



REVIEW

Shared Genetics of Psychiatric Disorders [version 1; peer review: 2 approved]

Tova Fuller, Victor Reus

Department of Psychiatry, UCSF Weill Institute for Neurosciences, University of California, San Francisco School of Medicine, San Francisco, CA, USA

V1 **First published:** 12 Sep 2019, 8(F1000 Faculty Rev):1626 (<https://doi.org/10.12688/f1000research.18130.1>)
Latest published: 12 Sep 2019, 8(F1000 Faculty Rev):1626 (<https://doi.org/10.12688/f1000research.18130.1>)

Abstract

Until recently, advances in understanding the genetic architecture of psychiatric disorders have been impeded by a historic, and often mandated, commitment to the use of traditional, and unvalidated, categorical diagnoses in isolation as the relevant phenotype. Such studies typically required lengthy structured interviews to delineate differences in the character and duration of behavioral symptomatology amongst disorders that were thought to be etiologic, and they were often underpowered as a result. Increasing acceptance of the fact that co-morbidity in psychiatric disorders is the rule rather than the exception has led to alternative designs in which shared dimensional symptomatology is analyzed as a quantitative trait and to association analyses in which combined polygenic risk scores are computationally compared across multiple traditional categorical diagnoses to identify both distinct and unique genetic and environmental elements. Increasing evidence that most mental disorders share many common genetic risk variants and environmental risk modifiers suggests that the broad spectrum of psychiatric pathology represents the pleiotropic display of a more limited series of pathologic events in neuronal development than was originally believed, regulated by many common risk variants and a smaller number of rare ones.

Keywords

psychiatry, transdiagnostic, genetics, genomics, polygenic, risk

Open Peer Review

Reviewer Status

	Invited Reviewers	
	1	2
version 1 published 12 Sep 2019		

F1000 Faculty Reviews are written by members of the prestigious **F1000 Faculty**. They are commissioned and are peer reviewed before publication to ensure that the final, published version is comprehensive and accessible. The reviewers who approved the final version are listed with their names and affiliations.

- Yong-Gang Yao**, University of Chinese Academy of Sciences, Kunming, China
- Eske Derks**, QIMR Berghofer, Brisbane, Australia

Any comments on the article can be found at the end of the article.

Corresponding author: Victor Reus (victor.reus@ucsf.edu)

Author roles: Fuller T: Formal Analysis, Writing – Original Draft Preparation, Writing – Review & Editing; Reus V: Conceptualization, Formal Analysis, Funding Acquisition, Supervision, Writing – Original Draft Preparation, Writing – Review & Editing

Competing interests: No competing interests were disclosed.

Grant information: This work was supported by The National Institute of Mental Health NIMH grants 1R01MH113078, 2R01MH0838784 and 5R25MH060482.

The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Copyright: © 2019 Fuller T and Reus V. This is an open access article distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

How to cite this article: Fuller T and Reus V. **Shared Genetics of Psychiatric Disorders [version 1; peer review: 2 approved]** F1000Research 2019, 8(F1000 Faculty Rev):1626 (<https://doi.org/10.12688/f1000research.18130.1>)

First published: 12 Sep 2019, 8(F1000 Faculty Rev):1626 (<https://doi.org/10.12688/f1000research.18130.1>)

Introduction

Investigation of the underlying genetic risk of individual mental disorders has been hampered by a number of factors, including a lack of validity for current categorical diagnoses and a high rate of co-morbidity amongst disorders, as well as the operational difficulty in accruing a sufficient number of subjects satisfying rigidly defined diagnostic requirements. In recent years, investigators have recognized that what was initially perceived as a problem may in fact represent a strength and that alternative approaches, focusing on genetic analysis of shared intermediate risk phenotypes in quantitative traits, such as cognition, dimensional symptomatology, and cortical structure and function, may represent a more direct probe of causality¹⁻³. Such approaches have in turn engendered new statistical methods of analysis⁴⁻⁶. To this end, Plana-Ripoll *et al.*⁷, in a large-scale study encompassing almost 84 million person years, have convincingly shown that co-morbidity is present across all psychiatric disorders and is bi-directional, meaning that the risk for any given additional mental disorder is increased by the presence of the first. Seemingly disparate psychiatric disorders then are likely to share common genetic risk variants and, depending on gene dosage and the additional contribution of rare variants and environmental modulation, represent pleiotropic versions of a pathology network that is more shared than distinct.

Shared individual variants

One method of identifying overlap between disorders is to find individual variants shared by two or more disorders. A genome-wide association study (GWAS) of individuals with autism spectrum disorder (ASD) found a significant overlap with schizophrenia (SCZ) at 8p11.23, 3p25.3 (*ATP2B2*), and 3p13 (*FOXP1*)⁸. However, while the authors collected around 16,500 cases and approximately 16,000 controls, they did not find individual variants exceeding their appropriate GWAS threshold in the discovery set.

Similarly, in an older study, McCarthy *et al.* found copy number variation (CNV) duplications of 16p11.2 associated with SCZ as well as bipolar disorder (BPD) and depression⁹. At the same time, the microduplications were rare, and the power to detect significance was low.

Xiao *et al.*¹⁰ used prior research identifying two single nucleotide polymorphisms (SNPs), rs2709370 and rs6785, in the cAMP responsive element-binding (CREB)-1 gene to study associations with BPD, major depressive disorder (MDD), and SCZ. A meta-analysis found both SNPs were associated with increased risk of BPD ($p = 2.33 \times 10^{-4}$ and 6.33×10^{-5} , respectively). Likewise, an association with SCZ (3.96×10^{-5} and 2.44×10^{-5}) and MDD ($p = 0.0144$ and 0.0314) were identified. A number of studies demonstrating similar genetic overlap between other combinations of mental, medical, and neurologic disorders have also recently appeared¹¹⁻²³.

Determining overlap using polygenic summary statistics

Since each individual locus has a small contribution to disease risk in complex disorders, creating corresponding issues

with power that hinder identification, efforts have focused on polygenic attempts to determine shared risk. The methods covered below to estimate overlap in genetic loading include linkage disequilibrium score regression (LDSR) and polygenic risk scores (PRS)²⁴.

LDSR utilizes GWAS data to determine a linkage equilibrium score, defined as the sum of LD r^2 with all other SNPs, as well as to find heritability estimates and determine genetic correlations with different phenotypes. The common variant heritability (h^2_g) of each disorder, or the proportion of phenotypic variance, is potentially explainable by an optimal linear predictor formed using additive effects of autosomal SNPs. The optimal predictors for two phenotypes can be correlated²⁵. The LDSR approach has limitations. If LD scores in the reference population approximate those in the target population, this will increase measurement error of the LDSR. Another issue of bias arises if LD scores in the reference population are increased or decreased with respect to those of the target population²⁶.

A PRS may, for example, prune and threshold associating statistics from a GWAS, then choose the best polygenic score based on a set of candidate polygenic scores for each disease. The GWAS is performed in the discovery sample with a PRS assigned to individuals for a given disorder (risk alleles weighted by their odds ratios). The coefficient of determination from regression analysis, R^2 , is pruned by significance thresholds (P_T). The best polygenic score is often based on the maximal AUC. There are also limitations for the PRS method: the discovery sample must be as large as the original sample and both must be of significant size. The phenotype should be homogeneous (a problem in such disorders as MDD), and the level of genetic variation explained by common variants must be high as well²⁷.

As an example of these methods, one GWAS on alcohol dependence found genetic correlations based on LDSR with depressive symptoms, a diagnosis of MDD, attention deficit hyperactivity disorder (ADHD), SCZ, neuroticism, and subjective well-being at the $p = 10^{-5}$ level or better²⁸. Likewise, a study using a summary statistic to determine polygenic risk correlated among 24 disorders found a strong overlap between SCZ and BPD, both of which were associated with depression²⁹. Similar associations have been reported for ADHD and eating disorders³⁰ and between substance abuse and psychotic disorders^{31,32}.

In children, a PRS was used to determine the shared contribution among ADHD, several pediatric psychiatric disorders, depression, panic disorder, and generalized anxiety disorder (GAD)³³. In sum, Brikell and colleagues identified a general psychopathology factor suggesting a vulnerability to multiple disorders in children. Another study used PRS to determine overlap between SCZ and ASD with social communication difficulties at 8 and 17 years old³⁴.

A similar polygenic approach was employed by Selzam *et al.*³⁵ to posit a shared dimension which contributes to multiple disorders. A principal components analysis found a general

“p” factor on which all disorders loaded that explained up to 60% of the variance, with SCZ, BPD, and depression the highest-loading disorders.

A large study by The Brainstorm Consortium (265,218 cases and 784,643 controls) published results from a GWAS demonstrating similarities among different psychiatric disorders and, in contrast, demonstrating differences with neurological disorders, except migraine²⁵. This study determined the common variant heritability of 17 disorders including multiple psychiatric disorders from disparate domains such as affective disorders, anxiety disorders, SCZ, ADHD, post-traumatic stress disorder (PTSD), and ASD. Findings demonstrated SCZ was genetically correlated with most of the other psychiatric disorders (average genetic correlation [r_g] = 0.40), while MDD was correlated with all. Clinically, these results are consistent with shared treatment guidelines for both MDD and anxiety disorders, shared symptomatology of depression with PTSD, and co-existence of mood disorders and SCZ in schizoaffective disorder. The aforementioned findings with migraine included an association between migraine and ADHD ($r_g = 0.26$, $p = 8.81 \times 10^{-8}$), migraine and Tourette Syndrome ($r_g = 0.19$, $p = 1.80 \times 10^{-5}$), and migraine and MDD ($r_g = 0.32$, $p = 1.42 \times 10^{-22}$).

The above findings regarding neurological disease and its overlap with psychiatric pathology were replicated in at least one GWAS determining genetic overlap between MDD and migraine³⁶. LDSR was also used to demonstrate a 14.3% genetic correlation between SCZ and amyotrophic lateral sclerosis (ALS), with PRS for SCZ explaining 0.12% of the phenotypic variance in ALS, corresponding to a modest odds ratio of 1.08–1.26³⁷. While there is little shared heritability with other neurological diseases, depression has a PRS associated with those of heart failure and ischemic disease, consistent with known phenomena such as depression after myocardial infarction³⁸.

An alternative approach has been to look at subphenotypes, such as rapid cycling and presence of psychosis in both BPD and SCZ patients^{39–41}. Smeland *et al.*¹⁴ took a somewhat different approach, examining how both SCZ and BPD compared in association with genes linked to cognitive performance. A number of unique associations were found, with most for BPD predicting better performance and for SCZ worse performance.

Gene networking

Analysis of gene networks has built on transcription data to identify correlated transcripts/genes that form modules. These modules built from different transcripts that correlate with one another over different individuals form putative pathways of genes working in concert. The benefit of using such a method is a dimensional reduction analysis; rather than looking at single genes, the module “eigengene”, which roughly approximates the first principal component, is used for a group of genes hypothesized to be functioning in concert based on a

pattern of up- or down-regulation together. Such gene networking approaches have demonstrated shared and differential module expression in BPD, ASD, ADHD, alcoholism, depression, and SCZ^{39,42–44}.

Expression studies of SCZ using post-mortem brain samples have been limited in size, but in a study of 92 medicated and 29 antipsychotic-free SCZ patients and 118 healthy controls, hierarchical clustering of 5,000 preselected transcripts was used to find modules of genes. Two in particular were highly expressed in the brain, and a statistic, k -within, was used to find hub genes in one module specifically related to SCZ⁴⁵.

Conclusions

Although recent advances in identifying shared risk architecture are exciting, the timeline for clinical translation remains opaque. The number of implicated common risk variants is large and continues to grow, their individual effect sizes remain small, and methods for determining which rare variants are causally related and which are merely incidental are limited, as is our understanding of the role of epigenetic factors. Articulation of relevant pathologic pathways and spatiotemporal characterization of altered expression in development awaits further research, making potential therapeutic interventions based on these findings even more distant in the future. The first dramatic effect is likely to be in diagnostic classification and in how we consider matching patients to treatments and predicting prognosis.

A limitation of many of these studies is the use of mostly European ancestry, making results difficult to extrapolate to other populations. Power also continues to be an issue in detecting more rare variants, specifically in GWAS studies looking to replicate individual SNP or CNV findings.

One area of psychopathology not yet explored is that of personality disorders; there is known overlap, for example, between borderline personality disorder and MDD, anxiety disorders, and PTSD, although large-scale investigation of the genetics of core personality constructs has thus far resulted in conflicting findings. It might also be useful to further characterize the contribution from environmental experiences shared across disorders through concomitant use of SNP, CNV, and transcriptomic data.

Could shared heritability lead to neuroanatomical correlates? One natural step in this regard is to examine transdiagnostic neuroanatomical similarities coinciding with shared genetics, as Gong *et al.*⁴⁶ did, finding that SCZ, MDD, PTSD, and obsessive-compulsive disorder shared greater gray matter volume in the putamen on MRI ($P < 0.001$), which correlated with severity of symptoms. Similarly, van der Meer *et al.*⁴⁷ were able to link SCZ-associated genes to specific changes in hippocampal subfield volumes that were distinct from those seen in Alzheimer’s disease. Recent reports from the ENIGMA Consortium lend additional support to this avenue of inquiry^{48,49}.

References



1. Martin J, Taylor MJ, Lichtenstein P: **Assessing the evidence for shared genetic risks across psychiatric disorders and traits.** *Psychol Med.* 2018; **48**(11): 1759–1774.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
2. Davis LK: **Common knowledge: shared genetics in psychiatry.** *Nat Neurosci.* 2019; **22**(3): 331–332.
[PubMed Abstract](#) | [Publisher Full Text](#)
3. Corponi F, Bonassi S, Vieta E, *et al.*: **Genetic basis of psychopathological dimensions shared between schizophrenia and bipolar disorder.** *Prog Neuropsychopharmacol Biol Psychiatry.* 2019; **89**: 23–29.
[PubMed Abstract](#) | [Publisher Full Text](#)
4. Frei O, Holland D, Smeland OB, *et al.*: **Bivariate causal mixture model quantifies polygenic overlap between complex traits beyond genetic correlation.** *Nat Commun.* 2019; **10**(1): 2417.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
5. Pei G, Sun H, Dai Y, *et al.*: **Investigation of multi-trait associations using pathway-based analysis of GWAS summary statistics.** *BMC Genomics.* 2019; **20**(Suppl 1): 79.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
6. Zhan X, Zhao N, Plantinga A, *et al.*: **Powerful Genetic Association Analysis for Common or Rare Variants with High-Dimensional Structured Traits.** *Genetics.* 2017; **206**(4): 1779–1790.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
7. Plana-Ripoll O, Pedersen CB, Holtz Y, *et al.*: **Exploring Comorbidity Within Mental Disorders Among a Danish National Population.** *JAMA Psychiatry.* 2019; **76**(3): 259–270.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
8. Autism Spectrum Disorders Working Group of The Psychiatric Genomics Consortium: **Meta-analysis of GWAS of over 16,000 individuals with autism spectrum disorder highlights a novel locus at 10q24.32 and a significant overlap with schizophrenia.** *Mol Autism.* 2017; **8**: 21.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
9. McCarthy SE, Makarov V, Kirov G, *et al.*: **Microduplications of 16p11.2 are associated with schizophrenia.** *Nat Genet.* 2009; **41**(11): 1223–7.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
10. Xiao X, Zhang C, Grigoriou-Serbanescu M, *et al.*: **The cAMP responsive element-binding (CREB)-1 gene increases risk of major psychiatric disorders.** *Mol Psychiatry.* 2018; **23**(9): 1957–1967.
[PubMed Abstract](#) | [Publisher Full Text](#) | [F1000 Recommendation](#)
11. Drange OK, Smeland OB, Shadrin AA, *et al.*: **Genetic Overlap Between Alzheimer's Disease and Bipolar Disorder Implicates the MARK2 and VAC14 Genes.** *Front Neurosci.* 2019; **13**: 220.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
12. Postolache TT, Del Bosque-Plata L, Jabbour S, *et al.*: **Co-shared genetics and possible risk gene pathway partially explain the comorbidity of schizophrenia, major depressive disorder, type 2 diabetes, and metabolic syndrome.** *Am J Med Genet B Neuropsychiatr Genet.* 2019; **180**(3): 186–203.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
13. Schork AJ, Won H, Appadurai V, *et al.*: **A genome-wide association study of shared risk across psychiatric disorders implicates gene regulation during fetal neurodevelopment.** *Nat Neurosci.* 2019; **22**(3): 353–361.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
14. Smeland OB, Bahrami S, Frei O, *et al.*: **Genome-wide analysis reveals extensive genetic overlap between schizophrenia, bipolar disorder, and intelligence.** *Mol Psychiatry.* 2019.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
15. Xu C, Cao H, Liu D: **Integrative analysis of shared genetic pathogenesis by obsessive-compulsive and eating disorders.** *Mol Med Rep.* 2018; **19**(3): 1761–1766.
[PubMed Abstract](#) | [Publisher Full Text](#)
16. Hackinger S, Prins B, Mamakou V, *et al.*: **Evidence for genetic contribution to the increased risk of type 2 diabetes in schizophrenia.** *Transl Psychiatry.* 2018; **8**(1): 252.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
17. Benros ME, Mortensen PB: **Role of Infection, Autoimmunity, Atopic Disorders, and the Immune System in Schizophrenia: Evidence from Epidemiological and Genetic Studies.** *Curr Top Behav Neurosci.* 2019; 1–19.
[PubMed Abstract](#) | [Publisher Full Text](#)
18. Gabrielli AP, Manzardo AM, Butler MG: **GeneAnalytics Pathways and Profiling of Shared Autism and Cancer Genes.** *Int J Mol Sci.* 2019; **20**(5): pii: E1166.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
19. Tylee DS, Sun J, Hess JL, *et al.*: **Genetic correlations among psychiatric and immune-related phenotypes based on genome-wide association data.** *Am J Med Genet B Neuropsychiatr Genet.* 2018; **177**(7): 641–657.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
20. Yilmaz Z, Halvorsen M, Bryois J, *et al.*: **Examination of the shared genetic basis of anorexia nervosa and obsessive-compulsive disorder.** *Mol Psychiatry.* 2018.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
21. Knowles EEM, Curran JE, Meikle PJ, *et al.*: **Disentangling the genetic overlap between cholesterol and suicide risk.** *Neuropsychopharmacology.* 2018; **43**(13): 2556–2563.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
22. Zuber V, Jönsson EG, Frei O, *et al.*: **Identification of shared genetic variants between schizophrenia and lung cancer.** *Sci Rep.* 2018; **8**(1): 674.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
23. Gui H, Li M, Sham PC, *et al.*: **Genetic overlap between epilepsy and schizophrenia: Evidence from cross phenotype analysis in Hong Kong Chinese population.** *Am J Med Genet B Neuropsychiatr Genet.* 2018; **177**(1): 86–92.
[PubMed Abstract](#) | [Publisher Full Text](#)
24. Martin AR, Daly MJ, Robinson EB, *et al.*: **Predicting Polygenic Risk of Psychiatric Disorders.** *Biol Psychiatry.* 2019; **86**(2): 97–109.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
25. Brainstorm Consortium, Anttila V, Bulik-Sullivan B, *et al.*: **Analysis of shared heritability in common disorders of the brain.** *Science.* 2018; **360**(6395): pii: eaap8757.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
26. Bulik-Sullivan BK, Loh PR, Finucane HK, *et al.*: **LD Score regression distinguishes confounding from polygenicity in genome-wide association studies.** *Nat Genet.* 2015; **47**(3): 291–5.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
27. Chalmer MA, Esserliind AL, Olesen J, *et al.*: **Polygenic risk score: use in migraine research.** *J Headache Pain.* 2018; **19**(1): 29.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
28. Walters RK, Polimanti R, Johnson EC, *et al.*: **Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders.** *Nat Neurosci.* 2018; **21**(12): 1656–69.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
29. Bulik-Sullivan B, Finucane HK, Anttila V, *et al.*: **An atlas of genetic correlations across human diseases and traits.** *Nat Genet.* 2015; **47**(11): 1236–41.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
30. Yao S, Kuja-Halkola R, Martin J, *et al.*: **Associations Between Attention-Deficit/Hyperactivity Disorder and Various Eating Disorders: A Swedish Nationwide Population Study Using Multiple Genetically Informative Approaches.** *Biol Psychiatry.* 2019; pii: S0006-3223(19)31371-X.
[PubMed Abstract](#) | [Publisher Full Text](#) | [F1000 Recommendation](#)
31. Gurriarán X, Rodríguez-López J, Flórez G, *et al.*: **Relationships between substance abuse/dependence and psychiatric disorders based on polygenic scores.** *Genes Brain Behav.* 2019; **18**(3): e12504.
[PubMed Abstract](#) | [Publisher Full Text](#) | [F1000 Recommendation](#)
32. Foo JC, Streit F, Treutlein J, *et al.*: **Shared genetic etiology between alcohol dependence and major depressive disorder.** *Psychiatr Genet.* 2018; **28**(4): 66–70.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
33. Brikell I, Larsson H, Lu Y, *et al.*: **The contribution of common genetic risk variants for ADHD to a general factor of childhood psychopathology.** *Mol Psychiatry.* 2018; **44**: 2223.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
34. St Pourcain B, Robinson EB, Anttila V, *et al.*: **ASD and schizophrenia show distinct developmental profiles in common genetic overlap with population-based social communication difficulties.** *Mol Psychiatry.* 2018; **23**(2): 263–70.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
35. Selzam S, Coleman JRI, Caspi A, *et al.*: **A polygenic p factor for major psychiatric disorders.** *Transl Psychiatry.* 2018; **8**(1): 205.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
36. Yang Y, Zhao H, Boomsma DI, *et al.*: **Molecular genetic overlap between migraine and major depressive disorder.** *Eur J Hum Genet.* 2018; **26**(8): 1202–16.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
37. McLaughlin RL, Schijven D, van Rheenen W, *et al.*: **Genetic correlation between amyotrophic lateral sclerosis and schizophrenia.** *Nat Commun.* 2017; **8**: 14774.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
38. McCoy TH, Castro VM, Snapper L, *et al.*: **Polygenic loading for major depression is associated with specific medical comorbidity.** *Transl Psychiatry.* 2017; **7**(9): e1238.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
39. Gandal MJ, Haney JR, Parikshak NN, *et al.*: **Shared molecular neuropathology across major psychiatric disorders parallels polygenic overlap.** *Science.* 2018; **359**(6376): 693–7.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)

40. **F** Bipolar Disorder and Schizophrenia Working Group of the Psychiatric Genomics Consortium: **Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes**. *Cell*. 2018; **173**(7): 1705–1715.e16.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
41. **F** Ranlund S, Calafato S, Thygesen JH, *et al.*: **A polygenic risk score analysis of psychosis endophenotypes across brain functional, structural, and cognitive domains**. *Am J Med Genet B Neuropsychiatr Genet*. 2018; **177**(1): 21–34.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
42. **F** Hammerschlag AR, de Leeuw CA, Middeldorp CM, *et al.*: **Synaptic and brain-expressed gene sets relate to the shared genetic risk across five psychiatric disorders**. *Psychol Med*. 2019; **42**: 1–11.
[PubMed Abstract](#) | [Publisher Full Text](#) | [F1000 Recommendation](#)
43. **F** Guan J, Cai JJ, Ji G, *et al.*: **Commonality in dysregulated expression of gene sets in cortical brains of individuals with autism, schizophrenia, and bipolar disorder**. *Transl Psychiatry*. 2019; **9**(1): 152.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
44. **F** Zhu K, Ou Yang TH, Dorie V, *et al.*: **Meta-analysis of expression and methylation signatures indicates a stress-related epigenetic mechanism in multiple neuropsychiatric disorders**. *Transl Psychiatry*. 2019; **9**(1): 32.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
45. de Jong S, Boks MP, Fuller TF, *et al.*: **A gene co-expression network in whole blood of schizophrenia patients is independent of antipsychotic-use and enriched for brain-expressed genes**. *PLoS One*. 2012; **7**(6): e39498.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
46. **F** Gong Q, Scarpazza C, Dai J, *et al.*: **A transdiagnostic neuroanatomical signature of psychiatric illness**. *Neuropsychopharmacology*. 2019; **44**(5): 869–75.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
47. **F** van der Meer D, Rokicki J, Kaufmann T, *et al.*: **Brain scans from 21,297 individuals reveal the genetic architecture of hippocampal subfield volumes**. *Mol Psychiatry*. 2018; **35**: 625.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
48. **F** van der Merwe C, Jahanshad N, Cheung JW, *et al.*: **Concordance of genetic variation that increases risk for anxiety disorders and posttraumatic stress disorders and that influences their underlying neurocircuitry**. *J Affect Disord*. 2019; **245**: 885–96.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)
49. **F** Walton E, Hibar D, Yilmaz Z, *et al.*: **Exploration of Shared Genetic Architecture Between Subcortical Brain Volumes and Anorexia Nervosa**. *Mol Neurobiol*. 2019; **56**(7): 5146–56.
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#) | [F1000 Recommendation](#)

Open Peer Review

Current Peer Review Status:  

Editorial Note on the Review Process

F1000 Faculty Reviews are written by members of the prestigious F1000 Faculty. They are commissioned and are peer reviewed before publication to ensure that the final, published version is comprehensive and accessible. The reviewers who approved the final version are listed with their names and affiliations.

The reviewers who approved this article are:

Version 1

1 **Eske Derks**

Translational Neurogenomics Laboratory, QIMR Berghofer, Brisbane, QLD, Australia

Competing Interests: No competing interests were disclosed.

2 **Yong-Gang Yao**

Kunming College of Life Science, University of Chinese Academy of Sciences, Kunming, China

Competing Interests: No competing interests were disclosed.

The benefits of publishing with F1000Research:

- Your article is published within days, with no editorial bias
- You can publish traditional articles, null/negative results, case reports, data notes and more
- The peer review process is transparent and collaborative
- Your article is indexed in PubMed after passing peer review
- Dedicated customer support at every stage

For pre-submission enquiries, contact research@f1000.com

F1000Research