# Conditional GWAS analysis to identify disorder-specific SNPs for psychiatric disorders

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**Abstract**
Substantial genetic liability is shared across psychiatric disorders but less is known about risk variants that are specific to a given disorder. We used multi-trait conditional and joint analysis (mtCOJO) to adjust GWAS summary statistics of one disorder for the effects of genetically correlated traits to identify putative disorder-specific SNP associations. We applied mtCOJO to summary statistics for five psychiatric disorders from the Psychiatric Genomics Consortium – schizophrenia (SCZ), bipolar disorder (BIP), major depression (MD), attention-deficit hyperactivity disorder (ADHD) and autism (AUT). Most genome-wide significant variants for these disorders had evidence of pleiotropy (i.e., impact on multiple psychiatric disorders) and hence have reduced mtCOJO conditional effect sizes. However, subsets of genome-wide significant variants had larger conditional effect sizes consistent with disorder-specific effects: 15 of 130 genome-wide significant variants for schizophrenia, 5 of 40 for major depression, 3 of 11 for ADHD and 1 of 2 for autism. We show that decreased expression of *VPS29* in the brain may increase risk to SCZ only and increased expression of *CSE1L* is associated with SCZ and MD, but not with BIP. Likewise, decreased expression of *PCDHA7* in the brain is linked to increased risk of MD but decreased risk of SCZ and BIP.

**Introduction**

Pervasive sharing of genetic risk factors between common psychiatric disorders (i.e. pleiotropy) has now been unequivocably demonstrated from genome-wide association studies (GWAS), as quantified by estimates of genetic correlation ($r_g$) [1, 2]. The $r_g$ estimates are highest between schizophrenia and bipolar disorder (0.67, standard error (s.e.) = 0.03) but are > 0.15 for any combination of the five common disorders of schizophrenia (SCZ), bipolar disorder (BIP), ADHD, Major Depression (MD) and autism spectrum disorders (AUT) [2, 3]. Cross-diagnosis analyses can leverage power to identify genetic risk loci shared across classical diagnostic boundaries [4] and can increase power for risk prediction of disorders in independent samples [5, 6]. The shared genetic basis for psychiatric disorders contributes to an evidence base supporting a trans-diagnostic approach in clinical practice [7]. Nonetheless, traditional diagnostic classes reflect real symptom differences at patient presentation even though it can be difficult to classify some individuals given a high-degree of concurrent and longitudinal comordibity. Since $r_g$ estimates are higher between data sets of the same disorder than between data sets of different disorders [4, 8] it implies some real biological basis to the classical diagnostic classes. Hence, a key question of importance in psychiatry is identification of genetic factors that are disorder specific rather than those shared across classical diagnostic groupings. Identifying such variants could aid in understanding the biological pathways that underlie the constellation of symptoms seen in each disorder.

One method for identifying disorder-specific variants is to conduct a case-case GWAS with cases of one disorder compared to cases of another. The SCZ/BIP working group of the Psychiatric Genomics Consortium (PGC) conducted an association analysis comparing in logistic regression SCZ (N=23,585) vs BIP (N=15,270) cases to identify variants specific to each disorder. The cases were matched on ancestry and genotyping platform, hence the sample sizes were smaller than those available for the disorder specific GWAS which limits the statistical power. Conducting such analysis requires access to the raw genotypes which is not always feasible for all cohorts due to privacy laws. Methods that use summary statistics can utilise larger sample sizes without the need to provide access to raw daa to researchers. In addition, case-case GWAS can identify differences between pairs of disorders[9], but does not generalize to the multivariate space to identify SNPs primarily associated one disorder.

We conditioned the effect of SNPs estimated for one disorder on those of other disorders using multi-trait, conditional and joint analysis (mtCOJO)[10], a summary-statistics based method that accounts for overlap in samples contributing to the disorder specific

GWAS. We report results from conditional analyses of 5 psychiatric disorders: SCZ, BIP, MD, ADHD and AUT using association summary statistics from meta-analyses conducted by the Psychiatric Genomics Consortium (PGC) including data from 23andMe. Each disorder is conditioned on the other four disorders in one model.

**Methods**

We applied the mtCOJO method as described in Zhu et al. [10]. This method approximates a conditional analysis where the effect of a SNP on a disease is conditioned upon the covariates of the disease, but only requires summary statistics as input. As an example, if we are interested in estimating the effect of a SNP (*z*) on risk to schizophrenia (*y*) accounting for the effect of a covarying factor such as bipolar (*x*), we condition upon the effect of bipolar on schizophrenia $\hat{b}_{xy}$, as estimated using Generalised Summary-based Mendelian Randomisation (GSMR). This can be extended to condition upon multiple covarying diseases so that the effect of the SNP on risk on the disorder of interest is estimated conditional upon the covariates on the disorder (see **Supplementary Material** for detailed description of the method).

To identify independent genome-wide significant SNPs for use as genetic instruments in mtCOJO analysis, each dataset was clumped to select independent genome-wide significant (GWS) SNPs ($p < 5 \times 10^{-8}$) using 7,762 unrelated individuals from the Atherosclerosis Risk In Community (ARIC) dataset[11], imputed to 1000Genomes Phase III as an LD reference sample. GWS SNPs more than 1MB apart or with an $r^2$ value < 0.05 were considered to be independent. GSMR accounts for any remaining LD between instruments. GSMR analysis with filtering to remove SNPs with outlier pleiotropic effects (compared to other GWS SNPs) using the HEIDI test [12] was performed with each disorder included both as an exposure and an outcome in combination with the other disorders. Owing to having fewer than 10 independent GWS SNPs, independent SNPs significant at $p < 10^{-7}$ were used for GSMR analysis with autism as the exposure variable. In order to compare the estimated effects of one disorder on another from MR, we derived a conversion of the estimated effects from GSMR to the liability scale (see **Supplementary Material, Supplementary Figure 1**).

We performed mtCOJO analysis (implemented in GCTA[13] (http://cnsgenomics.com/software/gcta/#mtCOJO) of 5 genetically correlated psychiatric

disorders using the results from large genome-wide association studies from the Psychiatric GWAS consortium (**Table 1),** running the analysis in turn with each disorder as the outcome with the other disorders as covariates. A total of 5,275,400 SNPs with matching alleles that were in common across the 5 disorders were used for further analysis. Indels were excluded from the analysis.

For each disorder, SNP effects conditional upon the other disorders were calculated. Results were uploaded to FUMA for annotation [14]. Ranking SNPs according to the difference between the marginal and conditional effect sizes for each disorder is not necessarily meaningful because, for example, a SNP that has a low estimated marginal effect, so no effect on the outcome trait, will have a large conditional effect if the SNP has a large effect on the covariate traits. For the purposes of identifying which SNPs show evidence of disorder-specificity, we focus on presenting results for SNPs that were GWS with the outcome disorder in the original GWAS. We further estimated whether the difference between the conditional and raw effect size of each SNP was significant (Supplementary Material).

**MAGMA gene-set analysis**

MAGMA gene-set analysis[15] as implemented in FUMA was used to investigate which sets of biologically related genes show the strongest evidence of association in the conditional analyses.

**Genetic Correlation**

LD-score regression [16] was used to estimate the genetic correlation between the conditional and unadjusted GWAS results.

**Summary Mendelian Randomisation**

To investigate the potential functional relevance of SNPs with disorder-specific effects, we applied the SMR approach [12], integrating eQTL (SNP-gene expression association) and mQTL (SNP_DNA methylation association) to the results from the conditional analyses. eQTL data from brain tissue were derived from a meta-analysis of the GTEx study, the Common Mind Consortium (CMC) and the Religious Orders Study and Memory and Aging Project (ROSMAP). The details of the meta-analysis have been described elsewhere[17]. Using meta-analysis results across brain tissues and studies is justified owing to the high correlation

in effect sizes between tissues[17]. Only genes with a cis-eQTL with $p_{eQTL} < 5 \times 10^{-8}$ were included in the analysis. Experiment-wide significance accounting for testing multiple SNPs across multiple traits was set at $p_{SMR} = 1.9 \times 10^{-06}$ and the threshold for no evidence of heterogeneity due to pleiotropy at $p_{HEIDI} > 0.01$. Individual-level genotypes from the ARIC data (n = 7,762 unrelated individuals) [11] were used to estimate LD for the HEIDI test.

To test for the effects of disorder-specific variants on DNA methylation, we used SMR to integrating trait association data with meta-analysed brain mQTL data set from Jaffe et al. (n = 526) ROSMAP (n = 486) and fetal brain mQTL data from Hannon et al [18]. Only probes with at least one cis-mQTL with $p < 5 \times 10^{-8}$ were included in the SMR analysis. Probes that passed the significance threshold of $1.56 \times 10^{-7}$ and did not show evidence of heterogeneity as indicated by the HEIDI test were considered to be significant.

### Cell-type specificity for disorders

To gain insight into the cell types that are important for each disorder, we evaluated whether genes associated with specific brain cell-types are enriched for association with each of the disorders. Using data from single-cell sequencing experiments in mice, the cell-type specificity of each gene was calculated by comparing the expression of a gene in a given cell-type to that across all cell types [19]. MAGMA was used to calculate gene-based association statistics and to evaluate whether genes with high specificity in a given cell-type are enriched for association with a disorder. The enrichment analysis was performed for both unadjusted and conditional GWAS for all 5 disorders. To investigate whether there was a significant change in the cell-type enrichment after conditioning, MAGMA analysis was performed using the enrichment Z-scores from the unadjusted GWAS as covariates in the analysis and a conditional enrichment for all level 1 cell types analysed in Skene et al. [19] was estimated.

### Code Availability

Scripts used to generate the results are available on request from the corresponding author

## Results

### Baseline statistics

After merging GWAS summary statistics for the five psychiatric disorders 5,275,400 autosomal SNPs remained (**Table 1**). The number of independent genome-wide significant SNPs annotated by FUMA [14] is much greater for SCZ (M =130) compared to the other

disorders (M =16, 40, 11, 2 for BIP, MD, ADHD, AUT respectively) reflecting mostly sample size, but also genetic architecture, and population risk. Linkage disequilibrium score regression (LDSC) estimates of SNP-based heritability on the liability scale and genetic correlations were all significantly different from zero (**Table 2**). Genetic correlations were highest between SCZ and BIP ($r_g$ = 0.67 (s.e. = 0.03)) and lowest between BIP and ADHD ($r_g$ = 0.15 (s.e. = 0.04)). The LD-score regression intercept was significantly greater than zero for the majority of pairs of disorders reflecting sample overlap in the GWAS studies. The intercept was highest between ADHD and AUT due to substantial overlap in controls. See Supplementary Material for discussion of interpretation of results in the context of sample overlap.

The GSMR analyses highlights some asymmetries in the estimates of the causal effects of one disorder on another (**Table 3**). In particular, the estimated liability $\hat{b}_{xy}$ when considering MD as an exposure for each trait is higher than the estimates in the reverse direction. One explanation is that since MD is so common and is frequently comorbid with other disorders that MD samples include those diagnosed and undiagnosed with other disorders. However, if model assumptions are violated it may have greater impact when there is a large difference in lifetime risk between the pairs of disorder. However, countering this, we find a higher $\hat{b}_{xy}$ from AUT to ADHD than from ADHD to AUT, but the standard errors on estimates are much higher for these disorders. Interpretation of these $\hat{b}_{xy}$ estimates depends on the nature of the shared genetic contributions to psychiatric disorders that may reflect a complex mix of types of pleiotropy, where some sets shared of variants may have more correlated effect sizes than other sets of shared variants.

**Changes in Genetic Correlation**

The impact of the conditioning is demonstrated by the changes in the estimates of $\hat{r_g}$ comparing original and conditional GWAS results. The $\hat{r_g}$ between SCZ conditional on the other disorders (denoted $SCZ_{cond}$) and SCZ remained high at 0.93, while between $SCZ_{cond}$ and BIP it was much reduced (from 0.67 prior to conditioning to 0.36, after conditioning). It is noted that $b_{zy}$ is eliminated in the conditional analysis only if the SNP effect is mediated by trait *x*. Therefore, there is remaining genetic correlation because of pleiotropic SNP effects. A similar pattern of changes in genetic correlation with other traits was seen for the analyses with the other disorders as the outcome variable (**Supplementary Table 1**).

**mtCOJO genome-wide significant SNP results**

As expected because of pleiotropy between disorders, conditional analysis leads to a reduction in the mean test statistic across all SNPs in the genome and hence the number of independent SNPs reaching the significance threshold ($5x10^{-8}$) is reduced (**Table 1**). For each disorder, we present results for all independent SNPs significant in the unadjusted analysis or the conditional analysis **(Supplementary Table 2)**. GWS SNPs that are more significantly associated in the conditional analysis than the unadjusted analysis are shown in **Table 4**. A larger conditional effect size suggests that these variants are disorder-specific or have heterogeneous effects across disorders.

Given that SCZ is the disorder with the largest number of significant SNPs and for which the power to detect changes in effects is largest, we focus mostly on the results from the SCZ conditional analysis. Of the 130 SNPs from the unadjusted SCZ GWAS, five were more significant after adjusting for the other disorders (all of which had opposite direction of effects for BIP – **Supplementary Table 2**) and a further eight had a larger estimated effect size after conditioning. Forest plots for the four most significant SCZ SNPs from the conditional analysis (two of which were associated $p<5x10^{-8}$ in the unadjusted analysis) are shown in **Figure 1**.

For all disorders except for AUT, a number of SNPs surpass the significance threshold that were not significant in the original GWAS. For schizophrenia, ten SNPs that were significant in the conditional analysis and not in the original GWAS (**Table 4**). All 10 SNPs have opposite effects for BIP, so that the allele that predisposes to SCZ is in the protective direction for BIP. Although these opposite effects could be due to ascertainment, among them are variants in or near genes with annotated biological functions that are potentially relevant for SCZ. For instance a SNP that was significant in the conditional analysis (rs2973038 – $p_{adj} = 1.28 \times 10^{-08}$; $p_{scz} = 1.72 \times 10^{-06}$ ) is located in the Glial Cell Derived Neurotrophic Factor (*GDNF*), a gene that encodes a protein that enhances the survival of midbrain dopaminergic neurons [20], and is expressed during development [21].

All SNPs that were associated with BIP at $p< 5x10^{-8}$ in the original GWAS were less significant in the conditional analysis, showing evidence that they have some pleiotropic effect across disorders. Notably, this includes genes involved in calcium signalling, dopaminergic signalling and synaptic plasticity, indicating these processes may be important across psychiatric disorders. Three SNPs that were not significant in the BIP GWAS were

significant in the conditional analysis (**Table 4**, **Supplementary Table 2, Supplementary Figure 2**).

For each of the remaining disorders (MD, ADHD and AUT), we found that a small proportion of the existing significant SNPs had larger conditional effect sizes and one MD SNP and two ADHD SNPs that were not significant in the original GWAS became significant after conditioning (**Table 4**, **Supplementary Table 2).** However the difference in effect size after conditioning is not statistically significant for these SNPs, due to low statistical power (Supplementary Table 2). Forest plots for significant SNPs that had increased conditional effect sizes are shown in **Supplementary Figures 3-5**

**SMR analysis**

Changes in the expression of 9 genes were significantly associated with the 5 disorders (0 for BIP, 5 for SCZ, 3 for MD and 1 for ADHD, 0 for AUT) after conditioning and removal of genes in the MHC (**Supplementary Tables 3-4**), and a total of 72 DNA methylation sites (2 for BIP, 18 for SCZ, 37 for MD, 8 for ADHD, and 6 for AUT) were significantly associated with the 5 conditional traits (**Supplementary Table 3-4**).

Significant SMR results for gene expression where the associated SNP is more significant in the conditional analysis are presented in **Supplementary Table 3**. Three out of 5 significant SMR associations for SCZ were with SNPs where the conditional significance was greater than in the unadjusted analysis. One SNP - rs3759384 – is associated with decreased expression of *VPS29* in the brain and significantly increased risk for SCZ in the unadjusted analysis and has a larger conditional effect size (**Supplementary Figure 6**), indicating that *VPS29* may be linked to the development of SCZ and not other disorders. The VPS29 protein is a component of the retromer complex which prevents the degradation of certain proteins including signalling receptors, ion channels and small molecule transporters. The complex is essential for maintenance of neurons and has been implicated in the etiology of a number of neurodegenerative disorders [22].

One of the three associations for MD was with a SNP (rs7732179) with greater significance in the conditional analysis. The same variant shows evidence of association with SCZ but with opposite directions of effect ($b_{SCZ}$ = -0.045; $p_{SCZ}$ = 1.7 x $10^{-6}$ and $b_{BIP}$ = -0.029; $p_{BIP}$ = 0.027). The A allele confers risk to MDD but is protective for SCZ and BIP (**Supplementary Figure 7**). The SNP is associated with expression of *PCDHA7* in the brain. This gene encodes a member of the protocadherin family of genes located together on chromosome 5. A significant association was also found in this region in the DNA

methylation analysis of MD. Little is known about the exact function of these genes, however they are concentrated at the synaptic junction suggesting a key role in neuronal signalling [23].

Out of 72 significant DNA methylation sites, 34 were associated with SNPs with higher significance in the conditional analyses (1 for BIP, 3 for SCZ, 21 for MD, 4 for ADHD and 5 for AUT) (**Supplementary Table 3**). It is noteworthy that one variant (rs2064853) was significantly associated with both SCZ and MD and DNA methylation near the *CSE1L* gene, but with opposite alleles increasing risk to each disorder (**Supplementary Figure 8**).

We investigated whether genes identified in the gene expression SMR or that are the closest gene to a significant methylation site are the primary target for FDA-approved drugs. We identified two genes that are targeted by medications. The serotonin receptor gene *HTR1D* which was identified in the DNA methylation analysis for MD is the primary target of the migraine drug naratriptan. Individuals with migraine are at 2-4 fold higher risk of developing depression and these results may suggest that triptans, used to treat migraines, could also be effective for MD.

The second drug target identified is with *MPL* and ADHD. This gene is targeted by romiplostim, an orphan drug developed for treatment of chronic idiopathic thrombocytopenic purpura.

**MAGMA gene-set analyses**

We conducted MAGMA gene-set analysis in FUMA to identify pathways and gene-sets that are enriched for association with the disorders after conditional analyses and to identify which sets become more or less significant after conditioning. Results for each disorder are presented in **Supplementary Table 5**. After conservative Bonferroni correction for the number of gene-sets tested for each disorder, three gene sets were significant - two for SCZ conditional analysis and one for AUT. For SCZ, the two significant sets were go:establishment of localization in the cell and GO:Dendrite, of which establishment of localization had a more significant p-value in the conditional analysis (**Supplementary Table 5**). For AUT, the gene-set GO:Dendrite_morphogenesis was significant after multiple testing and had a more significant p-value in the conditional analysis, potentially implicating genes expressed in dendrites in autism-specific pathology.

**Cell-type specificity for disorders**

The results from the cell-type enrichment analyses of raw and conditional analyses are shown in **Figure 2**. Consistent with previous results, the original SCZ results were enriched in medium spiny neurons (MSNs), pyramidal CA1 cells, pyramidal SS1 cells, interneurons and serotonergic neurons (**Supplementary Table 6**). All of these cell types also show some evidence of association with BIP and to a lesser extent MD, consistent with the genetic correlation between disorders and hence show reduced enrichment in the SCZ conditional analysis. All enriched cell-types for SCZ remained significant after conditioning except for serotonergic neurons, indicating that genes specific to this cell-type may increase risk to all five disorders. Enrichment in interneurons was found for SCZ, BIP and MDD indicating their potential importance across all 3 disorders. After conditioning, this cell-type was still significantly enriched in SCZ and MDD, but not BIP. This may reflect that the sample size of the BIP analysis is smaller than for SCZ and MDD.

**Discussion:**

Our goal was to identify genetic variants that show disorder specific association by conducting a summary statistics based GWAS analysis for each of five psychiatric disorders conditioning on GWAS results from the other disorders. As expected, given the high degree of pleiotropy across disorders, compared to original GWAS results the number of SNPs associated at the threshold of genome-wide significance is very much reduced for each conditional GWAS. We utilise mtCOJO as a method that uses summary statistics to quickly screen for SNP associations. Functional annotation can help prioritise the associations of most interest. It will be important to understand why a variant increases risk only to that disorder and not to others.

By integrating conditional GWAS results with SNP-gene expression and SNP-methylation results, we identify decreased expression of *VPS29* as a potential biological mechanism underlying schizophrenia. The variant that increases risk to SCZ and is associated with decreased expression of VPS29 in brain tissue shows no evidence for association with other psychiatric disorders. The retromer complex, of which is VPS29 is a subunit, is highly conserved across eukaryotes. The complex plays a role in the recycling, delivery and degradation of proteins in the cell and is crucial in the maintenance of cell homeostasis[24]. Rare exonic mutations in members of the complex have been associated with Parkinson's Disease and post-mortem studies have revealed decreased expression of all members of the complex in the brains of patients with Parkinson's and Alzheimer's disease. The expression

of all three members of the complex is linked such that decreasing expression of one leads to decreased expression of all of them. Knocking down VPS35 using siRNA leads to elevated generation of amyloid-beta and reduced synaptic transmission[25, 26]. There is therefore considerable interest in identifying pharmacological agents that prevent the degradation of the retromer complex as a therapeutic mechanism for neurodegenerative disease. Small molecule screens have identified potential therapeutic agents that have shown promise in vitro[27]. Our results provide that such compounds may of interest in targeting biological mechnisms specific to schizophrenia.

Furthermore, SNPs associated with decreased expression of *PCDH7* and decreased methylation near other members of the protocadherin gene family on chromosome 5 may increase risk of MD, but be protective for SCZ and BIP. The protocadherins are a large family of genes involved in cell-cell adhesion that are primarily expressed in the nervous system. They play a major role in the development of the nervous system and in regulating dendritic branching. The PCDHA7 gene is part of a complex cluster of protocadherin alpha genes in the same genomic locus. The expression of the different isoforms at the locus is controlled by upstream CpG sites. Owing to their functional role in nervous system development and their location in linkage peaks, the PCDHA genes have been investigated as candidate genes for bipolar and schizophrenia[28]. Moreover, an epigenetic study of concordant and discordant MZ twins for depression showed that affected twins had increased variation in methylation in the PCDHA region, highlighting instability in this region as a potential mechanism underlying depression[29]. Further studies of the role of the PCDHA gene cluster in psychopathology are warranted.

Methylation in the promoter of the CSE1L gene, whose encoded protein influences cellular proliferation and has been linked to progression of a number of cancers, shows evidence of increasing risk to SCZ but being protective for MD.

Consistent with the large degree of pleiotropy between disorders, we found that most of the significant biological pathways for each disorder had reduced significance after conditioning. Pathway analysis of conditional results identified a potential role for genes expressed in dendrites in both autism and schizophrenia. Likewise, for the cell-type enrichment analysis, there was a reduction in the enrichment for most cell types in each disorder after conditioning. For SCZ, the previously identified enrichments in pyramidal SS1 and CA1 cells as well as medium spiny neurons remained significant after conditioning, despite also showing evidence for enrichment in BIP. The largest change in enrichment was

for serotonergic neurons, indicating that genes highly expressed there are important across all psychiatric disorders.

We provide an analysis framework for conditional cross-disorder analyses using summary statistics. Our study was motivated to improve on the SCZ case vs. BIP case analyses that utilised PGC cohorts for which both SCZ and BIP genotyped samples were available [30], but which necessarily excluded 28% of cases that could not be allocated into matched cohorts. They identified 5 SNPs associated at $p<5x10^{-8}$. We conducted an analysis of SCZ conditional on BIP and performed a lookup of those SNPs in the unadjusted and adjusted results. All but one (rs200005157) of their associated SNPs were matched directly or to an LD proxy (**Supplementary Table 7)**. All show increased statistical significance in the conditional analysis. We identified more disorder-specific SNPs (10 specific to SCZ) consistent with the larger sample sizes afforded from using summary statistics, highlighting that mtCOJO is an efficient method for screening for disorder-specific SNPs for two or more related disorders. An in depth discussion of the mtCOJO method is given in the **Supplementary Material.**

**Limitations**

There are a number of limitations to our analyses that should be considered. Although methods that utilise summary statistics have several advantages, they also depend upon the summary statistics being generated accurately. In this instance, all studies have gone through the same quality control and analysis pipeline meaning that systematic differences between studies are unlikely. It is not clear how misdiagnosis of cases would impact upon the results.

There are also substantial differences in sample size between the GWAS of different disorders, with SCZ and MD having a larger sample size than the other disorders, which may disproportionately influence the results. This is shown by most of the significant differences in effect sizes between the raw and conditional results being for SCZ. The disorders that have the most genome-wide significant SNPs will also have the most accurate estimates of their effects on the disorders. As sample sizes increase for some of the other disorders, the results for those disorders will become more accurate.

In order to reduce the burden of multiple testing in the SMR analysis, we only included SNPs that are associated at the genome-wide significant level with gene expression or methylation in cis. Relaxing the statistical threshold for inclusion may have identified more SNPs with effects on gene expression in brain with the trade-off of increasing the experiment-wide significance level.

## Conclusion

In conclusion, our results suggest that mtCOJO is an efficient method for identifying variants with disorder-specific effects and they represent a small fraction of variants identified for each disorder to date, reflecting the high degree of pleiotropy between disorders. Nonetheless, we identify several loci that have evidence of being disorder-specific. Further research in human studies should focus on whether the disorder-specific variants associate with specific symptoms in mixed clinical populations.


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## Conflict of Interest Statement

P.F.S. is on the advisory committee at Lundbeck, is a Scientific Advisory Board member at Pfizer and has received speaker reimbursement and grant funding from Roche. J.H.-L. is a Scientific Advisor at Cartana and has received grant funding from Roche.

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## FIGURE LEGENDS

Figure 1 – Forest plots for the 4 most significant SNPs in SCZ mtCOJO analysis with larger conditional effect sizes

Figure 2 Results from brain cell-type enrichment analyses of raw and conditional GWAS analyses

## Tables

Table 1. Summary of datasets used and results from conditional GWAS analysis

| Disorder | Cases | Controls | No. SNPs in original study | No GWS SNPs in merged data | Study reference | No. GWS SNPs in Published Study | Assumed Lifetime Disease Risk | GWS loci in conditional GWAS | New GWS loci | GWS SNPs from unadjusted GWAS with larger conditional effect size |
|---|---|---|---|---|---|---|---|---|---|---|
| **SCZ** | 40,675 | 64,643 | 5,471,613 | 130 | Pardinas et al 2018 | 145 | 0.01 | 43 | 10 | 15 |
| **BIP** | 20,352 | 31,358 | 9,498,970 | 16 | Stahl et al 2018 BioRxiv | 19 | 0.01 | 4 | 3 | 0 |
| **MD** | 135,458 | 344,901 | 10,468,943 | 40 | Wray et al 2018 | 44 | 0.15 | 15 | 1 | 5 |
| **ADHD** | 19,099 | 34,194 | 6,755,648 | 11 | Demontis et al BioRxiv | 12 | 0.05 | 5 | 2 | 3 |
| **AUT** | 18,381 | 27,969 | 7,539,669 | 2 | Grove et al BioRxiv | 3 | 0.01 | 1 | 0 | 1 |

Table 2. Estimated SNP-based heritability on the liability scale, genetic correlation and LD-score intercepts estimated from LD-score regression

| | SCZ | BIP | MDD | ADHD | AUT |
|---|---|---|---|---|---|
| SCZ | **0.23 (0.01)** | *0.21 (0.01)* | *0.03 (0.01)* | 0.02 (0.01) | 0.008 (0.01) |
| BIP | 0.67 (0.02) | **0.19 (0.01)** | *0.05 (0.007)* | *0.03 (0.006)* | 0.009 (0.008) |
| MD | 0.36 (0.02) | 0.35 (0.02) | **0.08 (0.004)** | *0.10 (0.008)* | *0.09 (0.008)* |
| ADHD | 0.18 (0.03) | 0.15 (0.04) | 0.43 (0.03) | **0.22 (0.01)** | *0.35 (0.008)* |
| AUT | 0.23 (0.05) | 0.15 (0.05) | 0.43 (0.04) | 0.36 (0.05) | **0.12 (0.01)** |

LD-score SNP-based heritability on the liability scale and standard error reported on diagonal

$r_g$ and standard error reported below the diagonal
Bivariate ldsc intercept reported above the diagonal. Value significantly greater than zero (in italics) quantify sample overlap

Table 3. GSMR estimates of causal effect of each psychiatric disorder on the others with

conversion to the log odds ratio and liability scales

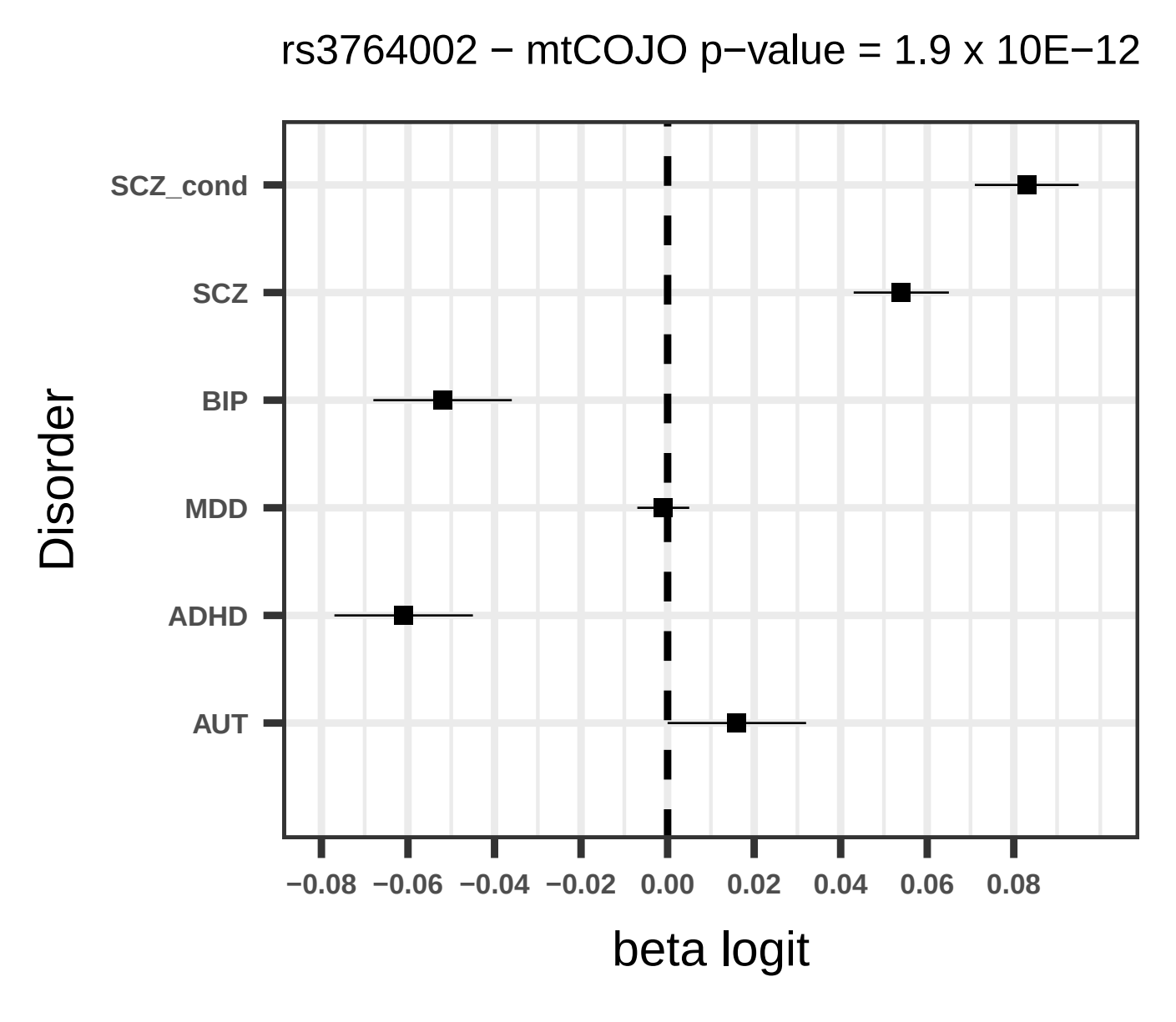
| Exposure | Outcome | N SNPs | bxy | bxy_se | bxy_liability | OR | bxy_pval |
|---|---|---|---|---|---|---|---|
| SCZ | BIP | 111 | 0.417 | 0.019 | 0.417 | 3.06 | 5.0E-109 |
| SCZ | MD | 111 | 0.074 | 0.007 | 0.109 | 1.22 | 4.9E-26 |
| SCZ | ADHD | 111 | 0.054 | 0.019 | 0.066 | 1.16 | 5.2E-03 |
| SCZ | AUT | 111 | 0.144 | 0.019 | 0.144 | 1.47 | 2.9E-09 |
| BIP | SCZ | 16 | 0.498 | 0.039 | 0.498 | 3.82 | 1.6E-37 |
| BIP | MD | 16 | 0.091 | 0.016 | 0.134 | 1.28 | 2.0E-08 |
| BIP | ADHD | 16 | 0.028 | 0.043 | 0.034 | 1.08 | 5.2E-01 |
| BIP | AUT | 16 | 0.123 | 0.046 | 0.123 | 1.39 | 7.4E-03 |
| MD | SCZ | 40 | 0.414 | 0.059 | 0.281 | 2.13 | 2.7E-12 |
| MD | BIP | 40 | 0.600 | 0.068 | 0.408 | 2.97 | 1.1E-18 |
| MD | ADHD | 40 | 0.402 | 0.072 | 0.339 | 2.09 | 2.9E-08 |
| MD | AUT | 40 | 0.463 | 0.078 | 0.314 | 2.33 | 3.7E-11 |
| ADHD | BIP | 13 | 0.135 | 0.052 | 0.109 | 1.34 | 8.9E-03 |
| ADHD | MD | 13 | 0.086 | 0.019 | 0.102 | 1.21 | 9.1E-06 |
| ADHD | SCZ | 13 | 0.156 | 0.043 | 0.126 | 1.40 | 2.8E-04 |
| ADHD | AUT | 11 | 0.333 | 0.060 | 0.269 | 2.06 | 2.9E-08 |
| AUT | SCZ | 11 | 0.063 | 0.041 | 0.063 | 1.19 | 1.3E-01 |
| AUT | BIP | 11 | 0.053 | 0.057 | 0.053 | 1.15 | 2.9E-01 |
| AUT | MD | 11 | 0.011 | 0.021 | 0.016 | 1.03 | 5.9E-01 |
| AUT | ADHD | 11 | 0.413 | 0.062 | 0.512 | 3.03 | 3.60E-11 |

* Estimates using autism as the exposure used instruments with $p < 10E-06$ due to lack of genome-wide significant SNPs for autism

Table 4. Results for SNPs that were genome-wide significant in the conditional analysis and have larger estimated conditional effect sizes than in the original GWAS

| Disorder | SNP | CHR | Position | A1 | Adjusted beta | SE Adjusted beta | Unadjusted beta | SE Unadjusted beta | Adjusted p-value | Unadjusted p-value | nearestGene |
|---|---|---|---|---|---|---|---|---|---|---|---|
| SCZ | rs3764002 | 12 | 108618630 | C | 0.083 | 0.012 | 0.054 | 0.011 | 1.94E-12 | 6.05E-07 | WSCD2 |
| SCZ | rs6095357 | 20 | 47523865 | A | -0.069 | 0.011 | -0.048 | 0.010 | 1.17E-10 | 1.21E-06 | ARFGEF2 |
| SCZ | rs7790864 | 7 | 28478625 | A | -0.062 | 0.011 | -0.044 | 0.010 | 6.33E-09 | 7.18E-06 | CREB5 |
| SCZ | rs1054972 | 19 | 1852582 | A | 0.076 | 0.013 | 0.053 | 0.012 | 6.42E-09 | 1.32E-05 | KLF16 |
| SCZ | rs2867673 | 7 | 71752652 | T | 0.060 | 0.010 | 0.049 | 0.010 | 9.44E-09 | 4.11E-07 | CALN1 |
| SCZ | rs6564668 | 16 | 79457393 | C | -0.060 | 0.010 | -0.038 | 0.010 | 1.05E-08 | 7.94E-05 | RP11-467I7.1 |
| SCZ | rs11922765 | 3 | 95047279 | G | -0.060 | 0.010 | -0.044 | 0.010 | 1.22E-08 | 4.36E-06 | RPS18P6 |
| SCZ | rs2973038 | 5 | 37833781 | C | 0.066 | 0.012 | 0.051 | 0.011 | 1.28E-08 | 1.72E-06 | GDNF |
| SCZ | rs10903945 | 10 | 363275 | C | 0.057 | 0.010 | 0.040 | 0.010 | 3.13E-08 | 3.30E-05 | DIP2C |
| SCZ | rs10282935 | 8 | 38703797 | A | 0.058 | 0.011 | 0.041 | 0.010 | 3.97E-08 | 3.17E-05 | TACC1 |
| SCZ | rs6701877 | 1 | 174015259 | G | -0.096 | 0.014 | -0.073 | 0.013 | 1.47E-11 | 2.37E-08 | RP11-160H22.3 |
| SCZ | rs7372313 | 3 | 135872958 | G | -0.069 | 0.010 | -0.062 | 0.010 | 4.26E-11 | 1.54E-10 | MSL2 |
| SCZ | rs1765142 | 11 | 30378559 | C | 0.065 | 0.011 | 0.058 | 0.010 | 1.54E-09 | 1.13E-08 | ARL14EP |
| SCZ | rs55646993 | 7 | 105017864 | G | -0.062 | 0.010 | -0.053 | 0.010 | 2.23E-09 | 3.83E-08 | SRPK2 |
| SCZ | rs150437760 | 14 | 59981768 | A | 0.131 | 0.024 | 0.121 | 0.022 | 3.71E-08 | 4.58E-08 | CCDC175 |
| BIP | rs125545112 | 9 | 23352293 | T | -0.083 | 0.014 | -0.066 | 0.014 | 1.55E-09 | 1.28E-06 | ELAVL2 |
| BIP | rs6891181 | 5 | 80849101 | T | -0.081 | 0.014 | -0.075 | 0.014 | 1.49E-08 | 1.27E-07 | SSBP2 |
| BIP | rs122689110 | 10 | 111878510 | T | -0.097 | 0.018 | -0.091 | 0.018 | 3.29E-08 | 2.73E-07 | ADD3 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| MD | rs11697370 | 20 | 47731767 | T | -0.031 | 0.005 | -0.023 | 0.005 | 3.31E-09 | 3.53E-06 | STAU1 |
| MD | rs27732 | 5 | 87992576 | A | 0.034 | 0.005 | 0.031 | 0.005 | 1.22E-11 | 1.87E-10 | MEF2C |
| MD | rs1806153 | 11 | 31850105 | T | 0.037 | 0.006 | 0.036 | 0.006 | 8.78E-10 | 1.18E-09 | RCN1 |
| MD | rs1354115 | 9 | 2983774 | A | 0.029 | 0.005 | 0.028 | 0.005 | 1.72E-08 | 2.37E-08 | CARM1P1 |
| MD | rs301799 | 1 | 8489302 | T | -0.028 | 0.005 | -0.026 | 0.005 | 2.49E-08 | 4.68E-08 | RERE |
| ADHD | rs78648104 | 6 | 50683009 | T | 0.136 | 0.023 | 0.124 | 0.025 | 4.31E-09 | 3.60E-07 | TFAP2D |
| ADHD | rs2244336 | 10 | 8831827 | C | 0.071 | 0.013 | 0.069 | 0.014 | 3.81E-08 | 3.67E-07 | ENSG00000270234 |
| ADHD | rs12410444 | 1 | 44188719 | A | 0.107 | 0.014 | 0.106 | 0.015 | 4.23E-15 | 3.85E-13 | ST3GAL3 |
| ADHD | rs13023832 | 2 | 215219808 | A | 0.133 | 0.020 | 0.117 | 0.021 | 1.23E-11 | 1.62E-08 | SPAG16 |
| ADHD | rs281320 | 15 | 47769424 | T | -0.080 | 0.013 | -0.074 | 0.013 | 1.84E-10 | 3.14E-08 | SEMA6D |
| AUT | rs10099100 | 8 | 10576775 | C | 0.084 | 0.014 | 0.084 | 0.015 | 1.20E-09 | 1.07E-08 | SOX7 |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SCZ
BIP
MDD
ADHD
AUT
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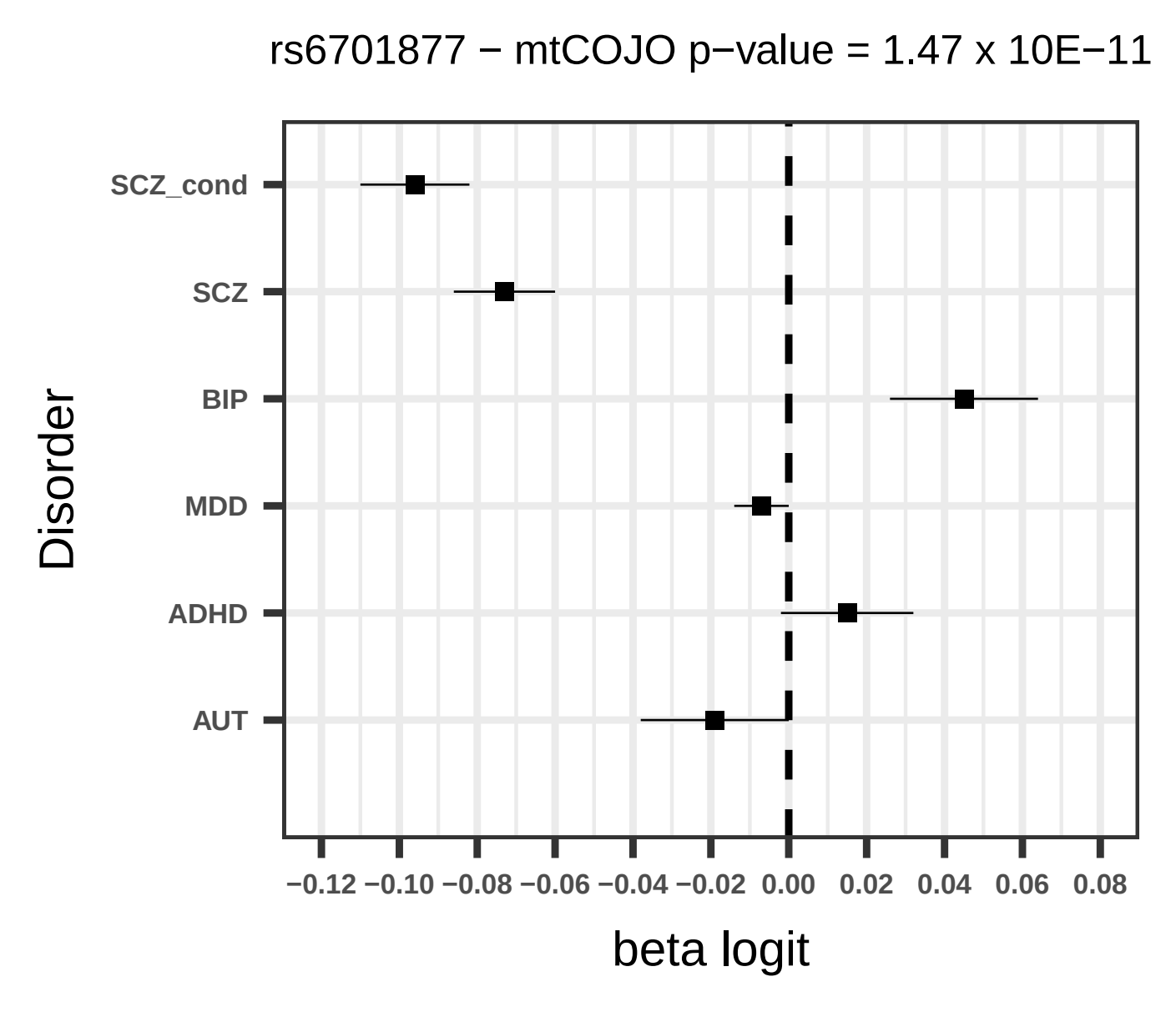
−0.06
−0.04
−0.02
0.00
0.02
0.04
0.06
0.08
beta logit


rs6701877 − mtCOJO p−value = 1.47 x 10E−11
Disorder
SCZ_cond
SCZ
BIP
MDD
ADHD
AUT
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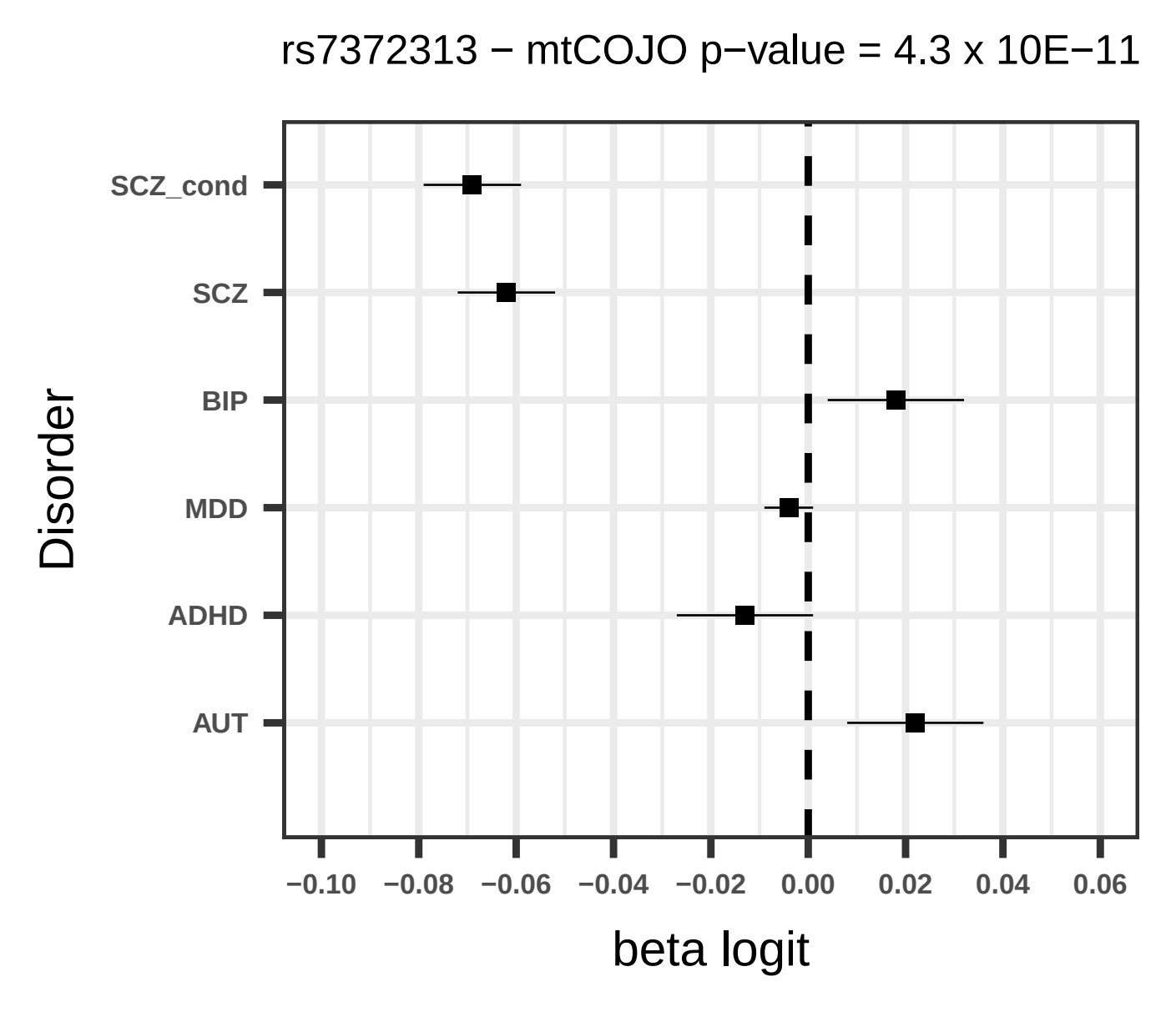
−0.06
−0.04
−0.02
0.00
0.02
0.04
0.06
0.08
beta logit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SCZ
BIP
MDD
ADHD
AUT
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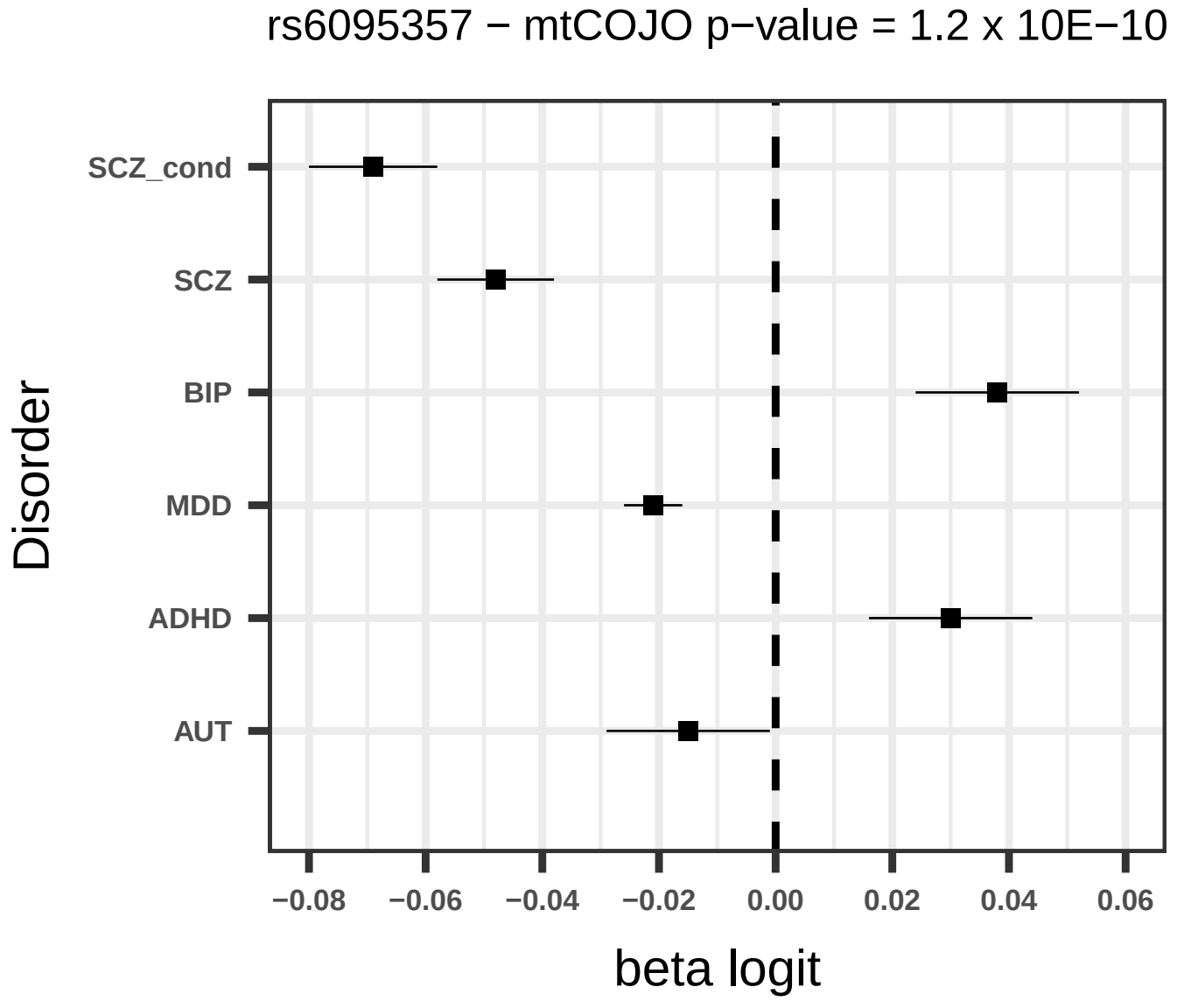
−0.06
−0.04
−0.02
0.00
0.02
0.04
0.06
beta logit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SCZ
BIP
MDD
ADHD
AUT
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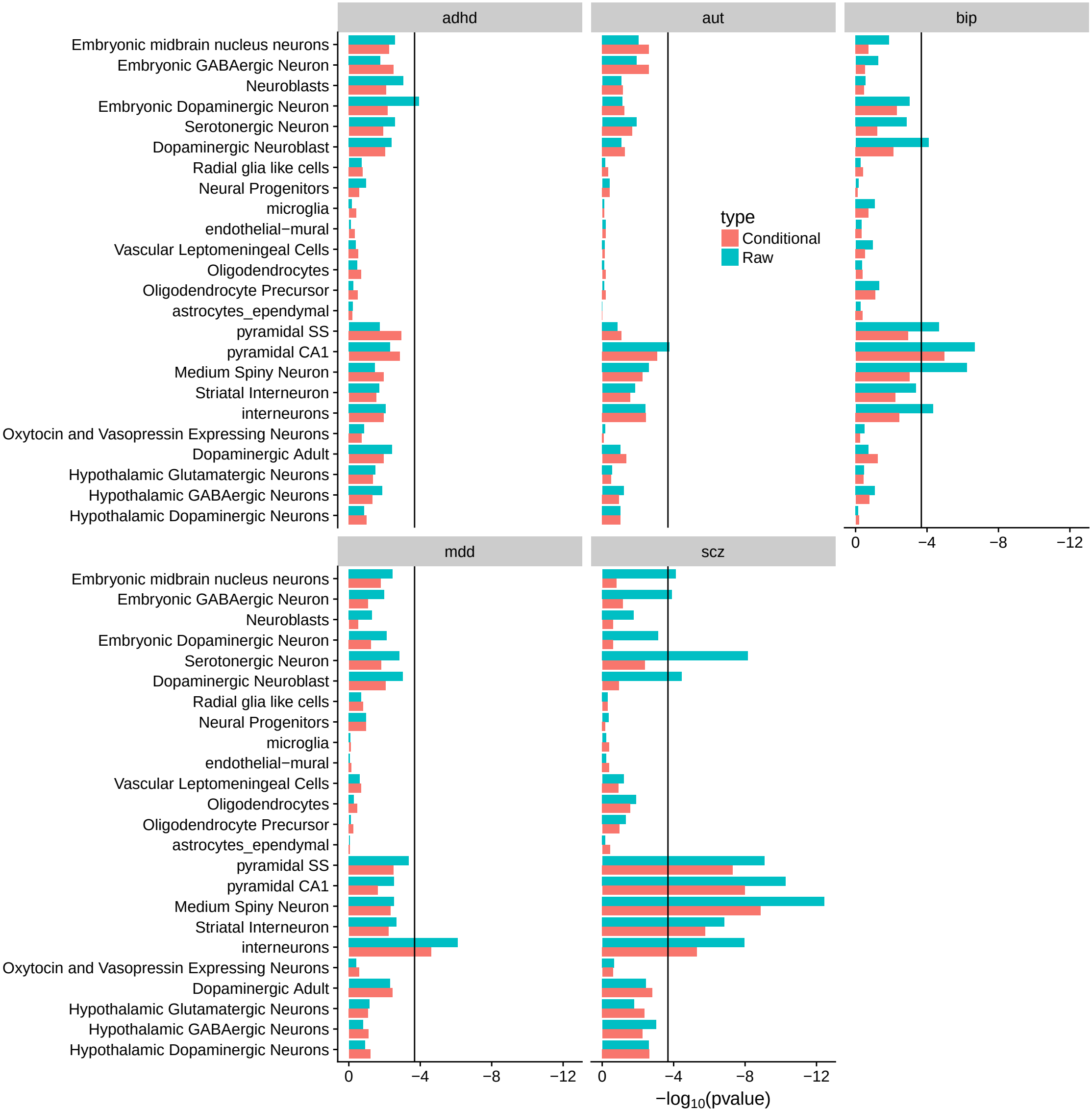
−0.04
−0.02
0.00
0.02
0.04
0.06
beta logit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aut
bip
mdd
scz
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Embryonic GABAergic Neuron
Neuroblasts
Embryonic Dopaminergic Neuron
Serotonergic Neuron
Dopaminergic Neuroblast
Radial glia like cells
Neural Progenitors
microglia
endothelial−mural
Vascular Leptomeningeal Cells
Oligodendrocytes
Oligodendrocyte Precursor
astrocytes_ependymal
pyramidal SS
pyramidal CA1
Medium Spiny Neuron
Striatal Interneuron
interneurons
Oxytocin and Vasopressin Expressing Neurons
Dopaminergic Adult
Hypothalamic Glutamatergic Neurons
Hypothalamic GABAergic Neurons
Hypothalamic Dopaminergic Neurons
type
Conditional
Raw
0
−4
−8
−12
−log10(pvalue)

**Supplementary Methods**

**Table of Contents**



## 1. Discussion of mtCOJO method for conditional GWAS analysis

### Multi-trait, conditional and joint analysis (mtCOJO)

We used the mtCOJO methodology[1] to conduct a conditional GWAS analysis of psychiatric disorders. mtCOJO was developed to generate GWAS summary statistics results for a target trait conditional on a covariate trait, recognising that the covariate trait is frequently not recorded in the individuals measured for the target trait. The mtCOJO method allows conditioning on the exposure by borrowing information from independently collected data, with the data linked through their SNP associations. Briefly, for two traits (*y* and *x*) with association effects for SNP z ( $\hat{b}_{zy}$ and $\hat{b}_{zx}$ respectively) the association effect estimates for trait *y* conditional on trait *x* is estimated as $\hat{b}_{zy}|\hat{b}_{xy} = \hat{b}_{zy} - \hat{b}_{zx}\hat{b}_{xy}$ (see Zhu et al. [1] for details), where $\hat{b}_{xy}$ is the effect of trait *x* on trait *y*, as estimated in generalised summary-based Mendelian randomisation (GSMR) analyses. If exposure trait *x* is causal of the outcome trait *y* or the two traits are pleiotropically related, we expect the genetic correlation estimated from the conditional GWAS result for trait *y* and that for trait *x* to be reduced by a factor proportional to the estimated effect of *x* on *y*. In a special case that if traits *x* and *y* are genetically identical we expect this correlation to be zero.

Classical MR analyses have the hypothesis of causality of an exposure trait on an outcome trait. Here, when the two disease traits are psychiatric disorders, we have no hypothesis of causality, but rather use GSMR to demonstrate significant bi-directional association of SNPs that are GWS in one disorder with those in another disorder and to estimate the weights for mtCOJO.

mtCOJO allows the analysis conditioning on multiple covarying diseases, so that the effect of a SNP on risk on the disorder of interest conditional upon the covariates on the disorder, is given by $\hat{b}_{zy}|\hat{\mathbf{b}}_{xy} = \hat{b}_{zy} - \hat{\mathbf{b}}_{zx}^{t}\hat{\mathbf{b}}_{xy}$ where $\hat{b}_{zy}$ is the SNP effect on the disease, $\hat{\mathbf{b}}_{xy}$ is a *t*-length vector with the *i*-th element $\hat{b}_{x_i y}$ being the effect of $x_i$ on the disease when all the covariates are fitted jointly, and $\hat{\mathbf{b}}_{zx}$ is a *t*-length vector of SNP effects on **x.** The method is robust to sample overlap between studies.

If the genetic correlation between two disorders is not driven by causality but a large number of pleiotropic effects (generally in the same direction) because of shared genetic pathways, then the GSMR $\hat{b}_{xy}$ reflects an average pleiotropic association between the two disorders. Nonetheless, conditioning on the average effect has meaning, and our conditional results can be used in pathway analyses to identify functionally relevant pathways that are associated with a disorder after accounting for effects of covarying disorders.
While it is possible that differences in quality control analysis or calling/imputation of SNPs across studies could lead to heterogeneity in the results and thus significant effects in the conditional analysis, these datasets were generated using the same analysis pipeline developed by the Psychiatric GWAS Consortium, and hence the likelihood of such heterogeneity is reduced.

**Estimating the significance of the difference between raw and conditional estimates.**

From Zhu et al, we know that the difference between the raw and the conditional estimates is $\hat{d} = \hat{b}_{zy} - \hat{b}_{zy}|\hat{\mathbf{b}}_{xy} = \hat{\mathbf{b}}_{zx}^{t}\hat{\mathbf{b}}_{xy}$, where $\hat{b}_{zx}$, $\hat{b}_{zy}$ and $\hat{b}_{xy}$ are defined the same as above. Therefore, the variance of the difference can be written as $\text{var}(\hat{d}) = \text{var}(\hat{\mathbf{b}}_{zx}^{t}\hat{\mathbf{b}}_{xy}) = \hat{\mathbf{b}}_{xy}^{t}\mathbf{V}_{zx}\hat{\mathbf{b}}_{xy}$ with $\mathbf{V}_{zx}$ being the (co)variance matrix of $\hat{b}_{zx}$[1]. The significance of the difference can be estimated using the test-statistic $T_d = \hat{d}^2/\text{var}(\hat{d})$.

If there is a single covariate trait, $\hat{d} = \hat{b}_{zx}\hat{b}_{xy}$ and $\text{var}(\hat{d}) = \text{var}(\hat{b}_{zx}\hat{b}_{xy}) = \hat{b}_{xy}^2\text{var}(\hat{b}_{zx})$.The significance of the difference can be tested as $T_d = \frac{\hat{d}^2}{\text{var}(\hat{d})} = \frac{(\hat{b}_{zx}\hat{b}_{xy})^2}{\hat{b}_{xy}^2\text{var}(\hat{b}_{zx})} = \frac{\hat{b}_{zx}^2}{\text{var}(\hat{b}_{zx})}$. Therefore, it suggests the significance of the difference depends on the p-value of SNP effect on the covariate trait. So for a SNP where the estimated effect size in the

covariate traits is very small (no association), we do not expect to see large changes between the raw and conditional estimates.

**Interpreting results in the context of sample overlap**

From Zhu et al, the joint effects of the covarying traits on the outcome trait are given by

$\mathbf{b}_{xy} = \mathbf{D}^{-\frac{1}{2}}\mathbf{R}_x^{-1}\mathbf{D}^{\frac{1}{2}}\boldsymbol{\beta}_{xy}$

where $\mathbf{R}_x = \{r_{g(x_i,x_j)}\}$ is a $t \times t$ matrix with $r_{g(x_i,x_j)}$ being the genetic correlation between covariates *i* and *j*, **D** is a $t \times t$ diagonal matrix with the *i*-th diagonal element $h^2_{SNP(x_i)}$ being the SNP-based heritability for the *i*-th covariate. We estimate $h^2_{SNP(x_j)}$ and $r_{g(x_i,x_j)}$ from GWAS summary data using the LDSC. The calculated genetic correlations are free of bias caused by sample overlap. It is possible that the marginal effects $\boldsymbol{\beta}_{xy}$ could be biased upwards due to sample overlap. However, as we are estimating the joint effects across 4 disorders, any bias would be diluted as the joint effects will be smaller than the marginal effects and the other marginal effects are largely free from bias due to sample overlap.

The sampling variance of the mtCOJO test statistic $\hat{b}_{zy}|\hat{\mathbf{b}}_{xy}$ is approximately

$\mathrm{var}(\hat{b}_{zy}|\hat{\mathbf{b}}_{xy}) = \mathrm{var}(\hat{b}_{zy}) + \hat{\mathbf{b}}_{xy}^t\mathbf{V}_{zx}\hat{\mathbf{b}}_{xy} - 2\hat{\mathbf{b}}_{xy}^t\mathrm{cov}(\hat{b}_{zy}, \hat{\mathbf{b}}_{zx})$

where $\mathbf{V}_{zx} = \mathrm{var}(\hat{\mathbf{b}}_{zx})$, and $\mathrm{cov}(\hat{b}_{zy}, \hat{\mathbf{b}}_{zx})$ is a *t*-length vector with the *i*-th element $\mathrm{cov}(\hat{b}_{zy}, \hat{b}_{zx_i})$ being the covariance between $\hat{b}_{zy}$ and $\hat{b}_{zx_i}$. We know from our previous study[17] that $\mathrm{cov}(\hat{b}_{zy}, \hat{b}_{zx_i}) = \rho_{x_iy}r_{p(x_i,y)}\sqrt{\mathrm{var}(\hat{b}_{zx_i})\mathrm{var}(\hat{b}_{zy})}$ where $\rho_{x_iy}$ is the proportion of sample overlap between $x_i$ and $y$ and $r_{p(x_i,y)}$ is the phenotypic correlation between $x_i$ and $y$. More generally, if there is a sample overlap between $y$ and $\mathbf{x}$, $\rho_{x_iy}r_{p(x_i,y)}$ can be approximated by the intercept of a bivariate LDSC analysis between $x_i$ and $y$ (ref[30]). $\mathbf{V}_{zx}$ is the sampling variance-covariance of $\hat{\mathbf{b}}_{zx}$ with the *ij*-th element $\mathrm{cov}(\hat{b}_{zx(i)}, \hat{b}_{zx(j)}) = \rho_{x_ix_j}r_{p(x_i,x_j)}\sqrt{\mathrm{var}(\hat{b}_{zx_i})\mathrm{var}(\hat{b}_{zx_j})}$ where $\rho_{x_ix_j}r_{p(x_i,x_j)}$ can also be approximated by the intercept of a bivariate LDSC analysis between $x_i$ and $x_j$. Therefore the covariance between traits due to sample overlap is accounted for in estimating the sampling variance of the mtCOJO test-statistic.

Although the test statistic accounts for the sample overlap, the effect size estimate of the effect of trait x conditional on trait y may be conservative (under-estimated) due to sample overlap. The conditional estimate is given by $\hat{b}_{zy}|\hat{\mathbf{b}}_{xy} = \hat{b}_{zy} -$

$\hat{\mathbf{b}}_{zx}^{t}\hat{\mathbf{b}}_{xy}$. We have shown that any bias in estimating $\hat{\mathbf{b}}_{xy}$ is likely to be small. However, if there is covariance between $\hat{b}_{zy}$ and one or more of the elements of $\hat{\mathbf{b}}_{zx}^{t}$ this could bias the conditional estimates. However, for positively correlated traits with sample overlap, as is the case for ADHD and autism in this analysis, the bias will be downwards, such that more loci may appear to be shared across disorders, rather than disorder-specific. The implications for the interpretation of these analyses are that if the GWAS studies were conducted in completely independent samples, we may have detected more disorder-specific loci for autism and ADHD. However, given the relatively small sample size of the ADHD and autism studies compared to the other disorders, it is probable that the number of extra loci identified would be small.

**2. Discussion of pathway analysis results**

Across the five disorders, there were 3 Gene Ontology terms that were more significant after conditioning. The GO Biological Process – Establishment of Localization of the Cell – was more significantly enriched in schizophrenia after conditioning. This is a broad process that includes 1,925 genes and so it is not obvious as to how it may relate to the pathological mechanism of schizophrenia. Among the sub-categories of this process are axonal dopamine secretion, neurotransmitter reuptake and secretion, and postsynaptic neurotransmitter receptor cycle, so it may be of relevance to the pathophysiology of SCZ. *VPS29* which was identified in the SMR analysis is part of this GO category.

Two other GO terms were significant after conditioning and accounting for multiple testing. across all disorders. Both relate to dendrites. The GO category "dendrite" was associated with SCZ but was less significant after conditioning. A related GO biological process "dendrite morphogenesis" was more significantly associated with autism after conditioning ($p\_adj = 2.9 \times 10^{-6}$, $p\_unadj = 1.9 \times 10^{-04}$). This change in significance does not appear to be driven by the variant near SOX7 that was more significant after conditioning (Table 4). Decreased branching of dendrites in hippocampal neurons has been found in patients with autism [2]

**3. Summary of estimates of $b_{xy}$ for all combinations of quantitative and binary traits**

When estimating $b_{xy}$ using GSMR in instances where the exposure trait and outcome trait are quantitative traits and the effect sizes have been standardised, the effect estimate is directly interpretable as SD units of y per SD unit of x. When using disease traits as exposures, $b_{xy}$ is

estimated on the logit scale and used in mtCOJO. The estimates on the logit scale can be difficult to interpret when disorders have a different prevalence and the proportion of cases and controls used in the GWAS is different from the population prevalence We derive transformations to make the $b_{xy}$ estimates interpretable when the exposure trait is a disease.

The key transformations of the $b_{xy}$ on the logit scale to the logOR and liability scale are

$$\hat{b}_{xy(\text{logOR})} = \frac{v_{K_x}}{K_x(1-K_x)}\hat{b}_{xy(logit)}$$

$$\hat{b}_{xy(liab)} = \frac{v_{K_x}K_y(1-K_y)}{v_{K_y}K_x(1-K_x)}\hat{b}_{xy(logit)}$$

where $K_x$ is the lifetime risk of the exposure trait and $K_y$ is the lifetime risk of the outcome trait and $v_K$ is the height of the normal distribution at the truncation point on the liability scale corresponding to risk *K*. $\hat{b}_{xy(logOR)}$ can be interpreted as the log of the odds ratio of *y* per 1 SD increase in liability in *x*. The estimate on the liability scale can be interpreted as the increase in liability in to disorder *y* per 1 SD increase in liability to *x*. Note that when two disorders have the same assumed prevalence, as is the case with schizophrenia and bipolar, $\hat{b}_{xy(logit)} = \hat{b}_{xy(liab)}$ . See the derivation below.

For two traits (*y* and *x*) with association effect sizes for SNP z ($\hat{b}_{zx}$ and $\hat{b}_{zy}$, respectively) the association effect size estimates for trait *y* conditional on trait *x* $(\hat{b}_{zy}|x)$ is estimated as $\hat{b}_{zy}|x \approx \hat{b}_{zy}|\hat{\mathbf{b}}_{xy} = \hat{b}_{zy} - \hat{b}_{zx}\hat{b}_{xy}$ , where $\hat{\mathbf{b}}_{xy} = \{\hat{b}_{xy(1)}, \hat{b}_{xy(2)}, \cdots, \hat{b}_{xy(m)}\}$ with $\hat{b}_{xy(i)} = \hat{b}_{zy(i)}/\hat{b}_{zx(i)}$, and $\hat{\mathbf{b}}_{xy} \sim N(\mathbf{1}b_{xy}, \mathbf{V})$ where $\mathbf{1}$ is an *m*×1 vector of ones and $\mathbf{V}$ is the variance-covariance matrix of $\hat{\mathbf{b}}_{xy}$, and *m* is the number of genome-wide significant SNPs selected as independently associated with trait *x*. $\hat{b}_{xy}$ is the effect of trait *x* on trait *y*, which can be calculated through GSMR analysis, $\hat{b}_{xy} = (\mathbf{1}'\mathbf{V}^{-1}\mathbf{1})^{-1}\mathbf{1}'\mathbf{V}^{-1}\hat{\mathbf{b}}_{xy}$ [1].

When trait *x* is a dichotomous trait we denote the population lifetime risk as $K_x$, $v_{K_x}$ as height of the normal curve when truncated at $K_x$, and the proportion of cases in the samples used to generate the SNP effects as $P_x$. The effect size estimated from logistic regression of *x* on SNP

*z* is on the logit scale $\hat{b}_{zx(logit(x))}$, such that exp($\hat{b}_{zx(logit(x))}$) is the odds ratio of the SNP for cases of disease *x*. From Lloyd-Jones et al[3], the relationship between $\hat{b}_{zx(logit(x))}$and $\hat{b}_{zx}$ on the observed scale from a case-control sample with proportion of cases $P_x$ ($\hat{b}_{zx(01[P_x])}$) is

$b_{zx(01[P_x])} \approx P_x(1-P_x)b_{zx(logit(x))}$

From Lee et al. 2011 [4] and Dempster and Lerner[5] the relationship between $\hat{b}_{zx}$ on the liability scale and ( $\hat{b}_{zx(liab)}$) and $\hat{b}_{zx(01[P_x])}$ is

$\hat{b}_{zx(liab)} = \frac{K_x(1-K_x)}{v_{K_x}P_x(1-P_x)}\hat{b}_{zx(01[P_x])}$.

Hence $\hat{b}_{zx(liab)} = \frac{K_x(1-K_x)}{v_{K_x}}\hat{b}_{zx(logit(x))}$.

So when *y* is a quantitative trait and *x* binary, the $\hat{b}_{xy}$ calculated from available summary statistics is $\frac{\hat{b}_{zy}}{\hat{b}_{zx(logit(x))}} = \hat{b}_{xy(y:logit(x))}$. A more interpretable regression coefficient is $\hat{b}_{xy(liab)} = \frac{\hat{b}_{zy}}{\hat{b}_{zx(liab)}} = \frac{v_{K_x}}{K_x(1-K_x)}\hat{b}_{xy(y:logit(x))}$. Similarly, if *y* is a dichotomous phenotype, the $\hat{b}_{xy}$ calculated from available summary statistics is $\frac{\hat{b}_{zy(logit(y))}}{\hat{b}_{zx(logit(x))}} = \hat{b}_{xy(logit(y):logit(x))}$, a more interpretable regression coefficient is either as logit of *y* per phenotypic liability SD unit of *x*: $\hat{b}_{xy(logit(y):liab(x))} = \frac{v_{K_x}}{K_x(1-K_x)}\hat{b}_{xy(logit(y):logit(x))}$ , or as phenotypic liability SD unit of *y* per phenotypic liability SD unit of *x*, $\hat{b}_{xy(liab(y):liab(x))} = \frac{\hat{b}_{zy(liab)}}{\hat{b}_{zx(liab)}} = \frac{v_{K_x}K_y(1-K_y)}{v_{K_y}K_x(1-K_x)}\hat{b}_{xy(logit(y):logit(x))}$. So, for schizophrenia and bipolar disorder since we assume $K_x = K_y$ = 0.01, then $\hat{b}_{xy(liab(y):liab(x))} = \hat{b}_{xy(logit(y):logit(x))}$. The interpretation and scaling of $\hat{b}_{xy}$ for any combination of binary and quantitative traits is summarised in **Supplementary Table 9**.

**Supplementary Table 9.**

| a) Units of $\hat{b}_{xy}$ given $\hat{b}_{xy(i)} = \hat{b}_{zy(i)}/\hat{b}_{zx(i)}$<br>b) Scale of estimation | **Trait y is quantitative**<br>**Linear regression GWAS**<br>$\hat{b}_{zy}$**:** Allelic effect in phenotypic SD units of *y* | **Trait y is binary disease**<br>**Logistic regression GWAS**<br>$\hat{b}_{zy(logit(y))}$**:** Allelic effect in ln(OR) of *y* |
|---|---|---|
| **Trait x is quantitative**<br>**Linear regression GWAS**<br>$\hat{b}_{zx}$**:** Allelic effect in phenotypic SD units of *x* | Estimated as $\hat{b}_{xy}$<br><br>$\hat{b}_{xy}$ in phenotypic SD units of *y* per phenotypic SD unit of *x* | $\hat{b}_{xy(logit\ (y):x)}$<br><br>$\hat{b}_{xy}$ value is logit SD units for disease *y* per phenotypic SD of trait *x* |
| **Trait x is binary disease** | Estimated as $\hat{b}_{xy(y:logit(x))}$ | Estimated as $\hat{b}_{xy(logit(y):logit(x))}$ |

| | | |
|---|---|---|
| $\hat{b}_{zx(logit(x))}$: Allelic effect in ln(OR) of *x* | $\hat{b}_{xy(y:liab(x))} = \frac{v_{K_x}}{K_x(1-K_x)}\hat{b}_{xy(y:logit(x))}$<br>$\hat{b}_{xy}$ in SD unit of *y* per logit SD unit of *x* | $\hat{b}_{xy(logit(y):liab(x))} = \frac{v_{K_x}}{K_x(1-K_x)}\hat{b}_{xy(logit(y):logit(x))}$<br>$\hat{b}_{xy}$ in logit SD units for disease *y* per phenotypic liability SD unit of *x*<br><br>$\hat{b}_{xy(liab(y):liab(x))} = \frac{v_{K_x}K_y(1-K_y)}{v_{K_y}K_x(1-K_x)}\hat{b}_{xy(logit(y):logit(x))}$<br>$\hat{b}_{xy}$ in SD units of liability of *y* per SD unit of liability to *x* |

**4. Simulations to confirm derivations**

In order to confirm the derivations summarised in Supplementary Table 10, we performed a series of simulations. We simulated 100 SNPs from a binomial distribution $z \sim B(2, p)$ with $p$ being the allele frequency of a SNP $p \sim U(0.01,0.5)$. We simulated an exposure phenotype under a liability-threshold model in ($n$=500,000 individuals) $x_{liab} = b_{zx}z + e$, $b_{zx} \sim N(0,1)$, $e \sim N(0, \sigma_e^2)$, where $\sigma_e^2 = \text{var}(zb_{zx})(\frac{1}{R_{zx}^2} - 1)$, with $R_{zx}^2$ was the variance in *x* explained by *z*. We set $R_{zx}^2 = 0.2$. *x* was then standardized with mean 0 and variance 1. Ten different sets of cases and controls were assigned to the underlying simulated liability according to various disease prevalences ($K$) from 0.01 to 0.1. The sample size of cases was $n_{cases} = nK$ and that of controls was $n_{controls} = n_{cases}(\frac{1}{P} - 1)$, where $P$ was sample prevalence, $P \sim U(0.1, 0.5)$. The cases and controls were randomly sampled from the whole population. In the simulation, we estimated $\hat{b}_{zx(liab)}$ from the whole population by linear regression and $\hat{b}_{zx(logit)}$ from the ascertained sample by logistic regression. $\hat{b}_{zx(logit)}$ was then transformed to the liability scale. The simulation was replicated 1,000 times. The comparison of estimated and transformed $\hat{b}_{zx(liab)}$ is shown in Supplementary Figure 8.

In the second set of simulations, a dichotomous exposure phenotype was simulated as above with 4 different prevalences ($K_x$ = 0.01, 0.04, 0.07 and 0.1) A outcome phenotype *y* with 200,000 individuals was simulated under the model $y_{liab} = x_{liab}b_{xy(liab)} + e_{y(liab)}$, where $e_{y(liab)} \sim N(0, \sigma^2_{e_{y(liab)}})$. $\sigma^2_{e_{y(liab)}} = \text{var}(x_{liab}b_{xy(liab)})(\frac{1}{R_{xy}^2} - 1)$ with $R_{xy}^2$ being the variance in *y* explained by *x*, $R_{xy}^2 = 0.05$. *y* was then standardized. We generated an ascertained sample for y using the same method as above. The four prevalences were the same as for disease *x*, $K_y$ = (0.01, 0.04, 0.07, 0.1). We estimated $\hat{b}_{xy(logit(y):logit(x))}$ by GSMR where

$\hat{b}_{zx(logit(x))}$ and $\hat{b}_{zy(logit(y))}$ were estimated in the ascertained samples by logistic regression. $\hat{b}_{xy(logit)}$ was then transformed to $\hat{b}_{xy(liab)}$. The simulation was performed 1,000 times.

Because both *x* and *y* were standardized, the expected value of $\hat{b}_{xy(liab)} = \sqrt{R^2_{xy}} = 0.223$.

**Supplementary Table 10** shows the results from the simulation.

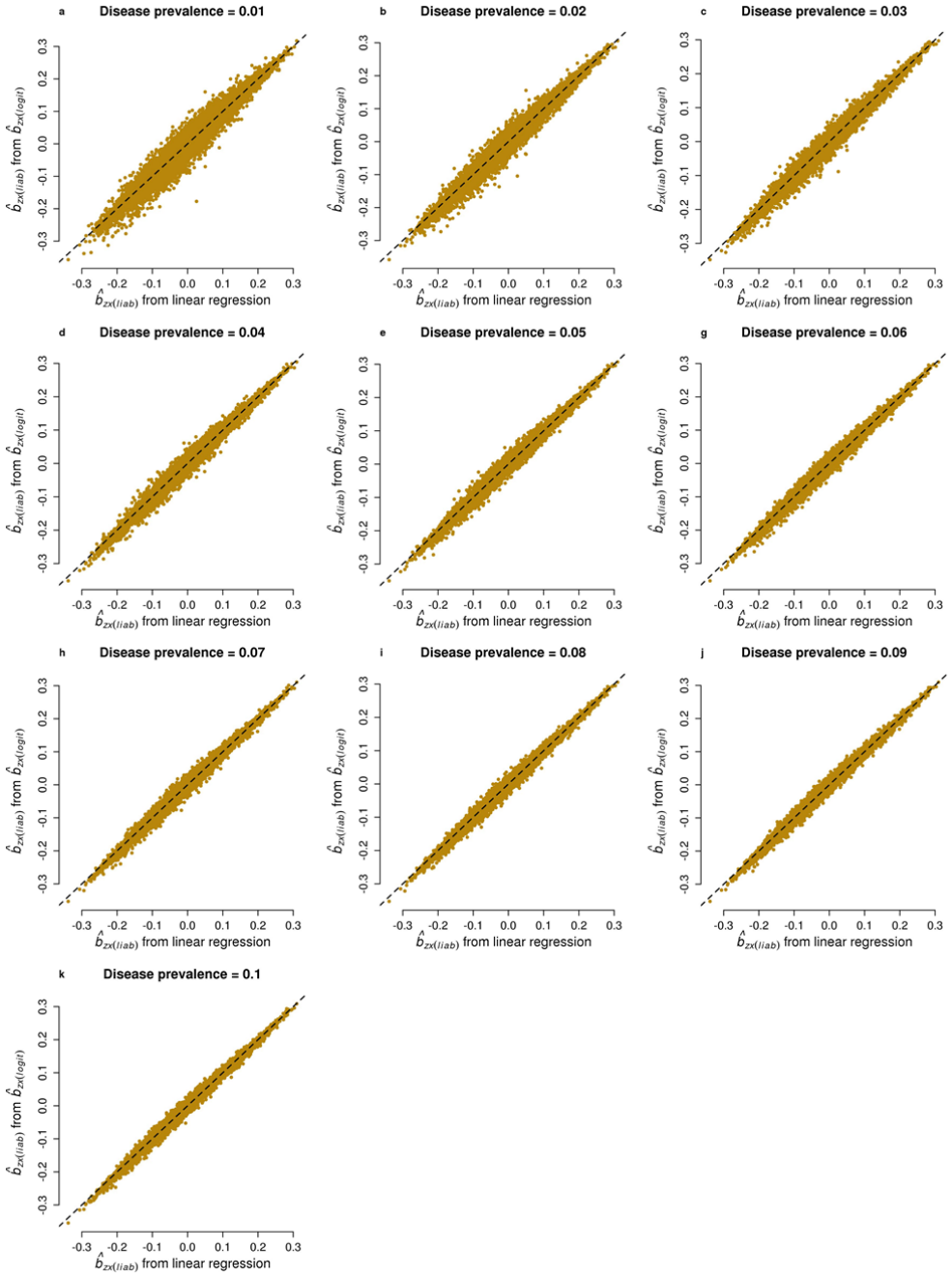
$\hat{b}_{xy(liab)}$ estimated from the logit scale. True $\hat{b}_{xy(liab)}$ is 0.223 which generated $\hat{b}_{xy(logit)}$ ranging from 0.156 to 0.304 depending of Kx, Ky combinations

| Disease prevalence | Scale | $K_y = 0.01$ | $K_y = 0.04$ | $K_y = 0.07$ | $K_y = 0.10$ |
|---|---|---|---|---|---|
| $K_x = 0.01$ | logit | 0.214 (0.0007) | 0.180 (0.0004) | 0.165 (0.0003) | 0.156 (0.0002) |
| | liability | 0.214 (0.0007) | 0.215 (0.0004) | 0.216 (0.0004) | 0.216 (0.0003) |
| $K_x = 0.04$ | logit | 0.263 (0.0009) | 0.220 (0.0004) | 0.202 (0.0003) | 0.191 (0.0003) |
| | liability | 0.219 (0.0007) | 0.220 (0.0004) | 0.220 (0.0004) | 0.220 (0.0003) |
| $K_x = 0.07$ | logit | 0.287 (0.0009) | 0.240 (0.0005) | 0.221 (0.0004) | 0.209 (0.0003) |
| | liability | 0.220 (0.0007) | 0.221 (0.0004) | 0.221 (0.0004) | 0.221 (0.0003) |
| $K_x = 0.10$ | logit | 0.304 (0.0010) | 0.254 (0.0005) | 0.234 (0.0004) | 0.221 (0.0003) |
| | liability | 0.220 (0.0007) | 0.221 (0.0004) | 0.221 (0.0004) | 0.221 (0.0003) |

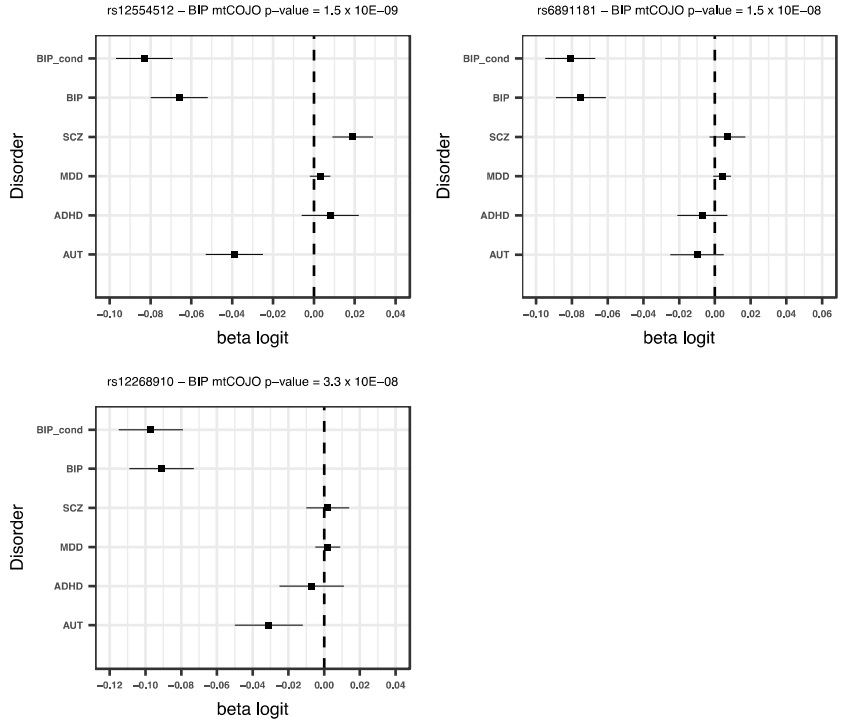
The simulations show that the transformation to the liability scale from the logit scale is a good approximation of the true estimate of $\hat{b}_{xy(liab)}$. The estimate is slightly downward biased and the bias is greater when the prevalence of the exposure trait is low.

## Supplementary Figures

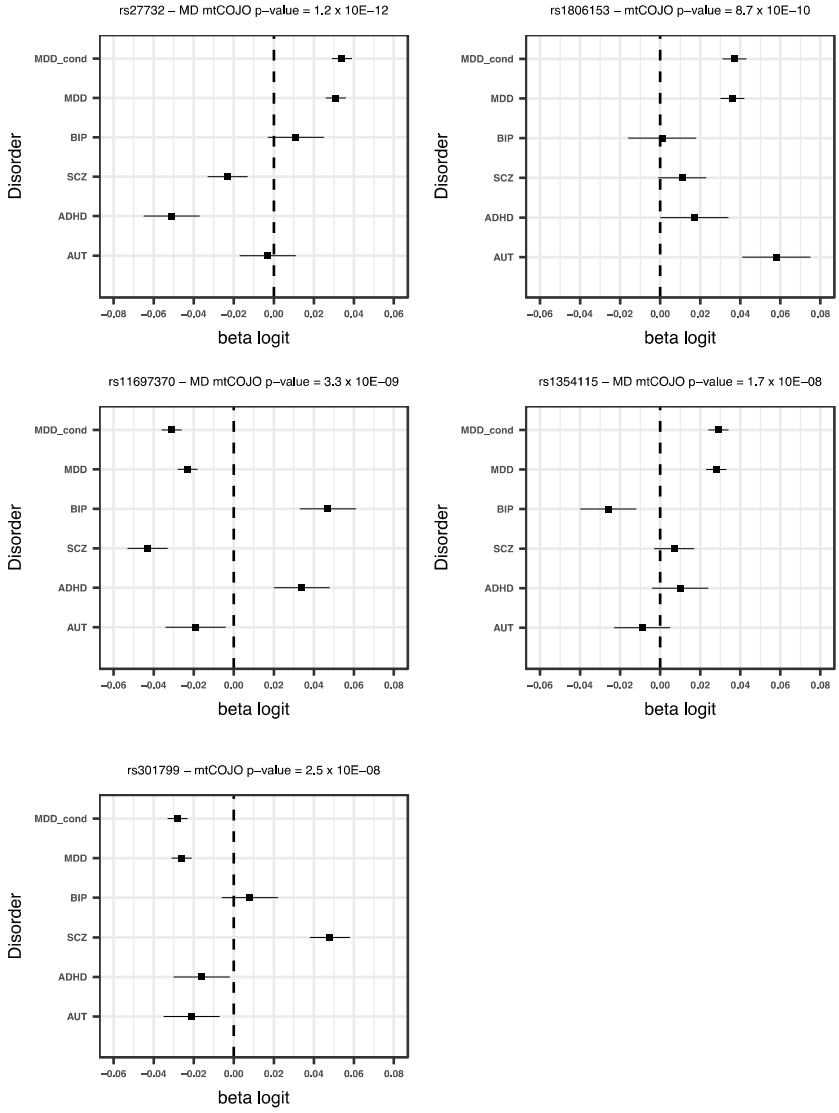
Supplementary Figure 1. Results from simulations to estimate $b_{xy}$ on the liability scale using derived transformation



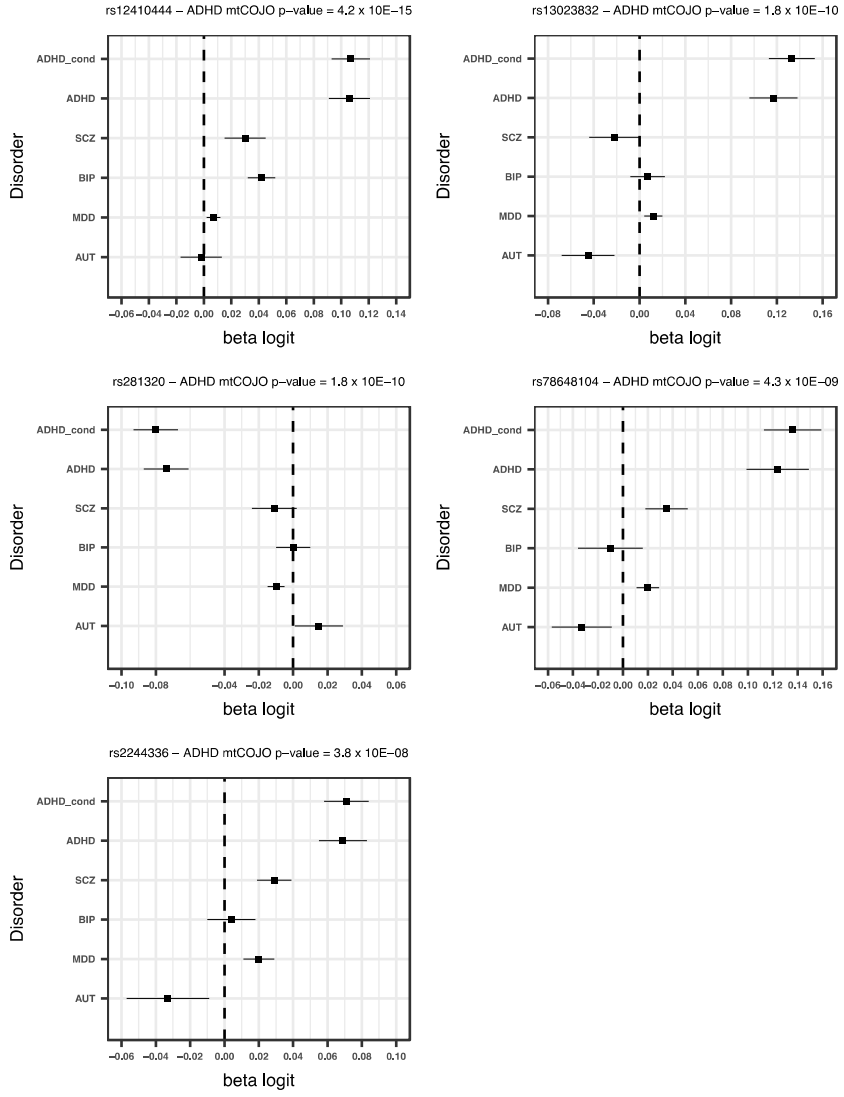
Supplementary Figure 2a-c. Significant SNPs from bipolar conditional analysis. All SNPs were not significant in the raw bipolar GWAS



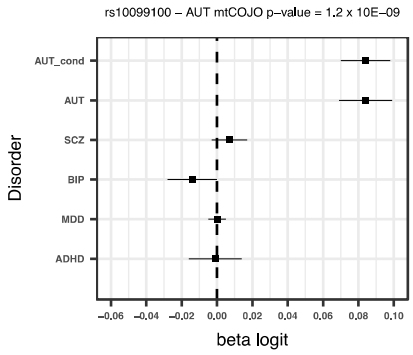
Supplementary Figure 3(a-e) Genome-wide significant SNPs from mtCOJO analysis of major depression with larger conditional effect sizes



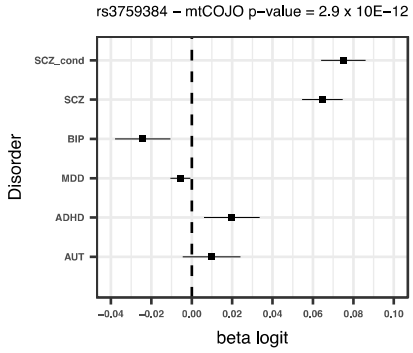
Supplementary Figure 4(a-e) Genome-wide significant SNPs from mtCOJO analysis of ADHD with larger conditional effect sizes.



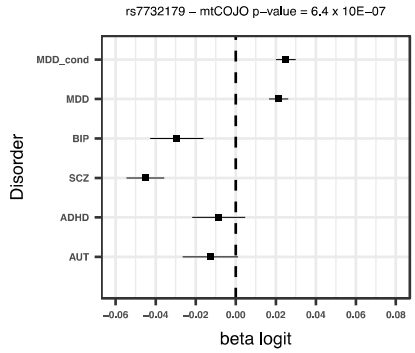
Supplementary Figure 5. Genome-wide significant SNP from mtCOJO analysis of AUT with larger conditional effect size.



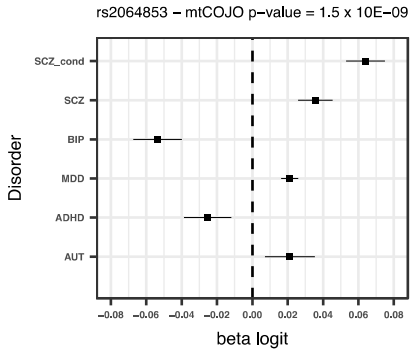
Supplementary Figure 6. Forest plot for mtCOJO analysis of rs3759384 – an eQTL for VPS29 – that was significant in SMR analysis.



Supplementary Figure 7. Forest plot for mtCOJO analysis of rs2064853 – an eQTL for PCDHA7 in brain– that was significant in SMR analysis and has opposite effects on MD and SCZ



Supplementary Figure 8. Forest plot for mtCOJO analysis of rs2064853 – an mQTL for DNA methylation in the promotor of the CSE1L gene – that was significant in SMR analysis and has opposite effects on SCZ and BIP



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Supplementary Table 2. Comparison between conditional and raw results for five psychiatric dis
Variants that are genome-wide significant in the adjusted analysis and have larger conditional e
SNPs where b_diff < 0 are SNPs with larger conditional effect size than raw effect size.

| Disorder | SNP | chr | pos | A1_scz | b_scz_adj | se_scz_adj |
|---|---|---|---|---|---|---|
| SCZ | rs3764002 | 12 | 108618630 | C | 0.083 | 0.012 |
| SCZ | rs6095357 | 20 | 47523865 | A | -0.069 | 0.011 |
| SCZ | rs7790864 | 7 | 28478625 | A | -0.062 | 0.011 |
| SCZ | rs1054972 | 19 | 1852582 | A | 0.076 | 0.013 |
| SCZ | rs2867673 | 7 | 71752652 | T | 0.060 | 0.010 |
| SCZ | rs6564668 | 16 | 79457393 | C | -0.060 | 0.010 |
| SCZ | rs11922765 | 3 | 95047279 | G | -0.060 | 0.010 |
| SCZ | rs2973038 | 5 | 37833781 | C | 0.066 | 0.012 |
| SCZ | rs10903945 | 10 | 363275 | C | 0.057 | 0.010 |
| SCZ | rs10282935 | 8 | 38703797 | A | 0.058 | 0.011 |
| SCZ | rs6701877 | 1 | 174015259 | G | -0.096 | 0.014 |
| SCZ | rs7372313 | 3 | 135872958 | G | -0.069 | 0.010 |
| SCZ | rs1765142 | 11 | 30378559 | C | 0.065 | 0.011 |
| SCZ | rs55646993 | 7 | 105017864 | G | -0.062 | 0.010 |
| SCZ | rs150437760 | 14 | 59981768 | A | 0.131 | 0.024 |
| SCZ | rs13201681 | 6 | 28394680 | C | -0.196 | 0.019 |
| SCZ | rs2660304 | 1 | 98512127 | G | 0.106 | 0.013 |
| SCZ | rs4766428 | 12 | 110723245 | C | 0.081 | 0.011 |
| SCZ | rs6065094 | 20 | 37453194 | A | -0.074 | 0.011 |
| SCZ | rs12293670 | 11 | 124612932 | A | 0.072 | 0.011 |
| SCZ | rs11783093 | 8 | 27425349 | C | -0.094 | 0.015 |
| SCZ | rs4129585 | 8 | 143312933 | A | 0.066 | 0.010 |
| SCZ | rs2851447 | 12 | 123665113 | G | -0.074 | 0.012 |
| SCZ | rs7432375 | 3 | 136288405 | G | -0.066 | 0.011 |
| SCZ | rs13135092 | 4 | 103198082 | A | -0.125 | 0.020 |
| SCZ | rs34796896 | 3 | 180623255 | G | -0.078 | 0.013 |
| SCZ | rs6002655 | 22 | 42603814 | C | 0.063 | 0.011 |
| SCZ | rs7951870 | 11 | 46373311 | T | -0.082 | 0.014 |
| SCZ | rs11874716 | 18 | 52750688 | T | 0.061 | 0.010 |
| SCZ | rs16867576 | 5 | 88746331 | A | 0.094 | 0.016 |
| SCZ | rs4144797 | 2 | 233562197 | T | 0.063 | 0.011 |
| SCZ | rs12416331 | 10 | 104928914 | T | -0.106 | 0.018 |
| SCZ | rs7632834 | 3 | 17886678 | T | -0.060 | 0.010 |
| SCZ | rs4936215 | 11 | 133852684 | A | 0.075 | 0.013 |
| SCZ | rs12129573 | 1 | 73768366 | C | 0.061 | 0.011 |
| SCZ | rs9461856 | 6 | 33395199 | G | 0.059 | 0.010 |
| SCZ | rs10503253 | 8 | 4180844 | C | 0.071 | 0.013 |
| SCZ | rs62334820 | 4 | 176855221 | C | 0.073 | 0.013 |
| SCZ | rs1353545 | 3 | 60287845 | G | 0.061 | 0.011 |

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|---|---|---|---|---|---|---|
| SCZ | rs7632921 | 3 | 71543758 | G | -0.058 | 0.011 |
| SCZ | rs2949006 | 2 | 200715388 | T | 0.071 | 0.013 |
| SCZ | rs7129727 | 11 | 57484660 | G | 0.061 | 0.011 |
| SCZ | rs9607782 | 22 | 41587556 | T | 0.067 | 0.012 |
| SCZ | rs17465671 | 16 | 63712719 | C | -0.058 | 0.011 |
| SCZ | rs301818 | 1 | 8503242 | G | 0.060 | 0.011 |
| SCZ | rs7596038 | 2 | 58383820 | C | -0.056 | 0.010 |
| SCZ | rs10148671 | 14 | 29469373 | T | -0.059 | 0.011 |
| SCZ | rs12705761 | 7 | 110976264 | G | -0.058 | 0.011 |
| SCZ | rs1451488 | 2 | 199990107 | A | -0.056 | 0.010 |
| SCZ | rs58950470 | 11 | 65383755 | G | 0.059 | 0.011 |
| SCZ | rs2053079 | 19 | 30987423 | A | -0.064 | 0.012 |
| SCZ | rs2007044 | 12 | 2344960 | A | -0.056 | 0.010 |
| SCZ | rs2917569 | 11 | 132568255 | T | 0.056 | 0.010 |
| SCZ | rs1899543 | 11 | 24406419 | A | -0.055 | 0.010 |
| SCZ | rs12668848 | 7 | 2020995 | G | -0.055 | 0.010 |
| SCZ | rs9403484 | 6 | 143651969 | C | 0.064 | 0.012 |
| SCZ | rs14403 | 1 | 243663893 | C | -0.065 | 0.013 |
| SCZ | rs36043959 | 8 | 111472014 | G | 0.065 | 0.013 |
| SCZ | rs1473594 | 8 | 60696526 | T | 0.053 | 0.010 |
| SCZ | rs6680011 | 1 | 95840866 | A | -0.073 | 0.014 |
| SCZ | rs1080500 | 3 | 53175017 | G | -0.056 | 0.011 |
| SCZ | rs7701440 | 5 | 60620980 | T | -0.051 | 0.010 |
| SCZ | rs3743078 | 15 | 78894759 | C | -0.060 | 0.012 |
| SCZ | rs12129719 | 1 | 66324512 | G | 0.052 | 0.011 |
| SCZ | rs12628643 | 22 | 40015493 | C | 0.053 | 0.011 |
| SCZ | rs2332700 | 14 | 72417326 | C | 0.057 | 0.012 |
| SCZ | rs7789569 | 7 | 104927586 | T | 0.052 | 0.011 |
| SCZ | rs760608 | 6 | 114719447 | G | -0.056 | 0.012 |
| SCZ | rs7216638 | 17 | 2156453 | T | -0.053 | 0.011 |
| SCZ | rs2905432 | 19 | 19484295 | G | -0.051 | 0.011 |
| SCZ | rs1319017 | 9 | 84736303 | G | 0.052 | 0.011 |
| SCZ | rs215411 | 4 | 23423603 | T | 0.052 | 0.011 |
| SCZ | rs7499750 | 16 | 13749265 | A | 0.057 | 0.012 |
| SCZ | rs7801375 | 7 | 131567263 | A | -0.067 | 0.014 |
| SCZ | rs10791097 | 11 | 130718630 | T | 0.048 | 0.010 |
| SCZ | rs36104021 | 12 | 103361112 | C | 0.078 | 0.017 |
| SCZ | rs12704290 | 7 | 86427626 | G | -0.075 | 0.016 |
| SCZ | rs1120004 | 12 | 23633432 | T | 0.055 | 0.012 |
| SCZ | rs7142769 | 14 | 104228841 | C | 0.051 | 0.011 |
| SCZ | rs7893279 | 10 | 18745105 | T | 0.077 | 0.017 |
| SCZ | rs10520163 | 4 | 170626552 | T | 0.047 | 0.010 |
| SCZ | rs12148337 | 15 | 70589272 | T | 0.047 | 0.010 |

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|---|---|---|---|---|---|---|
| SCZ | rs281299 | 15 | 47686081 | C | 0.048 | 0.011 |
| SCZ | rs6434928 | 2 | 198304577 | G | -0.049 | 0.011 |
| SCZ | rs4650963 | 1 | 177309490 | G | 0.070 | 0.016 |
| SCZ | rs1191551 | 14 | 30000405 | T | 0.056 | 0.013 |
| SCZ | rs6035706 | 20 | 20821005 | A | -0.050 | 0.011 |
| SCZ | rs211829 | 7 | 110048893 | T | 0.047 | 0.011 |
| SCZ | rs4925114 | 17 | 17711270 | A | 0.049 | 0.011 |
| SCZ | rs2514218 | 11 | 113392994 | C | -0.049 | 0.011 |
| SCZ | rs2970610 | 1 | 44097530 | T | 0.048 | 0.011 |
| SCZ | rs11646127 | 16 | 29966277 | G | -0.047 | 0.011 |
| SCZ | rs6800435 | 3 | 10804551 | C | 0.070 | 0.016 |
| SCZ | rs324015 | 12 | 57490100 | T | -0.054 | 0.012 |
| SCZ | rs2910032 | 5 | 152540354 | C | -0.045 | 0.010 |
| SCZ | rs12898315 | 15 | 61854003 | G | 0.045 | 0.010 |
| SCZ | rs4240748 | 12 | 92246786 | C | -0.046 | 0.011 |
| SCZ | rs17514846 | 15 | 91416550 | A | -0.045 | 0.011 |
| SCZ | rs10985817 | 9 | 101071090 | T | -0.060 | 0.014 |
| SCZ | rs2161711 | 16 | 71359066 | A | 0.058 | 0.014 |
| SCZ | rs1339227 | 6 | 73155701 | C | -0.046 | 0.011 |
| SCZ | rs16902086 | 5 | 45285752 | A | -0.046 | 0.011 |
| SCZ | rs489939 | 3 | 161470592 | G | -0.045 | 0.011 |
| SCZ | rs7010876 | 8 | 89264751 | T | -0.048 | 0.012 |
| SCZ | rs10783624 | 12 | 39522907 | C | -0.046 | 0.011 |
| SCZ | rs3735025 | 7 | 137074844 | T | 0.044 | 0.011 |
| SCZ | rs35346733 | 3 | 2521322 | G | 0.055 | 0.013 |
| SCZ | rs704373 | 3 | 63867355 | A | 0.045 | 0.011 |
| SCZ | rs6694545 | 1 | 30437268 | A | 0.049 | 0.012 |
| SCZ | rs13121251 | 4 | 143829759 | T | 0.045 | 0.011 |
| SCZ | rs217287 | 6 | 84407466 | C | -0.042 | 0.010 |
| SCZ | rs1975802 | 16 | 68285847 | A | -0.053 | 0.014 |
| SCZ | rs783540 | 15 | 83254708 | A | -0.040 | 0.010 |
| SCZ | rs11685299 | 2 | 225391296 | C | -0.043 | 0.011 |
| SCZ | rs28374258 | 1 | 190949551 | T | 0.050 | 0.013 |
| SCZ | rs9881798 | 3 | 16846967 | A | -0.040 | 0.011 |
| SCZ | rs133047 | 22 | 41027819 | T | 0.066 | 0.017 |
| SCZ | rs12991836 | 2 | 145141541 | A | -0.041 | 0.011 |
| SCZ | rs56873913 | 19 | 50091199 | T | 0.048 | 0.013 |
| SCZ | rs2077586 | 2 | 73161551 | A | 0.045 | 0.012 |
| SCZ | rs12447860 | 16 | 58642638 | T | -0.039 | 0.011 |
| SCZ | rs11587347 | 1 | 239198959 | C | -0.066 | 0.018 |
| SCZ | rs2410572 | 8 | 18421474 | G | -0.038 | 0.010 |
| SCZ | rs10196799 | 2 | 185640728 | A | 0.038 | 0.010 |
| SCZ | rs1042992 | 8 | 26269191 | C | 0.049 | 0.014 |

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|---|---|---|---|---|---|---|
| SCZ | rs55669358 | 8 | 34312412 | T | -0.065 | 0.018 |
| SCZ | rs9545047 | 13 | 79859456 | A | 0.037 | 0.011 |
| SCZ | rs10156310 | 8 | 38209129 | A | 0.045 | 0.013 |
| SCZ | rs56145559 | 2 | 73623439 | C | 0.044 | 0.013 |
| SCZ | rs634940 | 6 | 93077500 | G | 0.041 | 0.012 |
| SCZ | rs11993663 | 8 | 10032894 | C | 0.036 | 0.011 |
| SCZ | rs7225476 | 17 | 78561603 | G | 0.034 | 0.010 |
| SCZ | rs13169274 | 5 | 137855305 | T | -0.035 | 0.010 |
| SCZ | rs893949 | 11 | 134296384 | C | -0.030 | 0.011 |
| SCZ | rs12908161 | 15 | 85207825 | A | 0.033 | 0.012 |
| SCZ | rs11584091 | 1 | 150101169 | C | -0.038 | 0.014 |
| SCZ | rs75968099 | 3 | 36858583 | C | 0.029 | 0.011 |
| SCZ | rs35604463 | 14 | 99712032 | G | -0.028 | 0.011 |
| SCZ | rs7191183 | 16 | 9900057 | T | -0.029 | 0.011 |
| SCZ | rs112509803 | 7 | 24735004 | G | 0.030 | 0.016 |

| Disorder | SNP | chr | pos | A1_bip | b_bip_adj | se_bip_adj |
|---|---|---|---|---|---|---|
| BIP | rs12554512 | 9 | 23352293 | T | -0.083 | 0.014 |
| BIP | rs6891181 | 5 | 80849101 | T | -0.081 | 0.014 |
| BIP | rs12268910 | 10 | 111878510 | T | -0.097 | 0.018 |
| BIP | rs9834970 | 3 | 36856030 | T | -0.074 | 0.013 |
| BIP | rs73496688 | 11 | 79156748 | A | 0.103 | 0.019 |
| BIP | rs111444407 | 19 | 19358207 | T | 0.099 | 0.018 |
| BIP | rs11724116 | 4 | 162294038 | T | -0.099 | 0.019 |
| BIP | rs884301 | 17 | 53367464 | T | 0.072 | 0.014 |
| BIP | rs329319 | 5 | 133906609 | A | 0.073 | 0.014 |
| BIP | rs2314398 | 2 | 97413488 | C | 0.071 | 0.014 |
| BIP | rs10455979 | 6 | 166995260 | C | -0.064 | 0.014 |
| BIP | rs174592 | 11 | 61618608 | A | -0.064 | 0.014 |
| BIP | rs55648125 | 6 | 50816718 | A | -0.098 | 0.021 |
| BIP | rs138321 | 22 | 41209304 | A | 0.059 | 0.013 |
| BIP | rs2302417 | 3 | 52814256 | A | -0.058 | 0.014 |
| BIP | rs71395455 | 15 | 85153804 | A | 0.063 | 0.015 |
| BIP | rs13231398 | 7 | 110197412 | C | -0.091 | 0.022 |
| BIP | rs17150022 | 7 | 24771777 | T | -0.078 | 0.020 |
| BIP | rs10744560 | 12 | 2387099 | T | 0.038 | 0.014 |

| Disorder | SNP | chr | pos | A1_mdd | b_md_adj | se_md_adj |
|---|---|---|---|---|---|---|
| MD | rs11697370 | 20 | 47731767 | T | -0.031 | 0.005 |
| MD | rs27732 | 5 | 87992576 | A | 0.034 | 0.005 |
| MD | rs1806153 | 11 | 31850105 | T | 0.037 | 0.006 |
| MD | rs1354115 | 9 | 2983774 | A | 0.029 | 0.005 |
| MD | rs301799 | 1 | 8489302 | T | -0.028 | 0.005 |

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|---|---|---|---|---|---|---|
| MD | rs12552 | 13 | 53625781 | A | 0.040 | 0.005 |
| MD | rs1432639 | 1 | 72813218 | A | 0.038 | 0.005 |
| MD | rs8025231 | 15 | 37648402 | A | -0.031 | 0.005 |
| MD | rs915057 | 14 | 64686207 | A | -0.030 | 0.005 |
| MD | rs11135349 | 5 | 164523472 | A | -0.028 | 0.005 |
| MD | rs12958048 | 18 | 53101598 | A | 0.030 | 0.005 |
| MD | rs4904738 | 14 | 42179732 | T | -0.028 | 0.005 |
| MD | rs12129573 | 1 | 73768366 | A | 0.029 | 0.005 |
| MD | rs12666117 | 7 | 109105611 | A | 0.027 | 0.005 |
| MD | rs159963 | 1 | 8504421 | A | -0.028 | 0.005 |
| MD | rs16854051 | 4 | 42123892 | T | -0.033 | 0.006 |
| MD | rs1363104 | 5 | 103917797 | C | 0.027 | 0.005 |
| MD | rs10149470 | 14 | 104017953 | A | -0.027 | 0.005 |
| MD | rs4261101 | 1 | 90796053 | A | -0.028 | 0.005 |
| MD | rs2389016 | 1 | 80799329 | T | 0.029 | 0.005 |
| MD | rs7430565 | 3 | 158107180 | A | -0.026 | 0.005 |
| MD | rs10959913 | 9 | 11544964 | T | 0.031 | 0.006 |
| MD | rs6905391 | 6 | 28262686 | A | -0.037 | 0.007 |
| MD | rs5758265 | 22 | 41617897 | A | 0.029 | 0.006 |
| MD | rs11643192 | 16 | 72214276 | A | 0.026 | 0.005 |
| MD | rs4074723 | 12 | 23947737 | A | -0.026 | 0.005 |
| MD | rs7198928 | 16 | 7666402 | T | 0.027 | 0.005 |
| MD | rs2005864 | 14 | 75377692 | T | 0.026 | 0.005 |
| MD | rs7029033 | 9 | 126682068 | T | 0.048 | 0.010 |
| MD | rs10950398 | 7 | 12264871 | A | 0.025 | 0.005 |
| MD | rs62099069 | 18 | 36883737 | A | -0.025 | 0.005 |
| MD | rs4869056 | 5 | 166992078 | A | -0.025 | 0.005 |
| MD | rs7856424 | 9 | 119733595 | T | -0.027 | 0.005 |
| MD | rs1226412 | 2 | 157111313 | T | 0.030 | 0.006 |
| MD | rs4143229 | 13 | 44327799 | A | -0.045 | 0.009 |
| MD | rs11682175 | 2 | 57987593 | T | -0.023 | 0.005 |
| MD | rs11663393 | 18 | 50614732 | A | 0.024 | 0.005 |
| MD | rs8063603 | 16 | 6310645 | A | -0.025 | 0.005 |
| MD | rs77135925 | 17 | 27495269 | T | -0.041 | 0.009 |
| MD | rs61867293 | 10 | 106563924 | T | -0.028 | 0.006 |
| MD | rs7200826 | 16 | 13066833 | T | 0.025 | 0.006 |

| Disorder | SNP | chr | pos | A1_adhd | b_adhd_adj | se_adhd_adj |
|---|---|---|---|---|---|---|
| ADHD | rs78648104 | 6 | 50683009 | T | 0.136 | 0.023 |
| ADHD | rs2244336 | 10 | 8831827 | C | 0.071 | 0.013 |
| ADHD | rs12410444 | 1 | 44188719 | A | 0.107 | 0.014 |
| ADHD | rs13023832 | 2 | 215219808 | A | 0.133 | 0.020 |
| ADHD | rs281320 | 15 | 47769424 | T | -0.080 | 0.013 |

| | | | | | | |
|---|---|---|---|---|---|---|
| ADHD | rs74760947 | 8 | 34352610 | A | -0.168 | 0.030 |
| ADHD | rs4858241 | 3 | 20669071 | T | 0.071 | 0.013 |
| ADHD | rs1427829 | 12 | 89760744 | A | 0.066 | 0.013 |
| ADHD | rs10262192 | 7 | 114091753 | A | 0.063 | 0.012 |
| ADHD | rs212178 | 16 | 72578131 | A | -0.090 | 0.019 |
| ADHD | rs11591402 | 10 | 106747354 | A | -0.067 | 0.015 |
| ADHD | rs4916723 | 5 | 87854395 | A | -0.050 | 0.013 |
| ADHD | rs2391769 | 1 | 96978961 | A | -0.045 | 0.013 |

| Disorder | SNP | chr | pos | A1_aut | b_aut_adj | se_aut_adj |
|---|---|---|---|---|---|---|
| AUT | rs10099100 | 8 | 10576775 | C | 0.084 | 0.014 |
| AUT | rs910805 | 20 | 21248116 | A | 0.077 | 0.015 |

;orders

ffect sizes than raw effect sizes are highlighted in blue

| p_scz_adj | b_scz_unadj | se_scz_unadj | p_scz_unadj | b_scz_diff | se_diff | p_diff |
|---|---|---|---|---|---|---|
| 1.94E-12 | 0.054 | 0.011 | 6.05E-07 | -0.029 | 0.007 | 8.68E-05 |
| 1.17E-10 | -0.048 | 0.010 | 1.21E-06 | -0.021 | 0.007 | 1.47E-03 |
| 6.33E-09 | -0.044 | 0.010 | 7.18E-06 | -0.018 | 0.007 | 7.04E-03 |
| 6.42E-09 | 0.053 | 0.012 | 1.32E-05 | -0.024 | 0.008 | 3.93E-03 |
| 9.44E-09 | 0.049 | 0.010 | 4.11E-07 | -0.011 | 0.006 | 8.49E-02 |
| 1.05E-08 | -0.038 | 0.010 | 7.94E-05 | -0.022 | 0.006 | 7.15E-04 |
| 1.22E-08 | -0.044 | 0.010 | 4.36E-06 | -0.015 | 0.006 | 1.82E-02 |
| 1.28E-08 | 0.051 | 0.011 | 1.72E-06 | -0.015 | 0.007 | 3.96E-02 |
| 3.13E-08 | 0.040 | 0.010 | 3.30E-05 | -0.017 | 0.006 | 5.64E-03 |
| 3.97E-08 | 0.041 | 0.010 | 3.17E-05 | -0.017 | 0.006 | 7.55E-03 |
| 1.47E-11 | -0.073 | 0.013 | 2.37E-08 | -0.023 | 0.009 | 9.69E-03 |
| 4.26E-11 | -0.062 | 0.010 | 1.54E-10 | -0.007 | 0.006 | 2.80E-01 |
| 1.54E-09 | 0.058 | 0.010 | 1.13E-08 | -0.008 | 0.007 | 2.27E-01 |
| 2.23E-09 | -0.053 | 0.010 | 3.83E-08 | -0.009 | 0.006 | 1.49E-01 |
| 3.71E-08 | 0.121 | 0.022 | 4.58E-08 | -0.010 | 0.014 | 4.92E-01 |
| 5.98E-26 | -0.235 | 0.017 | 1.32E-41 | 0.039 | 0.011 | 4.71E-04 |
| 1.56E-15 | 0.108 | 0.012 | 2.18E-18 | 0.003 | 0.008 | 7.46E-01 |
| 6.00E-14 | 0.076 | 0.010 | 2.68E-14 | -0.005 | 0.007 | 4.67E-01 |
| 2.03E-11 | -0.085 | 0.010 | 7.91E-17 | 0.011 | 0.007 | 9.75E-02 |
| 6.98E-11 | 0.081 | 0.010 | 1.70E-15 | 0.009 | 0.007 | 1.71E-01 |
| 1.30E-10 | -0.093 | 0.014 | 7.64E-12 | 0.000 | 0.009 | 9.57E-01 |
| 1.62E-10 | 0.082 | 0.010 | 9.26E-18 | 0.016 | 0.006 | 1.26E-02 |
| 2.45E-10 | -0.087 | 0.011 | 5.55E-16 | 0.013 | 0.007 | 6.11E-02 |
| 2.96E-10 | -0.068 | 0.010 | 4.07E-12 | 0.001 | 0.006 | 8.26E-01 |
| 3.58E-10 | -0.149 | 0.018 | 7.87E-16 | 0.024 | 0.012 | 5.20E-02 |
| 1.57E-09 | -0.083 | 0.012 | 3.19E-12 | 0.006 | 0.008 | 4.71E-01 |
| 3.01E-09 | 0.075 | 0.010 | 2.15E-14 | 0.012 | 0.006 | 5.91E-02 |
| 3.16E-09 | -0.093 | 0.013 | 2.99E-13 | 0.012 | 0.008 | 1.72E-01 |
| 3.52E-09 | 0.072 | 0.010 | 8.44E-14 | 0.010 | 0.006 | 1.09E-01 |
| 5.23E-09 | 0.101 | 0.015 | 1.65E-11 | 0.007 | 0.010 | 4.91E-01 |
| 5.87E-09 | 0.082 | 0.010 | 4.33E-16 | 0.019 | 0.007 | 4.76E-03 |
| 7.02E-09 | -0.145 | 0.017 | 7.09E-18 | 0.040 | 0.011 | 3.59E-04 |
| 8.54E-09 | -0.058 | 0.010 | 2.52E-09 | -0.002 | 0.006 | 7.23E-01 |
| 8.72E-09 | 0.091 | 0.012 | 5.32E-14 | 0.016 | 0.008 | 3.69E-02 |
| 8.93E-09 | 0.076 | 0.010 | 8.94E-15 | 0.015 | 0.007 | 1.92E-02 |
| 9.21E-09 | 0.071 | 0.010 | 1.68E-13 | 0.011 | 0.006 | 7.57E-02 |
| 1.52E-08 | 0.066 | 0.012 | 9.60E-09 | -0.005 | 0.008 | 5.35E-01 |
| 1.69E-08 | 0.081 | 0.012 | 9.60E-12 | 0.009 | 0.008 | 2.75E-01 |
| 2.10E-08 | 0.059 | 0.010 | 5.67E-09 | -0.002 | 0.007 | 7.33E-01 |

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|---|---|---|---|---|---|---|
| 4.11E-08 | -0.057 | 0.010 | 9.52E-09 | -0.001 | 0.006 | 8.17E-01 |
| 4.33E-08 | 0.100 | 0.012 | 3.69E-17 | 0.029 | 0.008 | 2.46E-04 |
| 4.50E-08 | 0.063 | 0.010 | 1.47E-09 | 0.001 | 0.007 | 8.71E-01 |
| 4.61E-08 | 0.081 | 0.011 | 5.54E-13 | 0.015 | 0.008 | 5.20E-02 |
| 5.08E-08 | -0.058 | 0.010 | 4.14E-09 | 0.000 | 0.006 | 9.93E-01 |
| 5.10E-08 | 0.060 | 0.010 | 3.79E-09 | 0.000 | 0.007 | 9.82E-01 |
| 5.52E-08 | -0.067 | 0.010 | 2.37E-12 | 0.011 | 0.006 | 8.73E-02 |
| 6.76E-08 | -0.063 | 0.010 | 5.46E-10 | 0.004 | 0.007 | 5.41E-01 |
| 6.96E-08 | -0.066 | 0.010 | 5.11E-11 | 0.007 | 0.007 | 2.61E-01 |
| 7.22E-08 | -0.067 | 0.010 | 4.75E-12 | 0.011 | 0.006 | 9.62E-02 |
| 8.72E-08 | 0.057 | 0.010 | 2.07E-08 | -0.002 | 0.007 | 8.10E-01 |
| 9.65E-08 | -0.071 | 0.011 | 1.82E-10 | 0.007 | 0.007 | 3.67E-01 |
| 9.74E-08 | -0.089 | 0.010 | 5.63E-20 | 0.033 | 0.006 | 3.98E-07 |
| 9.89E-08 | 0.061 | 0.010 | 3.11E-10 | 0.005 | 0.006 | 4.29E-01 |
| 1.05E-07 | -0.058 | 0.009 | 1.23E-09 | 0.003 | 0.006 | 6.28E-01 |
| 1.13E-07 | -0.085 | 0.010 | 1.11E-18 | 0.030 | 0.006 | 3.19E-06 |
| 1.68E-07 | 0.064 | 0.011 | 1.41E-08 | 0.000 | 0.007 | 9.77E-01 |
| 1.80E-07 | -0.074 | 0.012 | 1.71E-10 | 0.009 | 0.008 | 2.58E-01 |
| 2.89E-07 | 0.080 | 0.012 | 4.07E-12 | 0.016 | 0.008 | 4.37E-02 |
| 3.25E-07 | 0.064 | 0.010 | 3.33E-11 | 0.011 | 0.006 | 9.63E-02 |
| 3.98E-07 | -0.074 | 0.013 | 2.83E-08 | 0.001 | 0.009 | 9.50E-01 |
| 5.40E-07 | -0.072 | 0.010 | 2.71E-12 | 0.016 | 0.007 | 2.32E-02 |
| 7.61E-07 | -0.072 | 0.010 | 3.72E-14 | 0.021 | 0.006 | 6.42E-04 |
| 7.82E-07 | -0.078 | 0.011 | 3.11E-12 | 0.018 | 0.007 | 1.42E-02 |
| 9.83E-07 | 0.054 | 0.010 | 3.35E-08 | 0.002 | 0.007 | 7.27E-01 |
| 1.03E-06 | 0.070 | 0.010 | 3.03E-12 | 0.017 | 0.007 | 9.52E-03 |
| 1.37E-06 | 0.070 | 0.011 | 1.52E-10 | 0.013 | 0.007 | 7.99E-02 |
| 1.93E-06 | 0.065 | 0.010 | 7.00E-11 | 0.014 | 0.007 | 3.90E-02 |
| 1.94E-06 | -0.061 | 0.011 | 1.90E-08 | 0.005 | 0.007 | 4.85E-01 |
| 1.98E-06 | -0.065 | 0.010 | 4.59E-10 | 0.011 | 0.007 | 9.52E-02 |
| 2.16E-06 | -0.069 | 0.010 | 6.62E-12 | 0.017 | 0.007 | 8.89E-03 |
| 2.36E-06 | 0.066 | 0.010 | 7.82E-11 | 0.014 | 0.007 | 3.55E-02 |
| 2.70E-06 | 0.058 | 0.010 | 1.40E-08 | 0.006 | 0.007 | 3.51E-01 |
| 2.89E-06 | 0.071 | 0.011 | 4.24E-10 | 0.014 | 0.007 | 6.73E-02 |
| 3.04E-06 | -0.077 | 0.013 | 6.27E-09 | 0.010 | 0.009 | 2.28E-01 |
| 3.12E-06 | 0.063 | 0.010 | 3.29E-11 | 0.015 | 0.006 | 1.72E-02 |
| 3.36E-06 | 0.090 | 0.016 | 7.31E-09 | 0.012 | 0.010 | 2.36E-01 |
| 3.40E-06 | -0.114 | 0.015 | 3.57E-14 | 0.039 | 0.010 | 8.75E-05 |
| 3.41E-06 | 0.062 | 0.011 | 1.42E-08 | 0.007 | 0.007 | 3.19E-01 |
| 3.80E-06 | 0.077 | 0.010 | 4.51E-14 | 0.026 | 0.007 | 1.00E-04 |
| 4.09E-06 | 0.111 | 0.015 | 4.80E-13 | 0.035 | 0.010 | 7.19E-04 |
| 4.87E-06 | 0.053 | 0.010 | 2.81E-08 | 0.006 | 0.006 | 3.55E-01 |
| 5.79E-06 | 0.054 | 0.010 | 1.16E-08 | 0.008 | 0.006 | 2.30E-01 |

| | | | | | | |
|---|---|---|---|---|---|---|
| 5.87E-06 | 0.055 | 0.010 | 2.19E-08 | 0.007 | 0.007 | 2.98E-01 |
| 6.34E-06 | -0.073 | 0.010 | 3.62E-13 | 0.024 | 0.007 | 4.19E-04 |
| 7.54E-06 | 0.082 | 0.014 | 1.16E-08 | 0.012 | 0.010 | 1.98E-01 |
| 8.02E-06 | 0.073 | 0.012 | 4.12E-10 | 0.017 | 0.008 | 2.97E-02 |
| 8.08E-06 | -0.060 | 0.010 | 7.24E-09 | 0.010 | 0.007 | 1.66E-01 |
| 8.44E-06 | 0.059 | 0.010 | 2.29E-09 | 0.012 | 0.007 | 7.60E-02 |
| 8.59E-06 | 0.057 | 0.010 | 2.64E-08 | 0.008 | 0.007 | 2.40E-01 |
| 8.87E-06 | -0.073 | 0.010 | 2.42E-12 | 0.023 | 0.007 | 4.93E-04 |
| 9.27E-06 | 0.068 | 0.010 | 1.39E-11 | 0.020 | 0.007 | 3.01E-03 |
| 1.04E-05 | -0.071 | 0.010 | 5.52E-13 | 0.024 | 0.007 | 2.22E-04 |
| 1.05E-05 | 0.082 | 0.015 | 2.00E-08 | 0.012 | 0.010 | 2.27E-01 |
| 1.08E-05 | -0.072 | 0.011 | 1.42E-10 | 0.018 | 0.008 | 1.72E-02 |
| 1.18E-05 | -0.063 | 0.010 | 3.72E-11 | 0.018 | 0.006 | 3.93E-03 |
| 1.40E-05 | 0.057 | 0.010 | 2.51E-09 | 0.012 | 0.006 | 5.55E-02 |
| 1.96E-05 | -0.056 | 0.010 | 2.15E-08 | 0.010 | 0.007 | 1.38E-01 |
| 2.03E-05 | -0.069 | 0.010 | 2.55E-12 | 0.023 | 0.007 | 3.97E-04 |
| 2.09E-05 | -0.080 | 0.013 | 1.02E-09 | 0.020 | 0.009 | 2.25E-02 |
| 2.17E-05 | 0.070 | 0.013 | 4.22E-08 | 0.012 | 0.008 | 1.57E-01 |
| 2.23E-05 | -0.063 | 0.010 | 3.76E-10 | 0.017 | 0.007 | 1.15E-02 |
| 2.56E-05 | -0.066 | 0.010 | 5.55E-11 | 0.020 | 0.007 | 2.93E-03 |
| 2.80E-05 | -0.057 | 0.010 | 1.24E-08 | 0.012 | 0.007 | 7.16E-02 |
| 3.11E-05 | -0.062 | 0.011 | 6.51E-09 | 0.014 | 0.007 | 5.16E-02 |
| 3.56E-05 | -0.060 | 0.010 | 5.44E-09 | 0.014 | 0.007 | 4.00E-02 |
| 3.84E-05 | 0.065 | 0.010 | 7.02E-11 | 0.020 | 0.007 | 1.95E-03 |
| 4.27E-05 | 0.087 | 0.012 | 2.42E-12 | 0.032 | 0.008 | 9.34E-05 |
| 4.61E-05 | 0.065 | 0.010 | 1.39E-10 | 0.020 | 0.007 | 3.19E-03 |
| 5.23E-05 | 0.077 | 0.011 | 6.20E-12 | 0.028 | 0.007 | 2.10E-04 |
| 6.08E-05 | 0.057 | 0.010 | 4.06E-08 | 0.012 | 0.007 | 7.80E-02 |
| 6.13E-05 | -0.069 | 0.010 | 9.53E-13 | 0.027 | 0.006 | 2.30E-05 |
| 8.92E-05 | -0.069 | 0.013 | 3.56E-08 | 0.016 | 0.008 | 5.41E-02 |
| 1.04E-04 | -0.059 | 0.010 | 8.45E-10 | 0.019 | 0.006 | 3.73E-03 |
| 1.06E-04 | -0.060 | 0.010 | 3.86E-09 | 0.017 | 0.007 | 1.03E-02 |
| 1.13E-04 | 0.073 | 0.012 | 6.35E-10 | 0.024 | 0.008 | 2.69E-03 |
| 1.31E-04 | -0.054 | 0.010 | 2.81E-08 | 0.014 | 0.006 | 3.34E-02 |
| 1.39E-04 | 0.094 | 0.016 | 3.47E-09 | 0.028 | 0.011 | 9.28E-03 |
| 1.44E-04 | -0.061 | 0.010 | 6.46E-10 | 0.020 | 0.007 | 3.14E-03 |
| 1.56E-04 | 0.070 | 0.012 | 2.58E-09 | 0.022 | 0.008 | 6.46E-03 |
| 1.61E-04 | 0.061 | 0.011 | 2.96E-08 | 0.016 | 0.007 | 2.53E-02 |
| 2.13E-04 | -0.062 | 0.010 | 3.28E-10 | 0.023 | 0.006 | 3.56E-04 |
| 2.19E-04 | -0.103 | 0.017 | 4.82E-10 | 0.037 | 0.011 | 7.69E-04 |
| 2.22E-04 | -0.055 | 0.010 | 1.07E-08 | 0.016 | 0.006 | 9.08E-03 |
| 2.52E-04 | 0.056 | 0.010 | 4.51E-09 | 0.018 | 0.006 | 4.22E-03 |
| 2.75E-04 | 0.073 | 0.012 | 3.67E-09 | 0.024 | 0.008 | 4.21E-03 |

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|---|---|---|---|---|---|---|
| 3.44E-04 | -0.095 | 0.017 | 1.37E-08 | 0.030 | 0.011 | 5.71E-03 |
| 4.01E-04 | 0.056 | 0.010 | 1.15E-08 | 0.019 | 0.006 | 4.09E-03 |
| 4.10E-04 | 0.073 | 0.012 | 5.56E-10 | 0.028 | 0.008 | 4.01E-04 |
| 4.86E-04 | 0.072 | 0.012 | 1.01E-09 | 0.027 | 0.008 | 3.81E-04 |
| 6.73E-04 | 0.063 | 0.011 | 1.30E-08 | 0.023 | 0.007 | 1.91E-03 |
| 7.97E-04 | 0.055 | 0.010 | 3.40E-08 | 0.019 | 0.007 | 4.81E-03 |
| 8.45E-04 | 0.052 | 0.010 | 4.86E-08 | 0.018 | 0.006 | 5.32E-03 |
| 9.01E-04 | -0.060 | 0.010 | 7.06E-10 | 0.025 | 0.006 | 8.66E-05 |
| 3.82E-03 | -0.053 | 0.010 | 2.98E-08 | 0.023 | 0.007 | 5.00E-04 |
| 5.43E-03 | 0.067 | 0.011 | 9.41E-10 | 0.034 | 0.007 | 1.79E-06 |
| 7.39E-03 | -0.081 | 0.013 | 8.63E-10 | 0.043 | 0.009 | 4.68E-07 |
| 8.31E-03 | 0.066 | 0.010 | 9.41E-11 | 0.037 | 0.007 | 2.26E-08 |
| 9.88E-03 | -0.056 | 0.010 | 1.66E-08 | 0.029 | 0.006 | 1.03E-05 |
| 9.91E-03 | -0.060 | 0.010 | 6.31E-09 | 0.031 | 0.007 | 6.25E-06 |
| 6.02E-02 | 0.084 | 0.015 | 2.31E-08 | 0.053 | 0.010 | 6.67E-08 |

| p_bip_adj | b_bip_unadj | se_bip_unadj | p_bip_unadj | b_bip_diff | se_bip_diff | p_bip_diff |
|---|---|---|---|---|---|---|
| 1.55E-09 | -0.066 | 0.014 | 1.28E-06 | -0.016 | 0.005 | 1.034E-03 |
| 1.49E-08 | -0.075 | 0.014 | 1.27E-07 | -0.005 | 0.005 | 3.045E-01 |
| 3.29E-08 | -0.091 | 0.018 | 2.73E-07 | -0.006 | 0.006 | 3.142E-01 |
| 2.52E-08 | -0.101 | 0.013 | 5.53E-14 | 0.027 | 0.005 | 2.934E-08 |
| 5.28E-08 | 0.109 | 0.019 | 1.05E-08 | 0.006 | 0.007 | 4.209E-01 |
| 6.25E-08 | 0.117 | 0.018 | 2.40E-10 | 0.017 | 0.007 | 9.750E-03 |
| 1.37E-07 | -0.104 | 0.019 | 3.27E-08 | 0.005 | 0.007 | 4.042E-01 |
| 1.60E-07 | 0.080 | 0.014 | 5.80E-09 | 0.008 | 0.005 | 9.837E-02 |
| 1.66E-07 | 0.079 | 0.014 | 1.54E-08 | 0.006 | 0.005 | 2.062E-01 |
| 7.83E-07 | 0.084 | 0.014 | 5.92E-09 | 0.013 | 0.005 | 1.015E-02 |
| 2.94E-06 | -0.075 | 0.014 | 4.60E-08 | 0.011 | 0.005 | 2.115E-02 |
| 4.95E-06 | -0.077 | 0.014 | 3.66E-08 | 0.013 | 0.005 | 8.251E-03 |
| 5.00E-06 | -0.117 | 0.022 | 4.92E-08 | 0.019 | 0.008 | 1.241E-02 |
| 1.15E-05 | 0.079 | 0.014 | 4.69E-09 | 0.020 | 0.005 | 2.927E-05 |
| 1.66E-05 | -0.079 | 0.014 | 4.93E-09 | 0.021 | 0.005 | 1.356E-05 |
| 1.75E-05 | 0.082 | 0.015 | 1.93E-08 | 0.020 | 0.005 | 2.065E-04 |
| 3.31E-05 | -0.121 | 0.022 | 3.36E-08 | 0.030 | 0.008 | 1.223E-04 |
| 1.30E-04 | -0.113 | 0.020 | 2.70E-08 | 0.035 | 0.007 | 1.715E-06 |
| 6.26E-03 | 0.083 | 0.014 | 2.92E-09 | 0.045 | 0.005 | 5.766E-19 |

| p_md_adj | b_md_unadj | se_md_unadj | p_md_unadj | b_md_diff | se_md_diff | p_md_diff |
|---|---|---|---|---|---|---|
| 3.31E-09 | -0.023 | 0.005 | 3.53E-06 | 0.007 | 0.002 | 2.04E-05 |
| 1.22E-11 | 0.031 | 0.005 | 1.87E-10 | 0.003 | 0.002 | 5.96E-02 |
| 8.78E-10 | 0.036 | 0.006 | 1.18E-09 | 0.001 | 0.002 | 5.10E-01 |
| 1.72E-08 | 0.028 | 0.005 | 2.37E-08 | 0.001 | 0.002 | 5.53E-01 |
| 2.49E-08 | -0.026 | 0.005 | 4.68E-08 | 0.001 | 0.002 | 4.70E-01 |

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|---|---|---|---|---|---|---|
| 1.66E-15 | 0.043 | 0.005 | 6.07E-19 | 0.003 | 0.002 | 4.15E-02 |
| 9.37E-14 | 0.039 | 0.005 | 4.55E-15 | 0.001 | 0.002 | 7.61E-01 |
| 3.39E-10 | -0.034 | 0.005 | 2.36E-12 | 0.003 | 0.002 | 9.49E-02 |
| 4.30E-09 | -0.030 | 0.005 | 7.61E-10 | 0.000 | 0.002 | 8.73E-01 |
| 1.08E-08 | -0.029 | 0.005 | 1.09E-09 | 0.001 | 0.002 | 5.48E-01 |
| 1.75E-08 | 0.034 | 0.005 | 3.61E-11 | 0.004 | 0.002 | 1.96E-02 |
| 1.82E-08 | -0.029 | 0.005 | 2.57E-09 | 0.000 | 0.002 | 8.04E-01 |
| 3.35E-08 | 0.034 | 0.005 | 4.01E-12 | 0.006 | 0.002 | 3.91E-04 |
| 4.07E-08 | 0.027 | 0.005 | 1.35E-08 | 0.000 | 0.002 | 9.28E-01 |
| 4.44E-08 | -0.027 | 0.005 | 3.19E-08 | 0.001 | 0.002 | 6.61E-01 |
| 7.02E-08 | -0.035 | 0.006 | 3.58E-09 | 0.002 | 0.002 | 4.23E-01 |
| 7.30E-08 | 0.031 | 0.005 | 7.38E-11 | 0.005 | 0.002 | 4.22E-03 |
| 8.21E-08 | -0.029 | 0.005 | 3.05E-09 | 0.002 | 0.002 | 2.73E-01 |
| 9.60E-08 | -0.029 | 0.005 | 1.04E-08 | 0.001 | 0.002 | 5.90E-01 |
| 1.19E-07 | 0.031 | 0.005 | 1.02E-08 | 0.001 | 0.002 | 4.11E-01 |
| 1.32E-07 | -0.029 | 0.005 | 2.87E-09 | 0.003 | 0.002 | 1.16E-01 |
| 1.39E-07 | 0.033 | 0.006 | 5.06E-09 | 0.002 | 0.002 | 2.15E-01 |
| 1.75E-07 | -0.044 | 0.007 | 1.35E-10 | 0.007 | 0.002 | 2.51E-03 |
| 1.87E-07 | 0.031 | 0.005 | 7.55E-09 | 0.002 | 0.002 | 3.22E-01 |
| 1.88E-07 | 0.027 | 0.005 | 3.36E-08 | 0.001 | 0.002 | 7.15E-01 |
| 2.27E-07 | -0.027 | 0.005 | 3.12E-08 | 0.001 | 0.002 | 6.46E-01 |
| 2.81E-07 | 0.028 | 0.005 | 1.00E-08 | 0.002 | 0.002 | 2.60E-01 |
| 3.09E-07 | 0.028 | 0.005 | 6.73E-09 | 0.002 | 0.002 | 1.68E-01 |
| 5.75E-07 | 0.052 | 0.009 | 2.74E-08 | 0.004 | 0.003 | 2.01E-01 |
| 7.05E-07 | 0.027 | 0.005 | 2.55E-08 | 0.002 | 0.002 | 1.58E-01 |
| 7.90E-07 | -0.028 | 0.005 | 1.31E-08 | 0.003 | 0.002 | 8.82E-02 |
| 9.49E-07 | -0.029 | 0.005 | 6.80E-09 | 0.003 | 0.002 | 4.49E-02 |
| 9.64E-07 | -0.031 | 0.005 | 8.48E-09 | 0.004 | 0.002 | 3.70E-02 |
| 1.17E-06 | 0.033 | 0.006 | 2.38E-08 | 0.004 | 0.002 | 8.27E-02 |
| 1.84E-06 | -0.051 | 0.009 | 2.51E-08 | 0.006 | 0.003 | 4.57E-02 |
| 2.81E-06 | -0.028 | 0.005 | 4.68E-09 | 0.005 | 0.002 | 3.05E-03 |
| 2.88E-06 | 0.028 | 0.005 | 1.65E-08 | 0.004 | 0.002 | 1.29E-02 |
| 4.58E-06 | -0.031 | 0.005 | 6.87E-09 | 0.006 | 0.002 | 1.11E-03 |
| 5.10E-06 | -0.049 | 0.009 | 9.36E-09 | 0.009 | 0.003 | 3.37E-03 |
| 6.33E-06 | -0.037 | 0.006 | 6.97E-10 | 0.009 | 0.002 | 1.15E-05 |
| 1.06E-05 | 0.031 | 0.006 | 2.43E-08 | 0.006 | 0.002 | 2.42E-03 |

| p_adhd_adj | b_adhd_unac | se_adhd_una | p_adhd_una | b_adhd_diff | se_adhd_diff | p_adhd_diff |
|---|---|---|---|---|---|---|
| 4.31E-09 | 0.124 | 0.025 | 3.60E-07 | 0.011 | 0.010 | 0.272 |
| 3.81E-08 | 0.069 | 0.014 | 3.67E-07 | 0.001 | 0.006 | 0.843 |
| 4.23E-15 | 0.106 | 0.015 | 3.85E-13 | 0.002 | 0.006 | 0.768 |
| 1.23E-11 | 0.117 | 0.021 | 1.62E-08 | 0.016 | 0.009 | 0.091 |
| 1.84E-10 | -0.074 | 0.013 | 3.14E-08 | 0.006 | 0.006 | 0.279 |

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|---|---|---|---|---|---|---|
| 1.85E-08 | -0.180 | 0.032 | 1.35E-08 | 0.011 | 0.014 | 0.404 |
| 8.95E-08 | 0.079 | 0.014 | 1.74E-08 | 0.008 | 0.006 | 0.160 |
| 1.73E-07 | 0.080 | 0.013 | 1.82E-09 | 0.014 | 0.006 | 0.012 |
| 5.17E-07 | 0.073 | 0.013 | 2.89E-08 | 0.011 | 0.006 | 0.060 |
| 1.70E-06 | -0.115 | 0.020 | 7.68E-09 | 0.025 | 0.009 | 0.005 |
| 1.35E-05 | -0.093 | 0.016 | 1.34E-08 | 0.026 | 0.007 | 0.000 |
| 9.75E-05 | -0.077 | 0.014 | 1.58E-08 | 0.027 | 0.006 | 0.000 |
| 4.55E-04 | -0.075 | 0.014 | 3.96E-08 | 0.030 | 0.006 | 0.000 |

| p_aut_adj | b_aut_unadj | se_aut_unad | p_aut_unadj | b_aut_diff | se_aut_diff | p_aut_diff |
|---|---|---|---|---|---|---|
| 1.20E-09 | 0.084 | 0.015 | 1.07E-08 | 0.000 | 0.020 | 0.494 |
| 3.22E-07 | -0.096 | 0.016 | 2.04E-09 | -0.004 | 0.022 | 0.447 |

| b_mdd_una | se_mdd_una | p_mdd_unad | b_bip_unadj | se_bip_unadj | p_bip_unadj | b_adhd_unad |
|---|---|---|---|---|---|---|
| -0.001 | 0.006 | 8.96E-01 | -0.052 | 0.016 | 9.04E-04 | -0.061 |
| -0.021 | 0.005 | 2.98E-05 | 0.038 | 0.014 | 6.28E-03 | 0.030 |
| 0.001 | 0.005 | 8.94E-01 | 0.037 | 0.014 | 7.93E-03 | 0.034 |
| -0.007 | 0.006 | 2.49E-01 | -0.049 | 0.017 | 4.74E-03 | 0.011 |
| -0.002 | 0.005 | 6.44E-01 | -0.019 | 0.014 | 1.73E-01 | -0.058 |
| 0.002 | 0.005 | 6.51E-01 | 0.042 | 0.014 | 2.03E-03 | 0.023 |
| 0.008 | 0.005 | 1.21E-01 | 0.030 | 0.014 | 2.95E-02 | 0.021 |
| 0.009 | 0.006 | 1.09E-01 | -0.029 | 0.015 | 5.63E-02 | 0.009 |
| -0.007 | 0.005 | 1.80E-01 | -0.036 | 0.013 | 8.00E-03 | -0.004 |
| -0.008 | 0.005 | 9.68E-02 | -0.036 | 0.014 | 9.59E-03 | -0.036 |
| -0.007 | 0.007 | 3.44E-01 | 0.045 | 0.019 | 1.73E-02 | 0.015 |
| -0.004 | 0.005 | 4.39E-01 | 0.018 | 0.014 | 1.73E-01 | -0.013 |
| -0.005 | 0.005 | 3.14E-01 | -0.019 | 0.014 | 1.77E-01 | -0.005 |
| -0.004 | 0.005 | 4.16E-01 | 0.019 | 0.013 | 1.49E-01 | -0.034 |
| 0.025 | 0.011 | 1.85E-02 | -0.030 | 0.031 | 3.30E-01 | 0.053 |
| -0.048 | 0.009 | 1.781E-08 | -0.093 | 0.024 | 8.44E-05 | 0.022 |
| -0.001 | 0.006 | 9.402E-01 | 0.012 | 0.017 | 4.72E-01 | -0.019 |
| 0.012 | 0.005 | 1.333E-02 | -0.012 | 0.014 | 3.89E-01 | 0.020 |
| -0.008 | 0.005 | 9.646E-02 | -0.026 | 0.014 | 6.46E-02 | 0.013 |
| 0.006 | 0.005 | 2.251E-01 | 0.021 | 0.014 | 1.44E-01 | 0.027 |
| -0.004 | 0.007 | 5.462E-01 | 0.005 | 0.018 | 7.75E-01 | -0.053 |
| 0.013 | 0.005 | 5.957E-03 | 0.037 | 0.014 | 6.05E-03 | -0.010 |
| 0.005 | 0.006 | 3.560E-01 | -0.032 | 0.015 | 3.49E-02 | 0.032 |
| -0.006 | 0.005 | 2.297E-01 | 0.000 | 0.014 | 9.88E-01 | -0.011 |
| -0.009 | 0.009 | 3.103E-01 | -0.055 | 0.026 | 3.29E-02 | -0.017 |
| 0.004 | 0.006 | 4.913E-01 | -0.011 | 0.017 | 5.09E-01 | 0.002 |
| 0.013 | 0.005 | 8.991E-03 | 0.026 | 0.014 | 5.87E-02 | 0.029 |
| -0.015 | 0.007 | 2.654E-02 | -0.023 | 0.018 | 2.03E-01 | -0.042 |
| 0.022 | 0.005 | 7.027E-06 | 0.021 | 0.014 | 1.17E-01 | 0.019 |
| -0.001 | 0.007 | 9.184E-01 | 0.015 | 0.021 | 4.87E-01 | 0.023 |
| -0.014 | 0.005 | 6.512E-03 | 0.041 | 0.014 | 3.89E-03 | -0.034 |
| -0.034 | 0.009 | 6.645E-05 | -0.081 | 0.024 | 6.45E-04 | -0.049 |
| -0.007 | 0.005 | 1.221E-01 | 0.010 | 0.013 | 4.76E-01 | -0.027 |
| 0.005 | 0.006 | 3.963E-01 | 0.030 | 0.017 | 6.77E-02 | 0.040 |
| 0.034 | 0.005 | 4.006E-12 | 0.031 | 0.014 | 2.36E-02 | 0.043 |
| 0.012 | 0.005 | 1.458E-02 | 0.031 | 0.013 | 1.88E-02 | -0.029 |
| 0.002 | 0.006 | 7.136E-01 | -0.008 | 0.017 | 6.34E-01 | -0.018 |
| 0.018 | 0.006 | 3.814E-03 | 0.017 | 0.017 | 3.12E-01 | 0.036 |
| -0.003 | 0.005 | 6.216E-01 | -0.004 | 0.014 | 7.94E-01 | -0.002 |

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|---|---|---|---|---|---|---|
| 0.001 | 0.005 | 8.281E-01 | 0.005 | 0.014 | 6.96E-01 | -0.040 |
| 0.014 | 0.006 | 2.073E-02 | 0.063 | 0.017 | 2.10E-04 | 0.003 |
| 0.024 | 0.005 | 3.240E-06 | 0.001 | 0.015 | 9.21E-01 | 0.043 |
| 0.028 | 0.006 | 2.078E-06 | 0.035 | 0.016 | 2.79E-02 | 0.004 |
| -0.004 | 0.005 | 4.192E-01 | 0.002 | 0.014 | 8.71E-01 | -0.017 |
| -0.022 | 0.005 | 2.388E-05 | 0.002 | 0.014 | 8.78E-01 | -0.015 |
| -0.023 | 0.005 | 1.824E-06 | -0.024 | 0.014 | 7.40E-02 | -0.012 |
| -0.007 | 0.005 | 1.701E-01 | -0.009 | 0.014 | 5.34E-01 | 0.013 |
| 0.004 | 0.005 | 4.753E-01 | -0.019 | 0.014 | 1.83E-01 | 0.028 |
| -0.012 | 0.005 | 1.466E-02 | -0.027 | 0.014 | 4.67E-02 | 0.030 |
| 0.000 | 0.005 | 9.645E-01 | 0.001 | 0.014 | 9.48E-01 | -0.014 |
| 0.007 | 0.006 | 2.328E-01 | -0.014 | 0.016 | 3.58E-01 | 0.020 |
| -0.016 | 0.005 | 1.002E-03 | -0.067 | 0.014 | 8.44E-07 | -0.007 |
| 0.001 | 0.005 | 8.327E-01 | 0.011 | 0.014 | 4.45E-01 | 0.011 |
| 0.001 | 0.005 | 7.741E-01 | -0.006 | 0.013 | 6.49E-01 | -0.003 |
| 0.013 | 0.005 | 1.109E-02 | -0.063 | 0.014 | 3.38E-06 | -0.001 |
| 0.004 | 0.006 | 4.755E-01 | 0.006 | 0.016 | 6.87E-01 | -0.021 |
| -0.005 | 0.006 | 4.140E-01 | -0.018 | 0.016 | 2.60E-01 | -0.005 |
| 0.004 | 0.006 | 5.089E-01 | 0.036 | 0.017 | 2.76E-02 | 0.010 |
| -0.011 | 0.005 | 1.866E-02 | 0.024 | 0.014 | 7.17E-02 | -0.013 |
| 0.000 | 0.007 | 9.538E-01 | 0.000 | 0.019 | 9.97E-01 | -0.015 |
| -0.008 | 0.005 | 9.360E-02 | -0.041 | 0.015 | 5.96E-03 | 0.011 |
| 0.000 | 0.005 | 9.827E-01 | -0.043 | 0.013 | 1.42E-03 | -0.002 |
| 0.004 | 0.006 | 4.973E-01 | -0.038 | 0.016 | 1.61E-02 | -0.019 |
| 0.003 | 0.005 | 5.613E-01 | 0.002 | 0.014 | 8.81E-01 | 0.039 |
| 0.010 | 0.005 | 4.392E-02 | 0.036 | 0.014 | 1.10E-02 | 0.002 |
| 0.025 | 0.006 | 6.194E-06 | 0.032 | 0.016 | 3.63E-02 | -0.001 |
| 0.013 | 0.005 | 1.286E-02 | 0.029 | 0.014 | 3.93E-02 | 0.043 |
| -0.001 | 0.005 | 8.141E-01 | -0.011 | 0.015 | 4.81E-01 | -0.010 |
| -0.002 | 0.005 | 7.088E-01 | -0.026 | 0.015 | 7.58E-02 | 0.004 |
| 0.006 | 0.005 | 2.381E-01 | -0.035 | 0.014 | 1.38E-02 | -0.035 |
| 0.008 | 0.005 | 1.029E-01 | 0.028 | 0.014 | 5.09E-02 | 0.033 |
| 0.009 | 0.005 | 7.206E-02 | 0.020 | 0.014 | 1.61E-01 | -0.023 |
| 0.029 | 0.006 | 2.652E-07 | 0.035 | 0.016 | 2.68E-02 | 0.012 |
| -0.003 | 0.007 | 6.161E-01 | -0.028 | 0.018 | 1.26E-01 | 0.021 |
| -0.011 | 0.005 | 2.887E-02 | 0.029 | 0.014 | 3.09E-02 | 0.019 |
| 0.016 | 0.008 | 3.960E-02 | 0.023 | 0.022 | 2.91E-01 | 0.007 |
| 0.007 | 0.007 | 3.183E-01 | -0.088 | 0.021 | 2.39E-05 | 0.020 |
| 0.001 | 0.006 | 8.396E-01 | 0.015 | 0.015 | 3.14E-01 | -0.003 |
| 0.008 | 0.005 | 9.886E-02 | 0.059 | 0.014 | 3.17E-05 | -0.001 |
| 0.007 | 0.008 | 3.722E-01 | 0.075 | 0.022 | 5.49E-04 | 0.033 |
| 0.010 | 0.005 | 3.290E-02 | 0.015 | 0.013 | 2.52E-01 | 0.005 |
| 0.020 | 0.005 | 3.392E-05 | 0.015 | 0.013 | 2.77E-01 | 0.025 |

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|---|---|---|---|---|---|---|
| 0.010 | 0.005 | 4.959E-02 | 0.012 | 0.014 | 3.83E-01 | 0.023 |
| -0.023 | 0.005 | 8.091E-06 | -0.052 | 0.014 | 2.68E-04 | -0.018 |
| 0.025 | 0.007 | 5.559E-04 | 0.034 | 0.020 | 9.97E-02 | -0.017 |
| 0.007 | 0.006 | 2.030E-01 | 0.033 | 0.016 | 4.13E-02 | 0.042 |
| -0.002 | 0.005 | 7.420E-01 | -0.021 | 0.015 | 1.45E-01 | -0.004 |
| 0.020 | 0.005 | 3.618E-05 | 0.028 | 0.014 | 4.19E-02 | 0.018 |
| -0.014 | 0.005 | 6.005E-03 | 0.018 | 0.014 | 2.01E-01 | -0.039 |
| -0.025 | 0.005 | 4.895E-07 | -0.048 | 0.014 | 6.96E-04 | -0.020 |
| 0.007 | 0.005 | 1.748E-01 | 0.033 | 0.014 | 2.09E-02 | 0.079 |
| -0.008 | 0.005 | 8.274E-02 | -0.053 | 0.014 | 1.33E-04 | -0.018 |
| 0.004 | 0.008 | 5.611E-01 | 0.022 | 0.021 | 3.05E-01 | 0.052 |
| 0.005 | 0.006 | 4.077E-01 | -0.041 | 0.016 | 1.08E-02 | 0.017 |
| -0.002 | 0.005 | 6.684E-01 | -0.039 | 0.013 | 3.26E-03 | -0.022 |
| 0.002 | 0.005 | 7.111E-01 | 0.030 | 0.013 | 2.36E-02 | -0.038 |
| -0.003 | 0.005 | 6.158E-01 | -0.021 | 0.014 | 1.42E-01 | 0.000 |
| -0.018 | 0.005 | 2.199E-04 | -0.047 | 0.014 | 7.60E-04 | -0.040 |
| -0.002 | 0.007 | 7.479E-01 | -0.037 | 0.018 | 4.47E-02 | -0.039 |
| -0.005 | 0.006 | 3.864E-01 | 0.020 | 0.018 | 2.52E-01 | 0.035 |
| -0.015 | 0.005 | 2.895E-03 | -0.037 | 0.014 | 8.24E-03 | -0.016 |
| 0.000 | 0.005 | 9.840E-01 | -0.044 | 0.014 | 2.32E-03 | 0.003 |
| -0.001 | 0.005 | 8.197E-01 | -0.029 | 0.014 | 3.71E-02 | 0.018 |
| 0.007 | 0.005 | 2.121E-01 | -0.027 | 0.015 | 7.19E-02 | -0.011 |
| -0.009 | 0.005 | 7.845E-02 | -0.031 | 0.014 | 3.09E-02 | -0.008 |
| -0.005 | 0.005 | 3.530E-01 | 0.049 | 0.014 | 5.01E-04 | -0.016 |
| 0.009 | 0.006 | 1.665E-01 | 0.068 | 0.017 | 8.75E-05 | 0.013 |
| 0.002 | 0.005 | 6.236E-01 | 0.045 | 0.014 | 1.85E-03 | 0.005 |
| 0.003 | 0.006 | 6.178E-01 | 0.058 | 0.016 | 2.67E-04 | 0.015 |
| 0.015 | 0.005 | 4.842E-03 | 0.026 | 0.015 | 7.82E-02 | 0.005 |
| 0.011 | 0.005 | 2.991E-02 | -0.058 | 0.014 | 2.14E-05 | -0.005 |
| -0.011 | 0.007 | 7.749E-02 | -0.037 | 0.018 | 3.71E-02 | 0.026 |
| -0.007 | 0.005 | 1.486E-01 | -0.040 | 0.014 | 3.33E-03 | -0.007 |
| 0.001 | 0.005 | 8.984E-01 | -0.031 | 0.014 | 3.29E-02 | -0.022 |
| 0.012 | 0.006 | 5.821E-02 | 0.049 | 0.017 | 3.36E-03 | 0.044 |
| 0.002 | 0.005 | 6.768E-01 | -0.029 | 0.014 | 3.20E-02 | -0.032 |
| 0.026 | 0.008 | 7.199E-04 | 0.063 | 0.023 | 5.83E-03 | 0.003 |
| -0.002 | 0.005 | 6.389E-01 | -0.045 | 0.014 | 1.77E-03 | 0.016 |
| -0.010 | 0.006 | 8.187E-02 | 0.045 | 0.017 | 7.07E-03 | 0.004 |
| 0.011 | 0.006 | 3.824E-02 | 0.035 | 0.016 | 2.42E-02 | -0.002 |
| -0.004 | 0.005 | 4.287E-01 | -0.046 | 0.014 | 6.51E-04 | -0.012 |
| -0.021 | 0.008 | 1.149E-02 | -0.088 | 0.023 | 1.63E-04 | 0.030 |
| -0.001 | 0.005 | 8.240E-01 | -0.031 | 0.013 | 2.06E-02 | -0.024 |
| 0.008 | 0.005 | 7.987E-02 | 0.040 | 0.014 | 2.65E-03 | -0.023 |
| 0.002 | 0.006 | 7.320E-01 | 0.055 | 0.018 | 2.25E-03 | -0.017 |

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|---|---|---|---|---|---|---|
| -0.009 | 0.008 | 2.959E-01 | -0.053 | 0.023 | 2.37E-02 | -0.102 |
| 0.012 | 0.005 | 1.475E-02 | 0.041 | 0.014 | 2.59E-03 | -0.009 |
| 0.013 | 0.006 | 2.861E-02 | 0.060 | 0.017 | 3.40E-04 | 0.036 |
| 0.010 | 0.006 | 9.554E-02 | 0.059 | 0.016 | 3.03E-04 | 0.011 |
| 0.012 | 0.006 | 2.471E-02 | 0.050 | 0.015 | 1.16E-03 | 0.006 |
| -0.009 | 0.005 | 6.844E-02 | 0.033 | 0.014 | 2.01E-02 | 0.020 |
| 0.010 | 0.005 | 3.773E-02 | 0.040 | 0.013 | 2.85E-03 | 0.000 |
| -0.004 | 0.005 | 4.252E-01 | -0.052 | 0.014 | 1.19E-04 | -0.026 |
| 0.005 | 0.005 | 3.036E-01 | -0.052 | 0.014 | 2.30E-04 | 0.016 |
| 0.014 | 0.005 | 9.316E-03 | 0.081 | 0.015 | 7.75E-08 | -0.015 |
| -0.010 | 0.007 | 1.127E-01 | -0.089 | 0.018 | 1.07E-06 | -0.013 |
| -0.005 | 0.005 | 2.872E-01 | 0.081 | 0.014 | 6.44E-09 | -0.024 |
| -0.012 | 0.005 | 1.557E-02 | -0.059 | 0.014 | 1.67E-05 | -0.029 |
| -0.007 | 0.005 | 2.013E-01 | -0.067 | 0.015 | 4.54E-06 | -0.018 |
| 0.028 | 0.008 | 3.286E-04 | 0.114 | 0.021 | 4.92E-08 | 0.055 |

| b_mdd_una | se_mdd_una | p_mdd_unad | b_scz_unadj | se_scz_unadj | p_scz_unadj | b_adhd_unac |
|---|---|---|---|---|---|---|
| 0.003 | 0.005 | 4.95E-01 | 0.019 | 0.010 | 5.54E-02 | 0.008 |
| 0.004 | 0.005 | 4.94E-01 | 0.007 | 0.010 | 4.94E-01 | -0.007 |
| 0.002 | 0.007 | 8.14E-01 | 0.002 | 0.012 | 8.61E-01 | -0.007 |
| -0.058 | 0.010 | 8.33E-10 | -0.006 | 0.005 | 2.08E-01 | 0.023 |
| 0.032 | 0.014 | 2.24E-02 | 0.006 | 0.007 | 4.20E-01 | -0.004 |
| 0.062 | 0.013 | 3.26E-06 | -0.012 | 0.007 | 7.96E-02 | 0.013 |
| -0.003 | 0.013 | 8.45E-01 | -0.005 | 0.007 | 4.58E-01 | 0.042 |
| 0.010 | 0.010 | 3.29E-01 | 0.006 | 0.005 | 2.48E-01 | 0.016 |
| 0.023 | 0.010 | 2.10E-02 | -0.001 | 0.005 | 8.07E-01 | -0.005 |
| 0.046 | 0.010 | 7.44E-06 | -0.007 | 0.005 | 1.98E-01 | 0.017 |
| -0.027 | 0.010 | 4.70E-03 | -0.009 | 0.005 | 6.41E-02 | -0.002 |
| -0.008 | 0.010 | 4.53E-01 | -0.025 | 0.005 | 4.95E-07 | -0.005 |
| -0.055 | 0.016 | 3.81E-04 | -0.013 | 0.008 | 9.92E-02 | -0.064 |
| 0.039 | 0.010 | 4.96E-05 | 0.019 | 0.005 | 7.06E-05 | -0.006 |
| -0.060 | 0.010 | 3.48E-10 | -0.010 | 0.005 | 3.57E-02 | -0.005 |
| 0.060 | 0.011 | 1.31E-08 | 0.014 | 0.005 | 8.69E-03 | -0.010 |
| -0.046 | 0.016 | 3.10E-03 | -0.013 | 0.008 | 9.46E-02 | -0.017 |
| -0.076 | 0.015 | 1.67E-07 | -0.029 | 0.007 | 8.10E-05 | -0.054 |
| 0.087 | 0.010 | 5.00E-18 | 0.016 | 0.005 | 1.67E-03 | -0.005 |

| b_scz_unad | se_scz_unadj | p_scz_unadj | b_bip_unadj | se_bip_unadj | p_bip_unadj | b_adhd_unac |
|---|---|---|---|---|---|---|
| -0.043 | 0.010 | 1.99E-05 | 0.047 | 0.014 | 7.06E-04 | 0.034 |
| -0.023 | 0.010 | 1.94E-02 | 0.011 | 0.014 | 4.19E-01 | -0.051 |
| 0.011 | 0.012 | 3.27E-01 | 0.001 | 0.017 | 9.57E-01 | 0.017 |
| 0.007 | 0.010 | 5.05E-01 | -0.026 | 0.014 | 6.15E-02 | 0.010 |
| 0.048 | 0.010 | 7.12E-07 | 0.008 | 0.014 | 5.60E-01 | -0.016 |

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|---|---|---|---|---|---|---|
| -0.010 | 0.010 | 3.19E-01 | 0.031 | 0.013 | 1.94E-02 | 0.029 |
| 0.026 | 0.010 | 9.00E-03 | 0.008 | 0.014 | 5.44E-01 | 0.016 |
| -0.006 | 0.010 | 5.25E-01 | -0.014 | 0.013 | 2.83E-01 | -0.008 |
| -0.008 | 0.010 | 4.40E-01 | 0.001 | 0.014 | 9.66E-01 | -0.019 |
| -0.010 | 0.010 | 3.03E-01 | 0.003 | 0.014 | 8.27E-01 | -0.006 |
| 0.039 | 0.010 | 1.36E-04 | 0.029 | 0.014 | 4.39E-02 | 0.009 |
| -0.004 | 0.010 | 6.64E-01 | -0.006 | 0.014 | 6.36E-01 | -0.006 |
| 0.076 | 0.010 | 8.94E-15 | 0.031 | 0.014 | 2.36E-02 | 0.043 |
| 0.027 | 0.010 | 5.20E-03 | -0.001 | 0.014 | 9.43E-01 | 0.003 |
| 0.050 | 0.010 | 3.67E-07 | 0.002 | 0.014 | 8.71E-01 | -0.016 |
| -0.032 | 0.012 | 8.70E-03 | -0.015 | 0.017 | 3.78E-01 | -0.037 |
| 0.028 | 0.009 | 3.00E-03 | 0.033 | 0.013 | 1.33E-02 | 0.057 |
| -0.028 | 0.010 | 3.80E-03 | -0.035 | 0.014 | 1.01E-02 | -0.015 |
| -0.002 | 0.010 | 8.47E-01 | -0.010 | 0.014 | 4.93E-01 | -0.007 |
| 0.026 | 0.011 | 1.53E-02 | 0.017 | 0.015 | 2.40E-01 | 0.001 |
| 0.002 | 0.010 | 8.57E-01 | -0.029 | 0.014 | 3.18E-02 | -0.016 |
| -0.012 | 0.011 | 2.72E-01 | 0.018 | 0.016 | 2.69E-01 | -0.007 |
| -0.134 | 0.014 | 2.90E-22 | -0.067 | 0.019 | 4.86E-04 | -0.005 |
| 0.064 | 0.011 | 1.58E-09 | 0.024 | 0.016 | 1.26E-01 | 0.001 |
| 0.009 | 0.010 | 3.82E-01 | 0.047 | 0.014 | 5.48E-04 | -0.025 |
| -0.030 | 0.010 | 2.40E-03 | 0.002 | 0.014 | 8.96E-01 | -0.013 |
| 0.005 | 0.010 | 5.95E-01 | 0.026 | 0.014 | 6.20E-02 | -0.009 |
| 0.030 | 0.010 | 1.80E-03 | 0.009 | 0.014 | 4.88E-01 | 0.016 |
| 0.013 | 0.018 | 4.70E-01 | 0.017 | 0.025 | 5.00E-01 | 0.019 |
| 0.016 | 0.010 | 9.29E-02 | 0.014 | 0.014 | 3.06E-01 | 0.000 |
| -0.014 | 0.010 | 1.62E-01 | -0.024 | 0.014 | 7.64E-02 | -0.012 |
| 0.009 | 0.010 | 3.86E-01 | -0.024 | 0.014 | 8.98E-02 | -0.034 |
| -0.022 | 0.010 | 3.53E-02 | -0.017 | 0.015 | 2.39E-01 | -0.024 |
| 0.011 | 0.012 | 3.60E-01 | 0.024 | 0.017 | 1.42E-01 | 0.023 |
| -0.042 | 0.017 | 1.27E-02 | -0.034 | 0.025 | 1.70E-01 | -0.032 |
| -0.066 | 0.010 | 3.05E-12 | -0.037 | 0.013 | 5.89E-03 | -0.023 |
| 0.041 | 0.010 | 2.70E-05 | 0.017 | 0.014 | 1.99E-01 | 0.028 |
| -0.024 | 0.010 | 2.07E-02 | -0.049 | 0.014 | 6.36E-04 | -0.040 |
| 0.015 | 0.018 | 3.94E-01 | -0.070 | 0.024 | 4.09E-03 | -0.021 |
| -0.057 | 0.012 | 2.97E-06 | -0.045 | 0.017 | 7.56E-03 | -0.085 |
| -0.013 | 0.011 | 2.38E-01 | 0.049 | 0.015 | 1.13E-03 | 0.020 |

| b_mdd_una | se_mdd_una | p_mdd_unad | b_scz_unadj | se_scz_unadj | p_scz_unadj | b_bip_unadj |
|---|---|---|---|---|---|---|
| 0.020 | 0.009 | 2.30E-02 | -0.010 | 0.026 | 6.85E-01 | 0.035 |
| 0.003 | 0.005 | 5.06E-01 | 0.004 | 0.014 | 7.42E-01 | 0.029 |
| 0.007 | 0.005 | 1.74E-01 | 0.042 | 0.010 | 6.51E-05 | 0.030 |
| 0.012 | 0.008 | 1.27E-01 | 0.007 | 0.015 | 6.33E-01 | -0.022 |
| -0.010 | 0.005 | 4.51E-02 | 0.000 | 0.010 | 9.92E-01 | -0.011 |

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|---|---|---|---|---|---|---|
| -0.014 | 0.012 | 2.48E-01 | -0.111 | 0.023 | 1.96E-06 | -0.124 |
| 0.010 | 0.005 | 3.80E-02 | -0.013 | 0.010 | 1.91E-01 | 0.012 |
| 0.007 | 0.005 | 1.28E-01 | -0.016 | 0.010 | 8.71E-02 | 0.003 |
| 0.013 | 0.005 | 8.15E-03 | 0.017 | 0.010 | 6.90E-02 | 0.019 |
| -0.002 | 0.008 | 8.35E-01 | 0.005 | 0.015 | 7.34E-01 | 0.028 |
| -0.027 | 0.006 | 2.47E-06 | -0.045 | 0.012 | 1.23E-04 | -0.042 |
| 0.009 | 0.005 | 5.62E-02 | -0.005 | 0.010 | 5.78E-01 | 0.008 |
| 0.001 | 0.005 | 8.65E-01 | 0.016 | 0.010 | 1.09E-01 | -0.015 |

| se_mdd_un | p_mdd_unad | b_scz_unadj | se_scz_unadj | p_scz_unadj | b_bip_unadj | se_bip_unadj |
|---|---|---|---|---|---|---|
| 0.005 | 9.34E-01 | 0.007 | 0.010 | 5.10E-01 | -0.014 | 0.014 |
| 0.006 | 0.5195 | -0.032 | 0.011 | 3.90E-03 | -0.003 | 0.016 |

| se_adhd_una | p_adhd_unac | b_aut_unadj | se_aut_unad | p_aut_unadj | nearestGene |
|---|---|---|---|---|---|
| 0.016 | 1.34E-04 | 0.016 | 0.016 | 3.08E-01 | WSCD2 |
| 0.014 | 3.05E-02 | -0.015 | 0.014 | 2.90E-01 | ARFGEF2 |
| 0.014 | 1.45E-02 | 0.038 | 0.015 | 8.72E-03 | CREB5 |
| 0.018 | 5.31E-01 | 0.038 | 0.018 | 3.21E-02 | KLF16 |
| 0.013 | 9.76E-06 | -0.029 | 0.014 | 3.44E-02 | CALN1 |
| 0.013 | 8.53E-02 | -0.015 | 0.014 | 2.94E-01 | RP11-467I7.1 |
| 0.013 | 1.21E-01 | -0.004 | 0.014 | 7.91E-01 | RPS18P6 |
| 0.015 | 5.32E-01 | 0.036 | 0.016 | 2.30E-02 | GDNF |
| 0.013 | 7.63E-01 | 0.018 | 0.014 | 1.89E-01 | DIP2C |
| 0.013 | 7.89E-03 | -0.030 | 0.014 | 3.12E-02 | TACC1 |
| 0.017 | 3.99E-01 | -0.019 | 0.019 | 3.11E-01 | RP11-160H22.3 |
| 0.014 | 3.27E-01 | 0.022 | 0.014 | 1.21E-01 | MSL2 |
| 0.014 | 7.20E-01 | -0.022 | 0.015 | 1.27E-01 | ARL14EP |
| 0.014 | 1.36E-02 | -0.047 | 0.014 | 8.06E-04 | SRPK2 |
| 0.029 | 6.22E-02 | -0.027 | 0.029 | 3.63E-01 | CCDC175 |
| 0.022 | 0.326 | -0.035 | 0.023 | 1.29E-01 | ZSCAN23 |
| 0.017 | 0.242 | 0.040 | 0.017 | 2.20E-02 | MIR137HG |
| 0.014 | 0.150 | 0.002 | 0.014 | 8.59E-01 | ATP2A2 |
| 0.014 | 0.374 | -0.001 | 0.015 | 9.31E-01 | PPP1R16B |
| 0.014 | 0.053 | 0.047 | 0.015 | 1.31E-03 | NRGN |
| 0.018 | 0.004 | -0.029 | 0.019 | 1.21E-01 | GULOP |
| 0.013 | 0.469 | 0.008 | 0.014 | 5.90E-01 | TSNARE1 |
| 0.016 | 0.036 | 0.010 | 0.016 | 5.58E-01 | MPHOSPH9 |
| 0.014 | 0.421 | 0.017 | 0.014 | 2.20E-01 | STAG1 |
| 0.029 | 0.565 | -0.061 | 0.029 | 3.44E-02 | SLC39A8 |
| 0.017 | 0.888 | 0.013 | 0.017 | 4.69E-01 | FXR1 |
| 0.014 | 0.040 | 0.031 | 0.014 | 3.05E-02 | TCF20 |
| 0.018 | 0.017 | -0.031 | 0.018 | 9.42E-02 | DGKZ |
| 0.013 | 0.161 | 0.005 | 0.014 | 7.17E-01 | CTD-2171N6.1 |
| 0.019 | 0.240 | 0.033 | 0.020 | 9.65E-02 | MEF2C-AS1 |
| 0.014 | 0.015 | -0.033 | 0.015 | 2.19E-02 | GIGYF2 |
| 0.023 | 0.030 | 0.000 | 0.024 | 9.97E-01 | NT5C2 |
| 0.013 | 0.043 | 0.015 | 0.014 | 2.73E-01 | NA |
| 0.017 | 0.017 | 0.006 | 0.017 | 7.36E-01 | IGSF9B |
| 0.014 | 0.001 | 0.026 | 0.014 | 7.23E-02 | RP4-598G3.1 |
| 0.013 | 0.028 | 0.027 | 0.014 | 5.18E-02 | SYNGAP1 |
| 0.016 | 0.279 | -0.001 | 0.017 | 9.43E-01 | CSMD1 |
| 0.016 | 0.025 | 0.024 | 0.017 | 1.43E-01 | GPM6A |
| 0.015 | 0.903 | 0.011 | 0.015 | 4.47E-01 | FHIT |

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|---|---|---|---|---|---|
| 0.014 | 0.004 | -0.036 | 0.014 | 9.87E-03 | FOXP1 |
| 0.017 | 0.839 | -0.005 | 0.018 | 7.80E-01 | FTCDNL1 |
| 0.014 | 0.002 | 0.037 | 0.015 | 1.16E-02 | TMX2:TMX2-CTNND1 |
| 0.016 | 0.791 | 0.025 | 0.016 | 1.16E-01 | ENSG00000231993 |
| 0.014 | 0.222 | -0.001 | 0.014 | 9.51E-01 | ENSG00000259864 |
| 0.014 | 0.282 | 0.011 | 0.015 | 4.48E-01 | RERE |
| 0.013 | 0.376 | -0.011 | 0.014 | 4.43E-01 | VRK2 |
| 0.014 | 0.363 | 0.022 | 0.015 | 1.35E-01 | ENSG00000258028 |
| 0.014 | 0.045 | 0.009 | 0.015 | 5.36E-01 | IMMP2L |
| 0.014 | 0.026 | 0.009 | 0.014 | 5.34E-01 | ENSG00000230407 |
| 0.014 | 0.331 | 0.024 | 0.015 | 9.83E-02 | PCNXL3 |
| 0.016 | 0.204 | 0.023 | 0.016 | 1.59E-01 | ZNF536 |
| 0.014 | 0.611 | 0.030 | 0.014 | 3.59E-02 | CACNA1C |
| 0.013 | 0.402 | 0.011 | 0.014 | 4.45E-01 | OPCML |
| 0.013 | 0.805 | -0.001 | 0.014 | 9.48E-01 | ENSG00000207252 |
| 0.013 | 0.939 | -0.002 | 0.014 | 8.63E-01 | MAD1L1 |
| 0.016 | 0.176 | 0.028 | 0.016 | 9.06E-02 | AIG1 |
| 0.016 | 0.773 | 0.000 | 0.017 | 9.88E-01 | AKT3 |
| 0.016 | 0.557 | 0.038 | 0.017 | 2.36E-02 | ENSG00000253107 |
| 0.014 | 0.321 | 0.004 | 0.014 | 7.96E-01 | ENSG00000253413 |
| 0.019 | 0.415 | -0.008 | 0.020 | 6.68E-01 | ENSG00000237954 |
| 0.015 | 0.449 | -0.047 | 0.015 | 1.27E-03 | RFT1 |
| 0.013 | 0.859 | 0.032 | 0.014 | 2.26E-02 | ZSWIM6 |
| 0.016 | 0.216 | -0.018 | 0.016 | 2.80E-01 | CHRNA3 |
| 0.014 | 0.005 | 0.026 | 0.014 | 6.87E-02 | PDE4B |
| 0.014 | 0.875 | -0.014 | 0.015 | 3.32E-01 | CACNA1I |
| 0.015 | 0.937 | 0.034 | 0.016 | 3.37E-02 | RGS6 |
| 0.014 | 0.002 | 0.050 | 0.015 | 5.61E-04 | SRPK2 |
| 0.015 | 0.492 | -0.014 | 0.016 | 3.82E-01 | RP3-399L15.3 |
| 0.014 | 0.801 | -0.007 | 0.014 | 6.02E-01 | SMG6 |
| 0.014 | 0.010 | -0.027 | 0.014 | 5.55E-02 | GATAD2A |
| 0.014 | 0.022 | 0.017 | 0.015 | 2.62E-01 | ENSG00000235377 |
| 0.014 | 0.099 | 0.026 | 0.015 | 6.98E-02 | RFPL4AP3 |
| 0.016 | 0.448 | 0.057 | 0.017 | 5.67E-04 | ENSG00000262267 |
| 0.018 | 0.246 | -0.026 | 0.019 | 1.60E-01 | ENSG00000233263 |
| 0.013 | 0.148 | 0.000 | 0.014 | 9.76E-01 | ENSG00000254842 |
| 0.021 | 0.735 | -0.031 | 0.022 | 1.52E-01 | ASCL1 |
| 0.020 | 0.314 | -0.030 | 0.021 | 1.57E-01 | GRM3 |
| 0.015 | 0.845 | -0.005 | 0.016 | 7.39E-01 | SOX5 |
| 0.014 | 0.924 | 0.026 | 0.014 | 7.28E-02 | PPP1R13B |
| 0.021 | 0.116 | 0.051 | 0.022 | 2.17E-02 | CACNB2 |
| 0.013 | 0.701 | 0.030 | 0.014 | 2.90E-02 | CLCN3 |
| 0.013 | 0.059 | 0.006 | 0.014 | 6.67E-01 | ENSG00000259503 |

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|---|---|---|---|---|---|
| 0.014 | 0.112 | 0.001 | 0.015 | 9.37E-01 | ENSG00000259221 |
| 0.014 | 0.211 | -0.021 | 0.015 | 1.48E-01 | SF3B1 |
| 0.021 | 0.410 | 0.032 | 0.021 | 1.32E-01 | ENSG00000224968 |
| 0.016 | 0.009 | 0.028 | 0.016 | 8.27E-02 | PRKD1 |
| 0.015 | 0.768 | -0.013 | 0.015 | 3.88E-01 | MRPS11P1 |
| 0.014 | 0.198 | 0.045 | 0.014 | 1.60E-03 | AC003088.1 |
| 0.014 | 0.007 | -0.034 | 0.015 | 1.88E-02 | RAI1 |
| 0.014 | 0.164 | 0.006 | 0.015 | 6.54E-01 | DRD2 |
| 0.014 | 0.000 | 0.010 | 0.015 | 4.92E-01 | PTPRF |
| 0.013 | 0.169 | -0.033 | 0.014 | 1.86E-02 | TMEM219 |
| 0.021 | 0.013 | 0.028 | 0.022 | 2.06E-01 | LINC00606 |
| 0.016 | 0.259 | -0.002 | 0.016 | 8.95E-01 | STAT6 |
| 0.013 | 0.098 | -0.032 | 0.014 | 2.13E-02 | AC091969.1 |
| 0.013 | 0.004 | -0.012 | 0.014 | 4.01E-01 | ENSG00000259616 |
| 0.014 | 0.982 | 0.006 | 0.014 | 6.66E-01 | ENSG00000258224 |
| 0.014 | 0.004 | -0.015 | 0.014 | 2.91E-01 | FURIN |
| 0.018 | 0.026 | 0.002 | 0.019 | 9.18E-01 | GABBR2 |
| 0.018 | 0.058 | 0.002 | 0.019 | 9.26E-01 | ENSG00000221237 |
| 0.014 | 0.249 | -0.026 | 0.015 | 7.58E-02 | RIMS1 |
| 0.014 | 0.813 | -0.002 | 0.015 | 8.89E-01 | HCN1 |
| 0.014 | 0.187 | -0.011 | 0.014 | 4.60E-01 | ENSG00000240354 |
| 0.015 | 0.449 | 0.006 | 0.016 | 6.90E-01 | MMP16 |
| 0.015 | 0.566 | -0.019 | 0.015 | 2.09E-01 | ENSG00000258144 |
| 0.014 | 0.259 | 0.030 | 0.015 | 4.19E-02 | DGKI |
| 0.018 | 0.457 | 0.006 | 0.018 | 7.36E-01 | CNTN4 |
| 0.014 | 0.728 | 0.023 | 0.015 | 1.26E-01 | ATXN7 |
| 0.015 | 0.326 | 0.001 | 0.016 | 9.46E-01 | RP11-111I12.1 |
| 0.015 | 0.731 | -0.006 | 0.015 | 7.07E-01 | RP11-284M14.1 |
| 0.013 | 0.708 | -0.009 | 0.014 | 5.01E-01 | SNAP91 |
| 0.018 | 0.153 | 0.018 | 0.019 | 3.28E-01 | PLA2G15 |
| 0.014 | 0.590 | -0.006 | 0.014 | 6.92E-01 | CPEB1 |
| 0.014 | 0.114 | 0.037 | 0.015 | 1.22E-02 | CUL3 |
| 0.016 | 0.007 | 0.037 | 0.017 | 3.22E-02 | HNRNPA1P46 |
| 0.014 | 0.017 | -0.047 | 0.014 | 9.30E-04 | ENSG00000229271 |
| 0.021 | 0.903 | 0.018 | 0.022 | 4.18E-01 | MKL1 |
| 0.014 | 0.257 | 0.006 | 0.015 | 6.98E-01 | ZEB2 |
| 0.016 | 0.786 | 0.004 | 0.016 | 8.06E-01 | NOSIP:PRRG2 |
| 0.015 | 0.883 | -0.012 | 0.015 | 4.24E-01 | EMX1 |
| 0.014 | 0.381 | 0.015 | 0.014 | 2.77E-01 | CNOT1 |
| 0.024 | 0.210 | -0.030 | 0.024 | 2.24E-01 | ENSG00000227854 |
| 0.013 | 0.066 | 0.009 | 0.014 | 5.00E-01 | PSD3 |
| 0.014 | 0.095 | -0.023 | 0.014 | 9.50E-02 | ZNF804A |
| 0.017 | 0.315 | 0.004 | 0.018 | 8.49E-01 | BNIP3L |

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|---|---|---|---|---|---|
| 0.023 | 0.000 | -0.015 | 0.024 | 5.51E-01 | ENSG00000253108 |
| 0.014 | 0.491 | -0.006 | 0.014 | 6.89E-01 | RBM26 |
| 0.016 | 0.021 | 0.044 | 0.017 | 7.30E-03 | WHSC1L1 |
| 0.016 | 0.493 | 0.012 | 0.017 | 4.61E-01 | ALMS1 |
| 0.016 | 0.692 | 0.016 | 0.016 | 3.06E-01 | ENSG00000261038 |
| 0.014 | 0.136 | -0.040 | 0.015 | 5.36E-03 | MSRA |
| 0.013 | 0.996 | 0.016 | 0.014 | 2.35E-01 | RPTOR |
| 0.013 | 0.053 | -0.018 | 0.014 | 1.97E-01 | ETF1 |
| 0.014 | 0.230 | -0.003 | 0.014 | 8.48E-01 | ENSG00000255545 |
| 0.015 | 0.290 | 0.050 | 0.015 | 1.12E-03 | SEC11A |
| 0.018 | 0.476 | 0.029 | 0.018 | 1.18E-01 | VPS45 |
| 0.014 | 0.085 | -0.007 | 0.014 | 6.13E-01 | TRANK1 |
| 0.014 | 0.037 | -0.012 | 0.014 | 3.72E-01 | BCL11B |
| 0.015 | 0.209 | -0.024 | 0.015 | 1.14E-01 | GRIN2A |
| 0.022 | 0.011 | 0.058 | 0.022 | 9.67E-03 | MPP6 |

| se_adhd_una | p_adhd_unac | b_aut_unadj | se_aut_unad | p_aut_unadj | nearestGene |
|---|---|---|---|---|---|
| 0.014 | 5.51E-01 | -0.039 | 0.014 | 6.05E-03 | ELAVL2 |
| 0.014 | 6.08E-01 | -0.010 | 0.015 | 5.10E-01 | SSBP2 |
| 0.018 | 6.89E-01 | -0.031 | 0.019 | 9.76E-02 | ADD3 |
| 0.013 | 8.50E-02 | 0.013 | 0.014 | 3.59E-01 | TRANK1 |
| 0.019 | 8.43E-01 | 0.051 | 0.020 | 9.11E-03 | TENM4 |
| 0.019 | 4.82E-01 | 0.027 | 0.020 | 1.64E-01 | NCAN |
| 0.018 | 1.76E-02 | 0.032 | 0.018 | 8.12E-02 | ENSG00000249568 |
| 0.014 | 2.57E-01 | -0.007 | 0.014 | 6.22E-01 | HLF |
| 0.014 | 7.08E-01 | 0.013 | 0.014 | 3.51E-01 | JADE2 |
| 0.014 | 2.22E-01 | 0.026 | 0.015 | 7.69E-02 | LMAN2L |
| 0.014 | 8.97E-01 | -0.018 | 0.014 | 1.96E-01 | RPS6KA2 |
| 0.014 | 7.03E-01 | 0.008 | 0.014 | 6.04E-01 | FADS2 |
| 0.021 | 2.31E-03 | -0.067 | 0.022 | 1.95E-03 | TFAP2B |
| 0.014 | 6.61E-01 | 0.010 | 0.014 | 4.63E-01 | SLC25A17 |
| 0.013 | 6.79E-01 | -0.042 | 0.014 | 2.60E-03 | ITIH1 |
| 0.014 | 5.06E-01 | 0.051 | 0.015 | 7.29E-04 | ZSCAN2 |
| 0.022 | 4.39E-01 | 0.033 | 0.023 | 1.50E-01 | AC003088.1 |
| 0.021 | 1.09E-02 | -0.053 | 0.022 | 1.55E-02 | DFNA5 |
| 0.014 | 7.44E-01 | -0.025 | 0.015 | 8.50E-02 | CACNA1C-IT3 |

| se_adhd_una | p_adhd_unac | b_aut_unadj | se_aut_unad | p_aut_unadj | nearestGene |
|---|---|---|---|---|---|
| 0.014 | 1.48E-02 | -0.019 | 0.015 | 1.98E-01 | STAU1 |
| 0.014 | 1.90E-04 | -0.003 | 0.014 | 8.03E-01 | MEF2C |
| 0.017 | 3.10E-01 | 0.058 | 0.017 | 6.59E-04 | RCN1 |
| 0.014 | 4.90E-01 | -0.009 | 0.014 | 5.22E-01 | CARM1P1 |
| 0.014 | 2.48E-01 | -0.021 | 0.014 | 1.41E-01 | RERE |

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|---|---|---|---|---|---|
| 0.013 | 2.91E-02 | 0.032 | 0.0141 | 2.18E-02 | OLFM4 |
| 0.014 | 2.44E-01 | 0.036 | 0.0142 | 1.04E-02 | RPL31P12 |
| 0.013 | 5.39E-01 | 0.014 | 0.014 | 3.15E-01 | ENSG00000259434 |
| 0.013 | 1.51E-01 | -0.026 | 0.014 | 6.74E-02 | ESR2:SYNE2 |
| 0.014 | 6.52E-01 | 0.013 | 0.014 | 3.69E-01 | CTC-340A15.2 |
| 0.014 | 5.16E-01 | -0.004 | 0.0148 | 7.78E-01 | TCF4 |
| 0.014 | 6.75E-01 | -0.013 | 0.014 | 3.46E-01 | LRFN5 |
| 0.014 | 1.49E-03 | 0.026 | 0.0143 | 7.23E-02 | RP4-598G3.1 |
| 0.013 | 8.36E-01 | 0.007 | 0.0139 | 6.22E-01 | ENSG00000234273 |
| 0.014 | 2.54E-01 | -0.021 | 0.0141 | 1.36E-01 | RERE |
| 0.017 | 2.71E-02 | -0.060 | 0.0176 | 6.59E-04 | BEND4 |
| 0.013 | 1.63E-05 | 0.062 | 0.0139 | 7.48E-06 | RP11-6N13.1 |
| 0.014 | 2.86E-01 | -0.056 | 0.0142 | 8.49E-05 | RNU7-160P |
| 0.014 | 6.06E-01 | -0.011 | 0.0144 | 4.67E-01 | RNU6-695P |
| 0.015 | 9.26E-01 | 0.011 | 0.0153 | 4.86E-01 | ENSG00000266033 |
| 0.013 | 2.30E-01 | -0.025 | 0.014 | 7.67E-02 | RSRC1 |
| 0.015 | 6.22E-01 | -0.031 | 0.0161 | 5.80E-02 | ENSG00000230365 |
| 0.019 | 7.77E-01 | -0.025 | 0.0197 | 2.06E-01 | PGBD1 |
| 0.015 | 9.60E-01 | 0.024 | 0.0155 | 1.20E-01 | L3MBTL2 |
| 0.014 | 6.86E-02 | 0.035 | 0.0142 | 1.31E-02 | PMFBP1 |
| 0.014 | 3.37E-01 | -0.010 | 0.0144 | 4.78E-01 | SOX5 |
| 0.014 | 4.89E-01 | -0.005 | 0.0143 | 7.22E-01 | RBFOX1 |
| 0.013 | 2.36E-01 | 0.004 | 0.0141 | 7.50E-01 | RPS6KL1 |
| 0.024 | 4.33E-01 | -0.014 | 0.0253 | 5.87E-01 | DENND1A |
| 0.013 | 9.76E-01 | -0.017 | 0.014 | 2.16E-01 | TMEM106B |
| 0.014 | 3.91E-01 | -0.008 | 0.0144 | 5.53E-01 | LINC00669 |
| 0.014 | 1.33E-02 | -0.025 | 0.0143 | 7.84E-02 | TENM2 |
| 0.015 | 1.02E-01 | 0.000 | 0.0153 | 9.94E-01 | ASTN2 |
| 0.017 | 1.67E-01 | 0.012 | 0.0174 | 4.84E-01 | NR4A2 |
| 0.025 | 1.88E-01 | -0.002 | 0.0271 | 9.35E-01 | ENOX1 |
| 0.013 | 7.85E-02 | -0.024 | 0.014 | 8.48E-02 | ENSG00000271615 |
| 0.013 | 3.44E-02 | 0.005 | 0.0139 | 7.09E-01 | DCC |
| 0.015 | 6.30E-03 | -0.042 | 0.015 | 5.62E-03 | ENSG00000260411 |
| 0.024 | 3.72E-01 | 0.018 | 0.0252 | 4.65E-01 | MYO18A |
| 0.017 | 2.96E-07 | -0.051 | 0.017 | 2.86E-03 | SORCS3 |
| 0.015 | 2.01E-01 | 0.003 | 0.0159 | 8.61E-01 | SHISA9 |

| se_bip_unadj | p_bip_unadj | b_aut_unadj | se_aut_unadj | p_aut_unadj | nearestGene |
|---|---|---|---|---|---|
| 0.017 | 4.69E-02 | -0.033 | 0.024 | 1.69E-01 | TFAP2D |
| 0.010 | 3.60E-03 | -0.003 | 0.014 | 8.11E-01 | ENSG00000270234 |
| 0.015 | 4.32E-02 | -0.002 | 0.015 | 8.73E-01 | ST3GAL3 |
| 0.022 | 3.13E-01 | -0.045 | 0.023 | 4.84E-02 | SPAG16 |
| 0.013 | 4.00E-01 | 0.015 | 0.014 | 2.60E-01 | SEMA6D |

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|---|---|---|---|---|---|
| 0.033 | 1.93E-04 | -0.042 | 0.033 | 2.12E-01 | ENSG00000253108 |
| 0.014 | 3.84E-01 | 0.020 | 0.014 | 1.55E-01 | RNU6-815P |
| 0.013 | 8.09E-01 | 0.035 | 0.014 | 1.25E-02 | ENSG00000271327 |
| 0.014 | 1.59E-01 | 0.026 | 0.014 | 5.78E-02 | FOXP2 |
| 0.022 | 2.09E-01 | -0.057 | 0.021 | 7.26E-03 | AC004158.2 |
| 0.016 | 9.85E-03 | -0.063 | 0.017 | 1.46E-04 | SORCS3 |
| 0.014 | 5.70E-01 | -0.067 | 0.014 | 1.92E-06 | LINC00461 |
| 0.014 | 2.92E-01 | -0.077 | 0.015 | 1.14E-07 | EEF1A1P11 |

| p_bip_unadj | b_adhd_unac | se_adhd_una | p_adhd_unac | nearestGene |
|---|---|---|---|---|
| 3.31E-01 | -0.001 | 0.015 | 9.23E-01 | SOX7 |
| 8.29E-01 | -0.054 | 0.015 | 3.58E-04 | ZNF877P |