Supplementary Material

Table of Contents

Tables

Figures

Overview

The MDD2000+ project comprises a total of 2431 cases with MDD and 3673 screened controls from different sources and genotyped on different platforms (main paper ***Tables 1*** and ***2***). Samples were provided by the Queensland Institute of Medical Research (QIMR, Australia), the Netherlands Study of Anxiety and Depression (NESDA), the Netherlands Twin Registry (NTR), the University of Edinburgh (UoE, United Kingdom), and the Molecular Genetics of Schizophrenia (MGS) study (controls only, United States). Genotyping was conducted on different Illumina and Affymetrix platforms and because the overlap in genotyped single nucleotide polymorphisms (SNPs) is limited, association analysis is based on a set of >1M imputed SNPs. The numbers of SNPs for each analysis set (main table ***Table 1***), represents genotyped SNPs surviving all quality control (QC) criteria that were used for imputation. Differing QC measures were applied to each sample (described below), before imposing uniform QC across all sample sets as described in the main paper.

Genotyping and initial quality control for the QIMR I317, I370 and I610 samples

The QIMR Genetic Epidemiology Laboratory collects a wide range of phenotypic variables on twin individuals and their family members. DNA samples from some of these subjects have been submitted for genotyping under projects funded with focus on a number of primary phenotypes. The QIMR samples genotyped on Illumina platforms are described in detail in Medland et al (1) (see their Table 2 projects 1-4,6). The Illumina platforms corresponding to the I317, I370 and I610 sample sets are the Illumina 317k, Illumina HumanCNV370-Quadv3 and the Illumina Human610-Quad respectively. QC steps for each project (1) included rejection of SNPs with Bead Studio Gen Call Scores < 0.7, SNP call rate < 0.95, Hardy Weinberg Equlibrium (HWE) test $p < 10^{-6}$, and SNPs with minor allele frequency (MAF) < 0.01. The different genotyping projects included overlapping individuals and families. After merging of the QIMR Illumina projects, the data were screened for missingness within individuals (removal of individuals where > 0.05 of genotyped SNPs failed), pedigree, sex errors, and Mendelian errors (genotypes for all family members for a given SNP were removed on detection of errors). Non-European ancestry outliers were removed. After QC, where one individual from a monozygotic (MZ) twin pair had been genotyped, duplicate genotypes were assigned to the ungenotyped co-twin. All but one of the genotyping projects represented the community samples of twins interviewed. One sample (Project 3 in Medland Table 2), contributing to analysis set I610, was a sample of migraine cases and non-migraine controls. Individuals interviewed in the NAG/IRPG studies (see METHODS) featured in all analysis sets (Table 1) but they were preferentially genotyped in the I370 analysis ste where they comprise 92% of the QIMR samples. Individuals interviewed Individuals surviving QC and satisfying the case and control definitions of section 2i) were selected as QIMR cases and controls and uploaded for joint analysis of all data.

Genotyping and initial quality control for the I370 NTR controls

In total 1405 individuals were submitted for genotyping to the Institute of Human Genetics, LIFE & BRAIN Center, University of Bonn, Germany on the Human610-Quad platform. Of these 577 satisfied the criteria for controls. No QC was applied to the genotypes prior to uploading of 657,366 SNPs for joint MDD2000+ analysis. Given that the ratio of controls:cases was ~2.5:1 for QIMR samples in the I610 set, it was decided to impute the NTR controls together with the QIMR samples in the I370 set where the ratio of controls:cases was much lower, hence only a subset of the genotyped SNPs was used.

Genotyping and initial quality control for A6.0 case sample

DNA from 1874 samples with MDD (1248 QIMR, 160 NESDA/NTR and 466 UoE) were submitted for genotyping to the Translational Genomics Research Institute (Tgen), Phoenix, Arizona. Since these samples have not been described elsewhere, we provide full details of the QC process. DNA samples were shipped on 96 well plates, 20uL per sample at 50ng of DNA per uL. At Tgen samples were re-plated ensuring that each centre was proportionally represented on each plate. A single QC sample was allocated to a standard position on each of the 21 plates.

Genotypes were initially called at Tgen using Affymetrix's Genotyping Console Software which runs the Birdseed v2 algorithm plate by plate. Only samples with a contrast statistic > 0.4 were included. Samples with a Birdseed call rate < 97.0 were excluded iteratively, each time excluding the sample with the lowest call rate. Samples with poor genotyping results were replated and the process repeated (using two additional plates). Genotypes were provided by Tgen for 1867 samples (1827 after subtracting deliberate duplicates and QC controls).

We calculated identity-by-state (IBS) matrix from the genotypes of autosomal markers and calculated the mean identity between all sample pairs. This provided evidence for contamination of a small number of samples (high mean IBS between

adjacent plated samples). These samples were excluded and genotypes were recalled plate by plate using the BirdSeed v2 algorithm as implemented in the BirdSuite software (2, 3). Individual genotypes were filtered after calling, changing the confidence score threshold from the default of 0.1 the more stringent value of 0.02. This threshold was established by investigating the effect of a range of thresholds on a number of QC measures. The QC checks listed in ***Table S1*** Stages 1-3 were performed at each threshold level. We compared the number of SNPs dropped at each stage and compared the quantile-quantile (Q-Q) plot from HWE tests of the SNPs surviving all QC steps. A genomic inflation of HWE test statistics is commonly observed in other data sets using the Affymetrix chips reflecting residual batch effects. We found that more stringent thresholds preferentially excluded poor performing SNPs i.e. the proportion of SNPs failing QC Stages 2 and 3 decreased as the confidence score threshold became more stringent.

Importantly, a total of 327 individuals had been previously genotyped on an Illumina platform and we used the 268 of these that had excellent dm.all_qc statistics (from program apt-geno-qc in the Affymetrix Power Tools) of 0.95 or higher to investigate genotype discordancy on SNPs genotyped in common across the platforms (Stage 4). We chose a confidence score threshold of 0.02 as the best balance between SNP numbers and genotype confidence. In total 646,601 SNPs remained. This represents about 70,000 SNPs fewer than often used in other studies using the Affymetrix 6.0 chip (e.g.(4)). However, we believe the extra stringency is justified because only cases were genotyped on this platform. The default confidence score threshold was used for calling individuals' genotypes for the SNPs that survived this QC step. As an additional check, sex for all samples was derived using the program apt-geno-qc (directly from the CEL files) and also by examining chrX and chrY.

Samples were required to have ≥95% call rate across all SNPs before entering the QC process. This threshold was also imposed post SNP QC resulting with the loss of 254 samples. Many studies would not impose such stringent QC, but using the 327 of the QIMR samples already been genotyped on an Illumina platform we were able to undertake additional checks not usually possible (***Table S1***, Stage 4). Discordance rates relative to the Illumina genotyping varied widely between samples (with a maximum of ~4.7% but a median of only ~0.13%), and imposing ≥95% call rate post QC eliminated 39 of the 45 most discordant samples.

Next, we merged the QIMR A6.0 genotypes with the full merged QIMR Illumina genotype data (1) (of which the I317, I370 and I610 QIMR sets used here are a subset) for the subset of ~138k SNPs which were overlapping and strand-unambiguous. Since family members of the unrelated individuals in the A6.0 sample had been genotyped on the Illumina platforms we used pairwise IBS analysis to verify that the genotyped individuals bore the expected relationship to their families. This identified two otherwise unknown sample mixups (a swap plus a mislabeled sample) and tested the quality of deliberate repeats. These checks also identified 20 pairs of related samples amongst the QIMR set: repeat genotypings (4 pairs representing multiple recruitments of the same individual); MZ (1 pair); siblings (7 pairs); parent/child (1 pair); avuncular (3 pairs) ; 1st cousins (4 pairs). All of the first degree relationships and multiple recruitments were already recorded in our database, and one member of each pair was dropped.

Additional samples were excluded if they were identified as gross ancestry outliers using Principal Component Analysis (PCA) when analysed together with genotype data from 16 global populations sourced from HapMap Phase 3 (HM3) (11 populations) and a previously published study of Northern European genetic diversity (GEUT- 5 populations) (5) using the same methods described in Medland et al (1). PCA was conducted using the autosomal SNPs that were genotyped in common between the A6.0 cases, HM3 and GEUT populations with the further proviso that SNP missing rates were < 2.5% in all individual cohorts and populations. A total of ~73K SNPs fulfilled these requirements. The EIGENSOFT package was used to conduct the PCA (6). Only those individuals in the 16 reference populations (n = 2317) were included in the initial PCA used to generate the top 10 Eigenvectors or Principal Components (PCs). The A6.0 cases were then projected onto this 'genetic space' background. The A6.0 case individuals cluster with Europeans as expected and the QIMR, NESDA/NTR and UoE samples cluster together. However, a few individuals show evidence of African or Asian ancestry. We calculated the mean and standard deviations for PC1 and PC2 of the non-Australian European reference and excluded any MDD2000 individuals more than 6 standard deviations from these means as ancestry outliers. A total of 15 QIMR, 7 NESDA/NTR and 5 UoE individuals that had survived QC were excluded as outliers.

Table S1 SNP and sample QC criteria for A6.0 case sample.

	SNPs removed	SNPs remaining
Stage 1		
No. SNPs called/genotyped		909,622
Monomorphic or MAF < 1%	145,911	
Not mapped reliably (includes Affymetrix proprietary probes)	4,049	
>5% missing	103,645	656,017
Stage 2		
Allele frequency difference on one plate vs rest ($P<10^{-6}$) removed only for the failing plate.	≤ 64 on each plate	
Stage 3		
$p< 10^{-6}$ for Hardy-Weinberg exact test, either across all samples and/or by plate.	519	
Minor allele frequency < 1%	71	
Positive controls on two or more plates disagreed with the consensus genotype for controls on the remaining plates	102	
Non-random genotypic failures as inferred by the flanking haplotypic background PLINK --mishap test ($P<10^{-10}$)	8090	647,235
Stage 4		
High discordance (>1% of individuals) for 268 individuals with Affymetrix contrast statistics ≥0.95 with an Illumina platform (see ii below) (strand-unambiguous SNPs genotyped on both platforms)	579	
Allele frequency differences ($P< 10^{-8}$) between the QIMR cases genotyped on Affymetrix vs 1205 unrelated cases genotyped on Ilumina platform (for same 137761 SNPs tested previously)	0	
Strand ambiguity, AT or CG SNPs with allele frequency close to 0.5	55	**646,601**

a: 646,601 SNPs comprised 621,111 autosomal, 25347 X and 143 Y chromosome SNPs
Following all QC procedures 646,601 SNPs for 1001 QIMR, 139 NESDA/NTR and 375 UoE MDD cases were included in the next stage of analysis.

Genotyping and initial quality control for the A6.0 control (MGS) sample

A6.0 controls comprised samples screened negative for major psychiatric disorders as part of the Molecular Genetics of Schizophrenia (MGS) study genotyped on the Affymetrix 6.0 at the Broad Institute Center for Genotyping and Analysis in two batches. Permission to access the genotypes was granted from the data access committees of the NIMH (GENRED controls) and dbGAP (GAIN schizophrenia controls) repositories. Only the samples (1636 controls) surviving the QC steps described in Shi et al (7) were used.

Statistical power

For a complex disease with lifetime population prevalence of *K*, assume a causal variant having two alleles (A and a) with frequencies of *p* and (1-*p*) . Let $(1-p)^2$, $2p(1-p)$ and p^2 be the frequencies of genotypes aa, Aa and AA (in Hardy-Weinberg equilibrium), with risks of f_0, f_1 and f_2. If we assume a multiplicative model then $f_1 = f_0 \lambda$ and $f_2 = f_0 \lambda^2$ where λ is the relative risk with respect to the causal variant. Let p_{case} and $p_{control}$ be the frequency of allele A in cases and controls, respectively, defined so that $Kp_{case} + (1-K)\, p_{control} = p$,

$p_{case} = \frac{p\lambda}{1+p(\lambda-1)}$ and $p_{control} = \frac{p}{1-K}\left(1 - \frac{K\lambda}{1+p(\lambda-1)}\right)$.

If the number of cases and controls in the sample are N_{case} and $N_{control}$, respectively then $N = N_{case} + N_{control}$ and $v = N_{case}/N$. The non-centrality parameter (NCP) of the X^2 test of association is

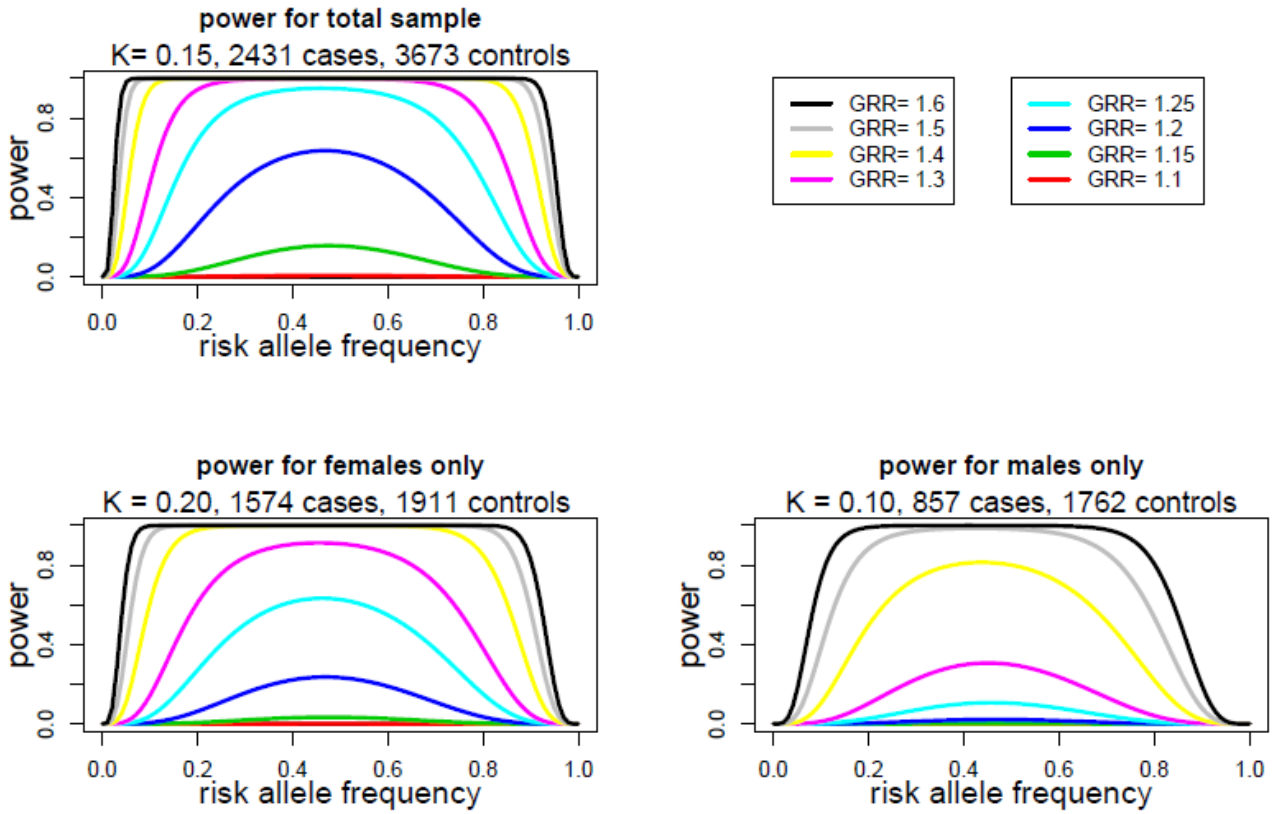
$$\text{NCP} = \frac{N^2(p_{case}-p_{control})^2}{Var(\hat{p}_{case}-\hat{p}_{control})} = \frac{2Nv(1-v)(p_{case}-p_{control})^2}{\bar{p}(1-\bar{p})} = \frac{2Nv(1-v)p^2(1-p)^2(\lambda-1)^2}{(1+p(\lambda-1))^2(1-K)^2\bar{p}(1-\bar{p})}, \quad [1]$$

[1]

where $\bar{p} = v\, p_{case} + (1-v)\, p_{control}$

We calculate power as the normal probability p(Z > T+√NCP), where Z ~N(0,1) and T is the normal deviate corresponding to the type I probability level, ie 5e-8 for genome-wide association. Power curves are presented in FigureS1. The estimated power is from equation [1], the same as from the Genetic Power Calculator(8).

Figure S1. Power curves for the total, male and female only study samples for different genotype relative risks (GRR= λ).



Comparing the power of case control studies of MDD and schizophrenia (SCZ)

From equation [1] we can write a NCP for the association test of a case-control study of MDD or SCZ. We assume both have equal proportions of cases in their samples (*v*), and the associated variant for each disorder has frequency, *p*.

$$NCP_{SCZ} = \frac{2N_{SCZ}v(1-v)p^2(1-p)^2(\lambda_{SCZ}-1)^2}{(1+p(\lambda_{SCZ}-1))^2(1-K_{SCZ})^2\bar{p}_{SCZ}(1-\bar{p}_{SCZ})}$$

and

$$NCP_{MDD} = \frac{2N_{MDD}v(1-v)p^2(1-p)^2(\lambda_{MDD}-1)^2}{(1+p(\lambda_{MDD}-1))^2(1-K_{MDD})^2\bar{p}_{MDD}(1-\bar{p}_{MDD})}$$

Following Yang et al (9), under the liability threshold model, we consider variants which explain the same proportion (q^2) of phenotypic variance on the liability scale so that

$$q^2 = 2p(1-p)\frac{(\lambda_{MDD}-1)^2}{i_{MDD}^2} = 2p(1-p)\frac{(\lambda_{SCZ}-1)^2}{i_{SCZ}^2}$$

where i_{SCZ} *and* i_{MDD} are the mean phenotypic liability of individuals with SCZ and MDD respectively, calculated as $i = z/K$ where z is the height of the standard normal curve at the truncation of proportion *K*. Therefore,

$$\lambda_{MDD} = 1 + \frac{i_{MDD}}{i_{SCZ}}(\lambda_{SCZ}-1)$$

i.e. a risk variant for schizophrenia $\lambda_{SCZ} = 1.20$ explains the same proportion of variance in liability as a risk variant of equal frequency in the population for MDD of $\lambda_{MDD} = 1.11$, assuming disease prevalence, K_{SCZ} = 0.007 and K_{MDD} = 0.15 so that i_{SCZ} = 2.78 and i_{MDD} = 1.55. The increase in sample size for a case control study for MDD to detect a risk variant which explains the same proportion of the variance in liability

$$\frac{N_{MDD}}{N_{SCZ}} = \frac{(\lambda_{SCZ}-1)^2}{(\lambda_{MDD}-1)^2}\frac{(1-K_{MDD})^2}{(1-K_{SCZ})^2}\frac{(1+p(\lambda_{MDD}-1))^2}{(1+p(\lambda_{SCZ}-1))^2}\frac{\overline{p}_{MDD}(1-\overline{p}_{MDD})}{\overline{p}_{SCZ}(1-\overline{p}_{SCZ})}$$

$$= \frac{i_{SCZ}^2}{i_{MDD}^2}\frac{(1-K_{MDD})^2}{(1-K_{SCZ})^2}\frac{(1+p\,\frac{i_{MDD}}{i_{SCZ}}(\lambda_{SCZ}-1))^2}{(1+p(\lambda_{SCZ}-1))^2}\frac{\overline{p}_{MDD}(1-\overline{p}_{MDD})}{\overline{p}_{SCZ}(1-\overline{p}_{SCZ})} \qquad [2]$$

$$\approx \frac{i_{SCZ}^2}{i_{MDD}^2}\frac{(1-K_{MDD})^2}{(1-K_{SCZ})^2} \qquad [3]$$

The increased sample size required for MDD to detect a variant that explains the same proportion of phenotypic liability as a variant for SCZ is demonstrated using equation [2] in Figure S2 (assuming both studies have equal proportion of cases). Using the approximation of equation [3] $\frac{N_{MDD}}{N_{SCZ}} \approx 2.4$.

Hospital-based MDD cohorts may represent a more extreme phenotype, with both lower prevalence and higher heritability (10). Using a prevalence for such clinical samples to be K_{MDD} = 0.06 (the average across sexes (11)) still requires a sample size ~1.8 times (equation [3])greater for a case control study of MDD compared to one for schizophrenia.

This comparison only accounts for the difference in prevalence rates and hence the lower difference in mean liability between cases (*i*) and controls (-iK/(1-K)) i.e. , K_{SCZ} = 0.007 and K_{MDD} = 0.15 the difference in mean liability between cases and controls is 2.78 s.d units for SCZ and 1.57 s.d. units for MDD. If we assume that the number and frequency of risk variants underlying SCZ and MDD is the same then the difference in heritability must reflect lower effect sizes in MDD. In

this case the ratio of NMDD/NSCZ can be derived by equating the NCP on equal proportions of genetic variance explained (i.e. scaling q2 by the heritability) so that equation [3] is inflated by the ratio of heritabilities $\frac{h^2_{SCZ}}{h^2_{MDD}}$, which may be as great as a factor of 2, ie sample sizes 4-5 times those for schizophrenia may be needed for MDD.

Figure S2 Ratio of sample size for a case-control study for MDD compared to one for SCZ assuming variants of equal population frequency that explain an equal proportion of the phenotypic variance.

A sample size of ~2.4 times greater (equation [3]) is needed for MDD compared to to detect variants that explain the same proportion of variance in *phenotypic* liability and that have the same frequency in the total population, expressed in terms of genotypic relative risk in SCZ (GRR = λ_{SCZ}).

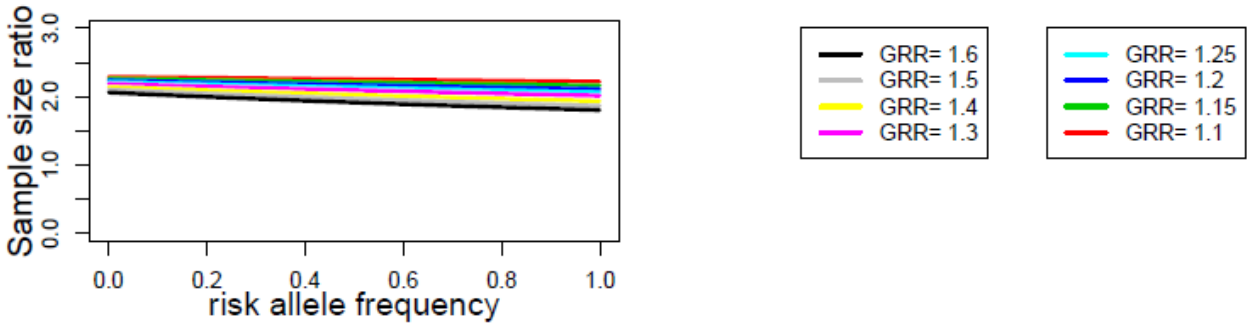


Figure S3 Manhattan Plot for full analysis of 2431 major depression cases and 3673 controls.

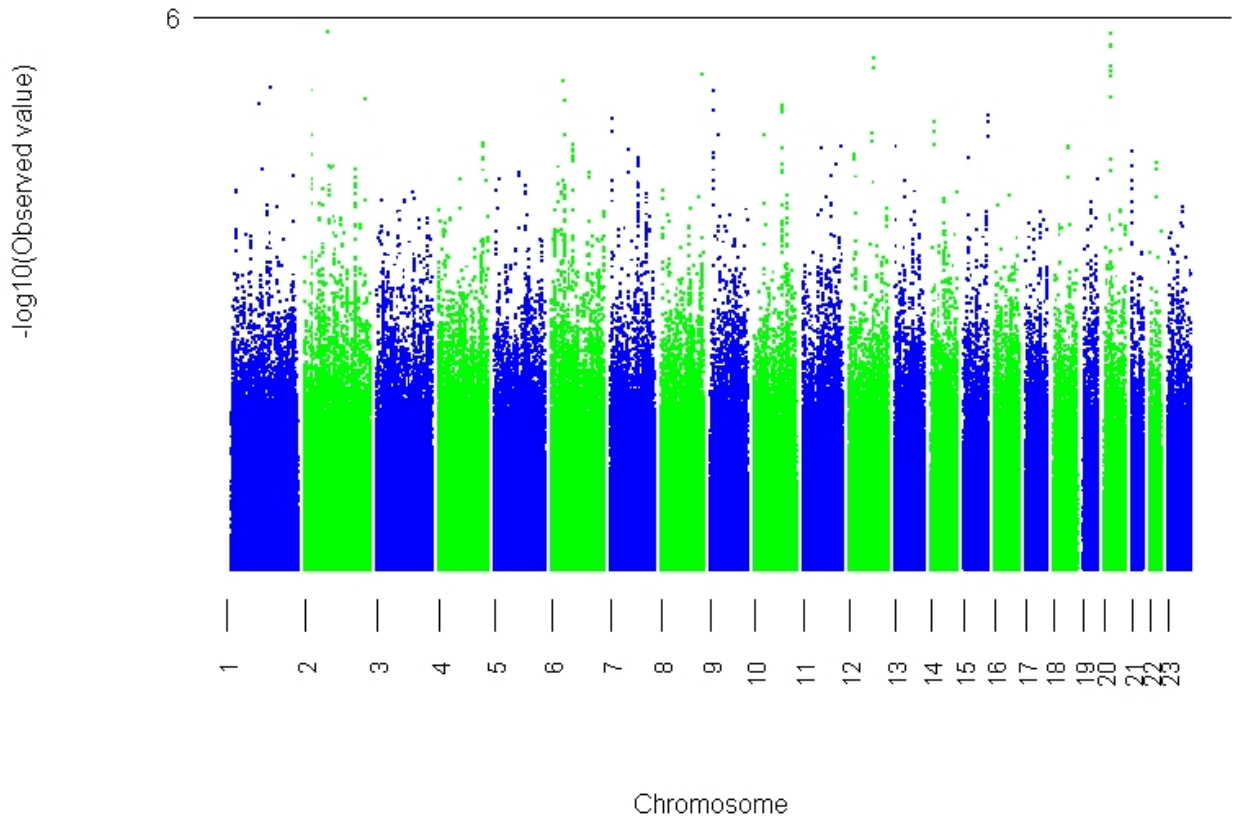


Figure S4 QQ plot from association of i) male only and ii) female only analyses

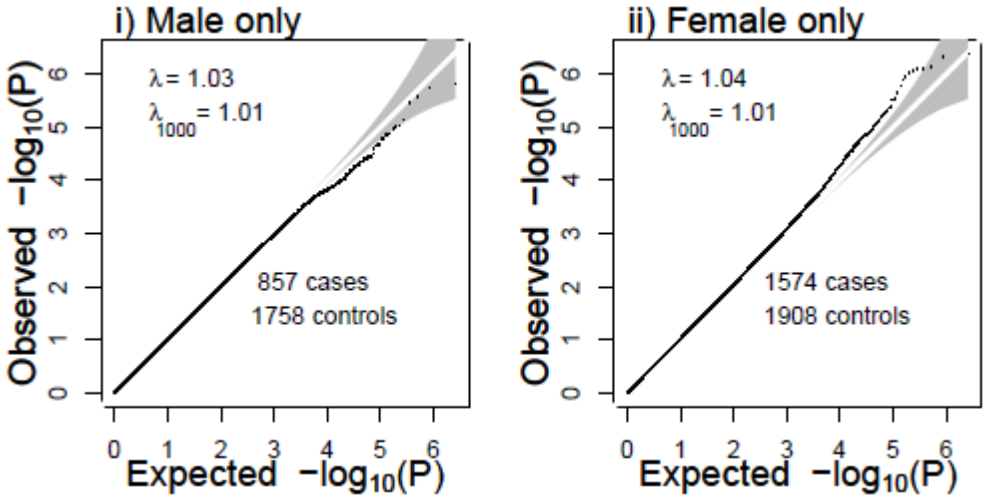


Table S2 SNPs in the PCLO region investigated by analysis set and sample source.

The gene *PCLO* gene, a novel but plausible candidate, identified in the GAIN MDD study (1) located on chromosome 7q11.23-q21.3 and bounded by two other plausible candidate genes *CACNA2D1* and *SEMA3E* . The most associated *PCLO* SNPs were rs2715148 and the non-synonymous rs2522833.
The most associated *PCLO* SNPs were rs2715148 and the non-synonymous rs2522833. The GAIN MDD sample comprises cases and controls from the Dutch NESDA and NTR studies, the same studies which contribute 127 cases and 577 controls to MDD2000+.
In addition, two of the replication samples comprised cases and controls from UoE and QIMR, the latter showing support for association across the region with p = 0.076 and 0.028 for rs2715148 and rs2522833, respectively.
Here we explore the 16 SNPs in our genotype set that were among the 30 SNPs considered in the GAIN MDD replication study, investigating allele frequency and association by analysis set and sample source.
This investigation shows that the genotyping results here are consistent with those presented in Sullivan et al (2009) for QIMR samples, but that the choice of different QIMR study participants
(overlap with MDD2000+ of 562 cases and 264 controls), the ascertainment of QIMR samples reflected in the summary statistics of Table 2 in the main text, and the combining of samples from different sources results in the lack of association in the total MDD2000+ sample.

		QIMR sample (Sullivan et al)			MDD2000+			A6.0									I317 (QIMR)			I370				I610 (QIMR)				ALL
SNP	Associated allele FWD strand	Freq controls [N = 1039]	Freq cases [N = 969]	P	Freq Cont [N=3673]	Freq Case [N=2431]	P	Freq Cont (MGS) [N=1636]	Freq All Case [N=1441]	Freq QIMR case [N=941]	Freq UoE Case [N=373]	Freq NESDA/ NTR Case [N=127]	P All case	P QIMR case	P UoE Case	P NESDA/ NTR case	Freq Cont [N=237]	Freq Case [N=-84]	P	Freq All Cont [N=1372]	Freq QIMR Cont [N=795]	Freq Case (QIMR) [N=737]	P	Freq Contr [N=428]	Freq Case [N=169]	p	P QIMR
rs7780196	G	0.41	0.46	**3.2E-03**	0.44	0.43	2.7E-01	0.43	0.44	0.44	0.43	0.44	1.2E-01	1.0E-01	2.9E-01	6.3E-01	0.42	0.37	1.9E-01	0.45	0.46	0.41	**1.9E-03**	0.45	0.44	6.9E-01	**7.0E-04**
rs10954689	T	0.44	0.49	**3.4E-03**	0.47	0.47	5.5E-01	0.45	0.48	0.49	0.46	0.46	8.2E-02	**2.6E-02**	6.8E-01	7.0E-01	0.48	0.47	9.3E-01	0.48	0.48	0.46	2.9E-01	0.48	0.46	4.5E-01	2.9E-01
rs12672552	T	0.89	0.90	7.4E-01	0.89	0.89	4.4E-01	0.89	0.89	0.89	0.91	0.88	9.7E-01	6.2E-01	1.6E-01	5.9E-01	0.87	0.86	6.1E-01	0.90	0.91	0.89	4.1E-01	0.91	0.90	5.8E-01	2.4E-01
rs6948464	C	0.64	0.65	2.9E-01	0.65	0.65	8.8E-01	0.65	0.65	0.66	0.64	0.64	8.1E-01	7.4E-01	3.3E-01	8.2E-01	0.66	0.65	7.4E-01	0.64	0.65	0.64	9.7E-01	0.66	0.65	7.5E-01	5.5E-01
rs13227462	G	0.95	0.95	7.9E-01	0.94	0.94	4.0E-01	0.94	0.95	0.94	0.95	0.96	**1.3E-02**	1.3E-01	**3.9E-02**	**3.6E-02**	0.94	0.93	7.5E-01	0.95	0.94	0.94	9.2E-02	0.94	0.94	9.1E-01	3.6E-01
rs6979066	A	0.33	0.37	**6.7E-03**	0.35	0.35	9.9E-01	0.34	0.36	0.37	0.36	0.34	7.9E-02	5.4E-02	2.4E-01	6.2E-01	0.33	0.32	8.2E-01	0.37	0.37	0.34	7.3E-02	0.37	0.34	2.7E-01	**3.8E-02**
rs6965452	G	0.84	0.86	**4.4E-02**	0.85	0.85	3.2E-01	0.84	0.86	0.86	0.85	0.87	**3.2E-03**	**8.2E-03**	8.7E-02	3.0E-01	0.84	0.83	7.2E-01	0.86	0.85	0.84	5.9E-02	0.84	0.84	9.6E-01	2.5E-01
rs12668093	C	0.85	0.86	6.8E-01	0.85	0.85	3.2E-01	0.85	0.85	0.85	0.87	0.82	6.7E-01	5.1E-01	3.4E-01	1.7E-01	0.82	0.84	7.6E-01	0.86	0.87	0.86	5.5E-01	0.87	0.84	2.0E-01	4.3E-01
rs2522833	C	0.41	0.45	**2.5E-02**	0.43	0.44	5.1E-01	0.42	0.44	0.45	0.42	0.43	**4.9E-02**	**1.2E-02**	8.4E-01	7.6E-01	0.43	0.42	9.4E-01	0.44	0.45	0.42	2.0E-01	0.45	0.43	5.2E-01	1.7E-01
rs13233504	T	0.20	0.21	2.7E-01	0.21	0.21	8.9E-01	0.21	0.21	0.22	0.20	0.19	9.8E-01	5.2E-01	8.6E-01	1.7E-01	0.19	0.21	4.3E-01	0.21	0.21	0.21	7.3E-01	0.21	0.20	9.5E-01	6.5E-01
rs2888018	G	0.32	0.33	5.7E-01	0.33	0.33	4.9E-01	0.33	0.34	0.34	0.31	0.34	5.9E-01	2.1E-01	3.7E-01	7.4E-01	0.33	0.33	9.4E-01	0.33	0.32	0.32	9.9E-01	0.31	0.34	2.7E-01	9.8E-01
rs10954694	C	0.35	0.37	1.9E-01	0.37	0.37	9.7E-01	0.35	0.38	0.38	0.38	0.34	8.1E-02	5.6E-02	1.6E-01	4.7E-01	0.35	0.32	4.2E-01	0.38	0.39	0.36	2.2E-01	0.40	0.35	1.0E-01	1.5E-01
rs9690648	T	0.93	0.93	9.7E-01	0.93	0.94	4.4E-01	0.93	0.93	0.93	0.94	0.91	6.9E-01	8.0E-01	4.4E-01	2.7E-01	0.93	0.96	1.6E-01	0.94	0.94	0.94	4.9E-01	0.93	0.92	3.6E-01	3.5E-01
rs6959723	A	0.81	0.82	4.8E-01	0.81	0.81	7.3E-01	0.80	0.82	0.82	0.80	0.82	6.6E-02	**4.0E-02**	6.0E-01	6.4E-01	0.82	0.77	2.4E-01	0.83	0.82	0.80	**3.3E-02**	0.81	0.80	8.7E-01	8.4E-02
rs7799260	G	0.52	0.53	4.2E-01	0.52	0.52	9.3E-01	0.51	0.53	0.54	0.50	0.52	3.1E-01	7.5E-02	6.2E-01	8.6E-01	0.52	0.46	1.8E-01	0.53	0.53	0.51	5.4E-01	0.54	0.52	4.2E-01	3.9E-01
rs12669254	T	0.91	0.92	3.3E-01	0.91	0.91	3.4E-01	0.91	0.91	0.91	0.93	0.90	6.5E-01	7.2E-01	**2.1E-02**	4.7E-01	0.91	0.90	6.8E-01	0.92	0.92	0.91	8.3E-02	0.92	0.91	5.3E-01	6.3E-02

16 out of the 30 SNPs used in the replication study undertaken Sullivan et al (2009) were included in our final imputed SNP set.
562 MDD cases and 264 controls were in common between the QIMR replication sample used in Sullivan et al (2009) and MDD2000+, of which 404 MDD cases were included in the A6.0 analysis set.
For SNPs directly genotyped in MDD2000+ the maximum discordance in genotypes was 2.
In Sullivan et al (2009) UoE cases vs UoE controls showed association of p = 4.0E-03 and p =7E-02 for SNPs rs13227462 and rs 12669254, respectively; these were the only 2 SNPs of the 16 to have p < 0.05 in the Sullivan et al (2009) paper for UoE samples
The lack of support for PCLO by the total MDD2000+ does not imply any inconsistency with the results reported in Sullivan et al (2009).

Table S3 Regions containing at least on SNP with a p-value of $p<10^{-5}$ in the meta-analysis of associations from the MDD2000+, GAIN and UK samples.

					Frequency	OR				P				
CHR	SNP	BP	A1	A2	MDD2000+	MDD2000+	GAIN	UK	Meta	MDD2000+	GAIN	UK	Meta	Gene +/- 50kb
1	rs7513908	8225206	A	G	0.17	1.18	1.11	1.18	1.16	1.2E-03	1.2E-01	1.4E-02	1.9E-05	
1	rs12407717	30198601	T	C	0.12	1.18	1.11	1.25	1.17	5.7E-03	1.4E-01	3.6E-03	4.0E-05	
1	rs11579964	222605563	T	C	0.16	0.84	0.84	0.84	0.84	3.5E-03	1.4E-02	1.0E-02	4.4E-06	*CNIH4 NVL WDR26*
3	rs581190	62821149	A	G	0.44	1.16	1.09	1.08	1.11	2.5E-04	9.0E-02	1.5E-01	4.3E-05	*CADPS*
3	rs12714788	72739803	C	A	0.27	0.87	0.84	0.96	0.88	1.1E-03	1.8E-03	4.9E-01	2.6E-05	
3	rs7647854	186359477	G	A	0.16	1.22	1.20	1.12	1.19	5.0E-04	7.4E-03	1.1E-01	4.6E-06	*C3orf70, EHHADH*
4	rs1826690	70386855	G	A	0.25	0.96	0.82	0.80	0.88	4.3E-01	8.1E-04	1.4E-04	1.9E-05	
5	rs1990950	156853334	T	G	0.40	1.09	1.17	1.10	1.12	2.5E-02	2.4E-03	6.5E-02	4.9E-05	*UGT2B4*
6	rs6568842	114907070	A	G	0.15	1.19	1.13	1.17	1.17	1.0E-03	8.4E-02	3.6E-02	2.6E-05	*ADAM19,ICHTHYIN*
10	rs7100942	25863759	A	C	0.43	1.12	1.09	1.13	1.11	4.2E-03	8.3E-02	1.8E-02	4.8E-05	*GPR158*
16	rs11075236	14372157	C	A	0.34	1.09	1.14	1.16	1.12	3.4E-02	1.4E-02	5.6E-03	3.3E-05	
16	rs3852700	65829359	C	T	0.07	1.28	1.19	1.22	1.24	1.5E-03	6.9E-02	4.4E-02	3.7E-05	*E2F4, ELMO3, EXOC3L, FHOD1, LRRC29, SLC9A5,TMEM208*
16	rs12446956	72059037	C	T	0.13	1.22	1.15	1.28	1.22	6.4E-04	6.1E-02	2.0E-03	1.1E-06	*SYT4*
18	rs12457996	39126271	C	T	0.23	0.88	0.88	0.84	0.87	5.3E-03	2.3E-02	4.5E-03	5.7E-06	
18	rs9951150	50972122	G	A	0.45	1.12	1.08	1.15	1.12	5.0E-03	1.0E-01	5.0E-03	2.6E-05	
19	rs2116877	11219440	C	T	0.11	0.86	0.85	0.79	0.84	1.6E-02	4.3E-02	4.4E-03	2.9E-05	*DOCK6,LOC55908, TSPAN16*
20	rs1539470	59771861	C	A	0.21	0.91	0.83	0.89	0.88	4.2E-02	1.5E-03	4.8E-02	4.3E-05	
22	rs5755867	34403989	C	T	0.04	1.51	1.32	1.17	1.36	9.2E-05	5.5E-02	2.5E-01	2.3E-05	*APOL5,APOL6*
23	rs17282946	120144590	A	G	0.05	0.78	0.83	0.78	0.79	9.4E-04	1.4E-01	4.7E-02	4.0E-05	

a: INFO =0.7; all other INFO statistics for MDD2000 and GAIN > 0.8

REFERENCES

1. Medland SE, Nyholt DR, Painter JN, McEvoy BP, McRae AF, Zhu G *et al.* Common variants in the trichohyalin gene are associated with straight hair in Europeans. *Am J Hum Genet* 2009 Nov; **85**(5)**:** 750-755.

2. Korn JM, Kuruvilla FG, McCarroll SA, Wysoker A, Nemesh J, Cawley S *et al.* Integrated genotype calling and association analysis of SNPs, common copy number polymorphisms and rare CNVs. *Nat Genet* 2008 Oct; **40**(10)**:** 1253-1260.

3. McCarroll SA, Kuruvilla FG, Korn JM, Cawley S, Nemesh J, Wysoker A *et al.* Integrated detection and population-genetic analysis of SNPs and copy number variation. *Nat Genet* 2008 Oct; **40**(10)**:** 1166-1174.

4. Purcell SM, Wray NR, Stone JL, Visscher PM, O'Donovan MC, Sullivan PF *et al.* Common polygenic variation contributes to risk of schizophrenia and bipolar disorder. *Nature* 2009 Aug 6; **460**(7256)**:** 748-752.

5. McEvoy BP, Montgomery GW, McRae AF, Ripatti S, Perola M, Spector TD *et al.* Geographical structure and differential natural selection among North European populations. *Genome Res* 2009 May; **19**(5)**:** 804-814.

6. Price AL, Patterson NJ, Plenge RM, Weinblatt ME, Shadick NA, Reich D. Principal components analysis corrects for stratification in genome-wide association studies. *Nat Genet* 2006 Aug; **38**(8)**:** 904-909.

7. Cross-Disorder Phenotype Group of the Psychiatric GC, Craddock N, Kendler K, Neale M, Nurnberger J, Purcell S *et al.* Dissecting the phenotype in genome-wide association studies of psychiatric illness. *Br J Psychiatry* 2009 Aug; **195**(2)**:** 97-99.

8. Purcell S, Cherny SS, Sham PC. Genetic Power Calculator: design of linkage and association genetic mapping studies of complex traits. *Bioinformatics* 2003 Jan; **19**(1)**:** 149-150.

9. Yang J, Wray NR, Visscher PM. Comparing apples and oranges: equating the power of case-control and quantitative trait association studies. *Genet Epidemiol* 2009 Nov 13.

10. McGuffin P, Cohen S, Knight J. Homing in on depression genes. *American Journal of Psychiatry* 2007 Feb; **164**(2)**:** 195-197.

11. McGuffin P, Katz R, Watkins S, Rutherford J. A hospital-based twin register of the heritability of DSM-IV unipolar depression. *Archives of General Psychiatry* 1996 Feb; **53**(2)**:** 129-136.

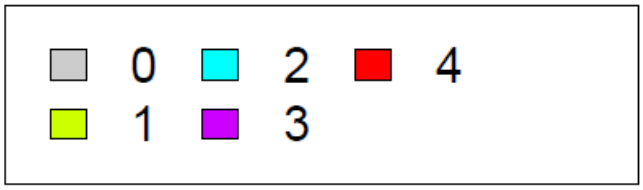
12. Sullivan PF, de Geus EJC, Willemsen G, James MR, Smit JH, Zandbelt T *et al.* Genome-wide association for major depressive disorder: a possible role for the presynaptic protein piccolo. *Molecular Psychiatry* 2009 Apr; **14**(4)**:** 359-375.

Supplementary Figures

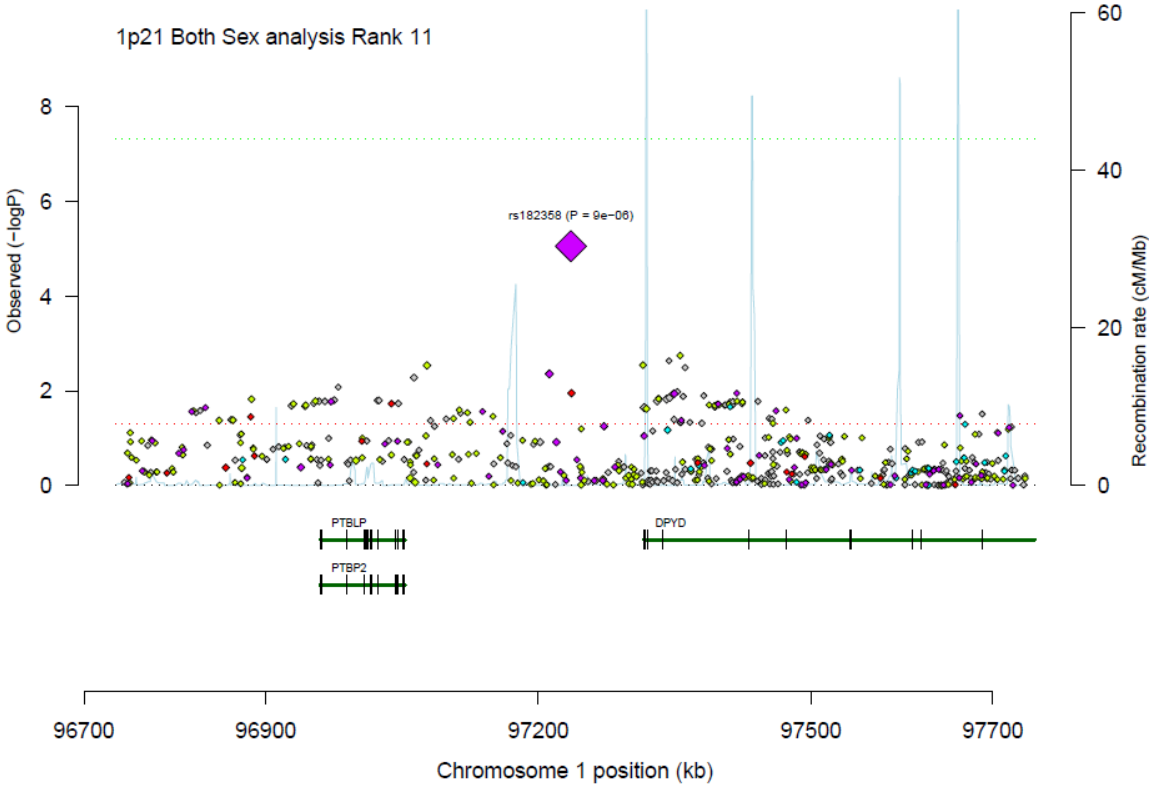
Regional association plots for all regions containing a SNP associated $p < 5 \times 10^{-5}$ and INFO > 0.3. The regional association plots are based on a concept developed by Paul de Bakker for the genome-wide association study by the Diabetes Genetics Initiative (1).

For each top SNP region there are two plots

- 1Mb region about the most associated SNP, plotting –log10(p) for each SNP, the position of genes in the region and the recombination rate across the region that bound haplotype blocks. The plotted SNPs are colour coded by the number of analysis sets in which they are imputed (legend). The size of the diamonds reflects the magnitude of r^2 linkage disequilibrium between the SNP and the labelled top associated SNP of the region. Genes within 50kb of these SNPs are listed. Colour coding for SNPs: number of sets in which the SNP was imputed (0 = imputed in all analysis sets, 4= genotyped in all analysis sets).



- Forest plots showing Odds Ratios (OR) and their 95% Confidence Intervals (L95-U95)for each contributing analysis set. I/G: I=Imputed, G=Genotyped. INFO: ratio of observed genotypic variance calculated from dosage scores, to expected genotypic variance based on mean dosage score, a measure of imputation quality. Fcon, Fcas: minor allele frequency in controls and cases.



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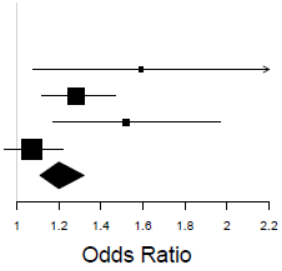
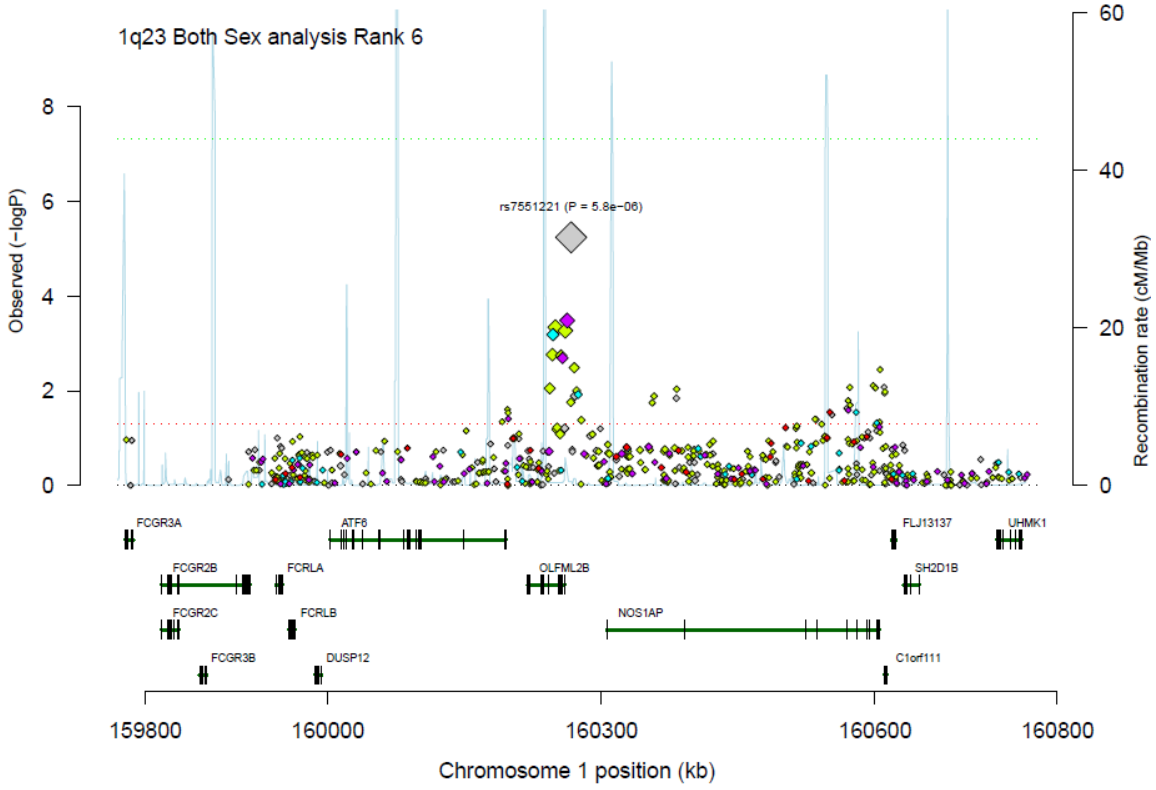
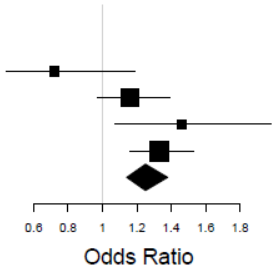
rs182358								
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	G	0.99	0.019	0.470	0.565	1.59	1.08	2.33
I370	G	0.98	0.00033	0.494	0.550	1.28	1.12	1.47
I610	I	1.03	0.0017	0.443	0.541	1.52	1.17	1.97
A6.0	G	0.71	0.28	0.495	0.517	1.07	0.94	1.22
All	**-**	**0.85**	**8.9e−06**	**0.487**	**0.530**	**1.20**	**1.11**	**1.32**

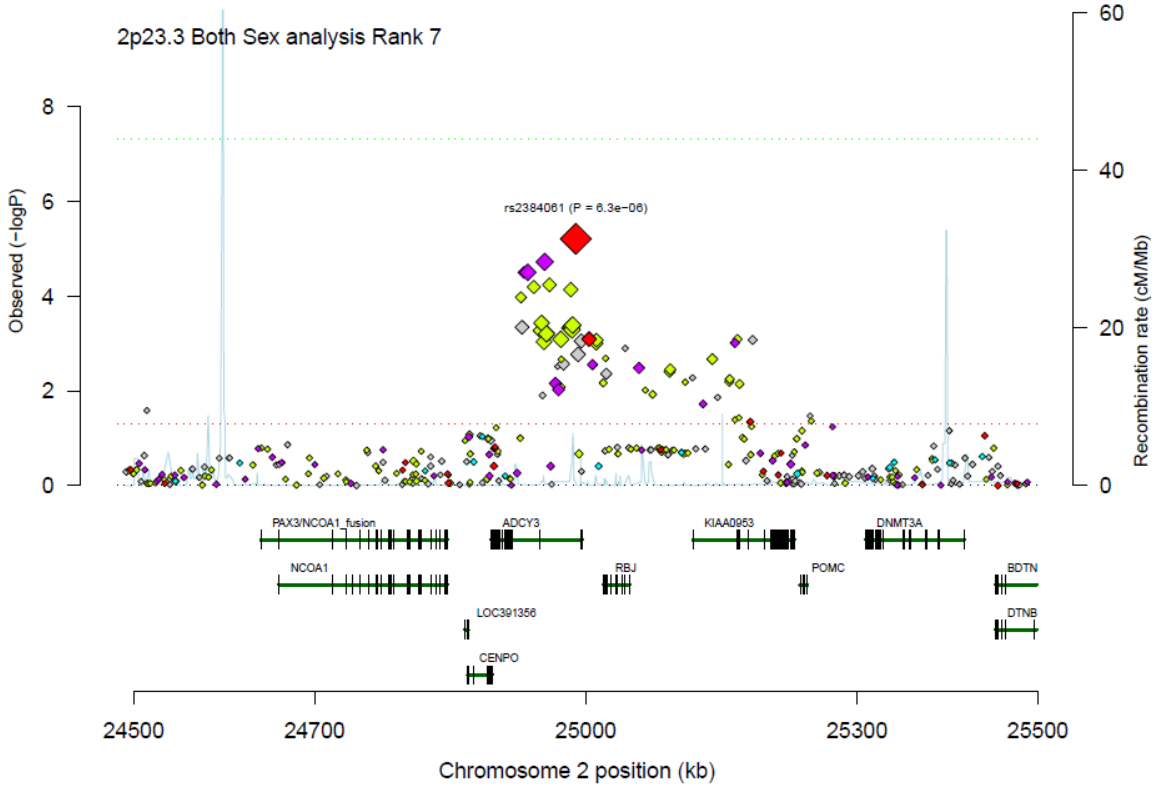




rs7551221

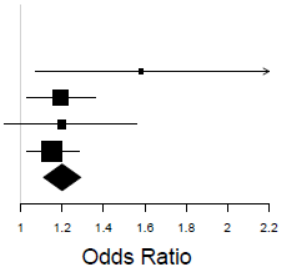
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	I	0.9	0.2	0.218	0.198	0.72	0.44	1.19
I370	I	0.86	0.096	0.199	0.216	1.16	0.97	1.39
I610	I	0.98	0.017	0.202	0.265	1.46	1.07	1.98
A6.0	I	0.96	3e−05	0.193	0.227	1.33	1.16	1.53
All	**-**	**0.93**	**5.8e−06**	**0.198**	**0.225**	**1.25**	**1.14**	**1.38**

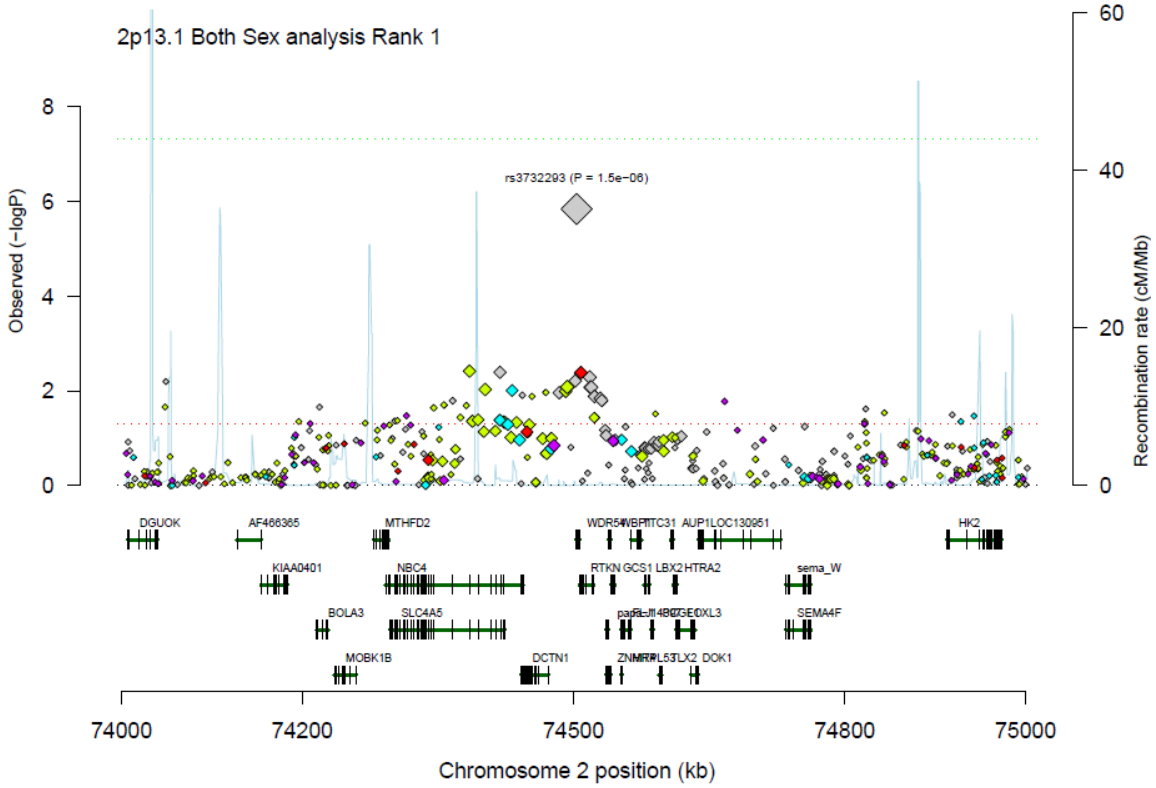




rs2384061

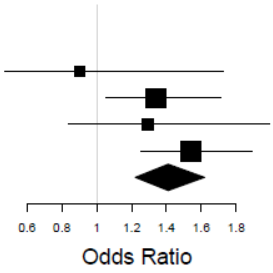
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	G	0.97	0.022	0.382	0.482	1.58	1.07	2.34
I370	G	0.95	0.015	0.394	0.446	1.19	1.03	1.36
I610	G	0.96	0.19	0.430	0.467	1.20	0.92	1.56
A6.0	G	0.99	0.013	0.392	0.438	1.15	1.03	1.28
All	**-**	**0.98**	**6.3e−06**	**0.397**	**0.444**	**1.20**	**1.11**	**1.29**

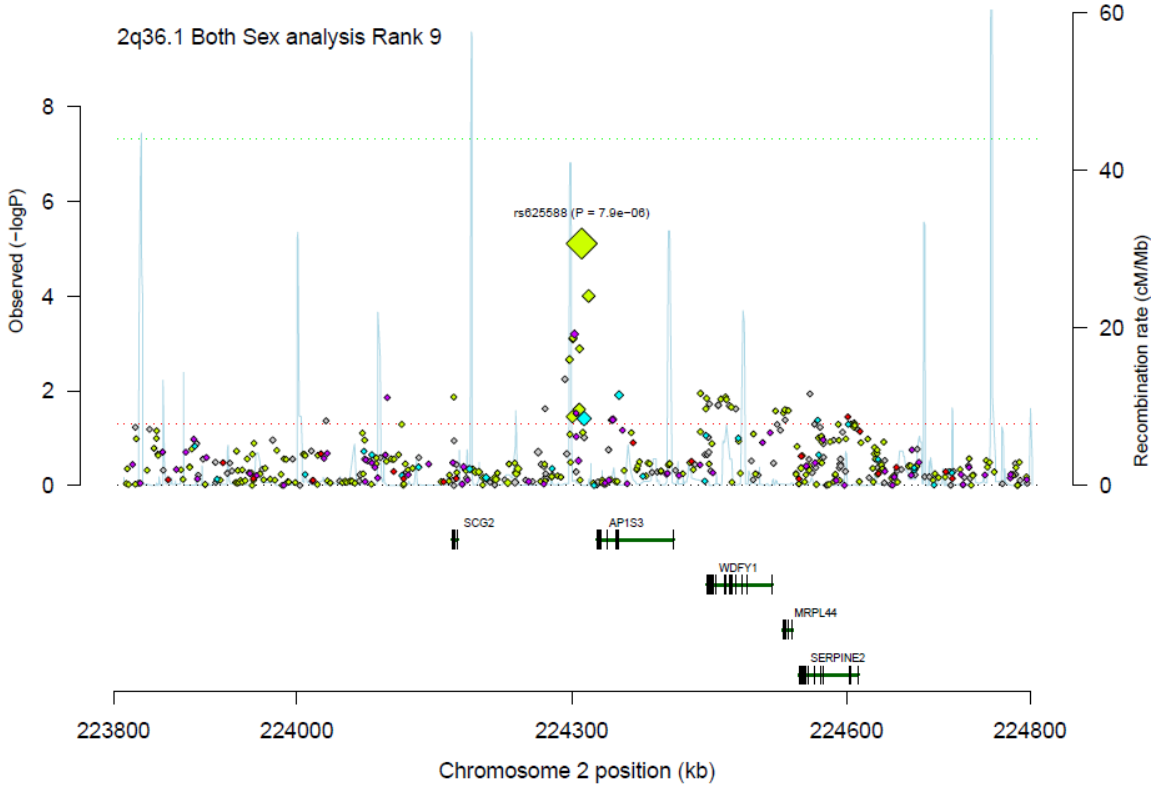




rs3732293

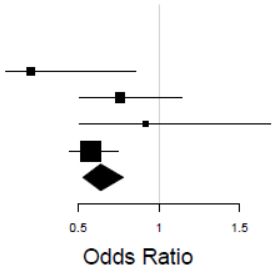
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	I	0.94	0.75	0.1010	0.0970	0.90	0.47	1.73
I370	I	0.96	0.018	0.0720	0.0990	1.34	1.05	1.71
I610	I	1.09	0.24	0.0810	0.0970	1.29	0.84	1.99
A6.0	I	1	3.8e−05	0.0620	0.0900	1.54	1.25	1.89
All	**-**	**0.99**	**1.5e−06**	**0.0705**	**0.0935**	**1.41**	**1.22**	**1.62**

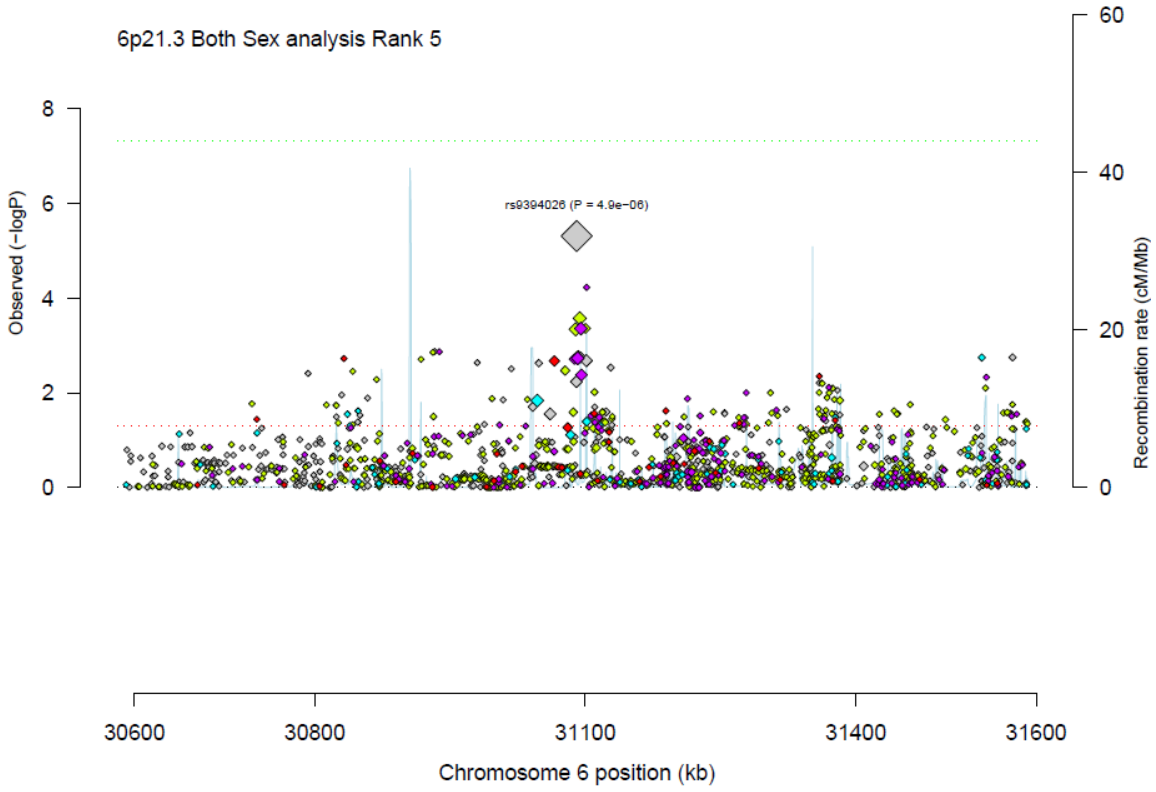




rs625588

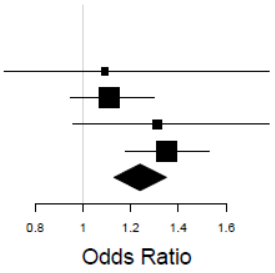
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	I	0.8	0.031	0.0540	0.0200	0.21	0.05	0.86
I370	I	0.63	0.18	0.0540	0.0440	0.76	0.51	1.14
I610	G	1.05	0.79	0.0490	0.0450	0.92	0.51	1.69
A6.0	I	1.01	2.8e−05	0.0640	0.0370	0.58	0.45	0.75
All	**-**	**0.87**	**7.9e−06**	**0.0579**	**0.0391**	**0.64**	**0.53**	**0.78**

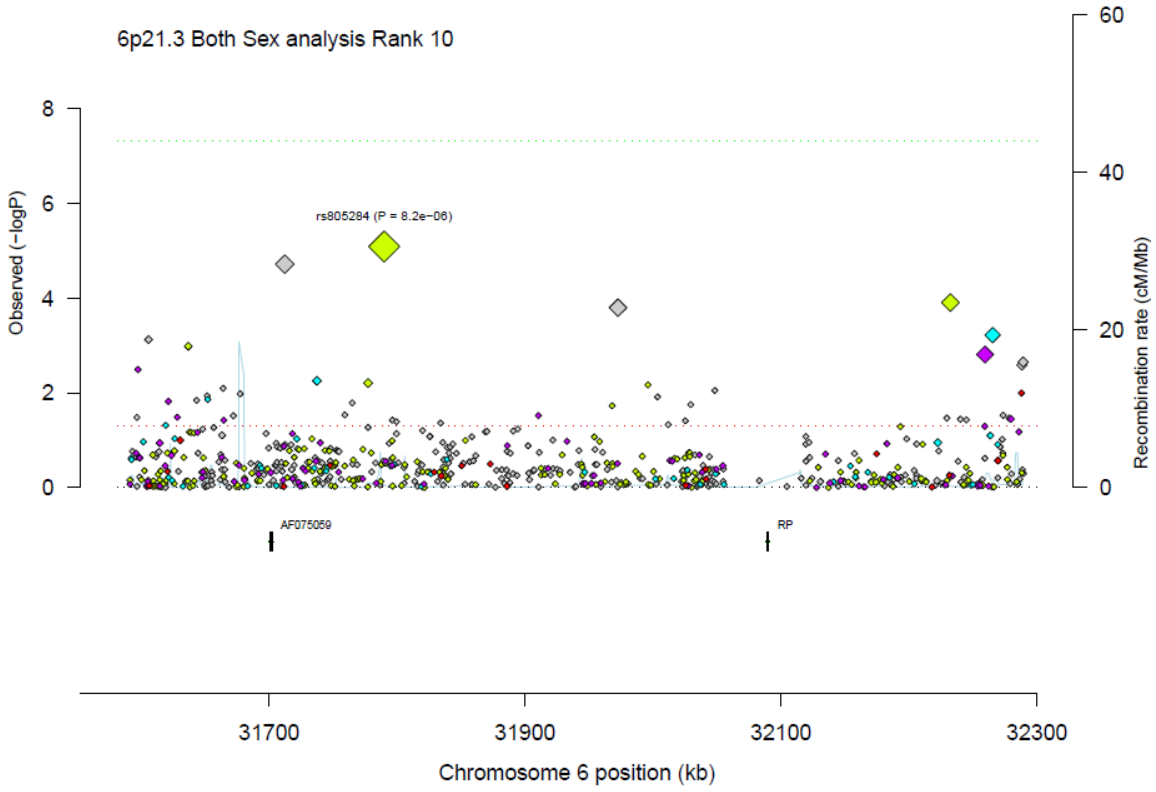




rs9394026

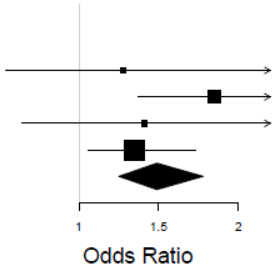
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	I	0.86	0.73	0.230	0.227	1.09	0.67	1.78
I370	I	0.99	0.19	0.220	0.239	1.11	0.95	1.30
I610	I	0.98	0.09	0.217	0.259	1.31	0.96	1.78
A6.0	I	0.98	5.1e−06	0.209	0.255	1.35	1.18	1.53
All	**-**	**0.98**	**4.9e−06**	**0.215**	**0.249**	**1.24**	**1.13**	**1.35**

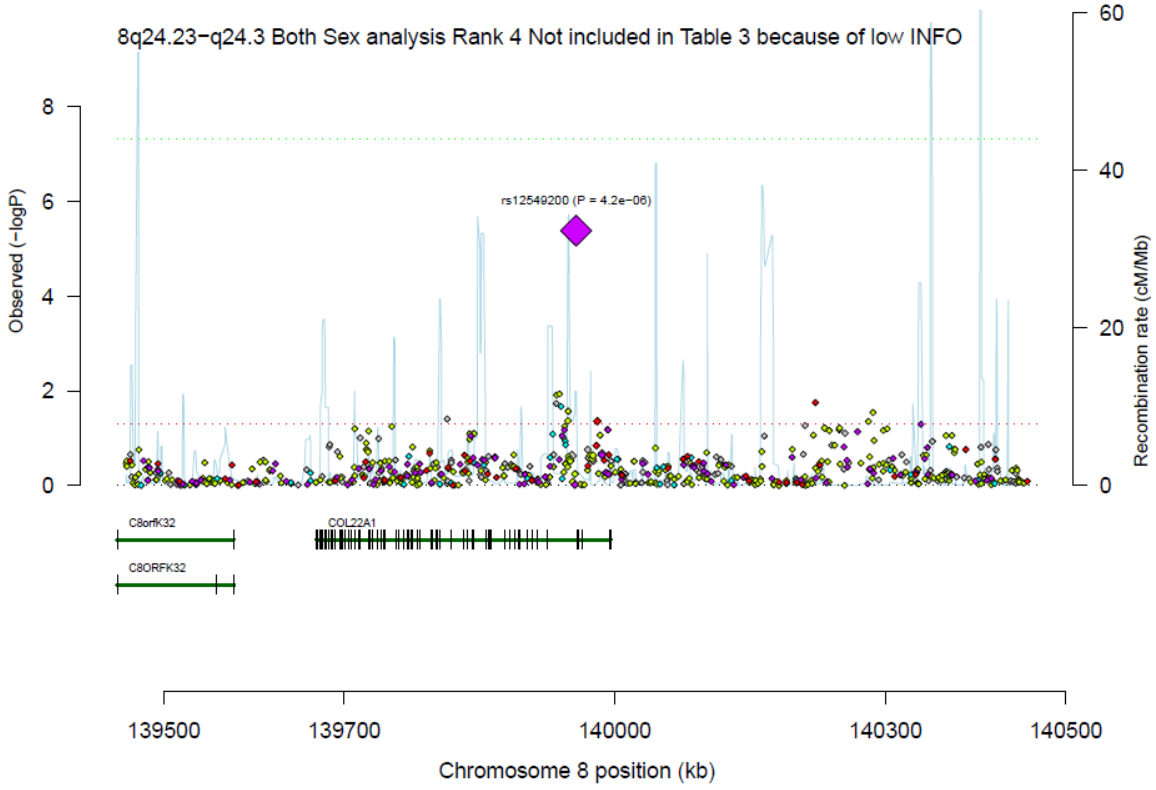




rs805284

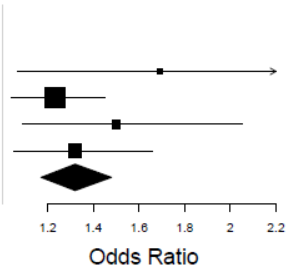
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	I	1.01	0.58	0.0490	0.0530	1.28	0.54	3.02
I370	I	0.96	5.7e−05	0.0400	0.0730	1.85	1.37	2.49
I610	G	0.71	0.39	0.0340	0.0420	1.41	0.64	3.12
A6.0	I	1.01	0.015	0.0410	0.0620	1.35	1.06	1.73
All	**-**	**0.97**	**8.2e−06**	**0.0403**	**0.0636**	**1.49**	**1.25**	**1.78**

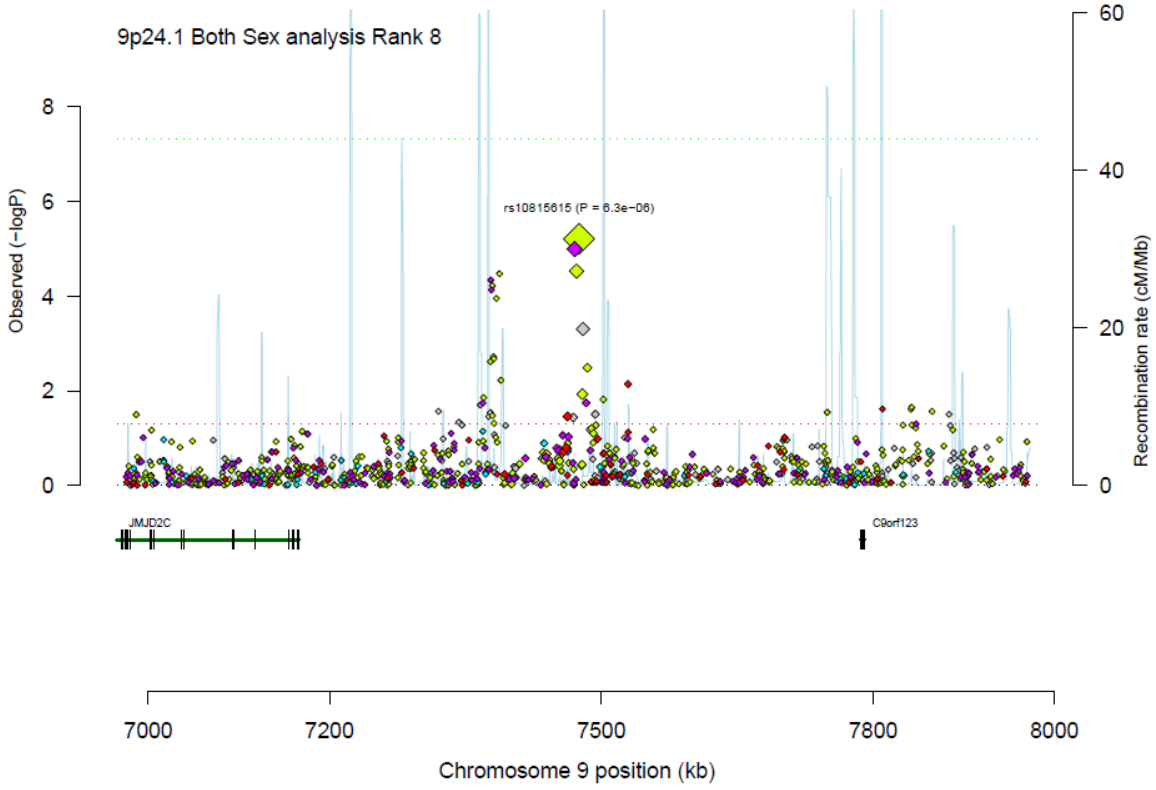




rs12549200

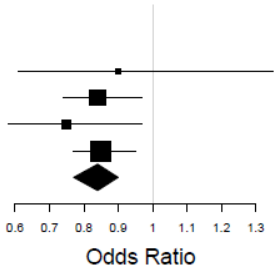
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	G	0.95	0.026	0.194	0.268	1.69	1.07	2.69
I370	G	1.01	0.016	0.182	0.218	1.23	1.04	1.45
I610	I	1.02	0.013	0.178	0.237	1.50	1.09	2.05
A6.0	G	0.35	0.017	0.183	0.199	1.32	1.05	1.66
All	**-**	**0.68**	**4.2e−06**	**0.183**	**0.210**	**1.32**	**1.17**	**1.48**

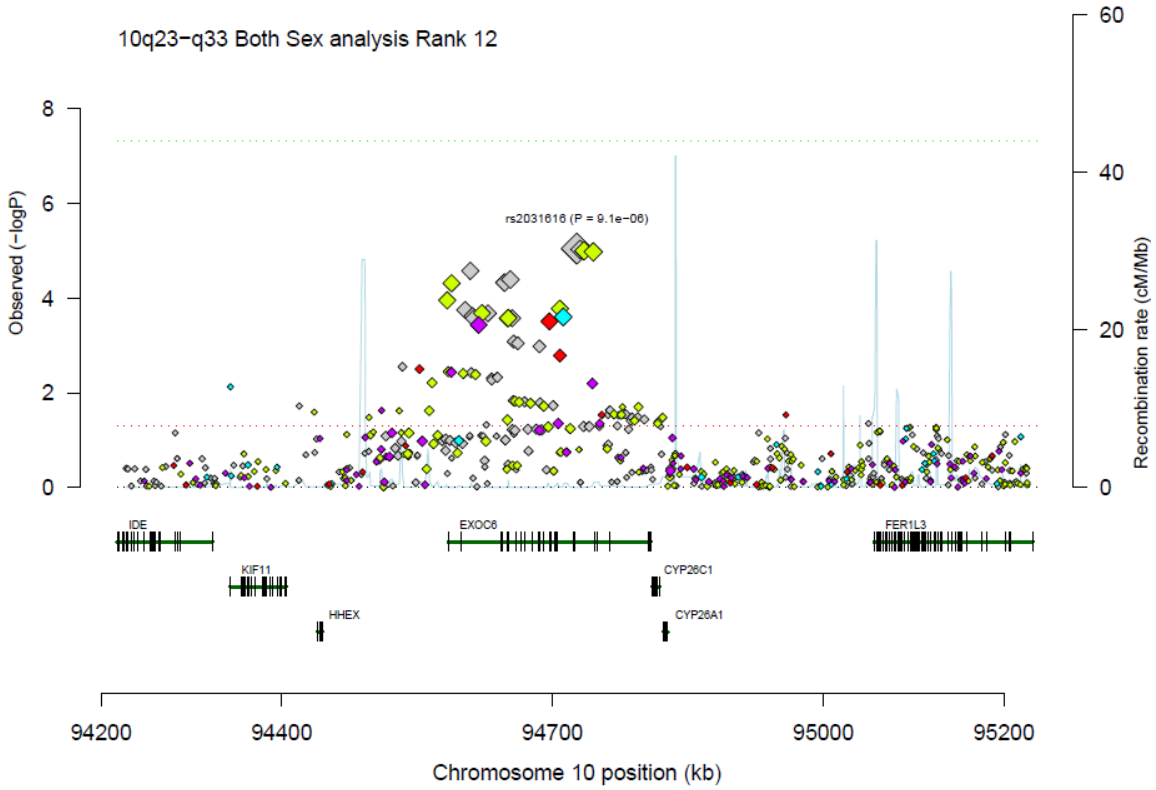




rs10815615

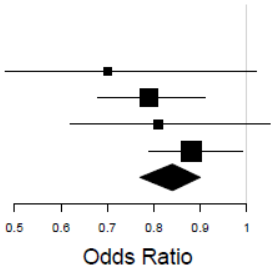
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	I	0.93	0.62	0.462	0.432	0.90	0.61	1.35
I370	G	0.97	0.014	0.474	0.434	0.84	0.74	0.97
I610	I	1.01	0.03	0.474	0.408	0.75	0.58	0.97
A6.0	I	0.98	0.0045	0.481	0.437	0.85	0.77	0.95
All	**-**	**0.97**	**6.3e−06**	**0.476**	**0.434**	**0.84**	**0.77**	**0.90**

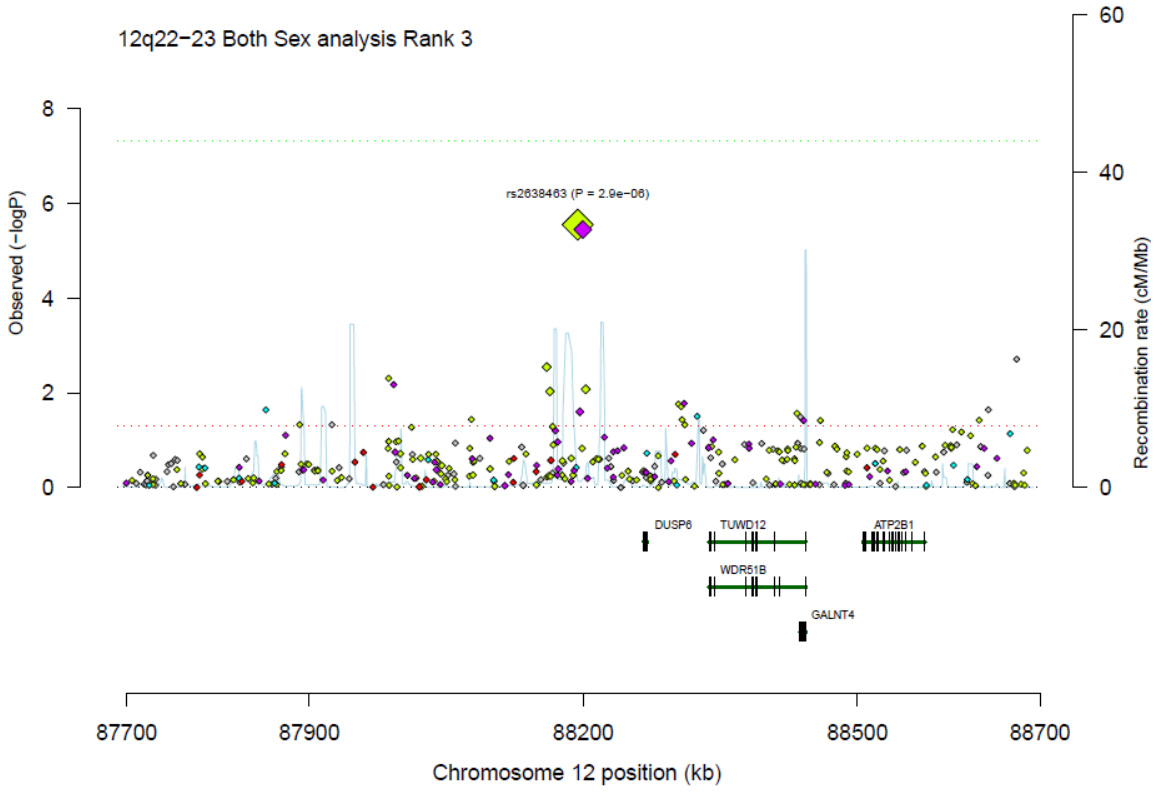




rs2031616

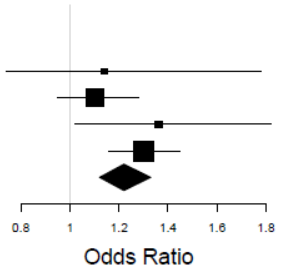
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	I	1.14	0.063	0.370	0.293	0.70	0.48	1.02
I370	I	0.95	0.0011	0.399	0.342	0.79	0.68	0.91
I610	I	1.04	0.11	0.407	0.356	0.81	0.62	1.05
A6.0	I	0.97	0.029	0.410	0.379	0.88	0.79	0.99
All	**-**	**0.98**	**9.1e−06**	**0.403**	**0.363**	**0.84**	**0.77**	**0.90**

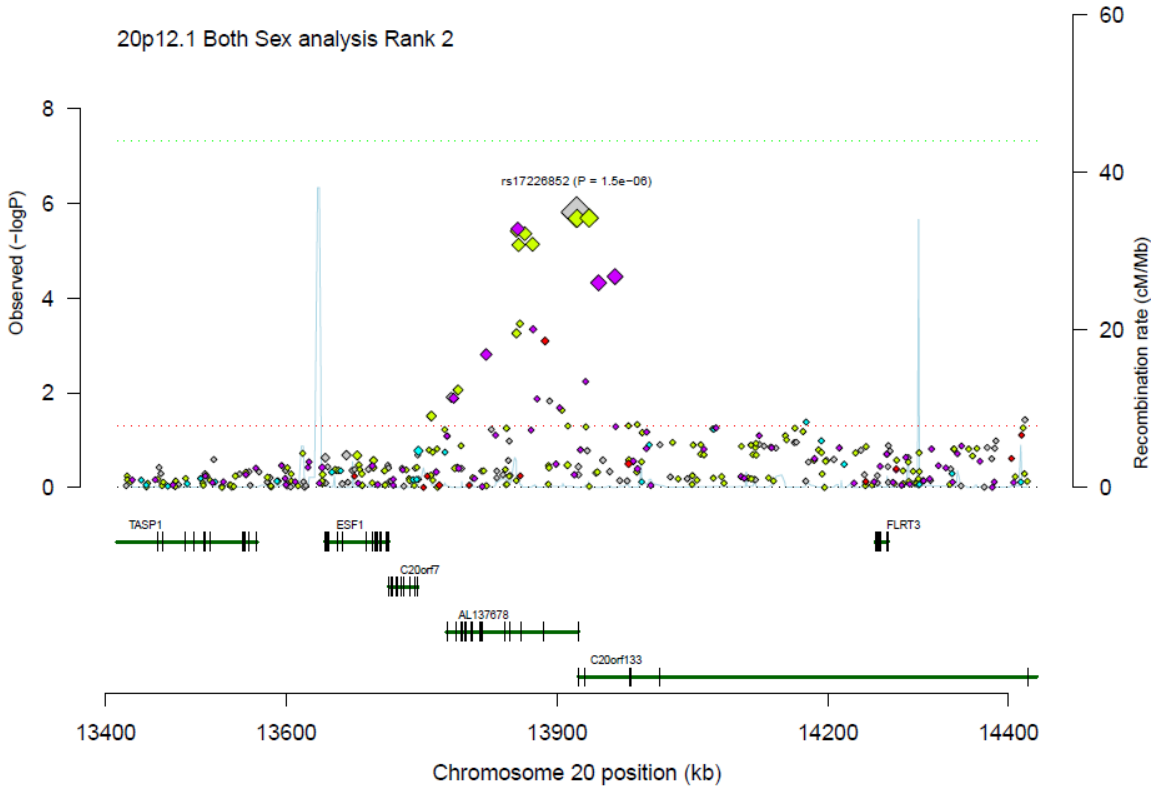




rs2638463

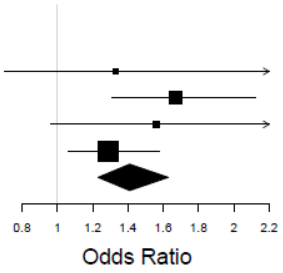
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	I	0.95	0.55	0.281	0.294	1.14	0.74	1.78
I370	I	0.91	0.21	0.302	0.308	1.10	0.95	1.28
I610	G	0.9	0.036	0.315	0.381	1.36	1.02	1.82
A6.0	I	1.02	8.7e−06	0.296	0.338	1.30	1.16	1.45
All	**-**	**0.97**	**2.9e−06**	**0.299**	**0.330**	**1.22**	**1.12**	**1.33**

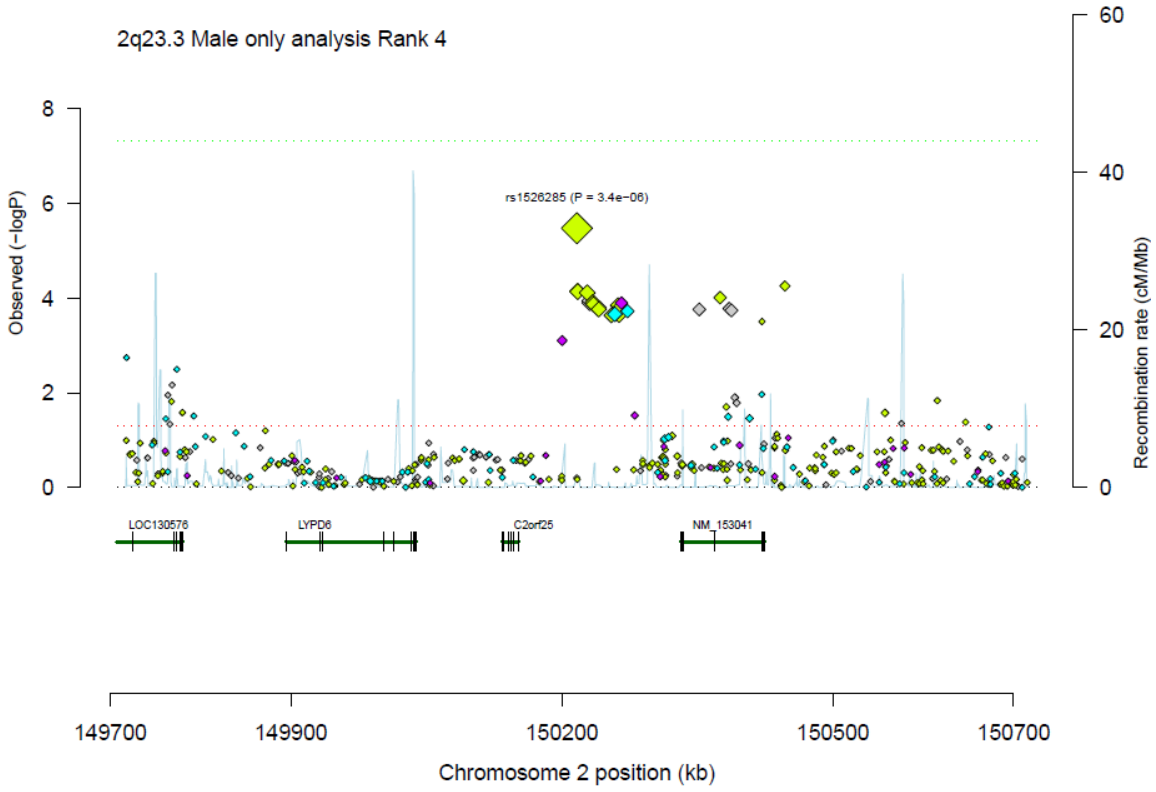




rs17226852

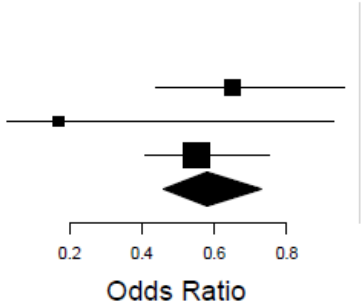
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	I	0.98	0.39	0.080	0.1020	1.33	0.70	2.55
I370	I	0.95	3e−05	0.070	0.1080	1.67	1.31	2.12
I610	I	1.01	0.072	0.060	0.0860	1.56	0.96	2.55
A6.0	I	0.96	0.013	0.069	0.0900	1.29	1.06	1.58
All	**-**	**0.96**	**1.5e−06**	**0.069**	**0.0956**	**1.41**	**1.23**	**1.63**

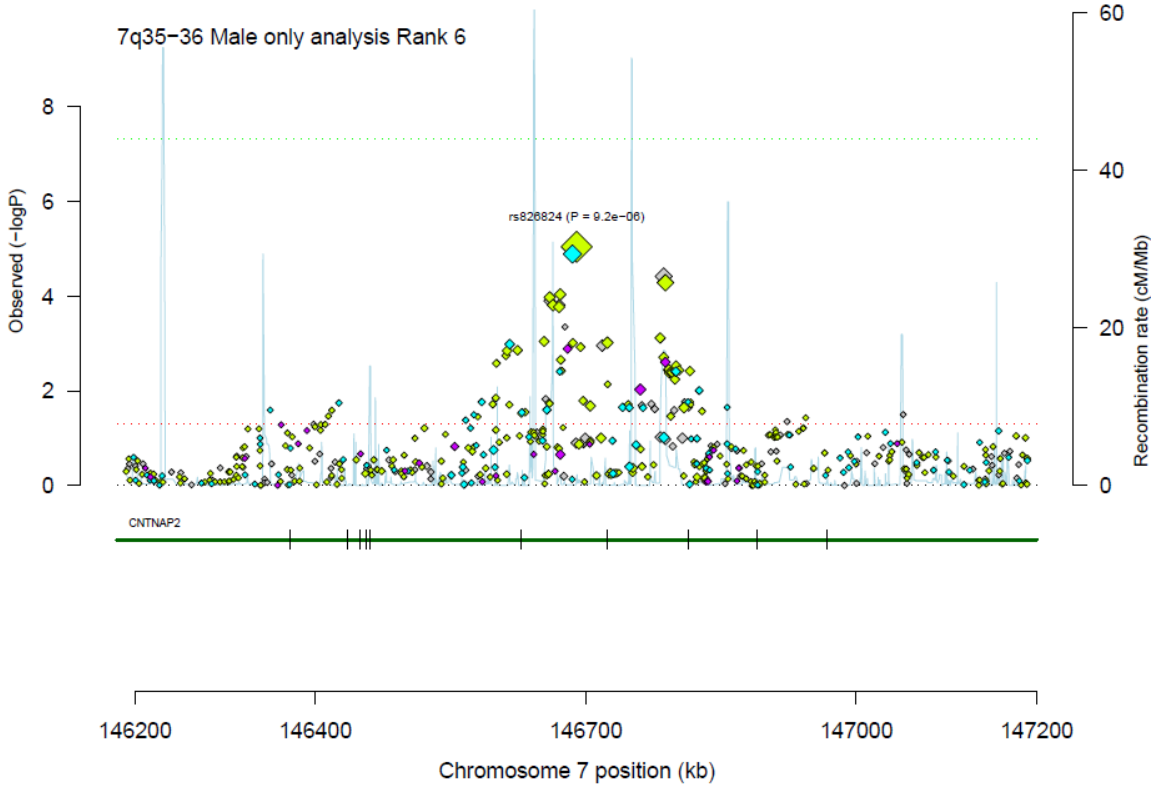




rs1526285

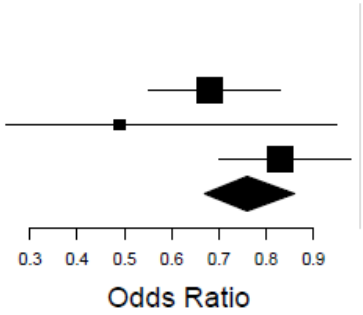
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I370	I	0.9	0.031	0.102	0.0730	0.65	0.44	0.96
I610	I	0.92	0.041	0.095	0.0330	0.17	0.03	0.93
A6.0	G	0.99	0.00016	0.111	0.0680	0.55	0.41	0.75
All	**-**	**0.95**	**3.4e−06**	**0.106**	**0.0683**	**0.58**	**0.46**	**0.73**

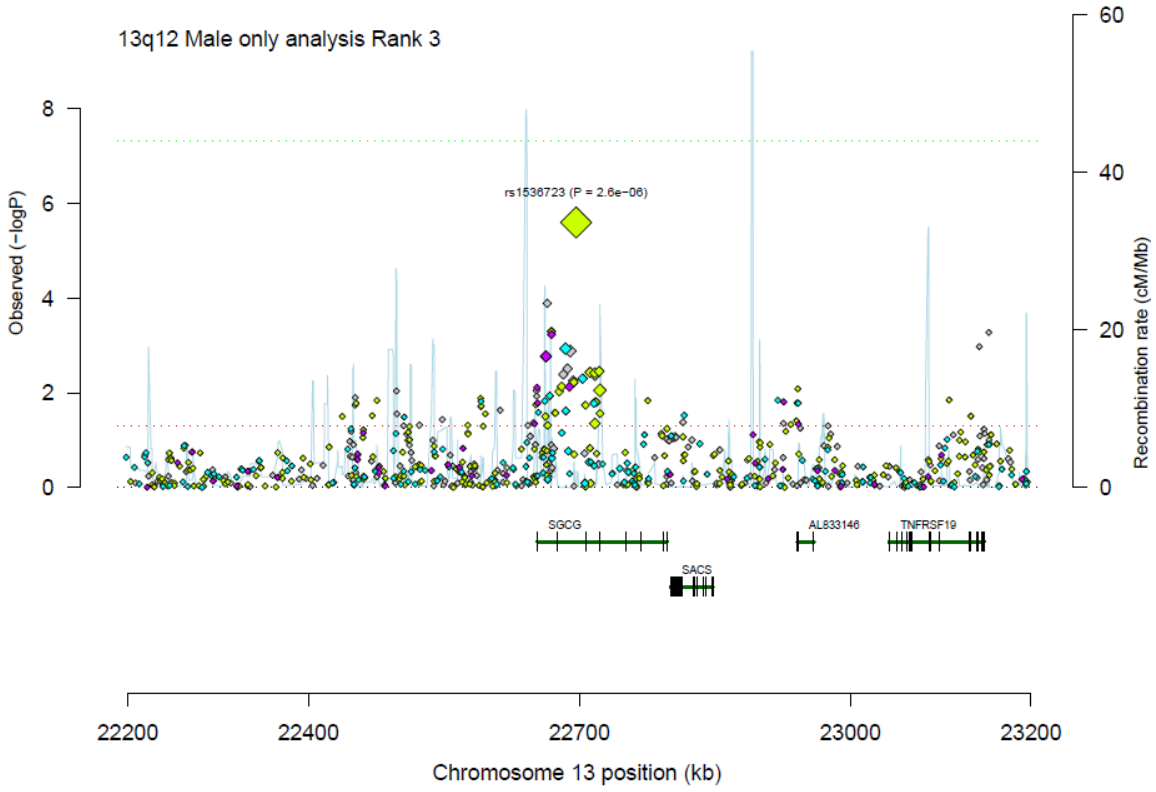




rs826824

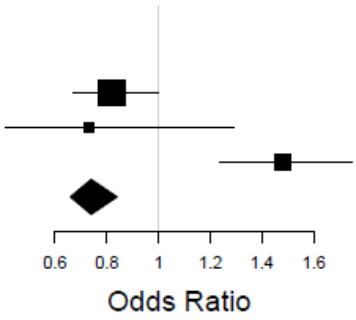
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I370	I	1	0.00017	0.482	0.397	0.68	0.55	0.83
I610	I	0.89	0.036	0.424	0.290	0.49	0.25	0.95
A6.0	G	0.97	0.032	0.477	0.432	0.83	0.70	0.98
All	**-**	**0.98**	**9.2e−06**	**0.475**	**0.412**	**0.76**	**0.67**	**0.86**

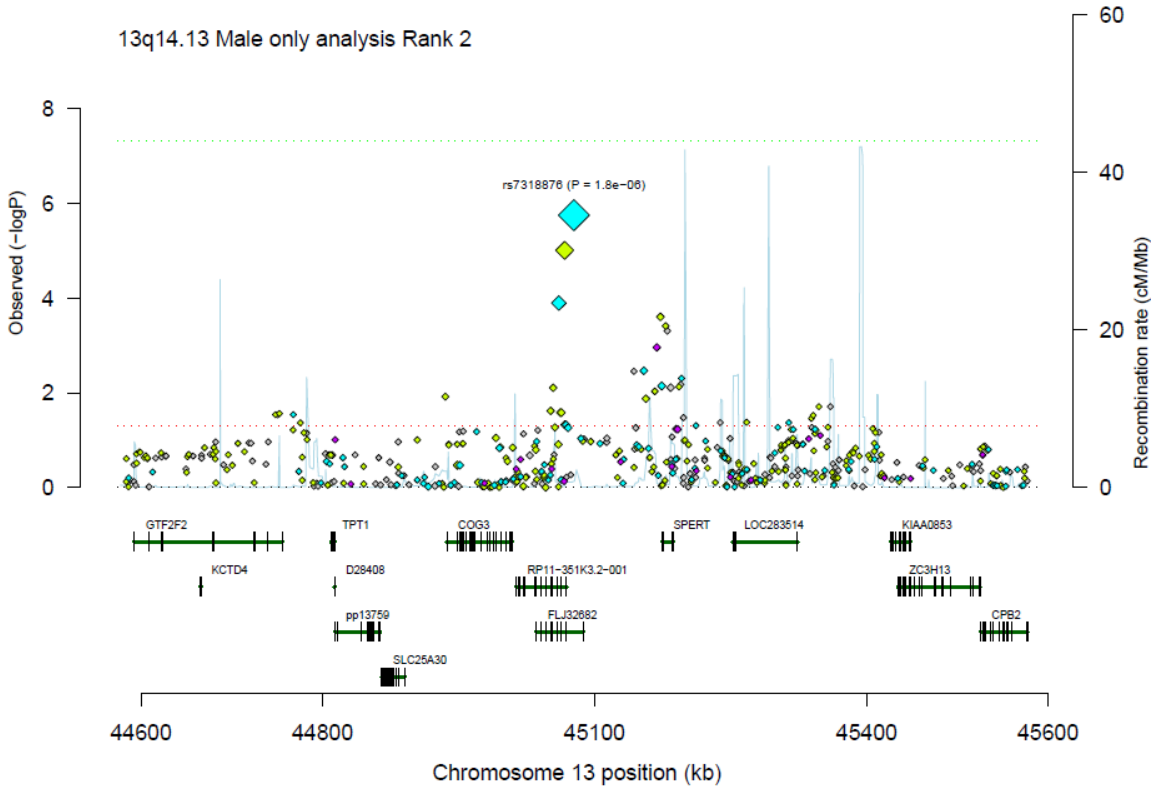




rs1536723

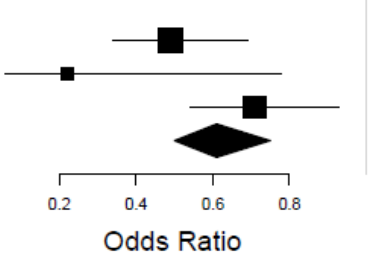
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I370	G	0.96	0.052	0.463	0.424	0.82	0.67	1.00
I610	I	1.03	0.28	0.481	0.408	0.73	0.41	1.29
A6.0	I	0.95	9.9e−06	0.496	0.583	1.48	1.24	1.75
All	**-**	**0.96**	**2.6e−06**	**0.482**	**0.515**	**0.74**	**0.66**	**0.84**

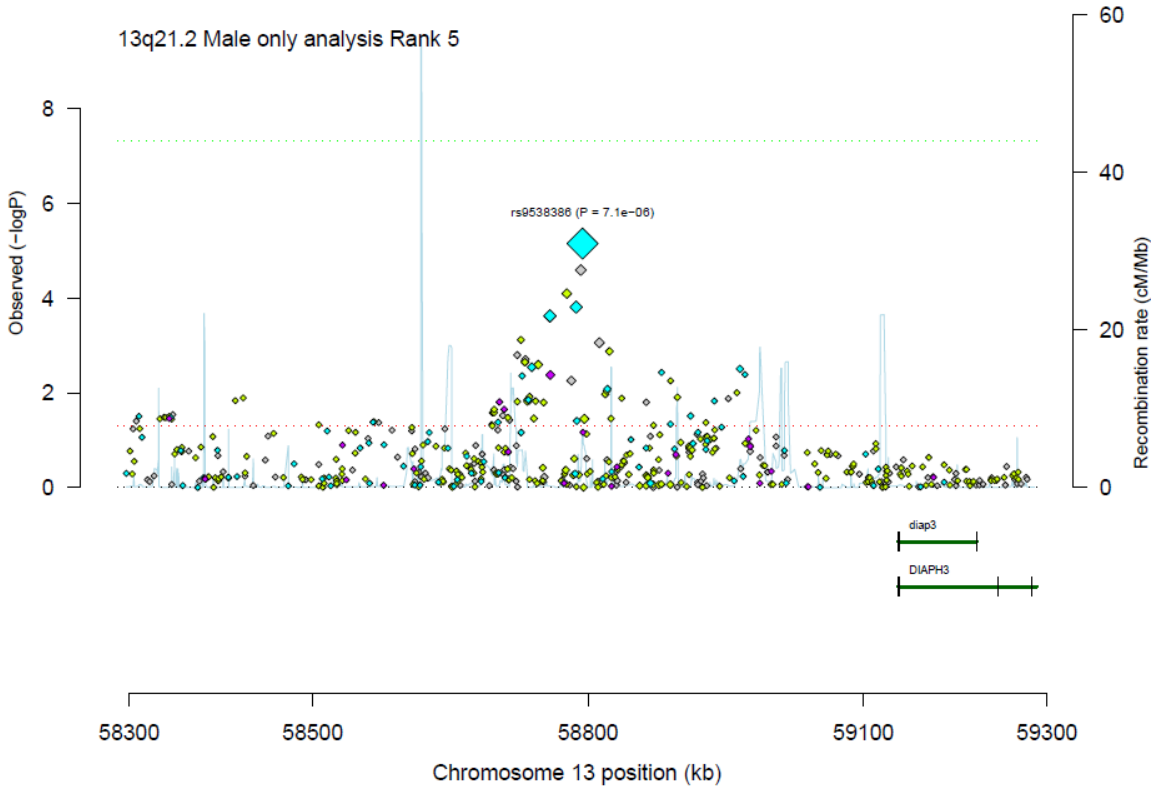




rs7318876

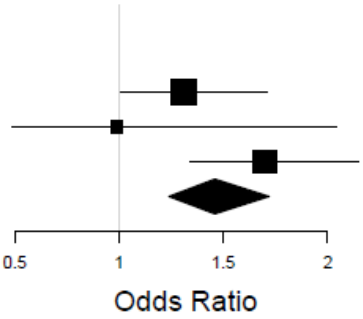
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I370	G	0.97	6.2e−05	0.133	0.0750	0.49	0.34	0.69
I610	G	0.91	0.019	0.148	0.0530	0.22	0.06	0.78
A6.0	I	0.99	0.012	0.119	0.0990	0.71	0.54	0.93
All	**-**	**0.98**	**1.8e−06**	**0.127**	**0.0879**	**0.61**	**0.50**	**0.75**

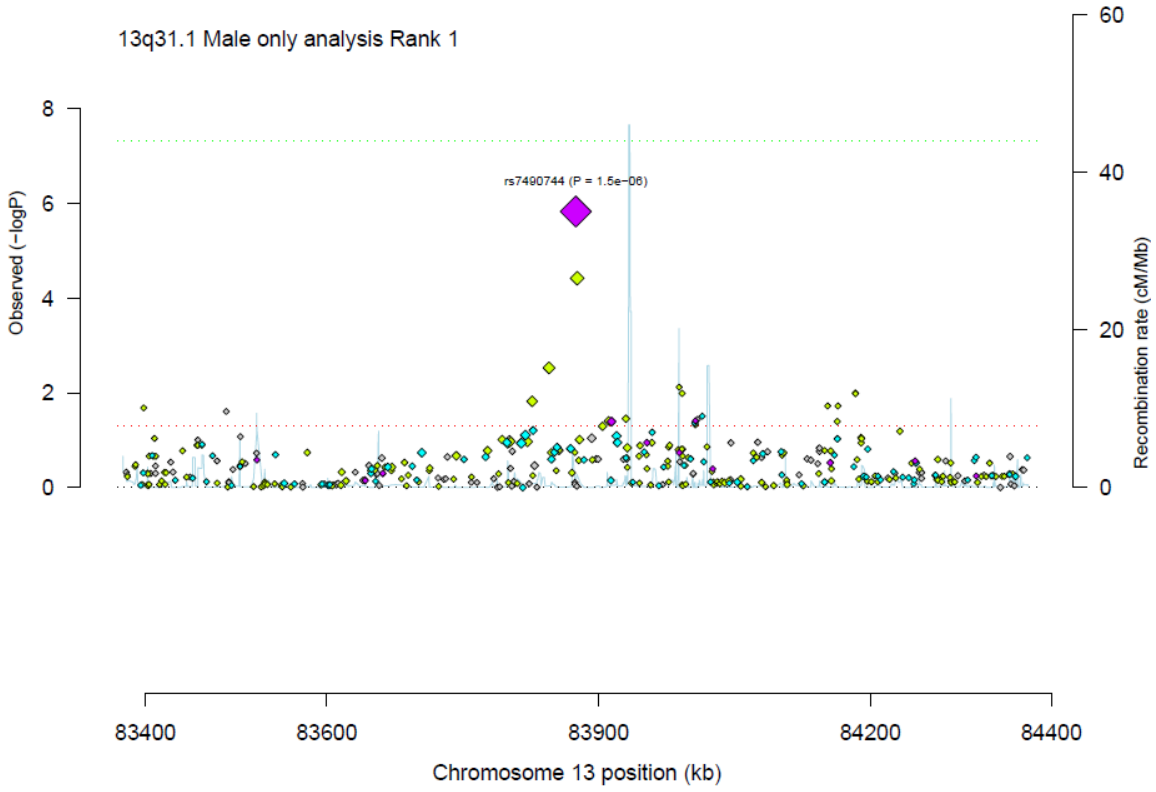




rs9538386

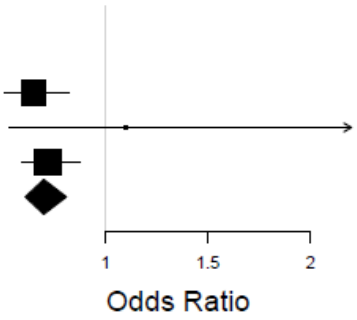
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I370	G	0.97	0.043	0.160	0.183	1.31	1.01	1.71
I610	G	1.05	0.99	0.186	0.184	0.99	0.49	2.04
A6.0	I	0.88	1e−05	0.154	0.204	1.70	1.34	2.15
All	**-**	**0.92**	**7.1e−06**	**0.159**	**0.195**	**1.46**	**1.24**	**1.72**

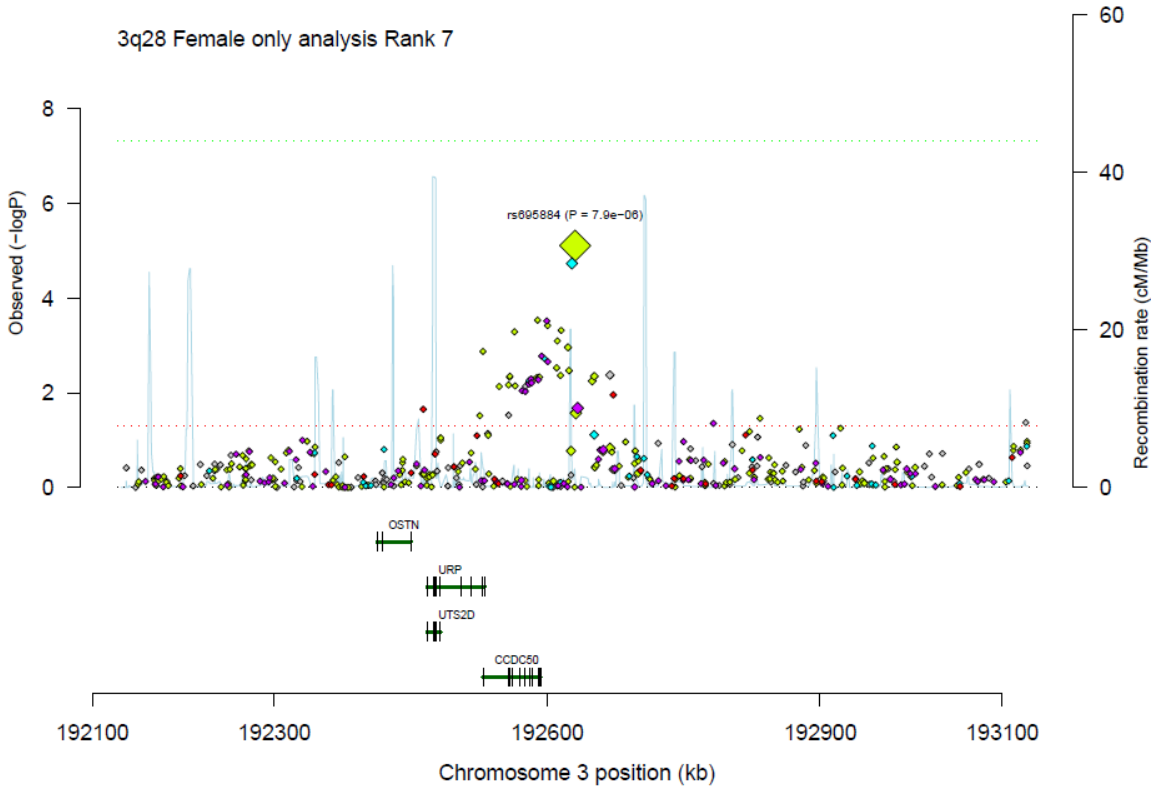




rs7490744

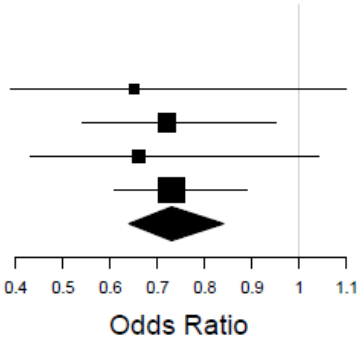
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I370	G	1.03	0.00031	0.272	0.202	0.65	0.51	0.82
I610	G	0.95	0.8	0.205	0.224	1.10	0.53	2.27
A6.0	G	1	0.0011	0.272	0.202	0.72	0.59	0.88
All	**-**	**1.01**	**1.5e−06**	**0.267**	**0.203**	**0.70**	**0.61**	**0.81**

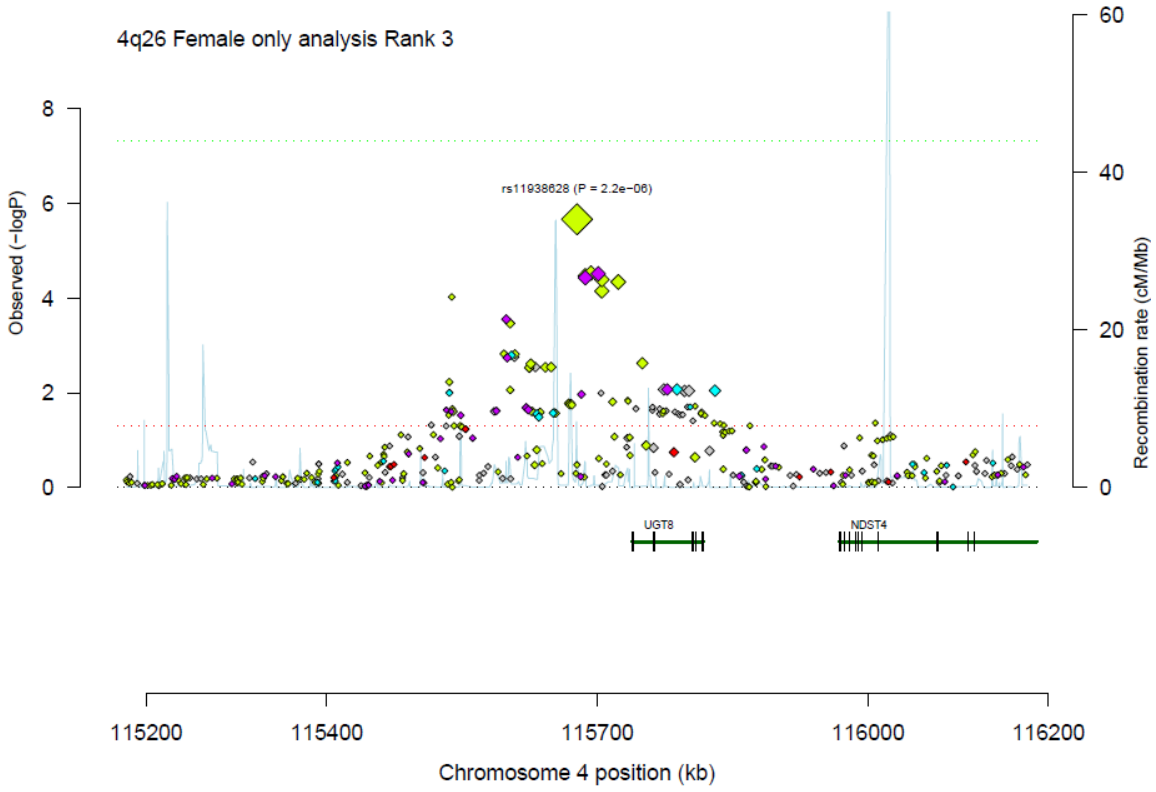




rs695884

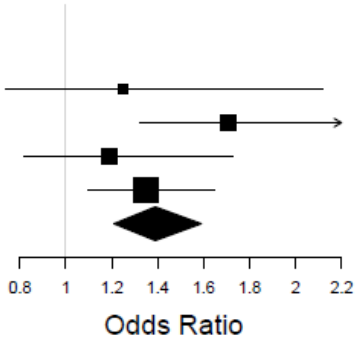
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	I	0.99	0.11	0.213	0.163	0.65	0.39	1.10
I370	I	0.95	0.019	0.163	0.143	0.72	0.54	0.95
I610	G	0.98	0.071	0.174	0.128	0.66	0.43	1.04
A6.0	I	1	0.0017	0.200	0.154	0.73	0.61	0.89
All	**-**	**0.99**	**7.9e-06**	**0.185**	**0.149**	**0.73**	**0.64**	**0.84**

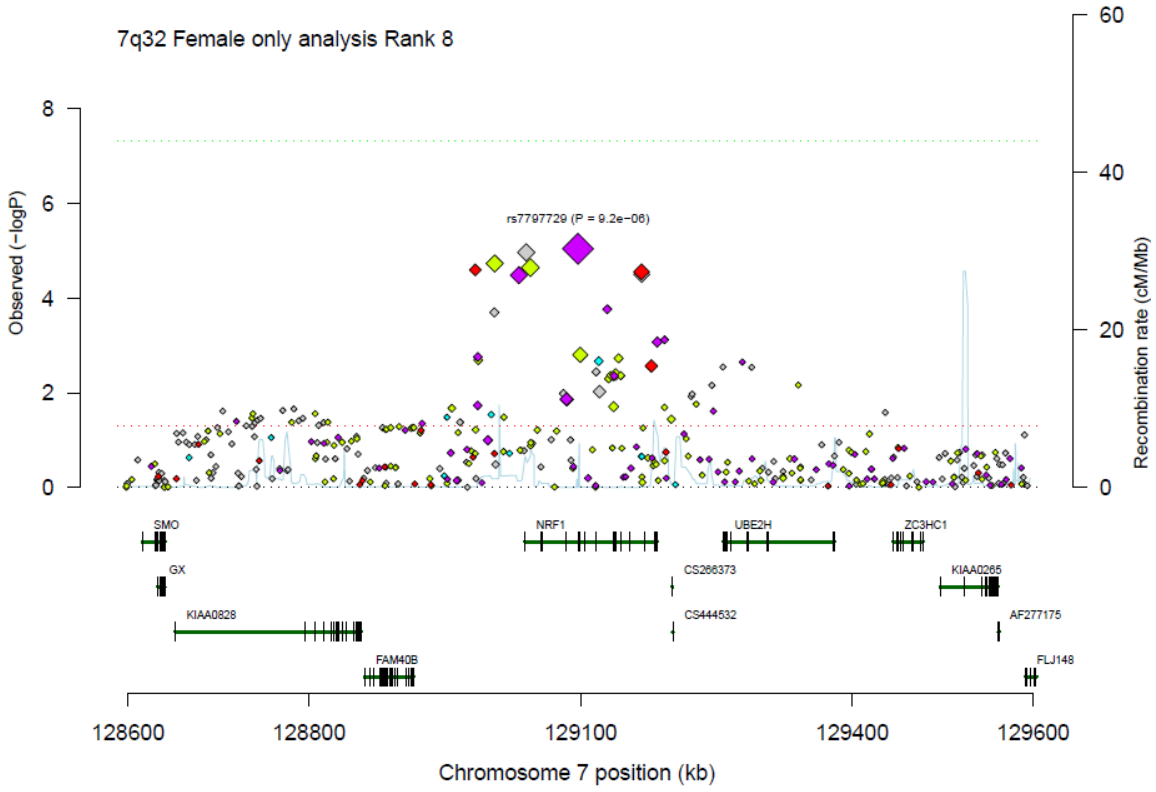




rs11938628

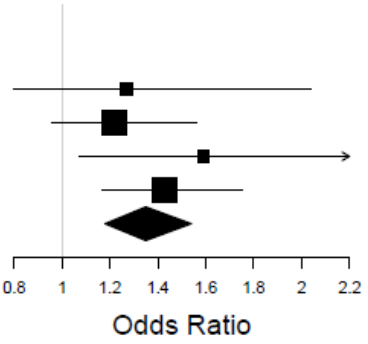
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	I	0.97	0.4	0.158	0.188	1.25	0.74	2.12
I370	G	0.95	4.4e−05	0.142	0.215	1.71	1.32	2.21
I610	I	1.04	0.36	0.176	0.202	1.19	0.82	1.73
A6.0	I	0.98	0.0039	0.145	0.182	1.35	1.10	1.65
All	**-**	**0.97**	**2.2e−06**	**0.150**	**0.193**	**1.39**	**1.21**	**1.59**

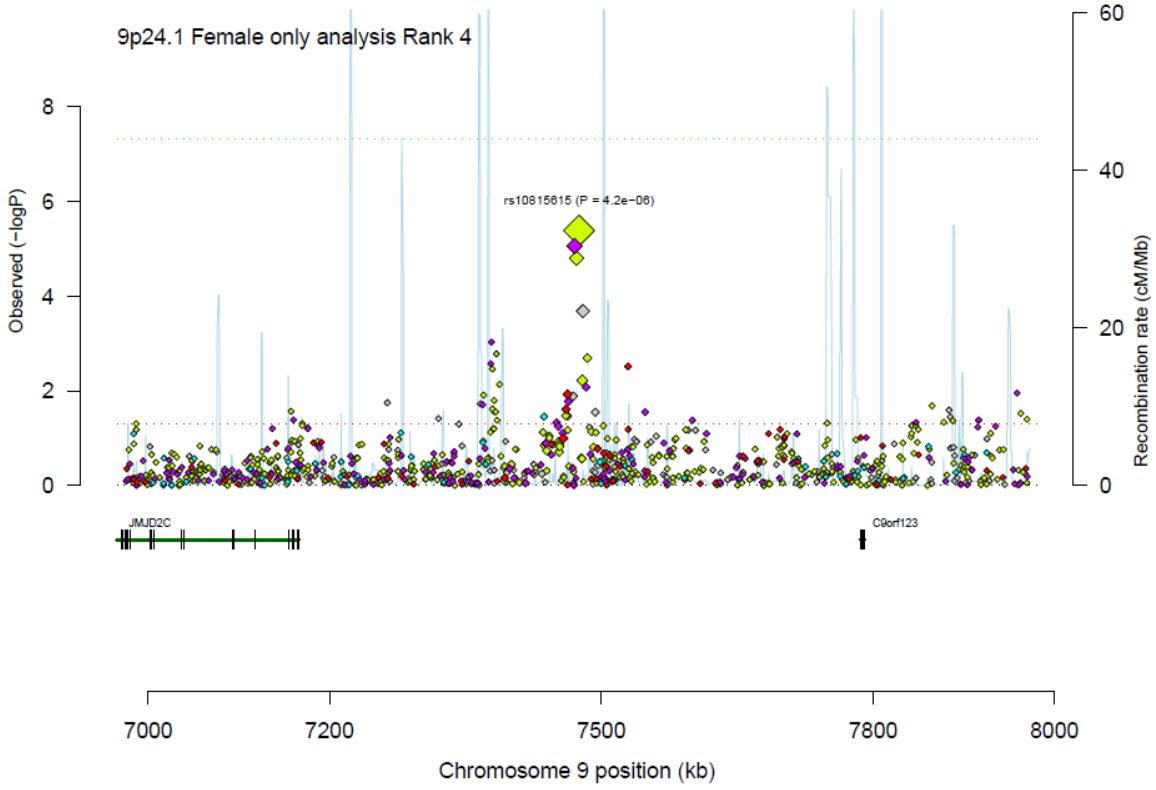




rs7797729

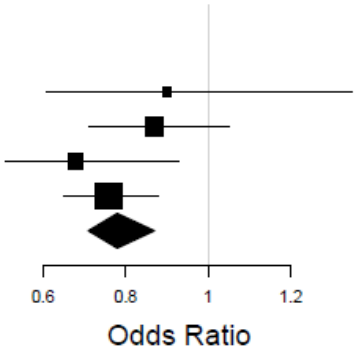
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	G	1.05	0.31	0.177	0.196	1.27	0.80	2.04
I370	G	1.02	0.1	0.160	0.197	1.22	0.96	1.56
I610	I	0.98	0.02	0.150	0.214	1.59	1.07	2.35
A6.0	G	1.04	5e−04	0.132	0.181	1.43	1.17	1.75
All	**-**	**1.03**	**9.2e−06**	**0.150**	**0.189**	**1.35**	**1.18**	**1.54**

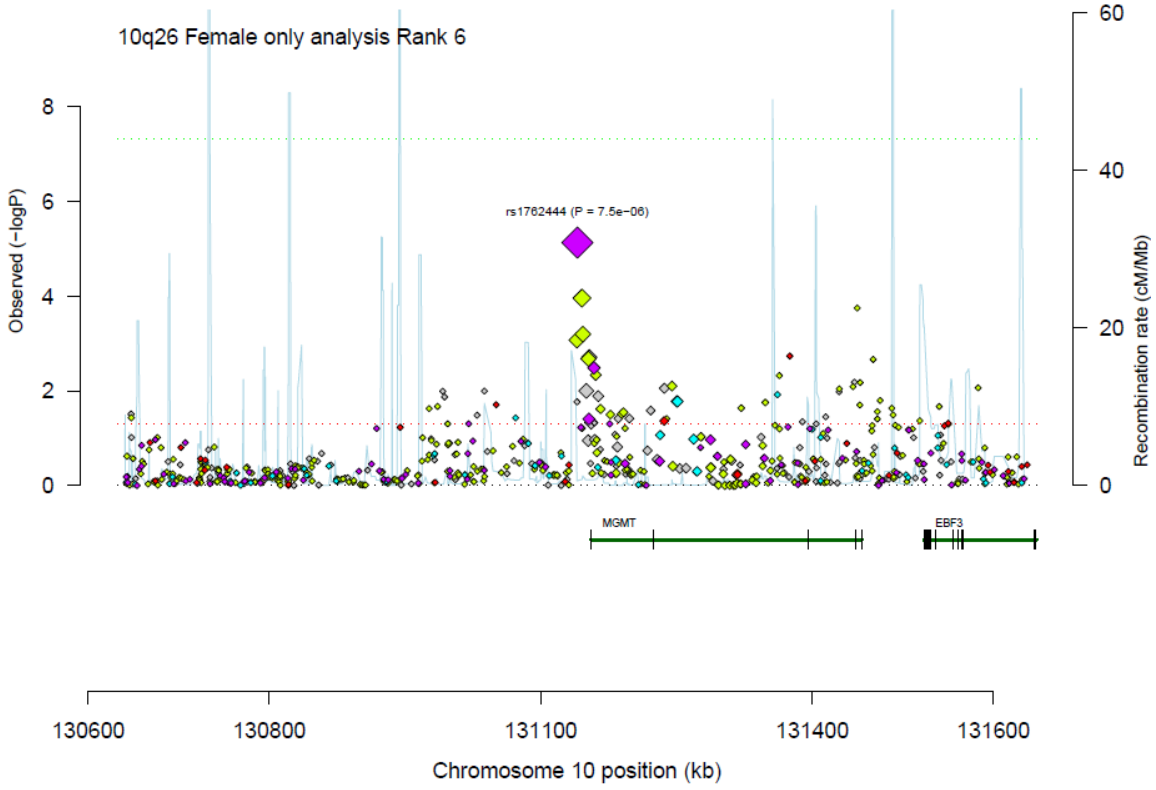




rs10815615

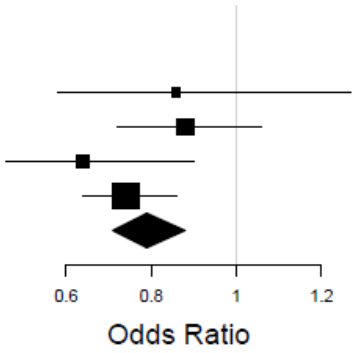
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	I	0.93	0.62	0.462	0.432	0.90	0.61	1.35
I370	G	0.97	0.14	0.452	0.419	0.87	0.71	1.05
I610	I	1.04	0.014	0.476	0.389	0.68	0.51	0.93
A6.0	I	0.95	0.00035	0.507	0.436	0.76	0.65	0.88
All	**-**	**0.97**	**4.2e−06**	**0.478**	**0.427**	**0.78**	**0.71**	**0.87**

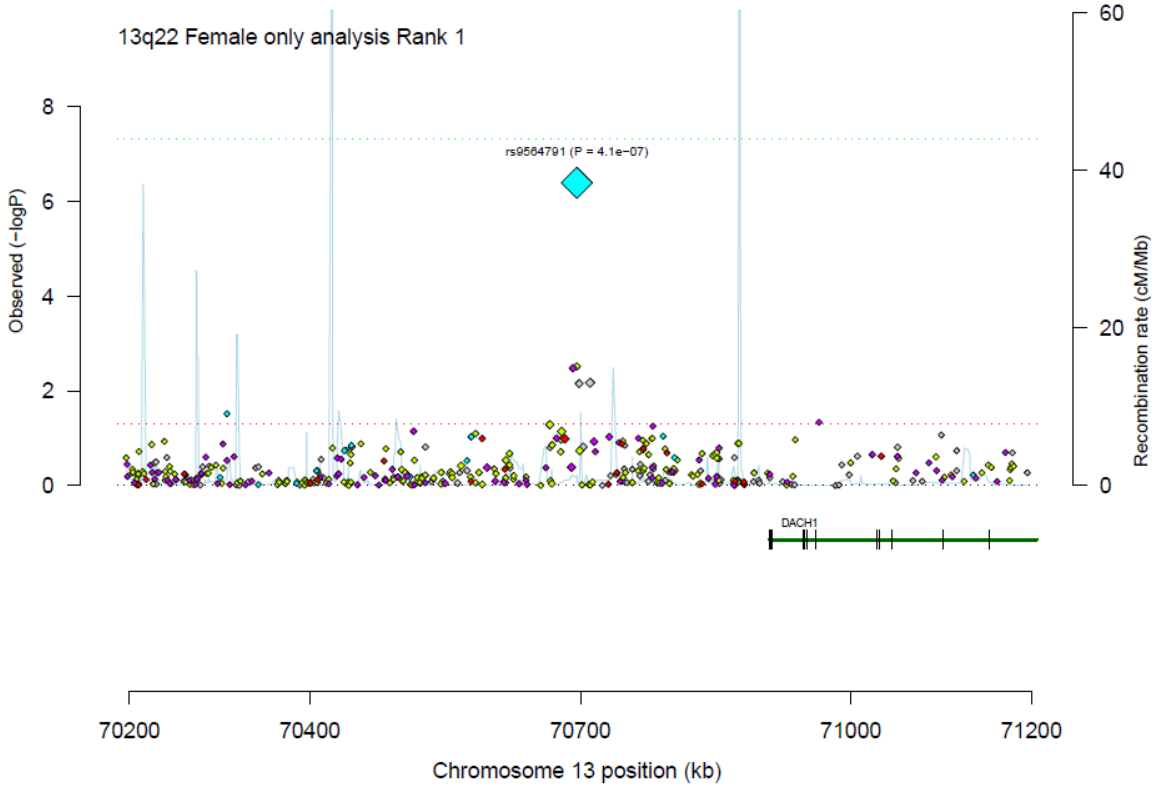




rs1762444

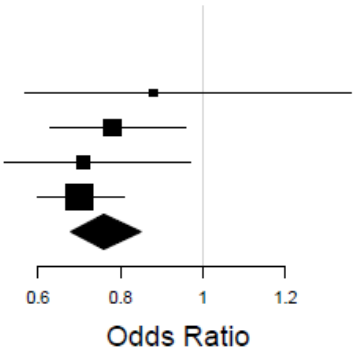
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	G	1	0.44	0.416	0.387	0.86	0.58	1.27
I370	G	1.02	0.17	0.392	0.371	0.88	0.72	1.06
I610	I	0.98	0.0096	0.389	0.294	0.64	0.46	0.90
A6.0	G	1.01	0.00012	0.419	0.350	0.74	0.64	0.86
All	**-**	**1.01**	**7.5e-06**	**0.405**	**0.353**	**0.79**	**0.71**	**0.88**

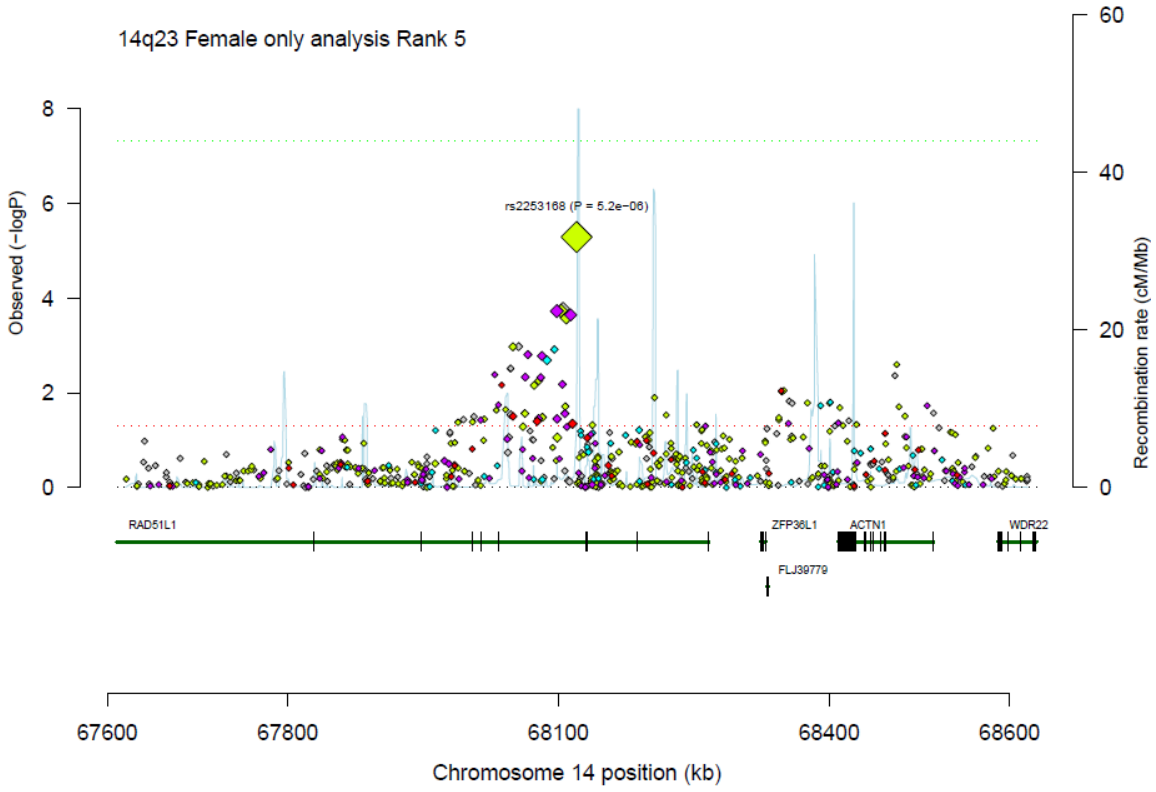




rs9564791

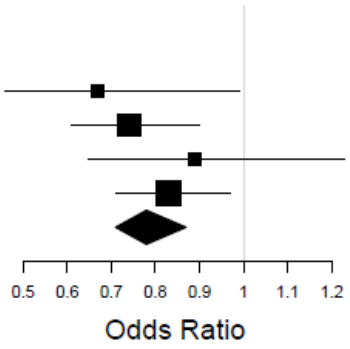
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	I	0.82	0.58	0.401	0.381	0.88	0.57	1.36
I370	G	0.87	0.017	0.433	0.396	0.78	0.63	0.96
I610	G	1.03	0.033	0.407	0.332	0.71	0.52	0.97
A6.0	I	1.01	2.7e−06	0.446	0.370	0.70	0.60	0.81
All	**-**	**0.95**	**4.1e−07**	**0.430**	**0.374**	**0.76**	**0.68**	**0.85**

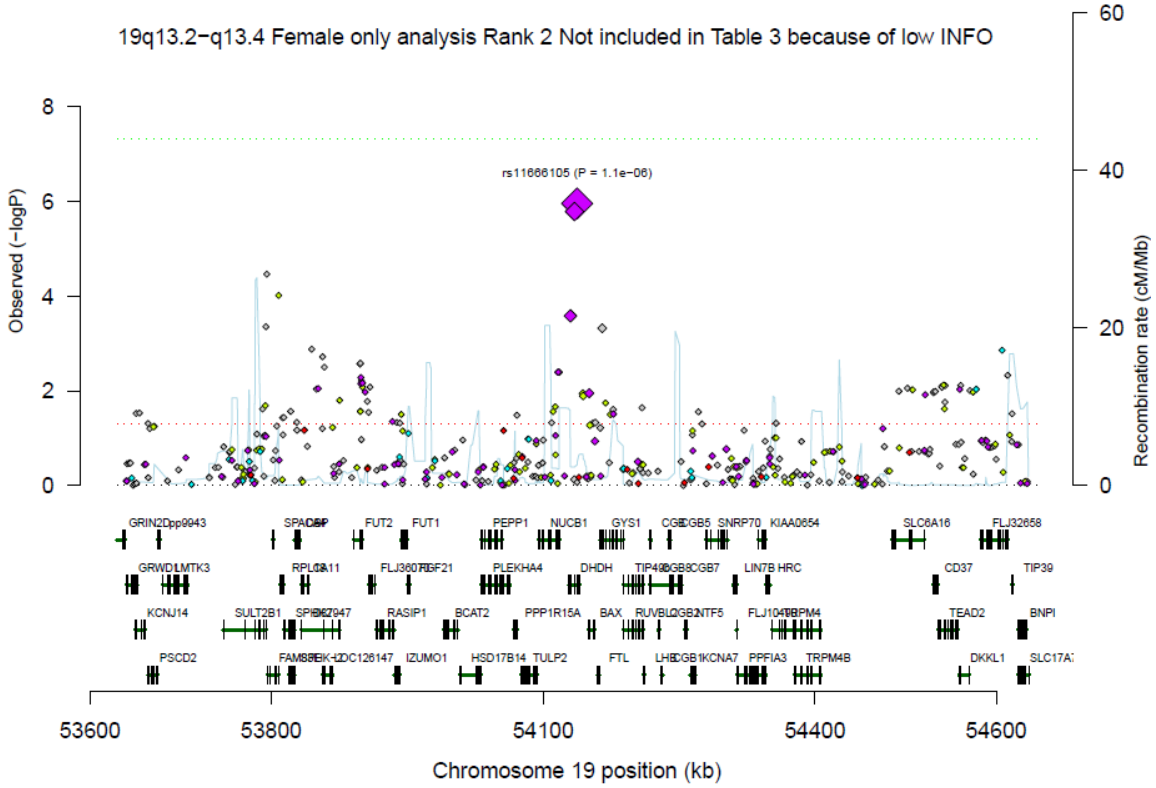




rs2253168

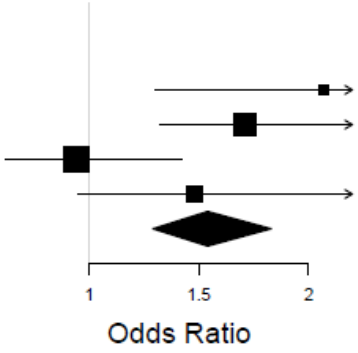
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	I	1	0.043	0.454	0.354	0.67	0.46	0.99
I370	G	1	0.0023	0.429	0.368	0.74	0.61	0.90
I610	I	0.97	0.48	0.394	0.363	0.89	0.65	1.23
A6.0	I	0.95	0.018	0.433	0.378	0.83	0.71	0.97
All	**-**	**0.97**	**5.2e−06**	**0.428**	**0.373**	**0.78**	**0.71**	**0.87**

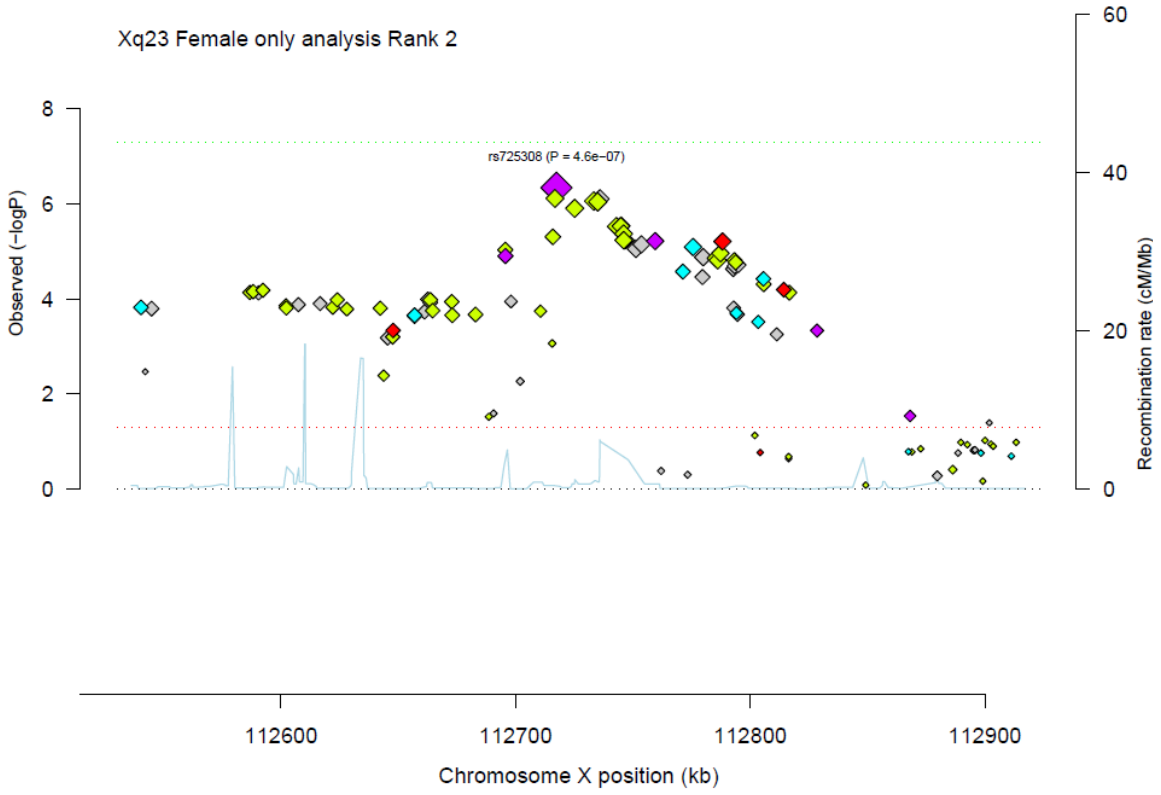




rs11666105

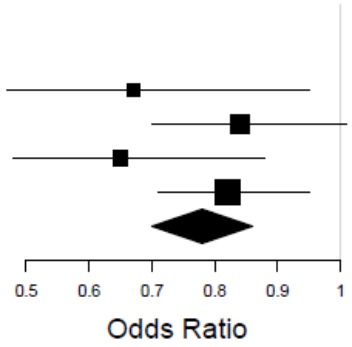
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	G	1.01	0.0021	0.143	0.250	2.07	1.30	3.30
I370	G	0.98	4.4e−05	0.138	0.209	1.71	1.32	2.22
I610	I	0.97	0.77	0.169	0.164	0.94	0.62	1.42
A6.0	G	0.19	0.084	0.175	0.185	1.48	0.95	2.31
All	**−**	**0.59**	**1.1e−06**	**0.157**	**0.193**	**1.54**	**1.29**	**1.83**

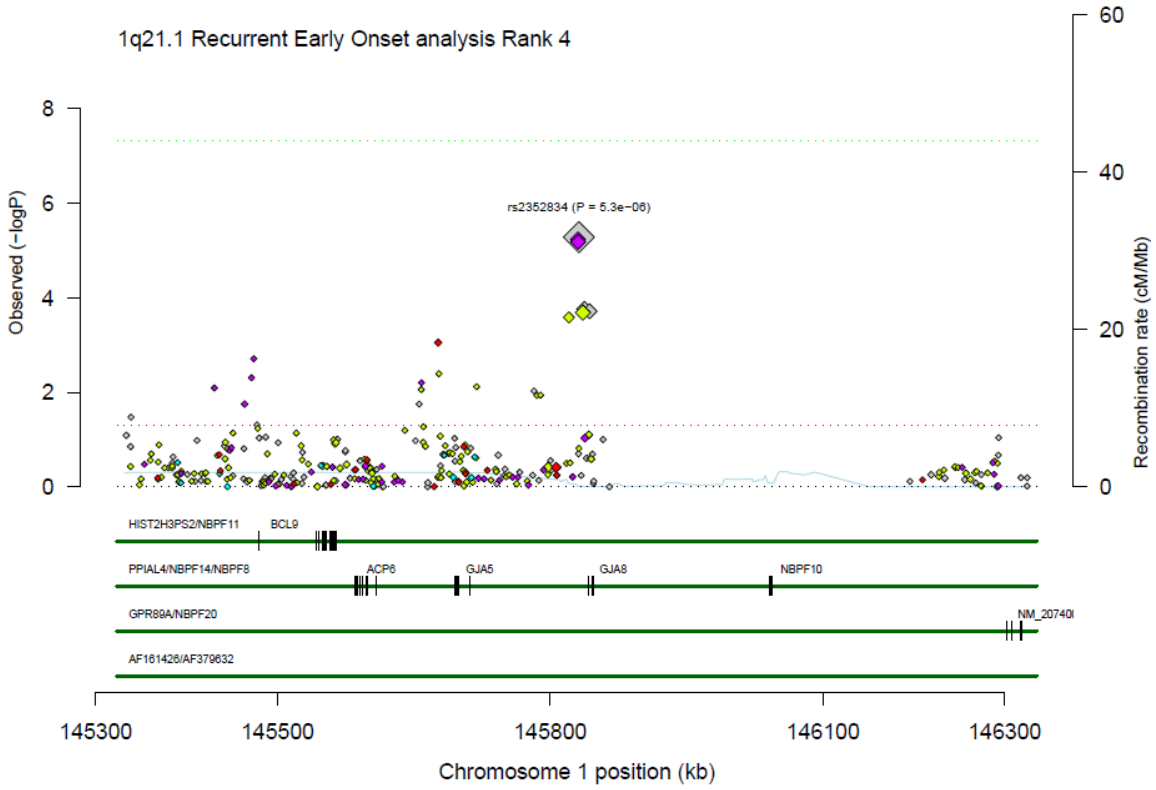




rs725308

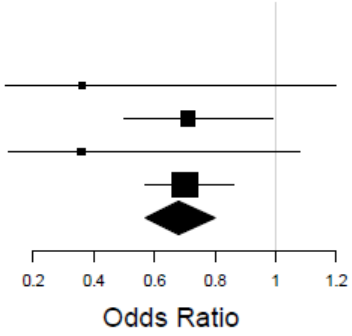
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	G	1.04	0.027	0.492	0.393	0.67	0.47	0.95
I370	G	1.02	0.068	0.475	0.439	0.84	0.70	1.01
I610	G	0.98	0.0055	0.486	0.386	0.65	0.48	0.88
A6.0	I	1	0.0082	0.458	0.407	0.82	0.71	0.95
All	**-**	**1.01**	**4.6e−07**	**0.472**	**0.413**	**0.78**	**0.70**	**0.86**

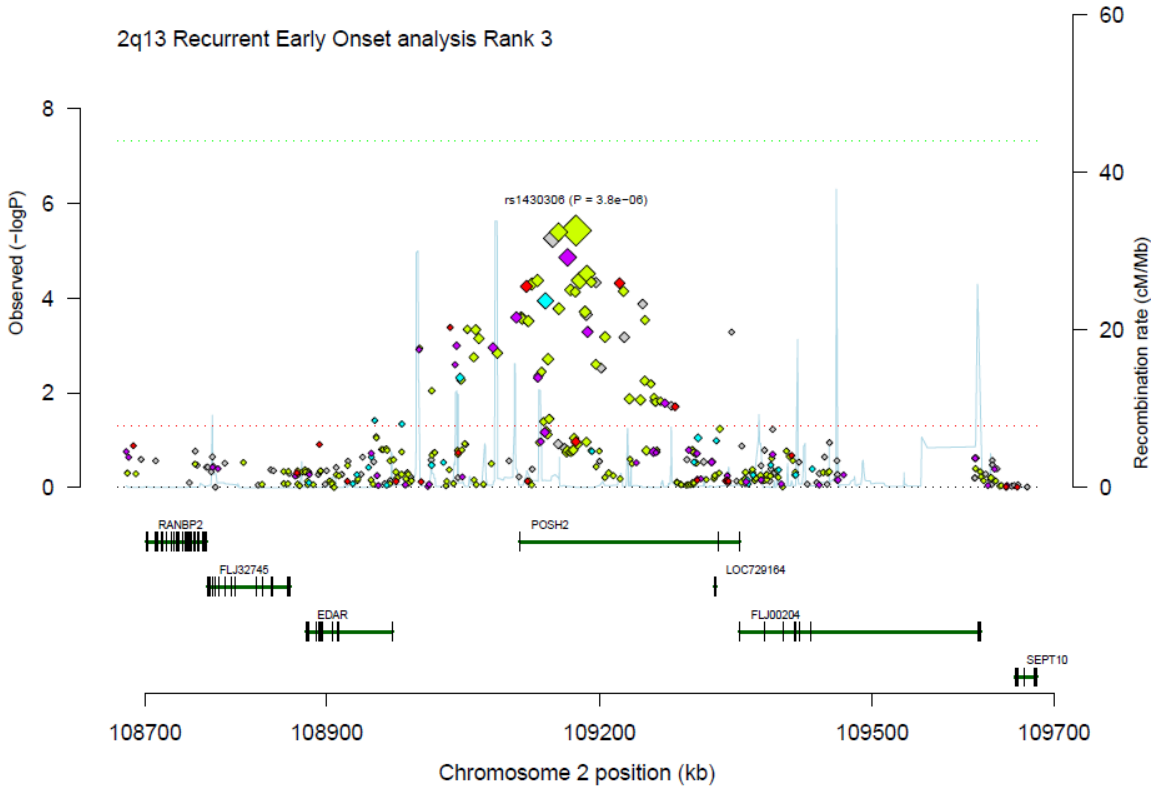




rs2352834

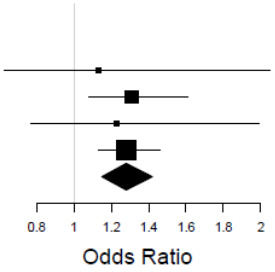
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	I	1.05	0.096	0.136	0.0480	0.36	0.11	1.20
I370	I	0.99	0.043	0.118	0.0890	0.71	0.50	0.99
I610	I	1.01	0.069	0.116	0.0450	0.36	0.12	1.08
A6.0	I	0.98	0.00088	0.129	0.0980	0.70	0.57	0.86
All	**-**	**0.99**	**7.9e-06**	**0.124**	**0.0925**	**0.68**	**0.57**	**0.80**

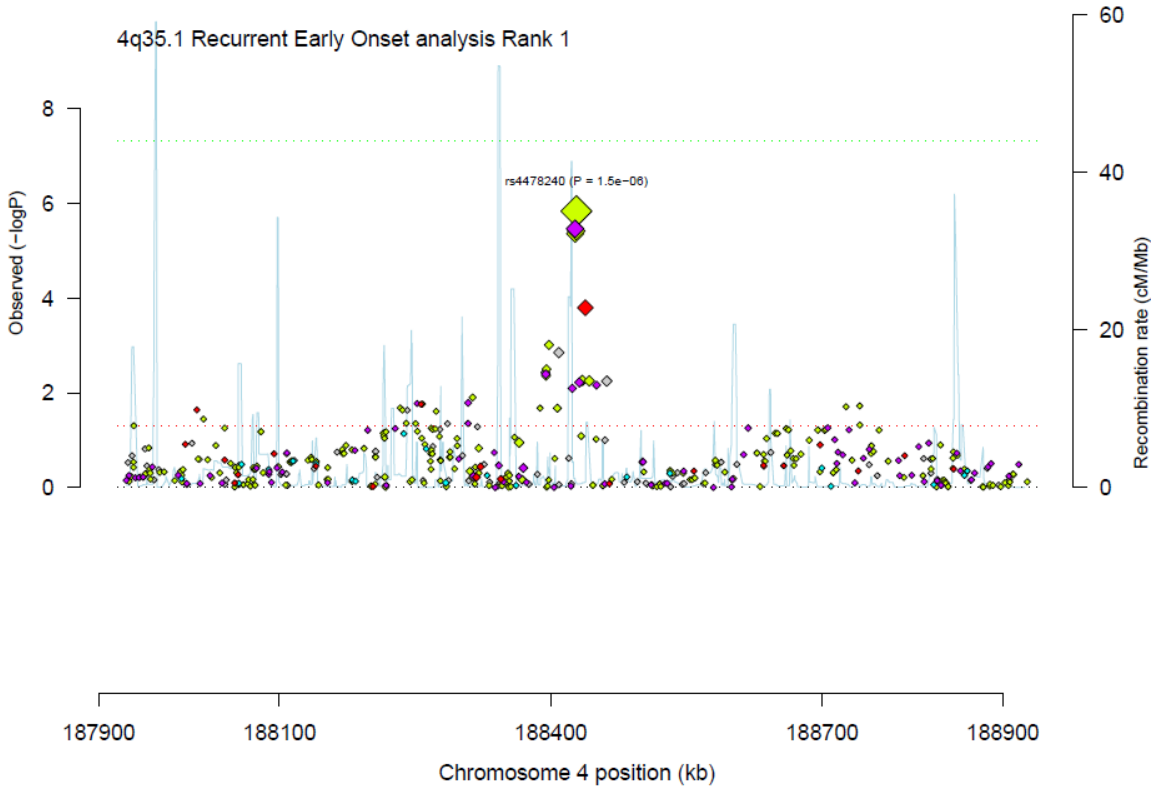




rs1430306

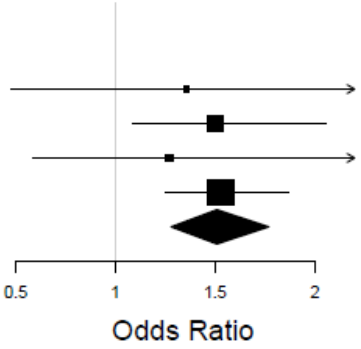
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	I	0.98	0.68	0.438	0.454	1.13	0.63	2.05
I370	I	0.98	0.0074	0.410	0.464	1.31	1.08	1.61
I610	G	0.95	0.39	0.423	0.456	1.23	0.77	1.99
A6.0	I	0.97	0.00019	0.402	0.460	1.28	1.13	1.46
All	**-**	**0.98**	**3.3e−06**	**0.410**	**0.461**	**1.28**	**1.15**	**1.42**

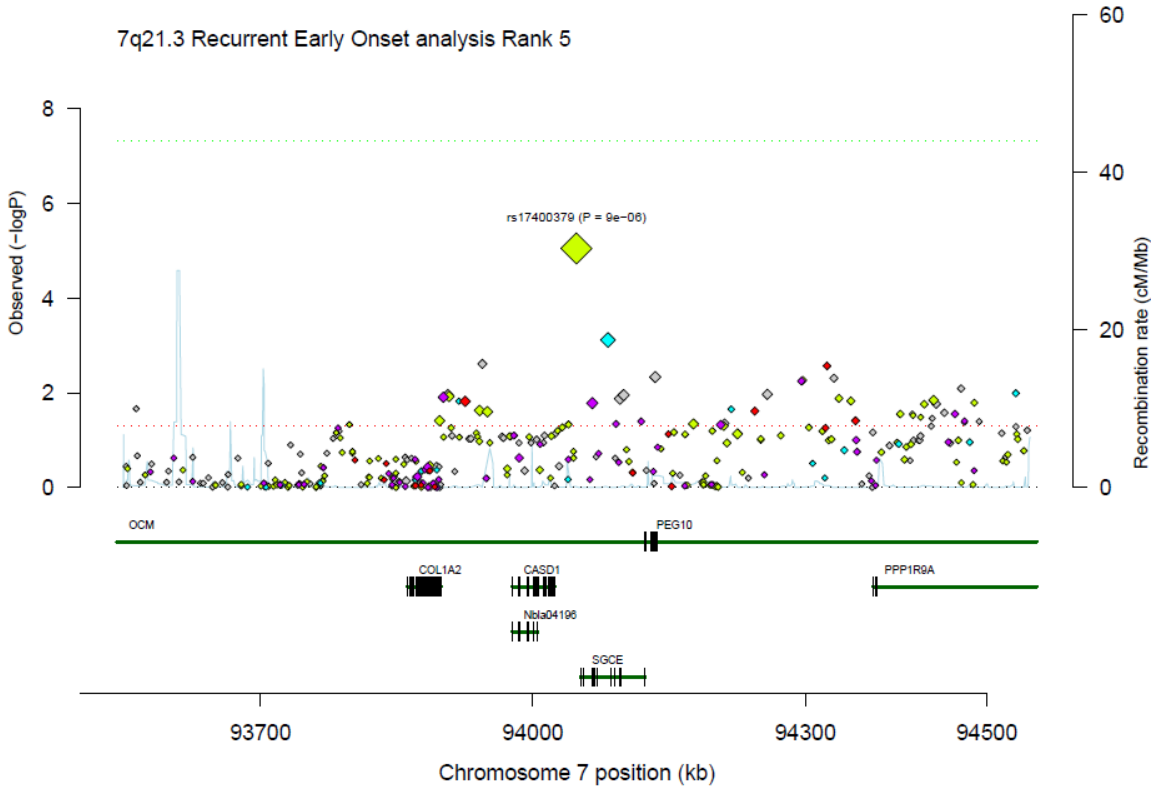




rs4478240

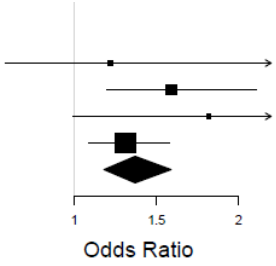
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	I	1.02	0.57	0.0800	0.092	1.36	0.48	3.83
I370	I	0.95	0.012	0.0880	0.122	1.50	1.09	2.06
I610	G	0.96	0.54	0.0960	0.109	1.27	0.59	2.72
A6.0	I	1.03	3.9e−05	0.0900	0.124	1.53	1.25	1.87
All	**-**	**0.99**	**6.8e−07**	**0.0893**	**0.122**	**1.51**	**1.28**	**1.77**

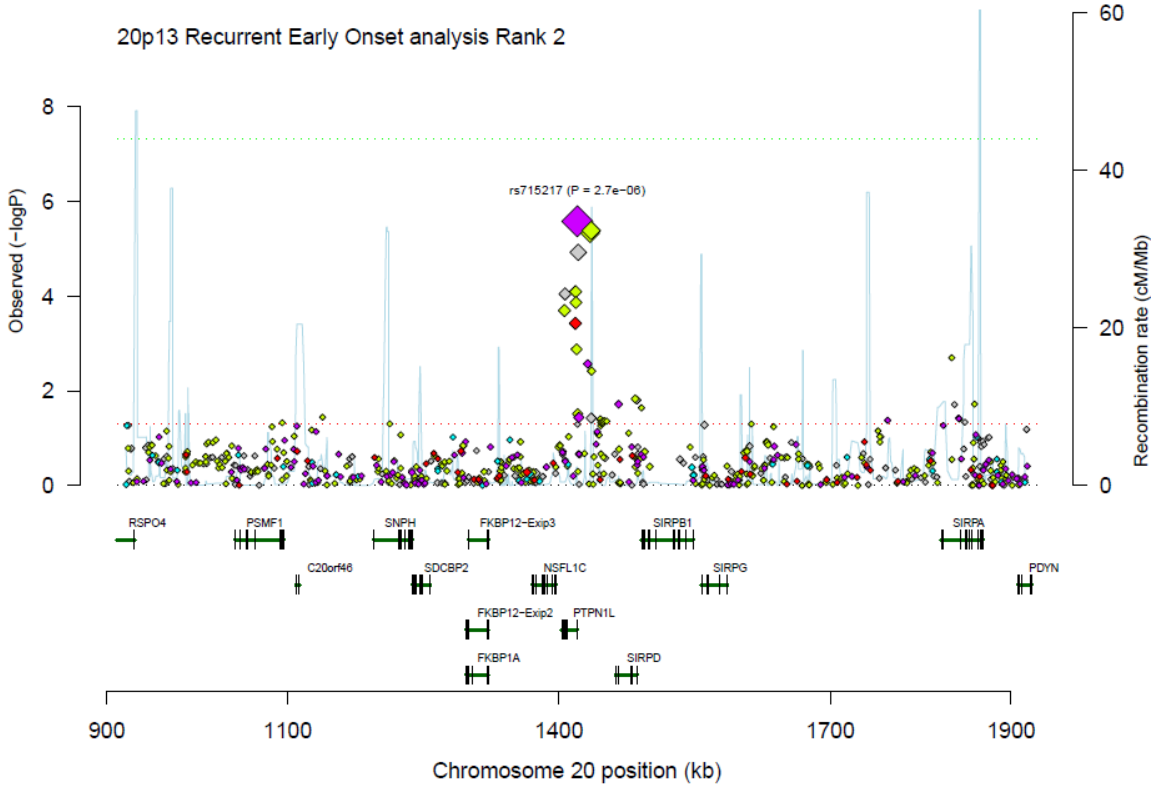




rs17400379

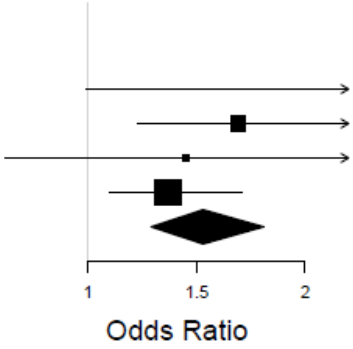
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	I	0.93	0.6	0.152	0.195	1.22	0.58	2.60
I370	G	0.83	0.0014	0.135	0.183	1.59	1.20	2.11
I610	I	0.96	0.053	0.133	0.211	1.82	0.99	3.36
A6.0	I	0.91	0.0047	0.130	0.164	1.31	1.09	1.58
All	**-**	**0.89**	**2.7e−05**	**0.134**	**0.171**	**1.37**	**1.18**	**1.59**

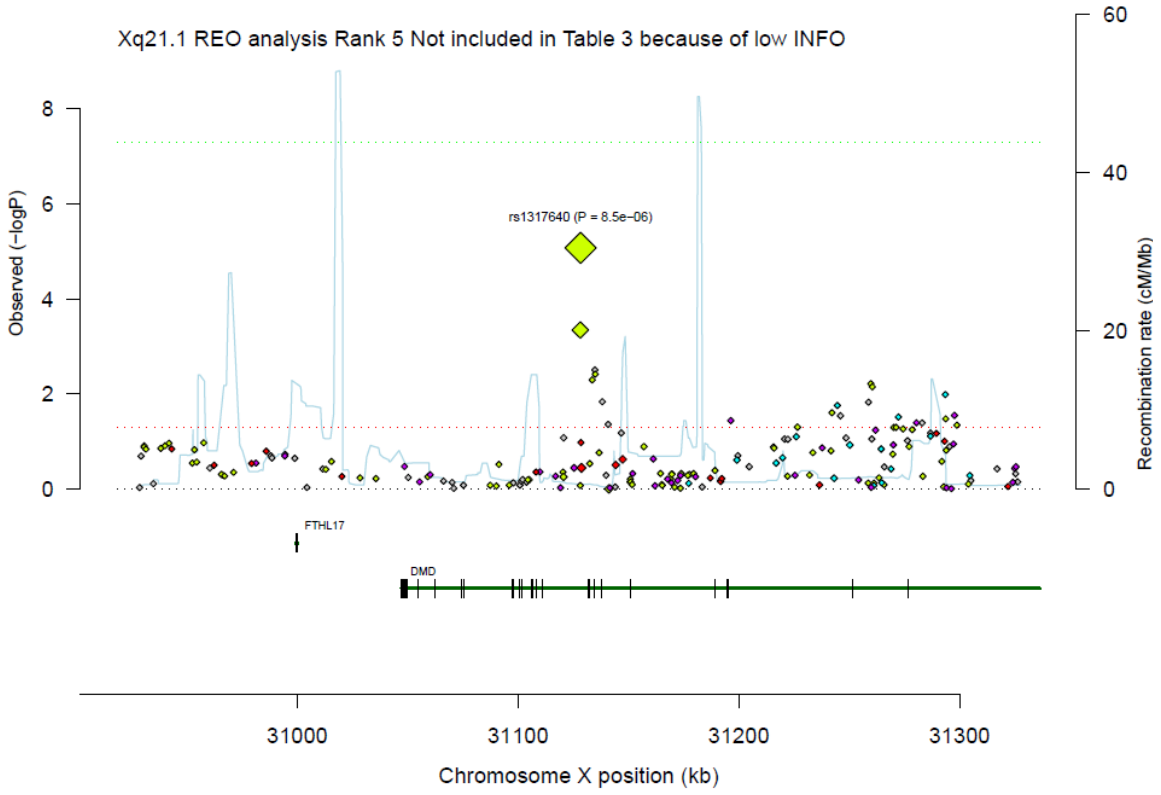




rs715217

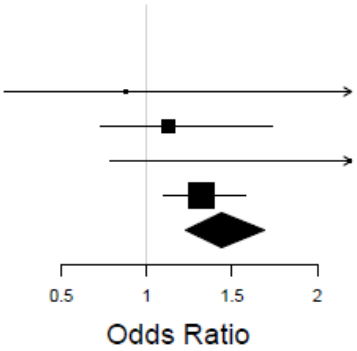
Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	G	1	0.054	0.0550	0.129	2.53	0.99	6.51
I370	I	1	0.0012	0.0760	0.121	1.69	1.23	2.32
I610	G	0.93	0.39	0.0740	0.091	1.45	0.62	3.41
A6.0	G	1	0.005	0.0830	0.103	1.37	1.10	1.71
All	**-**	**0.99**	**1.4e−06**	**0.0775**	**0.107**	**1.53**	**1.29**	**1.81**

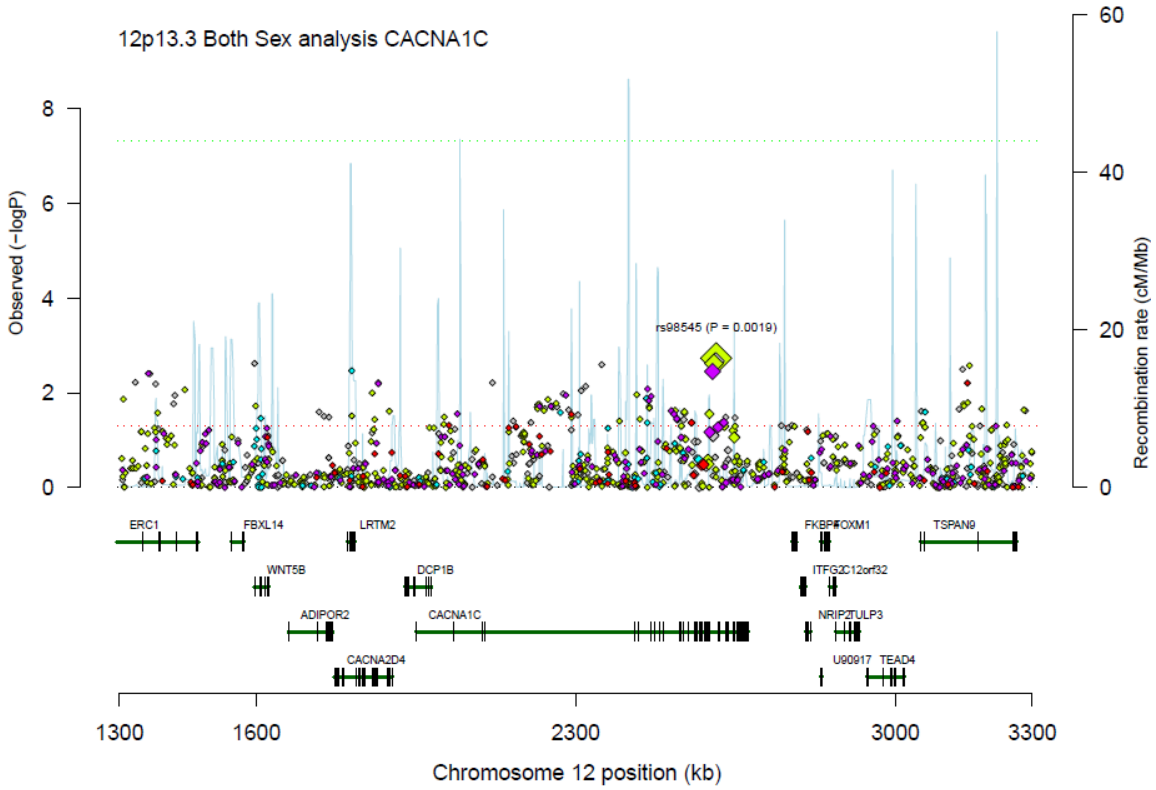


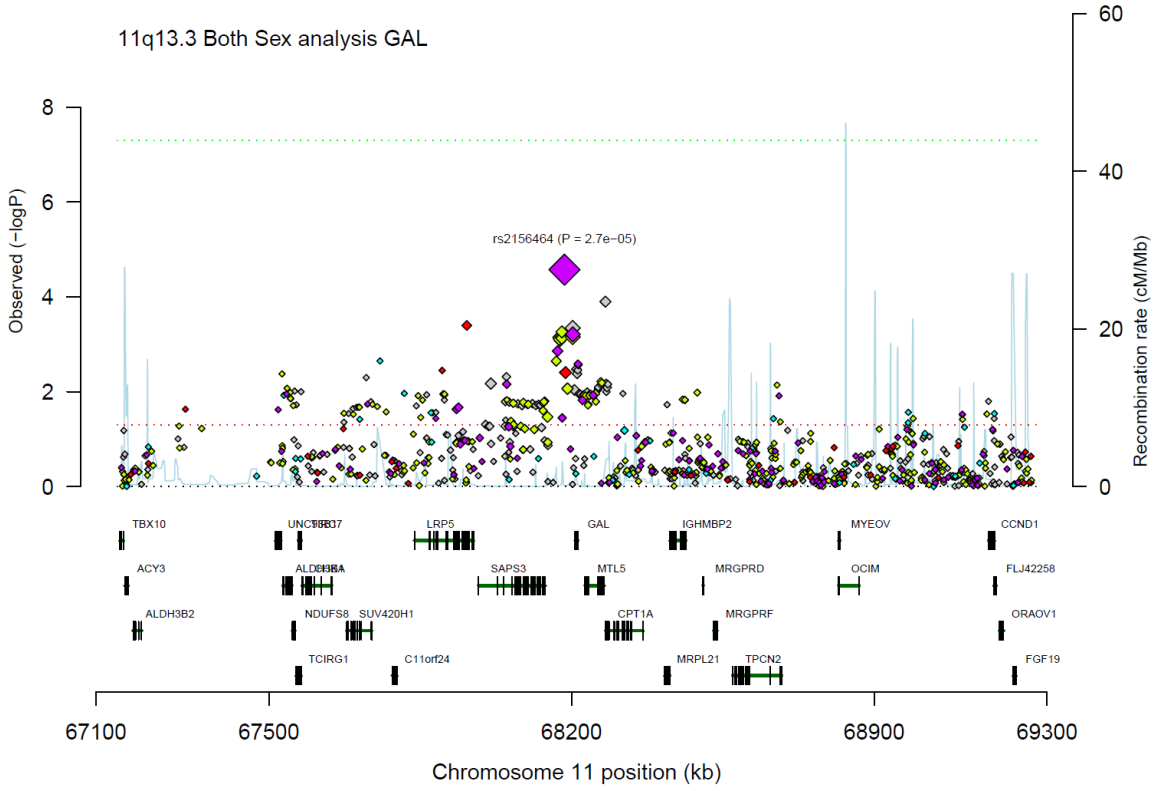


rs1317640

Set	I/G	INFO	P	Fcon	Fcas	OR	L95	U95
I317	I	2	0.88	0.059	0.056	0.88	0.17	4.61
I370	I	1	0.59	0.062	0.063	1.13	0.73	1.74
I610	I	1	0.13	0.043	0.071	2.19	0.79	6.10
A6.0	G	1	0.0031	0.072	0.104	1.32	1.10	1.58
All	**-**	**3**	**8.5e-06**	**0.064**	**0.092**	**1.44**	**1.23**	**1.69**




12p13.3 Both Sex analysis CACNA1C
Observed (−logP)
Recombination rate (cM/Mb)
rs98545 (P = 0.0019)
ERC1
FBXL14
LRTM2
FKBP8
FOXM1
TSPAN9
WNT5B
DCP1B
ITFG2
C12orf32
ADIPOR2
CACNA1C
NRIP2
TULP3
CACNA2D4
U90917
TEAD4
1300
1600
2300
3000
3300
Chromosome 12 position (kb)


11q13.3 Both Sex analysis GAL
Observed (−logP)
Recombination rate (cM/Mb)
rs2156464 (P = 2.7e−05)
TBX10
LRP5
GAL
IGHMBP2
MYEOV
CCND1
ACY3
SAPS3
MTL5
MRGPRD
OCIM
FLJ42258
ALDH3B2
NDUFS8
SUV420H1
CPT1A
MRGPRF
ORAOV1
TCIRG1
C11orf24
MRPL21
TPCN2
FGF19
67100
67500
68200
68900
69300
Chromosome 11 position (kb)

Reference

1. Saxena R, Voight BF, Lyssenko V, Burtt NP, de Bakker PIW, Chen H *et al.* Genome-wide association analysis identifies loci for type 2 diabetes and triglyceride levels. *Science* 2007; **316:** 1331-1336.

Totals	UK GWAS	GENRED / STARD	GAIN-MDD	Chr		Gene	No.SNP	No.Sim	Start BP	Stop BP	Test Stat	P	Alternative Name
	0	0	1		1	IL10	60	1.00E+05	2.05E+08	2.05E+08	195.51	0.0017	
	0	0	1		6	OPRM1	202	1.00E+05	1.54E+08	1.55E+08	498.2	0.002	
	1	0	1		6	HTR1B	59	1.00E+05	78228666	78229839	159.71	0.0058	
	1	0	0		9	GRIN1	50	1.00E+05	1.39E+08	1.39E+08	121.11	0.0211	
	1	1	0		12	CACNA1C	435	1.00E+05	2032676	2677376	666.79	0.0286	
	1	0	0		10	FGFR2	129	1.00E+05	1.23E+08	1.23E+08	218.16	0.0306	
	0	0	1		17	NGFR	61	1.00E+05	44927653	44947371	102.15	0.0309	
	1	0	0		14	PRKCH	212	1.00E+05	60858267	61087451	370.64	0.0318	
	0	1	0		19	APOE	50	1.00E+05	50100878	50104490	98.731	0.0362	
	0	0	1		22	TCF20	46	1.00E+05	40885962	40941389	112.84	0.0428	AR1
	1	0	0		10	HTR7	101	1.00E+05	92490555	92607651	227.17	0.0485	
	0	0	1		19	GMIP	52	1.00E+05	19601284	19615455	101.8	0.0618	
	0	0	1		11	PDE2A	106	1.00E+05	71964832	72063060	180.16	0.065	
	1	0	1		10	ADRA2A	54	1.00E+05	1.13E+08	1.13E+08	89.071	0.0775	
	1	0	0		1	PSMB4	40	1.00E+05	1.5E+08	1.5E+08	81.221	0.0828	
	1	0	1		5	NR3C1	119	1.00E+05	1.43E+08	1.43E+08	192.05	0.0934	
	1	1	1		12	GNB3	70	1.00E+05	6819635	6826818	107.42	0.0939	
	0	1	0		2	DNAJB2	54	1.00E+05	2.2E+08	2.2E+08	103.76	0.0942	
	0	1	0		6	ROS1	138	1.00E+05	1.18E+08	1.18E+08	210.26	0.0942	
	0	0	1		4	CCKAR	71	1.00E+05	26092115	26101140	105.42	0.1159	
	0	0	1		2	GAD1	63	1000	1.71E+08	1.71E+08	103.28	0.118	
	0	0	1		7	TAC1	40	1000	97199206	97207720	69.889	0.121	
	1	0	0		17	PER1	66	1000	7984512	7996478	101.26	0.126	
	1	0	1		2	PDE11A	296	1000	1.78E+08	1.79E+08	437.88	0.127	
	1	0	0		17	STAT3	74	1000	37718868	37794039	122.23	0.127	
	1	0	0		5	ADRA1B	68	1000	1.59E+08	1.59E+08	98.388	0.13	
	1	0	0		2	ZNF804A	104	1000	1.85E+08	1.86E+08	164.74	0.134	
	1	0	0		17	GRIN2C	56	1000	70349762	70367602	96.058	0.144	
	1	0	0		7	ABCB1	171	1000	86970883	87180500	243.28	0.157	
	1	0	0		5	GRIA1	263	1000	1.53E+08	1.53E+08	346.94	0.159	
	0	1	0		15	NTRK3	233	1000	86220991	86600665	313.25	0.163	
	0	1	0		12	PTPRR	235	1000	69318128	69600851	294.42	0.178	
	0	1	0		22	SYN3	462	1000	31238539	31732683	567.86	0.182	
	1	0	0		1	GRIK3	132	1000	37033714	37272431	175.93	0.183	
	0	0	1		15	GABRA5	72	1000	24663150	24776749	92.621	0.187	
	1	0	0		6	GRIK2	304	1000	1.02E+08	1.03E+08	373.89	0.188	
	1	0	0		11	GRIK4	297	1000	1.2E+08	1.2E+08	356.28	0.194	
	1	0	0		8	ADRA1A	171	1000	26661583	26778839	212.33	0.196	
	0	1	1		16	ADCY9	157	1000	3952652	4106187	191.25	0.201	
	0	0	1		2	IL1B	48	1000	1.13E+08	1.13E+08	64.87	0.206	
	1	0	0		2	PDE1A	225	1000	1.83E+08	1.83E+08	292.47	0.224	
	0	0	1		17	CCL2	65	1000	29606408	29608333	86.139	0.231	
	0	0	1		6	TNF	134	1000	31651328	31654091	162.4	0.232	
	1	1	1		12	TPH2	101	1000	70618892	70712488	129.92	0.24	
	0	0	1		1	OPRD1	50	1000	29011240	29062795	61.764	0.241	
	0	0	1		6	CNR1	78	1000	88906303	88911775	94.031	0.242	
	0	0	1		12	DUSP6	44	1000	88265967	88270427	55.053	0.252	
	0	0	1		11	CCKBR	76	1000	6237541	6249932	92.823	0.258	
	0	0	1		10	CYP2C9	83	1000	96688404	96739138	104.02	0.259	
	1	0	0		9	GRIN3A	161	1000	1.03E+08	1.04E+08	202.99	0.267	
	0	1	0		13	HS6ST3	342	1000	95541093	96289813	398.05	0.274	
	0	0	1		14	ESR2	99	1000	63763503	63875021	116.74	0.275	
	0	0	1		5	CRHBP	54	1000	76284435	76301055	63.412	0.289	
	0	0	1		1	DISC1	308	1000	2.3E+08	2.3E+08	338.38	0.301	
	0	0	1		7	NOS3	60	1000	1.5E+08	1.5E+08	67.188	0.307	
	1	1	1		22	COMT	100	1000	18309308	18336530	112.46	0.315	
	1	0	0		7	LEP	82	1000	1.28E+08	1.28E+08	87.977	0.318	
	0	0	1		3	CCK	65	1000	42274321	42281399	74.545	0.322	
	1	0	0		12	GRIN2B	380	1000	13605676	14024289	407.83	0.331	
	1	0	0		4	ADRA2C	36	1000	3738093	3740051	39.375	0.334	
	1	0	0		1	LEPR	141	1000	65658905	65875410	157.58	0.336	
	1	0	0		4	GRIA2	76	1000	1.58E+08	1.59E+08	82.81	0.337	
	1	0	1		16	SLC6A2	122	1000	54248056	54295201	133.81	0.339	
	1	1	1		11	BDNF	62	1000	27633017	27699872	67.205	0.343	
	0	1	0		3	CD47	69	1000	1.09E+08	1.09E+08	73.596	0.346	
	0	0	1		18	GNAL	141	1000	11679264	11871919	150.17	0.351	
	0	0	1		12	NOS1	151	1000	1.16E+08	1.16E+08	158.81	0.357	
	0	0	1		11	TH	62	1000	2141734	2149611	64.34	0.359	
	1	0	0	X		GRIA3	179	1000	1.22E+08	1.22E+08	193.59	0.363	
	0	0	1		6	PDE10A	303	1000	1.66E+08	1.66E+08	318.61	0.363	
	0	1	0		20	PHACTR3	220	1000	57612997	57856161	227.98	0.363	
	1	0	0		5	FGFR4	46	1000	1.76E+08	1.76E+08	48.378	0.372	
	1	0	0		12	PSMD9	60	1000	1.21E+08	1.21E+08	61.743	0.376	
	0	1	0		3	VGLL4	157	1000	11572543	11737220	163.31	0.389	
	1	0	0		3	GSK3B	150	1000	1.21E+08	1.21E+08	146.99	0.4	
	0	1	0		12	TSPAN8	54	1000	69805143	69838046	52.298	0.409	
	1	0	1	X		HTR2C	78	1000	1.14E+08	1.14E+08	62.797	0.421	
	1	0	1		4	DRD5	34	1000	9392355	9394731	31.241	0.424	
	0	1	1		1	MTHFR	100	1000	11768373	11788702	93.659	0.434	
	1	0	1		21	PDE9A	142	1000	42946930	43068687	144.62	0.452	
	0	0	1		7	CHRM2	113	1000	1.36E+08	1.36E+08	109.21	0.453	
	1	0	0		21	GRIK1	268	1000	29831124	30234153	260.64	0.455	
	0	0	1		4	PDE5A	94	1000	1.21E+08	1.21E+08	73.311	0.457	
	1	0	0		14	AKT1	48	1000	1.04E+08	1.04E+08	42.193	0.469	
	1	0	0		2	ADRA2B	26	1000	96142349	96145615	19.813	0.477	
	0	0	1		2	POMC	44	1000	25237225	25245063	36.917	0.485	
	1	1	0		10	ANK3	282	1000	61458164	61819494	260.73	0.5	
	0	0	1		8	PENK	46	1000	57516069	57521143	38.054	0.505	
	1	0	0		11	CD3E	53	1000	1.18E+08	1.18E+08	44.298	0.527	
	1	0	0		2	HTR2B	42	1000	2.32E+08	2.32E+08	28.919	0.527	
	1	1	1		3	DRD3	76	1000	1.15E+08	1.15E+08	63.034	0.538	
	1	0	0		16	GRIN2A	434	1000	9762922	10184112	386.5	0.538	
	0	0	1	X		GABRA3	68	1000	1.51E+08	1.51E+08	49.743	0.547	
	1	0	1		5	HTR1A	29	1000	63292033	63293302	20.519	0.564	
	0	0	1		15	CHRNA7	85	1000	30110017	30248527	69.87	0.569	
	0	0	1		16	HP	57	1000	70646008	70652456	40.625	0.569	
	0	1	0		4	FBXO8	64	1000	1.75E+08	1.75E+08	53.81	0.572	
	0	1	0		13	DGKH	206	1000	41520888	41701888	170.83	0.574	
	1	0	1		11	HTR3A	85	1000	1.13E+08	1.13E+08	70.291	0.58	
	1	0	0		19	GRIN2D	57	1000	53589943	53640000	44.753	0.581	
	1	0	0		19	GSK3A	22	1000	47426177	47438576	13.153	0.581	
	1	0	0		9	NTRK2	263	1000	86473285	86828325	225.86	0.581	
	0	1	0		14	SLC25A2	403	1000	36218828	36711616	357.92	0.586	

UKGWAS Lewis et al American J of Psychiatry 2010

GENRED/STARD Shi et al, Shyn et al,GenRed and STARD, Mol Psych 2010

GAIN-MDD Sullivan et al, 2009, Molecular Psychiatry using list from Lopez-Lanul, 2007

No. Sim No. of simulations used for the gene-based test
More simulations are undertaken for more associated genes

Start BP start and end position of the genes

Stop BP the gene-based test used +/- 50Kb from these boundaries

TestStat Testi statistic from VEGAS

P P- value for the gene

For columns UKGWAS, GENRED/STARD amd GAIN-MDD
Flag 1 = included in their candidate gene list
Flag 0 = not included in their candidate gene list

Candidate genes containing no SNPs in our data:
DXS7 FACL4 TACR

	0	0	1		5	GABRA6	37	1000	1.61E+08	1.61E+08	22.749	0.592	
	1	0	0		17	TBX21	48	1000	43165608	43178484	33.268	0.593	
	1	0	1		11	HTR3B	74	1000	1.13E+08	1.13E+08	56.674	0.596	
	0	0	1		12	OASL	59	1000	1.2E+08	1.2E+08	46.209	0.599	
	0	0	1		20	GNAS	84	1000	56848189	56919645	68.033	0.603	
	1	0	1		7	IL6	83	1000	22733342	22738145	65.06	0.607	
	1	0	0		19	GRIK5	33	1000	47194312	47261797	24.158	0.608	
	0	1	0		18	MYO5B	322	1000	45603098	45975382	269.54	0.608	
	1	0	1		17	CRHR1	75	1000	41217448	41268973	46.032	0.624	
	1	1	1		17	SLC6A4	62	1000	25549031	25586841	45.225	0.624	
	1	0	0		2	CREB1	65	1000	2.08E+08	2.08E+08	42.531	0.633	
	0	0	1		14	SERPINA	133	1000	94148466	94160143	107.65	0.641	ACCT
	0	0	1		7	NPY	102	1000	24290333	24298002	73.167	0.642	
	0	0	1		5	PAM	77	1000	1.02E+08	1.02E+08	42.684	0.657	
	0	0	1		20	LBP	103	1000	36408298	36439067	81.933	0.661	
	0	0	1		4	WFS1	91	1000	6322477	6355893	65.402	0.671	
	1	0	1		11	TPH1	41	1000	17999113	18018885	20.107	0.678	
	1	0	0		6	OLIG3	56	1000	1.38E+08	1.38E+08	40.846	0.681	
	0	1	1		6	GABBR1	145	1000	29677983	29708941	99.934	0.703	
	0	0	1		1	PLA2G2A	47	1000	20174517	20179496	31.327	0.708	
	0	0	1		2	CTLA4	47	1000	2.04E+08	2.04E+08	24.833	0.71	
	0	0	1		13	DAOA	87	1000	1.05E+08	1.05E+08	64.171	0.711	G72
	1	0	0		2	PER2	68	1000	2.39E+08	2.39E+08	45.809	0.718	
	0	1	0		2	EHD3	116	1000	31310706	31344764	82.794	0.722	
	0	0	1		8	FZD3	62	1000	28407691	28477880	38.489	0.725	
	0	0	1		6	DTNBP1	126	1000	15631017	15771250	84.035	0.739	
	1	0	0		4	FGFR3	24	1000	1764836	1780396	14.392	0.751	
	0	0	1		17	ACE	58	1000	58908165	58928711	33.664	0.753	
	1	1	1		13	HTR2A	127	1000	46305513	46368176	89.118	0.761	
	0	0	1		12	M6PR	52	1000	8984230	8993519	24.748	0.762	
	0	1	0		4	NFKB1	97	1000	1.04E+08	1.04E+08	52.626	0.766	
	1	0	0		5	HTR4	123	1000	1.48E+08	1.48E+08	71.15	0.774	
	0	1	0		1	SMG7	72	1000	1.82E+08	1.82E+08	40.246	0.784	
	0	0	1		7	CRHR2	72	1000	30659387	30688665	44.595	0.8	
	0	0	1		7	DDC	150	1000	50493627	50600648	84.104	0.807	
	1	0	0		3	SLC6A1	111	1000	11009419	11055935	77.647	0.807	
	0	1	0		2	KLHL29	141	1000	23608557	23931483	91.92	0.808	
	0	1	0		12	KCNC2	109	1000	73720162	73889778	65.41	0.811	
	1	0	0		8	FGFR1	59	1000	38387812	38445509	30.023	0.819	
	1	0	1		7	HTR5A	88	1000	1.54E+08	1.55E+08	40.731	0.826	
	0	0	1	X		GPR50	40	1000	1.5E+08	1.5E+08	24.995	0.828	
	1	1	1		11	DRD4	50	1000	627304	630703	24.959	0.835	
	1	0	1		12	P2RX7	101	1000	1.2E+08	1.2E+08	52.151	0.838	
	0	0	1		10	ADRB1	54	1000	1.16E+08	1.16E+08	26.007	0.848	
	1	0	1		4	CLOCK	78	1000	55993416	56107754	22.067	0.849	
	0	1	0		7	NFE2L3	49	1000	26158384	26192432	23.907	0.854	
	1	0	1		5	DRD1	83	1000	1.75E+08	1.75E+08	45.755	0.861	
	1	0	1		1	AVPR1B	18	1000	2.04E+08	2.04E+08	4.8212	0.863	
	0	1	0		12	CCND2	94	1000	4253198	4284777	57.914	0.864	
	1	0	0		12	AVPR1A	59	1000	61826482	61832857	20.828	0.871	
	1	0	0		7	PCLO	199	1000	82221256	82630133	117.05	0.875	
	0	0	1		12	P2RX4	76	1000	1.2E+08	1.2E+08	38.792	0.876	
	0	0	1		12	LRP1	64	1000	55808548	55893392	30.355	0.884	
	0	0	1		8	OPRK1	87	1000	54300828	54326747	38.999	0.889	
	0	1	0		4	UGT2A1	120	1000	70488723	70548006	50.923	0.897	
	1	0	0		11	GRIA4	178	1000	1.05E+08	1.05E+08	86.124	0.904	
	1	0	1	X		MAOA	38	1000	43400352	43491012	9.8451	0.906	
	0	1	0		3	ITPR1	360	1000	4510033	4864286	244.1	0.908	
	0	0	1	X		MAOB	32	1000	43510800	43626665	10.329	0.909	
	1	0	0		1	PER3	95	1000	7767349	7827824	41.986	0.909	
	1	0	1		11	DRD2	120	1000	1.13E+08	1.13E+08	50.28	0.915	
	0	0	1		22	ADORA2	41	1000	23153529	23168325	9.9477	0.917	
	0	0	1		12	CAMKK2	64	1000	1.2E+08	1.2E+08	27.924	0.922	
	0	0	1		11	CNTF	39	1000	58146720	58149778	10.241	0.923	
	0	0	1		2	SPAG16	405	1000	2.14E+08	2.15E+08	224.28	0.926	D2S294
	1	0	0		21	OLIG2	65	1000	33320108	33323370	29.665	0.936	
	0	1	0		16	MMP2	114	1000	54070581	54098087	47.783	0.944	
	0	1	0		12	CHST11	498	1000	1.03E+08	1.04E+08	301.87	0.947	
	1	0	0		21	OLIG1	47	1000	33364442	33366596	18.693	0.959	
	0	0	1		6	ESR1	279	1000	1.52E+08	1.52E+08	149.57	0.96	
	1	0	0		6	FKBP5	61	1000	35649344	35764692	15.013	0.964	
	0	0	1		10	PDE6C	108	1000	95362334	95415419	42.377	0.973	
	0	0	1		1	HTR6	76	1000	19864366	19878642	25.92	0.978	
	1	1	1		5	SLC6A3	90	1000	1445909	1498538	33.82	0.985	
	0	0	1		4	GYPA	34	1000	1.45E+08	1.45E+08	7.8437	0.988	
	0	1	0		13	TDRD3	90	1000	59869122	60046012	22.91	0.99	
Total	84	41	98										

Supplementary File 1 (.pdf) Supplementary methods and results

Supplementary File 2 (.pdf) Supplementary Figures: Regional Association Plots for all regions containing a SNP associated $p < 5 \times 10^{-5}$ and forest plots by analysis set for the most associated SNP in each region.

Supplementary File 3 (.xlsx) Association results for all SNP associated with $p<0.0001$

Supplementary File 4 (.xlsx) Gene-based test results for candidate genes.