841	0	9.54E-06	0	0	CB

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Brwd2	755081	7	136763885	RS36353338	7	66.26522	1.13E+08	1.32221	1.13728	0	9.62E-06	0	0	CB
Brp44l	352176	17	8476774	17.013.500	17	8.4	13900467	0.38294	0.33334	0	9.68E-06	0	0	CB
Slc37a3	714138	6	39302665	d6mit123	6	39.56321	56801586	3.20445	2.78542	0	9.84E-06	0	0	CB
Hydin	806251	8	112934349	D8MIT215	8	87.84173	1.18E+08	0.67982	0.58898	0	9.89E-06	0.0005	0.041856	CB
Sacm1l	856978	9	123469684	D9Mit18	9	96.97845	1.2E+08	1.6359	1.49993	0	9.90E-06	0	0	CB
Rplp0	646516	5	116013318	D5MIT10	5	65.80535	1.05E+08	1.07444	0.76295	0	1.00E-05	0.0005	0.041856	Shared
Ctso	528017	3	81758406	RS31036560	3	62.868	73719554	1.02461	1.38207	0	1.04E-05	0	0	Shared
Mkks	504932	2	136706086	D2Mit274	2	62.95823	1.14E+08	1.41571	1.54907	0	1.04E-05	0	0	CB
Vps13a	434568	19	16789546	D19MIT96	19	21.38792	21916083	0.91434	1.07556	0	1.04E-05	0.0005	0.041856	CB
Gpd1l	878814	9	114826138	D9MIT201	9	91.42427	1.17E+08	0.41317	0.47839	0	1.14E-05	0.0005	0.041856	Shared
Acaa1a	855863	9	119251862	D9Mit18	9	96.97845	1.2E+08	3.82715	4.55826	0	1.15E-05	0	0	CB
Smarca2	423472	19	26758317	D19MIT13	19	37.09408	32713513	0.36703	0.4513	0	1.15E-05	0.0005	0.041856	CB
unassigned	375150	17	33158455	D17MIT180	17	63.0586	51571276	0.16008	0.09049	0	1.16E-05	0.0005	0.041856	CB
Zfp94	760490	7	25087964	07.013.915	7	8.7	15600169	1.25422	1.14617	0	1.17E-05	0	0	CB
Mrpl30	4460	1	37950784	D1Mit374	1	27.02859	34816928	1.59953	1.41732	0	1.23E-05	0	0	Shared
Cmbl	285683	15	31519469	15.028.723	15	14.88113	28708166	0.30226	0.43697	0	1.26E-05	0.0005	0.041856	Shared
unassigned	521790	3	35687495	D3MIT6	3	28.26274	48687327	1.72016	2.00371	0	1.32E-05	0	0	CB
Ift74	581670	4	94352372	04.098.998	4	75.01299	99172673	2.16828	1.78724	0	1.44E-05	0.0005	0.041856	CB
Tbc1d9	800317	8	85765440	D8MIT346	8	54.67316	85454038	1.30659	1.57327	0	1.48E-05	0.0005	0.041856	CB
G2e3	169432	12	52458019	D12Mit2	12	26.67403	42747379	2.09016	2.44245	0	1.50E-05	0.0005	0.041856	Shared
Tex9	870581	9	72322150	D9MIT107	9	53.50038	73315075	0.88415	1.04022	0	1.51E-05	0.0005	0.041856	CB
Apbb2	664872	5	66791495	D5MIT352	5	30.68587	35957616	0.46707	0.55721	0	1.61E-05	0.0005	0.041856	CB
unassigned	739993	7	53338057	D7MIT248	7	39.99047	80656343	1.51387	1.30109	0	1.64E-05	0.0005	0.041856	CB
4833420G17Rik	220869	13	120251273	d13mit151	13	74.51442	1.16E+08	3.75267	2.79153	0	1.67E-05	0.0005	0.041856	Shared
Rnf167	121148	11	70464027	D11MIT320	11	39.87138	70766870	0.9967	1.15396	0	1.72E-05	0.0005	0.041856	Shared
Gabra5	767251	7	64669013	D7MIT267	7	18.29809	30331965	1.60234	1.97742	0	1.74E-05	0.0005	0.041856	CB
Hydin	806344	8	113122869	D8MIT47	8	79.10975	1.09E+08	1.8871	2.35799	0	1.78E-05	0	0	Shared
Trappc2l	808802	8	125137831	D8MIT42	8	102.8893	1.29E+08	1.61273	1.45287	0	1.78E-05	0.0005	0.041856	CB
unassigned	687898	6	34338451	RS49937148	6	13.13583	22510745	3.0939	2.71469	0	2.01E-05	0.0005	0.041856	Shared
Camk2d	536873	3	126432325	RS30160288	3	119.3825	1.26E+08	1.13014	1.28331	0	2.09E-05	0	0	CB
H2-Q2	358667	17	35482626	D17MIT51	17	53.34361	43641790	0.01596	0.01236	0	2.41E-05	0	0	Shared
Pigk	542060	3	152449218	D3Mit19	3	140.7312	1.57E+08	4.48639	5.72729	0	4.07E-05	0.0005	0.041856	CB

Appendix B: SCG cis-sQTL

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Luzp2	741243	7	62313420	07.056.455	7	36.40088	63842351	0.267	1.28228	0	3.16E-60	0	0	Shared
Elmod2	823265	8	85846596	D8MIT346	8	54.673156	85454038	0.17504	1.13973	0	3.60E-58	0	0	Shared
Dst	3735	1	34301287	D1Mit374	1	27.028585	34816928	0.22896	1.29561	0	5.69E-58	0	0	Shared
Decr1	598925	4	15846376	04.013.290	4	8.3	13290000	0.42952	1.25063	0	3.47E-55	0	0	Shared
Phkb	801157	8	88446043	D8MIT45	8	58.440058	89829274	0.23427	1.09964	0	8.70E-54	0	0	Shared
Fubp1	541883	3	1.52E+08	D3MIT147	3	137.32386	148408373	0.14133	1.09519	0	1.04E-52	0	0	Shared
Acsl1	794594	8	47603622	08.046.718	8	30.746529	46304537	0.0129	0.35278	0	4.09E-52	0	0	Shared
Astn2	606487	4	65719549	rs13477756	4	50.524248	68030949	0.10411	0.76355	0	5.44E-52	0	0	Shared
Tnks	816022	8	35952750	D8MIT94	8	19.424222	32452130	0.12876	0.6703	0	8.73E-49	0	0	Shared
Scfd1	169466	12	52516530	D12MIT285	12	30.221464	55750112	0.65612	1.97247	0	9.12E-49	0	0	Shared
Epb4.1l1	473393	2	1.56E+08	02.161.464	2	113.50933	161598295	0.45074	1.08937	0	1.32E-48	0	0	Shared
Ikbkap	604611	4	56785906	04.053.650	4	40.480187	53641772	0.47449	1.62661	0	2.35E-48	0	0	Shared
Calm3	759889	7	17504984	07.013.915	7	8.7	15600169	0.48039	0.90187	0	7.02E-48	0	0	Shared
Faim2	317186	15	99341014	D15MIT44	15	76.945032	98951714	0.722	1.28466	0	1.59E-47	0	0	Shared
unassigned	823691	8	87366940	D8MIT45	8	58.440058	89829274	0.66647	1.7865	0	3.88E-47	0	0	Shared
H2-D1	358652	17	35400786	17.034.150	17	51.1372	34678889	3.53782	1.99907	0	5.97E-47	0	0	Shared
Pmpcb	629687	5	21262242	D5MIT294	5	15.58331	20863135	0.14366	0.68525	0	1.39E-46	0	0	Shared
Dlg2	747244	7	99535430	07.088.976	7	61.08266	96249318	0.94658	1.45579	0	2.10E-46	0	0	Shared
Mcam	839488	9	43948488	D9MIT247	9	25.36975	36940492	0.38883	1.00441	0	3.53E-45	0	0	Shared
Nub1	630339	5	24213621	05.018.430	5	14.15919	18423994	0.45206	0.97147	0	4.09E-45	0	0	Shared
Dhx36	551036	3	62288882	03.060.525	3	40.51916	60240993	0.03926	0.42586	0	1.74E-44	0	0	Shared
unassigned	475893	2	1.67E+08	02.168.990	2	151.40532	169124295	0.22775	0.6056	0	1.25E-43	0	0	Shared
Srpk2	657646	5	23046202	D5MIT294	5	15.58331	20863135	0.81719	1.35194	0	1.69E-43	0	0	Shared
Dlat	865416	9	50446044	09.046.588	9	34.49446	46645088	0.8017	1.89964	0	4.37E-43	0	0	Shared
Sacm1l	856973	9	1.23E+08	D9Mit18	9	96.97845	120198563	0.04	0.44489	0	4.56E-43	0	0	Shared
Scoc	823281	8	85961971	D8MIT346	8	54.673156	85454038	0.1028	0.65756	0	7.17E-42	0	0	Shared
Fam20c	652127	5	1.39E+08	05.132.979	5	112.26584	133170167	1.1234	2.98411	0	7.99E-42	0	0	Shared
unassigned	667701	5	86445069	RS33085156	5	79.13497	90112330	0.17058	0.71316	0	8.50E-42	0	0	Shared
Epb4.9	273543	14	71015069	D14MIT39	14	54.529907	69166099	0.3637	1.03307	0	7.40E-40	0	0	Shared
Slc4a4	640797	5	89608686	RS33085156	5	79.13497	90112330	0.99765	1.64769	0	9.87E-40	0	0	Shared
unassigned	646512	5	1.16E+08	d5mit158	5	69.85959	115413178	1.28393	1.74481	0	3.28E-39	0	0	Shared
Rbms1	489847	2	60594523	D2MIT61	2	35.12792	60528325	0.73393	1.25096	0	8.56E-39	0	0	Shared
unassigned	810432	8	1.31E+08	D8MIT42	8	102.88933	129076217	0.14385	0.39074	0	7.80E-38	0	0	Shared
unassigned	649422	5	1.26E+08	D5MIT95	5	98.81753	125309605	0.4471	0.86287	0	8.94E-38	0	0	Shared
unassigned	650242	5	1.3E+08	D5MIT95	5	98.81753	125309605	0.20083	0.49899	0	3.68E-37	0	0	Shared
Ppap2a	219830	13	1.14E+08	D13MIT53	13	72.69389	113084631	2.34845	1.62383	0	4.25E-37	0	0	Shared
unassigned	604618	4	56789435	04.053.650	4	40.480187	53641772	0.48579	1.11913	0	1.02E-36	0	0	Shared
Otud6b	598773	4	14749848	04.013.290	4	8.3	13290000	0.46716	0.84961	0	1.08E-36	0	0	Shared
Stxbp1	484928	2	32667544	D2MIT296	2	21.50213	31180075	1.15728	0.81455	0	1.99E-36	0	0	Shared
H2-K1	375403	17	34136863	17.034.150	17	51.1372	34678889	1.54952	0.99903	0	5.02E-36	0	0	Shared
Ddx55	649093	5	1.25E+08	D5MIT95	5	98.81753	125309605	1.00077	1.56402	0	1.18E-35	0	0	Shared
H2-Aa	375490	17	34420135	17.034.150	17	51.1372	34678889	1.66325	2.92125	0	1.42E-35	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Tspyl2	935130	X	1.49E+08	DXMit216	X	58.906126	140336696	1.13381	2.30516	3.58703	2.14E-35	0	0	Shared
unassigned	656632	5	17319862	D5MIT294	5	15.58331	20863135	0.46476	0.92566	0	3.51E-35	0	0	SCG
unassigned	776895	7	1.2E+08	RS36353338	7	66.26522	112706514	0.47042	1.13519	0	1.50E-34	0	0	Shared
unassigned	800309	8	85745155	D8MIT346	8	54.673156	85454038	0.71443	1.3064	0	3.03E-34	0	0	Shared
unassigned	457361	2	71693712	RS28322831	2	43.67748	71063776	0.78186	1.3139	0	4.21E-34	0	0	Shared
unassigned	739972	7	53309586	D7MIT228	7	28.11811	47279833	0.42157	0.69807	0	1.22E-33	0	0	Shared
Mtor	594480	4	1.48E+08	D4MIT232	4	109.11827	144647559	0.34705	0.72467	0	1.25E-33	0	0	Shared
Gpr137b-ps	222308	13	12708077	D13Mit207	13	8.688726	16526195	0.31797	1.18397	0	1.48E-33	0	0	Shared
Elovl4	872585	9	83676795	09.079.053	9	64.60162	79115123	0.37558	0.66549	0	4.22E-33	0	0	Shared
Ptprd	607395	4	75627986	D4MIT132	4	51.331896	70333587	1.20207	2.29876	0	4.66E-33	0	0	Shared
unassigned	841168	9	50608199	D9MIT285	9	25.81754	40462577	0.5853	1.31168	0	6.39E-33	0	0	Shared
Bmpr1a	266534	14	35260958	14.027.409	14	32.019685	29395320	0.40412	0.62936	0	1.29E-32	0	0	Shared
Akap6	169755	12	54038131	D12MIT285	12	30.221464	55750112	0.12997	0.2967	0	2.60E-32	0	0	Shared
unassigned	872972	9	86489867	09.079.053	9	64.60162	79115123	0.87364	1.16372	0	2.93E-32	0	0	Shared
Amph	203688	13	19186642	D13Mit207	13	8.688726	16526195	0.17741	0.48772	0	3.11E-32	0	0	Shared
Mcam	839481	9	43945317	D9MIT285	9	25.81754	40462577	0.36069	0.73201	0	1.27E-31	0	0	Shared
Arhgef12	863418	9	42786290	D9MIT285	9	25.81754	40462577	0.35047	0.75678	0	1.57E-31	0	0	Shared
Cmbl	285683	15	31519469	15.028.723	15	14.881134	28708166	0.21471	0.38036	0	2.58E-31	0	0	Shared
Nmt2	444205	2	3243533	D2MIT1	2	2.4	3803361	0.42387	0.81926	0	9.08E-31	0	0	Shared
Mcam	839493	9	43950250	D9MIT247	9	25.36975	36940492	0.47078	0.65341	0	1.07E-30	0	0	Shared
Tnpo2	800970	8	87568935	D8MIT45	8	58.440058	89829274	1.8247	2.50023	0	1.11E-30	0	0	Shared
unassigned	582778	4	99634261	04.098.998	4	75.012985	99172673	0.57615	1.32946	0	1.81E-30	0	0	Shared
Tardbp	622399	4	1.48E+08	D4MIT232	4	109.11827	144647559	0.23776	0.61417	0	2.08E-30	0	0	Shared
unassigned	915598	X	1.31E+08	DXMIT172	X	47.924609	119197077	0.87752	1.16935	1.47685	2.83E-30	0	0	Shared
Ssfa2	458864	2	79500390	D2MIT75	2	46.41465	80424883	0.64231	1.24886	0	7.77E-30	0	0	Shared
unassigned	376248	17	36255677	17.034.150	17	51.1372	34678889	0.65686	1.70962	0	1.44E-29	0	0	Shared
Kif1a	46477	1	94970408	RS30388122	1	66.387403	94920500	0.94152	1.3534	0	1.48E-29	0	0	Shared
unassigned	752306	7	1.26E+08	RS36353338	7	66.26522	112706514	0.63272	1.33454	0	1.57E-29	0	0	Shared
Cdkal1	225033	13	29417906	RS29514367	13	20.539234	29499372	0.46436	0.84804	0	2.14E-29	0	0	Shared
Atp1a2	58692	1	1.74E+08	01.183.109	1	96.118477	183202456	2.62918	2.04717	0	2.41E-29	0	0	Shared
Etfb	738842	7	50708210	D7MIT228	7	28.11811	47279833	0.20765	0.3928	0	4.18E-29	0	0	Shared
Ap2a1	765109	7	52161064	D7MIT228	7	28.11811	47279833	1.22396	1.68717	0	7.62E-29	0	0	Shared
Rpl13a	765280	7	52381560	D7MIT228	7	28.11811	47279833	1.55967	2.01935	0	8.74E-29	0	0	Shared
unassigned	29374	1	1.87E+08	01.183.109	1	96.118477	183202456	0.27659	1.04135	0	9.89E-29	0	0	Shared
Capn7	247295	14	32176692	D14MIT174	14	33.327106	32460166	1.56843	2.40026	0	1.05E-28	0	0	Shared
unassigned	765273	7	52378646	D7MIT228	7	28.11811	47279833	0.18598	0.61833	0	1.05E-28	0	0	Shared
Svop	673598	5	1.15E+08	d5mit158	5	69.85959	115413178	0.65872	0.95551	0	1.57E-28	0	0	Shared
Ap2b1	124727	11	83156223	D11MIT320	11	39.87138	70766870	0.47965	0.95434	0	1.75E-28	0	0	Shared
Pafah1b1	149108	11	74491023	D11MIT320	11	39.87138	70766870	0.57216	1.05714	0	1.87E-28	0	0	Shared
Ttc35	287826	15	43343302	15.046.034	15	20.554602	46035472	2.31981	1.62497	0	1.95E-28	0	0	Shared
C920025E04Rik	376226	17	36246596	D17MIT51	17	53.34361	43641790	0.23735	0.48201	0	3.13E-28	0	0	SCG
Tln2	869509	9	67156692	D9MIT336	9	49.6331	65425671	0.94649	0.63534	0	3.25E-28	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
1600012F09Rik	223010	13	18081424	D13Mit207	13	8.688726	16526195	2.13196	1.64122	0	3.40E-28	0	0	Shared
unassigned	375399	17	34136077	17.034.150	17	51.1372	34678889	1.47648	1.09041	0	5.57E-28	0	0	Shared
Mmd	126542	11	90121218	D11MIT285	11	55.01615	89789103	0.68304	0.89531	0	9.41E-28	0	0	Shared
Uchl1	637596	5	67073860	05.049.898	5	44.23678	50000991	0.24329	0.32109	0	1.11E-27	0	0	Shared
unassigned	841413	9	51875677	09.046.588	9	34.49446	46645088	1.21474	1.56975	0	1.19E-27	0	0	Shared
Fam135a	34512	1	24064051	rs13475769	1	16.197578	24958696	0.76294	0.3649	0	1.60E-27	0	0	Shared
Clstn1	594819	4	1.49E+08	D4MIT232	4	109.11827	144647559	0.73278	0.89033	0	1.64E-27	0	0	Shared
Gtf2a1	195507	12	92808207	D12MIT194	12	54.38605	92525886	1.05047	0.58782	0	1.71E-27	0	0	Shared
Pkn1	823332	8	86201446	D8MIT45	8	58.440058	89829274	0.34252	0.56954	0	1.94E-27	0	0	Shared
Il6st	219731	13	1.13E+08	D13MIT53	13	72.69389	113084631	1.55051	1.25982	0	2.98E-27	0	0	Shared
Anxa5	547434	3	36356389	03.033.871	3	22.08075	33578373	1.48573	1.10117	0	4.52E-27	0	0	Shared
Epb4.9	273542	14	71014723	D14MIT39	14	54.529907	69166099	0.58442	0.8834	0	5.82E-27	0	0	Shared
Gde1	778086	7	1.26E+08	RS36353338	7	66.26522	112706514	0.43317	0.71183	0	7.64E-27	0	0	Shared
Ddr1	376093	17	35826947	17.034.150	17	51.1372	34678889	0.63032	1.14024	0	8.29E-27	0	0	Shared
Etfdh	553208	3	79426692	D3MIT98	3	51.73848	85985423	0.41107	0.58286	0	1.52E-26	0	0	Shared
Acad10	675311	5	1.22E+08	D5MIT95	5	98.81753	125309605	0.09647	0.32553	0	3.07E-26	0	0	Shared
Gm5077	727994	6	1.25E+08	d6mit366	6	77.49561	115192871	0.92481	1.83713	0	6.17E-26	0	0	SCG
Rbbp5	19840	1	1.34E+08	01.136.071	1	77.74879	136151166	0.22985	0.96332	0	7.41E-26	0	0	Shared
Lsm8	685312	6	18798736	06.016.672	6	10.4	16672000	0.16857	0.50085	0	7.61E-26	0	0	Shared
Ctnnd2	285463	15	30816886	15.028.723	15	14.881134	28708166	1.11147	1.76996	0	1.15E-25	0	0	Shared
Ddost	592343	4	1.38E+08	04.133.005	4	97.642221	133288839	1.6171	1.15679	0	1.28E-25	0	0	Shared
Alg9	841161	9	50587075	D9MIT247	9	25.36975	36940492	0.78692	1.22803	0	2.02E-25	0	0	Shared
Tbc1d9	800329	8	85788784	D8MIT346	8	54.673156	85454038	0.34152	0.62166	0	2.12E-25	0	0	Shared
Pink1	619917	4	1.38E+08	04.133.005	4	97.642221	133288839	3.56313	2.77544	0	2.29E-25	0	0	SCG
Fyco1	880707	9	1.24E+08	D9MIT151	9	100.11619	121386992	0.51294	0.9919	0	2.78E-25	0	0	Shared
Txnl1	413359	18	63823769	D18MIT152	18	47.63475	62096421	0.05283	0.2944	0	2.79E-25	0	0	Shared
H13	471809	2	1.53E+08	D2MIT285	2	110.63716	152683037	1.24952	1.79136	0	2.91E-25	0	0	Shared
Sidt2	864411	9	45755922	D9MIT285	9	25.81754	40462577	0.54634	0.83012	0	4.08E-25	0	0	Shared
unassigned	876293	9	1.05E+08	D9MIT24	9	73.18313	103132731	0.67011	0.87419	0	4.45E-25	0	0	Shared
unassigned	831688	8	1.27E+08	D8MIT42	8	102.88933	129076217	0.6364	1.01529	0	4.63E-25	0	0	Shared
unassigned	129549	11	1.02E+08	11.104.430	11	62.15042	104475224	0.64663	1.11036	0	1.64E-24	0	0	Shared
Faim2	317197	15	99351141	D15MIT44	15	76.945032	98951714	0.4405	0.61432	0	1.86E-24	0	0	Shared
Kcnab2	623479	4	1.52E+08	D4MIT42	4	117.10129	150944103	1.39145	1.86346	0	2.63E-24	0	0	Shared
Atm	866080	9	53264615	D9MIT248	9	44.87553	58210366	0.26792	0.49461	0	4.23E-24	0	0	Shared
unassigned	622178	4	1.47E+08	D4MIT232	4	109.11827	144647559	0.90484	1.27271	0	4.40E-24	0	0	Shared
Ndrg3	508846	2	1.57E+08	D2MIT423	2	107.80753	148685450	0.01997	0.13675	0	4.84E-24	0	0	Shared
Gmfb	267956	14	47435274	14.042.462	14	41.894152	44159798	2.17993	1.80698	0	5.72E-24	0	0	Shared
Cog6	549553	3	52804404	D3MIT6	3	28.26274	48687327	1.30982	2.13076	0	5.81E-24	0	0	Shared
unassigned	26870	1	1.74E+08	01.183.109	1	96.118477	183202456	1.30236	1.6553	0	7.80E-24	0	0	Shared
unassigned	3715	1	34269037	D1Mit374	1	27.028585	34816928	1.01518	1.27449	0	9.20E-24	0	0	Shared
Vwa5a	838533	9	38550716	D9MIT285	9	25.81754	40462577	0.54542	0.28307	0	1.06E-23	0	0	Shared
Lamc1	54398	1	1.55E+08	D1Mit102	1	80.039245	149096650	0.95782	1.3549	0	1.75E-23	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
3830406C13Rik	243434	14	13133662	14.008.937	14	5.6	10975728	1.69629	2.39622	0	2.11E-23	0	0	Shared
4833420G17Rik	220876	13	1.2E+08	D13MIT78	13	76.842169	119618032	0.6235	0.98782	0	2.12E-23	0	0	Shared
Ndufs8	431235	19	3911183	19.000.325	19	0.2	325000	1.13398	0.8702	0	2.31E-23	0	0	Shared
unassigned	780345	7	1.36E+08	07.122.234	7	82.95546	129586366	0.84526	1.34956	0	2.37E-23	0	0	Shared
Psma3	172158	12	72094004	12.065.348	12	37.44045	65530382	0.16226	0.6265	0	2.84E-23	0	0	Shared
Pik3c2a	777663	7	1.24E+08	RS36353338	7	66.26522	112706514	0.15329	0.40175	0	3.02E-23	0	0	Shared
unassigned	529269	3	87535632	D3MIT49	3	73.77602	89036582	0.03351	0.12849	0	4.33E-23	0	0	Shared
Ift52	474783	2	1.63E+08	D2MIT411	2	112.97352	159412163	0.30532	0.57088	0	5.16E-23	0	0	Shared
Dapk1	211792	13	60824384	13.061.624	13	39.879786	61715738	0.45676	0.68189	0	5.46E-23	0	0	Shared
unassigned	635789	5	53153771	D5MIT183	5	47.99434	53728383	0.95712	0.54103	0	7.64E-23	0	0	SCG
Tjp1	768212	7	72457221	07.056.455	7	36.40088	63842351	0.32862	0.55542	0	1.06E-22	0	0	Shared
H2-K1	375394	17	34133422	17.034.150	17	51.1372	34678889	0.68415	0.90009	0	1.16E-22	0	0	Shared
unassigned	508606	2	1.56E+08	02.161.464	2	113.50933	161598295	0.92142	1.25814	0	1.23E-22	0	0	Shared
Avil	84584	10	1.26E+08	D10Mit14	10	93.102537	118098315	1.01261	0.75674	0	1.54E-22	0	0	SCG
Sqrdl	465950	2	1.23E+08	RS27258455	2	126.73188	129951321	1.10779	1.48556	0	1.70E-22	0	0	Shared
Cul4a	789102	8	13136337	08.010.585	8	4.520052	10585028	0.08989	0.19061	0	2.46E-22	0	0	Shared
unassigned	385958	17	87834568	D17MIT76	17	95.2661	86033231	0.54728	0.78876	0	3.32E-22	0	0	Shared
Cst3	506956	2	1.49E+08	D2MIT285	2	110.63716	152683037	0.97189	0.88508	0	4.40E-22	0	0	Shared
Ece1	592082	4	1.38E+08	04.133.005	4	97.642221	133288839	0.94659	1.27122	0	5.37E-22	0	0	Shared
Thbs2	371126	17	14824854	D17Mit213	17	12.20714	16752157	0.33168	0.64305	0	5.93E-22	0	0	Shared
unassigned	761788	7	29756636	D7MIT267	7	18.29809	30331965	0.54379	0.78585	0	6.06E-22	0	0	Shared
Timm17a	51812	1	1.37E+08	01.136.071	1	77.74879	136151166	0.79872	1.22846	0	6.31E-22	0	0	Shared
Gm8909	376294	17	36304417	17.034.150	17	51.1372	34678889	34.63203	61.10456	0	6.61E-22	0	0	Shared
Ilf3	835195	9	21193014	09.014.560	9	12.99047	14614051	1.10019	0.86047	0	1.08E-21	0	0	Shared
Snrpd2	734804	7	19738036	07.013.915	7	8.7	15600169	0.04967	0.13573	0	1.32E-21	0	0	Shared
Timm17a	51813	1	1.37E+08	D1MIT1001	1	72.841454	130944135	0.6475	0.46804	0	1.46E-21	0	0	Shared
Usp48	591923	4	1.37E+08	04.133.005	4	97.642221	133288839	2.18148	1.58353	0	1.48E-21	0	0	Shared
Gsr	792625	8	34790752	D8Mit191	8	23.020658	36243839	0.09561	0.19383	0	1.67E-21	0	0	Shared
Lrrc68	785850	7	20116744	07.013.915	7	8.7	15600169	0.83298	1.27313	0	1.70E-21	0	0	Shared
unassigned	675710	5	1.23E+08	D5MIT95	5	98.81753	125309605	0.12109	0.48551	0	1.74E-21	0	0	Shared
unassigned	377546	17	45706082	17.034.150	17	51.1372	34678889	2.15923	1.81377	0	2.14E-21	0	0	Shared
Tekt2	616782	4	1.26E+08	D4MIT308	4	84.360247	123838543	0.28647	0.1313	0	2.18E-21	0	0	Shared
unassigned	554317	3	85942677	D3MIT49	3	73.77602	89036582	0.64169	0.77088	0	2.19E-21	0	0	Shared
Myo1c	122621	11	75482705	D11MIT320	11	39.87138	70766870	0.68547	1.11198	0	2.39E-21	0	0	Shared
Arl6ip1	777905	7	1.25E+08	RS36353338	7	66.26522	112706514	0.58963	0.77911	0	2.64E-21	0	0	Shared
Cdc40	91987	10	40570761	D10MIT184	10	40.059568	42088505	1.53173	2.23962	0	2.83E-21	0	0	Shared
Fyco1	880706	9	1.24E+08	D9Mit18	9	96.97845	120198563	0.89969	1.32522	0	2.95E-21	0	0	Shared
Ank	284935	15	27501213	15.028.723	15	14.881134	28708166	1.13198	1.31337	0	2.96E-21	0	0	SCG
unassigned	717204	6	57463755	06.057.998	6	39.56321	58018416	0.81391	1.14711	0	3.20E-21	0	0	Shared
Gla	932986	X	1.31E+08	DXMIT132	X	55.816704	138191357	0.75244	0.99311	1.17717	3.79E-21	0	0	Shared
Herc2	741488	7	63411776	D7MIT228	7	28.11811	47279833	0.16677	0.28585	0	3.86E-21	0	0	Shared
unassigned	232337	13	64470306	13.061.624	13	39.879786	61715738	0.46412	0.6816	0	3.90E-21	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Srp68	160621	11	1.16E+08	D11MIT214	11	79.65651	114991785	1.45866	1.03692	0	4.68E-21	0	0	Shared
Habp4	212220	13	64287025	13.061.624	13	39.879786	61715738	0.97524	1.22014	0	5.43E-21	0	0	Shared
Kif1b	622609	4	1.49E+08	D4MIT232	4	109.11827	144647559	1.11379	1.32161	0	6.07E-21	0	0	Shared
Freq	450213	2	31142807	D2MIT296	2	21.50213	31180075	1.39373	1.01877	0	6.65E-21	0	0	Shared
Cst3	506963	2	1.49E+08	D2MIT285	2	110.63716	152683037	0.97133	1.12437	0	9.02E-21	0	0	Shared
Crnkl1	506361	2	1.46E+08	D2MIT285	2	110.63716	152683037	1.1499	0.72354	0	9.09E-21	0	0	Shared
Lsm14a	763129	7	35132948	D7MIT228	7	28.11811	47279833	0.27285	0.5215	0	1.08E-20	0	0	Shared
Pion	629533	5	20733848	D5MIT294	5	15.58331	20863135	0.24094	0.96351	0	1.13E-20	0	0	Shared
3110007F17Rik	932158	X	1.21E+08	DXMit79	X	50.813632	127398406	8.61243	0.86067	0.70853	1.18E-20	0	0	SCG
Dlat	865423	9	50457743	D9MIT247	9	25.36975	36940492	0.52959	0.76863	0	1.31E-20	0	0	Shared
Adhfe1	682	1	9543733	RS32728630	1	6.020495	9632792	0.98958	1.53846	0	1.34E-20	0	0	Shared
Mccc1	547329	3	35877847	03.033.871	3	22.08075	33578373	2.17146	1.41399	0	2.06E-20	0	0	Shared
unassigned	607116	4	71787476	D4MIT132	4	51.331896	70333587	0.32048	0.56861	0	2.46E-20	0	0	Shared
Sacm1l	856989	9	1.23E+08	D9MIT151	9	100.11619	121386992	1.45762	1.86324	0	3.12E-20	0	0	Shared
Zfpm1	808688	8	1.25E+08	D8MIT42	8	102.88933	129076217	2.52044	1.76592	0	4.42E-20	0	0	Shared
A730017C20Rik	397289	18	59235505	D18MIT152	18	47.63475	62096421	1.15655	1.39245	0	5.35E-20	0	0	Shared
Fuz	739446	7	52154407	D7MIT228	7	28.11811	47279833	0.23699	0.49221	0	6.35E-20	0	0	Shared
Wdr36	392132	18	33007270	D18Mit68	18	14.5139	21594126	0.54458	0.87652	0	9.43E-20	0	0	Shared
unassigned	775342	7	1.13E+08	RS36353338	7	66.26522	112706514	1.3132	1.00711	0	1.20E-19	0	0	Shared
Actr10	172140	12	72063093	D12MIT91	12	43.26798	72843829	1.54752	1.05827	0	1.22E-19	0	0	Shared
Nipa1	767081	7	63252886	07.056.455	7	36.40088	63842351	0.06973	0.16339	0	1.52E-19	0	0	Shared
Tgfb1i1	754816	7	1.35E+08	07.122.234	7	82.95546	129586366	1.90626	1.43856	0	1.62E-19	0	0	SCG
Arhgef10l	620398	4	1.4E+08	04.133.005	4	97.642221	133288839	1.09514	0.65552	0	2.89E-19	0	0	Shared
Tarsl2	742622	7	72797146	07.056.455	7	36.40088	63842351	1.81399	2.42092	0	3.17E-19	0	0	Shared
Tmem222	618465	4	1.33E+08	D4Mit203	4	89.732314	129249262	0.62503	0.93348	0	3.26E-19	0	0	Shared
Syt17	778023	7	1.26E+08	RS36353338	7	66.26522	112706514	0.78654	1.01175	0	3.33E-19	0	0	Shared
Ctso	528017	3	81758406	D3MIT98	3	51.73848	85985423	0.93501	1.2546	0	3.97E-19	0	0	Shared
unassigned	755075	7	1.37E+08	07.122.234	7	82.95546	129586366	0.32137	0.498	0	4.02E-19	0	0	Shared
Gsr	792622	8	34780401	D8MIT94	8	19.424222	32452130	1.46054	1.15056	0	4.21E-19	0	0	SCG
Lgi2	663261	5	52955222	d5mit233	5	46.33401	53088465	2.05827	1.2716	0	4.70E-19	0	0	Shared
unassigned	765271	7	52377978	D7MIT228	7	28.11811	47279833	1.45049	1.2319	0	4.88E-19	0	0	Shared
Ndufs2	58398	1	1.73E+08	01.183.109	1	96.118477	183202456	0.45311	0.60544	0	5.10E-19	0	0	Shared
Psme4	112806	11	30718107	D11MIT186	11	23.608	35049231	0.7708	0.50858	0	5.32E-19	0	0	Shared
Cse1l	475884	2	1.67E+08	02.168.990	2	151.40532	169124295	0.62507	0.95352	0	5.57E-19	0	0	Shared
Lix1	353795	17	17580648	17.021.019	17	14.36839	21451267	0.9052	0.776	0	5.70E-19	0	0	SCG
Kif1b	622630	4	1.49E+08	D4MIT232	4	109.11827	144647559	0.85771	0.6779	0	6.13E-19	0	0	Shared
Ptov1	765050	7	52118446	D7MIT228	7	28.11811	47279833	0.32462	0.4897	0	6.80E-19	0	0	Shared
Nipal3	619242	4	1.35E+08	D4MIT170	4	99.940854	138171253	0.9809	1.18214	0	7.12E-19	0	0	Shared
Psmd6	262351	14	14944830	14.008.937	14	5.6	10975728	0.2247	0.36531	0	7.37E-19	0	0	Shared
Ece1	592069	4	1.37E+08	04.133.005	4	97.642221	133288839	2.23853	1.8114	0	7.63E-19	0	0	Shared
Fus	754680	7	1.35E+08	d7mit109	7	91.14939	143706746	0.70009	1.04242	0	8.55E-19	0	0	Shared
unassigned	497867	2	1.05E+08	D2MIT100	2	54.19426	106377525	0.16574	0.29497	0	9.05E-19	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Mlh1	878103	9	1.11E+08	D9MIT212	9	79.88305	108543415	0.85826	2.00832	0	9.89E-19	0	0	Shared
Ablim1	442644	19	57114983	D19MIT103	19	59.411152	53838656	0.68287	0.45389	0	1.04E-18	0	0	Shared
Ank2	562245	3	1.27E+08	RS30160288	3	119.38247	125981675	0.36487	0.52339	0	1.12E-18	0	0	Shared
Htt	632825	5	35248195	D5MIT352	5	30.68587	35957616	1.22237	0.94634	0	1.33E-18	0	0	Shared
Th1l	477441	2	1.74E+08	D2MIT148	2	167.77989	178535250	0.63987	0.98323	0	1.50E-18	0	0	Shared
unassigned	616789	4	1.26E+08	D4MIT308	4	84.360247	123838543	1.47234	0.94691	0	1.51E-18	0	0	SCG
Nomo1	739974	7	53312044	D7MIT228	7	28.11811	47279833	1.26412	1.71139	0	1.53E-18	0	0	Shared
C4a	375623	17	34866361	17.034.150	17	51.1372	34678889	0.40399	0.55586	0	1.62E-18	0	0	Shared
Dst	3747	1	34317012	D1Mit374	1	27.028585	34816928	0.87748	1.16828	0	1.76E-18	0	0	Shared
Mllt11	556275	3	95024337	D3MIT49	3	73.77602	89036582	0.37161	0.5091	0	1.80E-18	0	0	Shared
Bbs7	547502	3	36509494	03.033.871	3	22.08075	33578373	0.4773	1.01391	0	1.86E-18	0	0	Shared
unassigned	643541	5	1.04E+08	D5MIT239	5	66.11023	107842159	0.59573	1.03999	0	1.91E-18	0	0	Shared
Lars	409649	18	42410483	D18MIT202	18	28.05292	43551589	1.37348	1.0651	0	1.97E-18	0	0	Shared
Tardbp	622400	4	1.48E+08	D4MIT232	4	109.11827	144647559	0.469	0.77848	0	2.46E-18	0	0	Shared
Papss1	538000	3	1.31E+08	D3MIT256	3	103.27598	136014535	0.41303	0.25815	0	3.00E-18	0	0	Shared
Iars2	61137	1	1.87E+08	01.183.109	1	96.118477	183202456	0.09454	0.29725	0	3.37E-18	0	0	Shared
Hiatl1	232467	13	65173381	13.061.624	13	39.879786	61715738	0.43997	0.71493	0	3.59E-18	0	0	Shared
Entpd4	254060	14	69965580	D14MIT39	14	54.529907	69166099	0.87198	1.131	0	3.61E-18	0	0	Shared
Acap3	596643	4	1.55E+08	D4MIT42	4	117.10129	150944103	0.29147	0.69864	0	4.40E-18	0	0	Shared
Ivd	464751	2	1.19E+08	D2Mit274	2	62.95823	114283330	0.45483	0.64056	0	4.57E-18	0	0	Shared
Klraq1	368437	17	88961521	D17MIT76	17	95.2661	86033231	0.45484	0.65025	0	5.00E-18	0	0	Shared
Stx3	420873	19	11849858	19.013.429	19	11.129219	13436471	0.5997	0.84183	0	5.14E-18	0	0	Shared
Sergef	765878	7	53771038	D7MIT228	7	28.11811	47279833	1.15371	1.67079	0	5.38E-18	0	0	Shared
Spg21	844575	9	65323695	D9MIT336	9	49.6331	65425671	1.679	1.28742	0	6.45E-18	0	0	Shared
2010005J08Rik	135463	11	5622442	D11MIT2	11	7.6	12218640	3.61214	2.63416	0	6.84E-18	0	0	Shared
unassigned	260011	14	1.19E+08	RS31252045	14	77.831601	111376384	0.88032	1.28515	0	6.86E-18	0	0	Shared
Herc2	741461	7	63376940	D7Mit232	7	35.20811	59868792	0.71514	0.95471	0	7.93E-18	0	0	Shared
Fh1	59276	1	1.78E+08	01.183.109	1	96.118477	183202456	1.53866	1.26299	0	9.81E-18	0	0	Shared
Sik2	865534	9	50704772	D9MIT285	9	25.81754	40462577	0.47997	0.74854	0	9.99E-18	0	0	Shared
Trmt2b	932892	X	1.31E+08	DXMit79	X	50.813632	127398406	0.23368	0.3629	0.52955	9.99E-18	0	0	Shared
unassigned	241139	13	1.15E+08	D13MIT53	13	72.69389	113084631	1.44352	1.02349	0	1.25E-17	0	0	Shared
Smarcc1	853798	9	1.1E+08	09.105.291	9	79.88305	105335230	0.64695	0.32396	0	1.39E-17	0	0	Shared
9030624J02Rik	752340	7	1.26E+08	RS36353338	7	66.26522	112706514	1.19708	1.60643	0	1.61E-17	0	0	SCG
Efcab2	27990	1	1.8E+08	01.183.109	1	96.118477	183202456	0.97544	1.89626	0	1.64E-17	0	0	Shared
unassigned	186939	12	36748507	D12MIT60	12	21.025423	35474805	1.32918	1.18877	0	1.72E-17	0	0	Shared
Sema6d	466108	2	1.24E+08	D2Mit274	2	62.95823	114283330	2.12898	1.66522	0	2.09E-17	0	0	Shared
Rplp0	646516	5	1.16E+08	d5mit158	5	69.85959	115413178	1.06836	0.83126	0	2.16E-17	0	0	Shared
Abi3bp	329423	16	56652250	D16MIT139	16	56.627807	65669762	0.69104	1.02991	0	2.30E-17	0	0	SCG
Uevld	766067	7	54190268	D7MIT228	7	28.11811	47279833	0.89289	0.46989	0	2.40E-17	0	0	SCG
Degs1	60652	1	1.84E+08	01.183.109	1	96.118477	183202456	1.19373	0.96278	0	2.65E-17	0	0	Shared
unassigned	876980	9	1.08E+08	09.105.291	9	79.88305	105335230	1.09246	0.79393	0	2.74E-17	0	0	SCG
4833420G17Rik	220873	13	1.2E+08	D13MIT78	13	76.842169	119618032	0.97185	1.65984	0	2.75E-17	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	232581	13	67001532	13.061.624	13	39.879786	61715738	0.03522	0.10636	0	2.79E-17	0	0	Shared
Nomo1	739977	7	53316253	D7MIT228	7	28.11811	47279833	0.59587	0.77325	0	2.91E-17	0	0	Shared
Armcx1	915599	X	1.31E+08	DXMIT172	X	47.924609	119197077	1.1176	1.0244	0.97793	3.34E-17	0	0	SCG
Dclk2	554419	3	86640246	D3MIT49	3	73.77602	89036582	0.23113	0.7608	0	3.73E-17	0	0	Shared
Dixdc1	865456	9	50495466	D9MIT247	9	25.36975	36940492	0.23991	0.49444	0	3.78E-17	0	0	Shared
Dst	3676	1	34221942	D1Mit374	1	27.028585	34816928	1.42444	1.20005	0	3.78E-17	0	0	Shared
Rps3a	554315	3	85941922	D3MIT49	3	73.77602	89036582	0.61794	0.49928	0	3.93E-17	0	0	Shared
unassigned	806517	8	1.14E+08	D8MIT215	8	87.841725	118384638	1.43082	1.84882	0	4.36E-17	0	0	Shared
Slc7a5	830908	8	1.24E+08	D8MIT42	8	102.88933	129076217	0.56801	0.80779	0	5.20E-17	0	0	Shared
Chd4	704122	6	1.25E+08	D6MIT194	6	87.57626	128115503	1.75627	1.35167	0	5.24E-17	0	0	Shared
Pim1	356546	17	29631661	17.034.150	17	51.1372	34678889	1.03309	1.27174	0	5.80E-17	0	0	SCG
Gm13152	594123	4	1.47E+08	D4MIT232	4	109.11827	144647559	0.73686	0.60079	0	6.15E-17	0	0	Shared
Fam163b	483546	2	26969083	02.021.696	2	18.06443	21699873	0.46413	0.89494	0	6.35E-17	0	0	Shared
unassigned	409645	18	42403316	18.038.678	18	24.45192	38711680	2.19796	1.71537	0	7.75E-17	0	0	Shared
Vwf	704353	6	1.26E+08	D6MIT194	6	87.57626	128115503	0.65013	0.91578	0	7.97E-17	0	0	SCG
Pam	47051	1	99718478	01.102.953	1	66.387402	103022030	0.31989	0.39861	0	8.58E-17	0	0	Shared
unassigned	569106	3	88716553	D3MIT49	3	73.77602	89036582	1.08773	0.83814	0	9.72E-17	0	0	Shared
Cerk	313939	15	85981968	D15MIT262	15	57.212355	87111041	0.46778	0.67872	0	1.04E-16	0	0	Shared
unassigned	765282	7	52382363	D7MIT228	7	28.11811	47279833	0.75523	0.64891	0	1.04E-16	0	0	SCG
Acad9	521871	3	35974171	03.033.871	3	22.08075	33578373	0.98682	0.80635	0	1.09E-16	0	0	Shared
Mfn2	622163	4	1.47E+08	D4MIT232	4	109.11827	144647559	1.72003	2.11814	0	1.13E-16	0	0	Shared
unassigned	765283	7	52382980	D7MIT228	7	28.11811	47279833	1.3142	1.14925	0	1.33E-16	0	0	Shared
Gm14288	513504	2	1.77E+08	D2MIT148	2	167.77989	178535250	20.99272	25.2943	0	1.41E-16	0	0	Shared
Crispld1	1942	1	17743059	rs13475769	1	16.197578	24958696	0.21172	0.40257	0	1.42E-16	0	0	Shared
Ints1	679635	5	1.4E+08	05.132.979	5	112.26584	133170167	1.59296	1.18149	0	1.74E-16	0	0	Shared
H2-D1	358662	17	35404155	D17MIT51	17	53.34361	43641790	1.99384	2.43322	0	1.82E-16	0	0	Shared
Entpd4	254072	14	69982125	D14MIT39	14	54.529907	69166099	0.76348	0.99994	0	1.88E-16	0	0	Shared
unassigned	235672	13	90201563	13.096.920	13	58.796863	96589256	1.01118	0.63962	0	1.98E-16	0	0	Shared
Tln2	869533	9	67202255	D9MIT248	9	44.87553	58210366	0.60344	0.9185	0	2.00E-16	0	0	Shared
Tor1aip1	55128	1	1.58E+08	D1Mit102	1	80.039245	149096650	0.67743	0.41365	0	2.06E-16	0	0	Shared
Hyou1	839553	9	44190547	D9MIT2	9	25.36976	37202486	0.802	0.94947	0	2.16E-16	0	0	SCG
Itgav	459300	2	83632718	D2MIT75	2	46.41465	80424883	2.43831	2.04792	0	2.41E-16	0	0	SCG
Sfxn4	443435	19	60934587	D19MIT103	19	59.411152	53838656	0.23409	0.72646	0	2.54E-16	0	0	Shared
unassigned	167097	12	33652322	D12MIT60	12	21.025423	35474805	1.12958	1.32444	0	2.60E-16	0	0	Shared
Lyst	202916	13	13801795	D13Mit207	13	8.688726	16526195	0.06153	0.16644	0	2.67E-16	0	0	Shared
Rpl13a	765281	7	52381937	D7MIT228	7	28.11811	47279833	0.93942	1.1047	0	2.72E-16	0	0	Shared
unassigned	506063	2	1.44E+08	D2MIT423	2	107.80753	148685450	0.66226	1.15699	0	2.73E-16	0	0	Shared
Sacm1l	856985	9	1.23E+08	D9Mit18	9	96.97845	120198563	0.25002	0.47904	0	2.90E-16	0	0	Shared
Tekt2	616790	4	1.26E+08	D4MIT308	4	84.360247	123838543	0.65918	0.916	0	3.04E-16	0	0	SCG
unassigned	622226	4	1.47E+08	D4MIT232	4	109.11827	144647559	1.22308	1.34392	0	3.30E-16	0	0	Shared
unassigned	673934	5	1.16E+08	d5mit158	5	69.85959	115413178	1.09567	1.23672	0	3.72E-16	0	0	Shared
Elmo2	510635	2	1.65E+08	02.168.990	2	151.40532	169124295	0.52327	0.69091	0	3.85E-16	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Mcam	839485	9	43947784	D9MIT247	9	25.36975	36940492	1.29045	1.1746	0	4.16E-16	0	0	SCG
Sap130	391774	18	31795648	18.038.678	18	24.45192	38711680	1.19152	0.91475	0	4.22E-16	0	0	Shared
3110007F17Rik	932163	X	1.21E+08	DXMit79	X	50.813632	127398406	16.15454	2.13245	2.11723	4.43E-16	0	0	SCG
Amacr	283070	15	10924705	15.010.846	15	8.803289	10831030	0.53166	0.88817	0	4.64E-16	0	0	Shared
Gmfb	267954	14	47434596	14.042.462	14	41.894152	44159798	0.07127	0.16092	0	4.74E-16	0	0	Shared
Zfp459	232747	13	67509198	13.061.624	13	39.879786	61715738	0.39177	0.58972	0	5.26E-16	0	0	Shared
unassigned	678149	5	1.35E+08	D5MIT95	5	98.81753	125309605	1.24072	0.93748	0	5.38E-16	0	0	Shared
Dpp8	844348	9	64901585	D9MIT248	9	44.87553	58210366	0.65661	0.45962	0	6.13E-16	0	0	Shared
Gm447	663239	5	52765915	d5mit233	5	46.33401	53088465	1.07406	1.69508	0	6.16E-16	0	0	Shared
Zfp180	735114	7	24886474	07.013.915	7	8.7	15600169	0.04127	0.13198	0	6.29E-16	0	0	Shared
Gpr137b-ps	222313	13	12712036	D13Mit207	13	8.688726	16526195	0.49759	0.69967	0	6.70E-16	0	0	Shared
Zfp426	859124	9	20280854	09.014.560	9	12.99047	14614051	1.44194	0.9319	0	7.32E-16	0	0	Shared
unassigned	778044	7	1.26E+08	RS36353338	7	66.26522	112706514	0.8192	1.15368	0	7.40E-16	0	0	Shared
Zdhhc18	618582	4	1.33E+08	D4Mit203	4	89.732314	129249262	1.51034	1.8712	0	8.54E-16	0	0	Shared
AI314180	605167	4	58855449	D4MIT164	4	42.389612	59415112	1.13208	0.86414	0	9.04E-16	0	0	Shared
Mfn2	622152	4	1.47E+08	D4MIT232	4	109.11827	144647559	0.99283	1.15984	0	9.14E-16	0	0	Shared
Psmc4	761456	7	28827675	D7MIT294	7	15.72036	28074461	1.89329	1.37887	0	1.06E-15	0	0	Shared
Col5a2	37724	1	45443684	D1MIT236	1	37.41892	45435458	1.47498	2.09932	0	1.20E-15	0	0	SCG
Acacb	646046	5	1.15E+08	d5mit158	5	69.85959	115413178	0.75062	0.58456	0	1.21E-15	0	0	SCG
Erc1	727177	6	1.2E+08	d6mit366	6	77.49561	115192871	0.79874	1.12176	0	1.38E-15	0	0	Shared
Scfd1	169470	12	52523937	D12MIT285	12	30.221464	55750112	0.12873	0.26425	0	1.41E-15	0	0	Shared
Snx31	304122	15	36485274	15.028.723	15	14.881134	28708166	4.76307	3.43888	0	1.53E-15	0	0	SCG
Ctnnal1	604666	4	56851843	04.053.650	4	40.480187	53641772	1.39612	1.80758	0	1.62E-15	0	0	Shared
Lphn1	800495	8	86442832	D8MIT45	8	58.440058	89829274	1.84755	2.19877	0	1.74E-15	0	0	Shared
unassigned	153083	11	89849855	D11MIT285	11	55.01615	89789103	0.46376	0.67117	0	1.78E-15	0	0	SCG
Acad9	521890	3	35989871	03.033.871	3	22.08075	33578373	0.70719	0.9141	0	1.80E-15	0	0	SCG
unassigned	869287	9	66368535	D9MIT336	9	49.6331	65425671	0.44165	0.24605	0	1.85E-15	0	0	Shared
unassigned	657341	5	21545301	D5MIT294	5	15.58331	20863135	0.51355	0.77624	0	1.94E-15	0	0	Shared
Clip4	365100	17	72177038	D17Mit152	17	74.19469	65689824	0.60793	0.9924	0	1.97E-15	0	0	Shared
Terf1	1673	1	15809070	D1MIT169	1	18.851745	24071806	0.38102	0.58419	0	2.24E-15	0	0	Shared
Itgb4	132956	11	1.16E+08	D11MIT214	11	79.65651	114991785	0.93782	1.30077	0	2.28E-15	0	0	SCG
Gsr	792635	8	34807822	D8MIT94	8	19.424222	32452130	0.92824	1.13225	0	2.43E-15	0	0	Shared
Uevld	766070	7	54193327	D7MIT228	7	28.11811	47279833	1.15128	1.72826	0	2.46E-15	0	0	Shared
Lamc1	54407	1	1.55E+08	D1Mit102	1	80.039245	149096650	0.44683	0.64142	0	2.48E-15	0	0	Shared
Abcc9	731667	6	1.43E+08	D6Mit14	6	101.60848	145604376	2.00422	1.4985	0	2.60E-15	0	0	SCG
unassigned	646513	5	1.16E+08	d5mit158	5	69.85959	115413178	1.1803	1.34036	0	2.60E-15	0	0	Shared
unassigned	870307	9	71499011	D9MIT107	9	53.50038	73315075	2.08282	1.59052	0	2.62E-15	0	0	Shared
4933428G20Rik	128090	11	97351568	D11MIT289	11	59.90287	94741466	1.22987	0.83072	0	2.80E-15	0	0	Shared
Fxyd6	839870	9	45200759	D9MIT247	9	25.36975	36940492	1.0745	0.93852	0	3.05E-15	0	0	Shared
Snx14	873324	9	88276609	09.079.053	9	64.60162	79115123	0.48939	0.71196	0	3.09E-15	0	0	Shared
Lztfl1	880650	9	1.24E+08	D9MIT151	9	100.11619	121386992	0.36863	0.48846	0	3.19E-15	0	0	Shared
Matn2	286146	15	34285329	15.028.723	15	14.881134	28708166	0.80635	1.07435	0	3.25E-15	0	0	SCG

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	358724	17	35534330	D17MIT51	17	53.34361	43641790	5.96875	4.63207	0	3.26E-15	0	0	Shared
Abcb10	831529	8	1.26E+08	D8MIT42	8	102.88933	129076217	0.82547	1.21422	0	3.32E-15	0	0	Shared
Rap1gap	592009	4	1.37E+08	D4MIT170	4	99.940854	138171253	1.39566	1.06551	0	3.71E-15	0	0	Shared
Phldb1	863979	9	44534109	D9MIT247	9	25.36975	36940492	0.93361	1.26984	0	3.72E-15	0	0	Shared
Rplp0	646514	5	1.16E+08	d5mit158	5	69.85959	115413178	2.44458	1.9488	0	3.72E-15	0	0	Shared
Tyro3	465070	2	1.2E+08	RS27258455	2	126.73188	129951321	3.74789	3.21915	0	4.17E-15	0	0	SCG
Aars	806520	8	1.14E+08	D8MIT215	8	87.841725	118384638	0.83192	1.02581	0	4.35E-15	0	0	Shared
Cyp2b10	735768	7	26702323	07.017.531	7	12.92437	18957827	0.26344	0.62387	0	4.49E-15	0	0	SCG
Supt16h	269183	14	52802746	14.042.462	14	41.894152	44159798	0.40751	0.56538	0	4.55E-15	0	0	Shared
Ankrd52	85298	10	1.28E+08	D10Mit14	10	93.102537	118098315	1.10364	1.54926	0	4.71E-15	0	0	Shared
unassigned	375344	17	33960076	17.034.150	17	51.1372	34678889	1.29154	0.8335	0	5.10E-15	0	0	Shared
Pion	629536	5	20752769	D5MIT294	5	15.58331	20863135	0.98365	1.72922	0	5.16E-15	0	0	Shared
Psmc3ip	156253	11	1.01E+08	11.104.430	11	62.15042	104475224	0.41227	0.89544	0	5.43E-15	0	0	Shared
Tspo	294653	15	83404445	D15MIT262	15	57.212355	87111041	0.09815	0.13951	0	6.17E-15	0	0	SCG
unassigned	775344	7	1.13E+08	RS36353338	7	66.26522	112706514	0.66547	0.50725	0	6.19E-15	0	0	Shared
Ldlr	835402	9	21541685	09.014.560	9	12.99047	14614051	1.11289	1.23571	0	6.39E-15	0	0	SCG
Plcb3	432622	19	7039798	19.000.325	19	0.2	325000	3.02196	2.56149	0	6.74E-15	0	0	Shared
unassigned	269114	14	52704074	D14Mit183	14	42.794969	52629891	0.51447	0.715	0	7.88E-15	0	0	Shared
Tekt2	616786	4	1.26E+08	D4MIT308	4	84.360247	123838543	0.99978	1.57158	0	8.11E-15	0	0	Shared
Ube4b	622672	4	1.49E+08	D4MIT232	4	109.11827	144647559	0.41533	0.33352	0	8.50E-15	0	0	Shared
Myo1b	38271	1	51851170	D1MIT236	1	37.41892	45435458	0.83435	1.09812	0	8.85E-15	0	0	SCG
Tln2	869528	9	67189863	D9MIT336	9	49.6331	65425671	1.34347	1.10815	0	9.17E-15	0	0	SCG
Dcun1d1	547278	3	35791949	03.033.871	3	22.08075	33578373	0.65566	0.47492	0	9.39E-15	0	0	Shared
Fbxo38	413154	18	62686883	D18MIT152	18	47.63475	62096421	1.03947	0.70956	0	9.78E-15	0	0	Shared
Golt1b	707081	6	1.42E+08	D6Mit14	6	101.60848	145604376	1.42933	1.17107	0	1.13E-14	0	0	Shared
unassigned	730521	6	1.37E+08	D6MIT194	6	87.57626	128115503	0.08985	0.12782	0	1.18E-14	0	0	SCG
Exosc10	594496	4	1.48E+08	D4MIT232	4	109.11827	144647559	1.57008	2.08834	0	1.26E-14	0	0	Shared
Heatr5a	188685	12	53040809	D12MIT285	12	30.221464	55750112	0.85002	1.14013	0	1.44E-14	0	0	Shared
Sept3	294402	15	82114133	D15MIT67	15	36.957676	70032295	2.39466	1.69569	0	1.46E-14	0	0	Shared
Trmt6	504267	2	1.33E+08	D2MIT423	2	107.80753	148685450	0.20718	0.29079	0	1.49E-14	0	0	Shared
unassigned	114671	11	43249397	D11MIT51	11	25.39412	36205252	1.19094	1.79619	0	1.55E-14	0	0	Shared
Arntl	751303	7	1.2E+08	RS36353338	7	66.26522	112706514	1.1439	1.95316	0	1.58E-14	0	0	Shared
Rapgef5	182005	12	1.19E+08	D12MIT7	12	66.696627	104970690	0.22629	0.41745	0	1.58E-14	0	0	Shared
Cntfr	601963	4	41633829	d4mit238	4	33.232784	45243003	1.6106	1.20714	0	1.65E-14	0	0	Shared
Dars2	56178	1	1.63E+08	D1MIT507	1	89.469987	166978064	0.53703	0.85419	0	1.72E-14	0	0	Shared
unassigned	592078	4	1.38E+08	04.133.005	4	97.642221	133288839	1.43876	1.17862	0	1.72E-14	0	0	SCG
unassigned	42583	1	74488176	D1MIT24	1	52.918275	74458254	0.94175	1.56253	0	1.82E-14	0	0	Shared
Ddx19a	828651	8	1.14E+08	D8MIT215	8	87.841725	118384638	0.67049	0.95204	0	2.08E-14	0	0	Shared
Insr	810534	8	3192588	D8MIT155	8	3.1	4976602	0.9668	1.19527	0	2.27E-14	0	0	SCG
Acad9	521873	3	35975650	03.033.871	3	22.08075	33578373	3.01848	2.4949	0	2.28E-14	0	0	Shared
Ghitm	266910	14	37939147	D14MIT174	14	33.327106	32460166	1.08086	1.32515	0	2.35E-14	0	0	Shared
Elac2	119494	11	64801562	D11Mit4	11	39.42453	68422759	0.45646	0.78334	0	2.45E-14	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	355011	17	24857413	D17Mit213	17	12.20714	16752157	1.33379	1.19963	0	2.45E-14	0	0	Shared
Pcdhgb5	393358	18	37891248	18.038.678	18	24.45192	38711680	0.47276	0.64256	0	2.53E-14	0	0	Shared
unassigned	630230	5	24005856	05.018.430	5	14.15919	18423994	0.55762	0.70528	0	2.77E-14	0	0	Shared
Tkt	246939	14	31372951	D14MIT174	14	33.327106	32460166	1.27048	1.09894	0	2.83E-14	0	0	Shared
unassigned	333318	16	90876250	16.083.701	16	79.82369	83818653	1.00633	1.44567	0	3.28E-14	0	0	SCG
Park2	352684	17	11749519	17.013.500	17	8.4	13900467	0.49647	0.64385	0	3.47E-14	0	0	Shared
Lamc1	54414	1	1.55E+08	D1Mit102	1	80.039245	149096650	1.71197	1.44287	0	3.92E-14	0	0	SCG
unassigned	23903	1	1.61E+08	D1Mit102	1	80.039245	149096650	1.50064	1.86452	0	4.09E-14	0	0	Shared
unassigned	219878	13	1.14E+08	d13mit151	13	74.514424	116341977	0.9003	0.62836	0	5.14E-14	0	0	Shared
Pigt	475193	2	1.64E+08	02.168.990	2	151.40532	169124295	0.87679	0.73061	0	5.36E-14	0	0	Shared
Apobec1	727741	6	1.23E+08	d6mit366	6	77.49561	115192871	0.43769	0.70173	0	5.84E-14	0	0	SCG
unassigned	739477	7	52255454	D7MIT267	7	18.29809	30331965	2.05436	2.64091	0	6.19E-14	0	0	Shared
Aldh4a1	592746	4	1.39E+08	04.133.005	4	97.642221	133288839	0.47481	0.7097	0	6.26E-14	0	0	Shared
Tada3l	725760	6	1.13E+08	d6mit366	6	77.49561	115192871	3.21222	2.58633	0	6.35E-14	0	0	Shared
unassigned	144915	11	58747963	D11Mit4	11	39.42453	68422759	1.17317	1.48925	0	6.69E-14	0	0	Shared
Ap4s1	169560	12	52831896	D12MIT285	12	30.221464	55750112	0.11236	0.19928	0	6.97E-14	0	0	Shared
Inpp5f	754921	7	1.36E+08	07.122.234	7	82.95546	129586366	0.31196	0.41982	0	7.42E-14	0	0	Shared
Bat5	358549	17	35235845	17.034.150	17	51.1372	34678889	1.87903	2.14018	0	7.60E-14	0	0	Shared
Vldlr	423643	19	27318692	D19MIT96	19	21.387917	21916083	1.30513	0.93816	0	7.74E-14	0	0	Shared
Arntl	751325	7	1.2E+08	RS36353338	7	66.26522	112706514	0.26674	0.46803	0	7.86E-14	0	0	Shared
unassigned	329753	16	58456005	D16Mit125	16	48.358705	42377567	1.99252	1.60369	0	8.42E-14	0	0	Shared
unassigned	869261	9	65953299	D9MIT336	9	49.6331	65425671	2.24974	2.84997	0	9.21E-14	0	0	Shared
Gsr	792623	8	34782010	D8MIT94	8	19.424222	32452130	3.86052	3.24695	0	9.22E-14	0	0	SCG
Hcrtr1	617709	4	1.3E+08	D4Mit203	4	89.732314	129249262	1.36204	1.65255	0	9.27E-14	0	0	SCG
Cntnap2	690188	6	45870805	D6Mit272	6	27.2529	44382847	1.27952	1.01289	0	9.29E-14	0	0	Shared
unassigned	393371	18	37918039	18.038.678	18	24.45192	38711680	0.71251	0.97414	0	9.48E-14	0	0	SCG
Ankrd27	737787	7	36392142	D7MIT228	7	28.11811	47279833	1.70748	1.45768	0	9.78E-14	0	0	Shared
Ldhb	731599	6	1.42E+08	D6MIT194	6	87.57626	128115503	0.82346	0.69942	0	9.98E-14	0	0	SCG
Clpx	844485	9	65149668	D9MIT248	9	44.87553	58210366	1.67407	1.25324	0	1.05E-13	0	0	Shared
unassigned	761790	7	29757516	D7MIT267	7	18.29809	30331965	0.85039	0.97814	0	1.07E-13	0	0	Shared
unassigned	607123	4	71802352	rs13477756	4	50.524248	68030949	0.72076	0.93987	0	1.18E-13	0	0	Shared
unassigned	672389	5	1.09E+08	D5MIT239	5	66.11023	107842159	0.63623	1.08451	0	1.22E-13	0	0	Shared
5033411D12Rik	222833	13	17067999	D13Mit207	13	8.688726	16526195	0.29331	0.49026	0	1.26E-13	0	0	Shared
unassigned	298557	15	1E+08	D15MIT44	15	76.945032	98951714	0.53998	0.63526	0	1.26E-13	0	0	SCG
Ift74	581659	4	94321532	D4Mit166	4	66.232947	93616234	0.15235	0.39169	0	1.28E-13	0	0	Shared
Itpr2	732606	6	1.46E+08	D6Mit14	6	101.60848	145604376	1.16302	1.5312	0	1.33E-13	0	0	Shared
unassigned	869536	9	67209081	D9MIT107	9	53.50038	73315075	0.1475	0.22991	0	1.35E-13	0	0	SCG
unassigned	285907	15	32947010	15.028.723	15	14.881134	28708166	0.05148	0.13447	0	1.36E-13	0	0	Shared
Kif1b	622602	4	1.49E+08	D4MIT42	4	117.10129	150944103	0.47074	0.39999	0	1.43E-13	0	0	SCG
unassigned	604763	4	57084092	04.053.650	4	40.480187	53641772	0.07564	0.15067	0	1.44E-13	0	0	Shared
Fn3krp	134526	11	1.21E+08	D11MIT214	11	79.65651	114991785	0.24039	0.39224	0	1.47E-13	0	0	Shared
Ikbkap	604617	4	56788312	D4MIT164	4	42.389612	59415112	0.70299	0.99287	0	1.61E-13	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	866559	9	54891734	09.046.588	9	34.49446	46645088	0.80914	1.03415	0	1.73E-13	0	0	SCG
Tmc7	778070	7	1.26E+08	RS36353338	7	66.26522	112706514	0.71786	0.57288	0	1.77E-13	0	0	SCG
unassigned	284932	15	27497233	15.028.723	15	14.881134	28708166	1.04434	1.21748	0	1.89E-13	0	0	SCG
Pcx	418758	19	4602515	19.000.325	19	0.2	325000	1.47094	1.2807	0	2.00E-13	0	0	Shared
Rgs17	63473	10	4505049	rs13480474	10	1.8	4403267	0.25656	0.37187	0	2.21E-13	0	0	Shared
Tmem179	199424	12	1.14E+08	D12MIT7	12	66.696627	104970690	1.28543	0.99396	0	2.29E-13	0	0	Shared
Acacb	646017	5	1.15E+08	d5mit158	5	69.85959	115413178	3.37435	2.87765	0	2.32E-13	0	0	SCG
Fbxo44	622301	4	1.48E+08	D4MIT232	4	109.11827	144647559	2.50215	2.15651	0	2.35E-13	0	0	Shared
Arcn1	863987	9	44549877	D9MIT2	9	25.36976	37202486	0.86964	0.6436	0	2.53E-13	0	0	SCG
Stx2	677108	5	1.29E+08	D5MIT95	5	98.81753	125309605	1.23709	0.86103	0	2.53E-13	0	0	Shared
unassigned	715766	6	50272811	D6Mit272	6	27.2529	44382847	0.39111	0.51681	0	2.70E-13	0	0	Shared
Atp11b	521818	3	35733226	03.033.871	3	22.08075	33578373	1.52079	1.23128	0	2.73E-13	0	0	Shared
Macrod1	419763	19	7272022	D19Mit68	19	0.200001	3645155	1.34569	1.90372	0	2.77E-13	0	0	Shared
Ccdc104	139314	11	29121599	D11MIT186	11	23.608	35049231	0.91263	0.75739	0	2.78E-13	0	0	SCG
unassigned	765674	7	53173607	D7MIT228	7	28.11811	47279833	1.71929	2.14664	0	2.80E-13	0	0	SCG
Slc5a2	780256	7	1.35E+08	07.122.234	7	82.95546	129586366	1.28925	1.57697	0	2.83E-13	0	0	Shared
unassigned	255589	14	77981950	RS31380922	14	61.610758	78742431	0.71942	0.873	0	2.98E-13	0	0	Shared
Pkd2	643836	5	1.05E+08	D5MIT239	5	66.11023	107842159	0.89549	1.13148	0	3.21E-13	0	0	Shared
Pex16	460768	2	92217852	D2MIT75	2	46.41465	80424883	2.03695	1.64906	0	3.29E-13	0	0	Shared
Soat1	55254	1	1.58E+08	01.183.109	1	96.118477	183202456	0.47219	0.6181	0	3.38E-13	0	0	SCG
Sumf1	725019	6	1.08E+08	D6MIT328	6	75.24789	112729344	0.61082	0.71834	0	3.44E-13	0	0	Shared
unassigned	594081	4	1.47E+08	D4MIT232	4	109.11827	144647559	1.3601	1.77444	0	3.52E-13	0	0	SCG
Rpain	121282	11	70787304	D11MIT320	11	39.87138	70766870	0.12797	0.35806	0	3.54E-13	0	0	Shared
Scg3	871227	9	75531463	D9MIT107	9	53.50038	73315075	1.31944	2.0698	0	3.54E-13	0	0	Shared
Fau	419274	19	6058251	D19Mit68	19	0.200001	3645155	0.53096	0.6352	0	3.61E-13	0	0	Shared
Mphosph10	768045	7	71521483	07.056.455	7	36.40088	63842351	0.12375	0.24561	0	3.81E-13	0	0	Shared
unassigned	240771	13	1.14E+08	D13MIT53	13	72.69389	113084631	2.54866	2.14118	0	3.97E-13	0	0	Shared
Slc7a8	269591	14	55348184	D14Mit183	14	42.794969	52629891	0.8206	1.1818	0	4.14E-13	0	0	Shared
unassigned	555088	3	88716546	D3MIT49	3	73.77602	89036582	1.10875	0.88306	0	4.34E-13	0	0	Shared
Fam103a1	745709	7	88914316	D7MIT350	7	57.28732	90734599	1.03066	1.57197	0	4.48E-13	0	0	SCG
Ralgps2	55376	1	1.59E+08	D1Mit102	1	80.039245	149096650	3.77748	3.11355	0	4.65E-13	0	0	SCG
Ankrd54	311859	15	78891594	15.088.295	15	61.334066	88297664	0.79017	1.24947	0	4.73E-13	0	0	Shared
Ubash3b	862971	9	40836137	D9MIT247	9	25.36975	36940492	2.58872	2.15933	0	4.86E-13	0	0	Shared
Pcdhgb8	393374	18	37923645	18.038.678	18	24.45192	38711680	0.83936	1.10374	0	5.01E-13	0	0	Shared
Tmem25	864012	9	44601875	09.046.588	9	34.49446	46645088	0.40327	0.5389	0	5.02E-13	0	0	Shared
Ank2	562258	3	1.27E+08	RS30160288	3	119.38247	125981675	0.29094	0.44039	0	5.25E-13	0	0	Shared
Csrp1	20713	1	1.38E+08	01.136.071	1	77.74879	136151166	2.60658	2.25846	0	5.56E-13	0	0	SCG
Bxdc2	300710	15	10409364	15.010.846	15	8.803289	10831030	0.86497	0.54419	0	5.62E-13	0	0	Shared
unassigned	651913	5	1.39E+08	05.132.979	5	112.26584	133170167	0.82957	1.10472	0	6.82E-13	0	0	Shared
Oasl2	646285	5	1.15E+08	d5mit158	5	69.85959	115413178	0.61207	0.85436	0	7.02E-13	0	0	SCG
Crtc3	771127	7	87754784	D7MIT350	7	57.28732	90734599	1.37574	1.03871	0	7.18E-13	0	0	SCG
unassigned	169471	12	52527127	12.065.348	12	37.44045	65530382	2.33595	1.86671	0	7.44E-13	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	237837	13	1E+08	13.096.920	13	58.796863	96589256	0.83538	1.01475	0	7.53E-13	0	0	Shared
Mrpl46	770533	7	85920100	D7MIT350	7	57.28732	90734599	0.77635	0.90411	0	7.54E-13	0	0	Shared
H2-T22	893539	17	36177176	17.034.150	17	51.1372	34678889	0.67841	0.39984	0	8.05E-13	0	0	Shared
Abi1	517414	2	22808995	D2MIT81	2	18.06443	24644623	1.35456	1.19215	0	8.12E-13	0	0	Shared
Herc2	741514	7	63440235	D7Mit232	7	35.20811	59868792	2.01533	2.38612	0	8.20E-13	0	0	Shared
Itga6	457352	2	71684038	RS28322831	2	43.67748	71063776	0.72601	0.58988	0	8.68E-13	0	0	SCG
Oprm1	85852	10	3517332	rs13480474	10	1.8	4403267	9.23074	6.68693	0	9.24E-13	0	0	SCG
unassigned	735243	7	25205344	07.013.915	7	8.7	15600169	0.35459	0.56211	0	9.42E-13	0	0	Shared
unassigned	459334	2	83697846	D2MIT75	2	46.41465	80424883	0.71775	0.55086	0	9.55E-13	0	0	Shared
3110007F17Rik	932162	X	1.21E+08	DXMit79	X	50.813632	127398406	9.3369	0.41606	0.20625	9.64E-13	0	0	SCG
Gns	83722	10	1.21E+08	D10Mit14	10	93.102537	118098315	1.06526	1.29136	0	9.76E-13	0	0	Shared
Rit2	407422	18	31372324	18.038.678	18	24.45192	38711680	0.80519	0.96425	0	1.08E-12	0	0	Shared
Ddost	592346	4	1.38E+08	D4MIT170	4	99.940854	138171253	0.89928	1.02758	0	1.10E-12	0	0	Shared
unassigned	358650	17	35400148	17.034.150	17	51.1372	34678889	1.2079	1.05367	0	1.16E-12	0	0	Shared
unassigned	63848	10	5917528	RS38343005	10	4.536629	11465792	0.52197	0.73961	0	1.21E-12	0	0	Shared
Uggt1	35852	1	36249256	D1Mit374	1	27.028585	34816928	0.78293	0.62989	0	1.24E-12	0	0	Shared
Oxr1	287650	15	41633131	15.028.723	15	14.881134	28708166	0.86042	1.19076	0	1.33E-12	0	0	SCG
Tbc1d2b	873576	9	90122245	d9mit198	9	66.50428	91176808	2.70709	2.20717	0	1.33E-12	0	0	SCG
Otud7a	742267	7	70880685	D7MIT228	7	28.11811	47279833	0.45616	0.59549	0	1.38E-12	0	0	Shared
Nrip1	347072	16	76351884	D16MIT188	16	69.332085	76817838	0.0443	0.16761	0	1.54E-12	0	0	Shared
Strn4	734376	7	17407878	07.013.915	7	8.7	15600169	0.3173	0.48079	0	1.54E-12	0	0	Shared
Dvl2	120878	11	69819647	D11MIT320	11	39.87138	70766870	1.25852	0.92892	0	1.62E-12	0	0	Shared
unassigned	630110	5	23646144	D5MIT294	5	15.58331	20863135	0.88896	1.06228	0	1.70E-12	0	0	SCG
Snx7	560865	3	1.18E+08	D3MIT315	3	89.68246	115544553	0.38021	0.22839	0	1.80E-12	0	0	Shared
Eef1a1	871803	9	78328468	d9mit198	9	66.50428	91176808	0.51956	0.41788	0	1.81E-12	0	0	Shared
Prune2	421768	19	17286794	19.013.429	19	11.129219	13436471	1.23263	0.97648	0	1.86E-12	0	0	SCG
unassigned	179284	12	1.07E+08	D12MIT7	12	66.696627	104970690	1.89172	1.42793	0	1.91E-12	0	0	Shared
Zfp94	760491	7	25088809	07.013.915	7	8.7	15600169	0.57404	0.81332	0	1.93E-12	0	0	Shared
Dennd4a	844267	9	64683761	D9MIT336	9	49.6331	65425671	2.21666	1.78992	0	2.02E-12	0	0	Shared
Strap	706340	6	1.38E+08	D6MIT194	6	87.57626	128115503	1.08227	1.27215	0	2.07E-12	0	0	Shared
Gpr137b-ps	222307	13	12707467	D13Mit207	13	8.688726	16526195	0.24187	0.43259	0	2.13E-12	0	0	Shared
Tesk1	574617	4	43458612	d4mit238	4	33.232784	45243003	4.01833	3.30054	0	2.13E-12	0	0	SCG
Mef2a	768572	7	74438480	D7Mit232	7	35.20811	59868792	0.37633	0.54481	0	2.16E-12	0	0	Shared
unassigned	375928	17	35308913	D17MIT51	17	53.34361	43641790	0.27889	0.59053	0	2.16E-12	0	0	SCG
Mcam	839490	9	43948963	09.046.588	9	34.49446	46645088	0.94904	1.09482	0	2.24E-12	0	0	SCG
4933407N01Rik	139641	11	30848307	D11MIT186	11	23.608	35049231	0.78729	0.62563	0	2.26E-12	0	0	Shared
Golga3	645148	5	1.11E+08	D5MIT239	5	66.11023	107842159	1.45314	1.80653	0	2.26E-12	0	0	Shared
Snap91	873049	9	86699346	09.079.053	9	64.60162	79115123	0.82384	0.99006	0	2.28E-12	0	0	SCG
Angptl4	375335	17	33915337	17.034.150	17	51.1372	34678889	1.93778	1.62033	0	2.46E-12	0	0	SCG
Kif21a	314992	15	90822148	15.090.122	15	63.155859	90124664	0.60971	0.50653	0	2.51E-12	0	0	Shared
Bcat1	732273	6	1.45E+08	D6Mit14	6	101.60848	145604376	0.40743	0.32184	0	2.57E-12	0	0	Shared
Cmpk1	613725	4	1.15E+08	RS27499066	4	79.437135	114673522	0.67882	0.55008	0	2.71E-12	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Ctnnbip1	594776	4	1.49E+08	D4MIT232	4	109.11827	144647559	2.04484	1.54179	0	2.88E-12	0	0	Shared
unassigned	265758	14	32000456	D14MIT174	14	33.327106	32460166	1.05553	1.21515	0	2.99E-12	0	0	Shared
unassigned	598928	4	15851373	04.013.290	4	8.3	13290000	1.23929	1.43303	0	3.22E-12	0	0	Shared
unassigned	622632	4	1.49E+08	D4MIT232	4	109.11827	144647559	0.61943	0.44991	0	3.65E-12	0	0	Shared
Skiv2l2	240774	13	1.14E+08	D13MIT213	13	69.659242	109037352	1.93603	2.29583	0	3.72E-12	0	0	SCG
Mcam	839484	9	43947502	D9MIT247	9	25.36975	36940492	1.33953	1.22528	0	3.77E-12	0	0	SCG
Gtf2h1	740165	7	54052803	D7MIT228	7	28.11811	47279833	0.08341	0.1644	0	3.88E-12	0	0	Shared
unassigned	440768	19	46626029	19.046.444	19	55.551107	46465179	0.85923	0.63554	0	3.91E-12	0	0	Shared
unassigned	376245	17	36254575	17.034.150	17	51.1372	34678889	0.05128	0.10335	0	4.03E-12	0	0	Shared
Ppp5c	759912	7	17592463	07.013.915	7	8.7	15600169	0.75466	0.90405	0	4.19E-12	0	0	Shared
unassigned	357203	17	31667864	17.034.150	17	51.1372	34678889	0.38986	0.32549	0	4.38E-12	0	0	Shared
Prkag2	658064	5	24368792	05.018.430	5	14.15919	18423994	1.38726	1.87916	0	4.40E-12	0	0	Shared
Pclo	628644	5	14668995	D5MIT123	5	4.1	6556176	1.79137	1.24793	0	4.65E-12	0	0	Shared
Gnl3l	934962	X	1.47E+08	DXMit79	X	50.813632	127398406	1.61017	1.4686	1.28744	4.66E-12	0	0	SCG
Skiv2l2	240772	13	1.14E+08	D13MIT53	13	72.69389	113084631	1.02945	1.3622	0	4.68E-12	0	0	SCG
Exoc6	425761	19	37668201	D19MIT13	19	37.094077	32713513	0.55364	0.36394	0	4.76E-12	0	0	Shared
unassigned	742651	7	72845901	07.056.455	7	36.40088	63842351	0.85817	1.09642	0	4.79E-12	0	0	SCG
unassigned	286529	15	36105232	15.028.723	15	14.881134	28708166	3.11846	2.1924	0	4.80E-12	0	0	Shared
Mecr	590286	4	1.31E+08	D4Mit203	4	89.732314	129249262	2.39944	2.11415	0	5.16E-12	0	0	Shared
Akr7a5	592552	4	1.39E+08	D4Mit203	4	89.732314	129249262	0.95943	0.70035	0	5.28E-12	0	0	SCG
1500032L24Rik	294430	15	82178344	D15MIT67	15	36.957676	70032295	1.57216	1.70168	0	5.45E-12	0	0	Shared
Lancl1	41409	1	67085080	D1MIT132	1	55.208767	77143053	1.78711	2.1704	0	5.75E-12	0	0	Shared
H2-Aa	375489	17	34419724	17.034.150	17	51.1372	34678889	0.95145	0.73331	0	5.79E-12	0	0	SCG
1200011I18Rik	274825	14	76507173	14.067.129	14	52.822413	68793727	0.93032	0.73594	0	5.90E-12	0	0	Shared
Vwf	704351	6	1.26E+08	D6MIT194	6	87.57626	128115503	0.42522	0.54885	0	6.10E-12	0	0	SCG
Tnks	816009	8	35914689	D8Mit191	8	23.020658	36243839	0.70264	0.89912	0	6.25E-12	0	0	Shared
Ncor1	146141	11	62148003	D11Mit4	11	39.42453	68422759	0.62099	0.75013	0	6.54E-12	0	0	Shared
unassigned	448712	2	26874857	D2MIT81	2	18.06443	24644623	0.78229	0.62995	0	6.58E-12	0	0	Shared
A730017C20Rik	397288	18	59232216	D18MIT152	18	47.63475	62096421	1.17558	0.9876	0	6.71E-12	0	0	Shared
Bpnt1	29411	1	1.87E+08	01.183.109	1	96.118477	183202456	0.37062	0.2527	0	6.80E-12	0	0	Shared
Acacb	646029	5	1.15E+08	d5mit158	5	69.85959	115413178	1.70863	1.42786	0	6.98E-12	0	0	SCG
unassigned	139631	11	30834760	D11MIT51	11	25.39412	36205252	1.9499	1.54698	0	7.03E-12	0	0	Shared
unassigned	806684	8	1.14E+08	D8MIT47	8	79.109749	109368069	0.02603	0.03864	0	7.03E-12	0	0	Shared
Ece1	592081	4	1.38E+08	D4MIT170	4	99.940854	138171253	1.46729	1.18637	0	7.05E-12	0	0	Shared
Gtf2h3	649118	5	1.25E+08	D5MIT95	5	98.81753	125309605	0.92356	1.35883	0	7.05E-12	0	0	Shared
Clcn6	622221	4	1.47E+08	D4MIT232	4	109.11827	144647559	0.82918	0.6764	0	7.31E-12	0	0	SCG
Tekt2	616783	4	1.26E+08	D4MIT308	4	84.360247	123838543	1.82553	1.35759	0	7.55E-12	0	0	SCG
Mlh1	878090	9	1.11E+08	09.105.291	9	79.88305	105335230	0.16898	0.12329	0	7.61E-12	0	0	SCG
Pygl	191251	12	71302845	12.065.348	12	37.44045	65530382	1.32489	1.14733	0	8.12E-12	0	0	SCG
Cela1	317539	15	1.01E+08	D15MIT44	15	76.945032	98951714	0.27539	0.54973	0	8.37E-12	0	0	Shared
unassigned	220871	13	1.2E+08	D13MIT78	13	76.842169	119618032	6.03235	4.0452	0	8.73E-12	0	0	Shared
Scg5	499290	2	1.14E+08	02.109.360	2	59.82539	109399318	0.35126	0.49298	0	8.76E-12	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Herc2	741513	7	63440004	07.056.455	7	36.40088	63842351	2.79112	3.20405	0	8.99E-12	0	0	SCG
Stat2	85210	10	1.28E+08	D10Mit14	10	93.102537	118098315	0.58402	0.74495	0	8.99E-12	0	0	Shared
unassigned	755904	7	1.4E+08	07.122.234	7	82.95546	129586366	0.24915	0.36152	0	9.37E-12	0	0	Shared
Vps11	863828	9	44162234	D9MIT247	9	25.36975	36940492	0.69598	0.82493	0	9.72E-12	0	0	SCG
Ppil4	64162	10	7540825	RS33543047	10	4.53663	12164362	1.2204	0.94063	0	9.89E-12	0	0	Shared
App	348011	16	85173545	16.083.701	16	79.82369	83818653	0.8802	1.0554	0	1.03E-11	0	0	Shared
Zfp426	859121	9	20276149	09.014.560	9	12.99047	14614051	0.86655	0.59829	0	1.04E-11	0	0	Shared
Ptprf	614906	4	1.18E+08	RS27499066	4	79.437135	114673522	0.96555	0.70377	0	1.08E-11	0	0	SCG
Coq2	670444	5	1.01E+08	D5MIT10	5	65.80535	104668024	1.10958	0.87398	0	1.20E-11	0	0	SCG
unassigned	148368	11	70775198	D11MIT320	11	39.87138	70766870	0.1484	0.07245	0	1.22E-11	0	0	Shared
Lrrfip2	854197	9	1.11E+08	09.105.291	9	79.88305	105335230	2.60141	3.34192	0	1.27E-11	0	0	Shared
unassigned	529915	3	89052885	D3MIT49	3	73.77602	89036582	1.6778	1.45633	0	1.31E-11	0	0	Shared
Pcdhga4	393337	18	37844872	18.038.678	18	24.45192	38711680	1.15885	0.79475	0	1.32E-11	0	0	Shared
4833420G17Rik	220869	13	1.2E+08	D13MIT53	13	72.69389	113084631	7.34179	4.74307	0	1.44E-11	0	0	Shared
Lactb	869414	9	66822546	D9MIT336	9	49.6331	65425671	3.02747	3.65277	0	1.47E-11	0	0	SCG
Svop	673596	5	1.15E+08	D5MIT239	5	66.11023	107842159	1.46593	1.25138	0	1.48E-11	0	0	Shared
unassigned	433762	19	11851079	19.009.231	19	7.749799	9238445	1.16975	0.80343	0	1.54E-11	0	0	Shared
Erc1	727148	6	1.2E+08	d6mit366	6	77.49561	115192871	0.09159	0.21434	0	1.57E-11	0	0	Shared
Ppp2r5e	192270	12	76594414	12.065.348	12	37.44045	65530382	1.49788	1.18264	0	1.67E-11	0	0	Shared
Tekt2	616785	4	1.26E+08	D4MIT308	4	84.360247	123838543	1.14631	1.55578	0	1.67E-11	0	0	SCG
Gm5665	231895	13	62807064	RS30012306	13	43.697138	70428413	1.61556	1.03965	0	1.72E-11	0	0	Shared
Atf6b	358269	17	34784619	D17MIT51	17	53.34361	43641790	1.00014	1.17475	0	1.74E-11	0	0	SCG
Ecsit	859833	9	21888514	09.014.560	9	12.99047	14614051	1.33737	0.89512	0	1.76E-11	0	0	Shared
Wdtc1	618506	4	1.33E+08	D4Mit203	4	89.732314	129249262	0.33358	0.527	0	1.76E-11	0	0	Shared
Slc9a3r1	132545	11	1.15E+08	D11MIT214	11	79.65651	114991785	1.54595	1.38247	0	1.86E-11	0	0	SCG
Psg16	734480	7	17678998	07.013.915	7	8.7	15600169	1.32553	1.62805	0	2.06E-11	0	0	Shared
Ralgps2	55354	1	1.59E+08	D1Mit102	1	80.039245	149096650	0.98582	1.22139	0	2.13E-11	0	0	SCG
unassigned	730500	6	1.37E+08	D6MIT194	6	87.57626	128115503	0.39269	0.5477	0	2.13E-11	0	0	Shared
Fkbp9	692579	6	56801357	d6mit123	6	39.56321	56801586	0.80558	1.06505	0	2.18E-11	0	0	Shared
Trf	875818	9	1.03E+08	D9MIT24	9	73.18313	103132731	0.867	1.0175	0	2.18E-11	0	0	SCG
unassigned	287666	15	41656691	15.046.034	15	20.554602	46035472	1.69783	1.44638	0	2.22E-11	0	0	SCG
unassigned	831306	8	1.26E+08	D8MIT42	8	102.88933	129076217	0.26587	0.47944	0	2.22E-11	0	0	Shared
Tmod1	575341	4	46073842	d4mit238	4	33.232784	45243003	0.53009	0.62266	0	2.25E-11	0	0	Shared
Gpr137b	222333	13	13459856	D13Mit207	13	8.688726	16526195	1.65722	1.24884	0	2.30E-11	0	0	Shared
Dctn6	815836	8	35153817	D8MIT94	8	19.424222	32452130	0.89613	1.05943	0	2.55E-11	0	0	Shared
Mios	683980	6	8172486	06.016.672	6	10.4	16672000	1.46529	1.96096	0	2.60E-11	0	0	Shared
Lasp1	128206	11	97677036	D11MIT289	11	59.90287	94741466	2.64554	2.30232	0	2.65E-11	0	0	Shared
Soat1	55261	1	1.58E+08	D1Mit102	1	80.039245	149096650	0.23391	0.11925	0	2.67E-11	0	0	Shared
Ube4b	622693	4	1.49E+08	D4MIT232	4	109.11827	144647559	0.86052	0.75603	0	2.85E-11	0	0	Shared
Tbc1d9	800326	8	85782896	D8MIT346	8	54.673156	85454038	2.06718	1.89049	0	2.87E-11	0	0	Shared
Slc38a11	490672	2	65201432	D2MIT61	2	35.12792	60528325	2.39448	3.16828	0	3.01E-11	0	0	SCG
Rmnd1	63860	10	5935618	rs13480474	10	1.8	4403267	0.03353	0.06154	0	3.27E-11	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	737027	7	31097761	07.017.531	7	12.92437	18957827	2.01108	2.31384	0	3.29E-11	0	0	Shared
Tanc1	454967	2	59484857	D2MIT61	2	35.12792	60528325	0.15695	0.26042	0	3.49E-11	0	0	Shared
unassigned	504034	2	1.32E+08	D2MIT285	2	110.63716	152683037	0.92803	0.80025	0	3.60E-11	0	0	Shared
Smarca4	835333	9	21441880	D9MIT250	9	5.2	8393623	0.91638	0.76073	0	3.73E-11	0	0	SCG
2610301G19Rik	273270	14	70538154	D14MIT39	14	54.529907	69166099	0.74588	1.04129	0	3.74E-11	0	0	SCG
Zdhhc13	740320	7	56059724	07.056.455	7	36.40088	63842351	0.43778	0.56626	0	4.19E-11	0	0	Shared
Ank2	562259	3	1.27E+08	D3MIT256	3	103.27598	136014535	1.54325	1.32364	0	4.26E-11	0	0	Shared
Klc1	180949	12	1.13E+08	D12MIT7	12	66.696627	104970690	2.06171	1.81599	0	4.34E-11	0	0	SCG
Eif3k	761793	7	29762226	07.017.531	7	12.92437	18957827	0.58968	0.48158	0	4.39E-11	0	0	Shared
Tceb1	33407	1	16638045	rs13475769	1	16.197578	24958696	1.14079	0.91315	0	4.64E-11	0	0	SCG
Dnttip2	536280	3	1.22E+08	D3MIT57	3	88.53548	115533310	2.4601	2.89326	0	4.68E-11	0	0	Shared
unassigned	277936	14	1.04E+08	14.095.016	14	67.370818	96532085	0.06989	0.17549	0	4.73E-11	0	0	Shared
Ncstn	58619	1	1.74E+08	01.183.109	1	96.118477	183202456	0.3172	0.40942	0	4.74E-11	0	0	Shared
unassigned	358676	17	35460995	D17MIT51	17	53.34361	43641790	1.87737	2.61974	0	4.79E-11	0	0	SCG
Fam103a1	745708	7	88914219	D7MIT350	7	57.28732	90734599	1.67476	1.99011	0	5.08E-11	0	0	SCG
unassigned	377547	17	45706800	17.034.150	17	51.1372	34678889	1.18459	1.26928	0	5.12E-11	0	0	SCG
Rad23b	576747	4	55383302	04.053.650	4	40.480187	53641772	0.6028	0.7873	0	5.32E-11	0	0	Shared
Uevld	766058	7	54182791	D7MIT228	7	28.11811	47279833	0.25936	0.42218	0	5.43E-11	0	0	Shared
Pcmt1	86497	10	7364125	rs13480474	10	1.8	4403267	1.02779	0.92961	0	5.58E-11	0	0	SCG
Abi3bp	329431	16	56668399	D16MIT139	16	56.627807	65669762	3.01776	2.32884	0	5.72E-11	0	0	SCG
unassigned	745706	7	88913014	D7MIT350	7	57.28732	90734599	1.17353	0.92121	0	5.75E-11	0	0	SCG
unassigned	444537	2	4684380	D2MIT1	2	2.4	3803361	0.6994	0.93066	0	5.99E-11	0	0	SCG
5930434B04Rik	448708	2	26871015	D2Mit297	2	25.96707	42461006	1.16306	1.33958	0	6.01E-11	0	0	SCG
Leprotl1	815866	8	35200601	D8MIT292	8	21.904548	35848067	0.83749	0.95957	0	6.12E-11	0	0	SCG
Anxa2	845572	9	69330783	D9MIT107	9	53.50038	73315075	1.57405	1.40342	0	6.33E-11	0	0	Shared
Fam179b	171338	12	66107317	12.065.348	12	37.44045	65530382	1.94432	1.43003	0	6.36E-11	0	0	Shared
unassigned	419265	19	6050295	19.000.325	19	0.2	325000	0.91436	0.65628	0	6.47E-11	0	0	SCG
Ptprg	243390	14	13069556	14.008.937	14	5.6	10975728	1.35099	1.63835	0	6.60E-11	0	0	SCG
Echdc1	67901	10	29065758	RS29329200	10	39.498733	40791505	0.2283	0.13121	0	6.64E-11	0	0	SCG
Rnf34	648519	5	1.23E+08	D5MIT95	5	98.81753	125309605	1.48826	1.75037	0	6.80E-11	0	0	SCG
unassigned	812749	8	15900807	D8Mit191	8	23.020658	36243839	0.38453	0.60711	0	6.82E-11	0	0	Shared
Herc2	741451	7	63359198	D7Mit232	7	35.20811	59868792	1.84908	2.09421	0	7.09E-11	0	0	SCG
unassigned	482630	2	24555402	D2MIT81	2	18.06443	24644623	3.47047	3.00376	0	7.17E-11	0	0	SCG
Clpx	844490	9	65157969	09.046.588	9	34.49446	46645088	1.76779	2.11569	0	7.19E-11	0	0	Shared
unassigned	279680	14	1.19E+08	RS31252045	14	77.831601	111376384	0.70913	0.95201	0	7.58E-11	0	0	Shared
Tnfrsf21	359724	17	43201976	17.034.150	17	51.1372	34678889	0.88588	1.04352	0	7.63E-11	0	0	Shared
Klc1	180952	12	1.13E+08	D12MIT7	12	66.696627	104970690	2.01039	1.83044	0	7.73E-11	0	0	SCG
Ece1	592083	4	1.38E+08	04.133.005	4	97.642221	133288839	1.03804	1.22905	0	7.75E-11	0	0	SCG
G2e3	169432	12	52458019	D12MIT285	12	30.221464	55750112	1.60853	2.10433	0	8.24E-11	0	0	Shared
Gpd1l	878814	9	1.15E+08	D9MIT201	9	91.42427	117345284	0.45595	0.55697	0	8.50E-11	0	0	Shared
Cul3	43878	1	80273021	D1MIT134	1	59.854045	80264451	1.91082	1.65119	0	8.52E-11	0	0	Shared
BC037034	679279	5	1.39E+08	05.132.979	5	112.26584	133170167	1.40202	1.196	0	8.84E-11	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Pbrm1	247165	14	31867368	D14Mit183	14	42.794969	52629891	0.47598	0.60536	0	8.94E-11	0	0	Shared
Tbl3	372817	17	24838065	17.021.019	17	14.36839	21451267	0.921	1.1174	0	9.08E-11	0	0	SCG
Nlrx1	863752	9	44072809	D9MIT247	9	25.36975	36940492	1.30772	0.97086	0	9.58E-11	0	0	SCG
Setdb1	556340	3	95130084	D3MIT49	3	73.77602	89036582	0.23527	0.34663	0	9.75E-11	0	0	Shared
unassigned	863827	9	44161870	D9MIT2	9	25.36976	37202486	0.53108	0.68424	0	9.76E-11	0	0	Shared
Oxr1	287649	15	41632043	15.046.034	15	20.554602	46035472	0.4602	0.61857	0	9.78E-11	0	0	SCG
Rbm45	458349	2	76221526	D2MIT75	2	46.41465	80424883	0.59386	0.46059	0	9.83E-11	0	0	Shared
Polr3f	469981	2	1.44E+08	RS27267029	2	129.56131	136669427	0.82114	0.60913	0	9.88E-11	0	0	Shared
unassigned	465177	2	1.2E+08	D2MIT395	2	91.61399	119350649	2.611	2.07826	0	1.01E-10	0	0	Shared
Tgfb1i1	754818	7	1.35E+08	07.122.234	7	82.95546	129586366	1.51376	1.71883	0	1.03E-10	0	0	SCG
Dph1	149246	11	74994105	D11Mit4	11	39.42453	68422759	0.64941	0.8304	0	1.08E-10	0	0	SCG
Commd2	550399	3	57450637	D3MIT67	3	34.10534	52956484	0.51764	0.3384	0	1.09E-10	0	0	Shared
2210418O10Rik	513494	2	1.77E+08	D2MIT148	2	167.77989	178535250	0.81015	0.53825	0	1.13E-10	0	0	Shared
unassigned	285680	15	31515258	15.028.723	15	14.881134	28708166	3.66045	3.03265	0	1.13E-10	0	0	SCG
Cd1d1	554435	3	86799889	D3MIT98	3	51.73848	85985423	0.66474	0.89351	0	1.17E-10	0	0	SCG
Capza2	685120	6	17600003	06.016.672	6	10.4	16672000	0.00509	0.02713	0	1.18E-10	0	0	Shared
Ralgps1	485087	2	33023702	D2MIT296	2	21.50213	31180075	1.7153	1.31866	0	1.23E-10	0	0	Shared
Sdk1	652818	5	1.42E+08	05.132.979	5	112.26584	133170167	0.30401	0.45808	0	1.23E-10	0	0	Shared
Gm447	663240	5	52766784	d5mit233	5	46.33401	53088465	1.03749	0.93718	0	1.26E-10	0	0	Shared
unassigned	46813	1	97550361	RS50560599	1	67.504828	116681037	0.64691	0.83712	0	1.26E-10	0	0	SCG
Hspg2	591837	4	1.37E+08	D4MIT170	4	99.940854	138171253	0.52253	0.64691	0	1.27E-10	0	0	SCG
Psg16	734473	7	17659482	07.013.915	7	8.7	15600169	2.22341	1.70798	0	1.29E-10	0	0	Shared
unassigned	782806	7	1.47E+08	d7mit109	7	91.14939	143706746	1.40399	1.16858	0	1.32E-10	0	0	SCG
Herc2	741469	7	63389966	D7Mit232	7	35.20811	59868792	0.14027	0.18783	0	1.34E-10	0	0	Shared
Lrp1	107191	10	1.27E+08	D10Mit14	10	93.102537	118098315	1.29618	1.03636	0	1.35E-10	0	0	Shared
Atp6v1a	342862	16	44107842	D16MIT60	16	28.756136	32704177	0.79256	0.86887	0	1.37E-10	0	0	SCG
Acer2	580769	4	86563530	D4MIT348	4	56.036646	82826651	0.66973	0.83261	0	1.43E-10	0	0	Shared
Cd59a	462218	2	1.04E+08	D2MIT100	2	54.19426	106377525	0.09586	0.15827	0	1.43E-10	0	0	SCG
unassigned	531138	3	94681317	D3MIT49	3	73.77602	89036582	1.10113	0.88421	0	1.48E-10	0	0	Shared
Aars	806508	8	1.14E+08	D8MIT215	8	87.841725	118384638	2.05049	1.80379	0	1.50E-10	0	0	SCG
unassigned	561727	3	1.23E+08	RS30160288	3	119.38247	125981675	0.21798	0.37195	0	1.51E-10	0	0	Shared
unassigned	839570	9	44207304	D9MIT247	9	25.36975	36940492	1.38722	1.5647	0	1.51E-10	0	0	SCG
Fxyd6	839871	9	45204063	D9MIT247	9	25.36975	36940492	0.52534	0.58625	0	1.58E-10	0	0	Shared
Prkag2	658077	5	24386513	D5MIT348	5	18.20559	24424937	0.74575	0.89127	0	1.58E-10	0	0	Shared
Kcnh2	657841	5	23827063	D5MIT294	5	15.58331	20863135	0.91238	1.13626	0	1.62E-10	0	0	SCG
unassigned	562274	3	1.27E+08	D3MIT256	3	103.27598	136014535	0.74019	0.92658	0	1.72E-10	0	0	Shared
Sergef	765906	7	53889153	07.056.455	7	36.40088	63842351	0.68005	0.92614	0	1.79E-10	0	0	Shared
Rnf14	393609	18	38472871	18.038.678	18	24.45192	38711680	0.19843	0.10873	0	1.81E-10	0	0	Shared
Rcan3	619222	4	1.35E+08	D4MIT170	4	99.940854	138171253	0.68539	0.84961	0	1.85E-10	0	0	Shared
Chd1	353553	17	15843920	17.013.500	17	8.4	13900467	0.13823	0.26193	0	1.87E-10	0	0	Shared
Exoc1	639258	5	76989369	d5mit233	5	46.33401	53088465	1.71815	1.33989	0	1.92E-10	0	0	Shared
Mcam	839483	9	43947251	D9MIT247	9	25.36975	36940492	1.67251	1.53112	0	1.92E-10	0	0	SCG

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Ssfa2	458868	2	79502467	D2MIT75	2	46.41465	80424883	0.60554	0.75771	0	1.92E-10	0	0	Shared
Aebp2	706804	6	1.41E+08	D6MIT194	6	87.57626	128115503	3.64139	2.90972	0	2.02E-10	0	0	Shared
2010321M09Rik	844325	9	64829849	D9MIT248	9	44.87553	58210366	0.62552	0.46148	0	2.05E-10	0	0	Shared
Mios	683981	6	8174559	06.016.672	6	10.4	16672000	2.00625	2.54805	0	2.06E-10	0	0	Shared
Tekt2	616791	4	1.26E+08	D4MIT308	4	84.360247	123838543	1.49347	1.15097	0	2.11E-10	0	0	SCG
Zfp52	354363	17	21675584	17.021.019	17	14.36839	21451267	3.21347	2.23854	0	2.18E-10	0	0	Shared
Acta2	437896	19	34322956	D19MIT46	19	37.543065	33009697	1.24102	1.08913	0	2.24E-10	0	0	SCG
Cep192	399044	18	68040964	D18MIT208	18	45.2796	61019946	0.19224	0.36491	0	2.46E-10	0	0	Shared
Gm13251	594080	4	1.47E+08	D4MIT232	4	109.11827	144647559	0.63846	0.43951	0	2.47E-10	0	0	Shared
unassigned	262357	14	14949509	14.008.937	14	5.6	10975728	1.27634	1.13646	0	2.47E-10	0	0	SCG
unassigned	863830	9	44163015	D9MIT285	9	25.81754	40462577	0.85615	1.02474	0	2.49E-10	0	0	Shared
1700029I01Rik	594083	4	1.47E+08	D4MIT232	4	109.11827	144647559	0.93533	1.1843	0	2.50E-10	0	0	Shared
Dst	3773	1	34352315	D1Mit374	1	27.028585	34816928	1.71971	2.05154	0	2.59E-10	0	0	Shared
Tmem131	36086	1	36869033	D1MIT236	1	37.41892	45435458	1.217	0.96347	0	2.69E-10	0	0	Shared
unassigned	55119	1	1.58E+08	01.136.071	1	77.74879	136151166	2.50177	2.81061	0	2.73E-10	0	0	SCG
unassigned	349345	16	91714848	16.083.701	16	79.82369	83818653	0.39604	0.53453	0	2.78E-10	0	0	Shared
Tln2	869534	9	67202870	D9MIT248	9	44.87553	58210366	1.0589	0.90672	0	2.81E-10	0	0	SCG
unassigned	844764	9	65981296	D9MIT336	9	49.6331	65425671	0.90613	0.73631	0	2.83E-10	0	0	Shared
unassigned	521872	3	35974829	03.033.871	3	22.08075	33578373	0.75046	0.57748	0	2.86E-10	0	0	Shared
Phf2	228908	13	48918356	D13MIT13	13	37.017532	56582797	1.42562	1.16167	0	2.97E-10	0	0	Shared
Slc4a8	298648	15	1.01E+08	D15MIT44	15	76.945032	98951714	0.51594	0.66235	0	2.97E-10	0	0	SCG
unassigned	24427	1	1.63E+08	D1Mit102	1	80.039245	149096650	1.04373	0.77624	0	3.08E-10	0	0	Shared
unassigned	275017	14	77435806	RS31380922	14	61.610758	78742431	0.86961	1.331	0	3.09E-10	0	0	SCG
unassigned	167896	12	37979163	D12Mit2	12	26.674029	42747379	5.34477	4.38054	0	3.19E-10	0	0	SCG
unassigned	294431	15	82178900	D15MIT262	15	57.212355	87111041	0.94356	0.8658	0	3.25E-10	0	0	SCG
unassigned	812884	8	16358266	08.010.585	8	4.520052	10585028	0.21634	0.34637	0	3.25E-10	0	0	Shared
C920025E04Rik	376237	17	36248330	17.034.150	17	51.1372	34678889	0.31905	0.52714	0	3.29E-10	0	0	SCG
Manbal	473601	2	1.57E+08	D2MIT285	2	110.63716	152683037	0.94929	0.82462	0	3.31E-10	0	0	SCG
Vps13a	434575	19	16800063	19.013.429	19	11.129219	13436471	0.49455	0.32281	0	3.47E-10	0	0	Shared
Faim2	317192	15	99344842	D15MIT44	15	76.945032	98951714	2.03537	1.91394	0	3.53E-10	0	0	Shared
unassigned	761796	7	29765417	07.017.531	7	12.92437	18957827	2.05402	1.8083	0	3.54E-10	0	0	Shared
Dctn1	695797	6	83140488	RS30909511	6	57.9854	83140362	1.16814	0.94251	0	3.55E-10	0	0	Shared
Lrp1b	486936	2	41644500	D2Mit297	2	25.96707	42461006	1.7147	2.34073	0	3.68E-10	0	0	Shared
unassigned	367896	17	86887648	D17MIT76	17	95.2661	86033231	1.11194	1.26305	0	3.73E-10	0	0	Shared
Aars	806527	8	1.14E+08	D8MIT47	8	79.109749	109368069	0.78149	0.95498	0	3.82E-10	0	0	Shared
unassigned	741494	7	63419348	D7Mit232	7	35.20811	59868792	0.54268	0.6709	0	3.89E-10	0	0	Shared
Dst	3749	1	34320148	D1Mit374	1	27.028585	34816928	1.1631	1.38178	0	3.92E-10	0	0	Shared
Scarb2	669182	5	92880375	D5MIT239	5	66.11023	107842159	2.22488	1.93584	0	3.96E-10	0	0	SCG
Scg5	499314	2	1.14E+08	D2MIT100	2	54.19426	106377525	0.43908	0.31377	0	3.99E-10	0	0	Shared
Snx31	304121	15	36485032	15.028.723	15	14.881134	28708166	0.53501	0.90049	0	4.03E-10	0	0	SCG
Bin1	392032	18	32536723	18.038.678	18	24.45192	38711680	0.69776	0.83943	0	4.04E-10	0	0	Shared
Vrk3	739352	7	52007489	D7MIT228	7	28.11811	47279833	1.0905	1.52669	0	4.13E-10	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Oprm1	85860	10	3557623	rs13480474	10	1.8	4403267	5.97343	4.92617	0	4.24E-10	0	0	SCG
Fam125b	485258	2	33683224	D2MIT81	2	18.06443	24644623	2.68468	2.33279	0	4.53E-10	0	0	SCG
Gpr180	259873	14	1.19E+08	RS31252045	14	77.831601	111376384	0.72996	0.93404	0	4.55E-10	0	0	Shared
Ret	726688	6	1.18E+08	d6mit366	6	77.49561	115192871	1.10545	0.95916	0	4.67E-10	0	0	SCG
unassigned	630144	5	23683772	D5MIT294	5	15.58331	20863135	0.21585	0.36644	0	4.67E-10	0	0	Shared
Iars2	61140	1	1.87E+08	01.183.109	1	96.118477	183202456	0.22995	0.34404	0	4.77E-10	0	0	Shared
Inpp5a	757295	7	1.47E+08	d7mit109	7	91.14939	143706746	2.80241	2.4337	0	4.84E-10	0	0	SCG
unassigned	102134	10	95012355	D10MIT117	10	70.67248	87027855	0.84613	0.65248	0	5.09E-10	0	0	Shared
Eif4g3	592124	4	1.38E+08	D4MIT170	4	99.940854	138171253	0.93602	0.77414	0	5.11E-10	0	0	SCG
Pcolce	679080	5	1.38E+08	05.132.979	5	112.26584	133170167	0.32371	0.24737	0	5.12E-10	0	0	SCG
Polr3f	469989	2	1.44E+08	D2MIT395	2	91.61399	119350649	0.33317	0.46015	0	5.23E-10	0	0	Shared
Pttg1	141628	11	43234624	D11MIT51	11	25.39412	36205252	1.31942	1.79376	0	5.43E-10	0	0	SCG
unassigned	833257	9	6168431	D9MIT250	9	5.2	8393623	1.20598	1.57392	0	5.43E-10	0	0	Shared
unassigned	731788	6	1.43E+08	D6Mit14	6	101.60848	145604376	0.5258	0.40075	0	5.50E-10	0	0	Shared
Aldh3b1	431248	19	3921489	19.000.325	19	0.2	325000	2.19102	1.63635	0	5.73E-10	0	0	SCG
Gys2	731568	6	1.42E+08	D6Mit14	6	101.60848	145604376	1.83216	1.3355	0	5.74E-10	0	0	SCG
Phldb1	863956	9	44502498	D9MIT248	9	44.87553	58210366	0.95715	0.73401	0	5.95E-10	0	0	SCG
unassigned	934096	X	1.39E+08	DXMit216	X	58.906126	140336696	0.38384	0.30242	0.24478	6.10E-10	0	0	SCG
Lrba	528942	3	86108192	D3MIT98	3	51.73848	85985423	1.49804	1.81742	0	6.15E-10	0	0	SCG
unassigned	191181	12	71152100	D12MIT91	12	43.26798	72843829	2.68586	2.14276	0	6.26E-10	0	0	SCG
Cep290	80609	10	1E+08	d10Mit96	10	80.833163	99019575	1.13972	1.49784	0	6.30E-10	0	0	SCG
Spg21	844576	9	65328190	09.046.588	9	34.49446	46645088	1.6308	1.82525	0	6.32E-10	0	0	SCG
Kif5c	453440	2	49550291	D2MIT61	2	35.12792	60528325	1.61219	1.81436	0	6.40E-10	0	0	Shared
Gramd1a	762817	7	31919052	07.013.915	7	8.7	15600169	0.93829	1.13601	0	6.52E-10	0	0	SCG
Rin2	470314	2	1.46E+08	D2MIT423	2	107.80753	148685450	1.74869	1.29879	0	6.52E-10	0	0	SCG
Npl	54494	1	1.55E+08	D1Mit102	1	80.039245	149096650	0.6632	0.87954	0	6.53E-10	0	0	SCG
Notch2	532092	3	97921128	03.106.773	3	82.33049	106447862	1.01624	0.80688	0	7.16E-10	0	0	Shared
unassigned	156252	11	1.01E+08	11.104.430	11	62.15042	104475224	0.13792	0.10551	0	7.36E-10	0	0	SCG
Aph1b	869366	9	66670054	D9MIT336	9	49.6331	65425671	3.50187	3.07862	0	7.41E-10	0	0	Shared
Myo6	847891	9	80113942	D9MIT123	9	55.0405	73379633	0.68989	1.18234	0	7.43E-10	0	0	Shared
Mrpl46	770536	7	85926295	D7MIT350	7	57.28732	90734599	1.89644	1.54779	0	7.57E-10	0	0	Shared
unassigned	707137	6	1.43E+08	D6Mit14	6	101.60848	145604376	1.00733	0.89548	0	7.64E-10	0	0	SCG
Hcrtr1	617715	4	1.3E+08	D4Mit203	4	89.732314	129249262	0.99131	0.84478	0	7.65E-10	0	0	SCG
Aph1b	869343	9	66624084	D9MIT248	9	44.87553	58210366	1.17032	0.94174	0	7.74E-10	0	0	SCG
unassigned	254228	14	70534696	14.067.129	14	52.822413	68793727	1.0271	1.34918	0	7.76E-10	0	0	Shared
Cntnap2	690223	6	46120194	06.036.921	6	24.99854	36940848	0.98653	0.80101	0	7.92E-10	0	0	Shared
Ppp2r1a	354186	17	21093955	17.021.019	17	14.36839	21451267	0.9768	1.06516	0	8.00E-10	0	0	SCG
Cd59b	462211	2	1.04E+08	RS27416022	2	74.76293	93628229	0.03076	0.01831	0	8.34E-10	0	0	Shared
Actr10	172125	12	72048453	D12MIT91	12	43.26798	72843829	1.18389	1.02169	0	8.36E-10	0	0	SCG
unassigned	761798	7	29766601	D7MIT294	7	15.72036	28074461	0.80959	0.72483	0	8.39E-10	0	0	Shared
Acsl1	794589	8	47596745	08.046.718	8	30.746529	46304537	1.38067	1.59976	0	8.46E-10	0	0	SCG
Dzip1	279645	14	1.19E+08	RS31252045	14	77.831601	111376384	0.74856	1.10208	0	8.49E-10	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Ece1	592075	4	1.38E+08	04.133.005	4	97.642221	133288839	1.7265	1.51258	0	8.55E-10	0	0	SCG
Sorl1	863188	9	41898031	D9mit90	9	20.19926	32308040	0.61117	0.76309	0	8.65E-10	0	0	SCG
Zfp109	760464	7	25022117	D7MIT294	7	15.72036	28074461	0.77948	1.14244	0	8.73E-10	0	0	Shared
Rims2	287232	15	39342832	15.046.034	15	20.554602	46035472	0.45674	0.68776	0	8.74E-10	0	0	Shared
Dapk1	211778	13	60797618	13.061.624	13	39.879786	61715738	1.82967	2.10477	0	8.78E-10	0	0	SCG
Efcab2	27983	1	1.8E+08	01.183.109	1	96.118477	183202456	3.55688	2.34555	0	9.16E-10	0	0	SCG
unassigned	497697	2	1.04E+08	D2MIT100	2	54.19426	106377525	1.88924	1.64112	0	9.63E-10	0	0	Shared
Bivm	5816	1	44184516	D1MIT236	1	37.41892	45435458	0.53316	0.77252	0	9.74E-10	0	0	Shared
Igf1r	743201	7	75359807	D7Mit232	7	35.20811	59868792	0.45458	0.60073	0	9.79E-10	0	0	Shared
unassigned	256891	14	87885889	D14Mit194	14	66.469555	94235479	2.09963	1.72837	0	9.96E-10	0	0	Shared
Pak3	916971	X	1.4E+08	DXMIT172	X	47.924609	119197077	0.91882	1.05695	1.30819	9.97E-10	0	0	Shared
unassigned	567033	3	1.52E+08	D3MIT147	3	137.32386	148408373	0.35034	0.47398	0	1.04E-09	0	0	Shared
Cyb5r3	313068	15	82984701	D15Mit107	15	49.400965	84216927	0.93066	1.01522	0	1.07E-09	0	0	SCG
Xrcc6	294265	15	81859552	D15MIT262	15	57.212355	87111041	1.7918	1.50208	0	1.13E-09	0	0	Shared
Pik3c3	391645	18	30462574	D18Mit68	18	14.5139	21594126	0.62971	0.45829	0	1.14E-09	0	0	Shared
Fam45a	430885	19	60890817	D19MIT103	19	59.411152	53838656	1.36618	1.15606	0	1.15E-09	0	0	Shared
Mycbp2	277925	14	1.04E+08	RS31252045	14	77.831601	111376384	1.1903	1.03611	0	1.17E-09	0	0	SCG
unassigned	594742	4	1.49E+08	D4MIT42	4	117.10129	150944103	1.70834	1.42638	0	1.17E-09	0	0	Shared
Bbs7	547495	3	36501753	03.033.871	3	22.08075	33578373	3.46103	2.9059	0	1.20E-09	0	0	Shared
Magi1	722699	6	93742345	RS30909511	6	57.9854	83140362	1.59359	1.19038	0	1.24E-09	0	0	SCG
3830406C13Rik	243436	14	13134119	14.008.937	14	5.6	10975728	2.17384	1.90827	0	1.28E-09	0	0	Shared
Fam163a	55152	1	1.58E+08	01.136.071	1	77.74879	136151166	1.14599	1.07792	0	1.30E-09	0	0	SCG
Calm3	759887	7	17502987	07.013.915	7	8.7	15600169	0.48709	0.57861	0	1.33E-09	0	0	SCG
Bmpr1a	266533	14	35257135	14.027.409	14	32.019685	29395320	0.59315	0.69206	0	1.34E-09	0	0	Shared
Cd209a	810664	8	3748861	D8MIT155	8	3.1	4976602	2.48163	1.87137	0	1.37E-09	0	0	SCG
Ube2l6	459462	2	84642947	D2MIT75	2	46.41465	80424883	1.10883	1.28048	0	1.37E-09	0	0	SCG
Clcn6	622222	4	1.47E+08	D4MIT232	4	109.11827	144647559	1.03327	1.18185	0	1.38E-09	0	0	SCG
Sergef	765859	7	53698559	D7MIT228	7	28.11811	47279833	1.19324	0.97037	0	1.38E-09	0	0	Shared
Snap91	873061	9	86719691	09.079.053	9	64.60162	79115123	1.25371	1.57599	0	1.41E-09	0	0	Shared
unassigned	302658	15	27666174	15.028.723	15	14.881134	28708166	0.48111	0.72313	0	1.41E-09	0	0	Shared
Add1	632697	5	34953204	D5MIT388	5	29.38073	33660748	0.81097	0.67704	0	1.42E-09	0	0	Shared
unassigned	764973	7	51907943	D7MIT228	7	28.11811	47279833	0.87618	1.12728	0	1.53E-09	0	0	SCG
unassigned	419762	19	7271604	D19Mit68	19	0.200001	3645155	1.16494	1.37616	0	1.56E-09	0	0	SCG
Acss3	103388	10	1.06E+08	d10Mit96	10	80.833163	99019575	1.44042	1.80439	0	1.59E-09	0	0	SCG
Zfp111	760466	7	24983171	07.017.531	7	12.92437	18957827	0.99375	1.11794	0	1.67E-09	0	0	Shared
unassigned	188699	12	53062196	D12MIT285	12	30.221464	55750112	0.39261	0.52105	0	1.69E-09	0	0	SCG
H2-T10	893542	17	36178849	17.034.150	17	51.1372	34678889	1.93297	2.17598	0	1.75E-09	0	0	Shared
Larp7	562424	3	1.27E+08	D3MIT315	3	89.68246	115544553	1.89724	2.47522	0	1.76E-09	0	0	SCG
Enox1	255595	14	77992652	D14MIT39	14	54.529907	69166099	0.8434	1.02164	0	1.77E-09	0	0	Shared
Sae1	759733	7	16912528	07.013.915	7	8.7	15600169	0.62113	0.7385	0	1.77E-09	0	0	SCG
Txndc9	36358	1	38047072	D1Mit374	1	27.028585	34816928	2.01233	1.71477	0	1.77E-09	0	0	SCG
Rnls	437777	19	33464416	D19MIT46	19	37.543065	33009697	2.13492	1.42866	0	1.78E-09	0	0	SCG

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Slc25a12	491927	2	71113238	D2MIT61	2	35.12792	60528325	0.98005	1.07031	0	1.86E-09	0	0	SCG
unassigned	245170	14	22650891	14.008.937	14	5.6	10975728	0.09243	0.06879	0	1.86E-09	0	0	Shared
unassigned	51876	1	1.37E+08	01.136.071	1	77.74879	136151166	0.90861	1.03924	0	1.94E-09	0	0	SCG
Serinc3	510096	2	1.63E+08	02.168.990	2	151.40532	169124295	0.14671	0.20362	0	2.03E-09	0	0	Shared
Entpd4	254071	14	69981373	14.067.129	14	52.822413	68793727	1.27236	1.14995	0	2.14E-09	0	0	SCG
Rims2	287225	15	39308017	15.046.034	15	20.554602	46035472	0.31898	0.46022	0	2.21E-09	0	0	SCG
Wrn	815656	8	34395609	D8MIT94	8	19.424222	32452130	0.28662	0.45859	0	2.25E-09	0	0	Shared
Nfs1	508608	2	1.56E+08	D2MIT423	2	107.80753	148685450	0.70329	0.9123	0	2.30E-09	0	0	Shared
Wdr17	818993	8	55775543	08.046.718	8	30.746529	46304537	1.42082	1.16997	0	2.33E-09	0	0	Shared
unassigned	167070	12	33535117	D12MIT60	12	21.025423	35474805	1.08971	1.23857	0	2.33E-09	0	0	SCG
A630033E08Rik	372142	17	22984137	17.021.019	17	14.36839	21451267	1.04117	0.95324	0	2.34E-09	0	0	SCG
Eltd1	541741	3	1.51E+08	D3MIT147	3	137.32386	148408373	3.82723	3.24339	0	2.35E-09	0	0	Shared
Tagln2	26985	1	1.74E+08	01.183.109	1	96.118477	183202456	0.5113	0.59513	0	2.47E-09	0	0	SCG
Clcn3	819619	8	63417350	D8MIT68	8	37.448528	59469763	1.01637	0.8901	0	2.52E-09	0	0	SCG
Mcf2l	788991	8	13009502	08.010.585	8	4.520052	10585028	0.32724	0.47453	0	2.53E-09	0	0	Shared
Chmp1a	831286	8	1.26E+08	D8MIT42	8	102.88933	129076217	2.39041	2.10434	0	2.54E-09	0	0	SCG
Mms19	439541	19	42024473	D19MIT103	19	59.411152	53838656	2.09126	1.84565	0	2.59E-09	0	0	Shared
Stk32c	782460	7	1.46E+08	D7MIT223	7	99.51497	151795777	1.5301	1.72172	0	2.66E-09	0	0	SCG
Nop14	660203	5	35000559	D5MIT352	5	30.68587	35957616	2.14431	1.61296	0	2.68E-09	0	0	Shared
Slc25a32	304712	15	38927532	15.046.034	15	20.554602	46035472	0.04659	0.07199	0	2.73E-09	0	0	SCG
Ptplad1	868994	9	64838800	D9MIT336	9	49.6331	65425671	1.74321	1.36786	0	2.87E-09	0	0	Shared
Arg1	89839	10	24647118	RS29316281	10	22.943971	25167321	0.82254	0.50507	0	2.94E-09	0	0	SCG
Stx12	618383	4	1.32E+08	D4Mit203	4	89.732314	129249262	0.88849	0.75491	0	2.95E-09	0	0	Shared
Cdc5l	377498	17	45545311	17.034.150	17	51.1372	34678889	1.72723	1.03251	0	2.96E-09	0	0	Shared
Pygb	471399	2	1.51E+08	D2MIT285	2	110.63716	152683037	1.08683	0.96674	0	3.03E-09	0	0	SCG
Oxr1	287677	15	41682928	15.046.034	15	20.554602	46035472	2.7052	2.35364	0	3.09E-09	0	0	SCG
1500035H01Rik	839707	9	44592044	D9MIT247	9	25.36975	36940492	2.84585	2.56854	0	3.11E-09	0	0	Shared
Mms19	439566	19	42040762	19.046.444	19	55.551107	46465179	1.01067	0.82652	0	3.12E-09	0	0	Shared
Oxsr1	879650	9	1.19E+08	D9MIT201	9	91.42427	117345284	1.19519	0.89586	0	3.13E-09	0	0	Shared
Ptgir	734441	7	17494068	07.013.915	7	8.7	15600169	1.17058	1.43734	0	3.22E-09	0	0	SCG
Pla2g7	359888	17	43736032	17.034.150	17	51.1372	34678889	2.22222	1.75023	0	3.24E-09	0	0	Shared
Pdxp	318749	15	78748930	D15MIT262	15	57.212355	87111041	1.05329	1.1656	0	3.29E-09	0	0	SCG
Abcc9	731677	6	1.43E+08	D6Mit14	6	101.60848	145604376	1.78353	1.32868	0	3.33E-09	0	0	Shared
Pnpla6	787324	8	3530995	08.010.585	8	4.520052	10585028	0.92873	1.07242	0	3.35E-09	0	0	Shared
unassigned	631847	5	32000542	D5MIT388	5	29.38073	33660748	3.17414	3.8344	0	3.37E-09	0	0	Shared
unassigned	477150	2	1.73E+08	D2MIT113	2	164.04086	173180172	1.59784	1.29496	0	3.39E-09	0	0	SCG
unassigned	646510	5	1.16E+08	d5mit158	5	69.85959	115413178	0.71948	0.5522	0	3.39E-09	0	0	Shared
Clcn6	622219	4	1.47E+08	D4MIT232	4	109.11827	144647559	0.66418	0.79081	0	3.62E-09	0	0	SCG
Rnaseh2a	823762	8	87483931	D8MIT45	8	58.440058	89829274	1.01835	0.81321	0	3.66E-09	0	0	Shared
Soat1	55244	1	1.58E+08	D1Mit102	1	80.039245	149096650	0.73991	0.91024	0	3.72E-09	0	0	Shared
Sema3d	628370	5	12524251	D5MIT348	5	18.20559	24424937	0.33723	0.48328	0	3.77E-09	0	0	Shared
unassigned	443336	19	60605034	D19MIT103	19	59.411152	53838656	1.66979	1.46209	0	3.85E-09	0	0	SCG

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	728618	6	1.27E+08	d6mit366	6	77.49561	115192871	0.37589	0.3228	0	3.88E-09	0	0	SCG
Rbp4	438587	19	38198519	D19MIT13	19	37.094077	32713513	1.15056	1.42897	0	3.91E-09	0	0	SCG
Herc2	741457	7	63368415	D7MIT248	7	39.99047	80656343	0.82481	0.99235	0	3.95E-09	0	0	Shared
unassigned	738320	7	46789950	07.056.455	7	36.40088	63842351	1.35823	1.17192	0	4.04E-09	0	0	Shared
unassigned	283480	15	12781634	D15MIT13	15	2.1	3410212	1.04651	0.8877	0	4.08E-09	0	0	SCG
Gng8	734437	7	17480308	07.013.915	7	8.7	15600169	47.95471	13.51704	0	4.17E-09	0	0	SCG
unassigned	298646	15	1.01E+08	D15MIT44	15	76.945032	98951714	0.7508	1.11127	0	4.30E-09	0	0	Shared
Amph	203689	13	19187925	RS29514367	13	20.539234	29499372	2.76097	2.48569	0	4.32E-09	0	0	SCG
unassigned	679647	5	1.4E+08	05.132.979	5	112.26584	133170167	2.44764	2.04949	0	4.50E-09	0	0	Shared
Ifi203	59038	1	1.76E+08	01.183.109	1	96.118477	183202456	2.3244	1.7157	0	4.54E-09	0	0	SCG
unassigned	251292	14	56199524	D14MIT39	14	54.529907	69166099	1.12899	0.92058	0	4.74E-09	0	0	SCG
unassigned	262855	14	19102221	14.008.937	14	5.6	10975728	2.24161	2.05343	0	4.82E-09	0	0	Shared
unassigned	273474	14	70892080	14.067.129	14	52.822413	68793727	0.66459	0.85141	0	4.85E-09	0	0	Shared
Mtf2	644689	5	1.09E+08	D5MIT239	5	66.11023	107842159	1.26613	1.04385	0	4.88E-09	0	0	Shared
Copa	26792	1	1.74E+08	01.183.109	1	96.118477	183202456	0.35055	0.51079	0	5.12E-09	0	0	SCG
Lamc1	54421	1	1.55E+08	D1Mit102	1	80.039245	149096650	0.89269	0.76615	0	5.27E-09	0	0	Shared
Mbnl2	260199	14	1.21E+08	RS31252045	14	77.831601	111376384	1.47547	1.63111	0	5.32E-09	0	0	SCG
Zmynd8	510780	2	1.66E+08	02.168.990	2	151.40532	169124295	1.00652	0.83386	0	5.40E-09	0	0	SCG
unassigned	865451	9	50490342	D9MIT71	9	37.69738	50007830	1.13217	1.55343	0	5.63E-09	0	0	Shared
Rnasen	283518	15	12843670	D15MIT13	15	2.1	3410212	1.97506	1.70623	0	5.73E-09	0	0	SCG
Cadps	262132	14	13290206	14.008.937	14	5.6	10975728	0.40162	0.32447	0	5.78E-09	0	0	SCG
unassigned	219732	13	1.13E+08	D13MIT53	13	72.69389	113084631	1.30098	1.16739	0	5.78E-09	0	0	Shared
unassigned	223009	13	18078835	D13Mit207	13	8.688726	16526195	0.4676	0.52446	0	5.80E-09	0.0005	0.0455118	Shared
unassigned	173536	12	77402410	D12MIT143	12	49.408846	80981262	0.60577	0.77987	0	5.83E-09	0	0	Shared
Zfyve21	180973	12	1.13E+08	D12MIT7	12	66.696627	104970690	1.79642	1.38292	0	5.84E-09	0	0	Shared
Heatr5a	188682	12	53025990	12.065.348	12	37.44045	65530382	1.11085	0.9688	0	5.90E-09	0	0	SCG
Trim3	775382	7	1.13E+08	RS36353338	7	66.26522	112706514	0.96898	1.10649	0	5.94E-09	0	0	Shared
unassigned	594520	4	1.48E+08	D4MIT232	4	109.11827	144647559	0.10184	0.147	0	5.94E-09	0.0005	0.0455118	Shared
Ap2b1	124728	11	83160164	D11MIT320	11	39.87138	70766870	0.56502	0.62443	0	6.12E-09	0	0	SCG
unassigned	506960	2	1.49E+08	D2MIT423	2	107.80753	148685450	1.44709	1.65417	0	6.17E-09	0	0	SCG
Svep1	605004	4	58097388	D4MIT164	4	42.389612	59415112	1.2971	1.62302	0	6.36E-09	0	0	Shared
Sypl	167104	12	33660792	D12MIT60	12	21.025423	35474805	6.24609	5.40002	0	6.40E-09	0	0	SCG
Nt5c2	440867	19	46973114	D19MIT88	19	44.411348	37331405	1.20604	0.86932	0	6.44E-09	0	0	Shared
Hmgcl	591417	4	1.36E+08	D4MIT170	4	99.940854	138171253	1.13657	1.46659	0	6.46E-09	0	0	Shared
Abcg4	863761	9	44085552	D9MIT285	9	25.81754	40462577	0.52019	0.6928	0	6.47E-09	0	0	Shared
unassigned	51861	1	1.37E+08	D1MIT1001	1	72.841454	130944135	0.30653	0.41052	0	7.09E-09	0	0	Shared
Kif21a	314972	15	90796770	D15MIT67	15	36.957676	70032295	1.59429	1.45958	0	7.30E-09	0	0	SCG
Chrna5	842018	9	54852157	09.046.588	9	34.49446	46645088	0.64052	0.80044	0	7.32E-09	0	0	SCG
Scoc	823278	8	85958553	D8MIT346	8	54.673156	85454038	1.99848	1.68964	0	7.32E-09	0	0	SCG
Vps11	863833	9	44164312	D9MIT71	9	37.69738	50007830	1.39595	1.22274	0	7.36E-09	0	0	SCG
Rplp0	646518	5	1.16E+08	d5mit158	5	69.85959	115413178	0.07122	0.04727	0	7.37E-09	0	0	SCG
unassigned	735172	7	25039807	D7MIT267	7	18.29809	30331965	0.28361	0.42992	0	7.47E-09	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	735113	7	24882270	07.013.915	7	8.7	15600169	1.06743	0.91421	0	7.52E-09	0	0	SCG
Agap3	630212	5	23982476	D5MIT348	5	18.20559	24424937	0.95404	1.19834	0	7.55E-09	0.0005	0.0455118	Shared
Hspg2	591857	4	1.37E+08	04.133.005	4	97.642221	133288839	0.54715	0.42081	0	7.69E-09	0	0	SCG
Kif21a	314952	15	90769446	15.090.122	15	63.155859	90124664	0.82363	0.94	0	7.69E-09	0	0	SCG
H2-K1	375405	17	34137139	17.034.150	17	51.1372	34678889	1.15157	0.88408	0	7.72E-09	0	0	SCG
Mrpl3	852187	9	1.05E+08	D9MIT212	9	79.88305	108543415	1.16729	1.37917	0	7.90E-09	0	0	Shared
Heatr5a	188661	12	52995283	D12MIT285	12	30.221464	55750112	0.55608	0.69913	0	8.00E-09	0	0	SCG
Rbm45	458346	2	76218439	RS28322831	2	43.67748	71063776	1.25905	1.46643	0	8.30E-09	0	0	Shared
unassigned	870300	9	71489091	D9MIT107	9	53.50038	73315075	0.4463	0.58075	0	8.50E-09	0	0	Shared
Pygl	191244	12	71298385	12.065.348	12	37.44045	65530382	1.95075	1.68069	0	8.53E-09	0	0	SCG
unassigned	863810	9	44145828	D9MIT2	9	25.36976	37202486	0.94905	1.04632	0	8.66E-09	0	0	SCG
Scoc	823279	8	85961110	D8MIT346	8	54.673156	85454038	0.67657	0.48587	0	8.95E-09	0	0	Shared
Tnks	816011	8	35916296	D8Mit191	8	23.020658	36243839	1.17615	1.32586	0	8.95E-09	0	0	SCG
Met	685084	6	17483912	RS51272439	6	10.78458	19888102	1.50252	1.16273	0	9.05E-09	0	0	SCG
Extl3	272175	14	65677822	14.067.129	14	52.822413	68793727	1.31315	1.17098	0	9.25E-09	0	0	SCG
unassigned	602848	4	46133203	d4mit238	4	33.232784	45243003	0.48584	0.70928	0	9.56E-09	0	0	Shared
Noc3l	438750	19	38888596	D19MIT103	19	59.411152	53838656	0.8691	0.64318	0	9.65E-09	0	0	Shared
unassigned	29409	1	1.87E+08	01.183.109	1	96.118477	183202456	0.7236	0.84388	0	9.70E-09	0	0	SCG
Nav1	51921	1	1.37E+08	D1MIT1001	1	72.841454	130944135	1.53777	1.35965	0	9.76E-09	0	0	SCG
Psmb3	128178	11	97574758	D11MIT289	11	59.90287	94741466	0.50029	0.58502	0	9.79E-09	0	0	Shared
Serinc3	510098	2	1.63E+08	02.168.990	2	151.40532	169124295	0.18334	0.24622	0	9.81E-09	0	0	Shared
Cpne5	374110	17	29313107	D17Mit213	17	12.20714	16752157	3.54377	3.00257	0	9.88E-09	0	0	SCG
Spg21	844572	9	65316600	09.046.588	9	34.49446	46645088	0.7014	0.82966	0	1.00E-08	0	0	SCG
Stip1	432707	19	7103158	19.000.325	19	0.2	325000	0.50179	0.32798	0	1.02E-08	0	0	Shared
Tmem18	166585	12	31275393	D12MIT60	12	21.025423	35474805	0.81486	0.88362	0	1.04E-08	0	0	Shared
unassigned	358656	17	35403088	17.034.150	17	51.1372	34678889	2.90669	3.15137	0	1.04E-08	0	0	Shared
Polr2b	639538	5	77755573	D5MIT309	5	58.78964	79931746	0.8787	0.67347	0	1.05E-08	0	0	SCG
9330182L06Rik	628180	5	9421506	D5MIT123	5	4.1	6556176	0.87023	0.98717	0	1.06E-08	0	0	Shared
Chl1	699974	6	1.04E+08	d6mit366	6	77.49561	115192871	0.71283	0.59585	0	1.09E-08	0	0	SCG
Tubb5	376127	17	35971780	D17MIT51	17	53.34361	43641790	0.59799	0.53053	0	1.12E-08	0	0	SCG
unassigned	150405	11	78783348	D11MIT320	11	39.87138	70766870	0.61186	0.79353	0	1.15E-08	0	0	SCG
Epb4.1l4a	407889	18	33987766	18.038.678	18	24.45192	38711680	0.93169	1.16039	0	1.20E-08	0	0	SCG
Efcab2	27974	1	1.8E+08	01.183.109	1	96.118477	183202456	43.90255	22.68129	0	1.21E-08	0	0	SCG
Pafah2	591045	4	1.34E+08	D4MIT170	4	99.940854	138171253	0.56591	0.74317	0	1.22E-08	0	0	SCG
Ldlr	835410	9	21550529	09.014.560	9	12.99047	14614051	0.69379	0.62997	0	1.23E-08	0	0	SCG
Matn2	286152	15	34318505	D15MIT143	15	21.458543	51985414	1.42865	1.24943	0	1.24E-08	0	0	SCG
unassigned	51822	1	1.37E+08	01.102.953	1	66.387402	103022030	0.76901	0.85836	0	1.30E-08	0	0	Shared
Gsr	792626	8	34791965	D8MIT94	8	19.424222	32452130	0.55578	0.67448	0	1.31E-08	0	0	Shared
unassigned	766062	7	54186329	07.056.455	7	36.40088	63842351	2.31446	1.86301	0	1.32E-08	0	0	SCG
St3gal6	345031	16	58473537	D16MIT185	16	54.394402	60434381	1.0095	0.84044	0	1.33E-08	0	0	Shared
unassigned	277921	14	1.04E+08	D14Mit194	14	66.469555	94235479	0.55288	0.69035	0	1.39E-08	0	0	SCG
unassigned	851664	9	1.03E+08	D9MIT212	9	79.88305	108543415	0.75804	0.82634	0	1.39E-08	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Cadps	262131	14	13286709	14.008.937	14	5.6	10975728	1.96394	1.84114	0	1.40E-08	0	0	SCG
Ccbl2	540051	3	1.42E+08	03.141.220	3	108.244	140945577	2.0505	1.64824	0	1.43E-08	0	0	Shared
Gbp2	540004	3	1.42E+08	D3MIT351	3	107.46572	139262419	1.35473	1.09085	0	1.43E-08	0	0	SCG
Dhx9	54490	1	1.55E+08	D1MIT1001	1	72.841454	130944135	0.84116	0.74175	0	1.44E-08	0	0	Shared
Dixdc1	865440	9	50471403	09.046.588	9	34.49446	46645088	2.12527	2.64698	0	1.47E-08	0	0	Shared
Sorbs1	438962	19	40427019	19.046.444	19	55.551107	46465179	1.23592	1.06114	0	1.50E-08	0	0	Shared
Nudcd3	135648	11	6093283	D11MIT2	11	7.6	12218640	0.9727	1.08389	0	1.51E-08	0	0	Shared
Tapbp	357849	17	34065596	17.034.150	17	51.1372	34678889	0.48564	0.40616	0	1.51E-08	0	0	SCG
Hspg2	591825	4	1.37E+08	D4MIT170	4	99.940854	138171253	1.01861	1.19797	0	1.54E-08	0	0	SCG
unassigned	275015	14	77433993	RS31380922	14	61.610758	78742431	2.31125	1.76435	0	1.56E-08	0	0	SCG
unassigned	801075	8	88017105	D8MIT45	8	58.440058	89829274	1.79783	1.54349	0	1.58E-08	0	0	SCG
Dusp10	29172	1	1.86E+08	01.183.109	1	96.118477	183202456	1.14762	0.90878	0	1.60E-08	0	0	SCG
unassigned	324781	16	31829459	D16MIT60	16	28.756136	32704177	0.77351	0.95134	0	1.69E-08	0	0	Shared
unassigned	598926	4	15846894	RS28262872	4	8.826905	18026684	1.34962	1.22367	0	1.70E-08	0	0	SCG
unassigned	600879	4	34522438	D4mit94	4	20.993383	33951862	1.31269	1.09993	0	1.70E-08	0	0	SCG
Ghitm	266917	14	37946837	14.027.409	14	32.019685	29395320	0.81071	0.90572	0	1.74E-08	0	0	SCG
Nomo1	739992	7	53336798	D7MIT228	7	28.11811	47279833	0.87373	0.72515	0	1.74E-08	0	0	Shared
Gtf2h1	740173	7	54068059	D7MIT228	7	28.11811	47279833	1.18384	1.62409	0	1.76E-08	0	0	Shared
Nckipsd	853302	9	1.09E+08	D9MIT212	9	79.88305	108543415	1.56558	1.31086	0	1.76E-08	0	0	Shared
Csmd1	812814	8	16081653	D8MIT155	8	3.1	4976602	1.22394	0.91779	0	1.77E-08	0	0	Shared
Imp4	3812	1	34501316	D1Mit374	1	27.028585	34816928	0.47597	0.57946	0	1.78E-08	0	0	SCG
Folh1	772323	7	93905470	D7MIT350	7	57.28732	90734599	0.43068	0.64449	0	1.81E-08	0	0	Shared
Ppp2r5d	378086	17	46821475	17.034.150	17	51.1372	34678889	1.79816	1.58746	0	1.81E-08	0	0	SCG
Oprm1	85851	10	3516218	rs13480474	10	1.8	4403267	8.48998	6.24193	0	1.82E-08	0	0	SCG
Mllt11	556274	3	95024110	D3MIT49	3	73.77602	89036582	1.61696	1.52354	0	1.83E-08	0	0	Shared
Terf1	1676	1	15823485	rs13475769	1	16.197578	24958696	0.47463	0.64196	0	1.86E-08	0	0	Shared
Akirin2	573389	4	34513583	D4mit94	4	20.993383	33951862	0.7368	0.91485	0	1.89E-08	0	0	Shared
Osbpl3	715781	6	50303065	D6Mit272	6	27.2529	44382847	1.20824	1.06481	0	1.91E-08	0	0	SCG
Stt3b	878864	9	1.15E+08	D9MIT201	9	91.42427	117345284	0.67453	0.81945	0	1.91E-08	0	0	SCG
Pnpla6	787336	8	3538213	D8MIT155	8	3.1	4976602	0.6819	0.81676	0	2.00E-08	0	0	Shared
unassigned	284931	15	27494796	15.028.723	15	14.881134	28708166	1.26082	1.41324	0	2.01E-08	0	0	SCG
Myo1b	38255	1	51825862	rs13475894	1	45.460824	63625006	0.49982	0.66731	0	2.03E-08	0	0	SCG
Gal	431059	19	3411129	19.000.325	19	0.2	325000	2.76789	3.31305	0	2.07E-08	0	0	SCG
Tars	300945	15	11322916	15.010.846	15	8.803289	10831030	1.09245	1.41399	0	2.07E-08	0	0	SCG
Ostf1	434902	19	18655563	19.013.429	19	11.129219	13436471	1.0916	1.25117	0	2.08E-08	0	0	SCG
Ece1	592088	4	1.38E+08	04.133.005	4	97.642221	133288839	0.2907	0.37723	0	2.10E-08	0	0	SCG
Flot1	358813	17	35962382	17.034.150	17	51.1372	34678889	0.83205	0.95038	0	2.11E-08	0	0	SCG
Igf1r	743190	7	75340056	D7Mit232	7	35.20811	59868792	0.99538	0.86272	0	2.13E-08	0	0	Shared
Entpd4	254069	14	69980021	14.067.129	14	52.822413	68793727	2.07871	1.93036	0	2.18E-08	0	0	SCG
unassigned	54163	1	1.54E+08	D1Mit102	1	80.039245	149096650	0.6982	0.81847	0	2.19E-08	0	0	Shared
unassigned	232105	13	63624186	RS30012306	13	43.697138	70428413	1.0956	0.93046	0	2.19E-08	0	0	Shared
Alpl	619837	4	1.37E+08	D4MIT170	4	99.940854	138171253	1.16743	0.97751	0	2.24E-08	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Gpd1l	878819	9	1.15E+08	D9Mit18	9	96.97845	120198563	2.25379	1.99451	0	2.26E-08	0	0	SCG
Itga2	241240	13	1.16E+08	D13MIT78	13	76.842169	119618032	2.5157	1.88963	0	2.34E-08	0	0	SCG
Hspg2	591829	4	1.37E+08	04.133.005	4	97.642221	133288839	1.13537	1.31348	0	2.38E-08	0	0	SCG
Obscn	144949	11	58810673	D11MIT51	11	25.39412	36205252	3.58783	2.60621	0	2.38E-08	0	0	SCG
Hspg2	591830	4	1.37E+08	04.133.005	4	97.642221	133288839	1.46172	1.19032	0	2.40E-08	0	0	SCG
unassigned	335502	16	5249239	D16Mit131	16	4.5	7319135	2.64987	2.16977	0	2.40E-08	0	0	SCG
Atp1a2	58694	1	1.74E+08	01.183.109	1	96.118477	183202456	0.84671	0.79353	0	2.41E-08	0	0	SCG
unassigned	843756	9	62225180	D9MIT248	9	44.87553	58210366	0.98161	1.36597	0	2.42E-08	0	0	Shared
Cd97	823363	8	86249832	D8MIT346	8	54.673156	85454038	0.81121	0.98424	0	2.43E-08	0	0	SCG
unassigned	823875	8	87813387	D8MIT45	8	58.440058	89829274	0.68537	0.59624	0	2.43E-08	0	0	SCG
unassigned	400461	18	74963810	18.063.800	18	48.99442	63834285	1.21109	1.35086	0	2.48E-08	0	0	SCG
Ldlr	835399	9	21537953	09.014.560	9	12.99047	14614051	0.49094	0.43991	0	2.50E-08	0	0	SCG
unassigned	863815	9	44149236	D9MIT248	9	44.87553	58210366	1.36643	1.15457	0	2.51E-08	0	0	SCG
Tssc1	166179	12	29513618	D12MIT60	12	21.025423	35474805	1.74221	1.92067	0	2.53E-08	0	0	SCG
Col5a2	37718	1	45436983	D1MIT236	1	37.41892	45435458	1.31251	0.99214	0	2.56E-08	0	0	SCG
Slc38a11	490665	2	65192641	D2MIT61	2	35.12792	60528325	0.53283	0.4187	0	2.57E-08	0	0	SCG
2210418O10Rik	513495	2	1.77E+08	D2MIT148	2	167.77989	178535250	1.66933	1.37218	0	2.65E-08	0	0	Shared
Myo1c	122632	11	75486158	D11MIT51	11	25.39412	36205252	0.59775	0.67447	0	2.74E-08	0	0	SCG
Rps11	765272	7	52378220	D7MIT228	7	28.11811	47279833	0.66687	0.56859	0	2.76E-08	0	0	Shared
unassigned	762757	7	31836842	D7MIT294	7	15.72036	28074461	0.09505	0.06375	0	2.88E-08	0	0	Shared
unassigned	762815	7	31917885	07.056.455	7	36.40088	63842351	0.36575	0.48611	0	2.97E-08	0	0	Shared
unassigned	749893	7	1.13E+08	RS36353338	7	66.26522	112706514	0.90514	0.80537	0	3.02E-08	0	0	Shared
RP23-331L12.8	160083	11	1.15E+08	D11MIT214	11	79.65651	114991785	1.9792	1.32546	0	3.11E-08	0	0	SCG
unassigned	602280	4	43546307	d4mit238	4	33.232784	45243003	0.15201	0.11706	0	3.11E-08	0	0	Shared
Folh1	772325	7	93911456	D7MIT350	7	57.28732	90734599	0.34505	0.49768	0	3.15E-08	0	0	Shared
Usp22	145745	11	60977234	D11Mit4	11	39.42453	68422759	1.00503	0.84109	0	3.18E-08	0	0	SCG
Dst	3725	1	34282369	D1Mit374	1	27.028585	34816928	2.21688	2.43919	0	3.25E-08	0	0	SCG
unassigned	809152	8	1.26E+08	D8MIT42	8	102.88933	129076217	1.25089	1.05991	0	3.31E-08	0	0	Shared
Lyst	202910	13	13790606	D13Mit207	13	8.688726	16526195	0.42432	0.52482	0	3.32E-08	0	0	SCG
C920016K16Rik	357585	17	33139509	D17MIT51	17	53.34361	43641790	2.4787	1.77517	0	3.34E-08	0	0	SCG
Zfp93	735169	7	25061561	07.013.915	7	8.7	15600169	0.61448	0.71469	0	3.36E-08	0	0	Shared
Cd209a	810659	8	3745511	08.010.585	8	4.520052	10585028	0.33201	0.55815	0	3.46E-08	0	0	SCG
App	347988	16	85120913	16.083.701	16	79.82369	83818653	0.89921	1.00259	0	3.52E-08	0	0	SCG
Enpp1	89730	10	24384717	RS33702022	10	21.757861	24370362	0.81954	0.58059	0	3.55E-08	0	0	SCG
Zfp9	726792	6	1.18E+08	d6mit366	6	77.49561	115192871	1.31144	1.70649	0	3.60E-08	0	0	SCG
Nbn	571116	4	15903185	RS28262872	4	8.826905	18026684	2.24479	2.57759	0	3.63E-08	0	0	Shared
unassigned	731590	6	1.42E+08	06.149.619	6	105.50667	149491352	0.98692	1.06417	0	3.69E-08	0	0	SCG
Lsm8	685315	6	18803713	RS49937148	6	13.13583	22510745	1.17932	1.03051	0	3.76E-08	0	0	Shared
Pdrg1	507810	2	1.53E+08	D2MIT423	2	107.80753	148685450	1.00891	0.91748	0	3.80E-08	0	0	SCG
Cep164	864309	9	45583964	D9MIT247	9	25.36975	36940492	0.2287	0.36686	0	3.81E-08	0	0	Shared
unassigned	357883	17	34095177	17.034.150	17	51.1372	34678889	0.66514	0.84817	0	3.82E-08	0	0	SCG
Aagab	844000	9	63487400	D9MIT336	9	49.6331	65425671	0.63071	0.46584	0	3.84E-08	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Pik3cd	622788	4	1.49E+08	D4MIT42	4	117.10129	150944103	0.68232	0.54962	0	3.86E-08	0	0	SCG
Kars	829056	8	1.15E+08	D8MIT215	8	87.841725	118384638	0.68838	1.03283	0	3.87E-08	0	0	SCG
Iars2	61164	1	1.87E+08	01.183.109	1	96.118477	183202456	0.65424	0.88558	0	3.88E-08	0	0	Shared
unassigned	352818	17	12408095	17.013.500	17	8.4	13900467	0.76038	0.88555	0	3.97E-08	0	0	SCG
Agpat9	642927	5	1.01E+08	D5MIT239	5	66.11023	107842159	0.71087	0.9677	0	3.99E-08	0	0	SCG
Frmd4a	444476	2	4523188	D2MIT1	2	2.4	3803361	1.00554	1.18156	0	4.01E-08	0	0	SCG
Hps5	765995	7	54030194	D7Mit232	7	35.20811	59868792	1.60787	2.05019	0	4.02E-08	0	0	Shared
Il10ra	864212	9	45073575	D9MIT247	9	25.36975	36940492	0.5274	0.73474	0	4.08E-08	0	0	Shared
Cyp2b13	735803	7	26873667	07.013.915	7	8.7	15600169	0.94939	1.903	0	4.09E-08	0	0	SCG
Mrpl45	128019	11	97190552	11.104.430	11	62.15042	104475224	0.18383	0.26491	0	4.09E-08	0	0	SCG
unassigned	859128	9	20290587	09.014.560	9	12.99047	14614051	1.43471	1.61485	0	4.09E-08	0	0	SCG
Mdm4	51181	1	1.35E+08	D1MIT1001	1	72.841454	130944135	0.09065	0.05845	0	4.10E-08	0	0	Shared
Akap6	169823	12	54250618	D12Mit2	12	26.674029	42747379	0.9911	1.11275	0	4.14E-08	0	0	SCG
Lancl1	41393	1	67055810	D1MIT132	1	55.208767	77143053	0.62032	0.48963	0	4.15E-08	0	0	SCG
unassigned	604597	4	56771213	D4MIT164	4	42.389612	59415112	0.58237	0.78386	0	4.15E-08	0	0	Shared
Snx13	167580	12	35829011	D12MIT60	12	21.025423	35474805	1.43669	1.25346	0	4.18E-08	0	0	SCG
Arhgap5	169678	12	53660990	12.065.348	12	37.44045	65530382	1.1937	1.56588	0	4.20E-08	0	0	Shared
Mcam	839482	9	43946932	D9MIT247	9	25.36975	36940492	1.37081	1.26469	0	4.22E-08	0	0	SCG
Camk2d	536919	3	1.27E+08	RS30160288	3	119.38247	125981675	0.41064	0.478	0	4.33E-08	0	0	SCG
Mlh1	878108	9	1.11E+08	09.105.291	9	79.88305	105335230	0.81458	1.13589	0	4.33E-08	0	0	Shared
unassigned	539804	3	1.41E+08	D3MIT351	3	107.46572	139262419	0.58902	0.70858	0	4.38E-08	0	0	SCG
Ap2a1	765111	7	52162215	07.056.455	7	36.40088	63842351	1.19788	1.37088	0	4.41E-08	0	0	SCG
Bxdc2	300702	15	10406201	D15MIT13	15	2.1	3410212	0.52182	0.61448	0	4.43E-08	0	0	Shared
Ctnnbip1	594786	4	1.49E+08	D4MIT42	4	117.10129	150944103	1.00723	1.07689	0	4.46E-08	0	0	SCG
Gbp2	540002	3	1.42E+08	D3Mit19	3	140.73124	157273675	1.69607	1.42301	0	4.49E-08	0	0	SCG
Tubgcp3	811943	8	12641102	08.010.585	8	4.520052	10585028	1.04201	1.3621	0	4.54E-08	0	0	Shared
Nipal2	303735	15	34512479	15.028.723	15	14.881134	28708166	2.47303	3.10932	0	4.57E-08	0	0	Shared
Med23	67109	10	24629609	RS29322393	10	16.95714	19948509	0.8365	1.12269	0	4.59E-08	0	0	Shared
unassigned	166584	12	31273293	D12MIT60	12	21.025423	35474805	2.69038	2.50293	0	4.62E-08	0	0	Shared
unassigned	24431	1	1.63E+08	D1Mit102	1	80.039245	149096650	1.18911	1.35519	0	4.70E-08	0	0	Shared
Lactb	869412	9	66818463	D9MIT336	9	49.6331	65425671	1.52087	1.1971	0	4.91E-08	0	0	SCG
Foxo3	92276	10	41902288	RS37076985	10	29.161317	28876470	1.81752	2.1064	0	4.94E-08	0	0	SCG
unassigned	375491	17	34420888	D17MIT51	17	53.34361	43641790	2.21245	1.81714	0	4.99E-08	0	0	SCG
unassigned	630175	5	23876525	D5MIT348	5	18.20559	24424937	0.46801	0.67141	0	5.03E-08	0	0	Shared
unassigned	376253	17	36257872	17.034.150	17	51.1372	34678889	3.35996	2.82719	0	5.05E-08	0	0	SCG
Rpap1	500606	2	1.2E+08	D2MIT285	2	110.63716	152683037	1.07603	0.85538	0	5.12E-08	0	0	Shared
Cbl	863700	9	43959602	D9MIT247	9	25.36975	36940492	1.14167	1.00626	0	5.13E-08	0	0	SCG
Eef1a1	871799	9	78327432	d9mit198	9	66.50428	91176808	0.7757	0.8344	0	5.15E-08	0	0	SCG
unassigned	363795	17	66159827	D17Mit93	17	83.28793	74149996	0.74433	0.59122	0	5.19E-08	0	0	SCG
Abcf2	657978	5	24073003	D5MIT294	5	15.58331	20863135	0.74684	0.89785	0	5.21E-08	0	0	Shared
Dst	3744	1	34313082	D1Mit374	1	27.028585	34816928	2.64954	2.31749	0	5.41E-08	0	0	SCG
Fcgrt	765253	7	52357973	D7MIT228	7	28.11811	47279833	1.30458	1.51063	0	5.48E-08	0	0	SCG

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Obscn	144946	11	58809396	D11Mit4	11	39.42453	68422759	2.73559	1.7278	0	5.50E-08	0	0	SCG
unassigned	562428	3	1.27E+08	D3MIT57	3	88.53548	115533310	0.0866	0.06686	0	5.60E-08	0	0	Shared
Prmt3	740661	7	57112960	07.056.455	7	36.40088	63842351	0.46324	0.56288	0	5.63E-08	0	0	SCG
unassigned	840036	9	45734656	09.046.588	9	34.49446	46645088	0.50972	0.68381	0	5.65E-08	0	0	Shared
Tom1l1	153305	11	90532425	D11MIT289	11	59.90287	94741466	0.16234	0.25296	0	5.66E-08	0	0	Shared
Itga6	457334	2	71663622	RS27416022	2	74.76293	93628229	0.86596	0.7361	0	5.67E-08	0	0	SCG
Alg1	319314	16	5241408	16.010.089	16	7.349459	10175515	0.94044	0.80796	0	5.71E-08	0	0	Shared
unassigned	785919	7	20219334	07.013.915	7	8.7	15600169	0.58249	0.65666	0	5.79E-08	0	0	Shared
unassigned	594312	4	1.48E+08	D4MIT232	4	109.11827	144647559	1.17261	1.31585	0	5.80E-08	0	0	SCG
Brwd2	755073	7	1.37E+08	d7mit109	7	91.14939	143706746	0.88411	0.74433	0	5.87E-08	0	0	SCG
Utrn	87498	10	12410534	RS29347557	10	5.696346	12661713	0.98759	0.83226	0	5.87E-08	0	0	Shared
Sidt2	864417	9	45760700	D9MIT285	9	25.81754	40462577	0.50546	0.61886	0	5.89E-08	0	0	SCG
4932438A13Rik	522104	3	36928844	03.033.871	3	22.08075	33578373	0.20496	0.29784	0	5.99E-08	0	0	Shared
Nup155	282448	15	8071499	D15MIT13	15	2.1	3410212	1.39406	1.17799	0	6.04E-08	0	0	Shared
Npl	54506	1	1.55E+08	D1Mit102	1	80.039245	149096650	1.56552	1.17267	0	6.05E-08	0	0	SCG
Stxbp1	484929	2	32670403	RS27953638	2	27.96753	50041657	1.04441	1.12377	0	6.09E-08	0	0	SCG
Snx9	351740	17	5891784	17.013.500	17	8.4	13900467	0.87304	1.1186	0	6.12E-08	0	0	SCG
Trpc4ap	508378	2	1.55E+08	RS27267095	2	129.56131	136652019	0.77873	0.68559	0	6.22E-08	0	0	SCG
Rab6b	851801	9	1.03E+08	D9MIT107	9	53.50038	73315075	1.29634	1.16003	0	6.29E-08	0	0	Shared
unassigned	457343	2	71676258	RS28322831	2	43.67748	71063776	1.20623	1.11007	0	6.34E-08	0	0	SCG
Oxsm	262580	14	17071508	14.008.937	14	5.6	10975728	1.4517	1.66834	0	6.43E-08	0	0	SCG
Tipin	844134	9	64152315	D9MIT248	9	44.87553	58210366	0.79211	0.97873	0	6.44E-08	0	0	SCG
unassigned	156257	11	1.01E+08	11.104.430	11	62.15042	104475224	2.12078	1.6235	0	6.57E-08	0	0	Shared
Tspan5	539469	3	1.39E+08	03.141.220	3	108.244	140945577	0.78879	0.97594	0	6.79E-08	0	0	SCG
Ndufs4	241103	13	1.15E+08	d13mit151	13	74.514424	116341977	2.00921	2.39953	0	6.90E-08	0	0	SCG
Trf	875800	9	1.03E+08	D9MIT24	9	73.18313	103132731	0.43273	0.36644	0	6.94E-08	0	0	SCG
Dtd1	470028	2	1.44E+08	D2MIT285	2	110.63716	152683037	1.59295	1.92298	0	6.95E-08	0	0	Shared
Calm3	759883	7	17502179	07.013.915	7	8.7	15600169	1.17374	1.07381	0	6.96E-08	0	0	Shared
Pld1	520182	3	27987572	D3MIT304	3	14.40811	21370177	0.88161	1.15895	0	7.05E-08	0	0	Shared
H2-T10	376249	17	36256172	17.034.150	17	51.1372	34678889	0.22475	0.33049	0	7.12E-08	0	0	SCG
Mcam	839486	9	43947969	D9MIT285	9	25.81754	40462577	1.6649	1.52973	0	7.16E-08	0	0	SCG
unassigned	287674	15	41680186	15.046.034	15	20.554602	46035472	0.72777	0.89676	0	7.19E-08	0	0	SCG
unassigned	590551	4	1.32E+08	D4Mit203	4	89.732314	129249262	3.50111	3.10223	0	7.20E-08	0	0	SCG
Gdi1	910345	X	71552184	RS29086361	X	71.762464	95902327	0.43189	0.36975	0.29656	7.21E-08	0	0	Shared
Nnt	241773	13	1.2E+08	d13mit151	13	74.514424	116341977	0.95313	1.17866	0	7.39E-08	0	0	SCG
Man2a1	363606	17	65021284	17.059.041	17	71.70333	59495092	0.79005	0.90628	0	7.46E-08	0	0	SCG
Iars2	61145	1	1.87E+08	01.183.109	1	96.118477	183202456	0.5136	0.39195	0	7.47E-08	0	0	Shared
Tln2	869518	9	67170805	D9MIT336	9	49.6331	65425671	1.46995	1.30055	0	7.55E-08	0	0	SCG
Agpat9	642926	5	1.01E+08	D5MIT239	5	66.11023	107842159	0.55742	0.70663	0	7.58E-08	0	0	SCG
Eml2	734820	7	19776072	07.013.915	7	8.7	15600169	1.54152	1.41031	0	7.62E-08	0	0	SCG
Usp33	541958	3	1.52E+08	D3MIT147	3	137.32386	148408373	0.69043	0.86562	0	7.65E-08	0	0	SCG
unassigned	740179	7	54078161	D7MIT228	7	28.11811	47279833	0.71691	0.90386	0	7.74E-08	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Aldh4a1	592740	4	1.39E+08	D4MIT170	4	99.940854	138171253	1.5601	1.28787	0	7.76E-08	0	0	Shared
Ece1	592080	4	1.38E+08	04.133.005	4	97.642221	133288839	0.69352	0.54723	0	7.76E-08	0	0	SCG
Ghitm	266916	14	37946367	D14MIT174	14	33.327106	32460166	1.07897	0.98617	0	7.83E-08	0	0	SCG
unassigned	508607	2	1.56E+08	D2MIT423	2	107.80753	148685450	0.57954	0.69259	0	7.85E-08	0	0	SCG
Txnl1	413372	18	63841875	D18MIT152	18	47.63475	62096421	1.38253	1.54735	0	7.92E-08	0	0	SCG
unassigned	734868	7	19880754	07.013.915	7	8.7	15600169	1.7101	1.97975	0	8.05E-08	0	0	Shared
Pi4kb	531187	3	94788389	03.060.525	3	40.51916	60240993	0.81813	0.92661	0	8.57E-08	0	0	SCG
Hmgcs1	894205	13_random	116310	D13MIT78	13	76.842169	119618032	1.10109	1.20505	0	8.71E-08	0	0	Shared
Psmc4	761453	7	28827121	07.017.531	7	12.92437	18957827	2.33102	2.72855	0	8.73E-08	0	0	SCG
Cd37	765367	7	52491516	D7MIT228	7	28.11811	47279833	0.80589	1.03447	0	8.80E-08	0	0	SCG
Bbs7	547500	3	36509159	03.033.871	3	22.08075	33578373	3.2405	2.79818	0	8.85E-08	0	0	SCG
unassigned	367296	17	84175111	D17MIT76	17	95.2661	86033231	0.89207	0.99353	0	8.97E-08	0	0	Shared
unassigned	262854	14	19101849	14.008.937	14	5.6	10975728	0.70349	0.74764	0	9.01E-08	0	0	SCG
Slc18a2	430532	19	59337447	D19MIT103	19	59.411152	53838656	0.66864	0.74298	0	9.32E-08	0	0	SCG
unassigned	133741	11	1.19E+08	D11MIT214	11	79.65651	114991785	1.08433	0.7224	0	9.35E-08	0	0	SCG
Col3a1	5935	1	45382653	D1MIT236	1	37.41892	45435458	0.9352	1.13695	0	9.36E-08	0	0	SCG
Med8	587042	4	1.18E+08	RS27499066	4	79.437135	114673522	0.89789	0.67845	0	9.54E-08	0	0	SCG
unassigned	359144	17	37209306	D17Mit213	17	12.20714	16752157	1.61384	1.51845	0	9.72E-08	0	0	SCG
Laptm4b	286124	15	34207189	15.046.034	15	20.554602	46035472	0.7628	0.88479	0	9.74E-08	0	0	SCG
C530028O21Rik	704048	6	1.25E+08	D6MIT194	6	87.57626	128115503	0.72322	0.94533	0	9.88E-08	0	0	SCG
5033411D12Rik	222908	13	17786568	D13Mit207	13	8.688726	16526195	14.03415	9.93821	0	9.89E-08	0	0	Shared
Ank	284945	15	27520105	15.028.723	15	14.881134	28708166	0.88087	0.76935	0	1.00E-07	0	0	SCG
Ddost	592350	4	1.38E+08	D4MIT170	4	99.940854	138171253	0.68453	0.60938	0	1.00E-07	0	0	SCG
Nup133	831517	8	1.26E+08	D8MIT42	8	102.88933	129076217	0.79305	0.95831	0	1.00E-07	0	0	SCG
unassigned	459299	2	83632017	RS28322831	2	43.67748	71063776	0.98713	0.82306	0	1.00E-07	0	0	Shared
Trf	875807	9	1.03E+08	D9MIT347	9	74.99181	103159628	1.35977	1.51001	0	1.02E-07	0	0	Shared
Zfp459	232749	13	67514854	13.061.624	13	39.879786	61715738	5.25807	4.69778	0	1.02E-07	0	0	Shared
Chrnb4	866554	9	54884394	09.046.588	9	34.49446	46645088	1.1014	0.97819	0	1.05E-07	0	0	SCG
Mef2a	768573	7	74440267	D7MIT248	7	39.99047	80656343	1.19889	1.01522	0	1.05E-07	0	0	SCG
Rint1	630039	5	23317590	D5MIT294	5	15.58331	20863135	0.64262	0.84757	0	1.05E-07	0	0	Shared
Syne2	173463	12	77188751	12.065.348	12	37.44045	65530382	0.2998	0.42739	0	1.05E-07	0	0	Shared
Wapal	248145	14	35535457	D14MIT174	14	33.327106	32460166	1.72675	2.05245	0	1.05E-07	0	0	SCG
Dlat	865430	9	50466290	D9MIT248	9	44.87553	58210366	2.20482	2.04349	0	1.07E-07	0	0	SCG
Ppp5c	759922	7	17613047	07.013.915	7	8.7	15600169	0.29933	0.34639	0	1.07E-07	0	0	Shared
Actr3b	630542	5	25354208	D5MIT388	5	29.38073	33660748	1.20089	1.008	0	1.08E-07	0	0	SCG
Thy1	839421	9	43854069	09.046.588	9	34.49446	46645088	0.46956	0.58871	0	1.08E-07	0	0	SCG
unassigned	806519	8	1.14E+08	D8MIT215	8	87.841725	118384638	1.10403	1.23419	0	1.08E-07	0	0	SCG
Galnt11	630461	5	24771699	05.018.430	5	14.15919	18423994	0.84582	0.92642	0	1.09E-07	0	0	SCG
Lrp12	304846	15	39707675	15.046.034	15	20.554602	46035472	0.6312	0.77636	0	1.10E-07	0	0	SCG
Sass6	535263	3	1.16E+08	D3MIT315	3	89.68246	115544553	0.16932	0.23338	0	1.10E-07	0	0	Shared
Lrrk2	296486	15	91561910	15.090.122	15	63.155859	90124664	1.45419	1.22652	0	1.14E-07	0	0	Shared
Arhgef2	529684	3	88447268	D3MIT49	3	73.77602	89036582	0.5737	0.38977	0	1.15E-07	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Rasa1	235351	13	85395990	D13MIT125	13	47.516374	80862016	1.81561	1.52029	0	1.15E-07	0	0	Shared
Kif21a	314998	15	90828264	15.090.122	15	63.155859	90124664	0.66919	0.76858	0	1.17E-07	0	0	SCG
1700029I01Rik	594082	4	1.47E+08	D4MIT42	4	117.10129	150944103	4.57938	3.85818	0	1.19E-07	0	0	Shared
Echdc1	67891	10	29051632	RS37076985	10	29.161317	28876470	0.96036	1.14577	0	1.19E-07	0	0	Shared
Slc4a10	455466	2	62066681	RS28322831	2	43.67748	71063776	1.44996	1.85849	0	1.21E-07	0	0	SCG
Fundc2	910588	X	72639941	rs13483805	X	31.433568	87440160	0.58634	0.63598	0.68776	1.22E-07	0	0	Shared
Thnsl1	447405	2	21133614	D2MIT296	2	21.50213	31180075	1.00294	1.11946	0	1.22E-07	0	0	SCG
Tspo	294652	15	83404338	D15Mit107	15	49.400965	84216927	1.07176	0.98225	0	1.23E-07	0	0	SCG
Myo1c	122620	11	75482572	D11Mit4	11	39.42453	68422759	1.35917	1.20926	0	1.26E-07	0	0	SCG
Clstn1	594822	4	1.49E+08	D4MIT42	4	117.10129	150944103	1.41524	1.31169	0	1.31E-07	0	0	Shared
Rnf167	121148	11	70464027	D11MIT320	11	39.87138	70766870	0.85118	0.96172	0	1.31E-07	0.0005	0.0455118	Shared
Skiv2l2	240767	13	1.14E+08	d13mit151	13	74.514424	116341977	0.70794	0.50136	0	1.34E-07	0	0	Shared
Mamdc2	435664	19	23438292	19.013.429	19	11.129219	13436471	0.948	1.17488	0	1.35E-07	0	0	SCG
H2-Q2	358667	17	35482626	D17MIT51	17	53.34361	43641790	0.00662	0.00522	0	1.36E-07	0	0	Shared
Tshr	176913	12	92760432	D12MIT194	12	54.38605	92525886	0.67376	0.43637	0	1.36E-07	0	0	SCG
Patl1	420928	19	12006649	19.013.429	19	11.129219	13436471	1.27093	0.99713	0	1.38E-07	0	0	Shared
unassigned	474972	2	1.63E+08	02.168.990	2	151.40532	169124295	0.96648	1.15245	0	1.43E-07	0	0	Shared
Ptgir	734439	7	17491855	07.013.915	7	8.7	15600169	0.92314	0.70861	0	1.45E-07	0	0	SCG
unassigned	771180	7	87884641	D7MIT350	7	57.28732	90734599	0.74438	0.87724	0	1.46E-07	0	0	SCG
Bmpr1a	266536	14	35273696	14.027.409	14	32.019685	29395320	0.76762	0.62411	0	1.49E-07	0	0	Shared
Gcn1l1	646574	5	1.16E+08	d5mit158	5	69.85959	115413178	0.79442	1.01349	0	1.56E-07	0	0	Shared
Lyst	202882	13	13729814	D13Mit207	13	8.688726	16526195	1.32512	1.50628	0	1.58E-07	0	0	SCG
5033411D12Rik	222870	13	17415049	D13Mit207	13	8.688726	16526195	0.20532	0.30505	0	1.59E-07	0	0	Shared
Dpp6	630658	5	27231782	05.018.430	5	14.15919	18423994	0.43247	0.4882	0	1.60E-07	0	0	SCG
Pkn1	823336	8	86204887	D8MIT45	8	58.440058	89829274	2.58133	2.34198	0	1.62E-07	0	0	SCG
unassigned	823365	8	86251545	D8MIT45	8	58.440058	89829274	0.36236	0.48903	0	1.63E-07	0	0	SCG
Oplah	310841	15	76135124	D15MIT67	15	36.957676	70032295	1.20611	1.05204	0	1.66E-07	0	0	SCG
Rex2	594031	4	1.46E+08	D4MIT232	4	109.11827	144647559	3.46707	4.29384	0	1.68E-07	0	0	SCG
Dvl2	120879	11	69819818	D11Mit4	11	39.42453	68422759	4.01446	3.41746	0	1.69E-07	0	0	SCG
Lass5	317271	15	99569837	D15MIT44	15	76.945032	98951714	1.46168	1.30593	0	1.69E-07	0	0	SCG
Imp4	3808	1	34500412	D1Mit374	1	27.028585	34816928	1.36736	1.19734	0	1.71E-07	0	0	SCG
Mycbp2	277971	14	1.04E+08	RS31252045	14	77.831601	111376384	1.05688	1.15333	0	1.71E-07	0	0	SCG
Ebag9	288015	15	44468336	15.028.723	15	14.881134	28708166	1.63904	1.18768	0	1.72E-07	0	0	SCG
Cntnap2	690234	6	46184227	06.036.921	6	24.99854	36940848	0.98107	0.81447	0	1.73E-07	0	0	Shared
Pttg1	141634	11	43239103	11.041.143	11	25.39412	41113079	1.27839	0.96399	0	1.73E-07	0	0	Shared
9030625A04Rik	275011	14	77429355	RS31380922	14	61.610758	78742431	0.66683	0.9119	0	1.78E-07	0	0	Shared
unassigned	358725	17	35534845	17.034.150	17	51.1372	34678889	2.64583	3.17995	0	1.78E-07	0.0005	0.0455118	SCG
Dst	3661	1	34211384	D1Mit374	1	27.028585	34816928	1.60089	1.30458	0	1.83E-07	0	0	Shared
Mrps10	360839	17	47515589	D17MIT180	17	63.0586	51571276	0.78757	0.55925	0	1.87E-07	0	0	Shared
Limk1	678177	5	1.35E+08	D5MIT143	5	120.97554	151804668	0.68198	0.60685	0	1.88E-07	0	0	Shared
unassigned	594807	4	1.49E+08	D4MIT232	4	109.11827	144647559	1.44788	1.26111	0	1.89E-07	0	0	SCG
Prom1	661947	5	44392020	05.049.898	5	44.23678	50000991	0.64722	0.4021	0	1.90E-07	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	739533	7	52415005	D7MIT248	7	39.99047	80656343	0.48864	0.61829	0	1.94E-07	0	0	Shared
Hspg2	591852	4	1.37E+08	04.133.005	4	97.642221	133288839	1.44574	1.26348	0	1.95E-07	0	0	SCG
Tmbim1	42556	1	74335948	D1MIT132	1	55.208767	77143053	0.65323	0.58966	0	1.95E-07	0	0	SCG
Hapln1	215380	13	89744820	D13MIT125	13	47.516374	80862016	3.74928	5.06643	0	2.01E-07	0	0	SCG
Herc2	741487	7	63410388	07.056.455	7	36.40088	63842351	1.33938	1.52508	0	2.05E-07	0	0	SCG
C530028O21Rik	704041	6	1.25E+08	D6MIT194	6	87.57626	128115503	0.2133	0.15571	0	2.06E-07	0	0	SCG
Arg1	89833	10	24636589	RS29316281	10	22.943971	25167321	1.49909	1.88051	0	2.10E-07	0	0	Shared
Ahr	186877	12	36190955	D12MIT60	12	21.025423	35474805	1.79411	1.53115	0	2.12E-07	0	0	SCG
Nup188	449940	2	30177417	D2Mit297	2	25.96707	42461006	1.00633	1.20749	0	2.14E-07	0	0	Shared
unassigned	358525	17	35228629	17.021.019	17	14.36839	21451267	3.94199	3.59835	0	2.16E-07	0	0	SCG
Jag1	504980	2	1.37E+08	RS27267029	2	129.56131	136669427	0.50559	0.67147	0	2.20E-07	0	0	SCG
Mrps5	466871	2	1.27E+08	D2MIT395	2	91.61399	119350649	1.19493	0.93509	0	2.22E-07	0	0	Shared
Stk11ip	11687	1	75521998	D1MIT132	1	55.208767	77143053	0.88266	1.0256	0	2.23E-07	0	0	Shared
Slc24a3	470178	2	1.45E+08	D2MIT285	2	110.63716	152683037	1.96931	1.68572	0	2.25E-07	0	0	Shared
Akap9	627358	5	4039240	D5MIT123	5	4.1	6556176	1.05117	0.84234	0	2.27E-07	0	0	Shared
Arg1	89831	10	24635850	RS29365246	10	15.912841	19378741	0.63211	0.84494	0	2.29E-07	0	0	SCG
unassigned	731570	6	1.42E+08	D6Mit14	6	101.60848	145604376	1.33571	1.75191	0	2.29E-07	0.0005	0.0455118	SCG
Arhgef10	789606	8	14999328	08.010.585	8	4.520052	10585028	0.50909	0.64329	0	2.33E-07	0	0	SCG
Gpr137b	222317	13	12716187	D13Mit207	13	8.688726	16526195	0.42485	0.5145	0	2.36E-07	0	0	SCG
Ntrk3	770453	7	85605196	D7MIT350	7	57.28732	90734599	2.95006	3.37616	0	2.41E-07	0	0	SCG
unassigned	762829	7	31927908	D7Mit232	7	35.20811	59868792	3.38696	2.90629	0	2.42E-07	0	0	SCG
Unc13b	574425	4	43100779	d4mit238	4	33.232784	45243003	2.18785	1.74447	0	2.43E-07	0.0005	0.0455118	SCG
Dcun1d1	547279	3	35792323	D3MIT6	3	28.26274	48687327	0.99036	0.85515	0	2.46E-07	0	0	SCG
H2-T23	376238	17	36248542	D17MIT51	17	53.34361	43641790	1.77046	1.50644	0	2.49E-07	0	0	SCG
Hebp2	88490	10	18261100	RS29347557	10	5.696346	12661713	0.48477	0.63728	0	2.49E-07	0	0	SCG
Macf1	616097	4	1.23E+08	D4MIT308	4	84.360247	123838543	1.45093	1.6101	0	2.53E-07	0	0	SCG
Ptpn5	766149	7	54343863	D7MIT248	7	39.99047	80656343	1.77609	1.41809	0	2.53E-07	0.0005	0.0455118	Shared
Rbks	659522	5	31962321	D5MIT352	5	30.68587	35957616	1.01488	1.30422	0	2.54E-07	0	0	Shared
unassigned	211127	13	56838636	13.043.962	13	29.583286	44046397	1.12333	1.21783	0	2.55E-07	0	0	SCG
Gas5	24432	1	1.63E+08	D1Mit102	1	80.039245	149096650	0.68744	0.46549	0	2.56E-07	0	0	Shared
Dpt	25213	1	1.67E+08	D1MIT507	1	89.469987	166978064	1.52541	1.69858	0	2.58E-07	0.0005	0.0455118	SCG
Adamts12	283099	15	11001308	D15MIT13	15	2.1	3410212	0.71501	0.91661	0	2.61E-07	0	0	SCG
unassigned	559059	3	1.07E+08	RS37321647	3	42.80783	68043880	2.12962	2.29043	0	2.66E-07	0	0	SCG
unassigned	310342	15	74582822	D15MIT67	15	36.957676	70032295	0.42287	0.36111	0	2.67E-07	0	0	SCG
Heatr5a	188646	12	52978357	D12Mit2	12	26.674029	42747379	1.56234	1.37209	0	2.69E-07	0.0005	0.0455118	SCG
1110059E24Rik	435348	19	21672742	D19MIT96	19	21.387917	21916083	1.64831	2.0125	0	2.70E-07	0	0	Shared
Cpne5	374103	17	29298075	D17Mit213	17	12.20714	16752157	2.57386	2.08241	0	2.76E-07	0	0	SCG
Skiv2l2	240755	13	1.14E+08	d13mit151	13	74.514424	116341977	0.95235	0.81991	0	2.76E-07	0	0	SCG
Asb3	112889	11	31001049	D11MIT186	11	23.608	35049231	1.24177	1.03996	0	2.81E-07	0	0	Shared
Tmem63b	377647	17	45814880	17.034.150	17	51.1372	34678889	0.64439	0.77872	0	2.84E-07	0	0	Shared
Dis3l	868858	9	64154858	D9MIT336	9	49.6331	65425671	0.74105	0.59835	0	2.86E-07	0	0	SCG
unassigned	646396	5	1.16E+08	d5mit158	5	69.85959	115413178	1.22112	1.35841	0	2.91E-07	0	0	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Setd3	198402	12	1.09E+08	D12MIT7	12	66.696627	104970690	0.86613	0.99982	0	2.92E-07	0	0	SCG
Txndc9	36354	1	38041988	D1Mit374	1	27.028585	34816928	0.55884	0.66057	0	2.94E-07	0	0	SCG
Slc24a2	609176	4	86876220	D4MIT348	4	56.036646	82826651	1.64613	1.09459	0	2.98E-07	0	0	SCG
Ndufaf1	500559	2	1.19E+08	RS27258455	2	126.73188	129951321	0.65656	0.58059	0	2.99E-07	0	0	SCG
Spg21	844580	9	65332299	D9MIT107	9	53.50038	73315075	0.70492	0.61812	0	2.99E-07	0	0	SCG
unassigned	63865	10	5942789	rs13480474	10	1.8	4403267	2.09283	1.81556	0	3.01E-07	0	0	Shared
Ptprg	243384	14	13053106	D14MIT98	14	6.470372	17356225	1.22945	1.4796	0	3.02E-07	0.0005	0.0455118	Shared
Map3k6	590759	4	1.33E+08	D4Mit203	4	89.732314	129249262	0.3393	0.25829	0	3.04E-07	0.0005	0.0455118	SCG
Epb4.1l2	67222	10	25180600	RS33702022	10	21.757861	24370362	0.67638	0.79342	0	3.09E-07	0.0005	0.0455118	SCG
Spata5	522274	3	37427108	03.033.871	3	22.08075	33578373	0.65792	0.81755	0	3.14E-07	0	0	Shared
1700054N08Rik	831475	8	1.26E+08	D8MIT42	8	102.88933	129076217	1.21677	1.00698	0	3.22E-07	0	0	Shared
unassigned	621656	4	1.45E+08	D4MIT232	4	109.11827	144647559	1.35782	1.69424	0	3.26E-07	0	0	SCG
2610528E23Rik	344852	16	57323584	RS4187006	16	43.579253	51575793	0.9019	1.0943	0	3.27E-07	0	0	SCG
Sprn	782804	7	1.47E+08	d7mit109	7	91.14939	143706746	0.8259	0.85488	0	3.27E-07	0	0	SCG
unassigned	485462	2	34567890	D2Mit297	2	25.96707	42461006	2.31649	2.04829	0	3.31E-07	0	0	SCG
Ogdh	109025	11	6249115	D11MIT2	11	7.6	12218640	0.26289	0.30461	0	3.33E-07	0.0005	0.0455118	SCG
Zfp109	760462	7	25019398	07.017.531	7	12.92437	18957827	7.41619	6.48894	0	3.35E-07	0	0	Shared
Cog2	809483	8	1.27E+08	D8MIT42	8	102.88933	129076217	0.88567	1.08972	0	3.43E-07	0	0	Shared
Cmas	707131	6	1.43E+08	D6Mit14	6	101.60848	145604376	2.26862	2.41909	0	3.53E-07	0	0	SCG
Pim1	356538	17	29627940	D17Mit213	17	12.20714	16752157	1.01989	0.69011	0	3.53E-07	0	0	SCG
Ankrd27	737795	7	36400896	D7MIT228	7	28.11811	47279833	1.49087	1.37159	0	3.56E-07	0.0005	0.0455118	SCG
Glb1	854800	9	1.14E+08	D9MIT201	9	91.42427	117345284	0.46947	0.60137	0	3.56E-07	0	0	SCG
Sfrp5	439626	19	42276063	D19MIT46	19	37.543065	33009697	1.02429	1.15021	0	3.57E-07	0	0	SCG
Grid2	693267	6	63206770	06.036.921	6	24.99854	36940848	0.90497	1.09477	0	3.58E-07	0	0	SCG
Fam160b1	430052	19	57455105	D19MIT103	19	59.411152	53838656	1.85995	2.13763	0	3.73E-07	0.0005	0.0455118	SCG
Gm13157	593795	4	1.47E+08	D4MIT170	4	99.940854	138171253	14.31448	11.52756	0	3.73E-07	0	0	Shared
H47	742752	7	73228298	07.056.455	7	36.40088	63842351	0.58076	0.81626	0	3.76E-07	0	0	Shared
Coq2	670446	5	1.01E+08	D5MIT239	5	66.11023	107842159	0.88553	0.76344	0	3.80E-07	0	0	SCG
Emp1	705872	6	1.35E+08	D6MIT328	6	75.24789	112729344	0.85132	0.974	0	3.80E-07	0	0	SCG
Tie1	615039	4	1.18E+08	RS27499066	4	79.437135	114673522	0.88618	0.66119	0	3.82E-07	0	0	SCG
Atp11b	521786	3	35676947	D3MIT6	3	28.26274	48687327	0.60765	0.49457	0	3.84E-07	0	0	SCG
Gtf2h1	740167	7	54057165	D7MIT228	7	28.11811	47279833	1.2572	1.11659	0	3.84E-07	0	0	Shared
Esyt1	107502	10	1.28E+08	D10Mit14	10	93.102537	118098315	0.45414	0.52439	0	3.95E-07	0	0	SCG
H2-D1	358654	17	35402751	D17MIT51	17	53.34361	43641790	0.18948	0.27563	0	4.01E-07	0	0	SCG
Pde1c	717050	6	56128732	06.036.921	6	24.99854	36940848	1.12185	1.489	0	4.02E-07	0	0	SCG
Gtpbp1	293522	15	79546282	D15MIT67	15	36.957676	70032295	0.49978	0.62682	0	4.04E-07	0	0	Shared
C530028O21Rik	704050	6	1.25E+08	RS30909511	6	57.9854	83140362	1.2214	0.98938	0	4.08E-07	0	0	SCG
Arntl2	708003	6	1.47E+08	D6Mit14	6	101.60848	145604376	2.90956	2.1294	0	4.09E-07	0.0005	0.0455118	Shared
Atm	866078	9	53262826	D9MIT248	9	44.87553	58210366	1.71352	2.03906	0	4.13E-07	0	0	SCG
unassigned	296683	15	92084498	15.090.122	15	63.155859	90124664	1.39876	1.25127	0	4.14E-07	0	0	SCG
unassigned	433897	19	12556719	D19MIT96	19	21.387917	21916083	0.75333	0.63705	0	4.15E-07	0.0005	0.0455118	SCG
Mlh1	878101	9	1.11E+08	09.105.291	9	79.88305	105335230	1.06867	1.56027	0	4.19E-07	0	0	SCG

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Acsf2	153949	11	94430648	11.104.430	11	62.15042	104475224	0.6109	0.42246	0	4.20E-07	0	0	SCG
C330023M02Rik	648035	5	1.22E+08	D5MIT95	5	98.81753	125309605	2.73266	2.4207	0	4.22E-07	0	0	SCG
Ryr2	221969	13	11670091	D13Mit207	13	8.688726	16526195	0.50052	0.65453	0	4.24E-07	0.0005	0.0455118	SCG
unassigned	823763	8	87488863	D8MIT45	8	58.440058	89829274	1.15009	1.20501	0	4.26E-07	0	0	SCG
Efhb	379403	17	53540768	D17MIT51	17	53.34361	43641790	0.63997	0.73231	0	4.36E-07	0	0	SCG
unassigned	823007	8	83519359	D8MIT346	8	54.673156	85454038	0.54975	0.69871	0	4.36E-07	0.0005	0.0455118	SCG
Efhb	379402	17	53540104	D17MIT51	17	53.34361	43641790	0.53401	0.75016	0	4.37E-07	0	0	Shared
unassigned	742868	7	73854897	D7Mit232	7	35.20811	59868792	1.02949	0.92665	0	4.37E-07	0	0	SCG
Dctn1	695810	6	83144982	D6MIT328	6	75.24789	112729344	1.70473	1.54701	0	4.43E-07	0	0	SCG
unassigned	787318	8	3522670	D8MIT155	8	3.1	4976602	3.17766	2.94834	0	4.43E-07	0	0	SCG
Oprm1	85864	10	3587906	RS38621064	10	13.651095	17528671	0.92385	1.18277	0	4.48E-07	0	0	SCG
Fkbp9	692583	6	56818839	06.057.998	6	39.56321	58018416	0.94688	1.07719	0	4.51E-07	0	0	Shared
Pign	47635	1	1.07E+08	D1MIT1001	1	72.841454	130944135	3.66771	4.33216	0	4.54E-07	0.0005	0.0455118	SCG
Lass4	787616	8	4515556	D8MIT155	8	3.1	4976602	0.45646	0.39796	0	4.56E-07	0	0	SCG
Slc25a17	312487	15	81150063	D15Mit107	15	49.400965	84216927	0.83803	0.74292	0	4.59E-07	0	0	Shared
unassigned	765191	7	52268669	07.017.531	7	12.92437	18957827	0.30189	0.41866	0	4.59E-07	0	0	Shared
H2-T23	376231	17	36169554	17.034.150	17	51.1372	34678889	1.7563	1.52297	0	4.60E-07	0	0	SCG
Zfp748	232829	13	67646274	13.061.624	13	39.879786	61715738	0.35298	0.48154	0	4.63E-07	0	0	Shared
Steap4	627842	5	7978453	D5MIT388	5	29.38073	33660748	1.35331	1.53819	0	4.64E-07	0	0	SCG
Apbb1	775351	7	1.13E+08	RS36353338	7	66.26522	112706514	1.24163	1.34559	0	4.65E-07	0	0	SCG
Rbp4	438589	19	38199051	D19MIT13	19	37.094077	32713513	1.08424	0.70647	0	4.66E-07	0	0	SCG
Rps28	375345	17	33960181	17.034.150	17	51.1372	34678889	0.80853	0.89897	0	4.67E-07	0	0	Shared
Astn1	23905	1	1.61E+08	D1MIT1001	1	72.841454	130944135	1.17526	1.31207	0	4.76E-07	0.0005	0.0455118	SCG
Slc11a2	317413	15	1E+08	D15MIT44	15	76.945032	98951714	0.06984	0.12462	0	4.84E-07	0	0	Shared
Adam22	655809	5	8136816	D5MIT123	5	4.1	6556176	0.83224	0.98598	0	4.86E-07	0	0	SCG
Msi1	646455	5	1.16E+08	d5mit158	5	69.85959	115413178	0.49187	0.75709	0	4.95E-07	0	0	Shared
Syn3	100067	10	85929729	RS46745265	10	65.869576	69258223	0.64105	0.54336	0	5.08E-07	0	0	SCG
Heg1	325530	16	33735669	RS4187006	16	43.579253	51575793	0.53173	0.69618	0	5.10E-07	0.0005	0.0455118	SCG
Imp4	3813	1	34501860	rs13475894	1	45.460824	63625006	0.31449	0.43926	0	5.11E-07	0	0	Shared
Atp1a2	58703	1	1.74E+08	D1MIT1001	1	72.841454	130944135	0.93735	1.00546	0	5.13E-07	0	0	SCG
Zfp160	354207	17	21148649	D17Mit213	17	12.20714	16752157	0.1123	0.08831	0	5.19E-07	0	0	Shared
Dtd1	470032	2	1.44E+08	D2Mit274	2	62.95823	114283330	1.38164	1.18217	0	5.22E-07	0	0	Shared
Pacsin1	355983	17	27844825	D17Mit213	17	12.20714	16752157	3.31239	2.99464	0	5.25E-07	0.0005	0.0455118	SCG
Slc2a6	483520	2	26878247	D2MIT296	2	21.50213	31180075	0.87078	0.76729	0	5.36E-07	0.0005	0.0455118	SCG
unassigned	550403	3	57453910	RS37321647	3	42.80783	68043880	0.6546	0.8701	0	5.36E-07	0	0	Shared
Echdc1	67886	10	29033407	D10MIT184	10	40.059568	42088505	0.82497	0.68308	0	5.41E-07	0	0	SCG
H2-Ab1	358133	17	34404289	17.021.019	17	14.36839	21451267	0.66993	0.57961	0	5.42E-07	0	0	SCG
Sacm1l	856987	9	1.23E+08	D9MIT201	9	91.42427	117345284	0.52763	0.45958	0	5.42E-07	0.0005	0.0455118	Shared
Cnot10	878746	9	1.15E+08	D9MIT201	9	91.42427	117345284	0.42647	0.32264	0	5.49E-07	0	0	Shared
Rbp4	438583	19	38191308	D19MIT13	19	37.094077	32713513	0.35762	0.5151	0	5.56E-07	0	0	SCG
unassigned	765536	7	52780783	D7MIT228	7	28.11811	47279833	1.41215	1.68132	0	5.57E-07	0.0005	0.0455118	SCG
Mcam	839478	9	43944618	09.046.588	9	34.49446	46645088	0.46632	0.42873	0	5.66E-07	0	0	SCG

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Epb4.1l2	67262	10	25242462	RS29367295	10	20.727339	23573544	0.37266	0.29636	0	5.73E-07	0	0	SCG
unassigned	287675	15	41681832	15.046.034	15	20.554602	46035472	3.05129	2.65062	0	5.80E-07	0	0	SCG
Grwd1	765629	7	53080942	D7Mit232	7	35.20811	59868792	0.7926	0.9222	0	5.81E-07	0	0	SCG
Polr3h	312691	15	81755694	D15Mit107	15	49.400965	84216927	1.16827	1.5049	0	5.82E-07	0.0005	0.0455118	SCG
unassigned	395935	18	52647056	D18Mit123	18	38.31055	56130259	1.03623	1.22954	0	5.89E-07	0	0	Shared
unassigned	707058	6	1.42E+08	D6Mit14	6	101.60848	145604376	1.17879	0.91696	0	5.94E-07	0.0005	0.0455118	SCG
Clk1	39691	1	58476967	rs13475894	1	45.460824	63625006	2.26982	2.66516	0	5.95E-07	0	0	Shared
Golph3l	531447	3	95413596	D3MIT49	3	73.77602	89036582	1.12943	1.32123	0	5.95E-07	0	0	SCG
Gbf1	427731	19	46335227	19.046.444	19	55.551107	46465179	1.76664	1.61877	0	6.07E-07	0	0	SCG
Klrb1b	729174	6	1.29E+08	D6MIT194	6	87.57626	128115503	0.91014	1.48806	0	6.10E-07	0	0	SCG
unassigned	393375	18	37924112	D18MIT202	18	28.05292	43551589	0.42229	0.62787	0	6.11E-07	0	0	Shared
unassigned	354214	17	21162171	17.034.150	17	51.1372	34678889	1.06095	1.17846	0	6.20E-07	0.0005	0.0455118	Shared
Mcam	839479	9	43944980	D9MIT248	9	44.87553	58210366	0.97892	0.91724	0	6.22E-07	0	0	Shared
Cd97	823371	8	86254054	D8MIT45	8	58.440058	89829274	1.80627	1.54826	0	6.30E-07	0	0	SCG
Txnrd1	77130	10	82340028	D10MIT117	10	70.67248	87027855	2.17303	2.37697	0	6.34E-07	0	0	SCG
Cyb5r3	313071	15	82990779	D15Mit107	15	49.400965	84216927	0.86546	0.80852	0	6.36E-07	0	0	SCG
Med23	67108	10	24628440	RS33702022	10	21.757861	24370362	1.21497	1.04332	0	6.49E-07	0	0	Shared
Nrg1	815435	8	33028011	D8MIT292	8	21.904548	35848067	1.06659	0.96042	0	6.53E-07	0	0	SCG
Creb3	574639	4	43578349	d4mit238	4	33.232784	45243003	1.0316	0.90999	0	6.57E-07	0	0	Shared
unassigned	284553	15	25729763	15.028.723	15	14.881134	28708166	1.51714	1.7698	0	6.60E-07	0	0	SCG
Ostm1	69689	10	42416089	D10MIT184	10	40.059568	42088505	1.05618	1.19308	0	6.61E-07	0	0	SCG
Azi2	855522	9	1.18E+08	D9MIT201	9	91.42427	117345284	1.29728	1.48699	0	6.64E-07	0.0005	0.0455118	SCG
unassigned	562425	3	1.27E+08	D3MIT57	3	88.53548	115533310	0.95483	1.26047	0	6.68E-07	0	0	Shared
Pick1	293333	15	79060253	15.090.122	15	63.155859	90124664	0.7212	0.45475	0	6.69E-07	0	0	Shared
unassigned	176897	12	92638972	D12MIT7	12	66.696627	104970690	1.5499	1.1792	0	6.71E-07	0	0	SCG
Supt3h	360195	17	45175029	D17MIT51	17	53.34361	43641790	1.06469	0.867	0	6.80E-07	0	0	Shared
Sacm1l	856975	9	1.23E+08	D9Mit18	9	96.97845	120198563	2.65059	2.28874	0	6.81E-07	0.0005	0.0455118	SCG
Mrpl30	4460	1	37950784	D1Mit374	1	27.028585	34816928	1.87137	1.61351	0	6.85E-07	0	0	Shared
Tjp1	768211	7	72455899	D7MIT248	7	39.99047	80656343	0.89398	1.07668	0	6.86E-07	0	0	SCG
Svep1	605001	4	58085551	D4MIT164	4	42.389612	59415112	0.38616	0.54932	0	6.97E-07	0	0	Shared
Map2k4	146771	11	65569784	D11MIT51	11	25.39412	36205252	0.45542	0.37329	0	6.98E-07	0.0005	0.0455118	SCG
unassigned	35667	1	34874608	D1Mit374	1	27.028585	34816928	0.62381	0.72749	0	6.99E-07	0	0	SCG
Ddost	592344	4	1.38E+08	04.133.005	4	97.642221	133288839	1.26458	1.40894	0	7.04E-07	0	0	SCG
unassigned	312682	15	81745060	15.090.122	15	63.155859	90124664	0.54016	0.43489	0	7.11E-07	0	0	SCG
Ppih	615273	4	1.19E+08	RS27499066	4	79.437135	114673522	0.21111	0.14144	0	7.18E-07	0.0005	0.0455118	Shared
unassigned	491930	2	71114948	D2MIT61	2	35.12792	60528325	0.43724	0.48545	0	7.26E-07	0	0	Shared
Myo1e	845766	9	70224336	D9MIT107	9	53.50038	73315075	0.15017	0.20448	0	7.31E-07	0	0	Shared
6330439K17Rik	506127	2	1.44E+08	D2MIT411	2	112.97352	159412163	1.18566	1.04411	0	7.38E-07	0	0	SCG
Cpne5	374118	17	29341635	17.021.019	17	14.36839	21451267	0.94471	1.2422	0	7.39E-07	0.0005	0.0455118	SCG
Ryr2	222067	13	11884973	D13Mit207	13	8.688726	16526195	0.50495	0.61286	0	7.41E-07	0.0005	0.0455118	SCG
Enpp3	89780	10	24513423	D10Mit123	10	3.021254	9952319	1.4881	1.10132	0	7.42E-07	0	0	SCG
Iars2	61130	1	1.87E+08	01.183.109	1	96.118477	183202456	2.22996	1.96441	0	7.47E-07	0	0	SCG

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	474776	2	1.63E+08	D2MIT423	2	107.80753	148685450	2.23283	2.00933	0	7.50E-07	0.0005	0.0455118	SCG
Slc24a2	609142	4	86722026	D4MIT132	4	51.331896	70333587	5.10944	4.29236	0	7.56E-07	0.0005	0.0455118	SCG
Stab1	265698	14	31959862	14.027.409	14	32.019685	29395320	0.65203	0.80581	0	7.61E-07	0.0005	0.0455118	SCG
unassigned	354509	17	22514249	D17Mit213	17	12.20714	16752157	0.46001	0.54557	0	7.65E-07	0	0	SCG
Ifi204	58975	1	1.76E+08	01.183.109	1	96.118477	183202456	1.01019	1.47085	0	7.71E-07	0.0005	0.0455118	SCG
unassigned	432672	19	7069281	19.009.231	19	7.749799	9238445	1.94168	1.61654	0	7.76E-07	0	0	Shared
Ptplad1	868995	9	64840064	d9mit198	9	66.50428	91176808	2.93831	3.23154	0	7.78E-07	0.0005	0.0455118	SCG
unassigned	378092	17	46823654	17.034.150	17	51.1372	34678889	1.84924	2.07328	0	7.83E-07	0	0	SCG
Mmadhc	487940	2	50136633	D2MIT61	2	35.12792	60528325	1.55751	1.88796	0	7.94E-07	0	0	SCG
Extl2	535127	3	1.16E+08	D3MIT315	3	89.68246	115544553	1.36004	1.53121	0	8.20E-07	0	0	SCG
unassigned	740327	7	56072045	D7MIT228	7	28.11811	47279833	1.03564	1.20967	0	8.21E-07	0	0	Shared
unassigned	594824	4	1.49E+08	D4MIT232	4	109.11827	144647559	1.38408	1.27519	0	8.28E-07	0	0	SCG
Col4a1	811570	8	11217927	D8MIT155	8	3.1	4976602	0.48741	0.59614	0	8.38E-07	0	0	SCG
Ttc13	831681	8	1.27E+08	D8MIT42	8	102.88933	129076217	0.53349	0.41061	0	8.44E-07	0	0	SCG
Twf1	315779	15	94416927	D15MIT44	15	76.945032	98951714	0.48223	0.6328	0	8.51E-07	0	0	Shared
Skiv2l	375725	17	34978948	17.034.150	17	51.1372	34678889	1.07268	0.93352	0	8.59E-07	0	0	Shared
Aph1b	869346	9	66637462	D9MIT248	9	44.87553	58210366	1.81734	1.98231	0	8.71E-07	0.0005	0.0455118	SCG
Klk10	738942	7	51038838	D7MIT228	7	28.11811	47279833	0.74169	1.09613	0	8.85E-07	0	0	SCG
Nup37	78241	10	87610937	D10MIT117	10	70.67248	87027855	0.97681	1.16079	0	8.92E-07	0	0	Shared
Gucy1a3	553582	3	81909729	D3MIT49	3	73.77602	89036582	1.27228	1.38968	0	8.95E-07	0	0	Shared
Ppp2r1b	841214	9	50688797	09.046.588	9	34.49446	46645088	1.50832	1.68814	0	8.97E-07	0	0	SCG
Tln2	869538	9	67213759	D9MIT336	9	49.6331	65425671	0.17379	0.1018	0	8.99E-07	0	0	SCG
Igf1r	743202	7	75363299	07.056.455	7	36.40088	63842351	1.24015	1.41217	0	9.12E-07	0	0	SCG
Tekt2	616784	4	1.26E+08	D4MIT308	4	84.360247	123838543	0.69193	0.9149	0	9.17E-07	0	0	SCG
H2-T10	376228	17	36256376	D17MIT51	17	53.34361	43641790	1.27981	1.55264	0	9.23E-07	0	0	SCG
Gsk3b	326516	16	38170767	16.039.061	16	48.358704	39141781	0.65666	0.73145	0	9.60E-07	0	0	Shared
D730040F13Rik	604708	4	56936226	D4MIT164	4	42.389612	59415112	1.22533	1.38685	0	9.70E-07	0	0	SCG
Kcnab2	623496	4	1.52E+08	D4MIT42	4	117.10129	150944103	0.28248	0.46635	0	9.74E-07	0.0005	0.0455118	Shared
Apba2	742514	7	71895036	D7Mit232	7	35.20811	59868792	2.9493	2.67842	0	9.75E-07	0	0	SCG
H2-gs10	358707	17	35517447	D17MIT51	17	53.34361	43641790	1.31406	1.06368	0	9.77E-07	0	0	SCG
Acad9	521889	3	35989785	D3MIT6	3	28.26274	48687327	0.75939	0.84194	0	9.84E-07	0	0	SCG
Cpne5	374102	17	29297279	17.021.019	17	14.36839	21451267	2.19671	1.58145	0	9.94E-07	0	0	SCG
unassigned	679087	5	1.38E+08	05.132.979	5	112.26584	133170167	1.23045	1.3824	0	1.03E-06	0.0005	0.0455118	SCG
Smap2	615672	4	1.21E+08	04.098.998	4	75.012985	99172673	0.65982	0.79773	0	1.04E-06	0	0	Shared
Disp1	896018	1_random	69028	01.183.109	1	96.118477	183202456	0.35206	0.51459	0	1.05E-06	0	0	SCG
Notch2	532070	3	97876651	RS37321647	3	42.80783	68043880	0.73072	0.82759	0	1.05E-06	0	0	SCG
Sema7a	842781	9	57802349	D9MIT336	9	49.6331	65425671	1.17246	1.48388	0	1.05E-06	0	0	Shared
unassigned	622849	4	1.49E+08	D4MIT232	4	109.11827	144647559	1.46873	1.69998	0	1.05E-06	0	0	SCG
unassigned	630336	5	24209026	05.018.430	5	14.15919	18423994	1.1116	0.97624	0	1.07E-06	0	0	SCG
Atp6v1c1	287062	15	38621367	15.028.723	15	14.881134	28708166	1.2135	1.13085	0	1.09E-06	0.0005	0.0455118	SCG
Man1c1	618957	4	1.34E+08	D4MIT170	4	99.940854	138171253	2.34777	2.08865	0	1.09E-06	0	0	SCG
Tbx20	860276	9	24527792	09.014.560	9	12.99047	14614051	4.24987	3.75735	0	1.10E-06	0	0	SCG

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Arpc5	22876	1	1.55E+08	D1Mit102	1	80.039245	149096650	1.00388	1.08895	0	1.11E-06	0	0	Shared
Ptplad1	869011	9	64854371	09.046.588	9	34.49446	46645088	0.93717	0.73777	0	1.12E-06	0	0	SCG
unassigned	147724	11	69377142	D11Mit4	11	39.42453	68422759	2.20365	2.03704	0	1.13E-06	0	0	SCG
unassigned	722705	6	93765820	06.057.998	6	39.56321	58018416	1.91258	1.60767	0	1.13E-06	0	0	SCG
Coq2	670448	5	1.01E+08	D5MIT309	5	58.78964	79931746	2.51366	2.84293	0	1.14E-06	0	0	SCG
unassigned	219862	13	1.14E+08	D13MIT213	13	69.659242	109037352	1.46464	1.21526	0	1.14E-06	0	0	Shared
Nqo2	206517	13	34073295	RS29514367	13	20.539234	29499372	1.45106	1.33374	0	1.16E-06	0	0	SCG
Ndrg3	508842	2	1.57E+08	D2MIT411	2	112.97352	159412163	1.66639	1.83629	0	1.17E-06	0	0	SCG
Slc37a4	839576	9	44210958	D9MIT248	9	44.87553	58210366	1.07377	0.99661	0	1.17E-06	0	0	SCG
Vps52	357890	17	34098093	17.034.150	17	51.1372	34678889	1.63871	1.86434	0	1.18E-06	0.0005	0.0455118	Shared
Tbc1d23	344797	16	57199012	D16MIT139	16	56.627807	65669762	0.97935	1.12186	0	1.20E-06	0	0	Shared
Trak1	856349	9	1.21E+08	D9MIT151	9	100.11619	121386992	2.61971	2.23775	0	1.20E-06	0	0	Shared
Hcrtr1	617710	4	1.3E+08	D4MIT170	4	99.940854	138171253	1.92476	2.2385	0	1.26E-06	0	0	SCG
unassigned	3690	1	34231645	D1MIT169	1	18.851745	24071806	1.48377	1.64766	0	1.26E-06	0	0	Shared
Cyp2b9	735813	7	26986125	07.017.531	7	12.92437	18957827	0.71706	7.93013	0	1.27E-06	0	0	SCG
Ece1	592086	4	1.38E+08	D4MIT170	4	99.940854	138171253	1.3172	1.16438	0	1.28E-06	0	0	SCG
Heph	912240	X	93753378	DXMIT132	X	55.816704	138191357	2.55308	3.10527	3.31287	1.28E-06	0	0	SCG
Orc6l	801058	8	87829139	08.076.189	8	47.386767	75816827	1.41311	1.13984	0	1.28E-06	0.0005	0.0455118	SCG
unassigned	22873	1	1.55E+08	D1Mit102	1	80.039245	149096650	1.20724	1.03063	0	1.32E-06	0	0	SCG
Abcg4	863763	9	44086172	D9MIT247	9	25.36975	36940492	2.79639	2.48939	0	1.33E-06	0	0	SCG
Acap3	596639	4	1.55E+08	D4MIT42	4	117.10129	150944103	1.26472	1.11133	0	1.33E-06	0.0005	0.0455118	Shared
Alg9	841170	9	50610050	D9MIT285	9	25.81754	40462577	0.68361	0.84477	0	1.33E-06	0.0005	0.0455118	SCG
Cpne5	374101	17	29296898	17.034.150	17	51.1372	34678889	2.45844	2.00885	0	1.35E-06	0	0	SCG
Ercc2	734935	7	19979402	07.013.915	7	8.7	15600169	1.25281	1.0569	0	1.36E-06	0	0	SCG
unassigned	738266	7	38973801	07.056.455	7	36.40088	63842351	0.79139	0.88154	0	1.39E-06	0	0	SCG
Hps5	766002	7	54038537	D7MIT228	7	28.11811	47279833	0.55765	0.72215	0	1.41E-06	0.0005	0.0455118	Shared
unassigned	317398	15	1E+08	D15MIT44	15	76.945032	98951714	1.65849	1.52014	0	1.41E-06	0.0005	0.0455118	Shared
4930555I21Rik	591254	4	1.35E+08	D4MIT170	4	99.940854	138171253	13.77949	12.15204	0	1.42E-06	0.0005	0.0455118	SCG
Bmpr1a	266519	14	35238146	D14MIT174	14	33.327106	32460166	1.63851	1.4769	0	1.42E-06	0.0005	0.0455118	SCG
Pkd2	643814	5	1.05E+08	D5MIT239	5	66.11023	107842159	1.5791	1.34419	0	1.42E-06	0	0	Shared
unassigned	869248	9	65936386	D9MIT336	9	49.6331	65425671	0.94191	0.85408	0	1.43E-06	0	0	SCG
Kdm5b	20468	1	1.37E+08	D1Mit102	1	80.039245	149096650	0.6245	0.72071	0	1.44E-06	0	0	SCG
Mfn2	622160	4	1.47E+08	D4MIT232	4	109.11827	144647559	1.25136	1.18051	0	1.45E-06	0.0005	0.0455118	Shared
Mgp	730523	6	1.37E+08	D6MIT194	6	87.57626	128115503	2.18204	1.80779	0	1.45E-06	0	0	SCG
Lrp5	431138	19	3622605	19.000.325	19	0.2	325000	1.40254	1.0355	0	1.46E-06	0	0	SCG
Dpf2	432195	19	5902104	D19Mit68	19	0.200001	3645155	0.7349	0.64753	0	1.47E-06	0	0	SCG
6330416L07Rik	372060	17	22495897	17.021.019	17	14.36839	21451267	0.77985	0.87235	0	1.48E-06	0.0005	0.0455118	SCG
Rps25	839584	9	44218361	D9MIT248	9	44.87553	58210366	0.11946	0.17824	0	1.48E-06	0	0	SCG
unassigned	800346	8	85818218	D8MIT45	8	58.440058	89829274	0.99048	0.85843	0	1.48E-06	0	0	SCG
Arhgef4	3927	1	34866558	D1Mit374	1	27.028585	34816928	1.54577	1.72132	0	1.49E-06	0.0005	0.0455118	SCG
Gbp1	539971	3	1.42E+08	03.141.220	3	108.244	140945577	0.58692	0.80928	0	1.49E-06	0	0	SCG
Me1	873000	9	86571795	D9MIT123	9	55.0405	73379633	0.36181	0.30677	0	1.49E-06	0	0	SCG

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
P4hb	161801	11	1.2E+08	D11MIT214	11	79.65651	114991785	2.36312	2.17946	0	1.49E-06	0.0005	0.0455118	SCG
Enpp2	306582	15	54738393	D15MIT262	15	57.212355	87111041	1.93841	1.66064	0	1.52E-06	0.0005	0.0455118	SCG
Heatr5a	188694	12	53057136	D12Mit2	12	26.674029	42747379	0.75402	0.86697	0	1.52E-06	0.0005	0.0455118	SCG
Rad51l3	151223	11	82695306	D11MIT320	11	39.87138	70766870	1.08891	1.26924	0	1.56E-06	0	0	Shared
unassigned	538702	3	1.35E+08	D3MIT351	3	107.46572	139262419	1.72188	1.44912	0	1.56E-06	0.0005	0.0455118	Shared
Eif3m	497865	2	1.05E+08	D2MIT100	2	54.19426	106377525	0.34129	0.41686	0	1.57E-06	0.0005	0.0455118	SCG
Nid1	202850	13	13601015	D13Mit207	13	8.688726	16526195	1.38398	1.23815	0	1.57E-06	0	0	SCG
Ptprt	509803	2	1.62E+08	02.161.464	2	113.50933	161598295	0.73912	0.89978	0	1.58E-06	0	0	SCG
unassigned	29413	1	1.87E+08	01.183.109	1	96.118477	183202456	1.18388	1.28737	0	1.58E-06	0.0005	0.0455118	SCG
Heatr5a	188676	12	53019687	D12MIT60	12	21.025423	35474805	1.01077	0.91128	0	1.59E-06	0	0	SCG
Patl1	420933	19	12017131	19.013.429	19	11.129219	13436471	2.33682	1.81557	0	1.59E-06	0	0	SCG
unassigned	842874	9	58109204	D9MIT248	9	44.87553	58210366	0.58354	0.50912	0	1.59E-06	0	0	SCG
Rxfp1	553215	3	79448180	D3MIT98	3	51.73848	85985423	0.95383	0.79068	0	1.60E-06	0.0005	0.0455118	SCG
Tmod1	575349	4	46096435	d4mit238	4	33.232784	45243003	1.39774	1.31181	0	1.60E-06	0.0005	0.0455118	Shared
unassigned	129646	11	1.02E+08	D11MIT289	11	59.90287	94741466	0.50269	0.54594	0	1.62E-06	0	0	SCG
Lamc1	54419	1	1.55E+08	D1Mit102	1	80.039245	149096650	1.06177	0.94632	0	1.63E-06	0	0	SCG
Zfp239	702492	6	1.18E+08	d6mit366	6	77.49561	115192871	1.27459	1.02002	0	1.65E-06	0.0005	0.0455118	Shared
Pi4k2a	426757	19	42175154	D19MIT88	19	44.411348	37331405	0.3732	0.302	0	1.70E-06	0	0	Shared
unassigned	69270	10	40352717	RS29329200	10	39.498733	40791505	0.98366	1.27416	0	1.71E-06	0	0	SCG
Mkks	504933	2	1.37E+08	RS27267029	2	129.56131	136669427	3.17939	2.70815	0	1.77E-06	0.0005	0.0455118	SCG
unassigned	141633	11	43238162	RS26845852	11	16.78021	24370394	2.96852	4.16817	0	1.78E-06	0	0	Shared
unassigned	617736	4	1.3E+08	D4Mit203	4	89.732314	129249262	1.02555	1.1716	0	1.79E-06	0	0	SCG
unassigned	358554	17	35238306	17.034.150	17	51.1372	34678889	1.2034	1.11048	0	1.80E-06	0.0005	0.0455118	SCG
Exoc7	160645	11	1.16E+08	D11MIT214	11	79.65651	114991785	2.06492	1.81046	0	1.81E-06	0.0005	0.0455118	SCG
Vamp2	120503	11	68902612	D11MIT320	11	39.87138	70766870	0.19717	0.24296	0	1.84E-06	0	0	SCG
Ptprt	509767	2	1.61E+08	D2MIT411	2	112.97352	159412163	1.1923	1.01156	0	1.87E-06	0.0005	0.0455118	SCG
Sorl1	863190	9	41907255	D9MIT285	9	25.81754	40462577	0.58978	0.68742	0	1.90E-06	0	0	SCG
Srp9	28904	1	1.84E+08	01.183.109	1	96.118477	183202456	3.04805	3.3018	0	1.90E-06	0	0	SCG
unassigned	418895	19	4879843	D19Mit68	19	0.200001	3645155	1.18528	1.33187	0	1.90E-06	0	0	SCG
unassigned	298642	15	1.01E+08	D15Mit107	15	49.400965	84216927	1.37173	1.20669	0	1.93E-06	0	0	SCG
Syt16	173087	12	75286488	D12MIT91	12	43.26798	72843829	0.21943	0.17372	0	1.95E-06	0	0	SCG
App	347957	16	85040496	D16MIT189	16	73.832256	82534333	0.26528	0.37156	0	1.96E-06	0	0	SCG
Dnajc3	260017	14	1.19E+08	14.095.016	14	67.370818	96532085	0.45783	0.55867	0	1.99E-06	0	0	SCG
Sacm1l	856988	9	1.23E+08	D9MIT151	9	100.11619	121386992	0.92878	1.10493	0	2.01E-06	0	0	Shared
Vps52	357882	17	34094794	17.034.150	17	51.1372	34678889	0.64299	0.86213	0	2.04E-06	0.0005	0.0455118	Shared
Cysltr2	274218	14	73430220	D14Mit194	14	66.469555	94235479	2.03162	2.36752	0	2.05E-06	0	0	SCG
unassigned	632759	5	35141984	D5MIT352	5	30.68587	35957616	0.82167	0.67536	0	2.05E-06	0	0	SCG
Clk1	39692	1	58477974	D1MIT134	1	59.854045	80264451	2.08514	1.91034	0	2.06E-06	0	0	SCG
Rbms1	489890	2	60680401	RS28322831	2	43.67748	71063776	1.86032	2.09432	0	2.07E-06	0	0	SCG
Lgals9	150404	11	78781501	D11MIT320	11	39.87138	70766870	1.09384	0.92317	0	2.08E-06	0	0	SCG
Sucla2	254766	14	73968443	14.067.129	14	52.822413	68793727	1.19197	1.06133	0	2.08E-06	0.0005	0.0455118	SCG
Emp1	705873	6	1.35E+08	D6MIT194	6	87.57626	128115503	1.20594	1.08346	0	2.09E-06	0	0	SCG

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Rbp4	438584	19	38191368	D19MIT13	19	37.094077	32713513	12.68076	7.90425	0	2.09E-06	0.0005	0.0455118	SCG
Gtf2h1	740168	7	54059232	D7MIT228	7	28.11811	47279833	1.41719	1.28333	0	2.12E-06	0	0	Shared
Kif1b	622640	4	1.49E+08	D4MIT232	4	109.11827	144647559	1.18426	1.28702	0	2.13E-06	0	0	SCG
Pla2g6	311941	15	79127802	D15MIT262	15	57.212355	87111041	2.34678	2.61979	0	2.14E-06	0.0005	0.0455118	SCG
Siva1	181212	12	1.14E+08	D12MIT7	12	66.696627	104970690	1.08473	0.74647	0	2.15E-06	0.0005	0.0455118	Shared
RP23-331L12.8	160084	11	1.15E+08	D11MIT214	11	79.65651	114991785	0.7965	1.01169	0	2.16E-06	0.0005	0.0455118	SCG
Slc11a2	317392	15	1E+08	D15MIT44	15	76.945032	98951714	0.54723	0.47076	0	2.19E-06	0	0	Shared
Ccdc117	135422	11	5431336	D11MIT2	11	7.6	12218640	0.24772	0.26875	0	2.23E-06	0.0005	0.0455118	SCG
Ephb2	619531	4	1.36E+08	D4MIT170	4	99.940854	138171253	1.99514	1.76595	0	2.23E-06	0.0005	0.0455118	SCG
Ppfia2	81148	10	1.06E+08	d10Mit96	10	80.833163	99019575	1.7871	1.59108	0	2.30E-06	0	0	SCG
Vps11	863831	9	44163522	D9MIT285	9	25.81754	40462577	2.24425	2.44449	0	2.31E-06	0	0	SCG
Paip1	220864	13	1.2E+08	D13MIT78	13	76.842169	119618032	0.95352	0.81916	0	2.40E-06	0.0005	0.0455118	Shared
Slit1	439411	19	41723480	D19MIT96	19	21.387917	21916083	0.24251	0.31152	0	2.40E-06	0	0	SCG
unassigned	863747	9	44065088	D9MIT247	9	25.36975	36940492	1.40431	1.54713	0	2.42E-06	0.0005	0.0455118	SCG
Cep290	80610	10	1E+08	d10Mit96	10	80.833163	99019575	2.18138	1.61332	0	2.45E-06	0	0	SCG
Cadps	262224	14	13538169	D14MIT98	14	6.470372	17356225	0.66773	0.74903	0	2.53E-06	0.0005	0.0455118	SCG
Dpy19l3	763462	7	36493568	D7MIT228	7	28.11811	47279833	1.64483	1.34425	0	2.53E-06	0	0	Shared
Slamf9	26946	1	1.74E+08	01.183.109	1	96.118477	183202456	0.71405	0.88165	0	2.53E-06	0	0	SCG
unassigned	619485	4	1.36E+08	04.133.005	4	97.642221	133288839	1.42967	1.25264	0	2.54E-06	0.0005	0.0455118	SCG
Sacm1l	856980	9	1.23E+08	D9Mit18	9	96.97845	120198563	2.53337	2.231	0	2.61E-06	0	0	SCG
Gbe1	330640	16	70433797	16.065.697	16	59.663761	65778985	0.94418	0.81554	0	2.63E-06	0	0	SCG
Tgfbr3	671980	5	1.08E+08	D5MIT239	5	66.11023	107842159	1.44832	1.27933	0	2.63E-06	0	0	SCG
3110002H16Rik	388997	18	12334653	D18MIT222	18	9.2	14746018	0.79571	0.59647	0	2.66E-06	0.0005	0.0455118	SCG
Larp7	562436	3	1.27E+08	D3MIT315	3	89.68246	115544553	0.15199	0.12586	0	2.69E-06	0.0005	0.0455118	Shared
Poli	414835	18	70688356	D18MIT186	18	54.44325	72180072	0.19649	0.28245	0	2.70E-06	0	0	Shared
Bag3	754893	7	1.36E+08	07.122.234	7	82.95546	129586366	1.05503	1.17949	0	2.72E-06	0.0005	0.0455118	SCG
Oprm1	85838	10	3496546	rs13480474	10	1.8	4403267	2.58224	1.99079	0	2.75E-06	0	0	SCG
Parvb	294802	15	84113215	15.090.122	15	63.155859	90124664	1.51845	1.79912	0	2.78E-06	0.0005	0.0455118	SCG
Tjp1	768213	7	72457710	07.056.455	7	36.40088	63842351	0.98487	1.13331	0	2.82E-06	0.0005	0.0455118	SCG
Chd4	704137	6	1.25E+08	D6MIT194	6	87.57626	128115503	0.86311	0.95649	0	2.86E-06	0	0	SCG
Tmem2	422477	19	21904301	D19MIT96	19	21.387917	21916083	0.8411	1.00785	0	2.86E-06	0.0005	0.0455118	Shared
unassigned	439031	19	40627950	19.046.444	19	55.551107	46465179	0.90623	0.75405	0	2.87E-06	0	0	SCG
unassigned	574429	4	43114751	d4mit238	4	33.232784	45243003	2.01072	1.5812	0	2.95E-06	0	0	SCG
unassigned	274726	14	76130283	14.067.129	14	52.822413	68793727	3.17719	3.64331	0	2.98E-06	0	0	Shared
Cacna2d1	628811	5	15860404	D5MIT294	5	15.58331	20863135	0.99763	1.13008	0	3.01E-06	0	0	SCG
Mlh1	878092	9	1.11E+08	D9MIT212	9	79.88305	108543415	1.41191	1.05089	0	3.03E-06	0	0	SCG
Ppib	844723	9	65914234	D9MIT248	9	44.87553	58210366	1.00904	1.07834	0	3.07E-06	0	0	SCG
unassigned	274259	14	73602702	14.042.462	14	41.894152	44159798	1.14426	1.29367	0	3.07E-06	0	0	SCG
B230118H07Rik	497000	2	1.01E+08	D2MIT75	2	46.41465	80424883	2.49507	2.94044	0	3.12E-06	0	0	Shared
unassigned	622570	4	1.49E+08	D4MIT232	4	109.11827	144647559	1.33512	1.2181	0	3.13E-06	0.0005	0.0455118	SCG
Bmpr1a	266523	14	35242854	14.027.409	14	32.019685	29395320	1.90473	1.70026	0	3.15E-06	0	0	SCG
Atpbd4	499475	2	1.14E+08	D2Mit274	2	62.95823	114283330	0.92364	0.79467	0	3.24E-06	0.0005	0.0455118	Shared

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Evi5l	787482	8	4202970	D8MIT155	8	3.1	4976602	2.17783	1.9483	0	3.26E-06	0.0005	0.0455118	SCG
Pias3	531793	3	96504153	03.106.773	3	82.33049	106447862	0.1287	0.18326	0	3.28E-06	0	0	Shared
Wasf2	590709	4	1.33E+08	04.133.005	4	97.642221	133288839	2.35067	2.02112	0	3.32E-06	0	0	SCG
Ccnd2	728699	6	1.27E+08	D6MIT194	6	87.57626	128115503	1.44931	1.24036	0	3.38E-06	0.0005	0.0455118	Shared
Npc1	404674	18	12353519	D18MIT222	18	9.2	14746018	1.0364	0.91142	0	3.44E-06	0.0005	0.0455118	SCG
Snx29	320475	16	11738402	RS4164914	16	9.413247	15586358	1.58547	1.3991	0	3.49E-06	0	0	Shared
unassigned	675274	5	1.22E+08	D5MIT425	5	93.27848	120330450	1.1482	1.02789	0	3.53E-06	0	0	SCG
Stip1	432714	19	7110003	19.009.231	19	7.749799	9238445	1.39752	1.27599	0	3.55E-06	0.0005	0.0455118	SCG
Flii	145590	11	60538669	D11MIT320	11	39.87138	70766870	0.54975	0.48757	0	3.58E-06	0.0005	0.0455118	SCG
Psg16	734483	7	17683528	07.013.915	7	8.7	15600169	0.54443	0.46772	0	3.61E-06	0.0005	0.0455118	SCG
Nxf2	933062	X	1.31E+08	RS29300656	X	89.33472	153071529	0.54975	0.65857	2.18386	3.62E-06	0.0005	0.0455118	SCG
Gm6251	66126	10	19928698	D10Mit123	10	3.021254	9952319	0.02945	0.03827	0	3.66E-06	0.0005	0.0455118	SCG
Tmem70	1824	1	16667913	rs13475769	1	16.197578	24958696	0.24324	0.18159	0	3.66E-06	0	0	SCG
Tbl3	372815	17	24837334	D17Mit213	17	12.20714	16752157	2.39207	2.63929	0	3.73E-06	0.0005	0.0455118	SCG
Supt3h	360194	17	45173675	17.034.150	17	51.1372	34678889	1.77755	1.58517	0	3.76E-06	0.0005	0.0455118	SCG
Dpp8	844342	9	64891494	D9MIT107	9	53.50038	73315075	1.02399	1.15102	0	3.81E-06	0	0	SCG
unassigned	287222	15	39294174	D15MIT143	15	21.458543	51985414	1.49116	1.73946	0	3.83E-06	0	0	Shared
Akap6	169751	12	54012868	D12Mit2	12	26.674029	42747379	0.59007	0.55374	0	3.87E-06	0	0	SCG
Tmem18	166586	12	31275827	D12MIT60	12	21.025423	35474805	0.15519	0.17713	0	4.01E-06	0.0005	0.0455118	SCG
unassigned	839532	9	44141070	D9MIT285	9	25.81754	40462577	0.47844	0.54723	0	4.01E-06	0	0	SCG
Myo1c	122619	11	75481922	D11MIT289	11	59.90287	94741466	1.26004	1.12934	0	4.03E-06	0	0	SCG
Qtrt1	835219	9	21221509	09.014.560	9	12.99047	14614051	0.9613	1.18708	0	4.04E-06	0.0005	0.0455118	Shared
Igf1r	743183	7	75329648	D7Mit232	7	35.20811	59868792	1.12788	1.30705	0	4.05E-06	0	0	SCG
Syngr2	133437	11	1.18E+08	D11MIT214	11	79.65651	114991785	0.57794	0.62209	0	4.06E-06	0.0005	0.0455118	SCG
Sema5a	285804	15	32404140	D15MIT103	15	31.660276	63605769	0.2409	0.34168	0	4.11E-06	0.0005	0.0455118	Shared
unassigned	622655	4	1.49E+08	D4MIT232	4	109.11827	144647559	1.33902	1.23398	0	4.12E-06	0.0005	0.0455118	SCG
Gpc4	925233	X	49409842	DXMit119	X	34.986222	69655585	0.73475	0.77627	0.98954	4.19E-06	0	0	SCG
St6galnac3	567192	3	1.53E+08	D3Mit19	3	140.73124	157273675	1.32248	1.1614	0	4.25E-06	0.0005	0.0455118	SCG
Tnxb	358317	17	34846328	17.034.150	17	51.1372	34678889	1.41626	1.25309	0	4.28E-06	0.0005	0.0455118	SCG
Gm13152	594122	4	1.47E+08	D4MIT232	4	109.11827	144647559	0.85771	1.1064	0	4.32E-06	0.0005	0.0455118	Shared
Serpinb2	16866	1	1.09E+08	RS50560599	1	67.504828	116681037	1.69432	2.17726	0	4.42E-06	0.0005	0.0455118	SCG
Pnrc2	619339	4	1.35E+08	D4MIT170	4	99.940854	138171253	0.76995	0.70097	0	4.43E-06	0.0005	0.0455118	SCG
Kcnma1	264022	14	24324416	14.027.409	14	32.019685	29395320	1.80037	1.59772	0	4.45E-06	0.0005	0.0455118	SCG
Robo3	862482	9	37236669	D9MIT2	9	25.36976	37202486	1.20441	1.49031	0	4.48E-06	0.0005	0.0455118	SCG
Heatr1	202750	13	12514330	13.013.314	13	8.3	13614141	0.24657	0.32652	0	4.50E-06	0.0005	0.0455118	Shared
Tspan18	496119	2	93152152	D2MIT75	2	46.41465	80424883	0.27924	0.21045	0	4.50E-06	0	0	SCG
Gbf1	427734	19	46339349	D19MIT13	19	37.094077	32713513	1.18881	1.0821	0	4.54E-06	0	0	SCG
Nars	413504	18	64659431	18.063.800	18	48.99442	63834285	0.33843	0.38391	0	4.58E-06	0.0005	0.0455118	SCG
unassigned	20586	1	1.37E+08	RS50560599	1	67.504828	116681037	1.86057	1.77555	0	4.58E-06	0.0005	0.0455118	SCG
Bco2	865388	9	50358809	D9MIT250	9	5.2	8393623	1.56097	1.16623	0	4.62E-06	0	0	SCG
unassigned	54418	1	1.55E+08	D1Mit102	1	80.039245	149096650	1.04799	0.94562	0	4.75E-06	0.0005	0.0455118	SCG
unassigned	296499	15	91586444	15.090.122	15	63.155859	90124664	1.14411	1.33834	0	4.76E-06	0.0005	0.0455118	SCG

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
5930434B04Rik	448707	2	26869626	D2Mit297	2	25.96707	42461006	0.94045	1.0795	0	4.78E-06	0.0005	0.0455118	SCG
Hcrtr1	617714	4	1.3E+08	D4Mit203	4	89.732314	129249262	1.92547	1.6522	0	4.90E-06	0.0005	0.0455118	SCG
Slc25a33	622847	4	1.49E+08	D4MIT42	4	117.10129	150944103	2.25004	1.97287	0	4.91E-06	0	0	SCG
Ank2	562257	3	1.27E+08	03.141.220	3	108.244	140945577	0.72186	0.83455	0	5.04E-06	0	0	SCG
Stambp	720179	6	83520330	06.095.876	6	52.18486	95860531	1.17325	1.34581	0	5.06E-06	0.0005	0.0455118	SCG
Ubtf	156805	11	1.02E+08	D11MIT214	11	79.65651	114991785	4.52683	4.07605	0	5.12E-06	0	0	SCG
BC062109	670274	5	1.01E+08	D5MIT239	5	66.11023	107842159	1.42497	1.23972	0	5.15E-06	0	0	SCG
unassigned	134551	11	1.21E+08	D11MIT214	11	79.65651	114991785	1.2337	1.34424	0	5.15E-06	0	0	SCG
unassigned	42560	1	74337914	RS50560599	1	67.504828	116681037	0.96252	1.03856	0	5.22E-06	0.0005	0.0455118	SCG
Ahctf1	60105	1	1.82E+08	01.183.109	1	96.118477	183202456	0.6007	0.48739	0	5.25E-06	0	0	SCG
unassigned	864014	9	44603820	D9MIT2	9	25.36976	37202486	1.67223	1.52156	0	5.32E-06	0	0	Shared
Map3k5	66007	10	19796288	RS29316281	10	22.943971	25167321	0.62773	0.48002	0	5.36E-06	0.0005	0.0455118	Shared
Ankrd46	304096	15	36425642	15.046.034	15	20.554602	46035472	1.11912	0.99267	0	5.37E-06	0	0	SCG
Nfasc	51088	1	1.35E+08	D1MIT1001	1	72.841454	130944135	1.16731	1.28732	0	5.50E-06	0.0005	0.0455118	SCG
Heatr5a	188664	12	52998759	D12MIT285	12	30.221464	55750112	1.41666	1.25108	0	5.51E-06	0	0	SCG
Syt16	173039	12	75098758	D12MIT91	12	43.26798	72843829	4.86065	3.91542	0	5.51E-06	0	0	SCG
B230118H07Rik	496995	2	1.01E+08	RS28322831	2	43.67748	71063776	1.2071	1.0364	0	5.71E-06	0.0005	0.0455118	SCG
Zc3h15	459253	2	83502401	RS27416022	2	74.76293	93628229	2.15594	1.72082	0	5.73E-06	0	0	Shared
Leprotl1	815867	8	35200783	D8Mit191	8	23.020658	36243839	1.56512	1.43107	0	5.78E-06	0	0	SCG
Pign	47681	1	1.08E+08	D1MIT1001	1	72.841454	130944135	0.06268	0.05512	0	5.80E-06	0.0005	0.0455118	SCG
Pim1	356539	17	29628134	17.034.150	17	51.1372	34678889	3.29374	2.60191	0	5.94E-06	0.0005	0.0455118	SCG
unassigned	313070	15	82990410	15.088.295	15	61.334066	88297664	0.97595	1.05181	0	5.94E-06	0.0005	0.0455118	SCG
unassigned	214141	13	77064888	RS30012306	13	43.697138	70428413	0.34936	0.47049	0	5.95E-06	0.0005	0.0455118	Shared
Syngr2	133432	11	1.18E+08	D11MIT214	11	79.65651	114991785	1.38593	1.13249	0	5.98E-06	0	0	Shared
Lynx1	310341	15	74582306	15.090.122	15	63.155859	90124664	1.05878	1.2068	0	6.22E-06	0	0	SCG
Bmp1	273478	14	70894575	D14MIT39	14	54.529907	69166099	1.45404	1.2176	0	6.23E-06	0.0005	0.0455118	Shared
2900052N01Rik	840278	9	46734648	D9MIT248	9	44.87553	58210366	0.33067	0.45488	0	6.27E-06	0.0005	0.0455118	SCG
Prdx6	56229	1	1.63E+08	D1MIT507	1	89.469987	166978064	0.08068	0.11241	0	6.32E-06	0	0	Shared
Epb4.1l4b	604755	4	57076124	D4MIT164	4	42.389612	59415112	0.41064	0.52317	0	6.45E-06	0	0	SCG
Ptprn2	181826	12	1.18E+08	D12MIT194	12	54.38605	92525886	1.46732	1.60278	0	6.54E-06	0.0005	0.0455118	SCG
unassigned	191615	12	73185521	D12MIT91	12	43.26798	72843829	1.07029	0.81063	0	6.66E-06	0.0005	0.0455118	Shared
Dctn1	695796	6	83140200	D6MIT328	6	75.24789	112729344	1.12117	1.20618	0	6.83E-06	0.0005	0.0455118	SCG
unassigned	413134	18	62666768	D18Mit123	18	38.31055	56130259	0.86678	1.02305	0	6.95E-06	0.0005	0.0455118	SCG
Brwd2	755063	7	1.37E+08	d7mit109	7	91.14939	143706746	2.27226	2.58426	0	6.98E-06	0.0005	0.0455118	SCG
Ndrg3	508837	2	1.57E+08	D2MIT411	2	112.97352	159412163	0.68172	0.77019	0	7.04E-06	0	0	SCG
unassigned	541962	3	1.52E+08	D3Mit19	3	140.73124	157273675	1.06151	1.2518	0	7.04E-06	0.0005	0.0455118	Shared
Uqcrb	232584	13	67003676	13.061.624	13	39.879786	61715738	1.25404	1.18023	0	7.20E-06	0	0	SCG
Nfs1	508617	2	1.56E+08	D2MIT423	2	107.80753	148685450	2.14045	1.93362	0	7.27E-06	0.0005	0.0455118	Shared
Slc25a17	312491	15	81157474	D15MIT103	15	31.660276	63605769	1.18786	1.31776	0	7.36E-06	0.0005	0.0455118	SCG
unassigned	124608	11	82770796	11.072.405	11	39.87138	72402307	1.0462	0.89264	0	7.51E-06	0.0005	0.0455118	SCG
Dhx16	358870	17	36020973	17.013.500	17	8.4	13900467	1.89341	2.26106	0	7.62E-06	0	0	SCG
Ppp2r1b	841207	9	50678170	D9MIT285	9	25.81754	40462577	1.03873	0.93342	0	7.68E-06	0.0005	0.0455118	SCG

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Ppm1k	717209	6	57475086	06.095.876	6	52.18486	95860531	0.58238	0.52911	0	7.87E-06	0.0005	0.0455118	SCG
Nudt4	102132	10	95010571	d10Mit96	10	80.833163	99019575	1.70281	1.90392	0	7.91E-06	0	0	SCG
Tmem66	792769	8	35233281	D8MIT94	8	19.424222	32452130	0.60328	0.69308	0	8.10E-06	0	0	SCG
unassigned	622576	4	1.49E+08	D4MIT232	4	109.11827	144647559	0.82694	0.9274	0	8.12E-06	0.0005	0.0455118	SCG
Sdc2	285908	15	32953570	15.028.723	15	14.881134	28708166	2.38066	2.1554	0	8.20E-06	0	0	SCG
Utrn	87533	10	12485069	D10Mit123	10	3.021254	9952319	0.5924	0.72889	0	8.90E-06	0.0005	0.0455118	SCG
unassigned	800348	8	85821952	D8MIT346	8	54.673156	85454038	1.04654	1.13577	0	8.95E-06	0.0005	0.0455118	SCG
Zfp619	738321	7	46790755	D7Mit232	7	35.20811	59868792	0.99111	1.0308	0	9.00E-06	0.0005	0.0455118	SCG
unassigned	687898	6	34338451	d6mit123	6	39.56321	56801586	3.2344	2.73494	0	9.47E-06	0	0	Shared
H2-D1	358661	17	35403834	D17MIT231	17	38.54838	34672294	2.9372	3.11737	0	9.88E-06	0.0005	0.0455118	SCG
unassigned	358040	17	34326274	D17MIT51	17	53.34361	43641790	0.95154	1.02844	0	9.90E-06	0	0	SCG
Myo1e	845737	9	70174953	D9MIT248	9	44.87553	58210366	1.21047	1.38536	0	1.10E-05	0.0005	0.0455118	SCG
Gm9640	671513	5	1.06E+08	D5MIT239	5	66.11023	107842159	0.21338	0.37851	0	1.11E-05	0	0	SCG
Parp8	241515	13	1.18E+08	d13mit151	13	74.514424	116341977	0.78705	0.90058	0	1.13E-05	0.0005	0.0455118	Shared
unassigned	897406	17	35565124	D17MIT231	17	38.54838	34672294	0.4956	0.57361	0	1.25E-05	0.0005	0.0455118	SCG
Cpne5	374100	17	29296077	17.034.150	17	51.1372	34678889	1.27312	1.12186	0	1.34E-05	0.0005	0.0455118	SCG
Rit2	407412	18	31313381	D18Mit68	18	14.5139	21594126	1.48486	1.38824	0	1.41E-05	0.0005	0.0455118	SCG
Pms2	653260	5	1.45E+08	05.132.979	5	112.26584	133170167	0.97369	1.09385	0	1.44E-05	0.0005	0.0455118	SCG
Ccnb2	869989	9	70255527	D9MIT336	9	49.6331	65425671	0.20042	0.15376	0	1.50E-05	0	0	SCG
Tlr1	664514	5	65344823	d5mit233	5	46.33401	53088465	1.56807	1.64471	0	1.63E-05	0	0	SCG
unassigned	412638	18	60859627	D18Mit123	18	38.31055	56130259	2.21501	2.39134	0	1.89E-05	0.0005	0.0455118	SCG
unassigned	510107	2	1.63E+08	02.168.990	2	151.40532	169124295	1.39968	1.5301	0	2.87E-05	0.0005	0.0455118	SCG
Ahctf1	60106	1	1.82E+08	01.183.109	1	96.118477	183202456	0.65655	0.54559	0	3.60E-05	0	0	SCG
Dpagt1	839527	9	44137082	D9MIT250	9	5.2	8393623	2.21343	2.01651	0	5.07E-05	0.0005	0.0455118	SCG

APPENDIX C: TRANS-sQTL

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	276765	14	93593508	07.056.455	7	36.40088	63842351	1.91295	1.22501	0	2.79E-21	0	0	SCG
Gigyf1	651736	5	137961256	D4MIT232	4	109.11827	144647559	2.88773	2.0161	0	2.19E-19	0	0	Shared
Snrpd2	85003	10	127449225	07.013.915	7	8.7	15600169	0.02368	0.08157	0	3.52E-18	0	0	Shared
Gabra3	927240	X	69901352	D2MIT148	2	167.77989	178535250	0.2376	0.4547	0	4.08E-17	0	0	SCG
unassigned	859773	9	21793462	D17MIT180	17	63.0586	51571276	1.6804	2.61377	0	4.69E-15	0	0	Shared
unassigned	276767	14	93594843	D7MIT228	7	28.11811	47279833	2.00026	1.32526	0	9.48E-14	0	0	SCG
Scyl1	432135	19	5759273	D8MIT68	8	37.448528	59469763	0.98372	1.17867	0	2.22E-13	0	0	SCG
Col5a3	859274	9	20619310	D7MIT228	7	28.11811	47279833	1.6349	2.19098	0	5.08E-13	0	0	CB
unassigned	866561	9	54895932	D4MIT42	4	117.10129	150944103	0.8223	1.18868	0	1.50E-12	0	0	CB
unassigned	432061	19	5661566	02.168.990	2	151.40532	169124295	0.44776	0.65544	0	3.36E-12	0	0	CB
unassigned	276766	14	93594317	D7MIT248	7	39.99047	80656343	0.36163	0.47864	0	2.67E-11	0	0	SCG
Rnf19a	304031	15	36182786	D4MIT308	4	84.360247	123838543	2.34696	1.85228	0	4.80E-11	0	0	CB
Snrpd2	85002	10	127449157	07.013.915	7	8.7	15600169	1.03129	0.99272	0	6.60E-11	0	0	CB
Snrpd2	85003	10	127449225	07.013.915	7	8.7	15600169	0.03001	0.08708	0	1.70E-10	0	0	Shared
Mbtd1	126962	11	93793534	15.028.723	15	14.881134	28708166	0.86142	1.0406	0	2.01E-10	0	0	CB
unassigned	76858	10	80792701	19.000.325	19	0.2	325000	0.65336	0.94174	0	2.55E-10	0	0	CB
Gabra3	927233	X	69798038	D2MIT113	2	164.04086	173180172	0.64936	0.92583	0	5.11E-10	0	0	SCG
Tdrd1	429926	19	56916725	D17MIT76	17	95.2661	86033231	0.55914	0.76991	0	7.27E-10	0	0	CB
Gabra3	927221	X	69704936	D2MIT148	2	167.77989	178535250	1.15122	0.79618	0	8.69E-10	0	0	SCG
RP23-244H7.9	472320	2	153758444	19.046.444	19	55.551107	46465179	12.11525	15.23338	0	8.90E-10	0	0	CB
Cndp1	417509	18	84809683	D13Mit207	13	8.688726	16526195	2.42719	3.35617	0	1.07E-09	0	0	CB
Eps8l3	534147	3	107694614	19.000.325	19	0.2	325000	1.34805	1.96317	0	1.72E-09	0	0	CB
Scn11a	879809	9	119678883	D14Mit194	14	66.469555	94235479	3.70701	4.99808	0	1.82E-09	0	0	CB
Tnrc18	680284	5	143527799	D10Mit14	10	93.102537	118098315	0.69801	0.89392	0	2.09E-09	0	0	CB
Mbtd1	126961	11	93793159	15.028.723	15	14.881134	28708166	1.40978	1.68686	0	2.14E-09	0	0	CB
Ftl1	588498	4	125181716	D7MIT228	7	28.11811	47279833	0.52097	0.60986	0	2.49E-09	0	0	CB
Tlk2	130488	11	105045552	D4MIT232	4	109.11827	144647559	1.0292	1.27385	0	7.20E-09	0	0	SCG
Col14a1	289042	15	55277721	D7MIT228	7	28.11811	47279833	0.38465	0.55055	0	1.60E-08	0	0	CB
unassigned	583449	4	102268480	09.046.588	9	34.49446	46645088	1.01207	0.89703	0	1.85E-08	0	0	CB
Slc6a3	213494	13	73710263	D1MIT507	1	89.469987	166978064	1.58476	1.94468	0	2.67E-08	0	0	SCG
unassigned	842536	9	56984159	d6mit366	6	77.49561	115192871	0.23538	0.30178	0	2.92E-08	0	0	CB
unassigned	927217	X	69680401	D2MIT148	2	167.77989	178535250	1.69626	1.34728	0	3.86E-08	0	0	SCG
Olfr1013	459639	2	85610160	08.010.585	8	4.520052	10585028	8.24405	4.28856	0	6.74E-08	0	0	SCG
unassigned	779793	7	134005082	RS28322831	2	43.67748	71063776	0.88291	0.74105	0	7.80E-08	0	0	CB
A2m	703312	6	121611495	06.057.998	6	39.56321	58018416	1.08128	0.92024	0	7.97E-08	0	0	CB
Arhgap25	721101	6	87446224	D2MIT81	2	18.06443	24644623	0.83674	1.14822	0	8.09E-08	0	0	CB
unassigned	180099	12	110692618	RS28322831	2	43.67748	71063776	0.47044	0.61787	0	9.11E-08	0	0	SCG
Jak1	611305	4	100829563	D5MIT425	5	93.27848	120330450	0.87282	0.79574	0	9.77E-08	0	0	SCG
Chm	931832	X	110183188	rs13483805	X	31.433568	87440160	0.9009	1.00344	1.13556	1.04E-07	0	0	CB
Creb3l1	495807	2	91833441	D15MIT15	15	83.154738	102823545	1.34236	1.7501	0	1.19E-07	0	0	CB
Carf	8457	1	60165159	D3MIT256	3	103.27598	136014535	0.76588	0.87923	0	1.32E-07	0	0	CB

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Gabra3	927223	X	69721565	D2MIT148	2	167.77989	178535250	1.16115	1.6256	0	1.40E-07	0	0	SCG
Inpp5e	483308	2	26257233	09.046.588	9	34.49446	46645088	2.13038	2.74272	0	1.43E-07	0	0	SCG
Brca1	156428	11	101391105	d6mit366	6	77.49561	115192871	1.17711	1.6983	0	1.51E-07	0	0	CB
unassigned	562847	3	129389312	D9MIT151	9	100.11619	121386992	1.3615	1.79571	0	1.52E-07	0	0	Shared
Rab3il1	420312	19	10104643	05.132.979	5	112.26584	133170167	1.36378	1.57823	0	1.80E-07	0	0	SCG
Mcm8	468205	2	132664454	17.013.500	17	8.4	13900467	0.88555	1.14367	0	2.00E-07	0	0	SCG
unassigned	324913	16	31933964	D5MIT10	5	65.80535	104668024	0.37868	0.47157	0	2.33E-07	0	0	CB
Col23a1	116497	11	51386260	06.016.672	6	10.4	16672000	0.47385	0.34445	0	2.47E-07	0	0	SCG
Gigyf2	13870	1	89333391	D4MIT308	4	84.360247	123838543	2.53982	2.94672	0	2.63E-07	0	0	CB
Ttc39c	389150	18	12883449	D3Mit19	3	140.73124	157273675	2.52354	2.2863	0	2.69E-07	0	0	SCG
Gpr98	234919	13	81718154	18.063.800	18	48.99442	63834285	1.80017	1.28139	0	2.82E-07	0	0	SCG
Phex	935601	X	153612157	D2MIT81	2	18.06443	24644623	1.53151	0.95903	0	2.87E-07	0.0005	0.0418557	CB
4931406P16Rik	763096	7	35027284	01.183.109	1	96.118477	183202456	1.65797	1.86678	0	3.12E-07	0	0	SCG
Col4a3	12799	1	82638208	D3MIT49	3	73.77602	89036582	2.66322	3.93316	0	3.12E-07	0	0	CB
Glul	23125	1	155754172	D11MIT51	11	25.39412	36205252	0.8464	0.71716	0	3.33E-07	0	0	SCG
Hacl1	265977	14	32439605	D11MIT186	11	23.608	35049231	1.38203	2.1299	0	3.54E-07	0	0	SCG
Dyx1c1	846433	9	72816911	RS30267686	18	60.34946	81658329	1.48625	1.16433	0	3.60E-07	0	0	CB
Ank	284953	15	27524252	D17MIT51	17	53.34361	43641790	0.18124	0.14841	0	3.65E-07	0	0	SCG
Flt3	681282	5	148166584	D9Mit18	9	96.97845	120198563	1.4112	1.20195	0	3.72E-07	0	0	CB
Cyp2j5	610438	4	96297458	D9MIT2	9	25.36976	37202486	3.25386	2.40537	0	3.78E-07	0	0	SCG
Cnot6l	669541	5	96523182	D4MIT232	4	109.11827	144647559	1.08892	1.19899	0	3.80E-07	0	0	CB
Micall1	311880	15	78966068	D11MIT186	11	23.608	35049231	0.48942	0.39429	0	3.97E-07	0.0005	0.0455118	SCG
unassigned	899933	5	38651820	RS30267686	18	60.34946	81658329	0.64947	0.76125	0	4.18E-07	0	0	CB
Amigo1	534204	3	107989537	D8MIT47	8	79.109749	109368069	1.16318	1.38964	0	4.30E-07	0	0	CB
Capn9	809513	8	127118540	D19Mit68	19	0.200001	3645155	1.5963	2.07794	0	4.36E-07	0	0	SCG
Eefsec	721433	6	88305536	rs13475894	1	45.460824	63625006	1.13413	0.99232	0	4.76E-07	0	0	SCG
Abcb11	491404	2	69112057	D9MIT24	9	73.18313	103132731	0.54245	0.68985	0	4.85E-07	0	0	SCG
Cep192	399016	18	68009800	d7mit109	7	91.14939	143706746	0.54766	0.70113	0	5.30E-07	0	0	SCG
unassigned	535545	3	118265349	19.000.325	19	0.2	325000	2.30455	3.67336	0	5.76E-07	0.0005	0.0455118	Shared
unassigned	181354	12	114309697	D13Mit207	13	8.688726	16526195	1.14295	1.25143	0	6.28E-07	0	0	CB
unassigned	840767	9	48923300	D2MIT1	2	2.4	3803361	1.41251	1.13058	0	6.61E-07	0	0	CB
Gigyf1	651736	5	137961256	D4MIT232	4	109.11827	144647559	1.46703	1.22635	0	6.96E-07	0.0005	0.0418557	Shared
Atp12a	251515	14	56998862	D3MIT147	3	137.32386	148408373	3.20741	2.56031	0	7.01E-07	0	0	CB
unassigned	345334	16	60205242	04.013.290	4	8.3	13290000	0.60223	0.48186	0	7.04E-07	0	0	CB
Lhx8	567497	3	153984602	D2MIT61	2	35.12792	60528325	1.4798	1.25923	0	7.07E-07	0	0	SCG
Btbd16	755317	7	137933772	04.098.998	4	75.012985	99172673	1.08762	0.89292	0	7.26E-07	0	0	CB
unassigned	12877	1	82743230	D1Mit102	1	80.039245	149096650	1.31182	1.44353	0	7.31E-07	0	0	CB
Tcf25	809087	8	125906433	D11MIT186	11	23.608	35049231	1.65005	1.54152	0	7.65E-07	0	0	SCG
Rims2	287249	15	39398506	RS29347557	10	5.696346	12661713	0.60792	0.83862	0	7.67E-07	0	0	SCG
Gabra5	767263	7	64744228	D18MIT194	18	30.70688	43820481	1.275	1.12859	0	7.74E-07	0.0005	0.0418557	CB
Col17a1	441110	19	47723257	D2Mit297	2	25.96707	42461006	0.74887	0.59801	0	8.10E-07	0	0	CB

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Wdhd1	268092	14	47867771	09.046.588	9	34.49446	46645088	1.2495	0.89603	0	8.16E-07	0	0	SCG
Daxx	357825	17	34047395	D9MIT107	9	53.50038	73315075	1.09472	0.93016	0	8.32E-07	0.0005	0.0455118	SCG
unassigned	562847	3	129389312	D9MIT201	9	91.42427	117345284	1.45285	1.78763	0	8.55E-07	0	0	Shared
Dusp13	263685	14	22563991	D2MIT285	2	110.63716	152683037	1.72214	2.08697	0	8.61E-07	0	0	CB
Kif20b	425154	19	35024713	RS30160288	3	119.38247	125981675	2.1501	1.52943	0	8.85E-07	0	0	SCG
2610204M08Rik	181189	12	113853106	12.007.977	12	5	7957798	3.83849	3.33406	0	9.16E-07	0.0005	0.0418557	CB
Dysf	696200	6	84142920	14.027.409	14	32.019685	29395320	0.77384	0.59281	0	9.28E-07	0	0	CB
unassigned	148799	11	72354054	RS32210051	7	61.08266	99669474	0.9196	0.69723	0	9.42E-07	0	0	SCG
Xlr3a	927303	X	70336214	DXMit79	X	50.813632	127398406	1.85161	2.15798	3.1237	9.43E-07	0	0	CB
unassigned	616731	4	125862184	D7Mit232	7	35.20811	59868792	3.05495	2.71288	0	9.51E-07	0.0005	0.0418557	CB
Krt2	317951	15	101644378	D8MIT242	8	71.218548	104283476	0.79651	0.97489	0	9.57E-07	0	0	CB
Gsr	792629	8	34799818	D2Mit274	2	62.95823	114283330	1.18705	1.00097	0	9.60E-07	0.0005	0.0418557	CB
Nampt	167060	12	33515143	D5MIT95	5	98.81753	125309605	0.3394	0.28296	0	1.00E-06	0	0	CB
unassigned	641460	5	92832683	D9MIT71	9	37.69738	50007830	0.42172	0.30618	0	1.00E-06	0.0005	0.0455118	SCG
Hnrnpf	702515	6	117867521	RS50560599	1	67.504828	116681037	0.27547	0.2239	0	1.04E-06	0	0	SCG
unassigned	292555	15	76200416	13.043.962	13	29.583286	44046397	0.85234	1.00881	0	1.09E-06	0	0	SCG
unassigned	761790	7	29757516	D7MIT248	7	39.99047	80656343	0.89917	1.04987	0	1.09E-06	0.0005	0.0418557	CB
Slc25a26	698557	6	94553590	D7MIT350	7	57.28732	90734599	0.23216	0.30166	0	1.11E-06	0	0	SCG
unassigned	793786	8	42341340	RS30160288	3	119.38247	125981675	1.84459	1.59175	0	1.12E-06	0	0	SCG
Serpine1	678845	5	137539351	D19MIT96	19	21.387917	21916083	0.36376	0.4515	0	1.16E-06	0	0	CB
Fbxo36	13196	1	84836479	D5MIT10	5	65.80535	104668024	1.13345	1.32134	0	1.18E-06	0.0005	0.0418557	CB
Slc6a7	412755	18	61169103	RS46745265	10	65.869576	69258223	2.33741	2.82848	0	1.18E-06	0	0	SCG
Lrp1b	486912	2	41366928	D5MIT239	5	66.11023	107842159	0.75386	0.64107	0	1.19E-06	0	0	CB
unassigned	357343	17	32193163	D4MIT308	4	84.360247	123838543	1.95679	1.7504	0	1.22E-06	0.0005	0.0418557	CB
Tcea2	479044	2	181420497	D2Mit274	2	62.95823	114283330	1.43806	1.30079	0	1.23E-06	0.0005	0.0418557	CB
Zfp451	35486	1	33836748	09.046.588	9	34.49446	46645088	1.9993	1.80391	0	1.24E-06	0	0	CB
unassigned	477100	2	172840695	D10Mit123	10	3.021254	9952319	0.37367	0.30731	0	1.34E-06	0.0005	0.0455118	SCG
Hydin	806344	8	113122869	D8MIT292	8	21.904548	35848067	1.52146	1.99298	0	1.35E-06	0	0	SCG
Parvg	294837	15	84171324	D13Mit207	13	8.688726	16526195	1.33025	1.03042	0	1.37E-06	0	0	SCG
Eapa2	714782	6	42539702	RS4187006	16	43.579253	51575793	0.47613	0.37389	0	1.39E-06	0.0005	0.0418557	CB
Sipa1l3	762046	7	30133340	D15MIT103	15	31.660276	63605769	1.06714	0.91912	0	1.39E-06	0	0	SCG
unassigned	379786	17	56248081	rs13483805	X	31.433568	87440160	0.53278	0.52688	1.04164	1.41E-06	0.0005	0.0455118	SCG
unassigned	61414	1	188454668	D4MIT170	4	99.940854	138171253	0.80174	0.92943	0	1.46E-06	0	0	SCG
Mlxipl	651174	5	135613820	D2MIT285	2	110.63716	152683037	0.22446	0.16852	0	1.53E-06	0	0	SCG
Slamf6	26698	1	173872766	09.079.053	9	64.60162	79115123	2.16423	1.72067	0	1.55E-06	0	0	CB
Myo3a	447533	2	22219202	D1Mit102	1	80.039245	149096650	1.65084	2.20541	0	1.56E-06	0	0	CB
Ppfibp2	750241	7	114873359	16.010.089	16	7.349459	10175515	1.77651	1.98869	0	1.56E-06	0.0005	0.0418557	CB
Notch4	694143	6	68201951	D11MIT214	11	79.65651	114991785	0.87772	1.20141	0	1.60E-06	0	0	CB
Ftl1	588499	4	125182152	D7MIT228	7	28.11811	47279833	1.74904	1.59818	0	1.62E-06	0	0	SCG
Gata4	271753	14	63819213	D2MIT423	2	107.80753	148685450	0.45927	0.38795	0	1.66E-06	0.0005	0.0455118	SCG
unassigned	260104	14	119583607	D1MIT1001	1	72.841454	130944135	0.99932	1.28589	0	1.66E-06	0.0005	0.0455118	SCG

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Pik3r5	120263	11	68309792	06.095.876	6	52.18486	95860531	1.06832	0.81469	0	1.69E-06	0	0	CB
Top3a	145613	11	60572807	D9MIT336	9	49.6331	65425671	1.7096	2.02468	0	1.75E-06	0.0005	0.0418557	CB
Ephb3	322641	16	21219145	D3MIT49	3	73.77602	89036582	1.10177	1.25578	0	1.77E-06	0.0005	0.0455118	SCG
unassigned	234091	13	74469111	15.046.034	15	20.554602	46035472	1.31151	1.25869	0	1.77E-06	0	0	SCG
Oc90	308648	15	65715383	RS36353338	7	66.26522	112706514	1.04241	0.77796	0	1.83E-06	0.0005	0.0455118	SCG
unassigned	124716	11	83138263	RS26845852	11	16.78021	24370394	2.34539	2.15006	0	1.83E-06	0	0	CB
Cacna1e	54762	1	156408885	D5MIT95	5	98.81753	125309605	0.77884	0.60813	0	1.87E-06	0	0	SCG
BC107364	556687	3	96237617	D9mit90	9	20.19926	32308040	0.63084	0.55228	0	1.89E-06	0.0005	0.0455118	SCG
unassigned	379951	17	56586901	09.014.560	9	12.99047	14614051	0.70286	0.79126	0	1.90E-06	0	0	SCG
unassigned	80589	10	100004855	D15Mit107	15	49.400965	84216927	1.06503	1.41605	0	1.90E-06	0	0	SCG
Mx1	350604	16	97674387	D15MIT67	15	36.957676	70032295	6.31655	4.96673	0	1.96E-06	0	0	SCG
Myo15	118580	11	60337922	D2MIT81	2	18.06443	24644623	1.54984	1.11566	0	1.97E-06	0	0	CB
Serpina3n	178764	12	105651692	RS30160288	3	119.38247	125981675	1.17135	1.23258	0	2.01E-06	0.0005	0.0455118	SCG
AI182371	485645	2	34941227	RS33477935	X	5.766692	9574173	2.00157	2.37092	3.5434	2.12E-06	0	0	CB
unassigned	689496	6	41091183	RS29347557	10	5.696346	12661713	0.35796	0.42114	0	2.13E-06	0	0	SCG
Nlrp14	750092	7	114340693	RS30267686	18	60.34946	81658329	0.75211	0.57676	0	2.14E-06	0	0	SCG
Tcf12	870375	9	71706685	RS30909511	6	57.9854	83140362	1.01265	0.9072	0	2.18E-06	0	0	CB
unassigned	530378	3	90073502	17.021.019	17	14.36839	21451267	1.49986	1.70211	0	2.25E-06	0	0	CB
unassigned	782427	7	146090249	D5MIT95	5	98.81753	125309605	0.62916	0.54715	0	2.30E-06	0	0	CB
Ethe1	735324	7	25391225	D17Mit93	17	83.28793	74149996	1.68598	1.53882	0	2.36E-06	0.0005	0.0418557	CB
Lrp1b	486864	2	41044334	D17MIT180	17	63.0586	51571276	0.67738	0.58402	0	2.37E-06	0.0005	0.0418557	CB
Gys1	739674	7	52698906	RS28322831	2	43.67748	71063776	1.13755	0.99936	0	2.40E-06	0	0	SCG
Med23	67090	10	24613476	01.136.071	1	77.74879	136151166	1.19098	1.29294	0	2.42E-06	0.0005	0.0418557	CB
Slc23a3	42774	1	75125488	RS31036560	3	62.868	73719554	0.81958	0.99255	0	2.47E-06	0	0	SCG
Dffa	594680	4	148491518	D2MIT411	2	112.97352	159412163	0.95664	1.12183	0	2.48E-06	0.0005	0.0418557	CB
Phka2	919113	X	156992233	D2MIT100	2	54.19426	106377525	2.02284	1.69948	0	2.54E-06	0.0005	0.0418557	CB
Wnt2b	558524	3	104753937	D3Mit151	3	18.63179	31137265	0.37804	0.49274	0	2.58E-06	0.0005	0.0455118	SCG
unassigned	507645	2	152151898	RS29351336	10	22.94397	24605158	0.70675	0.79268	0	2.60E-06	0.0005	0.0418557	CB
Muc6	783255	7	148834492	D11Mit4	11	39.42453	68422759	1.59362	2.02246	0	2.61E-06	0.0005	0.0418557	CB
unassigned	456694	2	69707796	13.061.624	13	39.879786	61715738	2.11953	1.95051	0	2.69E-06	0	0	CB
Plxnd1	726326	6	115915897	RS29347557	10	5.696346	12661713	1.16391	1.02621	0	2.72E-06	0	0	SCG
Spg7	808938	8	125600774	D15Mit107	15	49.400965	84216927	0.92822	1.10092	0	2.73E-06	0	0	SCG
Bahcc1	134132	11	120146906	D9MIT248	9	44.87553	58210366	0.94451	0.76122	0	2.76E-06	0	0	SCG
Jag2	199544	12	114167104	D6MIT67	6	52.18486	97701794	0.36347	0.44624	0	2.77E-06	0.0005	0.0418557	CB
Tmem45b	861423	9	31236141	DXMIT132	X	55.816704	138191357	1.24711	1.29816	1.50149	2.82E-06	0	0	SCG
Slc39a7	375431	17	34165745	04.013.290	4	8.3	13290000	0.76064	0.66213	0	2.83E-06	0.0005	0.0418557	CB
unassigned	14211	1	90221927	D2Mit297	2	25.96707	42461006	1.05081	1.31669	0	2.84E-06	0	0	CB
Zfp609	869122	9	65545306	D6MIT274	6	30.88472	48676564	1.19481	1.08083	0	2.85E-06	0	0	CB
Fbxl13	657154	5	21006299	RS33477935	X	5.766692	9574173	0.95069	1.17999	1.63337	2.87E-06	0.0005	0.0418557	CB
Slc6a5	740690	7	57197148	11.072.405	11	39.87138	72402307	1.25683	1.47652	0	2.93E-06	0	0	CB
Osbpl11	325350	16	33206039	03.141.220	3	108.244	140945577	2.40021	2.20854	0	3.00E-06	0.0005	0.0455118	SCG

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	757952	7	148644435	D2MIT296	2	21.50213	31180075	0.68845	0.63391	0	3.03E-06	0	0	SCG
Plekha8	692085	6	54565210	D13MIT78	13	76.842169	119618032	2.40264	2.06146	0	3.09E-06	0	0	SCG
Tgm2	509151	2	157958177	D17MIT20	17	69.42766	57366870	0.57029	0.69636	0	3.09E-06	0.0005	0.0418557	CB
Cr2	63244	1	196967384	RS33625666	X	9.993891	12120156	0.67492	0.683	0.94996	3.16E-06	0	0	SCG
unassigned	919657	X	160707623	D5MIT239	5	66.11023	107842159	0.70767	0.89449	0	3.16E-06	0.0005	0.0418557	CB
unassigned	831284	8	125729944	RS30160288	3	119.38247	125981675	3.03607	2.76258	0	3.21E-06	0	0	SCG
Parp14	341351	16	35833307	D8MIT211	8	73.005637	105240821	1.0092	1.09774	0	3.53E-06	0.0005	0.0455118	SCG
Ndst4	536747	3	125411038	D15MIT143	15	21.458543	51985414	0.8914	1.08478	0	3.54E-06	0	0	CB
Cyp4f14	375110	17	33053933	D19MIT96	19	21.387917	21916083	0.19861	0.24705	0	3.57E-06	0.0005	0.0418557	CB
Mast3	821163	8	73304094	RS30160288	3	119.38247	125981675	0.58214	0.4912	0	3.58E-06	0.0005	0.0455118	SCG
Tspan11	704859	6	127873584	D13MIT250	13	36.468185	56424004	1.42196	1.17107	0	3.61E-06	0.0005	0.0455118	SCG
Plb1	632044	5	32657693	09.046.588	9	34.49446	46645088	5.34381	4.3916	0	3.65E-06	0	0	CB
unassigned	791140	8	26673724	RS30160288	3	119.38247	125981675	0.76282	0.71308	0	3.66E-06	0.0005	0.0455118	SCG
Crkrs	128288	11	98092298	rs13480474	10	1.8	4403267	1.20201	1.41298	0	3.67E-06	0.0005	0.0455118	SCG
Nr5a2	52262	1	138778874	D6MIT274	6	30.88472	48676564	0.93884	0.70673	0	3.75E-06	0	0	CB
unassigned	535545	3	118265349	19.000.325	19	0.2	325000	4.02149	6.88767	0	3.82E-06	0.0005	0.0418557	Shared
Chn1	492589	2	73559467	D5MIT95	5	98.81753	125309605	0.0683	0.04546	0	3.83E-06	0.0005	0.0418557	CB
unassigned	655890	5	8559502	D17MIT231	17	38.54838	34672294	1.52581	1.32639	0	3.83E-06	0.0005	0.0455118	SCG
unassigned	859773	9	21793462	D17MIT231	17	38.54838	34672294	0.99763	1.30986	0	3.84E-06	0.0005	0.0418557	Shared
Lama4	68802	10	38789761	11.104.430	11	62.15042	104475224	0.34945	0.25967	0	3.87E-06	0.0005	0.0418557	CB
unassigned	26555	1	173348870	d4mit238	4	33.232784	45243003	0.83624	0.75045	0	3.90E-06	0.0005	0.0418557	CB
Krt12	155521	11	99282073	06.036.921	6	24.99854	36940848	7.37576	6.64502	0	3.93E-06	0	0	SCG
Optc	51413	1	135798642	RS29347557	10	5.696346	12661713	1.17021	1.04554	0	3.94E-06	0.0005	0.0455118	SCG
Rbbp7	919449	X	159212485	D15MIT103	15	31.660276	63605769	1.3705	1.29484	0	3.94E-06	0	0	SCG
Rps6ka3	918764	X	155768503	14.027.409	14	32.019685	29395320	1.15625	0.97048	0	3.97E-06	0	0	CB
Optn	479462	2	4942275	04.098.998	4	75.012985	99172673	1.32724	1.18251	0	3.99E-06	0.0005	0.0418557	CB
unassigned	619029	4	134367245	06.095.876	6	52.18486	95860531	0.61633	0.56118	0	4.00E-06	0.0005	0.0455118	SCG
Cd83	208448	13	43892932	D9MIT248	9	44.87553	58210366	0.96469	1.20194	0	4.03E-06	0.0005	0.0455118	SCG
Dpysl4	757145	7	146276064	RS4165334	16	14.919414	23467678	0.57702	0.67823	0	4.19E-06	0.0005	0.0418557	CB
1700128F08Rik	833605	9	8241463	D13Mit207	13	8.688726	16526195	5.85209	6.71928	0	4.26E-06	0.0005	0.0418557	CB
unassigned	852554	9	106765582	rs13475894	1	45.460824	63625006	0.67096	0.60996	0	4.32E-06	0.0005	0.0418557	CB
Cpne4	852183	9	104935159	RS28262872	4	8.826905	18026684	1.42318	1.61748	0	4.33E-06	0.0005	0.0455118	SCG
Cdc123	479655	2	5728491	RS33477935	X	5.766692	9574173	2.06439	2.20188	2.37393	4.37E-06	0	0	CB
unassigned	816796	8	41596660	RS28262872	4	8.826905	18026684	0.27682	0.23807	0	4.37E-06	0	0	SCG
Col5a3	859240	9	20591549	15.028.723	15	14.881134	28708166	1.20153	1.44297	0	4.46E-06	0.0005	0.0418557	CB
Rela	419128	19	5638896	08.010.585	8	4.520052	10585028	0.85267	0.71434	0	4.47E-06	0.0005	0.0418557	CB
unassigned	359134	17	37199732	D12MIT285	12	30.221464	55750112	1.72809	1.79984	0	4.48E-06	0.0005	0.0455118	SCG
Gm13157	593778	4	145213129	D17Mit152	17	74.19469	65689824	1.32287	1.69643	0	4.54E-06	0	0	SCG
1300014I06Rik	226163	13	34744416	D5MIT425	5	93.27848	120330450	1.35959	1.72334	0	4.63E-06	0.0005	0.0418557	CB
unassigned	888270	13	61002779	RS33477935	X	5.766692	9574173	1.16197	1.24599	1.5987	4.67E-06	0.0005	0.0418557	CB
Tnc	606186	4	63628260	D1MIT132	1	55.208767	77143053	1.2687	1.59944	0	4.68E-06	0.0005	0.0455118	SCG

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
unassigned	395544	18	50023571	04.098.998	4	75.012985	99172673	0.32837	0.28271	0	4.72E-06	0	0	CB
Ccnb2	869997	9	70266852	RS33477935	X	5.766692	9574173	3.10044	3.41068	4.40056	4.80E-06	0.0005	0.0418557	CB
Socs6	417906	18	89056684	DXMIT132	X	55.816704	138191357	2.42069	2.62965	2.73297	4.87E-06	0	0	SCG
Med12	912915	X	98481577	02.109.360	2	59.82539	109399318	1.1146	1.21356	0	4.98E-06	0.0005	0.0418557	CB
Serpina3b	178750	12	105366224	D16Mit131	16	4.5	7319135	0.6854	0.54663	0	4.99E-06	0.0005	0.0455118	SCG
Lmcd1	701050	6	112279810	11.072.405	11	39.87138	72402307	0.77309	0.8604	0	5.03E-06	0	0	CB
Rngtt	573195	4	33416495	D2Mit274	2	62.95823	114283330	2.70888	2.44078	0	5.06E-06	0	0	CB
Gspt1	336553	16	11238968	RS29300656	X	89.33472	153071529	0.42303	0.47506	0.49705	5.07E-06	0	0	SCG
Odf2	449710	2	29756630	d9mit198	9	66.50428	91176808	1.60612	1.44972	0	5.11E-06	0.0005	0.0418557	CB
Sh3bp2	632673	5	34902995	D11MIT51	11	25.39412	36205252	1.59418	1.9102	0	5.20E-06	0.0005	0.0455118	SCG
Ubqln4	529629	3	88359779	RS28322831	2	43.67748	71063776	0.68225	0.5655	0	5.21E-06	0.0005	0.0418557	CB
Zbtb20	327404	16	43618521	rs13475894	1	45.460824	63625006	0.53916	0.61168	0	5.28E-06	0.0005	0.0455118	SCG
Aldh3a1	118761	11	61022141	02.021.696	2	18.06443	21699873	1.357	1.71586	0	5.66E-06	0	0	CB
Btn3a3	375521	17	34607006	D1MIT132	1	55.208767	77143053	4.03672	3.20178	0	5.66E-06	0.0005	0.0455118	SCG
Usf2	762712	7	31741176	D1MIT132	1	55.208767	77143053	0.78167	0.67265	0	5.69E-06	0.0005	0.0455118	SCG
Abca7	76260	10	79470451	15.046.034	15	20.554602	46035472	0.87397	0.7834	0	5.85E-06	0	0	SCG
unassigned	465160	2	119845425	RS51272439	6	10.78458	19888102	0.42493	0.34489	0	5.94E-06	0.0005	0.0418557	CB
Mertk	467127	2	128602022	RS33702022	10	21.757861	24370362	1.23146	1.06453	0	6.01E-06	0	0	SCG
unassigned	120836	11	69754271	D9MIT71	9	37.69738	50007830	1.08624	1.31682	0	6.02E-06	0	0	SCG
unassigned	75630	10	77012661	RS4165334	16	14.919414	23467678	1.01103	1.18185	0	6.03E-06	0	0	CB
Rplp0	826864	8	105388678	D5MIT309	5	58.78964	79931746	0.17974	0.13243	0	6.04E-06	0.0005	0.0418557	CB
Mical2	751054	7	119464877	04.013.290	4	8.3	13290000	0.67315	0.58426	0	6.09E-06	0.0005	0.0418557	CB
Commd10	395140	18	47247180	D1MIT1001	1	72.841454	130944135	1.15265	1.23912	0	6.37E-06	0.0005	0.0455118	SCG
Fanca	831366	8	125823910	D19MIT103	19	59.411152	53838656	1.9132	2.14609	0	6.59E-06	0.0005	0.0418557	CB
unassigned	824103	8	89031877	03.106.773	3	82.33049	106447862	1.74403	2.27798	0	6.63E-06	0.0005	0.0418557	CB
Trove2	53107	1	145612935	D7MIT350	7	57.28732	90734599	0.42139	0.46825	0	6.68E-06	0.0005	0.0455118	SCG
Smtnl1	494583	2	84657301	D11MIT320	11	39.87138	70766870	1.2103	1.46235	0	6.95E-06	0.0005	0.0455118	SCG
Fbxw15	877625	9	109458080	RS33477935	X	5.766692	9574173	0.97882	1.04939	2.15856	7.08E-06	0.0005	0.0418557	CB
Akap9	627366	5	4051048	D5MIT309	5	58.78964	79931746	0.48491	0.39687	0	7.11E-06	0.0005	0.0418557	CB
unassigned	429234	19	54062874	D1MIT507	1	89.469987	166978064	0.9328	0.88016	0	7.13E-06	0.0005	0.0455118	SCG
Ndufv2	381609	17	66432753	RS33477935	X	5.766692	9574173	2.57402	2.75018	3.60967	7.39E-06	0.0005	0.0418557	CB
Sfrs11	568098	3	157674988	04.013.290	4	8.3	13290000	1.7382	1.91138	0	7.64E-06	0	0	SCG
unassigned	218500	13	107739698	DXMIT132	X	55.816704	138191357	1.15768	1.25779	1.28081	7.70E-06	0	0	SCG
unassigned	506146	2	144370448	RS4165334	16	14.919414	23467678	1.48507	1.60467	0	7.85E-06	0.0005	0.0418557	CB
unassigned	510457	2	164678043	D2Mit274	2	62.95823	114283330	0.82456	0.72422	0	7.95E-06	0	0	CB
unassigned	815843	8	35160448	rs13480474	10	1.8	4403267	1.32358	1.17423	0	7.96E-06	0.0005	0.0455118	SCG
1700037C18Rik	334980	16	3906253	DXMIT132	X	55.816704	138191357	2.32834	2.49449	2.68613	7.99E-06	0.0005	0.0455118	SCG
Fam13a	717380	6	58904200	D10Mit123	10	3.021254	9952319	0.55559	0.64345	0	8.07E-06	0.0005	0.0455118	SCG
Nsun2	212841	13	69770452	RS29347557	10	5.696346	12661713	0.92306	1.05948	0	8.19E-06	0.0005	0.0455118	SCG
Egfr	110329	11	16769222	d6mit123	6	39.56321	56801586	1.01465	1.21514	0	8.28E-06	0.0005	0.0418557	CB
Dis3l	868881	9	64187353	D2Mit297	2	25.96707	42461006	0.76718	0.67778	0	8.41E-06	0.0005	0.0418557	CB

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
Ece1	592060	4	137460989	D12Mit2	12	26.674029	42747379	0.16389	0.20125	0	8.61E-06	0.0005	0.0418557	CB
Mslnl	355398	17	25881913	D2MIT81	2	18.06443	24644623	0.80172	0.6298	0	8.94E-06	0.0005	0.0418557	CB
Ap3s2	770865	7	87062117	D9MIT285	9	25.81754	40462577	0.70157	0.78517	0	8.96E-06	0.0005	0.0418557	CB
Lbxcor1	868488	9	62990052	03.060.525	3	40.51916	60240993	0.83861	0.70341	0	9.04E-06	0.0005	0.0418557	CB
Fnta	814521	8	27109526	01.183.109	1	96.118477	183202456	0.49347	0.59241	0	9.14E-06	0.0005	0.0418557	CB
unassigned	838335	9	37325088	RS29514367	13	20.539234	29499372	1.25295	1.45617	0	9.24E-06	0.0005	0.0418557	CB
Itga3	154111	11	94906360	d5mit158	5	69.85959	115413178	0.99574	0.86181	0	9.49E-06	0.0005	0.0455118	SCG
Dsg3	390118	18	20680524	d9mit198	9	66.50428	91176808	0.43594	0.55834	0	9.52E-06	0.0005	0.0455118	SCG
Slc26a4	186113	12	32213510	D11MIT186	11	23.608	35049231	1.34601	1.74996	0	9.53E-06	0.0005	0.0455118	SCG
Spag17	532428	3	99883995	D18Mit123	18	38.31055	56130259	1.58287	1.19268	0	9.76E-06	0.0005	0.0418557	CB
unassigned	704622	6	126924472	DXMit119	X	34.986222	69655585	1.70174	1.76494	1.90757	9.82E-06	0	0	CB
Saps2	296077	15	89083481	RS33477935	X	5.766692	9574173	1.13584	1.20005	1.37416	9.97E-06	0	0	CB
Pik3c2g	706610	6	139803796	RS30267686	18	60.34946	81658329	2.785	2.07153	0	9.99E-06	0	0	CB
Slc15a2	341549	16	36781663	RS29514367	13	20.539234	29499372	0.64614	0.46102	0	1.01E-05	0.0005	0.0418557	CB
Gm13547	450701	2	32152729	D2Mit274	2	62.95823	114283330	1.47605	1.31978	0	1.08E-05	0.0005	0.0418557	CB
Gpnmb	690951	6	48986758	D9MIT248	9	44.87553	58210366	1.26026	1.62798	0	1.09E-05	0	0	SCG
Plekhh2	367485	17	85000025	D7MIT223	7	99.51497	151795777	0.18882	0.23952	0	1.09E-05	0.0005	0.0418557	CB
unassigned	196810	12	101836253	DXMit216	X	58.906126	140336696	1.25398	1.26842	1.49313	1.09E-05	0	0	SCG
unassigned	875688	9	102489565	14.008.937	14	5.6	10975728	0.60133	0.46509	0	1.12E-05	0.0005	0.0418557	CB
unassigned	246595	14	29323349	D5MIT95	5	98.81753	125309605	0.60631	0.49273	0	1.12E-05	0.0005	0.0418557	CB
Enox1	255567	14	77907948	03.106.773	3	82.33049	106447862	0.89074	0.78577	0	1.13E-05	0.0005	0.0455118	SCG
Mrpl3	852188	9	104957926	RS50560599	1	67.504828	116681037	1.57301	1.42442	0	1.14E-05	0	0	CB
Thsd7b	19106	1	131327565	DXMIT68	X	20.022513	50676500	1.49262	1.31597	1.13421	1.18E-05	0.0005	0.0418557	CB
Epha3	345610	16	63552345	DXMIT68	X	20.022513	50676500	1.29476	1.20872	1.08693	1.20E-05	0	0	CB
Sec61a1	721488	6	88458570	D16MIT60	16	28.756136	32704177	0.40382	0.44275	0	1.25E-05	0	0	SCG
2810032G03Rik	163068	12	5422986	D2MIT75	2	46.41465	80424883	0.48128	0.42719	0	1.36E-05	0.0005	0.0455118	SCG
Baiap2l2	311932	15	79115905	15.028.723	15	14.881134	28708166	0.54932	0.39268	0	1.40E-05	0	0	CB
Serpinb3b	48006	1	109171558	rs13483805	X	31.433568	87440160	0.75995	0.81496	0.94396	1.43E-05	0.0005	0.0418557	CB
unassigned	425905	19	38214824	11.041.143	11	25.39412	41113079	1.66011	1.3118	0	1.44E-05	0.0005	0.0418557	CB
Fchsd2	748995	7	108334914	06.095.876	6	52.18486	95860531	0.79369	0.95206	0	1.60E-05	0.0005	0.0418557	CB
unassigned	386803	17	13168396	D6MIT67	6	52.18486	97701794	3.99076	3.62239	0	1.73E-05	0	0	CB
Hnf4g	517551	3	3648036	RS4164914	16	9.413247	15586358	0.85771	0.74348	0	1.74E-05	0	0	CB
unassigned	822905	8	83233496	RS30388122	1	66.387403	94920500	1.0871	0.94315	0	1.75E-05	0.0005	0.0455118	SCG
Taf8	378352	17	47635507	D9MIT248	9	44.87553	58210366	1.54257	1.26406	0	1.79E-05	0.0005	0.0455118	SCG
unassigned	349395	16	91927379	01.183.109	1	96.118477	183202456	3.79161	3.4434	0	1.82E-05	0.0005	0.0418557	CB
Suds3	674308	5	117549404	D2Mit297	2	25.96707	42461006	1.97249	2.1318	0	1.84E-05	0.0005	0.0418557	CB
Lck	617499	4	129233537	02.168.990	2	151.40532	169124295	0.79925	0.54949	0	1.85E-05	0.0005	0.0455118	SCG
unassigned	812809	8	16070242	D18MIT152	18	47.63475	62096421	0.4979	0.59747	0	1.90E-05	0.0005	0.0418557	CB
Pip5k1b	435920	19	24471139	02.109.360	2	59.82539	109399318	0.48389	0.57035	0	1.91E-05	0.0005	0.0418557	CB
unassigned	476162	2	167758368	D2Mit274	2	62.95823	114283330	1.25169	1.45987	0	1.98E-05	0.0005	0.0418557	CB
Ceacam10	735383	7	25565921	05.038.809	5	37.9822	38911990	1.04502	0.82119	0	2.66E-05	0.0005	0.0418557	CB

Gene Name	Affy Exon ID	Gene Chr	Start	SNP Name	SNP chr	SNP cM	SNP BP	Mean A	Mean B	Mean C	pval	perm pval	Q-Value	Tissue
LOC665506	689582	6	41498188	03.033.871	3	22.08075	33578373	0.6824	1.01029	0	3.02E-05	0.0005	0.0455118	SCG
Hk2	719940	6	82693939	rs13483805	X	31.433568	87440160	1.03691	1.12294	1.64758	3.07E-05	0.0005	0.0455118	SCG
Nrl	269850	14	56140962	RS29514367	13	20.539234	29499372	1.9264	1.48002	0	3.21E-05	0.0005	0.0418557	CB
Them5	530962	3	94147215	D14MIT174	14	33.327106	32460166	1.34041	1.63356	0	3.79E-05	0	0	SCG
unassigned	354967	17	24727883	RS33085156	5	79.13497	90112330	1.06203	1.14682	0	5.14E-05	0	0	CB
Rcor1	180677	12	112338131	D2Mit274	2	62.95823	114283330	1.01378	1.17254	0	5.26E-05	0.0005	0.0418557	CB

Appendix D: Differentially Expressed Genes on Chr 10 Between rs13480474 and rs38621064

Affy Exon ID	Gene Name	Chr	Start	End	Score(d)	Numerator(r)	Denominator(s+s0)	Fold Change	q-value(%)
6771894	1700052N19Rik	10	5891405	5917234	-15.51791318	-1.639127819	0.105628109	0.321050507	0
6772098	9130014G24Rik	10	10119700	10192112	7.275556853	0.686647059	0.094377251	1.609538469	0
6766063	Adat2	10	13272599	13283357	-7.948749746	-0.765784314	0.096340222	0.588133546	0
6772232	Aig1	10	13284586	13588776	-12.01787679	-1.087513725	0.090491336	0.470571638	0
6771912	Akap12	10	5987073	6176133	16.87517199	1.8412	0.109107036	3.583079366	0
6771974	BC013529	10	7487747	7512620	7.078151294	0.903383333	0.127629842	1.870447319	0
6766240	Cited2	10	17388397	17445443	-8.144889345	-0.826936275	0.101528239	0.563725106	0
6771884	Esr1	10	5317321	5734926	7.357559138	0.794760784	0.108019626	1.734789702	0
6765519	Fbxo5	10	4540597	4547321	-16.6677387	-1.935407843	0.116117002	0.261447315	0
6772255	Gpr126	10	14096075	14265690	16.05690041	1.692573529	0.105410975	3.232327836	0
6772111	Grm1	10	10373700	10827355	-45.42850744	-4.776705882	0.105147762	0.036481127	0
6766110	Hivep2	10	13686822	13871180	-21.87004343	-2.221265686	0.101566588	0.214453135	0
6765723	Katna1	10	7445719	7482947	-8.930754209	-0.883096078	0.098882587	0.542202594	0
6771920	Mthfd1l	10	6190432	6373616	-7.800864049	-0.783216667	0.100401271	0.581069781	0
6765513	Mtrf1l	10	4522345	4534257	-10.64393021	-1.130988235	0.106256638	0.456602848	0
6771862	Myct1	10	4739647	4805108	8.919158851	1.355338848	0.151958147	2.558572028	0
6766158	Nmbr	10	14425417	14593538	-10.97797893	-1.199652941	0.109278124	0.435380005	0
6765719	Nup43	10	7387314	7398740	-9.56759479	-0.994076471	0.103900352	0.502057159	0
6766046	Plagl1	10	12799942	12858141	-8.939814943	-0.839964706	0.093957729	0.558657236	0
6964522	Plekha1	10	5966499	5989649	-6.266266162	-0.665929412	0.106272124	0.630282534	0
6765730	Ppil4	10	7512702	7542923	-13.82428188	-1.509155882	0.109167036	0.351316713	0
6765596	Rmnd1	10	5914173	5965819	-7.676312019	-0.856103922	0.11152542	0.552442447	0
6772009	Sash1	10	8442015	8605779	-7.235022097	-0.739536275	0.102216174	0.598931836	0
6766038	Sf3b5	10	12725149	12728978	-5.439583437	-0.593240196	0.109059858	0.662852512	0
6765971	Shprh	10	10869117	10994635	-18.73549023	-1.829151961	0.097630323	0.281430002	0
6765533	Syne1	10	4795069	5022772	-34.28701736	-3.854034314	0.112405062	0.06915444	0
6765551	Syne1	10	5114700	5326491	-25.30454294	-2.53665	0.100244846	0.17234245	0
6771995	Ust	10	7700988	8238720	-19.0668414	-2.168240196	0.113717849	0.222481889	0
6771858	Vip	10	4698927	4712490	-9.463051364	-1.037989216	0.109688638	0.487005775	0
6772261	Vta1	10	14374564	14425366	-9.044375434	-0.903898039	0.099940349	0.534440765	0

Appendix E: Differentially Expressed Genes on Chr X Between rs33478059 and rs13483805

Affy Exon ID	Gene Name	Chr	Start	End	Score(d)	Numerator(r)	Denominator(s+s0)	Fold Change	q-value(%)
7016321	41888	X	34437417	34529670	-7.1284582	-0.799279412	0.112125145	0.574636121	0
7011581	7011581	X	58347008	58543840	-16.666181	-2.048864706	0.122935462	0.241674187	0
7012004	7012004	X	71536372	71540646	-24.51072	-2.757738848	0.112511538	0.147855637	0
7015691	7015691	X	12232010	12250707	-6.2755571	-0.687111765	0.109490162	0.621096023	0
7015921	7015921	X	18966486	19058445	-6.09867	-0.657665142	0.10783747	0.633903377	0
7011791	1110012L19Rik	X	67627723	67644643	-12.672797	-1.266585294	0.099945208	0.415642391	0
7011872	2610030H06Rik	X	69058168	69083230	-5.904341	-0.700686275	0.118673071	0.615279455	0
7011949	Abcd1	X	70961788	70983877	6.5828867	0.625112745	0.094960277	1.542331352	0
7011776	Aff2	X	66613516	67153727	-15.147926	-1.550069608	0.102328832	0.341493587	0
7010382	Agtr2	X	20967122	21066290	-8.6851753	-1.48204902	0.170641232	0.357980022	0
7016678	Apln	X	45371560	45388091	-9.8177105	-1.071326471	0.109121823	0.475881254	0
7017601	Arhgap4	X	71136553	71156672	-8.7210111	-0.874206863	0.100241458	0.545553708	0
7017156	Atp11c	X	57476141	57668082	-9.5952944	-1.161022549	0.120999159	0.447195461	0
7011937	Atp2b3	X	70748400	70839151	-19.041557	-2.011946078	0.105660798	0.247938449	0
7011964	Avpr2	X	71137128	71140831	-6.5217497	-0.703872549	0.10792695	0.613922075	0
7011936	Bgn	X	70719198	70741572	13.788077	1.983761765	0.143875156	3.955230476	0
7012082	Brcc3	X	72661987	72720210	-7.1954652	-0.749690196	0.10418926	0.594731256	0
7016427	C1galt1c1	X	35983714	35988348	-7.1544868	-0.893759804	0.124922978	0.538209662	0
7015746	Cask	X	13079890	13453907	-12.747624	-1.228997059	0.096409889	0.426613919	0
7010308	Chst7	X	19636358	19674759	7.6774334	1.006642157	0.131117016	2.009229214	0
7016421	Cul4b	X	35884726	35954257	-6.5715429	-0.765092157	0.116425042	0.58841578	0
7016903	Cxx1b	X	50972342	50973594	-9.2162432	-1.019627451	0.11063374	0.493243707	0
7016900	Cxx1b	X	50914317	50971063	-8.5547628	-0.941551961	0.110061726	0.520672472	0
7011286	Cxx1c	X	50911113	50912300	-8.5659276	-0.895435294	0.10453454	0.537584969	0
7011377	Ddx26b	X	53493656	53785810	-26.474674	-2.617423529	0.098865183	0.162958495	0
7012305	Dmd	X	80060191	82450372	-7.1564523	-0.825076471	0.115291269	0.564452283	0
7010644	Dock11	X	33428837	33641588	9.5270084	1.137084314	0.119353764	2.19936083	0
7011938	Dusp9	X	70829066	70888848	-5.5644047	-0.633593137	0.113865395	0.644569068	0
7015991	Elk1	X	20509913	20527742	-14.886632	-1.576385294	0.105892674	0.335320992	0
7017672	F8	X	72418085	72627655	-6.2412962	-0.608637255	0.097517764	0.655815882	0
7011922	F8a	X	70473367	70484234	-6.0372616	-0.606463725	0.100453445	0.656804663	0
7012008	Fam50a	X	71558328	71565472	-9.6040051	-0.957253922	0.099672367	0.51503632	0
7017134	Fgf13	X	56315322	56838739	-27.965611	-2.937002941	0.105021948	0.130579204	0

Affy Exon ID	Gene Name	Chr	Start	End	Score(d)	Numerator(r)	Denominator(s+s0)	Fold Change	q-value(%)
7011757	Fmr1	X	65931714	65971138	-14.103308	-1.564392157	0.110923778	0.338120137	0
7011759	Fmr1nb	X	66015035	66057730	-7.6007449	-0.777782429	0.102329763	0.583262639	0
7012080	Fundc2	X	72627654	72657164	-7.3118073	-0.906779412	0.124015771	0.533374437	0
7017520	Gabra3	X	69678823	69902177	-26.622599	-4.083233333	0.153374705	0.058996234	0
7011904	Gabrq	X	70070537	70135860	-19.558245	-2.198922549	0.112429441	0.21780024	0
7016826	Gpc3	X	49533241	49967162	12.514176	1.530377451	0.122291507	2.888614038	0
7016823	Gpc4	X	49377248	49518474	5.805814	0.669047059	0.115237425	1.590022366	0
7010835	Gria3	X	38713419	39031775	-15.470894	-1.890319608	0.122185544	0.269747294	0
7018041	Gyk	X	82947277	83072628	-4.7174752	-0.748244118	0.158611139	0.595327681	0
7017578	Haus7	X	70682657	70704368	-13.967935	-1.334115686	0.095512739	0.396635115	0
7012245	Hnrnpa3	X	77702055	77769327	-11.933646	-1.199530392	0.100516672	0.43541699	0
7016808	Hs6st2	X	48684904	49037701	-38.396052	-3.948120588	0.102826211	0.064788403	0
7011403	Htatsf1	X	54306487	54320351	-9.8087134	-1.091259804	0.111254123	0.469351344	0
7016760	Igsf1	X	47135718	47364086	-11.104975	-1.149252941	0.10348992	0.450858635	0
7010262	Kdm6a	X	17739721	17864129	-11.94447	-1.531666667	0.128232281	0.345877563	0
7017600	L1cam	X	71099125	71126114	15.15475	1.63575098	0.107936519	3.107492653	0
7017625	Lage3	X	71597511	71610378	-12.285164	-1.217864706	0.099132962	0.429918558	0
7011602	Ldoc1	X	58962697	58964122	-10.726857	-1.92326186	0.179294065	0.263657719	0
7017881	Mageb16	X	76868578	76916764	-11.635156	-1.192189216	0.102464399	0.437638263	0
7010183	Maoa	X	16195866	16284433	25.422115	2.760541176	0.108588179	6.77650399	0
7015831	Maob	X	16286284	16394490	15.58629	1.68310098	0.107985989	3.211174311	0
7017155	Mcf2	X	57309023	57432410	-4.9904974	-0.648133333	0.129873495	0.638105408	0
7010764	Mcts1	X	35533239	35968426	-13.220801	-1.657677451	0.125384042	0.316948984	0
7017610	Mecp2	X	71271948	71331009	-9.4776427	-0.95459902	0.100721145	0.515984982	0
7015697	Med14	X	12255799	12409111	-6.7383803	-0.678834314	0.100741466	0.624669799	0
7016891	Mospd1	X	50673981	50767501	-7.5966913	-0.977569608	0.128683604	0.507834528	0
7017678	Mtcp1	X	72650135	72661946	-17.731252	-1.80289902	0.10167917	0.286598106	0
7011840	Mtm1	X	68435080	68568856	-7.1869284	-0.740752941	0.103069475	0.598426952	0
7011848	Mtmr1	X	68617935	68674614	-12.514036	-1.304178431	0.104217251	0.40495165	0
7015835	Ndp	X	16462647	16551296	-15.043501	-1.635101961	0.108691585	0.321947653	0
7016317	Nkrf	X	34427486	34443529	-11.128667	-1.335156863	0.119974553	0.396348971	0
7011907	Nsdhl	X	70163860	70203867	11.690977	1.336257843	0.114298215	2.524955292	0
7010086	Nyx	X	12999720	13073747	-7.4258293	-0.761971569	0.102610973	0.589689917	0

Affy Exon ID	Gene Name	Chr	Start	End	Score(d)	Numerator(r)	Denominator(s+s0)	Fold Change	q-value(%)
7016555	Odz1	X	39885391	40783422	-25.848103	-3.134194118	0.121254318	0.113897334	0
7009963	OTTMUSG00000016789	X	10876350	10876879	-8.7117864	-0.866998721	0.0995202	0.54828628	0
7010342	Pctk1	X	20265095	20277005	-10.786061	-1.045581373	0.096938202	0.484449647	0
7017598	Pdzd4	X	71038710	71070298	-8.3155963	-0.87964902	0.105783035	0.543499638	0
7010327	Phf16	X	20002663	20097065	-8.7532364	-0.870217647	0.099416674	0.547064313	0
7011263	Phf6	X	50264971	50310120	-8.8259521	-1.016681373	0.11519226	0.494251972	0
7017585	Pnck	X	70901333	70905886	-20.748606	-2.321240196	0.111874514	0.200095386	0
7011913	Pnma3	X	70295321	70344040	-17.911905	-1.821579412	0.101696578	0.282911081	0
7004860	Ppp4r2	X	72478402	72481068	-8.9841742	-0.90212451	0.100412624	0.535098166	0
7011050	Rab33a	X	45871703	45885946	-14.457306	-1.600066176	0.110675262	0.329861847	0
7016797	Rap2c	X	48357109	48395257	-9.0998046	-0.924368627	0.101581151	0.526911062	0
7010334	Rbm10	X	20194725	20228006	-16.11967	-1.458160784	0.090458478	0.363956823	0
7017063	Rbmx	X	54636083	54646203	-18.000036	-1.833889216	0.101882532	0.280507409	0
7011052	Rbmx2	X	46048181	46072663	-9.5902224	-0.881189216	0.091884127	0.542919717	0
7017604	Renbp	X	71167489	71176226	-11.46552	-1.140795098	0.099497894	0.453509571	0
7010330	Rgn	X	20105813	20187018	-8.283218	-0.739352451	0.089259084	0.599008155	0
7016397	Rhox11	X	35429771	35443212	-5.6138428	-0.650175102	0.115816407	0.637202971	0
7016241	RP23-110D11.1	X	29873976	29947708	8.1705032	1.158356863	0.141773014	2.232030688	0
7016180	RP23-110D11.1	X	27219135	27251155	7.006284	1.02090098	0.145712189	2.029185815	0
7010519	RP23-110D11.1	X	29873976	29947708	6.2111002	0.864938235	0.139256847	1.821261694	0
7016201	RP23-110D11.1	X	28179838	28802127	5.8014037	0.837551961	0.144370571	1.787015268	0
7010326	Rp2h	X	19918213	19987087	-7.8111254	-0.805479412	0.103119509	0.572171914	0
7011870	Rpl30	X	69048965	69058120	-15.423717	-1.4764	0.095722713	0.359384477	0
7016849	Rps17	X	50125491	50125853	-5.3113275	-0.625038235	0.117680229	0.648402593	0
7011051	Slc25a14	X	45976631	46015992	-12.749539	-1.381697059	0.108372317	0.3837671	0
7010667	Slc25a5	X	34335597	34338795	-6.422152	-0.701678431	0.109259081	0.614856466	0
7011944	Slc6a8	X	70918489	70927839	-14.521642	-1.469707843	0.101208106	0.361055408	0
7015941	Slc9a7	X	19647347	19868923	-10.130603	-1.065132353	0.105140078	0.477928812	0
7017277	Slitrk4	X	61448373	61616480	-46.522124	-4.587444031	0.098607795	0.041595059	0
7016125	Slx	X	25714317	26129764	4.9381611	0.671889216	0.136060612	1.59315785	0
7016666	Smarca1	X	45152593	45246131	-5.7703747	-0.68109902	0.11803376	0.623689977	0
7011952	Srpk3	X	71019718	71024264	-7.7247407	-0.734884314	0.095133848	0.600866205	0
7011953	Ssr4	X	71031209	71037611	-6.518095	-0.69562549	0.106722208	0.617441565	0

Affy Exon ID	Gene Name	Chr	Start	End	Score(d)	Numerator(r)	Denominator(s+s0)	Fold Change	q-value(%)
7010856	Stag2	X	39502407	39696904	-7.934302	-0.923163725	0.116350969	0.527351308	0
7011760	Styx	X	66074291	66078458	-6.7176109	-0.686656863	0.102217421	0.621291894	0
7012001	Taz	X	71526854	71535672	-13.369218	-1.518077451	0.113550208	0.349150888	0
7011990	Tktl1	X	71422598	71453839	-6.6982491	-0.619239216	0.092447923	0.65101414	0
7012265	Tmem47	X	78316003	78527375	-5.7777114	-0.590837255	0.102261469	0.663957474	0
7009941	Tspan7	X	10062252	10237647	-12.102014	-1.153509804	0.095315521	0.449530278	0
7021194	Tspan7	X	10146857	10198936	-11.979488	-1.121980392	0.093658459	0.459462686	0
7010345	Usp11	X	20280969	20297664	-14.823849	-1.598220588	0.107814143	0.330284097	0
7011039	Utp14a	X	45610059	45640873	-10.376488	-1.016629412	0.097974321	0.494269774	0
7015993	Uxt	X	20528791	20539211	-10.655368	-1.148187255	0.1077567	0.451191797	0
7012085	Vbp1	X	72759521	72820597	-6.0970162	-0.861514706	0.141301035	0.550374409	0
7017550	Xlr3a	X	70331635	70342380	-4.8857872	-0.624485294	0.127816719	0.648651153	0
7011918	Xlr3b	X	70437494	70448638	-5.3506986	-0.794751961	0.148532373	0.576442271	0
7017570	Xlr3c	X	70499879	70510729	-7.2345138	-0.933933333	0.129094139	0.523429328	0
7017549	Xlr4c	X	70319683	70488431	-4.6422333	-0.589442157	0.126973834	0.664599836	0
7011033	Xpnpep2	X	45406797	45497158	9.6561108	0.905296078	0.093753696	1.872928829	0
7010647	Zcchc12	X	33735919	33752783	-6.719684	-0.93229902	0.138741498	0.524022615	0
7015994	Zfp182	X	20587696	20639422	-13.983985	-1.389979412	0.099397949	0.381570247	0
7011928	Zfp275	X	70555871	70604416	-6.9750291	-0.632255882	0.090645627	0.645166806	0
7016722	Zfp280c	X	45894803	45959666	-17.099891	-1.889732353	0.110511367	0.269857118	0
7015995	Zfp300	X	20656286	20666633	-15.524153	-1.649873529	0.106277845	0.318668091	0
7011378	Zfp449	X	53512877	53626498	5.4540681	0.666760784	0.122250177	1.587504613	0
7021322	Zic3	X	55267487	57679568	-24.442026	-2.463062745	0.100771629	0.181361138	0
7011464	Zic3	X	55236135	55294911	-22.446719	-2.270709804	0.101159988	0.207227906	0

Appendix F: cis-sQTL Co-localizing with SCNVs

Affy Exon ID	Gene Name	Chr	Start	End	Copy Number	Tissue	Strain
58978	Mnda	1	1.76E+08	1.76E+08	1	CB	129/SvJ
59038	Ifi203 /// LOC100862473 /// LOC100862472 /// Gm16340	1	1.76E+08	1.76E+08	3	SCG	Shared
160083	Cd300lh /// Gm11711 /// Gm11710	11	1.15E+08	1.15E+08	3	SCG	Shared
160084	Cd300lh	11	1.15E+08	1.15E+08	3	SCG	Shared
222307	Gpr137b-ps /// Gpr137b	13	12681000	12729999	1	Both	129/SvJ
222308	Gpr137b-ps	13	12681000	12729999	1	Both	129/SvJ
222313	Gpr137b-ps	13	12681000	12729999	1	Both	129/SvJ
222317	Gpr137b-ps /// Gpr137b	13	12681000	12729999	1	SCG	129/SvJ
222323	Gpr137b-ps	13	13437000	13472999	4	CB	129/SvJ
222333	Gpr137b	13	13437000	13472999	4	Both	129/SvJ
287225	Rims2	15	39307000	39314999	3	SCG	129/SvJ
351740	Snx9	17	5808000	5929999	1	SCG	Shared
358724	H2-Q9 /// LOC68395 /// H2-Q8 /// H2-Q7	17	35530000	35555999	4	Both	Shared
358725	H2-Q9 /// LOC68395 /// H2-Q8 /// H2-Q7	17	35530000	35555999	4	SCG	Shared
376226	C920025E04Rik	17	36226000	36276999	4	SCG	Shared
376228	C920025E04Rik	17	36226000	36276999	4	SCG	Shared
376237	---	17	36226000	36276999	4	SCG	Shared
376238	H2-T23	17	36226000	36276999	4	SCG	Shared
376245	H2-T9 /// H2-T10 /// H2-T22	17	36226000	36276999	4	Both	Shared
376248	H2-T10	17	36226000	36276999	4	Both	Shared
376249	H2-T10	17	36226000	36276999	4	SCG	Shared
376253	H2-T9 /// H2-T22 /// H2-T10	17	36226000	36276999	4	SCG	Shared
376254	H2-T9	17	36226000	36276999	4	CB	Shared
376264	---	17	36226000	36276999	4	CB	Shared
376271	---	17	36226000	36276999	4	CB	Shared
376294	Gm8909	17	36273000	36323999	1	Both	Shared
391774	Sap130	18	31778000	31796999	4	Both	Shared
513494	2210418O10Rik	2	1.76E+08	1.77E+08	1	Both	Shared
513495	2210418O10Rik	2	1.76E+08	1.77E+08	1	Both	Shared
513504	2210418O10Rik	2	1.76E+08	1.77E+08	1	Both	Shared
539971	Gbp1	3	1.42E+08	1.42E+08	4	SCG	129/SvJ

Affy Exon ID	Gene Name	Chr	Start	End	Copy Number	Tissue	Strain
540002	Gbp2 /// Gbp1	3	1.42E+08	1.42E+08	4	SCG	129/SvJ
593778	Gm13212	4	1.45E+08	1.45E+08	4	SCG	Shared
593795	Gm13212	4	1.47E+08	1.47E+08	6	Both	Shared
594031	Rex2 /// Gm13242 /// Zfp600	4	1.46E+08	1.46E+08	6	SCG	Shared
594075	Gm13139	4	1.47E+08	1.47E+08	3	CB	Shared
594080	1700029I01Rik /// Gm13251 /// Gm13139	4	1.47E+08	1.47E+08	5	Both	Shared
594081	1700029I01Rik /// Gm13251 /// Gm13139	4	1.47E+08	1.47E+08	5	SCG	Shared
594082	1700029I01Rik /// Gm13251 /// Gm13139	4	1.47E+08	1.47E+08	6	Both	Shared
594083	1700029I01Rik /// Gm13251 /// Gm13139	4	1.47E+08	1.47E+08	6	Both	Shared
594120	Gm13152	4	1.47E+08	1.47E+08	8	CB	Shared
594122	Gm13152 /// LOC100504917	4	1.47E+08	1.47E+08	8	Both	Shared
594123	Gm13152	4	1.47E+08	1.47E+08	8	Both	Shared
606487	Astn2	4	65708000	65742999	0	Both	129/SvJ
627366	Akap9	5	4048000	4058999	11	CB	Shared
658555	Speer4b	5	27819000	27832999	4	CB	129/SvJ
694143	LOC641050	6	68191000	68204999	6	CB	129/SvJ
735803	Cyp2b13	7	26768000	26985999	0	SCG	129/SvJ
759098	Vmn2r42	7	9335000	9574999	1	CB	Shared
759130	2810047C21Rik1	7	9317000	9338999	3	CB	129/SvJ
759202	Vmn2r42	7	9913000	9953999	3	CB	Shared
777620	Gm15483	7	1.23E+08	1.23E+08	1	CB	129/SvJ
840278	2900052N01Rik	9	46676000	46967999	3	SCG	129/SvJ
894205	Hmgcs1	13_randon	0	138999	1	CB	Shared
894212	Hmgcs1	13_randon	0	138999	1	CB	Shared
220886	4833420G17Rik	13	1.2E+08	1.2E+08	17	CB	FVB
312691	Polr3h	15	81750000	81761999	3	SCG	FVB
320444	---	16	11630000	11639999	4	CB	FVB
358650	H2-D1 /// 5430410E06Rik	17	35380000	35465999	4	Both	FVB
358652	H2-D1	17	35380000	35465999	4	Both	FVB
358654	H2-D1	17	35380000	35465999	4	SCG	FVB
358656	H2-D1	17	35380000	35465999	4	Both	FVB

Affy Exon ID	Gene Name	Chr	Start	End	Copy Number	Tissue	Strain
358661	H2-D1	17	35380000	35465999	4	SCG	FVB
358662	H2-D1	17	35380000	35465999	4	Both	FVB
358666	---	17	35462000	35490999	3	CB	FVB
358667	---	17	35462000	35490999	3	Both	FVB
358676	H2-Q1	17	35380000	35465999	4	SCG	FVB
375521	Btnl4	17	34602000	34635999	3	SCG	FVB
376231	H2-T23	17	36168000	36185999	1	SCG	FVB
630039	Rint1	5	23314000	23322999	4	Both	FVB
689496	---	6	41012000	41117999	0	SCG	FVB
738266	1600014C10Rik	7	38957000	38989999	16	SCG	FVB
872972	Me1	9	86486000	86494999	4	Both	FVB
893539	H2-T9	17	36168000	36185999	1	CB	FVB
893542	H2-T9	17	36168000	36185999	1	CB	FVB

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