Genome-wide significant locus for Research Diagnostic Criteria Schizoaffective Disorder Bipolar Type.

Elaine K Green[1], Arianna Di Florio[2, 3], Liz Forty[2], Katherine Gordon-Smith[4], Detelina Grozeva[5], Christine Fraser[2], Alex Richards[2], Jennifer L Moran[6], Shaun Purcell[6,7], Pamela Sklar[6,7] George Kirov[2], Michael J Owen[2], Michael C O'Donovan[2], Nick Craddock[2], Lisa Jones[4], Ian R Jones[2].

[1]School of Biomedical and Healthcare Sciences, Plymouth University Peninsula Schools of Medicine and Dentistry, Portland Square Building, Drake Circus, Plymouth PL4 8AA
[2]MRC Centre for Neuropsychiatric Genetics and Genomics, Institute of Psychological Medicine and Clinical Neurosciences, Cardiff University, Cardiff, CF24 4HQ, UK
[3]Department of Psychiatry, University of North Carolina at Chapel Hill, USA
[4]Department of Psychological Medicine, Worcester University, WR2 6AJ, UK
[5]Department of Medical Genetics, Cambridge Institute for Medical Research, University of Cambridge, Cambridge, UK
[6]Stanley Center for Psychiatric Research, The Broad Institute of MIT and Harvard, 7 Cambridge Center, Cambridge, MA 02142, USA
[7]Division of Psychiatric Genomics in the Department of Psychiatry, Friedman Brain Institute, and Institute for Genomics and Multiscale Biology, Icahn School of Medicine, Mount Sinai, New York, NY, USA

Running Title: GWS association with RDC-SABP.

*Correspondence: Dr E K Green, School of Biomedical and Healthcare Sciences, Plymouth University Peninsula Schools of Medicine and Dentistry, Portland Square Building, Drake Circus, Plymouth PL4 8AA. UK (Email: elaine.green@plymouth.ac.uk, tel: 44 (0)1752584465, fax: 44 (0)1752584605).

Abstract

Studies have suggested that Research Diagnostic Criteria for Schizoaffective Disorder Bipolar type (RDC-SABP) might identify a more genetically homogenous subgroup of bipolar disorder. Aiming to identify loci associated with RDC-SABP we have performed a replication study using independent RDC-SABP cases (n=144) and controls (n=6,559), focusing on the 10 loci that reached a P-value $<10^{-5}$ for RDC-SABP in the Wellcome Trust Case Control Consortium (WTCCC) bipolar disorder sample. Combining the WTCCC and replication datasets by meta-analysis (combined RDC-SABP, n=423, Controls, n=9,494) we observed genome-wide significant association at one SNP, rs2352974, located within the intron of the gene *TRAIP* on chromosome 3p21.31 (P-value, 4.37×10^{-8}). This locus did not reach genome-wide significance in bipolar disorder or schizophrenia large Psychiatric Genomic Consortium datasets, suggesting that it may represent a relatively specific genetic risk for the bipolar subtype of schizoaffective disorder.

Key Words:

Schizoaffective disorder bipolar type, *TRAIP*, Research Diagnostic Criteria, SABP

Introduction

In the recent years many successful large scale genome studies have identified genetic susceptibility loci, including common, rare and structural variants which confer risk individually to schizophrenia (SZ) and bipolar disorder (BD), and a combination of such disorders (PGC-BD, 2011; PGC-SZ, 2014; Kirov, 2015; Green *et al*., 2016). Often such studies, in addition to probands with BD and SZ, include a group which meet criteria for schizoaffective disorder. Traditional family studies have shown evidence of familial overlap between schizoaffective disorder and both SZ and BD, which has been confirmed by Scandinavian population registered based studies (Cardno & Owen, 2014). Depending on the proportion of cases diagnosed as schizoaffective disorder, the inclusion of these individuals may impact on the genetic findings when considering the relationship between SZ and BD (Cardno & Owen, 2014).

The concept and diagnostic criteria for Schizoaffective Disorder (SAD) have been controversial with DSM-IV-TR noting that the SAD category "fills a necessary and important hole in the diagnostic system, but unfortunately it does not do its job very well". The approaches taken by the various classification systems have differed, with Research Diagnostic Criteria (RDC) for schizoaffective disorder bipolar type broader than those proposed by the World Health Organisation and the American Psychiatric Association (Spitzer *et al*., (1978)). RDC does not require psychotic symptoms in the absence of a mood episode and rather gives a list of specific psychotic symptoms "suggesting schizophrenia" occurring in a manic episode that would point to a diagnosis of SABP. These differences result in more patients being diagnosed in the schizoaffective categories under RDC compared to the ICD and DSM systems.

Genetic studies focusing on individuals rated by Research Diagnostic Criteria as Schizoaffective Disorder Bipolar type (RDC-SABP) have previously been performed. Examining the Wellcome Trust Case Control Consortium dataset (WTCCC, 2007), we noted that RDC-SABP stood out from other subsets of the BD sample as having a significantly excess of strong association signals ($P<10^{-5}$) and hence 'may be of particular use to for identifying common susceptibility loci GWAS' (Hamshere *et al*., 2009). In addition, variation at genes encoding $GABA_A$–receptor subunits were associated with risk of RDC-SABP and this association was relatively specific to this diagnostic subset, with no association to SZ or BD (Craddock *et al*., 2010). This finding was replicated in an independent study (Breuer *et al*., 2011). Finally, polygenic score analysis of RDC-SABP using SZ derived polygenic scores showed that the polygenic influences on SZ had a greater overlap with SABP than those for the remaining BD individuals (Hamshere *et al*., 2011).

Aiming to identify loci that are associated with RDC-SABP at statistically stringent levels of significance (P-value $< 5x10^{-8}$) we have genotyped a replication sample using the Illumina Infinium

HD genotyping array, the ImmunoChip, focusing on the 10 SNPs that reached a P-value threshold of $< 10^{-5}$ in the WTCCC study (Hamshere *et al*., 2009), and combined the 2 datasets by meta-analysis (total RDC-SABP cases, n= 423 and controls, n= 9,494).

Materials and Methods

Samples

All participants were unrelated, white European, living in the British Isles. The protocols and procedures were approved by the relevant ethics review panels where patients were recruited.

Original WTCCC sample set.

The WTCCC bipolar disorder sample and dataset has been previously reported, and as such the sample and collection information is not included (WTCCC, 2007). Analyses of subsets of these BD samples, including those individuals rated as RDC-SABP have also been reported (n = 279) (Hamshere *et al*., 2009; Craddock *et al*., 2010; Green *et al*., 2010). RDC is a broader definition of SABP, and provide more delineation between individuals on the basis of the pattern of mood psychotic symptomatology than rating by DSM-IV (APA, 1994; Hamshere *et al*., 2011). Inter-rater reliability was formally assessed using 20 random cases. Mean kappa statistics were 0.86 for RDC.

Replication sample set

The independent replication RDC-SABP (n=144) sample set was part of the bipolar disorder sample, the BDRN sample (n=1,849). A description of this BD collection has been detailed in Green *et al*., (2013, 2016). WTCCC2 set was used as the control sample (n = 6,599), and the characteristics and recruitment of which have been described in WTCCC 2007. These controls are not screened to exclude the presence of psychiatric illness.

Genotyping

The genotyping was performed using the custom Illumina Infinium HD genotyping array, the ImmunoChip. The ImmunoChip BD genotyping study has been previously reported for the 1218 BD cases and 2913 controls (Green *et al*., 2013) but not for the subset of RDC SABP cases. Additional samples were genotyped at University College London (UCL) to increase the sample size, including 631 BD cases (44 RDC-SABP cases) and 3,646 WTCCC2 controls. In total, the replication RDC-SABP sample consists of 144 RDC-SABP cases and 6,556 WTCCC2 controls, which are independent of the original WTCCC GWAS.

This study focuses on 10 SNPs that were included on the ImmunoChip as part of the 'investigator-specific SNP selection for replication' and were independently associated SNPs ($r^2 < 0.2$) with an association signal of $P<10^{-5}$ for RDC-SABP cases against controls in our previous study Hamshere *et al*., 2009[12]. It is worth noting that in this study the Cochran-Armitage trend test of genotype distributions with disease was employed, whereas the data presented here was analysed using logistic regression of disease state with a genomic inflation factor (λ) of 1.06. As such the P-values and ORs stated may differ slightly from the original publication and the P-values for 2 SNPs are slightly $> 10^{-5}$. We note that following Principal Component analysis (data shown in supplementary methods) SNP rs2352974 remains genome-wide significant when combined with the replication dataset by meta-analysis.

Statistical analysis

A brief summary of the methodology is described here and more detailed description is available in the Supplementary Materials section. The BDRN sample set was genotyped on the ImmunoChip at either the Sanger Institute or UCL sequencing facility. The bipolar disorder dataset genotyped at the Sanger Institute has been published (Green *et al*., 2013) and this genotype calling and quality control pipeline was implemented for the sample genotyped at UCL. Briefly, the genotypes were called by GenoSNP software (Giannoulatou *et al*., 2008). The data management and quality control assessment was performed using PLINK (v1.07) (Purcell et al., 2007) and a series of shell scripts initially for all BD and control samples.

We planned to combine the data genotyped at the two centres. In order to highlight any potential 'batch effects' problems that might prevent the combining of the data, we included 9 identical samples from the first centre to be genotyped by UCL. The concordance rate for the 9 samples across overlapping SNPs (n=96,184) was very high reaching 99.997%. Thus we felt confident in combining the datasets.

From the total BD dataset, 144 RDC-SABP and controls were extracted (n = 6,556) and quality control analysis performed. Principal Component Analysis (PCA) was performed with Eigenstrat on the combined sample and any individual outliers that did not cluster near to the HapMap European individuals were removed in order to maximise the ethnic homogeneity of our sample (Patterson *et al*., 2006; Price *et al.,* 2006). The genomic inflation factor was calculated using 43K SNPs in relative linkage (α=1).

Meta-analysis

The RDC-SABP replication dataset was combined with the original RDC-SABP (WTCCC 2007) dataset by fixed-effects meta-analysis using PLINK (v1.07) (Purcell *et al*., 2007) to estimate a common odds ratio weighted by individual study standard errors (SE).

Results

An independent replication sample of 144 cases (RDC-SABP) and 6,559 controls SNPs were genotyped on the ImmunoChip Illumina array. We have focused on 10 SNPs that showed an independent association ($r^2 < 0.2$) signal at $P < 10^{-5}$ for RDC-SABP against controls in our previous study of the WTCCC dataset previously (Hamshere *et al*., (2009)). We combined our replication data with the WTCCC SNP data by fixed effect meta-analysis. SNP, rs2352974, on chromosome 3p21.31 met genome-wide association (P-value = 4.37×10^{-8}, OR=0.67). This SNP resides within the intronic region of the gene, *TRAIP* (TRAF interacting protein).

A meta-analysis of all SNPs on the ImmunoChip was also performed (data not presented). No additional individual SNP was associated at levels that exceed the accepted genome-wide levels of significance ($P < 5 \times 10^{-8}$).

SNP	CHR	BP	A1	A2	WTCCC RDC-SABP data				Immunochip, RDC_SABP data				Meta-analysis		Gene
					Cases MAF	Controls MAF	P-Value	OR [95%CI]	Cases MAF	Controls MAF	P-Value	OR	P-Value	OR	
rs4027132	2	12037492	G	A	0.357	0.459	7.69E-06	0.654 [0.546-0.783]	0.486	0.457	0.332	1.122 [0.889-1.417]	0.0038	0.807 [0.698-0.933]	*LPIN1* (70kb)
rs2352974	3	49890613	T	C	0.387	0.499	1.01E-06	0.631 [0.528-0.755]	0.413	0.493	0.0084	0.728 [0.575-0.922]	**4.37E-08**	**0.666 [0.569-0.780]**	***TRAIP* (0kb)**
rs4279178*	4	47068330	A	G	0.401	0.509	2.96E-06	0.647 [0.542-0.772]	0.444	0.482	0.208	0.860 [0.681-1.087]	8.24E-06	0.721 [0.624-0.832]	*GABRB1* (0kb)
rs7680321	4	47145107	C	T	0.136	0.079	1.02E-05	1.833 [1.412-2.381]	0.118	0.090	0.109	1.342 [0.937-1.923]	7.03E-06	1.606 [1.306-1.975]	*GABRB1* (0kb)
rs13154602	5	76395917	A	C	0.363	0.269	3.59E-06	1.578 [1.308-1.903]	0.267	0.282	0.574	0.927 [0.711-1.208]	6.35E-04	1.132 [1.123-1.534]	*ZBED3-ASI* (0kb)
rs1171115	6	84229623	C	T	0.357	0.264	9.81E-06	1.518 [1.268-1.817]	0.302	0.275	0.308	1.141 [0.885 -1.472]	3.00E-05	1.375 [1.184-1.597]	*PRSS35* (0kb)
rs7990962	13	43399245	G	A	0.253	0.173	6.92E-06	1.617 [1.319-1.983]	0.163	0.180	0.474	0.892 [0.654-1.218]	8.83E-04	1.343 [1.129-1.598]	*LINC01050*|*LINC00428* (24.5kb|17.3kb)
rs16942644	15	89612736	A	G	0.171	0.102	2.00E-06	1.815 [1.429-2.304]	0.135	0.111	0.197	1.252 [0.890-1.763]	4.00E-06	1.599 [1.310-1.952]	*ABHD2* (18.7kb)
rs4786811	16	6132787	G	A	0.041	0.014	1.10E-05	2.981 [1.858-4.785]	0.010	0.018	0.368	0.592 [0.189-1.855]	2.25E-04	2.324 [1.484 -3.638]	*RBFOX1* (0kb)
rs4818065	21	41037723	A	G	0.272	0.182	6.97E-07	1.685 [1.379-2.059]	0.184	0.187	0.905	0.982 [0.726-1.328]	5.63E-05	1.419 [1.197-1.683]	*B3GALT5* (2.9kb)

Table 1. Meta-analysis of WTCCC RDC-SABP (cases n=279, controls n=2,938) and ImmunoChip RDC-SABP data (cases n=144, controls n=9,497).

Abbreviations: CHR, chromosome; BP, position in base pairs for UCSC Build hg19; A1, allele 1; A2, allele 2; WTCCC, Wellcome Trust Case Control Consortium; MAF, minor allele frequency; OR, odds ratio; RDC, Research Diagnostic Criteria; SABP, Schizoaffective disorder, Bipolar type; Gene, gene symbol is followed by the distance between the SNP and the reference sequence gene location.
The SNPs listed are those with an independent association ($r^2 < 0.2$) signal at $P < 10^{-5}$ for Research Diagnostic Criteria Schizoaffective disorder, Bipolar type (RDC-SABP) against controls previously reported by Hamshere *et al*., (2009) analysed originally using the Cochran-Armitage Trend test, here an updated analysis of the WTCCC RDC-SABP dataset has been performed using logistic regression of disease state with a genomic inflation factor (λ) of 1.06, as such P-values and OR may alter slightly from the original publication. Note: rs4786811 is included in the meta-analysis although the MAF is < 0.05 in both cases and controls. rs6414684 was merged with rs4279178*.

Discussion

Combining an independent sample with our previous dataset (Hamshere *et al*., 2009), we report a novel locus reaching genome-wide significant association with RDC-SABP at the intronic SNP rs2352974 (P-Value = $4.37x10^{-8}$, OR= 0.67) on chromosome 3p21.31 at *TRAIP* (TRAF interacting protein). In comparison, this loci was not genome-wide significantly associated in either the large Psychiatric Genomics Consortium (PGC) BD (P=0.39, OR=1.01) or SZ meta-analysis data (P=0.037, OR=0.98) (PGC-BD, 2011, PGC-SZ, 2014), suggesting that it may be a relatively specific genetic risk for bipolar subtype of schizoaffective disorder. The gene *TRAIP* encodes an E3 RING ubiquitin ligase. A recent study has reported that mutations within *TRAIP* are associated with microcephalic primordial dwarfism, and identified *TRAIP* as a component of the DNA damage response replication blocking DNA lesions (Harley *et al*., 2016).

There is much debate around the clinical usefulness and the nosological status of diagnostic category schizoaffective disorder. Discussions include whether schizoaffective disorder is a form of schizophrenia, affective disorder, a combination of the two or should be regarded as a separate disease entity (Craddock *et al*., 2009). To add to this there are concerns over the poor reliability of diagnosis (Maj *et al*. 2000; Santelmann *et al*., 2015) and apparent low diagnostic stability over time (Schwartz *et al*., 2000; Laursen *et al*., 2005). Our findings here, of a susceptibility locus specific (i.e. not identified in BD or SZ datasets) for RDC-SABP, combined with our previous genetic findings for SABP do further support the notion that SABP is a partly independent diagnostic category, with some specific biological characteristics not shared with other phenotypes (Craddock *et al*., 2009, 2010; Hamshere *et al.*, 2009). Larger well phenotypically defined samples, although challenging to collect, we envisage will enable the identification of additional risk loci that are specific to SABP, and loci that also confer risk to both or either BD and/or SZ.

In summary, within our UK RDC-SABP sample we have identified a genome-wide significantly associated locus at an intronic SNP in *TRAIP*. Our findings further indicate the importance of research examining clinical diagnostic phenotypes, which in turn will be ultimately important for clinical practice.

Acknowledgements

We are indebted to all individuals who have participated in, or helped with, our research. We particularly thank those involved with Bipolar UK-the Bipolar Organization and the Bipolar Disorder Research Network (www.BDRN.org). Sample collection and analysis was supported by the Wellcome Trust (grant 078901) and a grant from the Stanley Medical Research Institute via the Stanley Centre for Psychiatric Research at the Broad Institute of MIT and Harvard. Genotyping was supported by the Wellcome Trust under WTCCC.

Conflict of Interest Disclosure

Michael C O'Donovan has received a consultancy fee from Roche for participation in a discussion about using genetics to identify drug targets.

References

American Psychiatric Association. Diagnostic and Statistical Manual of Mental Disorders (4th edn) (DSM-IV). APA, 1994.

Breuer R, Hamshere ML, Strohmaier J, Mattheisen M, Degenhardt F, Meier S, Paul T, O'Donovan MC, Mühleisen TW, Schulze TG, Nöthen MM, Cichon S, Craddock N, Rietschel M. 2011. Independent evidence for the selective influence of GABA(A) receptors on one component of the bipolar disorder phenotype. Mol Psychiatry 16: 587-589.

Cardno AG, Owen MJ. 2014. Genetic relationships between schizophrenia, bipolar disorder, and schizoaffective disorder. Schizophr Bull 40: 504-515.

Craddock N, O'Donovan MC, Owen MJ. 2009. Psychosis genetics: modeling the relationship between schizophrenia, bipolar disorder, and mixed (or "schizoaffective") psychoses. Schizophr Bull 35: 482-490.

Craddock N, Jones L, Jones IR, Kirov G, Green EK, Grozeva D, Moskvina V, Nikolov I, Hamshere ML, Vukcevic D, Caesar S, Gordon-Smith K, Fraser C, Russell E, Norton N, Breen G, St Clair D, Collier DA, Young AH, Ferrier IN, Farmer A, McGuffin P, Holmans PA; Wellcome Trust Case Control Consortium (WTCCC), Donnelly P, Owen MJ, O'Donovan MC. 2010. Strong genetic evidence for a selective influence of GABAA receptors on a component of the bipolar disorder phenotype. Mol Psychiatry 15: 146-153.

Giannoulatou E, Yau C, Colella S, Ragoussis J, Holmes CC. 2008. GenoSNP: a variational Bayes within sample SNP genotyping algorithm that does not require a reference population. Bioinformatics 24: 2209–2214.

Green EK, Hamshere M, Forty L, Gordon-Smith K, Fraser C, Russell E, Grozeva D, Kirov G, Holmans P, Moran JL, Purcell S, Sklar P, Owen MJ, O'Donovan MC, Jones L, WTCCC, Jones IR, Craddock N. 2013. Replication of bipolar disorder susceptibility alleles and identification of two novel genome-wide significant associations in a new bipolar disorder case-control sample. Mol Psychiatry 18: 1302-1307.

Green EK, Grozeva D, Moskvina V, Hamshere ML, Jones IR, Jones L, Forty L, Caesar S, Gordon-Smith K, Fraser C, Russell E, St Clair D, Young AH, Ferrier N, Farmer A, McGuffin P, Holmans PA, Owen MJ, O'Donovan MC, Craddock N. 2010. Variation at the GABAA receptor gene, Rho 1 (GABRR1) associated with susceptibility to bipolar schizoaffective disorder. Am J Med Genet B Neuropsychiatr Genet 153B: 1347-9.

Green EK, Rees E, Walters JT, Smith KG, Forty L, Grozeva D, Moran JL, Sklar P, Ripke S, Chambert KD, Genovese G, McCarroll SA, Jones I, Jones L, Owen MJ, O'Donovan MC, Craddock N, Kirov G. 2016. Copy number variation in bipolar disorder. Mol Psychiatry 21:89-93.

Giannoulatou E, Yau C, Colella S, Ragoussis J, Holmes CC. 2008. GenoSNP: a variational Bayes within sample SNP genotyping algorithm that does not require a reference population. Bioinformatics 24: 2209–2214.

Hamshere ML, Green EK, Jones IR, Jones L, Moskvina V, Kirov G, Grozeva D, Nikolov I, Vukcevic D, Caesar S, Gordon-Smith K, Fraser C, Russell E, Breen G, St Clair D, Collier DA, Young AH, Ferrier IN, Farmer A, McGuffin P; Wellcome Trust Case Control Consortium., Holmans PA, Owen MJ, O'Donovan MC, Craddock N. 2009. Genetic utility of broadly defined bipolar schizoaffective disorder as a diagnostic concept. Br J Psychiatry 195: 23-29.

Hamshere ML, O'Donovan MC, Jones IR, Jones L, Kirov G, Green EK, Moskvina V, Grozeva D, Bass N, McQuillin A, Gurling H, St Clair D, Young AH, Ferrier IN, Farmer A, McGuffin P, Sklar P, Purcell S, Holmans PA, Owen MJ, Craddock N. 2011. Polygenic dissection of the bipolar phenotype. Br J Psychiatry 198: 284-288.

Harley ME, Murina O, Leitch A, Higgs MR, Bicknell LS, Yigit G, Blackford AN, Zlatanou A, Mackenzie KJ, Reddy K, Halachev M, McGlasson S, Reijns MA, Fluteau A, Martin CA, Sabbioneda S, Elcioglu NH, Altmüller J, Thiele H, Greenhalgh L, Chessa L, Maghnie M, Salim M, Bober MB, Nürnberg P, Jackson SP, Hurles ME, Wollnik B, Stewart GS, Jackson AP. 2016. TRAIP promotes DNA damage response during genome replication and is mutated in primordial dwarfism. Nat Genet 48: 36-43

Kirov G. 2015. CNVs in neuropsychiatric disorders.Hum Mol Genet 24: R45-49.

Laursen TM, Labouriau R, Licht RW, Bertelsen A, Munk-Olsen T, Mortensen PB. 2005. Family history of psychiatric illness as a risk factor for schizoaffective disorder: a Danish register-based cohort study. Arch Gen Psychiatry 62: 841-848.

Malaspina D, Owen MJ, Heckers S, Tandon R, Bustillo J, Schultz S, Barch DM, Gaebel W, Gur RE, Tsuang M, Van Os J, Carpenter W. 2013. Schizoaffective Disorder in the DSM-5. Schizophr Res 150: 21-5.

Maj M, Pirozzi R, Formicola AM, Bartoli L, Bucci P. 2000. Reliability and validity of the DSM-IV diagnostic category of schizoaffective disorder: preliminary data. J Affect Disord 57: 95-8.

Psychiatric GWAS Consortium Bipolar Disorder Working Group, Sklar P, Ripke S, Scott LJ, Andreassen OA, Cichon S, Craddock N, Edenberg HJ Jr, Nurnberger JI, Rietschel M, Blackwood D, Corvin A, Flickinger M, Guan W, Mattingsdal M, McQuillen A, Kwan P, Wienker TF, Daly M, Dudbridge F, Holmans PA, Lin D, Burmeister M, Greenwood TA, Hamshere ML, Muglia P, Smith EN, Zandi PP, Nievergelt CM, McKinney R, Shilling PD, Schork NJ, Bloss CS, Foroud T, Koller DL, Gershon ES, Liu C, Badner JA, Scheftner WA, Lawson WB, Nwulia EA, Hipolito M, Coryell W, Rice J, Byerley W, McMahon FJ, Schulze TG, Berrettini W, Lohoff FW, Potash JB, Mahon PB, McInnis MG, Zöllner S, Zhang P, Craig DW, Szelinger S, Barrett TB, Breuer R, Meier S, Strohmaier J, Witt SH, Tozzi F, Farmer A, McGuffin P, Strauss J, Xu W, Kennedy JL, Vincent JB, Matthews K, Day R, Ferreira MA, O'Dushlaine C, Perlis R, Raychaudhuri S, Ruderfer D, Lee PH, Smoller JW, Li J, Absher D, Bunny WE, Barchas JD, Schatzberg AF, Jones EG, Meng F, Thompson RC, Watson SJ, Myers RM, Akil H, Boehnke M, Chambert K, Moran J, Scolnick E, Djurovic S, Melle I, Morken G, Gill M, Morris D, Quinn E, Mühleisen TW, Degenhardt FA, Mattheisen M, Schumacher J, Maier W, Steffans M, Propping P, Nöthen MM, Anjorin A, Bass N, Gurling H, Kandaswamy R, Lawrence J, McGhee K, McIntosh A, McLean AW, Muir WJ, Pickard BS, Breen G, St Clair D, Caesar S, Gordon-Smith K, Jones L, Fraser C, Green EK, Frozeva D, Jones IR, Kirov G, Moskvina V, Nikolov I, O'Donovan MC, Owen MJ, Collier DA, Elkin A, Williamson R, Young AH, Ferrier IN, Stefansson K, Stefansson H, Porgeirsson P, Steinberg S, Gustafsson Ó, Bergen SE, Nimgaonkar V, Hultman C, Landén M, Lichtenstein P, Sullivan P, Schalling M, Osby U, Backlund L, Frisén L, Langstrom N, Jamain S, Leboyer M, Etain B, Bellivier F, Petursson H, Sigurđsson E, Müller-Mysok B, Lucae S, Schwarz M, Fullerton JM, Schofield PR, Martin N, Montgomery GW, Lathrop M, Óskarsson H, Bauer M, Wright A, Mitchell PB, Hautzinger M, Reif A, Kelsoe JR, Purcell SM. 2011. Large-scale genome-wide association analysis of bipolar disorder identifies a new susceptibility locus near ODZ4. Nat Genet 43: 977-983.

Patterson N, Price AL, Reich D. 2006. Population structure and eigen analysis. PLoS Genet 2: e190.

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

Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MA, Bender D, Maller J, Sklar P, de Bakker PI, Daly MJ, Sham PC. 2007. PLINK: a tool set for whole-genome association and population-based linkage analyses. Am J Hum Genet 81:559–575.

Santelmann H, Franklin J, Bußhoff J, Baethge C. 2015. Test-retest reliability of schizoaffective disorder compared with schizophrenia, bipolar disorder, and unipolar depression--a systematic review and meta-analysis. Bipolar Disord. 17: 753-68.

Schwartz JE, Fennig S, Tanenberg-Karant M, Carlson G, Craig T, Galambos N, Lavelle J, Bromet EJ. 2000. Congruence of diagnoses 2 years after a first-admission diagnosis of psychosis. Arch Gen Psychiatry. 57: 593-600.

Schizophrenia Working Group of the Psychiatric Genomics Consortium. Ripke S, Neale BM, Corvin A, Walters JT, Farh KH, Holmans PA, Lee P, Bulik-Sullivan B, Collier DA, Huang H, Pers TH, Agartz I, Agerbo E, Albus M, Alexander M, Amin F, Bacanu SA, Begemann M, Belliveau RA Jr, Bene J, Bergen SE, Bevilacqua E, Bigdeli TB, Black DW, Bruggeman R, Buccola NG, Buckner RL, Byerley W, Cahn W, Cai G, Campion D, Cantor RM, Carr VJ, Carrera N, Catts SV, Chambert KD, Chan RC, Chen RY, Chen EY, Cheng W, Cheung EF, Chong SA, Cloninger CR, Cohen D, Cohen N, Cormican P, Craddock N, Crowley JJ, Curtis D, Davidson M, Davis KL, Degenhardt F, Del Favero J, Demontis D, Dikeos D, Dinan T, Djurovic S, Donohoe G, Drapeau E, Duan J, Dudbridge F, Durmishi N, Eichhammer P, Eriksson J, Escott-Price V, Essioux L, Fanous AH, Farrell MS, Frank J, Franke L, Freedman R, Freimer NB, Friedl M, Friedman JI, Fromer M, Genovese G, Georgieva L, Giegling I, Giusti-Rodríguez P, Godard S, Goldstein JI, Golimbet V, Gopal S, Gratten J, de Haan L, Hammer C, Hamshere ML, Hansen M, Hansen T, Haroutunian V, Hartmann AM, Henskens FA, Herms S, Hirschhorn JN, Hoffmann P, Hofman A, Hollegaard MV, Hougaard DM, Ikeda M, Joa I, Julià A, Kahn RS, Kalaydjieva L, Karachanak-Yankova S, Karjalainen J, Kavanagh D, Keller MC, Kennedy JL, Khrunin A, Kim Y, Klovins J, Knowles JA, Konte B, Kucinskas V, Ausrele Kucinskiene Z, Kuzelova-Ptackova H, Kähler AK, Laurent C, Keong JL, Lee SH, Legge SE, Lerer B, Li M, Li T, Liang KY, Lieberman J, Limborska S, Loughland CM, Lubinski J, Lönnqvist J, Macek M Jr, Magnusson PK, Maher BS, Maier W, Mallet J, Marsal S, Mattheisen M, Mattingsdal M, McCarley RW, McDonald C, McIntosh AM, Meier S, Meijer CJ, Melegh B, Melle I, Mesholam-Gately RI,

Metspalu A, Michie PT, Milani L, Milanova V, Mokrab Y, Morris DW, Mors O, Murphy KC, Murray RM, Myin-Germeys I, Müller-Myhsok B, Nelis M, Nenadic I, Nertney DA, Nestadt G, Nicodemus KK, Nikitina-Zake L, Nisenbaum L, Nordin A, O'Callaghan E, O'Dushlaine C, O'Neill FA, Oh SY, Olincy A, Olsen L, Van Os J, Pantelis C, Papadimitriou GN, Papiol S, Parkhomenko E, Pato MT, Paunio T, Pejovic-Milovancevic M, Perkins DO, Pietiläinen O, Pimm J, Pocklington AJ, Powell J, Price A, Pulver AE, Purcell SM, Quested D, Rasmussen HB, Reichenberg A, Reimers MA, Richards AL, Roffman JL, Roussos P, Ruderfer DM, Salomaa V, Sanders AR, Schall U, Schubert CR, Schulze TG, Schwab SG, Scolnick EM, Scott RJ, Seidman LJ, Shi J, Sigurdsson E, Silagadze T, Silverman JM, Sim K, Slominsky P, Smoller JW, So HC, Spencer CA, Stahl EA, Stefansson H, Steinberg S, Stogmann E, Straub RE, Strengman E, Strohmaier J, Stroup TS, Subramaniam M, Suvisaari J, Svrakic DM, Szatkiewicz JP, Söderman E, Thirumalai S, Toncheva D, Tosato S, Veijola J, Waddington J, Walsh D, Wang D, Wang Q, Webb BT, Weiser M, Wildenauer DB, Williams NM, Williams S, Witt SH, Wolen AR, Wong EH, Wormley BK, Xi HS, Zai CC, Zheng X, Zimprich F, Wray NR, Stefansson K, Visscher PM, Adolfsson R, Andreassen OA, Blackwood DH, Bramon E, Buxbaum JD, Børglum AD, Cichon S, Darvasi A, Domenici E, Ehrenreich H, Esko T, Gejman PV, Gill M, Gurling H, Hultman CM, Iwata N, Jablensky AV, Jönsson EG, Kendler KS, Kirov G, Knight J, Lencz T, Levinson DF, Li QS, Liu J, Malhotra AK, McCarroll SA, McQuillin A, Moran JL, Mortensen PB, Mowry BJ, Nöthen MM, Ophoff RA, Owen MJ, Palotie A, Pato CN, Petryshen TL, Posthuma D, Rietschel M, Riley BP, Rujescu D, Sham PC, Sklar P, St Clair D, Weinberger DR, Wendland JR, Werge T, Daly MJ, Sullivan PF, O'Donovan MC.2014. Biological insights from 108 schizophrenia-associated genetic loci. Nature 511: 421-427.

Spitzer RL, Endicott J, Robins E. 1978 Research diagnostic criteria: rationale and reliability. Arch Gen Psychiatry 1978; 35: 773–782.

Wellcome Trust Case Control Consortium. 2007. Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. Nature 44