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Methods for Mining Genome-Wide Phenotype Associations in a Functional Context

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Methods for Mining Genome-Wide Phenotype Associations in a Functional Context

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For Kai and Lena

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Abstract

Genome-wide association studies (GWAS) have linked various complex diseases to many dozens, sometimes hundreds, of individual genomic loci. Since these are generally of small effect and may lack both functional annotations and an obvious relation to other disease-associated regions, they are difficult to place in a functional context that advances our understanding of the disease. When considered only in isolation, disparate collections of trait associations provide little mechanistic insight. Thus, there is a pressing need for computational methods that use genome-wide molecular data to aggregate GWAS associations and extract functional insight from seemingly unrelated SNPs. To this end, we recently introduced Sherlock, a Bayesian method that detects gene-disease associations through pattern matching between eQTL results and the the full set of GWAS loci (He et al., 2013). Here we review the Bayesian formulation and present Empirical Sherlock, a robust, parameter-free approach to detecting associations between various molecular functions and GWAS traits. It uses an empirically-derived null distribution to associate subsets of GWAS loci, grouped by their relevance to a particular molecular function, with the GWAS trait. The method is easily generalizable to most any genome-wide functional characterization (e.g. DNA methylation, transcription factor binding, etc.), in addition to eQTL. By avoiding null distributions that assume a particular theoretical form for the input GWAS, Empirical Sherlock yields results are resistant to false discovery due to inflation of the output p-values. The core method requires no tunable parameters or prior probabilities and, when used with eQTL, permits an adjustment for pleiotropic SNPs that control the expression of many genes. In addition, Empirical Sherlock calculates significance directly, avoiding the inherent limitations of permutation-based tests. As we demonstrate using moderately-powered GWAS for Crohn's disease, type 2 diabetes, and Schizophrenia, it detects gene associations that are either validated through better-powered GWAS or supported by independent literature.

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Chapter 1

Introduction

The genetic underpinnings of complex disease have proven resistant to easy mapping using only the common polymorphisms directly implicated through genome-wide association studies (GWAS). Typically, such studies reveal large numbers of small effect loci that, in aggregate, explain only a small fraction of complex disease heritability. This discrepancy has generated considerable debate concerning the specific mechanisms of polygenic trait inheritance and the overall utility of the GWAS paradigm.[1] [2] [3] By assembling ever-larger disease cohorts, the power to resolve small effects through association studies improves, but this does not necessarily translate into superior mechanistic insight. The functional consequence of a given locus is often non-obvious, especially for the many associations located in intergenic regions. Even when accurate annotations are available, the challenge of assembling many dozens or hundreds of associated loci into a coherent picture of disease etiology is daunting. The ability to reliably map large numbers of associated loci onto a smaller number of functional elements constitutes a key component of a pipeline to convert disparate associations into meaningful disease insight.

For these reasons, there is much interest in mining GWAS results using a diverse array of genome-wide indicators of functional relevance. These include assays for chromatin structure, DNA methylation, transcription factor binding activity, and gene expression regulation, as made publicly available through the NHGRI's Encyclopedia of of DNA Elements (ENCODE) project and the NIH-funded Genotype-Tissue Expression (GTEx) program, among others.[4] [5] Taken together, they form a dictionary of genomic loci in terms of distinct but related molecular phenotypes that can be used to understand the key drivers of complex diseases and other traits. In typical use, however, these molecular definitions provide clues only one-by-one for the top GWAS SNPs (those near or above genome-wide significance).

Yet, to be especially useful, improved approaches for GWAS data mining must reflect both the need to gain functional insight and the need to aggregate many SNPs to explain a larger fraction of the inherited phenotypic variance. Although the degree to which missing heritability is captured by rare genetic variants, higher-order genetic interactions (epistasis), or small effects across many common SNPs is the subject of active debate, approaches that mine small effects from SNPs below genome-wide significance are highly attractive, since data is readily available from existing studies.[2] [6] [7] Several lines of evidence suggest that much additional information can be gleaned from common SNPs that fall below genome-wide statistical significance:

First, the number of statistically-significant small-effect loci associated with a given trait is limited primarily by the power of the studies involved, not necessarily by some intrinsic property of biological network architecture. An analysis of the current NHGRI GWAS Catalog reveals an exponential distribution of reported effect sizes, with a few large effect loci interspersed with large numbers of small effects.[8] Across all studies, the median odds ratio (OR) is well-below 1.3 (Fig. 1.1). With current and planned studies routinely targeting many tens of thousands of individuals in disease cohorts, the number of small effect loci that reach genome-wide significance will only increase.

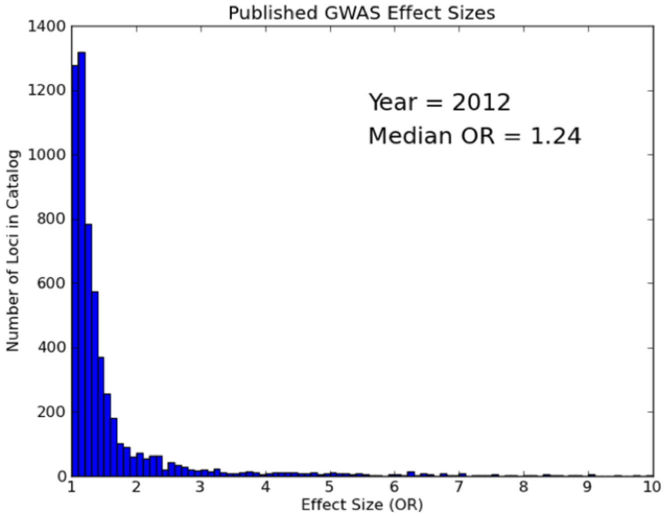


Figure 1.1: Histogram of of odds ratios from all entries in the GWAS catalog through 2012. Large effects are rare, while the number of small effects discovered relates largely to the statistical power of the GWAS studies undertaken.

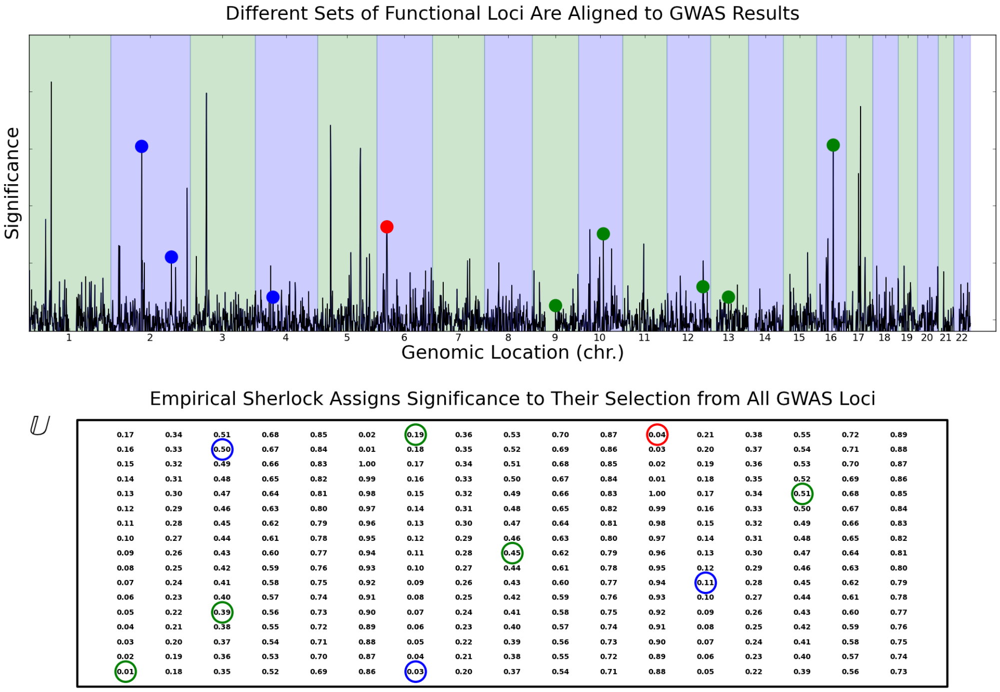
Second, work in model systems indicates that an accumulation of small effects can explain most heritability for some traits. For example, association studies performed in a panel of yeast segregants may achieve much higher statistical power than typical human GWAS. In a study of 46 traits, the inclusion of small effect loci enabled between 72% and 100% of the narrow-sense (additive) heritability to be explained.[9] Although epistasis appeared to contribute to phenotypic variation for many traits, additive effects constituted the dominant component of broad-sense heritability in most cases. For highly additive traits, it was possible to predict trait values using genotypes, but only when very small effect loci were included.

Lastly, recent efforts have demonstrated that the phenotypic variance explained by all SNPs in human GWAS, when considered in aggregate, can be significantly higher than that of just the top SNPs and may approach the heritability estimates of twin and pedigree studies.[3] For example, the heritability of human height is approximately 0.8, while the phenotypic variance accounted for by 180 top GWAS SNPs is only 0.1.[10] When all SNPs in a human height GWAS are considered simultaneously using mixed linear models, the variance explained approaches 0.5.[7] Similar results are reported for body mass index, QT interval, Schizophrenia, and other phenotypes.[11] [12] Although such approaches do not provide mechanistic insight, they suggest that one-half to one-third of the additive genetic variation in a population is actually tagged by common GWAS SNPs.[3]

With these issues in mind, we recently developed a Bayesian approach, named Sherlock, to mining all SNPs from GWAS using eQTL in various tissues.[13] Unlike predicate efforts, it makes use of both cis and trans eQTL loci, grouping multiple weak variants to implicate specific genes even in the absence of proximal disease associations.[14] [15] The eQTL data used are from healthy cohorts completely separate from the GWAS study, as opposed to alternate methods.[16] We demonstrated an enrichment for known and plausible disease genes in two GWAS and noted that, although the individual supporting SNPs may fall well-below genome-wide significance, they collectively provide sufficient statistical power to implicate the genes. This is consistent with observations that GWAS loci of modest effect can reside in regulatory regions with strong control over trait susceptibility that may represent ideal therapeutic targets.[17] [18] By aggregating SNPs and linking them to specific molecular functions, Sherlock provides insights that are absent from the top GWAS results considered in isolation. Much like its namesake detective, it collects numerous small clues to implicate the actual culprits responsible for complex disease and other polygenic traits.

Despite its promise, using Sherlock in practice necessitates careful attention when new GWAS or eQTL data sets are encountered. Various prior probabilities and cohort estimates are required, and a number of assumptions regarding the statistical properties of the input data are made. In particular, Sherlock's p-value calculation for the significance of GWAS and eQTL pattern overlap assumes that the null distribution for each locus is uniform. While small, low-powered studies may closely track a uniform distribution, real-world GWAS meta-analyses can exhibit significant inflation due to stratification and imputation artifacts, in addition to strong associations (and linked associations) from the study phenotype. This may cause an overestimation of a gene's statistical significance and systematic inflation of output p-values. An additional concern is the potential for inflation due to dependence between genes in an eQTL study. Sherlock makes an implicit assumption of independence between the genes it tests, and chance overlap of significant GWAS SNPs with pleiotropic eQTL loci — those affecting the expression of dozens or hundreds of genes — may violate this and yield false discoveries.

Here we present a more general solution to the multi-locus functional data mining problem called Empirical Sherlock. The core method involves essentially no tunable parameters and makes no assumptions regarding the distribution of input GWAS p-values. It constitutes a robust, general-purpose approach to testing function-trait associations using information gleaned from all GWAS SNPs, not just the top hits. After grouping GWAS loci using independent measures of molecular function, Empirical Sherlock calculates the significance of selecting these functional subsets from the pool of all GWAS SNPs. By using a simple scoring function and null distributions derived from the input GWAS, it enables a set-based test for trait association that avoids the strict thresholds required for single-SNP association under genome-wide significance. When applied to eQTL data, it recasts Bayesian Sherlock's pattern matching as a test of whether the SNPs that influence the expression of a given gene are collectively associated with the GWAS phenotype. Although demonstrated here using an array of eQTL tissue types, the method is applicable whenever genome-wide functional information can be used to group specific sets of GWAS loci together.



0.17	0.34	0.51	0.68	0.85	0.02	0.19	0.36	0.53	0.70	0.87	0.04	0.21	0.38	0.55	0.72	0.89
0.16	0.33	0.50	0.67	0.84	0.01	0.18	0.35	0.52	0.69	0.86	0.03	0.20	0.37	0.54	0.71	0.88
0.15	0.32	0.49	0.66	0.83	1.00	0.17	0.34	0.51	0.68	0.85	0.02	0.19	0.36	0.53	0.70	0.87
0.14	0.31	0.48	0.65	0.82	0.99	0.16	0.33	0.50	0.67	0.84	0.01	0.18	0.35	0.52	0.69	0.86
0.13	0.30	0.47	0.64	0.81	0.98	0.15	0.32	0.49	0.66	0.83	1.00	0.17	0.34	0.51	0.68	0.85
0.12	0.29	0.46	0.63	0.80	0.97	0.14	0.31	0.48	0.65	0.82	0.99	0.16	0.33	0.50	0.67	0.84
0.11	0.28	0.45	0.62	0.79	0.96	0.13	0.30	0.47	0.64	0.81	0.98	0.15	0.32	0.49	0.66	0.83
0.10	0.27	0.44	0.61	0.78	0.95	0.12	0.29	0.46	0.63	0.80	0.97	0.14	0.31	0.48	0.65	0.82
0.09	0.26	0.43	0.60	0.77	0.94	0.11	0.28	0.45	0.62	0.79	0.96	0.13	0.30	0.47	0.64	0.81
0.08	0.25	0.42	0.59	0.76	0.93	0.10	0.27	0.44	0.61	0.78	0.95	0.12	0.29	0.46	0.63	0.80
0.07	0.24	0.41	0.58	0.75	0.92	0.09	0.26	0.43	0.60	0.77	0.94	0.11	0.28	0.45	0.62	0.79
0.06	0.23	0.40	0.57	0.74	0.91	0.08	0.25	0.42	0.59	0.76	0.93	0.10	0.27	0.44	0.61	0.78
0.05	0.22	0.39	0.56	0.73	0.90	0.07	0.24	0.41	0.58	0.75	0.92	0.09	0.26	0.43	0.60	0.77
0.04	0.21	0.38	0.55	0.72	0.89	0.06	0.23	0.40	0.57	0.74	0.91	0.08	0.25	0.42	0.59	0.76
0.03	0.20	0.37	0.54	0.71	0.88	0.05	0.22	0.39	0.56	0.73	0.90	0.07	0.24	0.41	0.58	0.75
0.02	0.19	0.36	0.53	0.70	0.87	0.04	0.21	0.38	0.55	0.72	0.89	0.06	0.23	0.40	0.57	0.74
0.01	0.18	0.35	0.52	0.69	0.86	0.03	0.20	0.37	0.54	0.71	0.88	0.05	0.22	0.39	0.56	0.73

Figure 1.2: Top Row: Specific sets of genome-wide loci are implicated in molecular functions red, green, and blue through ENCODE, eQTL, or other independent data sets. These may align to GWAS loci with specific p-values for trait association, as indicated. Bottom Row: Empirical Sherlock tests the significance of the collection of GWAS p-values for each molecular function against chance selection from $\mathbb{U}$, the universal set of all independently-sorting GWAS loci. The method accurately accounts for wide variation in the size of functional sets and makes no assumptions regarding the underlying distribution of GWAS p-values.

Conceptually, the method is similar to Fisher's combined probability test, but it is architected to permit the use of an empirically-derived null distribution and empirical corrections when dependence between the functional elements is known.[19] It uses independently-segregating SNPs from the complete set of GWAS results to define a universal p-value set $\mathbb{U}$, from which subsets of p-values for functionally-linked loci are selected. This is illustrated in Figure 1.2, with the molecular functions red, green, and blue mapped to specific subsets of GWAS loci. If, for example, the green function is known, through independent means, to overlap five specific loci in the GWAS, Empirical Sherlock computes the significance of drawing this subset from $\mathbb{U}$ using a null distribution for any five loci drawn randomly from $\mathbb{U}$. By performing such calculations accurately, across sets of widely-varying size, from one to many hundreds of loci, without the use of tunable parameters or assumptions regarding the distribution of $\mathbb{U}$, Empirical Sherlock constitutes a robust, versatile method for mining GWAS results using a diverse collection of functional assays.

Traditional approaches to statistical testing were developed in an era prior to the advent of computers when only a small number of tests (e.g. fewer than ten) were typically made, necessitating reliance on assumed, theoretically-derived null distributions. When many samples of the input test statistic are available, as with the hundreds of thousands of SNPs in a typical GWAS, the use of an empirically-derived null distribution can prove appreciably more accurate.[20] This makes Empirical Sherlock highly resistant to false inflation, regardless of artifacts present in the input GWAS due to population stratification, the specifics of the association test, or other reasons. It also makes it easy-to-use and less-prone to error, as there is no need to adjust parameters based on specific study criteria. By achieving consistently low inflation, our method is particularly well-suited for large-scale GWAS data mining, where an input association study is analyzed using many potentially-informative molecular traits. These could include eQTL from dozens of primary human tissues through GTEx or many hundreds of traits available through ENCODE. With inflation well-controlled, it becomes feasible to incorporate a diverse collection of molecular traits into a pipeline and simply correct for the number of tests performed. Otherwise, if system parameters and improper assumptions interact in unpredictable ways to inflate the output, the problem of false positives is greatly exacerbated. Given that it is difficult to know *a priori* which tissues or molecular traits are relevant for a specific disease, our goal is a pipeline that automatically provides a robust indicator of disease association for many tissues and molecular traits — thereby discouraging guessing as strategy to reduce false discovery.

Chapter 2

Bayesian Sherlock Method

Our initial strategy for mining small effects in GWAS, named Sherlock, uses a Bayesian framework with tissue-specific eQTL to test the hypothesis of gene-phenotype association.[13] Unlike predicate efforts, it incorporates trans eQTL loci that are often ignored due to their typically smaller effect size and poor reproducibility.[15] [21] Since it computes the significance of GWAS-eQTL pattern matching using multiple loci – often several dozen or more – the alignment between GWAS and eQTL can be highly significant and indicative of trait-gene associations operating entirely through trans loci. In this chapter, we derive the original Sherlock method and discuss its use and performance with real data sets. In theory, this approach could be extended to work with other genome-wide functional indicators like ENCODE tracks, but the number of tunable parameters involved and performance problems when only a single locus or large numbers of loci are involved make this impractical. The original Sherlock method represents an important milestone in the development of a more general approach to functional, multi-locus GWAS data mining. It is described here in part to motivate the development of Empirical Sherlock — a general-purpose scheme that makes no assumptions regarding the input distribution and avoids the use of tunable parameters — in subsequent chapters of this thesis.

2.1 *Model Derivation*

Given a specific gene in an eQTL data set and GWAS data for a trait or disease of interest, Sherlock determines the statistical significance of the overlap in their genome-wide patterns of association. When loci strongly associated with expression of the gene match GWAS loci that show a pattern of association unexpected by chance, it may indicate a causal role for the gene in the phenotype. Thus, our input data consists of p-values for the eQTL of the gene, denoted as vector $\mathbf{x}$, and p-values for the GWAS, denoted as vector $\mathbf{y}$. We use binary indicator variables U_i and V_i to indicate association of SNP i with the expression and disease traits, respectively. Our goal is to use $\mathbf{x}$ and $\mathbf{y}$ to test hypotheses H_0, that the gene is not associated with the disease, and H_1, that the gene is associated with the disease. We do this using a Bayesain framework to determine the ratio of the probability of vectors $\mathbf{x}$ and $\mathbf{y}$ under H_1 (gene-disease association) and under H_0 (no gene-disease association). We use the posterior ratio:

$$\frac{P(H_1|x,y)}{P(H_0|x,y)} = \frac{P(H_1)}{P(H_0)}\frac{P(x,y|H_1)}{P(x,y|H_0)} \tag{2.1}$$

When only a small fraction of the molecular functions tested (e.g. genes in a large eQTL data set), the prior ratio of H_1 and H_0 (first term) can assumed to be small, although this may not hold in the most general case. The ratio of model evidence (second term) is the Bayes factor based on the probability of GWAS and functional data under H_1 and H_0. Here we describe our procedure for calculating the Bayes factor for each gene in our input functional data set. Assuming independence between the individual SNPs supporting each gene, the gene-level Bayes factor is simply the product of the SNP-level Bayes factors:

$$B_{gene} = \prod_{i=1}^{N} B_i = \prod_{i=1}^{N} \frac{P(x_i, y_i|H_1)}{P(x_i, y_i|H_0)} \tag{2.2}$$

As disused previously, independence is enforced through filtering or aggregating of input SNPs based on proximity, linkage, or both. The likelihood function for each SNP for a given hypothesis (H_1 or H_0) is determined by summing over hidden variables U_i and V_i

$$P(x_i, y_i|H) = \sum_{U_i,V_i} P(U_i)P(V_i|H,U_i)P(x_i|U_i)P(y_i|V_i) \tag{2.3}$$

where U_i is a Bernoulli random variable with success probability α, the prior probability of a SNP being associated with the expression trait. Likewise, V_i is a Bernoulli random variable with success probability β, the prior probability of a SNP being associated with the trait phenotype. We may use these hidden variables to separate the SNP-level Bayes factors in Equation 2 into gene expression and phenotypic trait components

$$B_{i,x} = \frac{P(x_i|U_i = 1)}{P(x_i|U_i = 0)} \qquad B_{i,y} = \frac{P(y_i|U_i = 1)}{P(y_i|U_i = 0)} \tag{2.4}$$

We use these below to simplify the expression for the Bayes factor of the i^{th} SNP. To derive this, we note that under the null hypothesis of no gene-disease relationship (H_0) the GWAS and eQTL data sets are independent and the likelihood function is

$$P(x_i, y_i|H_0) = P(x_i|H_0)P(y_i|H_0) \tag{2.5}$$

where the probability of the GWAS and eQTL summary statistics is given by

$$P(x_i|H_0) = (1-\alpha)P(x_i|U_i = 0) + \alpha P(x_i|U_i = 1) \tag{2.6}$$

$$P(y_i|H_0) = (1-\beta)P(y_i|V_i = 0) + \beta P(y_i|V_i = 1) \tag{2.7}$$

Under the alternate hypothesis (H_1) of non-random alignment between the GWAS and eQTL data sets the likelihood function is

$$P(x_i, y_i|H_1) = (1-\alpha)P(x_i|U_i = 0)P(y_i|H_0) + \alpha P(x_i|U_i = 1)P(y_i|V_i = 1) \tag{2.8}$$

The ratio of these likelihood functions under the two different hypotheses is the SNP-level Bayes factor from Equation 2:

$$B_i = \frac{P(x_i, y_i|H_1)}{P(x_i, y_i|H_0)} = \frac{(1-\alpha)P(x_i|U_i = 0)P(y_i|H_0) + \alpha P(x_i|U_i = 1)P(y_i|V_i = 1)}{P(x_i|H_0)P(y_i|H_0)}$$

This can be simplified by substituting the separate expression and phenotype Bayes factor components from Equation 3:

$$B_i = \frac{(1-\alpha)\frac{P(x_i|U_i=0)}{P(x_i|U_i=1)}}{\alpha + (1-\alpha)\frac{P(x_i|U_i=0)}{P(x_i|U_i=1)}} + \frac{\alpha\frac{P(x_i|U_i=1)}{P(x_i|U_i=0)}\frac{P(y_i|V_i=1)}{P(y_i|V_i=0)}}{[(1-\alpha)+\alpha\frac{P(x_i|U_i=1)}{P(x_i|U_i=0)}][(1-\beta)+\beta\frac{P(y_i|V_i=1)}{P(y_i|V_i=0)}]}$$

To reveal the final form:

$$B_i = \frac{1-\alpha}{1-\alpha+\alpha B_{i,x}} + \frac{\alpha B_{i,x}}{1-\alpha+\alpha\beta_{i,x}} \cdot \frac{B_{i,y}}{1-\beta+\beta B_{i,y}} \tag{2.9}$$

Thus, the Bayes factor for each gene tested depend only on the prior probability of SNP association with an expression trait (α), the prior probability of a SNP association with the phenotype (β), and the SNP-level Bayes factors for the expression and phenotype traits.

2.2 *Model Behavior and Parameter Estimation*

Here, to gain insight into the model, we examine the behavior of the gene-level Bayes factor in response to various combinations of strong or weak SNP-level associations in the GWAS and eQTL data. In Equation 2, if we use the logarithm of the SNP-level Bayes factors as our base score, the overall gene score becomes the sum of the individual SNP log Bayes factors.

Since prior probabilities α and β in Equation 9 are typically 0.01 or less, when a SNP is not associated with expression of a given gene, $B_{i,x} < 1$ and $\alpha B_{i,x} << 1$. Thus, regardless of the GWAS SNP significance, the score $S_i = log(B_i) \approx 0$, as expected.

Alternatively, when the eQTL SNP is very significant, $\alpha B_{i,x} >> 1$, and the score may be approximated as

$$S_i = log(B_i) = log\left(\frac{B_{i,y}}{1 + B_{i,y}}\right)$$

When the GWAS SNP is highly significant $\beta B_{i,y} >> 1$ and $S_i \approx log(1/\beta)$. This is a positive number that contributes to a higher gene-level Bayes factor but is bounded such that even very small GWAS p-values add no more than $log(1/\beta)$ to the gene score. Alternatively, when the GWAS SNP is not significant, $B_{i,y} < 1$ and $S_i \approx log(B_{i,y}) < 0$. This negative score represents reduced evidence of gene-phenotype association. In this manner, the gene-level log Bayes factor score comprises a number of SNP-level Bayes factors equal to the number of significant eQTL loci for the gene of interest. When the sum of these is approximately zero, it indicates that, in aggregate, the alignment between GWAS and eQTL data is unremarkable. When the sum of these is greater than zero, it indicates an alignment that favors the gene-disease association hypothesis (H_1) over the hypothesis of no gene-disease association (H_0).

Clearly, the selection of realistic values for the α and β priors is necessary for the proper determination of Bayes factors. Consistent with previous efforts, we estimate these based on an assumption of tag SNPs spread uniformly across the genome.[22] Assuming 1×10^6 SNPs spread across a genome of 3×10^9 base pairs, there are approximately 10^3 SNPs within ± 1 Mb of a gene start site. Assuming a single eQTL SNP in cis for each gene, we use a prior probability of $10^3/10^6 = 10^{-3}$ for α for cis association. When the eQTL SNPs is not proximal to the gene, we assume that it is one of many trans loci that association with the gene's expression. If genes have 50 trans loci on average, then the prior probability of trans association is $\alpha = 50/10^6 = 5 \times 10^{-5}$. For the prior probability of SNP association with the phenotype, we select $\beta = 10^{-3}$ based on the recognition that complex traits are likely associated with hundreds of loci.[10]

2.3 *Statistical Significance of Gene Bayes Factors*

To compute the statistical significance of gene Bayes factors, we employ a Bayes/non-Bayes compromise.[23] With this approach, a null distribution of possible gene Bayes factors is constructed through multiple randomizations of the GWAS case/control data. The gene's p-value is then estimated from its ranking in the collection of simulated Bayes factors. For efficiency, we use a proceed that approximates the results of random swapping of GWAS cases and controls.[24] The eQTL SNPs in haplotype block are sampled with a multivariate normal random vector with covariance that matches the linkage structure of the block. We permute only the GWAS data, since the structure inherent in eQTL and the absence of full summary statistics for most studies make preclude an easy bi-directional treatment. For each gene in our results, we report both the gene log Bayes factor (LBF) and the p-value from this procedure. Due to the finite number of permutations used, the minimum estimated p-value is approximately 1×10^{-7}.

2.4 *Summary of Results: Crohn's Disease*

We performed an analysis of a moderately-powered Crohn's disease GWAS using lymphoblastoid eQTL and attempted to replicate the results using a larger meta Crohn's GWAS [25] [26] [27] The top genes discovered using Bayesian Sherlock are listed in Table 2.1. Of these, three genes — ORMDL3, PTGER4, and SLC22A5 — were reported in the original GWAS paper and are supported by additional studies.[25] [28] These genes are discovered here through strong cis loci, as is expected for any gene that has been previously implicated directly using GWAS alone. The remaining genes in Table 2.1 are implicated entirely through trans loci, with the exception of UBE2L3 which is supported by both cis and trans loci.

The gene UBE2L3 has been implicated in numerous other autoimmune diseases, including systemic lupus erythematosus, celiac disease, and rheumatoid arthritis.[29] It was also implicated through an eQTL analysis of Crohn's GWAS results using only the cis loci. Here, we find supporting SNPs in both cis and trans.[14] The gene EFS has not been associated with Crohn's disease in humans, but knockout of the mouse homolog Efs yields an exaggerated T-cell mediated immune response and inflammatory lesions in the small intestine similar to Crohn's.[30] Additionally, the target of EFS, the kinase FYN, is marginally significant ($p = 9.2 \times 10^{-4}$) in our gene list, supported by separate trans loci.

Two other genes in the list have well-established immune functions and probable relations to autoimmune disease and IBD. IK encodes a cytokine that down regulates a class II MHC antigen whose aberrant expression is associated with autoimmune disease.[31] LYNX1 encodes a signaling peptide of nicotinic acetylcholine receptors (nAChR), a system that regulates the development and activation of T and B cells.[32] Smoking has been shown to affect IBD through $\alpha 7$ nAChR, a target of LYNX1, in a manner that ameliorates ulcerative colitis but exacerbates Crohn's disease.[33] Additionally, agonists of $\alpha 7$ nAChR affect disease severity in a murine model for colitis.[34]

All genes listed in Table 2.1 replicate when using a separate Crohn's GWAS at the level of $p < 0.05$, with the exception of IK.[26] Half of them (5 of 10) rank within the top 13 genes when combining the same GWAS and eQTL using our Empirical Sherlock method, with most of the discrepancy likely due to differing assumptions regarding linkage.

Gene	LBF	p-value	GWAS Hit	Supporting Evidence	p-value (rep.)
UBE2L3	7.8	2.2×10^{-6}	No	associated with celiac disease, rheumatoid arthritis, and lupus	4.2×10^{-6}
ORMDL3	5.7	3.3×10^{-5}	Yes	previously associated with Crohn's disease and ulcerative colitis	1.0×10^{-6}
PTGER4	5.6	3.7×10^{-5}	Yes	associated with Crohn's disease through GWAS	3.4×10^{-6}
IK	5.4	4.3×10^{-5}	No	regulates class II MHC antigen, which is associated with autoimmune diseases	7.5×10^{-1}
LYNX1	5.3	4.8×10^{-5}	No	agonist of non-neuronal nAchR pathway, which may be important for IBD	1.4×10^{-2}
NUDT4	5.3	4.8×10^{-5}	No	NA	3.4×10^{-5}
EFS	5.2	6.1×10^{-5}	No	knock-out mice exhibit symptoms similar to human Crohn's disease	3.9×10^{-2}
FAM96A	5.2	6.3×10^{-5}	No	NA	4.2×10^{-6}
SLC22A5	5.2	6.3×10^{-5}	Yes	previously associated with Crohn's disease	3.8×10^{-5}
ANAPC2	4.9	9.2×10^{-5}	No	NA	6.0×10^{-4}

Table 2.1: Top genes from Bayesain Sherlock analysis of Crohn's GWAS. Most genes replicate using a higher-power Crohn's study.

2.5 *Summary of Results: Type 2 Diabetes*

We performed a similar analysis using a Type 2 Diabetes GWAS and liver eQTL.[35] [36] Of the four genes shown in Table 2.2 at at $p < 10^{-4}$, two were previously implicated in T2D through GWAS and are discovered here through strong cis loci: TSPAN8 and JAZF1. The genes PRUB and GNB5 have not previously been implicated in T2D through GWAS, but other studies reveal these to be plausible candidate T2D genes. The expression of the mouse homolog Purb in multiple tissues (liver, adipose, muscle, and islet) has been shown to influence a number of metabolic phenotypes including fat mass, fat-to-body-weight ratio, glucose level, insulin level, glucose-to-insulin ratio, and oral glucose tolerance in mouse crosses.[16] [37] [38] [39] For the gene GNB5, haploinsufficiency (single copy deletion) of the mouse homolog caused late-onset obesity, insulin resistance, and liver steatosis — phenotypes strongly resembling human metabolic syndrome and T2D.[40] In addition, the closely-related gene GNB3 is associated with obesity, insulin resistance, and glucose tolerance in humans; it is one of the few genes shown to influence all of these traits simultaneously.[41]

Gene	LBF	p-value	GWAS Hit	Supporting Evidence
TSPAN8	6.1	9.4×10^{-6}	Yes	associated with T2D through GWAS
PURB	6.1	9.4×10^{-6}	No	expression is linked to T2D-related phenotypes
GNB5	5.0	8.9×10^{-5}	No	deletion leads to T2D symptoms
JAZF1	4.9	9.5×10^{-5}	Yes	associated with T2D through GWAS

Table 2.2: Top genes from Bayesain Sherlock analysis of T2D GWAS.

Chapter 3

Empirical Sherlock Method

Although Sherlock represents an important advance in our ability to aggregate trait associations and map them to molecular function, it incorporates various assumptions and prior probabilities that necessitate careful attention when new GWAS or eQTL are encountered. Chief among these is the assumption that the null distribution for each locus is uniform. As shown in Figure 3.1 (blue data), intentional violation of this assumption through artificial inflation of the top GWAS SNPs yields false inflation of output genes. This is particularly problematic, as significant inflation due to population stratification, imputation, and other issues is common in real-world GWAS. In addition, Sherlock assumes no dependence between functional elements (genes), an assumption that can be violated through chance alignment of significant GWAS SNPs and pleiotropic eQTL loci — those affecting the expression of dozens or hundreds of genes (Figure 3.1, green data). As discussed previously, Empirical Sherlock is designed to avoid false inflation by forming null distributions using the actual distribution of GWAS p-values. It requires essentially no tunable parameters and makes no assumptions concerning the form of the input data. In addition, it includes a provision for adjusting the distributions based on known dependencies between functional elements.

3.1 *Method Overview*

When testing the significance of a set of n functionally-related loci in a given GWAS, Empirical Sherlock uses a simple scheme to compute a score for the n p-values of the GWAS SNPs that best tag these loci. It then uses a convolution-based approach to construct an empirical null distribution for n p-values drawn randomly from the full set of GWAS p-values. Together, these are used to compute a p-value of association for the molecular function (e.g. expression of a specific gene in a given tissue) in the the GWAS. In certain instances, particularly with eQTL for many genes in a given tissue sample, this test may be performed repeatedly for

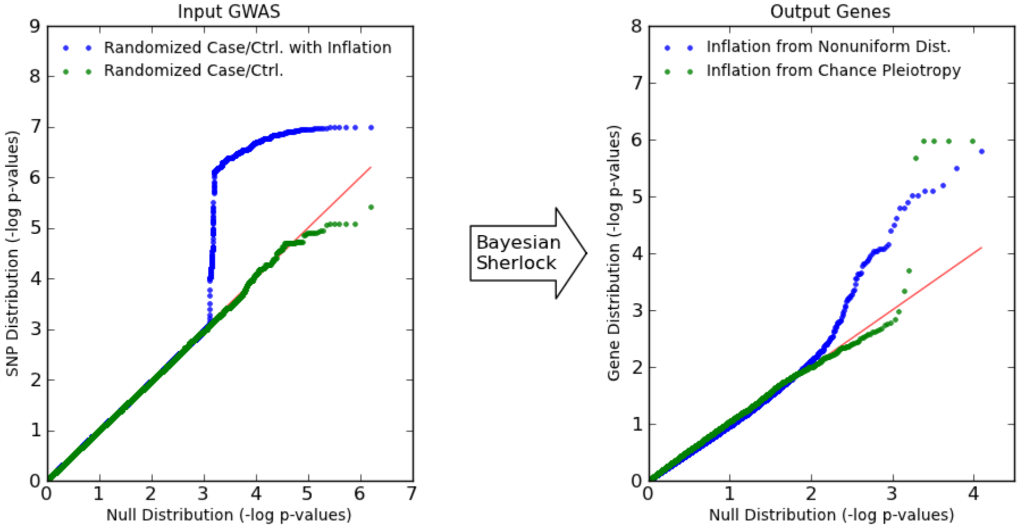


Figure 3.1: Violation of key Sherlock assumptions may yield false inflation of randomized case-control data, where zero inflation is expected: Artificial inflation of the top GWAS SNPs causes systematic inflation of output genes (blue data). Coincident overlap of significant GWAS SNPs and pleiotropic genes causes inflation of top results (green data). Empirical Sherlock is constructed to avoid these issues.

all functional elements in a study. If dependence between the sets of functional elements in a data set is detected — for example, due to pleiotropic loci that regulate many genes — a provision of adjusting the null distribution is included. Through extensive testing and simulation, we show that our empirical strategy produces a test statistic that highly resistant to false inflation. In this section, we describe the individual components of the Empirical Sherlock method in detail in the order in which they occur.

3.2 *Identifying Tag SNPs for Independent Blocks*

Empirical Sherlock is predicated on the assumption that the collection of SNPs tested are tagging independently segregating haplotype blocks in both the GWAS and eQTL cohorts. Understanding the true block structure of the cohorts is critical to accurately estimating gene significance. The inadvertent inclusion of dependent blocks can inflate the significance of genes by over-counting true associations; conversely, a conservative approach that enforces wide separation between tagging SNPs may miss many independent functional loci. The preferred approach to identifying independent blocks requires genotypes for both the GWAS and functional data to define block boundaries based on regions of rapid decay in linkage disequilibrium (LD).[42] However, since the difficulty of obtaining genotypes across an array of studies makes this impractical, we constructed a database of LD using Caucasian cohorts from the 1000 Genomes Project.[43] We use PLINK (v1.07) to compute r^2 linkage between common SNPs for 379 individuals in the CEPH, CEU, TSI, GBR, FIN, and IBS cohorts of 1000 Genomes release v3.20101123.[44] This permits the alignment of associated loci in the functional data to corresponding SNPs in GWAS data, and it enables the identification of independently-segregating tag SNPs in the combined data for use in the statistical test.

We first align the GWAS SNPs to all the loci present in a given functional data set that pass a specific threshold. For the eQTL data used here, the nominal threshold is typically SNP p-values $< 10^{-5}$. In other cases, this threshold could take the form of DNA binding affinity or essentially any criteria that can be used to assemble a set of functionally-related loci. If matching SNPs are not present in both data sets, we use the closest GWAS SNPs in r^2 LD > 0.85, if available. We then use an agglomerative clustering approach to identify non-overlapping blocks of SNPs in r^2 LD > 0.2.[45] From each block, the functional SNP with the strongest association is selected as a tag, and its corresponding GWAS SNP is included in the set subjected to statistical test. Since discrepancies between the various cohorts — GWAS, functional, and linkage — are inevitable, a minimum 100 kb distance between tag SNPs is enforced. In addition, we exclude SNPs from the human leukocyte antigen (HLA) region between 6p22.1 to 6p21.3 due to its complex linkage structure. Genes in the HLA are retained in the data and may appear in our top results through their trans eQTL loci.

3.3 *Core Statistical Method*

Once a set of GWAS SNPs related to a specific molecular function is identified, we compute a score s by simply combining their log p-values:

$$s = -\sum_{i=1}^{n} log_{10}(p_i) \tag{3.1}$$

This converts our collection of SNPs into a scalar quantity that, when referenced against the appropriate null distribution, indicates the statistical significance of selecting this subset from the pool of all independent GWAS loci. Our approach is analogous to Fisher's combined probability test using the scoring function $-2\sum_{i=1}^{n} log_e(p_i)$ which follows a χ^2 distribution with $2n$ degrees of freedom when p-values are drawn from a uniform distribution on (0,1).[46] With our method, instead of assuming a particular form for the distribution of GWAS p-values, we use discrete convolution to compute an empirically-derived distribution of scores when combining n p-values. Since s represents a specific score, we let S represent a random variable of all possible scores. We form the discrete probability distribution function (PDF) of S using bins of width b log units, where the probability of scores in the range $0 \leq s < b$ is the first element, $b \leq s < 2b$ is the second element, and so forth. Thus, $f_n[s] = P(S = s)$ is the discrete PDF for a score comprising n independent GWAS p-values. For the simplest case of scores involving only a single SNP, the PDF $f_1[s]$ is essentially a normalized histogram of p-values for all independent (unlinked) SNPs in the GWAS:

$$f_1[k] = \frac{1}{N} \sum_{i=1}^{N} I\left[kb \leq -log_{10}(p_i) < (k+1)b\right] \tag{3.2}$$

where I is the indicator function, N is the total number of SNPs, b is the bin width, and $k = s/b$ is the array index. In typical use, the minimum GWAS p-value is truncated at 10^{-10}, well below genome-wide significance, yielding 100 bins when spacing $b = 0.1$ is used. This single-locus PDF forms the basis from which null distributions for any arbitrary number of functionally-related loci are formed. Since the sum of two independent random variables has a PDF equal to the convolution of their individual probability distributions, scores involving two GWAS p-values have PDF $f_2 = f_1 * f_1$. In the general case for any value of $n > 1$, the PDF $f_n[s]$ is formed from $n - 1$ recursive convolutions of $f_1[s]$:

$$f_n[k] = \sum_{l=0}^{k} f_1[l] \cdot f_{n-1}\left[k - l\right] \tag{3.3}$$

where again $k = s/b$ is the array index and any array elements outside the possible score range are zero by definition. For the special case of a truly uniform p-value distribution, we may construct an exact continuous solution to the recursive convolution for n p-values:

$$f_n(s) = ln(10)^n \prod_{i=0}^{n-1} \frac{1}{i} s^{n-1} 10^{-s} \tag{3.4}$$

The derivation of equation 3.4 is provided in Appendix A. To motivate the use of our empirical approach, we compare this theoretical result to our empirical method for GWAS of differing power. For low-powered association studies with p-value distributions close to uniform, the tails of the distributions are similar, leading to roughly identical estimates of significance for a given score. For well-powered meta analyses that appear to contain inflation from various sources, significant differences in the distribution tails can lead to an appreciable overestimation of significance for high scores (Figure 3.3 in Performance Verification).

3.4 *Correcting for Pleiotropic and Sampling Effects*

Naively, the base score distribution $f_1[s]$ for a single SNP is constructed from the set of all independent p-values present in the input GWAS. However, if these include large numbers of imputed SNPs that do not align to those acutally genotyped in the functional assay (e.g. due to the use of primarily HapMap SNPs on microarrays), false inflation may occur. To avoid such problems, we typically form $f_1[s]$ from the set of all independently segregating SNPs that actually align to GWAS SNPs at least once across all elements in a given functional data set. For example, the set of all SNPs that align to eQTL for at least one gene across all genes in the collection (typically 10 to 15 thousand in a given tissue). This approach was used for the eQTL results we report here. Alternatively, both data sets could be imputed using identical cohorts and techniques, or if genotypes are unavailable, they could be trimmed to contain only the SNPs actually genotyped.

Another source of false inflation stems from a lack of true independence between functional elements across a given data set. For example, pleiotropic loci may appear to regulate hundreds of genes in the eQTL data for a given tissue. In our simulations, these loci may inflate the output test statistic due to chance alignment with significant GWAS SNPs; in our test matrix, this occurs at an appreciable level in perhaps five percent of the cases (see supplement). Since our method permits the use of a unique distribution f_1 for each p-value added to the score, it enables a simple scheme for reducing inflation by adjusting each distribution based on the number of functional elements affected by the locus. For the eQTL example, this involves conditioning the GWAS distribution based on the number of genes influenced by a locus across the entire eQTL data set. When chance alignment of pleiotropic loci and significant GWAS SNPs occurs, the overrepresentation of small p-values is reflected in the null distribution for affected genes. Thus, in practice, the actual distribution incorporated into an Empirical Sherlock score with eQTL data is conditioned on the number of genes that are regulated by the same locus:

$$f_{1|c}[k] = \frac{\sum_{i=1}^{n} I[kb \leq -log_{10}(p_i) < (k+1)b] \cap I[C_i = c]}{\sum_{i=1}^{n} I[C_i = c]} \tag{3.5}$$

where I is the indicator function, k is the index, b is the bin width, and the ith SNP is assigned gene count C_i while the locus in question has count c. Now the distribution contains only the p-values of SNPs that match the pleiotropy of the SNP being added to the score. With this change, instead of computing the significance of a set of SNPs drawn from GWAS, our method computes the significance of a set of SNPs drawn *given* their individual pleiotropies. In our simulations, this results in a minor change the significance and rank order of output genes in most cases but prevents systematic inflation whenever chance alignment of significant GWAS SNPs and pleiotropic loci occurs (see Results and supplement).

3.5 *Avoiding Arbitrary Thresholding of Functional Data*

Although our core method is parameter free, it uses sets of known functional loci as primary input. Since the assumptions used in forming these sets could bias the results in arbitrary ways, we employ a scheme to vary the set composition to minimize the importance of specific inclusion/exclusion criteria by scanning across a range of thresholds. For each gene in an eQTL, we select a range of eQTL SNP p-value thresholds, from 10^{-5} to 10^{-7} for loci genome-wide, plus 10^{-3} for loci in cis, defined here as within 1 Mb of the transcription start site. Gene significance is computed multiple times using different subsets of the aligned GWAS SNPs. From this collection of threshold-specific results, we select the smallest p-value, Bonferroni corrected, as the final gene p-value. Thus, by scanning across a range of thresholds, the importance of the specific criteria used to distinguish valid functional associations from background noise is minimized.

3.6 *Performance Verification*

Across a matrix of fifteen randomized case-control GWAS and six eQTL data sets, we note three instances of significant inflation due to chance alignment between highly pleiotropic eQTL loci and top GWAS SNPs. As shown in the top row of Figure 3.2, this may falsely suggest trait-gene association when pleiotropy is ignored. On the left, the PDF for each SNP in the convolution is $f_1[s]$, the unconditioned distribution of p-values in the universal set $\mathbb{U}$ for all independently-sorting GWAS SNPs. On the right, the individual PDFs are conditioned on the pleiotropy of each SNP added to the gene score. This reduces the systematic inflation in our examples, resulting in uniform output that falls within the 95% confidence envelope, as expected.

In general, uncorrected pleiotropic effects are secondary to inflation that stems from incorrect assumptions regarding the distribution of input GWAS p-values. Since Empirical Sherlock uses an empirically-derived null distribution, it is less prone to inflation than methods that assume various priors or specific theoretical forms for the distribution. In the bottom row of Figure 3.2, example Sherlock results (left side) exhibit marked inflation, while only the very highest ranked genes in Empirical Sherlock results (right side) exhibit elevated significance.

To understand the potential discrepancy between the uniform and empirical approaches, we calculate null

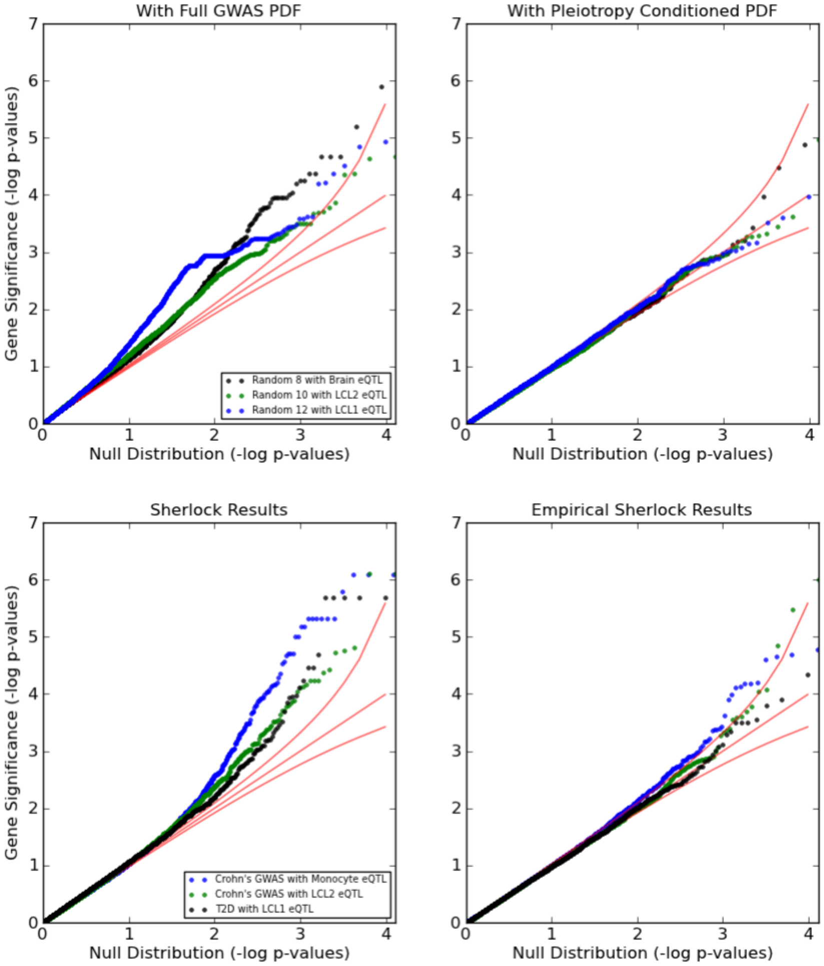


Figure 3.2: Top Row: The chance overlap of pleiotropic loci in functional data and significant SNPs from GWAS can result in improper inflation of output genes (left column). The use of PDFs conditioned on SNP pleiotropy brings the results of case-control randomization GWAS back towards the expected uniform output (right column). Bottom Row: Example results from our test data show reduced systematic inflation with Empirical Sherlock (right column) versus Sherlock (left column). Many fewer genes exceed the 95% confidence level (red envelope) when non-uniform GWAS and pleiotropy are properly accounted for.

distributions for functional data with one, three, and five SNPs in Figure 3.3. In blue are null distributions for our method when assuming a uniform distribution of GWAS p-values; in green are distributions derived from the actual distribution of p-values. On the left, a low-power GWAS yields right tails that closely match those under the uniform assumption and the discrepancy in an example gene p-value is small. On the right, a high-power GWAS can have markedly more strong associations than the uniform assumption, resulting in a discrepancy in the right tails and the example p-value.

In using Empirical Sherlock to mine GWAS with functional data sets, some spurious inflation of the test

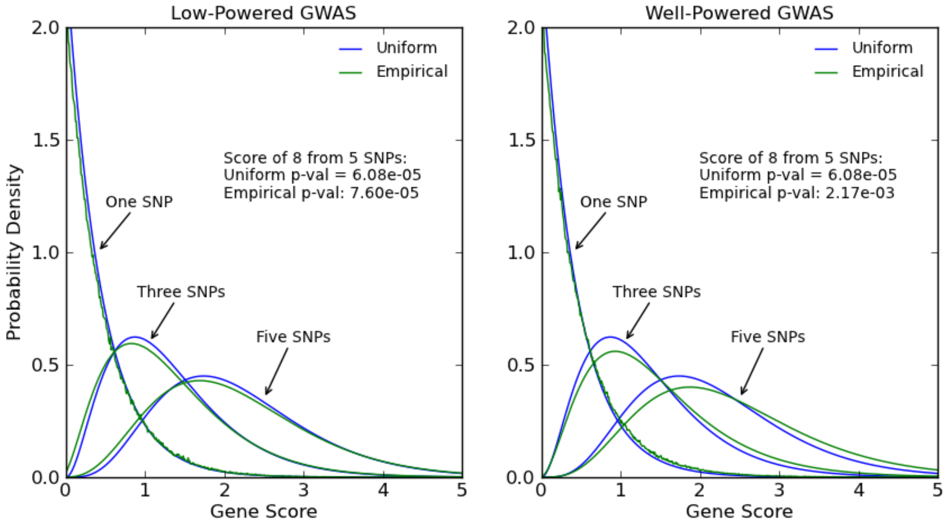


Figure 3.3: Top Row: For low-power GWAS, the uniform and empirical distributions may have similar tails and yield similar p-values (left column). For GWAS with inflation, the discrepancy in the null distribution tails, especially for mutli-SNPs genes, will yield substantial differences in the computed p-values (right column).

statistic will occur even if overall inflation of the output gene p-values is well controlled. To understand how this could affect decisions made in a high-throughput GWAS screening mode against large functional databases (for example, GTEx-derived eQTL), we constructed a matrix of 90 tests using randomized case-control GWAS: 15 false GWAS run against six eQTL data sets. We estimate the number of genes below a target false discovery rate (FDR) using the q-value approach of Storey.[47] We treat q-values below 0.25 as significant and tally the number of passing genes across our matrix, as shown in Table 3.4. From our simulations, this roughly corresponds to the point at which the distribution exceeds the 95% confidence interval for a uniform test statistic, as shown in Figure 3.4.

Across all GWAS and eQTL combinations, the average number of genes falsely implicated under these assumptions is 0.4 per test. We believe that this level of performance, especially when the results are further strengthened via a meta analysis across tissues, can provide the confidence necessary to devote resources towards validating the results of a computational screen.

GWAS	LCL1	LCL2	Monocyte	Adipose	Liver	Brain
random 1	0	2	0	2	1	0
random 2	0	2	0	0	0	0
random 3	1	1	1	0	0	0
random 4	0	0	0	1	1	0
random 5	0	1	1	0	0	1
random 6	1	0	1	0	0	0
random 7	0	0	2	0	0	0
random 8	0	0	0	0	1	2
random 9	1	0	0	0	1	0
random 10	0	1	0	0	0	1
random 11	0	0	0	0	0	0
random 12	0	0	0	1	0	0
random 13	4	0	0	0	0	0
random 14	1	1	1	1	1	0
random 15	0	0	3	0	0	0

Table 3.1: Using the q-value approach, we estimate the number of genes below a target FDR of 0.25 across our matrix of random GWAS and eQTL data sets. Since the GWAS are constructed through random assignment of case and control from 1000 Genomes data, any inflation present is spurious.

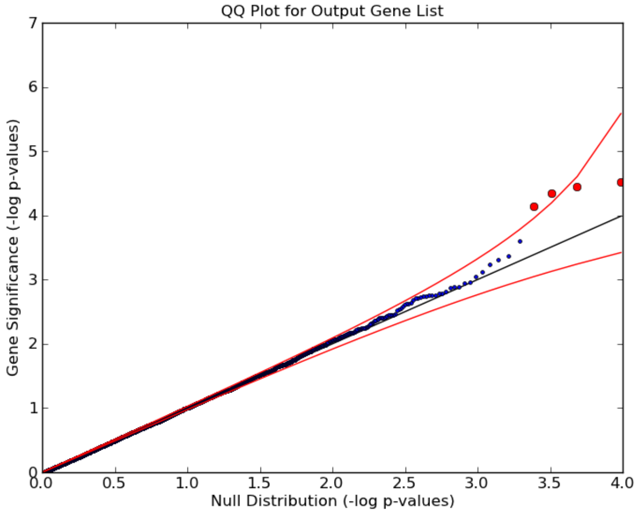


Figure 3.4: QQ plot for the worst case (GWAS random 13 with LCL1) identified in our test matrix: four marginally significant genes are found despite no real phenotype. Here, the q-value approach is used to distinguish significant genes (red circles) from non-significant genes (blue circles). As is typical, the overall distribution is well-behaved and bounded by the 95% confidence interval (red envelope). Even this rather minor level of top gene inflation is rare across our test matrix.

Chapter 4

Empirical Sherlock Analyses Using Multi-tissue eQTL

To demonstrate our method, we perform analyses using GWAS for Crohn's disease, type 2 diabetes (T2D), and schizophrenia. Since the Crohn's and T2D GWAS are from older, moderately powered meta analyses, they permit us to discover genes that are pre-validated through newer, better-powered studies. Since the schizophrenia GWAS used is from a large, unpublished meta analysis, we rely heavily on epidemiological studies of co-occurring disorders when interpreting the results. Our basic approach is similar for all three studies: First, we use Empirical Sherlock to compute gene p-values for all genes found across six eQTL data sets: two lymphoblastoid cell lines (LCLs), one primary monocyte, one liver tissue, one brain tissue, and one adipose tissue.[27] [48] [49] [36] [50] [51] Second, we rank the genes according to a meta analysis (Fisher's method) of their gene p-values from each eQTL data sets where the transcript was present. Since only partial overlap in gene regulatory networks across tissues is expected, we also seed the top results with genes having a p-value $< 10^{-4}$ in any single tissue. Next, we test these top-ranked genes for enrichment against categories of disease-associated genes using WebGestalt.[52] Finally, we discuss supporting evidence for the top genes not previously implicated in the disease of interest through GWAS. This may include evidence from published literature, pathway databases, or model systems. When possible, we also use the Mouse Genome Informatics (MGI) database of mutants and phenotypes to search for interesting validation targets.[53]

4.1 *Crohn's Disease*

Crohn's disease and ulcerative colitis are distinct phenotypes of inflammatory bowel disease (IBD [MIM 266600]), a chronic inflammatory disorder of the gastrointestinal tract that has been the subject of multiple, increasingly well-powered association studies.[54] [55] [56] [57] [58] [26] [25] Together these have implicated over 160 loci in IBD, explaining over 13% of the Crohn's disease variance.[55] Here we use our method with a moderately-powered Crohn's GWAS to boost its effective statistical power and identify genes previously found only in larger, higher-powered studies. This GWAS identified 22 probable Crohn's genes based on proximity to 31 replicated loci that pass a Boferroni $p < 0.05$ threshold for association.[25]

As shown in Table 4.1, our method identifies 41 genes with gene p-values below 10^{-4} in a single tissue or 10^{-2} in the meta analysis. Of these, only four were identified in the original GWAS: PTGER4, MST1, ATG16L1, and ORMDL3. The other known IBD genes (P4HA2, SLC22A4, SLC22A5, CARD9, UBE2L3, ZPBP2, ADO) were identified previously in GWAS with either twice the case cohort size or targeting a distinct cohort (e.g. Ashkenazim).[26] [57] Here, they are implicated through a combination of cis and trans loci, often across multiple tissues. For example, the gene P4HA2 is strongly implicated by cis loci in the Dixon LCL eQTL data set and no other, even though the transcript is present in 5 of 6 eQTL studies. The gene ZPBP2 is implicated entirely through cis loci in the Dixon LCL eQTL and entirely through trans loci in adipose eQTL. The gene SLC22A5 is implicated through a combination of both proximal loci and those over 1.5 MB from the gene's transcription start site in several data sets. A full list of supporting SNPs for the top Crohn's genes is provided in the supplement.

Our enrichment test for the top genes against categories of disease-associated genes is shown in Table 4.2. The most enriched disease categories are all related to IBD and similar intestinal inflammatory diseases, with Crohn's being the top hit. The enrichment is highly significant, with adjusted p-values of 2.7×10^{-12} to 1.6×10^{-6} (hypergeometric test). All supporting genes are drawn from the list of known IBD genes mentioned previously.

A survey of the remaining top genes — those not previously implicated through GWAS — reveals a number of plausible Crohn's genes, including several either previously implicated in IBD by other means or involving known diagnostic and therapeutic targets for Crohn's (e.g. TNF-α and IL6). The gene ZNF300P1 is implicated here through strong associations in liver eQTL at a GWAS locus that was subsequently mapped to the gene IRGM, although nine other candidate genes are nearby.[55] In a study of anti TNF-α therapy in pediatric IBD, variation in the gene BRWD1 was found most predictive of therapeutic response.[59] The gene MAPK8IP1 is an inflammatory pathway gene associated with survival in pancreatic cancer and with a putative role in type 2 diabetes.[60] [61] Here, it is strongly implicated via trans loci in the monocyte, Dixon LCL, and liver eQTL data sets, largely through a set of loci at 17q21. In a murine rheumatoid arthritis model, treatment with HYAL3 small interference RNAs (siRNAs) affected the release of inflammatory mediators

Gene	**Meta/Best p-value**	**Input Gene**	**Catalog Gene**	**Zeller (Monocyte)**	**Dixon (LCL)**	**Duan (LCL)**	**Schadt (Liver)**	**Myers (Brain)**	**Muther (Adipose)**
P4HA2	2.3×10^{-7}		Yes	NA	2.3×10^{-7}	5.7×10^{-1}	5.1×10^{-1}	5.9×10^{-1}	5.3×10^{-2}
AK096536	3.3×10^{-6}			NA	NA	NA	3.3×10^{-6}	NA	NA
PTGER4	3.3×10^{-6}	Yes	Yes	1.1×10^{-1}	3.3×10^{-6}	5.1×10^{-4}	4.4×10^{-1}	NA	7.9×10^{-1}
BRWD1	6.7×10^{-6}			5.2×10^{-1}	8.0×10^{-2}	8.3×10^{-1}	6.7×10^{-6}	NA	5.9×10^{-2}
ZFYVE16	1.1×10^{-5}			2.5×10^{-1}	3.4×10^{-1}	1.0	5.8×10^{-1}	5.6×10^{-1}	1.1×10^{-5}
DND1	1.4×10^{-5}			NA	1.4×10^{-1}	NA	1.4×10^{-5}	NA	8.7×10^{-1}
RBM6	1.4×10^{-5}			2.5×10^{-5}	1.4×10^{-5}	1.2×10^{-1}	7.2×10^{-1}	8.4×10^{-1}	5.6×10^{-1}
MAPK8IP1	1.7×10^{-5}			1.7×10^{-5}	4.0×10^{-4}	NA	1.3×10^{-4}	5.0×10^{-1}	NA
HYAL3	2.1×10^{-5}			2.1×10^{-5}	2.7×10^{-1}	9.7×10^{-2}	NA	NA	7.8×10^{-1}
SLC22A4	2.2×10^{-5}		Yes	2.2×10^{-5}	4.7×10^{-1}	NA	3.2×10^{-1}	8.7×10^{-2}	NA
SOX15	2.3×10^{-5}			1.8×10^{-2}	1.9×10^{-1}	NA	2.3×10^{-5}	5.8×10^{-1}	6.0×10^{-1}
PLEKHB2	3.3×10^{-5}			9.2×10^{-1}	9.6×10^{-1}	3.3×10^{-5}	6.5×10^{-1}	1.5×10^{-1}	1.8×10^{-2}
CLEC1B	6.3×10^{-5}			6.3×10^{-5}	4.1×10^{-1}	NA	1.0×10^{-1}	NA	5.9×10^{-1}
GAS6	6.4×10^{-5}			6.4×10^{-5}	2.6×10^{-1}	NA	3.4×10^{-1}	3.5×10^{-1}	2.9×10^{-1}
FALZ	6.6×10^{-5}			6.6×10^{-5}	NA	NA	4.1×10^{-1}	NA	NA
LRRC37A4	7.4×10^{-5}			7.4×10^{-5}	NA	NA	NA	NA	NA
USP4	7.9×10^{-5}			7.9×10^{-5}	4.1×10^{-1}	9.0×10^{-1}	4.7×10^{-2}	5.0×10^{-1}	8.3×10^{-1}
KCNJ13	8.5×10^{-5}			NA	8.5×10^{-5}	NA	8.6×10^{-1}	NA	7.7×10^{-1}
CDC42SE2	9.0×10^{-5}			3.8×10^{-4}	9.0×10^{-5}	2.8×10^{-1}	1.6×10^{-3}	NA	8.8×10^{-1}
SLC22A5	7.2×10^{-4}		Yes	1.0×10^{-4}	4.3×10^{-4}	6.9×10^{-2}	1.2×10^{-1}	3.1×10^{-1}	7.3×10^{-1}
CARD9	1.0×10^{-3}		Yes	2.0×10^{-3}	2.0×10^{-3}	4.9×10^{-3}	2.6×10^{-1}	7.0×10^{-1}	5.0×10^{-2}
UBE2L3	2.1×10^{-3}		Yes	1.4×10^{-3}	1.6×10^{-3}	1.1×10^{-3}	9.5×10^{-1}	8.0×10^{-1}	5.6×10^{-1}
BCAS3	2.4×10^{-3}			1.4×10^{-1}	5.1×10^{-1}	1.8×10^{-1}	3.1×10^{-3}	3.0×10^{-2}	1.2×10^{-3}
MST1	3.5×10^{-3}	Yes	Yes	1.3×10^{-3}	9.6×10^{-1}	NA	1.0×10^{-3}	NA	NA
SLC16A14	4.0×10^{-3}			NA	1.8×10^{-3}	NA	NA	NA	8.6×10^{-3}
ATG16L1	4.7×10^{-3}	Yes	Yes	9.5×10^{-1}	5.4×10^{-4}	6.1×10^{-1}	1.1×10^{-1}	1.5×10^{-3}	1.4×10^{-1}
ZPBP2	4.7×10^{-3}		Yes	NA	2.1×10^{-3}	NA	NA	NA	1.1×10^{-2}
CCNH	5.4×10^{-3}			5.4×10^{-3}	5.1×10^{-2}	1.0	2.0×10^{-1}	2.9×10^{-3}	4.0×10^{-1}
LIPG	5.9×10^{-3}			NA	2.3×10^{-1}	1.9×10^{-3}	4.6×10^{-3}	NA	2.6×10^{-1}
MOBK1B	7.0×10^{-3}			9.7×10^{-3}	NA	NA	5.1×10^{-3}	NA	NA
CYGB	7.2×10^{-3}			NA	1.3×10^{-2}	1.0	2.1×10^{-3}	6.8×10^{-1}	4.3×10^{-2}
INPP5E	7.2×10^{-3}			1.9×10^{-3}	3.7×10^{-3}	1.0×10^{-1}	5.0×10^{-1}	NA	3.5×10^{-1}
SALL4	7.8×10^{-3}			NA	3.8×10^{-1}	NA	2.6×10^{-2}	NA	6.9×10^{-4}
MC2R	7.8×10^{-3}			NA	3.6×10^{-1}	NA	NA	NA	1.7×10^{-4}
MEA1	7.9×10^{-3}			NA	3.8×10^{-1}	1.4×10^{-2}	1.9×10^{-2}	4.3×10^{-2}	3.7×10^{-2}
CSDE1	8.0×10^{-3}			4.1×10^{-3}	6.3×10^{-1}	2.4×10^{-3}	4.1×10^{-2}	1.2×10^{-1}	9.8×10^{-1}
IQWD1	8.3×10^{-3}			2.2×10^{-2}	NA	NA	3.1×10^{-3}	NA	NA
ORMDL3	9.0×10^{-3}	Yes	Yes	2.2×10^{-1}	2.8×10^{-4}	1.5×10^{-3}	8.2×10^{-1}	6.8×10^{-1}	7.7×10^{-1}
ADO	9.2×10^{-3}		Yes	6.9×10^{-4}	NA	8.9×10^{-2}	NA	3.3×10^{-1}	6.9×10^{-2}
NPTN	9.4×10^{-3}			3.7×10^{-1}	NA	3.6×10^{-2}	3.7×10^{-1}	2.6×10^{-2}	1.9×10^{-3}
TYW1	9.8×10^{-3}			3.7×10^{-2}	NA	5.7×10^{-1}	9.2×10^{-3}	4.0×10^{-1}	3.4×10^{-3}

Table 4.1: Significance of top Crohn's genes from a cross-tissue meta analysis. Of the top 41 genes, only four are identified in the input GWAS, but 11 are present in the current GWAS catalog for Crohn's and ulcerative colitis

upon stimulation with TNF-α.[62] Growth Arrest-Specific 6 (GAS6) has been implicated in the regulation of various systemic inflammatory responses and proposed as a biomarker for detecting early inflammation.[63] [64] [65] LRRC37A4P is a pseudogene in 17q21, the region associated with expression changes in MAPK8IP1. A systematic review of Crohn's literature for proteases and protease inhibitor activity identified USP4 as a probable Crohn's gene.[66] Endothelial lipase, the product of LIPG, has been associated with pro inflammatory citokines in numerous studies.[67] [68] The gene MOB1A/MATS1 regulates cell proliferation and apoptosis, and its expression is suppressed in colorectal cancer tissue.[69] MC2R is one of two melanocortins shown to regulate expression of the inflammation-related gene IL6 in adipocytes, the supporting eQTL tissue here.[70] IL6 is a marker that distinguishes Crohn's disease from ulcerative colitis and has been proposed as a target for Crohn's management through induced T lymphocyte apoptosis.[71] [72]

To underscore the importance of identifying genes through trait-associated perturbations in their entire regulatory network, versus simply their proximal loci, we searched for promising validation targets. Using the Mouse Genome Informatics (MGI) database of mutants and phenotypes, there are several entries from our top genes with Crohn's-relevant phenotypes.[53] Mutations in the murine homologs of both MST1 and ATG16L1 yield increased susceptibility to induced colitis (MP:0008537) with few additional phenotypes of note. Since both genes were previously implicated in Crohn's GWAS and are identified here almost entirely through cis loci, they do not represent particularly attractive targets for validating the unique, trans-specific nature of our findings. The genes SALL4 and CLEC1B, however, are implicated through trans loci and their murine knockouts exhibit a broad array of serious developmental disorders. Included among these are colonic enlargement (MP:0002731) for SALL4 and intestinal edema (MP:0003288) and abnormal small intestine morphology (MP:0000496) for CLEC1B. A murine model that retains these genes but modulates their expression in a tissue-specific or developmentally-specific manner via trans loci may exhibit a more limited phenotype consistent with Crohn's. These genes and similar genes discovered through improved input data could represent important, causative elements that remain hidden in transitional means of GWAS analysis.

Disease	**Genes**	**Number Found**	**Adjusted p-value**
Crohn Disease	ZPBP2 P4HA2 ORMDL3 CARD9 ATG16L1 PTGER4 MST1 SLC22A4 SLC22A5	9/167	2.7×10^{-12}
IBD	ZPBP2 P4HA2 ORMDL3 CARD9 ATG16L1 PTGER4 MST1 SLC22A4 SLC22A5	9/225	2.0×10^{-11}
Gastroenteritis	ZPBP2 ORMDL3 CARD9 ATG16L1 PTGER4 MST1 SLC22A4 SLC22A5	8/200	2.9×10^{-10}
Colitis, Ulcerative	MST1 SLC22A4 ORMDL3 CARD9 ATG16L1 SLC22A5 PTGER4	7/139	8.8×10^{-10}
Colitis	MST1 SLC22A4 ORMDL3 CARD9 ATG16L1 SLC22A5 PTGER4	7/153	1.4×10^{-9}
Cholangitis, Sclerosing	MST1 SLC22A4 CARD9 SLC22A5	4/28	1.3×10^{-7}
Cholangitis	MST1 SLC22A4 CARD9 SLC22A5	4/32	1.8×10^{-7}
Intestinal Diseases	MST1 SLC22A4 ORMDL3 CARD9 ATG16L1 SLC22A5 PTGER4	7/331	1.8×10^{-7}
Colonic Diseases	MST1 SLC22A4 CARD9 ATG16L1 SLC22A5 PTGER4	6/279	1.6×10^{-6}

Table 4.2: Category enrichment for top Crohn's genes. Top categories are highly significant and all related to Crohn's or similar conditions.

4.2 *Type 2 Diabetes*

Diabetes mellitus type 2 (T2D [MIM 125853]) is a metabolic disorder indicated by high blood sugar stemming from insulin resistance. Heritability estimates for T2D range from 0.3 to 0.6, with non-genetic factors playing an important role in determining if genetically predisposed individuals actually present with the disease.[73]

Although the subject of numerous large-scale GWAS, the loci discovered to date are of small effect and explain less than 10% of the trait variance.[3, 74] Here again, to demonstrate the utility of our method, we use an early mea-GWAS of moderate power, identifying 21 genes near 16 risk alleles, to search for functional overlap with an array of eQTL (Table 4.3).[35] The statistical significance of our top results is lower than in the Crohn's example, with only 19 genes passing our meta analysis threshold. Two of these, TSPAN8 and CDKN2B, were identified in the input GWAS. Third gene, TP53INP1, was first identified in a study with almost twice as many cases (8,130, versus 4,549) as the input GWAS.[74] Of the remaining top genes, five have either strong support from T2D comorbidities or murine models, or both (Table 4.4).

Gene	**Meta/Best p-value**	**Input Gene**	**Catalog Gene**	**Zeller (Monocyte)**	**Dixon (LCL)**	**Duan (LCL)**	**Schadt (Liver)**	**Myers (Brain)**	**Muther (Adipose)**
TSPAN8	3.2×10^{-5}	Yes	Yes	9.7×10^{-1}	2.6×10^{-1}	NA	3.2×10^{-5}	NA	NA
TRIB1	4.6×10^{-5}			4.0×10^{-1}	9.4×10^{-1}	4.6×10^{-5}	3.4×10^{-1}	8.5×10^{-1}	4.0×10^{-1}
BDH2	4.9×10^{-5}			NA	NA	NA	4.9×10^{-5}	7.8×10^{-1}	NA
S1PR4	5.4×10^{-5}			NA	NA	2.8×10^{-1}	NA	NA	5.4×10^{-5}
CDKN2B	7.7×10^{-5}	Yes	Yes	3.0×10^{-1}	7.7×10^{-5}	7.0×10^{-1}	NA	NA	2.2×10^{-2}
C20orf3	8.0×10^{-5}			NA	5.2×10^{-1}	6.2×10^{-1}	NA	7.3×10^{-1}	8.0×10^{-5}
RPP25	8.9×10^{-5}			5.1×10^{-1}	6.9×10^{-1}	8.6×10^{-1}	6.8×10^{-1}	8.9×10^{-5}	3.4×10^{-1}
TP53INP1	3.1×10^{-3}		Yes	3.7×10^{-3}	3.0×10^{-4}	2.7×10^{-2}	3.4×10^{-1}	9.2×10^{-1}	2.9×10^{-1}
DNA2	3.3×10^{-3}			3.7×10^{-2}	NA	NA	NA	NA	3.0×10^{-4}
ZNF121	3.7×10^{-3}			3.5×10^{-2}	NA	1.7×10^{-2}	NA	4.1×10^{-4}	7.3×10^{-1}
MITD1	5.2×10^{-3}			1.4×10^{-3}	NA	1.5×10^{-2}	1.4×10^{-1}	NA	NA
CMAS	5.7×10^{-3}			2.0×10^{-3}	4.0×10^{-2}	8.8×10^{-1}	7.1×10^{-1}	2.4×10^{-1}	10.0×10^{-4}
HOXB2	5.8×10^{-3}			2.4×10^{-2}	3.5×10^{-3}	2.3×10^{-1}	1.7×10^{-2}	NA	2.3×10^{-1}
SRBD1	7.1×10^{-3}			7.4×10^{-4}	NA	4.1×10^{-1}	4.1×10^{-1}	6.3×10^{-3}	NA
MYL2	7.3×10^{-3}			2.1×10^{-4}	8.7×10^{-2}	NA	3.4×10^{-1}	NA	NA
EIF2B2	8.6×10^{-3}			1.0×10^{-2}	8.8×10^{-2}	4.0×10^{-2}	2.6×10^{-2}	7.9×10^{-1}	4.5×10^{-2}
KIR2DS5	9.5×10^{-3}			1.2×10^{-4}	NA	NA	7.3×10^{-1}	NA	NA
BCAT2	9.5×10^{-3}			10.0×10^{-1}	7.2×10^{-1}	9.6×10^{-4}	8.4×10^{-1}	4.1×10^{-1}	1.9×10^{-4}
OGDHL	9.7×10^{-3}			NA	9.8×10^{-1}	1.3×10^{-4}	6.4×10^{-2}	3.3×10^{-1}	1.0×10^{-1}

Table 4.3: Top gene preditctions for Type 2 Diabetes. Only two of these were identified in the input GWAS, but several other genes have been implicated in phenotypes related to T2D

The gene TRIB1 is associated with obesity, triglycerides, and cholesterol levels, but not T2D, through multiple GWAS.[75, 76] It is implicated here through a number of modest trans associations on different chromosomes in Duan LCL. In murine studies, a high-fat diet leads to both hypertriglyceridemia and insulin resistance in the absence of Trib1 (the mouse homolog) in haematopoietic cells.[77] A missense variant in helicase/nuclease DNA2, along with non-coding variants in HK1, were recently linked to congenital hyperinsulinism in a pedigree study.[78] Since computational predictions suggest that the DNA2 amino acid substitution is benign, HK1 was proposed as the candidate gene. Our results indicate that DNA2 may be the more likely candidate. The gene SRBD1 is implicated by GWAS in glaucoma, one of several ophthalmic diseases with a significant, well-established overrepresentation in diabetic cohorts.[79] Here it is implicated by a combination of cis and trans across both monocyte and adipose eQTL. MYL2 was recently implicated in a GWAS for glycemic traits — known risk factors for T2D.[80]

As with Crohn's disease, knockout mice that exhibit relevant phenotypes may yield supporting evidence for top genes in our list and suggest targets for validating the importance of trans loci in the disease phenotype. Of the top 19 T2D genes, three are listed in the MGI database with phenotypes involving insulin or glucose.[53] Consistent with other murine studies, the knockout for the homolog of TRIB1 exhibits impaired glucose tolerance (MP:0005293) and insulin resistance (MP:0005331). Its inclusion in our results entirely through trans loci makes it an attractive target for validation studies. The murine knockout for the homolog of MYL2 exhibits a number of phenotypes, mostly cardiac related, but among these is abnormal glucose uptake (MP:0004039). Given its association with human glycemic traits, and its support here entirely through trans loci, it too represents a promising candidate for validation. Finally, the knockout for the homolog of BCAT2, a mitochondrial protein catalyzing amino acid production, displays a number of metabolic-related phenotypes, including increased insulin sensitivity (MP:0002891) and abnormal glucose homeostasis (MP:0002078). It is implicated here entirely through trans loci in both Duan LCL and adipose eQTL.

Disease	**Genes**	**Number Found**	**Adjusted p-value**
Insulin Resistance	CDKN2B TSPAN8 TRIB1	3/194	2.6×10^{-3}
Diabetes, Gestational	CDKN2B TSPAN8	2/70	5.0×10^{-3}
Central Nervous System Infections	EIF2B2 KIR2DS5	2/90	5.0×10^{-3}
Heart Diseases	CDKN2B MYL2 TRIB1	3/366	5.0×10^{-3}
Cardiovascular Diseases	CDKN2B MYL2 TRIB1	3/425	5.0×10^{-3}
Hyperglycemia	CDKN2B TSPAN8	2/117	6.2×10^{-3}
diabetes mellitus type 2 and obesity	CDKN2B TSPAN8	2/139	7.0×10^{-3}
Pathologic Processes	CDKN2B TSPAN8 KIR2DS5	3/561	7.0×10^{-3}
Li-Fraumeni syndrome	CDKN2B TP53INP1	2/171	7.3×10^{-3}

Table 4.4: Category enrichment for top T2D genes. Although of modest significance, the top categories include T2D comorbidities through genes not directly associated with T2D.

4.3 *Schizophrenia*

Schizophrenia [MIM 181500] is a common, highly-heritable psychosis with complex genetic underpinnings. It lacks a precise pathology, such as the amyloid plaques of Alzheimer's disease, and is likely an umbrella diagnosis for a collection of distinct etiologies. Heritability estimates for schizophrenia are as high as 0.8, but only 0.01 of the variance in liability is currently explained by top GWAS results.[81] [82] Here, we use an unpublished large-scale meta GWAS for schizophrenia to identify hidden genes through the Empirical Sherlock method. The significance of our top results is high, with 58 genes passing our threshold criteria, as shown in Table 4.5. As discussed below, the results are enriched for both known schizophrenia genes and genes associated with phenotypes known from epidemiological studies to co-occur with schizophrenia.

Gene	**Meta/Best p-value**	**Input Gene**	**Catalog Gene**	**Zeller (Monocyte)**	**Dixon (LCL)**	**Duan (LCL)**	**Schadt (Liver)**	**Myers (Brain)**	**Muther (Adipose)**
BTN3A2	6.5×10^{-14}		Yes	3.9×10^{-8}	2.7×10^{-12}	3.4×10^{-9}	6.5×10^{-14}	NA	NA
BTN2A1	3.0×10^{-11}			1.9×10^{-1}	3.0×10^{-11}	2.4×10^{-1}	4.6×10^{-1}	1.6×10^{-1}	8.1×10^{-1}
BTN3A1	6.2×10^{-11}		Yes	2.7×10^{-2}	2.1×10^{-4}	3.8×10^{-1}	6.2×10^{-11}	4.4×10^{-1}	9.5×10^{-2}
BTN3A3	3.0×10^{-10}			4.0×10^{-1}	3.0×10^{-10}	9.1×10^{-9}	2.0×10^{-7}	4.0×10^{-1}	7.3×10^{-2}
HLA-DRB4	4.9×10^{-10}			4.9×10^{-10}	NA	NA	NA	1.7×10^{-1}	NA
HLA-A	6.6×10^{-8}			6.6×10^{-8}	7.5×10^{-1}	NA	4.3×10^{-1}	3.7×10^{-1}	NA
BCAP29	1.3×10^{-7}			9.5×10^{-1}	5.3×10^{-1}	1.4×10^{-1}	1.3×10^{-7}	NA	8.6×10^{-1}
ZFP57	5.2×10^{-7}			6.9×10^{-2}	5.2×10^{-7}	NA	NA	NA	NA
GLT8D1	7.0×10^{-7}			7.2×10^{-1}	4.8×10^{-5}	3.8×10^{-2}	3.1×10^{-2}	7.0×10^{-7}	4.3×10^{-1}
PRSS16	1.2×10^{-6}		Yes	NA	1.2×10^{-6}	4.0×10^{-1}	NA	NA	NA
IER3	1.3×10^{-6}			1.3×10^{-6}	NA	3.8×10^{-1}	2.1×10^{-1}	8.1×10^{-1}	9.6×10^{-2}
OMG	1.6×10^{-6}			2.7×10^{-1}	1.0	NA	NA	9.9×10^{-1}	1.6×10^{-6}
USMG5	3.9×10^{-6}			3.9×10^{-6}	3.2×10^{-1}	7.1×10^{-1}	9.9×10^{-1}	NA	5.2×10^{-1}
BAG5	5.0×10^{-6}			5.0×10^{-6}	1.7×10^{-3}	8.1×10^{-1}	8.6×10^{-2}	2.9×10^{-1}	3.3×10^{-1}
HLA-A29.1	5.5×10^{-6}			5.5×10^{-6}	NA	NA	NA	NA	NA
C10orf32	6.0×10^{-6}			NA	6.0×10^{-6}	2.6×10^{-1}	3.3×10^{-2}	2.8×10^{-1}	1.0
AMN	6.7×10^{-6}			NA	6.7×10^{-6}	4.0×10^{-1}	2.3×10^{-1}	NA	NA
YARS2	8.8×10^{-6}			8.8×10^{-6}	NA	1.1×10^{-3}	5.8×10^{-1}	2.2×10^{-1}	NA
TMEM113	9.1×10^{-6}			NA	NA	NA	9.1×10^{-6}	NA	NA
BTN2A2	1.0×10^{-5}		Yes	6.8×10^{-1}	1.0×10^{-5}	2.4×10^{-1}	NA	NA	3.8×10^{-1}
HIST1H2BD	1.4×10^{-5}			1.4×10^{-5}	6.1×10^{-1}	2.0×10^{-1}	5.8×10^{-1}	5.3×10^{-1}	9.5×10^{-1}
IMMP2L	1.7×10^{-5}			4.6×10^{-3}	1.7×10^{-5}	NA	3.5×10^{-1}	8.2×10^{-1}	7.1×10^{-1}
GATAD2A	2.0×10^{-5}			2.0×10^{-5}	9.1×10^{-2}	8.7×10^{-1}	7.1×10^{-1}	6.0×10^{-1}	9.2×10^{-1}
KCNK12	2.1×10^{-5}			2.6×10^{-1}	6.2×10^{-1}	8.6×10^{-2}	2.7×10^{-1}	8.0×10^{-1}	2.1×10^{-5}
AK2	3.7×10^{-5}			2.4×10^{-1}	8.8×10^{-2}	2.9×10^{-1}	2.7×10^{-2}	9.0×10^{-2}	3.7×10^{-5}
BLK	4.1×10^{-5}			1.2×10^{-2}	4.1×10^{-5}	3.4×10^{-1}	1.0	NA	NA
HFM1	4.8×10^{-5}			NA	4.2×10^{-1}	NA	NA	NA	4.8×10^{-5}
LACTB2	5.0×10^{-5}			7.1×10^{-1}	3.9×10^{-1}	5.0×10^{-5}	7.2×10^{-1}	NA	6.0×10^{-1}
ITIH4	5.0×10^{-5}		Yes	3.4×10^{-1}	5.0×10^{-5}	7.5×10^{-1}	9.0×10^{-1}	7.9×10^{-1}	1.6×10^{-1}
CDK2AP1	6.4×10^{-5}			NA	6.4×10^{-5}	1.4×10^{-1}	1.6×10^{-4}	2.3×10^{-1}	NA
MPHOSPH9	6.6×10^{-5}			6.6×10^{-5}	8.7×10^{-5}	2.5×10^{-1}	1.8×10^{-1}	NA	NA
MUSTN1	7.7×10^{-5}			7.7×10^{-5}	10.0×10^{-1}	8.4×10^{-1}	8.3×10^{-1}	4.8×10^{-1}	3.0×10^{-1}
NARF	8.1×10^{-5}			5.1×10^{-2}	8.9×10^{-1}	8.1×10^{-5}	1.5×10^{-1}	2.9×10^{-1}	6.7×10^{-1}
GUCY1A2	8.2×10^{-5}			NA	8.2×10^{-5}	NA	5.4×10^{-1}	NA	2.8×10^{-1}
LOC378135	9.2×10^{-5}			NA	NA	NA	NA	9.2×10^{-5}	NA
ARL6IP4	9.2×10^{-5}			6.0×10^{-1}	9.2×10^{-5}	2.1×10^{-1}	7.2×10^{-1}	7.2×10^{-1}	8.2×10^{-1}
HLA-DQA2	7.7×10^{-4}			1.9×10^{-2}	6.0×10^{-2}	2.9×10^{-3}	1.6×10^{-3}	NA	NA
AS3MT	2.4×10^{-3}		Yes	4.4×10^{-4}	2.3×10^{-2}	NA	1.2×10^{-2}	NA	5.6×10^{-1}
HLA-DQA1	2.8×10^{-3}		Yes	1.3×10^{-3}	9.6×10^{-2}	2.9×10^{-3}	2.5×10^{-1}	NA	NA
ZSCAN16	3.2×10^{-3}			2.9×10^{-4}	NA	NA	NA	1.6×10^{-2}	2.2×10^{-1}
DCPS	3.4×10^{-3}			2.2×10^{-2}	9.1×10^{-1}	1.4×10^{-3}	4.3×10^{-3}	NA	1.9×10^{-1}
TBC1D5	3.9×10^{-3}			5.5×10^{-2}	2.3×10^{-3}	8.1×10^{-1}	4.9×10^{-3}	NA	6.0×10^{-2}
C22orf32	4.0×10^{-3}			NA	NA	1.9×10^{-3}	3.2×10^{-3}	NA	2.7×10^{-1}
ALMS1	5.1×10^{-3}			3.8×10^{-2}	6.0×10^{-4}	5.4×10^{-1}	4.5×10^{-1}	2.1×10^{-3}	8.2×10^{-1}
GUSBL2	5.7×10^{-3}			8.3×10^{-2}	NA	NA	3.9×10^{-4}	NA	NA
GFOD2	5.8×10^{-3}			1.3×10^{-4}	NA	NA	1.2×10^{-1}	5.5×10^{-2}	5.9×10^{-1}
TM9SF1	6.7×10^{-3}			2.6×10^{-1}	6.8×10^{-1}	4.5×10^{-3}	6.7×10^{-1}	2.6×10^{-4}	1.4×10^{-1}
VRK2	7.0×10^{-3}		Yes	7.3×10^{-3}	1.1×10^{-4}	9.6×10^{-1}	3.7×10^{-1}	NA	4.4×10^{-1}
CLP1	7.4×10^{-3}			2.1×10^{-4}	NA	1.2×10^{-1}	NA	NA	2.5×10^{-1}
CREB1	7.6×10^{-3}			3.8×10^{-1}	2.0×10^{-3}	1.4×10^{-2}	NA	1.2×10^{-1}	1.1×10^{-1}
HSP90AB2P	8.5×10^{-3}			1.3×10^{-1}	NA	NA	NA	NA	5.7×10^{-4}
C16orf70	8.7×10^{-3}			NA	NA	8.9×10^{-3}	2.2×10^{-3}	NA	4.4×10^{-1}
ASAH1	9.2×10^{-3}			1.3×10^{-1}	1.7×10^{-2}	2.5×10^{-1}	2.9×10^{-1}	1.2×10^{-3}	2.2×10^{-1}
EP300	9.3×10^{-3}			1.2×10^{-3}	2.1×10^{-1}	5.6×10^{-1}	1.1×10^{-3}	5.4×10^{-1}	4.9×10^{-1}
SERPIND1	9.3×10^{-3}			NA	5.3×10^{-3}	NA	1.7×10^{-2}	NA	NA
ZDHHC5	9.5×10^{-3}			4.7×10^{-3}	1.2×10^{-2}	1.0×10^{-1}	3.6×10^{-1}	5.2×10^{-2}	4.0×10^{-1}
PRMT7	9.7×10^{-3}			2.6×10^{-3}	7.3×10^{-1}	1.2×10^{-1}	6.1×10^{-3}	1.1×10^{-1}	3.2×10^{-1}
HGS	10.0×10^{-3}			1.9×10^{-2}	5.5×10^{-1}	1.6×10^{-2}	1.0	1.0×10^{-2}	1.7×10^{-1}

Table 4.5: Top gene predictions for Schizophrenia. Eleven of these are found in current GWAS catalog, while numerous other genes are associated with co-occurring conditions and other indicators of disease relevance.

Ignoring the eleven genes in Table 4.5 that have previously been associated with schizophrenia through

GWAS, we provide supporting evidence for the remaining genes through a variety of sources. The gene BCAP29 is associated with narcolepsy, a disorder with clinical manifestations similar to schizophrenia and subject to misdiagnosis.[83] Its inclusion here may indicate contamination of the case cohort through misdiagnosis, a common biological mechanism, or some combination of these. The gene ZFP57 is associated with Type 1 diabetes, one of several autoimmune disorders known, through strong epidemiological evidence, to co-occur with schizophrenia.[84] [85] Expression changes in the gene GLT8D1 were recently linked to psychiatric disorders in a Japanese cohort.[86] Expression changes in the mouse homolog of IER3 have been implicated in a lupus-like autoimmune disease, another condition co-occurring in schizophrenia.[87] [85] Since various studies suggest that myelin dysfunction is involved in the pathogenesis of schizophrenia, association studies have specifically targeted OMG and other myelin-related genes but failed to find strong, proximal schizophrenia associations.[88] Through Empirical Sherlock, it is implicated here in trans by two strong loci in adipose eQTL. Given recent success using adipose-derived Schwann cells in promoting myelination, this finding seems particularly noteworthy.[89] The gene BAG5 has been shown to inhibit a gene strongly implicated in early-onset Parkinson's disease that enhances dopaminergic neuron degeneration, a finding consistent with the well-established dopamine hypothesis of schizophrenia.[90] [91] Intragenic deletions have been shown to affect alternative transcripts of the gene IMMP2L in patients with Tourette syndrome, a comorbidity of schizophrenia.[92] [93] BLK is a well-studied lupus and autoimmune gene.[94] As a messenger molecule involved in signal transduction pathways associated with dopamine receptor subtypes, association studies have attempted to implicate CREB1 in schizophrenia directly.[95] Here, its significance is elevated in both LCL tissue types through a diverse collection of mostly trans loci. The gene ASAH1 has been reported as schizophrenia gene in a Han Chinese cohort.[96] EP300 is another autoimmune-related gene, linked to suppression of a lupus-like disease in a mouse model.[97]

As shown in Table 4.6, our analysis of overrepresented disease-associated genes includes various disorders known to co-occur with schizophrenia. These include type 1 diabetes, autoimmune hepatitis, and autoimmune Thyroiditis — disorders specifically identified as enriched in a large epidemiological study.[85] In addition, the list includes narcolepsy, a disease that may present with symptoms similar to schizophrenia, leading to a contamination of the study cohort through misdiagnosis.[83] Also included is an overrepresentation of genes linked with human immunodeficiency virus (HIV) infection, another condition known to be more common in schizophrenia cohorts.[98]

We also used the Kyoto encyclopedia of genes and genomes (KEGG) database to search for overrepresentation of pathways in schizophrenia.[99] This analysis was performed on a tissue-by-tissue basis, and only

Disease	Genes	Number Found	Adjusted p-value
Autoimmune Diseases	BLK HLA-DQA2 HLA-DRB4 PRSS16 HLA-DQA1 MPHOSPH9 HLA-A	7/414	7.0×10^{-5}
Vitiligo	KCNK12 HLA-DRB4 HLA-DQA1 HLA-A	4/55	7.0×10^{-5}
Diabetes Mellitus, Type 1	HLA-DQA2 HLA-DRB4 PRSS16 HLA-DQA1 HLA-A	5/169	1.0×10^{-4}
Disease Susceptibility	BLK HLA-DQA2 HLA-DRB4 BTN2A1 PRSS16 HLA-DQA1 PCLO HLA-A	8/825	2.0×10^{-4}
Genetic Predisposition to Disease	BLK HLA-DQA2 HLA-DRB4 BTN2A1 PRSS16 HLA-DQA1 PCLO HLA-A	8/808	2.0×10^{-4}
Myasthenia Gravis	PRSS16 HLA-DQA1 HLA-A	3/39	2.0×10^{-4}
Hepatitis, Autoimmune	HLA-DRB4 HLA-DQA1 HLA-A	3/36	2.0×10^{-4}
Disorders of Excessive Somnolence	BCAP29 HLA-DRB4 HLA-DQA1 PCLO	4/119	2.0×10^{-4}
Narcolepsy	BCAP29 HLA-DRB4 HLA-DQA1 PCLO	4/112	2.0×10^{-4}
HIV	EP300 HLA-DQA2 GLT8D1 HLA-DRB4 HGS HLA-DQA1 HIST1H2BD HLA-A	8/755	2.0×10^{-4}
Thyroiditis, Autoimmune	HLA-DRB4 HLA-DQA1 HLA-A	3/47	3.0×10^{-4}
AIDS	HLA-DQA2 HLA-DRB4 HLA-DQA1 HLA-A	4/136	3.0×10^{-4}
Simian AIDS	HLA-DQA2 HLA-DQA1 HLA-A	3/49	3.0×10^{-4}

Table 4.6: Top gene predictions for Schizophrenia Disease. Of these, only four were identified in the original GWAS, but 11 are found in current GWAS catalog for Schizophrenia/IBD.

results for monocyte eQTL were found to be statistically significant. In Table 4.7, Empirical Sherlock results are combined in a meta analysis based on the set of genes in each KEGG pathway. In Table 4.8, the eQTL loci for these genes are combined prior to analysis using Empirical Sherlock. In each case, multiple KEGG pathways show elevated significance, per the adjusted p-values. As expected, these are enriched for various autoimmune diseases. In addition, the alcohol use disorder (AUD) pathway is found to be significant; this condition is reported to be the most common co-occurring disorder in schizophrenic individuals.[100]

KEGG Pathway	p-value	Number	Definition
hsa05332	1.8×10^{-7}	36	Graft-versus-host disease
hsa05330	2.6×10^{-7}	31	Allograft rejection
hsa05320	1.7×10^{-6}	35	Autoimmune thyroid disease
hsa04940	2.7×10^{-6}	35	Type I diabetes mellitus
hsa04514	8.0×10^{-6}	100	Cell adhesion molecules (CAMs)
hsa05310	2.4×10^{-5}	24	Asthma
hsa05140	3.9×10^{-5}	64	Leishmaniasis
hsa04612	4.7×10^{-5}	73	Antigen processing and presentation

Table 4.7: Meta analysis for Empirical Sherlock results in monocyte eQTL when grouping genes in KEGG pathways.

KEGG Pathway	p-value	Definition
hsa05203	1.5×10^{-9}	Viral carcinogenesis
hsa05322	1.1×10^{-7}	Systemic lupus erythematosus
hsa05034	1.0×10^{-5}	Alcoholism
hsa05310	8.7×10^{-5}	Asthma
hsa05160	1.8×10^{-4}	Hepatitis C

Table 4.8: Empirical Sherlock results in monocyte eQTL when grouping loci using KEGG pathways.

Chapter 5

Discussion

Regardless of their sophistication, computational approaches alone cannot prove a causal link between a given disease and specific genes or other functional genomic elements. Rather, they assign statistical significance to various hypotheses that may require considerable time and expense to investigate. In the era of inexpensive genotyping and high-throughput functional genomic assays, with an ever-expanding list of potentially causal agents, general-purpose data mining methods must err on the side of caution. They should be constructed to do everything possible to prevent spurious correlations from masquerading as viable candidates, thereby distracting research efforts from more promising targets. In addition, such methods should be easy to use and not subject to inflation due to misconfiguration or simple user error. With this philosophy in mind, we designed Empirical Sherlock to make judicious use of *all* available data, both to reject spurious correlations and to discover functional elements hidden in a vast pool of modest associations. Key attributes of Empirical Sherlock include:

1. A statistical test that pools GWAS loci to incorporate information from all SNPs, including those typically discarded under strict thresholds for genome-wide significance.

2. A method that maps multiple associations onto a single functional element, gaining both useful insight and statistical power.

3. An approach that is easily extended to most any genome-wide functional assay (e.g. eQTL, DNA methylation, transcription factor binding, etc.).

4. The use of functional data from cohorts independent of the GWAS study, thereby reducing the tendency to discover reactive (versus potentially causal) functional associations.

5. The use of an empirically-derived null distribution that greatly reduces false discovery due to inflation and other biases present in input GWAS data.

6. The ability to define sets of functional loci using a range of thresholds, thereby minimizing potential biases due to a single, arbitrary cutoff.

7. The ability to condition the null distribution to correct for known dependencies between the elements tested (e.g. adjusting for known pleiotropic loci).

8. A method that involves essentially no tunable parameters or study-specific configuration.

In tests of our method using multiple eQTL studies across tissue types and moderately powered disease GWAS, the top results are enriched for genes that are either implicated through larger association studies or plausibly related to the trait through known comorbidities or mechanisms. In many instances, these genes are identified through an aggregation of multiple GWAS associations that fall well-below genome-wide significance, illustrating the boost in the effective statistical power that is possible when SNPs are tested as sets, versus individually. In our simulations, inflation that could lead to false gene discovery is well controlled, even in the presence of dependence between the supporting SNPs or significant inflation of the input GWAS.

The approach demonstrated here operates entirely on summary statistics, as restrictions on the transfer of individual human genotypes would severely hinder widespread adoption of computational methods that require them. However, when available, individual genotypes for both the GWAS and functional cohorts could improve the accuracy and utility of the analysis in several ways: First, as discussed in the context of tag SNP selection, genotypes can be used to better inform the partitioning of loci into haplotype blocks specific for the actual cohorts used. Second, the directionality of the functional SNPs supporting a given element can provide additional insight and statistical support to a given hypothesis. For example, if the case-associated alleles from GWAS always drive the expression of a given gene in the same direction, this coherence between supporting SNPs can boost confidence in the finding and provide a specific hypothesis to test. Finally, genotypes can enable the calculation of the phenotypic variance explained by supporting loci for top genes, lending enormous credibility in cases when this constitutes an appreciable fraction of total heritability. Although the p-values involved here suggest that most loci tag small effects, large numbers of them could be expected from a diverse survey across many tissues. That is, the regulatory networks reflected in the small number of eQTL data sets used here provide only sparse sampling of the possible ways that compromised regulation could contribute to a disease phenotype. Despite this, the supporting SNPs for our top Crohn's genes include over forty independent loci below 10^{-3}, even when ignoring adjacent tag SNPs that may prove independent with better linkage estimates.

The foundational methods of statistical inference developed by Pearson, Fisher, and their successors are predicated on data scarcity — situations that necessitate various estimates and assumptions regarding an unknown distribution from which samples are drawn. Much of modern research, however, involves collaborative, large-scale studies that generate thousands or millions of samples and, often, an equal number of hypotheses to test. Since our core method is appropriate for most any problem of statistical inference involving n draws from a distribution that is known empirically, it may have broad utility outside the field of genomic data integration. Thus, an obvious follow-up activity is the release of general-purpose libraries in R, Python, or C to test subset significance using our scoring function and null distributions constructed via recursive convolution of an empirical PDF.

When considering method optimization strategies in conjunction with a code release, several items are worth noting: The convolution operation is likely best performed using a Fast Fourier Transform (FFT) approach, versus a direct implementation, depending on the size of the arrays. For scores involving an n greater than several dozens elements (in our testing), the null distribution converges to a Gaussian as expected under the central limit theorem. An optimal computational strategy may therefore involve monitoring this convergence and constructing the null from summary statistics above a threshold value of n. Situations requiring element-specific PDFs conditioned to account for dependancies between sets may preclude this approach, depending on the accuracy desired. Another consideration is the number of bits needed to avoid undesirable quantization of very small p-values; semi-custom libraries are likely necessary to achieve the dynamic range required for the long, thin tails of some null distributions.

In this work, we have cast Empirical Sherlock as a tool for discovering the hidden drivers of common, complex disease through a reanalysis of well-powered association studies, but other compelling use cases exist. Primary among these is the extraction of functional insight from otherwise uninformative association studies that are inherently limited in their cohort size and statistical power. The field of pharmacogenomics, for example, is replete with studies of perhaps several hundred individuals who exhibit variation in metabolism or response to a given drug. In certain instances, a few key mutations of large effect may be responsible and therefore directly accessible through modest studies (e.g. variation in the genes VKORC1 and CYP2C9 and warfarin coagulation efficacy).[101] Yet, in other cases, variation may stem from a diverse collection of polymorphisms distributed across a complex pathway (e.g. the response of glucocorticoids in the treatment of asthma).[102] By integrating data from drug efficacy studies and a diverse collection of functional genomic elements (eQTL, various indicators of chromatin structure, etc.), our method could potentially advance both the development of novel pharmaceuticals and inform the re-purposing of existing compounds. Additionally, it could assist in the development of genotype-based indications and contraindications in the era of personalized medicine.

Although GWAS have dramatically increased the number of known loci for common disease in recent years, the difficulty of placing these into an informative context — and the realization that many more loci, of individually very small effect, are likely involved in disease etiology — limits the ability of association studies to drive improved therapeutic and preventive measures. The ever-expanding collection of genome-wide functional assays are of limited utility in addressing these issues when loci are considered only individually, isolated from the pathways and networks that they perturb. Empirical Sherlock is a straightforward means of testing trait associations for functional signatures in a manner that reflects the complex nature of gene-level and pathway-level regulation.

Appendix A

Null Distribution Under Uniform Assumption

For the case when the distribution of p-values in the universal set $\mathbb{U}$ is uniform, we derive an explicit expression for the null distribution for purposes of comparison against the empirical p-value distribution. As demonstrated previously, this can result in substantial differences in the statistical significance of top functional elements due to discrepancies in the distribution tails.

By definition, the distribution of GWAS p-values in the absence of association is uniform on the interval from 0 to 1. Let X denote a random variable (i.e. the p-value of an aligned SNP) and $f_X(x)$ denote the probability distribution function (PDF) of its possible values:

$$f_X(x) = \begin{cases} 1 & \text{for } 0 \leq x \leq 1 \\ 0 & \text{for } x < 0 \text{ or } x > 1 \end{cases}$$

Our score is based on log-transformed p-values. Let Y denote the transformed random variable and $f_Y(y)$ denote its distribution:

$$Y = -log_{10}(X) \qquad X = 10^{-Y}$$

$$\left|\frac{dx}{dy}\right| = 10^{-Y} ln(10)$$

We transform the distributions using:

$$f_Y(y) = f_X(x)\left|\frac{dx}{dy}\right|$$

Yielding:

$$f_Y(y) = \begin{cases} 10^{-Y} ln(10) \quad \text{for } y > 0 \\ 0 \quad \text{for } y \leq 0 \end{cases}$$

Since the gene score, S_{gene} is composed of independently segregating SNP blocks, the summation of these random variables (i.e. S_{block} scores) results in the convolution of their PDFs. We now include a subscript to denote the number of blocks added, with $f_Y(y) = f_{Y_1}(y)$. For genes with two blocks, the resulting PDF $f_{Y_2}(y)$ is:

$$f_{Y_2}(y) = f_{Y_1}(y) * f_{Y_1}(y) = (ln(10)^2) \int_0^y 10^{-\tau} 10^{-(y-\tau)} \, d\tau = ln(10)^2 y 10^{-y}$$

For scores composed of n blocks, we recursively compute the convolution of PDFs f_{Y_1} and $f_{Y_{n-1}}$, yielding:

$$f_{Y_n}(y) = f_{Y_{n-1}}(y) * f_{Y_1}(y) = ln(10)^n \prod_{i=0}^{n-1} \frac{1}{i} y^{n-1} 10^{-y}$$

For a given gene score, S_{gene}, composed of n SNP blocks, the statistical significance of GWAS-eQTL overlap is indicated by the p-value:

$$p = \int_{S_{gene}}^{\infty} f_{Y_n}(y) dy$$

Appendix B

Supporting SNPs for Top Crohn's Results

The supporting SNPs for all top Crohn's genes are provided here. The genes are listed in rank order, and only functional data yielding Empirical Sherlock p-values below 0.1 is shown. Thus, certain genes may have only one supporting eQTL data set listed, while others will have multiple listings if their Empirical Sherlock results are significant across multiple tissues. Definitions for each column in the supporting matrix are provided in Table B.1. All coordinates provided are for assembly hg19 / GRCh37 of the human genome. Minor allele frequencies (MAFs) given are from NCBI dbSNP build 135. Linkage disequilibrium is from our custom database, as described in Methods.

Table B.1: Explanation of Supporting SNP Information

BLK	Haplotype Block Number. These are not sequential, since only independently-sorting SNPs are retained.
PRX	Proximity of SNP to gene (cis or trans)
CHR	Chromosome
eQTL SNP	ID of eQTL SNP used
PL	SNP pleiotropy. The number of times this SNP is found in other genes in the eQTL data set.
Location	Location of the eQTL SNP
MAF	Minor allele frequency of the eQTL SNP. Used as a check for independence of adjacent tag SNPs.
GWAS SNP	ID of the GWAS SNP used
Location	Location of the aligned GWAS SNP
MAF	Minor allele frequency of the GWAS SNP
Delta	Distance in base pairs between the two SNPs
LD	Linkage disequilibrium (r^2) between the SNPs
eQTL pval	Used to define SNP sets at different thresholds, as per our method
GWAS pval	Used to construct the gene score. The summation of log(p-values) for this column is the gene score

Crohns Gene 1
P4HA2: prolyl 4-hydroxylase, alpha polypeptide II
Gene Location: chr5:131528303-131563556
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 2.3×10^{-7}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs1395835	9	234938888	0.37	rs1395835	234938888	0.37	0	1.00	1.0×10^{-5}	6.7×10^{-1}
3	trans	chr5	rs10063114	1	50890863	0.29	rs10063114	50890863	0.29	0	1.00	7.1×10^{-6}	5.2×10^{-1}
4	cis	chr5	rs4706020	1	130674076	0.15	rs4706020	130674076	0.15	0	1.00	4.0×10^{-4}	1.2×10^{-6}
7	cis	chr5	rs1858074	2	131371999	0.14	rs1858074	131371999	0.14	0	1.00	1.5×10^{-7}	9.3×10^{-5}
15	cis	chr5	rs1050152	1	131676320	0.23	rs2188962	131770805	0.16	94485	0.87	2.0×10^{-4}	4.6×10^{-9}
19	trans	chr10	rs6585818	2	124104924	0.11	rs6585818	124104924	0.11	0	1.00	3.1×10^{-6}	8.4×10^{-1}

Crohns Gene 1
P4HA2: prolyl 4-hydroxylase, alpha polypeptide II
Gene Location: chr5:131528303-131563556
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 5.3×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
4	trans	chr4	rs1916246	1	149829054	0.27	rs11736001	149813345	0.25	15709	0.94	2.5×10^{-6}	1.4×10^{-2}
10	trans	chr7	rs17245738	2	11746175	0.18	rs1405320	11737902	0.45	8273	0.92	7.1×10^{-6}	3.0×10^{-2}
11	trans	chr12	rs4964731	3	109057809	0.36	rs10861957	109056377	0.34	1432	0.95	5.8×10^{-6}	8.4×10^{-1}
15	trans	chr19	rs426132	2	18206681	0.19	rs426132	18206681	0.19	0	1.00	3.9×10^{-6}	3.9×10^{-1}

Crohns Gene 2
AK096536: Not Found in HUGO
Gene Location: Not Found:Not Found-Not Found
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 3.3×10^{-6}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr3	rs4686980	1	188302851	0.40	rs4686980	188302851	0.40	0	1.00	2.5×10^{-6}	8.4×10^{-1}
3	trans	chr4	rs4396948	1	160208630	0.46	rs4396948	160208630	0.46	0	1.00	6.8×10^{-6}	4.8×10^{-1}
10	trans	chr5	rs11957134	1	150230950	0.22	rs11957134	150230950	0.22	0	1.00	1.7×10^{-17}	1.1×10^{-10}
28	trans	chr5	rs6869405	1	150387736	0.08	rs6869405	150387736	0.08	0	1.00	3.0×10^{-8}	4.9×10^{-4}

Crohns Gene 3
PTGER4: prostaglandin E receptor 4 (subtype EP4)
Gene Location: chr5:40680031-40693837
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 3.3×10^{-6}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs9426379	1	29849150	0.15	rs9426379	29849150	0.15	0	1.00	7.0×10^{-6}	6.6×10^{-1}
2	trans	chr2	rs3901491	1	50976485	0.14	rs3901491	50976485	0.14	0	1.00	9.6×10^{-6}	1.4×10^{-1}
3	cis	chr5	rs1981843	1	40238857	0.15	rs1981843	40238857	0.15	0	1.00	6.0×10^{-5}	4.5×10^{-4}
8	cis	chr5	rs7720838	1	40486896	0.41	rs7720838	40486896	0.41	0	1.00	5.2×10^{-6}	4.9×10^{-17}

Crohns Gene 3
PTGER4: prostaglandin E receptor 4 (subtype EP4)
Gene Location: chr5:40680031-40693837
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 5.1×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs1048854	2	94643531	0.16	rs1048854	94643531	0.16	0	1.00	1.0×10^{-5}	6.0×10^{-1}
20	trans	chr2	rs3755521	1	95983226	0.27	rs889851	95980340	0.26	2886	1.00	9.0×10^{-7}	2.3×10^{-1}
22	trans	chr2	rs16858857	10	143969046	0.22	rs10176686	143929917	0.22	39129	0.97	1.0×10^{-5}	3.9×10^{-1}
24	trans	chr3	rs12486634	1	16693427	0.14	rs12106804	16693266	0.13	161	NA	1.0×10^{-5}	5.0×10^{-1}
27	trans	chr4	rs6826015	3	24579166	0.19	rs13111756	24557437	0.19	21729	1.00	6.0×10^{-6}	8.8×10^{-1}
29	trans	chr4	rs2631266	12	102947157	0.18	rs2631267	102948472	0.13	1315	0.95	1.0×10^{-6}	3.7×10^{-1}
30	trans	chr4	rs1994530	3	169311333	0.12	rs1994530	169311333	0.12	0	1.00	5.0×10^{-7}	8.5×10^{-1}
31	trans	chr5	rs4246742	6	1267356	0.47	rs4246742	1267356	0.47	0	1.00	1.0×10^{-5}	7.5×10^{-1}
34	trans	chr5	rs10056553	3	38713519	0.16	rs10056553	38713519	0.16	0	1.00	6.0×10^{-6}	5.4×10^{-1}
36	cis	chr5	rs7720838	1	40486896	0.41	rs7720838	40486896	0.41	0	1.00	5.0×10^{-5}	4.9×10^{-17}
43	trans	chr6	rs9478703	2	156692792	0.14	rs17087341	156690480	0.17	2312	0.88	8.0×10^{-6}	9.9×10^{-1}
48	trans	chr8	rs7017034	1	51959409	0.18	rs7017034	51959409	0.18	0	1.00	1.0×10^{-5}	3.3×10^{-1}
51	trans	chr11	rs4910002	1	11461388	0.43	rs4910003	11462298	0.45	910	0.86	1.0×10^{-5}	7.0×10^{-1}
54	trans	chr11	rs2467586	2	32637872	0.18	rs185689	32658926	0.19	21054	1.00	1.0×10^{-6}	1.3×10^{-1}
58	trans	chr12	rs1989893	3	47890354	0.28	rs10783194	47889340	0.27	1014	0.96	3.0×10^{-6}	9.8×10^{-1}
71	trans	chr16	rs11640800	3	11408046	0.12	rs2867945	11406018	0.13	2028	0.95	1.0×10^{-5}	6.0×10^{-1}
76	trans	chr18	rs10048330	1	54576032	0.30	rs4800954	54571013	0.30	5019	1.00	2.0×10^{-6}	9.8×10^{-1}
89	trans	chr20	rs2328144	1	17402680	0.45	rs6080690	17402109	0.40	571	0.99	2.0×10^{-6}	6.1×10^{-1}

Crohns Gene 4
BRWD1: bromodomain and WD repeat domain containing 1
Gene Location: chr21:40557403-40685712
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 8.0×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs761517	7	186961387	0.30	rs761517	186961387	0.30	0	1.00	2.9×10^{-6}	2.5×10^{-2}
2	trans	chr1	rs878947	7	212683565	0.24	rs878947	212683565	0.24	0	1.00	4.0×10^{-6}	6.1×10^{-1}
3	trans	chr1	rs11117760	162	217222118	0.50	rs11117760	217222118	0.50	0	1.00	5.8×10^{-6}	10.0×10^{-1}
4	trans	chr1	rs4658619	75	242271323	0.36	rs4658619	242271323	0.36	0	1.00	6.3×10^{-6}	3.0×10^{-1}
5	trans	chr4	rs7675286	18	36019457	0.29	rs7675286	36019457	0.29	0	1.00	1.0×10^{-5}	8.5×10^{-1}
9	trans	chr4	rs7665024	404	110289595	0.21	rs6533426	110293437	0.33	3842	0.96	6.7×10^{-7}	5.8×10^{-1}
11	trans	chr4	rs7677410	1	116684526	0.21	rs7677410	116684526	0.21	0	1.00	9.9×10^{-6}	2.6×10^{-1}
12	trans	chr6	rs6909472	16	113001768	0.23	rs6909472	113001768	0.23	0	1.00	7.5×10^{-6}	2.6×10^{-1}
13	trans	chr7	rs1229052	2	39000551	0.26	rs1229052	39000551	0.26	0	1.00	2.5×10^{-6}	3.1×10^{-3}
17	trans	chr8	rs1817107	1	82789609	0.30	rs1817107	82789609	0.30	0	1.00	2.4×10^{-6}	4.1×10^{-1}
21	trans	chr9	rs2026801	4	113905451	0.40	rs2026801	113905451	0.40	0	1.00	6.3×10^{-6}	1.7×10^{-1}
22	trans	chr12	rs3918347	50	109293320	0.42	rs3918347	109293320	0.42	0	1.00	8.0×10^{-6}	2.2×10^{-2}
23	trans	chr12	rs9668430	7	122623595	0.22	rs9668430	122623595	0.22	0	1.00	1.0×10^{-5}	4.5×10^{-1}
24	trans	chr14	rs2383301	8	32890538	0.08	rs2383301	32890538	0.08	0	1.00	4.5×10^{-6}	2.1×10^{-1}
26	trans	chr15	rs11070266	69	40644776	0.13	rs11070266	40644776	0.13	0	1.00	4.1×10^{-6}	5.5×10^{-2}
27	trans	chr17	rs1859360	51	51277058	0.36	rs1859360	51277058	0.36	0	1.00	3.5×10^{-7}	2.3×10^{-1}
28	trans	chr18	rs12607558	217	31754053	0.26	rs12607558	31754053	0.26	0	1.00	2.3×10^{-6}	6.2×10^{-1}
29	trans	chr18	rs9947963	8	75563973	0.24	rs9967336	75566182	0.26	2209	0.98	4.2×10^{-6}	8.0×10^{-1}
32	cis	chr21	rs459094	1	40007704	0.44	rs459094	40007704	0.44	0	1.00	8.0×10^{-4}	7.2×10^{-1}
33	cis	chr21	rs3171465	1	40552307	0.45	rs2297256	40558421	0.46	6114	0.97	1.2×10^{-8}	3.5×10^{-1}
64	cis	chr21	rs2837002	1	40763986	0.32	rs2837002	40763986	0.32	0	1.00	2.0×10^{-5}	4.2×10^{-1}
68	cis	chr21	rs2837263	2	41247892	0.16	rs2837263	41247892	0.16	0	1.00	3.0×10^{-4}	5.6×10^{-1}

Crohns Gene 4
BRWD1: bromodomain and WD repeat domain containing 1
Gene Location: chr21:40557403-40685712
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 6.7×10^{-6}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs7540036	1	205452224	0.30	rs7540036	205452224	0.30	0	1.00	8.1×10^{-7}	7.7×10^{-1}
2	trans	chr2	rs10930609	1	174482931	0.49	rs10930609	174482931	0.49	0	1.00	3.9×10^{-6}	5.3×10^{-1}
3	trans	chr2	rs12694164	8	210073135	0.41	rs1583758	210060812	0.35	12323	0.88	2.9×10^{-6}	7.1×10^{-1}
5	trans	chr5	rs7713629	1	113210609	0.32	rs7713629	113210609	0.32	0	1.00	5.0×10^{-6}	3.9×10^{-1}
6	trans	chr5	rs4921536	1	159327624	0.49	rs4921536	159327624	0.49	0	1.00	6.3×10^{-6}	7.2×10^{-1}
8	trans	chr6	rs2324753	1	85558462	0.34	rs2324753	85558462	0.34	0	1.00	7.5×10^{-6}	8.5×10^{-1}
9	trans	chr7	rs491554	1	140776614	0.32	rs491554	140776614	0.32	0	1.00	6.7×10^{-6}	8.4×10^{-1}
11	trans	chr9	rs4147239	1	22861227	0.37	rs4147239	22861227	0.37	0	1.00	9.2×10^{-6}	8.1×10^{-1}
12	trans	chr9	rs16918694	1	32865017	0.12	rs11790585	32874506	0.11	9489	0.98	2.9×10^{-6}	1.1×10^{-1}
14	trans	chr9	rs10867178	1	80924008	0.33	rs7874921	80925219	0.31	1211	1.00	5.1×10^{-6}	9.7×10^{-1}
17	trans	chr10	rs7919721	1	98158494	0.48	rs7919721	98158494	0.48	0	1.00	5.1×10^{-7}	5.3×10^{-1}
19	trans	chr11	rs1944812	2	126970429	0.34	rs1944812	126970429	0.34	0	1.00	6.5×10^{-6}	1.0×10^{-1}
23	trans	chr12	rs6539283	1	107222989	0.36	rs6539283	107222989	0.36	0	1.00	4.6×10^{-6}	1.5×10^{-1}
25	trans	chr13	rs9285295	1	75972846	0.41	rs9285295	75972846	0.41	0	1.00	6.9×10^{-6}	6.4×10^{-1}
26	trans	chr16	rs9922740	2	1566382	0.15	rs9922740	1566382	0.15	0	1.00	8.4×10^{-6}	4.4×10^{-1}
28	trans	chr17	rs4792849	1	43395178	0.29	rs4792849	43395178	0.29	0	1.00	1.3×10^{-6}	2.7×10^{-1}
31	trans	chr17	rs3946526	5	43541656	0.08	rs3946526	43541656	0.08	0	1.00	1.5×10^{-25}	3.0×10^{-2}
32	trans	chr17	rs2696425	2	43666906	0.42	rs2696425	43666906	0.42	0	1.00	1.4×10^{-38}	9.4×10^{-4}
55	trans	chr17	rs17762165	2	43778602	0.11	rs17762165	43778602	0.11	0	1.00	5.2×10^{-38}	1.3×10^{-3}
169	trans	chr17	rs2732646	1	44254379	0.07	rs2732646	44254379	0.07	0	1.00	2.3×10^{-39}	6.8×10^{-4}
197	trans	chr17	rs199535	3	44822662	0.11	rs199535	44822662	0.11	0	1.00	8.3×10^{-44}	6.2×10^{-4}
202	trans	chr18	rs17651098	1	36299007	0.19	rs11661303	36294734	0.19	4273	0.88	2.4×10^{-6}	3.7×10^{-1}
206	trans	chr19	rs1997563	3	51373190	0.41	rs1997563	51373190	0.41	0	1.00	4.3×10^{-7}	1.6×10^{-1}
207	trans	chr20	rs6119407	15	32403641	0.39	rs6119407	32403641	0.39	0	1.00	7.2×10^{-6}	2.0×10^{-1}
235	cis	chr21	rs8132424	2	40584412	0.49	rs8132424	40584412	0.49	0	1.00	1.1×10^{-17}	3.8×10^{-1}
262	cis	chr21	rs2836992	1	40735606	0.36	rs2836992	40735606	0.36	0	1.00	7.6×10^{-5}	7.2×10^{-1}

Crohns Gene 4
BRWD1: bromodomain and WD repeat domain containing 1
Gene Location: chr21:40557403-40685712
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 5.9×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs950283	2	94567223	0.33	rs950283	94567223	0.33	0	1.00	5.3×10^{-6}	2.8×10^{-1}
7	trans	chr2	rs6752908	1	69409222	0.43	rs6749826	69409029	0.43	193	0.98	6.6×10^{-6}	6.0×10^{-1}
9	trans	chr2	rs11123788	1	100205498	0.32	rs11123788	100205498	0.32	0	1.00	3.7×10^{-6}	7.8×10^{-2}
11	trans	chr7	rs6976686	1	135976504	0.44	rs11973908	135977244	0.45	740	1.00	8.4×10^{-7}	1.6×10^{-1}
40	trans	chr9	rs1359091	1	10367106	0.29	rs1359091	10367106	0.29	0	1.00	2.7×10^{-6}	1.2×10^{-1}
43	trans	chr17	rs12600635	1	17142896	0.16	rs12600635	17142896	0.16	0	1.00	4.5×10^{-6}	4.3×10^{-2}
48	trans	chr22	rs17606171	1	25544496	0.05	rs4476445	25531002	0.13	13494	0.85	5.1×10^{-6}	1.8×10^{-1}

Crohns Gene 5
ZFYVE16: zinc finger, FYVE domain containing 16
Gene Location: chr5:79703837-79775498
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 1.1×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs6760827	3	154776368	0.25	rs7606717	154773575	0.24	2793	0.92	9.0×10^{-6}	5.0×10^{-2}
3	trans	chr4	rs3111813	1	14275327	0.09	rs3111813	14275327	0.09	0	1.00	2.7×10^{-6}	1.6×10^{-1}
21	trans	chr4	rs11732304	1	118500850	0.07	rs11562866	118492252	0.06	8598	0.99	3.9×10^{-6}	5.3×10^{-1}
39	trans	chr5	rs4532399	1	40467272	0.49	rs4957300	40463739	0.48	3533	1.00	2.8×10^{-6}	7.7×10^{-19}
43	trans	chr6	rs9296686	2	52497672	0.41	rs9296686	52497672	0.41	0	1.00	4.7×10^{-6}	6.3×10^{-3}
46	trans	chr11	rs1939436	1	101610075	0.42	rs1939436	101610075	0.42	0	1.00	1.4×10^{-6}	4.1×10^{-1}
49	trans	chr12	rs1010096	6	27844230	0.36	rs1010096	27844230	0.36	0	1.00	9.9×10^{-6}	5.7×10^{-1}
52	trans	chr12	rs17109931	1	71986944	0.24	rs17109926	71978728	0.23	8216	0.98	6.4×10^{-6}	5.1×10^{-1}
53	trans	chr13	rs7981502	5	30164630	0.16	rs7981502	30164630	0.16	0	1.00	2.7×10^{-6}	6.4×10^{-3}
56	trans	chr13	rs9573848	125	76940976	0.13	rs12866529	76937109	0.19	3867	0.85	4.0×10^{-7}	6.2×10^{-1}
61	trans	chr14	rs10162454	36	75144618	0.28	rs10162454	75144618	0.28	0	1.00	6.4×10^{-6}	5.5×10^{-1}

Crohns Gene 6
DND1: dead end homolog 1 (zebrafish)
Gene Location: chr5:140050380-140053171
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 1.4×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs2944628	2	75697169	0.16	rs2944628	75697169	0.16	0	1.00	6.2×10^{-6}	2.0×10^{-1}
2	trans	chr4	rs231247	1	113359703	0.32	rs231247	113359703	0.32	0	1.00	8.8×10^{-6}	8.3×10^{-1}
5	trans	chr8	rs4424264	1	25487993	0.48	rs4424264	25487993	0.48	0	1.00	7.8×10^{-6}	4.1×10^{-3}
6	trans	chr11	rs963259	1	83944122	0.36	rs1454021	83942876	0.34	1246	0.97	1.2×10^{-6}	1.7×10^{-1}
9	trans	chr17	rs2157839	1	43151400	0.31	rs2157839	43151400	0.31	0	1.00	6.0×10^{-6}	4.1×10^{-1}
18	trans	chr17	rs3946526	5	43541656	0.08	rs3946526	43541656	0.08	0	1.00	7.4×10^{-37}	3.0×10^{-2}
19	trans	chr17	rs2696425	2	43666906	0.42	rs2696425	43666906	0.42	0	1.00	5.6×10^{-54}	9.4×10^{-4}
57	trans	chr17	rs17563827	1	43818222	0.12	rs17563827	43818222	0.12	0	1.00	1.7×10^{-52}	6.0×10^{-4}
189	trans	chr17	rs199535	3	44822662	0.11	rs199535	44822662	0.11	0	1.00	1.8×10^{-56}	6.2×10^{-4}

Crohns Gene 7
RBM6: RNA binding motif protein 6
Gene Location: chr3:49977476-50114685
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 2.5×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs7517092	3	238771226	0.14	rs7517092	238771226	0.14	0	1.00	7.0×10^{-6}	5.3×10^{-2}
3	cis	chr3	rs9827708	1	49649989	0.22	rs9827708	49649989	0.22	0	1.00	2.8×10^{-6}	5.3×10^{-7}
12	cis	chr3	rs2883059	1	49902160	0.30	rs2883059	49902160	0.30	0	1.00	3.2×10^{-26}	1.5×10^{-3}
16	cis	chr3	rs7628058	1	50039474	0.45	rs7628058	50039474	0.45	0	1.00	2.6×10^{-42}	6.2×10^{-4}
31	trans	chr5	rs7736506	5	159314364	0.39	rs6556461	159317458	0.40	3094	1.00	2.3×10^{-6}	6.3×10^{-1}
34	trans	chr6	rs504844	8	163551376	0.21	rs504844	163551376	0.21	0	1.00	1.3×10^{-6}	4.9×10^{-1}
35	trans	chr7	rs10281523	2	132821236	0.28	rs10281523	132821236	0.28	0	1.00	9.3×10^{-6}	8.0×10^{-2}
36	trans	chr16	rs2015762	3	22929538	0.34	rs208625	22928822	0.34	716	1.00	8.1×10^{-7}	8.7×10^{-1}
37	trans	chr20	rs6045861	20	19127331	0.21	rs6035231	19125010	0.24	2321	0.99	7.6×10^{-6}	3.2×10^{-2}

Crohns Gene 7
RBM6: RNA binding motif protein 6
Gene Location: chr3:49977476-50114685
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 1.4×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
4	trans	chr1	rs3753864	1	28390596	0.18	rs3753864	28390596	0.18	0	1.00	1.7×10^{-6}	5.9×10^{-1}
5	trans	chr2	rs1375866	79	23389576	0.32	rs1375866	23389576	0.32	0	1.00	4.5×10^{-6}	2.0×10^{-1}
7	trans	chr2	rs891270	1	41920954	0.28	rs891270	41920954	0.28	0	1.00	5.2×10^{-6}	5.0×10^{-1}
11	cis	chr3	rs11715915	1	49455330	0.26	rs11715915	49455330	0.26	0	1.00	4.0×10^{-5}	1.6×10^{-5}
28	cis	chr3	rs11714957	1	49776178	0.22	rs3749237	49770032	0.23	6146	1.00	4.0×10^{-5}	4.7×10^{-7}
49	cis	chr3	rs3774733	1	50037123	0.42	rs4688689	50035542	0.44	1581	1.00	1.2×10^{-12}	5.7×10^{-4}
73	cis	chr3	rs2236989	1	50505395	0.18	rs2236989	50505395	0.18	0	1.00	6.0×10^{-4}	9.6×10^{-1}
74	trans	chr6	rs2152076	28	118461619	0.38	rs2152076	118461619	0.38	0	1.00	2.0×10^{-6}	1.3×10^{-2}
76	trans	chr8	rs1615810	6	5567808	0.43	rs1615810	5567808	0.43	0	1.00	1.0×10^{-5}	3.2×10^{-3}
77	trans	chr11	rs2048092	2	6629530	0.48	rs2048092	6629530	0.48	0	1.00	9.8×10^{-6}	6.5×10^{-1}
78	trans	chr11	rs2953310	60	40137543	0.46	rs2953310	40137543	0.46	0	1.00	9.1×10^{-6}	9.2×10^{-1}
79	trans	chr12	rs261902	2	32476727	0.17	rs261902	32476727	0.17	0	1.00	4.6×10^{-7}	4.5×10^{-1}
80	trans	chr13	rs9513027	1	28648669	0.27	rs9513027	28648669	0.27	0	1.00	9.1×10^{-6}	5.9×10^{-3}
81	trans	chr17	rs2908948	1	11350711	0.24	rs2908948	11350711	0.24	0	1.00	9.9×10^{-6}	9.5×10^{-2}
82	trans	chr18	rs1789476	2	57146923	0.34	rs1789476	57146923	0.34	0	1.00	7.0×10^{-6}	6.3×10^{-1}
83	trans	chr19	rs2927438	41	45242107	0.18	rs2927438	45242107	0.18	0	1.00	2.3×10^{-6}	2.8×10^{-1}
84	trans	chr20	rs1022790	20	10730759	0.43	rs1022790	10730759	0.43	0	1.00	9.2×10^{-6}	6.5×10^{-1}

Crohns Gene 8
MAPK8IP1: mitogen-activated protein kinase 8 interacting protein 1
Gene Location: chr11:45907046-45928016
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 1.7×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs3773172	1	14511699	0.13	rs3773172	14511699	0.13	0	1.00	1.3×10^{-6}	4.1×10^{-1}
3	trans	chr4	rs2868879	1	85273102	0.48	rs2868879	85273102	0.48	0	1.00	1.2×10^{-6}	8.0×10^{-1}
4	trans	chr7	rs7457799	1	145180002	0.23	rs2372053	145182535	0.23	2533	1.00	5.5×10^{-6}	9.9×10^{-1}
6	trans	chr11	rs2668898	1	61725498	0.41	rs2668898	61725498	0.41	0	1.00	9.8×10^{-6}	8.6×10^{-3}
7	trans	chr15	rs426705	1	68249248	0.49	rs426705	68249248	0.49	0	1.00	1.8×10^{-6}	8.6×10^{-1}
11	trans	chr17	rs7213273	2	43155914	0.31	rs7213273	43155914	0.31	0	1.00	1.1×10^{-12}	5.9×10^{-1}
22	trans	chr17	rs11079502	3	43350666	0.48	rs2074292	43361491	0.48	10825	0.98	4.7×10^{-9}	4.7×10^{-2}
40	trans	chr17	rs17631676	3	43549526	0.10	rs17631303	43516402	0.08	33124	0.98	5.8×10^{-230}	1.3×10^{-1}
43	trans	chr17	rs2696425	2	43666906	0.42	rs2696425	43666906	0.42	0	1.00	0.	9.4×10^{-4}
63	trans	chr17	rs12150547	1	43775546	0.11	rs12150547	43775546	0.11	0	1.00	0.	2.0×10^{-3}
181	trans	chr17	rs1406068	2	44234526	0.10	rs1406068	44234526	0.10	0	1.00	0.	9.2×10^{-4}
196	trans	chr17	rs199436	2	44789285	0.42	rs199436	44789285	0.42	0	1.00	8.2×10^{-320}	2.8×10^{-3}
206	trans	chr21	rs2823756	1	17742330	0.34	rs2823756	17742330	0.34	0	1.00	6.3×10^{-6}	6.5×10^{-2}

Crohns Gene 8
MAPK8IP1: mitogen-activated protein kinase 8 interacting protein 1
Gene Location: chr11:45907046-45928016
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 4.0×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs11128543	38	1178831	0.39	rs11128543	1178831	0.39	0	1.00	1.2×10^{-6}	6.2×10^{-1}
4	trans	chr7	rs4077509	6	43658804	0.30	rs4077509	43658804	0.30	0	1.00	8.9×10^{-6}	6.4×10^{-2}
5	trans	chr17	rs11012	2	43513441	0.10	rs11012	43513441	0.10	0	1.00	3.0×10^{-8}	3.3×10^{-2}
6	trans	chr17	rs393152	1	43719143	0.27	rs393152	43719143	0.27	0	1.00	4.0×10^{-11}	1.1×10^{-3}
11	trans	chr17	rs242924	1	43885367	0.48	rs110402	43880047	0.49	5320	0.98	5.8×10^{-7}	5.7×10^{-1}
22	trans	chr17	rs7221390	2	44116950	0.12	rs7221390	44116950	0.12	0	1.00	7.1×10^{-11}	9.8×10^{-4}
28	trans	chr17	rs199533	1	44828931	0.10	rs199533	44828931	0.10	0	1.00	1.7×10^{-12}	3.5×10^{-4}
32	trans	chr20	rs4810479	3	44545048	0.44	rs4810479	44545048	0.44	0	1.00	1.5×10^{-6}	9.6×10^{-1}

Crohns Gene 8
MAPK8IP1: mitogen-activated protein kinase 8 interacting protein 1
Gene Location: chr11:45907046-45928016
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 1.3×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr4	rs547838	1	160009294	0.37	rs547838	160009294	0.37	0	1.00	4.4×10^{-6}	7.6×10^{-2}
2	trans	chr6	rs505347	1	103600715	0.36	rs505347	103600715	0.36	0	1.00	9.2×10^{-6}	4.0×10^{-1}
3	trans	chr7	rs258658	2	81725129	0.41	rs258664	81727029	0.39	1900	0.98	5.5×10^{-6}	7.8×10^{-1}
5	trans	chr7	rs310589	7	150892599	0.24	rs310589	150892599	0.24	0	1.00	5.0×10^{-6}	6.1×10^{-1}
7	trans	chr10	rs10821585	2	61516587	0.47	rs10128501	61508784	0.50	7803	0.94	3.1×10^{-7}	9.9×10^{-1}
9	trans	chr10	rs4918766	7	96711884	0.35	rs4918766	96711884	0.35	0	1.00	7.5×10^{-6}	1.4×10^{-1}
10	trans	chr15	rs4779101	2	79800041	0.33	rs4779101	79800041	0.33	0	1.00	7.9×10^{-7}	2.3×10^{-1}
11	trans	chr17	rs3946526	5	43541656	0.08	rs3946526	43541656	0.08	0	1.00	4.5×10^{-6}	3.0×10^{-2}
22	trans	chr17	rs17761207	1	43762255	0.11	rs17761207	43762255	0.11	0	1.00	1.2×10^{-7}	1.3×10^{-3}
114	trans	chr17	rs2732705	1	44351929	0.06	rs2732705	44351929	0.06	0	1.00	5.0×10^{-8}	4.5×10^{-4}
118	trans	chr21	rs9977811	1	15534637	0.25	rs9977811	15534637	0.25	0	1.00	3.4×10^{-6}	2.5×10^{-1}

Crohns Gene 9
HYAL3: hyaluronoglucosaminidase 3
Gene Location: chr3:50330258-50336899
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 2.1×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs3820667	1	109968410	0.48	rs3820667	109968410	0.48	0	1.00	8.6×10^{-6}	7.2×10^{-1}
3	trans	chr2	rs2696114	7	183528968	0.37	rs2696114	183528968	0.37	0	1.00	5.1×10^{-6}	7.9×10^{-1}
5	trans	chr3	rs12491849	2	48531227	0.22	rs12491849	48531227	0.22	0	1.00	2.3×10^{-6}	1.8×10^{-1}
6	trans	chr3	rs3172494	1	48731487	0.11	rs3172494	48731487	0.11	0	1.00	1.6×10^{-6}	7.1×10^{-1}
7	trans	chr3	rs5030795	1	49141116	0.07	rs9880088	49178990	0.08	37874	0.99	2.3×10^{-7}	2.2×10^{-3}
12	trans	chr3	rs4410472	1	49329090	0.44	rs4410472	49329090	0.44	0	1.00	1.2×10^{-8}	8.6×10^{-6}
23	cis	chr3	rs2131104	1	49696633	0.49	rs2131104	49696633	0.49	0	1.00	3.6×10^{-8}	4.9×10^{-7}
28	cis	chr3	rs2271960	2	49878078	0.40	rs2271960	49878078	0.40	0	1.00	5.7×10^{-7}	6.4×10^{-5}
38	cis	chr3	rs7635601	1	50044006	0.16	rs7615318	49987475	0.17	56531	0.94	6.7×10^{-16}	2.1×10^{-1}
52	cis	chr3	rs12632110	1	50224225	0.42	rs12632110	50224225	0.42	0	1.00	8.1×10^{-34}	1.9×10^{-1}
59	cis	chr3	rs4619816	2	51248198	0.49	rs4619816	51248198	0.49	0	1.00	8.0×10^{-15}	4.1×10^{-1}
61	trans	chr3	rs7620081	3	51500591	0.08	rs7620081	51500591	0.08	0	1.00	4.4×10^{-7}	7.1×10^{-1}
63	trans	chr5	rs2416492	1	117338365	0.39	rs2416492	117338365	0.39	0	1.00	8.3×10^{-6}	7.5×10^{-1}
64	trans	chr14	rs8011721	1	102986388	0.42	rs8011721	102986388	0.42	0	1.00	7.7×10^{-6}	8.5×10^{-1}
65	trans	chr15	rs17786786	3	71608619	0.29	rs17786786	71608619	0.29	0	1.00	3.4×10^{-7}	9.8×10^{-1}
68	trans	chr16	rs258097	2	55765906	0.29	rs258097	55765906	0.29	0	1.00	4.7×10^{-6}	3.0×10^{-1}

Crohns Gene 9
HYAL3: hyaluronoglucosaminidase 3
Gene Location: chr3:50330258-50336899
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 9.7×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs12751011	2	80078821	0.25	rs2127436	80079996	0.28	1175	0.99	3.0×10^{-6}	6.6×10^{-1}
9	trans	chr2	rs11127473	2	470329	0.37	rs12479270	458363	0.35	11966	0.91	8.0×10^{-6}	3.7×10^{-1}
11	trans	chr3	rs2873641	2	96563005	0.05	rs2873641	96563005	0.05	0	1.00	1.0×10^{-5}	3.1×10^{-2}
12	trans	chr3	rs1358024	2	133484188	0.20	rs1358024	133484188	0.20	0	1.00	4.0×10^{-7}	7.3×10^{-1}
13	trans	chr4	rs13150862	2	15420372	0.19	rs17385047	15433195	0.19	12823	0.96	8.0×10^{-6}	8.2×10^{-2}
18	trans	chr4	rs2608836	2	39486593	0.26	rs2608836	39486593	0.26	0	1.00	3.0×10^{-6}	5.2×10^{-3}
35	trans	chr4	rs975477	2	139539662	0.20	rs975477	139539662	0.20	0	1.00	3.0×10^{-7}	6.4×10^{-2}
37	trans	chr4	rs12499698	6	141808099	0.20	rs10519565	141796795	0.21	11304	0.98	3.0×10^{-6}	3.0×10^{-1}
40	trans	chr5	rs4262120	3	30563394	0.47	rs4262120	30563394	0.47	0	1.00	6.0×10^{-6}	2.3×10^{-1}
41	trans	chr5	rs2902316	2	129003982	0.20	rs3909548	128969615	0.06	34367	0.96	8.0×10^{-6}	9.7×10^{-1}
43	trans	chr7	rs7800747	2	35389499	0.12	rs7800747	35389499	0.12	0	1.00	7.0×10^{-6}	1.8×10^{-2}
45	trans	chr7	rs10951449	2	35596304	0.40	rs10951449	35596304	0.40	0	1.00	1.0×10^{-5}	5.5×10^{-1}
50	trans	chr9	rs1360410	8	18159671	0.19	rs1360410	18159671	0.19	0	1.00	8.0×10^{-6}	6.2×10^{-1}
54	trans	chr9	rs17792842	2	111761784	0.12	rs1772033	111769543	0.12	7759	0.96	1.0×10^{-5}	6.7×10^{-1}
55	trans	chr9	rs6477689	2	111880693	0.24	rs2805888	111880736	0.22	43	NA	2.0×10^{-6}	8.7×10^{-1}
58	trans	chr9	rs10818139	5	121099040	0.46	rs10818139	121099040	0.46	0	1.00	4.0×10^{-6}	4.1×10^{-1}
62	trans	chr12	rs7978413	14	94513816	0.24	rs7978413	94513816	0.24	0	1.00	2.0×10^{-6}	5.0×10^{-1}
65	trans	chr13	rs4326946	2	58689521	0.43	rs9537936	58647862	0.45	41659	0.99	1.0×10^{-5}	3.6×10^{-1}
67	trans	chr13	rs6491306	3	97445165	0.20	rs1924597	97440571	0.14	4594	0.90	3.0×10^{-6}	2.3×10^{-1}
75	trans	chr20	rs4813979	18	1178698	0.05	rs7266780	1183560	0.05	4862	1.00	1.0×10^{-5}	2.6×10^{-1}

Crohns Gene 10
SLC22A4: solute carrier family 22 (organic cation/ergothioneine transporter), member 4
Gene Location: chr5:131630144-131679899
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 2.2×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs11121289	3	9054049	0.10	rs11121289	9054049	0.10	0	1.00	3.3×10^{-6}	8.3×10^{-1}
3	trans	chr4	rs6842767	1	185104471	0.11	rs6552764	185104503	0.19	32	1.00	1.9×10^{-6}	3.9×10^{-1}
4	cis	chr5	rs3756295	2	130692840	0.48	rs3756295	130692840	0.48	0	1.00	4.1×10^{-6}	1.3×10^{-4}
9	cis	chr5	rs440970	3	131336287	0.38	rs440970	131336287	0.38	0	1.00	6.8×10^{-23}	7.2×10^{-3}
29	cis	chr5	rs4361509	1	131536753	0.23	rs4361509	131536753	0.23	0	1.00	3.9×10^{-27}	2.3×10^{-6}
90	cis	chr5	rs2227282	1	132013179	0.48	rs2227282	132013179	0.48	0	1.00	5.6×10^{-9}	1.2×10^{-1}
96	trans	chr9	rs2249710	1	130325264	0.43	rs2249710	130325264	0.43	0	1.00	4.4×10^{-6}	4.5×10^{-1}
97	trans	chr11	rs7122729	1	37303654	0.39	rs7122729	37303654	0.39	0	1.00	5.8×10^{-6}	6.1×10^{-1}
98	trans	chr22	rs3827336	3	33020998	0.11	rs3827336	33020998	0.11	0	1.00	8.3×10^{-6}	8.5×10^{-1}

Crohns Gene 10
SLC22A4: solute carrier family 22 (organic cation/ergothioneine transporter), member 4
Gene Location: chr5:131630144-131679899
GWAS Data: Barrett 2008
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 8.7×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr2	rs2716736	23	39947947	0.15	rs2716736	39947947	0.15	0	1.00	4.8×10^{-6}	1.0×10^{-2}

Crohns Gene 11
SOX15: SRY (sex determining region Y)-box 15
Gene Location: chr17:7491497-7493488
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 1.8×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs2365470	1	158751416	0.07	rs12497390	158727551	0.09	23865	0.99	6.6×10^{-6}	1.2×10^{-2}
2	trans	chr11	rs2155220	1	76266172	0.40	rs2155220	76266172	0.40	0	1.00	8.1×10^{-6}	1.3×10^{-2}
8	cis	chr17	rs12936934	4	7500765	0.17	rs9898876	7526962	0.18	26197	1.00	5.8×10^{-11}	6.0×10^{-1}

Crohns Gene 11
SOX15: SRY (sex determining region Y)-box 15
Gene Location: chr17:7491497-7493488
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 2.3×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs7582497	23	43638947	0.36	rs7582497	43638947	0.36	0	1.00	7.4×10^{-6}	3.0×10^{-1}
2	trans	chr2	rs3792106	2	234190740	0.47	rs3792106	234190740	0.47	0	1.00	4.9×10^{-6}	3.8×10^{-17}
5	trans	chr7	rs6462963	1	40230346	0.50	rs6462963	40230346	0.50	0	1.00	4.0×10^{-6}	4.1×10^{-2}

Crohns Gene 12
PLEKHB2: pleckstrin homology domain containing, family B (evectins) member 2
Gene Location: chr2:131862419-131907425
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 3.3×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr1	rs11209039	6	67751193	0.40	rs11209039	67751193	0.40	0	1.00	2.0×10^{-6}	6.1×10^{-13}
6	trans	chr1	rs3933049	43	242480885	0.26	rs6690240	242477096	0.25	3789	0.89	8.0×10^{-7}	3.4×10^{-1}
8	trans	chr2	rs2357888	15	11184914	0.50	rs2357888	11184914	0.50	0	1.00	2.0×10^{-6}	1.4×10^{-1}
9	trans	chr5	rs16889921	10	58813031	0.20	rs10514862	58797572	0.21	15459	1.00	7.0×10^{-6}	7.3×10^{-3}
10	trans	chr7	rs7794021	11	11398356	0.44	rs739774	11394751	0.37	3605	0.91	6.0×10^{-6}	2.3×10^{-2}
12	trans	chr9	rs7018646	56	126926031	0.17	rs7018646	126926031	0.17	0	1.00	7.0×10^{-7}	2.0×10^{-1}
15	trans	chr10	rs10734095	432	129084327	0.36	rs10734095	129084327	0.36	0	1.00	9.0×10^{-6}	1.4×10^{-1}
18	trans	chr12	rs4762869	20	22202346	0.22	rs11046274	22200916	0.26	1430	1.00	1.0×10^{-5}	6.2×10^{-1}
19	trans	chr21	rs12053716	2	19911397	0.12	rs1740194	19923715	0.18	12318	0.91	4.0×10^{-6}	1.8×10^{-1}

Crohns Gene 12
PLEKHB2: pleckstrin homology domain containing, family B (evectins) member 2
Gene Location: chr2:131862419-131907425
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 1.8×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs10181599	1	34056072	0.42	rs7561434	34062843	0.29	6771	0.97	6.5×10^{-6}	6.8×10^{-1}
2	trans	chr2	rs1367237	7	222218904	0.30	rs4674584	222211490	0.25	7414	1.00	9.5×10^{-6}	6.3×10^{-1}
8	trans	chr9	rs10971203	5	32899739	0.35	rs10971193	32896388	0.34	3351	1.00	4.8×10^{-6}	9.1×10^{-1}
9	trans	chr10	rs1334592	1	16447004	0.24	rs1334592	16447004	0.24	0	1.00	7.6×10^{-6}	2.9×10^{-1}
10	trans	chr11	rs570024	1	64215032	0.31	rs596308	64210652	0.35	4380	0.91	2.9×10^{-6}	3.2×10^{-5}
20	trans	chr12	rs11181929	5	43595873	0.37	rs1922765	43597224	0.37	1351	1.00	6.1×10^{-6}	2.7×10^{-1}
34	trans	chr13	rs912659	3	100259210	0.22	rs912659	100259210	0.22	0	1.00	5.7×10^{-6}	3.8×10^{-2}
40	trans	chr17	rs555355	3	75091219	0.20	rs716284	75075680	0.02	15539	0.99	5.1×10^{-6}	9.8×10^{-1}
41	trans	chr19	rs351967	7	789890	0.34	rs351967	789890	0.34	0	1.00	7.2×10^{-6}	2.5×10^{-1}

Crohns Gene 13
CLEC1B: C-type lectin domain family 1, member B
Gene Location: chr12:10145661-10151899
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 6.4×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs2668069	20	37976700	0.19	rs2668069	37976700	0.19	0	1.00	6.3×10^{-6}	1.4×10^{-1}
4	trans	chr3	rs12485738	174	56865776	0.37	rs12485738	56865776	0.37	0	1.00	1.8×10^{-15}	2.2×10^{-1}
13	trans	chr4	rs1485571	3	20067226	0.34	rs961521	20078019	0.37	10793	0.97	2.1×10^{-6}	1.2×10^{-2}
15	trans	chr5	rs10512734	1	40393605	0.48	rs10512734	40393605	0.48	0	1.00	6.1×10^{-6}	8.8×10^{-17}
36	cis	chr12	rs4764188	1	10158924	0.32	rs4764188	10158924	0.32	0	1.00	1.1×10^{-9}	8.1×10^{-1}
37	trans	chr12	rs10506328	1	54687232	0.16	rs10506328	54687232	0.16	0	1.00	1.1×10^{-6}	4.5×10^{-2}

Crohns Gene 13
CLEC1B: C-type lectin domain family 1, member B
Gene Location: chr12:10145661-10151899
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 10.0×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr1	rs12085479	1	51199116	0.40	rs12085479	51199116	0.40	0	1.00	7.3×10^{-6}	2.8×10^{-3}
3	trans	chr3	rs696078	2	22944157	0.29	rs696078	22944157	0.29	0	1.00	5.1×10^{-6}	8.4×10^{-1}
4	trans	chr4	rs828152	1	17063564	0.26	rs828151	17063786	0.30	222	NA	8.2×10^{-6}	9.3×10^{-1}
5	trans	chr4	rs353173	1	68779749	0.30	rs353170	68781464	0.28	1715	1.00	5.9×10^{-6}	8.7×10^{-1}
6	trans	chr5	rs11135114	2	160187121	0.29	rs7726599	160187078	0.34	43	NA	4.4×10^{-6}	5.5×10^{-2}

Crohns Gene 14
GAS6: growth arrest-specific 6
Gene Location: chr13:114523521-114567046
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 6.5×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
3	trans	chr1	rs4839053	4	111111149	0.35	rs4839053	111111149	0.35	0	1.00	9.5×10^{-7}	5.2×10^{-2}
5	trans	chr4	rs9998195	3	5026576	0.16	rs4689977	5022496	0.16	4080	0.98	9.7×10^{-6}	1.5×10^{-1}
6	trans	chr5	rs9292777	1	40437948	0.47	rs9292777	40437948	0.47	0	1.00	1.2×10^{-6}	5.5×10^{-22}
7	trans	chr5	rs7732173	2	75477663	0.13	rs7732173	75477663	0.13	0	1.00	3.2×10^{-6}	4.6×10^{-1}
12	trans	chr5	rs307311	1	84693620	0.19	rs307311	84693620	0.19	0	1.00	6.2×10^{-6}	2.0×10^{-1}

Crohns Gene 15
FALZ: Not Found in HUGO
Gene Location: Not Found:Not Found-Not Found
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 6.6×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs13321458	1	68610030	0.17	rs13321458	68610030	0.17	0	1.00	9.4×10^{-6}	2.3×10^{-1}
3	trans	chr5	rs2398624	1	3714522	0.23	rs2398624	3714522	0.23	0	1.00	9.5×10^{-6}	6.5×10^{-1}
4	trans	chr11	rs4754859	1	97058949	0.48	rs4754859	97058949	0.48	0	1.00	8.1×10^{-6}	1.4×10^{-1}
14	trans	chr17	rs17631676	3	43549526	0.10	rs17631303	43516402	0.08	33124	0.98	6.1×10^{-57}	1.3×10^{-1}
56	trans	chr17	rs17563827	1	43818222	0.12	rs17563827	43818222	0.12	0	1.00	8.0×10^{-78}	6.0×10^{-4}
110	trans	chr17	rs17572893	1	44064208	0.05	rs17572893	44064208	0.05	0	1.00	9.3×10^{-76}	1.1×10^{-3}
154	trans	chr17	rs2668624	1	44352872	0.10	rs2668624	44352872	0.10	0	1.00	1.7×10^{-85}	6.0×10^{-4}
158	trans	chr17	rs199448	1	44809001	0.10	rs199448	44809001	0.10	0	1.00	3.5×10^{-92}	6.4×10^{-4}
162	trans	chr18	rs7231138	1	72616636	0.12	rs10514147	72613208	0.10	3428	1.00	2.4×10^{-6}	8.0×10^{-1}
165	trans	chr20	rs6019504	2	47514595	0.13	rs6019504	47514595	0.13	0	1.00	8.9×10^{-6}	3.4×10^{-1}

Crohns Gene 16
LRRC37A4: Not Found in HUGO
Gene Location: chr17:43583248-43597889
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 7.4×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
3	trans	chr1	rs11118121	1	218719755	0.23	rs11118121	218719755	0.23	0	1.00	8.6×10^{-6}	5.6×10^{-1}
6	trans	chr2	rs1037221	1	177401482	0.08	rs1037221	177401482	0.08	0	1.00	3.9×10^{-7}	4.0×10^{-1}
7	trans	chr5	rs4867686	1	172150990	0.21	rs4867686	172150990	0.21	0	1.00	6.2×10^{-6}	5.5×10^{-2}
8	trans	chr6	rs17084394	2	154033562	0.10	rs17084394	154033562	0.10	0	1.00	7.0×10^{-6}	6.2×10^{-1}
10	trans	chr7	rs39075	1	29276692	0.43	rs39075	29276692	0.43	0	1.00	8.1×10^{-6}	9.1×10^{-1}
11	trans	chr7	rs810532	3	73505188	0.26	rs810532	73505188	0.26	0	1.00	3.1×10^{-7}	6.8×10^{-1}
13	trans	chr8	rs7460992	1	17929475	0.29	rs7460992	17929475	0.29	0	1.00	3.6×10^{-6}	5.8×10^{-1}
14	trans	chr8	rs309843	1	29848666	0.09	rs309843	29848666	0.09	0	1.00	2.6×10^{-6}	5.0×10^{-1}
15	trans	chr9	rs4837360	1	132109628	0.38	rs4837360	132109628	0.38	0	1.00	1.4×10^{-6}	3.8×10^{-1}
16	trans	chr11	rs4758006	1	7645720	0.32	rs4758006	7645720	0.32	0	1.00	3.5×10^{-7}	8.0×10^{-1}
19	cis	chr17	rs1558085	1	42854208	0.46	rs1558085	42854208	0.46	0	1.00	9.3×10^{-7}	9.0×10^{-1}
26	cis	chr17	rs7213273	2	43155914	0.31	rs7213273	43155914	0.31	0	1.00	1.1×10^{-6}	5.9×10^{-1}
32	cis	chr17	rs11079502	3	43350666	0.48	rs2074292	43361491	0.48	10825	0.98	9.6×10^{-13}	4.7×10^{-2}
47	cis	chr17	rs17631676	3	43549526	0.10	rs17631303	43516402	0.08	33124	0.98	6.0×10^{-208}	1.3×10^{-1}
50	cis	chr17	rs2696425	2	43666906	0.42	rs2696425	43666906	0.42	0	1.00	0.	9.4×10^{-4}
69	cis	chr17	rs17688434	1	43772540	0.05	rs17688434	43772540	0.05	0	1.00	0.	1.8×10^{-3}
183	cis	chr17	rs1406068	2	44234526	0.10	rs1406068	44234526	0.10	0	1.00	0.	9.2×10^{-4}
198	trans	chr17	rs199436	2	44789285	0.42	rs199436	44789285	0.42	0	1.00	1.2×10^{-179}	2.8×10^{-3}
208	trans	chr17	rs2165846	1	44941366	0.37	rs2165846	44941366	0.37	0	1.00	4.7×10^{-6}	8.5×10^{-2}
209	trans	chr18	rs1284194	1	13667707	0.38	rs1149356	13666768	0.36	939	1.00	9.0×10^{-6}	9.9×10^{-1}
210	trans	chr20	rs6111042	2	16291006	0.45	rs6111042	16291006	0.45	0	1.00	7.5×10^{-6}	8.9×10^{-1}
211	trans	chr21	rs2164171	2	27789058	0.25	rs2164171	27789058	0.25	0	1.00	2.9×10^{-6}	7.4×10^{-1}

Crohns Gene 17
USP4: ubiquitin specific peptidase 4 (proto-oncogene)
Gene Location: chr3:49314576-49377536
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 7.9×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
11	cis	chr3	rs4077495	2	48756512	0.13	rs4077495	48756512	0.13	0	1.00	4.7×10^{-21}	2.2×10^{-3}
14	cis	chr3	rs9990153	1	49291883	0.09	rs9990153	49291883	0.09	0	1.00	9.8×10^{-28}	4.1×10^{-3}
29	cis	chr3	rs9858542	2	49701983	0.24	rs9858542	49701983	0.24	0	1.00	2.9×10^{-11}	1.9×10^{-7}
32	cis	chr3	rs739983	2	50178011	0.39	rs739983	50178011	0.39	0	1.00	1.2×10^{-6}	4.6×10^{-1}
33	trans	chr3	rs9869826	3	50998816	0.12	rs9869826	50998816	0.12	0	1.00	4.5×10^{-17}	5.9×10^{-1}
34	trans	chr3	rs7620081	3	51500591	0.08	rs7620081	51500591	0.08	0	1.00	7.4×10^{-16}	7.1×10^{-1}

Crohns Gene 17
USP4: ubiquitin specific peptidase 4 (proto-oncogene)
Gene Location: chr3:49314576-49377536
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 4.7×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs12402327	4	14583625	0.13	rs12402327	14583625	0.13	0	1.00	5.4×10^{-6}	1.1×10^{-1}
3	trans	chr7	rs12535198	133	85473354	0.20	rs9640974	85470182	0.23	3172	1.00	2.5×10^{-6}	3.8×10^{-1}
5	trans	chr12	rs1388658	9	27154542	0.40	rs10400476	27151891	0.39	2651	1.00	2.8×10^{-6}	3.2×10^{-2}

Crohns Gene 18
KCNJ13: potassium inwardly-rectifying channel, subfamily J, member 13
Gene Location: chr2:233630511-233641275
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 8.5×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs6712128	1	177770340	0.29	rs6755532	177769869	0.28	471	1.00	9.7×10^{-6}	3.2×10^{-1}
2	cis	chr2	rs2697766	3	233268715	0.39	rs2697766	233268715	0.39	0	1.00	7.0×10^{-4}	8.7×10^{-1}
4	trans	chr4	rs17017359	1	91575828	0.10	rs17017359	91575828	0.10	0	1.00	5.5×10^{-6}	6.3×10^{-2}
5	trans	chr8	rs1011158	1	9104831	0.48	rs1011158	9104831	0.48	0	1.00	5.5×10^{-6}	3.4×10^{-1}
6	trans	chr10	rs1539089	2	102221424	0.21	rs1539089	102221424	0.21	0	1.00	7.5×10^{-6}	1.3×10^{-1}
7	trans	chr16	rs3826103	1	12664929	0.48	rs890893	12664137	0.45	792	0.91	4.5×10^{-6}	2.8×10^{-3}
9	trans	chr16	rs6500331	1	50808726	0.45	rs6500331	50808726	0.45	0	1.00	7.7×10^{-6}	6.0×10^{-10}
10	trans	chr18	rs4940927	2	57732689	0.32	rs4940927	57732689	0.32	0	1.00	4.8×10^{-6}	1.6×10^{-1}

Crohns Gene 19
CDC42SE2: CDC42 small effector 2
Gene Location: chr5:130599701-130730382
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 3.8×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
3	cis	chr5	rs12516376	1	129720170	0.19	rs12516376	129720170	0.19	0	1.00	1.3×10^{-6}	2.2×10^{-3}
32	cis	chr5	rs12153520	1	130418134	0.15	rs12153520	130418134	0.15	0	1.00	1.0×10^{-13}	1.0×10^{-2}
46	cis	chr5	rs3756295	2	130692840	0.48	rs3756295	130692840	0.48	0	1.00	2.0×10^{-9}	1.3×10^{-4}
53	cis	chr5	rs440970	3	131336287	0.38	rs440970	131336287	0.38	0	1.00	3.5×10^{-11}	7.2×10^{-3}
63	trans	chr7	rs11767371	3	45248653	0.17	rs11767371	45248653	0.17	0	1.00	3.5×10^{-6}	4.6×10^{-1}
64	trans	chr22	rs6004306	1	25230909	0.23	rs6004306	25230909	0.23	0	1.00	9.3×10^{-6}	3.8×10^{-1}

Crohns Gene 19
CDC42SE2: CDC42 small effector 2
Gene Location: chr5:130599701-130730382
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 9.0×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs780235	38	233674529	0.31	rs780235	233674529	0.31	0	1.00	1.5×10^{-6}	3.8×10^{-1}
2	trans	chr2	rs1386352	2	173046754	0.38	rs1386352	173046754	0.38	0	1.00	8.3×10^{-6}	5.2×10^{-1}
3	trans	chr5	rs6893661	3	34732224	0.45	rs6893661	34732224	0.45	0	1.00	2.9×10^{-7}	2.7×10^{-1}
4	trans	chr5	rs716971	3	35795738	0.49	rs716971	35795738	0.49	0	1.00	5.5×10^{-6}	6.6×10^{-2}
5	trans	chr5	rs10942328	3	82737843	0.19	rs10942328	82737843	0.19	0	1.00	7.1×10^{-7}	1.3×10^{-1}
6	cis	chr5	rs10520079	1	129820038	0.12	rs10520079	129820038	0.12	0	1.00	5.5×10^{-6}	1.3×10^{-5}
8	cis	chr5	rs1978235	1	129921388	0.41	rs1978235	129921388	0.41	0	1.00	7.0×10^{-5}	4.2×10^{-3}
10	cis	chr5	rs10477723	1	130187390	0.42	rs10477723	130187390	0.42	0	1.00	1.1×10^{-4}	7.4×10^{-4}
25	cis	chr5	rs4706009	1	130536044	0.17	rs4706009	130536044	0.17	0	1.00	2.8×10^{-23}	4.4×10^{-2}
37	cis	chr5	rs1291602	1	130766662	0.10	rs1291602	130766662	0.10	0	1.00	8.2×10^{-33}	8.4×10^{-2}
71	cis	chr5	rs440970	1	131336287	0.38	rs440970	131336287	0.38	0	1.00	4.7×10^{-10}	7.2×10^{-3}
90	trans	chr6	rs354532	3	111548813	0.48	rs354532	111548813	0.48	0	1.00	6.2×10^{-6}	4.5×10^{-1}
91	trans	chr7	rs4255023	1	73239618	0.43	rs4255023	73239618	0.43	0	1.00	2.8×10^{-6}	2.2×10^{-1}
93	trans	chr7	rs10228290	1	155879851	0.30	rs10228290	155879851	0.30	0	1.00	3.9×10^{-6}	8.6×10^{-1}
95	trans	chr8	rs1390943	1	20081890	0.41	rs1390943	20081890	0.41	0	1.00	2.0×10^{-6}	9.2×10^{-2}
97	trans	chr9	rs10979066	7	110597519	0.23	rs10979066	110597519	0.23	0	1.00	2.6×10^{-6}	2.1×10^{-1}
99	trans	chr10	rs496776	1	29515598	0.34	rs496776	29515598	0.34	0	1.00	2.1×10^{-6}	8.3×10^{-1}
100	trans	chr11	rs6589872	1	121158100	0.45	rs6589872	121158100	0.45	0	1.00	6.5×10^{-6}	9.5×10^{-2}
101	trans	chr12	rs4883169	12	8725426	0.23	rs4883169	8725426	0.23	0	1.00	6.0×10^{-6}	8.0×10^{-1}
102	trans	chr13	rs1571070	14	103374377	0.48	rs1571070	103374377	0.48	0	1.00	7.8×10^{-6}	3.5×10^{-1}
103	trans	chr14	rs2383301	8	32890538	0.08	rs2383301	32890538	0.08	0	1.00	5.7×10^{-6}	2.1×10^{-1}
104	trans	chr15	rs8027435	3	98624886	0.50	rs8027435	98624886	0.50	0	1.00	4.2×10^{-6}	2.3×10^{-1}
105	trans	chr16	rs9923450	2	9102388	0.35	rs9923450	9102388	0.35	0	1.00	1.8×10^{-6}	7.8×10^{-1}
107	trans	chr16	rs6498567	1	15771601	0.29	rs6498567	15771601	0.29	0	1.00	6.3×10^{-6}	1.3×10^{-3}
108	trans	chr16	rs27590	18	65845916	0.15	rs27590	65845916	0.15	0	1.00	5.2×10^{-6}	9.4×10^{-1}
109	trans	chr19	rs2305767	1	17294296	0.23	rs2305767	17294296	0.23	0	1.00	1.0×10^{-5}	6.4×10^{-1}
110	trans	chr20	rs6137426	17	2227433	0.27	rs6137426	2227433	0.27	0	1.00	2.4×10^{-6}	1.6×10^{-1}

Crohns Gene 19
CDC42SE2: CDC42 small effector 2
Gene Location: chr5:130599701-130730382
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 1.6×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs12026921	4	213464445	0.27	rs12026921	213464445	0.27	0	1.00	2.2×10^{-6}	6.3×10^{-1}
2	trans	chr2	rs17049685	1	58906501	0.10	rs17049685	58906501	0.10	0	1.00	9.5×10^{-6}	10.0×10^{-1}
6	cis	chr5	rs10035791	1	129891761	0.14	rs10035791	129891761	0.14	0	1.00	1.6×10^{-5}	2.0×10^{-3}
61	cis	chr5	rs2079511	1	130560128	0.10	rs2079511	130560128	0.10	0	1.00	2.3×10^{-13}	2.8×10^{-2}
68	cis	chr5	rs31251	1	130833946	0.24	rs31251	130833946	0.24	0	1.00	4.9×10^{-9}	1.9×10^{-4}
74	cis	chr5	rs440970	1	131336287	0.38	rs440970	131336287	0.38	0	1.00	5.1×10^{-6}	7.2×10^{-3}
77	trans	chr7	rs1860477	2	146738312	0.30	rs1860477	146738312	0.30	0	1.00	5.8×10^{-6}	6.9×10^{-1}
78	trans	chr12	rs11063789	1	5748324	0.38	rs2159950	5732481	0.31	15843	0.89	8.4×10^{-6}	1.8×10^{-1}
79	trans	chr13	rs9514827	7	108919403	0.30	rs9514827	108919403	0.30	0	1.00	3.5×10^{-6}	7.7×10^{-1}
80	trans	chr16	rs8055161	14	82443459	0.11	rs8055161	82443459	0.11	0	1.00	6.2×10^{-6}	9.9×10^{-1}
82	trans	chr16	rs918727	4	86590080	0.36	rs918727	86590080	0.36	0	1.00	3.1×10^{-6}	3.0×10^{-1}
85	trans	chr20	rs11698656	2	8819136	0.38	rs6140742	8819112	0.39	24	1.00	5.6×10^{-6}	6.0×10^{-2}

Crohns Gene 20
SLC22A5: solute carrier family 22 (organic cation/carnitine transporter), member 5
Gene Location: chr5:131705400-131731306
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 1.0×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
3	trans	chr5	rs2460164	1	90058190	0.37	rs2460164	90058190	0.37	0	1.00	6.3×10^{-6}	8.4×10^{-1}
4	trans	chr5	rs11242022	1	129661649	0.39	rs11242022	129661649	0.39	0	1.00	8.5×10^{-6}	4.0×10^{-1}
7	trans	chr5	rs12518350	1	130096260	0.34	rs12518350	130096260	0.34	0	1.00	5.9×10^{-6}	1.9×10^{-2}
30	trans	chr5	rs7728773	1	130446419	0.31	rs7728773	130446419	0.31	0	1.00	2.5×10^{-6}	3.6×10^{-4}
32	trans	chr5	rs6875363	1	130581195	0.19	rs6875363	130581195	0.19	0	1.00	9.0×10^{-9}	4.1×10^{-3}
36	cis	chr5	rs867150	2	130743668	0.13	rs867150	130743668	0.13	0	1.00	8.2×10^{-7}	7.8×10^{-2}
63	cis	chr5	rs440970	3	131336287	0.38	rs440970	131336287	0.38	0	1.00	3.1×10^{-27}	7.2×10^{-3}
111	cis	chr5	rs10900805	1	131580851	0.15	rs10900805	131580851	0.15	0	1.00	8.0×10^{-8}	9.0×10^{-2}
128	cis	chr5	rs2631360	1	131707429	0.32	rs4705938	131694077	0.22	13352	0.97	6.7×10^{-85}	1.5×10^{-6}
173	cis	chr5	rs11242127	1	132055504	0.42	rs11242127	132055504	0.42	0	1.00	2.0×10^{-8}	1.6×10^{-1}
174	trans	chr7	rs2125404	6	34697388	0.17	rs2125404	34697388	0.17	0	1.00	1.3×10^{-6}	6.3×10^{-1}
175	trans	chr10	rs2210461	1	110386320	0.22	rs2210461	110386320	0.22	0	1.00	2.3×10^{-7}	3.5×10^{-1}
178	trans	chr17	rs17705445	2	36131437	0.27	rs17705445	36131437	0.27	0	1.00	4.4×10^{-6}	2.8×10^{-1}
180	trans	chr21	rs458744	2	27574648	0.18	rs463164	27578868	0.14	4220	1.00	3.0×10^{-6}	5.3×10^{-1}

Crohns Gene 20
SLC22A5: solute carrier family 22 (organic cation/carnitine transporter), member 5
Gene Location: chr5:131705400-131731306
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 4.3×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs10490083	1	202877944	0.17	rs10490083	202877944	0.17	0	1.00	1.1×10^{-7}	1.5×10^{-1}
2	trans	chr2	rs6717510	12	225087829	0.33	rs6717510	225087829	0.33	0	1.00	7.3×10^{-6}	9.3×10^{-1}
3	trans	chr4	rs1812310	2	5221578	0.12	rs1812310	5221578	0.12	0	1.00	6.6×10^{-6}	7.6×10^{-3}
6	cis	chr5	rs1858074	2	131371999	0.14	rs1858074	131371999	0.14	0	1.00	4.0×10^{-5}	9.3×10^{-5}
22	cis	chr5	rs11950562	1	131652529	0.27	rs4705938	131694077	0.22	41548	0.99	1.8×10^{-8}	1.5×10^{-6}
35	cis	chr5	rs803218	12	132216264	0.46	rs803218	132216264	0.46	0	1.00	2.0×10^{-5}	7.6×10^{-1}
38	trans	chr13	rs1343794	1	72663889	0.24	rs1343794	72663889	0.24	0	1.00	7.4×10^{-6}	5.2×10^{-2}
39	trans	chr14	rs225995	33	30493712	0.45	rs225995	30493712	0.45	0	1.00	9.2×10^{-6}	7.7×10^{-1}
40	trans	chr19	rs6509732	1	53702508	0.41	rs6509732	53702508	0.41	0	1.00	5.2×10^{-6}	5.4×10^{-1}
43	trans	chr22	rs5769520	2	49671776	0.38	rs5769520	49671776	0.38	0	1.00	8.4×10^{-6}	2.3×10^{-1}

Crohns Gene 20
SLC22A5: solute carrier family 22 (organic cation/carnitine transporter), member 5
Gene Location: chr5:131705400-131731306
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 6.9×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr4	rs2612533	2	42712114	0.28	rs2612533	42712114	0.28	0	1.00	1.0×10^{-5}	1.2×10^{-2}
3	trans	chr5	rs6595948	1	129669537	0.32	rs6876137	129673206	0.40	3669	0.87	1.0×10^{-5}	1.3×10^{-2}
5	cis	chr5	rs13190293	2	131566926	0.28	rs2077380	131568617	0.27	1691	1.00	2.0×10^{-5}	2.1×10^{-2}
15	trans	chr16	rs2885415	18	395396	0.17	rs2885415	395396	0.17	0	1.00	4.0×10^{-6}	5.9×10^{-1}
19	trans	chr16	rs16962966	10	13919235	0.10	rs16962966	13919235	0.10	0	1.00	1.0×10^{-5}	3.7×10^{-1}
22	trans	chr17	rs11658605	3	33714452	0.18	rs11658605	33714452	0.18	0	1.00	1.0×10^{-5}	7.6×10^{-1}

Crohns Gene 21
CARD9: caspase recruitment domain family, member 9
Gene Location: chr9:139257440-139268133
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 2.0×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr4	rs13126694	1	159098784	0.50	rs13126694	159098784	0.50	0	1.00	6.9×10^{-6}	8.0×10^{-1}
3	trans	chr9	rs7871007	1	106423251	0.34	rs7871007	106423251	0.34	0	1.00	8.5×10^{-6}	4.3×10^{-2}
13	cis	chr9	rs3812584	2	139312719	0.40	rs4487900	139303301	0.44	9418	0.86	1.1×10^{-57}	1.3×10^{-4}
28	trans	chr12	rs10777222	1	90444741	0.45	rs10777222	90444741	0.45	0	1.00	6.2×10^{-6}	1.9×10^{-2}
29	trans	chr20	rs6038917	29	7649535	0.29	rs6038917	7649535	0.29	0	1.00	7.5×10^{-6}	3.8×10^{-2}

Crohns Gene 21
CARD9: caspase recruitment domain family, member 9
Gene Location: chr9:139257440-139268133
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 2.0×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr5	rs248457	1	150582456	0.35	rs248457	150582456	0.35	0	1.00	9.8×10^{-6}	1.7×10^{-1}
2	trans	chr5	rs4569911	1	160235125	0.38	rs4569911	160235125	0.38	0	1.00	1.7×10^{-6}	3.1×10^{-1}
4	trans	chr7	rs6966421	1	155329530	0.28	rs6966421	155329530	0.28	0	1.00	9.0×10^{-6}	3.2×10^{-1}
6	cis	chr9	rs7019243	4	138988568	0.38	rs7019243	138988568	0.38	0	1.00	2.0×10^{-4}	7.8×10^{-2}
26	cis	chr9	rs1127152	2	139335599	0.31	rs1127152	139335599	0.31	0	1.00	7.6×10^{-14}	2.2×10^{-4}
30	trans	chr11	rs422756	5	131380656	0.13	rs422756	131380656	0.13	0	1.00	3.9×10^{-6}	1.2×10^{-2}
31	trans	chr17	rs7210298	3	57541627	0.39	rs7210298	57541627	0.39	0	1.00	8.9×10^{-6}	4.4×10^{-4}

Crohns Gene 21
CARD9: caspase recruitment domain family, member 9
Gene Location: chr9:139257440-139268133
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 4.9×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
4	trans	chr3	rs6794649	2	153478423	0.22	rs6794649	153478423	0.22	0	1.00	8.0×10^{-6}	6.0×10^{-2}
7	trans	chr6	rs6923735	2	3417643	0.37	rs9405639	3419149	0.37	1506	0.90	1.0×10^{-6}	9.9×10^{-6}
15	trans	chr6	rs4895539	2	139056007	0.37	rs4895539	139056007	0.37	0	1.00	4.0×10^{-6}	3.5×10^{-1}
18	trans	chr9	rs10962740	2	16940390	0.31	rs7469270	16942496	0.25	2106	0.97	3.0×10^{-6}	6.0×10^{-1}
26	trans	chr12	rs2046524	21	24969054	0.21	rs3198082	24969363	0.47	309	1.00	7.0×10^{-6}	4.7×10^{-2}
27	trans	chr12	rs1813801	2	99188822	0.45	rs2036225	99190372	0.45	1550	0.89	4.0×10^{-6}	1.0
32	trans	chr13	rs1324914	4	74634972	0.43	rs1324914	74634972	0.43	0	1.00	6.0×10^{-7}	4.8×10^{-1}
41	trans	chr17	rs1110195	2	71964906	0.20	rs1110195	71964906	0.20	0	1.00	6.0×10^{-6}	8.4×10^{-2}
43	trans	chr19	rs4802863	3	52268972	0.35	rs4802863	52268972	0.35	0	1.00	5.0×10^{-6}	3.0×10^{-1}
44	trans	chr22	rs1894490	2	49594779	0.45	rs5770018	49595560	0.25	781	0.87	4.0×10^{-6}	6.2×10^{-1}

Crohns Gene 21
CARD9: caspase recruitment domain family, member 9
Gene Location: chr9:139257440-139268133
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 5.0×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs10170736	5	14528490	0.44	rs1829065	14528016	0.44	474	0.99	5.3×10^{-6}	9.9×10^{-1}
2	trans	chr3	rs1403501	2	152674921	0.41	rs1403501	152674921	0.41	0	1.00	7.3×10^{-6}	3.8×10^{-2}
3	trans	chr16	rs226046	1	21304147	0.25	rs226046	21304147	0.25	0	1.00	9.4×10^{-6}	2.4×10^{-1}
5	trans	chr17	rs9894429	2	79596811	0.35	rs9894429	79596811	0.35	0	1.00	6.7×10^{-6}	1.8×10^{-2}

Crohns Gene 22
UBE2L3: ubiquitin-conjugating enzyme E2L 3
Gene Location: chr22:21921956-21978323
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 1.4×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr9	rs10973939	25	38626309	0.12	rs10973939	38626309	0.12	0	1.00	9.4×10^{-6}	9.6×10^{-1}
3	trans	chr14	rs7147439	1	105523663	0.42	rs3809470	105531945	0.43	8282	0.96	5.8×10^{-6}	3.1×10^{-2}
5	cis	chr22	rs460106	1	21806401	0.48	rs460106	21806401	0.48	0	1.00	1.5×10^{-17}	4.6×10^{-2}
9	cis	chr22	rs2283790	1	21956653	0.27	rs2283790	21956653	0.27	0	1.00	1.3×10^{-76}	1.7×10^{-6}
15	trans	chr22	rs5756414	5	37330779	0.50	rs5756414	37330779	0.50	0	1.00	2.9×10^{-6}	3.2×10^{-1}

Crohns Gene 22
UBE2L3: ubiquitin-conjugating enzyme E2L 3
Gene Location: chr22:21921956-21978323
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 1.6×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs2271019	113	200861003	0.46	rs2062847	200849360	0.45	11643	0.96	5.6×10^{-6}	9.0×10^{-1}
2	trans	chr2	rs2119047	48	184633519	0.40	rs2119047	184633519	0.40	0	1.00	4.5×10^{-6}	4.6×10^{-1}
3	trans	chr3	rs4855516	59	68858280	0.17	rs4855516	68858280	0.17	0	1.00	9.3×10^{-7}	5.2×10^{-1}
5	trans	chr4	rs1485006	60	94397988	0.48	rs1485006	94397988	0.48	0	1.00	7.8×10^{-7}	1.9×10^{-1}
8	trans	chr4	rs1557804	27	110278816	0.28	rs1557804	110278816	0.28	0	1.00	3.6×10^{-6}	7.5×10^{-1}
11	trans	chr10	rs10829156	10	18950555	0.17	rs10829156	18950555	0.17	0	1.00	8.3×10^{-6}	8.8×10^{-1}
12	trans	chr11	rs1405732	3	95378495	0.13	rs1405732	95378495	0.13	0	1.00	1.4×10^{-6}	4.1×10^{-1}
13	trans	chr18	rs371346	3	44250955	0.23	rs371346	44250955	0.23	0	1.00	5.2×10^{-6}	3.4×10^{-1}
16	trans	chr20	rs753381	120	39797465	0.28	rs753381	39797465	0.28	0	1.00	4.9×10^{-7}	3.3×10^{-2}
21	cis	chr22	rs5998672	1	21966442	0.37	rs4821116	21973319	0.21	6877	0.92	3.8×10^{-7}	3.9×10^{-6}

Crohns Gene 22
UBE2L3: ubiquitin-conjugating enzyme E2L 3
Gene Location: chr22:21921956-21978323
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 1.1×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
4	trans	chr1	rs2791521	12	86917500	0.42	rs4656100	86917944	0.43	444	0.96	2.0×10^{-6}	2.8×10^{-1}
5	trans	chr1	rs1910296	3	238827051	0.19	rs1910296	238827051	0.19	0	1.00	9.0×10^{-6}	9.2×10^{-1}
7	trans	chr3	rs7635040	3	108099860	0.05	rs7635040	108099860	0.05	0	1.00	1.0×10^{-5}	2.6×10^{-1}
9	trans	chr5	rs7735939	1	84212395	0.44	rs7735799	84212340	0.33	55	0.94	2.0×10^{-6}	2.7×10^{-4}
73	trans	chr11	rs1945848	57	106519130	0.15	rs1945848	106519130	0.15	0	1.00	5.0×10^{-6}	4.0×10^{-1}
77	trans	chr11	rs11215797	17	115978780	0.18	rs1426387	115974172	0.28	4608	0.96	4.0×10^{-6}	6.1×10^{-1}
78	trans	chr13	rs1330045	41	86515953	0.15	rs7322119	86485397	0.18	30556	0.98	3.0×10^{-6}	3.0×10^{-1}
81	trans	chr14	rs12887971	3	99556336	0.20	rs8008908	99552095	0.18	4241	0.99	7.0×10^{-6}	9.2×10^{-1}
82	trans	chr16	rs12786	56	2902832	0.33	rs11076863	2897411	0.23	5421	0.93	1.0×10^{-5}	8.7×10^{-1}
97	cis	chr22	rs12484550	2	21941915	0.23	rs5754217	21939675	0.38	2240	0.92	6.0×10^{-6}	2.5×10^{-6}

Crohns Gene 23
BCAS3: breast carcinoma amplified sequence 3
Gene Location: chr17:58755171-59470199
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 3.1×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr2	rs690249	1	8447979	0.36	rs690249	8447979	0.36	0	1.00	3.0×10^{-6}	1.9×10^{-1}
3	trans	chr3	rs541653	145	74321141	0.34	rs541653	74321141	0.34	0	1.00	8.4×10^{-6}	3.1×10^{-1}
4	trans	chr5	rs2070729	3	131819921	0.38	rs2070729	131819921	0.38	0	1.00	5.0×10^{-6}	1.1×10^{-4}
5	trans	chr11	rs2448276	155	80110511	0.35	rs2448276	80110511	0.35	0	1.00	1.8×10^{-6}	10.0×10^{-1}
6	trans	chr14	rs2295307	1	24765622	0.31	rs2295307	24765622	0.31	0	1.00	8.5×10^{-6}	1.7×10^{-1}

Crohns Gene 23
BCAS3: breast carcinoma amplified sequence 3
Gene Location: chr17:58755171-59470199
GWAS Data: Barrett 2008
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 3.0×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs13374930	3	219553947	0.23	rs13374930	219553947	0.23	0	1.00	8.3×10^{-6}	2.4×10^{-1}
3	trans	chr2	rs6545814	1	25131316	0.46	rs6545814	25131316	0.46	0	1.00	4.5×10^{-6}	1.4×10^{-3}
5	trans	chr3	rs13084750	3	184094724	0.14	rs13084750	184094724	0.14	0	1.00	6.7×10^{-6}	4.4×10^{-1}
7	trans	chr5	rs10044936	1	140653258	0.04	rs10044936	140653258	0.04	0	1.00	1.2×10^{-6}	9.6×10^{-2}
9	trans	chr6	rs9321180	1	130102959	0.23	rs9321180	130102959	0.23	0	1.00	8.5×10^{-6}	3.4×10^{-1}
10	trans	chr7	rs13240515	2	112948157	0.21	rs13240515	112948157	0.21	0	1.00	9.3×10^{-6}	3.9×10^{-1}

Crohns Gene 23
BCAS3: breast carcinoma amplified sequence 3
Gene Location: chr17:58755171-59470199
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 1.2×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs2280406	1	49941436	0.38	rs2230590	49936102	0.49	5334	0.97	8.2×10^{-6}	2.1×10^{-4}
7	trans	chr3	rs2301166	1	50148305	0.43	rs2240327	50113034	0.43	35271	1.00	7.0×10^{-6}	4.0×10^{-4}
9	trans	chr10	rs4453146	1	58342471	0.19	rs7909510	58343819	0.20	1348	0.95	5.6×10^{-6}	4.3×10^{-2}
12	trans	chr15	rs11635196	1	37264182	0.38	rs11635196	37264182	0.38	0	1.00	2.3×10^{-6}	3.6×10^{-1}

Crohns Gene 24
MST1: macrophage stimulating 1 (hepatocyte growth factor-like)
Gene Location: chr3:49721379-49726196
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 1.3×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
4	cis	chr3	rs9863142	2	49366741	0.16	rs9863142	49366741	0.16	0	1.00	9.3×10^{-10}	1.3×10^{-5}
5	trans	chr4	rs6449005	1	14193404	0.14	rs6449005	14193404	0.14	0	1.00	8.5×10^{-6}	10.0×10^{-1}
8	trans	chr5	rs233379	2	13581311	0.08	rs233379	13581311	0.08	0	1.00	3.3×10^{-6}	5.1×10^{-2}
10	trans	chr6	rs4546496	3	99664966	0.42	rs17059246	99662743	0.42	2223	0.99	6.0×10^{-6}	3.2×10^{-1}
11	trans	chr7	rs6461799	1	24406742	0.24	rs6461799	24406742	0.24	0	1.00	6.1×10^{-6}	1.4×10^{-2}
14	trans	chr16	rs889558	3	57172629	0.14	rs889558	57172629	0.14	0	1.00	6.7×10^{-6}	8.9×10^{-2}

Crohns Gene 24
MST1: macrophage stimulating 1 (hepatocyte growth factor-like)
Gene Location: chr3:49721379-49726196
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 1.0×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs6739276	1	239946756	0.42	rs6739276	239946756	0.42	0	1.00	6.6×10^{-6}	5.0×10^{-1}
7	cis	chr3	rs11718165	1	49696797	0.20	rs11718165	49696797	0.20	0	1.00	4.1×10^{-9}	4.6×10^{-7}
14	trans	chr4	rs901113	1	21276080	0.25	rs2322884	21275195	0.21	885	0.99	2.6×10^{-6}	5.4×10^{-1}
16	trans	chr5	rs10471414	1	49960673	0.49	rs10471414	49960673	0.49	0	1.00	5.2×10^{-6}	5.7×10^{-1}
21	trans	chr7	rs10273103	9	83009942	0.24	rs3801479	83014996	0.18	5054	0.98	4.6×10^{-7}	1.3×10^{-1}
23	trans	chr8	rs6558533	1	1709918	0.21	rs6558527	1702911	0.21	7007	0.91	5.8×10^{-6}	9.6×10^{-1}
26	trans	chr12	rs12308045	1	53165178	0.17	rs4919706	53177573	0.18	12395	0.89	4.5×10^{-6}	2.4×10^{-1}
28	trans	chr18	rs12605002	1	27237820	0.31	rs12605002	27237820	0.31	0	1.00	5.4×10^{-6}	7.6×10^{-2}

Crohns Gene 25
SLC16A14: solute carrier family 16, member 14 (monocarboxylic acid transporter 14)
Gene Location: chr2:230899689-230933715
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 1.8×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	cis	chr2	rs13397985	2	231091223	0.12	rs13397985	231091223	0.12	0	1.00	6.0×10^{-4}	1.8×10^{-5}
2	trans	chr16	rs2520126	2	26579841	0.35	rs2520126	26579841	0.35	0	1.00	8.1×10^{-6}	6.4×10^{-1}

Crohns Gene 25
SLC16A14: solute carrier family 16, member 14 (monocarboxylic acid transporter 14)
Gene Location: chr2:230899689-230933715
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 8.6×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs4255332	1	152958745	0.39	rs1611753	152956381	0.45	2364	1.00	6.7×10^{-6}	3.8×10^{-1}
2	trans	chr4	rs1563849	3	42632678	0.17	rs1563849	42632678	0.17	0	1.00	9.0×10^{-6}	2.5×10^{-3}
5	trans	chr10	rs10829269	1	27830676	0.28	rs7096275	27832854	0.26	2178	0.99	5.3×10^{-6}	3.8×10^{-2}

Crohns Gene 26
ATG16L1: autophagy related 16-like 1 (S. cerevisiae)
Gene Location: chr2:234160216-234204320
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 5.4×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs1457341	2	81389365	0.43	rs1457341	81389365	0.43	0	1.00	1.7×10^{-6}	2.7×10^{-1}
4	trans	chr2	rs849526	3	206592695	0.44	rs849526	206592695	0.44	0	1.00	5.4×10^{-6}	8.2×10^{-1}
10	cis	chr2	rs1000141	1	234242347	0.36	rs1000141	234242347	0.36	0	1.00	4.0×10^{-5}	8.5×10^{-10}
11	trans	chr3	rs11130377	1	53722874	0.26	rs11130377	53722874	0.26	0	1.00	2.5×10^{-6}	2.2×10^{-1}
12	trans	chr5	rs10520006	10	127999225	0.26	rs10520006	127999225	0.26	0	1.00	3.9×10^{-6}	7.8×10^{-1}
14	trans	chr8	rs6651315	5	69618167	0.38	rs7016101	69611629	0.45	6538	0.98	8.7×10^{-6}	5.7×10^{-1}
17	trans	chr17	rs8249	1	33289937	0.45	rs1482103	33287651	0.45	2286	1.00	4.9×10^{-6}	8.5×10^{-1}
18	trans	chr18	rs8090058	2	33769406	0.20	rs8090058	33769406	0.20	0	1.00	4.6×10^{-6}	3.8×10^{-1}

Crohns Gene 26
ATG16L1: autophagy related 16-like 1 (S. cerevisiae)
Gene Location: chr2:234160216-234204320
GWAS Data: Barrett 2008
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 1.5×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	cis	chr2	rs6431262	1	234199537	0.42	rs6431262	234199537	0.42	0	1.00	2.2×10^{-7}	1.2×10^{-6}
2	trans	chr5	rs1806081	2	9201631	0.14	rs1806081	9201631	0.14	0	1.00	6.7×10^{-6}	3.7×10^{-1}
3	trans	chr8	rs2514332	5	99110123	0.12	rs2514332	99110123	0.12	0	1.00	1.8×10^{-6}	4.2×10^{-1}

Crohns Gene 27
ZPBP2: zona pellucida binding protein 2
Gene Location: chr17:38024454-38034149
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 2.1×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	cis	chr17	rs1008723	1	38066267	0.36	rs1008723	38066267	0.36	0	1.00	3.0×10^{-4}	2.4×10^{-4}

Crohns Gene 27
ZPBP2: zona pellucida binding protein 2
Gene Location: chr17:38024454-38034149
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 1.1×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
6	trans	chr2	rs12053361	2	212355500	0.39	rs4672615	212356992	0.35	1492	1.00	4.6×10^{-6}	7.4×10^{-1}
10	trans	chr3	rs2304442	1	49322027	0.47	rs2304442	49322027	0.47	0	1.00	3.2×10^{-6}	1.2×10^{-5}
21	trans	chr5	rs1345420	1	82934244	0.27	rs12657861	82929501	0.27	4743	0.99	8.5×10^{-6}	3.1×10^{-1}
28	trans	chr11	rs1144396	2	102679052	0.41	rs1144396	102679052	0.41	0	1.00	7.5×10^{-6}	9.2×10^{-1}
30	trans	chr12	rs10880314	1	42940836	0.39	rs1669947	42942234	0.42	1398	1.00	4.3×10^{-6}	6.3×10^{-1}
33	trans	chr14	rs7143581	1	91136964	0.39	rs881218	91130502	0.40	6462	0.99	5.5×10^{-6}	4.7×10^{-2}
37	trans	chr16	rs2276330	1	68857289	0.07	rs2276330	68857289	0.07	0	1.00	7.0×10^{-6}	2.5×10^{-1}
40	trans	chr16	rs12447903	2	84554990	0.46	rs11866096	84555319	0.48	329	0.90	8.7×10^{-6}	1.5×10^{-1}
41	trans	chr19	rs6511937	1	9327778	0.31	rs10407714	9319223	0.34	8555	0.99	2.1×10^{-6}	3.3×10^{-1}

Crohns Gene 28
CCNH: cyclin H
Gene Location: chr5:86690078-86708721
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 5.5×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs2014788	4	14126453	0.34	rs2014788	14126453	0.34	0	1.00	6.6×10^{-6}	1.7×10^{-2}
2	trans	chr1	rs7538112	2	201463838	0.41	rs515384	201464807	0.36	969	0.91	8.8×10^{-7}	4.4×10^{-3}
4	trans	chr15	rs636751	2	35012584	0.41	rs636751	35012584	0.41	0	1.00	9.0×10^{-6}	5.7×10^{-2}
5	trans	chr17	rs9909601	6	33817422	0.24	rs6505476	33811033	0.24	6389	0.91	2.1×10^{-7}	2.6×10^{-1}

Crohns Gene 28
CCNH: cyclin H
Gene Location: chr5:86690078-86708721
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 5.2×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr4	rs2048542	6	45076915	0.16	rs2048542	45076915	0.16	0	1.00	7.2×10^{-7}	3.0×10^{-2}
3	trans	chr4	rs9307834	14	76453850	0.47	rs10020976	76431119	0.30	22731	0.87	2.6×10^{-6}	3.5×10^{-1}
4	trans	chr12	rs1713595	1	128881424	0.29	rs1713595	128881424	0.29	0	1.00	8.0×10^{-6}	7.8×10^{-2}

Crohns Gene 28
CCNH: cyclin H
Gene Location: chr5:86690078-86708721
GWAS Data: Barrett 2008
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 2.9×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
7	trans	chr2	rs11685920	215	42203826	0.17	rs11686998	42188641	0.19	15185	0.94	3.6×10^{-6}	4.6×10^{-1}
8	trans	chr2	rs1522909	5	138871234	0.07	rs1522909	138871234	0.07	0	1.00	3.3×10^{-6}	8.1×10^{-4}
11	trans	chr3	rs1661532	16	3805368	0.21	rs1661532	3805368	0.21	0	1.00	2.4×10^{-7}	2.4×10^{-2}
19	trans	chr7	rs7792327	17	33912480	0.02	rs7792327	33912480	0.02	0	1.00	8.2×10^{-6}	8.6×10^{-2}
21	trans	chr9	rs1331355	50	12359463	0.31	rs1331355	12359463	0.31	0	1.00	4.9×10^{-6}	9.0×10^{-1}
23	trans	chr9	rs7041366	16	72569410	0.49	rs7041366	72569410	0.49	0	1.00	2.9×10^{-6}	7.4×10^{-1}
24	trans	chr11	rs7130359	33	26745739	0.06	rs7130359	26745739	0.06	0	1.00	6.2×10^{-6}	3.5×10^{-1}
27	trans	chr13	rs17826945	27	81176558	0.05	rs17826945	81176558	0.05	0	1.00	5.6×10^{-6}	6.9×10^{-2}
28	trans	chr15	rs11635236	46	90850762	0.47	rs11635236	90850762	0.47	0	1.00	5.3×10^{-7}	1.2×10^{-1}
29	trans	chr17	rs2160115	11	55165612	0.34	rs2160115	55165612	0.34	0	1.00	7.9×10^{-6}	5.3×10^{-1}
31	trans	chr20	rs6132977	8	2825972	0.10	rs6132977	2825972	0.10	0	1.00	1.5×10^{-6}	2.9×10^{-2}

Crohns Gene 29
LIPG: lipase, endothelial
Gene Location: chr18:47088426-47119278
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 1.9×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr1	rs11209039	6	67751193	0.40	rs11209039	67751193	0.40	0	1.00	1.0×10^{-5}	6.1×10^{-13}
4	trans	chr1	rs7535386	1	85962610	0.43	rs1361714	85960156	0.44	2454	0.88	3.0×10^{-6}	6.6×10^{-1}
6	trans	chr1	rs1637941	2	230715075	0.44	rs886984	230717402	0.47	2327	0.97	4.0×10^{-6}	6.2×10^{-1}
8	trans	chr4	rs4693083	1	84241316	0.19	rs11099594	84240847	0.18	469	1.00	1.0×10^{-5}	2.3×10^{-1}
9	trans	chr5	rs11749605	1	94409482	0.41	rs1895865	94431710	0.40	22228	0.93	3.0×10^{-6}	8.7×10^{-1}
15	trans	chr6	rs207268	1	90826709	0.49	rs207269	90828169	0.41	1460	1.00	3.0×10^{-6}	4.3×10^{-3}
18	trans	chr9	rs2025324	1	7102389	0.39	rs2025324	7102389	0.39	0	1.00	1.0×10^{-5}	7.1×10^{-1}
19	trans	chr9	rs13440274	6	28251718	0.19	rs13440446	28251541	0.21	177	0.87	1.0×10^{-5}	6.3×10^{-2}
21	trans	chr11	rs1508522	1	42435951	0.35	rs1508523	42436149	0.38	198	NA	6.0×10^{-6}	8.7×10^{-1}
22	trans	chr11	rs4483608	1	76413086	0.28	rs7127747	76412663	0.37	423	0.99	7.0×10^{-6}	2.4×10^{-2}
40	trans	chr18	rs2628207	2	63546386	0.24	rs2628209	63546551	0.26	165	1.00	5.0×10^{-6}	3.9×10^{-1}
46	trans	chr20	rs1540753	4	20040919	0.18	rs725466	20036075	0.18	4844	1.00	1.0×10^{-6}	5.2×10^{-1}
49	trans	chr20	rs2300204	1	32588773	0.34	rs2284378	32588095	0.21	678	1.00	7.0×10^{-6}	7.7×10^{-1}
51	trans	chr22	rs134187	1	28641134	0.26	rs134187	28641134	0.26	0	1.00	8.0×10^{-6}	7.3×10^{-1}

Crohns Gene 29
LIPG: lipase, endothelial
Gene Location: chr18:47088426-47119278
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 4.6×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
3	trans	chr3	rs161923	1	7832927	0.37	rs162211	7823055	0.33	9872	0.97	1.5×10^{-6}	8.1×10^{-1}
4	trans	chr4	rs2110177	1	27442060	0.25	rs2110177	27442060	0.25	0	1.00	3.6×10^{-6}	8.9×10^{-1}
6	trans	chr8	rs2956957	1	1554539	0.21	rs2956957	1554539	0.21	0	1.00	6.3×10^{-6}	2.4×10^{-1}
7	trans	chr13	rs620909	1	90110725	0.37	rs620909	90110725	0.37	0	1.00	3.7×10^{-6}	1.1×10^{-1}
8	trans	chr17	rs1024611	1	32579788	0.38	rs991804	32587725	0.42	7937	0.99	8.3×10^{-6}	4.0×10^{-6}

Crohns Gene 30
MOBK1B: Not Found in HUGO
Gene Location: Not Found:Not Found-Not Found
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 9.7×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs1033846	1	18073505	0.38	rs1033846	18073505	0.38	0	1.00	4.4×10^{-6}	9.7×10^{-1}
2	trans	chr1	rs3888717	1	33595289	0.21	rs12031625	33590873	0.23	4416	0.96	5.6×10^{-6}	4.9×10^{-1}
3	trans	chr1	rs943520	1	53965176	0.11	rs943520	53965176	0.11	0	1.00	6.7×10^{-6}	2.6×10^{-1}
6	trans	chr2	rs10168005	1	88445815	0.17	rs10168005	88445815	0.17	0	1.00	2.9×10^{-6}	5.5×10^{-1}
9	trans	chr2	rs7600308	1	138453808	0.25	rs9283455	138458639	0.47	4831	0.87	5.9×10^{-6}	1.0×10^{-1}
13	trans	chr2	rs6754477	1	159620326	0.20	rs1913900	159617573	0.18	2753	0.99	4.7×10^{-6}	2.9×10^{-2}
14	trans	chr3	rs4678765	1	35360207	0.20	rs4678765	35360207	0.20	0	1.00	3.4×10^{-6}	2.0×10^{-1}
16	trans	chr3	rs11918416	3	63505191	0.35	rs11918416	63505191	0.35	0	1.00	6.8×10^{-8}	3.0×10^{-1}
22	trans	chr4	rs3775868	1	68446302	0.11	rs3775868	68446302	0.11	0	1.00	1.1×10^{-6}	8.9×10^{-1}
23	trans	chr4	rs10004000	1	175692458	0.22	rs11727514	175682850	0.23	9608	0.94	2.3×10^{-6}	4.1×10^{-2}
24	trans	chr5	rs10076745	1	8653313	0.33	rs10076745	8653313	0.33	0	1.00	2.5×10^{-6}	1.0×10^{-1}
26	trans	chr5	rs274550	5	131728712	0.29	rs274552	131727346	0.48	1366	0.96	2.1×10^{-6}	8.5×10^{-5}
27	trans	chr6	rs2273621	1	97058553	0.41	rs6902835	97063005	0.40	4452	0.98	6.0×10^{-6}	1.8×10^{-1}
28	trans	chr6	rs4946889	1	108332377	0.12	rs4946889	108332377	0.12	0	1.00	1.1×10^{-8}	5.5×10^{-2}
29	trans	chr7	rs11976167	2	70856174	0.11	rs11976167	70856174	0.11	0	1.00	2.7×10^{-6}	6.2×10^{-1}
31	trans	chr9	rs439660	2	4733368	0.09	rs439660	4733368	0.09	0	1.00	3.2×10^{-6}	1.7×10^{-1}
33	trans	chr10	rs10763550	1	52330352	0.30	rs10763566	52341930	0.30	11578	0.98	2.6×10^{-6}	8.2×10^{-1}
36	trans	chr10	rs17119214	1	107371475	0.18	rs17119214	107371475	0.18	0	1.00	6.0×10^{-10}	3.0×10^{-1}
44	trans	chr12	rs11115214	1	82574691	0.34	rs3994835	82529437	0.28	45254	0.87	1.2×10^{-6}	3.5×10^{-1}
45	trans	chr14	rs8011939	1	28004044	0.38	rs8011939	28004044	0.38	0	1.00	9.4×10^{-6}	1.0×10^{-1}
46	trans	chr14	rs1884093	1	63713182	0.49	rs6573499	63704649	0.48	8533	0.97	1.1×10^{-6}	3.4×10^{-2}
48	trans	chr18	rs2048031	2	61475561	0.12	rs2048031	61475561	0.12	0	1.00	8.1×10^{-7}	5.0×10^{-1}
51	trans	chr19	rs358550	2	32987942	0.16	rs358539	32996606	0.13	8664	0.92	1.4×10^{-6}	5.0×10^{-1}

Crohns Gene 30
MOBK1B: Not Found in HUGO
Gene Location: Not Found:Not Found-Not Found
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 5.1×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs6697764	25	94738846	0.30	rs11165110	94752469	0.31	13623	1.00	7.0×10^{-6}	7.1×10^{-1}
2	trans	chr2	rs6755028	58	128195442	0.34	rs6754999	128195387	0.39	55	NA	2.8×10^{-6}	2.6×10^{-1}
4	trans	chr2	rs908919	3	154519277	0.09	rs908919	154519277	0.09	0	1.00	6.8×10^{-6}	2.5×10^{-2}
8	trans	chr3	rs1661506	3	3809709	0.46	rs1661506	3809709	0.46	0	1.00	2.0×10^{-6}	2.2×10^{-1}
11	trans	chr4	rs10470814	8	25191232	0.40	rs7661189	25250165	0.29	58933	0.92	2.3×10^{-6}	1.4×10^{-3}

Crohns Gene 31
CYGB: cytoglobin
Gene Location: chr17:74523439-74533782
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 1.3×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs921323	136	23413122	0.35	rs1562755	23409862	0.31	3260	1.00	9.8×10^{-6}	1.4×10^{-1}
2	trans	chr2	rs3768729	23	46592006	0.46	rs3768729	46592006	0.46	0	1.00	5.9×10^{-6}	6.3×10^{-2}
4	trans	chr2	rs4552182	3	219184872	0.40	rs10932774	219191569	0.30	6697	0.98	4.2×10^{-6}	3.3×10^{-2}
5	trans	chr7	rs3111446	106	112198998	0.21	rs3111446	112198998	0.21	0	1.00	5.5×10^{-6}	2.6×10^{-2}
6	trans	chr7	rs41622	4	120428607	0.17	rs42333	120422982	0.17	5625	1.00	8.8×10^{-6}	8.5×10^{-2}
7	trans	chr8	rs1982135	2	58826865	0.13	rs1982135	58826865	0.13	0	1.00	2.9×10^{-6}	1.9×10^{-1}
8	trans	chr8	rs10101981	13	136177949	0.19	rs11167077	136187340	0.19	9391	0.85	7.0×10^{-6}	9.2×10^{-2}
9	trans	chr10	rs6480848	132	78741306	0.17	rs6480848	78741306	0.17	0	1.00	1.8×10^{-6}	3.4×10^{-1}
10	trans	chr10	rs1927157	45	114635381	0.11	rs1927157	114635381	0.11	0	1.00	6.9×10^{-6}	6.2×10^{-1}
11	trans	chr13	rs9576809	56	40038354	0.39	rs9576809	40038354	0.39	0	1.00	1.0×10^{-5}	5.5×10^{-1}
12	trans	chr17	rs5025290	10	20205817	0.11	rs5025290	20205817	0.11	0	1.00	4.7×10^{-6}	9.2×10^{-1}
13	trans	chr17	rs1799873	23	38976998	0.31	rs7211017	38957953	0.31	19045	0.99	6.5×10^{-6}	2.5×10^{-1}
15	cis	chr17	rs9913445	2	74791146	0.27	rs9913445	74791146	0.27	0	1.00	5.0×10^{-4}	2.2×10^{-2}

Crohns Gene 31
CYGB: cytoglobin
Gene Location: chr17:74523439-74533782
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 2.1×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr5	rs17135753	2	112928779	0.21	rs17135753	112928779	0.21	0	1.00	5.1×10^{-6}	2.0×10^{-1}
2	trans	chr6	rs9460635	1	21455153	0.48	rs9460635	21455153	0.48	0	1.00	3.7×10^{-6}	2.1×10^{-5}
3	trans	chr7	rs1229653	6	26432559	0.11	rs1229653	26432559	0.11	0	1.00	5.8×10^{-6}	1.9×10^{-1}
4	trans	chr11	rs3134402	1	122784817	0.43	rs3134402	122784817	0.43	0	1.00	9.8×10^{-7}	9.3×10^{-2}

Crohns Gene 31
CYGB: cytoglobin
Gene Location: chr17:74523439-74533782
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 4.3×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs2933251	1	148406799	0.19	rs2933251	148406799	0.19	0	1.00	8.9×10^{-6}	1.4×10^{-2}
3	trans	chr6	rs2299088	17	16516192	0.18	rs2299088	16516192	0.18	0	1.00	1.3×10^{-6}	4.9×10^{-1}

Crohns Gene 32
INPP5E: inositol polyphosphate-5-phosphatase, 72 kDa
Gene Location: chr9:139323066-139334256
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 1.9×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
17	cis	chr9	rs10781538	1	139320929	0.36	rs11145756	139364585	0.39	43656	0.93	3.5×10^{-290}	1.5×10^{-4}
32	trans	chr10	rs11007890	2	30359297	0.13	rs16931056	30387015	0.10	27718	0.96	8.2×10^{-7}	5.7×10^{-2}

Crohns Gene 32
INPP5E: inositol polyphosphate-5-phosphatase, 72 kDa
Gene Location: chr9:139323066-139334256
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 3.7×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr6	rs11756587	1	158572975	0.14	rs11756587	158572975	0.14	0	1.00	1.6×10^{-6}	2.1×10^{-1}
3	cis	chr9	rs7019243	4	138988568	0.38	rs7019243	138988568	0.38	0	1.00	3.0×10^{-4}	7.8×10^{-2}
15	cis	chr9	rs10870194	2	139327034	0.39	rs1127152	139335599	0.31	8565	0.86	7.0×10^{-10}	2.2×10^{-4}

Crohns Gene 33
SALL4: sal-like 4 (Drosophila)
Gene Location: chr20:50400582-50419048
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 2.6×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs927727	1	29793205	0.50	rs927727	29793205	0.50	0	1.00	8.0×10^{-6}	3.1×10^{-1}
3	trans	chr2	rs7595902	2	20074271	0.29	rs11676372	20072512	0.29	1759	1.00	9.7×10^{-6}	1.8×10^{-1}
4	trans	chr17	rs12453065	2	51007436	0.33	rs12453065	51007436	0.33	0	1.00	1.0×10^{-7}	3.9×10^{-3}

Crohns Gene 33
SALL4: sal-like 4 (Drosophila)
Gene Location: chr20:50400582-50419048
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 6.9×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr5	rs1023518	1	131793772	0.28	rs1023518	131793772	0.28	0	1.00	4.9×10^{-6}	6.1×10^{-7}
6	trans	chr16	rs2911279	1	81593274	0.32	rs2911276	81595186	0.34	1912	1.00	8.9×10^{-6}	2.9×10^{-1}
8	trans	chr16	rs1424045	2	82560643	0.21	rs4569270	82557069	0.24	3574	0.89	6.3×10^{-6}	6.6×10^{-1}
9	trans	chr19	rs2292455	1	1526613	0.31	rs2292455	1526613	0.31	0	1.00	9.9×10^{-6}	9.5×10^{-1}

Crohns Gene 34
MC2R: melanocortin 2 receptor (adrenocorticotropic hormone)
Gene Location: chr18:13882042-13915535
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 1.7×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
6	trans	chr1	rs2793810	1	179162353	0.44	rs2171958	179176398	0.48	14045	0.90	5.1×10^{-6}	1.6×10^{-1}
11	trans	chr10	rs10761659	1	64445564	0.47	rs10761659	64445564	0.47	0	1.00	4.3×10^{-6}	2.8×10^{-10}

Crohns Gene 35
MEA1: male-enhanced antigen 1
Gene Location: chr6:42979966-42981618
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 1.4×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
4	trans	chr10	rs11196301	615	84634847	0.14	rs11196301	84634847	0.14	0	1.00	9.0×10^{-6}	6.6×10^{-1}
7	trans	chr12	rs11049693	2	28677944	0.25	rs11049685	28665708	0.25	12236	0.93	1.0×10^{-5}	5.5×10^{-3}

Crohns Gene 35
MEA1: male-enhanced antigen 1
Gene Location: chr6:42979966-42981618
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 1.9×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr2	rs6740430	1	48314490	0.39	rs6740430	48314490	0.39	0	1.00	5.1×10^{-6}	1.0×10^{-2}
4	trans	chr10	rs681088	3	79232842	0.45	rs681088	79232842	0.45	0	1.00	3.8×10^{-6}	9.7×10^{-2}

Crohns Gene 35
MEA1: male-enhanced antigen 1
Gene Location: chr6:42979966-42981618
GWAS Data: Barrett 2008
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 4.4×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
4	trans	chr2	rs17019050	1	80577921	0.35	rs17019050	80577921	0.35	0	1.00	2.2×10^{-6}	5.4×10^{-3}
7	trans	chr2	rs11678557	1	230002180	0.17	rs11678557	230002180	0.17	0	1.00	7.6×10^{-6}	1.8×10^{-1}
13	trans	chr13	rs9596150	9	50138309	0.30	rs9596150	50138309	0.30	0	1.00	1.2×10^{-6}	3.9×10^{-1}

Crohns Gene 35
MEA1: male-enhanced antigen 1
Gene Location: chr6:42979966-42981618
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 3.7×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr15	rs17637182	6	26017543	0.25	rs8029176	26021544	0.25	4001	0.92	9.5×10^{-7}	2.7×10^{-2}

Crohns Gene 36
CSDE1: cold shock domain containing E1, RNA-binding
Gene Location: chr1:115259533-115300671
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 4.1×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	cis	chr1	rs17013385	1	115646444	0.16	rs12739537	115650070	0.15	3626	1.00	4.1×10^{-6}	1.1×10^{-1}
4	trans	chr2	rs10496675	2	129914648	0.07	rs10496675	129914648	0.07	0	1.00	9.0×10^{-6}	2.0×10^{-1}
5	trans	chr5	rs12187740	4	129317778	0.45	rs4315958	129311522	0.48	6256	0.98	3.2×10^{-6}	9.0×10^{-3}
6	trans	chr8	rs7017881	1	120047857	0.30	rs6469804	120044829	0.25	3028	0.94	2.1×10^{-6}	3.6×10^{-3}
7	trans	chr10	rs2804118	5	6958808	0.18	rs2804118	6958808	0.18	0	1.00	3.4×10^{-6}	7.2×10^{-1}
8	trans	chr16	rs17226979	3	50949161	0.01	rs17226979	50949161	0.01	0	1.00	3.4×10^{-7}	5.3×10^{-3}
13	trans	chr17	rs17700008	6	45863591	0.24	rs17700008	45863591	0.24	0	1.00	6.1×10^{-8}	7.5×10^{-1}

Crohns Gene 36
CSDE1: cold shock domain containing E1, RNA-binding
Gene Location: chr1:115259533-115300671
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 2.4×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs4846126	30	12663304	0.44	rs4846126	12663304	0.44	0	1.00	4.0×10^{-6}	3.5×10^{-4}
5	trans	chr3	rs347594	130	11249528	0.39	rs430353	11254071	0.42	4543	0.97	5.0×10^{-6}	9.3×10^{-1}
6	trans	chr3	rs2363520	572	24948515	0.26	rs10865801	24929802	0.27	18713	0.97	4.0×10^{-6}	6.8×10^{-1}
7	trans	chr4	rs6534204	45	121623193	0.19	rs1874442	121623057	0.13	136	0.86	8.0×10^{-6}	8.1×10^{-1}
15	trans	chr5	rs251292	13	65190626	0.49	rs251292	65190626	0.49	0	1.00	4.0×10^{-7}	6.5×10^{-2}
27	trans	chr6	rs1698216	82	8269155	0.48	rs621896	8269415	0.46	260	1.00	1.0×10^{-5}	8.1×10^{-1}
40	trans	chr7	rs10248053	65	103164653	0.43	rs10248053	103164653	0.43	0	1.00	5.0×10^{-6}	3.7×10^{-4}
41	trans	chr7	rs2188420	76	106486243	0.22	rs17153527	106495809	0.12	9566	0.87	3.0×10^{-6}	5.6×10^{-1}
42	trans	chr8	rs4737234	9	55878470	0.24	rs4737805	55877790	0.32	680	0.86	1.0×10^{-5}	7.9×10^{-1}
46	trans	chr10	rs11196301	615	84634847	0.14	rs11196301	84634847	0.14	0	1.00	3.0×10^{-7}	6.6×10^{-1}
49	trans	chr10	rs10734095	432	129084327	0.36	rs10734095	129084327	0.36	0	1.00	5.0×10^{-6}	1.4×10^{-1}
53	trans	chr11	rs10899646	5	79253944	0.22	rs10899649	79260312	0.29	6368	0.94	1.0×10^{-5}	9.8×10^{-1}
60	trans	chr13	rs11842161	70	108246475	0.28	rs957788	108257220	0.30	10745	0.99	3.0×10^{-6}	7.6×10^{-2}
62	trans	chr15	rs7183705	13	102015259	0.12	rs7165891	102020488	0.09	5229	0.90	6.0×10^{-6}	2.0×10^{-1}
64	trans	chr17	rs1531564	44	73110279	0.48	rs1531564	73110279	0.48	0	1.00	1.0×10^{-5}	9.3×10^{-1}
65	trans	chr18	rs11662013	93	2096769	0.13	rs7245336	2096905	0.12	136	NA	2.0×10^{-6}	7.8×10^{-1}
66	trans	chr18	rs2728508	343	23180056	0.33	rs17525	23177706	0.31	2350	0.95	1.0×10^{-5}	8.5×10^{-1}

Crohns Gene 36
CSDE1: cold shock domain containing E1, RNA-binding
Gene Location: chr1:115259533-115300671
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 4.1×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	cis	chr1	rs8453	1	115259599	0.09	rs8453	115259599	0.09	0	1.00	2.2×10^{-7}	1.4×10^{-1}
3	trans	chr1	rs4068473	6	166629905	0.49	rs10494466	166625743	0.40	4162	1.00	7.8×10^{-6}	5.8×10^{-2}
4	trans	chr1	rs6694387	3	172292205	0.34	rs6694387	172292205	0.34	0	1.00	2.9×10^{-7}	2.9×10^{-1}
6	trans	chr6	rs9295456	1	19991446	0.19	rs9295456	19991446	0.19	0	1.00	5.7×10^{-6}	1.6×10^{-2}
7	trans	chr14	rs2810068	3	54030396	0.32	rs2810068	54030396	0.32	0	1.00	4.6×10^{-6}	8.2×10^{-1}
8	trans	chr14	rs7156012	1	83371030	0.49	rs7156012	83371030	0.49	0	1.00	4.5×10^{-6}	1.3×10^{-1}

Crohns Gene 37
IQWD1: Not Found in HUGO
Gene Location: Not Found:Not Found-Not Found
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 2.2×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs6659595	35	245816096	0.31	rs6659595	245816096	0.31	0	1.00	1.1×10^{-6}	3.5×10^{-1}
4	trans	chr7	rs36876	6	14977994	0.11	rs36876	14977994	0.11	0	1.00	6.0×10^{-6}	2.3×10^{-1}
6	trans	chr15	rs4906708	1	25617979	0.46	rs4906708	25617979	0.46	0	1.00	8.3×10^{-6}	1.4×10^{-1}
10	trans	chr17	rs212492	30	32730455	0.29	rs212492	32730455	0.29	0	1.00	3.5×10^{-7}	8.4×10^{-2}
12	trans	chr22	rs2239749	12	37331305	0.49	rs2239749	37331305	0.49	0	1.00	8.3×10^{-6}	6.4×10^{-3}

Crohns Gene 37
IQWD1: Not Found in HUGO
Gene Location: Not Found:Not Found-Not Found
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 3.1×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs16827337	1	150546608	0.24	rs16827337	150546608	0.24	0	1.00	7.9×10^{-6}	8.0×10^{-3}
3	trans	chr8	rs4316157	20	12632951	0.42	rs4316157	12632951	0.42	0	1.00	9.5×10^{-6}	6.7×10^{-2}
4	trans	chr11	rs12280457	17	3243367	0.39	rs6578334	3242223	0.38	1144	0.95	8.0×10^{-6}	5.6×10^{-1}
5	trans	chr14	rs17100254	9	33621512	0.17	rs17100254	33621512	0.17	0	1.00	2.8×10^{-6}	6.5×10^{-3}

Crohns Gene 38
ORMDL3: ORM1-like 3 (S. cerevisiae)
Gene Location: chr17:38077295-38083884
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 2.8×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr5	rs346648	1	135724494	0.29	rs346644	135718134	0.28	6360	1.00	9.6×10^{-6}	4.6×10^{-1}
2	cis	chr17	rs7214151	1	37507772	0.33	rs7214151	37507772	0.33	0	1.00	6.0×10^{-4}	1.0×10^{-1}
9	cis	chr17	rs879606	1	37781849	0.36	rs879606	37781849	0.36	0	1.00	4.0×10^{-4}	2.2×10^{-3}
26	cis	chr17	rs907091	1	37921742	0.49	rs9303277	37976469	0.49	54727	0.97	8.9×10^{-25}	3.1×10^{-5}
41	cis	chr17	rs7219923	1	38074518	0.45	rs7216389	38069949	0.34	4569	0.97	6.8×10^{-26}	1.2×10^{-4}
58	cis	chr17	rs7211770	1	38289003	0.40	rs7211770	38289003	0.40	0	1.00	6.0×10^{-4}	5.3×10^{-1}
60	cis	chr17	rs13695	1	38545193	0.11	rs13695	38545193	0.11	0	1.00	6.0×10^{-6}	5.5×10^{-2}

Crohns Gene 38
ORMDL3: ORM1-like 3 (S. cerevisiae)
Gene Location: chr17:38077295-38083884
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 1.5×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
3	trans	chr1	rs6681988	1	107930365	0.45	rs6681988	107930365	0.45	0	1.00	5.0×10^{-6}	3.3×10^{-1}
4	trans	chr1	rs11264845	1	157871097	0.46	rs7545948	157879381	0.48	8284	0.98	3.0×10^{-6}	3.1×10^{-1}
8	trans	chr1	rs1051740	6	226019633	0.29	rs1051740	226019633	0.29	0	1.00	1.0×10^{-5}	4.6×10^{-1}
10	trans	chr1	rs12731570	1	231981938	0.16	rs12735632	231982016	0.16	78	1.00	3.0×10^{-6}	6.8×10^{-1}
17	trans	chr1	rs4129118	1	241928698	0.39	rs6696527	241926150	0.31	2548	0.99	2.0×10^{-6}	3.8×10^{-1}
30	trans	chr2	rs17050260	1	59803819	0.16	rs11682929	59808603	0.16	4784	0.98	3.0×10^{-6}	2.2×10^{-1}
32	trans	chr2	rs10497705	1	190492014	0.47	rs10497705	190492014	0.47	0	1.00	7.0×10^{-6}	3.8×10^{-1}
34	trans	chr3	rs2174746	9	153098443	0.15	rs2174746	153098443	0.15	0	1.00	1.0×10^{-6}	3.9×10^{-1}
36	trans	chr5	rs11955062	2	97021670	0.22	rs1560323	97028011	0.27	6341	0.96	1.0×10^{-5}	1.9×10^{-1}
38	trans	chr5	rs3846728	1	131436217	0.28	rs27437	131436961	0.34	744	0.88	4.0×10^{-6}	3.8×10^{-6}
43	trans	chr5	rs420460	1	150548930	0.50	rs420460	150548930	0.50	0	1.00	1.0×10^{-6}	4.5×10^{-1}
48	trans	chr6	rs1418309	2	22500073	0.48	rs7742591	22501947	0.49	1874	1.00	1.0×10^{-7}	1.1×10^{-1}
57	trans	chr6	rs736476	1	134727620	0.34	rs736476	134727620	0.34	0	1.00	5.0×10^{-6}	5.7×10^{-1}
59	trans	chr7	rs17164126	1	11287195	0.15	rs2040798	11290286	0.14	3091	0.99	8.0×10^{-6}	6.8×10^{-1}
63	trans	chr8	rs17053106	4	24952142	0.13	rs7837627	24953723	0.12	1581	1.00	1.0×10^{-5}	8.8×10^{-1}
65	trans	chr9	rs4740888	1	7396956	0.31	rs4740888	7396956	0.31	0	1.00	9.0×10^{-7}	7.4×10^{-1}
66	trans	chr9	rs6475540	8	21595717	0.31	rs12343168	21600424	0.31	4707	0.88	5.0×10^{-6}	4.0×10^{-1}
70	trans	chr9	rs1330828	5	85134671	0.46	rs7043482	85135915	0.42	1244	0.97	1.0×10^{-5}	2.3×10^{-1}
80	trans	chr10	rs404311	3	30898024	0.43	rs448247	30896831	0.45	1193	0.99	9.0×10^{-6}	1.9×10^{-2}
85	trans	chr10	rs7917438	1	120535370	0.18	rs6585507	120538000	0.18	2630	1.00	1.0×10^{-5}	5.1×10^{-1}
86	trans	chr11	rs4752741	2	1716153	0.21	rs11040310	1716663	0.21	510	0.94	1.0×10^{-5}	7.4×10^{-1}
87	trans	chr11	rs7112561	59	6739109	0.48	rs12284429	6739407	0.48	298	1.00	6.0×10^{-6}	2.5×10^{-1}
88	trans	chr11	rs4237757	1	7670249	0.25	rs4237757	7670249	0.25	0	1.00	7.0×10^{-6}	5.9×10^{-1}
93	trans	chr11	rs12286870	16	107776667	0.20	rs10466556	107803708	0.17	27041	0.89	2.0×10^{-7}	6.2×10^{-1}
95	trans	chr12	rs17659860	4	29558615	0.14	rs17659860	29558615	0.14	0	1.00	1.0×10^{-5}	7.3×10^{-1}
98	trans	chr12	rs1514668	8	43527634	0.31	rs1849785	43527723	0.31	89	1.00	7.0×10^{-6}	5.4×10^{-1}
102	trans	chr13	rs11838655	29	22695311	0.47	rs11838655	22695311	0.47	0	1.00	7.0×10^{-6}	4.9×10^{-1}
103	trans	chr13	rs9510622	2	23774923	0.34	rs9510623	23775454	0.34	531	1.00	7.0×10^{-6}	9.4×10^{-1}
105	trans	chr13	rs1041304	1	35140485	0.40	rs1041304	35140485	0.40	0	1.00	1.0×10^{-5}	1.6×10^{-1}
108	trans	chr13	rs6561566	1	50445012	0.12	rs9526614	50443558	0.10	1454	0.97	9.0×10^{-6}	4.8×10^{-1}
110	trans	chr13	rs1323450	1	50602282	0.26	rs9535416	50624140	0.26	21858	0.93	6.0×10^{-6}	7.0×10^{-1}
111	trans	chr14	rs10139382	2	24300497	0.26	rs10139382	24300497	0.26	0	1.00	2.0×10^{-6}	9.3×10^{-1}
113	trans	chr16	rs6564677	1	79595556	0.13	rs6564677	79595556	0.13	0	1.00	9.0×10^{-6}	9.5×10^{-2}
115	trans	chr17	rs739439	3	26723822	0.10	rs739439	26723822	0.10	0	1.00	1.0×10^{-5}	8.7×10^{-1}
124	cis	chr17	rs12936231	1	38029120	0.46	rs12936231	38029120	0.46	0	1.00	4.0×10^{-10}	9.8×10^{-6}
156	trans	chr17	rs2606189	2	77213331	0.14	rs2606188	77213668	0.16	337	1.00	5.0×10^{-6}	6.7×10^{-3}
160	trans	chr19	rs8109837	1	28471060	0.25	rs10405619	28466735	0.25	4325	1.00	8.0×10^{-6}	5.2×10^{-1}
161	trans	chr19	rs11083655	1	29239956	0.24	rs11083656	29242418	0.24	2462	0.99	9.0×10^{-6}	6.8×10^{-1}
164	trans	chr20	rs6050267	1	25019099	0.16	rs6050267	25019099	0.16	0	1.00	3.0×10^{-6}	6.0×10^{-2}

Crohns Gene 39
ADO: 2-aminoethanethiol (cysteamine) dioxygenase
Gene Location: chr10:64564515-64568239
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 6.9×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr5	rs3797642	31	76748926	0.12	rs3797642	76748926	0.12	0	1.00	4.9×10^{-6}	4.3×10^{-2}
3	trans	chr6	rs387233	3	67316395	0.05	rs388232	67322556	0.08	6161	1.00	1.6×10^{-6}	6.5×10^{-1}
6	cis	chr10	rs382424	1	64489774	0.37	rs224147	64485815	0.49	3959	0.98	5.4×10^{-7}	2.4×10^{-9}
13	trans	chr10	rs2901990	1	98120109	0.21	rs2901990	98120109	0.21	0	1.00	3.8×10^{-7}	8.2×10^{-1}

Crohns Gene 39
ADO: 2-aminoethanethiol (cysteamine) dioxygenase
Gene Location: chr10:64564515-64568239
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 8.9×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
3	trans	chr2	rs4233884	64	10835457	0.26	rs4614910	10829416	0.32	6041	0.88	2.0×10^{-6}	2.4×10^{-1}
5	trans	chr2	rs1867750	4	119920455	0.28	rs1867750	119920455	0.28	0	1.00	5.0×10^{-6}	8.0×10^{-1}
6	trans	chr3	rs12493081	28	26806108	0.50	rs3912610	26806383	0.48	275	0.98	6.0×10^{-6}	2.9×10^{-1}
19	trans	chr3	rs1489617	8	177790092	0.47	rs2902414	177767236	0.32	22856	0.86	9.0×10^{-6}	1.1×10^{-4}
25	trans	chr5	rs166280	2	55818087	0.26	rs166280	55818087	0.26	0	1.00	9.0×10^{-6}	5.4×10^{-1}
26	trans	chr5	rs13175611	118	68242039	0.49	rs13175611	68242039	0.49	0	1.00	2.0×10^{-6}	5.4×10^{-1}
29	trans	chr6	rs7738608	1	16384665	0.50	rs7738608	16384665	0.50	0	1.00	1.0×10^{-5}	7.1×10^{-1}
31	trans	chr6	rs10807344	10	46625635	0.13	rs10807344	46625635	0.13	0	1.00	1.0×10^{-5}	4.4×10^{-1}
32	trans	chr6	rs332591	12	48007346	0.34	rs112500	48007492	0.35	146	1.00	1.0×10^{-5}	7.6×10^{-1}
38	trans	chr6	rs9370233	17	53684912	0.28	rs9395878	53668237	0.27	16675	0.98	2.0×10^{-6}	4.4×10^{-1}
55	trans	chr7	rs217013	159	140988611	0.45	rs217013	140988611	0.45	0	1.00	4.0×10^{-6}	3.8×10^{-1}
58	trans	chr8	rs1485532	3	13825467	0.22	rs1485532	13825467	0.22	0	1.00	6.0×10^{-6}	2.5×10^{-1}
62	trans	chr10	rs11598809	3	93527090	0.13	rs17107019	93526562	0.13	528	1.00	2.0×10^{-6}	9.8×10^{-1}
67	trans	chr11	rs10501143	6	35841576	0.18	rs10501143	35841576	0.18	0	1.00	9.0×10^{-6}	3.2×10^{-1}
70	trans	chr11	rs1945848	57	106519130	0.15	rs1945848	106519130	0.15	0	1.00	7.0×10^{-6}	4.0×10^{-1}
72	trans	chr12	rs10881072	1	47585115	0.44	rs10881072	47585115	0.44	0	1.00	1.0×10^{-5}	2.0×10^{-2}
73	trans	chr12	rs1629940	19	103193521	0.32	rs1629940	103193521	0.32	0	1.00	1.0×10^{-5}	1.3×10^{-1}
74	trans	chr12	rs7295928	3	108280027	0.16	rs11609659	108296260	0.15	16233	0.86	1.0×10^{-5}	1.8×10^{-1}
76	trans	chr13	rs1860836	4	57177656	0.30	rs9569497	57183350	0.24	5694	0.98	1.0×10^{-5}	8.8×10^{-1}
78	trans	chr14	rs8012757	6	50477578	0.19	rs8012757	50477578	0.19	0	1.00	9.0×10^{-6}	9.3×10^{-1}
79	trans	chr14	rs4903749	2	78778726	0.13	rs4903741	78766644	0.12	12082	0.99	8.0×10^{-6}	9.0×10^{-1}
80	trans	chr15	rs4556743	1	94585444	0.27	rs8042025	94590544	0.31	5100	0.85	5.0×10^{-6}	5.1×10^{-1}
83	trans	chr16	rs2269911	2	3065924	0.19	rs2269911	3065924	0.19	0	1.00	7.0×10^{-6}	5.5×10^{-1}
87	trans	chr16	rs12929956	30	55741501	0.20	rs12929956	55741501	0.20	0	1.00	6.0×10^{-6}	7.8×10^{-2}
89	trans	chr17	rs4480854	1	49632782	0.47	rs4480854	49632782	0.47	0	1.00	1.0×10^{-5}	5.0×10^{-2}
97	trans	chr19	rs7254617	101	40791512	0.23	rs10418932	40800288	0.22	8776	0.98	9.0×10^{-7}	8.4×10^{-1}
107	trans	chr21	rs4816344	11	30847259	0.10	rs4816344	30847259	0.10	0	1.00	4.0×10^{-6}	2.4×10^{-1}

Crohns Gene 39
ADO: 2-aminoethanethiol (cysteamine) dioxygenase
Gene Location: chr10:64564515-64568239
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 6.9×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr1	rs12403887	6	91699151	0.20	rs12403887	91699151	0.20	0	1.00	6.8×10^{-6}	1.3×10^{-1}
5	trans	chr7	rs977480	32	112304167	0.44	rs977480	112304167	0.44	0	1.00	7.2×10^{-6}	8.5×10^{-2}
19	trans	chr10	rs7081017	48	69954451	0.50	rs6480311	69956848	0.49	2397	0.85	1.2×10^{-6}	8.5×10^{-1}

Crohns Gene 40
NPTN: neuroplastin
Gene Location: chr15:73852343-73925753
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 3.6×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr2	rs1357343	1	57573557	0.12	rs4233968	57487947	0.11	85610	0.94	1.0×10^{-5}	1.0×10^{-2}
3	trans	chr2	rs4675800	7	242502642	0.33	rs4675800	242502642	0.33	0	1.00	8.0×10^{-6}	3.1×10^{-2}
4	trans	chr4	rs4608765	15	87259268	0.46	rs4611890	87259006	0.46	262	1.00	1.0×10^{-5}	4.4×10^{-1}
5	trans	chr4	rs11722147	16	158671867	0.15	rs1904949	158663069	0.24	8798	0.95	6.0×10^{-6}	6.2×10^{-1}
11	trans	chr7	rs11973211	117	140984375	0.34	rs4726446	140990727	0.32	6352	0.98	8.0×10^{-7}	2.2×10^{-1}
21	trans	chr10	rs11252653	28	4717336	0.24	rs313455	4694013	0.19	23323	0.91	3.0×10^{-7}	4.9×10^{-1}
24	trans	chr10	rs11196301	615	84634847	0.14	rs11196301	84634847	0.14	0	1.00	2.0×10^{-6}	6.6×10^{-1}
27	trans	chr11	rs11218469	13	121810205	0.38	rs12577788	121813931	0.38	3726	0.98	1.0×10^{-5}	7.8×10^{-2}
33	trans	chr12	rs1498616	17	17548363	0.14	rs1498616	17548363	0.14	0	1.00	8.0×10^{-6}	2.5×10^{-1}
37	trans	chr14	rs17715699	1	57181499	0.40	rs17715699	57181499	0.40	0	1.00	9.0×10^{-6}	3.5×10^{-1}
38	trans	chr20	rs6015426	2	57638815	0.41	rs6070709	57639099	0.37	284	1.00	7.0×10^{-6}	7.2×10^{-1}
39	trans	chr21	rs366592	2	17334568	0.30	rs366592	17334568	0.30	0	1.00	5.0×10^{-6}	4.3×10^{-2}
40	trans	chr22	rs5760874	10	25536642	0.12	rs4476445	25531002	0.13	5640	1.00	1.0×10^{-5}	1.8×10^{-1}

Crohns Gene 40
NPTN: neuroplastin
Gene Location: chr15:73852343-73925753
GWAS Data: Barrett 2008
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 2.6×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs6764079	22	14260674	0.26	rs6764079	14260674	0.26	0	1.00	7.1×10^{-6}	1.8×10^{-1}
2	trans	chr3	rs12494994	64	99822536	0.17	rs12494994	99822536	0.17	0	1.00	3.8×10^{-6}	7.4×10^{-1}
6	trans	chr9	rs7045505	12	79249761	0.09	rs7045505	79249761	0.09	0	1.00	7.0×10^{-6}	2.8×10^{-2}
7	trans	chr10	rs998139	55	8425531	0.27	rs998139	8425531	0.27	0	1.00	9.5×10^{-7}	2.7×10^{-1}
8	trans	chr16	rs1482247	29	59591788	0.48	rs1482247	59591788	0.48	0	1.00	7.4×10^{-6}	1.6×10^{-1}

Crohns Gene 40
NPTN: neuroplastin
Gene Location: chr15:73852343-73925753
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 1.9×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
4	trans	chr1	rs3790566	1	67814440	0.41	rs3790567	67822377	0.41	7937	0.99	2.8×10^{-6}	1.5×10^{-3}
9	trans	chr1	rs1195865	205	81678117	0.26	rs2972002	81679010	0.36	893	0.96	4.1×10^{-7}	5.1×10^{-1}
13	trans	chr3	rs3811725	1	183562276	0.41	rs6775202	183576600	0.49	14324	1.00	9.2×10^{-6}	4.5×10^{-2}
17	trans	chr6	rs6934007	6	3549706	0.13	rs6934461	3549996	0.16	290	1.00	2.5×10^{-6}	7.2×10^{-2}
20	trans	chr9	rs10815644	52	7598892	0.15	rs13285544	7595558	0.14	3334	0.95	8.5×10^{-6}	9.6×10^{-1}
21	trans	chr10	rs10997950	15	69912278	0.32	rs7081820	69914009	0.31	1731	0.98	2.0×10^{-6}	7.6×10^{-2}
33	trans	chr21	rs2409416	17	32975321	0.46	rs2409416	32975321	0.46	0	1.00	3.4×10^{-6}	3.3×10^{-1}

Crohns Gene 41
TYW1: tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)
Gene Location: chr7:66461816-66704498
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 3.7×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
4	cis	chr7	rs17137288	2	66581995	0.28	rs17137288	66581995	0.28	0	1.00	9.4×10^{-7}	5.6×10^{-1}
17	trans	chr7	rs2960920	1	72083747	0.25	rs2960920	72083747	0.25	0	1.00	1.3×10^{-8}	2.6×10^{-1}
21	trans	chr7	rs4483038	1	72211476	0.41	rs4483038	72211476	0.41	0	1.00	6.8×10^{-11}	2.9×10^{-3}

Crohns Gene 41
TYW1: tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)
Gene Location: chr7:66461816-66704498
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 9.2×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	cis	chr7	rs1880278	1	66617560	0.26	rs6966142	66616604	0.25	956	0.98	6.8×10^{-5}	5.8×10^{-1}
3	trans	chr7	rs4318932	1	72043041	0.45	rs4318932	72043041	0.45	0	1.00	1.4×10^{-8}	2.9×10^{-3}
7	trans	chr7	rs4483038	1	72211476	0.41	rs4483038	72211476	0.41	0	1.00	4.3×10^{-18}	2.9×10^{-3}
15	trans	chr14	rs17108853	4	79653170	0.05	rs17108853	79653170	0.05	0	1.00	7.5×10^{-6}	1.2×10^{-1}
16	trans	chr17	rs1242507	1	17365399	0.37	rs1242507	17365399	0.37	0	1.00	9.5×10^{-6}	8.2×10^{-1}
18	trans	chr20	rs6123832	3	57418071	0.41	rs6123832	57418071	0.41	0	1.00	4.9×10^{-6}	9.3×10^{-1}

Crohns Gene 41
TYW1: tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)
Gene Location: chr7:66461816-66704498
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 3.5×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
18	trans	chr7	rs7798532	1	72282003	0.39	rs7798532	72282003	0.39	0	1.00	1.9×10^{-6}	9.3×10^{-4}

Details for Top T2D Genes

The supporting SNPs for all top T2D genes are provided here. The genes are listed in rank order, and only functional data yielding Empirical Sherlock p-values below 0.1 is shown. Thus, certain genes may have only one supporting eQTL data set listed, while others will have multiple listings if their Empirical Sherlock results are significant across multiple tissues. Definitions for each column in the supporting matrix are provided in Table C.1. All coordinates provided are for assembly hg19 / GRCh37 of the human genome. Minor allele frequencies (MAFs) given are from NCBI dbSNP build 135. Linkage disequilibrium is from our custom database, as described in Methods.

Table B.2: Explanation of Supporting SNP Information

BLK	Haplotype Block Number. These are not sequential, since only independently-sorting SNPs are retained.
PRX	Proximity of SNP to gene (cis or trans)
CHR	Chromosome
eQTL SNP	ID of eQTL SNP used
PL	SNP pleiotropy. The number of times this SNP is found in other genes in the eQTL data set.
Location	Location of the eQTL SNP
MAF	Minor allele frequency of the eQTL SNP. Used as a check for independence of adjacent tag SNPs.
GWAS SNP	ID of the GWAS SNP used
Location	Location of the aligned GWAS SNP
MAF	Minor allele frequency of the GWAS SNP
Delta	Distance in base pairs between the two SNPs
LD	Linkage disequilibrium (r^2) between the SNPs
eQTL pval	Used to define SNP sets at different thresholds, as per our method
GWAS pval	Used to construct the gene score. The summation of log(p-values) for this column is the gene score

T2D Gene 1
TSPAN8: tetraspanin 8
Gene Location: chr12:71518876-71551779
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 3.2×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr4	rs6841355	1	25538772	0.46	rs6841355	25538772	0.46	0	1.00	5.7×10^{-6}	3.7×10^{-1}
2	trans	chr5	rs30656	1	129010769	0.31	rs30656	129010769	0.31	0	1.00	9.7×10^{-6}	6.2×10^{-1}
3	trans	chr6	rs9381214	2	42693959	0.42	rs7764439	42689755	0.40	4204	1.00	9.7×10^{-6}	6.2×10^{-1}
4	trans	chr8	rs281713	1	108545055	0.36	rs281713	108545055	0.36	0	1.00	3.6×10^{-6}	6.8×10^{-1}
13	trans	chr11	rs10789859	2	111960533	0.36	rs10789859	111960533	0.36	0	1.00	1.3×10^{-6}	3.8×10^{-1}
14	cis	chr12	rs7965899	1	71298675	0.31	rs7965899	71298675	0.31	0	1.00	9.9×10^{-6}	1.0×10^{-2}
33	cis	chr12	rs1512988	1	71454999	0.28	rs1512988	71454999	0.28	0	1.00	6.3×10^{-19}	3.2×10^{-5}
56	trans	chr18	rs11151091	1	75589532	0.47	rs1542953	75591080	0.49	1548	0.99	4.8×10^{-6}	6.1×10^{-1}

T2D Gene 2
TRIB1: tribbles homolog 1 (Drosophila)
Gene Location: chr8:126442562-126450644
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 4.6×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs9306867	51	18283243	0.42	rs9306867	18283243	0.42	0	1.00	9.0×10^{-7}	9.2×10^{-1}
4	trans	chr4	rs11932673	1	57833203	0.17	rs9942208	57833671	0.18	468	0.99	4.0×10^{-7}	8.0×10^{-1}
7	trans	chr5	rs6870959	1	148496513	0.29	rs6870959	148496513	0.29	0	1.00	1.0×10^{-5}	1.1×10^{-2}
9	trans	chr6	rs12211400	2	130007477	0.49	rs12211400	130007477	0.49	0	1.00	8.0×10^{-6}	4.1×10^{-1}
13	trans	chr7	rs13307299	2	67228631	0.43	rs13307299	67228631	0.43	0	1.00	1.0×10^{-5}	1.9×10^{-1}
14	trans	chr9	rs1008878	1	22036112	0.17	rs1008878	22036112	0.17	0	1.00	6.0×10^{-6}	2.6×10^{-5}
18	trans	chr9	rs10115497	2	107303592	0.20	rs10115497	107303592	0.20	0	1.00	7.0×10^{-6}	4.7×10^{-1}
21	trans	chr10	rs12255547	1	78852296	0.12	rs12255547	78852296	0.12	0	1.00	1.0×10^{-5}	4.8×10^{-2}
22	trans	chr12	rs10777420	1	93027171	0.15	rs10777420	93027171	0.15	0	1.00	1.0×10^{-5}	5.4×10^{-1}
26	trans	chr16	rs8060901	6	9570666	0.35	rs8060901	9570666	0.35	0	1.00	6.0×10^{-6}	3.7×10^{-3}

T2D Gene 3
BDH2: 3-hydroxybutyrate dehydrogenase, type 2
Gene Location: chr4:103998781-104021024
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 4.9×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs1496042	71	152159773	0.47	rs1496042	152159773	0.47	0	1.00	8.1×10^{-6}	10.0×10^{-1}
2	trans	chr4	rs2087864	7	4803437	0.22	rs2087864	4803437	0.22	0	1.00	8.8×10^{-6}	2.0×10^{-1}
4	cis	chr4	rs3775972	2	104004362	0.16	rs2306478	104003148	0.16	1214	0.96	7.1×10^{-6}	3.0×10^{-3}
12	cis	chr4	rs6815702	5	104127786	0.32	rs6815702	104127786	0.32	0	1.00	2.9×10^{-6}	1.5×10^{-3}
14	trans	chr6	rs9394588	10	39349059	0.10	rs9394588	39349059	0.10	0	1.00	5.0×10^{-6}	3.2×10^{-1}
15	trans	chr7	rs7334	117	55278852	0.45	rs7334	55278852	0.45	0	1.00	2.6×10^{-6}	4.3×10^{-3}
16	trans	chr9	rs6475184	1	17857109	0.14	rs6475184	17857109	0.14	0	1.00	4.3×10^{-6}	8.6×10^{-1}
19	trans	chr10	rs4463750	20	14686790	0.41	rs4463750	14686790	0.41	0	1.00	7.5×10^{-6}	4.3×10^{-1}
20	trans	chr11	rs10734174	3	95847064	0.22	rs10734174	95847064	0.22	0	1.00	5.6×10^{-6}	7.5×10^{-1}
21	trans	chr11	rs660222	8	110010175	0.50	rs660222	110010175	0.50	0	1.00	6.2×10^{-7}	4.8×10^{-1}
23	trans	chr12	rs7308077	7	96907972	0.08	rs7308077	96907972	0.08	0	1.00	7.7×10^{-6}	1.8×10^{-2}
24	trans	chr12	rs11111760	34	104163898	0.19	rs11111760	104163898	0.19	0	1.00	9.0×10^{-6}	7.7×10^{-1}
25	trans	chr17	rs11868596	2	54745339	0.11	rs11868596	54745339	0.11	0	1.00	6.5×10^{-6}	6.9×10^{-1}
26	trans	chr18	rs2276378	10	12892169	0.31	rs2276378	12892169	0.31	0	1.00	8.0×10^{-6}	8.7×10^{-1}
27	trans	chr20	rs6044715	1	17249788	0.24	rs6044715	17249788	0.24	0	1.00	2.9×10^{-6}	4.0×10^{-1}

T2D Gene 4
S1PR4: sphingosine-1-phosphate receptor 4
Gene Location: chr19:3178735-3180330
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 5.4×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs4375990	1	24774912	0.45	rs4375990	24774912	0.45	0	1.00	6.2×10^{-6}	6.4×10^{-2}
2	trans	chr12	rs10879240	1	71443285	0.45	rs10879240	71443285	0.45	0	1.00	3.4×10^{-6}	2.9×10^{-6}
3	trans	chr20	rs8122333	2	744032	0.09	rs8122333	744032	0.09	0	1.00	4.4×10^{-6}	1.2×10^{-1}

T2D Gene 5
CDKN2B: cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)
Gene Location: chr9:22002901-22009312
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 7.7×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs616415	1	232481252	0.23	rs616415	232481252	0.23	0	1.00	8.8×10^{-6}	5.4×10^{-1}
2	trans	chr3	rs2700331	2	9266056	0.33	rs2700331	9266056	0.33	0	1.00	1.4×10^{-6}	9.8×10^{-1}
3	trans	chr3	rs323629	81	151927593	0.44	rs323629	151927593	0.44	0	1.00	5.8×10^{-6}	7.1×10^{-1}
5	cis	chr9	rs2383208	1	22132076	0.24	rs2383208	22132076	0.24	0	1.00	7.0×10^{-4}	9.8×10^{-7}
7	trans	chr12	rs7954630	1	102290154	0.44	rs7954630	102290154	0.44	0	1.00	6.8×10^{-6}	5.8×10^{-1}
8	trans	chr13	rs1759875	1	38384014	0.11	rs1759875	38384014	0.11	0	1.00	7.8×10^{-6}	2.3×10^{-1}
9	trans	chr13	rs9516155	11	93704206	0.23	rs9516155	93704206	0.23	0	1.00	5.7×10^{-6}	3.9×10^{-2}
11	trans	chr14	rs11622292	2	90066327	0.33	rs11622292	90066327	0.33	0	1.00	7.4×10^{-6}	1.1×10^{-1}
12	trans	chr16	rs7192327	14	80818428	0.35	rs7192327	80818428	0.35	0	1.00	6.3×10^{-6}	5.2×10^{-1}
13	trans	chr18	rs3884522	4	71400098	0.07	rs3884522	71400098	0.07	0	1.00	1.0×10^{-5}	8.4×10^{-1}

T2D Gene 5
CDKN2B: cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)
Gene Location: chr9:22002901-22009312
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 2.2×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs4072897	7	241342330	0.33	rs4072897	241342330	0.33	0	1.00	1.9×10^{-6}	3.0×10^{-1}
17	trans	chr2	rs7595947	200	52264332	0.30	rs7595947	52264332	0.30	0	1.00	5.6×10^{-9}	5.2×10^{-1}
26	trans	chr6	rs7763423	1	5523888	0.49	rs7763423	5523888	0.49	0	1.00	2.7×10^{-6}	3.3×10^{-2}
30	trans	chr7	rs11772778	1	17191458	0.12	rs11772778	17191458	0.12	0	1.00	8.8×10^{-6}	9.5×10^{-2}
31	trans	chr7	rs11972506	4	150496668	0.44	rs11972506	150496668	0.44	0	1.00	2.6×10^{-6}	4.7×10^{-1}
32	trans	chr12	rs10784637	4	68034947	0.45	rs10784637	68034947	0.45	0	1.00	5.8×10^{-6}	2.7×10^{-1}
34	trans	chr13	rs943559	5	73715341	0.42	rs943559	73715341	0.42	0	1.00	9.5×10^{-7}	2.8×10^{-1}
38	trans	chr13	rs3736867	1	99061378	0.47	rs2291176	99062686	0.49	1308	0.96	2.2×10^{-6}	1.3×10^{-2}
43	trans	chr14	rs12436725	7	94047444	0.11	rs12436725	94047444	0.11	0	1.00	6.6×10^{-7}	9.0×10^{-1}

T2D Gene 6
C20orf3: chromosome 20 open reading frame 3
Gene Location: chr20:24943579-24973425
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 8.0×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr3	rs3850194	3	171608370	0.19	rs3850194	171608370	0.19	0	1.00	7.9×10^{-6}	1.5×10^{-1}
3	trans	chr14	rs2287400	1	75182937	0.31	rs2287400	75182937	0.31	0	1.00	8.4×10^{-6}	7.1×10^{-4}
6	trans	chr14	rs17093914	1	75363641	0.28	rs17093914	75363641	0.28	0	1.00	8.0×10^{-6}	4.0×10^{-4}

T2D Gene 7
RPP25: ribonuclease P/MRP 25kDa subunit
Gene Location: chr15:75247442-75249775
GWAS Data: Barrett 2008
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 8.9×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs17204920	2	107346018	0.05	rs17204920	107346018	0.05	0	1.00	7.0×10^{-6}	2.7×10^{-2}
2	trans	chr5	rs34386	1	107511903	0.25	rs34386	107511903	0.25	0	1.00	5.4×10^{-6}	3.0×10^{-1}
4	trans	chr8	rs16910959	1	83705317	0.14	rs16910959	83705317	0.14	0	1.00	3.8×10^{-6}	2.0×10^{-1}
5	trans	chr9	rs2383208	1	22132076	0.24	rs2383208	22132076	0.24	0	1.00	6.4×10^{-6}	9.8×10^{-7}

T2D Gene 8
TP53INP1: tumor protein p53 inducible nuclear protein 1
Gene Location: chr8:95938199-95961615
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 3.7×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr5	rs6871819	1	171577700	0.40	rs6871819	171577700	0.40	0	1.00	4.2×10^{-6}	5.0×10^{-1}
2	cis	chr8	rs2241505	1	95686279	0.44	rs2241505	95686279	0.44	0	1.00	1.1×10^{-6}	2.6×10^{-1}
22	cis	chr8	rs1453377	1	95969947	0.44	rs1453377	95969947	0.44	0	1.00	1.1×10^{-26}	5.9×10^{-3}
33	cis	chr8	rs6471513	1	96100175	0.29	rs6471513	96100175	0.29	0	1.00	2.8×10^{-8}	2.4×10^{-2}
36	trans	chr21	rs2831165	36	29174612	0.15	rs2831165	29174612	0.15	0	1.00	9.9×10^{-7}	6.5×10^{-1}
37	trans	chr22	rs11704670	1	49583035	0.16	rs11704670	49583035	0.16	0	1.00	7.5×10^{-6}	7.2×10^{-2}

T2D Gene 8
TP53INP1: tumor protein p53 inducible nuclear protein 1
Gene Location: chr8:95938199-95961615
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 3.0×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs4845141	7	206972072	0.49	rs12565617	206962637	0.47	9435	0.96	7.0×10^{-6}	6.9×10^{-1}
2	trans	chr2	rs10864875	1	122853426	0.29	rs10864875	122853426	0.29	0	1.00	6.9×10^{-7}	7.3×10^{-1}
3	trans	chr7	rs1799011	9	78529329	0.28	rs1799011	78529329	0.28	0	1.00	2.8×10^{-6}	2.0×10^{-1}
4	cis	chr8	rs4734291	1	95820594	0.37	rs4734291	95820594	0.37	0	1.00	7.0×10^{-4}	1.2×10^{-4}
8	cis	chr8	rs481887	1	95967838	0.26	rs481887	95967838	0.26	0	1.00	3.7×10^{-6}	4.4×10^{-3}
15	trans	chr11	rs2174164	2	16443567	0.20	rs2174164	16443567	0.20	0	1.00	7.7×10^{-6}	6.1×10^{-1}
16	trans	chr20	rs6063071	5	45737763	0.31	rs6063071	45737763	0.31	0	1.00	1.8×10^{-6}	2.1×10^{-1}

T2D Gene 8
TP53INP1: tumor protein p53 inducible nuclear protein 1
Gene Location: chr8:95938199-95961615
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 2.7×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
3	trans	chr2	rs13414678	2	154029978	0.48	rs13414678	154029978	0.48	0	1.00	7.0×10^{-7}	1.3×10^{-1}
9	trans	chr2	rs7578480	4	154190729	0.28	rs7578480	154190729	0.28	0	1.00	9.0×10^{-6}	3.0×10^{-1}
11	trans	chr2	rs4673101	20	225255374	0.49	rs4673101	225255374	0.49	0	1.00	4.0×10^{-6}	3.2×10^{-1}
13	trans	chr4	rs4608765	12	87259268	0.46	rs4608765	87259268	0.46	0	1.00	1.0×10^{-5}	1.5×10^{-1}
14	trans	chr5	rs13175611	115	68242039	0.49	rs13175611	68242039	0.49	0	1.00	7.0×10^{-6}	9.3×10^{-1}
16	trans	chr6	rs9370238	1	53726183	0.44	rs9370238	53726183	0.44	0	1.00	8.0×10^{-6}	7.2×10^{-1}
19	trans	chr9	rs627947	11	3981076	0.39	rs4740746	3981029	0.38	47	NA	5.0×10^{-7}	9.5×10^{-4}
21	trans	chr10	rs10994191	1	52489148	0.12	rs10994191	52489148	0.12	0	1.00	1.0×10^{-5}	1.9×10^{-1}
23	trans	chr13	rs4770836	18	26037909	0.27	rs4770836	26037909	0.27	0	1.00	3.0×10^{-6}	9.9×10^{-2}
25	trans	chr16	rs1004792	3	3094261	0.16	rs1004792	3094261	0.16	0	1.00	2.0×10^{-6}	8.7×10^{-1}
28	trans	chr18	rs11152377	3	60972446	0.25	rs11152377	60972446	0.25	0	1.00	7.0×10^{-6}	4.9×10^{-1}

T2D Gene 9
DNA2: DNA replication helicase 2 homolog (yeast)
Gene Location: chr10:70173820-70231879
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 3.7×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr5	rs6873702	1	108015658	0.12	rs6873702	108015658	0.12	0	1.00	3.8×10^{-7}	1.0×10^{-1}
3	cis	chr10	rs12217591	2	70251287	0.16	rs12217591	70251287	0.16	0	1.00	5.5×10^{-7}	4.7×10^{-2}

T2D Gene 9
DNA2: DNA replication helicase 2 homolog (yeast)
Gene Location: chr10:70173820-70231879
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 3.0×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
4	trans	chr2	rs12467485	1	19773375	0.34	rs12467485	19773375	0.34	0	1.00	5.1×10^{-6}	1.1×10^{-1}
5	trans	chr2	rs6715117	1	167021197	0.38	rs6715117	167021197	0.38	0	1.00	8.5×10^{-6}	5.0×10^{-1}
6	trans	chr3	rs1694014	1	21982433	0.31	rs1694014	21982433	0.31	0	1.00	6.3×10^{-6}	1.4×10^{-1}
13	trans	chr3	rs1452075	1	62481063	0.01	rs1452075	62481063	0.01	0	1.00	1.0×10^{-6}	5.7×10^{-6}
27	trans	chr5	rs6888875	1	173275898	0.45	rs6888875	173275898	0.45	0	1.00	3.6×10^{-6}	4.9×10^{-1}

T2D Gene 10
ZNF121: zinc finger protein 121
Gene Location: chr19:9676291-9695209
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 3.5×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr7	rs2043731	2	51170012	0.47	rs2043731	51170012	0.47	0	1.00	3.1×10^{-6}	1.2×10^{-2}
4	trans	chr7	rs10255738	1	126036578	0.15	rs10255738	126036578	0.15	0	1.00	7.4×10^{-6}	1.8×10^{-1}
5	trans	chr8	rs6981891	1	55391896	0.21	rs6981891	55391896	0.21	0	1.00	6.3×10^{-6}	2.0×10^{-1}
6	trans	chr9	rs7861073	1	6447439	0.27	rs7861073	6447439	0.27	0	1.00	5.8×10^{-6}	7.4×10^{-1}
20	trans	chr9	rs12343129	2	116345565	0.09	rs12343129	116345565	0.09	0	1.00	1.8×10^{-6}	1.4×10^{-1}
21	trans	chr18	rs1379641	4	30982868	0.09	rs1379641	30982868	0.09	0	1.00	2.3×10^{-7}	1.9×10^{-1}
23	trans	chr22	rs7287124	1	29239157	0.44	rs7287124	29239157	0.44	0	1.00	4.2×10^{-6}	1.0×10^{-1}
24	trans	chr22	rs4821705	1	38152929	0.03	rs4821705	38152929	0.03	0	1.00	1.9×10^{-6}	7.8×10^{-1}

T2D Gene 10
ZNF121: zinc finger protein 121
Gene Location: chr19:9676291-9695209
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 1.7×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs11809479	268	18712161	0.40	rs11809479	18712161	0.40	0	1.00	2.0×10^{-7}	8.1×10^{-1}
3	trans	chr2	rs4669775	6	11850369	0.38	rs4669775	11850369	0.38	0	1.00	3.0×10^{-6}	2.3×10^{-1}
5	trans	chr3	rs13070090	4	943915	0.19	rs13070090	943915	0.19	0	1.00	8.0×10^{-6}	7.3×10^{-1}
6	trans	chr3	rs12493197	19	24919200	0.15	rs12493197	24919200	0.15	0	1.00	4.0×10^{-6}	7.7×10^{-1}
8	trans	chr4	rs1358440	11	11275561	0.28	rs1358440	11275561	0.28	0	1.00	1.0×10^{-5}	9.5×10^{-1}
9	trans	chr4	rs11726974	7	21307467	0.30	rs11726974	21307467	0.30	0	1.00	1.0×10^{-5}	3.9×10^{-2}
11	trans	chr5	rs153706	7	16882242	0.39	rs153706	16882242	0.39	0	1.00	1.0×10^{-5}	1.7×10^{-2}
12	trans	chr5	rs34306	91	67578745	0.16	rs34306	67578745	0.16	0	1.00	1.0×10^{-5}	7.3×10^{-1}
13	trans	chr8	rs7009857	3	11167233	0.07	rs7009857	11167233	0.07	0	1.00	1.0×10^{-5}	1.1×10^{-3}
14	trans	chr8	rs11784534	3	103203083	0.10	rs11784534	103203083	0.10	0	1.00	1.0×10^{-5}	3.1×10^{-1}
15	trans	chr11	rs16909992	13	11732004	0.41	rs16909992	11732004	0.41	0	1.00	3.0×10^{-6}	2.6×10^{-1}
17	trans	chr11	rs825993	6	97261585	0.15	rs825993	97261585	0.15	0	1.00	1.0×10^{-5}	2.0×10^{-1}
18	trans	chr18	rs12953614	18	23148637	0.34	rs12953614	23148637	0.34	0	1.00	9.0×10^{-6}	1.5×10^{-1}

T2D Gene 10
ZNF121: zinc finger protein 121
Gene Location: chr19:9676291-9695209
GWAS Data: Barrett 2008
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 4.1×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs1470579	1	185529080	0.47	rs1470579	185529080	0.47	0	1.00	3.8×10^{-6}	3.1×10^{-7}
2	trans	chr5	rs731432	1	133131036	0.41	rs731432	133131036	0.41	0	1.00	4.8×10^{-6}	7.2×10^{-1}
3	trans	chr8	rs4732754	1	27650428	0.42	rs4732754	27650428	0.42	0	1.00	7.1×10^{-6}	7.0×10^{-1}
8	trans	chr14	rs17104686	1	37024142	0.26	rs17104686	37024142	0.26	0	1.00	4.0×10^{-7}	3.4×10^{-1}
15	trans	chr20	rs6034740	1	17086061	0.14	rs6034740	17086061	0.14	0	1.00	9.8×10^{-6}	4.0×10^{-2}

T2D Gene 11
MITD1: MIT, microtubule interacting and transport, domain containing 1
Gene Location: chr2:99785725-99797492
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 1.4×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
4	cis	chr2	rs13396584	3	99611768	0.19	rs13396584	99611768	0.19	0	1.00	2.0×10^{-8}	6.1×10^{-2}
17	cis	chr2	rs4851196	1	99858556	0.22	rs4851196	99858556	0.22	0	1.00	4.4×10^{-9}	2.2×10^{-2}
21	trans	chr5	rs256840	1	155924030	0.48	rs256840	155924030	0.48	0	1.00	5.8×10^{-6}	3.6×10^{-1}
22	trans	chr7	rs6962125	3	156231520	0.05	rs6962125	156231520	0.05	0	1.00	2.6×10^{-6}	1.1×10^{-1}
23	trans	chr10	rs12248765	2	11142727	0.46	rs12248765	11142727	0.46	0	1.00	8.6×10^{-7}	3.5×10^{-3}
25	trans	chr16	rs11074593	2	10214306	0.21	rs11074593	10214306	0.21	0	1.00	6.6×10^{-6}	6.1×10^{-1}

T2D Gene 11
MITD1: MIT, microtubule interacting and transport, domain containing 1
Gene Location: chr2:99785725-99797492
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 1.5×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs1386979	201	7848731	0.21	rs1386979	7848731	0.21	0	1.00	1.0×10^{-5}	5.3×10^{-1}
3	trans	chr7	rs11766554	650	79784997	0.09	rs11766554	79784997	0.09	0	1.00	2.0×10^{-6}	3.6×10^{-1}
5	trans	chr8	rs2720687	10	129043368	0.13	rs2720687	129043368	0.13	0	1.00	1.0×10^{-5}	10.0×10^{-2}
8	trans	chr10	rs11196301	614	84634847	0.14	rs11196301	84634847	0.14	0	1.00	1.0×10^{-5}	7.7×10^{-2}
14	trans	chr15	rs12912208	32	62354570	0.46	rs8029942	62353458	0.44	1112	0.96	9.0×10^{-7}	2.3×10^{-2}
17	trans	chr20	rs3761184	56	42969798	0.22	rs3761184	42969798	0.22	0	1.00	1.0×10^{-5}	7.3×10^{-1}

T2D Gene 12
CMAS: cytidine monophosphate N-acetylneuraminic acid synthetase
Gene Location: chr12:22199158-22218602
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 2.0×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs924753	53	15706124	0.48	rs924753	15706124	0.48	0	1.00	9.5×10^{-7}	2.9×10^{-1}
6	trans	chr7	rs1419840	2	34448659	0.41	rs1419840	34448659	0.41	0	1.00	1.6×10^{-6}	4.0×10^{-1}
8	trans	chr13	rs4770734	2	25336128	0.15	rs4770734	25336128	0.15	0	1.00	8.6×10^{-6}	2.9×10^{-4}
9	trans	chr14	rs1950420	17	27141020	0.47	rs1950420	27141020	0.47	0	1.00	5.7×10^{-6}	6.5×10^{-1}
10	trans	chr17	rs295073	33	32780576	0.28	rs295073	32780576	0.28	0	1.00	4.1×10^{-6}	1.6×10^{-1}

T2D Gene 12
CMAS: cytidine monophosphate N-acetylneuraminic acid synthetase
Gene Location: chr12:22199158-22218602
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 4.0×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs2226099	14	183449357	0.18	rs2226099	183449357	0.18	0	1.00	1.8×10^{-6}	3.2×10^{-1}
2	trans	chr5	rs4957054	3	575683	0.21	rs4957054	575683	0.21	0	1.00	9.0×10^{-6}	2.7×10^{-1}
3	trans	chr5	rs4865585	147	53999767	0.23	rs4865585	53999767	0.23	0	1.00	3.1×10^{-6}	3.6×10^{-1}
4	trans	chr9	rs869487	2	35615896	0.48	rs869487	35615896	0.48	0	1.00	7.1×10^{-6}	3.7×10^{-2}
5	trans	chr11	rs512225	3	124539236	0.09	rs512225	124539236	0.09	0	1.00	7.4×10^{-6}	7.0×10^{-2}
6	cis	chr12	rs3847888	2	23134279	0.13	rs3847888	23134279	0.13	0	1.00	6.0×10^{-4}	8.7×10^{-1}
7	trans	chr15	rs1664476	17	57667027	0.44	rs1664476	57667027	0.44	0	1.00	7.9×10^{-6}	6.5×10^{-1}

T2D Gene 12
CMAS: cytidine monophosphate N-acetylneuraminic acid synthetase
Gene Location: chr12:22199158-22218602
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 10.0×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
3	trans	chr2	rs1039835	12	30510752	0.36	rs1039835	30510752	0.36	0	1.00	3.2×10^{-6}	2.9×10^{-3}
5	trans	chr2	rs2241736	2	47187393	0.29	rs2241736	47187393	0.29	0	1.00	6.1×10^{-6}	6.9×10^{-1}
6	trans	chr2	rs9309438	139	70842774	0.33	rs9309438	70842774	0.33	0	1.00	9.2×10^{-6}	1.6×10^{-1}
7	trans	chr2	rs12328639	18	211676323	0.15	rs12328639	211676323	0.15	0	1.00	6.3×10^{-6}	6.3×10^{-2}
9	trans	chr4	rs1497401	24	143321490	0.45	rs1497401	143321490	0.45	0	1.00	6.9×10^{-6}	3.8×10^{-1}
13	trans	chr5	rs1839246	63	120061858	0.08	rs1839246	120061858	0.08	0	1.00	1.2×10^{-6}	8.3×10^{-1}
14	trans	chr5	rs2112409	1	170199979	0.40	rs2112409	170199979	0.40	0	1.00	8.0×10^{-6}	1.4×10^{-2}
15	trans	chr5	rs12654838	3	171127612	0.16	rs12654838	171127612	0.16	0	1.00	8.7×10^{-6}	1.5×10^{-1}
16	trans	chr6	rs12210303	84	131137148	0.17	rs12210303	131137148	0.17	0	1.00	6.9×10^{-6}	4.7×10^{-2}
17	trans	chr6	rs543363	120	131451112	0.10	rs543363	131451112	0.10	0	1.00	9.1×10^{-6}	1.6×10^{-1}
18	trans	chr7	rs12534598	20	107220096	0.31	rs12534598	107220096	0.31	0	1.00	6.5×10^{-6}	4.0×10^{-2}
20	trans	chr8	rs13271489	3	9803712	0.29	rs13271489	9803712	0.29	0	1.00	1.3×10^{-6}	4.6×10^{-2}
23	trans	chr10	rs1342766	13	9074500	0.23	rs1342766	9074500	0.23	0	1.00	9.7×10^{-6}	4.9×10^{-1}
24	trans	chr14	rs2184667	123	27780446	0.12	rs2184667	27780446	0.12	0	1.00	3.4×10^{-7}	8.3×10^{-1}
38	trans	chr15	rs12915189	47	91114376	0.40	rs12915189	91114376	0.40	0	1.00	9.1×10^{-7}	2.8×10^{-1}

T2D Gene 13
HOXB2: homeobox B2
Gene Location: chr17:46620018-46622393
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 2.4×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs11580758	1	63588694	0.07	rs11580758	63588694	0.07	0	1.00	8.9×10^{-6}	8.4×10^{-1}
2	trans	chr1	rs4846580	2	219897941	0.33	rs4846580	219897941	0.33	0	1.00	7.2×10^{-6}	8.5×10^{-1}
7	trans	chr2	rs1439929	1	224397999	0.13	rs1439929	224397999	0.13	0	1.00	4.5×10^{-6}	9.5×10^{-1}
8	trans	chr3	rs6798938	1	113218206	0.20	rs6798938	113218206	0.20	0	1.00	8.1×10^{-6}	8.7×10^{-1}
9	trans	chr4	rs1110342	2	179273888	0.36	rs1110342	179273888	0.36	0	1.00	1.3×10^{-6}	5.3×10^{-1}
14	trans	chr9	rs10979284	2	110987440	0.21	rs10979284	110987440	0.21	0	1.00	1.6×10^{-6}	4.6×10^{-1}
15	trans	chr9	rs12375949	1	124617900	0.44	rs12375949	124617900	0.44	0	1.00	9.0×10^{-6}	5.3×10^{-1}
16	trans	chr10	rs1925700	1	23419522	0.42	rs1925700	23419522	0.42	0	1.00	7.0×10^{-7}	2.1×10^{-3}
18	trans	chr12	rs2302728	1	2774668	0.39	rs2302728	2774668	0.39	0	1.00	6.8×10^{-6}	9.5×10^{-1}
19	trans	chr15	rs4470099	1	68766146	0.35	rs4470099	68766146	0.35	0	1.00	6.1×10^{-6}	9.2×10^{-1}
26	trans	chr17	rs9904967	1	45536875	0.38	rs9904967	45536875	0.38	0	1.00	8.1×10^{-10}	5.4×10^{-2}
68	cis	chr17	rs7220520	2	46167942	0.29	rs7220520	46167942	0.29	0	1.00	4.2×10^{-16}	7.8×10^{-4}
116	cis	chr17	rs12939811	1	46607958	0.13	rs12939811	46607958	0.13	0	1.00	2.0×10^{-204}	6.7×10^{-3}
130	cis	chr17	rs1320283	1	46807134	0.46	rs1320283	46807134	0.46	0	1.00	3.2×10^{-13}	7.3×10^{-1}
132	cis	chr17	rs16945851	1	47114482	0.07	rs2241932	47130230	0.07	15748	1.00	5.0×10^{-7}	9.1×10^{-1}
133	trans	chr22	rs760627	1	29459634	0.47	rs760627	29459634	0.47	0	1.00	2.0×10^{-6}	9.4×10^{-1}

T2D Gene 13
HOXB2: homeobox B2
Gene Location: chr17:46620018-46622393
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 3.5×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr3	rs10490775	1	62036724	0.11	rs10490775	62036724	0.11	0	1.00	8.8×10^{-6}	1.2×10^{-1}
3	trans	chr4	rs1390347	1	176724385	0.49	rs1390347	176724385	0.49	0	1.00	6.7×10^{-7}	4.1×10^{-1}
6	trans	chr6	rs7759336	1	130567718	0.37	rs7759336	130567718	0.37	0	1.00	1.0×10^{-5}	8.8×10^{-1}
16	cis	chr17	rs12449653	1	46473686	0.32	rs12449653	46473686	0.32	0	1.00	2.0×10^{-4}	8.9×10^{-3}
22	cis	chr17	rs1042815	1	46620288	0.49	rs1042815	46620288	0.49	0	1.00	7.9×10^{-10}	2.4×10^{-3}
26	trans	chr20	rs6081600	2	19437539	0.27	rs6081600	19437539	0.27	0	1.00	8.9×10^{-6}	9.9×10^{-1}

T2D Gene 13
HOXB2: homeobox B2
Gene Location: chr17:46620018-46622393
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 1.7×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs10917360	3	23539010	0.30	rs10917360	23539010	0.30	0	1.00	6.1×10^{-6}	10.0×10^{-2}
3	trans	chr7	rs12538253	1	75388031	0.24	rs12538253	75388031	0.24	0	1.00	6.6×10^{-6}	5.6×10^{-1}
6	cis	chr17	rs8079617	1	46610028	0.11	rs8079617	46610028	0.11	0	1.00	5.2×10^{-7}	6.8×10^{-3}
13	trans	chr17	rs4794409	4	51084543	0.40	rs4794409	51084543	0.40	0	1.00	3.5×10^{-6}	1.8×10^{-1}

T2D Gene 14
SRBD1: S1 RNA binding domain 1
Gene Location: chr2:45615818-45838433
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 7.4×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	cis	chr2	rs3911086	3	45575726	0.22	rs3911086	45575726	0.22	0	1.00	9.0×10^{-7}	6.9×10^{-3}
12	cis	chr2	rs4525744	1	45772725	0.49	rs4525744	45772725	0.49	0	1.00	2.6×10^{-10}	5.5×10^{-3}
17	trans	chr3	rs9811594	2	160745935	0.30	rs9811594	160745935	0.30	0	1.00	4.5×10^{-6}	4.5×10^{-2}
18	trans	chr13	rs9548906	2	40308690	0.47	rs4133063	40307119	0.47	1571	1.00	6.1×10^{-6}	1.0×10^{-1}

T2D Gene 14
SRBD1: S1 RNA binding domain 1
Gene Location: chr2:45615818-45838433
GWAS Data: Barrett 2008
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 6.3×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr5	rs17157849	19	104639792	0.24	rs17157849	104639792	0.24	0	1.00	4.7×10^{-7}	8.5×10^{-2}
2	trans	chr7	rs10253978	1	33554672	0.09	rs10253978	33554672	0.09	0	1.00	9.5×10^{-6}	1.1×10^{-2}

T2D Gene 15
MYL2: myosin, light chain 2, regulatory, cardiac, slow
Gene Location: chr12:111348623-111358404
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 2.1×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr5	rs2407759	1	54197973	0.36	rs2407759	54197973	0.36	0	1.00	3.8×10^{-6}	4.5×10^{-1}
2	trans	chr6	rs9368222	1	20686996	0.28	rs9368222	20686996	0.28	0	1.00	5.2×10^{-6}	1.5×10^{-11}
3	trans	chr8	rs9298276	1	77218289	0.22	rs9298276	77218289	0.22	0	1.00	9.7×10^{-6}	2.4×10^{-1}
4	trans	chr10	rs2768327	1	119247667	0.48	rs2768327	119247667	0.48	0	1.00	3.4×10^{-6}	7.6×10^{-1}
5	trans	chr11	rs4148898	1	45674599	0.35	rs4148903	45672725	0.31	1874	0.99	4.3×10^{-6}	3.1×10^{-2}
6	trans	chr14	rs10140164	1	55406123	0.43	rs10140164	55406123	0.43	0	1.00	4.0×10^{-6}	6.6×10^{-1}

T2D Gene 15
MYL2: myosin, light chain 2, regulatory, cardiac, slow
Gene Location: chr12:111348623-111358404
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 8.7×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr5	rs331746	1	124852713	0.47	rs331746	124852713	0.47	0	1.00	8.7×10^{-6}	5.6×10^{-2}
2	trans	chr22	rs2041607	1	17450515	0.32	rs2041607	17450515	0.32	0	1.00	1.0×10^{-5}	2.4×10^{-1}

T2D Gene 16
EIF2B2: eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa
Gene Location: chr14:75469611-75476294
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 1.0×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr4	rs1842259	1	136504466	0.20	rs1842259	136504466	0.20	0	1.00	3.7×10^{-6}	4.4×10^{-1}
7	trans	chr12	rs11175490	3	65034845	0.05	rs11175490	65034845	0.05	0	1.00	9.1×10^{-6}	8.5×10^{-2}
8	cis	chr14	rs8017803	2	75108422	0.45	rs8017803	75108422	0.45	0	1.00	2.4×10^{-8}	4.3×10^{-1}
18	cis	chr14	rs2058919	2	75310812	0.44	rs2058919	75310812	0.44	0	1.00	3.1×10^{-7}	10.0×10^{-4}
38	cis	chr14	rs175057	1	75489632	0.40	rs175057	75489632	0.40	0	1.00	6.8×10^{-80}	1.3×10^{-1}
64	cis	chr14	rs7148230	2	75677699	0.34	rs9805950	75678634	0.29	935	0.94	6.3×10^{-6}	1.6×10^{-1}
67	trans	chr21	rs741792	2	41254150	0.18	rs741792	41254150	0.18	0	1.00	8.9×10^{-6}	9.8×10^{-1}

T2D Gene 16
EIF2B2: eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa
Gene Location: chr14:75469611-75476294
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 8.8×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs3770565	1	216876828	0.23	rs3770565	216876828	0.23	0	1.00	1.0×10^{-5}	7.6×10^{-2}
2	cis	chr14	rs8185	2	75408789	0.22	rs8185	75408789	0.22	0	1.00	9.0×10^{-4}	3.0×10^{-1}
9	cis	chr14	rs175444	2	75601782	0.33	rs175444	75601782	0.33	0	1.00	1.1×10^{-4}	1.5×10^{-1}

T2D Gene 16
EIF2B2: eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa
Gene Location: chr14:75469611-75476294
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 4.0×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr4	rs2289164	1	147878242	0.49	rs2289164	147878242	0.49	0	1.00	5.0×10^{-6}	2.4×10^{-1}
9	trans	chr5	rs12109629	1	93359702	0.10	rs12109629	93359702	0.10	0	1.00	8.0×10^{-6}	6.9×10^{-1}
13	trans	chr5	rs1363438	20	119580326	0.36	rs1363438	119580326	0.36	0	1.00	2.0×10^{-6}	5.9×10^{-2}
29	trans	chr7	rs7796305	1	36764846	0.40	rs7796305	36764846	0.40	0	1.00	1.0×10^{-5}	6.5×10^{-1}
30	trans	chr7	rs2160195	1	38404971	0.15	rs2160195	38404971	0.15	0	1.00	2.0×10^{-6}	2.6×10^{-1}
31	trans	chr8	rs10100187	10	11257495	0.49	rs10100187	11257495	0.49	0	1.00	7.0×10^{-6}	1.7×10^{-1}
32	trans	chr9	rs10868811	8	72979246	0.31	rs10868811	72979246	0.31	0	1.00	2.0×10^{-6}	3.1×10^{-1}
33	trans	chr9	rs3780269	1	134457580	0.16	rs3780269	134457580	0.16	0	1.00	1.0×10^{-5}	8.9×10^{-2}
34	trans	chr10	rs11005041	4	57576058	0.39	rs11005041	57576058	0.39	0	1.00	5.0×10^{-6}	4.7×10^{-1}
35	trans	chr10	rs3922824	1	107150600	0.35	rs3922824	107150600	0.35	0	1.00	1.0×10^{-5}	7.4×10^{-2}
36	trans	chr10	rs1891115	32	124524751	0.50	rs1891115	124524751	0.50	0	1.00	9.0×10^{-6}	1.8×10^{-1}
37	trans	chr12	rs7953165	6	46431015	0.45	rs7953165	46431015	0.45	0	1.00	9.0×10^{-6}	8.0×10^{-2}
43	trans	chr14	rs11624780	6	74406611	0.39	rs11624780	74406611	0.39	0	1.00	5.0×10^{-7}	6.0×10^{-1}
71	cis	chr14	rs4556	1	75476071	0.45	rs4556	75476071	0.45	0	1.00	6.0×10^{-6}	1.3×10^{-1}
89	trans	chr16	rs2082037	1	84528293	0.23	rs2082037	84528293	0.23	0	1.00	7.0×10^{-6}	8.2×10^{-1}
90	trans	chr18	rs9966932	8	7689368	0.41	rs9966932	7689368	0.41	0	1.00	1.0×10^{-5}	2.6×10^{-2}
91	trans	chr18	rs7504200	41	12247872	0.47	rs7504200	12247872	0.47	0	1.00	2.0×10^{-6}	8.8×10^{-1}
93	trans	chr19	rs3826834	20	48494445	0.16	rs3826834	48494445	0.16	0	1.00	2.0×10^{-6}	2.8×10^{-1}
94	trans	chr21	rs2833392	2	32763231	0.14	rs2833392	32763231	0.14	0	1.00	1.0×10^{-5}	9.5×10^{-1}

T2D Gene 16
EIF2B2: eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa
Gene Location: chr14:75469611-75476294
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 2.6×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr5	rs10056565	2	80619046	0.20	rs10056565	80619046	0.20	0	1.00	3.0×10^{-7}	1.2×10^{-1}
3	trans	chr5	rs11747001	13	132412299	0.16	rs11747001	132412299	0.16	0	1.00	6.2×10^{-6}	7.5×10^{-1}
5	trans	chr5	rs6860981	5	155605629	0.37	rs6860981	155605629	0.37	0	1.00	5.4×10^{-6}	6.1×10^{-1}
8	trans	chr8	rs1809498	19	21836384	0.34	rs1809498	21836384	0.34	0	1.00	2.3×10^{-6}	1.9×10^{-1}
11	trans	chr8	rs10105946	6	106664873	0.18	rs10105946	106664873	0.18	0	1.00	1.7×10^{-6}	2.4×10^{-1}
16	cis	chr14	rs175071	1	75498177	0.33	rs175071	75498177	0.33	0	1.00	2.5×10^{-7}	2.6×10^{-1}
35	cis	chr14	rs2300601	1	75639571	0.47	rs2300601	75639571	0.47	0	1.00	1.0×10^{-7}	5.2×10^{-2}
39	trans	chr18	rs621834	9	34351529	0.14	rs621834	34351529	0.14	0	1.00	1.7×10^{-6}	1.9×10^{-2}

T2D Gene 16
EIF2B2: eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa
Gene Location: chr14:75469611-75476294
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 4.5×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr1	rs10783087	1	98787759	0.41	rs10783087	98787759	0.41	0	1.00	1.3×10^{-6}	3.9×10^{-1}
4	trans	chr6	rs17178962	1	134832733	0.05	rs17178962	134832733	0.05	0	1.00	5.1×10^{-6}	6.7×10^{-3}
5	trans	chr7	rs7785072	1	29137502	0.34	rs7785072	29137502	0.34	0	1.00	3.5×10^{-7}	9.5×10^{-1}
39	trans	chr16	rs9935238	1	76158610	0.38	rs9935238	76158610	0.38	0	1.00	2.3×10^{-6}	1.0×10^{-1}

T2D Gene 17
KIR2DS5: killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 5
Gene Location: chr19:70096-113132
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 1.2×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr10	rs7921719	2	109602952	0.14	rs7921719	109602952	0.14	0	1.00	4.8×10^{-6}	4.9×10^{-1}
3	trans	chr10	rs12255372	1	114808902	0.19	rs12255372	114808902	0.19	0	1.00	3.3×10^{-6}	3.6×10^{-17}
4	trans	chr12	rs7972539	2	96821569	0.10	rs7972539	96821569	0.10	0	1.00	5.5×10^{-6}	6.3×10^{-1}
6	trans	chr13	rs1928375	1	35142537	0.23	rs1928375	35142537	0.23	0	1.00	8.0×10^{-6}	2.4×10^{-1}
9	trans	chr19	rs678846	7	55326613	0.18	rs678846	55326613	0.18	0	1.00	7.2×10^{-10}	5.6×10^{-1}

T2D Gene 18
BCAT2: branched chain amino-acid transaminase 2, mitochondrial
Gene Location: chr19:49298318-49314320
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 9.6×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr5	rs13179557	19	64165343	0.04	rs13179557	64165343	0.04	0	1.00	1.0×10^{-5}	2.0×10^{-2}
2	trans	chr5	rs11949445	26	64320495	0.12	rs11949445	64320495	0.12	0	1.00	5.0×10^{-6}	2.5×10^{-2}
4	trans	chr6	rs9296000	17	11383976	0.45	rs9296000	11383976	0.45	0	1.00	4.0×10^{-6}	4.1×10^{-1}
7	trans	chr6	rs12665609	6	37586488	0.12	rs12665609	37586488	0.12	0	1.00	1.0×10^{-5}	2.9×10^{-1}
10	trans	chr6	rs2236038	12	47206033	0.47	rs2236038	47206033	0.47	0	1.00	9.0×10^{-6}	3.3×10^{-1}
13	trans	chr8	rs7004533	7	142696491	0.11	rs7004533	142696491	0.11	0	1.00	1.0×10^{-5}	2.0×10^{-1}
14	trans	chr9	rs10973114	17	3696511	0.20	rs10973114	3696511	0.20	0	1.00	1.0×10^{-5}	2.8×10^{-1}
15	trans	chr10	rs4453159	4	110448849	0.45	rs4453159	110448849	0.45	0	1.00	8.0×10^{-6}	1.7×10^{-1}
16	trans	chr10	rs2421121	24	124488187	0.18	rs2421121	124488187	0.18	0	1.00	2.0×10^{-6}	2.3×10^{-2}
17	trans	chr11	rs11041703	12	8018591	0.09	rs11041703	8018591	0.09	0	1.00	1.0×10^{-5}	2.9×10^{-3}
18	trans	chr13	rs11842969	6	101214375	0.42	rs11842969	101214375	0.42	0	1.00	1.0×10^{-5}	1.9×10^{-1}
22	trans	chr16	rs171798	53	55744504	0.30	rs171798	55744504	0.30	0	1.00	1.0×10^{-6}	7.7×10^{-1}
25	trans	chr17	rs8072659	21	32016493	0.45	rs8072659	32016493	0.45	0	1.00	1.0×10^{-5}	6.5×10^{-1}

T2D Gene 18
BCAT2: branched chain amino-acid transaminase 2, mitochondrial
Gene Location: chr19:49298318-49314320
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 1.9×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr7	rs2079373	8	32119530	0.15	rs30585	32093550	0.17	25980	0.86	4.1×10^{-6}	1.3×10^{-1}
4	trans	chr14	rs10162454	15	75144618	0.28	rs10162454	75144618	0.28	0	1.00	4.7×10^{-8}	1.3×10^{-2}
30	trans	chr14	rs929579	3	75330697	0.32	rs929579	75330697	0.32	0	1.00	1.1×10^{-6}	5.0×10^{-4}

T2D Gene 19
OGDHL: oxoglutarate dehydrogenase-like
Gene Location: chr10:50942686-50970425
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 1.3×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
25	trans	chr1	rs7516544	1	173491431	0.36	rs7516544	173491431	0.36	0	1.00	2.0×10^{-7}	1.7×10^{-2}
33	trans	chr2	rs12614262	1	5630388	0.31	rs12614262	5630388	0.31	0	1.00	4.0×10^{-6}	8.3×10^{-1}
34	trans	chr5	rs12516173	1	173542308	0.21	rs12516173	173542308	0.21	0	1.00	1.0×10^{-5}	9.0×10^{-1}
38	trans	chr6	rs9295478	1	20716253	0.42	rs9295478	20716253	0.42	0	1.00	1.0×10^{-6}	1.5×10^{-5}
49	trans	chr7	rs13230639	1	11304855	0.08	rs13230639	11304855	0.08	0	1.00	3.0×10^{-7}	2.2×10^{-2}
57	trans	chr7	rs6970779	1	130681773	0.11	rs978061	130681534	0.13	239	NA	9.0×10^{-6}	6.3×10^{-1}
58	trans	chr8	rs289555	1	13246938	0.12	rs289555	13246938	0.12	0	1.00	1.0×10^{-5}	1.4×10^{-1}
59	trans	chr10	rs2756115	1	101508622	0.26	rs2756115	101508622	0.26	0	1.00	1.0×10^{-5}	7.8×10^{-2}
61	trans	chr19	rs10421681	1	13349110	0.43	rs10421681	13349110	0.43	0	1.00	3.0×10^{-6}	4.0×10^{-1}
64	trans	chr22	rs9614177	1	43925090	0.45	rs9614177	43925090	0.45	0	1.00	9.0×10^{-6}	4.3×10^{-1}

T2D Gene 19
OGDHL: oxoglutarate dehydrogenase-like
Gene Location: chr10:50942686-50970425
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 6.4×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs7601227	2	174879174	0.48	rs7601227	174879174	0.48	0	1.00	6.1×10^{-6}	5.9×10^{-1}
3	trans	chr4	rs11722994	3	21263330	0.24	rs11722994	21263330	0.24	0	1.00	1.4×10^{-6}	3.5×10^{-1}
5	trans	chr5	rs1530812	39	41000152	0.49	rs1530812	41000152	0.49	0	1.00	1.9×10^{-8}	1.1×10^{-1}
8	trans	chr5	rs2271214	3	178770718	0.19	rs2271214	178770718	0.19	0	1.00	6.7×10^{-6}	2.2×10^{-1}
10	trans	chr13	rs1811951	9	66015942	0.28	rs7337746	66016604	0.26	662	1.00	4.3×10^{-6}	3.6×10^{-1}
11	trans	chr18	rs621834	9	34351529	0.14	rs621834	34351529	0.14	0	1.00	2.8×10^{-6}	1.9×10^{-2}

Appendix C

Supporting SNPs for Top T2D Results

The supporting SNPs for all top T2D genes are provided here. The genes are listed in rank order, and only functional data yielding Empirical Sherlock p-values below 0.1 is shown. Thus, certain genes may have only one supporting eQTL data set listed, while others will have multiple listings if their Empirical Sherlock results are significant across multiple tissues. Definitions for each column in the supporting matrix are provided in Table C.1. All coordinates provided are for assembly hg19 / GRCh37 of the human genome. Minor allele frequencies (MAFs) given are from NCBI dbSNP build 135. Linkage disequilibrium is from our custom database, as described in Methods.

Table C.1: Explanation of Supporting SNP Information

BLK	Haplotype Block Number. These are not sequential, since only independently-sorting SNPs are retained.
PRX	Proximity of SNP to gene (cis or trans)
CHR	Chromosome
eQTL SNP	ID of eQTL SNP used
PL	SNP pleiotropy. The number of times this SNP is found in other genes in the eQTL data set.
Location	Location of the eQTL SNP
MAF	Minor allele frequency of the eQTL SNP. Used as a check for independence of adjacent tag SNPs.
GWAS SNP	ID of the GWAS SNP used
Location	Location of the aligned GWAS SNP
MAF	Minor allele frequency of the GWAS SNP
Delta	Distance in base pairs between the two SNPs
LD	Linkage disequilibrium (r^2) between the SNPs
eQTL pval	Used to define SNP sets at different thresholds, as per our method
GWAS pval	Used to construct the gene score. The summation of log(p-values) for this column is the gene score

T2D Gene 1
TSPAN8: tetraspanin 8
Gene Location: chr12:71518876-71551779
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 3.2×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr4	rs6841355	1	25538772	0.46	rs6841355	25538772	0.46	0	1.00	5.7×10^{-6}	3.7×10^{-1}
2	trans	chr5	rs30656	1	129010769	0.31	rs30656	129010769	0.31	0	1.00	9.7×10^{-6}	6.2×10^{-1}
3	trans	chr6	rs9381214	2	42693959	0.42	rs7764439	42689755	0.40	4204	1.00	9.7×10^{-6}	6.2×10^{-1}
4	trans	chr8	rs281713	1	108545055	0.36	rs281713	108545055	0.36	0	1.00	3.6×10^{-6}	6.8×10^{-1}
13	trans	chr11	rs10789859	2	111960533	0.36	rs10789859	111960533	0.36	0	1.00	1.3×10^{-6}	3.8×10^{-1}
14	cis	chr12	rs7965899	1	71298675	0.31	rs7965899	71298675	0.31	0	1.00	9.9×10^{-6}	1.0×10^{-2}
33	cis	chr12	rs1512988	1	71454999	0.28	rs1512988	71454999	0.28	0	1.00	6.3×10^{-19}	3.2×10^{-5}
56	trans	chr18	rs11151091	1	75589532	0.47	rs1542953	75591080	0.49	1548	0.99	4.8×10^{-6}	6.1×10^{-1}

T2D Gene 2
TRIB1: tribbles homolog 1 (Drosophila)
Gene Location: chr8:126442562-126450644
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 4.6×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs9306867	51	18283243	0.42	rs9306867	18283243	0.42	0	1.00	9.0×10^{-7}	9.2×10^{-1}
4	trans	chr4	rs11932673	1	57833203	0.17	rs9942208	57833671	0.18	468	0.99	4.0×10^{-7}	8.0×10^{-1}
7	trans	chr5	rs6870959	1	148496513	0.29	rs6870959	148496513	0.29	0	1.00	1.0×10^{-5}	1.1×10^{-2}
9	trans	chr6	rs12211400	2	130007477	0.49	rs12211400	130007477	0.49	0	1.00	8.0×10^{-6}	4.1×10^{-1}
13	trans	chr7	rs13307299	2	67228631	0.43	rs13307299	67228631	0.43	0	1.00	1.0×10^{-5}	1.9×10^{-1}
14	trans	chr9	rs1008878	1	22036112	0.17	rs1008878	22036112	0.17	0	1.00	6.0×10^{-6}	2.6×10^{-5}
18	trans	chr9	rs10115497	2	107303592	0.20	rs10115497	107303592	0.20	0	1.00	7.0×10^{-6}	4.7×10^{-1}
21	trans	chr10	rs12255547	1	78852296	0.12	rs12255547	78852296	0.12	0	1.00	1.0×10^{-5}	4.8×10^{-2}
22	trans	chr12	rs10777420	1	93027171	0.15	rs10777420	93027171	0.15	0	1.00	1.0×10^{-5}	5.4×10^{-1}
26	trans	chr16	rs8060901	6	9570666	0.35	rs8060901	9570666	0.35	0	1.00	6.0×10^{-6}	3.7×10^{-3}

T2D Gene 3
BDH2: 3-hydroxybutyrate dehydrogenase, type 2
Gene Location: chr4:103998781-104021024
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 4.9×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs1496042	71	152159773	0.47	rs1496042	152159773	0.47	0	1.00	8.1×10^{-6}	10.0×10^{-1}
2	trans	chr4	rs2087864	7	4803437	0.22	rs2087864	4803437	0.22	0	1.00	8.8×10^{-6}	2.0×10^{-1}
4	cis	chr4	rs3775972	2	104004362	0.16	rs2306478	104003148	0.16	1214	0.96	7.1×10^{-6}	3.0×10^{-3}
12	cis	chr4	rs6815702	5	104127786	0.32	rs6815702	104127786	0.32	0	1.00	2.9×10^{-6}	1.5×10^{-3}
14	trans	chr6	rs9394588	10	39349059	0.10	rs9394588	39349059	0.10	0	1.00	5.0×10^{-6}	3.2×10^{-1}
15	trans	chr7	rs7334	117	55278852	0.45	rs7334	55278852	0.45	0	1.00	2.6×10^{-6}	4.3×10^{-3}
16	trans	chr9	rs6475184	1	17857109	0.14	rs6475184	17857109	0.14	0	1.00	4.3×10^{-6}	8.6×10^{-1}
19	trans	chr10	rs4463750	20	14686790	0.41	rs4463750	14686790	0.41	0	1.00	7.5×10^{-6}	4.3×10^{-1}
20	trans	chr11	rs10734174	3	95847064	0.22	rs10734174	95847064	0.22	0	1.00	5.6×10^{-6}	7.5×10^{-1}
21	trans	chr11	rs660222	8	110010175	0.50	rs660222	110010175	0.50	0	1.00	6.2×10^{-7}	4.8×10^{-1}
23	trans	chr12	rs7308077	7	96907972	0.08	rs7308077	96907972	0.08	0	1.00	7.7×10^{-6}	1.8×10^{-2}
24	trans	chr12	rs11111760	34	104163898	0.19	rs11111760	104163898	0.19	0	1.00	9.0×10^{-6}	7.7×10^{-1}
25	trans	chr17	rs11868596	2	54745339	0.11	rs11868596	54745339	0.11	0	1.00	6.5×10^{-6}	6.9×10^{-1}
26	trans	chr18	rs2276378	10	12892169	0.31	rs2276378	12892169	0.31	0	1.00	8.0×10^{-6}	8.7×10^{-1}
27	trans	chr20	rs6044715	1	17249788	0.24	rs6044715	17249788	0.24	0	1.00	2.9×10^{-6}	4.0×10^{-1}

T2D Gene 4
S1PR4: sphingosine-1-phosphate receptor 4
Gene Location: chr19:3178735-3180330
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 5.4×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs4375990	1	24774912	0.45	rs4375990	24774912	0.45	0	1.00	6.2×10^{-6}	6.4×10^{-2}
2	trans	chr12	rs10879240	1	71443285	0.45	rs10879240	71443285	0.45	0	1.00	3.4×10^{-6}	2.9×10^{-6}
3	trans	chr20	rs8122333	2	744032	0.09	rs8122333	744032	0.09	0	1.00	4.4×10^{-6}	1.2×10^{-1}

T2D Gene 5
CDKN2B: cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)
Gene Location: chr9:22002901-22009312
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 7.7×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs616415	1	232481252	0.23	rs616415	232481252	0.23	0	1.00	8.8×10^{-6}	5.4×10^{-1}
2	trans	chr3	rs2700331	2	9266056	0.33	rs2700331	9266056	0.33	0	1.00	1.4×10^{-6}	9.8×10^{-1}
3	trans	chr3	rs323629	81	151927593	0.44	rs323629	151927593	0.44	0	1.00	5.8×10^{-6}	7.1×10^{-1}
5	cis	chr9	rs2383208	1	22132076	0.24	rs2383208	22132076	0.24	0	1.00	7.0×10^{-4}	9.8×10^{-7}
7	trans	chr12	rs7954630	1	102290154	0.44	rs7954630	102290154	0.44	0	1.00	6.8×10^{-6}	5.8×10^{-1}
8	trans	chr13	rs1759875	1	38384014	0.11	rs1759875	38384014	0.11	0	1.00	7.8×10^{-6}	2.3×10^{-1}
9	trans	chr13	rs9516155	11	93704206	0.23	rs9516155	93704206	0.23	0	1.00	5.7×10^{-6}	3.9×10^{-2}
11	trans	chr14	rs11622292	2	90066327	0.33	rs11622292	90066327	0.33	0	1.00	7.4×10^{-6}	1.1×10^{-1}
12	trans	chr16	rs7192327	14	80818428	0.35	rs7192327	80818428	0.35	0	1.00	6.3×10^{-6}	5.2×10^{-1}
13	trans	chr18	rs3884522	4	71400098	0.07	rs3884522	71400098	0.07	0	1.00	1.0×10^{-5}	8.4×10^{-1}

T2D Gene 5
CDKN2B: cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)
Gene Location: chr9:22002901-22009312
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 2.2×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs4072897	7	241342330	0.33	rs4072897	241342330	0.33	0	1.00	1.9×10^{-6}	3.0×10^{-1}
17	trans	chr2	rs7595947	200	52264332	0.30	rs7595947	52264332	0.30	0	1.00	5.6×10^{-9}	5.2×10^{-1}
26	trans	chr6	rs7763423	1	5523888	0.49	rs7763423	5523888	0.49	0	1.00	2.7×10^{-6}	3.3×10^{-2}
30	trans	chr7	rs11772778	1	17191458	0.12	rs11772778	17191458	0.12	0	1.00	8.8×10^{-6}	9.5×10^{-2}
31	trans	chr7	rs11972506	4	150496668	0.44	rs11972506	150496668	0.44	0	1.00	2.6×10^{-6}	4.7×10^{-1}
32	trans	chr12	rs10784637	4	68034947	0.45	rs10784637	68034947	0.45	0	1.00	5.8×10^{-6}	2.7×10^{-1}
34	trans	chr13	rs943559	5	73715341	0.42	rs943559	73715341	0.42	0	1.00	9.5×10^{-7}	2.8×10^{-1}
38	trans	chr13	rs3736867	1	99061378	0.47	rs2291176	99062686	0.49	1308	0.96	2.2×10^{-6}	1.3×10^{-2}
43	trans	chr14	rs12436725	7	94047444	0.11	rs12436725	94047444	0.11	0	1.00	6.6×10^{-7}	9.0×10^{-1}

T2D Gene 6
C20orf3: chromosome 20 open reading frame 3
Gene Location: chr20:24943579-24973425
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 8.0×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr3	rs3850194	3	171608370	0.19	rs3850194	171608370	0.19	0	1.00	7.9×10^{-6}	1.5×10^{-1}
3	trans	chr14	rs2287400	1	75182937	0.31	rs2287400	75182937	0.31	0	1.00	8.4×10^{-6}	7.1×10^{-4}
6	trans	chr14	rs17093914	1	75363641	0.28	rs17093914	75363641	0.28	0	1.00	8.0×10^{-6}	4.0×10^{-4}

T2D Gene 7
RPP25: ribonuclease P/MRP 25kDa subunit
Gene Location: chr15:75247442-75249775
GWAS Data: Barrett 2008
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 8.9×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs17204920	2	107346018	0.05	rs17204920	107346018	0.05	0	1.00	7.0×10^{-6}	2.7×10^{-2}
2	trans	chr5	rs34386	1	107511903	0.25	rs34386	107511903	0.25	0	1.00	5.4×10^{-6}	3.0×10^{-1}
4	trans	chr8	rs16910959	1	83705317	0.14	rs16910959	83705317	0.14	0	1.00	3.8×10^{-6}	2.0×10^{-1}
5	trans	chr9	rs2383208	1	22132076	0.24	rs2383208	22132076	0.24	0	1.00	6.4×10^{-6}	9.8×10^{-7}

T2D Gene 8
TP53INP1: tumor protein p53 inducible nuclear protein 1
Gene Location: chr8:95938199-95961615
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 3.7×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr5	rs6871819	1	171577700	0.40	rs6871819	171577700	0.40	0	1.00	4.2×10^{-6}	5.0×10^{-1}
2	cis	chr8	rs2241505	1	95686279	0.44	rs2241505	95686279	0.44	0	1.00	1.1×10^{-6}	2.6×10^{-1}
22	cis	chr8	rs1453377	1	95969947	0.44	rs1453377	95969947	0.44	0	1.00	1.1×10^{-26}	5.9×10^{-3}
33	cis	chr8	rs6471513	1	96100175	0.29	rs6471513	96100175	0.29	0	1.00	2.8×10^{-8}	2.4×10^{-2}
36	trans	chr21	rs2831165	36	29174612	0.15	rs2831165	29174612	0.15	0	1.00	9.9×10^{-7}	6.5×10^{-1}
37	trans	chr22	rs11704670	1	49583035	0.16	rs11704670	49583035	0.16	0	1.00	7.5×10^{-6}	7.2×10^{-2}

T2D Gene 8
TP53INP1: tumor protein p53 inducible nuclear protein 1
Gene Location: chr8:95938199-95961615
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 3.0×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs4845141	7	206972072	0.49	rs12565617	206962637	0.47	9435	0.96	7.0×10^{-6}	6.9×10^{-1}
2	trans	chr2	rs10864875	1	122853426	0.29	rs10864875	122853426	0.29	0	1.00	6.9×10^{-7}	7.3×10^{-1}
3	trans	chr7	rs1799011	9	78529329	0.28	rs1799011	78529329	0.28	0	1.00	2.8×10^{-6}	2.0×10^{-1}
4	cis	chr8	rs4734291	1	95820594	0.37	rs4734291	95820594	0.37	0	1.00	7.0×10^{-4}	1.2×10^{-4}
8	cis	chr8	rs481887	1	95967838	0.26	rs481887	95967838	0.26	0	1.00	3.7×10^{-6}	4.4×10^{-3}
15	trans	chr11	rs2174164	2	16443567	0.20	rs2174164	16443567	0.20	0	1.00	7.7×10^{-6}	6.1×10^{-1}
16	trans	chr20	rs6063071	5	45737763	0.31	rs6063071	45737763	0.31	0	1.00	1.8×10^{-6}	2.1×10^{-1}

T2D Gene 8
TP53INP1: tumor protein p53 inducible nuclear protein 1
Gene Location: chr8:95938199-95961615
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 2.7×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
3	trans	chr2	rs13414678	2	154029978	0.48	rs13414678	154029978	0.48	0	1.00	7.0×10^{-7}	1.3×10^{-1}
9	trans	chr2	rs7578480	4	154190729	0.28	rs7578480	154190729	0.28	0	1.00	9.0×10^{-6}	3.0×10^{-1}
11	trans	chr2	rs4673101	20	225255374	0.49	rs4673101	225255374	0.49	0	1.00	4.0×10^{-6}	3.2×10^{-1}
13	trans	chr4	rs4608765	12	87259268	0.46	rs4608765	87259268	0.46	0	1.00	1.0×10^{-5}	1.5×10^{-1}
14	trans	chr5	rs13175611	115	68242039	0.49	rs13175611	68242039	0.49	0	1.00	7.0×10^{-6}	9.3×10^{-1}
16	trans	chr6	rs9370238	1	53726183	0.44	rs9370238	53726183	0.44	0	1.00	8.0×10^{-6}	7.2×10^{-1}
19	trans	chr9	rs627947	11	3981076	0.39	rs4740746	3981029	0.38	47	NA	5.0×10^{-7}	9.5×10^{-4}
21	trans	chr10	rs10994191	1	52489148	0.12	rs10994191	52489148	0.12	0	1.00	1.0×10^{-5}	1.9×10^{-1}
23	trans	chr13	rs4770836	18	26037909	0.27	rs4770836	26037909	0.27	0	1.00	3.0×10^{-6}	9.9×10^{-2}
25	trans	chr16	rs1004792	3	3094261	0.16	rs1004792	3094261	0.16	0	1.00	2.0×10^{-6}	8.7×10^{-1}
28	trans	chr18	rs11152377	3	60972446	0.25	rs11152377	60972446	0.25	0	1.00	7.0×10^{-6}	4.9×10^{-1}

T2D Gene 9
DNA2: DNA replication helicase 2 homolog (yeast)
Gene Location: chr10:70173820-70231879
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 3.7×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr5	rs6873702	1	108015658	0.12	rs6873702	108015658	0.12	0	1.00	3.8×10^{-7}	1.0×10^{-1}
3	cis	chr10	rs12217591	2	70251287	0.16	rs12217591	70251287	0.16	0	1.00	5.5×10^{-7}	4.7×10^{-2}

T2D Gene 9
DNA2: DNA replication helicase 2 homolog (yeast)
Gene Location: chr10:70173820-70231879
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 3.0×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
4	trans	chr2	rs12467485	1	19773375	0.34	rs12467485	19773375	0.34	0	1.00	5.1×10^{-6}	1.1×10^{-1}
5	trans	chr2	rs6715117	1	167021197	0.38	rs6715117	167021197	0.38	0	1.00	8.5×10^{-6}	5.0×10^{-1}
6	trans	chr3	rs1694014	1	21982433	0.31	rs1694014	21982433	0.31	0	1.00	6.3×10^{-6}	1.4×10^{-1}
13	trans	chr3	rs1452075	1	62481063	0.01	rs1452075	62481063	0.01	0	1.00	1.0×10^{-6}	5.7×10^{-6}
27	trans	chr5	rs6888875	1	173275898	0.45	rs6888875	173275898	0.45	0	1.00	3.6×10^{-6}	4.9×10^{-1}

T2D Gene 10
ZNF121: zinc finger protein 121
Gene Location: chr19:9676291-9695209
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 3.5×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr7	rs2043731	2	51170012	0.47	rs2043731	51170012	0.47	0	1.00	3.1×10^{-6}	1.2×10^{-2}
4	trans	chr7	rs10255738	1	126036578	0.15	rs10255738	126036578	0.15	0	1.00	7.4×10^{-6}	1.8×10^{-1}
5	trans	chr8	rs6981891	1	55391896	0.21	rs6981891	55391896	0.21	0	1.00	6.3×10^{-6}	2.0×10^{-1}
6	trans	chr9	rs7861073	1	6447439	0.27	rs7861073	6447439	0.27	0	1.00	5.8×10^{-6}	7.4×10^{-1}
20	trans	chr9	rs12343129	2	116345565	0.09	rs12343129	116345565	0.09	0	1.00	1.8×10^{-6}	1.4×10^{-1}
21	trans	chr18	rs1379641	4	30982868	0.09	rs1379641	30982868	0.09	0	1.00	2.3×10^{-7}	1.9×10^{-1}
23	trans	chr22	rs7287124	1	29239157	0.44	rs7287124	29239157	0.44	0	1.00	4.2×10^{-6}	1.0×10^{-1}
24	trans	chr22	rs4821705	1	38152929	0.03	rs4821705	38152929	0.03	0	1.00	1.9×10^{-6}	7.8×10^{-1}

T2D Gene 10
ZNF121: zinc finger protein 121
Gene Location: chr19:9676291-9695209
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 1.7×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs11809479	268	18712161	0.40	rs11809479	18712161	0.40	0	1.00	2.0×10^{-7}	8.1×10^{-1}
3	trans	chr2	rs4669775	6	11850369	0.38	rs4669775	11850369	0.38	0	1.00	3.0×10^{-6}	2.3×10^{-1}
5	trans	chr3	rs13070090	4	943915	0.19	rs13070090	943915	0.19	0	1.00	8.0×10^{-6}	7.3×10^{-1}
6	trans	chr3	rs12493197	19	24919200	0.15	rs12493197	24919200	0.15	0	1.00	4.0×10^{-6}	7.7×10^{-1}
8	trans	chr4	rs1358440	11	11275561	0.28	rs1358440	11275561	0.28	0	1.00	1.0×10^{-5}	9.5×10^{-1}
9	trans	chr4	rs11726974	7	21307467	0.30	rs11726974	21307467	0.30	0	1.00	1.0×10^{-5}	3.9×10^{-2}
11	trans	chr5	rs153706	7	16882242	0.39	rs153706	16882242	0.39	0	1.00	1.0×10^{-5}	1.7×10^{-2}
12	trans	chr5	rs34306	91	67578745	0.16	rs34306	67578745	0.16	0	1.00	1.0×10^{-5}	7.3×10^{-1}
13	trans	chr8	rs7009857	3	11167233	0.07	rs7009857	11167233	0.07	0	1.00	1.0×10^{-5}	1.1×10^{-3}
14	trans	chr8	rs11784534	3	103203083	0.10	rs11784534	103203083	0.10	0	1.00	1.0×10^{-5}	3.1×10^{-1}
15	trans	chr11	rs16909992	13	11732004	0.41	rs16909992	11732004	0.41	0	1.00	3.0×10^{-6}	2.6×10^{-1}
17	trans	chr11	rs825993	6	97261585	0.15	rs825993	97261585	0.15	0	1.00	1.0×10^{-5}	2.0×10^{-1}
18	trans	chr18	rs12953614	18	23148637	0.34	rs12953614	23148637	0.34	0	1.00	9.0×10^{-6}	1.5×10^{-1}

T2D Gene 10
ZNF121: zinc finger protein 121
Gene Location: chr19:9676291-9695209
GWAS Data: Barrett 2008
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 4.1×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs1470579	1	185529080	0.47	rs1470579	185529080	0.47	0	1.00	3.8×10^{-6}	3.1×10^{-7}
2	trans	chr5	rs731432	1	133131036	0.41	rs731432	133131036	0.41	0	1.00	4.8×10^{-6}	7.2×10^{-1}
3	trans	chr8	rs4732754	1	27650428	0.42	rs4732754	27650428	0.42	0	1.00	7.1×10^{-6}	7.0×10^{-1}
8	trans	chr14	rs17104686	1	37024142	0.26	rs17104686	37024142	0.26	0	1.00	4.0×10^{-7}	3.4×10^{-1}
15	trans	chr20	rs6034740	1	17086061	0.14	rs6034740	17086061	0.14	0	1.00	9.8×10^{-6}	4.0×10^{-2}

T2D Gene 11
MITD1: MIT, microtubule interacting and transport, domain containing 1
Gene Location: chr2:99785725-99797492
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 1.4×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
4	cis	chr2	rs13396584	3	99611768	0.19	rs13396584	99611768	0.19	0	1.00	2.0×10^{-8}	6.1×10^{-2}
17	cis	chr2	rs4851196	1	99858556	0.22	rs4851196	99858556	0.22	0	1.00	4.4×10^{-9}	2.2×10^{-2}
21	trans	chr5	rs256840	1	155924030	0.48	rs256840	155924030	0.48	0	1.00	5.8×10^{-6}	3.6×10^{-1}
22	trans	chr7	rs6962125	3	156231520	0.05	rs6962125	156231520	0.05	0	1.00	2.6×10^{-6}	1.1×10^{-1}
23	trans	chr10	rs12248765	2	11142727	0.46	rs12248765	11142727	0.46	0	1.00	8.6×10^{-7}	3.5×10^{-3}
25	trans	chr16	rs11074593	2	10214306	0.21	rs11074593	10214306	0.21	0	1.00	6.6×10^{-6}	6.1×10^{-1}

T2D Gene 11

MITD1: MIT, microtubule interacting and transport, domain containing 1
Gene Location: chr2:99785725-99797492
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 1.5×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs1386979	201	7848731	0.21	rs1386979	7848731	0.21	0	1.00	1.0×10^{-5}	5.3×10^{-1}
3	trans	chr7	rs11766554	650	79784997	0.09	rs11766554	79784997	0.09	0	1.00	2.0×10^{-6}	3.6×10^{-1}
5	trans	chr8	rs2720687	10	129043368	0.13	rs2720687	129043368	0.13	0	1.00	1.0×10^{-5}	10.0×10^{-2}
8	trans	chr10	rs11196301	614	84634847	0.14	rs11196301	84634847	0.14	0	1.00	1.0×10^{-5}	7.7×10^{-2}
14	trans	chr15	rs12912208	32	62354570	0.46	rs8029942	62353458	0.44	1112	0.96	9.0×10^{-7}	2.3×10^{-2}
17	trans	chr20	rs3761184	56	42969798	0.22	rs3761184	42969798	0.22	0	1.00	1.0×10^{-5}	7.3×10^{-1}

T2D Gene 12

CMAS: cytidine monophosphate N-acetylneuraminic acid synthetase
Gene Location: chr12:22199158-22218602
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 2.0×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs924753	53	15706124	0.48	rs924753	15706124	0.48	0	1.00	9.5×10^{-7}	2.9×10^{-1}
6	trans	chr7	rs1419840	2	34448659	0.41	rs1419840	34448659	0.41	0	1.00	1.6×10^{-6}	4.0×10^{-1}
8	trans	chr13	rs4770734	2	25336128	0.15	rs4770734	25336128	0.15	0	1.00	8.6×10^{-6}	2.9×10^{-4}
9	trans	chr14	rs1950420	17	27141020	0.47	rs1950420	27141020	0.47	0	1.00	5.7×10^{-6}	6.5×10^{-1}
10	trans	chr17	rs295073	33	32780576	0.28	rs295073	32780576	0.28	0	1.00	4.1×10^{-6}	1.6×10^{-1}

T2D Gene 12

CMAS: cytidine monophosphate N-acetylneuraminic acid synthetase
Gene Location: chr12:22199158-22218602
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 4.0×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs2226099	14	183449357	0.18	rs2226099	183449357	0.18	0	1.00	1.8×10^{-6}	3.2×10^{-1}
2	trans	chr5	rs4957054	3	575683	0.21	rs4957054	575683	0.21	0	1.00	9.0×10^{-6}	2.7×10^{-1}
3	trans	chr5	rs4865585	147	53999767	0.23	rs4865585	53999767	0.23	0	1.00	3.1×10^{-6}	3.6×10^{-1}
4	trans	chr9	rs869487	2	35615896	0.48	rs869487	35615896	0.48	0	1.00	7.1×10^{-6}	3.7×10^{-2}
5	trans	chr11	rs512225	3	124539236	0.09	rs512225	124539236	0.09	0	1.00	7.4×10^{-6}	7.0×10^{-2}
6	cis	chr12	rs3847888	2	23134279	0.13	rs3847888	23134279	0.13	0	1.00	6.0×10^{-4}	8.7×10^{-1}
7	trans	chr15	rs1664476	17	57667027	0.44	rs1664476	57667027	0.44	0	1.00	7.9×10^{-6}	6.5×10^{-1}

T2D Gene 12

CMAS: cytidine monophosphate N-acetylneuraminic acid synthetase
Gene Location: chr12:22199158-22218602
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 10.0×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
3	trans	chr2	rs1039835	12	30510752	0.36	rs1039835	30510752	0.36	0	1.00	3.2×10^{-6}	2.9×10^{-3}
5	trans	chr2	rs2241736	2	47187393	0.29	rs2241736	47187393	0.29	0	1.00	6.1×10^{-6}	6.9×10^{-1}
6	trans	chr2	rs9309438	139	70842774	0.33	rs9309438	70842774	0.33	0	1.00	9.2×10^{-6}	1.6×10^{-1}
7	trans	chr2	rs12328639	18	211676323	0.15	rs12328639	211676323	0.15	0	1.00	6.3×10^{-6}	6.3×10^{-2}
9	trans	chr4	rs1497401	24	143321490	0.45	rs1497401	143321490	0.45	0	1.00	6.9×10^{-6}	3.8×10^{-1}
13	trans	chr5	rs1839246	63	120061858	0.08	rs1839246	120061858	0.08	0	1.00	1.2×10^{-6}	8.3×10^{-1}
14	trans	chr5	rs2112409	1	170199979	0.40	rs2112409	170199979	0.40	0	1.00	8.0×10^{-6}	1.4×10^{-2}
15	trans	chr5	rs12654838	3	171127612	0.16	rs12654838	171127612	0.16	0	1.00	8.7×10^{-6}	1.5×10^{-1}
16	trans	chr6	rs12210303	84	131137148	0.17	rs12210303	131137148	0.17	0	1.00	6.9×10^{-6}	4.7×10^{-2}
17	trans	chr6	rs543363	120	131451112	0.10	rs543363	131451112	0.10	0	1.00	9.1×10^{-6}	1.6×10^{-1}
18	trans	chr7	rs12534598	20	107220096	0.31	rs12534598	107220096	0.31	0	1.00	6.5×10^{-6}	4.0×10^{-2}
20	trans	chr8	rs13271489	3	9803712	0.29	rs13271489	9803712	0.29	0	1.00	1.3×10^{-6}	4.6×10^{-2}
23	trans	chr10	rs1342766	13	9074500	0.23	rs1342766	9074500	0.23	0	1.00	9.7×10^{-6}	4.9×10^{-1}
24	trans	chr14	rs2184667	123	27780446	0.12	rs2184667	27780446	0.12	0	1.00	3.4×10^{-7}	8.3×10^{-1}
38	trans	chr15	rs12915189	47	91114376	0.40	rs12915189	91114376	0.40	0	1.00	9.1×10^{-7}	2.8×10^{-1}

T2D Gene 13
HOXB2: homeobox B2
Gene Location: chr17:46620018-46622393
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 2.4×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs11580758	1	63588694	0.07	rs11580758	63588694	0.07	0	1.00	8.9×10^{-6}	8.4×10^{-1}
2	trans	chr1	rs4846580	2	219897941	0.33	rs4846580	219897941	0.33	0	1.00	7.2×10^{-6}	8.5×10^{-1}
7	trans	chr2	rs1439929	1	224397999	0.13	rs1439929	224397999	0.13	0	1.00	4.5×10^{-6}	9.5×10^{-1}
8	trans	chr3	rs6798938	1	113218206	0.20	rs6798938	113218206	0.20	0	1.00	8.1×10^{-6}	8.7×10^{-1}
9	trans	chr4	rs1110342	2	179273888	0.36	rs1110342	179273888	0.36	0	1.00	1.3×10^{-6}	5.3×10^{-1}
14	trans	chr9	rs10979284	2	110987440	0.21	rs10979284	110987440	0.21	0	1.00	1.6×10^{-6}	4.6×10^{-1}
15	trans	chr9	rs12375949	1	124617900	0.44	rs12375949	124617900	0.44	0	1.00	9.0×10^{-6}	5.3×10^{-1}
16	trans	chr10	rs1925700	1	23419522	0.42	rs1925700	23419522	0.42	0	1.00	7.0×10^{-7}	2.1×10^{-3}
18	trans	chr12	rs2302728	1	2774668	0.39	rs2302728	2774668	0.39	0	1.00	6.8×10^{-6}	9.5×10^{-1}
19	trans	chr15	rs4470099	1	68766146	0.35	rs4470099	68766146	0.35	0	1.00	6.1×10^{-6}	9.2×10^{-1}
26	trans	chr17	rs9904967	1	45536875	0.38	rs9904967	45536875	0.38	0	1.00	8.1×10^{-10}	5.4×10^{-2}
68	cis	chr17	rs7220520	2	46167942	0.29	rs7220520	46167942	0.29	0	1.00	4.2×10^{-16}	7.8×10^{-4}
116	cis	chr17	rs12939811	1	46607958	0.13	rs12939811	46607958	0.13	0	1.00	2.0×10^{-204}	6.7×10^{-3}
130	cis	chr17	rs1320283	1	46807134	0.46	rs1320283	46807134	0.46	0	1.00	3.2×10^{-13}	7.3×10^{-1}
132	cis	chr17	rs16945851	1	47114482	0.07	rs2241932	47130230	0.07	15748	1.00	5.0×10^{-7}	9.1×10^{-1}
133	trans	chr22	rs760627	1	29459634	0.47	rs760627	29459634	0.47	0	1.00	2.0×10^{-6}	9.4×10^{-1}

T2D Gene 13
HOXB2: homeobox B2
Gene Location: chr17:46620018-46622393
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 3.5×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr3	rs10490775	1	62036724	0.11	rs10490775	62036724	0.11	0	1.00	8.8×10^{-6}	1.2×10^{-1}
3	trans	chr4	rs1390347	1	176724385	0.49	rs1390347	176724385	0.49	0	1.00	6.7×10^{-7}	4.1×10^{-1}
6	trans	chr6	rs7759336	1	130567718	0.37	rs7759336	130567718	0.37	0	1.00	1.0×10^{-5}	8.8×10^{-1}
16	cis	chr17	rs12449653	1	46473686	0.32	rs12449653	46473686	0.32	0	1.00	2.0×10^{-4}	8.9×10^{-3}
22	cis	chr17	rs1042815	1	46620288	0.49	rs1042815	46620288	0.49	0	1.00	7.9×10^{-10}	2.4×10^{-3}
26	trans	chr20	rs6081600	2	19437539	0.27	rs6081600	19437539	0.27	0	1.00	8.9×10^{-6}	9.9×10^{-1}

T2D Gene 13
HOXB2: homeobox B2
Gene Location: chr17:46620018-46622393
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 1.7×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs10917360	3	23539010	0.30	rs10917360	23539010	0.30	0	1.00	6.1×10^{-6}	10.0×10^{-2}
3	trans	chr7	rs12538253	1	75388031	0.24	rs12538253	75388031	0.24	0	1.00	6.6×10^{-6}	5.6×10^{-1}
6	cis	chr17	rs8079617	1	46610028	0.11	rs8079617	46610028	0.11	0	1.00	5.2×10^{-7}	6.8×10^{-3}
13	trans	chr17	rs4794409	4	51084543	0.40	rs4794409	51084543	0.40	0	1.00	3.5×10^{-6}	1.8×10^{-1}

T2D Gene 14
SRBD1: S1 RNA binding domain 1
Gene Location: chr2:45615818-45838433
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 7.4×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	cis	chr2	rs3911086	3	45575726	0.22	rs3911086	45575726	0.22	0	1.00	9.0×10^{-7}	6.9×10^{-3}
12	cis	chr2	rs4525744	1	45772725	0.49	rs4525744	45772725	0.49	0	1.00	2.6×10^{-10}	5.5×10^{-3}
17	trans	chr3	rs9811594	2	160745935	0.30	rs9811594	160745935	0.30	0	1.00	4.5×10^{-6}	4.5×10^{-2}
18	trans	chr13	rs9548906	2	40308690	0.47	rs4133063	40307119	0.47	1571	1.00	6.1×10^{-6}	1.0×10^{-1}

T2D Gene 14
SRBD1: S1 RNA binding domain 1
Gene Location: chr2:45615818-45838433
GWAS Data: Barrett 2008
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 6.3×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr5	rs17157849	19	104639792	0.24	rs17157849	104639792	0.24	0	1.00	4.7×10^{-7}	8.5×10^{-2}
2	trans	chr7	rs10253978	1	33554672	0.09	rs10253978	33554672	0.09	0	1.00	9.5×10^{-6}	1.1×10^{-2}

T2D Gene 15
MYL2: myosin, light chain 2, regulatory, cardiac, slow
Gene Location: chr12:111348623-111358404
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 2.1×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr5	rs2407759	1	54197973	0.36	rs2407759	54197973	0.36	0	1.00	3.8×10^{-6}	4.5×10^{-1}
2	trans	chr6	rs9368222	1	20686996	0.28	rs9368222	20686996	0.28	0	1.00	5.2×10^{-6}	1.5×10^{-11}
3	trans	chr8	rs9298276	1	77218289	0.22	rs9298276	77218289	0.22	0	1.00	9.7×10^{-6}	2.4×10^{-1}
4	trans	chr10	rs2768327	1	119247667	0.48	rs2768327	119247667	0.48	0	1.00	3.4×10^{-6}	7.6×10^{-1}
5	trans	chr11	rs4148898	1	45674599	0.35	rs4148903	45672725	0.31	1874	0.99	4.3×10^{-6}	3.1×10^{-2}
6	trans	chr14	rs10140164	1	55406123	0.43	rs10140164	55406123	0.43	0	1.00	4.0×10^{-6}	6.6×10^{-1}

T2D Gene 15
MYL2: myosin, light chain 2, regulatory, cardiac, slow
Gene Location: chr12:111348623-111358404
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 8.7×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr5	rs331746	1	124852713	0.47	rs331746	124852713	0.47	0	1.00	8.7×10^{-6}	5.6×10^{-2}
2	trans	chr22	rs2041607	1	17450515	0.32	rs2041607	17450515	0.32	0	1.00	1.0×10^{-5}	2.4×10^{-1}

T2D Gene 16
EIF2B2: eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa
Gene Location: chr14:75469611-75476294
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 1.0×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr4	rs1842259	1	136504466	0.20	rs1842259	136504466	0.20	0	1.00	3.7×10^{-6}	4.4×10^{-1}
7	trans	chr12	rs11175490	3	65034845	0.05	rs11175490	65034845	0.05	0	1.00	9.1×10^{-6}	8.5×10^{-2}
8	cis	chr14	rs8017803	2	75108422	0.45	rs8017803	75108422	0.45	0	1.00	2.4×10^{-8}	4.3×10^{-1}
18	cis	chr14	rs2058919	2	75310812	0.44	rs2058919	75310812	0.44	0	1.00	3.1×10^{-7}	10.0×10^{-4}
38	cis	chr14	rs175057	1	75489632	0.40	rs175057	75489632	0.40	0	1.00	6.8×10^{-80}	1.3×10^{-1}
64	cis	chr14	rs7148230	2	75677699	0.34	rs9805950	75678634	0.29	935	0.94	6.3×10^{-6}	1.6×10^{-1}
67	trans	chr21	rs741792	2	41254150	0.18	rs741792	41254150	0.18	0	1.00	8.9×10^{-6}	9.8×10^{-1}

T2D Gene 16
EIF2B2: eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa
Gene Location: chr14:75469611-75476294
GWAS Data: Barrett 2008
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 8.8×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs3770565	1	216876828	0.23	rs3770565	216876828	0.23	0	1.00	1.0×10^{-5}	7.6×10^{-2}
2	cis	chr14	rs8185	2	75408789	0.22	rs8185	75408789	0.22	0	1.00	9.0×10^{-4}	3.0×10^{-1}
9	cis	chr14	rs175444	2	75601782	0.33	rs175444	75601782	0.33	0	1.00	1.1×10^{-4}	1.5×10^{-1}

T2D Gene 16
EIF2B2: eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa
Gene Location: chr14:75469611-75476294
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 4.0×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr4	rs2289164	1	147878242	0.49	rs2289164	147878242	0.49	0	1.00	5.0×10^{-6}	2.4×10^{-1}
9	trans	chr5	rs12109629	1	93359702	0.10	rs12109629	93359702	0.10	0	1.00	8.0×10^{-6}	6.9×10^{-1}
13	trans	chr5	rs1363438	20	119580326	0.36	rs1363438	119580326	0.36	0	1.00	2.0×10^{-6}	5.9×10^{-2}
29	trans	chr7	rs7796305	1	36764846	0.40	rs7796305	36764846	0.40	0	1.00	1.0×10^{-5}	6.5×10^{-1}
30	trans	chr7	rs2160195	1	38404971	0.15	rs2160195	38404971	0.15	0	1.00	2.0×10^{-6}	2.6×10^{-1}
31	trans	chr8	rs10100187	10	11257495	0.49	rs10100187	11257495	0.49	0	1.00	7.0×10^{-6}	1.7×10^{-1}
32	trans	chr9	rs10868811	8	72979246	0.31	rs10868811	72979246	0.31	0	1.00	2.0×10^{-6}	3.1×10^{-1}
33	trans	chr9	rs3780269	1	134457580	0.16	rs3780269	134457580	0.16	0	1.00	1.0×10^{-5}	8.9×10^{-2}
34	trans	chr10	rs11005041	4	57576058	0.39	rs11005041	57576058	0.39	0	1.00	5.0×10^{-6}	4.7×10^{-1}
35	trans	chr10	rs3922824	1	107150600	0.35	rs3922824	107150600	0.35	0	1.00	1.0×10^{-5}	7.4×10^{-2}
36	trans	chr10	rs1891115	32	124524751	0.50	rs1891115	124524751	0.50	0	1.00	9.0×10^{-6}	1.8×10^{-1}
37	trans	chr12	rs7953165	6	46431015	0.45	rs7953165	46431015	0.45	0	1.00	9.0×10^{-6}	8.0×10^{-2}
43	trans	chr14	rs11624780	6	74406611	0.39	rs11624780	74406611	0.39	0	1.00	5.0×10^{-7}	6.0×10^{-1}
71	cis	chr14	rs4556	1	75476071	0.45	rs4556	75476071	0.45	0	1.00	6.0×10^{-6}	1.3×10^{-1}
89	trans	chr16	rs2082037	1	84528293	0.23	rs2082037	84528293	0.23	0	1.00	7.0×10^{-6}	8.2×10^{-1}
90	trans	chr18	rs9966932	8	7689368	0.41	rs9966932	7689368	0.41	0	1.00	1.0×10^{-5}	2.6×10^{-2}
91	trans	chr18	rs7504200	41	12247872	0.47	rs7504200	12247872	0.47	0	1.00	2.0×10^{-6}	8.8×10^{-1}
93	trans	chr19	rs3826834	20	48494445	0.16	rs3826834	48494445	0.16	0	1.00	2.0×10^{-6}	2.8×10^{-1}
94	trans	chr21	rs2833392	2	32763231	0.14	rs2833392	32763231	0.14	0	1.00	1.0×10^{-5}	9.5×10^{-1}

T2D Gene 16
EIF2B2: eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa
Gene Location: chr14:75469611-75476294
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 2.6×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr5	rs10056565	2	80619046	0.20	rs10056565	80619046	0.20	0	1.00	3.0×10^{-7}	1.2×10^{-1}
3	trans	chr5	rs11747001	13	132412299	0.16	rs11747001	132412299	0.16	0	1.00	6.2×10^{-6}	7.5×10^{-1}
5	trans	chr5	rs6860981	5	155605629	0.37	rs6860981	155605629	0.37	0	1.00	5.4×10^{-6}	6.1×10^{-1}
8	trans	chr8	rs1809498	19	21836384	0.34	rs1809498	21836384	0.34	0	1.00	2.3×10^{-6}	1.9×10^{-1}
11	trans	chr8	rs10105946	6	106664873	0.18	rs10105946	106664873	0.18	0	1.00	1.7×10^{-6}	2.4×10^{-1}
16	cis	chr14	rs175071	1	75498177	0.33	rs175071	75498177	0.33	0	1.00	2.5×10^{-7}	2.6×10^{-1}
35	cis	chr14	rs2300601	1	75639571	0.47	rs2300601	75639571	0.47	0	1.00	1.0×10^{-7}	5.2×10^{-2}
39	trans	chr18	rs621834	9	34351529	0.14	rs621834	34351529	0.14	0	1.00	1.7×10^{-6}	1.9×10^{-2}

T2D Gene 16
EIF2B2: eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa
Gene Location: chr14:75469611-75476294
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 4.5×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr1	rs10783087	1	98787759	0.41	rs10783087	98787759	0.41	0	1.00	1.3×10^{-6}	3.9×10^{-1}
4	trans	chr6	rs17178962	1	134832733	0.05	rs17178962	134832733	0.05	0	1.00	5.1×10^{-6}	6.7×10^{-3}
5	trans	chr7	rs7785072	1	29137502	0.34	rs7785072	29137502	0.34	0	1.00	3.5×10^{-7}	9.5×10^{-1}
39	trans	chr16	rs9935238	1	76158610	0.38	rs9935238	76158610	0.38	0	1.00	2.3×10^{-6}	1.0×10^{-1}

T2D Gene 17
KIR2DS5: killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 5
Gene Location: chr19:70096-113132
GWAS Data: Barrett 2008
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 1.2×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr10	rs7921719	2	109602952	0.14	rs7921719	109602952	0.14	0	1.00	4.8×10^{-6}	4.9×10^{-1}
3	trans	chr10	rs12255372	1	114808902	0.19	rs12255372	114808902	0.19	0	1.00	3.3×10^{-6}	3.6×10^{-17}
4	trans	chr12	rs7972539	2	96821569	0.10	rs7972539	96821569	0.10	0	1.00	5.5×10^{-6}	6.3×10^{-1}
6	trans	chr13	rs1928375	1	35142537	0.23	rs1928375	35142537	0.23	0	1.00	8.0×10^{-6}	2.4×10^{-1}
9	trans	chr19	rs678846	7	55326613	0.18	rs678846	55326613	0.18	0	1.00	7.2×10^{-10}	5.6×10^{-1}

T2D Gene 18
BCAT2: branched chain amino-acid transaminase 2, mitochondrial
Gene Location: chr19:49298318-49314320
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 9.6×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr5	rs13179557	19	64165343	0.04	rs13179557	64165343	0.04	0	1.00	1.0×10^{-5}	2.0×10^{-2}
2	trans	chr5	rs11949445	26	64320495	0.12	rs11949445	64320495	0.12	0	1.00	5.0×10^{-6}	2.5×10^{-2}
4	trans	chr6	rs9296000	17	11383976	0.45	rs9296000	11383976	0.45	0	1.00	4.0×10^{-6}	4.1×10^{-1}
7	trans	chr6	rs12665609	6	37586488	0.12	rs12665609	37586488	0.12	0	1.00	1.0×10^{-5}	2.9×10^{-1}
10	trans	chr6	rs2236038	12	47206033	0.47	rs2236038	47206033	0.47	0	1.00	9.0×10^{-6}	3.3×10^{-1}
13	trans	chr8	rs7004533	7	142696491	0.11	rs7004533	142696491	0.11	0	1.00	1.0×10^{-5}	2.0×10^{-1}
14	trans	chr9	rs10973114	17	3696511	0.20	rs10973114	3696511	0.20	0	1.00	1.0×10^{-5}	2.8×10^{-1}
15	trans	chr10	rs4453159	4	110448849	0.45	rs4453159	110448849	0.45	0	1.00	8.0×10^{-6}	1.7×10^{-1}
16	trans	chr10	rs2421121	24	124488187	0.18	rs2421121	124488187	0.18	0	1.00	2.0×10^{-6}	2.3×10^{-2}
17	trans	chr11	rs11041703	12	8018591	0.09	rs11041703	8018591	0.09	0	1.00	1.0×10^{-5}	2.9×10^{-3}
18	trans	chr13	rs11842969	6	101214375	0.42	rs11842969	101214375	0.42	0	1.00	1.0×10^{-5}	1.9×10^{-1}
22	trans	chr16	rs171798	53	55744504	0.30	rs171798	55744504	0.30	0	1.00	1.0×10^{-6}	7.7×10^{-1}
25	trans	chr17	rs8072659	21	32016493	0.45	rs8072659	32016493	0.45	0	1.00	1.0×10^{-5}	6.5×10^{-1}

T2D Gene 18
BCAT2: branched chain amino-acid transaminase 2, mitochondrial
Gene Location: chr19:49298318-49314320
GWAS Data: Barrett 2008
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 1.9×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr7	rs2079373	8	32119530	0.15	rs30585	32093550	0.17	25980	0.86	4.1×10^{-6}	1.3×10^{-1}
4	trans	chr14	rs10162454	15	75144618	0.28	rs10162454	75144618	0.28	0	1.00	4.7×10^{-8}	1.3×10^{-2}
30	trans	chr14	rs929579	3	75330697	0.32	rs929579	75330697	0.32	0	1.00	1.1×10^{-6}	5.0×10^{-4}

T2D Gene 19
OGDHL: oxoglutarate dehydrogenase-like
Gene Location: chr10:50942686-50970425
GWAS Data: Barrett 2008
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 1.3×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
25	trans	chr1	rs7516544	1	173491431	0.36	rs7516544	173491431	0.36	0	1.00	2.0×10^{-7}	1.7×10^{-2}
33	trans	chr2	rs12614262	1	5630388	0.31	rs12614262	5630388	0.31	0	1.00	4.0×10^{-6}	8.3×10^{-1}
34	trans	chr5	rs12516173	1	173542308	0.21	rs12516173	173542308	0.21	0	1.00	1.0×10^{-5}	9.0×10^{-1}
38	trans	chr6	rs9295478	1	20716253	0.42	rs9295478	20716253	0.42	0	1.00	1.0×10^{-6}	1.5×10^{-5}
49	trans	chr7	rs13230639	1	11304855	0.08	rs13230639	11304855	0.08	0	1.00	3.0×10^{-7}	2.2×10^{-2}
57	trans	chr7	rs6970779	1	130681773	0.11	rs978061	130681534	0.13	239	NA	9.0×10^{-6}	6.3×10^{-1}
58	trans	chr8	rs289555	1	13246938	0.12	rs289555	13246938	0.12	0	1.00	1.0×10^{-5}	1.4×10^{-1}
59	trans	chr10	rs2756115	1	101508622	0.26	rs2756115	101508622	0.26	0	1.00	1.0×10^{-5}	7.8×10^{-2}
61	trans	chr19	rs10421681	1	13349110	0.43	rs10421681	13349110	0.43	0	1.00	3.0×10^{-6}	4.0×10^{-1}
64	trans	chr22	rs9614177	1	43925090	0.45	rs9614177	43925090	0.45	0	1.00	9.0×10^{-6}	4.3×10^{-1}

T2D Gene 19
OGDHL: oxoglutarate dehydrogenase-like
Gene Location: chr10:50942686-50970425
GWAS Data: Barrett 2008
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 6.4×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs7601227	2	174879174	0.48	rs7601227	174879174	0.48	0	1.00	6.1×10^{-6}	5.9×10^{-1}
3	trans	chr4	rs11722994	3	21263330	0.24	rs11722994	21263330	0.24	0	1.00	1.4×10^{-6}	3.5×10^{-1}
5	trans	chr5	rs1530812	39	41000152	0.49	rs1530812	41000152	0.49	0	1.00	1.9×10^{-8}	1.1×10^{-1}
8	trans	chr5	rs2271214	3	178770718	0.19	rs2271214	178770718	0.19	0	1.00	6.7×10^{-6}	2.2×10^{-1}
10	trans	chr13	rs1811951	9	66015942	0.28	rs7337746	66016604	0.26	662	1.00	4.3×10^{-6}	3.6×10^{-1}
11	trans	chr18	rs621834	9	34351529	0.14	rs621834	34351529	0.14	0	1.00	2.8×10^{-6}	1.9×10^{-2}

Appendix D

Supporting SNPs for Top Schizophrenia Results

The supporting SNPs for all top Schizophrenia genes are provided here. The genes are listed in rank order, and only functional data yielding Empirical Sherlock p-values below 0.1 is shown. Thus, certain genes may have only one supporting eQTL data set listed, while others will have multiple listings if their Empirical Sherlock results are significant across multiple tissues. Definitions for each column in the supporting matrix are provided in Table D.1. All coordinates provided are for assembly hg19 / GRCh37 of the human genome. Minor allele frequencies (MAFs) given are from NCBI dbSNP build 135. Linkage disequilibrium is from our custom database, as described in Methods.

Table D.1: Explanation of Supporting SNP Information

BLK	Haplotype Block Number. These are not sequential, since only independently-sorting SNPs are retained.
PRX	Proximity of SNP to gene (cis or trans)
CHR	Chromosome
eQTL SNP	ID of eQTL SNP used
PL	SNP pleiotropy. The number of times this SNP is found in other genes in the eQTL data set.
Location	Location of the eQTL SNP
MAF	Minor allele frequency of the eQTL SNP. Used as a check for independence of adjacent tag SNPs.
GWAS SNP	ID of the GWAS SNP used
Location	Location of the aligned GWAS SNP
MAF	Minor allele frequency of the GWAS SNP
Delta	Distance in base pairs between the two SNPs
LD	Linkage disequilibrium (r^2) between the SNPs
eQTL pval	Used to define SNP sets at different thresholds, as per our method
GWAS pval	Used to construct the gene score. The summation of log(p-values) for this column is the gene score

Schizophrenia Gene 1
BTN3A2: butyrophilin, subfamily 3, member A2
Gene Location: chr6:26365397-26378548
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 3.9×10^{-8}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr5	rs9292703	1	38321765	0.13	rs9292703	38321765	0.13	0	1.00	5.4×10^{-6}	4.2×10^{-1}
10	trans	chr6	rs1986731	1	25174070	0.16	rs1986731	25174070	0.16	0	1.00	4.3×10^{-13}	3.2×10^{-7}
16	cis	chr6	rs9295657	2	25419318	0.14	rs9295657	25419318	0.14	0	1.00	2.6×10^{-23}	2.0×10^{-4}
29	cis	chr6	rs2328879	1	25583103	0.48	rs2328879	25583103	0.48	0	1.00	1.5×10^{-12}	1.8×10^{-1}
37	cis	chr6	rs1883259	1	25683280	0.16	rs1883259	25683280	0.16	0	1.00	4.4×10^{-29}	4.2×10^{-2}
52	cis	chr6	rs2096386	1	25787817	0.48	rs2096386	25787817	0.48	0	1.00	9.3×10^{-12}	1.9×10^{-1}
92	cis	chr6	rs1009181	2	26158993	0.31	rs1009181	26158993	0.31	0	1.00	7.2×10^{-19}	8.9×10^{-2}
104	cis	chr6	rs9358932	2	26362705	0.07	rs9358932	26362705	0.07	0	1.00	3.0×10^{-154}	3.0×10^{-12}
149	cis	chr6	rs9379893	1	26584668	0.18	rs9379893	26584668	0.18	0	1.00	1.0×10^{-50}	5.3×10^{-8}
318	trans	chr7	rs7802651	3	52113844	0.05	rs7802651	52113844	0.05	0	1.00	5.2×10^{-6}	7.7×10^{-1}
319	trans	chr10	rs1329180	1	91930931	0.11	rs1329180	91930931	0.11	0	1.00	4.3×10^{-6}	6.8×10^{-1}

Schizophrenia Gene 1
BTN3A2: butyrophilin, subfamily 3, member A2
Gene Location: chr6:26365397-26378548
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 2.7×10^{-12}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	cis	chr6	rs9295657	3	25419318	0.14	rs9295657	25419318	0.14	0	1.00	6.4×10^{-9}	2.0×10^{-4}
7	cis	chr6	rs10105	2	25701903	0.22	rs10105	25701903	0.22	0	1.00	5.9×10^{-8}	2.9×10^{-6}
31	cis	chr6	rs1436310	2	25969958	0.50	rs1436310	25969958	0.50	0	1.00	7.0×10^{-4}	1.2×10^{-1}
59	cis	chr6	rs9379858	2	26367689	0.07	rs9379858	26367689	0.07	0	1.00	9.4×10^{-29}	2.2×10^{-12}
101	cis	chr6	rs9379897	4	26601526	0.13	rs9379897	26601526	0.13	0	1.00	4.1×10^{-21}	3.0×10^{-11}
110	cis	chr6	rs10946868	2	26887930	0.41	rs10946868	26887930	0.41	0	1.00	7.4×10^{-9}	6.0×10^{-8}
189	trans	chr12	rs2193149	3	13706502	0.20	rs2193149	13706502	0.20	0	1.00	1.4×10^{-6}	7.9×10^{-1}
190	trans	chr16	rs10500328	2	5807878	0.21	rs10500328	5807878	0.21	0	1.00	3.9×10^{-6}	9.8×10^{-1}
191	trans	chr16	rs3762872	1	86366644	0.48	rs3762872	86366644	0.48	0	1.00	8.6×10^{-6}	5.8×10^{-1}

Schizophrenia Gene 1
BTN3A2: butyrophilin, subfamily 3, member A2
Gene Location: chr6:26365397-26378548
GWAS Data: McCarroll 2012
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 3.4×10^{-9}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
10	trans	chr1	rs2043799	5	76549727	0.15	rs2043799	76549727	0.15	0	1.00	6.0×10^{-8}	7.6×10^{-1}
14	trans	chr2	rs850908	3	186220642	0.24	rs850908	186220642	0.24	0	1.00	3.0×10^{-6}	2.2×10^{-1}
16	trans	chr2	rs7572482	1	192015072	0.49	rs7572482	192015072	0.49	0	1.00	5.0×10^{-6}	1.0×10^{-1}
18	trans	chr2	rs4852014	2	239854389	0.41	rs4852014	239854389	0.41	0	1.00	4.0×10^{-6}	2.6×10^{-1}
19	trans	chr3	rs156166	6	6425168	0.24	rs156166	6425168	0.24	0	1.00	1.0×10^{-6}	5.7×10^{-1}
21	trans	chr3	rs7647735	3	66774036	0.47	rs7647735	66774036	0.47	0	1.00	4.0×10^{-6}	3.7×10^{-1}
24	trans	chr3	rs7618658	6	125171369	0.22	rs7618658	125171369	0.22	0	1.00	9.0×10^{-8}	3.7×10^{-1}
49	trans	chr3	rs12491993	2	152481845	0.14	rs12491993	152481845	0.14	0	1.00	7.0×10^{-6}	8.5×10^{-1}
59	trans	chr3	rs7640074	2	164562164	0.16	rs7640074	164562164	0.16	0	1.00	1.0×10^{-6}	8.3×10^{-1}
73	trans	chr3	rs17538705	1	181187581	0.45	rs17538705	181187581	0.45	0	1.00	6.0×10^{-6}	9.3×10^{-1}
75	trans	chr3	rs9883259	8	194769624	0.15	rs9883259	194769624	0.15	0	1.00	5.0×10^{-6}	9.5×10^{-1}
76	trans	chr4	rs6840829	2	4185610	0.48	rs6840829	4185610	0.48	0	1.00	9.0×10^{-6}	8.9×10^{-1}
78	trans	chr4	rs1512953	2	67359005	0.21	rs1512953	67359005	0.21	0	1.00	5.0×10^{-6}	5.9×10^{-1}
83	trans	chr4	rs4407532	2	122444046	0.38	rs4407532	122444046	0.38	0	1.00	3.0×10^{-7}	3.5×10^{-1}
88	trans	chr4	rs6856260	1	129611736	0.46	rs6856260	129611736	0.46	0	1.00	9.0×10^{-6}	4.5×10^{-2}
90	trans	chr5	rs6555279	2	4409626	0.47	rs6555279	4409626	0.47	0	1.00	6.0×10^{-6}	3.6×10^{-1}
94	trans	chr5	rs150628	2	9565135	0.29	rs150628	9565135	0.29	0	1.00	8.0×10^{-7}	4.6×10^{-1}
96	trans	chr5	rs193552	1	148172599	0.31	rs193552	148172599	0.31	0	1.00	1.0×10^{-5}	2.7×10^{-1}
97	trans	chr5	rs10037652	1	153846868	0.33	rs10037652	153846868	0.33	0	1.00	3.0×10^{-6}	4.5×10^{-1}
99	cis	chr6	rs6921589	1	25422369	0.14	rs6921589	25422369	0.14	0	1.00	8.0×10^{-7}	2.5×10^{-4}
104	cis	chr6	rs7771468	2	25713568	0.16	rs7771468	25713568	0.16	0	1.00	2.0×10^{-5}	1.2×10^{-5}
197	cis	chr6	rs12174602	2	26372827	0.08	rs12174602	26372827	0.08	0	1.00	1.0×10^{-22}	8.3×10^{-13}
252	cis	chr6	rs9467835	6	26678512	0.35	rs9467835	26678512	0.35	0	1.00	4.0×10^{-5}	8.3×10^{-8}
547	trans	chr6	rs7758787	2	133240024	0.23	rs7758787	133240024	0.23	0	1.00	9.0×10^{-6}	6.4×10^{-1}
549	trans	chr6	rs1413901	2	150355441	0.24	rs1413901	150355441	0.24	0	1.00	1.0×10^{-5}	5.7×10^{-3}
552	trans	chr7	rs2192675	2	13007537	0.15	rs2192675	13007537	0.15	0	1.00	1.0×10^{-6}	1.6×10^{-1}
555	trans	chr7	rs11983807	2	29811861	0.17	rs11983807	29811861	0.17	0	1.00	4.0×10^{-8}	5.5×10^{-2}
558	trans	chr8	rs10866941	2	2348747	0.28	rs10866941	2348747	0.28	0	1.00	6.0×10^{-6}	2.4×10^{-1}
562	trans	chr9	rs7047812	2	9726090	0.13	rs7047812	9726090	0.13	0	1.00	5.0×10^{-8}	2.1×10^{-1}
565	trans	chr9	rs10978698	2	109764204	0.27	rs10978698	109764204	0.27	0	1.00	3.0×10^{-6}	4.1×10^{-1}
570	trans	chr10	rs9665606	3	2517773	0.29	rs9665606	2517773	0.29	0	1.00	2.0×10^{-6}	9.9×10^{-1}
571	trans	chr10	rs10999379	1	72294836	0.15	rs10999379	72294836	0.15	0	1.00	1.0×10^{-5}	9.7×10^{-1}
573	trans	chr11	rs1491850	2	27749725	0.38	rs1491850	27749725	0.38	0	1.00	4.0×10^{-6}	1.5×10^{-1}
574	trans	chr12	rs4766193	2	4108513	0.11	rs4766193	4108513	0.11	0	1.00	5.0×10^{-6}	4.7×10^{-1}
576	trans	chr12	rs7132224	1	131356046	0.32	rs7132224	131356046	0.32	0	1.00	4.0×10^{-6}	3.5×10^{-1}
577	trans	chr14	rs1253696	1	52396047	0.49	rs1253696	52396047	0.49	0	1.00	5.0×10^{-6}	7.3×10^{-1}
578	trans	chr15	rs2461649	2	80351169	0.20	rs2461649	80351169	0.20	0	1.00	3.0×10^{-6}	9.6×10^{-1}
581	trans	chr16	rs12924453	6	11751499	0.25	rs12924453	11751499	0.25	0	1.00	3.0×10^{-6}	5.1×10^{-1}
583	trans	chr16	rs1875394	1	13090833	0.50	rs1875394	13090833	0.50	0	1.00	7.0×10^{-6}	8.4×10^{-1}
584	trans	chr16	rs7199094	2	86726926	0.30	rs7199094	86726926	0.30	0	1.00	1.0×10^{-5}	3.4×10^{-1}
586	trans	chr17	rs8073778	2	11626332	0.30	rs8073778	11626332	0.30	0	1.00	7.0×10^{-6}	1.8×10^{-1}
587	trans	chr17	rs9905479	1	16904915	0.22	rs9905479	16904915	0.22	0	1.00	6.0×10^{-6}	1.8×10^{-2}
588	trans	chr18	rs7238346	2	62729823	0.44	rs7238346	62729823	0.44	0	1.00	2.0×10^{-6}	4.3×10^{-1}
603	trans	chr18	rs12373402	2	68132998	0.45	rs12373402	68132998	0.45	0	1.00	4.0×10^{-7}	4.3×10^{-1}
604	trans	chr21	rs369327	2	29593200	0.48	rs369327	29593200	0.48	0	1.00	1.0×10^{-5}	1.1×10^{-1}
606	trans	chr21	rs2071049	2	37866480	0.44	rs2071049	37866480	0.44	0	1.00	8.0×10^{-7}	9.1×10^{-1}
608	trans	chr22	rs1883278	1	25494744	0.45	rs1883278	25494744	0.45	0	1.00	1.0×10^{-5}	4.0×10^{-2}

Schizophrenia Gene 1
BTN3A2: butyrophilin, subfamily 3, member A2
Gene Location: chr6:26365397-26378548
GWAS Data: McCarroll 2012
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 6.5×10^{-14}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs13413974	2	67762906	0.14	rs13413974	67762906	0.14	0	1.00	1.4×10^{-6}	1.0×10^{-2}
2	trans	chr2	rs1816698	1	124833536	0.21	rs1816698	124833536	0.21	0	1.00	9.9×10^{-6}	8.3×10^{-2}
4	trans	chr5	rs213510	1	94990558	0.34	rs213510	94990558	0.34	0	1.00	6.4×10^{-6}	4.4×10^{-1}
5	cis	chr6	rs7752195	1	25419094	0.08	rs7752195	25419094	0.08	0	1.00	1.6×10^{-7}	8.9×10^{-11}
13	cis	chr6	rs1324082	1	25801971	0.28	rs1324082	25801971	0.28	0	1.00	9.1×10^{-5}	7.7×10^{-8}
40	cis	chr6	rs9379851	1	26354780	0.08	rs9379851	26354780	0.08	0	1.00	5.6×10^{-22}	3.3×10^{-12}
68	cis	chr6	rs9393777	2	26942027	0.15	rs9393777	26942027	0.15	0	1.00	1.1×10^{-11}	7.9×10^{-12}
93	trans	chr6	rs1928274	2	46837390	0.33	rs1928274	46837390	0.33	0	1.00	8.7×10^{-6}	3.7×10^{-1}
95	trans	chr7	rs9969372	2	49067276	0.32	rs9969372	49067276	0.32	0	1.00	6.3×10^{-6}	1.5×10^{-1}
96	trans	chr11	rs1670642	2	21264711	0.21	rs1670642	21264711	0.21	0	1.00	3.7×10^{-6}	8.1×10^{-1}
97	trans	chr14	rs178452	16	80443279	0.36	rs178452	80443279	0.36	0	1.00	5.5×10^{-6}	5.5×10^{-1}

Schizophrenia Gene 2
BTN2A1: butyrophilin, subfamily 2, member A1
Gene Location: chr6:26458152-26469866
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 3.0×10^{-11}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs2271929	2	32134491	0.50	rs2271929	32134491	0.50	0	1.00	8.0×10^{-6}	7.9×10^{-1}
2	trans	chr2	rs3884557	16	141239854	0.19	rs3884557	141239854	0.19	0	1.00	5.4×10^{-6}	9.1×10^{-1}
3	trans	chr3	rs11128583	45	11970239	0.26	rs11128583	11970239	0.26	0	1.00	9.9×10^{-6}	3.0×10^{-1}
4	trans	chr3	rs2028740	6	78550688	0.38	rs2028740	78550688	0.38	0	1.00	7.3×10^{-6}	3.7×10^{-1}
5	trans	chr4	rs3108397	9	123018134	0.48	rs3108397	123018134	0.48	0	1.00	3.2×10^{-6}	2.8×10^{-2}
6	trans	chr5	rs6872400	1	104382896	0.30	rs6872400	104382896	0.30	0	1.00	9.7×10^{-7}	7.2×10^{-1}
8	trans	chr5	rs7705821	3	117894902	0.09	rs7705821	117894902	0.09	0	1.00	1.9×10^{-6}	4.5×10^{-3}
9	cis	chr6	rs1324087	1	25841408	0.18	rs1324087	25841408	0.18	0	1.00	4.0×10^{-5}	1.0×10^{-9}
29	cis	chr6	rs2093169	1	26495099	0.17	rs2093169	26495099	0.17	0	1.00	5.9×10^{-14}	1.2×10^{-10}
41	cis	chr6	rs9393777	2	26942027	0.15	rs9393777	26942027	0.15	0	1.00	4.6×10^{-9}	7.9×10^{-12}
77	trans	chr8	rs7009399	49	81903007	0.24	rs7009399	81903007	0.24	0	1.00	9.7×10^{-6}	5.2×10^{-1}
78	trans	chr9	rs1926728	48	78391161	0.47	rs1926728	78391161	0.47	0	1.00	5.3×10^{-6}	4.1×10^{-1}
79	trans	chr13	rs9552822	4	23669382	0.31	rs9552822	23669382	0.31	0	1.00	7.6×10^{-6}	8.8×10^{-1}
81	trans	chr13	rs9584386	6	97218033	0.18	rs9584386	97218033	0.18	0	1.00	5.0×10^{-6}	3.9×10^{-2}
82	trans	chr15	rs4924556	1	41878208	0.42	rs4924556	41878208	0.42	0	1.00	6.0×10^{-6}	5.4×10^{-1}
83	trans	chr21	rs4818773	5	46796831	0.23	rs4818773	46796831	0.23	0	1.00	7.6×10^{-8}	9.4×10^{-1}

Schizophrenia Gene 3
BTN3A1: butyrophilin, subfamily 3, member A1
Gene Location: chr6:26402464-26415444
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 2.7×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs880434	1	225624635	0.05	rs880434	225624635	0.05	0	1.00	1.9×10^{-6}	8.7×10^{-1}
9	trans	chr3	rs6442417	1	13907157	0.19	rs6442417	13907157	0.19	0	1.00	8.1×10^{-6}	2.7×10^{-1}
35	cis	chr6	rs2237236	1	26451553	0.49	rs2237236	26451553	0.49	0	1.00	2.0×10^{-16}	6.9×10^{-5}
43	trans	chr7	rs10239544	1	66897869	0.41	rs10239544	66897869	0.41	0	1.00	4.1×10^{-6}	2.4×10^{-1}

Schizophrenia Gene 3
BTN3A1: butyrophilin, subfamily 3, member A1
Gene Location: chr6:26402464-26415444
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 2.1×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs1980283	3	61788620	0.47	rs1980283	61788620	0.47	0	1.00	3.7×10^{-6}	5.5×10^{-2}
3	cis	chr6	rs214064	1	25540718	0.08	rs214064	25540718	0.08	0	1.00	2.0×10^{-4}	3.2×10^{-3}
7	cis	chr6	rs3923	1	25783315	0.49	rs3923	25783315	0.49	0	1.00	7.0×10^{-5}	1.4×10^{-1}
21	cis	chr6	rs12346	1	26097046	0.20	rs12346	26097046	0.20	0	1.00	3.0×10^{-4}	9.0×10^{-3}
39	cis	chr6	rs3198487	1	26414373	0.14	rs3198487	26414373	0.14	0	1.00	9.2×10^{-13}	7.6×10^{-1}
53	cis	chr6	rs9379897	4	26601526	0.13	rs9379897	26601526	0.13	0	1.00	7.5×10^{-6}	3.0×10^{-11}
59	trans	chr9	rs2259969	4	78942956	0.50	rs2259969	78942956	0.50	0	1.00	9.3×10^{-6}	10.0×10^{-1}
62	trans	chr9	rs2285317	3	118093492	0.34	rs2285317	118093492	0.34	0	1.00	1.2×10^{-6}	2.0×10^{-1}
63	trans	chr10	rs1938417	2	37687520	0.47	rs1938417	37687520	0.47	0	1.00	5.1×10^{-6}	8.9×10^{-1}
64	trans	chr12	rs2193149	3	13706502	0.20	rs2193149	13706502	0.20	0	1.00	5.0×10^{-6}	7.9×10^{-1}
65	trans	chr13	rs2026818	3	96631592	0.33	rs2026818	96631592	0.33	0	1.00	2.8×10^{-6}	7.1×10^{-4}
66	trans	chr17	rs8079271	3	16322364	0.49	rs8079271	16322364	0.49	0	1.00	6.7×10^{-6}	3.3×10^{-1}
67	trans	chr18	rs1785393	1	5559690	0.11	rs1785393	5559690	0.11	0	1.00	4.4×10^{-6}	6.7×10^{-1}

Schizophrenia Gene 3
BTN3A1: butyrophilin, subfamily 3, member A1
Gene Location: chr6:26402464-26415444
GWAS Data: McCarroll 2012
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 6.2×10^{-11}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs1529102	1	64495627	0.39	rs1529102	64495627	0.39	0	1.00	3.1×10^{-6}	4.9×10^{-1}
2	trans	chr4	rs13150491	1	189759434	0.34	rs13150491	189759434	0.34	0	1.00	4.0×10^{-6}	1.3×10^{-3}
4	cis	chr6	rs1892253	1	25782314	0.13	rs1892253	25782314	0.13	0	1.00	1.4×10^{-5}	1.0×10^{-10}
8	cis	chr6	rs9393708	2	26362643	0.07	rs9393708	26362643	0.07	0	1.00	5.0×10^{-9}	2.6×10^{-12}
26	cis	chr6	rs9393777	2	26942027	0.15	rs9393777	26942027	0.15	0	1.00	5.3×10^{-5}	7.9×10^{-12}
28	trans	chr6	rs4714484	11	41531223	0.20	rs4714484	41531223	0.20	0	1.00	1.3×10^{-6}	3.0×10^{-1}
29	trans	chr8	rs10749624	1	12792352	0.46	rs10749624	12792352	0.46	0	1.00	6.8×10^{-6}	5.4×10^{-1}
30	trans	chr10	rs7086330	2	85030339	0.48	rs7086330	85030339	0.48	0	1.00	9.1×10^{-6}	4.6×10^{-1}
31	trans	chr10	rs7083854	1	127264189	0.41	rs7083854	127264189	0.41	0	1.00	4.8×10^{-6}	4.9×10^{-1}
32	trans	chr20	rs2164169	1	206402	0.37	rs2164169	206402	0.37	0	1.00	3.3×10^{-6}	8.1×10^{-1}

Schizophrenia Gene 3
BTN3A1: butyrophilin, subfamily 3, member A1
Gene Location: chr6:26402464-26415444
GWAS Data: McCarroll 2012
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 9.5×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs10916258	1	228219882	0.21	rs10916258	228219882	0.21	0	1.00	8.3×10^{-6}	2.2×10^{-1}
3	trans	chr6	rs7766018	1	69869637	0.11	rs7766018	69869637	0.11	0	1.00	5.6×10^{-6}	4.7×10^{-4}
10	trans	chr10	rs6602325	1	8583805	0.35	rs6602325	8583805	0.35	0	1.00	8.4×10^{-6}	5.9×10^{-1}
11	trans	chr13	rs1751858	1	40969426	0.39	rs1751858	40969426	0.39	0	1.00	4.4×10^{-6}	3.7×10^{-1}
14	trans	chr20	rs12480756	1	4749032	0.10	rs12480756	4749032	0.10	0	1.00	6.2×10^{-6}	8.9×10^{-1}

Schizophrenia Gene 4
BTN3A3: butyrophilin, subfamily 3, member A3
Gene Location: chr6:26440699-26453643
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 3.0×10^{-10}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr6	rs9295657	3	25419318	0.14	rs9295657	25419318	0.14	0	1.00	9.0×10^{-8}	2.0×10^{-4}
4	cis	chr6	rs10105	2	25701903	0.22	rs10105	25701903	0.22	0	1.00	1.5×10^{-6}	2.9×10^{-6}
25	cis	chr6	rs1436310	2	25969958	0.50	rs1436310	25969958	0.50	0	1.00	7.0×10^{-4}	1.2×10^{-1}
38	cis	chr6	rs4145878	1	26198046	0.38	rs4145878	26198046	0.38	0	1.00	5.0×10^{-5}	5.5×10^{-3}
47	cis	chr6	rs9379858	2	26367689	0.07	rs9379858	26367689	0.07	0	1.00	1.1×10^{-27}	2.2×10^{-12}
68	cis	chr6	rs7763910	1	26472655	0.49	rs7763910	26472655	0.49	0	1.00	2.8×10^{-6}	5.8×10^{-4}
72	cis	chr6	rs9379897	4	26601526	0.13	rs9379897	26601526	0.13	0	1.00	4.1×10^{-21}	3.0×10^{-11}
138	trans	chr6	rs1008794	22	170335567	0.17	rs1008794	170335567	0.17	0	1.00	5.5×10^{-6}	7.5×10^{-1}
139	trans	chr7	rs1852210	9	45994256	0.43	rs1852210	45994256	0.43	0	1.00	5.4×10^{-6}	2.5×10^{-1}
141	trans	chr8	rs7824308	5	80070539	0.30	rs7824308	80070539	0.30	0	1.00	2.7×10^{-6}	1.6×10^{-2}
143	trans	chr16	rs10500328	2	5807878	0.21	rs10500328	5807878	0.21	0	1.00	4.7×10^{-6}	9.8×10^{-1}

Schizophrenia Gene 4
BTN3A3: butyrophilin, subfamily 3, member A3
Gene Location: chr6:26440699-26453643
GWAS Data: McCarroll 2012
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 9.1×10^{-9}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
10	trans	chr1	rs2043799	5	76549727	0.15	rs2043799	76549727	0.15	0	1.00	6.0×10^{-8}	7.6×10^{-1}
14	trans	chr2	rs300691	2	180171	0.21	rs300691	180171	0.21	0	1.00	9.0×10^{-6}	2.7×10^{-1}
15	trans	chr2	rs850908	3	186220642	0.24	rs850908	186220642	0.24	0	1.00	1.0×10^{-5}	2.2×10^{-1}
17	trans	chr2	rs4852014	2	239854389	0.41	rs4852014	239854389	0.41	0	1.00	4.0×10^{-6}	2.6×10^{-1}
18	trans	chr3	rs156166	6	6425168	0.24	rs156166	6425168	0.24	0	1.00	3.0×10^{-6}	5.7×10^{-1}
20	trans	chr3	rs7647735	3	66774036	0.47	rs7647735	66774036	0.47	0	1.00	4.0×10^{-6}	3.7×10^{-1}
23	trans	chr3	rs7618658	6	125171369	0.22	rs7618658	125171369	0.22	0	1.00	9.0×10^{-8}	3.7×10^{-1}
48	trans	chr3	rs12491993	2	152481845	0.14	rs12491993	152481845	0.14	0	1.00	7.0×10^{-6}	8.5×10^{-1}
58	trans	chr3	rs7640074	2	164562164	0.16	rs7640074	164562164	0.16	0	1.00	1.0×10^{-6}	8.3×10^{-1}
73	trans	chr3	rs9883259	8	194769624	0.15	rs9883259	194769624	0.15	0	1.00	5.0×10^{-6}	9.5×10^{-1}
74	trans	chr4	rs1867924	1	1671772	0.46	rs1867924	1671772	0.46	0	1.00	1.0×10^{-5}	1.3×10^{-1}
76	trans	chr4	rs1512953	2	67359005	0.21	rs1512953	67359005	0.21	0	1.00	5.0×10^{-6}	5.9×10^{-1}
80	trans	chr4	rs4407532	2	122444046	0.38	rs4407532	122444046	0.38	0	1.00	2.0×10^{-6}	3.5×10^{-1}
85	trans	chr4	rs3733260	8	129208259	0.13	rs3733260	129208259	0.13	0	1.00	1.0×10^{-5}	7.7×10^{-2}
86	trans	chr5	rs6555279	2	4409626	0.47	rs6555279	4409626	0.47	0	1.00	6.0×10^{-6}	3.6×10^{-1}
89	trans	chr5	rs150628	2	9565135	0.29	rs150628	9565135	0.29	0	1.00	3.0×10^{-6}	4.6×10^{-1}
91	trans	chr6	rs9295657	1	25419318	0.14	rs9295657	25419318	0.14	0	1.00	1.0×10^{-5}	2.0×10^{-4}
93	cis	chr6	rs7771468	2	25713568	0.16	rs7771468	25713568	0.16	0	1.00	2.0×10^{-5}	1.2×10^{-5}
185	cis	chr6	rs12174602	2	26372827	0.08	rs12174602	26372827	0.08	0	1.00	2.0×10^{-20}	8.3×10^{-13}
239	cis	chr6	rs9467835	6	26678512	0.35	rs9467835	26678512	0.35	0	1.00	1.0×10^{-4}	8.3×10^{-8}
502	trans	chr6	rs7758787	2	133240024	0.23	rs7758787	133240024	0.23	0	1.00	9.0×10^{-6}	6.4×10^{-1}
504	trans	chr6	rs1413901	2	150355441	0.24	rs1413901	150355441	0.24	0	1.00	1.0×10^{-5}	5.7×10^{-3}
509	trans	chr6	rs17086954	1	156337304	0.23	rs17086954	156337304	0.23	0	1.00	2.0×10^{-6}	9.4×10^{-1}
512	trans	chr7	rs2192675	2	13007537	0.15	rs2192675	13007537	0.15	0	1.00	2.0×10^{-6}	1.6×10^{-1}
515	trans	chr7	rs11983807	2	29811861	0.17	rs11983807	29811861	0.17	0	1.00	4.0×10^{-8}	5.5×10^{-2}
518	trans	chr8	rs10866941	2	2348747	0.28	rs10866941	2348747	0.28	0	1.00	6.0×10^{-6}	2.4×10^{-1}
522	trans	chr9	rs7047812	2	9726090	0.13	rs7047812	9726090	0.13	0	1.00	5.0×10^{-8}	2.1×10^{-1}
525	trans	chr9	rs10978698	2	109764204	0.27	rs10978698	109764204	0.27	0	1.00	3.0×10^{-6}	4.1×10^{-1}
530	trans	chr10	rs9665606	3	2517773	0.29	rs9665606	2517773	0.29	0	1.00	4.0×10^{-6}	9.9×10^{-1}
531	trans	chr11	rs1491850	2	27749725	0.38	rs1491850	27749725	0.38	0	1.00	1.0×10^{-5}	1.5×10^{-1}
532	trans	chr12	rs4766193	2	4108513	0.11	rs4766193	4108513	0.11	0	1.00	5.0×10^{-6}	4.7×10^{-1}
534	trans	chr13	rs9535553	1	51572734	0.33	rs9535553	51572734	0.33	0	1.00	1.0×10^{-5}	4.4×10^{-1}
535	trans	chr15	rs2461649	2	80351169	0.20	rs2461649	80351169	0.20	0	1.00	3.0×10^{-6}	9.6×10^{-1}
537	trans	chr16	rs12924453	6	11751499	0.25	rs12924453	11751499	0.25	0	1.00	9.0×10^{-6}	5.1×10^{-1}
538	trans	chr16	rs7199094	2	86726926	0.30	rs7199094	86726926	0.30	0	1.00	1.0×10^{-5}	3.4×10^{-1}
540	trans	chr17	rs8073778	2	11626332	0.30	rs8073778	11626332	0.30	0	1.00	7.0×10^{-6}	1.8×10^{-1}
545	trans	chr18	rs12373402	2	68132998	0.45	rs12373402	68132998	0.45	0	1.00	4.0×10^{-7}	4.3×10^{-1}
546	trans	chr21	rs369327	2	29593200	0.48	rs369327	29593200	0.48	0	1.00	1.0×10^{-5}	1.1×10^{-1}
547	trans	chr21	rs2071049	2	37866480	0.44	rs2071049	37866480	0.44	0	1.00	1.0×10^{-5}	9.1×10^{-1}

Schizophrenia Gene 4
BTN3A3: butyrophilin, subfamily 3, member A3
Gene Location: chr6:26440699-26453643
GWAS Data: McCarroll 2012
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 2.0×10^{-7}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs4513478	2	173626250	0.42	rs4513478	173626250	0.42	0	1.00	1.5×10^{-6}	8.1×10^{-1}
2	cis	chr6	rs9295661	1	25450026	0.07	rs9295661	25450026	0.07	0	1.00	7.5×10^{-5}	5.1×10^{-10}
18	cis	chr6	rs9393708	2	26362643	0.07	rs9393708	26362643	0.07	0	1.00	9.1×10^{-13}	2.6×10^{-12}
64	trans	chr6	rs1928274	2	46837390	0.33	rs1928274	46837390	0.33	0	1.00	9.0×10^{-6}	3.7×10^{-1}
65	trans	chr14	rs178452	16	80443279	0.36	rs178452	80443279	0.36	0	1.00	3.6×10^{-6}	5.5×10^{-1}

Schizophrenia Gene 4
BTN3A3: butyrophilin, subfamily 3, member A3
Gene Location: chr6:26440699-26453643
GWAS Data: McCarroll 2012
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 7.3×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr8	rs12679385	2	101810043	0.36	rs12679385	101810043	0.36	0	1.00	8.1×10^{-6}	5.8×10^{-1}
4	trans	chr13	rs9517119	2	98552547	0.18	rs9517119	98552547	0.18	0	1.00	1.4×10^{-6}	1.8×10^{-2}
6	trans	chr15	rs12050688	1	89712765	0.27	rs12050688	89712765	0.27	0	1.00	3.9×10^{-6}	4.5×10^{-2}

Schizophrenia Gene 5
HLA-DRB4: major histocompatibility complex, class II, DR beta 4
Gene Location: chr6:3846265-3860953
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 4.9×10^{-10}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs2391228	1	93606940	0.25	rs2391228	93606940	0.25	0	1.00	9.6×10^{-6}	8.1×10^{-1}
2	trans	chr4	rs11100365	1	162252857	0.21	rs11100365	162252857	0.21	0	1.00	3.0×10^{-6}	4.8×10^{-1}
3	trans	chr6	rs7752195	1	25419094	0.08	rs7752195	25419094	0.08	0	1.00	9.7×10^{-8}	8.9×10^{-11}
20	trans	chr6	rs9467704	2	26319486	0.20	rs9467704	26319486	0.20	0	1.00	2.2×10^{-11}	6.6×10^{-10}
30	trans	chr6	rs3799380	1	26467182	0.32	rs3799380	26467182	0.32	0	1.00	3.6×10^{-6}	2.3×10^{-11}
70	trans	chr6	rs791900	2	33672747	0.19	rs791900	33672747	0.19	0	1.00	6.0×10^{-8}	1.8×10^{-3}

Schizophrenia Gene 6
HLA-A: major histocompatibility complex, class I, A
Gene Location: chr6:29910246-29913661
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 6.6×10^{-8}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
4	trans	chr6	rs9295661	1	25450026	0.07	rs9295661	25450026	0.07	0	1.00	7.1×10^{-7}	5.1×10^{-10}
25	trans	chr6	rs10456045	1	26404958	0.21	rs10456045	26404958	0.21	0	1.00	6.0×10^{-7}	8.0×10^{-6}
118	trans	chr12	rs16945163	30	115641837	0.10	rs16945163	115641837	0.10	0	1.00	1.5×10^{-6}	3.9×10^{-1}
119	trans	chr17	rs11649888	3	31491925	0.07	rs11649888	31491925	0.07	0	1.00	1.6×10^{-6}	1.9×10^{-1}
120	trans	chr17	rs9892543	9	36067959	0.23	rs9892543	36067959	0.23	0	1.00	1.2×10^{-6}	9.6×10^{-1}
122	trans	chr18	rs1942922	1	57705339	0.34	rs1942922	57705339	0.34	0	1.00	3.9×10^{-6}	9.5×10^{-2}

Schizophrenia Gene 7
BCAP29: B-cell receptor-associated protein 29
Gene Location: chr7:107221203-107263762
GWAS Data: McCarroll 2012
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 1.3×10^{-7}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs11165406	4	95832611	0.36	rs11165406	95832611	0.36	0	1.00	4.8×10^{-6}	1.4×10^{-4}
2	trans	chr2	rs6760957	1	109230389	0.49	rs6760957	109230389	0.49	0	1.00	6.5×10^{-6}	1.5×10^{-1}
3	trans	chr2	rs3813817	1	174891414	0.49	rs3813817	174891414	0.49	0	1.00	7.6×10^{-6}	1.4×10^{-1}
4	trans	chr4	rs6533498	11	111112788	0.31	rs6533498	111112788	0.31	0	1.00	1.3×10^{-7}	4.2×10^{-1}
5	trans	chr4	rs7658791	1	182582942	0.30	rs7658791	182582942	0.30	0	1.00	5.3×10^{-6}	4.0×10^{-1}
6	trans	chr5	rs1459589	1	100697215	0.39	rs1459589	100697215	0.39	0	1.00	4.9×10^{-6}	3.0×10^{-1}
9	trans	chr5	rs13178130	1	133905829	0.41	rs13178130	133905829	0.41	0	1.00	7.9×10^{-7}	7.5×10^{-1}
10	trans	chr6	rs1348	3	10449258	0.17	rs1348	10449258	0.17	0	1.00	3.2×10^{-6}	8.7×10^{-1}
16	trans	chr7	rs2244351	1	50739526	0.48	rs2244351	50739526	0.48	0	1.00	1.4×10^{-6}	1.7×10^{-1}
17	trans	chr9	rs10809488	3	11467111	0.40	rs10809488	11467111	0.40	0	1.00	4.0×10^{-6}	7.2×10^{-2}
19	trans	chr10	rs10883728	2	104269301	0.34	rs10883728	104269301	0.34	0	1.00	2.3×10^{-6}	1.2×10^{-2}
22	trans	chr10	rs10883766	1	104464763	0.20	rs10883766	104464763	0.20	0	1.00	4.6×10^{-6}	3.2×10^{-6}
29	trans	chr10	rs284858	1	104573936	0.45	rs284858	104573936	0.45	0	1.00	5.0×10^{-8}	9.4×10^{-8}
47	trans	chr10	rs11191560	1	104869038	0.13	rs11191560	104869038	0.13	0	1.00	1.6×10^{-9}	1.2×10^{-11}
51	trans	chr11	rs12223458	1	11361458	0.18	rs12223458	11361458	0.18	0	1.00	9.2×10^{-6}	3.8×10^{-1}
52	trans	chr12	rs11610862	5	19814859	0.36	rs11610862	19814859	0.36	0	1.00	4.4×10^{-6}	5.6×10^{-1}
54	trans	chr12	rs12817819	7	90039326	0.07	rs12817819	90039326	0.07	0	1.00	1.9×10^{-7}	9.7×10^{-1}
56	trans	chr12	rs1347851	2	90566978	0.16	rs1347851	90566978	0.16	0	1.00	3.5×10^{-6}	4.1×10^{-2}
57	trans	chr13	rs10492674	4	88634590	0.42	rs10492674	88634590	0.42	0	1.00	3.2×10^{-6}	8.7×10^{-1}
58	trans	chr14	rs12437164	2	67995657	0.25	rs12437164	67995657	0.25	0	1.00	7.8×10^{-6}	1.4×10^{-1}
59	trans	chr14	rs7493141	1	86151263	0.35	rs7493141	86151263	0.35	0	1.00	2.7×10^{-6}	6.6×10^{-1}
63	trans	chr22	rs16982287	1	26925953	0.09	rs16982287	26925953	0.09	0	1.00	8.0×10^{-6}	7.1×10^{-1}

Schizophrenia Gene 8
ZFP57: zinc finger protein 57 homolog (mouse)
Gene Location: chr6:29640168-29644931
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 6.9×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr4	rs10019000	1	34488990	0.35	rs10019000	34488990	0.35	0	1.00	8.6×10^{-7}	1.7×10^{-1}
22	trans	chr9	rs7028812	1	3460842	0.14	rs7028812	3460842	0.14	0	1.00	9.8×10^{-6}	4.0×10^{-1}
24	trans	chr10	rs3852502	1	92836763	0.45	rs3852502	92836763	0.45	0	1.00	5.9×10^{-6}	1.4×10^{-4}
27	trans	chr11	rs10501835	1	95729876	0.25	rs10501835	95729876	0.25	0	1.00	5.4×10^{-6}	6.8×10^{-1}
29	trans	chr17	rs6503404	1	42923432	0.34	rs6503404	42923432	0.34	0	1.00	4.8×10^{-6}	3.8×10^{-1}
32	trans	chr17	rs7221059	1	74988444	0.20	rs7221059	74988444	0.20	0	1.00	8.1×10^{-6}	4.4×10^{-1}

Schizophrenia Gene 8
ZFP57: zinc finger protein 57 homolog (mouse)
Gene Location: chr6:29640168-29644931
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 5.2×10^{-7}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs13004835	1	193004176	0.26	rs13004835	193004176	0.26	0	1.00	4.2×10^{-6}	5.8×10^{-1}
4	trans	chr5	rs256287	44	34672299	0.12	rs256287	34672299	0.12	0	1.00	3.0×10^{-6}	5.7×10^{-1}
8	trans	chr6	rs12176317	2	26372786	0.07	rs12176317	26372786	0.07	0	1.00	8.3×10^{-8}	1.0×10^{-12}
10	trans	chr6	rs9393777	2	26942027	0.15	rs9393777	26942027	0.15	0	1.00	9.7×10^{-10}	7.9×10^{-12}

Schizophrenia Gene 9
GLT8D1: glycosyltransferase 8 domain containing 1
Gene Location: chr3:52728503-52740048
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 4.8×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs6542809	24	109912193	0.34	rs6542809	109912193	0.34	0	1.00	8.4×10^{-6}	8.7×10^{-1}
2	cis	chr3	rs1546737	1	52407041	0.20	rs1546737	52407041	0.20	0	1.00	7.0×10^{-4}	9.1×10^{-6}
37	cis	chr3	rs1042779	1	52821011	0.44	rs1042779	52821011	0.44	0	1.00	7.1×10^{-7}	1.5×10^{-7}
60	cis	chr3	rs3774421	3	53551010	0.17	rs3774421	53551010	0.17	0	1.00	8.0×10^{-4}	7.0×10^{-1}
61	trans	chr4	rs13102584	33	172701103	0.35	rs13102584	172701103	0.35	0	1.00	1.0×10^{-5}	5.4×10^{-1}
63	trans	chr8	rs10955132	120	98808157	0.46	rs10955132	98808157	0.46	0	1.00	2.4×10^{-6}	8.9×10^{-2}
65	trans	chr14	rs10438025	2	75183239	0.24	rs10438025	75183239	0.24	0	1.00	4.7×10^{-6}	4.0×10^{-1}
66	trans	chr14	rs4903268	1	75371060	0.19	rs4903268	75371060	0.19	0	1.00	9.1×10^{-6}	9.3×10^{-2}
68	trans	chr15	rs2311469	2	28069068	0.50	rs2311469	28069068	0.50	0	1.00	6.4×10^{-7}	6.1×10^{-1}

Schizophrenia Gene 9
GLT8D1: glycosyltransferase 8 domain containing 1
Gene Location: chr3:52728503-52740048
GWAS Data: McCarroll 2012
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 3.8×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs6732845	1	205132016	0.39	rs6732845	205132016	0.39	0	1.00	1.0×10^{-5}	8.3×10^{-4}
2	trans	chr3	rs10510699	154	39335450	0.09	rs10510699	39335450	0.09	0	1.00	4.0×10^{-6}	3.7×10^{-1}
3	trans	chr4	rs10517949	14	66759828	0.48	rs10517949	66759828	0.48	0	1.00	8.0×10^{-6}	3.7×10^{-1}
5	trans	chr4	rs10002279	17	112432021	0.11	rs10002279	112432021	0.11	0	1.00	2.0×10^{-6}	1.4×10^{-1}
14	trans	chr7	rs10278735	1	37803161	0.21	rs10278735	37803161	0.21	0	1.00	4.0×10^{-6}	4.7×10^{-1}
17	trans	chr8	rs13439240	1	97318660	0.05	rs13439240	97318660	0.05	0	1.00	1.0×10^{-5}	6.7×10^{-1}
18	trans	chr18	rs273742	4	23186088	0.39	rs273742	23186088	0.39	0	1.00	4.0×10^{-6}	9.2×10^{-4}
19	trans	chr18	rs2195046	19	64503443	0.30	rs2195046	64503443	0.30	0	1.00	6.0×10^{-6}	3.9×10^{-1}
20	trans	chr19	rs8099984	2	57843920	0.44	rs8099984	57843920	0.44	0	1.00	8.0×10^{-6}	9.8×10^{-1}

Schizophrenia Gene 9
GLT8D1: glycosyltransferase 8 domain containing 1
Gene Location: chr3:52728503-52740048
GWAS Data: McCarroll 2012
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 3.1×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr9	rs10814339	1	36154678	0.18	rs10814339	36154678	0.18	0	1.00	3.5×10^{-6}	1.4×10^{-2}
3	trans	chr9	rs1933584	2	84948300	0.38	rs1933584	84948300	0.38	0	1.00	10.0×10^{-6}	2.2×10^{-5}
4	trans	chr11	rs4936618	1	121223996	0.16	rs4936618	121223996	0.16	0	1.00	9.0×10^{-6}	7.0×10^{-1}
5	trans	chr13	rs9634554	2	106490187	0.12	rs9634554	106490187	0.12	0	1.00	6.2×10^{-6}	8.5×10^{-1}
6	trans	chr16	rs9927740	1	26883828	0.40	rs9927740	26883828	0.40	0	1.00	9.5×10^{-6}	5.2×10^{-1}
7	trans	chr20	rs6131592	5	14528513	0.06	rs6131592	14528513	0.06	0	1.00	9.0×10^{-6}	8.9×10^{-1}
8	trans	chr20	rs4564856	5	22297047	0.36	rs4564856	22297047	0.36	0	1.00	8.5×10^{-6}	3.1×10^{-1}

Schizophrenia Gene 9
GLT8D1: glycosyltransferase 8 domain containing 1
Gene Location: chr3:52728503-52740048
GWAS Data: McCarroll 2012
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 7.0×10^{-7}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
4	cis	chr3	rs352169	1	52236762	0.23	rs352169	52236762	0.23	0	1.00	4.1×10^{-9}	3.2×10^{-5}
11	cis	chr3	rs1961958	1	52585990	0.36	rs1961958	52585990	0.36	0	1.00	1.6×10^{-19}	1.1×10^{-6}
26	cis	chr3	rs2256332	1	52855865	0.49	rs2256332	52855865	0.49	0	1.00	9.0×10^{-8}	1.2×10^{-7}
42	trans	chr6	rs1998017	2	144317124	0.08	rs1998017	144317124	0.08	0	1.00	3.5×10^{-6}	8.1×10^{-1}
46	trans	chr10	rs2070968	1	73581560	0.39	rs2070968	73581560	0.39	0	1.00	6.2×10^{-6}	1.4×10^{-1}

Schizophrenia Gene 10
PRSS16: protease, serine, 16 (thymus)
Gene Location: chr6:27215501-27224399
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 1.2×10^{-6}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
3	cis	chr6	rs12176317	2	26372786	0.07	rs12176317	26372786	0.07	0	1.00	3.0×10^{-4}	1.0×10^{-12}
8	cis	chr6	rs12205310	1	26605864	0.08	rs12205310	26605864	0.08	0	1.00	1.3×10^{-4}	2.8×10^{-1}
10	cis	chr6	rs10946868	2	26887930	0.41	rs10946868	26887930	0.41	0	1.00	5.0×10^{-4}	6.0×10^{-8}

Schizophrenia Gene 11
IER3: immediate early response 3
Gene Location: chr6:30710975-30712327
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 1.3×10^{-6}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr3	rs2665540	2	68552308	0.16	rs2665540	68552308	0.16	0	1.00	6.8×10^{-6}	8.3×10^{-2}
8	trans	chr6	rs523383	1	25869848	0.24	rs523383	25869848	0.24	0	1.00	7.5×10^{-6}	1.2×10^{-9}
10	trans	chr6	rs10484435	2	26031811	0.06	rs10484435	26031811	0.06	0	1.00	2.7×10^{-6}	6.2×10^{-11}
13	trans	chr12	rs11117146	1	86382870	0.34	rs11117146	86382870	0.34	0	1.00	3.9×10^{-6}	1.2×10^{-1}

Schizophrenia Gene 11
IER3: immediate early response 3
Gene Location: chr6:30710975-30712327
GWAS Data: McCarroll 2012
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 9.6×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs300803	2	101514	0.48	rs300803	101514	0.48	0	1.00	1.4×10^{-6}	8.9×10^{-1}
4	trans	chr4	rs6852540	10	83623978	0.40	rs6852540	83623978	0.40	0	1.00	3.7×10^{-6}	1.6×10^{-2}
26	trans	chr13	rs9569649	6	57819477	0.20	rs9569649	57819477	0.20	0	1.00	1.5×10^{-7}	2.0×10^{-2}
28	trans	chr19	rs2302951	1	48954421	0.17	rs2302951	48954421	0.17	0	1.00	2.9×10^{-6}	5.9×10^{-1}

Schizophrenia Gene 12
OMG: oligodendrocyte myelin glycoprotein
Gene Location: chr17:29621667-29624380
GWAS Data: McCarroll 2012
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 1.6×10^{-6}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
6	trans	chr6	rs523383	1	25869848	0.24	rs523383	25869848	0.24	0	1.00	3.0×10^{-6}	1.2×10^{-9}
8	trans	chr14	rs17767434	2	71806727	0.05	rs17767434	71806727	0.05	0	1.00	1.7×10^{-6}	1.9×10^{-3}

Schizophrenia Gene 13
USMG5: up-regulated during skeletal muscle growth 5 homolog (mouse)
Gene Location: chr10:105148808-105156270
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 3.9×10^{-6}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs4855383	1	69340525	0.42	rs4855383	69340525	0.42	0	1.00	2.2×10^{-6}	6.0×10^{-1}
2	trans	chr7	rs11765559	1	135036378	0.35	rs11765559	135036378	0.35	0	1.00	3.7×10^{-6}	8.7×10^{-1}
6	trans	chr10	rs3758559	1	103445232	0.16	rs3758559	103445232	0.16	0	1.00	8.3×10^{-7}	5.3×10^{-1}
7	trans	chr10	rs10883712	1	103939305	0.49	rs10883712	103939305	0.49	0	1.00	3.9×10^{-8}	7.6×10^{-2}
11	cis	chr10	rs1572530	1	104193834	0.30	rs1572530	104193834	0.30	0	1.00	2.2×10^{-15}	2.0×10^{-2}
31	cis	chr10	rs10883757	1	104400133	0.23	rs10883757	104400133	0.23	0	1.00	1.7×10^{-7}	4.0×10^{-6}
45	cis	chr10	rs2482506	1	104563743	0.48	rs2482506	104563743	0.48	0	1.00	5.5×10^{-69}	8.6×10^{-2}
73	cis	chr10	rs11191499	1	104764271	0.14	rs11191499	104764271	0.14	0	1.00	7.8×10^{-53}	2.7×10^{-11}
107	cis	chr10	rs1163073	1	105022934	0.28	rs1163073	105022934	0.28	0	1.00	0.	3.4×10^{-2}
125	cis	chr10	rs4917391	1	105282664	0.19	rs4917391	105282664	0.19	0	1.00	3.4×10^{-19}	7.6×10^{-3}
136	cis	chr10	rs2145310	1	105463885	0.36	rs2145310	105463885	0.36	0	1.00	4.1×10^{-13}	3.2×10^{-1}
139	cis	chr10	rs515910	1	105966404	0.48	rs515910	105966404	0.48	0	1.00	5.8×10^{-6}	5.6×10^{-2}
141	trans	chr15	rs1036522	1	96684647	0.24	rs1036522	96684647	0.24	0	1.00	2.6×10^{-6}	3.0×10^{-1}

Schizophrenia Gene 14
BAG5: BCL2-associated athanogene 5
Gene Location: chr14:104022880-104029151
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 5.0×10^{-6}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr5	rs7700706	3	141294362	0.26	rs7700706	141294362	0.26	0	1.00	3.2×10^{-7}	6.1×10^{-1}
5	trans	chr7	rs2390811	2	23796656	0.45	rs2390811	23796656	0.45	0	1.00	1.4×10^{-6}	9.6×10^{-1}
9	trans	chr11	rs1554519	6	10904067	0.47	rs1554519	10904067	0.47	0	1.00	4.6×10^{-6}	3.2×10^{-1}
10	trans	chr13	rs9507401	4	25296819	0.37	rs9507401	25296819	0.37	0	1.00	9.1×10^{-6}	4.1×10^{-1}
25	cis	chr14	rs7148456	3	104028270	0.27	rs7148456	104028270	0.27	0	1.00	6.0×10^{-23}	3.1×10^{-8}
30	cis	chr14	rs3742365	1	104198251	0.42	rs3742365	104198251	0.42	0	1.00	2.2×10^{-10}	1.9×10^{-6}
47	trans	chr22	rs715629	8	32806595	0.31	rs715629	32806595	0.31	0	1.00	9.3×10^{-6}	1.9×10^{-2}

Schizophrenia Gene 14
BAG5: BCL2-associated athanogene 5
Gene Location: chr14:104022880-104029151
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 1.7×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs1488189	67	112711371	0.45	rs1488189	112711371	0.45	0	1.00	1.0×10^{-5}	2.0×10^{-1}
2	trans	chr6	rs7758080	66	149577079	0.37	rs7758080	149577079	0.37	0	1.00	1.0×10^{-5}	5.0×10^{-1}
3	trans	chr8	rs10282765	8	98411402	0.40	rs10282765	98411402	0.40	0	1.00	8.5×10^{-6}	9.9×10^{-1}
10	cis	chr14	rs2296482	2	104029819	0.23	rs2296482	104029819	0.23	0	1.00	7.0×10^{-5}	1.7×10^{-8}
14	cis	chr14	rs8702	1	104152352	0.46	rs8702	104152352	0.46	0	1.00	2.0×10^{-4}	1.5×10^{-1}
16	trans	chr16	rs193756	158	11326785	0.40	rs193756	11326785	0.40	0	1.00	5.1×10^{-6}	5.4×10^{-1}

Schizophrenia Gene 14
BAG5: BCL2-associated athanogene 5
Gene Location: chr14:104022880-104029151
GWAS Data: McCarroll 2012
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 8.6×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs4950932	1	203174864	0.26	rs4950932	203174864	0.26	0	1.00	4.9×10^{-6}	5.6×10^{-1}
2	trans	chr5	rs1295217	4	154958347	0.08	rs1295217	154958347	0.08	0	1.00	6.8×10^{-6}	6.6×10^{-1}
3	trans	chr6	rs13204241	1	145366647	0.32	rs13204241	145366647	0.32	0	1.00	6.6×10^{-6}	5.0×10^{-1}
4	trans	chr10	rs4751880	3	124015462	0.47	rs4751880	124015462	0.47	0	1.00	7.3×10^{-6}	7.5×10^{-1}
6	cis	chr14	rs7693	1	104023704	0.20	rs7693	104023704	0.20	0	1.00	9.0×10^{-8}	1.7×10^{-4}
18	trans	chr21	rs9636977	1	42277689	0.42	rs9636977	42277689	0.42	0	1.00	7.3×10^{-6}	1.1×10^{-1}

Schizophrenia Gene 15
HLA-A29.1: Not Found in HUGO
Gene Location: Not Found:Not Found-Not Found
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 5.5×10^{-6}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs17099155	1	77019986	0.13	rs17099155	77019986	0.13	0	1.00	7.6×10^{-6}	3.6×10^{-1}
2	trans	chr1	rs10733121	2	238639112	0.11	rs10733121	238639112	0.11	0	1.00	1.2×10^{-6}	6.2×10^{-1}
4	trans	chr3	rs6805378	3	142866513	0.48	rs6805378	142866513	0.48	0	1.00	5.1×10^{-6}	8.0×10^{-1}
8	trans	chr5	rs4368715	2	150351665	0.21	rs4368715	150351665	0.21	0	1.00	3.6×10^{-7}	9.6×10^{-1}
12	trans	chr5	rs6876263	1	155618395	0.34	rs6876263	155618395	0.34	0	1.00	3.9×10^{-6}	7.2×10^{-2}
15	trans	chr6	rs9461219	1	25836927	0.06	rs9461219	25836927	0.06	0	1.00	1.5×10^{-6}	5.3×10^{-12}
19	trans	chr6	rs6933583	1	26355283	0.26	rs6933583	26355283	0.26	0	1.00	5.3×10^{-11}	6.2×10^{-10}
88	trans	chr7	rs7801616	1	151452628	0.29	rs7801616	151452628	0.29	0	1.00	3.3×10^{-6}	8.4×10^{-2}
89	trans	chr10	rs7080061	1	97112861	0.45	rs7080061	97112861	0.45	0	1.00	3.5×10^{-6}	3.4×10^{-3}
90	trans	chr17	rs7207507	1	10283950	0.34	rs7207507	10283950	0.34	0	1.00	4.0×10^{-6}	4.3×10^{-1}

Schizophrenia Gene 16
C10orf32: chromosome 10 open reading frame 32
Gene Location: chr10:104613966-104624718
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 6.0×10^{-6}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs7527281	325	217203091	0.29	rs7527281	217203091	0.29	0	1.00	6.5×10^{-6}	2.2×10^{-2}
2	trans	chr3	rs4287886	687	29422762	0.42	rs4287886	29422762	0.42	0	1.00	1.3×10^{-6}	8.5×10^{-2}
3	trans	chr6	rs6932737	2	170351025	0.33	rs6932737	170351025	0.33	0	1.00	4.6×10^{-6}	7.8×10^{-1}
4	cis	chr10	rs12573077	1	104434630	0.27	rs12573077	104434630	0.27	0	1.00	2.0×10^{-5}	4.1×10^{-1}
18	cis	chr10	rs9527	1	104623578	0.17	rs9527	104623578	0.17	0	1.00	6.2×10^{-12}	1.2×10^{-4}
31	cis	chr10	rs10883824	1	104812897	0.40	rs10883824	104812897	0.40	0	1.00	4.5×10^{-7}	5.1×10^{-11}
49	cis	chr10	rs4918001	1	105013147	0.08	rs4918001	105013147	0.08	0	1.00	7.7×10^{-6}	1.2×10^{-1}

Schizophrenia Gene 16
C10orf32: chromosome 10 open reading frame 32
Gene Location: chr10:104613966-104624718
GWAS Data: McCarroll 2012
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 3.3×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr2	rs415838	1	77612535	0.33	rs415838	77612535	0.33	0	1.00	3.2×10^{-6}	2.4×10^{-1}
6	trans	chr3	rs1472176	1	102948106	0.44	rs1472176	102948106	0.44	0	1.00	1.6×10^{-6}	8.5×10^{-1}
18	cis	chr10	rs9527	1	104623578	0.17	rs9527	104623578	0.17	0	1.00	9.8×10^{-10}	1.2×10^{-4}
20	cis	chr10	rs12257935	1	104803062	0.08	rs12257935	104803062	0.08	0	1.00	9.8×10^{-6}	5.9×10^{-2}
22	trans	chr13	rs3098728	1	111410802	0.44	rs3098728	111410802	0.44	0	1.00	6.8×10^{-6}	6.6×10^{-1}

Schizophrenia Gene 17
AMN: amnionless homolog (mouse)
Gene Location: chr14:103388992-103397179
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 6.7×10^{-6}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr3	rs1541989	4	104575391	0.49	rs1541989	104575391	0.49	0	1.00	1.7×10^{-7}	2.1×10^{-1}
3	trans	chr6	rs2237165	2	16654023	0.36	rs2237165	16654023	0.36	0	1.00	7.3×10^{-6}	9.9×10^{-1}
5	trans	chr7	rs6947810	3	51804814	0.28	rs6947810	51804814	0.28	0	1.00	2.8×10^{-6}	9.9×10^{-1}
6	trans	chr7	rs6978354	1	116226422	0.47	rs6978354	116226422	0.47	0	1.00	9.6×10^{-6}	2.3×10^{-1}
7	trans	chr10	rs9419615	14	133491775	0.24	rs9419615	133491775	0.24	0	1.00	6.4×10^{-6}	9.0×10^{-1}
8	cis	chr14	rs2296482	2	104029819	0.23	rs2296482	104029819	0.23	0	1.00	3.0×10^{-4}	1.7×10^{-8}
10	cis	chr14	rs1187417	2	104310025	0.24	rs1187417	104310025	0.24	0	1.00	6.0×10^{-4}	2.1×10^{-7}

Schizophrenia Gene 18
YARS2: tyrosyl-tRNA synthetase 2, mitochondrial
Gene Location: chr12:32899477-32908887
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 8.8×10^{-6}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr3	rs7638292	1	171146484	0.47	rs7638292	171146484	0.47	0	1.00	7.0×10^{-6}	7.3×10^{-1}
5	trans	chr13	rs9559147	3	108398277	0.29	rs9559147	108398277	0.29	0	1.00	8.8×10^{-6}	8.9×10^{-1}
6	trans	chr16	rs12716974	2	29944832	0.36	rs12716974	29944832	0.36	0	1.00	3.4×10^{-6}	4.6×10^{-9}
16	trans	chr16	rs11642740	3	30060655	0.19	rs11642740	30060655	0.19	0	1.00	9.9×10^{-12}	9.4×10^{-6}

Schizophrenia Gene 18
YARS2: tyrosyl-tRNA synthetase 2, mitochondrial
Gene Location: chr12:32899477-32908887
GWAS Data: McCarroll 2012
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 1.1×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs961522	3	58272502	0.27	rs961522	58272502	0.27	0	1.00	1.0×10^{-5}	3.4×10^{-6}
3	trans	chr2	rs7593369	9	58493260	0.35	rs7593369	58493260	0.35	0	1.00	5.0×10^{-6}	2.3×10^{-4}
7	trans	chr9	rs10867453	1	72016960	0.22	rs10867453	72016960	0.22	0	1.00	8.0×10^{-6}	8.3×10^{-1}
11	trans	chr10	rs11196301	614	84634847	0.14	rs11196301	84634847	0.14	0	1.00	1.0×10^{-5}	9.4×10^{-1}
14	trans	chr18	rs12958819	170	77277405	0.14	rs12958819	77277405	0.14	0	1.00	1.0×10^{-6}	5.2×10^{-1}
18	trans	chr22	rs16981495	19	26589752	0.20	rs16981495	26589752	0.20	0	1.00	6.0×10^{-6}	3.6×10^{-1}

Schizophrenia Gene 19
TMEM113: Not Found in HUGO
Gene Location: Not Found:Not Found-Not Found
GWAS Data: McCarroll 2012
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 9.1×10^{-6}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
4	trans	chr3	rs352169	1	52236762	0.23	rs352169	52236762	0.23	0	1.00	2.3×10^{-16}	3.2×10^{-5}
11	trans	chr3	rs9311474	1	52338852	0.47	rs9311474	52338852	0.47	0	1.00	1.0×10^{-18}	3.4×10^{-8}
15	trans	chr3	rs13091025	1	52467324	0.06	rs13091025	52467324	0.06	0	1.00	5.4×10^{-6}	7.4×10^{-2}
48	trans	chr3	rs4687657	1	52852538	0.27	rs4687657	52852538	0.27	0	1.00	9.9×10^{-6}	1.5×10^{-6}
72	trans	chr6	rs2208601	1	55615326	0.12	rs2208601	55615326	0.12	0	1.00	2.9×10^{-6}	6.2×10^{-1}
74	trans	chr7	rs12701008	1	30220830	0.23	rs12701008	30220830	0.23	0	1.00	5.6×10^{-6}	4.6×10^{-1}
75	trans	chr10	rs1923396	1	4321300	0.40	rs1923396	4321300	0.40	0	1.00	5.4×10^{-6}	5.7×10^{-1}
76	trans	chr10	rs2448541	3	50014816	0.45	rs2448541	50014816	0.45	0	1.00	2.2×10^{-6}	2.7×10^{-1}

Schizophrenia Gene 20
BTN2A2: butyrophilin, subfamily 2, member A2
Gene Location: chr6:26383328-26395100
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 1.0×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs754894	1	203017087	0.34	rs754894	203017087	0.34	0	1.00	8.8×10^{-6}	2.7×10^{-2}
2	trans	chr1	rs10915949	1	226339764	0.35	rs10915949	226339764	0.35	0	1.00	9.4×10^{-6}	4.5×10^{-1}
3	trans	chr4	rs12642662	1	28470784	0.16	rs12642662	28470784	0.16	0	1.00	1.4×10^{-6}	1.5×10^{-1}
20	cis	chr6	rs4320356	1	26423560	0.49	rs4320356	26423560	0.49	0	1.00	1.1×10^{-6}	7.4×10^{-5}
33	cis	chr6	rs9379897	4	26601526	0.13	rs9379897	26601526	0.13	0	1.00	9.0×10^{-4}	3.0×10^{-11}
39	trans	chr8	rs7009399	49	81903007	0.24	rs7009399	81903007	0.24	0	1.00	1.5×10^{-7}	5.2×10^{-1}
41	trans	chr10	rs1047991	1	30629226	0.24	rs1047991	30629226	0.24	0	1.00	3.3×10^{-6}	2.0×10^{-1}
43	trans	chr15	rs9920881	3	35961254	0.30	rs9920881	35961254	0.30	0	1.00	5.1×10^{-6}	6.5×10^{-1}
45	trans	chr15	rs11858401	2	62452242	0.19	rs11858401	62452242	0.19	0	1.00	6.5×10^{-7}	9.2×10^{-1}

Schizophrenia Gene 21
HIST1H2BD: histone cluster 1, H2bd
Gene Location: chr6:26158348-26171576
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 1.4×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs2848122	1	89107189	0.27	rs2848122	89107189	0.27	0	1.00	9.9×10^{-6}	1.1×10^{-1}
2	trans	chr5	rs6871305	1	84065374	0.20	rs6871305	84065374	0.20	0	1.00	9.1×10^{-6}	1.4×10^{-1}
3	trans	chr5	rs255340	1	94137371	0.13	rs255340	94137371	0.13	0	1.00	9.3×10^{-6}	5.6×10^{-2}
6	cis	chr6	rs9295657	2	25419318	0.14	rs9295657	25419318	0.14	0	1.00	1.8×10^{-7}	2.0×10^{-4}
12	cis	chr6	rs17320614	1	25727921	0.16	rs17320614	25727921	0.16	0	1.00	4.3×10^{-7}	1.2×10^{-5}
30	cis	chr6	rs11758372	3	25959355	0.08	rs11758372	25959355	0.08	0	1.00	3.9×10^{-7}	5.8×10^{-1}
51	cis	chr6	rs1009181	2	26158993	0.31	rs1009181	26158993	0.31	0	1.00	3.5×10^{-125}	8.9×10^{-2}
73	cis	chr6	rs9358932	2	26362705	0.07	rs9358932	26362705	0.07	0	1.00	5.8×10^{-14}	3.0×10^{-12}
122	trans	chr9	rs11103117	1	138527913	0.17	rs11103117	138527913	0.17	0	1.00	6.9×10^{-6}	6.3×10^{-1}
123	trans	chr10	rs17682394	2	18564128	0.07	rs17682394	18564128	0.07	0	1.00	4.6×10^{-6}	7.8×10^{-1}
124	trans	chr10	rs2999427	1	47633512	0.38	rs2999427	47633512	0.38	0	1.00	3.8×10^{-6}	4.0×10^{-1}
126	trans	chr14	rs11157539	1	47547900	0.35	rs11157539	47547900	0.35	0	1.00	3.0×10^{-6}	2.8×10^{-1}
127	trans	chr15	rs16956820	1	31810241	0.12	rs16956820	31810241	0.12	0	1.00	8.9×10^{-6}	1.1×10^{-1}
128	trans	chr15	rs4547312	1	43632138	0.45	rs4547312	43632138	0.45	0	1.00	3.3×10^{-6}	9.4×10^{-4}

Schizophrenia Gene 22
IMMP2L: IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)
Gene Location: chr7:110303105-111202573
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 4.6×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr2	rs2166445	1	46492759	0.21	rs2166445	46492759	0.21	0	1.00	7.3×10^{-7}	8.3×10^{-1}
3	trans	chr5	rs17721860	1	58406871	0.03	rs17721860	58406871	0.03	0	1.00	6.4×10^{-6}	2.9×10^{-1}
7	cis	chr7	rs940818	1	110336323	0.49	rs940818	110336323	0.49	0	1.00	3.6×10^{-7}	8.0×10^{-1}
9	cis	chr7	rs799618	1	110485378	0.26	rs799618	110485378	0.26	0	1.00	6.8×10^{-51}	2.4×10^{-2}
47	cis	chr7	rs37715	1	110879251	0.40	rs37715	110879251	0.40	0	1.00	2.0×10^{-67}	2.4×10^{-8}
55	cis	chr7	rs37644	1	110982360	0.19	rs37644	110982360	0.19	0	1.00	2.6×10^{-7}	2.8×10^{-1}
69	cis	chr7	rs2528681	1	111288089	0.40	rs2528681	111288089	0.40	0	1.00	6.5×10^{-19}	2.6×10^{-2}
88	trans	chr9	rs1937935	2	25703720	0.37	rs1937935	25703720	0.37	0	1.00	3.0×10^{-6}	3.6×10^{-1}
89	trans	chr9	rs12378054	5	118411240	0.13	rs12378054	118411240	0.13	0	1.00	4.4×10^{-6}	9.5×10^{-1}
90	trans	chr13	rs10781825	1	22770518	0.25	rs10781825	22770518	0.25	0	1.00	4.3×10^{-6}	7.6×10^{-2}

Schizophrenia Gene 22
IMMP2L: IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)
Gene Location: chr7:110303105-111202573
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 1.7×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs2231856	1	157095470	0.21	rs2231856	157095470	0.21	0	1.00	6.0×10^{-7}	9.7×10^{-1}
2	trans	chr2	rs7423300	2	26647277	0.33	rs7423300	26647277	0.33	0	1.00	4.3×10^{-6}	8.4×10^{-1}
3	trans	chr2	rs4972710	4	173070217	0.23	rs4972710	173070217	0.23	0	1.00	7.4×10^{-6}	4.3×10^{-1}
4	trans	chr4	rs12645863	2	175457629	0.20	rs12645863	175457629	0.20	0	1.00	9.5×10^{-6}	5.1×10^{-1}
5	trans	chr5	rs2963672	2	175935316	0.31	rs2963672	175935316	0.31	0	1.00	4.5×10^{-6}	1.6×10^{-1}
6	trans	chr6	rs9462531	2	39303594	0.41	rs9462531	39303594	0.41	0	1.00	8.7×10^{-6}	3.6×10^{-1}
7	cis	chr7	rs1525501	2	109798853	0.24	rs1525501	109798853	0.24	0	1.00	1.3×10^{-4}	5.3×10^{-1}
14	cis	chr7	rs7795011	1	110602792	0.45	rs7795011	110602792	0.45	0	1.00	6.2×10^{-12}	6.3×10^{-4}
20	cis	chr7	rs214460	1	110851553	0.37	rs214460	110851553	0.37	0	1.00	3.3×10^{-7}	3.7×10^{-11}
32	trans	chr10	rs3125602	1	132753083	0.44	rs3125602	132753083	0.44	0	1.00	5.0×10^{-6}	3.0×10^{-1}
33	trans	chr13	rs9318474	2	24905769	0.19	rs9318474	24905769	0.19	0	1.00	2.4×10^{-6}	9.3×10^{-1}
34	trans	chr13	rs510342	11	28178525	0.38	rs510342	28178525	0.38	0	1.00	9.2×10^{-7}	5.5×10^{-1}
35	trans	chr14	rs12385910	10	64999970	0.19	rs12385910	64999970	0.19	0	1.00	4.8×10^{-6}	1.3×10^{-1}

Schizophrenia Gene 23
GATAD2A: GATA zinc finger domain containing 2A
Gene Location: chr19:19496641-19619741
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 2.0×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs17288929	7	56852389	0.16	rs17288929	56852389	0.16	0	1.00	9.2×10^{-6}	3.2×10^{-1}
2	trans	chr6	rs960270	1	18557074	0.43	rs960270	18557074	0.43	0	1.00	4.3×10^{-6}	1.8×10^{-1}
3	trans	chr12	rs10858945	1	90443482	0.45	rs10858945	90443482	0.45	0	1.00	5.2×10^{-6}	6.2×10^{-1}
11	cis	chr19	rs2916070	1	19524105	0.14	rs2916070	19524105	0.14	0	1.00	2.9×10^{-9}	2.6×10^{-4}
20	cis	chr19	rs4808967	1	19640524	0.45	rs4808967	19640524	0.45	0	1.00	1.1×10^{-11}	2.0×10^{-9}
26	trans	chr20	rs6125888	1	48699651	0.10	rs6125888	48699651	0.10	0	1.00	6.4×10^{-6}	8.0×10^{-1}

Schizophrenia Gene 23
GATAD2A: GATA zinc finger domain containing 2A
Gene Location: chr19:19496641-19619741
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 9.1×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs6734896	6	240486774	0.14	rs6734896	240486774	0.14	0	1.00	6.3×10^{-6}	5.1×10^{-1}
2	trans	chr3	rs4261862	14	1762176	0.28	rs4261862	1762176	0.28	0	1.00	9.3×10^{-6}	3.8×10^{-1}
5	trans	chr3	rs1543235	2	70285198	0.36	rs1543235	70285198	0.36	0	1.00	7.6×10^{-6}	2.7×10^{-2}
7	trans	chr7	rs2041369	6	31681563	0.26	rs2041369	31681563	0.26	0	1.00	5.9×10^{-6}	1.0×10^{-1}
12	trans	chr8	rs4304300	4	94605374	0.30	rs4304300	94605374	0.30	0	1.00	5.0×10^{-6}	6.8×10^{-2}
13	trans	chr9	rs624290	12	3928115	0.22	rs624290	3928115	0.22	0	1.00	5.1×10^{-6}	1.6×10^{-2}
14	trans	chr17	rs6502398	106	14735492	0.40	rs6502398	14735492	0.40	0	1.00	8.3×10^{-6}	4.6×10^{-1}
15	trans	chr17	rs4794538	1	52925502	0.12	rs4794538	52925502	0.12	0	1.00	7.3×10^{-6}	8.3×10^{-1}
16	cis	chr19	rs2238663	30	19256870	0.32	rs2238663	19256870	0.32	0	1.00	2.0×10^{-4}	9.8×10^{-1}
17	trans	chr21	rs2825977	1	21426885	0.39	rs2825977	21426885	0.39	0	1.00	4.3×10^{-6}	4.6×10^{-1}
18	trans	chr21	rs2298660	1	42845633	0.27	rs2298660	42845633	0.27	0	1.00	1.5×10^{-6}	9.3×10^{-2}

Schizophrenia Gene 24
KCNK12: potassium channel, subfamily K, member 12
Gene Location: chr2:47747914-47797470
GWAS Data: McCarroll 2012
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 8.6×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs1335740	1	76545965	0.11	rs1335740	76545965	0.11	0	1.00	7.0×10^{-6}	6.9×10^{-1}
13	trans	chr2	rs3930	14	53897525	0.24	rs3930	53897525	0.24	0	1.00	3.0×10^{-7}	2.6×10^{-3}
15	trans	chr2	rs6733199	2	220984680	0.22	rs6733199	220984680	0.22	0	1.00	1.0×10^{-5}	1.8×10^{-1}
16	trans	chr3	rs7619910	14	173556777	0.37	rs7619910	173556777	0.37	0	1.00	9.0×10^{-6}	2.4×10^{-2}
18	trans	chr4	rs4234711	1	5991384	0.23	rs4234711	5991384	0.23	0	1.00	6.0×10^{-6}	9.7×10^{-1}
19	trans	chr6	rs1977198	2	26466225	0.48	rs1977198	26466225	0.48	0	1.00	1.0×10^{-6}	4.4×10^{-4}
20	trans	chr6	rs13207327	1	168712643	0.23	rs13207327	168712643	0.23	0	1.00	8.0×10^{-6}	2.8×10^{-2}
24	trans	chr6	rs6917521	1	170350612	0.26	rs6917521	170350612	0.26	0	1.00	7.0×10^{-6}	8.3×10^{-1}
25	trans	chr8	rs11996339	3	29330180	0.46	rs11996339	29330180	0.46	0	1.00	8.0×10^{-6}	3.3×10^{-1}
27	trans	chr8	rs6471522	7	96202974	0.22	rs6471522	96202974	0.22	0	1.00	8.0×10^{-6}	5.5×10^{-1}
28	trans	chr10	rs196305	12	121377463	0.30	rs196305	121377463	0.30	0	1.00	9.0×10^{-6}	8.8×10^{-1}
29	trans	chr12	rs1500066	9	33123050	0.13	rs1500066	33123050	0.13	0	1.00	1.0×10^{-5}	1.8×10^{-1}
32	trans	chr13	rs7350672	2	70665192	0.18	rs7350672	70665192	0.18	0	1.00	6.0×10^{-7}	1.1×10^{-1}
42	trans	chr14	rs1872159	5	22947903	0.19	rs1872159	22947903	0.19	0	1.00	9.0×10^{-6}	8.9×10^{-1}
43	trans	chr15	rs6496209	1	97627184	0.42	rs6496209	97627184	0.42	0	1.00	1.0×10^{-5}	8.9×10^{-1}
44	trans	chr20	rs6089532	1	60442047	0.44	rs6089532	60442047	0.44	0	1.00	7.0×10^{-6}	8.9×10^{-1}
45	trans	chr21	rs3827232	1	43867059	0.25	rs3827232	43867059	0.25	0	1.00	1.0×10^{-5}	3.4×10^{-1}

Schizophrenia Gene 24
KCNK12: potassium channel, subfamily K, member 12
Gene Location: chr2:47747914-47797470
GWAS Data: McCarroll 2012
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 2.1×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
8	trans	chr1	rs12042444	1	73988149	0.41	rs12042444	73988149	0.41	0	1.00	7.9×10^{-6}	1.0×10^{-5}
11	trans	chr5	rs17805650	1	11490932	0.11	rs17805650	11490932	0.11	0	1.00	5.0×10^{-6}	1.2×10^{-1}
13	trans	chr5	rs3935014	1	38422991	0.14	rs3935014	38422991	0.14	0	1.00	2.0×10^{-6}	6.3×10^{-1}
14	trans	chr6	rs9478496	1	154333183	0.12	rs9478496	154333183	0.12	0	1.00	6.7×10^{-6}	9.7×10^{-1}
21	trans	chr7	rs4730472	1	110610696	0.47	rs4730472	110610696	0.47	0	1.00	8.1×10^{-7}	7.4×10^{-4}
29	trans	chr7	rs982256	1	110904226	0.45	rs982256	110904226	0.45	0	1.00	3.9×10^{-6}	1.5×10^{-11}
33	trans	chr10	rs1262016	1	79951957	0.13	rs1262016	79951957	0.13	0	1.00	7.6×10^{-6}	1.4×10^{-1}
35	trans	chr11	rs907606	1	1857112	0.31	rs907606	1857112	0.31	0	1.00	3.6×10^{-6}	8.6×10^{-1}
42	trans	chr17	rs9898020	1	53057715	0.41	rs9898020	53057715	0.41	0	1.00	1.5×10^{-6}	3.2×10^{-1}
43	trans	chr22	rs5750597	1	38741793	0.24	rs5750597	38741793	0.24	0	1.00	8.4×10^{-6}	3.2×10^{-1}

Schizophrenia Gene 25
AK2: adenylate kinase 2
Gene Location: chr1:33473540-33502512
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 8.8×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	cis	chr1	rs2358521	2	34381854	0.44	rs2358521	34381854	0.44	0	1.00	7.3×10^{-6}	1.9×10^{-1}
4	trans	chr1	rs199930	110	181741301	0.21	rs199930	181741301	0.21	0	1.00	5.0×10^{-7}	8.9×10^{-2}
6	trans	chr2	rs1818595	3	13168232	0.42	rs1818595	13168232	0.42	0	1.00	9.9×10^{-6}	8.4×10^{-1}
7	trans	chr2	rs2278754	88	46583187	0.25	rs2278754	46583187	0.25	0	1.00	1.0×10^{-5}	2.8×10^{-1}
8	trans	chr2	rs843212	2	156467786	0.29	rs843212	156467786	0.29	0	1.00	8.1×10^{-6}	1.9×10^{-1}
9	trans	chr2	rs1031808	134	157591413	0.25	rs1031808	157591413	0.25	0	1.00	5.0×10^{-6}	2.8×10^{-1}
10	trans	chr3	rs6804571	4	7136588	0.44	rs6804571	7136588	0.44	0	1.00	4.8×10^{-6}	7.3×10^{-2}
11	trans	chr3	rs6770632	14	8793724	0.23	rs6770632	8793724	0.23	0	1.00	1.0×10^{-5}	9.9×10^{-1}
12	trans	chr3	rs9843848	90	70647563	0.32	rs9843848	70647563	0.32	0	1.00	4.6×10^{-6}	1.2×10^{-1}
13	trans	chr3	rs4682479	1	112974641	0.26	rs4682479	112974641	0.26	0	1.00	8.6×10^{-6}	2.7×10^{-1}
14	trans	chr4	rs13121153	2	17104059	0.48	rs13121153	17104059	0.48	0	1.00	6.6×10^{-6}	4.0×10^{-1}
15	trans	chr4	rs12643250	15	40262582	0.37	rs12643250	40262582	0.37	0	1.00	1.0×10^{-5}	7.3×10^{-1}
16	trans	chr4	rs4861597	1	184931818	0.43	rs4861597	184931818	0.43	0	1.00	9.1×10^{-6}	9.2×10^{-1}
17	trans	chr5	rs254670	2	157232642	0.31	rs254670	157232642	0.31	0	1.00	1.4×10^{-6}	9.8×10^{-2}
20	trans	chr6	rs2025317	1	65556355	0.23	rs2025317	65556355	0.23	0	1.00	7.3×10^{-6}	5.9×10^{-1}
22	trans	chr7	rs1011559	3	20703948	0.15	rs1011559	20703948	0.15	0	1.00	1.7×10^{-6}	8.7×10^{-1}
23	trans	chr7	rs6973950	16	76941830	0.50	rs6973950	76941830	0.50	0	1.00	8.0×10^{-6}	2.7×10^{-1}
24	trans	chr7	rs4730529	27	111976914	0.35	rs4730529	111976914	0.35	0	1.00	3.1×10^{-6}	5.2×10^{-1}
25	trans	chr8	rs4320511	1	10870605	0.45	rs4320511	10870605	0.45	0	1.00	9.9×10^{-6}	7.5×10^{-2}
29	trans	chr9	rs1359095	7	10276100	0.46	rs1359095	10276100	0.46	0	1.00	7.7×10^{-8}	1.1×10^{-3}
30	trans	chr9	rs608895	3	127809723	0.30	rs608895	127809723	0.30	0	1.00	5.9×10^{-6}	4.3×10^{-1}
31	trans	chr10	rs12252294	2	125578734	0.27	rs12252294	125578734	0.27	0	1.00	9.0×10^{-7}	8.8×10^{-3}
32	trans	chr11	rs12365860	8	56381507	0.39	rs12365860	56381507	0.39	0	1.00	4.4×10^{-6}	3.0×10^{-1}
34	trans	chr14	rs10132292	5	37153185	0.39	rs10132292	37153185	0.39	0	1.00	1.8×10^{-6}	7.5×10^{-3}
36	trans	chr14	rs17092615	4	95973619	0.06	rs17092615	95973619	0.06	0	1.00	9.8×10^{-6}	3.3×10^{-1}
38	trans	chr16	rs1424203	22	60798217	0.29	rs1424203	60798217	0.29	0	1.00	1.0×10^{-6}	6.2×10^{-1}
39	trans	chr17	rs11869775	1	13234204	0.14	rs11869775	13234204	0.14	0	1.00	7.4×10^{-6}	1.8×10^{-1}
40	trans	chr20	rs7272481	42	19162559	0.10	rs7272481	19162559	0.10	0	1.00	5.4×10^{-6}	4.0×10^{-1}

Schizophrenia Gene 25
AK2: adenylate kinase 2
Gene Location: chr1:33473540-33502512
GWAS Data: McCarroll 2012
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 2.7×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs657359	32	14513609	0.20	rs657359	14513609	0.20	0	1.00	2.0×10^{-6}	8.5×10^{-1}
3	trans	chr1	rs4320729	2	24409191	0.30	rs4320729	24409191	0.30	0	1.00	2.3×10^{-6}	7.2×10^{-2}
5	trans	chr1	rs17369712	1	42862409	0.20	rs17369712	42862409	0.20	0	1.00	6.9×10^{-6}	2.4×10^{-3}
6	trans	chr1	rs606149	18	193921548	0.43	rs606149	193921548	0.43	0	1.00	5.9×10^{-6}	2.6×10^{-1}
8	trans	chr2	rs10498184	1	226220594	0.20	rs10498184	226220594	0.20	0	1.00	2.1×10^{-6}	5.5×10^{-1}
10	trans	chr4	rs4334819	1	6431416	0.22	rs4334819	6431416	0.22	0	1.00	4.4×10^{-6}	5.2×10^{-2}
11	trans	chr4	rs12641486	12	96725419	0.37	rs12641486	96725419	0.37	0	1.00	8.5×10^{-6}	1.5×10^{-1}
12	trans	chr6	rs199245	1	143337546	0.38	rs199245	143337546	0.38	0	1.00	8.0×10^{-6}	1.7×10^{-3}
13	trans	chr10	rs11005041	1	57576058	0.39	rs11005041	57576058	0.39	0	1.00	8.1×10^{-6}	1.9×10^{-1}
14	trans	chr15	rs8038785	4	39703982	0.34	rs8038785	39703982	0.34	0	1.00	3.8×10^{-6}	4.5×10^{-1}
15	trans	chr19	rs2386983	3	48549948	0.22	rs2386983	48549948	0.22	0	1.00	3.8×10^{-6}	5.5×10^{-1}

Schizophrenia Gene 25
AK2: adenylate kinase 2
Gene Location: chr1:33473540-33502512
GWAS Data: McCarroll 2012
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 9.0×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
3	trans	chr1	rs10799316	6	225668031	0.29	rs10799316	225668031	0.29	0	1.00	6.6×10^{-7}	6.8×10^{-1}
7	trans	chr3	rs787187	40	120030677	0.08	rs787187	120030677	0.08	0	1.00	1.5×10^{-6}	9.8×10^{-1}
8	trans	chr6	rs10456479	6	12244847	0.20	rs10456479	12244847	0.20	0	1.00	6.6×10^{-6}	9.9×10^{-1}
9	trans	chr6	rs1044670	3	56891979	0.06	rs1044670	56891979	0.06	0	1.00	3.5×10^{-6}	8.5×10^{-3}
14	trans	chr9	rs950349	68	32191134	0.04	rs950349	32191134	0.04	0	1.00	8.0×10^{-6}	2.2×10^{-1}
15	trans	chr10	rs17668159	28	101998830	0.08	rs7923115	102000220	0.07	1390	1.00	1.3×10^{-6}	7.0×10^{-3}
17	trans	chr11	rs1791847	3	21215845	0.21	rs1791847	21215845	0.21	0	1.00	3.8×10^{-6}	4.3×10^{-1}
21	trans	chr14	rs4904547	4	89794530	0.37	rs4904547	89794530	0.37	0	1.00	9.9×10^{-6}	9.6×10^{-1}
26	trans	chr18	rs16951170	45	47402488	0.09	rs645644	47402589	0.10	101	NA	9.9×10^{-6}	3.8×10^{-1}
27	trans	chr18	rs9646596	28	53049212	0.08	rs17510124	53068680	0.01	19468	0.95	7.4×10^{-6}	8.3×10^{-6}

Schizophrenia Gene 25
AK2: adenylate kinase 2
Gene Location: chr1:33473540-33502512
GWAS Data: McCarroll 2012
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 3.7×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs4657374	1	164760618	0.25	rs4657374	164760618	0.25	0	1.00	4.0×10^{-6}	3.9×10^{-3}
5	trans	chr2	rs4852929	4	69930569	0.23	rs4852929	69930569	0.23	0	1.00	5.7×10^{-6}	2.7×10^{-2}
13	trans	chr4	rs4863588	1	139619389	0.31	rs4863588	139619389	0.31	0	1.00	7.6×10^{-6}	9.6×10^{-1}
16	trans	chr8	rs11786333	2	4969414	0.07	rs11786333	4969414	0.07	0	1.00	6.6×10^{-6}	6.3×10^{-2}
17	trans	chr8	rs3105764	1	118734726	0.27	rs3105764	118734726	0.27	0	1.00	2.8×10^{-6}	3.7×10^{-1}
21	trans	chr9	rs4741428	3	14762247	0.08	rs10124839	14761260	0.08	987	0.98	6.5×10^{-7}	4.5×10^{-1}
25	trans	chr9	rs4877686	1	84765612	0.44	rs4877686	84765612	0.44	0	1.00	3.4×10^{-6}	2.0×10^{-5}
31	trans	chr9	rs2993516	1	84971118	0.38	rs2993516	84971118	0.38	0	1.00	4.4×10^{-6}	2.6×10^{-5}
33	trans	chr12	rs11058587	1	122646871	0.45	rs11058587	122646871	0.45	0	1.00	2.1×10^{-6}	2.8×10^{-3}
36	trans	chr16	rs3851706	3	15950647	0.32	rs3851706	15950647	0.32	0	1.00	9.6×10^{-6}	3.2×10^{-1}
37	trans	chr16	rs1991053	1	75788840	0.44	rs1991053	75788840	0.44	0	1.00	8.1×10^{-6}	5.1×10^{-1}
42	trans	chr18	rs9966702	6	59933157	0.38	rs9966702	59933157	0.38	0	1.00	9.9×10^{-7}	1.8×10^{-1}
45	trans	chr19	rs2239986	1	58231807	0.28	rs2239986	58231807	0.28	0	1.00	6.6×10^{-6}	5.1×10^{-2}

Schizophrenia Gene 26
BLK: B lymphoid tyrosine kinase
Gene Location: chr8:11351520-11422108
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 1.2×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs1016449	1	60156189	0.07	rs1016449	60156189	0.07	0	1.00	3.8×10^{-6}	4.1×10^{-1}
2	trans	chr4	rs2702385	1	179383805	0.22	rs2702385	179383805	0.22	0	1.00	1.8×10^{-6}	3.7×10^{-2}
3	trans	chr6	rs9296925	1	14134083	0.43	rs9296925	14134083	0.43	0	1.00	8.8×10^{-6}	3.1×10^{-1}
4	trans	chr6	rs17546195	1	68388068	0.07	rs17546195	68388068	0.07	0	1.00	6.4×10^{-6}	5.8×10^{-2}
5	trans	chr6	rs17519592	1	104875332	0.13	rs17519592	104875332	0.13	0	1.00	7.6×10^{-6}	4.7×10^{-1}
7	trans	chr6	rs2782573	1	119352714	0.34	rs2782573	119352714	0.34	0	1.00	8.8×10^{-6}	1.5×10^{-1}
8	trans	chr6	rs12173761	1	138623227	0.23	rs12173761	138623227	0.23	0	1.00	7.8×10^{-6}	8.1×10^{-1}
9	trans	chr6	rs10223845	2	164667149	0.14	rs10223845	164667149	0.14	0	1.00	3.5×10^{-7}	6.7×10^{-1}
10	trans	chr8	rs2980437	2	8094763	0.50	rs2980437	8094763	0.50	0	1.00	2.8×10^{-6}	9.1×10^{-6}
34	trans	chr8	rs4840426	1	9408978	0.47	rs4840426	9408978	0.47	0	1.00	9.1×10^{-6}	3.0×10^{-4}
44	cis	chr8	rs4841401	1	10489592	0.45	rs4841401	10489592	0.45	0	1.00	5.8×10^{-6}	8.6×10^{-2}
54	cis	chr8	rs17725480	1	11009317	0.16	rs17725480	11009317	0.16	0	1.00	3.5×10^{-8}	1.6×10^{-1}
98	cis	chr8	rs2736340	1	11343973	0.37	rs2736340	11343973	0.37	0	1.00	2.1×10^{-23}	4.4×10^{-2}
111	trans	chr8	rs10086626	2	130480381	0.24	rs10086626	130480381	0.24	0	1.00	2.3×10^{-6}	7.8×10^{-1}
113	trans	chr11	rs947916	3	123514821	0.17	rs947916	123514821	0.17	0	1.00	8.0×10^{-6}	6.0×10^{-1}
116	trans	chr12	rs10841840	1	21673513	0.20	rs10841840	21673513	0.20	0	1.00	4.4×10^{-7}	9.5×10^{-1}
117	trans	chr13	rs7981035	1	61124261	0.42	rs7981035	61124261	0.42	0	1.00	3.9×10^{-6}	8.7×10^{-1}
118	trans	chr22	rs9620595	1	26634750	0.13	rs9620595	26634750	0.13	0	1.00	8.2×10^{-6}	6.0×10^{-2}

Schizophrenia Gene 26
BLK: B lymphoid tyrosine kinase
Gene Location: chr8:11351520-11422108
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 4.1×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs6662274	2	107919366	0.49	rs6662274	107919366	0.49	0	1.00	1.0×10^{-5}	5.9×10^{-2}
2	trans	chr1	rs2317955	1	158315924	0.19	rs2317955	158315924	0.19	0	1.00	6.8×10^{-6}	5.3×10^{-1}
3	trans	chr1	rs7527281	325	217203091	0.29	rs7527281	217203091	0.29	0	1.00	6.3×10^{-7}	2.2×10^{-2}
4	trans	chr2	rs6736061	2	124755681	0.07	rs6736061	124755681	0.07	0	1.00	1.0×10^{-5}	1.2×10^{-1}
5	trans	chr3	rs10440120	2	12486964	0.28	rs10440120	12486964	0.28	0	1.00	5.9×10^{-8}	8.5×10^{-1}
6	trans	chr3	rs2720930	5	194789032	0.32	rs2720930	194789032	0.32	0	1.00	2.5×10^{-6}	3.0×10^{-2}
7	trans	chr7	rs6943558	1	12068095	0.17	rs6943558	12068095	0.17	0	1.00	5.1×10^{-6}	9.3×10^{-1}
8	trans	chr7	rs848013	1	12429488	0.47	rs848013	12429488	0.47	0	1.00	4.8×10^{-6}	2.0×10^{-1}
9	trans	chr7	rs2952763	1	52162898	0.46	rs2952763	52162898	0.46	0	1.00	1.2×10^{-6}	4.2×10^{-1}
13	trans	chr7	rs7789655	1	86481013	0.24	rs7789655	86481013	0.24	0	1.00	1.6×10^{-6}	1.3×10^{-4}
14	trans	chr8	rs2955587	1	8098079	0.41	rs2955587	8098079	0.41	0	1.00	7.7×10^{-8}	4.7×10^{-6}
38	trans	chr8	rs1994020	1	9038596	0.48	rs1994020	9038596	0.48	0	1.00	1.1×10^{-6}	1.5×10^{-3}
43	trans	chr8	rs10100760	1	9370559	0.37	rs10100760	9370559	0.37	0	1.00	7.6×10^{-6}	2.2×10^{-4}
44	trans	chr8	rs7015700	1	9527707	0.26	rs7015700	9527707	0.26	0	1.00	2.4×10^{-9}	4.2×10^{-2}
48	trans	chr8	rs1962448	1	9871971	0.21	rs1962448	9871971	0.21	0	1.00	2.7×10^{-6}	1.3×10^{-1}
53	trans	chr8	rs10903321	1	10069485	0.18	rs10903321	10069485	0.18	0	1.00	1.9×10^{-6}	3.8×10^{-2}
58	trans	chr8	rs14879	1	10286273	0.44	rs14879	10286273	0.44	0	1.00	9.9×10^{-6}	4.1×10^{-2}
64	cis	chr8	rs7816990	1	10463944	0.43	rs7816990	10463944	0.43	0	1.00	3.0×10^{-4}	2.3×10^{-2}
70	cis	chr8	rs6987083	1	10764045	0.14	rs6987083	10764045	0.14	0	1.00	4.5×10^{-7}	2.3×10^{-2}
84	cis	chr8	rs10100449	1	10899288	0.36	rs10100449	10899288	0.36	0	1.00	3.0×10^{-5}	8.2×10^{-2}
127	cis	chr8	rs4840568	1	11351019	0.44	rs4840568	11351019	0.44	0	1.00	8.9×10^{-27}	5.2×10^{-2}
144	cis	chr8	rs11784941	1	11486220	0.15	rs11784941	11486220	0.15	0	1.00	1.4×10^{-5}	9.5×10^{-1}
154	cis	chr8	rs904015	1	11646934	0.31	rs904015	11646934	0.31	0	1.00	3.0×10^{-5}	5.4×10^{-2}
163	cis	chr8	rs1132195	1	11850995	0.42	rs1132195	11850995	0.42	0	1.00	7.9×10^{-6}	5.3×10^{-3}
167	trans	chr13	rs17326684	18	22769539	0.18	rs17326684	22769539	0.18	0	1.00	1.9×10^{-6}	2.3×10^{-2}
168	trans	chr13	rs1998960	2	90280540	0.29	rs1998960	90280540	0.29	0	1.00	9.9×10^{-6}	3.3×10^{-1}
169	trans	chr14	rs2241441	1	79175334	0.44	rs2241441	79175334	0.44	0	1.00	3.2×10^{-6}	6.1×10^{-1}
173	trans	chr15	rs1050931	1	55497691	0.26	rs1050931	55497691	0.26	0	1.00	3.5×10^{-6}	1.4×10^{-1}
174	trans	chr15	rs10852164	1	92498444	0.34	rs10852164	92498444	0.34	0	1.00	1.0×10^{-5}	3.2×10^{-1}

Schizophrenia Gene 27
HFM1: HFM1, ATP-dependent DNA helicase homolog (S. cerevisiae)
Gene Location: chr1:91726322-91870426
GWAS Data: McCarroll 2012
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 4.8×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs1441855	1	108441113	0.12	rs1441855	108441113	0.12	0	1.00	8.0×10^{-6}	2.1×10^{-1}
2	trans	chr3	rs6442180	1	10588012	0.49	rs6442180	10588012	0.49	0	1.00	2.6×10^{-7}	3.4×10^{-3}
3	trans	chr3	rs3844291	1	52341215	0.31	rs3844291	52341215	0.31	0	1.00	8.7×10^{-6}	3.2×10^{-6}
5	trans	chr3	rs2071506	1	52826276	0.44	rs2071506	52826276	0.44	0	1.00	9.5×10^{-6}	3.0×10^{-7}
6	trans	chr16	rs11643520	1	24531718	0.05	rs11643520	24531718	0.05	0	1.00	5.3×10^{-6}	7.5×10^{-1}
7	trans	chr17	rs12450102	1	76248280	0.19	rs12450102	76248280	0.19	0	1.00	2.5×10^{-6}	4.7×10^{-1}

Schizophrenia Gene 28
LACTB2: lactamase, beta 2
Gene Location: chr8:71549500-71581447
GWAS Data: McCarroll 2012
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 5.0×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr4	rs6825268	3	26783453	0.42	rs6825268	26783453	0.42	0	1.00	1.0×10^{-5}	4.2×10^{-6}
2	trans	chr17	rs17588651	11	49881185	0.15	rs17588651	49881185	0.15	0	1.00	1.0×10^{-5}	2.0×10^{-3}

Schizophrenia Gene 29
ITIH4: inter-alpha-trypsin inhibitor heavy chain family, member 4
Gene Location: chr3:52847005-52864717
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 5.0×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs735881	23	75642987	0.22	rs735881	75642987	0.22	0	1.00	7.2×10^{-6}	3.4×10^{-1}
2	cis	chr3	rs352143	1	52264907	0.19	rs352143	52264907	0.19	0	1.00	6.0×10^{-4}	7.4×10^{-1}
4	cis	chr3	rs731831	1	52536514	0.30	rs731831	52536514	0.30	0	1.00	7.0×10^{-4}	1.9×10^{-6}
38	cis	chr3	rs1573815	1	52870132	0.27	rs1573815	52870132	0.27	0	1.00	1.9×10^{-9}	7.0×10^{-8}
60	trans	chr5	rs745878	2	105421213	0.29	rs745878	105421213	0.29	0	1.00	9.2×10^{-6}	8.3×10^{-1}
61	trans	chr7	rs7807424	1	20520093	0.14	rs7807424	20520093	0.14	0	1.00	9.4×10^{-6}	7.3×10^{-2}
62	trans	chr7	rs39036	240	89104422	0.26	rs39036	89104422	0.26	0	1.00	3.6×10^{-7}	1.5×10^{-1}
63	trans	chr10	rs1227086	49	73447555	0.27	rs1227086	73447555	0.27	0	1.00	3.0×10^{-6}	9.3×10^{-1}
64	trans	chr17	rs178853	1	29767195	0.36	rs178853	29767195	0.36	0	1.00	4.0×10^{-6}	8.2×10^{-2}

Schizophrenia Gene 30
CDK2AP1: cyclin-dependent kinase 2 associated protein 1
Gene Location: chr12:123745539-123756687
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 6.4×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs1377387	16	130221208	0.16	rs1377387	130221208	0.16	0	1.00	6.3×10^{-7}	4.9×10^{-1}
3	trans	chr5	rs11948763	3	28711056	0.11	rs11948763	28711056	0.11	0	1.00	9.8×10^{-7}	5.9×10^{-3}
5	trans	chr12	rs1997401	25	80589275	0.37	rs1997401	80589275	0.37	0	1.00	2.1×10^{-6}	1.5×10^{-1}
6	cis	chr12	rs940904	2	123491572	0.26	rs940904	123491572	0.26	0	1.00	8.0×10^{-4}	1.1×10^{-6}
10	cis	chr12	rs1727324	1	123698603	0.25	rs1727324	123698603	0.25	0	1.00	2.0×10^{-5}	7.6×10^{-6}

Schizophrenia Gene 30
CDK2AP1: cyclin-dependent kinase 2 associated protein 1
Gene Location: chr12:123745539-123756687
GWAS Data: McCarroll 2012
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 1.6×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr8	rs4386964	2	67395905	0.22	rs4386964	67395905	0.22	0	1.00	4.6×10^{-6}	9.5×10^{-1}
3	cis	chr12	rs7296418	1	123457619	0.33	rs7296418	123457619	0.33	0	1.00	2.4×10^{-9}	1.1×10^{-5}
21	cis	chr12	rs2695478	1	123689521	0.12	rs2695478	123689521	0.12	0	1.00	5.8×10^{-14}	7.3×10^{-6}

Schizophrenia Gene 31
MPHOSPH9: M-phase phosphoprotein 9
Gene Location: chr12:123640945-123706442
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 6.6×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs2602951	1	77791025	0.12	rs2602951	77791025	0.12	0	1.00	5.7×10^{-6}	4.3×10^{-1}
3	trans	chr3	rs4955646	1	169118180	0.15	rs4955646	169118180	0.15	0	1.00	7.4×10^{-6}	3.3×10^{-2}
4	cis	chr12	rs4275659	1	123447928	0.49	rs4275659	123447928	0.49	0	1.00	1.2×10^{-9}	9.3×10^{-6}
8	cis	chr12	rs1790116	1	123618544	0.36	rs1790116	123618544	0.36	0	1.00	3.0×10^{-16}	1.0×10^{-6}
27	trans	chr17	rs1019113	1	32548821	0.09	rs1019113	32548821	0.09	0	1.00	3.3×10^{-6}	5.0×10^{-1}

Schizophrenia Gene 31

MPHOSPH9: M-phase phosphoprotein 9
Gene Location: chr12:123640945-123706442
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 8.7×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs7555815	4	14603198	0.31	rs7555815	14603198	0.31	0	1.00	7.4×10^{-6}	7.8×10^{-1}
2	trans	chr2	rs2278754	88	46583187	0.25	rs2278754	46583187	0.25	0	1.00	1.7×10^{-8}	2.8×10^{-1}
3	trans	chr3	rs1881354	8	10958228	0.49	rs1881354	10958228	0.49	0	1.00	9.1×10^{-6}	9.7×10^{-1}
4	trans	chr3	rs4287886	687	29422762	0.42	rs4287886	29422762	0.42	0	1.00	1.3×10^{-6}	8.5×10^{-2}
5	trans	chr3	rs9817104	7	70624977	0.19	rs9817104	70624977	0.19	0	1.00	3.7×10^{-6}	5.3×10^{-1}
6	trans	chr6	rs652720	125	149540264	0.40	rs652720	149540264	0.40	0	1.00	7.4×10^{-6}	8.8×10^{-1}
7	trans	chr7	rs10254616	16	150565220	0.38	rs10254616	150565220	0.38	0	1.00	6.3×10^{-6}	6.9×10^{-1}
8	trans	chr9	rs1042486	69	126783433	0.37	rs1042486	126783433	0.37	0	1.00	7.6×10^{-6}	8.3×10^{-1}
11	cis	chr12	rs940904	2	123491572	0.26	rs940904	123491572	0.26	0	1.00	6.0×10^{-4}	1.1×10^{-6}
27	cis	chr12	rs1716160	1	123700225	0.37	rs1716160	123700225	0.37	0	1.00	7.0×10^{-5}	5.7×10^{-7}
31	cis	chr12	rs1716382	1	124624465	0.28	rs1716382	124624465	0.28	0	1.00	3.0×10^{-4}	3.9×10^{-1}
32	trans	chr13	rs9543238	27	73720118	0.48	rs9543238	73720118	0.48	0	1.00	6.2×10^{-6}	3.7×10^{-1}
33	trans	chr14	rs10140426	1	100376502	0.39	rs10140426	100376502	0.39	0	1.00	7.7×10^{-6}	2.4×10^{-2}
34	trans	chr17	rs1008620	8	70362790	0.17	rs1008620	70362790	0.17	0	1.00	8.8×10^{-7}	5.7×10^{-1}

Schizophrenia Gene 32

MUSTN1: musculoskeletal, embryonic nuclear protein 1
Gene Location: chr3:52867130-52869318
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 7.7×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs17660531	1	76547750	0.11	rs17660531	76547750	0.11	0	1.00	6.7×10^{-7}	7.1×10^{-1}
3	trans	chr1	rs4655438	3	216153094	0.34	rs4655438	216153094	0.34	0	1.00	7.8×10^{-6}	3.7×10^{-3}
4	cis	chr3	rs353547	1	52268866	0.37	rs353547	52268866	0.37	0	1.00	7.2×10^{-6}	1.0×10^{-6}
14	cis	chr3	rs2256332	1	52855865	0.49	rs2256332	52855865	0.49	0	1.00	8.0×10^{-11}	1.2×10^{-7}
21	cis	chr3	rs35671032	1	53006055	0.20	rs35671032	53006055	0.20	0	1.00	2.0×10^{-6}	7.6×10^{-2}
27	cis	chr3	rs2230493	1	53213657	0.10	rs2230493	53213657	0.10	0	1.00	5.2×10^{-6}	6.7×10^{-1}
30	trans	chr12	rs7970335	2	115561804	0.33	rs7970335	115561804	0.33	0	1.00	6.7×10^{-6}	3.8×10^{-1}
31	trans	chr15	rs12911496	8	62080200	0.33	rs12911496	62080200	0.33	0	1.00	7.8×10^{-6}	1.3×10^{-2}
32	trans	chr21	rs9305628	1	39244991	0.15	rs9305628	39244991	0.15	0	1.00	1.1×10^{-6}	2.9×10^{-1}

Schizophrenia Gene 33

NARF: nuclear prelamin A recognition factor
Gene Location: chr17:80416539-80446143
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 5.1×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
3	trans	chr10	rs12573122	17	6738313	0.13	rs12573122	6738313	0.13	0	1.00	4.9×10^{-6}	7.5×10^{-1}
4	trans	chr11	rs10833177	3	19829331	0.41	rs10833177	19829331	0.41	0	1.00	8.5×10^{-6}	1.4×10^{-1}
5	trans	chr11	rs10894433	30	131616001	0.43	rs10894433	131616001	0.43	0	1.00	1.9×10^{-6}	2.8×10^{-1}
6	trans	chr14	rs10135277	16	35823231	0.49	rs10135277	35823231	0.49	0	1.00	7.3×10^{-6}	7.3×10^{-5}
14	cis	chr17	rs8081734	1	80448533	0.35	rs8081734	80448533	0.35	0	1.00	2.2×10^{-16}	2.7×10^{-1}

Schizophrenia Gene 33
NARF: nuclear prelamin A recognition factor
Gene Location: chr17:80416539-80446143
GWAS Data: McCarroll 2012
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 8.1×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr1	rs3010228	6	11404632	0.40	rs3010228	11404632	0.40	0	1.00	5.0×10^{-7}	5.8×10^{-1}
3	trans	chr2	rs13387382	1	12744519	0.20	rs13387382	12744519	0.20	0	1.00	1.0×10^{-5}	8.6×10^{-3}
17	trans	chr2	rs11125729	1	57975170	0.35	rs11125729	57975170	0.35	0	1.00	2.0×10^{-6}	2.7×10^{-6}
68	trans	chr2	rs2678905	1	58135872	0.32	rs2678905	58135872	0.32	0	1.00	3.0×10^{-7}	6.7×10^{-9}
101	trans	chr2	rs7585086	1	154072062	0.26	rs7585086	154072062	0.26	0	1.00	4.0×10^{-6}	2.0×10^{-1}
102	trans	chr4	rs2631266	8	102947157	0.18	rs2631266	102947157	0.18	0	1.00	1.0×10^{-5}	7.1×10^{-1}
108	trans	chr5	rs6451994	7	21756851	0.33	rs6451994	21756851	0.33	0	1.00	1.0×10^{-6}	2.7×10^{-2}
123	trans	chr6	rs9349374	1	46714598	0.18	rs9349374	46714598	0.18	0	1.00	5.0×10^{-7}	6.2×10^{-2}
134	trans	chr6	rs647942	9	48026377	0.37	rs647942	48026377	0.37	0	1.00	1.0×10^{-6}	1.6×10^{-1}
135	trans	chr13	rs7989073	3	32014980	0.09	rs7989073	32014980	0.09	0	1.00	8.0×10^{-6}	2.4×10^{-1}
137	trans	chr14	rs891297	1	21026773	0.31	rs891297	21026773	0.31	0	1.00	1.0×10^{-5}	2.2×10^{-2}
145	trans	chr15	rs7181181	1	86809025	0.43	rs7181181	86809025	0.43	0	1.00	5.0×10^{-7}	1.6×10^{-1}
149	trans	chr16	rs171593	1	11248371	0.32	rs171593	11248371	0.32	0	1.00	5.0×10^{-6}	9.3×10^{-1}
151	cis	chr17	rs7209788	1	80415914	0.40	rs7209788	80415914	0.40	0	1.00	8.0×10^{-5}	4.5×10^{-1}
154	trans	chr18	rs1542005	2	54555401	0.13	rs1542005	54555401	0.13	0	1.00	1.0×10^{-5}	2.7×10^{-1}

Schizophrenia Gene 34
GUCY1A2: guanylate cyclase 1, soluble, alpha 2
Gene Location: chr11:106557909-106889171
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 8.2×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
3	trans	chr2	rs696815	1	198688084	0.30	rs696815	198688084	0.30	0	1.00	4.6×10^{-7}	4.4×10^{-6}
8	trans	chr2	rs2196176	1	198904914	0.33	rs2196176	198904914	0.33	0	1.00	6.1×10^{-7}	8.3×10^{-6}

Schizophrenia Gene 35
LOC378135: Not Found in HUGO
Gene Location: Not Found:Not Found-Not Found
GWAS Data: McCarroll 2012
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 9.2×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr2	rs1922378	2	35289777	0.12	rs1922378	35289777	0.12	0	1.00	4.0×10^{-6}	3.1×10^{-1}
7	trans	chr7	rs10954689	1	82402373	0.42	rs10954689	82402373	0.42	0	1.00	1.3×10^{-8}	1.3×10^{-4}
13	trans	chr7	rs2888019	1	82503409	0.31	rs2888019	82503409	0.31	0	1.00	1.1×10^{-7}	1.2×10^{-4}
20	trans	chr11	rs7935732	1	81316876	0.28	rs7935732	81316876	0.28	0	1.00	4.2×10^{-6}	4.8×10^{-2}
22	trans	chr12	rs12308436	2	115051318	0.12	rs12308436	115051318	0.12	0	1.00	5.5×10^{-6}	1.5×10^{-1}
24	trans	chr22	rs134169	1	28612399	0.17	rs134169	28612399	0.17	0	1.00	6.2×10^{-6}	3.4×10^{-5}

Schizophrenia Gene 36
ARL6IP4: ADP-ribosylation-like factor 6 interacting protein 4
Gene Location: chr12:123464879-123467460
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 9.2×10^{-5}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr5	rs6449870	5	66799242	0.41	rs6449870	66799242	0.41	0	1.00	2.1×10^{-6}	2.6×10^{-1}
2	trans	chr5	rs6596572	3	103725070	0.46	rs6596572	103725070	0.46	0	1.00	8.2×10^{-6}	6.8×10^{-1}
3	trans	chr8	rs9643233	11	129322437	0.39	rs9643233	129322437	0.39	0	1.00	1.7×10^{-6}	3.3×10^{-1}
4	trans	chr12	rs7973596	1	7817772	0.12	rs7973596	7817772	0.12	0	1.00	3.0×10^{-6}	5.4×10^{-1}
9	cis	chr12	rs4758670	2	122785249	0.47	rs4758670	122785249	0.47	0	1.00	2.0×10^{-4}	2.2×10^{-3}
10	cis	chr12	rs7305511	1	123498253	0.49	rs7305511	123498253	0.49	0	1.00	6.2×10^{-6}	9.1×10^{-6}
18	cis	chr12	rs1568428	1	123738876	0.49	rs1568428	123738876	0.49	0	1.00	1.5×10^{-5}	1.4×10^{-5}
23	trans	chr15	rs4984473	4	96533457	0.48	rs4984473	96533457	0.48	0	1.00	9.5×10^{-6}	9.9×10^{-1}
24	trans	chr18	rs1812572	1	1218622	0.43	rs1812572	1218622	0.43	0	1.00	8.2×10^{-6}	7.8×10^{-1}
25	trans	chr18	rs2949535	8	27857785	0.21	rs2949535	27857785	0.21	0	1.00	9.3×10^{-6}	2.5×10^{-1}

Schizophrenia Gene 37
HLA-DQA2: major histocompatibility complex, class II, DQ alpha 2
Gene Location: chr6:32709162-32714664
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 1.9×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs946471	2	216943125	0.21	rs946471	216943125	0.21	0	1.00	7.2×10^{-6}	8.3×10^{-1}
5	trans	chr5	rs6897337	1	103337484	0.31	rs6897337	103337484	0.31	0	1.00	6.5×10^{-6}	2.7×10^{-1}
6	trans	chr6	rs4145940	1	3885152	0.42	rs4145940	3885152	0.42	0	1.00	2.3×10^{-6}	5.6×10^{-1}
7	trans	chr6	rs17695342	1	85730991	0.08	rs17695342	85730991	0.08	0	1.00	5.4×10^{-6}	5.5×10^{-2}
10	trans	chr7	rs3753098	1	26198040	0.30	rs3753098	26198040	0.30	0	1.00	3.5×10^{-6}	2.2×10^{-2}
11	trans	chr7	rs2236426	1	138764233	0.21	rs2236426	138764233	0.21	0	1.00	4.7×10^{-6}	3.8×10^{-1}
13	trans	chr8	rs1566084	1	142624215	0.42	rs1566084	142624215	0.42	0	1.00	1.2×10^{-6}	1.9×10^{-3}
19	trans	chr10	rs7916957	2	22862069	0.18	rs7916957	22862069	0.18	0	1.00	6.8×10^{-6}	3.8×10^{-2}
20	trans	chr12	rs2231700	3	69653146	0.39	rs2231700	69653146	0.39	0	1.00	5.9×10^{-10}	6.9×10^{-1}
32	trans	chr18	rs101940	1	44168254	0.29	rs101940	44168254	0.29	0	1.00	8.4×10^{-6}	1.9×10^{-3}

Schizophrenia Gene 37
HLA-DQA2: major histocompatibility complex, class II, DQ alpha 2
Gene Location: chr6:32709162-32714664
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 6.0×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs1522374	4	152235530	0.25	rs1522374	152235530	0.25	0	1.00	2.5×10^{-6}	2.0×10^{-2}

Schizophrenia Gene 37
HLA-DQA2: major histocompatibility complex, class II, DQ alpha 2
Gene Location: chr6:32709162-32714664
GWAS Data: McCarroll 2012
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 2.9×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs12026071	8	17560646	0.13	rs12026071	17560646	0.13	0	1.00	1.0×10^{-5}	8.0×10^{-1}
3	trans	chr1	rs1441834	2	30173101	0.36	rs1441834	30173101	0.36	0	1.00	6.0×10^{-6}	9.5×10^{-1}
4	trans	chr1	rs11811702	2	33350183	0.37	rs11811702	33350183	0.37	0	1.00	5.0×10^{-7}	2.5×10^{-2}
5	trans	chr1	rs4660811	2	45035549	0.17	rs4660811	45035549	0.17	0	1.00	1.0×10^{-7}	7.1×10^{-2}
8	trans	chr1	rs17130873	6	84562324	0.07	rs17130873	84562324	0.07	0	1.00	8.0×10^{-7}	9.0×10^{-1}
9	trans	chr1	rs562044	2	110374054	0.39	rs562044	110374054	0.39	0	1.00	1.0×10^{-5}	8.0×10^{-1}
10	trans	chr1	rs2993437	2	202193981	0.45	rs2993437	202193981	0.45	0	1.00	7.0×10^{-6}	4.7×10^{-1}
14	trans	chr1	rs17187561	2	208742013	0.08	rs17187561	208742013	0.08	0	1.00	6.0×10^{-7}	1.4×10^{-1}
16	trans	chr1	rs7527372	2	218287335	0.15	rs7527372	218287335	0.15	0	1.00	5.0×10^{-6}	1.4×10^{-1}
17	trans	chr1	rs1294327	3	233426676	0.41	rs1294327	233426676	0.41	0	1.00	5.0×10^{-6}	2.1×10^{-1}
18	trans	chr2	rs12468225	2	24922359	0.26	rs12468225	24922359	0.26	0	1.00	1.0×10^{-5}	4.2×10^{-1}
29	trans	chr2	rs1396733	2	28642747	0.40	rs1396733	28642747	0.40	0	1.00	1.0×10^{-6}	3.4×10^{-1}
31	trans	chr2	rs6749108	2	43496986	0.32	rs6749108	43496986	0.32	0	1.00	4.0×10^{-6}	7.8×10^{-1}
32	trans	chr2	rs13021135	2	115914096	0.42	rs13021135	115914096	0.42	0	1.00	1.0×10^{-5}	5.1×10^{-1}
33	trans	chr2	rs12477083	2	129042639	0.31	rs12477083	129042639	0.31	0	1.00	1.0×10^{-5}	9.6×10^{-1}
34	trans	chr2	rs4972488	2	176712969	0.16	rs4972488	176712969	0.16	0	1.00	1.0×10^{-5}	9.8×10^{-1}
62	trans	chr2	rs3816196	2	190640475	0.41	rs3816196	190640475	0.41	0	1.00	5.0×10^{-7}	7.9×10^{-2}
74	trans	chr3	rs2600228	2	12908510	0.49	rs2600228	12908510	0.49	0	1.00	6.0×10^{-6}	6.8×10^{-1}
76	trans	chr3	rs7429789	2	54339768	0.08	rs7429789	54339768	0.08	0	1.00	1.0×10^{-5}	1.3×10^{-1}
78	trans	chr3	rs2320879	2	70708646	0.20	rs2320879	70708646	0.20	0	1.00	1.0×10^{-6}	2.7×10^{-2}
79	trans	chr3	rs558917	2	74350297	0.47	rs558917	74350297	0.47	0	1.00	1.0×10^{-5}	2.5×10^{-1}
81	trans	chr3	rs2399250	2	108619666	0.30	rs2399250	108619666	0.30	0	1.00	1.0×10^{-6}	2.2×10^{-1}
83	trans	chr3	rs11711220	2	122679372	0.30	rs11711220	122679372	0.30	0	1.00	1.0×10^{-6}	9.8×10^{-1}
85	trans	chr3	rs1456680	2	147866568	0.24	rs1456680	147866568	0.24	0	1.00	1.0×10^{-5}	9.0×10^{-1}
86	trans	chr3	rs9878758	2	155053281	0.33	rs9878758	155053281	0.33	0	1.00	1.0×10^{-5}	7.0×10^{-1}
87	trans	chr4	rs10003471	2	92200866	0.08	rs10003471	92200866	0.08	0	1.00	3.0×10^{-6}	7.0×10^{-1}
89	trans	chr4	rs17013593	2	129593111	0.34	rs17013593	129593111	0.34	0	1.00	3.0×10^{-6}	7.8×10^{-1}
93	trans	chr4	rs1077094	2	159480698	0.25	rs1077094	159480698	0.25	0	1.00	1.0×10^{-5}	5.7×10^{-1}
96	trans	chr4	rs4690798	2	165926586	0.49	rs4690798	165926586	0.49	0	1.00	3.0×10^{-6}	1.4×10^{-1}
98	trans	chr4	rs11724690	2	186764747	0.21	rs11724690	186764747	0.21	0	1.00	3.0×10^{-6}	7.7×10^{-1}
100	trans	chr5	rs6899118	2	25795294	0.42	rs6899118	25795294	0.42	0	1.00	1.0×10^{-5}	5.4×10^{-1}
101	trans	chr5	rs10056342	2	133782662	0.30	rs10056342	133782662	0.30	0	1.00	7.0×10^{-7}	4.3×10^{-1}
104	trans	chr6	rs6936950	2	6910091	0.16	rs6936950	6910091	0.16	0	1.00	3.0×10^{-7}	7.6×10^{-1}
107	trans	chr6	rs9467714	10	26340785	0.20	rs9467714	26340785	0.20	0	1.00	1.0×10^{-6}	8.7×10^{-12}
151	trans	chr6	rs4714084	3	37585221	0.35	rs4714084	37585221	0.35	0	1.00	3.0×10^{-6}	3.0×10^{-1}
152	trans	chr6	rs7761797	2	127843293	0.21	rs7761797	127843293	0.21	0	1.00	1.0×10^{-5}	1.0×10^{-1}
153	trans	chr6	rs9478712	2	156858484	0.48	rs9478712	156858484	0.48	0	1.00	4.0×10^{-6}	2.0×10^{-1}
154	trans	chr7	rs2058430	2	2206110	0.41	rs2058430	2206110	0.41	0	1.00	1.0×10^{-5}	3.9×10^{-10}
156	trans	chr7	rs10261060	2	8556819	0.37	rs10261060	8556819	0.37	0	1.00	1.0×10^{-6}	4.5×10^{-1}
162	trans	chr7	rs7800834	2	9016752	0.47	rs7800834	9016752	0.47	0	1.00	7.0×10^{-6}	4.0×10^{-3}
163	trans	chr7	rs2717351	2	19019880	0.40	rs2717351	19019880	0.40	0	1.00	1.0×10^{-5}	2.6×10^{-1}
164	trans	chr7	rs2960632	2	52659243	0.47	rs2960632	52659243	0.47	0	1.00	6.0×10^{-6}	5.5×10^{-1}
165	trans	chr7	rs4718886	2	68898689	0.27	rs4718886	68898689	0.27	0	1.00	1.0×10^{-5}	1.2×10^{-1}
168	trans	chr7	rs11768402	2	95160853	0.16	rs11768402	95160853	0.16	0	1.00	4.0×10^{-6}	5.7×10^{-1}
170	trans	chr8	rs11574398	2	31025343	0.34	rs11574398	31025343	0.34	0	1.00	6.0×10^{-6}	9.4×10^{-2}
171	trans	chr8	rs7015004	3	40337012	0.11	rs7015004	40337012	0.11	0	1.00	1.0×10^{-5}	7.1×10^{-2}
172	trans	chr8	rs7817235	2	64524456	0.26	rs7817235	64524456	0.26	0	1.00	1.0×10^{-5}	7.5×10^{-4}
173	trans	chr8	rs12056881	4	140872156	0.36	rs12056881	140872156	0.36	0	1.00	4.0×10^{-6}	7.8×10^{-1}
175	trans	chr9	rs12553901	2	21868757	0.28	rs12553901	21868757	0.28	0	1.00	1.0×10^{-7}	3.7×10^{-1}
182	trans	chr9	rs12683669	2	28225331	0.24	rs12683669	28225331	0.24	0	1.00	3.0×10^{-6}	3.0×10^{-1}
184	trans	chr9	rs7029237	2	36530955	0.39	rs7029237	36530955	0.39	0	1.00	6.0×10^{-6}	3.1×10^{-2}
190	trans	chr9	rs4379560	2	94395743	0.25	rs4379560	94395743	0.25	0	1.00	3.0×10^{-7}	3.5×10^{-1}
193	trans	chr9	rs10124685	2	118152551	0.23	rs10124685	118152551	0.23	0	1.00	6.0×10^{-6}	1.5×10^{-2}
194	trans	chr10	rs6602250	2	7574766	0.43	rs6602250	7574766	0.43	0	1.00	1.0×10^{-5}	2.3×10^{-1}
196	trans	chr10	rs420512	2	30897544	0.43	rs420512	30897544	0.43	0	1.00	5.0×10^{-6}	7.0×10^{-1}
201	trans	chr10	rs12217983	2	62064858	0.25	rs12217983	62064858	0.25	0	1.00	4.0×10^{-6}	1.4×10^{-1}
203	trans	chr10	rs7090742	2	68375667	0.12	rs7090742	68375667	0.12	0	1.00	2.0×10^{-7}	2.4×10^{-1}
207	trans	chr10	rs12257526	2	87928843	0.22	rs12257526	87928843	0.22	0	1.00	8.0×10^{-7}	6.4×10^{-1}
209	trans	chr10	rs11197181	2	117115713	0.27	rs11197181	117115713	0.27	0	1.00	1.0×10^{-5}	3.7×10^{-2}
231	trans	chr10	rs2784812	2	117337716	0.43	rs2784812	117337716	0.43	0	1.00	3.0×10^{-6}	1.2×10^{-1}
256	trans	chr10	rs1926178	2	129592238	0.36	rs1926178	129592238	0.36	0	1.00	3.0×10^{-6}	6.3×10^{-1}
261	trans	chr10	rs12220782	2	131485205	0.34	rs12220782	131485205	0.34	0	1.00	1.0×10^{-5}	3.0×10^{-1}
262	trans	chr11	rs6578882	2	7599391	0.37	rs6578882	7599391	0.37	0	1.00	4.0×10^{-6}	7.8×10^{-1}
264	trans	chr11	rs2046715	2	38002138	0.18	rs2046715	38002138	0.18	0	1.00	9.0×10^{-7}	6.6×10^{-1}
290	trans	chr11	rs564404	2	58817625	0.40	rs564404	58817625	0.40	0	1.00	7.0×10^{-6}	1.7×10^{-1}
294	trans	chr11	rs604096	2	118475098	0.27	rs604096	118475098	0.27	0	1.00	1.0×10^{-7}	5.4×10^{-1}
297	trans	chr12	rs11836388	2	5813402	0.13	rs11836388	5813402	0.13	0	1.00	4.0×10^{-6}	8.0×10^{-1}
306	trans	chr12	rs7975434	2	16711116	0.22	rs7975434	16711116	0.22	0	1.00	6.0×10^{-7}	7.8×10^{-1}
307	trans	chr12	rs11615201	2	17396190	0.13	rs11615201	17396190	0.13	0	1.00	5.0×10^{-6}	1.4×10^{-1}
309	trans	chr12	rs256655	2	30949511	0.34	rs256655	30949511	0.34	0	1.00	1.0×10^{-5}	5.0×10^{-1}
310	trans	chr12	rs12307124	2	67627644	0.19	rs12307124	67627644	0.19	0	1.00	2.0×10^{-6}	1.4×10^{-1}
312	trans	chr13	rs7324017	2	47406845	0.25	rs7324017	47406845	0.25	0	1.00	1.0×10^{-5}	9.1×10^{-1}
313	trans	chr13	rs950725	2	92149352	0.45	rs950725	92149352	0.45	0	1.00	1.0×10^{-5}	8.9×10^{-1}
315	trans	chr13	rs2391642	2	109089806	0.49	rs2391642	109089806	0.49	0	1.00	1.0×10^{-5}	5.4×10^{-1}
316	trans	chr14	rs1885152	2	96325206	0.28	rs1885152	96325206	0.28	0	1.00	8.0×10^{-6}	7.6×10^{-1}
317	trans	chr15	rs2444961	2	33425360	0.49	rs2444961	33425360	0.49	0	1.00	4.0×10^{-6}	4.9×10^{-1}
318	trans	chr15	rs573441	2	35070865	0.42	rs573441	35070865	0.42	0	1.00	8.0×10^{-6}	3.1×10^{-1}
319	trans	chr15	rs12913899	2	77844635	0.48	rs12913899	77844635	0.48	0	1.00	5.0×10^{-6}	4.9×10^{-1}
320	trans	chr15	rs11635554	2	80858682	0.47	rs11635554	80858682	0.47	0	1.00	9.0×10^{-6}	7.9×10^{-1}
321	trans	chr15	rs7170502	2	93928380	0.32	rs7170502	93928380	0.32	0	1.00	4.0×10^{-6}	6.4×10^{-1}
322	trans	chr15	rs17626833	2	94210807	0.25	rs17626833	94210807	0.25	0	1.00	1.0×10^{-5}	4.8×10^{-1}
323	trans	chr16	rs12448497	2	13492184	0.39	rs12448497	13492184	0.39	0	1.00	2.0×10^{-6}	2.0×10^{-1}
324	trans	chr16	rs4624179	12	25779427	0.27	rs4624179	25779427	0.27	0	1.00	3.0×10^{-6}	8.7×10^{-1}
325	trans	chr16	rs9939450	2	28301487	0.42	rs9939450	28301487	0.42	0	1.00	8.0×10^{-6}	4.9×10^{-1}
329	trans	chr16	rs12716977	2	30482803	0.40	rs12716977	30482803	0.40	0	1.00	2.0×10^{-6}	1.6×10^{-2}
332	trans	chr17	rs2531851	2	9200415	0.32	rs2531851	9200415	0.32	0	1.00	5.0×10^{-6}	2.2×10^{-2}
335	trans	chr17	rs17619645	2	14291895	0.24	rs17619645	14291895	0.24	0	1.00	7.0×10^{-6}	2.5×10^{-2}
337	trans	chr17	rs1971154	2	74121442	0.29	rs1971154	74121442	0.29	0	1.00	2.0×10^{-6}	1.3×10^{-1}
341	trans	chr17	rs7222745	2	80907253	0.46	rs7222745	80907253	0.46	0	1.00	6.0×10^{-6}	8.7×10^{-1}
345	trans	chr18	rs2000698	2	35108655	0.39	rs2000698	35108655	0.39	0	1.00	1.0×10^{-5}	3.3×10^{-2}
346	trans	chr18	rs8091972	2	63924393	0.22	rs8091972	63924393	0.22	0	1.00	1.0×10^{-5}	4.4×10^{-1}

Schizophrenia Gene 37
HLA-DQA2: major histocompatibility complex, class II, DQ alpha 2
Gene Location: chr6:32709162-32714664
GWAS Data: McCarroll 2012
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 1.6×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr10	rs4290163	1	104610926	0.43	rs4290163	104610926	0.43	0	1.00	9.3×10^{-6}	6.7×10^{-8}
2	trans	chr11	rs513438	2	82967963	0.29	rs513438	82967963	0.29	0	1.00	3.9×10^{-7}	2.3×10^{-1}

Schizophrenia Gene 38
AS3MT: arsenic (+3 oxidation state) methyltransferase
Gene Location: chr10:104613966-104661655
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 4.4×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs284267	1	10656351	0.24	rs284267	10656351	0.24	0	1.00	2.6×10^{-6}	1.8×10^{-1}
2	trans	chr1	rs1517753	1	71838498	0.29	rs1517753	71838498	0.29	0	1.00	5.0×10^{-6}	1.8×10^{-1}
3	trans	chr3	rs744230	1	5126013	0.36	rs744230	5126013	0.36	0	1.00	1.3×10^{-6}	1.1×10^{-1}
6	trans	chr3	rs12631325	5	24241510	0.09	rs12631325	24241510	0.09	0	1.00	3.7×10^{-6}	6.5×10^{-1}
7	trans	chr5	rs10060454	1	30672798	0.04	rs10056722	30665766	0.04	7032	0.97	3.5×10^{-6}	1.5×10^{-1}
10	trans	chr6	rs4716037	1	16057517	0.32	rs4716037	16057517	0.32	0	1.00	4.3×10^{-6}	2.6×10^{-1}
11	trans	chr7	rs6943205	1	71179316	0.35	rs6943205	71179316	0.35	0	1.00	5.0×10^{-7}	9.2×10^{-1}
12	trans	chr7	rs10949778	4	155213122	0.07	rs10949778	155213122	0.07	0	1.00	6.2×10^{-8}	3.9×10^{-1}
14	trans	chr8	rs328092	2	26339139	0.08	rs328092	26339139	0.08	0	1.00	6.1×10^{-6}	2.5×10^{-1}
17	cis	chr10	rs7086205	1	104202729	0.13	rs7086205	104202729	0.13	0	1.00	2.0×10^{-11}	4.3×10^{-1}
43	cis	chr10	rs17784294	1	104479385	0.23	rs17784294	104479385	0.23	0	1.00	1.3×10^{-22}	2.0×10^{-1}
66	cis	chr10	rs4917985	1	104624072	0.42	rs4917985	104624072	0.42	0	1.00	1.4×10^{-44}	1.2×10^{-12}
96	cis	chr10	rs4917995	2	104845443	0.11	rs4917995	104845443	0.11	0	1.00	2.0×10^{-7}	2.0×10^{-1}
113	cis	chr10	rs1163072	1	105024378	0.38	rs1163072	105024378	0.38	0	1.00	5.5×10^{-6}	2.6×10^{-4}
114	cis	chr10	rs2986016	1	105215016	0.13	rs2986016	105215016	0.13	0	1.00	2.4×10^{-7}	1.2×10^{-1}
119	trans	chr11	rs17150147	2	55956773	0.10	rs17150147	55956773	0.10	0	1.00	2.6×10^{-6}	8.7×10^{-1}
122	trans	chr12	rs11062678	1	3592467	0.30	rs11062678	3592467	0.30	0	1.00	9.1×10^{-7}	7.3×10^{-1}
124	trans	chr14	rs926099	1	78737743	0.15	rs926099	78737743	0.15	0	1.00	6.5×10^{-6}	8.0×10^{-2}
126	trans	chr21	rs11911479	4	19541320	0.10	rs11911479	19541320	0.10	0	1.00	3.0×10^{-6}	8.3×10^{-1}
127	trans	chr21	rs2827188	1	23359814	0.14	rs2827188	23359814	0.14	0	1.00	7.9×10^{-6}	3.0×10^{-1}

Schizophrenia Gene 38
AS3MT: arsenic (+3 oxidation state) methyltransferase
Gene Location: chr10:104613966-104661655
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 2.3×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
10	cis	chr10	rs4919690	1	104616500	0.19	rs4919690	104616500	0.19	0	1.00	4.1×10^{-7}	2.1×10^{-4}
19	cis	chr10	rs11191487	1	104734623	0.09	rs11191487	104734623	0.09	0	1.00	1.1×10^{-4}	6.9×10^{-3}
44	trans	chr19	rs2290652	1	35175208	0.27	rs2290652	35175208	0.27	0	1.00	3.5×10^{-7}	8.9×10^{-1}

Schizophrenia Gene 38
AS3MT: arsenic (+3 oxidation state) methyltransferase
Gene Location: chr10:104613966-104661655
GWAS Data: McCarroll 2012
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 1.2×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr9	rs10962269	1	16074726	0.28	rs10962269	16074726	0.28	0	1.00	4.5×10^{-6}	5.9×10^{-1}
3	trans	chr11	rs11035429	6	39746931	0.48	rs11035429	39746931	0.48	0	1.00	5.0×10^{-6}	1.6×10^{-3}
5	trans	chr11	rs2581928	2	57202790	0.19	rs2581928	57202790	0.19	0	1.00	7.0×10^{-7}	8.1×10^{-3}

Schizophrenia Gene 39
HLA-DQA1: major histocompatibility complex, class II, DQ alpha 1
Gene Location: chr6:32605182-32611429
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 1.3×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr6	rs9393708	1	26362643	0.07	rs9393708	26362643	0.07	0	1.00	7.0×10^{-6}	2.6×10^{-12}
35	trans	chr6	rs658429	1	124803536	0.14	rs658429	124803536	0.14	0	1.00	9.8×10^{-6}	2.2×10^{-1}
36	trans	chr12	rs2160512	1	16519020	0.26	rs2160512	16519020	0.26	0	1.00	8.2×10^{-6}	3.2×10^{-1}
39	trans	chr12	rs2398486	1	130278402	0.28	rs2398486	130278402	0.28	0	1.00	2.0×10^{-6}	8.5×10^{-1}

Schizophrenia Gene 39
HLA-DQA1: major histocompatibility complex, class II, DQ alpha 1
Gene Location: chr6:32605182-32611429
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 9.6×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs1160305	3	234009231	0.40	rs1160305	234009231	0.40	0	1.00	3.7×10^{-7}	8.9×10^{-1}
2	trans	chr2	rs4832481	1	17122737	0.40	rs4832481	17122737	0.40	0	1.00	6.3×10^{-6}	7.3×10^{-1}
3	trans	chr2	rs4314021	1	22639186	0.23	rs4314021	22639186	0.23	0	1.00	3.0×10^{-6}	4.3×10^{-5}
4	trans	chr3	rs1522374	4	152235530	0.25	rs1522374	152235530	0.25	0	1.00	2.5×10^{-6}	2.0×10^{-2}
6	cis	chr6	rs2076310	3	33166034	0.40	rs2076310	33166034	0.40	0	1.00	2.0×10^{-4}	2.1×10^{-2}
10	trans	chr6	rs501241	2	103652391	0.22	rs501241	103652391	0.22	0	1.00	6.4×10^{-6}	1.4×10^{-1}
11	trans	chr6	rs9371268	2	153153293	0.15	rs9371268	153153293	0.15	0	1.00	9.7×10^{-6}	7.5×10^{-2}
12	trans	chr10	rs718947	1	126739149	0.26	rs718947	126739149	0.26	0	1.00	1.3×10^{-6}	6.6×10^{-1}
13	trans	chr11	rs3741277	2	6702409	0.36	rs3741277	6702409	0.36	0	1.00	2.0×10^{-7}	2.3×10^{-1}
16	trans	chr11	rs1355889	2	22613389	0.36	rs1355889	22613389	0.36	0	1.00	2.8×10^{-7}	8.5×10^{-1}
19	trans	chr12	rs1148540	1	58688712	0.35	rs1148540	58688712	0.35	0	1.00	2.0×10^{-6}	4.9×10^{-1}
20	trans	chr16	rs11647618	1	25381812	0.46	rs11647618	25381812	0.46	0	1.00	6.7×10^{-6}	1.8×10^{-1}
21	trans	chr16	rs11645670	1	85146305	0.13	rs11645670	85146305	0.13	0	1.00	3.6×10^{-7}	2.0×10^{-1}
22	trans	chr18	rs1421125	1	22057911	0.24	rs1421125	22057911	0.24	0	1.00	1.0×10^{-5}	9.8×10^{-1}
23	trans	chr18	rs11662719	1	48183313	0.31	rs11662719	48183313	0.31	0	1.00	2.4×10^{-6}	2.2×10^{-1}

Schizophrenia Gene 39
HLA-DQA1: major histocompatibility complex, class II, DQ alpha 1
Gene Location: chr6:32605182-32611429
GWAS Data: McCarroll 2012
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 2.9×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs12026071	8	17560646	0.13	rs12026071	17560646	0.13	0	1.00	1.0×10^{-5}	8.0×10^{-1}
3	trans	chr1	rs1441834	2	30173101	0.36	rs1441834	30173101	0.36	0	1.00	6.0×10^{-6}	9.5×10^{-1}
4	trans	chr1	rs11811702	2	33350183	0.37	rs11811702	33350183	0.37	0	1.00	5.0×10^{-7}	2.5×10^{-2}
5	trans	chr1	rs4660811	2	45035549	0.17	rs4660811	45035549	0.17	0	1.00	1.0×10^{-7}	7.1×10^{-2}
8	trans	chr1	rs17130873	6	84562324	0.07	rs17130873	84562324	0.07	0	1.00	8.0×10^{-7}	9.0×10^{-1}
9	trans	chr1	rs562044	2	110374054	0.39	rs562044	110374054	0.39	0	1.00	1.0×10^{-5}	8.0×10^{-1}
10	trans	chr1	rs2993437	2	202193981	0.45	rs2993437	202193981	0.45	0	1.00	7.0×10^{-6}	4.7×10^{-1}
14	trans	chr1	rs17187561	2	208742013	0.08	rs17187561	208742013	0.08	0	1.00	6.0×10^{-7}	1.4×10^{-1}
16	trans	chr1	rs7527372	2	218287335	0.15	rs7527372	218287335	0.15	0	1.00	5.0×10^{-6}	1.4×10^{-1}
17	trans	chr1	rs1294327	3	233426676	0.41	rs1294327	233426676	0.41	0	1.00	5.0×10^{-6}	2.1×10^{-1}
18	trans	chr2	rs12468225	2	24922359	0.26	rs12468225	24922359	0.26	0	1.00	1.0×10^{-5}	4.2×10^{-1}
29	trans	chr2	rs1396733	2	28642747	0.40	rs1396733	28642747	0.40	0	1.00	1.0×10^{-6}	3.4×10^{-1}
31	trans	chr2	rs6749108	2	43496986	0.32	rs6749108	43496986	0.32	0	1.00	4.0×10^{-6}	7.8×10^{-1}
32	trans	chr2	rs13021135	2	115914096	0.42	rs13021135	115914096	0.42	0	1.00	1.0×10^{-5}	5.1×10^{-1}
33	trans	chr2	rs12477083	2	129042639	0.31	rs12477083	129042639	0.31	0	1.00	1.0×10^{-5}	9.6×10^{-1}
34	trans	chr2	rs4972488	2	176712969	0.16	rs4972488	176712969	0.16	0	1.00	1.0×10^{-5}	9.8×10^{-1}
62	trans	chr2	rs3816196	2	190640475	0.41	rs3816196	190640475	0.41	0	1.00	5.0×10^{-7}	7.9×10^{-2}
74	trans	chr3	rs2600228	2	12908510	0.49	rs2600228	12908510	0.49	0	1.00	6.0×10^{-6}	6.8×10^{-1}
76	trans	chr3	rs7429789	2	54339768	0.08	rs7429789	54339768	0.08	0	1.00	1.0×10^{-5}	1.3×10^{-1}
78	trans	chr3	rs2320879	2	70708646	0.20	rs2320879	70708646	0.20	0	1.00	1.0×10^{-6}	2.7×10^{-2}
79	trans	chr3	rs558917	2	74350297	0.47	rs558917	74350297	0.47	0	1.00	1.0×10^{-5}	2.5×10^{-1}
81	trans	chr3	rs2399250	2	108619666	0.30	rs2399250	108619666	0.30	0	1.00	1.0×10^{-6}	2.2×10^{-1}
83	trans	chr3	rs11711220	2	122679372	0.30	rs11711220	122679372	0.30	0	1.00	1.0×10^{-6}	9.8×10^{-1}
85	trans	chr3	rs1456680	2	147866568	0.24	rs1456680	147866568	0.24	0	1.00	1.0×10^{-5}	9.0×10^{-1}
86	trans	chr3	rs9878758	2	155053281	0.33	rs9878758	155053281	0.33	0	1.00	1.0×10^{-5}	7.0×10^{-1}
87	trans	chr4	rs10003471	2	92200866	0.08	rs10003471	92200866	0.08	0	1.00	3.0×10^{-6}	7.0×10^{-1}
89	trans	chr4	rs17013593	2	129593111	0.34	rs17013593	129593111	0.34	0	1.00	3.0×10^{-6}	7.8×10^{-1}
93	trans	chr4	rs1077094	2	159480698	0.25	rs1077094	159480698	0.25	0	1.00	1.0×10^{-5}	5.7×10^{-1}
96	trans	chr4	rs4690798	2	165926586	0.49	rs4690798	165926586	0.49	0	1.00	3.0×10^{-6}	1.4×10^{-1}
98	trans	chr4	rs11724690	2	186764747	0.21	rs11724690	186764747	0.21	0	1.00	3.0×10^{-6}	7.7×10^{-1}
100	trans	chr5	rs6899118	2	25795294	0.42	rs6899118	25795294	0.42	0	1.00	1.0×10^{-5}	5.4×10^{-1}
101	trans	chr5	rs10056342	2	133782662	0.30	rs10056342	133782662	0.30	0	1.00	7.0×10^{-7}	4.3×10^{-1}
104	trans	chr6	rs6936950	2	6910091	0.16	rs6936950	6910091	0.16	0	1.00	3.0×10^{-7}	7.6×10^{-1}
107	trans	chr6	rs9467714	10	26340785	0.20	rs9467714	26340785	0.20	0	1.00	1.0×10^{-6}	8.7×10^{-12}
151	trans	chr6	rs4714084	3	37585221	0.35	rs4714084	37585221	0.35	0	1.00	3.0×10^{-6}	3.0×10^{-1}
152	trans	chr6	rs7761797	2	127843293	0.21	rs7761797	127843293	0.21	0	1.00	1.0×10^{-5}	1.0×10^{-1}
153	trans	chr6	rs9478712	2	156858484	0.48	rs9478712	156858484	0.48	0	1.00	4.0×10^{-6}	2.0×10^{-1}
154	trans	chr7	rs2058430	2	2206110	0.41	rs2058430	2206110	0.41	0	1.00	1.0×10^{-5}	3.9×10^{-10}
156	trans	chr7	rs10261060	2	8556819	0.37	rs10261060	8556819	0.37	0	1.00	1.0×10^{-6}	4.5×10^{-1}
162	trans	chr7	rs7800834	2	9016752	0.47	rs7800834	9016752	0.47	0	1.00	7.0×10^{-6}	4.0×10^{-3}
163	trans	chr7	rs2717351	2	19019880	0.40	rs2717351	19019880	0.40	0	1.00	1.0×10^{-5}	2.6×10^{-1}
164	trans	chr7	rs2960632	2	52659243	0.47	rs2960632	52659243	0.47	0	1.00	6.0×10^{-6}	5.5×10^{-1}
165	trans	chr7	rs4718886	2	68898689	0.27	rs4718886	68898689	0.27	0	1.00	1.0×10^{-5}	1.2×10^{-1}
168	trans	chr7	rs11768402	2	95160853	0.16	rs11768402	95160853	0.16	0	1.00	4.0×10^{-6}	5.7×10^{-1}
170	trans	chr8	rs11574398	2	31025343	0.34	rs11574398	31025343	0.34	0	1.00	6.0×10^{-6}	9.4×10^{-2}
171	trans	chr8	rs7015004	3	40337012	0.11	rs7015004	40337012	0.11	0	1.00	1.0×10^{-5}	7.1×10^{-2}
172	trans	chr8	rs7817235	2	64524456	0.26	rs7817235	64524456	0.26	0	1.00	1.0×10^{-5}	7.5×10^{-4}
173	trans	chr8	rs12056881	4	140872156	0.36	rs12056881	140872156	0.36	0	1.00	4.0×10^{-6}	7.8×10^{-1}
175	trans	chr9	rs12553901	2	21868757	0.28	rs12553901	21868757	0.28	0	1.00	1.0×10^{-7}	3.7×10^{-1}
182	trans	chr9	rs12683669	2	28225331	0.24	rs12683669	28225331	0.24	0	1.00	3.0×10^{-6}	3.0×10^{-1}
184	trans	chr9	rs7029237	2	36530955	0.39	rs7029237	36530955	0.39	0	1.00	6.0×10^{-6}	3.1×10^{-2}
190	trans	chr9	rs4379560	2	94395743	0.25	rs4379560	94395743	0.25	0	1.00	3.0×10^{-7}	3.5×10^{-1}
193	trans	chr9	rs10124685	2	118152551	0.23	rs10124685	118152551	0.23	0	1.00	6.0×10^{-6}	1.5×10^{-2}
194	trans	chr10	rs6602250	2	7574766	0.43	rs6602250	7574766	0.43	0	1.00	1.0×10^{-5}	2.3×10^{-1}
196	trans	chr10	rs420512	2	30897544	0.43	rs420512	30897544	0.43	0	1.00	5.0×10^{-6}	7.0×10^{-1}
201	trans	chr10	rs12217983	2	62064858	0.25	rs12217983	62064858	0.25	0	1.00	4.0×10^{-6}	1.4×10^{-1}
203	trans	chr10	rs7090742	2	68375667	0.12	rs7090742	68375667	0.12	0	1.00	2.0×10^{-7}	2.4×10^{-1}
207	trans	chr10	rs12257526	2	87928843	0.22	rs12257526	87928843	0.22	0	1.00	8.0×10^{-7}	6.4×10^{-1}
209	trans	chr10	rs11197181	2	117115713	0.27	rs11197181	117115713	0.27	0	1.00	1.0×10^{-5}	3.7×10^{-2}
231	trans	chr10	rs2784812	2	117337716	0.43	rs2784812	117337716	0.43	0	1.00	3.0×10^{-6}	1.2×10^{-1}
256	trans	chr10	rs1926178	2	129592238	0.36	rs1926178	129592238	0.36	0	1.00	3.0×10^{-6}	6.3×10^{-1}
261	trans	chr10	rs12220782	2	131485205	0.34	rs12220782	131485205	0.34	0	1.00	1.0×10^{-5}	3.0×10^{-1}
262	trans	chr11	rs6578882	2	7599391	0.37	rs6578882	7599391	0.37	0	1.00	4.0×10^{-6}	7.8×10^{-1}
264	trans	chr11	rs2046715	2	38002138	0.18	rs2046715	38002138	0.18	0	1.00	9.0×10^{-7}	6.6×10^{-1}
290	trans	chr11	rs564404	2	58817625	0.40	rs564404	58817625	0.40	0	1.00	7.0×10^{-6}	1.7×10^{-1}
294	trans	chr11	rs604096	2	118475098	0.27	rs604096	118475098	0.27	0	1.00	1.0×10^{-7}	5.4×10^{-1}
297	trans	chr12	rs11836388	2	5813402	0.13	rs11836388	5813402	0.13	0	1.00	4.0×10^{-6}	8.0×10^{-1}
306	trans	chr12	rs7975434	2	16711116	0.22	rs7975434	16711116	0.22	0	1.00	6.0×10^{-7}	7.8×10^{-1}
307	trans	chr12	rs11615201	2	17396190	0.13	rs11615201	17396190	0.13	0	1.00	5.0×10^{-6}	1.4×10^{-1}
309	trans	chr12	rs256655	2	30949511	0.34	rs256655	30949511	0.34	0	1.00	1.0×10^{-5}	5.0×10^{-1}
310	trans	chr12	rs12307124	2	67627644	0.19	rs12307124	67627644	0.19	0	1.00	2.0×10^{-6}	1.4×10^{-1}
312	trans	chr13	rs7324017	2	47406845	0.25	rs7324017	47406845	0.25	0	1.00	1.0×10^{-5}	9.1×10^{-1}
313	trans	chr13	rs950725	2	92149352	0.45	rs950725	92149352	0.45	0	1.00	1.0×10^{-5}	8.9×10^{-1}
315	trans	chr13	rs2391642	2	109089806	0.49	rs2391642	109089806	0.49	0	1.00	1.0×10^{-5}	5.4×10^{-1}
316	trans	chr14	rs1885152	2	96325206	0.28	rs1885152	96325206	0.28	0	1.00	8.0×10^{-6}	7.6×10^{-1}
317	trans	chr15	rs2444961	2	33425360	0.49	rs2444961	33425360	0.49	0	1.00	4.0×10^{-6}	4.9×10^{-1}
318	trans	chr15	rs573441	2	35070865	0.42	rs573441	35070865	0.42	0	1.00	8.0×10^{-6}	3.1×10^{-1}
319	trans	chr15	rs12913899	2	77844635	0.48	rs12913899	77844635	0.48	0	1.00	5.0×10^{-6}	4.9×10^{-1}
320	trans	chr15	rs11635554	2	80858682	0.47	rs11635554	80858682	0.47	0	1.00	9.0×10^{-6}	7.9×10^{-1}
321	trans	chr15	rs7170502	2	93928380	0.32	rs7170502	93928380	0.32	0	1.00	4.0×10^{-6}	6.4×10^{-1}
322	trans	chr15	rs17626833	2	94210807	0.25	rs17626833	94210807	0.25	0	1.00	1.0×10^{-5}	4.8×10^{-1}
323	trans	chr16	rs12448497	2	13492184	0.39	rs12448497	13492184	0.39	0	1.00	2.0×10^{-6}	2.0×10^{-1}
324	trans	chr16	rs4624179	12	25779427	0.27	rs4624179	25779427	0.27	0	1.00	3.0×10^{-6}	8.7×10^{-1}
325	trans	chr16	rs9939450	2	28301487	0.42	rs9939450	28301487	0.42	0	1.00	8.0×10^{-6}	4.9×10^{-1}
329	trans	chr16	rs12716977	2	30482803	0.40	rs12716977	30482803	0.40	0	1.00	2.0×10^{-6}	1.6×10^{-2}
332	trans	chr17	rs2531851	2	9200415	0.32	rs2531851	9200415	0.32	0	1.00	5.0×10^{-6}	2.2×10^{-2}
335	trans	chr17	rs17619645	2	14291895	0.24	rs17619645	14291895	0.24	0	1.00	7.0×10^{-6}	2.5×10^{-2}
337	trans	chr17	rs1971154	2	74121442	0.29	rs1971154	74121442	0.29	0	1.00	2.0×10^{-6}	1.3×10^{-1}
341	trans	chr17	rs7222745	2	80907253	0.46	rs7222745	80907253	0.46	0	1.00	6.0×10^{-6}	8.7×10^{-1}
345	trans	chr18	rs2000698	2	35108655	0.39	rs2000698	35108655	0.39	0	1.00	1.0×10^{-5}	3.3×10^{-2}
346	trans	chr18	rs8091972	2	63924393	0.22	rs8091972	63924393	0.22	0	1.00	1.0×10^{-5}	4.4×10^{-1}

Schizophrenia Gene 40
ZSCAN16: zinc finger and SCAN domain containing 16
Gene Location: chr6:28092386-28097856
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 2.9×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr4	rs6840808	1	26028508	0.10	rs6840808	26028508	0.10	0	1.00	6.5×10^{-6}	2.3×10^{-1}
2	trans	chr7	rs10226475	1	2226162	0.39	rs10226475	2226162	0.39	0	1.00	1.3×10^{-6}	7.8×10^{-11}

Schizophrenia Gene 40
ZSCAN16: zinc finger and SCAN domain containing 16
Gene Location: chr6:28092386-28097856
GWAS Data: McCarroll 2012
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 1.6×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr3	rs17700761	2	97087767	0.05	rs17700761	97087767	0.05	0	1.00	7.0×10^{-6}	4.6×10^{-2}
3	trans	chr7	rs12704584	6	90600097	0.26	rs12704584	90600097	0.26	0	1.00	6.0×10^{-6}	5.3×10^{-1}
6	trans	chr10	rs10509617	1	92822616	0.13	rs10509617	92822616	0.13	0	1.00	5.6×10^{-7}	3.9×10^{-4}
7	trans	chr11	rs1563899	2	115438446	0.33	rs1563899	115438446	0.33	0	1.00	8.7×10^{-6}	8.8×10^{-1}
8	trans	chr12	rs17774142	4	4710600	0.26	rs17774142	4710600	0.26	0	1.00	7.4×10^{-6}	2.8×10^{-1}
9	trans	chr14	rs4255714	1	52175433	0.06	rs4255714	52175433	0.06	0	1.00	5.6×10^{-6}	4.2×10^{-1}
10	trans	chr17	rs6504299	6	46579605	0.10	rs6504299	46579605	0.10	0	1.00	8.8×10^{-6}	7.2×10^{-3}

Schizophrenia Gene 41
DCPS: decapping enzyme, scavenger
Gene Location: chr11:126173646-126215644
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 2.2×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs7600852	5	24247686	0.08	rs7600852	24247686	0.08	0	1.00	2.8×10^{-6}	9.0×10^{-1}
2	trans	chr2	rs11687036	13	33753366	0.42	rs11687036	33753366	0.42	0	1.00	6.4×10^{-6}	6.7×10^{-1}
6	trans	chr3	rs6802313	4	149900094	0.39	rs6802313	149900094	0.39	0	1.00	9.2×10^{-6}	5.7×10^{-1}
7	trans	chr5	rs889229	6	58479300	0.50	rs889229	58479300	0.50	0	1.00	2.2×10^{-7}	1.8×10^{-2}
8	trans	chr9	rs11144203	32	77670081	0.12	rs11144203	77670081	0.12	0	1.00	4.2×10^{-6}	10.0×10^{-1}
9	trans	chr10	rs1058348	203	11302345	0.12	rs1058348	11302345	0.12	0	1.00	7.1×10^{-6}	6.1×10^{-1}
12	cis	chr11	rs11220426	1	126125154	0.08	rs11220426	126125154	0.08	0	1.00	3.5×10^{-8}	2.1×10^{-1}
17	trans	chr12	rs839120	57	86557927	0.14	rs839120	86557927	0.14	0	1.00	7.4×10^{-6}	7.9×10^{-1}
19	trans	chr14	rs10135277	16	35823231	0.49	rs10135277	35823231	0.49	0	1.00	5.6×10^{-6}	7.3×10^{-5}
20	trans	chr14	rs1262319	2	99475583	0.33	rs1262319	99475583	0.33	0	1.00	2.6×10^{-6}	4.6×10^{-1}
22	trans	chr20	rs6071589	2	37444221	0.47	rs6071589	37444221	0.47	0	1.00	6.8×10^{-6}	1.1×10^{-2}

Schizophrenia Gene 41
DCPS: decapping enzyme, scavenger
Gene Location: chr11:126173646-126215644
GWAS Data: McCarroll 2012
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 1.4×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs1435042	2	154019476	0.20	rs1435042	154019476	0.20	0	1.00	1.0×10^{-5}	1.1×10^{-1}
4	trans	chr3	rs1289736	4	107950892	0.43	rs1289736	107950892	0.43	0	1.00	3.0×10^{-6}	6.3×10^{-1}
5	trans	chr3	rs12492285	1	142953595	0.22	rs12492285	142953595	0.22	0	1.00	9.0×10^{-6}	6.4×10^{-1}
9	trans	chr9	rs1319017	1	84736303	0.41	rs1319017	84736303	0.41	0	1.00	7.0×10^{-6}	8.7×10^{-6}
35	trans	chr9	rs10867839	1	84891286	0.44	rs10867839	84891286	0.44	0	1.00	6.0×10^{-6}	1.9×10^{-5}
60	trans	chr12	rs1064319	2	119866533	0.28	rs1064319	119866533	0.28	0	1.00	8.0×10^{-6}	1.1×10^{-1}
61	trans	chr20	rs2145552	1	19862248	0.34	rs2145552	19862248	0.34	0	1.00	1.0×10^{-5}	5.2×10^{-1}

Schizophrenia Gene 41
DCPS: decapping enzyme, scavenger
Gene Location: chr11:126173646-126215644
GWAS Data: McCarroll 2012
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 4.3×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs12738201	1	75275749	0.48	rs12738201	75275749	0.48	0	1.00	2.6×10^{-6}	3.8×10^{-1}
2	trans	chr1	rs12724113	4	160328804	0.19	rs12724113	160328804	0.19	0	1.00	6.8×10^{-6}	1.6×10^{-2}
3	trans	chr9	rs10511575	2	12924111	0.17	rs10511575	12924111	0.17	0	1.00	8.9×10^{-6}	6.6×10^{-2}
4	trans	chr10	rs7075964	1	111631265	0.19	rs7075964	111631265	0.19	0	1.00	4.0×10^{-6}	9.4×10^{-1}
7	trans	chr11	rs1352307	1	47168254	0.03	rs1352307	47168254	0.03	0	1.00	1.7×10^{-6}	1.4×10^{-6}
9	trans	chr17	rs2378871	2	59638769	0.34	rs2378871	59638769	0.34	0	1.00	7.8×10^{-6}	5.8×10^{-1}

Schizophrenia Gene 42
TBC1D5: TBC1 domain family, member 5
Gene Location: chr3:17198653-17741512
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 5.5×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs6667619	1	208077220	0.33	rs6667619	208077220	0.33	0	1.00	2.6×10^{-7}	2.0×10^{-1}
2	trans	chr2	rs10198062	3	100635663	0.13	rs10198062	100635663	0.13	0	1.00	1.7×10^{-6}	10.0×10^{-1}
4	trans	chr2	rs6435309	1	206736522	0.25	rs6435309	206736522	0.25	0	1.00	4.7×10^{-6}	8.8×10^{-1}
5	trans	chr3	rs9826795	2	25250866	0.21	rs9826795	25250866	0.21	0	1.00	3.2×10^{-6}	4.3×10^{-1}
7	trans	chr3	rs9289439	2	132860651	0.19	rs9289439	132860651	0.19	0	1.00	3.2×10^{-6}	3.8×10^{-1}
13	trans	chr6	rs6913034	2	14352513	0.36	rs6913034	14352513	0.36	0	1.00	4.4×10^{-6}	5.9×10^{-1}
14	trans	chr6	rs16888579	2	77803487	0.14	rs16888579	77803487	0.14	0	1.00	2.3×10^{-8}	9.5×10^{-1}
18	trans	chr6	rs9456433	1	160025456	0.30	rs9456433	160025456	0.30	0	1.00	4.5×10^{-7}	2.2×10^{-2}
23	trans	chr7	rs7785481	1	16357439	0.33	rs7785481	16357439	0.33	0	1.00	6.5×10^{-6}	8.4×10^{-2}
24	trans	chr10	rs452121	2	6776447	0.29	rs452121	6776447	0.29	0	1.00	9.7×10^{-7}	4.3×10^{-1}
25	trans	chr10	rs4750655	4	15531257	0.08	rs4750655	15531257	0.08	0	1.00	5.6×10^{-6}	2.6×10^{-1}
27	trans	chr10	rs1578875	1	45550145	0.36	rs1578875	45550145	0.36	0	1.00	8.8×10^{-6}	5.6×10^{-1}
28	trans	chr11	rs12576528	1	123136864	0.30	rs12576528	123136864	0.30	0	1.00	5.9×10^{-6}	7.7×10^{-1}
30	trans	chr11	rs3758927	2	133829644	0.47	rs3758927	133829644	0.47	0	1.00	2.8×10^{-6}	4.4×10^{-8}
31	trans	chr12	rs10842800	5	26986748	0.18	rs10842800	26986748	0.18	0	1.00	5.1×10^{-6}	3.6×10^{-2}
32	trans	chr15	rs16962603	1	36421965	0.05	rs16962603	36421965	0.05	0	1.00	9.6×10^{-6}	9.2×10^{-1}
34	trans	chr15	rs1675996	2	67261513	0.13	rs1675996	67261513	0.13	0	1.00	1.3×10^{-7}	5.3×10^{-1}
35	trans	chr20	rs1316918	2	11642094	0.19	rs1316918	11642094	0.19	0	1.00	3.5×10^{-6}	2.9×10^{-1}
36	trans	chr20	rs6110220	1	14245838	0.16	rs6110220	14245838	0.16	0	1.00	2.1×10^{-6}	3.0×10^{-1}

Schizophrenia Gene 42
TBC1D5: TBC1 domain family, member 5
Gene Location: chr3:17198653-17741512
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 2.3×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs4949911	1	86062911	0.29	rs4949911	86062911	0.29	0	1.00	5.7×10^{-7}	6.9×10^{-1}
2	trans	chr2	rs880848	28	70872293	0.49	rs880848	70872293	0.49	0	1.00	4.3×10^{-6}	5.4×10^{-2}
3	trans	chr3	rs6767752	40	11960905	0.36	rs6767752	11960905	0.36	0	1.00	3.7×10^{-7}	4.6×10^{-1}
5	cis	chr3	rs3796301	2	16242101	0.17	rs3796301	16242101	0.17	0	1.00	5.0×10^{-4}	5.0×10^{-1}
6	cis	chr3	rs4260417	2	16737497	0.09	rs4260417	16737497	0.09	0	1.00	9.0×10^{-4}	7.4×10^{-1}
11	cis	chr3	rs2733516	1	17252724	0.29	rs2733516	17252724	0.29	0	1.00	1.4×10^{-10}	9.7×10^{-4}
36	cis	chr3	rs4470554	1	17671037	0.32	rs4470554	17671037	0.32	0	1.00	6.8×10^{-12}	1.2×10^{-3}
45	trans	chr5	rs698060	1	87086376	0.28	rs698060	87086376	0.28	0	1.00	7.1×10^{-7}	1.1×10^{-1}
46	trans	chr12	rs3918347	49	109293320	0.42	rs3918347	109293320	0.42	0	1.00	6.4×10^{-6}	3.3×10^{-2}
47	trans	chr14	rs1951533	1	30055573	0.26	rs1951533	30055573	0.26	0	1.00	6.0×10^{-6}	3.4×10^{-4}
48	trans	chr16	rs11642346	28	10058574	0.31	rs11642346	10058574	0.31	0	1.00	3.6×10^{-6}	5.2×10^{-3}
49	trans	chr17	rs1708623	1	17156087	0.49	rs1708623	17156087	0.49	0	1.00	1.0×10^{-5}	7.2×10^{-1}
50	trans	chr18	rs1561698	1	47859326	0.49	rs1561698	47859326	0.49	0	1.00	8.1×10^{-6}	2.8×10^{-1}
51	trans	chr21	rs2828223	59	24902544	0.39	rs2828223	24902544	0.39	0	1.00	3.0×10^{-6}	3.6×10^{-2}

Schizophrenia Gene 42
TBC1D5: TBC1 domain family, member 5
Gene Location: chr3:17198653-17741512
GWAS Data: McCarroll 2012
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 4.9×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs3789484	2	6391313	0.38	rs3789484	6391313	0.38	0	1.00	2.8×10^{-6}	5.1×10^{-1}
3	trans	chr1	rs1436175	1	224908366	0.49	rs1436175	224908366	0.49	0	1.00	6.4×10^{-7}	1.8×10^{-2}
4	trans	chr2	rs2433388	5	64493619	0.37	rs2433388	64493619	0.37	0	1.00	5.9×10^{-6}	4.7×10^{-1}
6	cis	chr3	rs11720982	1	17193348	0.46	rs11720982	17193348	0.46	0	1.00	1.4×10^{-7}	2.5×10^{-3}
24	cis	chr3	rs728022	1	17305303	0.30	rs728022	17305303	0.30	0	1.00	2.4×10^{-19}	8.2×10^{-4}
66	cis	chr3	rs11708664	1	17791027	0.17	rs11708664	17791027	0.17	0	1.00	4.8×10^{-6}	5.2×10^{-2}
78	cis	chr3	rs9757046	2	18040913	0.35	rs9757046	18040913	0.35	0	1.00	4.8×10^{-5}	6.7×10^{-2}
79	trans	chr5	rs11956685	1	31839074	0.30	rs11956685	31839074	0.30	0	1.00	3.4×10^{-6}	7.3×10^{-2}
80	trans	chr5	rs4704609	3	79402443	0.22	rs4704609	79402443	0.22	0	1.00	7.0×10^{-6}	3.8×10^{-1}
81	trans	chr5	rs4429870	1	164391457	0.28	rs4429870	164391457	0.28	0	1.00	9.2×10^{-6}	1.6×10^{-1}
82	trans	chr6	rs9395787	1	13444738	0.33	rs9395787	13444738	0.33	0	1.00	6.6×10^{-6}	3.9×10^{-2}
83	trans	chr9	rs10512121	2	84352443	0.35	rs10512121	84352443	0.35	0	1.00	8.5×10^{-6}	5.1×10^{-2}
86	trans	chr14	rs2295849	1	59781644	0.35	rs2295849	59781644	0.35	0	1.00	1.4×10^{-6}	2.9×10^{-1}
89	trans	chr20	rs6136614	2	19058170	0.35	rs6136614	19058170	0.35	0	1.00	3.0×10^{-6}	4.7×10^{-1}

Schizophrenia Gene 42
TBC1D5: TBC1 domain family, member 5
Gene Location: chr3:17198653-17741512
GWAS Data: McCarroll 2012
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 6.0×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr4	rs2322549	15	143317027	0.45	rs2322549	143317027	0.45	0	1.00	1.2×10^{-6}	5.0×10^{-2}
10	trans	chr5	rs6451234	7	35896984	0.27	rs6451234	35896984	0.27	0	1.00	7.2×10^{-7}	1.3×10^{-1}
22	trans	chr5	rs2961804	1	50402124	0.21	rs2961804	50402124	0.21	0	1.00	3.4×10^{-6}	3.6×10^{-1}
31	trans	chr8	rs1025395	1	8836603	0.48	rs1025395	8836603	0.48	0	1.00	8.0×10^{-7}	7.1×10^{-4}
45	trans	chr8	rs7845483	11	125682525	0.46	rs7845483	125682525	0.46	0	1.00	9.0×10^{-6}	6.8×10^{-1}
47	trans	chr9	rs7847334	1	120989782	0.33	rs7847334	120989782	0.33	0	1.00	1.9×10^{-6}	9.9×10^{-2}
50	trans	chr14	rs10137571	8	59505553	0.29	rs10137571	59505553	0.29	0	1.00	1.5×10^{-6}	8.8×10^{-1}
63	trans	chr16	rs4146819	1	69923563	0.28	rs4146819	69923563	0.28	0	1.00	3.8×10^{-6}	2.1×10^{-1}

Schizophrenia Gene 43
C22orf32: chromosome 22 open reading frame 32
Gene Location: chr22:42475694-42480288
GWAS Data: McCarroll 2012
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 1.9×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs3125297	1	212800586	0.24	rs3125297	212800586	0.24	0	1.00	7.0×10^{-6}	8.6×10^{-1}
2	trans	chr1	rs10925721	9	238811915	0.14	rs10925721	238811915	0.14	0	1.00	8.0×10^{-7}	9.8×10^{-1}
14	trans	chr3	rs13325716	132	56882063	0.07	rs13325716	56882063	0.07	0	1.00	2.0×10^{-6}	7.5×10^{-2}
15	trans	chr3	rs6441111	7	156821808	0.42	rs6441111	156821808	0.42	0	1.00	6.0×10^{-6}	1.2×10^{-1}
16	trans	chr4	rs2215809	3	15440633	0.14	rs2215809	15440633	0.14	0	1.00	1.0×10^{-5}	1.5×10^{-1}
17	trans	chr5	rs11948899	2	167848199	0.39	rs11948899	167848199	0.39	0	1.00	1.0×10^{-5}	9.8×10^{-1}
18	trans	chr6	rs2236041	3	42130318	0.21	rs2236041	42130318	0.21	0	1.00	6.0×10^{-6}	5.4×10^{-1}
21	trans	chr7	rs12700592	1	25214405	0.27	rs12700592	25214405	0.27	0	1.00	1.0×10^{-5}	5.0×10^{-1}
23	trans	chr7	rs11766731	2	35429465	0.20	rs11766731	35429465	0.20	0	1.00	2.0×10^{-6}	2.6×10^{-1}
39	trans	chr7	rs758250	1	151079871	0.25	rs758250	151079871	0.25	0	1.00	2.0×10^{-6}	4.2×10^{-1}
40	trans	chr8	rs12682045	3	6118677	0.08	rs12682045	6118677	0.08	0	1.00	1.0×10^{-5}	1.8×10^{-2}
41	trans	chr9	rs10081631	4	84391174	0.33	rs10081631	84391174	0.33	0	1.00	2.0×10^{-6}	7.7×10^{-1}
42	trans	chr9	rs7866942	28	132912105	0.29	rs7866942	132912105	0.29	0	1.00	1.0×10^{-5}	5.0×10^{-3}
43	trans	chr10	rs12772598	9	84626053	0.07	rs12772598	84626053	0.07	0	1.00	4.0×10^{-6}	9.3×10^{-1}
44	trans	chr10	rs12359546	2	95019423	0.46	rs12359546	95019423	0.46	0	1.00	9.0×10^{-6}	8.2×10^{-1}
45	trans	chr11	rs12577418	1	17101554	0.26	rs12577418	17101554	0.26	0	1.00	8.0×10^{-6}	5.4×10^{-4}
52	trans	chr11	rs542274	3	17207433	0.42	rs542274	17207433	0.42	0	1.00	1.0×10^{-6}	3.1×10^{-4}
61	trans	chr11	rs11039130	1	47229316	0.13	rs11039130	47229316	0.13	0	1.00	6.0×10^{-7}	9.4×10^{-1}
66	trans	chr12	rs35049	5	31162232	0.28	rs35049	31162232	0.28	0	1.00	8.0×10^{-6}	3.9×10^{-1}
68	trans	chr12	rs2681487	1	90023847	0.10	rs2681487	90023847	0.10	0	1.00	1.0×10^{-6}	2.2×10^{-1}
70	trans	chr12	rs12427047	2	90213070	0.23	rs12427047	90213070	0.23	0	1.00	9.0×10^{-6}	4.2×10^{-1}
72	trans	chr14	rs227433	2	70387376	0.37	rs227433	70387376	0.37	0	1.00	1.0×10^{-5}	3.0×10^{-1}
73	trans	chr15	rs1434675	1	46576123	0.36	rs1434675	46576123	0.36	0	1.00	1.0×10^{-5}	5.1×10^{-1}
74	trans	chr15	rs7178965	10	70514433	0.26	rs7178965	70514433	0.26	0	1.00	7.0×10^{-6}	6.2×10^{-1}
75	trans	chr15	rs1020501	1	96565598	0.34	rs1020501	96565598	0.34	0	1.00	1.0×10^{-5}	4.5×10^{-1}
76	trans	chr19	rs2682543	3	43982467	0.27	rs2682543	43982467	0.27	0	1.00	1.0×10^{-5}	8.0×10^{-1}
78	cis	chr22	rs12157312	1	42290177	0.14	rs12157312	42290177	0.14	0	1.00	2.0×10^{-5}	4.0×10^{-2}
98	cis	chr22	rs133303	1	42395242	0.48	rs133303	42395242	0.48	0	1.00	1.0×10^{-4}	4.6×10^{-5}
131	cis	chr22	rs6002621	2	42511002	0.31	rs6002621	42511002	0.31	0	1.00	8.0×10^{-10}	7.5×10^{-5}

Schizophrenia Gene 43
C22orf32: chromosome 22 open reading frame 32
Gene Location: chr22:42475694-42480288
GWAS Data: McCarroll 2012
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 3.2×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr10	rs17129781	19	114203593	0.11	rs17129781	114203593	0.11	0	1.00	6.3×10^{-6}	3.2×10^{-1}
2	trans	chr15	rs1845931	28	86634961	0.36	rs1845931	86634961	0.36	0	1.00	3.5×10^{-6}	4.7×10^{-3}
3	trans	chr19	rs10853822	2	51247694	0.13	rs10853822	51247694	0.13	0	1.00	6.7×10^{-6}	8.6×10^{-1}
4	cis	chr22	rs1801311	1	42486723	0.38	rs1801311	42486723	0.38	0	1.00	6.9×10^{-7}	5.0×10^{-5}

Schizophrenia Gene 44
ALMS1: Alstrom syndrome 1
Gene Location: chr2:73612885-73837046
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 3.8×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs12122125	2	45767431	0.43	rs12122125	45767431	0.43	0	1.00	8.6×10^{-6}	6.3×10^{-1}
2	trans	chr2	rs907136	3	54894649	0.13	rs907136	54894649	0.13	0	1.00	2.6×10^{-6}	1.7×10^{-2}
3	trans	chr2	rs3791659	2	56134800	0.46	rs3791659	56134800	0.46	0	1.00	2.0×10^{-6}	3.6×10^{-1}
7	cis	chr2	rs6720094	1	73588076	0.46	rs6720094	73588076	0.46	0	1.00	1.5×10^{-15}	5.4×10^{-4}
52	trans	chr2	rs7608315	1	163213723	0.24	rs7608315	163213723	0.24	0	1.00	7.7×10^{-6}	1.6×10^{-1}
53	trans	chr4	rs295224	6	161227411	0.36	rs295224	161227411	0.36	0	1.00	4.0×10^{-6}	9.7×10^{-1}
54	trans	chr7	rs4721669	2	17942808	0.09	rs4721669	17942808	0.09	0	1.00	4.8×10^{-6}	6.4×10^{-1}
55	trans	chr8	rs12156311	1	6025992	0.15	rs12156311	6025992	0.15	0	1.00	6.4×10^{-6}	6.3×10^{-1}
57	trans	chr9	rs7871770	1	110307465	0.46	rs7871770	110307465	0.46	0	1.00	5.4×10^{-6}	1.9×10^{-1}
59	trans	chr11	rs11211945	1	106722896	0.11	rs11211945	106722896	0.11	0	1.00	6.0×10^{-7}	1.8×10^{-1}
60	trans	chr15	rs1371385	1	90005699	0.47	rs1371385	90005699	0.47	0	1.00	4.5×10^{-6}	3.0×10^{-2}
61	trans	chr16	rs9923068	1	17872588	0.18	rs9923068	17872588	0.18	0	1.00	9.5×10^{-6}	2.3×10^{-2}

Schizophrenia Gene 44
ALMS1: Alstrom syndrome 1
Gene Location: chr2:73612885-73837046
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 6.0×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs662145	210	55529828	0.29	rs662145	55529828	0.29	0	1.00	5.6×10^{-6}	9.8×10^{-2}
2	trans	chr2	rs751759	1	68350615	0.44	rs751759	68350615	0.44	0	1.00	4.7×10^{-6}	4.2×10^{-2}
3	cis	chr2	rs1522926	1	73591241	0.43	rs1522926	73591241	0.43	0	1.00	2.1×10^{-6}	5.8×10^{-4}
22	cis	chr2	rs11688718	1	73760939	0.43	rs11688718	73760939	0.43	0	1.00	1.9×10^{-6}	4.6×10^{-3}
34	trans	chr5	rs10475399	90	7898094	0.49	rs10475399	7898094	0.49	0	1.00	3.3×10^{-6}	6.0×10^{-2}
35	trans	chr5	rs4292454	36	42623245	0.41	rs4292454	42623245	0.41	0	1.00	6.8×10^{-6}	5.1×10^{-1}
36	trans	chr6	rs1953635	6	140933310	0.34	rs1953635	140933310	0.34	0	1.00	8.5×10^{-6}	4.5×10^{-1}
42	trans	chr7	rs1358064	184	86941669	0.15	rs1358064	86941669	0.15	0	1.00	1.0×10^{-6}	1.6×10^{-2}
43	trans	chr9	rs1930503	9	7820315	0.33	rs1930503	7820315	0.33	0	1.00	2.0×10^{-6}	2.0×10^{-1}
44	trans	chr11	rs12574668	1	46422686	0.19	rs12574668	46422686	0.19	0	1.00	1.0×10^{-5}	7.1×10^{-7}
45	trans	chr12	rs7488953	1	129932796	0.34	rs7488953	129932796	0.34	0	1.00	3.3×10^{-6}	2.5×10^{-2}
46	trans	chr13	rs7997166	8	51675480	0.12	rs7997166	51675480	0.12	0	1.00	1.6×10^{-6}	5.6×10^{-1}
47	trans	chr21	rs2828223	59	24902544	0.39	rs2828223	24902544	0.39	0	1.00	6.1×10^{-6}	3.6×10^{-2}
48	trans	chr22	rs133642	14	48710319	0.15	rs133642	48710319	0.15	0	1.00	1.8×10^{-6}	9.2×10^{-1}

Schizophrenia Gene 44
ALMS1: Alstrom syndrome 1
Gene Location: chr2:73612885-73837046
GWAS Data: McCarroll 2012
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 2.1×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	cis	chr2	rs6720094	2	73588076	0.46	rs6720094	73588076	0.46	0	1.00	3.2×10^{-6}	5.4×10^{-4}
10	cis	chr2	rs13391552	1	73818936	0.29	rs13391552	73818936	0.29	0	1.00	4.7×10^{-10}	6.9×10^{-5}
14	trans	chr4	rs10032131	3	131252392	0.18	rs10032131	131252392	0.18	0	1.00	6.3×10^{-6}	5.8×10^{-1}
15	trans	chr8	rs970294	1	20442235	0.30	rs970294	20442235	0.30	0	1.00	9.6×10^{-6}	3.1×10^{-1}
16	trans	chr10	rs719748	3	7731885	0.42	rs719748	7731885	0.42	0	1.00	9.2×10^{-6}	8.9×10^{-1}
17	trans	chr10	rs11819196	7	18697657	0.34	rs11819196	18697657	0.34	0	1.00	9.5×10^{-6}	7.7×10^{-1}
18	trans	chr10	rs11191389	4	104523018	0.33	rs11191389	104523018	0.33	0	1.00	2.9×10^{-6}	1.2×10^{-3}
20	trans	chr15	rs12905054	6	33356768	0.42	rs12905054	33356768	0.42	0	1.00	3.8×10^{-6}	2.5×10^{-1}
21	trans	chr16	rs6498594	1	16073437	0.11	rs6498594	16073437	0.11	0	1.00	4.9×10^{-6}	6.3×10^{-1}

Schizophrenia Gene 45
GUSBL2: Not Found in HUGO
Gene Location: Not Found:Not Found-Not Found
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 8.3×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs10192105	5	229366942	0.19	rs10192105	229366942	0.19	0	1.00	3.5×10^{-6}	6.7×10^{-1}
2	trans	chr3	rs17061232	4	59804978	0.10	rs17061232	59804978	0.10	0	1.00	2.5×10^{-7}	1.4×10^{-1}
3	trans	chr4	rs1402671	4	140944844	0.22	rs1402671	140944844	0.22	0	1.00	5.1×10^{-6}	8.2×10^{-1}
5	trans	chr8	rs1488935	3	38133793	0.26	rs1488935	38133793	0.26	0	1.00	6.2×10^{-6}	1.7×10^{-4}
6	trans	chr11	rs10793047	6	69828633	0.34	rs10793047	69828633	0.34	0	1.00	9.6×10^{-6}	4.9×10^{-1}
7	trans	chr18	rs606618	3	40531433	0.48	rs606618	40531433	0.48	0	1.00	2.0×10^{-6}	3.3×10^{-1}

Schizophrenia Gene 45
GUSBL2: Not Found in HUGO
Gene Location: Not Found:Not Found-Not Found
GWAS Data: McCarroll 2012
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 3.9×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
4	trans	chr2	rs2890484	4	15176554	0.15	rs2890484	15176554	0.15	0	1.00	3.9×10^{-6}	5.3×10^{-1}
5	trans	chr2	rs1365480	2	64622008	0.34	rs1365480	64622008	0.34	0	1.00	8.5×10^{-6}	1.9×10^{-1}
8	trans	chr6	rs7773938	1	26474044	0.17	rs7773938	26474044	0.17	0	1.00	1.1×10^{-6}	5.6×10^{-11}
11	trans	chr11	rs571955	6	104751269	0.45	rs571955	104751269	0.45	0	1.00	8.2×10^{-6}	6.1×10^{-1}
12	trans	chr14	rs10133637	2	85994291	0.25	rs10133637	85994291	0.25	0	1.00	4.4×10^{-6}	7.0×10^{-1}
14	trans	chr15	rs7173588	1	38910544	0.27	rs7173588	38910544	0.27	0	1.00	3.6×10^{-6}	2.7×10^{-1}
15	trans	chr15	rs17269397	6	58857378	0.30	rs17269397	58857378	0.30	0	1.00	2.1×10^{-6}	2.9×10^{-2}

Schizophrenia Gene 46
GFOD2: glucose-fructose oxidoreductase domain containing 2
Gene Location: chr16:67708435-67753273
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 1.3×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs12096757	17	245816799	0.44	rs12096757	245816799	0.44	0	1.00	4.6×10^{-6}	4.5×10^{-3}
2	trans	chr2	rs17034382	4	68002521	0.24	rs17034382	68002521	0.24	0	1.00	9.2×10^{-6}	5.8×10^{-1}
3	trans	chr11	rs11021758	1	11312500	0.14	rs11021758	11312500	0.14	0	1.00	8.4×10^{-7}	5.0×10^{-1}
5	cis	chr16	rs3868143	1	67328453	0.26	rs3868143	67328453	0.26	0	1.00	1.0×10^{-8}	2.9×10^{-2}
15	cis	chr16	rs17686899	9	67627635	0.03	rs17686899	67627635	0.03	0	1.00	1.4×10^{-6}	3.0×10^{-2}
17	cis	chr16	rs9928374	1	67811930	0.08	rs8049622	67800927	0.14	11003	0.97	3.7×10^{-10}	5.8×10^{-3}
23	cis	chr16	rs10468274	1	67922342	0.32	rs10468274	67922342	0.32	0	1.00	3.0×10^{-29}	3.6×10^{-4}
27	cis	chr16	rs7200986	1	68099946	0.47	rs7200986	68099946	0.47	0	1.00	1.9×10^{-8}	6.2×10^{-4}
33	cis	chr16	rs8058517	2	68379860	0.13	rs8058517	68379860	0.13	0	1.00	4.4×10^{-7}	3.2×10^{-4}

Schizophrenia Gene 46
GFOD2: glucose-fructose oxidoreductase domain containing 2
Gene Location: chr16:67708435-67753273
GWAS Data: McCarroll 2012
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 5.5×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
6	trans	chr5	rs4836433	34	128361955	0.39	rs4836433	128361955	0.39	0	1.00	3.1×10^{-6}	3.1×10^{-1}
7	trans	chr8	rs17310732	16	99415437	0.11	rs17310732	99415437	0.11	0	1.00	2.6×10^{-6}	9.0×10^{-1}
8	trans	chr9	rs1415686	12	106236224	0.13	rs1415686	106236224	0.13	0	1.00	4.3×10^{-6}	3.6×10^{-1}
11	trans	chr11	rs550700	5	96823102	0.30	rs550700	96823102	0.30	0	1.00	5.1×10^{-6}	5.2×10^{-4}

Schizophrenia Gene 47
TM9SF1: transmembrane 9 superfamily member 1
Gene Location: chr14:24657924-24664882
GWAS Data: McCarroll 2012
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 4.5×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs9306867	51	18283243	0.42	rs9306867	18283243	0.42	0	1.00	1.0×10^{-6}	2.7×10^{-2}
2	trans	chr3	rs500985	6	8077017	0.25	rs500985	8077017	0.25	0	1.00	1.0×10^{-5}	7.5×10^{-2}
3	trans	chr3	rs327183	4	107898529	0.37	rs327183	107898529	0.37	0	1.00	1.0×10^{-5}	8.2×10^{-2}
4	trans	chr5	rs2956571	5	17224497	0.36	rs2956571	17224497	0.36	0	1.00	9.0×10^{-7}	8.7×10^{-1}
5	trans	chr6	rs9399295	3	140171922	0.42	rs9399295	140171922	0.42	0	1.00	6.0×10^{-6}	3.5×10^{-1}
8	trans	chr8	rs10094736	1	17130582	0.32	rs10094736	17130582	0.32	0	1.00	4.0×10^{-6}	6.7×10^{-7}
11	trans	chr11	rs4963157	1	776335	0.08	rs4963157	776335	0.08	0	1.00	1.0×10^{-5}	3.2×10^{-1}

Schizophrenia Gene 47
TM9SF1: transmembrane 9 superfamily member 1
Gene Location: chr14:24657924-24664882
GWAS Data: McCarroll 2012
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 2.6×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr12	rs10848635	1	2316195	0.32	rs10848635	2316195	0.32	0	1.00	6.9×10^{-6}	4.9×10^{-11}
4	trans	chr16	rs10521135	1	26281716	0.36	rs10521135	26281716	0.36	0	1.00	2.5×10^{-6}	1.4×10^{-1}

Schizophrenia Gene 48
VRK2: vaccinia related kinase 2
Gene Location: chr2:58273776-58387055
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 7.3×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	cis	chr2	rs1460255	1	57978858	0.23	rs1460255	57978858	0.23	0	1.00	6.9×10^{-8}	2.2×10^{-6}
14	cis	chr2	rs884669	1	58134604	0.31	rs884669	58134604	0.31	0	1.00	3.2×10^{-7}	2.6×10^{-2}
37	cis	chr2	rs12713377	1	58472110	0.45	rs12713377	58472110	0.45	0	1.00	1.7×10^{-14}	6.3×10^{-1}
44	trans	chr9	rs12379948	2	10512117	0.22	rs12379948	10512117	0.22	0	1.00	6.1×10^{-6}	8.9×10^{-1}
46	trans	chr20	rs3966739	3	13001715	0.49	rs3966739	13001715	0.49	0	1.00	9.6×10^{-7}	9.5×10^{-2}

Schizophrenia Gene 48
VRK2: vaccinia related kinase 2
Gene Location: chr2:58273776-58387055
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 1.1×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs10495536	11	6580745	0.11	rs10495536	6580745	0.11	0	1.00	6.3×10^{-6}	3.8×10^{-1}
2	cis	chr2	rs12991325	1	58016879	0.38	rs12991325	58016879	0.38	0	1.00	8.0×10^{-4}	1.1×10^{-6}
3	cis	chr2	rs12620940	1	58311684	0.21	rs12620940	58311684	0.21	0	1.00	3.0×10^{-5}	2.6×10^{-5}
9	trans	chr9	rs10758368	3	36310778	0.42	rs10758368	36310778	0.42	0	1.00	7.2×10^{-6}	1.4×10^{-4}
10	trans	chr11	rs1425193	1	55135435	0.22	rs1425193	55135435	0.22	0	1.00	2.8×10^{-6}	3.9×10^{-1}
15	trans	chr11	rs4939542	3	55729751	0.23	rs4939542	55729751	0.23	0	1.00	3.7×10^{-6}	8.7×10^{-1}
16	trans	chr13	rs7337698	1	23587128	0.42	rs7337698	23587128	0.42	0	1.00	1.0×10^{-5}	2.6×10^{-1}
17	trans	chr14	rs880433	6	28488693	0.34	rs880433	28488693	0.34	0	1.00	5.5×10^{-6}	8.8×10^{-1}
18	trans	chr22	rs733573	1	49090452	0.41	rs733573	49090452	0.41	0	1.00	4.0×10^{-6}	1.5×10^{-1}

Schizophrenia Gene 49
CLP1: CLP1, cleavage and polyadenylation factor I subunit, homolog (S. cerevisiae)
Gene Location: chr11:57425215-57429337
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 2.1×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr10	rs11189245	1	99267673	0.35	rs11189245	99267673	0.35	0	1.00	7.1×10^{-6}	6.0×10^{-1}
2	cis	chr11	rs576859	2	57480623	0.27	rs576859	57480623	0.27	0	1.00	1.2×10^{-6}	3.6×10^{-6}
4	cis	chr11	rs7117205	1	57641883	0.17	rs7117205	57641883	0.17	0	1.00	2.3×10^{-6}	6.2×10^{-6}

Schizophrenia Gene 50
CREB1: cAMP responsive element binding protein 1
Gene Location: chr2:208394615-208470284
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 2.0×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs4659339	16	118281822	0.28	rs4659339	118281822	0.28	0	1.00	2.7×10^{-6}	8.6×10^{-2}
2	trans	chr1	rs10754573	1	236677586	0.47	rs10754573	236677586	0.47	0	1.00	2.2×10^{-7}	5.6×10^{-1}
3	trans	chr2	rs2278754	88	46583187	0.25	rs2278754	46583187	0.25	0	1.00	2.8×10^{-6}	2.8×10^{-1}
4	trans	chr2	rs11895039	31	75640402	0.19	rs11895039	75640402	0.19	0	1.00	7.1×10^{-6}	3.0×10^{-1}
5	cis	chr2	rs4673360	2	207508741	0.39	rs4673360	207508741	0.39	0	1.00	5.0×10^{-4}	9.8×10^{-1}
6	cis	chr2	rs6721035	2	208272732	0.22	rs6721035	208272732	0.22	0	1.00	1.0×10^{-4}	1.3×10^{-2}
13	cis	chr2	rs2551949	1	208477852	0.13	rs2551949	208477852	0.13	0	1.00	2.0×10^{-5}	2.3×10^{-3}
14	cis	chr2	rs4375849	3	209000170	0.36	rs4375849	209000170	0.36	0	1.00	2.0×10^{-4}	1.9×10^{-1}
19	trans	chr3	rs4287886	687	29422762	0.42	rs4287886	29422762	0.42	0	1.00	1.3×10^{-6}	8.5×10^{-2}
20	trans	chr3	rs4563418	43	88479786	0.24	rs4563418	88479786	0.24	0	1.00	1.0×10^{-5}	9.6×10^{-1}
21	trans	chr4	rs7665024	404	110289595	0.21	rs7665024	110289595	0.21	0	1.00	7.8×10^{-6}	7.9×10^{-1}
22	trans	chr4	rs7677486	10	185336852	0.37	rs7677486	185336852	0.37	0	1.00	1.5×10^{-6}	4.5×10^{-2}
29	trans	chr7	rs1358064	184	86941669	0.15	rs1358064	86941669	0.15	0	1.00	8.8×10^{-7}	1.6×10^{-2}
30	trans	chr8	rs2946505	1	12811152	0.31	rs2946505	12811152	0.31	0	1.00	6.8×10^{-6}	1.0×10^{-4}
31	trans	chr9	rs7031908	2	6635045	0.21	rs7031908	6635045	0.21	0	1.00	5.0×10^{-6}	9.3×10^{-2}
32	trans	chr10	rs6480848	132	78741306	0.17	rs6480848	78741306	0.17	0	1.00	4.5×10^{-6}	1.7×10^{-2}
33	trans	chr10	rs10882381	73	95777488	0.41	rs10882381	95777488	0.41	0	1.00	3.5×10^{-6}	6.2×10^{-1}
35	trans	chr12	rs1874799	18	30202163	0.27	rs1874799	30202163	0.27	0	1.00	7.0×10^{-8}	2.7×10^{-1}
37	trans	chr15	rs12916537	14	82298536	0.27	rs12916537	82298536	0.27	0	1.00	5.9×10^{-7}	3.6×10^{-2}
38	trans	chr16	rs7197547	49	10136244	0.35	rs7197547	10136244	0.35	0	1.00	6.7×10^{-6}	4.5×10^{-1}
39	trans	chr18	rs1789595	2	53775254	0.18	rs1789595	53775254	0.18	0	1.00	8.1×10^{-6}	2.6×10^{-5}

Schizophrenia Gene 50
CREB1: cAMP responsive element binding protein 1
Gene Location: chr2:208394615-208470284
GWAS Data: McCarroll 2012
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: $1.4{\times}10^{-2}$

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
4	trans	chr1	rs863036	18	159117109	0.36	rs863036	159117109	0.36	0	1.00	$2.0{\times}10^{-6}$	$7.2{\times}10^{-1}$
6	trans	chr1	rs868963	32	211083168	0.14	rs868963	211083168	0.14	0	1.00	$7.0{\times}10^{-6}$	$2.5{\times}10^{-1}$
13	trans	chr1	rs11582507	1	211191894	0.25	rs11582507	211191894	0.25	0	1.00	$5.0{\times}10^{-6}$	$10.0{\times}10^{-1}$
16	trans	chr4	rs6534204	45	121623193	0.19	rs6534204	121623193	0.19	0	1.00	$6.0{\times}10^{-6}$	$3.0{\times}10^{-3}$
18	trans	chr5	rs10074520	49	122579735	0.11	rs10074520	122579735	0.11	0	1.00	$1.0{\times}10^{-5}$	$8.7{\times}10^{-1}$
19	trans	chr5	rs13357245	58	134904639	0.18	rs13357245	134904639	0.18	0	1.00	$4.0{\times}10^{-6}$	$8.7{\times}10^{-1}$
20	trans	chr6	rs11760067	44	135094272	0.06	rs11760067	135094272	0.06	0	1.00	$7.0{\times}10^{-6}$	$3.8{\times}10^{-2}$
21	trans	chr7	rs13246748	68	31258775	0.06	rs13246748	31258775	0.06	0	1.00	$3.0{\times}10^{-6}$	$3.0{\times}10^{-2}$
22	trans	chr7	rs1476865	246	68423676	0.46	rs1476865	68423676	0.46	0	1.00	$4.0{\times}10^{-6}$	$7.6{\times}10^{-2}$
23	trans	chr9	rs7033997	18	115708851	0.38	rs7033997	115708851	0.38	0	1.00	$5.0{\times}10^{-6}$	$2.3{\times}10^{-2}$
24	trans	chr12	rs11043499	207	17705237	0.41	rs11043499	17705237	0.41	0	1.00	$5.0{\times}10^{-6}$	$3.2{\times}10^{-1}$
25	trans	chr15	rs1471745	2	59574243	0.30	rs1471745	59574243	0.30	0	1.00	$8.0{\times}10^{-6}$	$1.0{\times}10^{-2}$
27	trans	chr17	rs2071167	60	42287519	0.42	rs2071167	42287519	0.42	0	1.00	$6.0{\times}10^{-6}$	$2.8{\times}10^{-1}$
28	trans	chr18	rs4129498	21	23001714	0.29	rs4129498	23001714	0.29	0	1.00	$1.0{\times}10^{-5}$	$3.8{\times}10^{-2}$
48	trans	chr18	rs2728508	171	23180056	0.33	rs2728508	23180056	0.33	0	1.00	$3.0{\times}10^{-6}$	$8.8{\times}10^{-3}$

Schizophrenia Gene 51
HSP90AB2P: heat shock protein 90kDa alpha (cytosolic), class B member 2, pseudogene
Gene Location: chr4:13335036-13339925
GWAS Data: McCarroll 2012
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: $5.7{\times}10^{-4}$

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr4	rs10517394	1	58271686	0.12	rs10517394	58271686	0.12	0	1.00	$8.5{\times}10^{-6}$	$8.1{\times}10^{-1}$
2	trans	chr8	rs17687067	1	17036201	0.20	rs17687067	17036201	0.20	0	1.00	$5.6{\times}10^{-6}$	$3.9{\times}10^{-8}$

Schizophrenia Gene 52
C16orf70: chromosome 16 open reading frame 70
Gene Location: chr16:67143914-67182442
GWAS Data: McCarroll 2012
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: $8.9{\times}10^{-3}$

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr9	rs7866942	28	132912105	0.29	rs7866942	132912105	0.29	0	1.00	$2.0{\times}10^{-6}$	$5.0{\times}10^{-3}$
4	trans	chr10	rs11196301	614	84634847	0.14	rs11196301	84634847	0.14	0	1.00	$2.0{\times}10^{-7}$	$9.4{\times}10^{-1}$
13	trans	chr13	rs529628	2	101968332	0.33	rs529628	101968332	0.33	0	1.00	$5.0{\times}10^{-6}$	$2.3{\times}10^{-3}$
30	trans	chr22	rs2413450	10	37470224	0.42	rs2413450	37470224	0.42	0	1.00	$1.0{\times}10^{-5}$	$6.2{\times}10^{-2}$

Schizophrenia Gene 52
C16orf70: chromosome 16 open reading frame 70
Gene Location: chr16:67143914-67182442
GWAS Data: McCarroll 2012
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: $2.2{\times}10^{-3}$

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs6749177	1	38677701	0.48	rs6749177	38677701	0.48	0	1.00	$7.4{\times}10^{-6}$	$6.2{\times}10^{-3}$
2	trans	chr2	rs6545415	1	54728082	0.23	rs6545415	54728082	0.23	0	1.00	$7.2{\times}10^{-6}$	$9.5{\times}10^{-1}$
4	trans	chr2	rs2941591	1	54908044	0.27	rs2941591	54908044	0.27	0	1.00	$2.1{\times}10^{-6}$	$5.4{\times}10^{-1}$
5	trans	chr2	rs4128869	1	181738631	0.31	rs4128869	181738631	0.31	0	1.00	$3.9{\times}10^{-7}$	$5.1{\times}10^{-1}$
8	trans	chr3	rs13319027	5	31522212	0.24	rs13319027	31522212	0.24	0	1.00	$2.6{\times}10^{-7}$	$6.4{\times}10^{-2}$
10	trans	chr4	rs4374629	1	99411783	0.41	rs4374629	99411783	0.41	0	1.00	$8.0{\times}10^{-7}$	$2.9{\times}10^{-1}$
11	trans	chr6	rs17262993	1	22207494	0.30	rs17262993	22207494	0.30	0	1.00	$8.5{\times}10^{-6}$	$5.6{\times}10^{-1}$
12	trans	chr6	rs7773994	2	37572144	0.48	rs7773994	37572144	0.48	0	1.00	$1.1{\times}10^{-6}$	$6.8{\times}10^{-1}$
16	cis	chr16	rs9926387	1	66483806	0.43	rs9926387	66483806	0.43	0	1.00	$7.0{\times}10^{-6}$	$1.4{\times}10^{-3}$
17	cis	chr16	rs896086	3	66607188	0.25	rs896086	66607188	0.25	0	1.00	$6.5{\times}10^{-7}$	$5.6{\times}10^{-1}$
33	cis	chr16	rs187431	1	66906871	0.33	rs187431	66906871	0.33	0	1.00	$1.1{\times}10^{-9}$	$4.3{\times}10^{-3}$
37	cis	chr16	rs9033	1	67181999	0.40	rs9033	67181999	0.40	0	1.00	$3.9{\times}10^{-17}$	$1.5{\times}10^{-3}$
39	cis	chr16	rs6979	1	67691668	0.41	rs6979	67691668	0.41	0	1.00	$5.8{\times}10^{-7}$	$1.5{\times}10^{-3}$
41	trans	chr18	rs17483463	1	6007275	0.08	rs17483463	6007275	0.08	0	1.00	$8.5{\times}10^{-6}$	$3.2{\times}10^{-1}$
43	trans	chr18	rs11152432	1	62064688	0.26	rs11152432	62064688	0.26	0	1.00	$7.9{\times}10^{-6}$	$5.1{\times}10^{-1}$

Schizophrenia Gene 53
ASAH1: N-acylsphingosine amidohydrolase (acid ceramidase) 1
Gene Location: chr8:17913924-17941879
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 1.7×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs662145	210	55529828	0.29	rs662145	55529828	0.29	0	1.00	8.5×10^{-7}	9.8×10^{-2}
2	trans	chr2	rs11675680	8	225974764	0.22	rs11675680	225974764	0.22	0	1.00	2.4×10^{-6}	8.8×10^{-1}
3	trans	chr3	rs9865782	2	113652774	0.43	rs9865782	113652774	0.43	0	1.00	2.6×10^{-7}	6.5×10^{-1}
4	trans	chr3	rs6767984	108	151208044	0.16	rs6767984	151208044	0.16	0	1.00	2.2×10^{-6}	7.8×10^{-2}
6	trans	chr5	rs2407508	2	53637054	0.41	rs2407508	53637054	0.41	0	1.00	3.7×10^{-6}	3.9×10^{-1}
7	trans	chr5	rs888926	12	179738101	0.35	rs888926	179738101	0.35	0	1.00	5.5×10^{-6}	4.7×10^{-1}
8	trans	chr8	rs1059611	2	19824563	0.13	rs1059611	19824563	0.13	0	1.00	1.1×10^{-6}	7.7×10^{-2}
9	trans	chr9	rs690552	7	93344344	0.38	rs690552	93344344	0.38	0	1.00	1.0×10^{-5}	9.0×10^{-2}
11	trans	chr17	rs7215531	1	56493374	0.24	rs7215531	56493374	0.24	0	1.00	2.6×10^{-6}	2.1×10^{-4}
12	trans	chr18	rs12607558	217	31754053	0.26	rs12607558	31754053	0.26	0	1.00	5.7×10^{-6}	1.5×10^{-2}
13	trans	chr19	rs4933000	5	22730026	0.15	rs4933000	22730026	0.15	0	1.00	4.2×10^{-6}	8.6×10^{-4}
14	trans	chr20	rs8122984	8	58352921	0.49	rs8122984	58352921	0.49	0	1.00	7.5×10^{-6}	5.8×10^{-1}

Schizophrenia Gene 53
ASAH1: N-acylsphingosine amidohydrolase (acid ceramidase) 1
Gene Location: chr8:17913924-17941879
GWAS Data: McCarroll 2012
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 1.2×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs1050492	2	226820500	0.48	rs1050492	226820500	0.48	0	1.00	7.3×10^{-6}	4.0×10^{-1}
2	trans	chr7	rs3800917	3	2167939	0.31	rs3800917	2167939	0.31	0	1.00	9.8×10^{-6}	2.2×10^{-12}
3	trans	chr10	rs10510046	1	120453168	0.20	rs10510046	120453168	0.20	0	1.00	7.4×10^{-6}	3.4×10^{-1}
4	trans	chr11	rs10750347	4	126695833	0.10	rs10750347	126695833	0.10	0	1.00	6.5×10^{-6}	1.1×10^{-1}
5	trans	chr15	rs1021190	2	46713266	0.43	rs1021190	46713266	0.43	0	1.00	7.1×10^{-6}	3.4×10^{-1}
6	trans	chr22	rs9306345	45	40832375	0.20	rs9306345	40832375	0.20	0	1.00	7.3×10^{-6}	3.2×10^{-2}

Schizophrenia Gene 54
EP300: E1A binding protein p300
Gene Location: chr22:41488613-41576081
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 1.2×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr4	rs16841112	2	7767318	0.18	rs16841112	7767318	0.18	0	1.00	10.0×10^{-6}	1.9×10^{-1}
3	trans	chr9	rs698467	5	109809787	0.35	rs698467	109809787	0.35	0	1.00	8.1×10^{-6}	4.4×10^{-1}
5	trans	chr10	rs10788706	14	48480371	0.22	rs10788706	48480371	0.22	0	1.00	2.2×10^{-8}	2.7×10^{-3}
6	trans	chr10	rs17106495	52	82285533	0.10	rs17106495	82285533	0.10	0	1.00	3.9×10^{-6}	5.6×10^{-1}
7	trans	chr12	rs11609833	1	95313638	0.09	rs11609833	95313638	0.09	0	1.00	4.7×10^{-6}	3.8×10^{-1}
9	trans	chr13	rs1928949	8	66774824	0.24	rs1928949	66774824	0.24	0	1.00	2.2×10^{-7}	3.9×10^{-1}
10	trans	chr17	rs12450955	5	4077980	0.29	rs12450955	4077980	0.29	0	1.00	1.9×10^{-6}	8.2×10^{-1}
11	cis	chr22	rs4821990	1	41438710	0.21	rs4821990	41438710	0.21	0	1.00	1.6×10^{-7}	7.2×10^{-6}
15	cis	chr22	rs2235852	1	41661154	0.40	rs2235852	41661154	0.40	0	1.00	1.6×10^{-6}	1.9×10^{-4}

Schizophrenia Gene 54
EP300: E1A binding protein p300
Gene Location: chr22:41488613-41576081
GWAS Data: McCarroll 2012
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 1.1×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
2	trans	chr2	rs7600002	5	64513207	0.40	rs7600002	64513207	0.40	0	1.00	3.2×10^{-6}	1.1×10^{-1}
3	trans	chr2	rs2084872	1	208969865	0.23	rs2084872	208969865	0.23	0	1.00	1.1×10^{-6}	5.3×10^{-1}
4	trans	chr7	rs765001	1	14118349	0.41	rs765001	14118349	0.41	0	1.00	2.6×10^{-6}	1.4×10^{-1}
5	trans	chr9	rs11143080	1	74656309	0.34	rs11143080	74656309	0.34	0	1.00	7.5×10^{-7}	5.8×10^{-2}
6	cis	chr22	rs926914	1	41418154	0.22	rs926914	41418154	0.22	0	1.00	4.8×10^{-6}	3.8×10^{-6}
14	cis	chr22	rs2024566	1	41697338	0.24	rs2024566	41697338	0.24	0	1.00	3.7×10^{-6}	3.5×10^{-4}

Schizophrenia Gene 55
SERPIND1: serpin peptidase inhibitor, clade D (heparin cofactor), member 1
Gene Location: chr22:21128382-21142008
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 5.3×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs6690415	41	242374995	0.46	rs6690415	242374995	0.46	0	1.00	1.1×10^{-6}	6.5×10^{-1}
2	trans	chr2	rs1027003	41	108723751	0.18	rs1027003	108723751	0.18	0	1.00	4.8×10^{-6}	2.8×10^{-1}
3	trans	chr11	rs7949686	1	38809822	0.40	rs7949686	38809822	0.40	0	1.00	1.0×10^{-5}	3.8×10^{-2}
4	trans	chr11	rs921872	2	86724086	0.47	rs921872	86724086	0.47	0	1.00	1.0×10^{-5}	1.3×10^{-3}
5	trans	chr11	rs1389235	10	129390680	0.26	rs1389235	129390680	0.26	0	1.00	7.0×10^{-6}	3.6×10^{-3}
6	trans	chr12	rs2398555	5	132214488	0.26	rs2398555	132214488	0.26	0	1.00	8.3×10^{-6}	3.8×10^{-1}
7	cis	chr22	rs178297	1	21353328	0.42	rs178297	21353328	0.42	0	1.00	4.0×10^{-4}	2.5×10^{-1}

Schizophrenia Gene 55
SERPIND1: serpin peptidase inhibitor, clade D (heparin cofactor), member 1
Gene Location: chr22:21128382-21142008
GWAS Data: McCarroll 2012
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 1.7×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs1321119	3	55950886	0.13	rs1321119	55950886	0.13	0	1.00	8.8×10^{-6}	8.9×10^{-1}
2	trans	chr2	rs12479151	9	158726555	0.45	rs12479151	158726555	0.45	0	1.00	3.6×10^{-6}	5.9×10^{-1}
4	trans	chr7	rs17199659	1	34851829	0.10	rs17199659	34851829	0.10	0	1.00	7.6×10^{-6}	3.6×10^{-1}
5	trans	chr12	rs11177527	8	69558981	0.15	rs11177527	69558981	0.15	0	1.00	8.3×10^{-6}	10.0×10^{-1}
6	trans	chr12	rs6538520	3	95003358	0.44	rs6538520	95003358	0.44	0	1.00	4.2×10^{-6}	1.9×10^{-2}
7	trans	chr20	rs6079468	2	14498396	0.14	rs6079468	14498396	0.14	0	1.00	9.7×10^{-6}	1.8×10^{-5}

Schizophrenia Gene 56
ZDHHC5: zinc finger, DHHC-type containing 5
Gene Location: chr11:57435473-57468659
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 4.7×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr5	rs116364	1	6699224	0.43	rs116364	6699224	0.43	0	1.00	9.4×10^{-6}	2.3×10^{-1}
2	trans	chr7	rs10227043	4	138538228	0.15	rs10227043	138538228	0.15	0	1.00	5.3×10^{-7}	1.1×10^{-1}
7	cis	chr11	rs576859	2	57480623	0.27	rs576859	57480623	0.27	0	1.00	1.8×10^{-14}	3.6×10^{-6}

Schizophrenia Gene 56
ZDHHC5: zinc finger, DHHC-type containing 5
Gene Location: chr11:57435473-57468659
GWAS Data: McCarroll 2012
Functional Data: Dixon 2007 LCL eQTL
Empirical Sherlock p-value: 1.2×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs3890745	38	2553624	0.46	rs3890745	2553624	0.46	0	1.00	3.2×10^{-6}	1.9×10^{-2}
2	trans	chr1	rs4245671	13	96258121	0.47	rs4245671	96258121	0.47	0	1.00	1.8×10^{-6}	3.6×10^{-1}
3	trans	chr4	rs1390066	16	67809075	0.38	rs1390066	67809075	0.38	0	1.00	7.0×10^{-6}	6.8×10^{-1}
4	trans	chr6	rs1079114	7	6894224	0.48	rs1079114	6894224	0.48	0	1.00	1.0×10^{-5}	1.3×10^{-1}
5	trans	chr6	rs7755431	5	43937518	0.35	rs7755431	43937518	0.35	0	1.00	5.8×10^{-6}	2.1×10^{-1}
6	trans	chr6	rs2170534	1	149273772	0.40	rs2170534	149273772	0.40	0	1.00	5.8×10^{-6}	7.4×10^{-1}
7	trans	chr8	rs1035665	185	72604032	0.50	rs1035665	72604032	0.50	0	1.00	2.3×10^{-7}	2.8×10^{-1}
12	cis	chr11	rs1783979	2	57468129	0.26	rs1783979	57468129	0.26	0	1.00	2.3×10^{-6}	2.3×10^{-4}
25	trans	chr17	rs6502398	106	14735492	0.40	rs6502398	14735492	0.40	0	1.00	1.3×10^{-6}	4.6×10^{-1}
26	trans	chr21	rs363544	3	31050277	0.41	rs363544	31050277	0.41	0	1.00	1.7×10^{-6}	1.5×10^{-2}

Schizophrenia Gene 56
ZDHHC5: zinc finger, DHHC-type containing 5
Gene Location: chr11:57435473-57468659
GWAS Data: McCarroll 2012
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 5.2×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
3	trans	chr1	rs4300250	1	199628473	0.20	rs4300250	199628473	0.20	0	1.00	4.3×10^{-6}	4.2×10^{-2}
4	trans	chr1	rs2553737	1	199777749	0.48	rs2553737	199777749	0.48	0	1.00	3.2×10^{-6}	6.2×10^{-1}
12	trans	chr3	rs2609860	1	146260900	0.25	rs2609860	146260900	0.25	0	1.00	7.9×10^{-6}	6.5×10^{-1}
13	trans	chr5	rs6860055	56	16306110	0.15	rs12521410	16306059	0.17	51	NA	6.8×10^{-7}	1.1×10^{-1}
17	trans	chr7	rs4723598	1	36953196	0.13	rs4723598	36953196	0.13	0	1.00	4.1×10^{-6}	3.3×10^{-1}
20	trans	chr8	rs6601285	57	8937942	0.07	rs4841096	8938003	0.07	61	NA	6.8×10^{-7}	1.1×10^{-5}
53	trans	chr9	rs1330304	2	16714629	0.50	rs1330304	16714629	0.50	0	1.00	8.1×10^{-6}	8.7×10^{-2}
75	trans	chr15	rs2899662	2	61076219	0.21	rs2899662	61076219	0.21	0	1.00	5.5×10^{-6}	2.0×10^{-1}

Schizophrenia Gene 57
PRMT7: protein arginine methyltransferase 7
Gene Location: chr16:68344876-68391169
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 2.6×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr1	rs605025	2	155887772	0.15	rs605025	155887772	0.15	0	1.00	8.1×10^{-6}	2.9×10^{-2}
4	trans	chr3	rs6776854	7	16457973	0.22	rs6776854	16457973	0.22	0	1.00	4.8×10^{-6}	7.2×10^{-1}
6	trans	chr3	rs6809606	18	59568658	0.09	rs6809606	59568658	0.09	0	1.00	2.3×10^{-7}	3.1×10^{-1}
8	trans	chr6	rs6913034	2	14352513	0.36	rs6913034	14352513	0.36	0	1.00	1.9×10^{-6}	5.9×10^{-1}
11	trans	chr6	rs6908127	2	151003757	0.18	rs6908127	151003757	0.18	0	1.00	8.3×10^{-7}	5.7×10^{-2}
15	trans	chr8	rs2622554	2	56290516	0.12	rs2622554	56290516	0.12	0	1.00	2.7×10^{-6}	4.1×10^{-1}
17	trans	chr9	rs10985811	1	101070487	0.26	rs10985811	101070487	0.26	0	1.00	9.0×10^{-8}	8.1×10^{-5}
18	trans	chr10	rs17372040	3	4779264	0.02	rs17372040	4779264	0.02	0	1.00	4.3×10^{-6}	7.5×10^{-1}
19	trans	chr13	rs12863903	100	96638651	0.10	rs12863903	96638651	0.10	0	1.00	1.5×10^{-6}	8.0×10^{-4}
20	trans	chr13	rs354447	1	106924526	0.24	rs354447	106924526	0.24	0	1.00	4.8×10^{-6}	2.3×10^{-1}
21	trans	chr14	rs35576618	12	37490875	0.01	rs976171	37526827	0.13	35952	0.91	4.5×10^{-6}	4.9×10^{-1}
24	cis	chr16	rs2271293	1	67902070	0.08	rs2271293	67902070	0.08	0	1.00	2.0×10^{-6}	2.3×10^{-2}
33	cis	chr16	rs7190134	1	68381516	0.12	rs7190134	68381516	0.12	0	1.00	5.2×10^{-10}	9.0×10^{-4}
34	trans	chr17	rs692198	49	41071396	0.38	rs692198	41071396	0.38	0	1.00	5.3×10^{-6}	4.7×10^{-1}
36	trans	chr17	rs12942446	3	68953037	0.16	rs12942446	68953037	0.16	0	1.00	3.6×10^{-6}	8.1×10^{-3}
38	trans	chr18	rs12954483	6	52734527	0.11	rs12954483	52734527	0.11	0	1.00	6.4×10^{-8}	3.8×10^{-3}

Schizophrenia Gene 57
PRMT7: protein arginine methyltransferase 7
Gene Location: chr16:68344876-68391169
GWAS Data: McCarroll 2012
Functional Data: Schadt 2008 Liver eQTL
Empirical Sherlock p-value: 6.1×10^{-3}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
13	cis	chr16	rs1465467	2	68398432	0.42	rs1465467	68398432	0.42	0	1.00	3.3×10^{-8}	1.7×10^{-4}
17	trans	chr18	rs2036736	14	9047864	0.30	rs2036736	9047864	0.30	0	1.00	2.9×10^{-6}	6.5×10^{-1}

Schizophrenia Gene 58
HGS: hepatocyte growth factor-regulated tyrosine kinase substrate
Gene Location: chr17:79650961-79669151
GWAS Data: McCarroll 2012
Functional Data: Zeller 2010 Monocyte eQTL
Empirical Sherlock p-value: 1.9×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs13032036	10	113382594	0.03	rs13032036	113382594	0.03	0	1.00	8.1×10^{-6}	6.7×10^{-2}
4	trans	chr2	rs6738261	3	229333848	0.48	rs6738261	229333848	0.48	0	1.00	4.9×10^{-6}	3.9×10^{-4}
5	trans	chr6	rs12191268	1	148798457	0.05	rs12191268	148798457	0.05	0	1.00	2.4×10^{-6}	6.4×10^{-1}
6	trans	chr7	rs354075	4	149329991	0.17	rs354075	149329991	0.17	0	1.00	6.9×10^{-6}	1.2×10^{-1}

Schizophrenia Gene 58
HGS: hepatocyte growth factor-regulated tyrosine kinase substrate
Gene Location: chr17:79650961-79669151
GWAS Data: McCarroll 2012
Functional Data: Duan 2008 LCL eQTL
Empirical Sherlock p-value: 1.6×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr10	rs10994415	7	62322034	0.17	rs10994415	62322034	0.17	0	1.00	1.0×10^{-5}	8.5×10^{-4}

Schizophrenia Gene 58
HGS: hepatocyte growth factor-regulated tyrosine kinase substrate
Gene Location: chr17:79650961-79669151
GWAS Data: McCarroll 2012
Functional Data: Myers 2007 Brain eQTL
Empirical Sherlock p-value: 1.0×10^{-2}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs11690661	1	153774953	0.18	rs11690661	153774953	0.18	0	1.00	9.3×10^{-6}	1.7×10^{-4}
2	trans	chr4	rs4303991	24	124478871	0.40	rs4303991	124478871	0.40	0	1.00	7.3×10^{-6}	1.1×10^{-3}
3	trans	chr5	rs4836433	34	128361955	0.39	rs4836433	128361955	0.39	0	1.00	8.1×10^{-6}	3.1×10^{-1}
4	trans	chr6	rs11510517	2	117851218	0.34	rs11510517	117851218	0.34	0	1.00	9.2×10^{-6}	3.1×10^{-1}
5	trans	chr7	rs1968201	18	102807435	0.07	rs1968201	102807435	0.07	0	1.00	3.1×10^{-6}	8.0×10^{-1}
6	trans	chr10	rs7894214	2	98393929	0.31	rs7894214	98393929	0.31	0	1.00	3.4×10^{-6}	9.9×10^{-1}

Schizophrenia Gene 59
SPATA18: spermatogenesis associated 18
Gene Location: chr4:52917592-52963458
GWAS Data: McCarroll 2012
Functional Data: MuTHER 2011 Adipose eQTL
Empirical Sherlock p-value: 4.2×10^{-4}

BLK	PRX	CHR	eQTL SNP	PL	Location	MAF	GWAS SNP	Location	MAF	Delta	LD	eQTL pval	GWAS pval
1	trans	chr2	rs4505525	1	122628522	0.13	rs4505525	122628522	0.13	0	1.00	6.5×10^{-6}	4.9×10^{-1}
3	trans	chr5	rs11951404	1	55926837	0.13	rs11951404	55926837	0.13	0	1.00	3.4×10^{-6}	1.0×10^{-2}
5	trans	chr6	rs13217257	2	148266755	0.05	rs13217257	148266755	0.05	0	1.00	9.8×10^{-6}	3.7×10^{-1}
11	trans	chr8	rs16939417	1	78009433	0.35	rs16939417	78009433	0.35	0	1.00	8.2×10^{-7}	1.9×10^{-1}
15	trans	chr19	rs9304900	3	2873439	0.43	rs9304900	2873439	0.43	0	1.00	3.2×10^{-6}	2.7×10^{-1}
46	trans	chr19	rs7245983	1	19657632	0.41	rs7245983	19657632	0.41	0	1.00	4.5×10^{-6}	1.3×10^{-9}
47	trans	chr19	rs11672983	1	55383051	0.31	rs11672983	55383051	0.31	0	1.00	2.7×10^{-6}	7.8×10^{-1}

Bibliography

[1] Manolio, T. A., Collins, F. S., Cox, N. J., Goldstein, D. B., Hindorff, L. A., Hunter, D. J., McCarthy, M. I., Ramos, E. M., Cardon, L. R., Chakravarti, A., et al. (2009). Finding the missing heritability of complex diseases. Nature *461*, 747–753.

[2] McClellan, J. and King, M.-C. (2010). Genetic heterogeneity in human disease. Cell *141*, 210–217.

[3] Visscher, P. M., Brown, M. A., McCarthy, M. I., and Yang, J. (2012). Five Years of GWAS Discovery. The American Journal of Human Genetics *90*, 7–24.

[4] ENCODE Project Consortium. (2004). The ENCODE (ENCyclopedia Of DNA Elements) Project. Science *306*, 636–640.

[5] GTEx Consortium. (2013). The Genotype-Tissue Expression (GTEx) project. Nature Publishing Group *45*, 580–585.

[6] Zuk, O., Hechter, E., Sunyaev, S. R., and Lander, E. S. (2012). The mystery of missing heritability: Genetic interactions create phantom heritability. Proceedings of the National Academy of Sciences pp. 1–6.

[7] Yang, J., Benyamin, B., Mcevoy, B. P., Gordon, S., Henders, A. K., Nyholt, D. R., Madden, P. A., Heath, A. C., Martin, N. G., Montgomery, G. W., et al. (2010). Common SNPs explain a large proportion of the heritability for human height. Nature genetics *42*, 565–569.

[8] Hindorff, L. A., Sethupathy, P., Junkins, H. A., Ramos, E. M., Mehta, J. P., Collins, F. S., and Manolio, T. A. (2009). Potential etiologic and functional implications of genome-wide association loci for human diseases and traits. Proceedings of the National Academy of Sciences of the United States of America *106*, 9362–9367.

[9] Bloom, J. S., Ehrenreich, I. M., Loo, W. T., Lite, T.-L. V., and Kruglyak, L. (2013). Finding the sources of missing heritability in a yeast cross. Nature pp. 1–6.

[10] Lango Allen, H., Estrada, K., Lettre, G., Berndt, S. I., Weedon, M. N., Rivadeneira, F., Willer, C. J., Jackson, A. U., Vedantam, S., Raychaudhuri, S., et al. (2010). Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature *467*, 832–838.

[11] Yang, J., Manolio, T. A., Pasquale, L. R., Boerwinkle, E., Caporaso, N., Cunningham, J. M., de Andrade, M., Feenstra, B., Feingold, E., Hayes, M. G., et al. (2011). Genome partitioning of genetic variation for complex traits using common SNPs. Nature genetics *43*, 519–525.

[12] Consortium, T. I. S. (2009). Common polygenic variation contributes to risk of schizophrenia and bipolar disorder. Nature *460*, 748–752.

[13] He, X., Fuller, C. K., Song, Y., Meng, Q., Zhang, B., Yang, X., and Li, H. (2013). Sherlock: Detecting Gene-Disease Associations by Matching Patterns of Expression QTL and GWAS. The American Journal of Human Genetics *92*, 667–680.

[14] Fransen, K., Visschedijk, M. C., Van Sommeren, S., Fu, J. Y., Franke, L., Festen, E. A. M., Stokkers, P. C. F., Van Bodegraven, A. A., Crusius, J. B. A., Hommes, D. W., et al. (2010). Analysis of SNPs with an effect on gene expression identifies UBE2L3 and BCL3 as potential new risk genes for Crohn's disease. Human molecular genetics *19*, 3482–3488.

[15] Montgomery, S. B. S. and Dermitzakis, E. T. E. (2011). From expression QTLs to personalized transcriptomics. Transactions of the IRE Professional Group on *12*, 277–282.

[16] Schadt, E., Lamb, J., Yang, X., Zhu, J., and Edwards, S. (2005). An integrative genomics approach to infer causal associations between gene expression .... Nature genetics.

[17] Hardison, R. C. and Blobel, G. A. (2013). Genetics. GWAS to therapy by genome edits? Science *342*, 206–207.

[18] Bauer, D. E., Kamran, S. C., Lessard, S., Xu, J., and Fujiwara, Y. (2013). An Erythroid Enhancer of BCL11A Subject to Genetic Variation Determines Fetal Hemoglobin Level. Science.

[19] Fisher, S. R. A. (1925). Statistical Methods for Research Workers. Oliver and Boyd Edinburgh.

[20] Efron, B. (2004). Large-Scale Simultaneous Hypothesis Testing. Journal of the American Statistical Association *99*, 96–104.

[21] Fransen, K., Visschedijk, M. C., van Sommeren, S., Fu, J. Y., Franke, L., Festen, E. A. M., Stokkers, P. C. F., van Bodegraven, A. A., Crusius, J. B. A., Hommes, D. W., et al. (2010). Analysis of SNPs with an effect on gene expression identifies UBE2L3 and BCL3 as potential new risk genes for Crohn's disease. Human molecular genetics *19*, 3482–3488.

[22] Stephens, M. and Balding, D. J. (2009). Modelling: Bayesian statistical methods for genetic association studies. Nature Reviews Genetics *10*, 681–690.

[23] Servin, B. and Stephens, M. (2007). Imputation-based analysis of association studies: candidate regions and quantitative traits. PLoS Genetics *3*, e114.

[24] Liu, J. Z., Mcrae, A. F., Nyholt, D. R., Medland, S. E., Wray, N. R., Brown, K. M., Investigators, A., Hayward, N. K., Montgomery, G. W., Visscher, P. M., et al. (2010). A Versatile Gene-Based Test for Genome-wide Association Studies. The American Journal of Human Genetics *87*, 139–145.

[25] Barrett, J. C., Hansoul, S., Nicolae, D. L., Cho, J. H., Duerr, R. H., Rioux, J. D., Brant, S. R., Silverberg, M. S., Taylor, K. D., Barmada, M. M., et al. (2008). Genome-wide association defines more than 30 distinct susceptibility loci for Crohn's disease. Nature genetics *40*, 955–962.

[26] Franke, A., Mcgovern, D. P. B., Barrett, J. C., Wang, K., Radford-Smith, G. L., Ahmad, T., Lees, C. W., Balschun, T., Lee, J., Roberts, R., et al. (2010). Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci. Nature Publishing Group *42*, 1118–1125.

[27] Duan, S., Huang, R., Zhang, W., Bleibel, W., Roe, C., Clark, T., Chen, T., Schweitzer, A., Blume, J., and Cox, N. (2008). Genetic architecture of transcript-level variation in humans. The American Journal of Human Genetics *82*, 1101–1113.

[28] Lees, C. W., Barrett, J. C., Parkes, M., and Satsangi, J. (2011). New IBD genetics: common pathways with other diseases. Gut *60*, 1739–1753.

[29] Zhernakova, A., Stahl, E. A., Trynka, G., Raychaudhuri, S., Festen, E. A., Franke, L., Westra, H.-J., Fehrmann, R. S. N., Kurreeman, F. A. S., Thomson, B., et al. (2011). Meta-Analysis of Genome-Wide Association Studies in Celiac Disease and Rheumatoid Arthritis Identifies Fourteen Non-HLA Shared Loci. PLoS Genetics *7*.

[30] Donlin, L., Danzl, N., Wanjalla, C., and Alexandropoulos, K. (2005). Deficiency in expression of the signaling protein Sin/Efs leads to T-lymphocyte activation and mucosal inflammation. Molecular and Cellular Biology *25*, 11035.

[31] Muraoka, M., Hasegawa, H., Kohno, M., Inoue, A., Miyazaki, T., Terada, M., Nose, M., and Yasukawa, M. (2006). IK cytokine ameliorates the progression of lupus nephritis in MRL/lpr mice. Arthritis and Rheumatism *54*, 3591–3600.

[32] Moriwaki, Y., Yoshikawa, K., Fukuda, H., Fujii, Y. X., Misawa, H., and Kawashima, K. (2007). Immune system expression of SLURP-1 and SLURP-2, two endogenous nicotinic acetylcholine receptor ligands. Life Sciences *80*, 2365–2368.

[33] Galitovskiy, V., Qian, J., Chernyavsky, A. I., Marchenko, S., Gindi, V., Edwards, R. A., and Grando, S. A. (2011). Cytokine-induced alterations of $\alpha7$ nicotinic receptor in colonic CD4 T cells mediate dichotomous response to nicotine in murine models of Th1/Th17- versus Th2-mediated colitis. Journal of immunology (Baltimore, Md. : 1950) *187*, 2677–2687.

[34] Snoek, S. A., Verstege, M. I., van der Zanden, E. P., Deeks, N., Bulmer, D. C., Skynner, M., Lee, K., Te Velde, A. A., Boeckxstaens, G. E., and de Jonge, W. J. (2010). Selective $\alpha7$ nicotinic acetylcholine receptor agonists worsen disease in experimental colitis. British journal of pharmacology *160*, 322–333.

[35] Zeggini, E., Scott, L. J., Saxena, R., Voight, B. F., Marchini, J. L., Hu, T., de Bakker, P. I. W., Abecasis, G. R., Almgren, P., Andersen, G., et al. (2008). Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. Nature Publishing Group *40*, 638–645.

[36] Schadt, E., Molony, C., Chudin, E., Hao, K., Yang, X., Lum, P., Kasarskis, A., Zhang, B., Wang, S., and Suver, C. (2008). Mapping the genetic architecture of gene expression in human liver. PLoS Biol *6*, e107.

[37] Chen, Y., Zhu, J., Lum, P. Y., Yang, X., Pinto, S., MacNeil, D. J., Zhang, C., Lamb, J., Edwards, S., Sieberts, S. K., et al. (2008). Variations in DNA elucidate molecular networks that cause disease. Nature *452*, 429–435.

[38] Derry, J. M. J., Zhong, H., Molony, C., MacNeil, D., GuhaThakurta, D., Zhang, B., Mudgett, J., Small, K., El Fertak, L., Guimond, A., et al. (2010). Identification of Genes and Networks Driving Cardiovascular and Metabolic Phenotypes in a Mouse F2 Intercross. PLoS One *5*.

[39] Yang, X., Deignan, J. L., Qi, H., Zhu, J., Qian, S., Zhong, J., Torosyan, G., Majid, S., Falkard, B., Kleinhanz, R. R., et al. (2009). Validation of candidate causal genes for obesity that affect shared metabolic pathways and networks. Nature Publishing Group *41*, 415–423.

[40] Wang, Q., Levay, K., Chanturiya, T., Dvoriantchikova, G., Anderson, K. L., Bianco, S. D. C., Ueta, C. B., Molano, R. D., Pileggi, A., Gurevich, E. V., et al. (2011). Targeted deletion of one or two copies of the G protein beta subunit G beta 5 gene has distinct effects on body weight and behavior in mice. Faseb Journal *25*, 3949–3957.

[41] Kopf, D., Cheng, L. S. C., Blandau, P., Hsueh, W., Raffel, L. J., Buchanan, T. A., Xiang, A. H., Davis, R. C., Rotter, J. I., and Lehnerta, H. (2008). Association of insulin sensitivity and glucose tolerance with the c.825C ¿ T variant of the G protein beta-3 subunit gene. Journal of Diabetes and Its Complications *22*, 205–209.

[42] Anderson, E. C. and Novembre, J. (2003). Finding haplotype block boundaries by using the minimum-description-length principle. The American Journal of Human Genetics *73*, 336–354.

[43] 1000 Genomes Project Consortium, Abecasis, G. R., Auton, A., Brooks, L. D., DePristo, M. A., Durbin, R. M., Handsaker, R. E., Kang, H. M., Marth, G. T., and McVean, G. A. (2012). An integrated map of genetic variation from 1,092 human genomes. Nature *491*, 56–65.

[44] Purcell, S., Neale, B., Todd-Brown, K., Thomas, L., Ferreira, M. A. R., Bender, D., Maller, J., Sklar, P., de Bakker, P. I. W., Daly, M. J., et al. (2007). PLINK: A Tool Set for Whole-Genome Association and Population-Based Linkage Analyses. The American Journal of Human Genetics *81*, 559–575.

[45] Hastie, T., Tibshirani, R., and Friedman, J. (2009). The Elements of Statistical Learning. Data Mining, Inference, and Prediction, Second Edition. (Springer).

[46] Van Zwet, W. R. and Oosterhoff, J. (1967). On the combination of independent test statistics. The Annals of Mathematical Statistics pp. 659–680.

[47] Storey, J. D. and Tibshirani, R. (2003). Statistical significance for genomewide studies. Proceedings of the National Academy of Sciences of the United States of America *100*, 9440–9445.

[48] Dixon, A., Liang, L., Moffatt, M., Chen, W., Heath, S., Wong, K., Taylor, J., Burnett, E., Gut, I., and Farrall, M. (2007). A genome-wide association study of global gene expression. Nature genetics *39*, 1202–1207.

[49] Zeller, T., Wild, P., Szymczak, S., Rotival, M., Schillert, A., Castagne, R., Maouche, S., Germain, M., Lackner, K., Rossmann, H., et al. (2010). Genetics and Beyond – The Transcriptome of Human Monocytes and Disease Susceptibility. PLoS One *5*, e10693.

[50] Myers, A. J., Gibbs, J. R., Webster, J. A., Rohrer, K., Zhao, A., Marlowe, L., Kaleem, M., Leung, D., Bryden, L., Nath, P., et al. (2007). A survey of genetic human cortical gene expression. Nature genetics *39*, 1494–1499.

[51] Grundberg, E., Small, K. S., Hedman, Å. K., Nica, A. C., Buil, A., Keildson, S., Bell, J. T., Yang, T.-P., Meduri, E., Barrett, A., et al. (2012). Mapping cis- and trans-regulatory effects across multiple tissues in twins. Nature genetics *44*, 1084–1089.

[52] Wang, J., Duncan, D., Shi, Z., and Zhang, B. (2013). WEB-based GEne SeT AnaLysis Toolkit (WebGestalt): update 2013. Nucleic Acids Research *41*, W77–83.

[53] Blake, J. A., Bult, C. J., Eppig, J. T., Kadin, J. A., Richardson, J. E., and Mouse Genome Database Group. (2014). The Mouse Genome Database: integration of and access to knowledge about the laboratory mouse. Nucleic Acids Research *42*, D810–7.

[54] Yamazaki, K., Umeno, J., Takahashi, A., Hirano, A., Johnson, T. A., Kumasaka, N., Morizono, T., Hosono, N., Kawaguchi, T., Takazoe, M., et al. (2013). A genome-wide association study identifies 2 susceptibility Loci for Crohn's disease in a Japanese population. Gastroenterology *144*, 781–788.

[55] Jostins, L., Ripke, S., Weersma, R. K., Duerr, R. H., McGovern, D. P., Hui, K. Y., Lee, J. C., Schumm, L. P., Sharma, Y., Anderson, C. A., et al. (2012). Host-microbe interactions have shaped the genetic architecture of inflammatory bowel disease. Nature *491*, 119–124.

[56] Julià, A., Domènech, E., Ricart, E., Tortosa, R., García-Sánchez, V., Gisbert, J. P., Nos Mateu, P., Gutiérrez, A., Gomollón, F., Mendoza, J. L., et al. (2013). A genome-wide association study on a southern European population identifies a new Crohn's disease susceptibility locus at RBX1-EP300. Gut pp. –.

[57] Kenny, E. E. E., Pe'er, I. I., Karban, A. A., Ozelius, L. L., Mitchell, A. A. A., Ng, S. M. S., Erazo, M. M., Ostrer, H. H., Abraham, C. C., Abreu, M. T. M., et al. (2012). A genome-wide scan of Ashkenazi Jewish Crohn's disease suggests novel susceptibility loci. PLoS Genetics *8*, e1002559–e1002559.

[58] Festen, E. A. M., Goyette, P., Green, T., Boucher, G., Beauchamp, C., Trynka, G., Dubois, P. C., Lagacé, C., Stokkers, P. C. F., Hommes, D. W., et al. (2011). A meta-analysis of genome-wide association scans identifies IL18RAP, PTPN2, TAGAP, and PUS10 as shared risk loci for Crohn's disease and celiac disease. PLoS Genetics *7*, e1001283–e1001283.

[59] Dubinsky, M. C., Mei, L., Friedman, M., Dhere, T., Haritunians, T., Hakonarson, H., Kim, C., Glessner, J., Targan, S. R., and McGovern, D. P. (2010). Genome wide association (GWA) predictors of antiTNFα therapeutic responsiveness in pediatric inflammatory bowel disease. Inflammatory Bowel Diseases *16*, 1357–1366.

[60] Reid-Lombardo, K. M., Fridley, B. L., Bamlet, W. R., Cunningham, J. M., Sarr, M. G., and Petersen, G. M. (2013). Survival Is Associated With Genetic Variation in Inflammatory Pathway Genes Among Patients With Resected and Unresected Pancreatic Cancer. Annals of Surgery *257*, 1096–1102.

[61] Waeber, G., Delplanque, J., Bonny, C., Mooser, V., Steinmann, M., Widmann, C., Maillard, A., Miklossy, J., Dina, C., Hani, E. H., et al. (2000). The gene MAPK8IP1, encoding islet-brain-1, is a candidate for type 2 diabetes. Nature Publishing Group *24*, 291–295.

[62] Campo, G. M., Avenoso, A., D'Ascola, A., Scuruchi, M., Prestipino, V., Nastasi, G., Calatroni, A., and Campo, S. (2012). The inhibition of hyaluronan degradation reduced pro-inflammatory cytokines in mouse synovial fibroblasts subjected to collagen-induced arthritis. Journal of Cellular Biochemistry *113*, 1852–1867.

[63] Hsiao, F.-C., Lin, Y.-F., Hsieh, P.-S., Chu, N.-F., Shieh, Y.-S., Hsieh, C.-H., Lee, C.-H., and Hung, Y.-J. (2013). Circulating Growth Arrest-Specific 6 Protein Is Associated With Adiposity, Systemic Inflammation, and Insulin Resistance Among Overweight and Obese Adolescents. Journal of Clinical Endocrinology & Metabolism *98*, E267–E274.

[64] Hurtado, B. and Garcia de Frutos, P. (2010). GAS6 in systemic inflammatory diseases: with and without infection. Critical Care *14*.

[65] Kuo, F.-C., Hung, Y.-J., Shieh, Y.-S., Hsieh, C.-H., Hsiao, F.-C., and Lee, C.-H. (2014). The levels of plasma growth arrest-specific protein 6 is associated with insulin sensitivity and inflammation in women. Diabetes research and clinical practice.

[66] Cleynen, I., Jüni, P., Bekkering, G. E., Nüesch, E., Mendes, C. T., Schmied, S., Wyder, S., Kellen, E., Villiger, P. M., Rutgeerts, P., et al. (2011). Genetic Evidence Supporting the Association of Protease and Protease Inhibitor Genes with Inflammatory Bowel Disease: A Systematic Review. PLoS One *6*, e24106.

[67] Paradis, M.-E. M., Badellino, K. O. K., Rader, D. J. D., Deshaies, Y. Y., Couture, P. P., Archer, W. R. W., Bergeron, N. N., and Lamarche, B. B. (2006). Endothelial lipase is associated with inflammation in humans. Journal of Lipid Research *47*, 2808–2813.

[68] Hara, T., Ishida, T., Kojima, Y., Tanaka, H., Yasuda, T., Shinohara, M., Toh, R., and Hirata, K.-i. (2011). Targeted deletion of endothelial lipase increases HDL particles with anti-inflammatory properties both in vitro and in vivo. Journal of Lipid Research *52*, 57–67.

[69] Kosaka, Y., Mimori, K., Tanaka, F., Inoue, H., Watanabe, M., and Mori, M. (2007). Clinical significance of the loss of MATS1 mRNA expression in colorectal cancer. International Journal of Oncology *31*, 333–338.

[70] Jun, D.-J., Na, K.-Y., Kim, W., Kwak, D., Kwon, E.-J., Yoon, J. H., Yea, K., Lee, H., Kim, J., Suh, P.-G., et al. (2010). Melanocortins induce interleukin 6 gene expression and secretion through melanocortin receptors 2 and 5 in 3T3-L1 adipocytes. Journal of molecular endocrinology *44*, 225–236.

[71] Mahida, Y. R., Kurlac, L., Gallagher, A., and Hawkey, C. J. (1991). High circulating concentrations of interleukin-6 in active Crohn's disease but not ulcerative colitis. Gut *32*, 1531–1534.

[72] Van Den Brande, J. M. H., Peppelenbosch, M. P., and Van Deventer, S. J. H. (2002). Treating Crohn's disease by inducing T lymphocyte apoptosis. Annals of the New York Academy of Sciences *973*, 166–180.

[73] Poulsen, P., Kyvik, K. O., Vaag, A., and Beck-Nielsen, H. (1999). Heritability of type II (non-insulin-dependent) diabetes mellitus and abnormal glucose tolerance–a population-based twin study. Diabetologia *42*, 139–145.

[74] Voight, B. F., Scott, L. J., Steinthorsdottir, V., Morris, A. P., Dina, C., Welch, R. P., Zeggini, E., Huth, C., Aulchenko, Y. S., Thorleifsson, G., et al. (2010). Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Publishing Group *42*, 579–589.

[75] Comuzzie, A. G., Cole, S. A., Laston, S. L., Voruganti, V. S., Haack, K., Gibbs, R. A., and Butte, N. F. (2012). Novel genetic loci identified for the pathophysiology of childhood obesity in the Hispanic population. PLoS One *7*, e51954.

[76] Waterworth, D. M., Ricketts, S. L., Song, K., Chen, L., Zhao, J. H., Ripatti, S., Aulchenko, Y. S., Zhang, W., Yuan, X., Lim, N., et al. (2010). Genetic variants influencing circulating lipid levels and risk of coronary artery disease. Arteriosclerosis, thrombosis, and vascular biology *30*, 2264–2276.

[77] Akira, S., Misawa, T., Satoh, T., and Saitoh, T. (2013). Macrophages control innate inflammation. Diabetes Obesity & Metabolism *15*, 10–18.

[78] Pinney, S. E., Ganapathy, K., Bradfield, J., Stokes, D., Sasson, A., Mackiewicz, K., Boodhansingh, K., Hughes, N., Becker, S., Givler, S., et al. (2013). Dominant Form of Congenital Hyperinsulinism Maps to HK1 Region on 10q. Hormone Research in Paediatrics *80*, 18–27.

[79] Goldacre, M. J., Wotton, C. J., and Keenan, T. D. L. (2012). Risk of selected eye diseases in people admitted to hospital for hypertension or diabetes mellitus: record linkage studies - Authors' response. British Journal of Ophthalmology *96*, 1534–1534.

[80] Go, M. J., Hwang, J.-Y., Kim, Y. J., Hee Oh, J., Kim, Y.-J., Heon Kwak, S., Soo Park, K., Lee, J., Kim, B.-J., Han, B.-G., et al. (2013). New susceptibility loci in MYL2, C12orf51 and OAS1 associated with 1-h plasma glucose as predisposing risk factors for type 2 diabetes in the Korean population. Journal of Human Genetics *58*, 362–365.

[81] Lichtenstein, P., Yip, B. H., Björk, C., Pawitan, Y., Cannon, T. D., Sullivan, P. F., and Hultman, C. M. (2009). Common genetic influences for schizophrenia and bipolar disorder: a population-based study of 2 million nuclear families. Lancet *373*.

[82] Visscher, P. M., Goddard, M. E., Derks, E. M., and Wray, N. R. (2012). Evidence-based psychiatric genetics, AKA the false dichotomy between common and rare variant hypotheses. Molecular Psychiatry *17*, 474–485.

[83] Talih, F. R. (2011). Narcolepsy presenting as schizophrenia: a literature review and two case reports. Innovations in clinical neuroscience *8*, 30–34.

[84] Baglivo, I., Esposito, S., De Cesare, L., Sparago, A., Anvar, Z., Riso, V., Cammisa, M., Fattorusso, R., Grimaldi, G., and Riccio, A. (2013). Genetic and epigenetic mutations affect the DNA binding capability of human ZFP57 in transient neonatal diabetes type 1. FEBS letters *587*, 1474–1481.

[85] Benros, M. E., Nielsen, P. R., Nordentoft, M., Eaton, W. W., Dalton, S. O., and Mortensen, P. B. (2011). Autoimmune diseases and severe infections as risk factors for schizophrenia: a 30-year population-based register study. American Journal of Psychiatry *168*, 1303–1310.

[86] Sasayama, D., Hori, H., Yamamoto, N., Nakamura, S., Teraishi, T., Tatsumi, M., Hattori, K., Ota, M., Higuchi, T., and Kunugi, H. (2014). ITIH3 polymorphism may confer susceptibility to psychiatric disorders by altering the expression levels of GLT8D1. Journal of psychiatric research *50*, 79–83.

[87] Zhang, Y., Schlossman, S. F., Edwards, R. A., Ou, C.-N., Gu, J., and Wu, M. X. (2002). Impaired apoptosis, extended duration of immune responses, and a lupus-like autoimmune disease in IEX-1-transgenic mice. Proceedings of the National Academy of Sciences of the United States of America *99*, 878–883.

[88] Jitoku, D., Hattori, E., Iwayama, Y., Yamada, K., Toyota, T., Kikuchi, M., Maekawa, M., Nishikawa, T., and Yoshikawa, T. (2011). Association study of Nogo-related genes with schizophrenia in a Japanese case-control sample. American journal of medical genetics. Part B, Neuropsychiatric genetics : the official publication of the International Society of Psychiatric Genetics *156B*, 581–592.

[89] Tomita, K., Madura, T., Mantovani, C., and Terenghi, G. (2012). Differentiated adipose-derived stem cells promote myelination and enhance functional recovery in a rat model of chronic denervation. Journal of Neuroscience Research *90*, 1392–1402.

[90] Kalia, S. K., Lee, S., Smith, P. D., Liu, L., Crocker, S. J., Thorarinsdottir, T. E., Glover, J. R., Fon, E. A., Park, D. S., and Lozano, A. M. (2004). BAG5 Inhibits Parkin and Enhances Dopaminergic Neuron Degeneration. Neuron *44*, 931–945.

[91] Howes, O. D. and Kapur, S. (2009). The Dopamine Hypothesis of Schizophrenia: Version III–The Final Common Pathway. Schizophrenia Bulletin *35*, 549–562.

[92] Bertelsen, B., Melchior, L., Jensen, L. R., and Groth, C. (2014). Intragenic deletions affecting two alternative transcripts of the IMMP2L gene in patients with Tourette syndrome. European Journal of . . . .

[93] Kerbeshian, J., Peng, C.-Z., and Burd, L. (2009). Tourette syndrome and comorbid early-onset schizophrenia. Journal of psychosomatic research *67*, 515–523.

[94] Connolly, J. J. and Hakonarson, H. (2012). Role of Cytokines in Systemic Lupus Erythematosus: Recent Progress from GWAS and Sequencing. Journal of Biomedicine and Biotechnology *2012*, 1–17.

[95] Crisafulli, C., Chiesa, A., Han, C., Lee, S.-J., Shim, D. S., Balzarro, B., Andrisano, C., Sidoti, A., Patkar, A. A., Pae, C.-U., et al. (2012). Possible influence of CREB1, CREBBP and CREM variants on diagnosis and treatment outcome in patients with schizophrenia. Neuroscience letters *508*, 37–41.

[96] Zhang, H., Li, D., Su, Y., Jiang, S., Xu, Y., Jiang, K., and Cui, D. (2012). Identification of the N-acylsphingosine amidohydrolase 1 gene (ASAH1)for susceptibility to schizophrenia in a Han Chinese population. World Journal of Biological Psychiatry *13*, 106–113.

[97] Forster, N., Gallinat, S., Jablonska, J., Weiss, S., Elsässer, H.-P., and Lutz, W. (2007). p300 protein acetyltransferase activity suppresses systemic lupus erythematosus-like autoimmune disease in mice. Journal of immunology (Baltimore, Md. : 1950) *178*, 6941–6948.

[98] Walkup, J., Akincigil, A., Hoover, D. R., Siegel, M. J., Amin, S., and Crystal, S. (2011). Use of Medicaid data to explore community characteristics associated with HIV prevalence among beneficiaries with schizophrenia. Public health reports (Washington, D.C. : 1974) *126 Suppl 3*, 89–101.

[99] Ogata, H., Goto, S., Sato, K., Fujibuchi, W., Bono, H., and Kanehisa, M. (1999). KEGG: Kyoto Encyclopedia of Genes and Genomes. Nucleic Acids Research *27*, 29–34.

[100] Drake, R. E. and Mueser, K. T. (2002). Co-occurring alcohol use disorder and schizophrenia. Alcohol research and Health *26*, 99–102.

[101] Cooper, G. M., Johnson, J. A., Langaee, T. Y., Feng, H., Stanaway, I. B., Schwarz, U. I., Ritchie, M. D., Stein, C. M., Roden, D. M., Smith, J. D., et al. (2008). A genome-wide scan for common genetic variants with a large influence on warfarin maintenance dose. Blood *112*, 1022–1027.

[102] Miller, S. M. and Ortega, V. E. (2013). Pharmacogenetics and the Development of Personalized Approaches for Combination Therapy in Asthma. Current Allergy and Asthma Reports *13*, 443–452.

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