

A genome-wide association analysis of a broad psychosis phenotype identifies three loci for further investigation.

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ABSTRACT

Background: Genome-wide association studies (GWAS) have identified several loci associated with schizophrenia and/or bipolar disorder. We performed a GWAS of psychosis, as a broad syndrome, rather than within specific diagnostic categories.

Methods: 1,239 cases with schizophrenia, schizoaffective or psychotic bipolar disorder, 857 of their unaffected relatives and 2,739 healthy controls were genotyped with the Affymetrix 6.0 SNP array. Analyses of 695,193 SNPs were conducted using UNPHASED, which combines information across families and unrelated individuals. We attempted to replicate signals we found in 23 genomic regions using existing data on non-overlapping samples from the Psychiatric GWAS Consortium (PGC) and SGENE-plus cohorts (10,352 schizophrenia patients and 24,474 controls).

Results: No individual SNP showed compelling evidence for association with psychosis in our data. However, we observed a trend for association with same risk alleles at loci previously associated with schizophrenia (one-sided $P=0.003$). A polygenic score analysis found that the PGC's panel of SNPs associated with schizophrenia significantly predicted disease status in our sample ($P=5 \times 10^{-14}$) and explained approximately 2% of the phenotypic variance.

Conclusion: Although narrowly-defined phenotypes have their advantages, we believe new loci may also be discovered through meta-analysis across broad phenotypes. The novel statistical methodology we introduced to model effect size heterogeneity between studies should help future GWAS that combine association evidence from related phenotypes. By applying these approaches we highlight three loci that warrant further investigation. We found that SNPs conveying risk for schizophrenia are also predictive of disease status in our data.

INTRODUCTION

Psychotic disorders including schizophrenia, bipolar and schizoaffective disorders affect approximately 3% of the general population (1-6) and constitute the most severe forms of mental diseases. Characteristic symptoms include hallucinations, delusional beliefs as well as severe mood variations and cognitive impairments, all of which can lead to major changes in behaviour and ability to function. According to the WHO's World Health Report, these psychotic disorders are ranked within the top seven leading causes of disability in young adults (7).

The genetic architecture of schizophrenia and bipolar disorder has been shown to include common alleles of subtle effect and rare mutations of large effect, often involving genome copy number variation (8-11). Recent large-scale meta-analyses of schizophrenia (12), conducted by the Psychiatric GWAS Consortium (PGC) combined data from over 50,000 individuals from 17 international cohorts (13-25) and identified seven associated loci. Of these loci, five were new and the remaining two had been previously implicated. The strongest new finding in schizophrenia was within an intron of a putative primary transcript for *MIR137* (microRNA 137), a known regulator of neuronal development. Four other schizophrenia loci with strong statistical support contain predicted targets of *MIR137*, suggesting *MIR137*-mediated dysregulation as a previously unknown etiologic mechanism in schizophrenia. The meta-analysis (12) also confirmed the role of the major histocompatibility complex (MHC) region, as suggested in other studies (23, 24, 26, 27), as well as a marker in intron four of transcription factor 4 (*TCF4*) (24).

The PGC conducted a similar meta-analysis for bipolar disorder (28) including over 11,000 cases and 51,000 controls from previous association studies (15, 29-41). The

analysis confirmed an association with *CACNA1C* and identified a new intronic variant in *ODZ4*. An overlap in the polygenic component between schizophrenia and bipolar disorder was also found (42, 43). In a combined meta-analysis of both schizophrenia and bipolar disorder, three loci reached genome-wide significance: *CACNA1C*, *ANK3* and the *ITIH3-ITIH4* region (28).

As data accumulate, there is increasing evidence for overlap in the genetic component to risk between different psychiatric disorders (44-46). When combined with epidemiological and neuroimaging data (47-50), the shared genetic architecture supports the view of schizophrenia, bipolar disorder and other psychoses as related rather than aetiologically distinct entities (8, 12, 28, 46, 51-60). Motivated by these findings, we performed a GWAS of psychotic disorders including patients with schizophrenia, schizoaffective disorder and bipolar disorder with a history of psychotic symptoms.

METHODS AND MATERIALS

The cohort

Prior to any exclusion, the full dataset included 6,935 participants with 1,820 patients, 1,224 of their unaffected relatives and 3,891 healthy controls. These samples were collected through seven centres across Australia and Europe (Germany, Holland, Spain and UK). Participants provided written informed consent and the study was approved by the respective ethical committees at each of the seven participating centres. After quality control, the full sample included 4,835 participants of which 1,239, 857 and 2,739 were patients, their unaffected relatives and healthy controls, respectively. Further sample and centre details are provided in Supplementary Table 1.

Inclusion and exclusion criteria and phenotype definition

To allow for a DSM-IV (61) diagnosis to be ascertained or ruled out, all participants (including controls and unaffected family members) underwent a structured clinical interview with either the Schedule for Affective Disorders and Schizophrenia (SADS) or the Structured Clinical Interview for DSM Disorders (SCID) or the Schedules for Clinical Assessment in Neuropsychiatry (SCAN) (62-64). Of the cases passing quality control, 784 met criteria for schizophrenia, 113 for bipolar disorder with a history of psychotic symptoms, 110 for psychotic disorder not otherwise specified, 97 for schizophreniform disorder, 64 for schizoaffective disorder, 44 for brief psychotic disorder, 20 for delusional disorder and 7 for substance-induced psychosis. Participants in all groups were excluded if they had a history of neurological disease or head injury resulting in loss of consciousness.

DNA sample preparation

Genomic DNA obtained from blood for all participants was sent to the Wellcome Trust Sanger Institute (WTSI), Cambridge, UK. Samples were processed in 96-well plate format and each plate carried a positive and a negative control. DNA concentrations were quantified using a PicoGreen assay (Invitrogen) and an aliquot assayed by agarose gel electrophoresis. A sample passed quality control if the original DNA concentration was at least 50 ng/ μ l and the DNA was not degraded.

Genotyping methodology and quality control

In order to track sample identity, 30 SNPs including sex chromosome markers, were typed on the Sequenom platform prior to entry to the whole genome genotyping pipeline. Of the initial 6,935 samples, 347 failed quality control due to degraded or insufficient DNA or incorrect sex classification. The remaining samples were sent for

genotyping with the Genome-wide Human SNP Array 6.0 at Affymetrix Services Lab (<http://www.affymetrix.com>).

Data quality control (Supplementary Tables 2 & 3)

Genotype calling was conducted using the CHIAMO algorithm (65, 66) modified for use with the Affymetrix 6.0 genotyping array. We excluded 11,610 SNPs with a study-wide missing data rate over 5%. We removed 26,858 SNPs with four or more Mendelian inheritance errors identified with Pedstats (67). Further exclusion criteria were departure from Hardy-Weinberg equilibrium ($P < 10^{-6}$) or minor allele frequency (MAF) less than 0.02 with 2,404 and 145,097 SNPs removed, respectively. A total of 38,895 SNPs from the X or Y chromosomes or mitochondrial DNA were also excluded from the analysis. Finally, 9,499 poorly genotyped SNPs were removed following visual inspection of the genotyping intensity plots in the program Evoker (68).

We excluded 214 samples with more than 2% missing data across all SNPs. Another 70 samples were excluded due to divergent genome-wide heterozygosity (inbreeding coefficients were $F > 0.076$ or $F < -0.076$ as estimated with PLINK (42). Chromosomal sharing was inferred from a genome-wide subset of 71,677 SNPs and from each duplicate pair the sample with the most complete genotype data was kept. We removed 70 duplicates and monozygotic twins by excluding one of each pair of individuals showing identity by descent greater than 95%.

After quality control, 4,835 individuals remained. Initial analysis of the genotype data identified a high fraction of samples (approximately 30%), which showed very poor signal to noise ratio in the genotyping assay. As the experimental source of the problem was unclear, and to ensure a robust set of genotype calls, these samples were removed from further analysis. We note that the sample loss was randomly distributed across the

three clinical groups (32% of patients, 30% of relatives and 30% of controls; Chi square (2df) =3.2; P =0.20). Full details on the sample quality control are provided in Supplementary Table 2.

In addition to 3,490 unrelated individuals, there were 1,345 related individuals clustered in 462 families. The family size ranged between 2 and 5 with an average of 2.9 members. Of the families, 196 were control families, 243 had one affected case only, 21 families included two cases and another 2 families had three cases. Data from these individuals were analysed at 695,193 autosomal SNPs.

Population structure analysis

To investigate the genetic structure in the data we performed principal component analysis (PCA) of unrelated individuals using EIGENSOFT version 3.0 (69) on a thinned set of SNPs (see Supplementary Material). Owing to the multicenter nature of our study we assessed the need to include principal components (PCs) as covariates in statistical tests of association to control for population stratification (70). This was done by using PLINK (42) to calculate the genome-wide distribution of the association test statistic in the unrelated individuals using different numbers of PCs as covariates. Possible inflation in the test statistic was measured by the genomic control parameter λ , which is the ratio of the median of the observed test statistic distribution to that of its expectation under the null hypothesis (71).

Association analysis in our discovery sample

A genome-wide association analysis was conducted with UNPHASED v3.1.4. (72), which allows a combined analysis of both families and unrelated individuals, thus increasing statistical power. UNPHASED calculates separately the transmitted and un-transmitted alleles in families as well as the allelic frequencies in unrelated patients and controls,

giving a combined odds ratio (OR), 95% confidence interval and P value. The analysis included three PCs as covariates.

For SNPs showing association with psychosis in our data with $P < 1 \times 10^{-4}$, proxy SNPs were identified using the proxy report routine in PLINK (42). Only those SNPs that were in linkage disequilibrium ($r^2 \geq 0.5$) with and within 100 Kb distance from at least one such proxy SNP that showed association with psychosis with $P < 1 \times 10^{-2}$ were selected for the replication phase. These criteria reduced the possibility that the association signal was driven by an artifact at the most associated SNP.

We attempted to replicate 44 SNPs included in the catalogue of published GWAS (73), accessed January 2012, for schizophrenia or bipolar disorder with P values less than 1×10^{-7} . These SNPs and the studies that identified them are listed in Table 1. If a reported SNP was not genotyped directly in our data, we used the 1000 Genomes Project (74) data to identify the best tag (highest r^2) and orientated the haplotype to the risk allele so that the directions of the odds ratios were matched between our analysis and the previous studies. Where relevant information was not available the SNP was excluded from analysis.

Related effects meta-analysis

We attempted *in silico* replication with independent samples from the PGC and the SGENE+ consortia using both a fixed effects meta-analysis (42) and a Bayesian related effects approach (27). The Bayesian related effects model (Supplementary methods) was considered appropriate in this context since there are obvious sources of heterogeneity between the discovery and the replication datasets due to differing phenotype definitions and sample origins. To ensure that no samples were overlapping between the discovery and replication data sets, we used a subset of at least 13,000

SNPs to exclude 717 participants (51 cases, 642 controls, 24 relatives) from our primary study. Similarly, another 74 controls were excluded from the SGENE+ replication cohort. Only SGENE+ samples that were not part of the PGC study were included in our meta-analyses.

Polygenic score analysis

A polygenic score analysis was conducted using a thinned (on the basis of linkage disequilibrium) panel of 113,774 SNPs from the PGC-Schizophrenia meta-analysis. Of these SNPs, 72,635 were available in our data and we further added suitable proxies for another 19,434 SNPs, which were identified through the program SNAP (75) to have $r^2 > 0.9$ with the index SNP and to be within 500Kb distance. Of 4,835 samples passing the above described quality control filters we excluded 717 individuals that overlapped with the PGC sample and another 833 related participants. Therefore our polygenic analysis was based on a subset of 3,285 unrelated subjects comprising of 1,188 patients and 2,097 controls. The polygenic score for each individual was calculated from the number of risk alleles they carried for each SNP, weighted by the $\log(\text{OR})$ provided by the PGC, and summed across all the SNPs. Calculations were performed using the PLINK SNP scoring routine (42).

We used logistic regression, with the three population structure principal components and the centre of origin of the samples as covariates, to test whether the polygenic scores were predictive of case-control status in our study. Following Purcell et al (26), we reported the proportion of the variance of disease risk in our sample (as measured by Nagelkerke's pseudo- R^2) that could be explained by the panel of SNPs. We examined the proportion of the variance explained by our data at various P -value thresholds for the PGC-schizophrenia SNP list ($P < 0.01, 0.05, 0.1, 0.2, 0.3, 0.4$ and 0.5) (26, 43).

RESULTS

The primary goal of our study was to use published genome wide association study data in schizophrenia and bipolar disorder to facilitate discovery in a new sample with a broad psychosis phenotype. Firstly, we examine previously published loci in our dataset. We then go on to present our discovery association data followed by replication in independent samples, using a novel meta-analysis approach. Finally, we report a polygenic score analysis testing if a panel of SNPs associated specifically with schizophrenia are predictive of the broader phenotype in our sample.

Population structure

Analysis of our data via PCA showed that the major components of the genetic variation capture the geographic origin of the samples (Supplementary figure 1). The first principal component separates samples from Northern Spain (Santander) from the rest of the sample. We found it necessary to include the first three PCs as covariates in order to control for the confounding effects of population structure even though this may reduce power to detect associations. The genomic control parameter, λ , was equal to 1.030 and 1.374 with and without including the three PCs respectively.

Replication of previously published loci in our dataset

To ascertain the strength of association in our data at loci previously associated with schizophrenia and/or bipolar disorder, we systematically assessed the evidence at the SNPs most strongly correlated with the previously reported SNPs and their risk alleles (Table 1 and Figure 1) (12, 15, 21, 23, 24, 26, 28, 30, 33, 34, 37, 38, 66, 76-96). We observed evidence for association at several loci. These include multiple SNPs in the MHC region, most strongly at rs9272219 near *HLA-DQA1*. We also replicated association at *MIR137*, *MCTP1*, *NRGN* and *CDC68*. More generally, we observed a positive

correlation between previously reported effect sizes and those estimated here, most notably with schizophrenia associated loci where 19 out of the 24 loci had the same risk allele (one-sided $P = 0.003$). We note that this sign test remained significant ($P < 0.05$) after thinning to reduce correlation between SNPs and removing the SNPs within the MHC (see Supplementary Table 4).

Association analysis in our discovery sample

We did not identify any novel SNPs associated with psychosis as a broad phenotype with $P < 1 \times 10^{-7}$ from our data set. Figure 2 and supplementary figure 2 show respectively the quantile-quantile plots of the distribution of observed and expected P values and the Manhattan plot of all autosomal SNPs that passed quality control.

Independent replication of our discovery data

We selected 63 SNPs in 23 genomic regions (Supplementary Data) showing the strongest evidence for association in our discovery dataset ($P < 1 \times 10^{-4}$) and having at least one suitable proxy SNP also associated (see Methods). We then attempted *in silico* replication using the large independent (see Methods) datasets publicly available from the Psychiatric Genomics Consortium (51, 57, 97, 98) as well as with data provided by the SGENE+ Consortium (24, 25).

All of the selected 63 SNPs were present in at least one of the replication datasets and 53 SNPs were available in both collections giving a two-study independent replication dataset with 10,352 patients and 24,474 controls. By combining estimates of the logarithmic odds ratios weighted by their precision (i.e., inverse variance of the estimator) across discovery and replication cohorts, we conducted a three-study meta-analysis with a total of 11,540 patients, 833 of their unaffected relatives and 26,571 controls. Table 2 contains the SNPs that in the replication data showed an effect in the

same direction (with one-sided $P < 0.05$) as in the discovery data set and had either combined (discovery plus replication) fixed effects P value $< 10^{-3}$ or combined fixed effects or related effects Bayes factor > 100 . Regional association plots of these SNPs are included in Figure 3 and forest plots are given in Supplementary figure 3. Full details of the replication meta-analyses are presented in Supplementary Data.

Two out of five top regions in our discovery analysis, rs743393 (on chromosome 3) and rs968794 (on chromosome 7), showed effects in the same direction in the replication data with one-sided replication P values of 0.020 and 0.007, respectively. However, the combined fixed effects evidence of association at these loci is weak by the standards of GWAS (P values 7×10^{-4} and 8×10^{-5} , and Bayes factors 25 and 200, respectively). Bayes factors from the related effects model (440 and 7400, respectively), which allow heterogeneity in effect size across studies, are larger than those from the fixed effect model, but still fail to provide convincing levels of evidence for these associations. See (66) for interpreting Bayes factors in the GWAS context.

Polygenic score analysis

We performed a polygenic score analysis using the SNPs associated with schizophrenia in the Psychiatric Genomics Consortium study. Logistic regression analyses showed significantly higher scores for patients than controls ($P = 5 \times 10^{-14}$), and explained approximately 1.7% of Nagelkerke's pseudo-variance in our sample. For additional results on the polygenic component, see Supplementary material and Supplementary Figure 4.

DISCUSSION

Although extensive twin research has shown high heritability estimates ranging between 73-85% for schizophrenia, schizoaffective disorder and manic syndromes (99-103), compared to other neuropsychiatric diseases, the search for psychosis susceptibility genes has not been straightforward (104-110). Several loci have now been convincingly identified and more are expected to be found through the Psychiatric Genomics Consortium, a large international collaboration undertaking mega-analyses of the available data (8, 12, 28). In this context, our sample with 4,835 participants has modest power to detect new variants unequivocally (111) and thus it is not that surprising that we did not identify convincing novel associations with a broad psychosis phenotype. For example, our data provide less than 10% power at type I error of 1×10^{-7} for an allelic relative risk of 1.2 at a common SNP, and in practice power may be further reduced due to our broader disease phenotype and our use of principal component covariates to control for population structure. It has been estimated that for allelic odds ratios of 1.1 and 1.2 as many as 10,000 to over 20,000 subjects would be required to achieve 80% power at genome wide significance levels (112). We hope that our data set will be valuable in the future meta-analyses that are likely to identify further common variants for psychotic illnesses with convincing statistical evidence.

The loci for which we found the best evidence of association, given our data and the independent replication samples from the Psychiatric Genomics and SGENE+ consortia, are reported in Table 2 and their regional association plots are in Figure 3. These include rs743393 located in chromosome 3, which is near the Integrin alpha 9 gene (ITGA9), thought to codify for a membrane glycoprotein that mediates cell-cell and cell-matrix adhesion (22). SNP rs968794 in chromosome 7 is close to the NDUFA4 gene coding for a

protein that is involved in the mitochondrial membrane respiratory chain (23). Finally, rs4761708 is located in a gene desert in chromosome 12 flanked by recombination hotspots. Limited information is available on the role of these genes and whether they are causal in increasing the risk of developing psychosis. Further data is required to confirm the associations and to inform on underlying disease mechanisms.

While our sample was too small to identify new loci unequivocally, it had good power to replicate previously published signals with modest effects assuming they are consistent across psychosis phenotypes. The analysis of established schizophrenia loci shows that there is a trend for consistent association in our data (Figure 1). Also the polygenic score analysis showed that, compared to controls, our cases are enriched for alleles thought to convey risk for schizophrenia; the PGC's panel of SNPs significantly predicted case-control status in our study and explained around 2% of the phenotypic variance in our sample. This is comparable to previously reported figures in other European case-control and family based populations (26, 43) and is consistent with a highly polygenic model of disease risk. Larger data sets are required to determine whether these signals are specific to only some of the sub-phenotypes of psychosis or are present across them.

Schizophrenia and bipolar disorder are thought to be highly complex and polygenic, with potentially thousands of susceptibility genes of small effect and, particularly for schizophrenia, also with rare variants of larger effects (10, 14, 26, 52, 58, 107, 113-116). Previous GWAS have generally targeted a specific diagnostic category and the merit of analysing a psychosis spectrum is debatable. One of the challenges facing psychiatric genetics has been the heterogeneity of the diseases in question and studying a broader phenotype could exacerbate this problem. However, as GWAS data accumulate there is growing evidence of genetic overlap between schizophrenia and bipolar disorder (8, 12,

28, 44, 46, 51, 55, 56, 58-60). Therefore, as well as examining narrowly defined diseases it is of use to undertake cross-disorder analyses. Our replication of established schizophrenia hits in a broadly defined psychosis sample and polygenic analyses support this view.

Current benchmarks for establishing new associations usually insist on a combined discovery and replication P value of less than 5×10^{-8} using a fixed effects meta-analysis, which is the correct summary of the overall statistical evidence when the true effect size is exactly the same across the studies. However, when the effect size may genuinely differ between the studies due to, for example, differences in phenotype definition, patterns of linkage disequilibrium or environmental contributions, it is appropriate to assess association evidence with a model that allows for heterogeneity. Here we have used a Bayesian related effects model that assumes that the effects between the studies are similar (e.g. highly correlated on the log odds scale) but not necessarily the same. A computational advantage of this model is that it only requires the study-wide summary statistics (effect size and its standard error) and therefore we believe that it will be useful in future meta-analyses of existing GWAS data sets, for example across neuropsychiatric diseases.

In our study, we applied the related effects model to combine the discovery and replication results at 63 SNPs that had the most evidence in the discovery analysis. As expected, the related effects model assigns a higher probability than the fixed effects model to the event that these SNPs represent real associations (Supplementary Data). For any one SNP, this can be either because the association is a true-positive but heterogeneous and/or subject to a “winner’s curse” effect (117, 118), or because the association is a false-positive and appears heterogeneous due to a relatively strong discovery signal created by chance effects. Future studies are needed to determine

conclusively whether the SNPs reported in Table 2 and Figure 3 represent real associations.

The scenario described here, where a discovery analysis of a particular phenotype in a small sample attempts to replicate putative associations *in silico*, in much larger meta-analyses of similar phenotypes, is likely to become more common in human genetics as GWAS data accumulate. We note that stringent *P* value thresholds for combined discovery and replication meta-analysis make it challenging to identify new loci because loci with consistent effects across studies will have already been identified. Therefore in on-going genome-wide meta-analysis across related phenotypes, modelling effect heterogeneity where appropriate is arguably the most powerful approach to identify additional susceptibility loci.

In conclusion, although no individual SNPs reached convincing evidence of association with psychosis, our data contribute to the international effort to produce a cohort large enough to investigate both the shared and separate genetic bases of multiple psychotic disorders. Our polygenic score analysis indicates that the PGC-derived panel of SNPs conveying risk specifically for schizophrenia is also predictive of case-control status in our data, explaining around 2% of the phenotypic variance. We advocate the use of related effects models in large meta-analyses for summarising the evidence for association across independent studies of related phenotypes.

Table 1: Evidence in our discovery data at loci previously reported to be associated with schizophrenia and/or bipolar disorder.

Evidence for association at the best marker, as measured by correlation (r^2) in the 1000 Genomes Project data (74), of previously implicated loci. Where the previously reported SNP is not typed in our data we oriented the haplotypes to estimate the odds ratio for the risk allele allowing a one sided comparison. One-sided P values < 0.05 (for replication with the same risk allele) are highlighted in bold font. SCZ: Schizophrenia, BPD: Bipolar Disorder.

Chr	Position (b36)	Genes	SNP risk allele	Odds ratio	Phenot.	Previous studies	Best tag	r^2 1000 genomes	Frequency	P value (two-sided)	Odds ratio (95% CI)
1	98502934	<i>MIR137</i>	rs1625579-T	1.12	SCZ	(12)	rs1782810	0.975	0.8034	0.0641257	1.14 (0.99-1.31)
1	167903079	<i>BRP44, DCAF6</i>	rs10489202-A	1.23	SCZ	(21)	rs10489202	1.000	0.2312	0.310317	1.07 (0.94-1.21)
1	243608967	-	rs6703335-G	1.09	SCZ	(12)	rs6703335	1.000	0.4324	0.476216	0.96 (0.86-1.07)
2	58222928	<i>VRK2</i>	rs2312147-C	1.09	SCZ	(24, 76)	rs1518395	1.000	0.6172	0.740698	0.98 (0.88-1.1)
2	193984621	<i>PCGEM1</i>	rs17662626-A	1.2	SCZ	(12)	rs17666314	0.633	0.942	0.810016	1.03 (0.82-1.29)
3	36862980	-	rs4624519-T	1.09	SCZ	(12)	rs4624519	1.000	0.6264	0.709072	1.02 (0.91-1.14)
3	52821011	<i>ITIH1, NEK4</i>	rs1042779-A	1.19	BPD	(38, 119)	rs1042779	1.000	0.6237	0.357295	1.05 (0.94-1.18)
3	52855229	<i>ITIH3, ITIH4</i>	rs2239547-T	1.1	SCZ	(12)	rs1573815	0.786	0.7678	0.283078	1.07 (0.94-1.22)
3	180550702	<i>FXR1</i>	rs6782299-T	1.1	SCZ	(26)	rs6782299	1.000	0.7294	0.822086	1.01 (0.9-1.14)
4	103457418	<i>NFKB1</i>	rs230529-T	1.45	SCZ	(78)	rs230529	1.000	0.3895	0.363959	1.05 (0.94-1.17)
5	94154588	<i>MCTP1</i>	rs17418283-C	1.21	BPD	(38)	rs255339	0.834	0.2968	0.0838988	1.11 (0.99-1.25)
6	27143883	<i>MHC</i>	rs13194053-T	1.22	SCZ	(23, 26)	rs7745603	0.866	0.7697	0.103731	1.11 (0.98-1.27)
6	27248931	<i>MHC</i>	rs6932590-T	1.16	SCZ	(24, 26, 79, 80)	rs6938200	0.874	0.7947	0.219974	1.09 (0.95-1.25)
6	28227604	<i>MHC, NKAPL</i>	rs1635-G	1.28	SCZ	(81)	rs2299030	0.909	0.03693	0.265435	1.16 (0.89-1.52)
6	30174131	<i>MHC, TRIM26</i>	rs2021722-C	1.15	SCZ	(12)	rs2517611	1.000	0.8058	0.418896	0.95 (0.83-1.08)
6	32172993	<i>MHC, NOTCH4</i>	rs3131296-G	1.19	SCZ	(24, 80)	rs2071278	1.000	0.8534	0.61264	1.04 (0.89-1.22)
6	32602269	<i>MHC, HLA-DQA1</i>	rs9272219-G	1.14	SCZ	(23)	rs9272219	1.000	0.7105	0.0740771	1.12 (0.99-1.26)
6	89732101	<i>GABRR1</i>	rs12201676-C	1.31	SCZ & BPD	(82)	rs12201676	1.000	0.2452	0.211557	1.08 (0.96-1.22)
7	145959243	<i>CNTNAP2</i>	rs802568-C	2.03	SCZ & BPD	(82)	rs802568	1.000	0.02746	0.197092	1.22 (0.9-1.65)
7	156048649	<i>LOC393076</i>	rs10949808-T	1.27	SCZ & BPD	(82)	rs10949808	1.000	0.397	0.224947	1.07 (0.96-1.19)
8	4180844	<i>CSMD1</i>	rs10503253-A	1.16	SCZ	(12)	rs10103330	1.000	0.1993	0.807814	1.02 (0.89-1.16)

8	38031345	<i>LSM1, WHSC1L1</i>	rs16887244-A	1.19	SCZ	(21)	rs16887244	1.000	0.7614	0.436771	1.05 (0.93-1.19)
8	58840924	<i>FAM110B</i>	rs1992045-T	1.56	SCZ & BPD	(82)	rs1992045	1.000	0.07363	0.125349	0.85 (0.69-1.05)
8	89760311	<i>MMP16</i>	rs7004633-A	1.11	SCZ	(12, 83)	rs7005110	1.000	0.1925	0.914021	0.99 (0.87-1.14)
9	121359286	<i>ASTN2</i>	rs11789399-G	1.29	SCZ & BPD	(82)	rs11789399	1.000	0.4962	0.415783	0.96 (0.86-1.06)
10	62179812	<i>ANK3</i>	rs10994336-T	1.45	BPD	(33, 38, 84-87)	rs3808943	0.858	0.05389	0.209758	0.85 (0.66-1.1)
10	62279124	<i>ANK3</i>	rs10994397-T	1.22	BPD	(28)	rs3808943	0.858	0.05389	0.209758	0.85 (0.66-1.1)
10	104775908	<i>CNNM2</i>	rs7914558-G	1.22	SCZ	(12, 88)	rs10509757	1.000	0.5927	0.131729	1.09 (0.98-1.21)
10	104906211	<i>NT5C2</i>	rs11191580-T	1.2	SCZ	(12, 88)	rs11191580	1.000	0.9169	0.912034	1.01 (0.83-1.23)
11	17160148	-	rs4356203-G	1.09	SCZ	(12)	rs4356203	1.000	0.4236	0.342312	0.95 (0.85-1.06)
11	66551002	Multiple	rs10896135-G	1.12	BPD	(28)	rs4930390	1.000	0.2557	0.901194	0.99 (0.88-1.12)
11	79077193	<i>ODZ4</i>	rs12576775-G	1.14	BPD	(28)	rs7932890	1.000	0.1737	0.259849	1.08 (0.94-1.24)
11	98125404	<i>CNTN5</i>	rs2509843-C	1.27	SCZ & BPD	(82)	rs2848547	1.000	0.3711	0.400322	0.95 (0.86-1.06)
11	124606285	<i>NRGN</i>	rs12807809-T	1.15	SCZ	(24, 80, 89)	rs1939214	0.972	0.8282	0.0051205	1.23 (1.06-1.43)
12	2345295	<i>CACNA1C</i>	rs1006737-A	1.18	SCZ & BPD	(15, 33, 37, 38, 90)	rs1006737	1.000	0.3265	0.353821	1.05 (0.94-1.18)
12	2419896	<i>CANCNA1C</i>	rs4765913-A	1.14	BPD	(28)	rs4765914	0.935	0.8061	0.432068	0.95 (0.83-1.08)
13	42653437	<i>DGKH</i>	rs1012053-A	1.59	BPD	(91-93)	rs1170188	0.806	0.8133	0.26017	1.08 (0.94-1.24)
13	106651661	<i>DAOA</i>	rs4996815-C	1.28	SCZ & BPD	(82)	rs4996815	1.000	0.3576	0.737436	1.02 (0.91-1.14)
15	38995491	Multiple	rs12899449-A	1.2	BPD	(33)	rs12899449	1.000	0.7063	0.441365	1.05 (0.93-1.18)
16	23634026	Multiple	rs420259-A	2.08	BPD	(34, 66, 94, 95)	rs420259	1.000	0.7306	0.517701	0.96 (0.85-1.08)
18	52752017	<i>CCDC68</i>	rs12966547-G	1.4	SCZ	(12)	rs11874716	1.000	0.567	0.0379359	1.12 (1.01-1.25)
18	53058238	<i>TCF4</i>	rs17594526-T	1.44	SCZ	(26)	rs17594526	1.000	0.0321	0.915797	1.02 (0.76-1.36)
19	19361735	<i>NCAN</i>	rs1064395-A	1.17	SCZ & BPD	(30, 96)	rs1064395	1.000	0.1639	0.543254	0.96 (0.83-1.1)
20	19852503	<i>RIN2</i>	rs6046396-G	1.28	SCZ & BPD	(82)	rs6046396	1.000	0.3015	0.57124	1.03 (0.92-1.16)

Table 2: Loci where we found the strongest evidence of association.

Evidence of association across the discovery sample and the PCG and SGENE replication collections as also shown as a forest plot in Supplementary figure 3. We report P values, odds ratios (and 95% confidence intervals) for these cohorts and the combined evidence (using an inverse variance weighted fixed effects approach). We also show the log₁₀ Bayes factor (BF) for models assuming effects to be either the same (fixed) or related (allowing heterogeneity). Note that the discovery sample odds ratios and P values presented in this table are based on a sub-set of our sample that did not overlap with the replication cohorts, therefore the P values may vary from those presented in supplementary figure 2, which includes all our discovery dataset.

Chr.	SNP (risk allele)	Position (Build 36)	Discovery <i>P</i> Odds ratio (95% CI)	Replication <i>P</i> Odds ratio (95% CI)	Combined <i>P</i> Odds ratio (95% CI)	log ₁₀ BF same	log ₁₀ BF related
3	rs743393-C	37718972	9.40E-06 1.301 (1.157 - 1.462)	0.039 1.043 (1.002 - 1.085)	7.40E-04 1.067 (1.028 - 1.108)	1.43	2.64
7	rs968794-A	10856010	8.30E-07 1.324 (1.184 - 1.480)	0.014 1.050 (1.010 - 1.091)	8.40E-05 1.076 (1.037 - 1.116)	2.3	3.87
12	rs4761708-C	92276217	1.40E-04 1.291 (1.130 - 1.476)	0.024 1.058 (1.007 - 1.110)	6.40E-04 1.083 (1.034 - 1.133)	1.56	2.18

FIGURE LEGENDS**Figure 1: Replication of previously published associated schizophrenia (SZ) and bipolar disorder (BP) loci.**

Reported odds ratios from the literature (x axis) plotted against the odds ratios estimated from our data as listed in Table 1 (y axis). The dotted line indicates an odds ratio of 1 in our data. Points above the line indicate the same direction of effect in previous studies and our data. Black circles indicate SNPs that replicate (P one-sided < 0.05) in our study. Triangles denote SNPs within the MHC region. Sign tests for an enrichment of effect in the same direction are presented for loci previously associated with schizophrenia, bipolar disorder or both. Further details on the sign tests are available in Supplementary Table 4.

Figure 2: Quantile-quantile plots of the distribution of observed and expected P value at all autosomal SNPs passing quality control. The genomic control lambda value was 1.03. This represents analyses conducted on our entire discovery sample (n=4835).

Figure 3: Regional association plots for the three SNPs reported in Table 2.

The plots show the evidence of association in our discovery data at genotyped SNPs. The SNP listed in Table 2 is indicated with a diamond and flanking SNPs (circles) are coloured according to their correlations (r^2) with this SNP measured in HapMap.

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