UCSF
UC San Francisco Previously Published Works

Title

Variation and genetic control of gene expression in primary immunocytes across inbred mouse strains.

Permalink

https://escholarship.org/uc/item/2w43r09r

Journal

Journal of immunology (Baltimore, Md. : 1950), 193(9)

ISSN

0022-1767

Authors

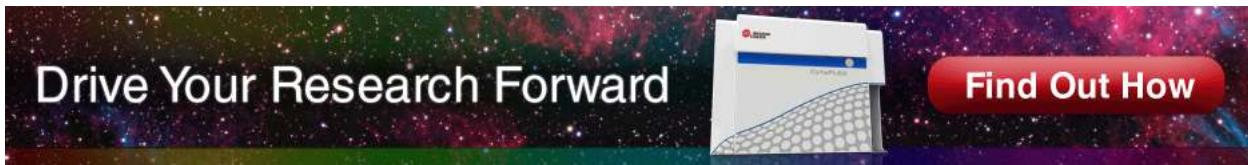Mostafavi, Sara
Ortiz-Lopez, Adriana
Bogue, Molly A
et al.

Publication Date

2014-11-01

DOI

10.4049/jimmunol.1401280

Peer reviewed

The Journal of Immunology

Variation and Genetic Control of Gene Expression in Primary Immunocytes across Inbred Mouse Strains

Sara Mostafavi, Adriana Ortiz-Lopez, Molly A. Bogue, Kimie Hattori, Cristina Pop, Daphne Koller, Diane Mathis, Christophe Benoist and The Immunological Genome Consortium

Supplementary Material	**http://www.jimmunol.org/content/suppl/2014/09/28/jimmunol.1401280.DCSupplemental.html**
References	This article **cites 56 articles**, 23 of which you can access for free at: http://www.jimmunol.org/content/193/9/4485.full#ref-list-1
Subscriptions	Information about subscribing to *The Journal of Immunology* is online at: http://jimmunol.org/subscriptions
Permissions	Submit copyright permission requests at: http://www.aai.org/ji/copyright.html
Email Alerts	Receive free email-alerts when new articles cite this article. Sign up at: http://jimmunol.org/cgi/alerts/etoc

Variation and Genetic Control of Gene Expression in Primary Immunocytes across Inbred Mouse Strains

Sara Mostafavi,* Adriana Ortiz-Lopez,[†] Molly A. Bogue,[‡] Kimie Hattori,[†]
Cristina Pop,* Daphne Koller,* Diane Mathis,[†] Christophe Benoist,[†] and
The Immunological Genome Consortium[1]

To determine the breadth and underpinning of changes in immunocyte gene expression due to genetic variation in mice, we performed, as part of the Immunological Genome Project, gene expression profiling for CD4^{+} T cells and neutrophils purified from 39 inbred strains of the Mouse Phenome Database. Considering both cell types, a large number of transcripts showed significant variation across the inbred strains, with 22% of the transcriptome varying by 2-fold or more. These included 119 loci with apparent complete loss of function, where the corresponding transcript was not expressed in some of the strains, representing a useful resource of "natural knockouts." We identified 1222 cis-expression quantitative trait loci (cis-eQTL) that control some of this variation. Most (60%) cis-eQTLs were shared between T cells and neutrophils, but a significant portion uniquely impacted one of the cell types, suggesting cell type–specific regulatory mechanisms. Using a conditional regression algorithm, we predicted regulatory interactions between transcription factors and potential targets, and we demonstrated that these predictions overlap with regulatory interactions inferred from transcriptional changes during immunocyte differentiation. Finally, comparison of these and parallel data from CD4^{+} T cells of healthy humans demonstrated intriguing similarities in variability of a gene's expression: the most variable genes tended to be the same in both species, and there was an overlap in genes subject to strong cis-acting genetic variants. We speculate that this "conservation of variation" reflects a differential constraint on intraspecies variation in expression levels of different genes, either through lower pressure for some genes, or by favoring variability for others. *The Journal of Immunology*, 2014, 193: 4485–4496.

F or more than a century, inbred mice have played a unique role in biomedical research. Their group homogeneity, phenotypic reproducibility, and genetic stability over time have led to key discoveries in essentially every area of biomedical research (1), including the discovery of fundamental concepts of immunology such as histocompatibility, MHC restriction, or genetic susceptibility to autoimmune diseases. The nearly homogeneous nature of an inbred strain's genome underlies the extraordinary power of targeted germline modifications, and it has supported mapping of loci associated with disease or phenotypic traits. The genomes of laboratory strains have been molded by strong selective pressures

linked to their domestication by mouse fanciers in China and Europe, then to inbreeding and allele fixation in biomedical research colonies. These genomes incorporate segments from several origins (2), as now clearly established by the decoding of the complete genome of the reference C57BL/6J, followed by a number of other inbred strains (3, 4). Efforts to standardize and integrate phenotypic and genetic information, as exemplified by the Mouse Phenome Database (MPD) project (5), are also helping to exploit the full potential of inbred strains in biomedical research.

The Immunological Genome (ImmGen) project is an international collaboration of laboratories that collectively perform a thorough dissection of gene expression and its regulation in the immune system of the mouse. Genome-wide gene expression data have been collected for ~250 immunological cell types of the mouse, yielding insights into genomic correlates of immunocyte differentiation and lineages (6). The assembled data also enabled predictions about regulatory networks that underlie mouse hematopoiesis (7). The first phase of the ImmGen project mainly used the reference C57BL/6J strain, and it thus focused on identifying changes in gene expression during differentiation and activation in the context of a unique genome. However, there is much value in analyzing the impact of functional genetic variation on gene expression levels. Variants influencing gene expression are pervasive in mammalian species and comprise a large majority of the disease-related variants identified in genome-wide association studies (8). Combined analysis of gene expression and genotype data across a genetically diverse population is a powerful means to understand the impact of genotypic variation on cellular processes, and ultimately to build mechanistic models that link genetic variation to detailed cellular processes in a context-specific manner (8, 9). Several comparative analyses of gene expression have been performed across inbred mouse strains (10–14)

*Department of Computer Science, Stanford University, Stanford, CA 94305;
[†]Division of Immunology, Department of Microbiology and Immunobiology, Harvard Medical School, Boston, MA 02115; and [‡]The Jackson Laboratory, Bar Harbor, ME 04609

[1]All authors and their affiliations appear at the end of this article.

The online version of this article contains supplemental material.

Abbreviations used in this article: cis-eQTL, cis-expression quantitative trait locus; eQTL, expression quantitative trait locus; FDR, false discovery rate; GN, granulocyte (polymorphonuclear neutrophil); ImmGen (Project), Immunological Genome (Project); ImmVar (Project), Immune Variation (Project); MAD, mean absolute deviation; MPD, Mouse Phenome Database; PC, principal component; SNP, single nucleotide polymorphism; T4, CD4^{+} T cell; TF, transcription factor; TSS, transcription start site; TV, true variability.

but were of limited breadth and/or performed in cell types not directly relevant to ImmGen.

In terms of understanding human disease, whereas the mouse models have been invaluable in establishing fundamental paradigms of immunologic function, caution has been suggested in translating findings from the mouse to the human immune system (15). Similarities and differences have been reported in the genomic underpinning of immune lineages of humans and mice, whether at steady-state or after cell activation (16–19). A direct comparison of the genetic underpinning of these differences would also be valuable in ascertaining what mouse models can be usefully applied to understand human diseases and their genetics.

To better understand the effect of genetic variation on the mouse immune system, we generated RNA expression data for 39 of the main inbred strains in the MPD "Priority Strain Panel." Using rigorous ImmGen standard operating procedures, genome-wide expression data were generated for two immunological cell types, CD4$^+$ T cells (T4) and polymorphonuclear neutrophils (granulocytes, GN). These were chosen to represent the main lymphoid and myeloid branches of the immune system, as well as its adaptive and innate facets. This effort paralleled a study of similar design in an ethnically diverse population of healthy humans, the Immune Variation (ImmVar) study, where genotype and gene expression data were collected for T4 and CD14$^+$CD16$^-$ monocytes (20–22). This matching study design allowed us to compare transcriptional variability and its roots in the two species. In the present study, we first report on the impact of genetic background on gene expression levels in mouse T4 and GN, identify *cis* expression quantitative trait loci (*cis*-eQTLs), and chart regulatory interactions that can be inferred from the perturbation of the regulatory network by genetic variation. Second, we compare the impact of functional variation in humans and mice by exploring the overlap between expression variability and its genetics in the two species.

Materials and Methods
Gene expression and genotype data

Inbred mouse strains from the MDP Priority Strain Panel, representing 39 strains, were obtained from The Jackson Laboratory (Bar Harbor, ME) at 5 wk of age. All mice were bred in The Jackson Laboratory under specific pathogen-free conditions. CD3$^+$CD4$^+$CD62L$^+$ naive T splenocytes and CD11b$^+$Ly6G$^+$ bone marrow GN were sorted from pools of two to three mice. Two biological replicates were generated for each strain using the ImmGen standard operating protocol (http://www.immgen.org). Gene expression data were generated for bone marrow GN and T4 using Affymetrix ST1.0 microarrays, the platform used for the main ImmGen compendium, resulting in the quantification of expression levels for 25,134 probes corresponding to 21,951 unique genes. Data were processed and normalized using the ImmGen standard operating protocol (http://www.immgen.org). When indicated, data were filtered to only include genes with >0.95 probability of expression (or a mean of >120 expression on the intensity scale; see standard operating protocol). This filtering criteria resulted in 11,598 and 11,285 expressed transcripts in T4 and GN, respectively, with 131,85 transcripts expressed in one or the other, and 9,698 transcripts expressed in both cell types. A threshold for absence of expression was also set at <0.05 probability of expression (or a <42 expression level on intensity scale). Genotype data were obtained from the mouse HapMap genotype resource (http://mouse.cs.ucla.edu/mousehapmap) (23). Only genotyped single nucleotide polymorphisms (SNPs) with minor allele frequency of >0.05 and a ≤10% missing rate (resulting in a total of 96,779 SNPs) were used in this study.

Defining the true variability metric, bimodality in gene expression, and complete loss of function loci

All analyses were performed in the MATLAB computing environment (R2013a, version 8.1.0.604). At least two biological replicates were available for each mouse and each cell type (for the strains for which there were more than two replicates, we randomly chose two of the replicates for

this analysis). For the true variability (TV) metric, two quantities were computed for each gene and each cell type using the log-transformed data: 1) the between-strains mean absolute deviation (MAD), which was divided by the mean gene expression level for that gene; and 2) the average of within-strains MAD, where the MAD for each strain was computed using the two replicates for that strain and then divided by the mean gene expression level for that gene. The TV score for each gene was defined as the difference between the first quantity, representing both meaningful and unwanted variability, and the second quantity, representing the unwanted variability. We note that there are two main differences between the TV metric proposed here and a standard ANOVA approach: first, we chose to quantify variability using MAD as opposed to variance because the latter gives more weight to extreme values. Second, as opposed to an associated F-statistic in ANOVA, where the test statistics (interpreted as the true variability score) is the ratio of two variances, here we use the difference of the two MADs as the score. We chose to use the difference so to emphasize the magnitude of the variability, in addition to the relative variability of the within-strains and between-strains MAD.

Bimodal genes were identified using two criteria: the first criterion was based on the assessment of the fit of a mixture of Gaussian distributions with two components to expression levels across the strains, and the second criterion used a threshold on the fold difference between high- and low-expressing strains. The mixture of Gaussians were fit using MATLAB's *gmdistribution* function (R2013a, version 8.1.0.604). A likelihood ratio test was used to assign a bimodality *p* value to each gene by comparing the likelihood of a mixture of Gaussian distributions with two components with simply the fit of a single Gaussian distribution. Genes with bimodality $p < 10^{-6}$ and at least a 2-fold difference in top two high-expressing and bottom two low-expressing strains were identified as bimodal. Complete loss-of-function loci were identified as those bimodal genes that additionally satisfied a strict threshold on expression levels: an expression of <42 (corresponding to <0.05 probability of expression) for at least two strains and expression >120 (corresponding to >0.95 probability of expression) for at least two strains.

eQTL association mapping for mice

It is well appreciated that genetic association studies in inbred strains are impacted by population stratification, which violates the assumptions of standard statistical tests and leads to an abundance of false positive associations (and therefore an inflation of association *p* values) (24). To account for population stratification, we used linear regression, regressing out the effect of the top two genotype PCs from log gene expression data. We chose two PCs by quantifying the inflation of observed *p* values using the λ statistic (25) as we varied the number of removed genotype PCs from one to five. A *cis* window of 1 Mb centered on transcription start site (TSS) was used to identify all *cis* SNPs for each gene.

Joint analysis. To increase statistical power, for the joint analysis, residual expression data (after removing genotype PCs, see above) from both cell types were concatenated (after removing mean expression for each cell type separately), resulting in a dataset with 2 × 39 samples and 13,185 expressed transcripts (expressed in at least one cell type). For each SNP-gene pair, the Wilcoxon rank sum statistic (as implemented in MATLAB R2013a, version 8.1.0.604) was used to test whether the expression of the gene was significantly different between strains with the reference or the alternative allele at the given SNP. Ten thousand permutations were performed for each SNP-gene pair, permuting the assignment of SNP values to strains while keeping intact the correspondence between genotype assigned to the T4 and GN sample for the same strain (thus accounting for "repeated" samples). A gene-level *p* value was assigned that accounted for the number of tested SNPs per gene by using the minimum permutation *p* value across all tested SNPs for that gene as the null distribution (26, 27). The final set of *cis*-eQTLs was defined by setting a 5% false discovery rate (FDR) threshold on the gene-level *p* values.

Cell-specific eQTL analysis. Cell-specific eQTLs were identified by testing the significance of an interaction term between genotype and cell type indicator in a linear regression setting, where the fit of the baseline model (no interaction) with one that additionally included a cell type indicator by genotype interaction term was assessed using an F test. In particular, we model the expression level of gene *g* in tissue *t* for strain *i* as $x_{g,t,i} = \alpha_{g,t} + \beta_g s_i + \gamma_{g,t} s_i$ where $\alpha_{g,t}$ is genotype-independent tissue-specific effect for tissue *t* and gene *g*, β_g is the tissue-shared genotype effect, and $\gamma_{g,t}$ represents the cell-specific genotype effect for tissue *t*. As above, gene-level *p* values were computed using 10,000 permutations (permuting the assignment of genotype values to the strains).

Constructing regulatory networks in mouse and validation using Ontogenet links

For constructing regulatory networks, genes expressed in both cell types and identified to have nonnegligible TV scores (as per Supplemental Fig. 1A) were used, which resulted in 3675 analyzed genes. Among these, 164 are transcription factors (TFs; as defined in Ref. 7). Two networks (one for each cell type) were constructed using stepwise regression, where a sparse set of TFs (regulators) was identified for each target gene (set of targets includes both TFs and nonregulatory genes). More specifically, for each target gene, stepwise regression was performed using all regulators (excluding autoregulation), and inferred regulators were identified using a 5% FDR to correct for the number of TFs tested for each target. A "joint network" was also constructed using the same approach but applied on concatenated expression data form both cell types (after removing mean gene expression from each cell type). Networks were constructed on genotype PC–corrected data.

We used the joint network constructed from T4 and GN data to compare the coexpression-based links derived in the present study with those derived from the ImmGen data (using the Ontogenet algorithm; see Ref. 7). We decided to use the joint network, as we observed a high degree of overlap between networks constructed individually from each cell type (see *Results*), and to identify persistent, and thus more likely true positive, relationships. Regulatory interactions and modules defined by Ontogenet were downloaded from the ImmGen Web site (http://www.immgen.org). Note that in Ref. 7, two types of modules were defined: initially 81 larger "coarse-grained modules" were defined, and subsequently some of these modules were refined into smaller modules with more coherent expression, resulting in 334 "fine modules." Coarse modules were constructed to capture the mechanisms that coregulate a larger set of genes in one cell-lineage, whereas fine modules were constructed to capture the distinct regulatory mechanism controlling only a smaller subset of these genes in the sublineage(s). Only "fine modules" and their "top regulators," representing more functionally specific gene groups and links, were used in the present analyses. Based on these data, a list of 4083 testable links connecting the top regulators to all genes in their assigned module was generated. First, the replication rate for this list was computed by assigning a p value to each link in the present study based on the coexpression of the corresponding regulator-target pair, and then assessing the proportion of true-positive p values using Storey's π_1 (28). To correct for the overall inflation of p values between all pairs of genes, as is often observed in coexpression data, we used the distribution of p values for coexpression of all gene/gene pairs as the null distribution to assign a p value to each of the 4083 links. Second, the links identified in this study were tested for consistency with those identified by the Ontogenet algorithm on the ImmGen data using a hypergeomtric test. This test identified regulators whose inferred targets were also coregulated (i.e., assigned to the same module) according to Ontogenet. Third, we computed the proportion of links identified in the present study that were also reported by Ontogenet and used the hypergeometric test to compute a p value for the overlap.

Gene expression, genotype, and eQTL discovery in human

Genotype and gene expression for T4 and neutrophils were obtained from the ImmVar study. As done for the mouse data, *cis*-eQTLs were defined using a 1-Mb window centered on the TSS. Gene expression data were corrected for three genotype PCs and 30 expression PCs (to increase statistical power by removing variability due to environmental or nonlocal genetic factors). The number of removed expression PCs was set by evaluating the improvement in number of *cis*-eQTLs that were detected based on data from one ("training") chromosome (chromosome 18). In particular, to select the number of PCs that are removed, the number of *cis*-eQTL discoveries in raw data was compared to PC-corrected data where we varied the number of removed PCs from 1 to 50. In order to avoid overfitting, we optimized the number of removed PCs based on *cis*-eQTL discovery on just one chromosome (and not the whole dataset). As previously observed (29), the improvement in *cis*-eQTL discovery greatly increased with removal of PCs, and there was a stable plateauing effect when we removed 20–40 PCs (see, for example, Ref. 21). As described for the mouse data above, in the joint eQTL analysis, gene expression data from both cell types were combined and a gene-level p value was computed for each gene using permutation analysis (1000 permutations per gene). In this case, the Spearman rank correlation was used as the test statistic.

Constructing regulatory networks for human/mouse comparison

Stepwise regression was used to construct a regulatory network for T4 data. For this analysis, we used the set of genes expressed in both humans and

mice (in T4) and were considered to have nonnegligible TV scores for T4 data in mice (as defined by Supplemental Fig. 1A), which resulted in a set of 3407, of which 183 are TFs. For constructing the network, human data were corrected for batch, population structure (three genotype PCs), gender, and age, whereas mouse data were corrected for two genotype PCs (mouse data were done in one batch, and the mice had identical gender and age). Significant links were identified at a 5% FDR.

The replication rate of links identified in one species onto the other was computed using the π_1 statistic to quantify the proportion of true-positives among the coexpression p values for the relevant links (links being replicated). As above, coexpression p values were adjusted using the distribution of all coexpression p values as the null.

The stepwise regression approach above identifies regulatory links in a target-centric manner, identifying "top" regulators for each target. Additionally, in a TF-centric manner, top targets for each TF were identified based on the ranking of their coexpression value (Pearson correlation coefficient) with the given TF. In particular, two analyses were conducted. First, for each TF in mice (humans), the top 10 targets were defined based on coexpression values, and the overlap of these targets was assessed in the top $n = [10, 20, 30, 50]$ targets for the same TF in human (mouse). The significance of the overlaps was determined using the hypergeometric test and corrected for the number of TFs tested. Second, the evidence for conservation of the top $n = [10, 20, 30, 50]$ targets of each TF in mice (humans) was assessed in humans by using the Wilcoxon rank sum test to compare the distribution of the coexpression values for the top n targets compared with the distribution of coexpression values between that TF and all genes.

Results

The mice tested in the present study included 35 classic laboratory inbred strains (*Mus musculus domesticus*) that represent all the major branches of the inbred tree (1) and four "wild-derived" strains (CAST/EiJ, PWD/PhJ, JF1/Ms, and MSM/Ms, which are representative of the *Mus musculus castaneus*, *Mus musculus musculus*, and *Mus musculus molossinus*, respectively). Gene expression data for bone marrow GN and T4 were quantified using Affymetrix ST1.0 microarrays (see *Materials and Methods*). Matching genotype data were obtained from the Mouse HapMap Genotype Imputation Resource (30) and included 132,285 genotyped SNPs (see *Materials and Methods*). Because we did not attempt in the present study to identify causal variants owing to the limitations imposed by the relatively large size of linkage disequilibrium blocks in inbred mice, the analyses only used genotyped SNPs for computational efficiency. All expression data can be browsed or accessed on the ImmGen Web site (http://www.immgen.org).

Extent and distribution of expression variation across strains

We first investigated the nature and extent of the transcript variability across the inbred strain panel. Overall we observed some variability in expression levels for most genes (58% of tested genes, or 8,544 genes in T4–or 39% of genes–and 10,006 genes in GN–46% of genes–at 5% FDR; Supplemental Fig. 1A). Of these, 2508 genes in T4 and 3711 genes in GN had >2-fold difference between the highest two and lowest two expressing strains. Some of the most variable genes correspond to retroviral elements (*Mela*, *EG665955*), and some correspond to loci with known copy number variation (e.g., *Cd244*, *Trim12*, *Glo1*) (31). A TV score was computed for each gene (and per cell type) to identify transcripts whose variance across the strains could be attributed to meaningful differences, by factoring out technical factors and unwanted variability (Fig. 1A, Supplemental Fig. 1A). In practice we computed a TV score for each gene by contrasting a measure of within-strain variability (computed from biological replicates) to between-strain variability (see *Materials and Methods*). We validated the reproducibility of these TV scores 1) by comparing them to TV quantified from a previous gene expression dataset from macrophages for the Hybrid Mouse Diversity Panel, which included 22 of the strains tested here (11); and 2) by assessing the
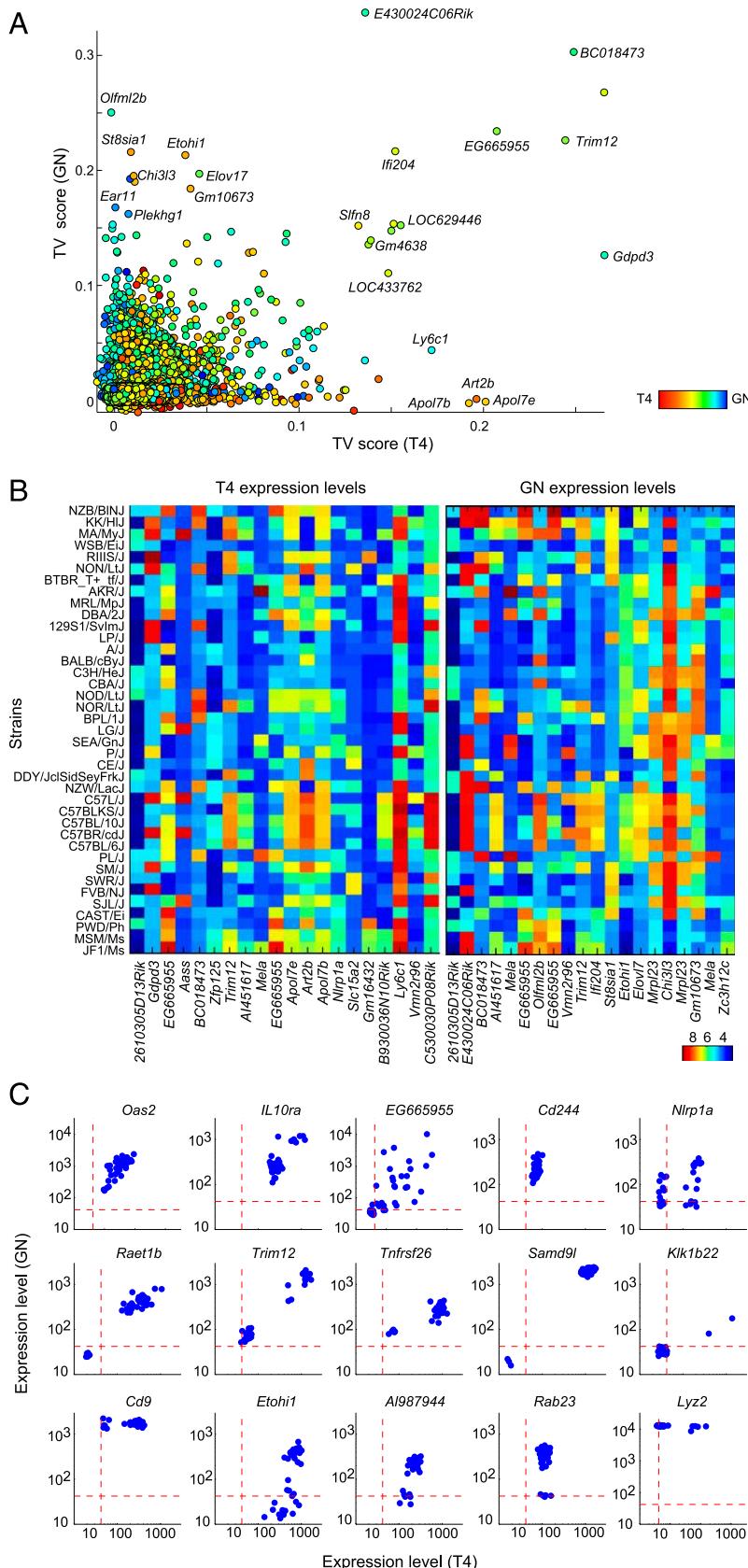
FIGURE 1. The extent and patterns of gene expression variation between inbred mice. A TV score was quantified for each transcript by contrasting a measure of between-strain variability, computed using biological replicates for each strain, with that of within-strain variability. (**A**) TV scores plotted per transcript based on T4 and GN data; each point represents a transcript. Colors depict preferential expression in T4 (red) or GN (blue) as quantified by the difference between mean expression levels. (**B**) Heat map of expression levels for the top 20 most variable transcripts based on T4 and GN data. (**C**) Examples of three types of "variation patterns." For each example transcript, each point represents a (mouse) strain, x-axis shows expression in T4, and y-axis shows expression in GN.

correspondence with reported variability in DNAase hypersensivity sites in eight inbred strains (32). Reassuringly, we found a significant correlation between the TV scores in GN and T4 with those computed from macrophage data (Spearman $\rho = 0.26$ for GN and $\rho = 0.2$ for T4, $p < 10^{-100}$) (Supplemental Fig. 1B). We

also observed significantly higher TV scores for genes previously identified to have variable DNase sites nearby, compared with the background TV scores ($p < 10^{-3}$; Supplemental Fig. 1C).

The distribution of expression across the strains for variable genes covered a wide range with varying patterns (Fig. 1B, 1C). In

most cases, a continuous spectrum was observed, hinting at a complex genetic determinism (Fig. 1C, *top row*). In others, bimodal patterns were observed, which we quantified by assessing the fit of a Gaussian mixture model to the expression pattern of each gene (433 and 567 such bimodal genes for T4 and GN expression, respectively, were identified at a Bonferroni-corrected $p < 0.05$; Fig. 1C; see *Materials and Methods*). We also searched for instances of complete loss of function by using a combination of the bimodality test and expression <0.05 probability of expression in at least two strains (see *Materials and Methods*). Overall, we identified 67 and 53 complete loss-of-function loci in T4 and GN, respectively, of which 10 lost expression in both cells (Fig. 1C, *middle row*; a complete list of loss-of-function loci is available from http://www.immgen.org). An example gene displaying such an on/off pattern was *Raet1b*, which encodes an NK cell lectin-like receptor ligand; it was silent in five of the strains but highly expressed in all others. This pattern was consistent for T4 and GN, likely reflecting the variation in composition of the $Rae1\alpha-\varepsilon$ family, and more generally the multiplicity of targets of NKG2D (33). There were also several instances of "conditional loss-of-function" loci whose expression was sometimes absent in one cell type but present in all strains in the other cell type (Fig. 1C, *bottom row*); for example, *Rab23* transcripts were absent in GNs for some of strains, but present in all T4s. Several of these strains can thus serve as "natural knockouts" or "natural knockdowns" either directly or by backcrossing the segments involved.

We assessed the impact of genetic variation on gene expression at a global level by comparing the relationships between the strains inferred from gene expression data with known genealogies and with genotype-derived relationships (Fig. 2A). Simple examination of the parallel correlation maps of Fig. 2A showed a significant correspondence between strain relationships as derived from the gene expression data and strain genotypes (1, 34). Differences are sharper on the genotype than on the expression matrix, most trivially because the former inherently focuses on differences (SNPs) rather than on transcripts that are largely shared, and/or because most SNPs have no transcriptional consequence. As expected, the wild-derived strains (CAST/EiJ, PWD/PhJ, JF1/Ms, MSM/Ms) were more similar to each other than the classical inbred strains; the CAST/Ei strain, derived from *M. m. castaneus* species, was the most distant outlier, whereas the two *M. m. molossinus*–derived strains (JF1/Ms and MSM/Ms) were more closely related to each other. Other relationships expected from strain histories (35) include the "C57 black" group of strains, the high pairwise similarity between CBA and C3H, or between NOD and NOR, both of which derive from the same stock through selection for susceptibility or resistance to diabetes (36).

For a better handle on the number and identity of differentially expressed transcripts that underlie these relationships, we created a genotype-based dendrogram depicting the relationship between the strains and identified differentially expressed genes that characterized each group (Fig. 2B). The wild-derived group was associated with 2092 differentially expressed genes (5% FDR, of which 204 differ by a fold change >2). These "wild-specific" genes have a range of functionalities, as evidenced by the absence of enrichment for any particular functional category based on gene ontology analysis. Manual exploration of the top associations identified several suggestive differences: the marked underexpression of some TLRs (*Tlr1* and *Tlr7*) in T4 cells from wild-derived strains; several members of the NK family (*Klrd1*, *Klrb1f*) or of the IFN-response pathway (*Ifitm1*, *Ifitm2*) were uniquely expressed in wild-derived T4; and transcripts encoding cell-surface molecules whose distribution is normally restricted to

myeloid cells (*Atp1a3*, *CD163*, *Anxa3*) but were present in T4 from wild-derived strains.

We also noted an intriguing differential expression of *Eps8l1* in the C57 black group. Mutations in *Eps8* family members lead to diverse auditory phenotypes, and the C57 strains are known to develop age-related hearing loss (37). At its inception, this project aimed to find, in the genetic and gene expression data, correlates to the phenotypic traits of these mouse strains, as assembled in the MPD. Unfortunately, a systematic test for association between gene expression levels and an extensive set of behavioral and physiological traits (~1500 traits from the MPD) (38) did not yield significant findings when corrected for random association. Reasons for this may include the limited number of strains for which complete phenotypes were available, buffering of gene expression by regulatory networks, or that the two cell types examined are not relevant to the traits currently in the MPD.

Identifying cis-*eQTLs for neutrophils and T4*

By correlating local genotype and expression data for the mice, we next identified specific *cis* genetic variants that impact gene expression levels in T4 and/or GN (our study did not have the statistical power to detect *trans*-eQTLs). To eliminate broad population-based trends that can result in the inflation of association p values (30), we removed the effect of the top two PCs of the genotype, which represent population structure, from the gene expression data using linear regression. We chose two principal components by assessing the inflation factor λ(24) (see *Materials and Methods*). We performed a *cis*-eQTL analysis with the residuals of this fit, defining *cis* SNPs as mapping in a 1-Mb window from the transcription start site. To increase our power to detect eQTLs that are shared by the two cell types while also detecting cell-specific eQTLs, we performed two analyses: 1) in a "joint analysis," we combined data from the two cell types and evaluated the significance of each SNP-to-gene association using permutation analysis; and 2) in a "cell-specific" analysis, using an ANOVA model, we explicitly tested the significance of a cell-specific SNP effect (see *Materials and Methods*). In both cases, using permutation analysis, we obtained a gene-level p value that took into account the number of tested *cis* variants (26, 27, 39) and defined significant *cis*-eQTLs at 5% FDR based on these gene-level p values.

Using the joint analysis, we identified 1047 genes with *cis*-eQTLs (Fig. 3A, Supplemental Table I; available for browsing on the ImmGen server). The joint analysis increased our discovery power: we identified 262 eQTLs that were not detected in separate analyses of GN and T4 data (774 and 958 eQTLs in separate analysis of T4 and GN, respectively). We observed a significant correlation between *cis*-eQTL association strengths and TV (Spearman $\rho = 0.29$, $p < 10^{-100}$).

Previous studies have identified *cis*-eQTLs for inbred mice in various tissues, including liver (10, 12–14) and immunocytes (10, 11). We compared our set of *cis*-eQTLs with those identified in macrophages (11), which was the most relevant and comparably sized. Orozco et al. (11) identified 1937 genes (corresponding to 4897 SNP-gene pairs) with *cis*-eQTLs controlling transcripts in primary macrophages that were testable in this study. To robustly compare results, we used Storey's π_1 statistic (28) and observed a replication rate of 55% ($p < 0.001$ under permutation testing). This estimate of overlap is similar to those previously reported in the literature for studies involving different cell types or conditions (29, 40–42).

To identify cell-specific *cis*-eQTLs, which should denote genetic impact on cell-specific regulatory pathways, we considered 9698 genes that are expressed in both cell types. We identified 234
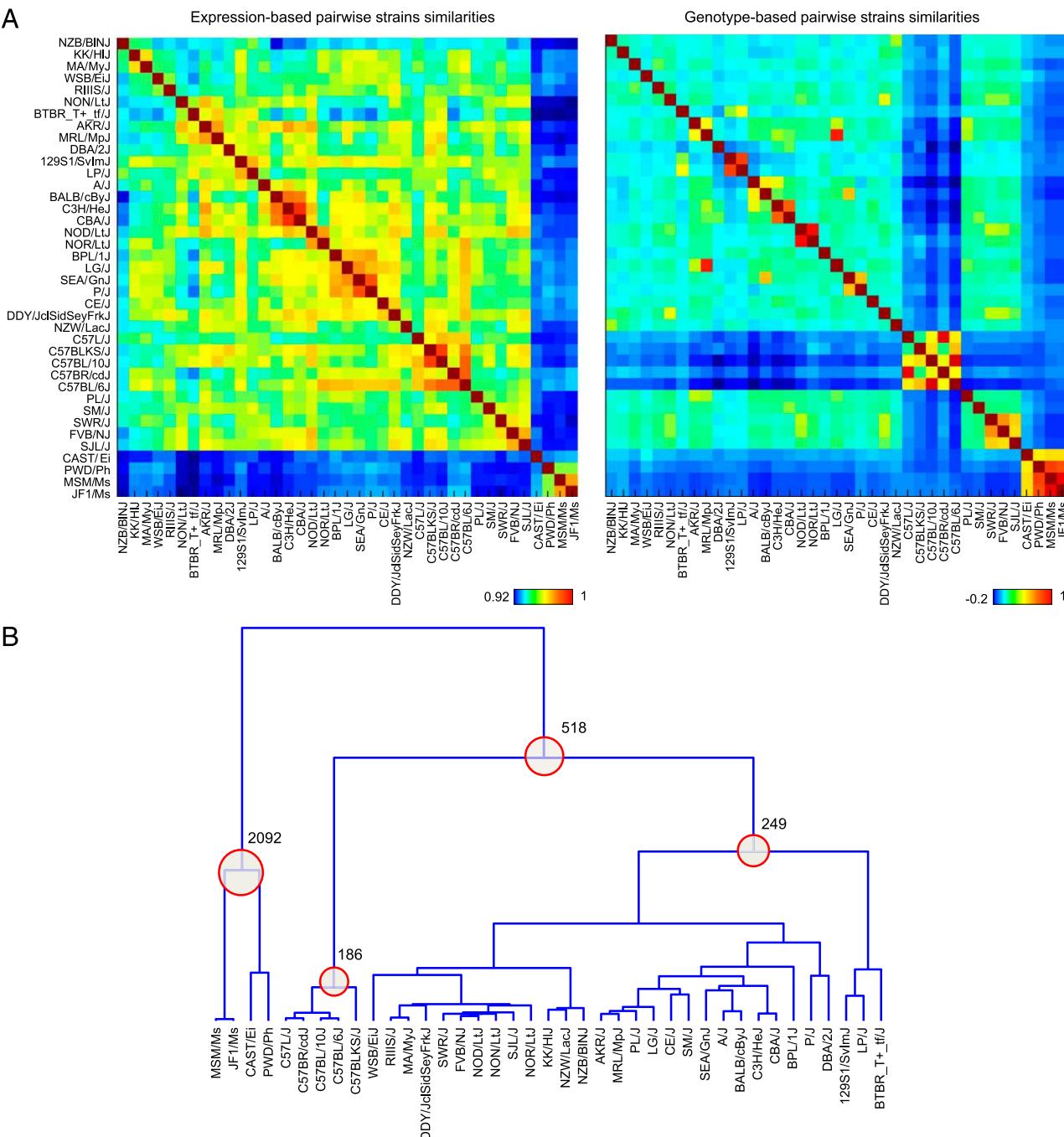
FIGURE 2. Expression-based and genotype-based strain similarities. (**A**) The similarity between each pair of strains was computed from genotype data or gene expression data using Spearman correlation. For expression data, all expressed genes were used in the computation. For genotype data, all variants satisfying the initial criteria (minor allele frequency > 0.05 and missing rate < 10%) were used. Each element in the heat map (matrix) represents the strength of the similarity between a pair of strains. Expression-based and genotype-based similarity heat maps follow the same row and column order. (**B**) The dendrogram was derived from a genotype-based similarity matrix using hierarchical agglomerative clustering. To account for strain-based scale differences between the distribution of similarities, pairwise strain distances for constructing the dendrogram were derived from ranked pairwise similarities for each strain. Each internal node in the dendrogram was used to define two groups (clusters) of strains, which are represented by descending leaves and nondescending leaves. Numbers of differentially expressed genes (defined using t test and a 5% FDR threshold) for groupings that yielded >100 differentially expressed genes at 5% FDR are shown.

significant cell-specific *cis*-eQTL, which indicates that ~30% of discovered *cis*-eQTLs are cell-specific (Fig. 3B), an estimate consistent with recent reports of tissue and cell type specificity of eQTLs in human studies (41, 42). For many genes with a cell-specific eQTL signal, we found major differences between effect sizes for the associated SNP in the two cell types (Fig. 3C). This analysis also identified 17 eQTLs where expression values cor-

relate in an opposite manner in the two cell types. For 10 of the 17 genes, the same top SNP was identified from both GN and T4 data. One of the strongest eQTLs with opposite directionality of effect was observed for *Pot1a* (Fig. 3D). The proportion of directional *cis*-eQTLs discovered in the present study is similar to those previously detected using primary immunocytes in humans (21, 43). This divergence may reflect the fact that a factor
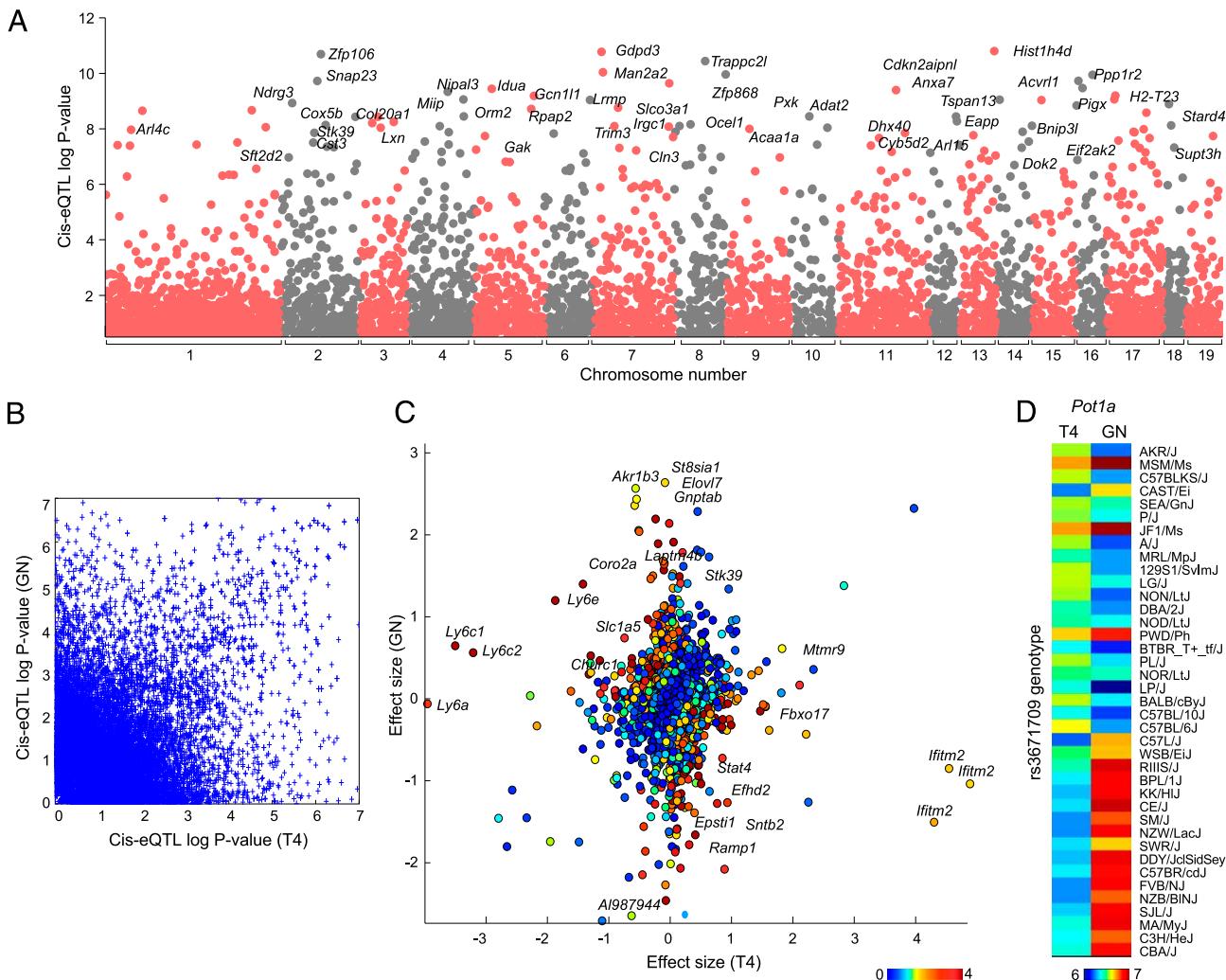
FIGURE 3. GN and T4 joint-discovered and cell-specific *cis*-eQTLs. (**A**) Association *p* values for each transcript and all of its *cis* SNPs (1 Mb from the TSS) were computed using the Wilcoxon rank sum test. Association statistics were computed from both T4 and GN data (joint analysis). Each point represents a transcript; only the best association for each transcript is shown. (**B**) For each cell type, association *p* values for SNP-transcript pairs were computed separately. The association *p* values are shown for the best GN SNP and best T4 SNP for each transcript (i.e., each transcript is represented twice). (**C**) Cell-specific SNP-transcript association *p* values were computed using an ANOVA model. Effect sizes for each transcript and each cell type were computed as the mean difference between strains with alternative and reference alleles. Colors depict the strength (negative $\log_{10}$ *p* value) of cell specificity at gene level. The figure shows effect size and association strengths for the best SNP for all expressed genes. (**D**) Heat map shows the expression levels for the gene *Pot1a* in GN and T4. Strains are sorted based on the genotype of the best SNP for *Pot1a*.

recruited to the same motif acts in an opposite manner in the two cells, but it is also possible that the SNP identified is in linkage disequilibrium with two different causal SNPs, each active in one cell type only.

Identifying regulatory links by coexpression analysis

Gene expression datasets that carry small "perturbations" such as those resulting from genetic variation can be fruitfully exploited to reverse-engineer the structure of genetic regulatory networks (44–46), with the caveat that relationships based solely on baseline coexpression cannot resolve causal from merely correlative associations. We constructed regulatory networks where we inferred interactions (links) between a set of 164 TFs and 3675 candidate downstream targets using stepwise regression. This analysis included only genes that were expressed in both cell types and had a nonnegligible TV score (as per Supplemental Fig. 1A). As above, to avoid artifacts from broad population structure, we used the genotype PC–corrected data. We identified 3462 and 3321 significant (5% FDR) links in T4 data and GN data, re-

spectively, and 4927 links in a joint network constructed using both T4 and GN data. For these networks, few regulatory hubs correlated with expression levels of a large number of targets (>100), and most TFs were linked to ≤15 targets (Fig. 4A, 4B). The major hubs mostly include chromatin modifiers and generic transcriptional activators such as *Smarcd1* and *Smarce1* (SWI/SNF-related chromatin regulators), *Asf1b* (a histone chaperone), *Phf21a* (a histone deacetylase), and the histone deubiquitinase *Mysm1* (Fig. 4B).

We evaluated the overlap between GN- and T4-inferred regulatory links using Storey's π_1 statistic (28). Considering only the interactions passing the statistical significance threshold in the discovery sample (5% FDR), we estimated replication rates of π_1 of 53 and 49% for T4 links in GN and vice versa, respectively, indicating that a large fraction of these associations is shared among the two cell types. Conversely, by directly testing the significance of a cell type–specific effect (see *Materials and Methods*), we estimated that 17% of total interactions are truly cell specific (at 5% FDR). With the interaction test, *Lmo2* was one of
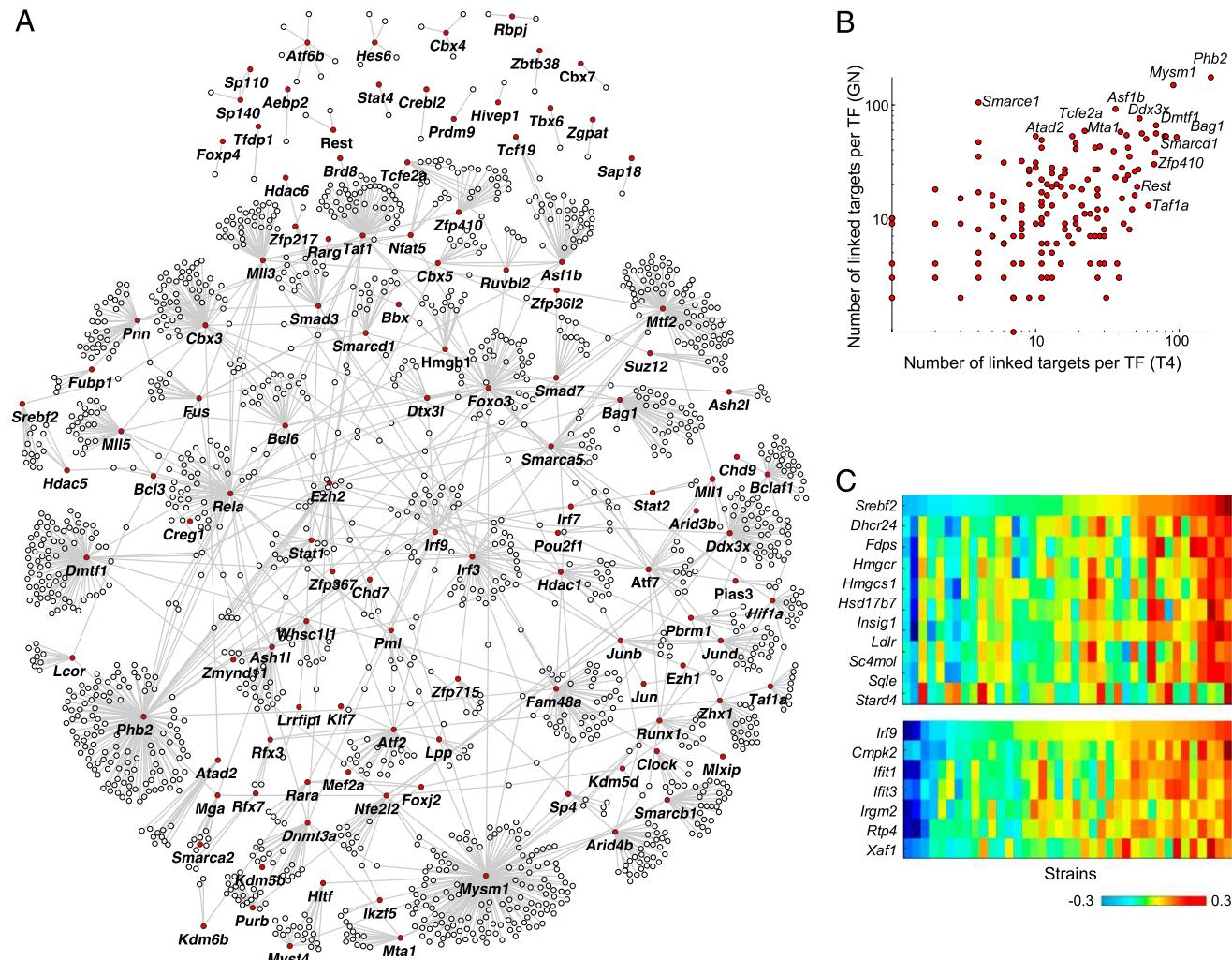
FIGURE 4. Analysis of gene coexpression in mice. (**A**) Overall network showing TF-target links discovered from T4 and GN data (joint network; for visualization purposes, figure only shows a limited set of the strongest links). TFs are marked in red. (**B**) Figure shows the node degree for each TF in T4 (*x*-axis) and GN (*y*-axis) networks. (**C**) Expression heat maps for selected regulators and their inferred targets; *top panel* shows data for *Srebf2* and nine of its targets, and the *bottom panel* shows data for *Irf9* and six of its targets (only targets that overlap with the Ontogenet predictions based on ImmGen data are shown).

the most differential regulatory hubs, with 51 inferred links in GN, but only four potential target genes in T4, which likely denotes a very specific role in GN (its targets in GN do not correspond to a distinct functional category in gene ontology analysis).

For an independent validation of coexpression relationships identifiable from this data, we compared a joint set of links identified from analysis of both cell types (joint network; see *Materials and Methods*) with a previous network constructed from the ImmGen compendium using the Ontogenet algorithm. Ontogenet exploits variation in expression through differentiation cascades to identify regulatory relationships (7). We hypothesized that true TF-target pairs identified by Ontogenet would also show evidence of coexpression when natural genetic variation was the network perturbant. First, we evaluated the strength of coexpression between pairs of TFs-targets previously identified by Ontogenet, and, using the π_1 statistic on adjusted *p* values for coexpression correlation coefficients (see *Materials and Methods*), we found that 27% of these links show evidence of coexpression. Conversely, we checked whether the targets of each TF are also more likely to belong to the same Ontogenet module by testing for significantly enriched Ontogenet modules among the predicted targets of each TF using the hypergeometric test. For 11 of the 127

TFs with at least 10 inferred targets, the targets were significantly enriched in an Ontogenet (fine) module at 5% FDR (Supplemental Table II). For example, *Srebf2*, which encodes a sterol regulatory TF, was associated with 33 genes in this study, 9 of which were part of the same module and predicted by Ontogenet to be regulated by *Srebf2* ($p < 10^{-15}$; Fig. 4C). Another well-known set of replicated links was between *Irf9* and six of its known targets within the IFN response signature ($p < 10^{-8}$; Fig. 4C). Although less robust to differences in inference method and sample sizes, we also directly evaluated the overlap between the inferred regulatory links in this study and those of Ontogenet, where we observed a modest (4%) but significant overlap (hypergeometric $p < 10^{-10}$).

Coexpression relationships that underlie the regulatory links in the present study are not conclusive of directionality. To disentangle causal from simply correlative associations in the present network, we examined the propagated influence of *cis* variants associated with the inferred TFs (47). In practice, we asked whether a *cis*-eQTL SNP for a TF was also correlated with the expression levels of the TF's inferred targets. Within the set of links identified in the joint network (4927 links), 230 links were testable, as they were incident to 1 of the 15 TFs for which

a *cis*-eQTL had been identified above; 50 links (22%) were "causally" supported, in that the genotype at the *cis*-eQTL was significantly associated with the expression of the TF's targets at 5% FDR.

Comparison of variation in gene expression in humans and mice

Comparative studies of gene expression patters across species have mainly focused on comparing similarities and differences in expression across tissues, cell types, or responses to triggers. In these studies, conserved cell type specificity or response to similar triggers across species is taken to indicate conserved functionality (19, 48–53). The impact of genetic variation in each species is averaged, smoothed, or factored out in such analyses. Instead, we sought to exploit the diversity of genetic background across inbred mice and across the human population sampled in the ImmVar study (which includes 360 healthy individuals from Asian, African, and European backgrounds with available expression data for CD4 and CD14 cells; the derivation and analysis of ImmVar datasets are detailed elsewhere; see Ref. 21). ImmVar was designed to match the present analysis in several respects (parallel profiling of T4 in both humans and mice). We took advantage of these congruent datasets to explore the similarities and differences

in expression variability, the impact of *cis* regulatory variation, and the inferred regulatory interactions in mice and humans. For this analysis, we considered 14,130 genes with one-to-one human/mouse orthology (MGI HMD_Human5 set) and restricted the analysis to 5,964 genes expressed in T4 (we only analyzed the T4 data, because of the exact correspondence of this cell type in our data from the two species).

First, we applied the same TV metric of variation discussed above to compare the variability in genes' expression in humans and mice. The TV scores were calculated for human genes by using replicate samples prepared from the same donor (collected at intervals ranging from 3 to 25 wk) after accounting for batch, age, and gender (using linear regression). The TV metric allowed us to eliminate genewise technical variability and only capture biological variability (responding to environmental and/or genetic cues). Human versus mouse comparison of the TV scores showed interesting patterns (Fig. 5A–C); some genes were variable in one species or the other, but in general there was a correlation between TV in mice and humans (Spearman $\rho = 0.16$, $p < 10^{-10}$). We categorized genes into five equally sized bins in each species based on TV scores and found significant predictability of TV scores in the second species based on the assigned bin in the first species (Fig. 5C; Wilcoxon rank sum test p values of 10^{-4} to 10^{-8}
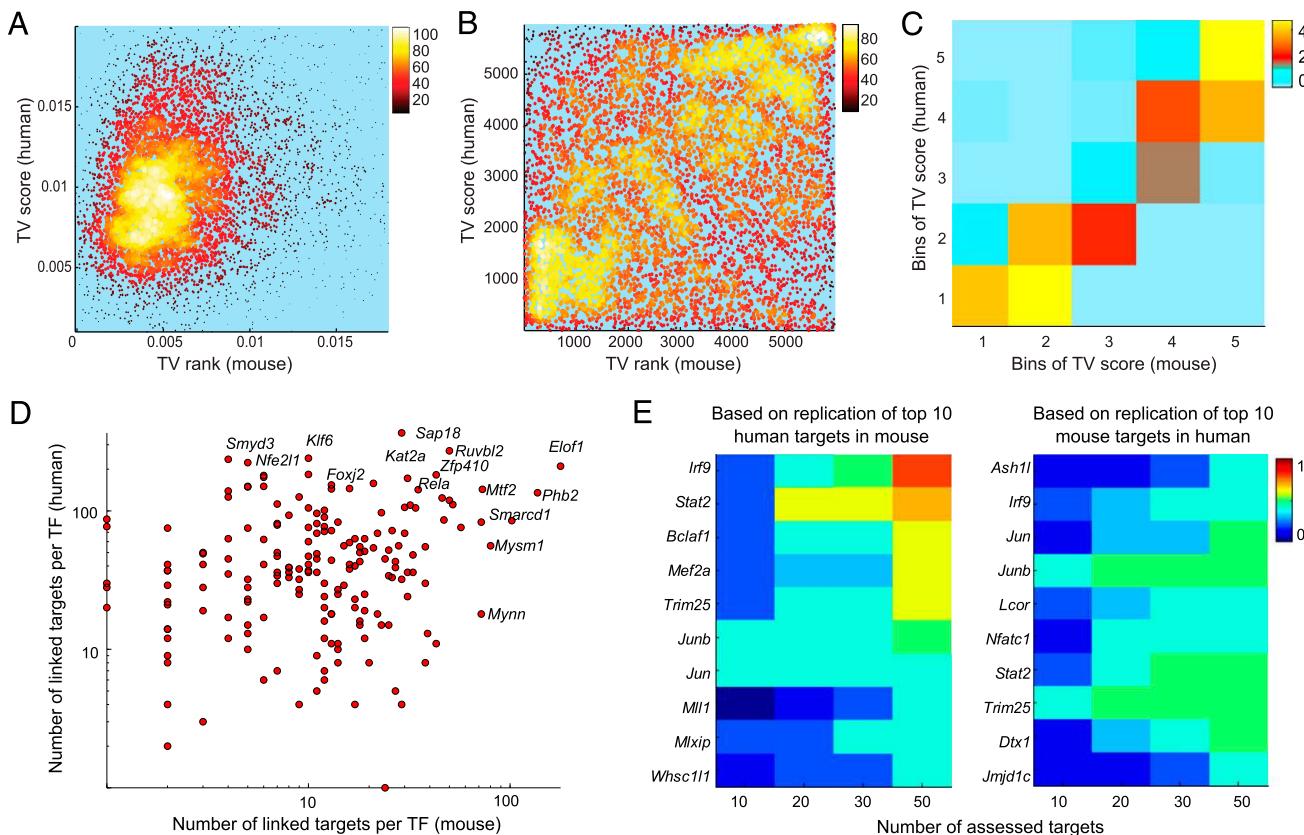
FIGURE 5. Sharing of variability and coexpression in mice and humans. (**A**) Density map of the scatter plot for TV scores (expressed genes only) in T4 of humans and mice (Spearman correlation $\rho = 0.16$). For visualization purpose, the figure is zoomed in on the high-density region. (**B**) Density map of the scatter plot for TV ranks (TV scores were transformed to ranks; in each species, highest TV score is assigned a rank of 5965). (**C**) To quantify the significance of the overlap of variable genes in the two species, mouse and human TV scores were each binned into five equally sized bins, and for each pair of TV bins (a square), the density of genes observed in that square was compared with density of genes in the same square under random mapping of human genes to mouse genes. Fifty thousand permutations (permuting the mapping between human and mouse genes) were performed to quantify the significance of the observed density in each square. Colors depict the strength of these p values (negative $\log_{10}$ p value). (**D**) Figure shows the network degree (number of inferred links) for each TF in the human and mouse networks. (**E**) Heat map summarizes the number of shared top targets for each TF in humana and mice. The top 10 targets for each TF in humans (mice) were first identified, and then the overlap with the top $n = [10, 20, 30, 40, 50]$ mouse (human) targets for the same TF was computed. Only regulators with at least 4 overlapping targets in the list of top 50 targets ($p < 10^{-6}$) are shown. The second plot shows the result where the top 10 targets for each regulator in mice were evaluated in human data.

for bins created in mice and humans, respectively); for example, 26% of the genes in the top bin (most variable) in one species are also categorized in the top bin the other species.

The variability captured by the TV metric encompasses environmental and other factors beyond the impact of genetic variation. To compare the extent of genetically determined variation in gene expression in both species, we evaluated the overlap of *cis*-eQTLs in humans and mice. Using the same methodology as above, we identified 2285 *cis*-eQTL genes in the human ImmVar datasets among the set of 7098 expressed genes in both species (either cell type) (eQTLs identified using the joint analysis; see *Materials and Methods*). Of the 674 genes associated with an eQTL discovered in mice for this set of expressed genes, 275 were also associated with an eQTL based on human data (hypergeometirc $p < 10^{-6}$), implying that genes that show a significant impact of local genetic variation tend to overlap in mice and humans, even though the variants themselves are certainly unrelated.

Next we compared gene regulatory networks constructed from the T4 dataset for both humans and mice. The motivation was to analyze the evolutionary conservation of these regulatory links, and from a practical standpoint to validate the inferences by confirmation in another species. For each species, we first constructed a network using stepwise regression as above (see *Materials and Methods*). At a global level, we observed a correlation between TFs' out-degree (the number of targets connected to each TF; Fig. 5D), with 38% of the top 20% hubs in one species shared with the second species ($p < 0.01$). As above, chromatin modifiers tend to be strong regulatory hubs in both species. We used the π_1 statistic to estimate the fraction of TF-to-target links identified in one species that are replicated in the second species. A 47% replication rate was observed for mouse links in the human T4 dataset, and a 19% replication rate was found for human links in the mouse dataset (permutation analysis $p < 0.001$) (Supplemental Fig. 2A, 2B). Finally, in a regulator-centric analysis, we also assessed the correspondence between top coexpressed links for each TF in the two species. To do so, we assessed the overlap and the distribution of coexpression values (correlation coefficients) for the top $n = [10, 20, 30, 50]$ targets of each TF in the second species (see *Materials and Methods*). Of the 189 TFs that were analyzed, we identified 17 TFs whose top 10 targets were highly conserved (hypergeometic test $p < 10^{-6}$; Fig. 5E), and the top targets of an additional set of 42 TFs showed significant evidence of high coexpression values in the second species (using the Wilcoxon rank sum test; Supplemental Fig. 2C, 2D). Among these highly conserved coexpression links, we identified well-known relationships, including coexpression between *Irf9* and IFN response genes *Dhx58, Ifi35, Irf1, Pml, Trafd1,* and *Stat2* and strong coexpression between *Jun* and *Fos* and known early response genes (*Ier2, Gadd45b*). We did not attempt to interpret the divergent regulatory links within these datasets: these are not conclusive of true differences, because multiple confounding factors can underlie such differences (different environmental influences, much smaller sample size for the mouse data, imperfect mapping of human to mouse probes). Overall, these comparisons show that many of the regulatory connections that can be inferred from the interindividual variation in expression profiles are conserved between these two mammalian species.

Discussion

Our motivation, in the context of the ImmGen and MDP programs, was threefold: to serve as a reference of genomic and genetic information relevant to the immune function in mice, to provide additional material for the dissection of genetic regulatory networks, and to provide a documented basis for comparison of the mouse and human immune systems.

In terms of resources, the present data provide useful information at several levels, and are all available interactively from the ImmGen and MDP Web browsers (http://www.immgen.org, http://phenome.jax.org). We detected a number of genes with a >2-fold change in expression across the strains (the empirical rule of thumb for functional significance). It will be interesting to see how these traits segregate in settings such as the Collaborative Cross strains, where the chromosomal segments can be traced in the recombinant chromosomes, allowing refinement of the genetic control and/or discovery of epistatic modifiers. Variation followed both bimodal and continuous expression patterns across mouse strains, including a few loci with complete loss of expression in some of the strains. As such, these can serve as a resource of natural knockdowns or natural knockouts (some affecting both cell types, others cell-specific). The 1222 *cis*-eQTLs detected in the two immunological cell types are also available through the dedicated ImmGen interface. However, the relatively large sizes of the linkage disequilibrium blocks in these inbred mouse strains, relative to outbred humans or mice (22), make it impossible to pinpoint with precision the causal variant, and the SNPs listed should only be considered as likely proxies of the truly relevant variant. Nevertheless, the patterns of variation and the eQTLs described here, and their conservation across species, may help to interpret differences in susceptibility to infection or autoimmune diseases, in a manner than translates to genetic in risk human populations.

The patterns of interstrain variability followed, as expected, the patterns of genetic distance and genealogical history between the strains. Wild-derived strains were predictably more distant from the classic inbred lines. Some of this genetic distance may be directly related to selective events during mouse domestication or to the input from non-*domesticus* subspecies. We previously reported that a variant at the *Il1b* locus, which leads to a 5- to 10-fold greater IL-1 response to stimulation through innate receptor pathways, is frequent in wild-derived strains but quite rare among classical inbred strains (54), and some of the expression variations uncovered in the present study may be of the same nature (e.g., *Tlr1* and *Tlr7*, although in this instance it is the wild-derived strains that show low or absent expression in T4). Some genes whose expression is normally confined to myeloid cells across the ImmGen compendium were expressed in T4 of the wild-derived strains. Some of these conditionally expressed genes are surprising, such as the expression of CD163, a scavenger receptor on macrophages whose function in T4 is not immediately obvious. We might speculate that this reflects a mode of innate sensing by T4 that was lost during domestication (interestingly, however, human T cells do not express these monocyte genes).

The distribution of *cis*-acting genetic variation was significantly correlated with the variation in expression for the most variable genes, although many of the genes with a high TV score did not show an active *cis*-eQTL. Recent literature indicates a larger impact for local sequence variation, which may have been detectable with larger sample sizes (29, 55), perhaps attainable with a larger study of outbred or Collaborative Cross mice. We note that the number of *cis*-eQTLs detected in the present study is more than what would be expected from an equally sized human dataset (28) where the effect of environment cannot be as effectively controlled.

The coexpression-based network estimated in this study extended the analysis of the regulatory networks of immunocytes initiated in ImmGen (7), and we observed a comforting degree of overlap between the two analyses. Although coexpression cannot formally identify causal directionality in a correlated pair (i.e., who controls whom), the selection of transcriptional regu-

lators provides a functional prior for directionality. Indeed, when we searched for causal chains of associations, by correlating a *cis* variant impacting the expression of a TF with the TF's downstream effects on its inferred targets, a significant portion (22%) of the testable links turned out to be causally driven. Interestingly, connections identified from interstrain variation more frequently involved generic regulators such as chromatin modifiers, which showed up in the present study as major hubs, than classic sequence-specific DNA-binding TFs and lineage determination factors (which were predictably more prevalent in the Ontogenet analysis). This difference is in line with the paucity of *cis*-eQTLs for classic TF regulators involved in differentiation or lineage determination, as previously shown in human cells (29, 56). One might speculate that a degree of "noise" in transcript level resulting from variations in redundant and pleiotropic factors is better tolerated (or even favored) than variation in more specific factors that form the blueprint of cell differentiation and lineage determination. This dominance of broad transcriptional regulators as major coexpression hubs was strikingly reproduced in the human datasets.

Finally, we observed sharing of the patterns of expression variability between humans and mice. Both genetic and nongenetic factors can result in expression variability, and we also observed significantly nonrandom overlaps in genes that are associated with *cis*-eQTLs in both species. From an evolutionary standpoint, this "conservation of variability" can be explained by species-shared strength of selection pressure on gene expression levels (57): variation in more redundant and/or less essential genes is better tolerated, and these characteristics would tend to be conserved. It is also possible that some of this species-shared variability is in genes whose intraspecies variation is favorable. The extraordinary diversification of coding sequence in MHC genes favors heterozygosity in individuals and diversity at the level of the species to best meet variable pathogen challenges (58). Similarly, it may be advantageous to diversify the levels of expression, and hence of response potential, in pathways of the immune system. Genes controlling activating and inhibitory NK receptors would plausibly fall in that category. From a mechanistic standpoint, one might also imagine different scenarios for the roots of this reproducible variability: some regions of the genome may be inherently noisier, a characteristic preserved during the evolutionary shuffling of syntenic chromosomal regions; regulatory feedback loops that control individual genes or sets of genes may be more or less robust; and microRNAs or other noncoding RNAs might make for a variable degree of control. Any of these mechanisms may have been, to an extent, preserved through 200 million years of evolution to conserve immunologically relevant variation.

Acknowledgments

ImmGen Consortium

David A. Blair,[1] Michael L. Dustin,[1] Susan A. Shinton,[2] Richard R. Hardy,[2] Tal Shay,[3] Aviv Regev,[3] Nadia Cohen,[4] Patrick Brennan,[4] Michael Brenner,[4] Francis Kim,[5] Tata Nageswara Rao,[5] Amy Wagers,[5] Tracy Heng,[6] Jeffrey Ericson,[6] Katherine Rothamel,[6] Adriana Ortiz-Lopez,[6] Diane Mathis,[6] Christophe Benoist,[6] Taras Kreslavsky,[7] Anne Fletcher,[7] Kutlu Elpek,[7] Angelique Bellemare-Pelletier,[7] Deepali Malhotra,[7] Shannon Turley,[7] Jennifer Miller,[8] Brian Brown,[8] Miriam Merad,[8] Emmanuel L. Gautier,[8,9] Claudia Jakubzick,[8] Gwendalyn J. Randolph,[8,9] Paul Monach,[10] Adam J. Best,[11] Jamie Knell,[11] Ananda Goldrath,[11] Vladimir Jojic,[12] Daphne Koller,[12] David Laidlaw,[13] Jim Collins,[14] Roi Gazit,[15] Derrick J. Rossi,[15] Nidhi Malhotra,[16] Katelyn Sylvia,[16] Joonsoo Kang,[16] Natalie A. Bezman,[17] Joseph C. Sun,[17] Gundula Min-Oo,[17] Charlie C. Kim,[17] Lewis L. Lanier[17]

[1]Skirball Institute of Biomolecular Medicine, New York University School of Medicine, New York, NY 10016. [2]Fox Chase Cancer Center, Philadelphia, PA 19111. [3]Broad Institute and Department of Biology, Massachusetts Institute of Technology, Cambridge, MA 02142. [4]Division of Rheumatology, Immunology and Allergy, Brigham and Women's Hospital, Boston, MA 02115. [5]Joslin Diabetes Center, Boston, MA 02215. [6]Division of Immunology, Department of Microbiology and Immunobiology, Harvard Medical School, Boston, MA 02115. [7]Dana Farber Cancer Institute and Harvard Medical School, Boston, MA 02115. [8]Icahn Medical Institute, Mount Sinai Hospital, New York, NY 10029. [9]Department of Pathology and Immunology, Washington University, St. Louis, MO 63110. [10]Department of Medicine, Boston University, Boston, MA 02118. [11]Division of Biological Sciences, University of California San Diego, La Jolla, CA 92093. [12]Computer Science Department, Stanford University, Stanford, CA 94305. [13]Computer Science Department, Brown University, Providence, RI 02912. [14]Department of Biomedical Engineering, Howard Hughes Medical Institute, Boston University, Boston, MA 02115. [15]Program in Molecular Medicine, Children's Hospital, Boston, MA 02115. [16]Department of Pathology, University of Massachusetts Medical School, Worcester, MA 01655. [17]Department of Microbiology and Immunology, University of California San Francisco, San Francisco, CA 94143.

Disclosures

References

1. Beck, J. A., S. Lloyd, M. Hafezparast, M. Lennon-Pierce, J. T. Eppig, M. F. Festing, and E. M. Fisher. 2000. Genealogies of mouse inbred strains. *Nat. Genet.* 24: 23–25.
2. Wade, C. M., and M. J. Daly. 2005. Genetic variation in laboratory mice. *Nat. Genet.* 37: 1175–1180.
3. Waterston, R. H., K. Lindblad-Toh, E. Birney, J. Rogers, J. F. Abril, P. Agarwal, R. Agarwala, R. Ainscough, M. Alexandersson, P. An, et al; Mouse Genome Sequencing Consortium. 2002. Initial sequencing and comparative analysis of the mouse genome. *Nature* 420: 520–562.
4. Keane, T. M., L. Goodstadt, P. Danecek, M. A. White, K. Wong, B. Yalcin, A. Heger, A. Agam, G. Slater, M. Goodson, et al. 2011. Mouse genomic variation and its effect on phenotypes and gene regulation. *Nature* 477: 289–294.
5. Bogue, M. A., and S. C. Grubb. 2004. The Mouse Phenome Project. *Genetica* 122: 71–74.
6. Heng, T. S., and M. W. Painter; Immunological Genome Project Consortium. 2008. The Immunological Genome Project: networks of gene expression in immune cells. *Nat. Immunol.* 9: 1091–1094.
7. Jojic, V., T. Shay, K. Sylvia, O. Zuk, X. Sun, J. Kang, A. Regev, D. Koller, A. J. Best, J. Knell, et al; Immunological Genome Project Consortium. 2013. Identification of transcriptional regulators in the mouse immune system. *Nat. Immunol.* 14: 633–643.
8. Montgomery, S. B., and E. T. Dermitzakis. 2011. From expression QTLs to personalized transcriptomics. *Nat. Rev. Genet.* 12: 277–282.
9. Civelek, M., and A. J. Lusis. 2014. Systems genetics approaches to understand complex traits. *Nat. Rev. Genet.* 15: 34–48.
10. Gerrits, A., Y. Li, B. M. Tesson, L. V. Bystrykh, E. Weersing, A. Ausema, B. Dontje, X. Wang, R. Breitling, R. C. Jansen, and G. de Haan. 2009. Expression quantitative trait loci are highly sensitive to cellular differentiation state. *PLoS Genet.* 5: e1000692.
11. Orozco, L. D., B. J. Bennett, C. R. Farber, A. Ghazalpour, C. Pan, N. Che, P. Wen, H. X. Qi, A. Mutukulu, N. Siemers, et al. 2012. Unraveling inflammatory responses using systems genetics and gene-environment interactions in macrophages. *Cell* 151: 658–670.
12. Bennett, B. J., C. R. Farber, L. Orozco, H. M. Kang, A. Ghazalpour, N. Siemers, M. Neubauer, I. Neuhaus, R. Yordanova, B. Guan, et al. 2010. A high-resolution association mapping panel for the dissection of complex traits in mice. *Genome Res.* 20: 281–290.
13. Aylor, D. L., W. Valdar, W. Foulds-Mathes, R. J. Buus, R. A. Verdugo, R. S. Baric, M. T. Ferris, J. A. Frelinger, M. Heise, M. B. Frieman, et al. 2011. Genetic analysis of complex traits in the emerging Collaborative Cross. *Genome Res.* 21: 1213–1222.
14. McClurg, P., J. Janes, C. Wu, D. L. Delano, J. R. Walker, S. Batalov, J. S. Takahashi, K. Shimomura, A. Kohsaka, J. Bass, et al. 2007. Genomewide association analysis in diverse inbred mice: power and population structure. *Genetics* 176: 675–683.
15. Davis, M. M. 2008. A prescription for human immunology. *Immunity* 29: 835–838.
16. Payne, K. J., and G. M. Crooks. 2007. Immune-cell lineage commitment: translation from mice to humans. *Immunity* 26: 674–677.
17. Odom, D. T., R. D. Dowell, E. S. Jacobsen, W. Gordon, T. W. Danford, K. D. MacIsaac, P. A. Rolfe, C. M. Conboy, D. K. Gifford, and E. Fraenkel. 2007. Tissue-specific transcriptional regulation has diverged significantly between human and mouse. *Nat. Genet.* 39: 730–732.

18. Ravasi, T., H. Suzuki, C. V. Cannistraci, S. Katayama, V. B. Bajic, K. Tan, A. Akalin, S. Schmeier, M. Kanamori-Katayama, N. Bertin, et al. 2010. An atlas of combinatorial transcriptional regulation in mouse and man. *Cell* 140: 744–752.

19. Shay, T., V. Jojic, O. Zuk, K. Rothamel, D. Puyraimond-Zemmour, T. Feng, E. Wakamatsu, C. Benoist, D. Koller, and A. Regev; ImmGen Consortium. 2013. Conservation and divergence in the transcriptional programs of the human and mouse immune systems. *Proc. Natl. Acad. Sci. USA* 110: 2946–2951.

20. Lee, M. N., C. Ye, A. C. Villani, T. Raj, W. Li, T. M. Eisenhaure, S. H. Imboywa, P. I. Chipendo, F. A. Ran, K. Slowikowski, et al. 2014. Common genetic variants modulate pathogen-sensing responses in human dendritic cells. *Science* 343: 1246980.

21. Raj, T., K. Rothamel, S. Mostafavi, C. Ye, M. N. Lee, J. M. Replogle, T. Feng, M. Lee, N. Asinovski, I. Frohlich, et al. 2014. Polarization of the effects of autoimmune and neurodegenerative risk alleles in leukocytes. *Science* 344: 519–523.

22. Ye, C. J., T. Feng, H. K. Kwon, T. Raj, M. T. Wilson, N. Asinovski, C. McCabe, M. H. Lee, I. Frohlich, H. I. Paik, et al. 2014. Intersection of population variation and autoimmunity genetics in human T cell activation. *Science* 345: 1254665.

23. Kirby, A., H. M. Kang, C. M. Wade, C. Cotsapas, E. Kostem, B. Han, N. Furlotte, E. Y. Kang, M. Rivas, M. A. Bogue, et al. 2010. Fine mapping in 94 inbred mouse strains using a high-density haplotype resource. *Genetics* 185: 1081–1095.

24. Kang, H. M., N. A. Zaitlen, C. M. Wade, A. Kirby, D. Heckerman, M. J. Daly, and E. Eskin. 2008. Efficient control of population structure in model organism association mapping. *Genetics* 178: 1709–1723.

25. Devlin, B., and K. Roeder. 1999. Genomic control for association studies. *Biometrics* 55: 997–1004.

26. Churchill, G. A., and R. W. Doerge. 1994. Empirical threshold values for quantitative trait mapping. *Genetics* 138: 963–971.

27. Stranger, B. E., S. B. Montgomery, A. S. Dimas, L. Parts, O. Stegle, C. E. Ingle, M. Sekowska, G. D. Smith, D. Evans, M. Gutierrez-Arcelus, et al. 2012. Patterns of *cis* regulatory variation in diverse human populations. *PLoS Genet.* 8: e1002639.

28. Storey, J. D., W. Xiao, J. T. Leek, R. G. Tompkins, and R. W. Davis. 2005. Significance analysis of time course microarray experiments. *Proc. Natl. Acad. Sci. USA* 102: 12837–12842.

29. Battle, A., S. Mostafavi, X. Zhu, J. B. Potash, M. M. Weissman, C. McCormick, C. D. Haudenschild, K. B. Beckman, J. Shi, R. Mei, et al. 2014. Characterizing the genetic basis of transcriptome diversity through RNA-sequencing of 922 individuals. *Genome Res.* 24: 14–24.

30. Kang, H. M., C. Ye, and E. Eskin. 2008. Accurate discovery of expression quantitative trait loci under confounding from spurious and genuine regulatory hotspots. *Genetics* 180: 1909–1925.

31. Orozco, L. D., S. J. Cokus, A. Ghazalpour, L. Ingram-Drake, S. Wang, A. van Nas, N. Che, J. A. Araujo, M. Pellegrini, and A. J. Lusis. 2009. Copy number variation influences gene expression and metabolic traits in mice. *Hum. Mol. Genet.* 18: 4118–4129.

32. Hosseini, M., L. Goodstadt, J. R. Hughes, M. S. Kowalczyk, M. de Gobbi, G. W. Otto, R. R. Copley, R. Mott, D. R. Higgs, and J. Flint. 2013. Causes and consequences of chromatin variation between inbred mice. *PLoS Genet.* 9: e1003570.

33. Champsaur, M., and L. L. Lanier. 2010. Effect of NKG2D ligand expression on host immune responses. *Immunol. Rev.* 235: 267–285.

34. Petkov, P. M., Y. Ding, M. A. Cassell, W. Zhang, G. Wagner, E. E. Sargent, S. Asquith, V. Crew, K. A. Johnson, P. Robinson, et al. 2004. An efficient SNP system for mouse genome scanning and elucidating strain relationships. *Genome Res.* 14: 1806–1811.

35. Morse, III, H. C. 1978. Introduction. In *Origins of inbred mice: proceedings of a workshop, Bethesda, Maryland, February 14-16.* H. C. Morse, ed. Academic Press, New York, p. 19–20.

36. Kikutani, H., and S. Makino. 1992. The murine autoimmune diabetes model: NOD and related strains. *Adv. Immunol.* 51: 285–322.

37. Zheng, Q. Y., K. R. Johnson, and L. C. Erway. 1999. Assessment of hearing in 80 inbred strains of mice by ABR threshold analyses. *Hear. Res.* 130: 94–107.

38. Grubb, S. C., C. J. Bult, and M. A. Bogue. 2014. Mouse phenome database. *Nucleic Acids Res.* 42: D825–D834.

39. Montgomery, S. B., M. Sammeth, M. Gutierrez-Arcelus, R. P. Lach, C. Ingle, J. Nisbett, R. Guigo, and E. T. Dermitzakis. 2010. Transcriptome genetics using second generation sequencing in a Caucasian population. *Nature* 464: 773–777.

40. Nica, A. C., L. Parts, D. Glass, J. Nisbet, A. Barrett, M. Sekowska, M. Travers, S. Potter, E. Grundberg, K. Small, et al; MuTHER Consortium. 2011. The architecture of gene regulatory variation across multiple human tissues: the MuTHER study. *PLoS Genet.* 7: e1002003.

41. Grundberg, E., K. S. Small, A. K. Hedman, A. C. Nica, A. Buil, S. Keildson, J. T. Bell, T. P. Yang, E. Meduri, A. Barrett, et al; Multiple Tissue Human Expression Resource (MuTHER) Consortium. 2012. Mapping *cis*- and *trans*-regulatory effects across multiple tissues in twins. *Nat. Genet.* 44: 1084–1089.

42. Flutre, T., X. Wen, J. Pritchard, and M. Stephens. 2013. A statistical framework for joint eQTL analysis in multiple tissues. *PLoS Genet.* 9: e1003486.

43. Fairfax, B. P., S. Makino, J. Radhakrishnan, K. Plant, S. Leslie, A. Dilthey, P. Ellis, C. Langford, F. O. Vannberg, and J. C. Knight. 2012. Genetics of gene expression in primary immune cells identifies cell type-specific master regulators and roles of HLA alleles. *Nat. Genet.* 44: 502–510.

44. Segal, E., M. Shapira, A. Regev, D. Pe'er, D. Botstein, D. Koller, and N. Friedman. 2003. Module networks: identifying regulatory modules and their condition-specific regulators from gene expression data. *Nat. Genet.* 34: 166–176.

45. Gardner, T. S., D. di Bernardo, D. Lorenz, and J. J. Collins. 2003. Inferring genetic networks and identifying compound mode of action via expression profiling. *Science* 301: 102–105.

46. Bar-Joseph, Z., G. K. Gerber, T. I. Lee, N. J. Rinaldi, J. Y. Yoo, F. Robert, D. B. Gordon, E. Fraenkel, T. S. Jaakkola, R. A. Young, and D. K. Gifford. 2003. Computational discovery of gene modules and regulatory networks. *Nat. Biotechnol.* 21: 1337–1342.

47. Zhu, J., B. Zhang, E. N. Smith, B. Drees, R. B. Brem, L. Kruglyak, R. E. Bumgarner, and E. E. Schadt. 2008. Integrating large-scale functional genomic data to dissect the complexity of yeast regulatory networks. *Nat. Genet.* 40: 854–861.

48. Miller, J. A., S. Horvath, and D. H. Geschwind. 2010. Divergence of human and mouse brain transcriptome highlights Alzheimer disease pathways. *Proc. Natl. Acad. Sci. USA* 107: 12698–12703.

49. Chan, E. T., G. T. Quon, G. Chua, T. Babak, M. Trochesset, R. A. Zirngibl, J. Aubin, M. J. Ratcliffe, A. Wilde, M. Brudno, et al. 2009. Conservation of core gene expression in vertebrate tissues. *J. Biol.* 8: 33.

50. Zheng-Bradley, X., J. Rung, H. Parkinson, and A. Brazma. 2010. Large scale comparison of global gene expression patterns in human and mouse. *Genome Biol.* 11: R124.

51. Su, A. I., T. Wiltshire, S. Batalov, H. Lapp, K. A. Ching, D. Block, J. Zhang, R. Soden, M. Hayakawa, G. Kreiman, et al. 2004. A gene atlas of the mouse and human protein-encoding transcriptomes. *Proc. Natl. Acad. Sci. USA* 101: 6062–6067.

52. Strand, A. D., A. K. Aragaki, Z. C. Baquet, A. Hodges, P. Cunningham, P. Holmans, K. R. Jones, L. Jones, C. Kooperberg, and J. M. Olson. 2007. Conservation of regional gene expression in mouse and human brain. *PLoS Genet.* 3: e59.

53. Enard, W., P. Khaitovich, J. Klose, S. Zöllner, F. Heissig, P. Giavalisco, K. Nieselt-Struwe, E. Muchmore, A. Varki, R. Ravid, et al. 2002. Intra- and interspecific variation in primate gene expression patterns. *Science* 296: 340–343.

54. Ohmura, K., A. Johnsen, A. Ortiz-Lopez, P. Desany, M. Roy, W. Besse, J. Rogus, M. Bogue, A. Puech, M. Lathrop, et al. 2005. Variation in IL-1β gene expression is a major determinant of genetic differences in arthritis aggressivity in mice. *Proc. Natl. Acad. Sci. USA* 102: 12489–12494.

55. Lappalainen, T., M. Sammeth, M. R. Friedländer, P. A. 't Hoen, J. Monlong, M. A. Rivas, M. Gonzàlez-Porta, N. Kurbatova, T. Griebel, P. G. Ferreira, et al; Geuvadis Consortium. 2013. Transcriptome and genome sequencing uncovers functional variation in humans. *Nature* 501: 506–511.

56. Ferraro, A., A. M. D'Alise, T. Raj, N. Asinovski, R. Phillips, A. Ergun, J. M. Replogle, A. Bernier, L. Laffel, B. E. Stranger, et al. 2014. Interindividual variation in human T regulatory cells. *Proc. Natl. Acad. Sci. USA* 111: E1111–E1120.

57. Georgi, B., B. F. Voight, and M. Bućan. 2013. From mouse to human: evolutionary genomics analysis of human orthologs of essential genes. *PLoS Genet.* 9: e1003484.

58. Parham, P., and T. Ohta. 1996. Population biology of antigen presentation by MHC class I molecules. *Science* 272: 67–74.

Supplementary Figure 1

A

B

C
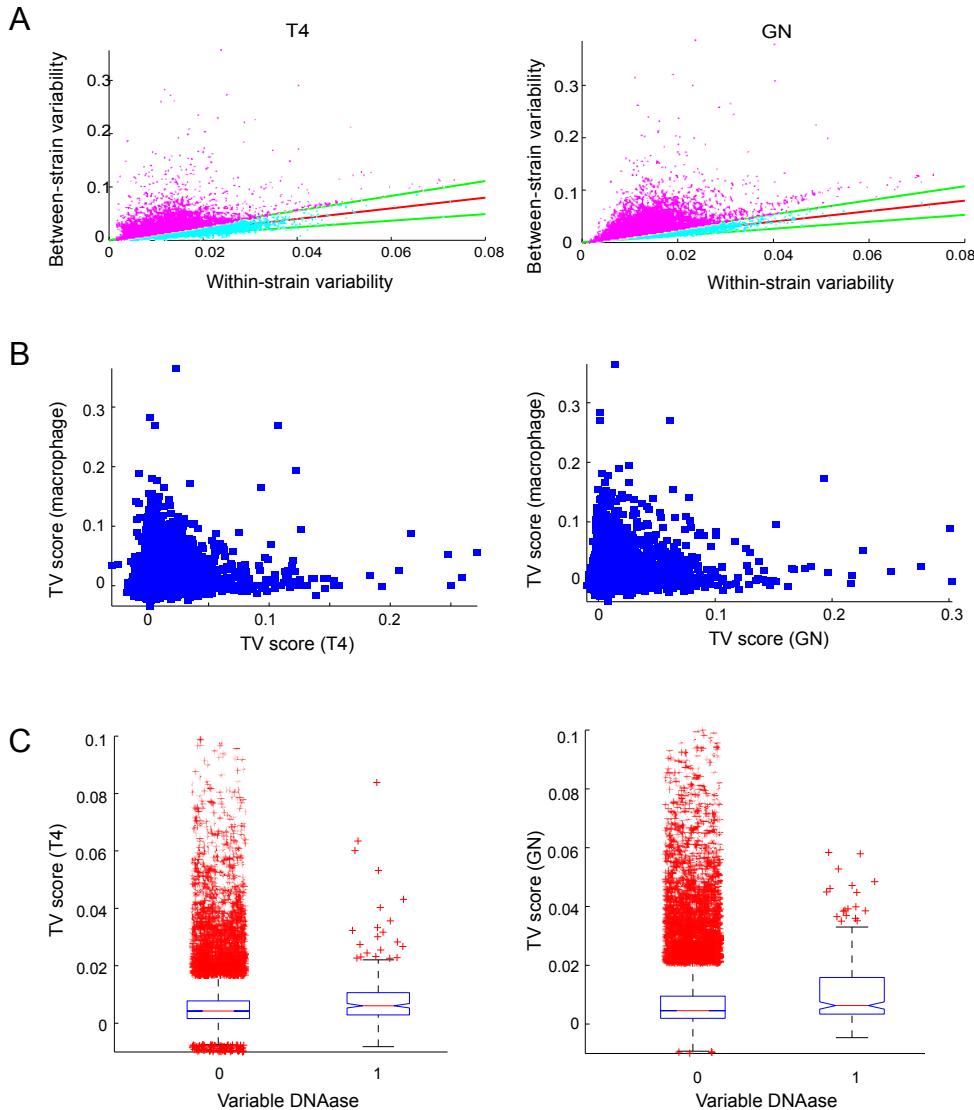
Figure S1. The True variation (TV) metric. (A) For each transcript, within strain-variability for each strain was computed as the absolute difference between replicates, averaged across all strains and divided by mean expression. Within-strain variability was computed as mean absolute deviation across the strains, and then divided by mean transcript expression. Each point represents a transcript. For identifying transcripts with high confidence TV scores, the distribution of negative TV scores (points below the red lines) was used to define a window around the line that corresponds to zero TV (defined by the green lines). The TV scores that lie in this window defined a "null" Gaussian distribution, which was used to compute the p-value for each TV score. **(B)** Scatter plot of TV scores computed from this study and a previous gene expression study in Macrophages (Orozco et al., 2012) (Spearman correlation rho=0.2 and P-value < 1e-100 for T4; rho=0.26 and P-value < 1e-200 for GN). **(C)** Transcripts are grouped into those with (group=1) or without (group=0) nearby variable DNAase sites (Hosseini *et al.*, 2013). Boxplots show the median, 25% and 75% quantiles of TV scores for each group.

Supplementary Figure 2
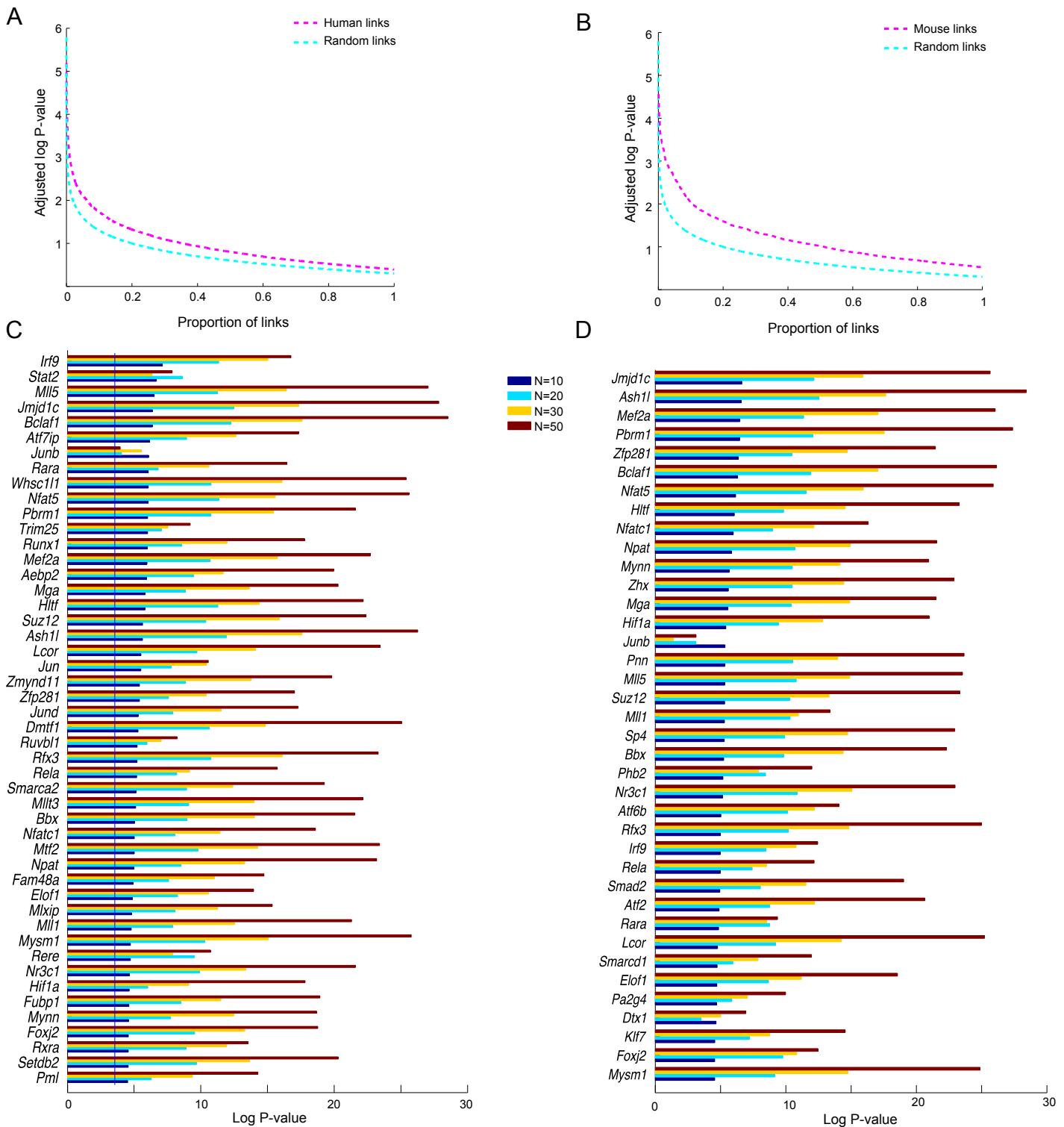
Figure S2. Cross-species replication of inferred regulatory links. (A-B) Inferred TF-target links from one species are assessed in the second species. Figure shows the CDF of log P-values for links identified in the "discovery" species as assessed in the "test" species. For sub-figure **(A)** links were identified in human and assessed in mouse. For sub-figure **(B)** links were identified in mouse and assessed in human. **(C-D)** For the top N={10, 20, 30, 50} targets of each TF in mouse (human), we computed the enrichment for high co-expression values (correlation coefficient) with its top N target in human (mouse) using the Wilcoxon rank sum test, and considering as background the correlation coefficients for associations between that TF and all other genes. Figures show the TFs whose targets are significantly "replicable" across species (using a 5% FDR threshold).

Table S1. Joint and cell-specific cis-eQTLs for 39 inbred mice using expression data from GN and T4 cells.

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10373944	Zmat5	11	4638506	rs29415458	4.0	2.1E-03	joint
10542750	Med21	6	146715724	rs30759086	4.0	2.1E-03	joint
10419288	Gch1	14	48580546	rs30713303	4.0	2.1E-03	joint
10521566	Tmem128	5	38961342	rs33252235	4.0	2.1E-03	joint
10565840	Neu3	7	106961689	rs3679473	4.0	2.1E-03	joint
10400109	Zfp277	12	41887752	rs33844949	4.0	2.1E-03	joint
10376899	Trim16	11	62701947	rs26940967	4.0	2.1E-03	joint
10512005	1810030N24Rik	4	34948296	rs27761123	4.0	2.1E-03	joint
10545401	Vamp5	6	71832725	rs6259011	4.0	2.1E-03	joint
10411882	Nln	13	105183198	rs29235759	4.0	2.1E-03	joint
10412701	3830406C13Rik	14	12267571	rs31142294	4.0	2.1E-03	joint
10578071	Wrn	8	34369548	rs3655839	4.0	2.1E-03	joint
10443421	Brpf3	17	29013324	rs33719751	4.0	2.1E-03	joint
10439881	5330426P16Rik	16	50274601	rs4185610	4.0	2.1E-03	joint
10490370	Psma7	2	178975820	rs27698946	4.0	2.1E-03	joint
10407387	Gm7120	13	120070017	rs29666531	4.0	2.1E-03	joint
10382692	2210020M01Rik	11	115762341	rs13481247	4.0	2.1E-03	joint
10441933	2210404J11Rik	17	15446299	rs33659635	4.0	2.1E-03	joint
10527732	Fry	5	151003034	rs29503742	4.0	2.1E-03	joint
10480379	Mrps5	2	128166258	rs27446019	4.0	2.1E-03	joint
10486595	Ttbk2	2	119572730	rs33016743	4.0	2.1E-03	joint
10572591	Ocel1	8	73228613	rs33447296	4.0	2.1E-03	joint
10543114	Rpa3	6	8407487	rs29916108	4.0	2.1E-03	joint
10579736	9130011J15Rik	8	75112482	rs6218496	4.0	2.1E-03	joint
10447038	1110001A16Rik	17	78951702	rs3670726	4.0	2.1E-03	joint
10484371	Calcrl	2	84433170	rs28044702	4.0	2.1E-03	joint
10439049	Pigx	16	32090262	rs4169922	4.0	2.1E-03	joint
10348432	Agap1	1	90689439	rs31441072	4.0	2.1E-03	joint
10407507	Rpl35a	16	33064622	rs4171166	4.0	2.1E-03	joint
10472820	Itga6	2	71432969	rs27985234	4.0	2.1E-03	joint
10396108	Arf6	12	71269636	rs29131427	4.0	2.1E-03	joint
10404928	C78339	13	46570016	rs29874743	4.0	2.1E-03	joint
10417869	Anxa7	14	21052836	rs30158307	4.0	2.1E-03	joint
10462539	Nudt15	14	73861463	rs30404670	4.0	2.1E-03	joint
10590365	Vipr1	9	121560327	rs33680295	4.0	2.1E-03	joint
10544570	Pcnp	16	55919183	rs4188086	4.0	2.1E-03	joint
10491136	Tnik	3	28081299	rs29644297	4.0	2.1E-03	joint
10441178	Itgb2l	16	97388863	rs4221351	4.0	2.1E-03	joint
10357808	Snrpe	1	135409223	rs32494351	4.0	2.1E-03	joint
10579313	Ssbp4	8	72270336	rs33223746	4.0	2.1E-03	joint
10542460	Dera	6	137667376	rs30224085	4.0	2.1E-03	joint
10523766	Lrrc8c	5	106106983	rs6178162	4.0	2.1E-03	joint
10427015	Acvr1b	15	100902918	rs6349436	4.0	2.1E-03	joint
10396699	Fntb	12	77911811	rs29176473	4.0	2.1E-03	joint
10557470	Gdpd3	7	133254825	rs31738440	4.0	2.1E-03	joint
10355246	Acadl	1	67123786	rs31844088	4.0	2.1E-03	joint
10575685	Nudt7	8	116236688	rs13479995	4.0	2.1E-03	joint
10479627	Tpd52l2	2	181207445	rs27671712	4.0	2.1E-03	joint
10441497	Tulp4	17	6114911	rs33599254	4.0	2.1E-03	joint
10504094	Galt	4	41694501	rs6405084	4.0	2.1E-03	joint
10374453	Glul	1	155590349	rs32454728	4.0	2.1E-03	joint

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10477815	Phf20	2	156176910	rs27336917	4.0	2.1E-03	joint
10479550	Ppdpf	2	181303721	rs27654429	4.0	2.1E-03	joint
10450723	H2-T10	17	36497056	mm37-17-36497056	4.0	2.1E-03	joint
10594636	Ppp1r2	16	31207323	rs4168855	4.0	2.1E-03	joint
10444821	H2-Q8	17	35649680	mm37-17-35649680	4.0	2.1E-03	joint
10564909	Man2a2	7	87376087	rs32350778	4.0	2.1E-03	joint
10475830	Mrps5	2	128166258	rs27446019	4.0	2.1E-03	joint
10530612	Fryl	5	73654644	rs6364064	4.0	2.1E-03	joint
10420787	Mtmr9	14	64848723	rs31448986	4.0	2.1E-03	joint
10407120	Rps3a	3	85019408	rs30804792	4.0	2.1E-03	joint
10359181	Tor3a	1	158217747	rs4136042	4.0	2.1E-03	joint
10508115	Stk40	4	125762193	rs27550222	4.0	2.1E-03	joint
10359386	Dars2	1	162766845	rs6175813	4.0	2.1E-03	joint
10532187	Gak	5	109077217	rs6310635	4.0	2.1E-03	joint
10512709	Mcart1	4	45382906	rs27862174	4.0	2.1E-03	joint
10365769	Hal	10	92626660	rs29373088	4.0	2.1E-03	joint
10450682	H2-T23	17	37073380	mm37-17-37073380	4.0	2.1E-03	joint
10565862	Pold3	7	106534630	rs31200487	4.0	2.1E-03	joint
10360884	Iars2	1	187103826	rs32415281	4.0	2.1E-03	joint
10462091	Klf9	19	22990922	rs30644836	4.0	2.1E-03	joint
10356475	Arl4c	1	90516874	rs30290928	4.0	2.1E-03	joint
10398721	2810002N01Rik	12	113604286	rs29156659	4.0	2.1E-03	joint
10412760	Il3ra	14	15375448	rs31072851	4.0	2.1E-03	joint
10489065	Ndrg3	2	156825245	rs33395615	4.0	2.1E-03	joint
10450694	H2-T22	17	37073380	mm37-17-37073380	4.0	2.1E-03	joint
10455007	Zmat2	18	36719667	rs29561436	4.0	2.1E-03	joint
10520833	Mrpl33	5	31585096	rs33153872	4.0	2.1E-03	joint
10520288	Galnt11	5	24509818	rs33486334	4.0	2.1E-03	joint
10475211	Haus2	2	119978910	rs27423349	4.0	2.1E-03	joint
10549171	5730419I09Rik	6	143094081	rs6368858	4.0	2.1E-03	joint
10373902	Gatsl3	11	3686755	rs26897275	4.0	2.1E-03	joint
10572449	Lsm4	8	73228613	rs33447296	4.0	2.1E-03	joint
10426999	Acvrl1	15	100943615	rs3673167	4.0	2.1E-03	joint
10427849	6030458C11Rik	15	12750495	rs31634346	4.0	2.1E-03	joint
10444824	H2-Q6	17	35306154	mm37-17-35306154	4.0	2.1E-03	joint
10549341	4933424B01Rik	6	146359925	rs30741186	4.0	2.1E-03	joint
10408331	Acot13	13	25677099	rs6265976	4.0	2.1E-03	joint
10386470	4930412M03Rik	11	60545490	rs29402619	4.0	2.1E-03	joint
10417538	Pdhb	14	9569951	rs31436768	4.0	2.1E-03	joint
10407072	Elovl7	13	109177164	rs29884548	4.0	2.1E-03	joint
10452980	Eif2ak2	17	78951702	rs3670726	4.0	2.1E-03	joint
10485963	Arhgap11a	2	114159060	rs27455022	4.0	2.1E-03	joint
10516605	Hdac1	4	129202096	rs31878418	4.0	2.1E-03	joint
10348299	5830472F04Rik	1	89469616	rs32481323	4.0	2.1E-03	joint
10366712	Ppm1h	10	121721932	rs29342476	4.0	2.1E-03	joint
10413125	Samd8	14	22411229	rs30456693	4.0	2.1E-03	joint
10540072	Ppp1r2	16	31207323	rs4168855	4.0	2.1E-03	joint
10375031	Snrnp25	11	32119734	rs29419622	4.0	2.1E-03	joint
10352815	Irf6	1	195302377	rs32792037	4.0	2.1E-03	joint
10467871	Dnmbp	19	43943259	rs30522915	4.0	2.1E-03	joint

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10524034	Idua	5	109824615	rs29624173	4.0	2.1E-03	joint
10457489	6030446N20Rik	18	12310824	rs30068698	4.0	2.1E-03	joint
10567412	Eri2	7	127003960	rs31824682	4.0	2.1E-03	joint
10567297	Itpripl2	7	125934386	rs6404036	4.0	2.1E-03	joint
10560592	Clptm1	7	19723345	rs31180331	4.0	2.1E-03	joint
10476163	Ptpra	2	130367115	rs13459166	4.0	2.1E-03	joint
10516211	Ndufs5	4	123115527	rs27553626	4.0	2.1E-03	joint
10418702	Sh3bp5	14	32161714	rs30675496	4.0	2.1E-03	joint
10451261	Abcc10	17	46678560	rs33699221	4.0	2.1E-03	joint
10408074	Hist1h4b	13	23495851	rs6314855	4.0	2.1E-03	joint
10430649	Cbx7	15	79769540	rs32338468	4.0	2.1E-03	joint
10518428	Clcn6	4	147224626	rs32194305	4.0	2.1E-03	joint
10402066	Foxn3	12	100827319	rs29203245	4.0	2.1E-03	joint
10528527	Fam126a	5	22620136	rs33156476	4.0	2.1E-03	joint
10566488	Trim3	7	112779528	rs31445876	4.0	2.1E-03	joint
10579181	Rfxank	8	72270336	rs33223746	4.0	2.1E-03	joint
10449356	AI413582	17	27626166	rs33172754	4.0	2.1E-03	joint
10506031	Nfia	4	97428004	rs28110080	4.0	2.1E-03	joint
10412562	Flnb	14	9018991	rs6291209	4.0	2.1E-03	joint
10573578	BC056474	8	87590219	rs13479871	4.0	2.1E-03	joint
10444830	H2-Q7	17	35374902	mm37-17-35374902	4.0	2.1E-03	joint
10481845	Fam125b	2	33737110	rs33026548	4.0	2.1E-03	joint
10472846	Pdk1	2	71602801	rs33268912	4.0	2.1E-03	joint
10377380	1500010J02Rik	11	69028313	rs3708219	4.0	2.1E-03	joint
10401138	Atp6v1d	12	80028884	rs6303798	4.0	2.1E-03	joint
10350733	Rgs16	1	155590349	rs32454728	4.0	2.1E-03	joint
10404496	Nqo2	13	34158199	rs29588682	4.0	2.1E-03	joint
10412345	Parp8	13	117064385	rs29511167	4.0	2.1E-03	joint
10408709	Ssr1	13	38142773	rs30018482	4.0	2.1E-03	joint
10500412	Gpr89	3	96711291	rs30609666	4.0	2.1E-03	joint
10564631	Slco3a1	7	81864105	rs31276257	4.0	2.1E-03	joint
10447004	Hdac1	4	129202096	rs31878418	4.0	2.1E-03	joint
10376721	Smcr8	11	60567566	rs13481050	4.0	2.1E-03	joint
10372988	Slc16a7	10	124421491	rs29362468	4.0	2.1E-03	joint
10597883	Ano10	9	122148100	rs30428866	4.0	2.1E-03	joint
10472195	Nudt15	14	73902085	rs30595135	4.0	2.1E-03	joint
10563094	Fcgrt	7	51942509	rs50417507	4.0	2.1E-03	joint
10507529	Med8	4	118078625	rs27495547	4.0	2.1E-03	joint
10566161	Trim68	7	110061966	rs32467515	4.0	2.1E-03	joint
10508468	2510006D16Rik	4	129405334	rs32527750	4.0	2.1E-03	joint
10545009	Pigy	6	57659921	rs30902330	4.0	2.1E-03	joint
10399036	Uevld	7	53452815	rs6157797	4.0	2.1E-03	joint
10440953	Donson	16	92081867	rs6285649	4.0	2.1E-03	joint
10366825	Agap2	10	126505512	rs29332499	4.0	2.1E-03	joint
10354470	Rpl15	14	18129273	rs30107859	4.0	2.1E-03	joint
10487380	Gm10766	2	127252844	rs27449840	4.0	2.1E-03	joint
10373728	Patz1	11	3686755	rs26897275	4.0	2.1E-03	joint
10444114	Vps52	17	33940053	mm37-17-33940053	4.0	2.1E-03	joint
10483809	Nfe2l2	2	75518588	rs27978430	4.0	2.1E-03	joint
10458033	Stard4	18	33400755	rs30210002	4.0	2.1E-03	joint
10480699	Dpp7	2	25077171	rs29620450	4.0	2.1E-03	joint
10476728	Dtd1	2	144392969	rs33423270	4.0	2.1E-03	joint
10589413	Nme6	9	109728187	rs29928493	4.0	2.1E-03	joint

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10418720	Mettl6	14	32399644	rs30837452	4.0	2.1E-03	joint
10473965	Arhgap1	2	91690031	rs29518200	4.0	2.1E-03	joint
10568169	Qprt	7	134217351	rs31543602	4.0	2.1E-03	joint
10439701	Abhd10	16	45411640	rs4181076	4.0	2.1E-03	joint
10407291	Arl15	13	114607122	rs30044459	4.0	2.1E-03	joint
10550833	Zfp180	7	25119077	rs32341931	4.0	2.1E-03	joint
10487359	Itpripl1	2	126900158	rs6284112	4.0	2.1E-03	joint
10377953	Kif1c	11	70469788	rs29431005	4.0	2.1E-03	joint
10492590	Ppm1l	3	69151930	rs30999878	4.0	2.1E-03	joint
10429926	Dgat1	15	76343291	rs31952352	4.0	2.1E-03	joint
10522467	Rasl11b	5	74200587	rs33081586	4.0	2.1E-03	joint
10354832	Ppil3	1	58465892	rs32150647	4.0	2.1E-03	joint
10437080	Ttc3	16	94603265	rs3721009	4.0	2.1E-03	joint
10590137	Acaa1a	9	119278549	rs33655475	4.0	2.1E-03	joint
10408162	Zfp322a	13	23445323	rs6243245	4.0	2.1E-03	joint
10397763	9030617O03Rik	12	102069254	rs29223317	4.0	2.1E-03	joint
10514896	2210012G02Rik	4	106543639	rs31903240	4.0	2.1E-03	joint
10542836	Klhdc5	6	147337897	rs30362969	4.0	2.1E-03	joint
10359754	Mpzl1	1	166987356	rs31420643	4.0	2.1E-03	joint
10539042	Polr1a	6	71251145	rs30964011	4.0	2.1E-03	joint
10361799	Adat2	10	13247820	rs29319120	4.0	2.1E-03	joint
10491952	Mgst2	3	51006281	rs30158371	4.0	2.1E-03	joint
10377851	Psmb6	11	70471151	rs26924498	4.0	2.1E-03	joint
10462035	Ldhb	6	142368838	rs6329892	4.0	2.1E-03	joint
10390258	Snx11	11	96767902	rs29387885	4.0	2.1E-03	joint
10529741	Rab28	5	41932526	rs33525655	4.0	2.1E-03	joint
10441646	Sft2d1	17	8485314	rs33080376	4.0	2.1E-03	joint
10488415	Cst3	2	148693899	rs33373524	4.0	2.1E-03	joint
10573747	Adcy7	8	91102075	rs32734138	4.0	2.1E-03	joint
10562439	Gpatch1	7	35726106	rs32290010	4.0	2.1E-03	joint
10488944	Uqcc	2	155324286	rs27338907	4.0	2.1E-03	joint
10536527	Capza2	6	17630608	rs30068139	4.0	2.1E-03	joint
10376427	2810021J22Rik	11	58681822	rs26971932	4.0	2.1E-03	joint
10417167	Clybl	14	122600010	rs30827652	4.0	2.1E-03	joint
10483381	Stk39	2	68155505	rs27972836	4.0	2.1E-03	joint
10565018	Iqgap1	7	87507588	rs32347321	4.0	2.1E-03	joint
10385966	Anxa6	11	55379765	rs26948271	4.0	2.1E-03	joint
10578582	D030016E14Rik	8	48527677	rs32595293	4.0	2.1E-03	joint
10466402	Eif4a1	11	68786528	rs29433934	4.0	2.1E-03	joint
10550169	Phf20	2	155159440	rs6325215	4.0	2.1E-03	joint
10371506	Stab2	10	86050898	rs29326301	4.0	2.1E-03	joint
10560695	Ceacam16	7	19623601	rs32365669	4.0	2.1E-03	joint
10553015	Bcat2	7	52879613	rs31194008	4.0	2.1E-03	joint
10401891	Ston2	12	93285469	rs3687366	4.0	2.1E-03	joint
10577144	Dcun1d2	8	13605017	rs6281754	4.0	2.1E-03	joint
10366350	Krr1	10	111250959	rs29375297	4.0	2.1E-03	joint
10542745	Fgfr1op2	6	146505005	rs30516598	4.0	2.1E-03	joint
10531952	Abcg3	5	105379107	rs33535604	4.0	2.1E-03	joint
10498576	Lxn	3	67242128	rs30900164	4.0	2.1E-03	joint
10412385	Mrps30	13	119074495	rs30030678	4.0	2.1E-03	joint
10441556	Gm1604b	17	7916760	rs33886934	4.0	2.1E-03	joint
10388227	Cyb5d2	11	72411477	rs26900597	4.0	2.1E-03	joint
10376796	Grap	11	61413334	rs3700615	4.0	2.1E-03	joint
10552622	2410002F23Rik	7	51330113	rs31469843	4.0	2.1E-03	joint
10553788	Atp10a	7	65384180	rs6274680	4.0	2.1E-03	joint

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10524621	Oasl2	5	115392734	rs32143931	4.0	2.1E-03	joint
10533285	Ptpn11	5	121658762	rs29505322	4.0	2.1E-03	joint
10591472	Cdc37	9	20724667	rs6306775	4.0	2.1E-03	joint
10545339	Mrpl35	6	71350429	rs30213915	4.0	2.1E-03	joint
10575102	Cirh1a	8	109164175	rs33180684	4.0	2.1E-03	joint
10475199	Snap23	2	119895277	rs27441680	4.0	2.1E-03	joint
10413059	Vcl	14	21732168	rs30797328	4.0	2.1E-03	joint
10442240	Zfp760	17	21606159	rs32491074	4.0	2.1E-03	joint
10540493	Edem1	6	108301923	rs29922131	4.0	2.1E-03	joint
10561842	Capns1	7	30911363	rs47397692	4.0	2.1E-03	joint
10545897	Dusp11	6	85980627	rs30653381	4.0	2.1E-03	joint
10579468	Haus8	8	72984250	rs33569542	4.0	2.1E-03	joint
10505451	Orm2	4	62920029	rs27905464	4.0	2.1E-03	joint
10550098	Wdr12	1	59779226	rs6336931	4.0	2.1E-03	joint
10508351	Phc2	4	128421457	rs27558242	4.0	2.1E-03	joint
10456158	Gm9949	18	62417011	rs29731574	4.0	2.1E-03	joint
10404053	Hist1h2bc	13	23495851	rs6314855	4.0	2.1E-03	joint
10367673	Plekhg1	10	6618400	mm37-10-6618400	4.0	2.1E-03	joint
10550674	Ercc2	7	19717530	rs31936053	4.0	2.1E-03	joint
10387372	Kdm6b	11	68786528	rs29433934	4.0	2.1E-03	joint
10441642	Brp44l	17	8510381	rs3694756	4.0	2.1E-03	joint
10392936	Nt5c	11	115369945	rs27031432	4.0	2.1E-03	joint
10576439	Cog2	8	126598718	rs3688669	4.0	2.1E-03	joint
10407481	Pfkp	13	6614495	rs6235987	4.0	2.1E-03	joint
10449644	Glo1	17	29917069	rs3693494	4.0	2.1E-03	joint
10385382	Sft2d1	17	8485314	rs33080376	4.0	2.1E-03	joint
10549097	Ldhb	6	142368838	rs6329892	4.0	2.1E-03	joint
10529671	Slc2a9	5	38842151	rs29778357	4.0	2.1E-03	joint
10527213	Daglb	5	144256790	rs33549671	4.0	2.1E-03	joint
10575619	Terf2ip	8	114025565	rs31309593	4.0	2.1E-03	joint
10552812	Irf3	7	52250686	rs32051036	4.0	2.1E-03	joint
10503917	Akirin2	4	34317853	rs27803858	4.0	2.1E-03	joint
10509777	Iffo2	4	138882720	rs31859712	4.0	2.1E-03	joint
10509858	Sdhb	4	140858826	rs32662580	4.0	2.1E-03	joint
10565582	Rps8	4	116499355	rs27513773	4.0	2.1E-03	joint
10485117	Creb3l1	2	91697689	rs27384575	4.0	2.1E-03	joint
10404913	Cap2	13	46641676	rs4136112	4.0	2.1E-03	joint
10378059	Txndc17	11	71854915	rs29412896	4.0	2.1E-03	joint
10486522	Zfp106	2	119895277	rs27441680	4.0	2.1E-03	joint
10350853	BC026585	1	159474767	rs3723483	4.0	2.1E-03	joint
10439955	Fam55c	16	55973781	rs4188156	4.0	2.1E-03	joint
10552945	Gys1	7	52238853	rs32431972	4.0	2.1E-03	joint
10487969	Trmt6	2	133015586	rs28288156	4.0	2.1E-03	joint
10390283	Cdk5rap3	11	96410911	rs27074446	4.0	2.1E-03	joint
10435443	Hspbap1	16	35800913	rs4173147	4.0	2.1E-03	joint
10474972	Chac1	2	119978910	rs27423349	4.0	2.1E-03	joint
10441509	Ppp1r2	16	31207323	rs4168855	4.0	2.1E-03	joint
10517301	Ldlrap1	4	134190126	rs6327269	4.0	2.1E-03	joint
10386359	Guk1	11	59023349	rs29412340	4.0	2.1E-03	joint
10511175	Aurkaip1	4	155224804	rs6247365	4.0	2.1E-03	joint
10362073	Sgk1	10	20605138	rs29377930	4.0	2.1E-03	joint
10541114	Rasgef1a	6	118431764	rs6284156	4.0	2.1E-03	joint
10420785	Mtmr9	14	64679008	rs31056052	4.0	2.1E-03	joint
10508686	Mecr	4	131411924	rs27589731	4.0	2.1E-03	joint

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10510422	Casz1	4	148277980	rs32695839	4.0	2.1E-03	joint
10377368	Rpl26	11	68740711	rs29456171	4.0	2.1E-03	joint
10412394	Nnt	13	120234690	rs29722117	4.0	2.1E-03	joint
10576152	Trappc2l	8	125143871	rs33245882	4.0	2.1E-03	joint
10471675	Glo1	17	29917069	rs3693494	4.0	2.1E-03	joint
10487208	Atp8b4	2	125525113	rs27435685	4.0	2.1E-03	joint
10408348	Mrs2	13	25643363	rs6412327	4.0	2.1E-03	joint
10572580	Use1	8	73890792	rs32668105	4.0	2.1E-03	joint
10407327	Emb	13	118116312	rs29571531	4.0	2.1E-03	joint
10560434	Qpctl	7	19717530	rs31936053	4.0	2.1E-03	joint
10465980	Sdhaf2	19	10728651	rs31091380	4.0	2.1E-03	joint
10385747	Phf15	11	52464276	rs26946582	4.0	2.1E-03	joint
10488722	Commd7	2	153439162	rs3720334	4.0	2.1E-03	joint
10544588	Gimap3	6	48583618	rs30123129	4.0	2.1E-03	joint
10439980	Pcnp	16	55975926	rs4151934	4.0	2.1E-03	joint
10477649	Acss2	2	154556635	rs29956539	4.0	2.1E-03	joint
10395672	Ap4s1	12	52771027	rs29158863	4.0	2.1E-03	joint
10446804	Slc30a6	17	75106216	rs33516919	4.0	2.1E-03	joint
10477966	Manbal	2	156968866	rs33154095	4.0	2.1E-03	joint
10517383	Nipal3	4	135048933	rs32938063	4.0	2.1E-03	joint
10423363	Ank	15	27437143	rs13482494	4.0	2.1E-03	joint
10502050	Alpk1	3	127216973	rs30661860	4.0	2.1E-03	joint
10532999	Sirt4	5	115563152	rs33137118	4.0	2.1E-03	joint
10387559	Senp3	11	68667674	rs29385375	4.0	2.1E-03	joint
10357436	Mcm6	1	130091676	rs32140455	4.0	2.1E-03	joint
10467956	Bloc1s2	19	44214333	rs3725175	4.0	2.1E-03	joint
10517009	Sytl1	4	132810523	rs32051931	4.0	2.1E-03	joint
10461898	Rfk	19	18123110	rs30308813	4.0	2.1E-03	joint
10518228	Vps13d	4	144667359	rs27601587	4.0	2.1E-03	joint
10582501	Fanca	8	125775590	rs33018881	4.0	2.1E-03	joint
10564888	Unc45a	7	87491970	rs31040534	4.0	2.1E-03	joint
10573733	Papd5	8	90914682	rs32837750	4.0	2.1E-03	joint
10531437	Scarb2	5	92902002	rs31776682	4.0	2.1E-03	joint
10560260	Sae1	7	17131895	rs32333995	4.0	2.1E-03	joint
10533644	Vps33a	5	123934329	rs29724748	4.0	2.1E-03	joint
10555407	Chchd8	7	107579311	rs3682987	4.0	2.1E-03	joint
10488912	Edem2	2	154635104	rs29542436	4.0	2.1E-03	joint
10450675	H2-T24	17	37091357	mm37-17-37091357	4.0	2.1E-03	joint
10404067	Hist1h4b	13	23495851	rs6314855	4.0	2.1E-03	joint
10388154	Med31	11	72565414	rs26887864	4.0	2.1E-03	joint
10385325	Pttg1	11	42800509	rs29426145	4.0	2.1E-03	joint
10547088	Mbd4	6	115802280	rs30657994	4.0	2.1E-03	joint
10491599	4932438A13Rik	3	37560742	rs30085634	4.0	2.1E-03	joint
10447668	Gm1604b	17	7916760	rs33886934	4.0	2.1E-03	joint
10470741	Coq4	2	29485035	rs27201282	4.0	2.1E-03	joint
10385941	Tnip1	11	54764694	rs29469382	4.0	2.1E-03	joint
10375903	Cdkn2aipnl	11	52336494	rs29436877	4.0	2.1E-03	joint
10472095	Bloc1s2	19	44214333	rs3725175	4.0	2.1E-03	joint
10394800	Bnip3l	14	67951761	rs30667567	4.0	2.1E-03	joint
10403455	Dip2c	13	9252397	rs29512540	4.0	2.1E-03	joint
10371959	Elk3	10	92811139	rs29365715	4.0	2.1E-03	joint
10450384	Msh5	17	35475871	mm37-17-35475871	4.0	2.1E-03	joint
10477644	Trp53inp2	2	156163688	rs27336985	4.0	2.1E-03	joint

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10437928	0610037P05Rik	16	14290071	rs4164042	4.0	2.1E-03	joint
10489107	Samhd1	2	156968866	rs33154095	4.0	2.1E-03	joint
10487660	Fam113a	2	129658845	rs27271340	4.0	2.1E-03	joint
10372844	Rassf3	10	120836412	rs29358003	4.0	2.1E-03	joint
10579347	Ifi30	8	72296612	rs33597694	4.0	2.1E-03	joint
10373740	Pik3ip1	11	4172536	rs29456423	4.0	2.1E-03	joint
10351026	Gas5	1	162985158	rs32696722	4.0	2.1E-03	joint
10494821	Tspan2	3	102023581	rs30911498	4.0	2.1E-03	joint
10446713	Snord53	17	71941288	rs33377370	4.0	2.1E-03	joint
10425333	Apobec3	15	79423472	rs32108677	4.0	2.1E-03	joint
10575074	Tmco7	8	109223808	rs33378496	4.0	2.1E-03	joint
10553403	Htatip2	7	56581972	rs6284895	4.0	2.1E-03	joint
10581835	Wdr59	8	114249223	rs6268367	4.0	2.1E-03	joint
10518385	Mfn2	4	147372444	rs33031209	4.0	2.1E-03	joint
10388065	Nlrp1b	11	70911360	rs3667647	4.0	2.1E-03	joint
10522060	Fam114a1	5	65318137	rs31442134	4.0	2.1E-03	joint
10459655	Poli	18	69746739	rs30006502	4.0	2.1E-03	joint
10412624	Pxk	14	8943486	rs30683468	4.0	2.1E-03	joint
10417708	Oxsm	14	16270126	rs30358912	4.0	2.1E-03	joint
10516590	Zbtb8a	4	129847468	rs8272673	4.0	2.1E-03	joint
10502191	Ostc	3	130017760	rs30746899	4.0	2.1E-03	joint
10498775	Golim4	3	75720362	rs3673084	4.0	2.1E-03	joint
10385995	Ccdc69	11	54056312	rs13496246	4.0	2.1E-03	joint
10345423	Plekhb2	1	34867218	rs13475803	4.0	2.1E-03	joint
10425999	Ttc38	15	85694078	rs3694980	4.0	2.1E-03	joint
10466676	1110059E24Rik	19	21701479	rs30753841	4.0	2.1E-03	joint
10582719	Sipa1l2	8	128036046	rs31995837	4.0	2.1E-03	joint
10547100	Plxnd1	6	116398018	rs29918692	4.0	2.1E-03	joint
10538617	Lancl2	6	57659921	rs30902330	4.0	2.1E-03	joint
10493335	5830417I10Rik	3	88439619	rs6293667	4.0	2.1E-03	joint
10427428	AW549877	15	3538844	rs31887977	4.0	2.1E-03	joint
10474950	Vps18	2	119067217	rs33499009	4.0	2.1E-03	joint
10486172	Fam82a2	2	119090181	rs33033614	4.0	2.1E-03	joint
10389561	Dhx40	11	86302643	rs13481137	4.0	2.1E-03	joint
10358050	Timm17a	1	137194760	rs32368271	4.0	2.1E-03	joint
10458607	Lars	18	42299973	rs3690709	4.0	2.1E-03	joint
10517287	Man1c1	4	134233017	rs28261585	4.0	2.1E-03	joint
10359713	Sft2d2	1	167155872	rs32112379	4.0	2.1E-03	joint
10368224	E030030I06Rik	10	21801862	rs6410365	4.0	2.1E-03	joint
10445360	Supt3h	17	44824943	rs33502191	4.0	2.1E-03	joint
10573583	Man2b1	8	87434336	rs32592383	4.0	2.1E-03	joint
10542140	Klrb1f	6	129003173	rs30175498	4.0	2.1E-03	joint
10386219	Zfp39	11	58785140	rs26971733	4.0	2.1E-03	joint
10389526	Cltc	11	86597129	rs29462930	4.0	2.1E-03	joint
10394778	Hpcal1	12	17631362	rs29158110	4.0	2.1E-03	joint
10410721	Arsk	13	76015019	rs3717315	4.0	2.1E-03	joint
10550906	Plaur	7	25119077	rs32341931	4.0	2.1E-03	joint
10425321	Apobec3	15	79423472	rs32108677	4.0	2.1E-03	joint
10539135	Capg	6	71927695	rs6334632	4.0	2.1E-03	joint
10562382	Lsm14a	7	35177898	rs32432896	4.0	2.1E-03	joint
10447569	Serac1	17	6073632	rs33278231	4.0	2.1E-03	joint
10381096	Igfbp4	11	98913177	rs13474434	4.0	2.1E-03	joint
10577070	Tubgcp3	8	12433957	rs6277651	4.0	2.1E-03	joint
10412830	Ngly1	14	16270126	rs30358912	4.0	2.1E-03	joint
10518019	Ddi2	4	141176275	rs32433574	4.0	2.1E-03	joint

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10408243	Hist1h4b	13	23495851	rs6314855	4.0	2.1E-03	joint
10497399	Pde7a	3	18777414	rs30656335	4.0	2.1E-03	joint
10361031	Rps6kc1	1	192727841	rs31891268	4.0	2.1E-03	joint
10422436	Dock9	14	122133056	rs31454088	4.0	2.1E-03	joint
10546294	Nup210	6	91045598	rs30118107	4.0	2.1E-03	joint
10542677	Etnk1	6	143094081	rs6368858	4.0	2.1E-03	joint
10560414	Ccdc61	7	18619279	rs31342300	4.0	2.1E-03	joint
10428103	Stk3	15	35170071	rs32384032	4.0	2.1E-03	joint
10502196	Rpl34	3	130074841	rs31432535	4.0	2.1E-03	joint
10419073	Tspan14	14	41788229	rs30521185	4.0	2.1E-03	joint
10581940	Kars	8	114582513	rs32903835	4.0	2.1E-03	joint
10457038	Gm10524	18	82902336	rs29869356	4.0	2.1E-03	joint
10347980	Itm2c	1	87842073	rs31340201	4.0	2.1E-03	joint
10523880	Rpap2	5	108056144	rs29731711	4.0	2.1E-03	joint
10590343	Trak1	9	121096052	rs30486572	4.0	2.1E-03	joint
10393544	Cyth1	11	118279115	rs29452076	4.0	2.1E-03	joint
10423921	Oxr1	15	41898649	rs3666046	4.0	2.1E-03	joint
10518372	Miip	4	147238192	rs27603697	4.0	2.1E-03	joint
10464251	Atrnl1	19	57499562	rs30752209	4.0	2.1E-03	joint
10512265	2310028H24Rik	4	41518071	rs32322824	4.0	2.1E-03	joint
10345504	Cox5b	1	36744537	rs31518923	4.0	2.1E-03	joint
10481474	Crat	2	30238684	rs27193651	4.0	2.1E-03	joint
10542636	Pyroxd1	6	142368838	rs6329892	4.0	2.1E-03	joint
10387545	Eif4a1	11	68786528	rs29433934	4.0	2.1E-03	joint
10582868	Sp110	1	87878515	rs3723583	4.0	2.1E-03	joint
10524723	Gcn1l1	5	115460516	rs33231931	4.0	2.1E-03	joint
10400023	Tspan13	12	36287512	rs29127252	4.0	2.1E-03	joint
10463462	Sfxn3	19	45007357	rs4137860	4.0	2.1E-03	joint
10511725	Cyb5r4	9	86905574	rs30179363	4.0	2.1E-03	joint
10348456	Cops8	1	92575832	rs32381743	4.0	2.1E-03	joint
10416334	Dok2	14	71043013	rs30346243	4.0	2.1E-03	joint
10572235	Lpar2	8	72296612	rs33597694	4.0	2.1E-03	joint
10555510	Pde2a	7	108164967	rs31037097	4.0	2.1E-03	joint
10400326	Eapp	12	55695070	rs29221983	4.0	2.1E-03	joint
10359190	Fam20b	1	158315445	rs32249484	4.0	2.1E-03	joint
10402648	Brp44l	17	8510381	rs3694756	4.0	2.1E-03	joint
10518226	Vps13d	4	144667359	rs27601587	4.0	2.1E-03	joint
10572432	Isyna1	8	72356159	rs33508509	4.0	2.1E-03	joint
10542650	Golt1b	6	142368838	rs6329892	4.0	2.1E-03	joint
10477052	2310046K01Rik	2	151814275	rs27346468	4.0	2.1E-03	joint
10412900	Nkiras1	14	19804543	rs31180136	4.0	2.1E-03	joint
10572637	Fam125a	8	73890792	rs32668105	4.0	2.1E-03	joint
10452978	Gm6548	17	79274540	rs33250776	4.0	2.1E-03	joint
10408044	Cox5b	1	36744537	rs31518923	4.0	2.1E-03	joint
10410355	A530054K11Rik	13	67680620	rs29242717	4.0	2.1E-03	joint
10557571	AI467606	7	134207826	rs31060001	4.0	2.1E-03	joint
10594631	Aph1b	9	66643110	rs33676273	4.0	2.1E-03	joint
10389522	Rpl13a	7	52174871	rs3653613	4.0	2.1E-03	joint
10595109	Lrrc1	9	77820103	rs30038899	4.0	2.1E-03	joint
10348277	Atg16l1	1	89473028	rs31425983	4.0	2.1E-03	joint
10542691	Lrmp	6	144898833	rs30843330	4.0	2.1E-03	joint
10516695	Tmem39b	4	129202096	rs31878418	4.0	2.1E-03	joint
10490116	Cass4	2	172199320	rs33292738	4.0	2.1E-03	joint
10560856	Irgc1	7	25119077	rs32341931	4.0	2.1E-03	joint
10566585	Gm1966	7	114170898	rs31636440	4.0	2.1E-03	joint

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10479514	Col20a1	2	180640406	rs27667839	4.0	2.1E-03	joint
10431601	Arsa	15	89507077	rs31625234	4.0	2.1E-03	joint
10404051	Hist1h4d	13	23495851	rs6314855	4.0	2.1E-03	joint
10485042	Zfp408	2	91690031	rs29518200	4.0	2.1E-03	joint
10503259	Trp53inp1	4	11088328	rs27747110	4.0	2.1E-03	joint
10421003	Bnip3l	14	67951761	rs30667567	4.0	2.1E-03	joint
10396306	Jkamp	12	73178478	rs29173056	4.0	2.1E-03	joint
10579070	Zfp868	8	72186510	rs33481582	4.0	2.1E-03	joint
10495596	Frrs1	3	116798243	rs6372496	4.0	2.1E-03	joint
10353783	Ccdc115	1	34541351	rs3682032	4.0	2.1E-03	joint
10511149	Mrpl20	4	155324980	rs3659087	4.0	2.1E-03	joint
10405693	Dapk1	13	60841065	rs30057268	4.0	2.1E-03	joint
10348558	Scly	1	93035701	rs3708228	4.0	2.1E-03	joint
10423593	Laptm4b	15	34936830	rs32011871	4.0	2.1E-03	joint
10546349	Xpc	6	91444913	rs6230067	4.0	2.1E-03	joint
10567964	Cln3	7	133254825	rs31738440	4.0	2.1E-03	joint
10346780	Eif4a1	11	68786528	rs29433934	4.0	2.1E-03	joint
10447167	Mta3	17	84078289	rs33367830	3.7	3.7E-03	joint
10387251	2310047M10Rik	11	69294200	rs29391628	3.7	3.7E-03	joint
10404262	Rps8	4	116499355	rs27513773	3.7	3.7E-03	joint
10551626	Lgals4	7	29645746	rs32308271	3.7	3.7E-03	joint
10411454	Sec61b	4	47855116	rs6239869	3.7	3.7E-03	joint
10590325	Ctnnb1	9	120980209	rs30379801	3.7	3.7E-03	joint
10384780	Fancl	11	25726666	rs26825351	3.7	3.7E-03	joint
10387689	Kctd11	11	70309221	rs29426113	3.7	3.7E-03	joint
10523778	D830014E11Rik	5	106106983	rs6178162	3.7	3.7E-03	joint
10436788	Hunk	16	90373659	rs4217360	3.7	3.7E-03	joint
10350753	Glul	1	155590349	rs32454728	3.7	3.7E-03	joint
10599576	Ppdpf	2	181222071	rs27671682	3.7	3.7E-03	joint
10398727	Klc1	12	112995775	rs29221416	3.7	3.7E-03	joint
10556082	Ppfibp2	7	114789328	rs31487343	3.7	3.7E-03	joint
10408902	Ccdc90a	13	43828565	rs29238723	3.7	3.7E-03	joint
10581558	Rps26	10	128411698	rs6208640	3.7	3.7E-03	joint
10572613	Mrpl34	8	73890792	rs32668105	3.7	3.7E-03	joint
10542665	Cmas	6	143094081	rs6368858	3.7	3.7E-03	joint
10424331	Trmt12	15	58616665	rs32180716	3.7	3.7E-03	joint
10458090	Reep5	18	34401782	rs29826401	3.7	3.7E-03	joint
10586368	Clpx	9	65128314	rs32878147	3.7	3.7E-03	joint
10581499	Chtf8	8	109164175	rs33180684	3.7	3.7E-03	joint
10446334	Glcci1	6	8584503	rs30759135	3.7	3.7E-03	joint
10396383	Slc38a6	12	74108934	rs33847664	3.7	3.7E-03	joint
10487109	Cep152	2	126175992	rs29956145	3.7	3.7E-03	joint
10396421	Hif1a	12	74991059	rs29202209	3.7	3.7E-03	joint
10349404	Mgat5	1	129293175	rs31595084	3.7	3.7E-03	joint
10347933	Sp140	1	87878515	rs3723583	3.7	3.7E-03	joint
10378572	Tlcd2	11	74506401	rs29396397	3.7	3.7E-03	joint
10584821	Cd3d	9	44883262	rs30360106	3.7	3.7E-03	joint
10576661	Itgb1	8	131207151	rs32965842	3.7	3.7E-03	joint
10474181	Abtb2	2	103534892	rs27393739	3.7	3.7E-03	joint
10540059	Slc41a3	6	90568670	rs30716113	3.7	3.7E-03	joint
10358982	Mr1	1	156349974	rs31193547	3.7	3.7E-03	joint
10461439	Fads1	19	10263233	rs30660123	3.7	3.7E-03	joint
10349648	Ctse	1	133716572	rs30622085	3.7	3.7E-03	joint
10441494	Tulp4	17	6114911	rs33599254	3.7	3.7E-03	joint
10509620	Capzb	4	138261770	rs27575260	3.7	3.7E-03	joint

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10504551	Rg9mtd3	4	45341933	rs27862264	3.7	3.7E-03	joint
10449225	Decr2	17	26440528	rs29522863	3.7	3.7E-03	joint
10493267	Arhgef2	3	88438299	rs31223164	3.7	3.7E-03	joint
10535124	Ints1	5	140250465	rs32295005	3.7	3.7E-03	joint
10441864	Mllt4	17	13820938	rs33887083	3.7	3.7E-03	joint
10587627	Cyb5r4	9	86943397	rs30034441	3.7	3.7E-03	joint
10498998	D930015E06Rik	3	83718097	rs30803680	3.7	3.7E-03	joint
10356293	A630001G21Rik	1	87819630	rs31991710	3.7	3.7E-03	joint
10556820	Tmem159	7	127065997	rs31984932	3.7	3.7E-03	joint
10551760	Zfp84	7	30787466	rs31088110	3.7	3.7E-03	joint
10467688	Exosc1	19	41961954	rs31120253	3.7	3.7E-03	joint
10499839	Snapin	3	89500015	rs31437137	3.7	3.7E-03	joint
10573461	Dnase2a	8	87434336	rs32592383	3.5	5.1E-03	joint
10450103	H2-Ke6	17	34312937	mm37-17-34312937	3.5	5.1E-03	joint
10502205	Hadh	3	131577261	rs30754910	3.5	5.1E-03	joint
10425808	Tspo	15	83476351	rs31718701	3.5	5.1E-03	joint
10547985	Cd27	6	125062474	rs30900624	3.5	5.1E-03	joint
10515416	Rps8	4	116499355	rs27513773	3.5	5.1E-03	joint
10427807	Sub1	15	12324856	rs32436445	3.5	5.1E-03	joint
10367626	1700052N19Rik	10	6320388	mm37-10-6320388	3.5	5.1E-03	joint
10496110	Papss1	3	131558405	rs30664155	3.5	5.1E-03	joint
10560304	Calm3	7	17644767	rs31135872	3.5	5.1E-03	joint
10421723	Dnajc15	14	77540081	rs31010036	3.5	5.1E-03	joint
10402800	Gpr132	12	114091939	rs29176738	3.5	5.1E-03	joint
10573790	Nod2	8	90876863	rs32548698	3.5	5.1E-03	joint
10498296	Commd2	3	57464323	rs30356334	3.5	5.1E-03	joint
10579833	Lsm6	8	80837427	rs33387239	3.5	5.1E-03	joint
10491106	Pld1	3	27805627	rs31049355	3.5	5.1E-03	joint
10491597	4932438A13Rik	3	37593832	rs31474324	3.5	5.1E-03	joint
10488608	Trib3	2	151493127	rs6226184	3.5	5.1E-03	joint
10563178	Cd37	7	51874922	rs31108361	3.5	5.1E-03	joint
10438975	AI480653	16	30521846	rs4168249	3.5	5.1E-03	joint
10555460	Stard10	7	108519175	rs31201581	3.5	5.1E-03	joint
10360391	Ifi203	1	176081804	rs13476248	3.5	5.1E-03	joint
10445033	Trim26	17	37003025	mm37-17-37003025	3.5	5.1E-03	joint
10538963	Rpl34	3	130577248	rs30804395	3.5	5.1E-03	joint
10384138	Tmed4	11	6168182	rs26899782	3.5	5.1E-03	joint
10569494	Tnfrsf22	7	150565771	rs6307236	3.5	5.1E-03	joint
10347915	Gm7609	1	84321318	rs6218295	3.5	5.1E-03	joint
10385893	Slc22a4	11	53866434	rs29483899	3.5	5.1E-03	joint
10547251	Bms1	6	118286718	rs30662648	3.5	5.1E-03	joint
10549375	Rps26	10	128411698	rs6208640	3.5	5.1E-03	joint
10442396	Abca3	17	24813221	rs33626149	3.5	5.1E-03	joint
10378253	Camkk1	11	72362875	rs29444620	3.5	5.1E-03	joint
10439744	Cd96	16	45873352	rs4182049	3.5	5.1E-03	joint
10460573	Eif1ad	19	5321056	rs31303058	3.5	5.1E-03	joint
10356267	A530032D15Rik	1	84321318	rs6218295	3.5	5.1E-03	joint
10550650	Ercc1	7	19743810	rs32247128	3.5	5.1E-03	joint
10347925	Gm7609	1	84321318	rs6218295	3.5	5.1E-03	joint
10375886	D930048N14Rik	11	51137809	rs29389999	3.5	5.1E-03	joint
10581926	Adat1	8	114582513	rs32903835	3.5	5.1E-03	joint
10578019	Nudc	4	132781978	rs27541373	3.5	5.1E-03	joint

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10572679	Glt25d1	8	73235564	rs33553972	3.5	5.1E-03	joint
10405248	Hrh2	13	54017849	rs29562820	3.5	5.1E-03	joint
10378068	Xaf1	11	71854915	rs29412896	3.5	5.1E-03	joint
10347672	Stk11ip	1	75610471	rs32497330	3.5	5.1E-03	joint
10502071	5730508B09Rik	3	127269817	rs31345996	3.5	5.1E-03	joint
10444788	H2-Q1	17	35374902	mm37-17-35374902	3.5	5.1E-03	joint
10551600	Hnrnpl	7	30275278	rs32425593	3.4	6.3E-03	joint
10373036	Os9	10	126549813	rs29382000	3.4	6.3E-03	joint
10569504	Tnfrsf23	7	151347350	rs31825474	3.4	6.3E-03	joint
10423498	Dap	15	31148809	rs6188331	3.4	6.3E-03	joint
10509562	Mul1	4	137620466	rs31969556	3.4	6.3E-03	joint
10479174	Rps8	4	116499355	rs27513773	3.4	6.3E-03	joint
10410287	Zfp458	13	67602610	rs29549507	3.4	6.3E-03	joint
10518520	Ubiad1	4	147549464	rs27648494	3.4	6.3E-03	joint
10431266	Cerk	15	85940133	rs31750172	3.4	6.3E-03	joint
10476197	Itpa	2	129897341	rs6366916	3.4	6.3E-03	joint
10514173	Rpl34	3	130577248	rs30804395	3.4	6.3E-03	joint
10444098	Wdr46	17	34513408	mm37-17-34513408	3.4	6.3E-03	joint
10428827	Tmem65	15	58848020	rs31921605	3.4	6.3E-03	joint
10582712	Egln1	8	126521082	rs33542690	3.4	6.3E-03	joint
10359405	Klhl20	1	162183761	rs30986132	3.4	6.3E-03	joint
10532310	4930522L14Rik	5	110375316	rs3653994	3.4	6.3E-03	joint
10354275	1700029F09Rik	1	43936501	rs32686522	3.4	6.3E-03	joint
10440186	Crybg3	16	58538819	rs4190408	3.4	6.3E-03	joint
10581729	Ddx19a	8	113875203	rs31300031	3.4	6.3E-03	joint
10401028	Sgpp1	12	76826539	rs29489631	3.4	6.3E-03	joint
10387768	Acadvl	11	68890200	rs29388602	3.4	6.3E-03	joint
10441787	Airn	17	13863978	rs33479838	3.4	6.3E-03	joint
10416653	Kbtbd7	14	80033649	rs31537501	3.4	6.3E-03	joint
10488020	Tmx4	2	134518263	rs27252412	3.4	6.3E-03	joint
10475630	Galk2	2	125890546	rs32903359	3.4	6.3E-03	joint
10462111	Gm9938	19	23049764	rs30886302	3.4	6.3E-03	joint
10516305	Mtap7d1	4	125927679	rs6211332	3.4	6.3E-03	joint
10568758	9430038I01Rik	7	144595282	rs31284615	3.4	6.3E-03	joint
10429568	Ly6c1	15	74816238	rs32227722	3.4	6.3E-03	joint
10406551	Ssbp2	13	91809780	rs29496982	3.4	6.3E-03	joint
10404036	Hist1h2bg	13	23495851	rs6314855	3.4	6.3E-03	joint
10560103	Rps8	4	116499355	rs27513773	3.4	6.3E-03	joint
10459643	4930503L19Rik	18	69780712	rs30205079	3.4	6.3E-03	joint
10428857	Mtss1	15	58916954	rs31957783	3.4	6.3E-03	joint
10557591	Itgal	7	134217351	rs31543602	3.4	6.3E-03	joint
10571657	Acsl1	8	47935070	rs33070153	3.4	6.3E-03	joint
10593015	Cd3g	9	44883262	rs30360106	3.4	6.3E-03	joint
10448748	Nubp2	17	25241162	rs33198520	3.4	6.3E-03	joint
10508936	Ubxn11	4	132781978	rs27541373	3.4	6.3E-03	joint
10346651	Bmpr2	1	60420877	rs6368854	3.4	6.3E-03	joint
10425781	Serhl	15	82937328	rs32113647	3.4	6.3E-03	joint
10444229	H2-DMa	17	34545041	mm37-17-34545041	3.4	6.3E-03	joint
10510574	Errfi1	4	150397589	rs32286055	3.4	6.3E-03	joint
10582669	Ttc13	8	126435623	rs6165611	3.4	6.3E-03	joint
10392953	Gga3	11	115463929	rs29440124	3.3	7.4E-03	joint
10379836	Mrm1	11	84626729	rs26953663	3.3	7.4E-03	joint

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10586347	Parp16	9	65290301	rs6401447	3.3	7.4E-03	joint
10422493	Gpr18	14	122352736	rs31421893	3.3	7.4E-03	joint
10419867	Homez	14	56219264	rs31330444	3.3	7.4E-03	joint
10441740	Agpat4	17	12046592	rs33428908	3.3	7.4E-03	joint
10506188	Pgm2	4	99642410	rs3718520	3.3	7.4E-03	joint
10353849	4632411B12Rik	1	35394655	rs32678805	3.3	7.4E-03	joint
10459405	Nars	18	64659744	rs29880738	3.3	7.4E-03	joint
10488575	Psmf1	2	150784906	rs6246702	3.3	7.4E-03	joint
10474596	Aven	2	112397798	rs27491356	3.3	7.4E-03	joint
10519857	Hgf	5	15877708	rs29561409	3.3	7.4E-03	joint
10348547	Ube2f	1	93035701	rs3708228	3.3	7.4E-03	joint
10473793	Psmc3	2	90863242	rs27402423	3.3	7.4E-03	joint
10476326	Cds2	2	132060646	rs27261466	3.3	7.4E-03	joint
10408097	Prss16	13	22036331	rs6298616	3.3	7.4E-03	joint
10572804	1700030K09Rik	8	74516271	rs32779910	3.3	7.4E-03	joint
10386723	Mapk7	11	62009810	rs29477724	3.3	7.4E-03	joint
10430834	Naga	15	82113966	rs3688247	3.3	7.4E-03	joint
10535532	Tecpr1	5	145070268	rs32354808	3.3	7.4E-03	joint
10546184	Plxna1	6	89208901	rs30173362	3.3	7.4E-03	joint
10502335	Bank1	3	135444878	rs30560563	3.3	7.4E-03	joint
10403466	Dip2c	13	9252397	rs29512540	3.3	7.4E-03	joint
10516520	Zfp362	4	128425092	rs6246370	3.3	7.4E-03	joint
10429573	Ly6c2	15	74816238	rs32227722	3.3	7.4E-03	joint
10525439	P2rx4	5	123295835	rs3667964	3.3	7.4E-03	joint
10496387	Dnajb14	3	137712099	rs30366050	3.3	7.4E-03	joint
10456501	Rnmt	18	68786652	rs30215286	3.3	7.4E-03	joint
10466304	Dtx4	19	12556585	rs30662339	3.3	7.4E-03	joint
10494735	Gdap2	3	100736041	rs3159669	3.3	7.4E-03	joint
10360648	Psen2	1	182527160	rs32640339	3.3	7.4E-03	joint
10367734	Ust	10	7013763	mm37-10-7013763	3.3	7.4E-03	joint
10436830	Ifnar2	16	91166074	rs4219004	3.3	7.4E-03	joint
10435048	Tctex1d2	16	32504485	rs4170352	3.3	7.4E-03	joint
10347254	Smarcal1	1	72644687	rs32375777	3.3	7.4E-03	joint
10518300	Tnfrsf1b	4	144665748	rs27601589	3.2	8.5E-03	joint
10475487	Slc28a2	2	122012502	rs27425615	3.2	8.5E-03	joint
10597627	Oxsr1	9	119278549	rs33655475	3.2	8.5E-03	joint
10572533	Myo9b	8	72977422	rs3662160	3.2	8.5E-03	joint
10398929	Btbd6	12	114259702	rs6202097	3.2	8.5E-03	joint
10380721	Scrn2	11	96901154	rs27023924	3.2	8.5E-03	joint
10551570	Sirt2	7	29659759	rs31834177	3.2	8.5E-03	joint
10440393	Samsn1	16	75757232	rs4205758	3.2	8.5E-03	joint
10371877	Slc25a3	10	90873147	rs29341914	3.2	8.5E-03	joint
10444658	Clic1	17	35199955	mm37-17-35199955	3.2	8.5E-03	joint
10404506	Ripk1	13	33231875	rs29731096	3.2	8.5E-03	joint
10594251	Kif23	9	61753431	rs30177109	3.2	8.5E-03	joint
10417130	Ubac2	14	122352736	rs31421893	3.2	8.5E-03	joint
10517687	Gm16287	4	138913105	rs27567958	3.2	8.5E-03	joint
10579724	Slc35e1	8	74148950	rs33257975	3.2	8.5E-03	joint
10577882	Hgsnat	8	26074626	rs33294613	3.2	8.5E-03	joint
10352348	Cnih4	1	182372120	rs32260232	3.2	8.5E-03	joint
10491083	Nceh1	3	27103506	rs3693773	3.2	8.5E-03	joint
10448016	Tcte3	17	15845030	rs33509212	3.2	8.5E-03	joint
10577096	Pcid2	8	12963299	rs6240019	3.2	8.5E-03	joint

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10526087	Sumf2	5	130265728	rs33177836	3.2	8.5E-03	joint
10446441	Ddx11	17	66117769	rs3724865	3.2	8.5E-03	joint
10349049	Zfp706	15	36914802	rs32412313	3.2	8.5E-03	joint
10447294	Prkce	17	86799227	rs33462874	3.2	8.5E-03	joint
10412773	Slc4a7	14	14647391	rs30256817	3.2	8.5E-03	joint
10429391	Slc45a4	15	73656388	rs31592859	3.2	8.5E-03	joint
10437712	Zc3h7a	16	11148720	rs4161657	3.2	8.5E-03	joint
10373498	Rps26	10	128411698	rs6208640	3.2	8.5E-03	joint
10442236	3110052M02Rik	17	21720906	rs31300897	3.2	9.6E-03	joint
10571114	Erlin2	8	28144682	rs33564919	3.2	9.6E-03	joint
10373027	Tspan31	10	126505512	rs29332499	3.2	9.6E-03	joint
10514956	Scp2	4	107172080	rs28163295	3.2	9.6E-03	joint
10476691	Polr3f	2	144392969	rs33423270	3.2	9.6E-03	joint
10396402	Prkch	12	74703805	rs29183372	3.2	9.6E-03	joint
10584435	Vwa5a	9	38271612	rs30127804	3.2	9.6E-03	joint
10475866	Bcl2l11	2	127962561	rs27432128	3.2	9.6E-03	joint
10568233	9130019O22Rik	7	135407911	rs31629325	3.2	9.6E-03	joint
10516296	Thrap3	4	125485262	rs32914111	3.2	9.6E-03	joint
10572301	Mef2b	8	72640167	rs33113956	3.2	9.6E-03	joint
10448023	Tcte3	17	15845030	rs33509212	3.2	9.6E-03	joint
10517083	Pigv	4	133297566	rs31809658	3.2	9.6E-03	joint
10524718	Rplp0	5	115720924	rs33443020	3.2	9.6E-03	joint
10593213	Rbm7	9	48368373	rs3717644	3.2	9.6E-03	joint
10457853	Ino80c	18	23647642	rs29954242	3.2	9.6E-03	joint
10362359	Pebp1	5	117930077	rs13478481	3.2	9.6E-03	joint
10503711	Casp8ap2	4	32723846	rs27806695	3.2	9.6E-03	joint
10453736	Unkl	17	25754240	rs33564606	3.2	9.6E-03	joint
10449631	Btbd9	17	31143300	rs33654565	3.2	9.6E-03	joint
10444236	H2-DMb2	17	33940053	mm37-17-33940053	3.2	9.6E-03	joint
10579049	Gm10033	8	72201228	rs32954892	3.2	9.6E-03	joint
10594540	Plekho2	9	65397210	rs6360660	3.1	1.1E-02	joint
10595803	Rnf7	9	96207157	rs30273712	3.1	1.1E-02	joint
10496302	Manba	3	134572525	rs31621856	3.1	1.1E-02	joint
10414590	Ear6	14	52703095	rs3691964	3.1	1.1E-02	joint
10453166	Cdkl4	17	80602577	rs29709987	3.1	1.1E-02	joint
10459844	Haus1	18	78935424	rs30015747	3.1	1.1E-02	joint
10377550	Trp53	11	70083661	rs26920974	3.1	1.1E-02	joint
10485685	Rpl35a	16	33064622	rs4171166	3.1	1.1E-02	joint
10475525	Pldn	2	122549260	rs3726940	3.1	1.1E-02	joint
10367945	Phactr2	10	13247820	rs29319120	3.1	1.1E-02	joint
10387222	Pfas	11	68711359	rs29468815	3.1	1.1E-02	joint
10409990	6720489N17Rik	13	63226418	rs13481846	3.1	1.1E-02	joint
10385034	Rpsa	9	119212345	rs33759597	3.1	1.1E-02	joint
10461909	BC016495	19	18728059	rs31138880	3.1	1.1E-02	joint
10399360	Rhob	12	8442395	rs29132841	3.1	1.1E-02	joint
10356269	Sp140	1	87878515	rs3723583	3.1	1.1E-02	joint
10542842	Ccdc91	6	147485122	rs3686286	3.1	1.1E-02	joint
10379953	4632419I22Rik	11	86469340	rs27012092	3.1	1.1E-02	joint
10511661	Otud6b	4	14209016	rs27728188	3.1	1.1E-02	joint
10410124	Ctsl	13	63620928	rs29783022	3.1	1.1E-02	joint
10565002	Crtc3	7	87904122	rs31362919	3.1	1.1E-02	joint
10504373	Gm12472	4	43663447	rs28320603	3.1	1.1E-02	joint
10453918	3110002H16Rik	18	11987071	rs29912712	3.1	1.1E-02	joint
10489391	Ada	2	163506876	rs29498451	3.1	1.1E-02	joint

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10441952	2210404J11Rik	17	14833162	rs33478834	3.1	1.1E-02	joint
10432488	Bcdin3d	15	99404944	rs3664324	3.0	1.1E-02	joint
10478169	Dhx35	2	158594917	rs27305491	3.0	1.1E-02	joint
10584634	Usp2	9	44322554	rs32609924	3.0	1.1E-02	joint
10410625	Sdha	13	74877462	rs29223975	3.0	1.1E-02	joint
10426909	Letmd1	15	100293660	rs3709293	3.0	1.1E-02	joint
10443021	Atp6v0e	17	27261107	rs33527411	3.0	1.1E-02	joint
10365749	Lta4h	10	93708378	rs29327254	3.0	1.1E-02	joint
10504831	Sec61b	4	47855116	rs6239869	3.0	1.1E-02	joint
10453049	Cdc42ep3	17	79838396	rs33604070	3.0	1.1E-02	joint
10534075	Psph	5	130496212	rs29631045	3.0	1.1E-02	joint
10437627	Rpl35a	16	33064622	rs4171166	3.0	1.1E-02	joint
10495896	Camk2d	3	126328000	rs30516581	3.0	1.1E-02	joint
10355974	Wdfy1	1	80634119	rs30204599	3.0	1.1E-02	joint
10565996	Inppl1	7	108769955	rs31326710	3.0	1.1E-02	joint
10408975	Kif13a	13	47007650	rs29811281	3.0	1.1E-02	joint
10495763	Gclm	3	122675914	rs30354722	3.0	1.1E-02	joint
10441706	1700010I14Rik	17	9218223	rs33285743	3.0	1.1E-02	joint
10586616	Vps13c	9	67622974	rs29697407	3.0	1.1E-02	joint
10443438	Pnpla1	17	28830413	rs6346412	3.0	1.1E-02	joint
10561837	Zfp146	7	31279600	rs31978143	3.0	1.1E-02	joint
10485340	Itpa	2	129897341	rs6366916	3.0	1.1E-02	joint
10559248	Tspan32	7	150565771	rs6307236	3.0	1.1E-02	joint
10502823	Dnajb4	3	152614030	rs31741345	3.0	1.1E-02	joint
10375864	Agxt2l2	11	50429501	rs26965588	3.0	1.1E-02	joint
10521798	Pacrgl	5	48496535	rs6411133	3.0	1.1E-02	joint
10447361	Ttc7	17	87443522	rs29798246	3.0	1.1E-02	joint
10497817	Anxa5	3	37264336	rs3151792	3.0	1.1E-02	joint
10366667	Gns	10	121142981	rs29359488	3.0	1.1E-02	joint
10389099	Rad51l3	11	82765715	rs29432702	3.0	1.2E-02	joint
10577544	Polb	8	23824528	rs4135461	3.0	1.2E-02	joint
10470936	Tbc1d13	2	30268649	rs13464645	3.0	1.2E-02	joint
10406757	Col4a3bp	13	97351492	rs29734096	3.0	1.2E-02	joint
10530503	Cnga1	5	72616926	rs31528146	3.0	1.2E-02	joint
10511325	Rps20	4	3584944	rs27682663	3.0	1.2E-02	joint
10462618	Ifit3	19	34756364	rs30367140	3.0	1.2E-02	joint
10350742	Rnasel	1	155614218	rs30564058	3.0	1.2E-02	joint
10368762	Cdc40	10	40358731	rs29374324	3.0	1.2E-02	joint
10361790	Fuca2	10	13247820	rs29319120	3.0	1.2E-02	joint
10411915	Ppwd1	13	105288962	rs29918048	3.0	1.2E-02	joint
10490256	Rps8	4	116499355	rs27513773	3.0	1.2E-02	joint
10549162	St8sia1	6	143094081	rs6368858	3.0	1.2E-02	joint
10457508	Npc1	18	12160804	rs3720444	3.0	1.2E-02	joint
10495147	Dennd2d	3	106973862	rs30133561	3.0	1.2E-02	joint
10439854	Bbx	16	50274601	rs4185610	3.0	1.2E-02	joint
10570236	Mcf2l	8	13605017	rs6281754	3.0	1.2E-02	joint
10396778	Mpp5	12	80028884	rs6303798	3.0	1.2E-02	joint
10561008	Ceacam1	7	26129230	rs32227353	3.0	1.3E-02	joint
10466606	Anxa1	19	20188567	rs30523372	3.0	1.3E-02	joint
10511282	Tnfrsf4	4	155383774	rs6284920	3.0	1.3E-02	joint
10403462	Dip2c	13	10248112	rs30048367	3.0	1.3E-02	joint
10595831	Zbtb38	9	96323590	rs30177765	3.0	1.3E-02	joint
10574276	Gpr97	8	97466278	rs32122721	3.0	1.3E-02	joint
10495107	Adora3	3	105169244	rs30595214	3.0	1.3E-02	joint
10353032	Rpa3	6	8407487	rs29916108	3.0	1.3E-02	joint

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10425923	Fam118a	15	85524208	rs32099700	3.0	1.3E-02	joint
10534216	Gtf2i	5	134788332	rs13486231	3.0	1.3E-02	joint
10522335	Atp10d	5	73228949	rs33387532	3.0	1.3E-02	joint
10383345	Fscn2	11	120032171	rs29483544	3.0	1.3E-02	joint
10399666	9030624G23Rik	12	25497826	rs29191921	3.0	1.3E-02	joint
10429298	Trappc9	15	72748734	rs32284145	3.0	1.3E-02	joint
10510624	Klhl21	4	150454218	rs31979269	3.0	1.3E-02	joint
10551120	Megf8	7	26101338	rs31480323	3.0	1.3E-02	joint
10532305	4930522L14Rik	5	110375316	rs3653994	3.0	1.3E-02	joint
10475718	Snrnp200	2	127059991	rs6346511	3.0	1.3E-02	joint
10344633	Tcea1	1	4768024	rs31791799	3.0	1.3E-02	joint
10390186	Abi3	11	95158270	rs29464862	3.0	1.3E-02	joint
10464218	Fam160b1	19	56947673	rs31052569	2.9	1.4E-02	joint
10530536	Tec	5	72733958	rs31531926	2.9	1.4E-02	joint
10512291	Dctn3	4	40754093	rs13477665	2.9	1.4E-02	joint
10534253	Gtf2ird1	5	134788332	rs13486231	2.9	1.4E-02	joint
10491486	Atp11b	3	35473242	rs29909670	2.9	1.4E-02	joint
10545751	Tex261	6	83761274	rs30416503	2.9	1.4E-02	joint
10474541	Nop10	2	112397798	rs27491356	2.9	1.4E-02	joint
10436783	Sod1	16	90255906	rs4217234	2.9	1.4E-02	joint
10457273	Kif5b	18	6228620	rs29822349	2.9	1.4E-02	joint
10561787	Zfp27	7	30527305	rs31148449	2.9	1.4E-02	joint
10435676	Gsk3b	16	38132341	rs4174411	2.9	1.4E-02	joint
10533007	Ccdc64	5	115646273	rs33589279	2.9	1.4E-02	joint
10419170	Txndc16	14	46392697	rs31241587	2.9	1.4E-02	joint
10389143	Slfn8	11	83244758	rs3662268	2.9	1.4E-02	joint
10426550	Tmem106c	15	97855998	rs31581769	2.9	1.4E-02	joint
10376507	4933439C10Rik	11	59078936	rs29399861	2.9	1.5E-02	joint
10350985	Mrps14	1	162145996	rs31342483	2.9	1.5E-02	joint
10381809	Itgb3	11	104518979	rs27038465	2.9	1.5E-02	joint
10407570	Zmynd11	13	10268521	rs36897899	2.9	1.5E-02	joint
10524018	Rpl34	3	130577248	rs30804395	2.9	1.5E-02	joint
10520250	Nub1	5	24509818	rs33486334	2.9	1.5E-02	joint
10399768	Ttc15	12	29398947	rs29212758	2.9	1.5E-02	joint
10532857	Gltp	5	115700264	rs29583537	2.9	1.5E-02	joint
10412711	Uqcrb	13	67687808	rs29834558	2.9	1.5E-02	joint
10566067	Rnf121	7	108223861	rs32200432	2.9	1.5E-02	joint
10573675	Lonp2	8	88671915	rs33300351	2.9	1.5E-02	joint
10406005	Irx2	13	72381078	rs30011210	2.9	1.5E-02	joint
10565759	Uvrag	7	106021716	rs31235564	2.9	1.6E-02	joint
10486710	Lcmt2	2	120910944	rs27454954	2.9	1.6E-02	joint
10491551	Exosc9	3	37352792	rs3158608	2.9	1.6E-02	joint
10542340	8430419L09Rik	6	134378973	rs30176386	2.9	1.6E-02	joint
10567022	Btbd10	7	121397206	rs31647638	2.9	1.6E-02	joint
10476969	Pygb	2	151492992	rs6225197	2.9	1.6E-02	joint
10530633	Sgcb	5	73776541	rs29548275	2.9	1.6E-02	joint
10436428	Mina	16	59432512	rs4191725	2.9	1.6E-02	joint
10360026	Uqcrb	13	67687808	rs29834558	2.9	1.6E-02	joint
10474006	Phf21a	2	92814299	rs13476640	2.9	1.6E-02	joint
10414548	Rnase6	14	51805763	rs30400951	2.9	1.6E-02	joint
10436865	Ifngr2	16	92081867	rs6285649	2.9	1.6E-02	joint
10529605	Wfs1	5	36410915	rs6161059	2.9	1.6E-02	joint
10550527	Irf2bp1	7	19623601	rs32365669	2.8	1.7E-02	joint
10374908	Rtn4	11	29625957	rs29420171	2.8	1.7E-02	joint
10540118	Lsm3	6	91444913	rs6230067	2.8	1.7E-02	joint

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10384123	Ddx56	11	6167406	rs13480847	2.8	1.7E-02	joint
10582008	2310061C15Rik	8	119617965	rs6227798	2.8	1.7E-02	joint
10407985	Gpr141	13	19885977	rs29635196	2.8	1.7E-02	joint
10360834	Hlx	1	186704249	rs31785670	2.8	1.7E-02	joint
10352320	Tmem63a	1	182871786	rs31674207	2.8	1.7E-02	joint
10458913	Cep120	18	54324899	rs30307241	2.8	1.7E-02	joint
10542714	Lyrm5	6	144557866	rs30617674	2.8	1.7E-02	joint
10533316	Erp29	5	121813345	rs33216974	2.8	1.8E-02	joint
10361846	Reps1	10	18317705	rs29317189	2.8	1.8E-02	joint
10595466	Pgm3	9	86687935	rs30423308	2.8	1.8E-02	joint
10436849	Ifnar1	16	91885909	rs4219533	2.8	1.8E-02	joint
10586441	Oaz2	9	65635795	rs30188336	2.8	1.8E-02	joint
10593050	Il10ra	9	44638009	rs29841687	2.8	1.8E-02	joint
10497773	Mccc1	3	36583994	rs3147048	2.8	1.8E-02	joint
10574423	A330008L17Rik	8	102923044	rs32321710	2.8	1.8E-02	joint
10506880	Kti12	4	108531685	rs28150412	2.8	1.8E-02	joint
10459854	F830208F22Rik	18	78248089	rs30177062	2.8	1.8E-02	joint
10376312	Larp1	11	57876912	rs29429879	2.8	1.9E-02	joint
10595529	4922501C03Rik	9	86905654	rs29695315	2.8	1.9E-02	joint
10410259	Uqcrb	13	67687808	rs29834558	2.8	1.9E-02	joint
10421749	Akap11	14	78779541	rs30323725	2.8	1.9E-02	joint
10495120	Ovgp1	3	106330732	rs31473892	2.8	1.9E-02	joint
10390271	Nfe2l1	11	96579189	rs6164096	2.8	1.9E-02	joint
10439642	Slc35a5	16	44481216	rs4179886	2.8	1.9E-02	joint
10476301	Smox	2	131291839	rs29930551	2.8	1.9E-02	joint
10430179	Apol7b	15	76561282	rs31682122	2.8	1.9E-02	joint
10486499	Tmem87a	2	120697778	rs27438933	2.8	1.9E-02	joint
10430956	Cyb5r3	15	82937328	rs32113647	2.8	1.9E-02	joint
10361156	Rcor3	1	193468580	rs30860614	2.8	1.9E-02	joint
10569485	Tnfrsf26	7	151022596	rs6318605	2.8	1.9E-02	joint
10593205	Rexo2	9	48213816	rs33643289	2.8	1.9E-02	joint
10594460	Dis3l	9	64155869	rs30015069	2.8	1.9E-02	joint
10535034	Zfp68	5	138958111	rs3661529	2.8	1.9E-02	joint
10479215	Rps8	4	116499355	rs27513773	2.7	2.0E-02	joint
10554926	Ccdc90b	7	100108654	rs31465001	2.7	2.0E-02	joint
10401172	Vti1b	12	80028884	rs6303798	2.7	2.0E-02	joint
10397818	Cpsf2	12	102260123	rs29206891	2.7	2.0E-02	joint
10461765	Lpxn	19	13296084	rs30317980	2.7	2.0E-02	joint
10398459	Ppp2r5c	12	111469066	rs29180355	2.7	2.0E-02	joint
10383867	Mtmr3	11	4442382	rs29417270	2.7	2.0E-02	joint
10497237	Pag1	3	9925725	rs30156006	2.7	2.0E-02	joint
10402835	Nudt14	12	114259747	rs29131909	2.7	2.0E-02	joint
10390640	Ikzf3	11	98281665	rs27070994	2.7	2.0E-02	joint
10517067	Sfn	4	132642384	rs33024223	2.7	2.0E-02	joint
10599346	Polr2k	15	36365406	rs32253436	2.7	2.0E-02	joint
10382376	Ttyh2	11	114532979	rs27029726	2.7	2.0E-02	joint
10542834	Gm5887	6	147022874	rs30765255	2.7	2.0E-02	joint
10469538	4930426L09Rik	2	18951036	rs29538801	2.7	2.0E-02	joint
10563780	E2f8	7	56609802	rs31628386	2.7	2.0E-02	joint
10521982	Cbfa2t2	2	154215872	rs6287924	2.7	2.1E-02	joint
10413008	Fut11	14	21555395	rs13472696	2.7	2.1E-02	joint
10345620	Mrpl30	1	38096577	rs32244279	2.7	2.1E-02	joint
10570429	Zfp828	8	14430267	rs6280829	2.7	2.1E-02	joint
10530151	Tlr6	5	65436811	rs31444586	2.7	2.1E-02	joint
10380719	Sp6	11	96444238	rs29434627	2.7	2.1E-02	joint

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10462005	Tmem2	19	21928881	rs31301051	2.7	2.1E-02	joint
10532989	Gatc	5	115471963	rs33324564	2.7	2.1E-02	joint
10505517	Tlr4	4	65694556	rs13477747	2.7	2.1E-02	joint
10503833	Rplp1	9	62560178	rs6339706	2.7	2.1E-02	joint
10501963	Ugt8a	3	125634898	rs30599218	2.7	2.1E-02	joint
10369206	Rps8	4	116499355	rs27513773	2.7	2.1E-02	joint
10409737	Agtpbp1	13	60473031	rs29589851	2.7	2.2E-02	joint
10544829	Jazf1	6	53059848	rs30752964	2.7	2.2E-02	joint
10353135	Ncoa2	1	13184872	rs31477656	2.7	2.2E-02	joint
10373000	Xrcc6bp1	10	126210709	rs29332948	2.7	2.2E-02	joint
10532753	Coro1c	5	114306753	rs33601130	2.7	2.2E-02	joint
10532802	Alkbh2	5	114599562	rs33429598	2.7	2.2E-02	joint
10397002	Sipa1l1	12	83338338	rs6330889	2.7	2.2E-02	joint
10472058	Rif1	2	51103744	rs33353352	2.7	2.2E-02	joint
10573703	Tmem188	8	90847735	rs33010793	2.7	2.2E-02	joint
10360737	Rpl35a	16	33064622	rs4171166	2.7	2.2E-02	joint
10405535	B230219D22Rik	13	54996852	rs29572215	2.7	2.2E-02	joint
10468231	Arl3	19	45941380	rs3718843	2.7	2.3E-02	joint
10502329	Cisd2	3	134956405	rs30604246	2.7	2.3E-02	joint
10498771	Pdcd10	3	76195638	rs30405476	2.7	2.3E-02	joint
10514732	Slc35d1	4	102090853	rs32197109	2.7	2.3E-02	joint
10427895	Basp1	15	25336862	rs3667619	2.7	2.3E-02	joint
10357790	Sox13	1	135409223	rs32494351	2.7	2.3E-02	joint
10565634	Myo7a	7	104967888	rs31747372	2.7	2.3E-02	joint
10453429	Pigf	17	87327330	rs6268795	2.7	2.3E-02	joint
10572212	Gmip	8	72463828	rs32629017	2.7	2.3E-02	joint
10444927	Nrm	17	35740822	mm37-17-35740822	2.7	2.3E-02	joint
10540472	Bhlhe40	6	108301859	rs30119858	2.7	2.3E-02	joint
10563050	Prr12	7	51570774	rs6405901	2.6	2.3E-02	joint
10420320	Cenpj	14	57152053	rs30604442	2.6	2.3E-02	joint
10390950	Gm11564	11	98865158	rs27102250	2.6	2.3E-02	joint
10594613	Usp3	9	66787809	rs33717498	2.6	2.3E-02	joint
10507908	Fhl3	4	124290513	rs27555528	2.6	2.3E-02	joint
10551065	D930028M14Rik	7	26101338	rs31480323	2.6	2.3E-02	joint
10550597	Fbxo46	7	19721583	rs6260413	2.6	2.3E-02	joint
10440406	Nrip1	16	76177962	rs4206160	2.6	2.3E-02	joint
10584941	Bace1	9	45087792	rs30359695	2.6	2.3E-02	joint
10396278	Daam1	12	73481149	rs3724186	2.6	2.3E-02	joint
10488382	Cd93	2	148207741	rs33143355	2.6	2.3E-02	joint
10440926	Dnajc28	16	92081867	rs6285649	2.6	2.3E-02	joint
10455483	Ythdc2	18	44838593	rs6281938	2.6	2.3E-02	joint
10552740	Nup62	7	52250686	rs32051036	2.6	2.4E-02	joint
10456798	Hdhd2	18	76374660	rs29672377	2.6	2.4E-02	joint
10505000	Nipsnap3a	4	53442816	rs27779509	2.6	2.4E-02	joint
10470462	Col5a1	2	28005358	rs27197977	2.6	2.4E-02	joint
10576305	Tcf25	8	125972572	rs33432761	2.6	2.4E-02	joint
10501832	Abcd3	3	122194084	rs30419088	2.6	2.4E-02	joint
10396694	Churc1	12	77873825	rs29183071	2.6	2.4E-02	joint
10542445	Strap	6	137446748	rs30843251	2.6	2.4E-02	joint
10546791	Sumf1	6	108479248	rs30229283	2.6	2.4E-02	joint
10396442	Snapc1	12	74991059	rs29202209	2.6	2.4E-02	joint
10393687	Azi1	11	120032171	rs29483544	2.6	2.4E-02	joint
10489186	Rpl35a	16	33064622	rs4171166	2.6	2.5E-02	joint
10402268	Lgmn	12	103631471	rs29171624	2.6	2.5E-02	joint

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10597900	Zfp445	9	122819320	rs29976441	2.6	2.5E-02	joint
10455989	Rbm22	18	61140136	rs6334696	2.6	2.5E-02	joint
10452937	Heatr5b	17	78951702	rs3670726	2.6	2.5E-02	joint
10583402	Zfp317	9	19270016	rs30162988	2.6	2.5E-02	joint
10499716	Ubap2l	3	90000401	rs30607762	2.6	2.5E-02	joint
10539907	Tpra1	6	89320559	rs30220244	2.6	2.5E-02	joint
10456995	Txnl4a	18	80987560	rs30301873	2.6	2.5E-02	joint
10394477	Laptm4a	12	9470091	rs29137060	2.6	2.5E-02	joint
10585860	Adpgk	9	59178045	rs29736662	2.6	2.5E-02	joint
10360040	Fcgr3	1	172970025	rs32678315	2.6	2.5E-02	joint
10449652	Dnahc8	17	29917069	rs3693494	2.6	2.5E-02	joint
10498155	Rps14	18	60666455	rs6324468	2.6	2.6E-02	joint
10464647	Tbc1d10c	19	4652712	rs30959235	2.6	2.6E-02	joint
10544002	Creb3l2	6	37481775	rs6330932	2.6	2.6E-02	joint
10520271	2900005J15Rik	5	24647720	rs29821175	2.6	2.6E-02	joint
10387525	Mpdu1	11	68786528	rs29433934	2.6	2.6E-02	joint
10520513	4930471M23Rik	5	31122738	rs29631774	2.6	2.6E-02	joint
10424411	Tsg101	7	53456332	rs31528732	2.6	2.6E-02	joint
10541885	Scnn1a	6	126168445	rs30954202	2.6	2.6E-02	joint
10360789	Degs1	1	184461100	rs31741702	2.6	2.6E-02	joint
10526735	Zscan21	5	138360832	rs8265976	2.6	2.6E-02	joint
10516652	Iqcc	4	129360089	rs27487632	2.6	2.6E-02	joint
10487513	Anapc1	2	127586140	rs33579568	2.6	2.6E-02	joint
10576274	Zfp276	8	125573046	rs6242679	2.6	2.6E-02	joint
10481368	Trub2	2	29485035	rs27201282	2.6	2.6E-02	joint
10407319	Rpl34	3	130266226	rs30911073	2.6	2.6E-02	joint
10556528	Pde3b	7	121440758	rs6256808	2.6	2.6E-02	joint
10455588	Hspe1	1	55612052	rs3723035	2.6	2.6E-02	joint
10382838	1810032O08Rik	11	116591416	rs29406603	2.6	2.6E-02	joint
10377612	Plscr3	11	69146229	rs29432944	2.6	2.6E-02	joint
10539080	St3gal5	6	72614156	rs30219729	2.6	2.7E-02	joint
10550394	Ptgir	7	17259509	rs31426810	2.6	2.7E-02	joint
10468311	Sh3pxd2a	19	47535259	rs30321371	2.6	2.7E-02	joint
10506274	Dnajc6	4	101392863	rs32490226	2.6	2.7E-02	joint
10503363	Rbm12b	4	11627403	rs31814977	2.6	2.7E-02	joint
10542079	Foxm1	6	128507691	rs29971833	2.6	2.7E-02	joint
10563615	Hps5	7	53720160	rs6364611	2.5	2.8E-02	joint
10435455	Rpl35a	16	33064622	rs4171166	2.5	2.8E-02	joint
10532921	Sppl3	5	116028399	rs33183771	2.5	2.8E-02	joint
10510129	Dhrs3	4	144870506	rs27627557	2.5	2.8E-02	joint
10435004	1500031L02Rik	16	32766708	rs4170615	2.5	2.8E-02	joint
10572669	Fam129c	8	73174378	rs32707454	2.5	2.8E-02	joint
10516884	Trnau1ap	4	132781978	rs27541373	2.5	2.8E-02	joint
10506134	Atg4c	4	98936968	rs28109068	2.5	2.8E-02	joint
10427454	Card6	15	5293817	rs6289794	2.5	2.8E-02	joint
10436348	Tomm70a	16	57510798	rs3709079	2.5	2.8E-02	joint
10415662	Rcbtb1	14	59629278	rs30907644	2.5	2.8E-02	joint
10460018	Zfp236	18	83598896	rs29578250	2.5	2.8E-02	joint
10348618	Asb1	1	93333537	rs31606310	2.5	2.8E-02	joint
10382470	Tmem104	11	114985564	rs29471047	2.5	2.8E-02	joint
10411306	Polk	13	97285071	rs29633246	2.5	2.8E-02	joint
10453260	Haao	17	84230336	rs33553636	2.5	2.9E-02	joint
10350247	Kif21b	1	138723844	rs30502059	2.5	2.9E-02	joint
10454842	Ube2d2	18	36778428	rs29625675	2.5	2.9E-02	joint
10417749	Ube2e1	14	18247303	rs30660151	2.5	2.9E-02	joint

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10556658	9030624J02Rik	7	125838946	rs32474210	2.5	2.9E-02	joint
10466439	Pebp1	5	117930077	rs13478481	2.5	2.9E-02	joint
10362129	Vnn3	10	23402924	rs29381450	2.5	2.9E-02	joint
10531208	Cox18	5	90681960	rs29508640	2.5	2.9E-02	joint
10349333	3110009E18Rik	1	122725754	rs30734173	2.5	3.0E-02	joint
10503134	Sdcbp	4	6797458	rs27674838	2.5	3.0E-02	joint
10444895	Flot1	17	35831079	mm37-17-35831079	2.5	3.0E-02	joint
10519151	Mib2	4	154887311	rs6201741	2.5	3.0E-02	joint
10552779	Fuz	7	52898483	rs32222012	2.5	3.0E-02	joint
10400941	Dhrs7	12	73178478	rs29173056	2.5	3.0E-02	joint
10455647	Tnfaip8	18	49339947	rs30246269	2.5	3.0E-02	joint
10596815	Rnf123	9	108042615	rs29989915	2.5	3.0E-02	joint
10517336	Clic4	4	134574671	rs6371478	2.5	3.0E-02	joint
10491603	4932438A13Rik	3	37560742	rs30085634	2.5	3.0E-02	joint
10514392	Tusc1	4	93185456	rs32755743	2.5	3.0E-02	joint
10425040	Apol7e	15	76545541	rs32342299	2.5	3.0E-02	joint
10416753	Pibf1	14	99106102	rs31252585	2.5	3.0E-02	joint
10524781	Rab35	5	116028399	rs33183771	2.5	3.0E-02	joint
10496438	Adh1	3	137721707	rs30882081	2.5	3.0E-02	joint
10553354	Nav2	7	56124204	rs32245660	2.5	3.0E-02	joint
10439058	Lrrc33	16	31342465	rs4168997	2.5	3.0E-02	joint
10456001	Rps14	18	60666455	rs6324468	2.5	3.0E-02	joint
10430945	Poldip3	15	82931730	rs31775148	2.5	3.0E-02	joint
10463632	Tmem180	19	45952834	rs3671238	2.5	3.0E-02	joint
10550978	Phldb3	7	25119077	rs32341931	2.5	3.0E-02	joint
10545001	Ppm1k	6	57659921	rs30902330	2.5	3.0E-02	joint
10510399	Masp2	4	147874905	rs27599611	2.5	3.0E-02	joint
10402140	Gm10431	12	102149223	rs29203855	2.5	3.0E-02	joint
10407792	Gpr137b-ps	13	12465870	rs3716238	2.5	3.0E-02	joint
10571274	Gsr	8	34097219	rs33386424	2.5	3.0E-02	joint
10501860	Fnbp1l	3	122367049	rs6217051	2.5	3.1E-02	joint
10449266	Itfg3	17	26440528	rs29522863	2.5	3.1E-02	joint
10507040	Spata6	4	111483605	rs27515792	2.5	3.1E-02	joint
10460057	Tshz1	18	84326190	rs29968809	2.5	3.1E-02	joint
10450699	H2-Q2	17	35374982	mm37-17-35374982	2.5	3.1E-02	joint
10594652	Lactb	9	66888400	rs30524357	2.5	3.1E-02	joint
10384145	H2afv	11	6168182	rs26899782	2.5	3.1E-02	joint
10505643	4930473A06Rik	4	83976236	rs28101086	2.5	3.1E-02	joint
10412251	Ndufs4	13	114824365	rs29547399	2.5	3.1E-02	joint
10444605	Vars	17	36100416	mm37-17-36100416	2.5	3.1E-02	joint
10419370	Exoc5	14	50085299	rs30596041	2.5	3.1E-02	joint
10587639	Nt5e	9	88068525	rs29885916	2.5	3.1E-02	joint
10509635	Akr7a5	4	139457637	rs27612037	2.5	3.1E-02	joint
10542264	2700089E24Rik	6	132335959	rs30712128	2.5	3.1E-02	joint
10593024	Cd3e	9	44789625	rs29749035	2.5	3.1E-02	joint
10351353	Cd247	1	167611765	rs31408859	2.5	3.1E-02	joint
10573082	Inpp4b	8	84724492	rs33367345	2.5	3.1E-02	joint
10442057	Riok2	17	17966665	rs29503159	2.5	3.1E-02	joint
10516943	Atpif1	4	132116095	rs32955860	2.5	3.1E-02	joint
10479228	Etohi1	2	178324499	rs33407067	2.5	3.1E-02	joint
10380477	Ppp1r9b	11	94582344	rs6366267	2.5	3.1E-02	joint
10563891	Nck2	1	44265387	rs6222550	2.4	3.2E-02	joint

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10526145	0610007L01Rik	5	131092689	rs33441667	2.4	3.2E-02	joint
10577230	Erich1	8	13605017	rs6281754	2.4	3.2E-02	joint
10520419	Ube3c	5	30100397	rs29564746	2.4	3.2E-02	joint
10447349	Cript	17	87443522	rs29798246	2.4	3.2E-02	joint
10555389	Ucp2	7	108164967	rs31037097	2.4	3.2E-02	joint
10527547	Mtif3	5	148016306	rs33127996	2.4	3.2E-02	joint
10392856	Nat9	11	115129532	rs29452428	2.4	3.2E-02	joint
10361104	Ppp2r5a	1	193264692	rs31727476	2.4	3.2E-02	joint
10567171	Rps13	7	123290980	rs3684383	2.4	3.3E-02	joint
10499309	Apoa1bp	3	87854631	rs31640799	2.4	3.3E-02	joint
10419082	5730469M10Rik	14	41249102	rs6360949	2.4	3.3E-02	joint
10507520	Hyi	4	118503791	rs27494641	2.4	3.3E-02	joint
10383999	Mrps24	11	5630318	rs26884997	2.4	3.3E-02	joint
10470050	Abca2	2	25362101	rs27210461	2.4	3.3E-02	joint
10544976	Kbtbd2	6	56681390	rs30760848	2.4	3.3E-02	joint
10475000	Rtf1	2	119403415	rs33072899	2.4	3.3E-02	joint
10508420	Yars	4	128659383	rs6334688	2.4	3.3E-02	joint
10517883	Necap2	4	140713786	rs32671622	2.4	3.3E-02	joint
10501048	2010016I18Rik	3	105421957	rs31691760	2.4	3.3E-02	joint
10461844	Gnaq	19	16185584	rs6342609	2.4	3.3E-02	joint
10579976	Elmod2	8	85934141	rs32919377	2.4	3.3E-02	joint
10578377	Frg1	8	42528102	rs3165545	2.4	3.3E-02	joint
10564507	Arrdc4	7	75206551	rs32453663	2.4	3.3E-02	joint
10483584	Mettl8	2	70937848	rs33174507	2.4	3.3E-02	joint
10358064	Ipo9	1	136413808	rs30869517	2.4	3.3E-02	joint
10372082	Nudt4	10	95008040	rs6196828	2.4	3.4E-02	joint
10354157	Chst10	1	38965805	rs6323941	2.4	3.4E-02	joint
10395612	G2e3	12	52583138	rs6267394	2.4	3.4E-02	joint
10407251	Ccno	13	114495733	rs29527544	2.4	3.4E-02	joint
10508392	Rnf19b	4	129125982	rs31775195	2.4	3.5E-02	joint
10454414	Pik3c3	18	30090864	rs13483275	2.4	3.5E-02	joint
10511290	Tnfrsf18	4	155388389	rs32224289	2.4	3.5E-02	joint
10494160	Tmod4	3	94933346	rs30257773	2.4	3.5E-02	joint
10550574	Dmpk	7	20015306	rs31098779	2.4	3.5E-02	joint
10408600	Serpinb6a	13	34249342	rs29237475	2.4	3.5E-02	joint
10488195	Rrbp1	2	143780025	rs27264453	2.4	3.5E-02	joint
10549361	Tm7sf3	6	146359925	rs30741186	2.4	3.5E-02	joint
10383282	Chmp6	11	119986865	rs27013742	2.4	3.5E-02	joint
10551347	Blvrb	7	28289392	rs31161692	2.4	3.5E-02	joint
10356968	Pam	1	100089736	rs6361718	2.4	3.5E-02	joint
10443598	Dnahc8	17	31117874	rs6282714	2.4	3.5E-02	joint
10586920	Rfx7	9	72307604	rs3718833	2.4	3.5E-02	joint
10585699	Fabp5	3	9912297	rs31388033	2.4	3.5E-02	joint
10562416	Cebpg	7	35554561	rs31595471	2.4	3.5E-02	joint
10384885	Spnb2	11	30083667	rs26860813	2.4	3.5E-02	joint
10518686	Pik3cd	4	148329368	rs32511975	2.4	3.5E-02	joint
10571849	Fbxo8	8	58429426	rs32873199	2.4	3.6E-02	joint
10576417	Galnt2	8	125798415	rs32995456	2.4	3.6E-02	joint
10440037	Nit2	16	56693973	rs4188876	2.4	3.6E-02	joint
10425092	Cyth4	15	79294488	rs3678019	2.4	3.6E-02	joint
10597518	Tgfbr2	9	116298298	rs29742003	2.4	3.6E-02	joint
10445241	Tnfrsf21	17	43827855	rs33244454	2.4	3.6E-02	joint
10483249	Galnt3	2	65936548	rs6232577	2.4	3.6E-02	joint
10492102	Spg20	3	54978078	rs6263547	2.4	3.6E-02	joint
10410345	Zfp748	13	67602610	rs29549507	2.4	3.6E-02	joint

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10432661	Galnt6	15	100539275	rs32185773	2.4	3.6E-02	joint
10504817	Tgfbr1	4	47310915	rs27845062	2.4	3.6E-02	joint
10428398	Eif3e	15	43077655	rs31580536	2.4	3.6E-02	joint
10460108	Gnpnat1	14	45899224	rs6284094	2.4	3.6E-02	joint
10594315	Fem1b	9	62226774	rs30481819	2.4	3.6E-02	joint
10508479	Ptp4a2	4	129847468	rs8272673	2.4	3.7E-02	joint
10565815	Gm4980	7	105859238	rs31710002	2.4	3.7E-02	joint
10560237	Gpr77	7	16822056	rs6348397	2.4	3.7E-02	joint
10444312	Btnl2	17	33887470	mm37-17-33887470	2.4	3.7E-02	joint
10408200	Hist1h4f	13	23495851	rs6314855	2.4	3.7E-02	joint
10585803	Stra6	9	58508540	rs6161783	2.4	3.7E-02	joint
10533085	Pebp1	5	117930077	rs13478481	2.4	3.7E-02	joint
10389134	Slfn9	11	82883421	rs28191176	2.3	3.7E-02	joint
10562578	Pop4	7	38996606	rs31864072	2.3	3.7E-02	joint
10433656	Mkl2	16	13343475	rs4163175	2.3	3.7E-02	joint
10400293	6530401N04Rik	12	52886510	rs29207736	2.3	3.7E-02	joint
10548884	Erp27	6	136108417	rs30574004	2.3	3.7E-02	joint
10529895	Qdpr	5	46415271	rs29633750	2.3	3.7E-02	joint
10518069	Efhd2	4	140713786	rs32671622	2.3	3.7E-02	joint
10468795	Rab11fip2	19	59979567	rs30957600	2.3	3.7E-02	joint
10399696	Rnf144a	12	26670102	rs33847601	2.3	3.7E-02	joint
10356601	Per2	1	92601941	rs6403530	2.3	3.7E-02	joint
10586252	Dennd4a	9	64888941	rs6227786	2.3	3.7E-02	joint
10572635	Sfn	4	132642384	rs33024223	2.3	3.7E-02	joint
10547926	Cops7a	6	125061813	rs30666174	2.3	3.8E-02	joint
10526848	A430033K04Rik	5	138623492	rs29727224	2.3	3.8E-02	joint
10361682	Ppil4	10	7511633	rs13465961	2.3	3.8E-02	joint
10390252	Gm11536	11	96410911	rs27074446	2.3	3.8E-02	joint
10509838	Padi2	4	140346796	rs28310621	2.3	3.8E-02	joint
10552832	Nosip	7	52250686	rs32051036	2.3	3.8E-02	joint
10407803	Gpr137b	13	12612567	rs29552398	2.3	3.9E-02	joint
10526508	Fis1	5	137814352	rs3150288	2.3	3.9E-02	joint
10376292	Larp1	11	57471055	rs29404065	2.3	3.9E-02	joint
10476834	Xrn2	2	147439021	rs27283473	2.3	3.9E-02	joint
10484999	Ddb2	2	90986721	rs33011122	2.3	3.9E-02	joint
10359677	Blzf1	1	166113450	rs31846431	2.3	3.9E-02	joint
10592471	Gramd1b	9	39499324	rs30324560	2.3	3.9E-02	joint
10391103	Jup	11	100860032	rs29414884	2.3	3.9E-02	joint
10556491	Far1	7	120138402	rs6185800	4.0	9.5E-03	cell_specific
10512005	1810030N24Rik	4	34367659	rs27803758	4.0	9.5E-03	cell_specific
10545401	Vamp5	6	71679431	rs30681710	4.0	9.5E-03	cell_specific
10518341	Ppp2r5a	1	193083622	rs30548840	4.0	9.5E-03	cell_specific
10439881	5330426P16Rik	16	50723786	rs4186115	4.0	9.5E-03	cell_specific
10390299	Pnpo	11	96444238	rs29434627	4.0	9.5E-03	cell_specific
10450723	H2-T10	17	35845027	mm37-17-35845027	4.0	9.5E-03	cell_specific
10579939	Usp38	8	83617706	rs33386427	4.0	9.5E-03	cell_specific
10519060	Tnfrsf14	4	154314843	rs33115581	4.0	9.5E-03	cell_specific
10416566	Epsti1	14	78095590	rs30781266	4.0	9.5E-03	cell_specific
10543471	Pot1a	6	25764203	rs3671709	4.0	9.5E-03	cell_specific
10477630	Dynlrb1	2	155347064	rs27324153	4.0	9.5E-03	cell_specific
10553301	Ldha	7	53338767	rs31872006	4.0	9.5E-03	cell_specific
10550365	Prkd2	7	17415743	rs32516878	4.0	9.5E-03	cell_specific
10587639	Nt5e	9	88236476	rs30435098	4.0	9.5E-03	cell_specific

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10400254	Heatr5a	12	52914832	rs29178695	4.0	9.5E-03	cell_specific
10346168	Stat4	1	52113607	rs6232649	4.0	9.5E-03	cell_specific
10461723	Fam111a	19	12661130	rs30614136	4.0	9.5E-03	cell_specific
10518069	Efhd2	4	141079421	rs27580162	4.0	9.5E-03	cell_specific
10456492	D18Ertd653e	18	68368898	rs30058399	4.0	9.5E-03	cell_specific
10486469	Vps39	2	120697778	rs27438933	4.0	9.5E-03	cell_specific
10549361	Tm7sf3	6	146606897	rs3724485	4.0	9.5E-03	cell_specific
10597627	Oxsr1	9	120065853	rs29831536	4.0	9.5E-03	cell_specific
10355967	Ap1s3	1	79481687	rs3659983	4.0	9.5E-03	cell_specific
10547140	Tmcc1	6	116153054	rs30316104	4.0	9.5E-03	cell_specific
10439936	Nfkbiz	16	55739724	rs4187896	4.0	9.5E-03	cell_specific
10530151	Tlr6	5	65381279	rs31444941	4.0	9.5E-03	cell_specific
10575120	Sntb2	8	109164175	rs33180684	4.0	9.5E-03	cell_specific
10542836	Klhdc5	6	147538222	rs30806561	4.0	9.5E-03	cell_specific
10456254	Nedd4l	18	65094902	rs29977382	4.0	9.5E-03	cell_specific
10483381	Stk39	2	68139594	rs33019425	4.0	9.5E-03	cell_specific
10553336	Zdhhc13	7	56010213	rs31326447	4.0	9.5E-03	cell_specific
10524631	Oasl1	5	115004548	rs29534493	4.0	9.5E-03	cell_specific
10396694	Churc1	12	77781590	rs29205494	4.0	9.5E-03	cell_specific
10525452	Rnf34	5	123324768	rs29525600	4.0	9.5E-03	cell_specific
10575102	Cirh1a	8	109264042	rs32899354	4.0	9.5E-03	cell_specific
10516823	Epb4.1	4	132229102	rs27593908	4.0	9.5E-03	cell_specific
10512774	Coro2a	4	46980565	rs27821784	4.0	9.5E-03	cell_specific
10526520	Plod3	5	137814352	rs3150288	4.0	9.5E-03	cell_specific
10430519	Csnk1e	15	79294488	rs3678019	4.0	9.5E-03	cell_specific
10577190	Rasa3	8	13605017	rs6281754	4.0	9.5E-03	cell_specific
10387536	Cd68	11	70469788	rs29431005	4.0	9.5E-03	cell_specific
10424676	Ly6e	15	75144538	rs31727411	4.0	9.5E-03	cell_specific
10551542	Fbxo17	7	29482328	rs31576129	4.0	9.5E-03	cell_specific
10358717	1700025G04Rik	1	154689249	rs6233546	4.0	9.5E-03	cell_specific
10420785	Mtmr9	14	64848723	rs31448986	4.0	9.5E-03	cell_specific
10466888	Glis3	19	28608123	rs30302551	4.0	9.5E-03	cell_specific
10510452	Dffa	4	148223345	rs3681476	4.0	9.5E-03	cell_specific
10532753	Coro1c	5	114354945	rs33661898	4.0	9.5E-03	cell_specific
10429573	Ly6c2	15	74732982	rs32479616	4.0	9.5E-03	cell_specific
10542275	Etv6	6	133828659	rs30018326	4.0	9.5E-03	cell_specific
10549162	St8sia1	6	143094081	rs6368858	4.0	9.5E-03	cell_specific
10510162	Ppp2r5a	1	193083622	rs30548840	4.0	9.5E-03	cell_specific
10574166	Cpne2	8	97095919	rs32098937	4.0	9.5E-03	cell_specific
10405757	2010111I01Rik	13	63058762	rs29584536	4.0	9.5E-03	cell_specific
10367717	BC013529	10	7464266	rs29326767	4.0	9.5E-03	cell_specific
10425302	Gtpbp1	15	79294488	rs3678019	4.0	9.5E-03	cell_specific
10377804	Arrb2	11	70750141	rs29485948	4.0	9.5E-03	cell_specific
10361104	Ppp2r5a	1	193105469	rs31308448	4.0	9.5E-03	cell_specific
10464128	Casp7	19	56466207	rs30353487	4.0	9.5E-03	cell_specific
10459925	Pqlc1	18	80683000	rs29623552	4.0	9.5E-03	cell_specific
10550332	Slc1a5	7	17415743	rs32516878	4.0	9.5E-03	cell_specific
10472738	Dcaf17	2	70937816	rs27971741	4.0	9.5E-03	cell_specific
10348537	Ramp1	1	93001662	rs30696327	4.0	9.5E-03	cell_specific
10547100	Plxnd1	6	116240441	rs30317040	4.0	9.5E-03	cell_specific
10427928	Trio	15	27768363	rs31749825	4.0	9.5E-03	cell_specific
10365601	Gnptab	10	87921997	rs29316311	4.0	9.5E-03	cell_specific
10381172	Stat5a	11	101697945	rs28234687	4.0	9.5E-03	cell_specific
10429568	Ly6c1	15	74732982	rs32479616	4.0	9.5E-03	cell_specific
10524955	Tesc	5	118241727	rs29675645	4.0	9.5E-03	cell_specific

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10493703	Jtb	3	89500015	rs31437137	4.0	9.5E-03	cell_specific
10421810	1190002H23Rik	14	79714035	rs6200299	4.0	9.5E-03	cell_specific
10454198	Rnf125	18	21090989	rs29579479	4.0	9.5E-03	cell_specific
10412830	Ngly1	14	16192800	rs30486858	4.0	9.5E-03	cell_specific
10407370	4833420G17Rik	13	120139786	rs30094125	4.0	9.5E-03	cell_specific
10510197	Ppp2r5a	1	193083622	rs30548840	4.0	9.5E-03	cell_specific
10546294	Nup210	6	90957129	rs30558656	4.0	9.5E-03	cell_specific
10457054	Zadh2	18	84292211	rs30065972	4.0	9.5E-03	cell_specific
10455472	Dcp2	18	44203666	rs29624632	4.0	9.5E-03	cell_specific
10350823	Abl2	1	158427217	rs30707627	4.0	9.5E-03	cell_specific
10353181	Lactb2	1	14206837	rs31958571	4.0	9.5E-03	cell_specific
10436830	Ifnar2	16	91420154	rs4219074	4.0	9.5E-03	cell_specific
10441055	Pigp	16	94603265	rs3721009	4.0	9.5E-03	cell_specific
10477808	Romo1	2	154970119	rs27326123	4.0	9.5E-03	cell_specific
10495252	Romo1	2	154970119	rs27326123	4.0	9.5E-03	cell_specific
10380751	Mrpl45	11	96832611	rs29446248	4.0	9.5E-03	cell_specific
10447294	Prkce	17	86686130	rs33242653	4.0	9.5E-03	cell_specific
10409767	Golm1	13	59400001	rs29784760	4.0	9.5E-03	cell_specific
10406598	Serinc5	13	93442535	rs29251705	4.0	9.5E-03	cell_specific
10405693	Dapk1	13	61666712	rs3718662	4.0	9.5E-03	cell_specific
10405263	4732471D19Rik	13	54513686	rs29850204	4.0	9.5E-03	cell_specific
10462603	Fas	19	34330781	rs31034447	4.0	9.5E-03	cell_specific
10423593	Laptm4b	15	34344001	rs31851117	4.0	9.5E-03	cell_specific
10501048	2010016I18Rik	3	106978693	rs30254304	4.0	9.5E-03	cell_specific
10475532	Sqrdl	2	122549260	rs3726940	3.7	1.4E-02	cell_specific
10577954	Rab11fip1	8	27979203	rs33034750	3.7	1.4E-02	cell_specific
10350977	4930523C07Rik	1	161122172	rs3719736	3.7	1.4E-02	cell_specific
10521440	Afap1	5	36436857	rs32582241	3.7	1.4E-02	cell_specific
10502299	Nfkb1	3	135803380	rs30938743	3.7	1.4E-02	cell_specific
10416371	Lpar6	14	73599680	rs30500077	3.7	1.4E-02	cell_specific
10437664	Dexi	16	10530544	rs4160897	3.7	1.4E-02	cell_specific
10503359	C430048L16Rik	4	12266574	rs32191648	3.7	1.4E-02	cell_specific
10350753	Glul	1	155614341	rs32575836	3.7	1.4E-02	cell_specific
10450075	H2-K1	17	33948803	mm37-17-33948803	3.7	1.4E-02	cell_specific
10376269	Galnt10	11	57194384	rs6235463	3.7	1.4E-02	cell_specific
10459912	Adnp2	18	81219995	rs29721638	3.7	1.4E-02	cell_specific
10547521	Atp6v1e1	6	121290936	rs30659335	3.7	1.4E-02	cell_specific
10424810	Gpaa1	15	75609284	rs6268783	3.7	1.4E-02	cell_specific
10563323	Nucb1	7	52760213	rs32277913	3.7	1.4E-02	cell_specific
10524004	Pcgf3	5	108241665	rs3718575	3.7	1.4E-02	cell_specific
10531952	Abcg3	5	104934161	rs33625455	3.7	1.4E-02	cell_specific
10563085	Fcgrt	7	52238853	rs32431972	3.7	1.4E-02	cell_specific
10416256	Bin3	14	70643331	rs6185468	3.7	1.4E-02	cell_specific
10554269	Abhd2	7	86363783	rs31691621	3.7	1.4E-02	cell_specific
10393728	Slc38a10	11	119986865	rs27013742	3.7	1.4E-02	cell_specific
10353167	Tram1	1	14206837	rs31958571	3.7	1.4E-02	cell_specific
10505008	Slc44a1	4	52502522	rs32306828	3.7	1.4E-02	cell_specific
10505028	Slc44a1	4	52502522	rs32306828	3.7	1.4E-02	cell_specific
10464153	Nhlrc2	19	56663472	rs45997356	3.7	1.4E-02	cell_specific
10396278	Daam1	12	72977231	rs29218894	3.7	1.4E-02	cell_specific
10378126	Ankfy1	11	72784506	rs26917883	3.7	1.4E-02	cell_specific
10382376	Ttyh2	11	114383904	rs27000532	3.7	1.4E-02	cell_specific
10556302	Ampd3	7	118046667	rs32256235	3.7	1.4E-02	cell_specific
10358389	Rgs2	1	145391712	rs32473980	3.7	1.4E-02	cell_specific

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10474006	Phf21a	2	92156887	rs27384975	3.7	1.4E-02	cell_specific
10528702	Prkag2	5	24469448	rs3705744	3.7	1.4E-02	cell_specific
10508936	Ubxn11	4	134026748	rs27547258	3.7	1.4E-02	cell_specific
10466925	Ak3	19	29225389	rs6366840	3.7	1.4E-02	cell_specific
10555681	Stim1	7	109583353	rs32441811	3.7	1.4E-02	cell_specific
10450212	Egfl8	17	34458128	mm37-17-34458128	3.5	1.8E-02	cell_specific
10375941	Vdac1	11	52259306	rs29402985	3.5	1.8E-02	cell_specific
10430770	Tob2	15	82396168	rs6362314	3.5	1.8E-02	cell_specific
10531529	Cnot6l	5	96265618	rs33565440	3.5	1.8E-02	cell_specific
10361620	Rmnd1	10	5898253	mm37-10-5898253	3.5	1.8E-02	cell_specific
10383235	A730011L01Rik	11	120030657	rs29474012	3.5	1.8E-02	cell_specific
10493711	Crtc2	3	89435945	rs31244910	3.5	1.8E-02	cell_specific
10513268	AI314180	4	58831823	rs6333919	3.5	1.8E-02	cell_specific
10487359	Itpripl1	2	127108723	rs33098756	3.5	1.8E-02	cell_specific
10560015	Rnf141	7	117852909	rs31752672	3.5	1.8E-02	cell_specific
10507908	Fhl3	4	124311705	rs32174150	3.5	1.8E-02	cell_specific
10509868	Atp13a2	4	140647159	rs27588207	3.5	1.8E-02	cell_specific
10477649	Acss2	2	156129718	rs27355705	3.5	1.8E-02	cell_specific
10481155	Rexo4	2	27703108	rs33304781	3.5	1.8E-02	cell_specific
10399061	Esyt2	12	117464677	rs6214666	3.5	1.8E-02	cell_specific
10457071	Cyb5	18	85447043	rs29679137	3.5	1.8E-02	cell_specific
10506870	Txndc12	4	107720590	rs33011000	3.5	1.8E-02	cell_specific
10367775	Stxbp5	10	9625228	rs29364104	3.5	1.8E-02	cell_specific
10478778	Arfgef2	2	166493958	rs27313367	3.4	2.2E-02	cell_specific
10420787	Mtmr9	14	64174110	rs30932330	3.4	2.2E-02	cell_specific
10344805	Cspp1	1	10247169	rs31048766	3.4	2.2E-02	cell_specific
10525893	Aacs	5	126184432	rs33584144	3.4	2.2E-02	cell_specific
10444439	Atf6b	17	33841940	mm37-17-33841940	3.4	2.2E-02	cell_specific
10389087	Rffl	11	82765715	rs29432702	3.4	2.2E-02	cell_specific
10385903	Pdlim4	11	53930025	rs29416948	3.4	2.2E-02	cell_specific
10572613	Mrpl34	8	73921071	rs32801300	3.4	2.2E-02	cell_specific
10550509	Pglyrp1	7	18888237	rs31948487	3.4	2.2E-02	cell_specific
10533285	Ptpn11	5	121690075	rs32188639	3.4	2.2E-02	cell_specific
10566580	Gm4759	7	114243647	rs31583245	3.4	2.2E-02	cell_specific
10555510	Pde2a	7	107768298	rs31749119	3.4	2.2E-02	cell_specific
10534990	Taf6	5	139065952	rs3687900	3.4	2.2E-02	cell_specific
10571274	Gsr	8	34902206	rs32869686	3.4	2.2E-02	cell_specific
10508992	Paqr7	4	134047858	rs27547127	3.4	2.2E-02	cell_specific
10374453	Glul	1	155614341	rs32575836	3.3	2.6E-02	cell_specific
10400718	Sos2	12	71269636	rs29131427	3.3	2.6E-02	cell_specific
10552210	Ankrd27	7	36114899	rs31949195	3.3	2.6E-02	cell_specific
10503845	Ube2j1	4	33149029	rs32496044	3.3	2.6E-02	cell_specific
10477739	Cep250	2	156229727	rs27336792	3.3	2.6E-02	cell_specific
10562368	4931406P16Rik	7	35399026	rs31939964	3.3	2.6E-02	cell_specific
10450675	H2-T24	17	36637612	mm37-17-36637612	3.3	2.6E-02	cell_specific
10372844	Rassf3	10	121077730	rs29327803	3.3	2.6E-02	cell_specific
10517373	Rcan3	4	134669683	rs28335132	3.3	2.6E-02	cell_specific
10423663	Vps13b	15	35755924	rs32146548	3.3	2.6E-02	cell_specific
10504865	Invs	4	48067605	rs6175060	3.3	2.6E-02	cell_specific
10454953	Tmco6	18	36663058	rs13483301	3.3	2.6E-02	cell_specific

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10444895	Flot1	17	36637612	mm37-17-36637612	3.2	2.9E-02	cell_specific
10412100	Map3k1	13	112607087	rs29808239	3.2	2.9E-02	cell_specific
10417749	Ube2e1	14	18208863	rs30662759	3.2	2.9E-02	cell_specific
10429564	Ly6a	15	74732872	rs32073945	3.2	2.9E-02	cell_specific
10535532	Tecpr1	5	144909341	rs32344365	3.2	2.9E-02	cell_specific
10597461	Cmtm7	9	114707961	rs33634484	3.2	2.9E-02	cell_specific
10546184	Plxna1	6	89271761	rs30475892	3.2	2.9E-02	cell_specific
10587854	Slc9a9	9	93753044	rs6339312	3.2	2.9E-02	cell_specific
10540059	Slc41a3	6	89655066	mm37-6-89655066	3.2	2.9E-02	cell_specific
10518570	Pgd	4	148522558	rs31807748	3.2	2.9E-02	cell_specific
10453678	Zeb1	18	5370959	rs29555170	3.2	2.9E-02	cell_specific
10421526	Rb1	14	73447674	rs30698679	3.1	3.2E-02	cell_specific
10579406	Arrdc2	8	72463828	rs32629017	3.1	3.2E-02	cell_specific
10412177	Skiv2l2	13	112869620	rs29241052	3.1	3.2E-02	cell_specific
10376755	Tnfrsf13b	11	59986632	rs29467518	3.1	3.2E-02	cell_specific
10421723	Dnajc15	14	78095590	rs30781266	3.1	3.2E-02	cell_specific
10348321	Dgkd	1	89797190	rs32265267	3.1	3.2E-02	cell_specific
10530215	1110003E01Rik	5	65381279	rs31444941	3.1	3.2E-02	cell_specific
10406530	Tmem167	13	89616620	rs29570900	3.1	3.2E-02	cell_specific
10494978	Ptpn22	3	103703663	rs30848500	3.1	3.2E-02	cell_specific
10566050	Il18bp	7	108176270	rs6344633	3.1	3.2E-02	cell_specific
10577230	Erich1	8	14430267	rs6280829	3.1	3.4E-02	cell_specific
10356475	Arl4c	1	90674018	rs31843138	3.1	3.4E-02	cell_specific
10350003	Cyb5r1	1	136255800	rs3658008	3.1	3.4E-02	cell_specific
10433735	Abcc1	16	13644224	rs4163486	3.1	3.4E-02	cell_specific
10344809	Cspp1	1	10247169	rs31048766	3.1	3.4E-02	cell_specific
10502469	Pdlim5	3	142648418	rs31101595	3.1	3.4E-02	cell_specific
10386723	Mapk7	11	62027215	rs29480195	3.1	3.4E-02	cell_specific
10450226	Ppt2	17	33841940	mm37-17-33841940	3.1	3.4E-02	cell_specific
10391207	Dhx58	11	100293380	rs29451902	3.1	3.4E-02	cell_specific
10476349	1110034G24Rik	2	133015586	rs28288156	3.1	3.4E-02	cell_specific
10353032	Rpa3	6	8456075	rs30173138	3.1	3.4E-02	cell_specific
10352459	Rab3gap2	1	186861978	rs6231754	3.1	3.4E-02	cell_specific
10569545	Nadsyn1	7	150565771	rs6307236	3.1	3.4E-02	cell_specific
10359034	Qsox1	1	158533664	rs6185284	3.1	3.4E-02	cell_specific
10546113	Sec61a1	6	89186890	rs30413806	3.0	3.7E-02	cell_specific
10562260	Gramd1a	7	31601749	rs31424765	3.0	3.7E-02	cell_specific
10566668	Socs6	18	88965286	rs30256508	3.0	3.7E-02	cell_specific
10493292	2810403A07Rik	3	88419784	rs31087596	3.0	3.7E-02	cell_specific
10553080	Car11	7	52898483	rs32222012	3.0	3.7E-02	cell_specific
10415778	Arl11	14	62106069	rs31516577	3.0	3.7E-02	cell_specific
10376568	Rai1	11	60811053	rs29390814	3.0	3.7E-02	cell_specific
10485405	Cd44	2	103260253	rs3726330	3.0	3.7E-02	cell_specific
10523647	Aff1	5	103823179	rs29674095	3.0	4.0E-02	cell_specific
10514133	Ttc39b	4	83360150	rs28103847	3.0	4.0E-02	cell_specific
10592535	Sorl1	9	41300061	rs29976434	3.0	4.0E-02	cell_specific
10488237	Snx5	2	143830449	rs33148264	3.0	4.0E-02	cell_specific
10475941	Zc3h6	2	127962561	rs27432128	3.0	4.0E-02	cell_specific
10405545	Pcbd2	13	56035920	rs30100717	3.0	4.0E-02	cell_specific
10469559	Msrb2	2	19175977	rs27153219	3.0	4.0E-02	cell_specific
10512655	Rnf38	4	43994971	rs27826309	2.9	4.3E-02	cell_specific
10407570	Zmynd11	13	9951889	rs6333172	2.9	4.3E-02	cell_specific

Probe ID	Gene Symbol	SNP Chrom (mm37)	SNP Position (mm37)	Best cis-eQTL SNP	Gene-level P-value (permutation analysis)	Q-value	Type
10574204	Arl2bp	8	97095919	rs32098937	2.9	4.3E-02	cell_specific
10391378	Ezh1	11	101570128	rs29467997	2.9	4.3E-02	cell_specific
10539135	Capg	6	71730411	rs30376556	2.9	4.3E-02	cell_specific
10436694	Rplp0	5	115834070	rs29733302	2.9	4.3E-02	cell_specific
10535477	Usp42	5	143694157	rs33060114	2.9	4.5E-02	cell_specific
10509168	E2f2	4	136101179	rs32603084	2.9	4.5E-02	cell_specific
10445442	Gtpbp2	17	46725237	rs33648198	2.9	4.5E-02	cell_specific
10368227	Ube2q2	9	54936087	rs6334610	2.9	4.5E-02	cell_specific
10535759	Lnx2	5	147886810	rs32380998	2.9	4.5E-02	cell_specific
10497920	Ankrd50	3	38688632	rs31426507	2.9	4.5E-02	cell_specific
10477897	Dlgap4	2	156470023	rs27339352	2.9	4.8E-02	cell_specific
10390271	Nfe2l1	11	96484370	rs27056717	2.9	4.8E-02	cell_specific
10585494	Ube2q2	9	54936087	rs6334610	2.9	4.8E-02	cell_specific
10585860	Adpgk	9	59930483	rs6395987	2.9	4.8E-02	cell_specific
10407222	Dhx29	13	112869620	rs29241052	2.9	4.8E-02	cell_specific
10486119	Plcb2	2	118657942	rs27440200	2.9	4.8E-02	cell_specific
10439005	Ppp1r2	16	32038501	rs4169852	2.9	4.8E-02	cell_specific

Table S2. The predicted regulatory links inferred by using expression data from T4 and GN cells (see Methods, joint T4_ GN network).

TF	Enriched for Ontogenet targets	Targets
Aebp2	NaN	Abl2,Cog5,Glis3,Mpp6,Vps13a,Xrn2,
Arid3b	NaN	Aoc2,Ccdc84,Dqx1,Iffo1,Il18bp,Klf11,Pcnxl3,Per2,Plekhg2,Ppm1b,Spg11,Tcirg1,Ttll3,
Arid4b	NaN	A830080D01Rik,Akap9,Ankrd12,Atp11b,Atp2b1,Atrx,Bod1l,C430048L16Rik,Capn7,Ccdc124,Ccpg1,Cdadc1,Chm,Cspp1,Enox2,Fam134b,Fbxl5,Ggps1,H2afx,Hn1,Il1rap,Ilf2,Kras,L3mbtl3,Lcorl,Mier3,Morf4l1,Mysm1,Ngly1,Pdha1,Phf14,Pppde1,Prei4,Pspc1,Rfx2,Rnf115,Rpl37a,Rps19,Rsrc2,Samd8,Ssbp4,St8sia4,Stard10,Taok1,Tgfbr1,Tmem63a,Top2b,Usp15,Usp53,Wdr20a,Zdhhc20,Zfp518,
Arid5b	NaN	5830417I10Rik,Acadm,B4galt5,Cdk5rap2,Dap,Dhrs7,Dock9,Dok2,Gm13819,Ldlrap1,St3gal1,Tmem8,Wdr46,
Asf1b	fine_module_55	0610010K14Rik,2310022A10Rik,2310061C15Rik,Aaas,Alg3,Atl2,Bub3,C230052I12Rik,Cbx3,Cbx5,Ccdc101,Ccnb2,Cdc20,Cks1b,Cks2,Csrp1,D2Ertd750e,Dbf4,Ddx11,Fancg,H2afx,Hdgf,Hint1,Hist1h2af,Hist1h2ak,Hist1h2ao,Hist1h2bb,Hist1h2bc,Hist1h4d,Hist2h4,Kpna2,LOC675534,Mcm2,Mcm5,Mcm7,Mrpl51,Mthfd2,Napa,Ncapd2,Nde1,Nudc,Nup35,Pcna,Polh,Pols,Pomt1,Ppia,Pppde2,Prim2,Psmc3,RP23-38E20.1,Rab18,Rangap1,Rfc4,Rpa3,Rrm1,Sec23b,Setdb1,Slc3a2,Slfn3,Smc2,St3gal4,Stip1,Stmn1,Taf6,Tagln2,Tcf19,Tuba1b,Tuba1c,Tubg1,Ubash3a,Usp39,Vars,Wdr61,l7Rn6,
Ash1l	NaN	1700081L11Rik,1700094D03Rik,Apc,Atp5e,Atp5o,B430203M17Rik,C030046E11Rik,C430014K11Rik,Cd200r1,Cox7a2l,D10Ertd641e,D930015E06Rik,Dera,Dmxl1,Dpp3,Etfb,Fryl,G6pc3,Gm7075,Insr,Itga4,Kidins220,LOC100044428,Luc7l2,Mga,Mycbp2,N4bp2l2,Nbeal1,Nipbl,Pgp,Phip,Pptc7,Prr8,Rev3l,Rpl19,Rufy2,Slc7a5,Snora62,Sra1,Ssfa2,Tnks,Tnrc6a,Trappc2l,Utrn,Whsc1l1,Zmynd11,
Ash2l	NaN	Anapc4,Cdca7l,Cdk4,D10Wsu52e,D2Ertd750e,Eif3b,Gart,Ggps1,Gpd1l,Ilf2,Itgb1,Itpripl1,Lair1,M6pr,Ncrna00117,Pdlim7,Plscr3,Pygb,Rasgrp4,Rbm3,Rpia,Rrm1,Rrp1,Snapin,Sod2,Sqle,Sumo3,Tm7sf3,Ube1l,Ufm1,
Atad2	NaN	2410129H14Rik,2610039C10Rik,B4galnt1,Bicd2,Cep57,Cradd,Dera,Dynll2,Dzip3,Elovl5,Fam3c,Fbxo22,G2e3,G3bp1,Gm6041,Hsp90b1,Ikbke,Immt,Lcmt1,Letm2,Ltv1,Map3k4,Mcph1,Mrpl15,Mrpl18,Myb,Nup155,Parp2,Pdp1,Pds5b,Rab28,Rexo4,Sgpp1,Smc2,Smc4,Srrt,Stt3b,Topbp1,Trim37,Vaultrc5,Zfp568,
Atf2	NaN	4930519P11Rik,A530054K11Rik,Cnot4,Dclre1c,Dennd4a,ENSMUSG00000074747,Eif4ebp3,Fbxo46,Gm10158,Gnrh1,Impact,Irgc1,Klf7,Klhl7,Lpp,Lrrc57,Lrrfip2,Mef2a,Mgat4a,N4bp2,Pdlim5,Pign,Qk,Rfx3,Rnasel,Rnf13,Rnpc3,Rpl5,Sdccag8,Slc38a9,Snord33,Snord35a,Ulk2,Uxt,Vps37a,Vrk2,Ywhag,Zcchc7,Zfp68,Zfp715,Zhx1,Zranb1,
Atf6	NaN	Bmp2k,Polr1a,
Atf6b	NaN	0610031J06Rik,0910001L09Rik,2410002I01Rik,4930471M23Rik,4930519P11Rik,5430437P03Rik,Abi3,Agpat1,Ap2s1,Aph1a,Atox1,Bri3bp,Chpf2,Ctdsp2,Dpm2,Dullard,Dyrk1b,Emp3,Fbxl6,Fis1,Fkbpl,Gngt2,Gpaa1,Gramd1a,Isyna1,Llgl1,Lrp10,Man2b2,Mov10,Mrpl4,Ndufa2,Nkiras2,Pcnxl3,Pigq,Ppt2,Rnf187,Shkbp1,Sirt2,Slc25a1,Slc35c2,Slc35e1,Slc39a3,Slc48a1,Tcfe2a,Tmem120a,Trpv2,Wbp1,Zfp358,
Atf7	NaN	2610110G12Rik,Aagab,Adamts10,Arhgef1,Arid3b,Atp13a1,BC031181,BC037034,BC037112,BC056474,C030016D13Rik,Chkb,Cic,Clcn6,Dcaf15,Depdc5,Dstyk,Fbl,Flt3l,Gabbr1,Lass2,Leng8,Mapk8ip3,Mbd6,Mll1,Ncln,Nf2,Nfrkb,Nisch,Nktr,Npm3,Papd5,Pex1,Pias3,Pigv,Polg2,Pou2f1,Runx1,Slc17a9,Slc35b3,Slc36a1,Srcap,Tecr,Tmem86b,Tpcn2,Whamm,Zfat,Zfp512,Zxdb,

TF	Enriched for Ontogenet targets	Targets
Atf7ip	NaN	Cwc22,Daglb,EG665955,Hps5,Ifit2,LOC100043377,Malt1,Mpzl3,Oas3,Pde2a,Plod1,Rps6ka5,
Bag1	NaN	0610009B22Rik,1110012L19Rik,1110057K04Rik,2010109K11Rik,2700060E02Rik,2810416G20Rik,2900064A13Rik,9630058J23Rik,Acot13,Adh5,Agpat5,Ahcyl2,Ankrd13a,Atp6v1g1,BC031781,Becn1,Cdgap,Col20a1,Cops4,Cops5,Ctr9,D10Ertd641e,D230037D09Rik,Dip2c,Dnajc15,Erp29,Fam175b,Fuca1,Gabpa,Gins4,Glipr2,Glud1,Gm13498,Gmcl1,Gtf2b,Hsd17b11,Iars2,Ifnar2,Ip6k2,Kctd10,Kctd2,Klhdc2,LOC677548,Lactb,Lcmt1,Llph,Lrrfip2,Map3k2,Mettl3,Mrpl18,Mrpl48,Mrps33,Mxd4,Ndufb6,Nipsnap3a,Nod1,Ostm1,Pdcd6,Pdcl3,Pdk3,Peci,Pfkfb3,Pgap2,Phb2,Pip4k2c,Plekhb2,Plk3,Ppp1r9b,Ppp3cc,Prkar1a,Psmc2,Psmd10,Psmd6,Ptpn9,Ptpra,Rap2c,Rassf3,Rdh11,Rrp1,Rtcd1,Sap30l,Sars,Sbds,Sdf4,Sec11c,Sec23b,Senp2,Senp3,Sft2d2,Shfm1,Slfn2,Slu7,Smarcd1,Srp9,Ssr1,Ssu72,Sugt1,Taf12,Tap2,Tax1bp3,Tbca,Tfdp1,Thra,Tmem19,Tmem41b,Tmem87b,Tsen34,Tspan5,Ufc1,Unc45a,Unc50,Utp23,Vcp,Vdac2,Vps29,Wdyhv1,Zbed4,
Bbx	NaN	4732471D19Rik,5330426P16Rik,9230105E10Rik,Abhd10,Akr7a5,Anxa7,Cdc42ep4,Commd8,Fchsd2,H2-D1,Hmgb1,LOC100043371,Mapkapk2,Parp3,Ptpn22,Snapc2,Tcfe2a,Wdtc1,Wrn,
Bcl3	NaN	8430419L09Rik,Adamtsl4,Ckb,Gm5617,H2-T24,Icam1,Jak3,Nat6,Nod1,Slc25a39,Socs3,
Bcl6	NaN	1110038D17Rik,Abhd1,Abtb2,Asb7,Atxn7l2,Ccdc50,Crip1,Dtx2,Extl3,Fam168a,Foxo3,Galm,Glipr1,Gm3771,Hsdl2,LOC100044416,Ppp2r5b,Rab19,Slc25a45,St13,St7l,Tubb5,Txndc9,Ulk2,Wdr81,Ypel5,Zdhhc7,
Bclaf1	NaN	1300010F03Rik,1810007M14Rik,4930522L14Rik,4930534B04Rik,A930005H10Rik,Bbx,Cep110,Chd9,Cpsf6,Ddhd2,Dicer1,Dlg1,Dopey1,Eml4,Fam178a,Fam36a,Gtpbp8,Ivns1abp,Lrba,Lrp6,Lysmd1,Ncapd3,Nnt,Pcm1,Prpf4b,Ranbp2,Rock2,Strbp,Tesc,Tmem184c,Trim24,Trpm7,Uba6,Uevld,Vps13a,Wwp1,Zfp280c,Zfp329,Zfp362,Zfp62,Zfp644,Zfp800,
Brd8	NaN	Bcr,Ddb2,Gm5299,Gm6560,Hus1,Laptm4b,Parp11,Trim41,Trim68,
Carm1	NaN	Armc7,Atxn7l2,C230052I12Rik,Disp1,Gpr65,H2-Ke6,Itm2c,Man2b2,Ndst2,Tmem141,Tnfrsf4,Ttc14,Zfp523,Zfp609,
Cbx3	NaN	2610030H06Rik,2700029M09Rik,4831426I19Rik,Acin1,Ap3s1,Arl6ip1,Ash2l,Atad2,Atp5c1,Atp6ap2,Brcc3,Cacybp,Ccdc72,Ccdc90a,Ccng1,Ccnh,Cct6a,Cct7,Commd6,Cops4,Cyb5,D5Wsu178e,Dcun1d2,Dek,Dgkz,Dnajb11,Eif2s1,Eif3e,Eri1,Ero1l,Exosc8,Fdft1,Fdps,Fut8,Gng10,H2afy,Hmgcr,Hnrnpab,Hprt1,Hps1,Hsdl2,Hspa5,Hspd1,Ilf2,Impa1,Iqsec1,Klf3,Larp7,Lta4h,Map4k3,Mat2a,Mdh1,Med31,Mgat2,Mis12,Mlxip,Mrpl32,Nat13,Ndufb6,Ndufc2,Nhp2l1,Nup107,Ola1,Olfr1419,Osbpl8,Pcyox1,Pdia6,Pold3,Ppp2r1b,Prdx1,Psma6,Psmd2,Ptges3,Ran,Rnf13,Sar1b,Sarnp,Sart1,Sfrs9,Slbp,Smc6,Snrpb2,Snx5,Socs4,Spcs2,Spcs3,St13,Strap,Syncrip,Tceb1,Thoc4,Trappc2,Txndc9,Uba2,Ube2w,Vdac3,Zdhhc17,Zfp35,Zfp644,Zfp664,Zmpste24,rp9,
Cbx4	NaN	2210016F16Rik,Adar,Adk,Alkbh5,Apobec1,Arid5b,Atp11c,Bat4,Brf1,Bub3,Def6,Dgkd,Dip2b,Flcn,Hnrnpab,Pbx2,Pcolce,Plekhg2,Ppp2r1b,Ptp4a2,Rab22a,Sec23ip,Stk11,Trim14,Vps37b,Zyg11b,
Cbx5	fine_module_63	2810417H13Rik,2900064A13Rik,3200002M19Rik,4930534B04Rik,Adam19,Ap4m1,Asf1b,Bcl2l13,Btbd12,Cdr2,Eif3c,Enpp4,Ezh2,Fam123a,Fam33a,Gins4,Hn1l,Mad2l1,Mast2,Mbnl3,Mipep,Mpp6,Nat5,Ncapd3,Nup50,Plk4,Pole4,Ppme1,Ppp2r5d,Rbbp8,Rnaseh2b,Srgap2,Tardbp,Tdp1,Tm9sf1,Tubb5,Vprbp,Wdr51b,Zbtb1,Zbtb43,
Cbx7	NaN	2810408P10Rik,Apobec3,
Chd3	NaN	Dad1,Dtd1,Phxr1,Pnet-ps,Slc25a36,Slc48a1,

TF	Enriched for Ontogenet targets	Targets
Chd7	NaN	Atg16l1,Bmp2k,Brp44l,Centb1,Cetn2,Eif3c,Fbxl20,Gbas,Kdm6b,LOC675534,Myo9b,Obfc1,Rpl26,Serac1,Sfmbt2,Slc4a1,Snx19,Stard5,Tmem85,Trpm7,Usp3,Xbp1,
Chd9	NaN	Appl2,
Churc1	NaN	Abcc5,Akr1a4,Drap1,Fbxo8,Fdps,Gm5617,Gtf2ird1,Krcc1,Nsdhl,Pcgf1,Trim23,
Clock	NaN	Acaa1a,Akap11,Gnptab,Prkd3,Rnf121,Thap3,Ublcp1,
Crebl2	NaN	Arrb1,Cul1,Golm1,Kbtbd2,Klf3,Lrrc8d,Map4k5,Mblac2,Oxr1,Snapin,Snrpb,Thoc6,Tubb2c,Usp28,Zbtb43,Zrsr1,
Creg1	NaN	2310047M10Rik,2510006D16Rik,4930471M23Rik,4930518I15Rik,Athl1,Atpgd1,Camk2b,Cars2,Dap3,Dcps,E230001N04Rik,Elovl7,Fryl,Gclm,Glipr1,Gna12,Gng5,Iscu,Kif1c,Med11,Mobkl1a,Pde1b,Pygo2,Rffl,Rnasek,Scnm1,Snap23,Tbc1d22b,Tecr,Tm2d2,Tmem154,Tsga10ip,Ttc7b,Txn2,Usp21,Vamp8,Zfp36l2,Zfp691,Zfp746,Znrf1,
Csda	NaN	Cks1b,Ddhd2,Kdsr,Klhdc5,Phka2,Rangap1,Wdr41,
Ddx3x	NaN	1110037F02Rik,1500012F01Rik,2810008M24Rik,Acadm,Adam10,Adrb2,Atf7ip,B230380D07Rik,Becn1,Birc2,Casd1,Ccnc,Ccng2,Cdc42ep3,Cdkn1b,Cept1,Cflar,Chmp5,Dnajb9,Efha1,Eif1a,Eif4e3,Exoc3,Fbxo33,Fkbpl,Frg1,Gm885,Hiatl1,Hist1h2bh,Hmgcs1,Hnrnph2,Hpvc-ps,Hspa13,Htt,Idh1,Idi1,Ifrd1,Inpp1,Kif3b,Klhl2,Lars,Lin7c,Lyrm5,Mast2,Mettl9,Nek7,Nudt4,Obfc2a,Pdcd10,Pdcl,Pgrmc1,Pnpla8,Prpf18,Psmb2,Pts,Purb,Rab27a,Rala,Rap2c,Rbm12b,Reep3,Rtn4,Safb2,Samsn1,Sc4mol,Scp2,Sdha,Sec23ip,Serf2,Serp1,Slu7,Snapc5,Snx4,Snx6,Sri,Tceb1,Tcp11l2,Tmem106b,Tpm4,Trappc6b,Trmt12,Twistnb,Uba3,Vamp4,Vamp7,Vbp1,Wsb1,Zmat2,
Dmtf1	NaN	1110020G09Rik,1200016B10Rik,2010106G01Rik,2310035C23Rik,2410025L10Rik,3110052M02Rik,Acot9,Alad,Ap4s1,Atp5g2,Atp7a,Atp8a1,Baz2b,Ccdc111,Ccnl1,Cep170,Clk4,Cln6,Cpeb2,Cpeb4,Dcaf6,Ddx26b,Dgkh,Dhx57,Dtx4,E130120F12Rik,Eif3k,Eif6,Exoc5,Fam13b,Fam188a,Fam48a,Fam82b,Far1,Fzr1,Garnl1,Gm12258,Gm4832,Gm5044,Gm5050,Gm5070,Gm5766,Gpatch8,Gpr65,Gprasp1,Hist1h1e,Hist1h2bc,Hist1h4c,Homer1,Jhdm1d,Jmjd8,Kdm4c,Krit1,Lemd3,Mobkl1a,Mudeng,Myo5a,Nufip2,Osbpl8,Pibf1,Ppdpf,Prpf39,Ptbp2,RP23-38E20.1,Rabgap1l,Rasa1,Rb1,Rc3h1,Rcan3,Rmrp,Rnf146,Rny3,Rp2h,Rpl24,Rpl7a,Rplp1,Rps23,Rps24,Rps27,Rps28,Sass6,Setd2,Sfrs18,Sike1,Slc35b3,Snora34,Snora52,Snora61,Snord118,Snord49a,Snx14,Socs4,Spata1,Stx17,Tatdn1,Tbce,Terc,Tmem160,Tmem62,Tmem87a,Trip11,Trip4,Trnt1,Vat1,Wdr26,Wdr44,Zbtb6,Zfc3h1,Zfml,Zfp51,Zfp595,Zmym5,Zufsp,
Dnmt3a	NaN	Apbb3,Bat2l,Eno3,Hif1an,Isca1,Kdm5b,Magi3,Maml2,Mgat5,Mta1,Pcnx,Pja1,Ptar1,Rad18,Ramp1,Rap1gds1,Rexo4,Rhoh,Rnf213,Slc37a1,Spata2,Trp53i13,
Dtx3l	fine_module_272	1200016B10Rik,2310061J03Rik,6330442E10Rik,Abcb7,Apobec3,Ate1,BC057170,Dcaf13,Ddx60,Foxo3,Frg1,Gbp2,Gm7774,Hdac1,Herc5,Ifih1,Il15ra,Irgm1,Isg20,Lsm6,Mrpl36,Nmi,OTTMUSG00000009332,Parp14,Pdcd10,Phkg2,Rab19,Slc30a6,Slfn5,Sptlc2,Tapbp,Trim21,Trim30,Txndc17,Vamp7,
E2f2	NaN	Dusp6,Zfp277,
Eed	NaN	4933424B01Rik,Actr6,Arhgap10,Btbd10,C330018D20Rik,Ccdc117,Ccdc45,D4Wsu53e,Dnaja1,Dnajc8,Fam102b,Gimap9,Hsd17b4,Ier5,Immp1l,Pcolce,Ptar1,Ubxn2a,Vbp1,Zfp595,Zfp706,
Etv6	NaN	Abr,Ampd2,Birc2,Bysl,Cd68,Xaf1,
Ezh1	NaN	Abca3,Ccdc45,Gadd45b,Jun,Klf3,Polg2,S100a13,Slc25a46,Snord35a,Tbc1d14,Ttbk2,Uqcr,

TF	Enriched for Ontogenet targets	Targets
Ezh2	NaN	1810074P20Rik,4933439F18Rik,Actn4,Agxt2l2,Atpif1,BC002199,BC052040,Cct5,Clic4,Cln6,Cops6,Ctdspl2,Depdc5,Dnm1l,Dpagt1,Fusip1,Ggta1,Gtf2i,H2afv,Lnx2,Lsm8,Mobkl2b,Ppm1g,Prkci,Rad18,Rala,Sfxn1,Slc43a3,Smarca5,Tmem188,Tor3a,Wdr26,Zc3h12d,Zfp367,
Fam48a	NaN	2810428I15Rik,5830472F04Rik,Akr1b3,Ankrd44,Anks3,Birc6,Clock,Cluap1,Cog5,Cstb,Dynll2,E130309D02Rik,Eif3i,Exoc6b,Fau,Fbxo6,Fnbp4,Gdi1,Gfm2,Gm10099,Gm11814,Gm12760,Gm3771,Gm5129,Gm5502,Gm7123,Gm8995,Grcc10,Hist3h2bb,Igfbp4,LOC100134980,Lgals3bp,Lsm6,Lsmd1,Map4k3,Mcts1,Mgea5,Mif,Mpst,Mrps11,Myeov2,Ndufa13,Ndufb9,Ndufc2,Ndufs8,Ninj1,Nktr,Oas1b,Ogt,Parp8,Pde1b,Polr2f,Ppm1d,Prdm9,Psmb5,Pygo2,Rbks,Rela,Rpl11,Rps12,Rps13,Rps29,Scarna17,Sec61g,Senp2,Slc25a27,Slc25a36,Slc35b2,Snapc3,Snord34,Snord35b,Snord82,Snrpd2,Snx29,Socs1,Tep1,Tmc4,Tmem194b,Tmem87b,Tomm7,Trim34,Tsga10ip,Tuba1a,Usp45,Vaultrc5,Wipi2,Yif1b,
Foxj2	NaN	3110003A17Rik,4930562F07Rik,4933437N03Rik,Ate1,Bat2,Bcl6,Brp44l,Chst12,Ctso,Dcaf13,Dusp7,Etv6,Fam33a,Fbrs,Gltscr1,Gm10091,Gnas,Hspa8,Macf1,Myo9b,Ndufb4,Rara,Rbms1,Rela,Rps7,Tbx6,
Foxn3	NaN	Coro1c,Leprot,Ndfip2,
Foxo3	NaN	0610037P05Rik,2010109K11Rik,9030624G23Rik,Abhd13,Acadsb,Acsl4,Ap3m2,Apobec1,Arf3,Arhgap15,Atp6v1c1,Bag1,Bcl6,Brd3,C030016D13Rik,C330007P06Rik,Ccnj,Cyb5d2,D730003I15Rik,Ddi2,Dennd2d,Dnmbp,Dtx3l,Fam103a1,Fbxl20,Gm5774,Hba-a1,Hba-a2,Hbb-b1,Hmbox1,Kif1b,Lass2,Lrrc57,Mrpl33,Nae1,Pacsin2,Pgm1,Pot1b,Pqlc3,Prr13,Pttg1ip,Rapgef2,Slc29a3,Sqrdl,Ssh2,Tuba1b,Tuba1c,Ufm1,Yipf5,Zfat,Zfp87,Zswim6,
Foxp4	NaN	Alg3,Bcorl1,Cat,Ccdc101,Cherp,Cog1,Crtc3,Ctsa,D330012F22Rik,Dapp1,Dnajb5,Dullard,Dvl3,Dynlrb1,Gaa,Hdac7,Khsrp,Lsmd1,Map4k1,Ncor2,Nfatc2,Pmf1,Prr12,Psmf1,Reep4,Rpl35a,Runx3,Slc35a4,Slfn2,Smg5,Taf6,Tmem63b,Tram2,Tyk2,Vps37c,Zfp335,Zfp362,Zmiz1,
Fubp1	fine_module_13	6720456H20Rik,A830080D01Rik,Aebp2,Akap9,Akt3,Ankib1,Ash1l,Atp13a3,Atp2a2,Bclaf1,Bloc1s1,Camk2b,Cib1,Erc1,Ergic3,Exoc4,Guk1,Hcst,Huwe1,Mad1l1,Mapre2,Ndufa8,Ocrl,Orai3,Pds5b,Phf20,Pold4,Ptar1,Rb1,Rps14,Slc20a1,Suhw4,Tmem68,Tnip1,Uqcrh,Use1,Yipf1,
Fus	NaN	Aak1,Anxa5,Banp,Cd46,Cirbp,D730040F13Rik,Fusip1,Gm16489,Hnrnpa1,Ift20,Mib2,Mrpl20,Sec63,Spryd3,Tdp1,Zc3h6,
Hdac1	NaN	1500041N16Rik,2510006D16Rik,Ak3,Ankrd50,C030046E11Rik,Dcp2,Dek,Gm4864,Gpr97,Hist1h4b,Hist1h4d,Hist1h4m,Ldlrap1,Pion,Rbm7,Tmem39b,Zfp828,
Hdac4	NaN	Cpeb2,Rnf160,Safb2,Slc25a30,Tbcel,Zbtb43,Zswim6,
Hdac5	NaN	2310011J03Rik,2310028H24Rik,Aldh4a1,Dctn2,Dennd3,Dnm1l,Fbxo46,Fuca1,Gadd45b,Gdi1,Inpp1,Lrrc68,Lsm10,Mboat7,Med22,Mical1,Mknk2,Naif1,Nfkbie,Ninj1,Pfas,Pitpnm1,Prex1,Ptp4a2,Pygo2,Rxra,Sema4b,Slc35a3,Smpd2,Tbc1d17,Tmem104,Tnfrsf1b,Tspo,Ttc7,Ulk1,Zfp426,
Hdac6	NaN	Adh5,Fam20b,Psmc2,Sfi1,
Hdac7	NaN	9930012K11Rik,A530032D15Rik,Adcy7,Arid4b,Bat2l,Cpped1,Fam38a,Gm10136,Gm10345,Gm15772,Gtf2i,Hmbox1,Lta4h,Micall1,Mll2,Mrpl54,Pkd1,Rltpr,Rnf13,Srcap,Tbc1d22b,Tet3,

TF	Enriched for Ontogenet targets	Targets
Hes6	NaN	1500032L24Rik,2010011I20Rik,2900010M23Rik,Abhd11,Abl1,Agpat1,Bscl2,Chmp1a,Ciapin1,Coro1c,Ctsb,Cyb5,D14Ertd449e,D17H6S53E,Dlg1,Dpp7,E230001N04Rik,Eif1b,Eml3,Entpd5,Entpd7,Exosc1,Fam108c,Fam132a,Gipc1,Gna12,Gpc1,Gstp1,Hmgxb3,Hspa13,Ilkap,Klhdc3,Manbal,Mrpl20,Mrpl34,Ndufa13,Nxn,Pgd,Pigx,Psme2,Rab19,Rfxank,Sf3b5,Slc26a2,St3gal2,Syngr2,Tagln2,Tmem160,Tmsb10,Tnf,Tubg1,Ube4b,Uqcr,Zfp386,
Hif1a	NaN	4933411K20Rik,Arf2,Cd200r1,Ctsc,Gclm,Kbtbd7,Larp4,Lipa,Lrrc58,Nampt,Snap29,Snapc1,Tmem106c,Tmem184c,Trrap,Ttll1,Zfp456,
Hivep1	NaN	2010016I18Rik,2410042D21Rik,9430008C03Rik,A430107D22Rik,Ccnyl1,Cpeb4,D15Wsu169e,Frrs1,Gprasp1,Hipk2,Lman2l,Mgat5,Olfml3,Pbx4,Pcnx,Phkb,Plcb2,Pnpla6,Pomt1,Ppm1h,Rtn4,Sipa1l1,Slfn1,Spred2,Stag1,Tet3,Ube4b,
Hltf	NaN	0610010K06Rik,9030607L17Rik,C1galt1,Ccnh,Cryzl1,Cwc22,Ercc6,Gm7079,Gna13,Gnptg,Hps3,Lgals8,Mcrs1,Nt5c2,Ntng2,Ptp4a3,Rg9mtd3,Sidt2,Smap1,Terf2ip,Tmod3,Zfp157,Zfp182,Zfp451,
Hmgb1	NaN	4930412M03Rik,Agpat5,Bbx,Btg2,Ccnl1,Gm2509,Gm8594,Gpr132,LOC677565,Ldlrap1,Mkl2,Naglu,Pot1b,Supt3h,Txndc12,
Id2	NaN	Ergic1,Gpr132,Lgals8,Ndfip2,Pole4,Prkx,Reep5,Rnf144a,Rnft1,Setd3,Tnfrsf13b,Zhx3,
Ikzf5	NaN	Aim1,BC032203,Cry1,Eftud1,Epm2aip1,Ifrg15,Mical3,Slc35d2,Tmem126b,Tns1,Usp38,Zbtb44,
Irf3	NaN	1810055G02Rik,Alkbh4,Alkbh6,Ap2m1,Arsa,Atp13a1,Atp6v1f,Bcat2,Cox5b,Crot,Dad1,Dcun1d2,Fcgrt,Fzr1,Gm11741,Gm6394,Gys1,Htatip2,Jhdm1d,Josd2,Lsm4,Mcart1,Nudt22,Nup62,Pold4,Psen2,Psmb5,Pygb,Rnasek,Rpia,Rpl13a,Slc36a1,Snord33,Snx15,St7l,Stk40,Tbc1d13,Tmem223,Tomm34,Tsta3,Uhrf2,Usp21,Wbscr22,Zfp715,
Irf7	NaN	1110032A03Rik,1810058I24Rik,2310047M10Rik,Alg12,Ccdc97,Crlf3,Dcaf11,Dhx58,Fbrs,Galnt10,Gm14251,Ifi27l2a,Impad1,Irf9,Oas3,Psmb8,Smpd1,Spsb3,Stat2,Tob1,Trappc2l,
Irf9	fine_module_269	1810006K21Rik,5830415L20Rik,Adar,Atp13a1,BC006779,Cenpq,Cln3,Cmpk2,Dhrs1,Dtx3l,Epsti1,Etohi1,H2-Q8,H2-T22,H2-T23,H2-T24,Hsh2d,Ifi35,Ifit1,Ifit3,Iqsec1,Irak4,Irf7,Irgm2,Lgals3bp,Lpcat4,Oas1b,Oas1g,Oas2,Oasl1,Parp12,Parp9,Pml,Pyroxd1,Rnasel,Rnf213,Rtp4,Stat1,Tap1,Trex1,Trim14,Trim25,Trim34,Ube1l,Usp18,Xaf1,Zbp1,Zbtb26,
Jun	NaN	Junb,Kcnn4,
Junb	NaN	Cenpv,Crot,Dusp1,Dusp5,Ezh1,Hexim1,Hist1h1c,Hist1h4m,Josd2,Jund,Mfsd8,Taok1,
Jund	fine_module_174	5031439G07Rik,Abcg1,Acot7,BC029214,Btg2,Dbp,Gm2a,Hnrnpa0,Hsh2d,Ier2,Ier5,Irs2,Itgb7,Jkamp,Junb,Ndufs6,Ocel1,Pag1,Sidt2,Whamm,Zdhhc3,
Kdm5b	NaN	Acadsb,Atp1a3,Chmp7,Cog2,Commd8,Dok2,Dynlt1,Idh3g,Impa1,Lpin2,Pdia4,Ppapdc1b,Rnf11,Ublcp1,Zfc3h1,
Kdm5d	fine_module_331	1700016K19Rik,Adcy7,Cdc2l6,Ddx3y,Eif2s3y,Idua,Rbm41,Stard4,Uty,Xrn2,Yipf5,
Kdm6b	NaN	1500010J02Rik,2700060E02Rik,C1galt1,Centb1,Chordc1,Cyb5d2,Dip2c,EG667078,Fam36a,Fcgrt,Gm10136,Gm15772,Gm9197,Kif1c,Lmbrd2,Napa,Ostc,Pcna,Phf21a,Pias3,Rara,Senp3,Sfn,Sh3bgrl,Trim8,Trp53i11,Ttc35,Ttc7b,Xaf1,Zdhhc18,Zfp335,Zfp398,Zfp746,
Klf10	NaN	Ak3,Arrdc4,Cpt1a,Dera,Fbxo22,Lpcat4,Slc35c1,Slc48a1,Snrpe,Sytl1,
Klf13	NaN	Bcl9,Ccnt1,D10Wsu52e,Eif3h,Gm4832,Gmfg,Iah1,Jund,Klhl18,Phip,Rprl1,Rprl2,St3gal1,Vaultrc5,Ywhah,
Klf3	NaN	Arrdc3,Ezh1,F630110N24Rik,Fam117b,Insr,Mylip,Rps6ka2,Sec23a,

TF	Enriched for Ontogenet targets	Targets
Klf7	NaN	Ap4e1,Gm4864,Hivep1,Rbm26,Samhd1,Thoc2,Ypel5,
Lcor	NaN	2700049A03Rik,4933426I21Rik,AI606181,Amn1,Ankrd13a,Bbs9,Cndp2,Crkrs,D16Ertd472e,D730040F13Rik,Ddit4,Dusp11,Dzip3,Fam160b1,Galnt2,Gm11285,Gm114,Gm5785,Gng12,Gpd2,Hbs1l,Impad1,Kctd10,LOC546695,Manba,Mdm4,Mmgt1,Narg1l,Nme3,Pigb,Rnf14,Samm50,Suhw4,Tmem65,Tshz3,Uhrf2,Zmynd8,
Lmo2	NaN	Rps9,Tmem184c,
Lpp	NaN	3110057O12Rik,4833420G17Rik,4933407H18Rik,Atxn1,Atxn7l1,Bloc1s2,Ccdc28a,Ctso,Gab3,Gdap10,Itpa,Mbd5,Mpp5,Prkar1a,Prune,Tatdn3,Tlr6,Tmem156,Tmem161b,Xrcc4,
Lrrfip1	NaN	2410089E03Rik,4930523C07Rik,G2e3,Grap,Hgsnat,ND6,
Mef2a	NaN	Adam9,Arhgap9,Arl6ip1,C230081A13Rik,Calcrl,Fdps,Galns,L1cam,Lrwd1,Mrpl12,Ran,Rnaseh2c,Rps9,
Mga	NaN	1190005F20Rik,1700047I17Rik1,4930432O21Rik,8430426H19Rik,Acpp,Ascc3,Ccdc92,Ccnc,Invs,Lcor,Map2k5,Mctp2,Nfe2l2,Setd3,Slc26a2,Smarca2,Tbc1d5,Thada,Tmed5,Tmod4,Uba3,Ylpm1,Zfp809,Zfp826,
Mll1	NaN	AU042671,Atf7,Atp5h,Dbi,Dgkd,Frat2,Gm16372,Med4,Mll2,Mrpl43,Pcmt1,Pgk1,Psmb4,Shc1,Spryd3,Zfp622,
Mll3	NaN	1190002H23Rik,2310011J03Rik,2900097C17Rik,4930518I15Rik,4930579G24Rik,4932438A13Rik,A230067G21Rik,Aak1,Ankrd16,Atp11a,BC021381,Basp1,Bcas3,Ccdc117,Cd46,Cdk5rap1,Cdt1,Cmah,ENSMUSG00000073622,Fam65b,Gm10640,Gm16494,Gm6041,Gpr52,H2afz,Hist1h2an,Hist1h4f,Hist2h2aa1,Hnrnph2,Hsn2,Huwe1,Hvcn1,Ipcef1,Lrrc59,Macf1,Maml2,Mfsd8,Mll2,Mll5,Ndufa11,Nfat5,Nhp2l1,Nop56,Nrbf2,Nudt3,Nup50,Olfr372,Parp9,Pgam1,Pgm1,Phf21a,Polr1d,Ppap2b,Rcc2,Rnf26,Rpl13a,Rpl3,Rpl34,Rps8,Serp1,Smg1,Snap29,Snrpg,Tmem71,Tpm3,Ttll4,Vps13b,Wasl,Ypel1,Zcchc11,Zfc3h1,Zfp182,Zfp236,Zfp407,
Mll5	fine_module_54	1810037I17Rik,2010111I01Rik,2210018M11Rik,2610039C10Rik,2810474O19Rik,9930021J03Rik,A530017D24Rik,A930024E05Rik,Actn4,Appbp2,Aprt,Asf1b,Ash1l,Bmpr2,Braf,C430010C01,Cd55,Chchd2,Diap2,Dmtf1,Fcho2,G3bp1,Gm10521,Gm12260,Gm12474,Gm9713,Gngt2,Hist2h3b,Hist3h2a,Hmgn2,Hnrnpa0,Hyou1,LOC100044416,Maml3,Mdh1,Mettl9,Mrpl30,Mrpl54,Myb,Myo9a,Ncoa1,Ndufaf1,Phxr1,Pnet-ps,Pold1,Pou5f2,Rangrf,Rbbp6,Rpl23a,Rpl27,Rpsa,Safb2,Scaper,Slc29a1,Sos1,Sos2,Tapbp,Tet2,Thoc4,Tnks1bp1,Tspo,Zbtb20,
Mlxip	NaN	Bat2l,Chuk,Commd2,Cyp4f13,Fnbp4,Fry,Il15ra,Mcts1,ND3,Ogt,Phc3,Rere,Scnm1,Sipa1l3,Tm2d1,Uba6,Vps33a,Wdr13,Znf512b,
Mta1	NaN	2410025L10Rik,3110001D03Rik,5930416I19Rik,Afg3l2,Aldh9a1,Amz2,Ap2a2,Arf2,Atp2a2,Bckdk,Bcl9,Cd84,Cdc23,Cdk2,Cndp2,Cox18,Cpsf1,Dicer1,Ehmt2,Eif1ad,Elmo2,Esyt1,Fbxl6,Galnt2,Gne,Gusb,Hdac6,Ifitm5,Igf2r,Igfbp4,Jmjd8,Kcnab2,Lrpap1,Map2k5,Map3k7,Map4k1,Mast2,Mcm7,Med24,Mif,Mrpl39,Ndufa9,Nup62,Patz1,Paxip1,Pigq,Polg,Ppp5c,Rad54l2,Rltpr,Rnf166,Sel1l,Smarcb1,Snhg1,Snord33,Srebf2,Stat2,Suv420h2,Tbcd,Tbl2,Zfp128,

TF	Enriched for Ontogenet targets	Targets
Mtf2	NaN	2410042D21Rik,4933433P14Rik,AW209491,Agps,Ankrd46,Arpc5,Atg4a,Atg5,Atl2,B3gnt2,Brd9,Bxdc5,Casp8ap2,Cct8,Cdk2ap2,Cldnd1,Cmas,Ctnnb1,Cugbp1,Cul1,Dcun1d5,Ddx3x,Dhx15,Dhx29,Dld,Dnajb14,Dnajc13,Eed,Efr3a,Erp44,Fam175b,Fam69a,Fyttd1,Gm7381,Gmcl1,Gmfb,Insig1,Ireb2,Isy1,Itga6,Kbtbd2,Krr1,LOC669999,Lcor,Llph,Lmbrd1,Ly75,Lypla1,Lypla2,Manea,Med6,Metap2,Mll2,Morc3,Mospd2,Mre11a,Mterfd1,Nars,Ndufaf1,Nup88,Nxt2,Ostm1,Otud6b,Oxsr1,Paip1,Pcmt1,Pik3cb,Polr2k,Polr3k,Ppig,Prdx3,Prmt10,Psmb4,Psmc6,Psmd1,Rab21,Rab22a,Rab2a,Rab5a,Rfc1,Rnf130,Rnf160,Rpe,Sec11c,Sept7,Sfrs3,Sgk3,Slc25a40,Slc35a3,Smarca5,Smc3,Smg1,Snx1,Sp140,Spast,Stx12,Sucla2,Sugt1,Sypl,Taf10,Tesk1,Tmbim4,Tmed5,Tmem161b,Tmem188,Tmem33,Tmem55a,Tmx1,Tmx3,Tmx4,Tnfaip8,Tpd52l2,Trdn,Trp53i13,Tspan13,Ttc15,Ube2v2,Ugdh,Ugp2,Uhrf2,Vrk1,Zcchc9,Zfp131,Zfp622,
Mxd4	NaN	1700081L11Rik,D030074E01Rik,Dctn3,Ddit4,Dynll1,Fam53b,Fnip1,Gpkow,Ier5,Itgb1bp1,Lrrc59,Mat2a,Mprip,Orc3l,Pgam1,Rbm25,Sesn3,Sfrs5,Spred2,Uggt1,Zfp771,
Myb	NaN	Casp7,Med21,Psmc6,Pwp1,Tiam1,Xylt1,
Mysm1	fine_module_235	1810074P20Rik,2210012G02Rik,2210404J11Rik,3110048L19Rik,4932441K18Rik,4933427D14Rik,5730419I09Rik,5830415L20Rik,6330416L07Rik,A230046K03Rik,A630047E20Rik,AI314180,Acbd5,Adam17,Ahsa2,Aim2,Anapc4,Angel2,Ap4b1,Apool,Appl1,Arhgap15,Arid4b,Armc8,Asah1,Ate1,Atp11c,Atp9b,Avl9,Azin1,Bclaf1,Bfar,Brf1,Brwd1,Ccdc75,Ccdc93,Cd84,Cdc73,Cep350,Chuk,Cir1,Col4a3bp,Crot,Csgalnact2,Cwf19l2,D030074E01Rik,D14Abb1e,Daam1,Dcaf17,Dcun1d1,Dhx36,Dhx40,Dmtf1,Dync1li2,Edem3,Ercc5,Esco1,Fam116a,Fam76b,Fbxo8,Fndc3a,Fnip1,Gcc2,Gls,Gm10459,Gm10673,Gm11270,Gm13213,Gm5488,Golga5,H2afz,Herc1,Herc3,Hist1h2ak,Hist2h4,Hltf,Hnrnph3,Ikzf5,Ireb2,Kat2b,Klhl5,Krcc1,Lins2,Lmbrd2,Lonp2,Man2a1,Map3k2,Map3k5,Map3k7,Mfn1,Mfsd7b,Mib1,Myst4,Nat12,Nmi,Nt5dc1,Ofd1,Oma1,Orc4l,Pcmtd1,Pex13,Pggt1b,Phc3,Phkb,Pigm,Pik3c2a,Pip4k2a,Pkn2,Ppm1b,Psme4,Pyroxd1,Rab11fip2,Rab12,Rabgap1,Rap1gds1,Rasa2,Rbm25,Rbm26,Rbm41,Rfesd,Ric8b,Rictor,Riok3,Rnf138,Rnf139,Rpl36al,Rps6ka3,S100pbp,Sacm1l,Scai,Scfd1,Sdccag1,Sel1l,Setx,Sfrs5,Slc37a3,Slk,Sltm,Smek2,Snapc1,Snx13,Sp4,Spag9,St7l,Styx,Syne1,Taf1b,Tardbp,Tbk1,Thoc2,Tia1,Tmed8,Trappc4,Trim23,Trio,Ttc13,Ttc14,Ube2w,Ube3a,Uimc1,Usp33,Vav3,Vps13c,Vps13d,Vps41,Vps54,Vti1b,Wdr37,Wdr77,Xiap,Zbtb1,Zbtb37,Zc3h7a,Zdhhc17,Zfand6,Zfp386,Zfp426,Zfp445,Zfp654,Zfp719,Zfp760,Zfp771,Zfp810,Zfp825,Zfyve16,Zrsr2,Zyg11b,
Myst4	NaN	1110038D17Rik,6030446N20Rik,Arhgap17,Atrnl1,Btbd9,Cytsa,Dip2b,Flot1,Galnt7,Hinfp,Hlcs,Ikbkb,Itgb1bp1,Kif13b,Lats2,Mtor,Nat13,Nhlrc2,Nlk,Pag1,Pfkfb3,Phactr2,Pik3c3,Syncrip,Trim26,Trim39,Trrap,Usp12,Zbtb34,
Nfat5	NaN	AU017193,Atp6v1c1,Atp8b4,Camk1d,Dennd1b,Erp27,Fyco1,Gm10388,Gm14335,Mll3,Mpzl3,Pigp,Pion,Pot1b,Ralgps1,Rb1cc1,Rbms1,Scarb1,Slc25a37,Tpi1,Ubn2,Zfp53,
Nfatc2	NaN	6330442E10Rik,AU017193,Atp6v0a2,Dusp5,Ssh1,Tnk2,Wdr61,Zfp467,
Nfe2l2	NaN	4930422I07Rik,6030499A19Rik,Ccdc56,Commd7,Cwf19l2,Gm1966,Hus1,Lmbrd2,Man2a2,Mga,Pdcd10,Reep4,Sec61b,Tnfrsf13b,Uty,Vamp7,Zbtb44,
Nfkbie	NaN	Actr5,Apeh,Arhgap17,Atg2a,Bcdin3d,Csprs,Dalrd3,Dctn3,Dhrs7,Fbxo42,Fhl3,Fmnl3,Galt,Gatsl3,Gcn1l1,Gfm2,Gm7609,Hinfp,Ltb,Manba,Nubp2,Pcnp,Prkce,Rbms1,Rfx5,Rgl2,Ring1,Rnf123,S100pbp,Slc35b2,Smox,Sphk2,Tcea1,
Nr4a1	NaN	Cst3,Dusp5,Jazf1,Rhbdd2,Trim8,
Patz1	NaN	Atp2a3,Bcr,Cabin1,E330009J07Rik,Map3k4,Mdc1,Rptor,Sema4b,Tap1,

TF	Enriched for Ontogenet targets	Targets
Pbrm1	NaN	AW554918,Abca7,Ap1s3,Arl6ip4,Bod1l,Bola2,Cblb,Cct6a,Dek,Dmxl1,Eif3j,Fam45a,Gm5774,Gm5775,Hipk3,Iars2,Lactb,Lin7c,Lrrc1,Mlf2,Oaz1,Ppp1ca,Psmd7,Ptpra,Rnu1b1,S100a13,Sars,Sec11c,Slc9a9,Ssh1,Synj2bp,Tmem120a,Tnpo1,Ttc35,Zfp710,
Pbx2	NaN	1110008F13Rik,2610039C10Rik,6720456B07Rik,Actn4,Ankrd13a,Arhgap9,BC037034,Cbx4,Ccdc88b,Cd151,Dpp3,Eif4e2,Frmd8,Got1,Hk1,Hspa4l,Hspd1,Klhl2,Mis12,Mlf2,Mocs1,Mrps15,Pcmtd1,Pip4k2b,Purb,Rbm6,Rbmx,Rgl2,Rnaseh2c,Rnf19b,Rnf5,Rpl3,Sema4f,Sh3gl1,Shc1,Slc27a4,Spsb3,Stard5,Stx12,Surf1,Tmem33,Tmem43,Trim41,Ywhag,
Phb2	NaN	0610007C21Rik,0610012G03Rik,1110008F13Rik,1110032A13Rik,1110037F02Rik,1500012F01Rik,1810058I24Rik,2410016O06Rik,2510006D16Rik,2610024G14Rik,2810428I15Rik,2900092E17Rik,4933421E11Rik,5730437N04Rik,6330442E10Rik,6720456B07Rik,9130011J15Rik,AI413582,ATP6,Acads,Acat1,Aco2,Acox1,Adpgk,Akr1b3,Alg5,Anapc13,Arl6ip4,Arl6ip5,Arpc1b,Atp5a1,Atp5g2,Atp5o,Atp6v0a2,Aurkaip1,Axin1,B430203M17Rik,Bag1,Bloc1s1,Bloc1s3,Bysl,C730025P13Rik,Calm3,Cars2,Cbx4,Cct2,Cct5,Cct7,Cdk5rap3,Cdkn2aipnl,Chchd7,Cib1,Cir1,Cnpy2,Cope,Cops6,Cops8,Cox5a,Cox7a2,Cpsf3l,Cpsf4,Crlf2,Cstf1,Ctsc,Dap3,Dclre1b,Dctn2,Dhps,Dhx58,Dpagt1,Dpp3,Dtx2,Dusp7,Dynlrb1,Ebp,Echs1,Edem3,Eef1b2,Ei24,Eif3b,Eif3f,Eif3g,Eif3h,Eif3i,Eif3k,Eif4b,Eif5a,Eif6,Elf2,Emg1,Eral1,Etfb,Fam100a,Fam125a,Frmd8,G530012D18Rik,Gba2,Glb1,Glo1,Glrx2,Gltp,Gm10209,Gm10459,Gm10785,Gm11681,Gm11741,Gm12000,Gm13819,Gm1943,Gm2173,Gm5921,Gm6274,Gm6394,Gm6540,Gm8624,Gns,Gpi1,Grcc10,Grn,Guk1,H2-Ke6,H2afv,Hax1,Hes6,Hn1,Hpvc-ps,Hsd17b10,Htra2,Ier2,Ifi35,Imp3,Jtb,Khsrp,Kptn,LOC100047557,Ldha,Lemd2,Lsm8,Lypla2,M6pr,Mapkapk2,Mars,Mdm4,Mea1,Mfsd1,Mgat2,Mlf2,Mrp63,Mrpl14,Mrpl23,Mrpl36,Mrpl43,Mta2,Mtch1,Mul1,Mus81,Ndufa10,Ndufa4,Ndufa8,Ndufaf3,Ndufb5,Ndufb9,Ndufs2,Ndufv1,Nfkbid,Nfu1,Nme3,Nop2,Nt5c,Nudt3,Oaz1,Ostc,Park7,Pctp,Pex11b,Pfdn5,Pgk1,Pgp,Pigm,Plekhj1,Polr2c,Polr2g,Ppm1g,Ppm1m,Ppp1ca,Ppp1r8,Ppp2r5b,Prdx3,Prkag1,Psmb10,Psmb4,Psmb9,Psmd5,Pttg1ip,Pwp1,Qars,Rnaset2a,Romo1,Rpl15,Rpl19,Rpl24,Rpl3,Rpl36,Rpl36a,Rpl36al,Rpl5,Rpl6,Rpl7,Rpl7a,Rps13,Rps14,Rps15a,Rps18,Rps2,Rps23,Rps27l,Rps4x,Rps7,Rsl24d1,Rwdd1,Samm50,Serf2,Sh3gl1,Shc1,Slc12a6,Slc25a39,Slc35a4,Slc38a10,Smc2,Smg5,Snord82,Snrpb,Snrpd2,Snx20,Sod2,Spsb3,Ssr2,Supt3h,Surf1,Surf4,Sys1,Taf10,Taz,Tbcb,Tex2,Tex261,Thoc5,Thoc6,Tm2d2,Tm9sf1,Tmem111,Tmem18,Tmem70,Tmem82,Tmem85,Tpra1,Trappc5,Trappc6b,Trdn,Triap1,Trim27,Trim35,Tubb2c,Txn2,Txndc11,Txndc17,Tyk2,Uqcrb,Uqcrh,Use1,Vps25,Xbp1,Yipf5,Ywhag,Zdhhc4,Zdhhc7,
Phf21a	NaN	Atg7,B430306N03Rik,Ddx3x,Dnajb1,Dynll1,Fbxl22,Gmcl1,Grik5,Hdac4,Hist1h4b,Hist1h4m,LOC100134980,Lass6,Mex3b,Mmgt2,Nanos1,Setd7,Vps37c,Zcchc9,Znrf1,
Pias3	NaN	2310035C23Rik,5730427N09Rik,6430526N21Rik,Abca7,Acap3,Apbb3,Arhgef11,Arrdc1,Atf7,B4galt3,BC059842,Clec16a,Cradd,Ern1,Ggt5,Gm3338,Gm6540,Gm6651,Gpatch8,Hspa1a,Icam2,Ndst2,P2rx4,Polr3c,Ppox,Prr8,Rpl36a,Rpl6,Rps6kb2,Setd1b,Sh2b1,Slco3a1,Tinf2,Zmiz1,
Pknox1	NaN	Calcrl,Heg1,Tbx6,
Pml	NaN	3110057O12Rik,BC048403,Leprot,Mfsd8,Mina,Nup210,Pign,Rnf14,Trak1,

TF	Enriched for Ontogenet targets	Targets
Pnn	fine_module_316	2610002M06Rik,4930453N24Rik,ATP6,AY036118,Agtpbp1,Camsap1l1,Cenpj,Cope,Cpne3,D19Ertd737e,Frmd8,Ftl1,Fubp1,Gbe1,Glud1,Gm10785,Gm5805,Gm7367,Got2,Hist1h2bb,Iqgap2,Kif5b,Lpgat1,Luc7l,Med24,Mettl3,Mkln1,Ndufa7,Pank2,Pih1d1,Pnrc2,Polb,Prpsap2,Ptpn2,Ranbp6,Riok2,Rprl1,Rprl2,Sec63,Sept2,Serp1,Sfpq,Sfrs7,Slc25a32,Slc30a9,Taf1,Tial1,Tmed4,Tmem77,Tmem82,Tmf1,Trim30,Ubxn2b,Usp16,Wdr5b,Zbed4,Zfp180,Zfp84,
Pou2f1	NaN	2810001A02Rik,Asb7,Atp6v1g1,Cfp,Cwf19l2,Dhx15,Dvl3,Fam125b,Fam76b,Gm9264,Hspa5,Ier5,Klhl20,Lclat1,Mkl2,Myst4,Phka2,Ptpn9,Rnf187,Sap130,Slc25a30,Socs3,Unkl,Zfp169,Zfp408,Zfp609,
Prdm9	NaN	3830406C13Rik,Acot2,Baiap2,Clec2d,Cul2,Mbtps2,Ndufs5,Pja2,Pts,Rabif,Rad51l3,Rnf170,Rtn4ip1,Rybp,Taf12,Tmem175,Tmem19,Wdr41,Zc3h6,
Pttg1	NaN	6530401N04Rik,Ap1s1,Eif5,
Purb	NaN	1600012H06Rik,2410129H14Rik,2810002D19Rik,2900097C17Rik,3110003A17Rik,5730508B09Rik,Abcc4,Alkbh5,Ankle2,Anp32a,Armc1,Atxn1l,BC013529,BC050254,BC056474,Bnip3,C78339,Cggbp1,Chchd2,Chmp1b,Chordc1,Cnot8,Coq10b,Creld2,Cugbp1,D1Ertd622e,Dld,Dnmt3a,ENSMUSG00000074747,Fmnl3,Gfpt1,Gm12058,Gm16372,Gm9713,Gmfb,Gnrh1,Hexim1,Hnrnpa0,Hnrpll,Ifi27l2a,Insig2,Josd1,Lig4,Mmgt1,Mrs2,Mta2,Nanos1,Nipa2,Nt5c3,Nt5dc3,Ormdl1,Pfdn2,Prf1,Prkar1a,Ptp4a2,Qk,Rell1,Ripk2,Rwdd4a,Setd3,Slain2,Slc25a20,Smc3,Smurf2,Snx18,Strm,Tmed1,Tmem123,Tmem19,Tmod3,Tra2a,Twsg1,Ubl3,Uspl1,
Rara	NaN	Acpl2,Atg2a,Carm1,Ccdc97,Crkrs,Cyth1,Fam100a,Foxj2,Fuz,Gnpda2,Gpr146,Hdac5,Hrh2,Hsp90aa1,Ifih1,Kdm6b,Lrch4,Nbeal2,Ncln,Ndufa4,Ntng2,Osgin1,Pddc1,Pdk2,Psmd6,Rtp4,Setd1b,Sipa1l2,Tbca,Tle3,Tmco6,Trub2,Zfp654,
Rarg	NaN	Irak2,Ptms,
Rbpj	NaN	1110057K04Rik,4930420K17Rik,AI316807,Arsk,Ccdc111,Dtx2,Exoc1,Gm10548,Haus2,Hspa1a,Lclat1,Luc7l2,Park7,Phyh,Rb1cc1,Scrn3,Setd3,Slc25a16,St6galnac2,Tmed1,Trdmt1,Vgll4,Zdhhc3,
Rela	NaN	0610010K14Rik,1810006K21Rik,2510002D24Rik,4932438A13Rik,Abtb2,Afmid,Alkbh4,Arf3,Atp5a1,Atp6v0e,BC021381,Bak1,Bcl3,Bloc1s2,Capns1,Cdk2ap1,Cic,Cmtm7,Creg1,Cstf1,Ctr9,Diablo,Dock10,Dym,Ebp,Eif5a,Frat1,Gm6181,Gvin1,Hexim2,Il10rb,Klhl6,Lrp10,Lsm10,Ly96,Mknk2,Mocs1,Mrpl4,Mrps21,Oas1c,Phip,Plod1,Pnpla2,Pspc1,Rgs3,Rras,Rusc1,Sap130,Scaper,Slc29a3,Smpd1,Spata2,Spred2,Tada3l,Tgfb1,Tmc6,Tmem184b,Trak1,Ulk1,Ypel1,
Rere	NaN	4732418C07Rik,Anp32a,Atn1,Cnot4,Dennd3,Exoc6b,Fam168a,Fus,Gm10397,Gm6548,Gng2,Irs2,Orai2,Parp12,Scai,Slc25a45,Wdr51b,Zmym5,
Rest	NaN	1110012L19Rik,2410042D21Rik,4833420G17Rik,Ada,Adam17,Ahsa1,Aktip,Angel2,Ankle2,Aprt,Atg5,Atp6ap2,BC050254,Cdc42se2,Ern1,Fam134b,Fundc1,Gm5921,Ifnar1,Kdm5b,Map2k1,Mbip,Nlk,Oxsm,Pdlim5,Pip4k2c,Pou5f2,Pppde1,Psmb10,Rnf115,Rps2,Slc17a9,Slc30a1,Smn1,Strap,Tgfbr1,Tmem41b,Vps33a,Wbp1,Zfp609,Zfp715,Zfp868,Zfyve16,
Rfx3	NaN	Atf2,Blvrb,Fas,Gm16489,Gtdc1,Hist1h2aa,Hist1h2af,Hist1h2ao,Hist1h4i,Nsun4,Rfx7,
Rfx5	NaN	5730419I09Rik,Ccdc84,Efcab4b,Efr3a,Exoc5,Hsd17b7,Insig2,Pcgf1,Pold3,Rbm22,Setd3,Snx32,Sumf1,Tinf2,Tmem184b,Vipr1,
Rfx7	NaN	2810002D19Rik,5033414D02Rik,Arl4c,B230380D07Rik,Bnip3l,Capn7,Cpped1,Cyb5r3,Dpy19l3,Fam175b,Fchsd2,Lcorl,Olfr1419,Pigx,Polr2f,
Runx1	NaN	1110012D08Rik,4932441K18Rik,Acrbp,BC037112,Bat2,Clec16a,Cpsf6,Cspp1,Gga3,Gltscr1,Gramd1a,Hectd1,Mlxip,Rps3,Slc46a3,Zfp771,
Runx3	NaN	Dap,Ddx41,Nat6,Rbm3,Smc4,

TF	Enriched for Ontogenet targets	Targets
Ruvbl2	NaN	0610031J06Rik,0610037L13Rik,1700017B05Rik,2700007P21Rik,A530013C23Rik,Anapc11,Ap1s1,Apeh,Ard1a,Arhgap15,Atp6ap2,Cct8,Cdca7l,Chtf8,Copg,Eif3l,Got1,H2-Q1,Higd2a,Hsp90ab1,Htatip2,Ict1,Irf2bp1,Metap1,Mrpl19,Mrps15,Mrps24,Mrrf,Nacc1,Nagpa,Naif1,Ndufa2,Ndufa3,Nf2,Orai3,Plod3,Polr2f,Pppde1,Prdx6,Ran,Rplp0,Rps3,Sdhb,Sigmar1,Spint2,Sssca1,Stk16,Tada3l,Tmem179b,Tmem43,Trmt112,Trrap,Ttc9c,Ttll1,Tusc4,Txnl4a,Ubfd1,Wbscr22,Zfand2a,
Rxra	NaN	Abca2,Bicd2,Ccdc23,Fbxo31,Nop16,Rpa3,Tesk1,Tsc22d3,Zfp217,
Sap18	NaN	0610010K06Rik,1700016K19Rik,9030617O03Rik,Abl1,Cluap1,Dstn,Fam46a,Fuca2,Gpr177,Rcor3,Rfx5,Slc16a6,Slc31a1,Smurf1,Tesk2,Tmem63a,Txndc16,
Scmh1	NaN	Acat1,H2-Q8,Isoc1,Mmadhc,Ofd1,Orc5l,Ppap2b,Sdhd,Spata1,Tmco6,Tmem141,Ylpm1,
Setd8	NaN	4732418C07Rik,5730403M16Rik,8430410A17Rik,A530054K11Rik,Abca1,Ccdc97,Cct2,Cstf1,Fam172a,Gm10673,Gtf3c6,Hspa8,Idh1,Inppl1,Kbtbd7,Mlec,Ppm1d,Prei4,Ptplb,Rwdd1,Sf3a1,Ssbp2,Thoc5,Tnfaip3,Tnks1bp1,Trim8,Tubgcp4,Zfp131,
Smad3	NaN	5330426P16Rik,Aacs,Anks3,Cables2,Cdyl2,Chst15,D2hgdh,Git1,Grap,Hdac6,Lrrc61,Orai2,Phf15,Pip5k1c,Pisd-ps1,Rab11fip1,Rarg,Rbm15b,Sept2,Stk40,Susd3,Tgfbr2,Vps37b,Zfp217,
Smad5	NaN	Adrb2,Irf7,Pnpla8,Stk39,
Smad7	NaN	AI987944,Aim1,Ash1l,Axin1,Ccnd2,Dexi,Dvl3,Mbp,Plxnd1,Sart1,Snapc3,Strap,Sypl,Trim30,Unc84a,Zfp36l2,
Smarca2	NaN	Afmid,Aldh4a1,B430319F04Rik,B4galnt1,Bcdin3d,Clic1,Ddx26b,Gm14251,Gm2701,Gm6712,Gm9197,Hexim2,Hnrpll,Hps3,Igf1r,Iqsec1,Kcnh3,Klhdc2,Mfsd6,Oas1c,Rmi1,Rshl2a,Sbds,Slc43a3,Sumo3,Trps1,U2af1l4,Uprt,
Smarca5	NaN	Abcb7,Acsl4,Arhgef1,Atl3,Cab39l,Cbx3,Dbf4,Dnajc1,Dnajc3,Gmps,Hccs,Hif1a,Hispd1,Idi1,Mapre1,Mbd6,Me2,Mtdh,Mtf2,Nmd3,Nr1h2,Nsdhl,Orc3l,Pbrm1,Plaa,Rev3l,Smarce1,Spnb2,Uggt1,Uxs1,Xrcc4,
Smarcb1	NaN	2210016F16Rik,2410042D21Rik,3200002M19Rik,5430437P03Rik,Agpat2,Alg1,Apoa1bp,Apool,Atp2a3,Atp5h,Baiap2,Btrc,Calr,Cbara1,Cd81,Cdc25a,Cdc37,Cdca7,Cdk2ap1,Cdk4,Cenpt,Centb1,Creld2,Cs,Ctnnbl1,Ctsb,Dcps,Ddx19a,Dguok,Dis3l,Dpp9,E130309D02Rik,Ercc2,Ergic3,Gm11270,Gm3365,Gsn,Haus4,Htt,Inpp5b,Ipo9,Irf3,Lpcat1,Mbtps2,Med11,Mlec,Mlst8,Mpi,Mpst,Mta1,Mtor,Nktr,Nmi,Nomo1,Nop10,Npm3,Nucb1,Nup88,Oma1,Parp16,Pdia4,Pgm2,Pja2,Pmf1,Pnp2,Prcp,Prkcsh,Psmb2,Psmc4,Psmd1,Psmd7,Ptp4a3,Pxmp4,Rad23b,Rai12,Rbms2,Rcn1,Rnf121,Rpn1,Ruvbl2,Rwdd4a,Sae1,Scnm1,Sf3a1,Srp68,Ubiad1,Uck1,Zfp157,
Smarcd1	NaN	1700012B15Rik,1810013D10Rik,2010007H12Rik,2310022A10Rik,2510003E04Rik,2610002J02Rik,2610002M06Rik,4933437N03Rik,5730403M16Rik,5730427N09Rik,8430410A17Rik,A730011L01Rik,AI606181,Acaa2,Adrb2,Akr1a4,Ampd2,Ap2m1,Ap4m1,Aph1a,Arfgap2,Arhgef12,Atmin,Atp1a1,BC004004,BC029214,BC031181,Bcl2l13,Bcs1l,Btd,Casp7,Cbx8,Ccdc53,Ccdc56,Cd151,Cetn2,Chpf2,Comt1,Cstb,Ctns,Ddx41,Dhrs1,Dnlz,Dpy19l3,Eif4e2,Esd,Extl3,Fam54b,Fam96a,Gba,Gbas,Gemin7,Glul,Gnpda2,Gstk1,Gstm4,Gtf3c6,Gyg,Hk1,Hyou1,Id2,Idh3g,Klf10,Lcmt2,Lipa,Lrrc14,Lrwd1,Mcrs1,Med6,Mrpl17,Mrpl45,Mrpl51,Mtif3,Mtmr9,Naglu,Ncdn,Ndufc2,Nme6,Npc1,Pank2,Pddc1,Pex13,Pi4k2a,Pigt,Pink1,Pip4k2b,Pofut2,Poldip2,Ppig,Ppme1,Prkaca,Psma5,Psma6,Psmc3,Psmd2,Ptplb,Rnf19b,Rnf5,Scly,Slc25a16,Slc25a45,Slc37a4,Slc4a1,Snx15,Spryd3,Sra1,Srd5a3,Stx6,Tatdn1,Tbcel,Tmem126a,Tmem175,Tmem185b,Tnks,Tor3a,Trappc4,Tsc2,Ube2l3,Usf1,Usp30,Usp39,Vdac1,Vdac3,Vwa5a,Wars,Wbp1,Wdr5b,Wdr61,Zbtb6,l7Rn6,
Smarce1	NaN	Aplp2,Cox7a2,Dhx57,Hibadh,Kif13b,Pcnp,Refbp2,Slc43a3,Sptlc2,Stx2,Tulp4,
Sp110	NaN	C130026I21Rik,G530012D18Rik,Il18bp,Kptn,Sp140,

TF	Enriched for Ontogenet targets	Targets
Sp140	NaN	2010007H12Rik,A530032D15Rik,Arhgef12,Asb3,Csprs,Fgfr1op2,Gm5617,Gm7609,Gm8613,Pdcl3,Sp110,
Sp4	NaN	AA987161,Arl15,Crebl2,Dpagt1,EG665955,Fam103a1,Fus,Hibch,Pja2,Rbm7,Rbpj,Tiparp,Tnfaip3,Zcchc11,Zfp39,Zfp748,
Srebf2	fine_module_312	Acaca,Agfg2,Arhgap1,Cirbp,Clcn6,Dhcr24,Fdft1,Fdps,Fusip1,H6pd,Hmgcr,Hmgcs1,Huwe1,Idh1,Idi1,Insig1,Ldlr,Ndst1,Nkiras2,Nsdhl,Nubp1,Pcyox1,Pcyt2,Prrc1,Rusc1,Sc4mol,Sc5d,Scarb1,Sgsh,Slc25a1,Slc35c1,Sqle,Stard4,
Stat1	NaN	Arsa,Aurkaip1,Cd274,Exoc4,Nlrc5,Pcgf5,Psmb9,Rev3l,Samhd1,
Stat2	NaN	1600014C10Rik,A430107D22Rik,Anapc11,B4galt7,BC056474,Bat2,Bnip3l,Camk2b,Ccdc91,Hdac7,Ints1,Jak3,Nfkbie,Pols,Psme1,Sec61b,Sema4a,Trafd1,Vars,Zfp408,
Stat4	NaN	Il4ra,
Suz12	NaN	AI987944,Arf6,B230219D22Rik,Birc6,Ccdc41,Ccnt1,Cenpb,Cops5,Cul2,Edem1,Emid1,Mex3c,Mphosph10,Tpr,Ube2q2,
Taf1	NaN	2310001H12Rik,2510003E04Rik,3110043O21Rik,4632419I22Rik,9430008C03Rik,AI314976,Acp2,Acsl1,Alg10b,Ap3m1,Ap4e1,Armc1,Atp1a3,Atp6v1c1,BC031353,Brd8,Brwd2,C330007P06Rik,Cbx5,Chka,Clasp2,Clpx,Cstf3,Ctdspl2,Ddx19a,Ddx3y,Ddx50,Dnajc10,Dnm1l,Dpy19l4,Eif2a,Fam172a,Fkbp5,Fmr1,Fusip1,Gabpa,Gopc,Gphn,Hace1,Herc5,Hspa4l,Htt,Ip6k2,Ipo9,Kctd9,Kif16b,Map4k5,Metap1,Mpp7,Mtap7d1,Nfx1,Nsf,Nvl,Pcgf5,Pebp1,Pias2,Pign,Pnn,Polr3f,Ppm1f,Ppp2r5c,Ppwd1,Rab18,Rad18,Rbmx,Rev1,Rmi1,Sc5d,Sec61b,Senp5,Sh3bgrl,Slc25a24,Slc36a4,Smc5,Srp54b,Srp54c,Ssbp1,Stag1,Suz12,Terf1,Tex10,Tfb2m,Thrap3,Tm2d1,Tsn,Txndc11,Ubfd1,Unc84a,Usp24,Wtap,Xpo1,Zcchc4,Zfp410,Zfp512,Zranb2,Zw10,
Taf1a	NaN	0610037L13Rik,2310004I24Rik,4833420G17Rik,9230112E08Rik,Aak1,Abcc5,Acad11,Alg5,Ccdc109a,Dcaf13,Efcab4b,Exoc1,Foxo3,Gm5512,Gm6134,Gtf2f2,Ilkap,Immt,Impad1,Kdsr,Kif3c,Larp4,Med4,Mmadhc,Mppe1,Mrpl39,Mtfmt,Nadsyn1,Nde1,Ndufv1,Nfrkb,Nqo2,Nxn,Orc5l,Pldn,Polr3b,Pon2,Prpf18,Psmf1,Rmnd1,Rpl36,Sec23a,Setdb1,Slc3a2,Tapt1,Tk2,Tmem68,Tomm34,Ttc9c,Ttll4,Ubr2,Yipf1,
Tbx6	NaN	4930522L14Rik,4932441K18Rik,9230112E08Rik,Abca2,Acrbp,Ascc3,Git1,Lrch4,Nbeal2,Nfkbid,Pknox1,Sfrs3,Ssx2ip,Suv420h2,Tmem86b,Tsc2,
Tcf19	NaN	1500032L24Rik,1810013D10Rik,B4galt3,Dad1,Emb,Etv6,H2afz,Jagn1,Lsm3,Marveld1,Mfsd10,Ndufs6,Nrm,Nubp1,Phb2,Pih1d1,Pkmyt1,Rcc2,Reep4,Ripk3,Rnf26,Sfxn1,Tcirg1,Yif1b,
Tcfe2a	NaN	2810001A02Rik,4831426I19Rik,4933439F18Rik,6430526N21Rik,A230046K03Rik,AA960436,Abl1,Acox1,Adcy3,Ap1s1,Ard1a,Atf6b,Atn1,Atp5g1,B4galnt1,Bat4,Btbd2,Ccdc115,Chmp1a,Crat,Dcaf15,Dpp9,F630110N24Rik,Fam117a,Fmr1,Foxp4,G530012D18Rik,Git1,Glipr1,Gltscr2,Gm15441,Hdgf,Ibtk,Lamp1,Med16,Mif4gd,Mospd3,Mpdu1,Mtf2,N4bp2l2,Nacc1,Ncdn,Ndufa11,Ndufv3,Nipbl,Nr1h2,Paqr7,Phkg2,Pigt,Pld3,Polr1d,Polr2c,Ppp2r5d,Prkaca,Ptger1,Rab37,Rpp21,Sh3bp1,Sirt6,Slc12a6,Slc24a6,Slc27a4,Snx13,Sssca1,Sys1,Tcirg1,Tmco4,Trex1,Tubb5,Was,Wdr81,Wsb2,Znf512b,
Tfdp1	NaN	1700054O19Rik,Aldh2,Ank,Atp6v1d,Cdc26,Cdk6,Entpd5,Gm5785,Gm6273,Hist1h1c,Hmgcs1,Metap2,Mrpl9,Nars,Ola1,Pdha1,Sdhd,Sh3bp5,Sh3glb1,Slc17a9,Slc35a3,Slc9a9,Tmem39b,
Thra	NaN	Ergic1,G6pc3,Glt25d1,Pdk2,Pnpla2,Ppdpf,Prkar1a,Tmem179b,Yif1b,Zfp410,
Trerf1	NaN	Eri1,Hiatl1,Nup107,Plxnd1,
Trim14	NaN	AU042671,B4galt1,Cct6a,Fbxo42,Gmfg,Ifi27l1,Mapre1,Mrpl9,ND4L,Pitpnm1,Rab24,Rap2a,Serinc5,Sike1,Sirt6,Tomm7,Zgpat,
Trim25	NaN	Apc,Bmf,Errfi1,Irf9,Krr1,Morc3,Mpp5,Tpd52l2,Zfp672,

TF	Enriched for Ontogenet targets	Targets
Trps1	NaN	2310001H12Rik,2310008H04Rik,4930522L14Rik,Acat1,Arhgap26,Csda,Elac1,Ly96,Twistnb,
Tsc22d3	NaN	2810474O19Rik,AI467606,Abhd15,Card6,Cxcr4,Dnajb1,Edem1,Exoc3,Fam46c,Fgfr1op2,Fkbp5,Haus8,Hint1,Papd5,Prdx6,Slc35e1,Timp2,
Whsc1l1	NaN	2900010M23Rik,A430078G23Rik,A430110L20Rik,AI413582,Acp5,Ada,Akap8l,Bak1,Bckdk,Ccdc32,Chd7,Ddx60,Dirc2,Glt8d3,Gm10091,Gm7774,Gnas,Gripap1,Heatr5a,Hist1h2bh,Hist2h2bb,Hspbap1,Klhl6,Lrrfip1,Mcts2,Mrps33,Ndufa10,Ndufa7,Ndufb4,Nt5e,Ppapdc1b,Prkab2,Psmb6,Rbm15b,Sema4b,Sgms1,Srgap2,Srpk2,Ssr2,Tmcc1,Traf5,Vamp1,Wdr13,
Xbp1	NaN	5730494M16Rik,9130401M01Rik,AI316807,Chmp5,Creld2,Dcun1d1,Fam48a,Fam76b,Garnl1,Gatsl3,Gnpda1,Isg20,Nubp2,Pdcl,Pdk3,Pfkl,Pgrmc1,Prpsap2,Slc31a1,Smpdl3a,Ubxn8,Znrd1,
Zbtb38	NaN	Cdc42ep4,Chst12,Dhcr24,Gm4638,Irf9,Morc3,Rnf7,Terf2ip,
Zfp217	NaN	1190005F20Rik,4933433P14Rik,Brpf3,D14Abb1e,Daglb,Erp44,Gcc2,Gm6041,Hdac5,Itfg3,Itgal,Itpk1,Mrpl24,Mthfr,Pacs2,Pbxip1,Pik3cd,Pim1,Rab11fip4,Rap2b,Sik1,Smad3,Smad7,Spast,Stim1,Tbc1d13,Thoc2,Tmem42,Tomm22,Uba2,Vgll4,Vps52,Zfp710,
Zfp367	NaN	1500010J02Rik,1700025G04Rik,Cep78,Cryl1,Hspb6,Mrp63,Nup37,Phkb,Poldip2,Scmh1,Slc1a5,
Zfp36l2	NaN	2310067B10Rik,AI316807,Abca7,Anks1,Csnk1e,Extl3,Gramd1b,Klf13,Map2k1,Orai3,Pbx2,Pip5k1c,Rpl23a,Tpcn1,Zc3h7a,
Zfp410	NaN	1500031L02Rik,5730494M16Rik,A530013C23Rik,Acaca,Aqr,Atpaf1,BC049349,Cables2,Cdadc1,Cdc16,Cdk5rap2,Chchd7,Copg,Cox11,Cyb5b,D1Ertd448e,Dennd4c,Diablo,Dnajc24,Eral1,Erlin2,Fam116a,Fam123a,Foxn3,Gm6950,Gm7413,Gmps,Gorasp2,Hint3,Ift20,Il10rb,Ints10,Klc1,Krtcap3,Lactb2,Magi3,Mapk8,Myo9a,Prr7,Rbbp8,Rhot1,Rps6ka5,Sap18,Seh1l,Slc10a7,Sos1,Stard3nl,Tet2,Thoc7,Tmem194,Tmem39a,Tnnt3,Tubgcp3,Tubgcp4,Ube2f,Ubn2,Uspl1,Wasl,Xpo7,Zadh2,Zdhhc13,Zdhhc6,Zfp672,Zhx3,Zwint,
Zfp422	NaN	Brd8,Dnahc8,Ifngr2,Mrfap1,Rab21,Tes,
Zfp691	NaN	1110006O24Rik,1300010F03Rik,1500041N16Rik,2810416G20Rik,Aaas,Adat2,Bscl2,C030046E11Rik,D11Wsu47e,Dhrs11,Gga3,Gltp,Idh3g,Pgm1,Rab12,Snx32,Stambpl1,Strada,Tusc4,Uxt,
Zfp715	NaN	1600014C10Rik,Asb3,Atf2,BC063263,Ctns,Erich1,Fam20b,Glt8d1,Gmip,Lass6,Plaa,Pop4,Rest,Rpl15,Sesn3,Sfrs12ip1,Spg11,Trib3,Ubash3b,Unc50,Zfp52,Zfp87,
Zgpat	NaN	AY036118,Adamts10,Atg16l1,C430010C01,Fam13b,Fam188a,Got2,Hps5,Ikbke,Itgb7,Lime1,Luc7l,Ncdn,Nisch,Pdcd2l,Pygo2,Shkbp1,Slc37a3,Smpd2,Srrt,Tbc1d1,Tmem39a,Zfp182,Zranb1,Zw10,rp9,
Zhx1	NaN	1110032A03Rik,2700007P21Rik,4732418C07Rik,4933407N01Rik,4933411K20Rik,4933421E11Rik,5730601F06Rik,Asxl2,Btrc,Ccng1,Cenpq,Cep57,Cetn2,Creg1,D230037D09Rik,Dapp1,Dguok,Dnajc13,Elmod2,Evi2a,Gnpda2,H2-Q1,H2-Q2,Ifi27l2a,Impad1,Kdm5d,Malt1,Mbip,Mbnl3,Mbtps2,Mut,Nsun3,Orc3l,Osgepl1,Papd4,Parp6,Pbrm1,Pou2f1,Prkx,Rnf170,Rnft1,Rnu73b,Rps18,Sec24a,Senp7,Sesn1,Sh3glb1,Shfm1,Snhg1,Snord49b,Sntb1,St3gal3,Taf1a,Zbtb26,Zfp277,Zfp398,Zfp759,
Zmynd11	NaN	Fut8,Gm2382,Larp7,Mthfs,Nf1,Prkci,Smad5,Stxbp5,Vps13b,Zfp451,