nature neuroscience

SUPPLEMENTARY INFORMATION

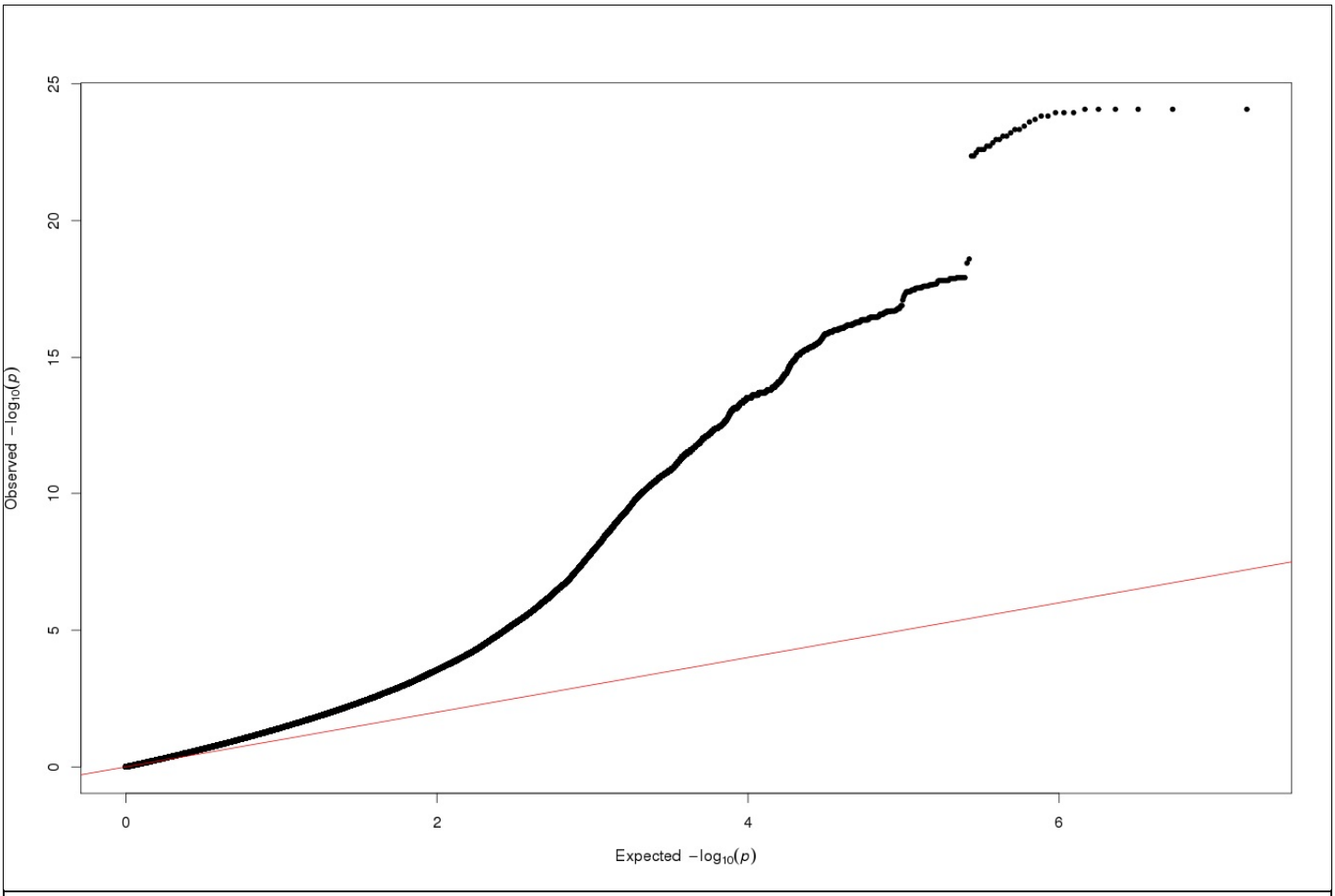
https://doi.org/10.1038/s41593-018-0326-7

In the format provided by the authors and unedited.

Genome-wide meta-analysis of depression identifies 102 independent variants and highlights the importance of the prefrontal brain regions

David M. Howard[1*], Mark J. Adams[1], Toni-Kim Clarke[1], Jonathan D. Hafferty[1], Jude Gibson[1], Masoud Shirali[1], Jonathan R. I. Coleman[2,3], Saskia P. Hagenaars[2,3], Joey Ward[4], Eleanor M. Wigmore[1], Clara Alloza[1], Xueyi Shen[1], Miruna C. Barbu[1], Eileen Y. Xu[1], Heather C. Whalley[1], Riccardo E. Marioni[5,6], David J. Porteous[5,6], Gail Davies[5,7], Ian J. Deary[5,7], Gibran Hemani[8], Klaus Berger[9], Henning Teismann[9], Rajesh Rawal[9], Volker Arolt[10], Bernhard T. Baune[11], Udo Dannlowski[10], Katharina Domschke[12], Chao Tian[13], David A. Hinds[13], 23andMe Research Team[14], Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium[14], Maciej Trzaskowski[15], Enda M. Byrne[15], Stephan Ripke[16,17,18], Daniel J. Smith[4], Patrick F. Sullivan[19,20,21], Naomi R. Wray[15], Gerome Breen[2,3], Cathryn M. Lewis[2,3] and Andrew M. McIntosh[1,7]

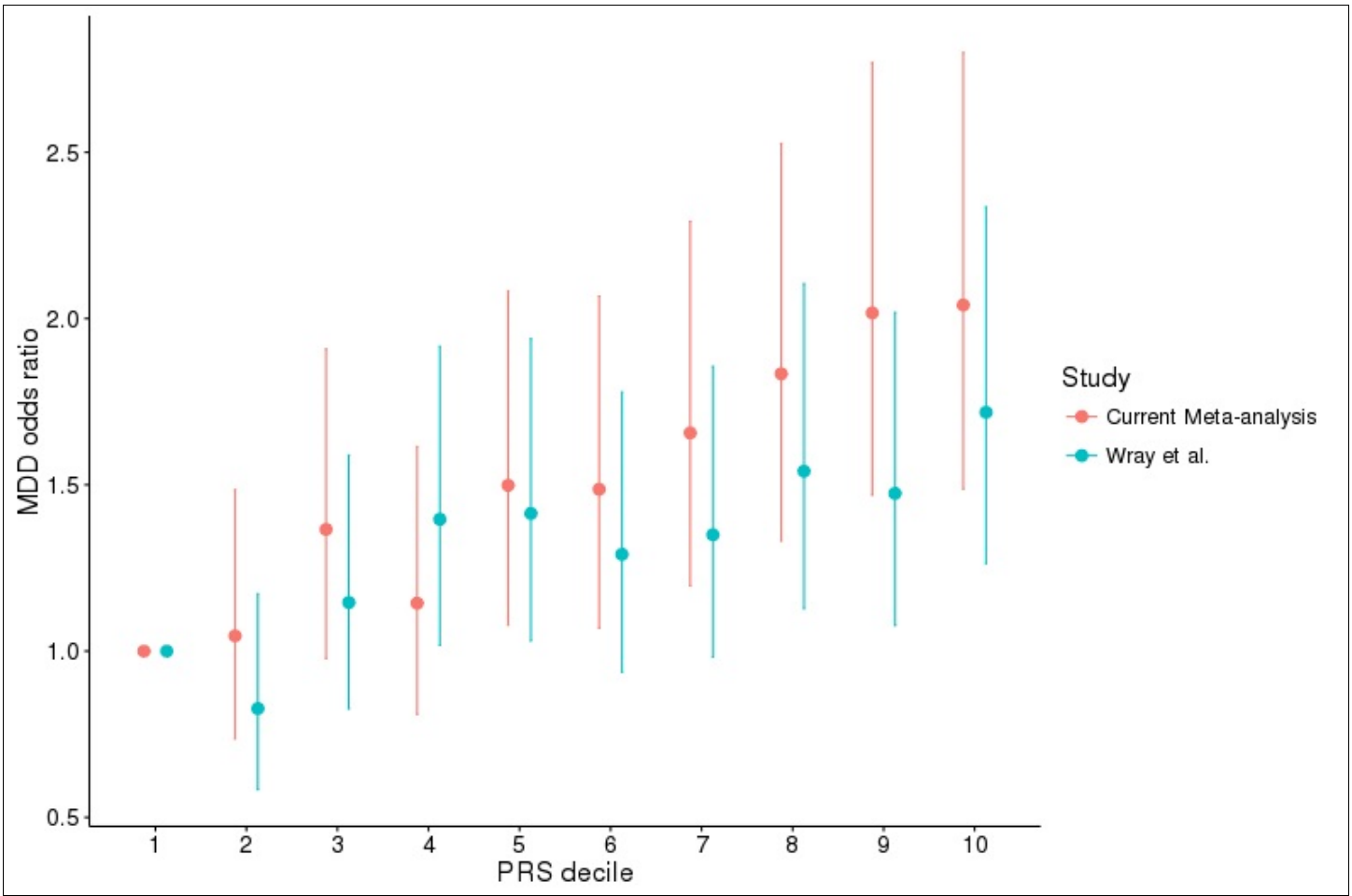
[1]Division of Psychiatry, University of Edinburgh, Royal Edinburgh Hospital, Edinburgh, UK. [2]Social Genetic and Developmental Psychiatry Centre, Institute of Psychiatry, Psychology & Neuroscience, King's College London, London, UK. [3]NIHR Biomedical Research Centre for Mental Health, South London and Maudsley NHS Trust, London, UK. [4]Institute of Health and Wellbeing, University of Glasgow, Glasgow, UK. [5]Centre for Cognitive Ageing and Cognitive Epidemiology, University of Edinburgh, Edinburgh, UK. [6]Centre for Genomic and Experimental Medicine, Institute of Genetics and Molecular Medicine, University of Edinburgh, Edinburgh, UK. [7]Department of Psychology, University of Edinburgh, Edinburgh, UK. [8]Medical Research Council (MRC) Integrative Epidemiology Unit, Population Health, Sciences, Bristol Medical School, University of Bristol, Bristol, UK. [9]Institute of Epidemiology & Social Medicine, University of Münster, Münster, Germany. [10]Department of Psychiatry, University of Münster, Münster, Germany. [11]Department of Psychiatry, University of Melbourne, Victoria, Australia. [12]Department of Psychiatry and Psychotherapy, Medical Center—University of Freiburg, Faculty of Medicine, University of Freiburg, Freiburg, Germany. [13]23andMe, Inc, Mountain View, CA, USA. [14]A list of members and affiliations appears in the Supplementary Note. [15]Queensland Brain Institute, University of Queensland, Brisbane, Queensland, Australia. [16]Department of Psychiatry, Charite Universitatsmedizin Berlin Campus Benjamin Franklin, Berlin, Germany. [17]Medical and Population Genetics, Broad Institute, Cambridge, MA, USA. [18]Analytic and Translational Genetics Unit, Massachusetts General Hospital, Boston, MA, USA. [19]Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, Stockholm, Sweden. [20]Department of Genetics, University of North Carolina, Chapel Hill, NC, USA. [21]Department of Psychiatry, University of North Carolina, Chapel Hill, NC, USA. *e-mail: D.Howard@ed.ac.uk



Supplementary Figure 1

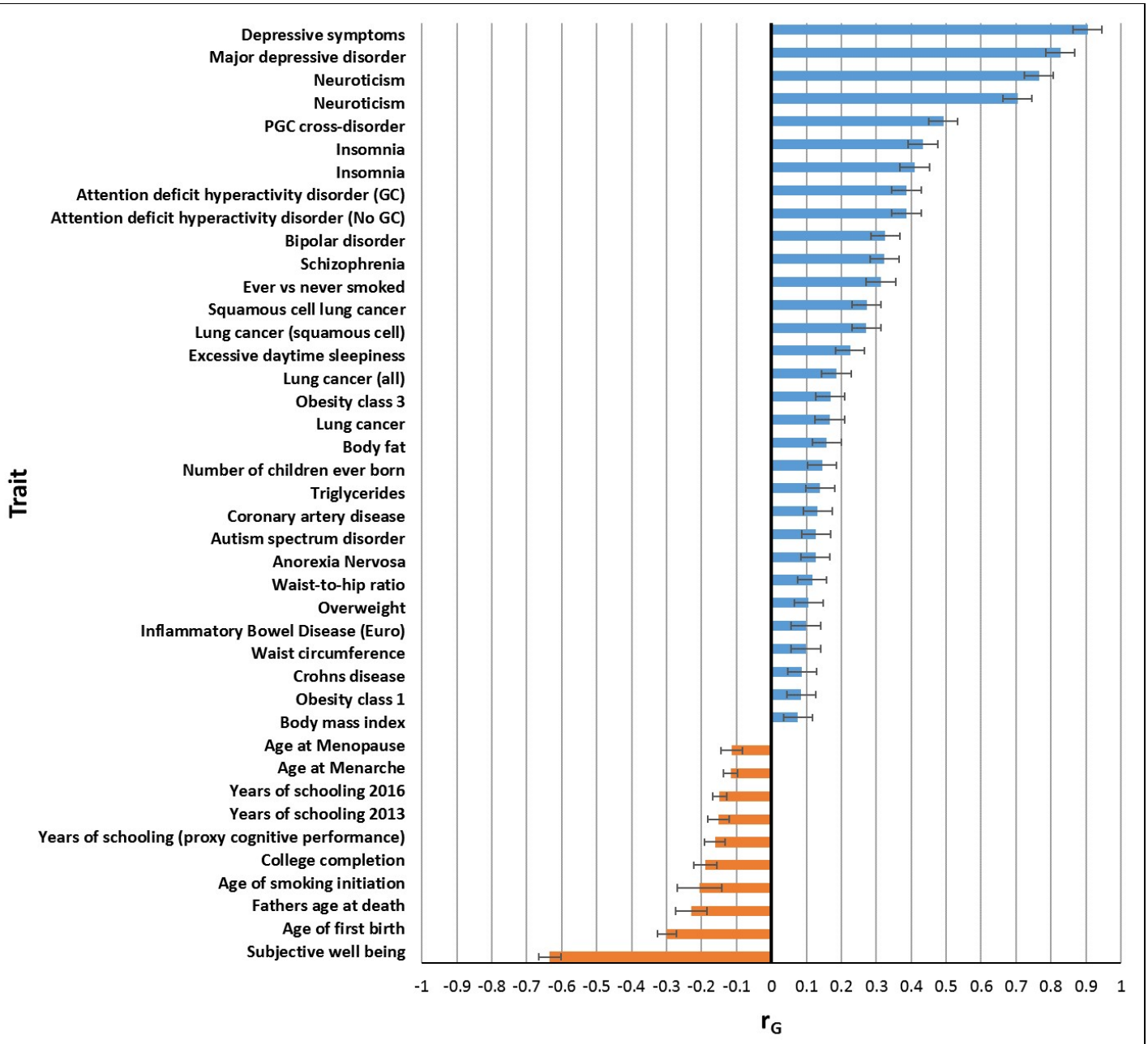
Quantile–quantile plot of the observed *P* values on those expected for each genetic variants association with depression in our meta-analysis (*n* = 807,553 individuals).

P-values were obtained from an inverse-variance weighted meta-analysis of summary statistics data from UK Biobank, Psychiatric Genomics Consortium and 23andMe. UK Biobank summary statistics were obtained using a linear association analysis with the results transformed to the logistic scale. Psychiatric Genomics Consortium and 23andMe data were analysed using an additive logistic model. All association analyses were two-sided tests.



Supplementary Figure 2

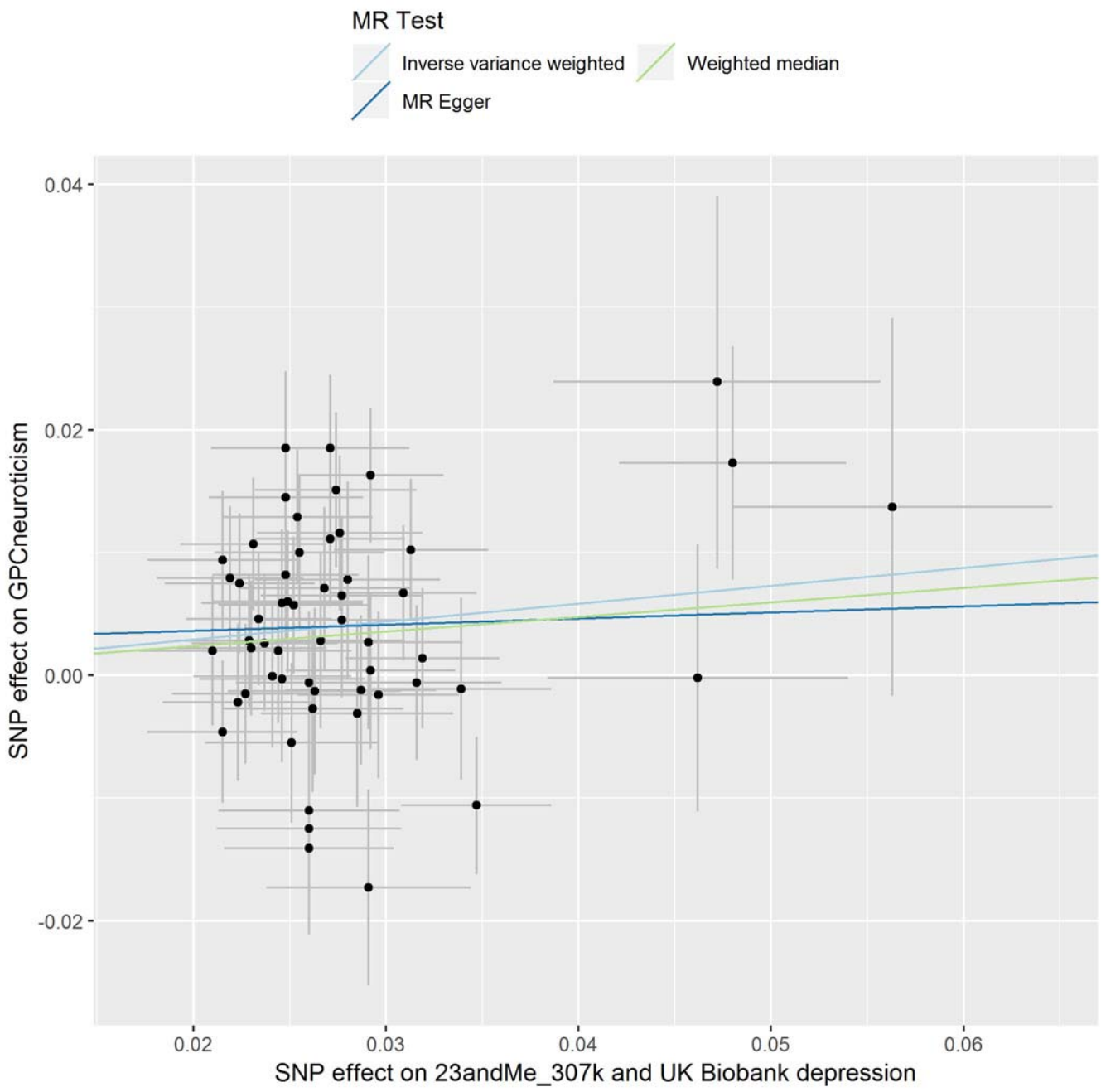
Odds ratios and 95% confidence intervals for major depressive disorder (MDD) in Generation Scotland (*n* = 6,946) based on polygenic risk score (PRS) deciles calculated from the current meta-analysis of depression (*n* = 765,884 individuals) and from summary statistics from the genome-wide association study of major depression conducted by Wray, et al. [9] (n = 453,779 individuals).



Supplementary Figure 3

Significant genetic correlations (r_G; $P < 0.01$, after false discovery rate correction for multiple testing) between depression (n = 807,553 individuals) and other behavioural and disease related traits using LD score regression.

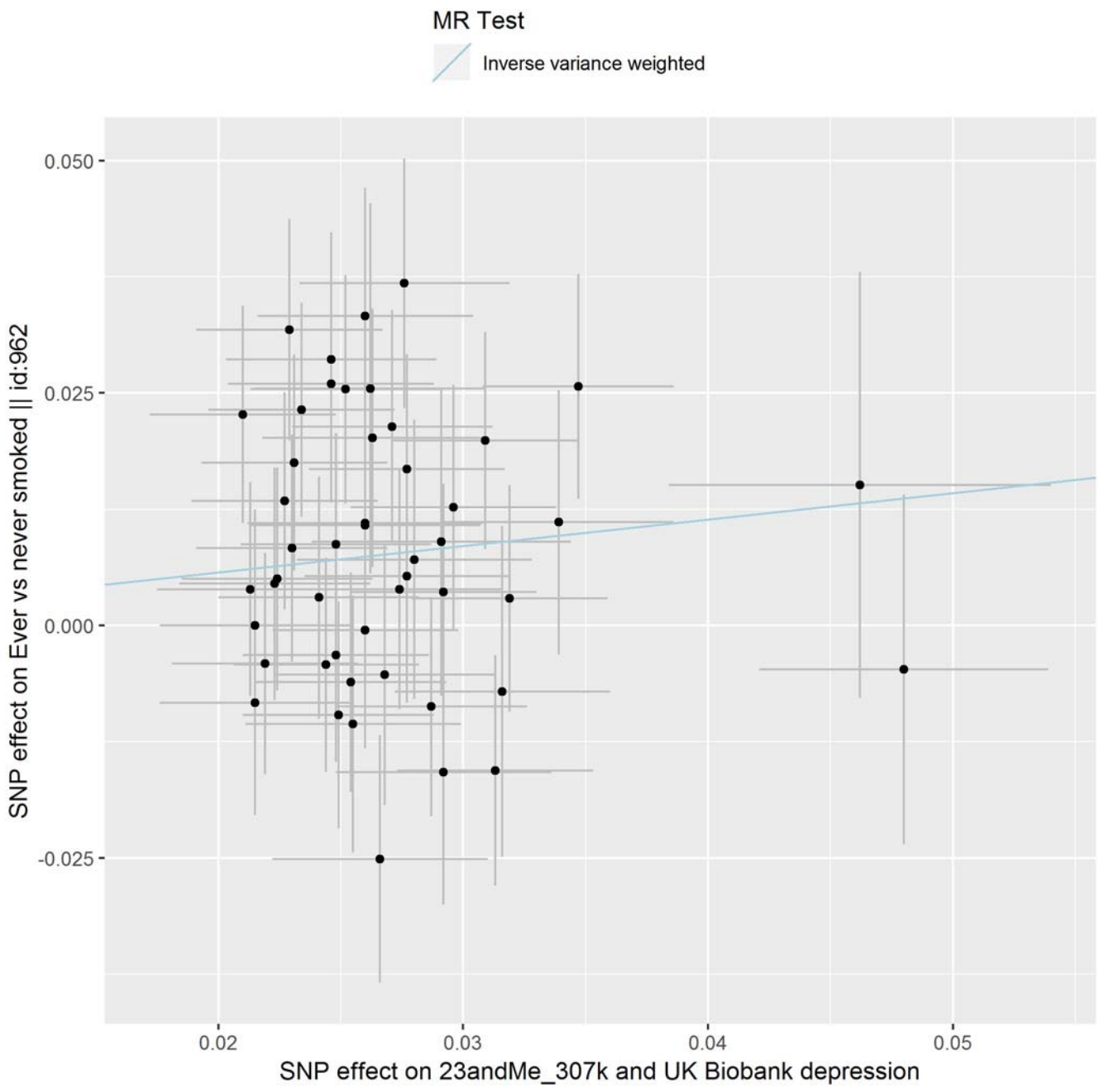
A negative r_G indicates that an earlier or lower value of a continuous trait (i.e. earlier father's age of death or lower subjective well being was associated with depression. A positive r_G indicates that a later or higher value of a continuous trait (i.e. higher triglyceride level) was associated with depression. *P*-values were calculated by testing whether r_G was significantly different from 0 using a two-sided test. The centre values are the genetic correlation for each trait and the error bars are the respective standard error. LD score regression implemented in LD Hub software (http://ldsc.broadinstitute.org/).



Supplementary Figure 4

Mendelian randomization test for a putative causal effect of depression (*n* = 629,934 individuals; 56 instrumental variables) on neuroticism (*n* = 29,496 twin pairs) using inverse weighted regression, MR Egger and a weighted median test.

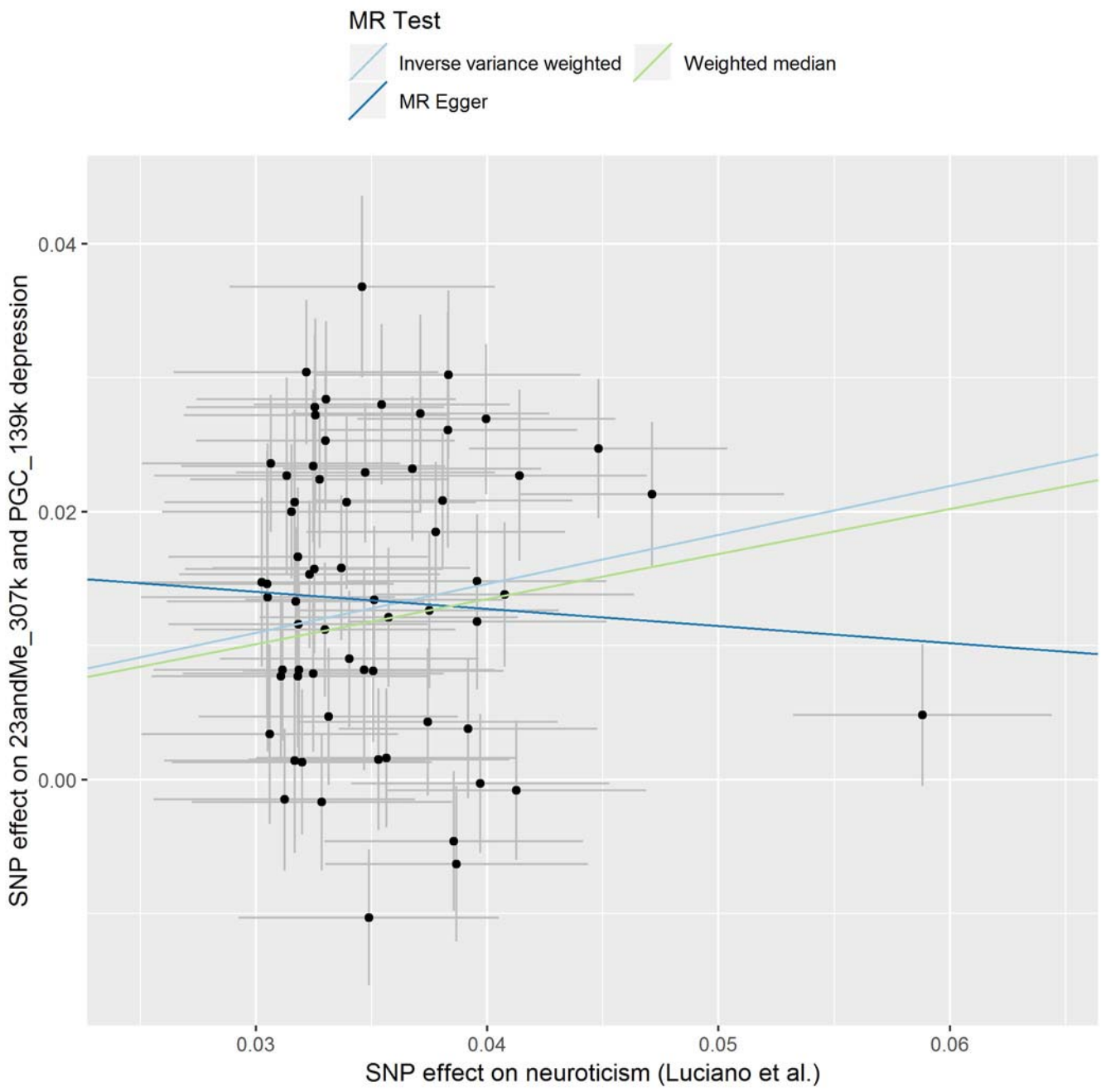
Centre values reflect the effect of each instrumental variable on each trait with the respective error bars reflecting the standard error of the variable's effect on each trait.



Supplementary Figure 5

Mendelian randomization analysis for a putative causal effect of depression (*n* = 629,934 individuals; 49 instrumental variables) on ever vs. never smoked (*n* = 69,409 individuals) using inverse weighted regression.

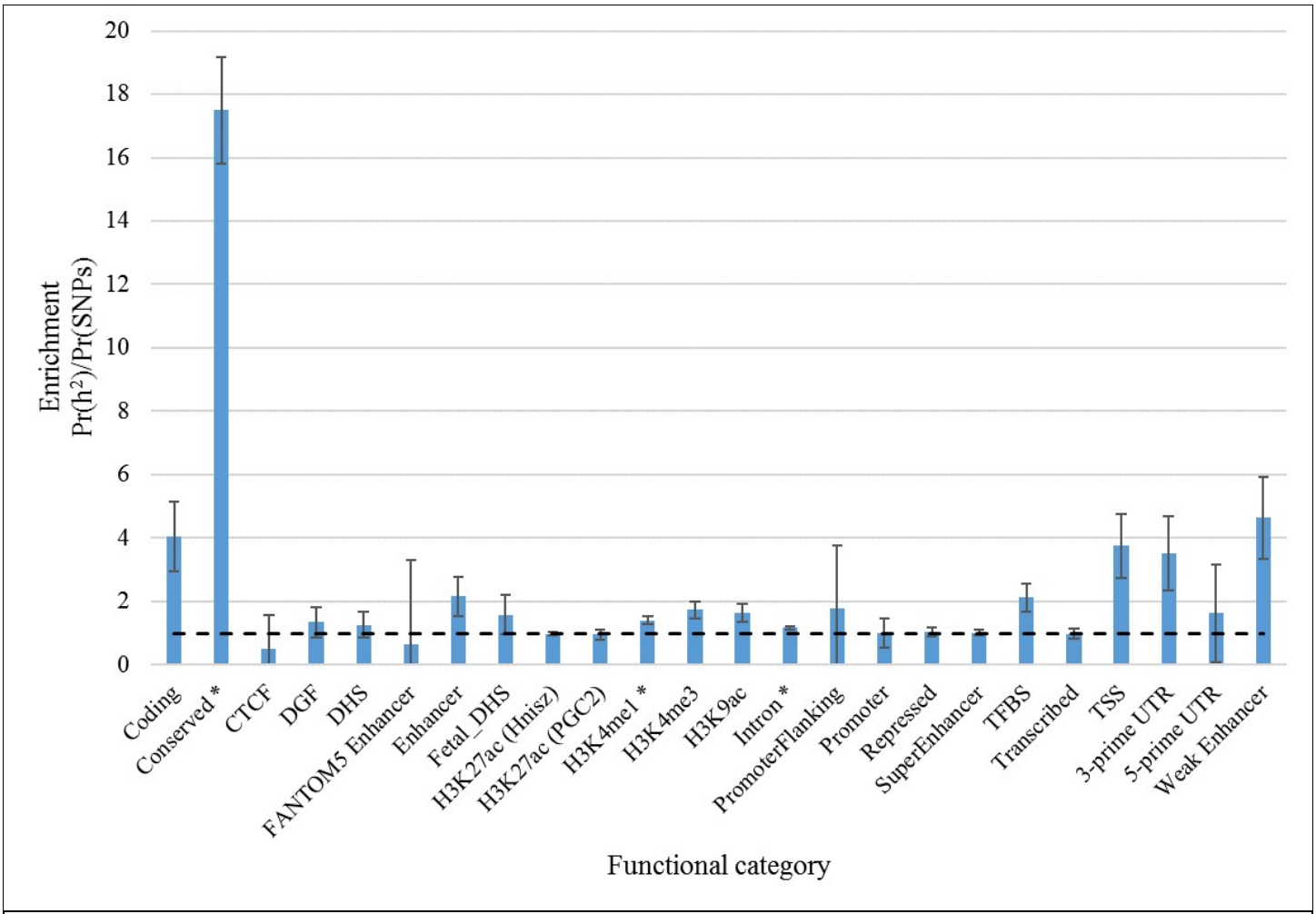
Centre values reflect the effect of each instrumental variable on each trait with the respective error bars reflecting the standard error of the variable's effect on each trait.



Supplementary Figure 6

Mendelian randomization test for a putative causal effect of neuroticism (*n* = 329,821 individuals; 65 instrumental variables) on depression (*n* = 537,701 individuals) using inverse weighted regression, MR Egger and a weighted median test.

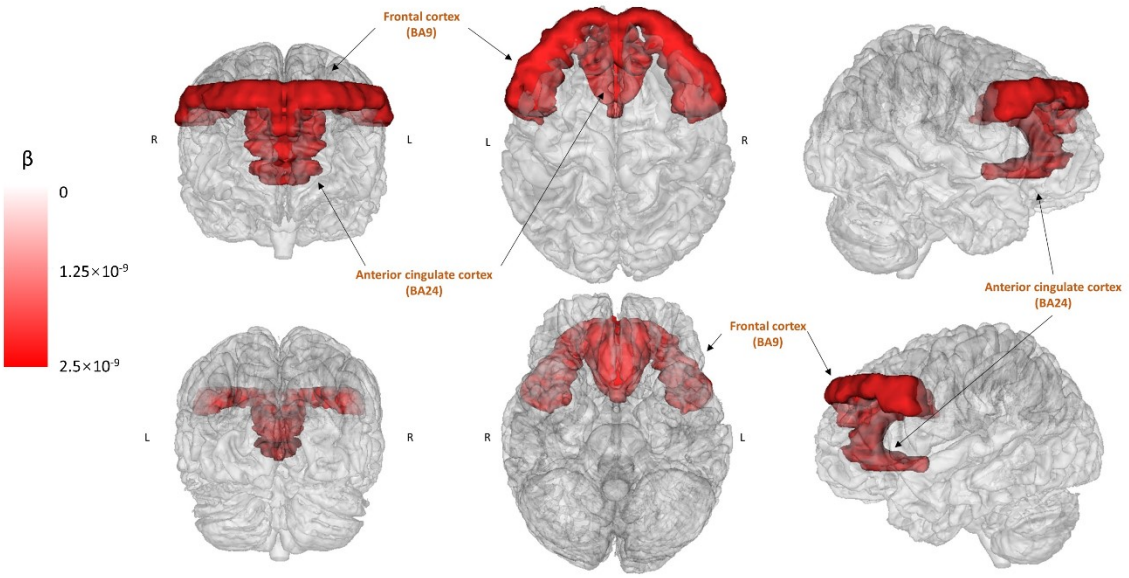
Centre values reflect the effect of each instrumental variable on each trait with the respective error bars reflecting the standard error of the variable's effect on each trait.



Supplementary Figure 7

Contribution of functional annotation of 24 categories to the heritability of depression (*n* = 807,553 individuals) based on the variants within each category.

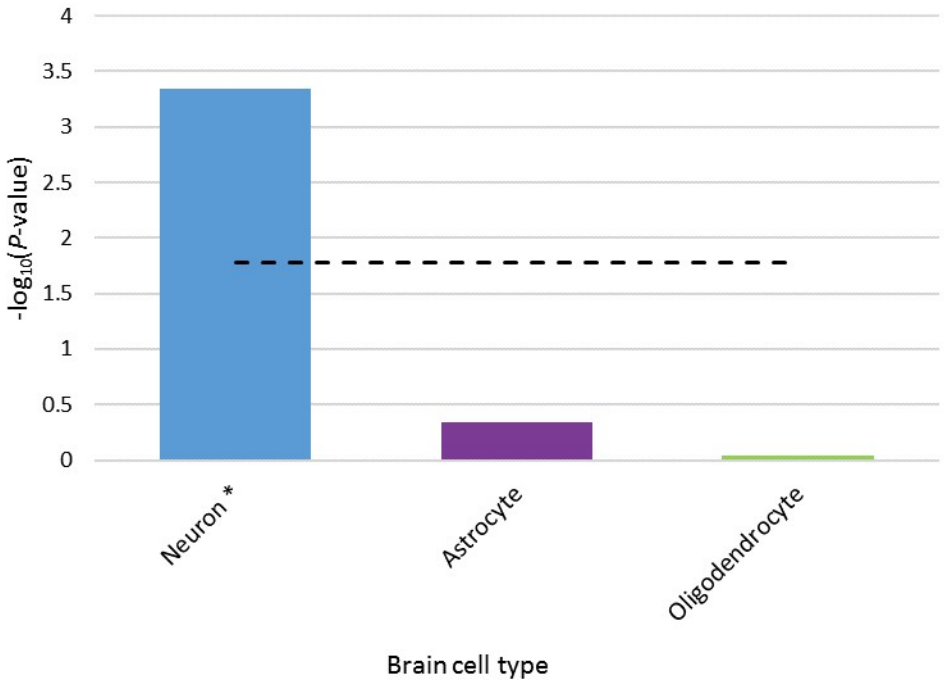
The enrichment of each functional category, shown on the y-axis, is calculated as the proportion of heritability assigned to a functional categories divided by the proportion of variants in that category ($Pr(h^2)/Pr(SNPs)$). Error bars represent jackknife standard errors for each the estimate of enrichment, and an asterisk indicates significant enrichment after Bonferroni correction for multiple testing (Conserved *P*-value = 2.55×10^{-17}; H3K4me1 *P*-value = 0.0015; Intron *P*-value = 0.0014). *P*-values were calculated using a one-sided test and tested whether there the estimate of enrichment was significantly different from zero enrichment. The dashed line represents the threshold for no enrichment.



Supplementary Figure 8

Enrichment estimate (β) of significantly enriched brain cell regions using GTEx overlaid on physical representation of brain anatomy (*n* = 807,553 individuals).

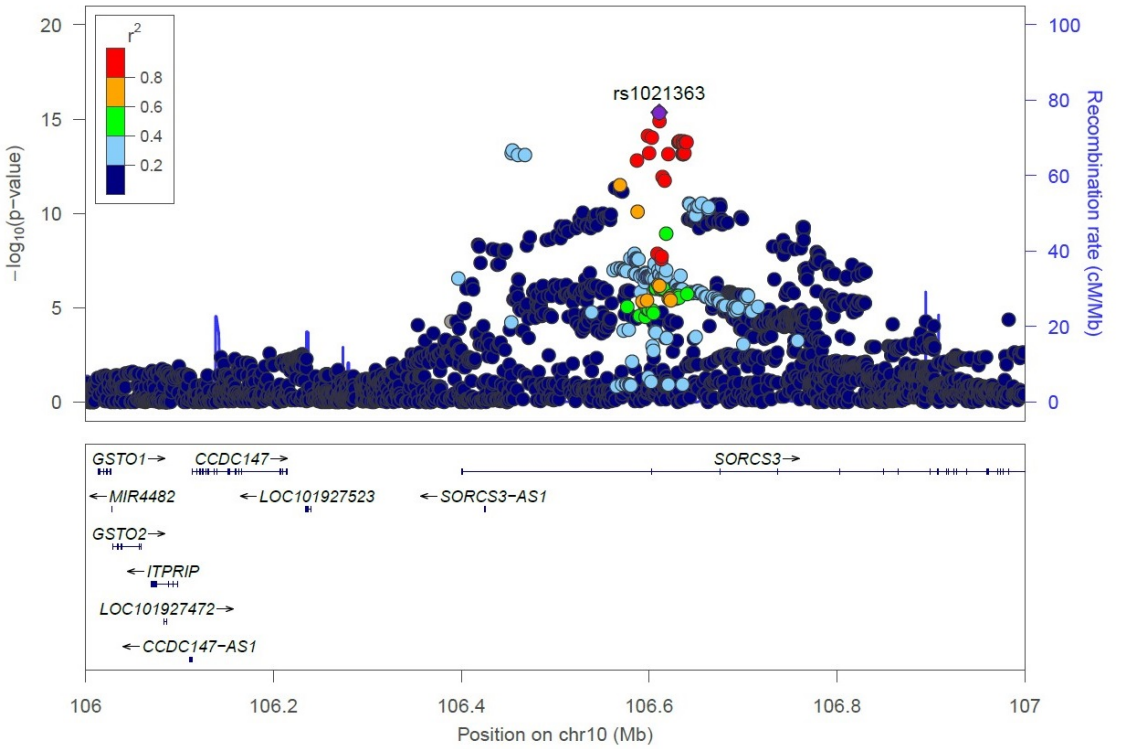
The pseudo-coloring highlights the coefficients of the brain regions in red that were significantly enriched ($P < 0.05$) for depression variants compared to no enrichment using a one-sided test and after Bonferroni correction for multiple testing.



Supplementary Figure 9

Stratified LD score regression analyses showing significance of enrichment estimates for 3 brain cell types in depression (*n* = 807,553 individuals).

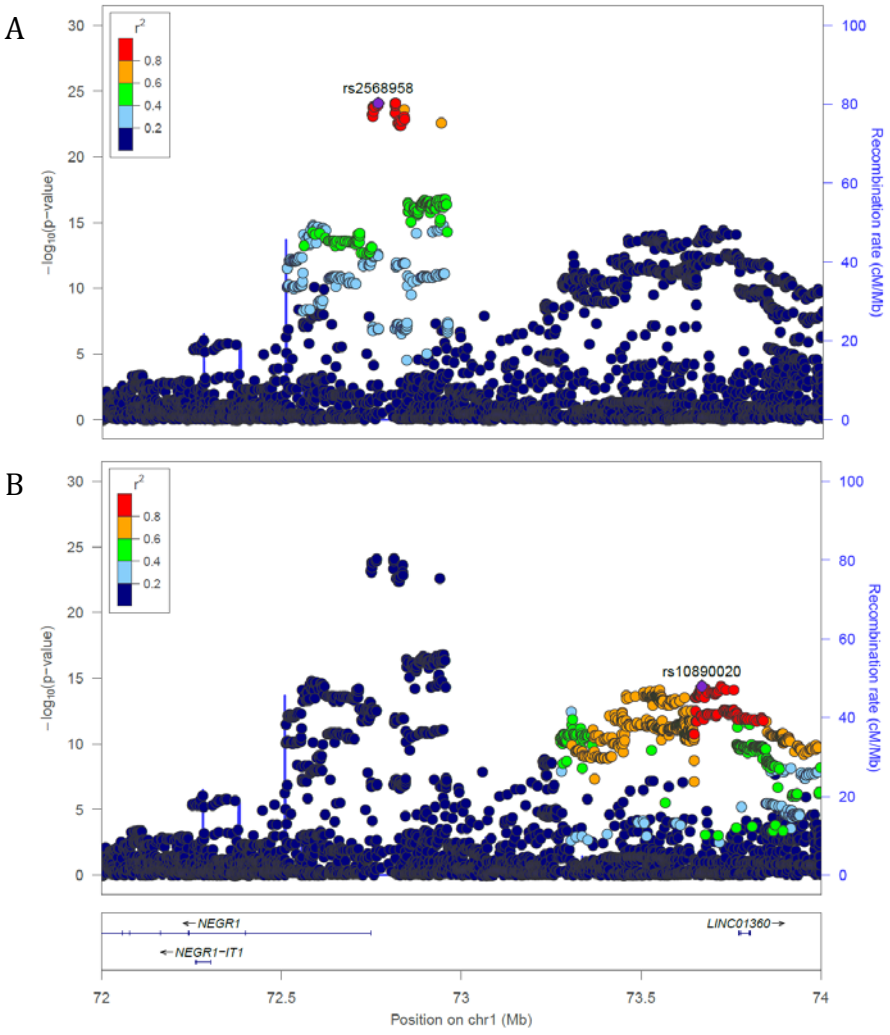
The dashed line represents the Bonferroni threshold for significance for multiple testing correction ($P = 0.0167$) and * indicates significant enrichment for that brain cell type (Neuron P-value = 4.52×10^{-4}). P-values were calculated based on evidence of enrichment compared to no enrichment using a one-sided test.



Supplementary Figure 10

Regional visualization plot centred on the independently-associated variant, rs1021363, close to the Sortilin-related VPS10 domain containing receptor 3 (*SORCS3*) gene on chromosome 10 (*n* = 807,553 individuals)

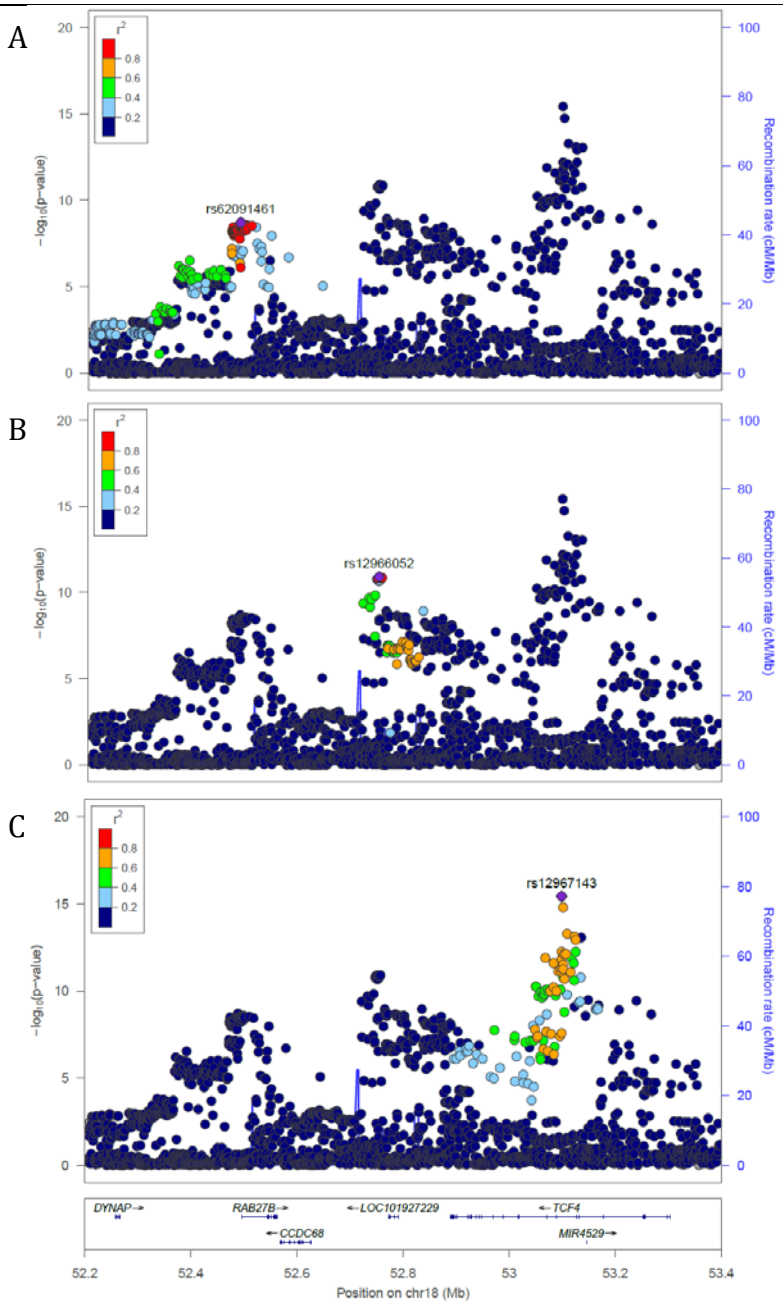
P-values were obtained from an inverse-variance weighted meta-analysis of summary statistics data from UK Biobank, Psychiatric Genomics Consortium and 23andMe. UK Biobank summary statistics were obtained using a linear association analysis with the results transformed to the logistic scale. Psychiatric Genomics Consortium and 23andMe data were analysed using an additive logistic model. All association analyses were two-sided tests. Recombination rates used in the plots are based on the European 1000 Genomes panel from November 2014.



Supplementary Figure 11

Regional visualization plots centred on independently-associated variants (A. rs2568958 and B. rs10890020) close to the neuronal growth regulator 1 (*NEGR1*) gene on chromosome 1 (*n* = 807,553 individuals).

P-values were obtained from an inverse-variance weighted meta-analysis of summary statistics data from UK Biobank, Psychiatric Genomics Consortium and 23andMe. UK Biobank summary statistics were obtained using a linear association analysis with the results transformed to the logistic scale. Psychiatric Genomics Consortium and 23andMe data were analysed using an additive logistic model. All association analyses were two-sided tests. Recombination rates used in the plots are based on the European 1000 Genomes panel from November 2014.



Supplementary Figure 12

Regional visualization plots centred on independently-associated variants (A. rs62091461, B. rs12966052, and C. rs12967143) close to the transcription factor 4 (*TCF4*) and *RAB27B* genes on chromosome 18 (*n* = 807,553 individuals).

P-values were obtained from an inverse-variance weighted meta-analysis of summary statistics data from UK Biobank, Psychiatric Genomics Consortium and 23andMe. UK Biobank summary statistics were obtained using a linear association analysis with the results transformed to the logistic scale. Psychiatric Genomics Consortium and 23andMe data were analysed using an additive logistic model. All association analyses were two-sided tests. Recombination rates used in the plots are based on the European 1000 Genomes panel from November 2014.

General directionality agreement of variants that have previously been associated with depression

Comparison with Hyde, et al. [1]

There were 17 variants associated with depression in the joint analysis conducted by Hyde, et al. [1]. All had an effect in the same direction in UK Biobank and 16 variants had an effect in the same direction in PGC_139k. In the current meta-analysis (which included the discovery cohort used by Hyde et al. [1]) all 17 variants had an effect in the same direction as that reported by Hyde et al.[1] with 14 variants maintaining $P < 5 \times 10^{-8}$ and 13 variants providing stronger evidence of an effect based on the observed lower *P*-values compared to Hyde et al. [1]. All 17 of the Hyde et al. [1] associated variants were within ± 1Mb of a significant variant ($P < 5 \times 10^{-8}$) in the current meta-analysis.

Comparison with Howard, et al. [2]

There were 17 associated variants reported for depression in UK Biobank by Howard, et al. [2] of which 16 were available in the current meta-analysis. Fifteen had an effect in the same direction in 23andMe_307k and 14 had an effect in the same direction in PGC_139k. In the current meta-analysis (which includes the broad depression phenotype from Howard, et al. [2]) the direction of effect for all 16 variants matched that observed by Howard, et al. [2]. Nine of the 16 variants maintained $P < 5 \times 10^{-8}$ in the meta-analysis and 8 variants had lower *P*-values for an association with depression compared to Howard, et al. [2]. Twelve out of the 16 variants (excluding the MHC region) identified in UK Biobank by Howard, et al. [2] were within ± 1Mb of a significant variant ($P < 5 \times 10^{-8}$) in the meta-analysis.

Comparison with Wray, et al. [3]

The Wray, et al. [3] analysis of PGC identified 44 variants associated with depression of which 38 were available in the current meta-analysis. The Wray, et al. [3] study included an earlier release of the UK Biobank data, 23andMe_307k and PGC_139k and it is not surprising that the direction of effect was consistent across all these studies and the current meta-analysis. There were 28 variants that maintained $P < 5 \times 10^{-8}$ in the meta-analysis and 22 variants had lower *P*-values compared to those reported by Wray, et al. [3]. Thirty six of the 43 significant variants (MHC region excluded) from Wray, et al. [3] were within ± 1Mb of a significant variant ($P < 5 \times 10^{-8}$) in the meta-analysis.

Cohort information for the 23andMe replication dataset

All participants within the replication dataset were drawn from the customer base of 23andMe, Inc. Saliva samples were used for DNA extraction and genotyping which was undertaken by the National Genetics Institute, a Clinical Laboratory Improvement Amendments licensed clinical laboratory and a subsidiary of Laboratory Corporation of America. Samples were genotyped on one of four platforms:

- The V1 and V2 platforms were versions of the Illumina HumanHap550+ BeadChip, with approximately 25,000 additional custom SNPs chosen by 23andMe, providing a total of about 560,000 SNPs
- The V3 platform had a total of about 950,000 SNPs and was based on the Illumina OmniExpress+ BeadChip, with custom SNPs selected to improve overlap with the V2 array.
- The V4 platform is a fully customized array of about 570,000 SNPs, including a lower redundancy subset of V2 and V3 SNPs and with additional coverage of lower allele frequency coding variation.

Those samples that had a call rate ≤ 98.5% were re-analysed and additional samples were obtained from individuals whose samples repeatedly failed on this criterion.

To prepare the genotype data for imputation, the data was phased using Finch which implements the Beagle haplotype graph-based phasing algorithm [4]. Prior to phasing each chromosome was split into chunks containing a maximum of 300,000 variants with an overlap of 10,000 variants on either side. The Minimac3 [5] imputation model parameters were estimated for each chunk using single batches of 10,000 individuals. A combined imputation panel based on the May 2015 release of the 1000 Genomes Phase 3 haplotypes [6] and the UK10K imputation reference panel[7] was used to improve imputation accuracy. The phased data was imputed against the chunked combined imputation panel using Minimac3.

Individuals were then excluded that had ≤ 97% European ancestry based on haplotype classification [8] and a segmental identity-by-descent (IBD) estimation algorithm [9] was used to identify a maximal set of unrelated individuals who were no closer than first cousins in an outbred population and unrelated to the 23andMe_307k cohort. The phenotype was the same as that used in the 23andMe_307k cohort and reported in Hyde, et al. [1] and was based on responses to web-based surveys with individuals that self-reported as having received a clinical diagnosis or treatment for depression classified as cases. This provided a total of 1,306,354

individuals (414,055 cases and 892,299 controls) with which to conduct an association analysis of the 102 variants found to be significant in the meta-analysis of PGC_139k, 23andMe_307k and UK Biobank. The association analysis was conducted using logistic regression and assuming additive allelic effects using imputed dosages. Age, sex, the top five principal components (to account for residual population structure), and genotype platform were fitted as covariates in the model. *P*-values were calculated using a likelihood ratio test.

All individuals in this replication cohort provided informed consent. The online surveys used to collect data by 23andMe, Inc. follow their human subjects protocol which has been reviewed and approved by Ethical & Independent Review Services, a private institutional review board (http://www.eandireview.com).

References

1. Hyde, C.L.*, et al.* Identification of 15 genetic loci associated with risk of major depression in individuals of European descent. *Nature Genetics* **48**, 1031-1036 (2016).
2. Howard, D.M.*, et al.* Genome-wide association study of depression phenotypes in UK Biobank identifies variants in excitatory synaptic pathways. *Nature Communications* **9**, 1470 (2018).
3. Wray, N.R.*, et al.* Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. *Nature Genetics* **50**, 668-681 (2018).
4. Browning, S.R. & Browning, B.L. Rapid and accurate haplotype phasing and missing-data inference for whole-genome association studies By use of localized haplotype clustering. *The American Journal of Human Genetics* **81**, 1084-1097 (2007).
5. Das, S.*, et al.* Next-generation genotype imputation service and methods. *Nature Genetics* **48**, 1284-1287 (2016).
6. The 1000 Genomes Project Consortium. A global reference for human genetic variation. *Nature* **526**, 68-74 (2015).
7. The UK10K Consortium.*, et al.* The UK10K project identifies rare variants in health and disease. *Nature* **526**, 82 (2015).
8. Durand, E.Y., Do, C.B., Mountain, J.L. & Macpherson, J.M. Ancestry composition: a novel, efficient pipeline for ancestry deconvolution. *bioRxiv* (2014).
9. Henn, B.M.*, et al.* Cryptic distant relatives are common in both isolated and cosmopolitan genetic samples. *PLOS ONE* **7**, e34267 (2012).

Members of the 23andMe Research Team and their affiliation

Michelle Agee 1
Robert K. Bell 1
Pierre Fontanillas 1
David A. Hinds 1
Yunxuan Jiang 1
Nadia K. Litterman 1
Elizabeth S. Noblin 1
G. David Poznik 1
Janie F. Shelton 1
Joyce Y. Tung 1
Catherine H. Wilson 1

Babak Alipanahi 1
Katarzyna Bryc 1
Nicholas A. Furlotte 1
Karen E. Huber 1
Aaron Kleinman 1
Matthew H. McIntyre 1
Carrie A.M. Northover 1
J. Fah Sathirapongsasuti 1
Suyash Shringarpure 1
Vladimir Vacic 1

Adam Auton 1
Sarah L. Elson 1
Barry Hicks 1
Ethan M. Jewett 1
Keng-Han Lin 1
Joanna L. Mountain 1
Steven J. Pitts 1
Olga V. Sazonova 1
Chao Tang 1
Xin Wang 1

1, 23andMe, Inc., Mountain View, CA, USA

Members of the Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium and their affiliations

Naomi R Wray* 1, 2
Stephan Ripke* 3, 4, 5
Manuel Mattheisen* 6, 7, 8, 9
Maciej Trzaskowski* 1
Enda M Byrne 1
Abdel Abdellaoui 10
Mark J Adams 11
Esben Agerbo 9, 12, 13
Tracy M Air 14
Till F M Andlauer 15, 16
Silviu-Alin Bacanu 17
Marie Bækvad-Hansen 9, 18
Aartjan T F Beekman 19
Tim B Bigdeli 17, 20
Elisabeth B Binder 15, 21
Douglas H R Blackwood 11
Julien Bryois 22
Henriette N Buttenschøn 8, 9, 23
Jonas Bybjerg-Grauholm 9, 18
Na Cai 24, 25
Enrique Castelao 26
Jane Hvarregaard Christensen 7, 8, 9
Toni-Kim Clarke 11
Jonathan R I Coleman 27
Lucía Colodro-Conde 28
Baptiste Couvy-Duchesne 2, 29
Nick Craddock 30
Gregory E Crawford 31, 32
Gail Davies 33
Ian J Deary 33
Franziska Degenhardt 34, 35
Eske M Derks 28
Nese Direk 36, 37
Conor V Dolan 10
Erin C Dunn 38, 39, 40
Thalia C Eley 27
Valentina Escott-Price 41
Farnush Farhadi Hassan Kiadeh 42
Hilary K Finucane 43, 44
Jerome C Foo 45
Andreas J Forstner 34, 35, 46, 47
Josef Frank 45
Héléna A Gaspar 27
Michael Gill 48
Fernando S Goes 49
Scott D Gordon 28
Jakob Grove 7, 8, 9, 50
Lynsey S Hall 11, 51
Christine Søholm Hansen 9, 18
Thomas F Hansen 52, 53, 54
Stefan Herms 34, 35, 47
Ian B Hickie 55
Per Hoffmann 34, 35, 47
Georg Homuth 56
Carsten Horn 57
Jouke-Jan Hottenga 10
David M Hougaard 9, 18
Marcus Ising 58
Rick Jansen 19
Ian Jones 59
Lisa A Jones 60
Eric Jorgenson 61
James A Knowles 62
Isaac S Kohane 63, 64, 65
Julia Kraft 4
Warren W. Kretzschmar 66
Jesper Krogh 67
Zoltán Kutalik 68, 69
Yihan Li 66
Penelope A Lind 28
Donald J MacIntyre 70, 71
Dean F MacKinnon 49
Robert M Maier 2
Wolfgang Maier 72
Jonathan Marchini 73
Hamdi Mbarek 10
Patrick McGrath 74
Peter McGuffin 27
Sarah E Medland 28
Divya Mehta 2, 75
Christel M Middeldorp 10, 76, 77
Evelin Mihailov 78
Yuri Milaneschi 19
Lili Milani 78
Francis M Mondimore 49
Grant W Montgomery 1
Sara Mostafavi 79, 80
Niamh Mullins 27
Matthias Nauck 81, 82
Bernard Ng 80
Michel G Nivard 10
Dale R Nyholt 83
Paul F O'Reilly 27
Hogni Oskarsson 84
Michael J Owen 59
Jodie N Painter 28
Carsten Bøcker Pedersen 9, 12, 13
Marianne Giørtz Pedersen 9, 12, 13
Roseann E. Peterson 17, 85
Erik Pettersson 22
Wouter J Peyrot 19
Giorgio Pistis 26
Danielle Posthuma 86, 87
Jorge A Quiroz 88
Per Qvist 7, 8, 9
John P Rice 89
Brien P. Riley 17
Margarita Rivera 27, 90
Saira Saeed Mirza 36
Robert Schoevers 91
Eva C Schulte 92, 93
Ling Shen 61
Jianxin Shi 94
Stanley I Shyn 95
Engilbert Sigurdsson 96
Grant C B Sinnamon 97
Johannes H Smit 19
Daniel J Smith 98
Hreinn Stefansson 99
Stacy Steinberg 99
Fabian Streit 45
Jana Strohmaier 45
Katherine E Tansey 100
Henning Teismann 101
Alexander Teumer 102
Wesley Thompson 9, 53, 103, 104
Pippa A Thomson 105
Thorgeir E Thorgeirsson 99
Matthew Traylor 106
Jens Treutlein 45
Vassily Trubetskoy 4
André G Uitterlinden 107
Daniel Umbricht 108
Sandra Van der Auwera 109
Albert M van Hemert 110
Alexander Viktorin 22
Peter M Visscher 1, 2
Yunpeng Wang 9, 53, 104
Bradley T. Webb 111
Shantel Marie Weinsheimer 9, 53

1, Institute for Molecular Bioscience, The University of Queensland, Brisbane, QLD, AU
2, Queensland Brain Institute, The University of Queensland, Brisbane, QLD, AU
3, Analytic and Translational Genetics Unit, Massachusetts General Hospital, Boston, MA, US
4, Department of Psychiatry and Psychotherapy, Universitätsmedizin Berlin Campus Charité Mitte, Berlin, DE
5, Medical and Population Genetics, Broad Institute, Cambridge, MA, US
6, Centre for Psychiatry Research, Department of Clinical Neuroscience, Karolinska Institutet, Stockholm, SE
7, Department of Biomedicine, Aarhus University, Aarhus, DK
8, iSEQ, Centre for Integrative Sequencing, Aarhus University, Aarhus, DK
9, iPSYCH, The Lundbeck Foundation Initiative for Integrative Psychiatric Research,, DK
10, Dept of Biological Psychology & EMGO+ Institute for Health and Care Research, Vrije Universiteit Amsterdam, Amsterdam, NL
11, Division of Psychiatry, University of Edinburgh, Edinburgh, GB
12, Centre for Integrated Register-based Research, Aarhus University, Aarhus, DK
13, National Centre for Register-Based Research, Aarhus University, Aarhus, DK
14, Discipline of Psychiatry, University of Adelaide, Adelaide, SA, AU
15, Department of Translational Research in Psychiatry, Max Planck Institute of Psychiatry, Munich, DE
16, Munich Cluster for Systems Neurology (SyNergy), Munich, DE
17, Department of Psychiatry, Virginia Commonwealth University, Richmond, VA, US
18, Center for Neonatal Screening, Department for Congenital Disorders, Statens Serum Institut, Copenhagen, DK
19, Department of Psychiatry, Vrije Universiteit Medical Center and GGZ inGeest, Amsterdam, NL
20, Virginia Institute for Psychiatric and Behavior Genetics, Richmond, VA, US
21, Department of Psychiatry and Behavioral Sciences, Emory University School of Medicine, Atlanta, GA, US
22, Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, Stockholm, SE
23, Department of Clinical Medicine, Translational Neuropsychiatry Unit, Aarhus University, Aarhus, DK
24, Human Genetics, Wellcome Trust Sanger Institute, Cambridge, GB
25, Statistical genomics and systems genetics, European Bioinformatics Institute (EMBL-EBI), Cambridge, GB
26, Department of Psychiatry, University Hospital of Lausanne, Prilly, Vaud, CH
27, Social Genetic and Developmental Psychiatry Centre, King's College London, London, GB
28, Genetics and Computational Biology, QIMR Berghofer Medical Research Institute, Brisbane, QLD, AU
29, Centre for Advanced Imaging, The University of Queensland, Brisbane, QLD, AU
30, Psychological Medicine, Cardiff University, Cardiff, GB
31, Center for Genomic and Computational Biology, Duke University, Durham, NC, US
32, Department of Pediatrics, Division of Medical Genetics, Duke University, Durham, NC, US
33, Centre for Cognitive Ageing and Cognitive Epidemiology, University of Edinburgh, Edinburgh, GB
34, Institute of Human Genetics, University of Bonn, Bonn, DE
35, Life&Brain Center, Department of Genomics, University of Bonn, Bonn, DE
36, Epidemiology, Erasmus MC, Rotterdam, Zuid-Holland, NL
37, Psychiatry, Dokuz Eylul University School Of Medicine, Izmir, TR
38, Department of Psychiatry, Massachusetts General Hospital, Boston, MA, US
39, Psychiatric and Neurodevelopmental Genetics Unit (PNGU), Massachusetts General Hospital, Boston, MA, US
40, Stanley Center for Psychiatric Research, Broad Institute, Cambridge, MA, US
41, Neuroscience and Mental Health, Cardiff University, Cardiff, GB
42, Bioinformatics, University of British Columbia, Vancouver, BC, CA
43, Department of Epidemiology, Harvard T.H. Chan School of Public Health, Boston, MA, US
44, Department of Mathematics, Massachusetts Institute of Technology, Cambridge, MA, US
45, Department of Genetic Epidemiology in Psychiatry, Central Institute of Mental Health, Medical Faculty Mannheim, Heidelberg University, Mannheim, Baden-Württemberg, DE
46, Department of Psychiatry (UPK), University of Basel, Basel, CH
47, Human Genomics Research Group, Department of Biomedicine, University of Basel, Basel, CH
48, Department of Psychiatry, Trinity College Dublin, Dublin, IE

49, Psychiatry & Behavioral Sciences, Johns Hopkins University, Baltimore, MD, US
50, Bioinformatics Research Centre, Aarhus University, Aarhus, DK
51, Institute of Genetic Medicine, Newcastle University, Newcastle upon Tyne, GB
52, Danish Headache Centre, Department of Neurology, Rigshospitalet, Glostrup, DK
53, Institute of Biological Psychiatry, Mental Health Center Sct. Hans, Mental Health Services Capital Region of Denmark, Copenhagen, DK
54, iPSYCH, The Lundbeck Foundation Initiative for Psychiatric Research, Copenhagen, DK
55, Brain and Mind Centre, University of Sydney, Sydney, NSW, AU
56, Interfaculty Institute for Genetics and Functional Genomics, Department of Functional Genomics, University Medicine and Ernst Moritz Arndt University Greifswald, Greifswald, Mecklenburg-Vorpommern, DE
57, Roche Pharmaceutical Research and Early Development, Pharmaceutical Sciences, Roche Innovation Center Basel, F. Hoffmann-La Roche Ltd, Basel, CH
58, Max Planck Institute of Psychiatry, Munich, DE
59, MRC Centre for Neuropsychiatric Genetics and Genomics, Cardiff University, Cardiff, GB
60, Department of Psychological Medicine, University of Worcester, Worcester, GB
61, Division of Research, Kaiser Permanente Northern California, Oakland, CA, US
62, Psychiatry & The Behavioral Sciences, University of Southern California, Los Angeles, CA, US
63, Department of Biomedical Informatics, Harvard Medical School, Boston, MA, US
64, Department of Medicine, Brigham and Women's Hospital, Boston, MA, US
65, Informatics Program, Boston Children's Hospital, Boston, MA, US
66, Wellcome Trust Centre for Human Genetics, University of Oxford, Oxford, GB
67, Department of Endocrinology at Herlev University Hospital, University of Copenhagen, Copenhagen, DK
68, Institute of Social and Preventive Medicine (IUMSP), University Hospital of Lausanne, Lausanne, VD, CH
69, Swiss Institute of Bioinformatics, Lausanne, VD, CH
70, Division of Psychiatry, Centre for Clinical Brain Sciences, University of Edinburgh, Edinburgh, GB
71, Mental Health, NHS 24, Glasgow, GB
72, Department of Psychiatry and Psychotherapy, University of Bonn, Bonn, DE
73, Statistics, University of Oxford, Oxford, GB
74, Psychiatry, Columbia University College of Physicians and Surgeons, New York, NY, US
75, School of Psychology and Counseling, Queensland University of Technology, Brisbane, QLD, AU
76, Child and Youth Mental Health Service, Children's Health Queensland Hospital and Health Service, South Brisbane, QLD, AU
77, Child Health Research Centre, University of Queensland, Brisbane, QLD, AU
78, Estonian Genome Center, University of Tartu, Tartu, EE
79, Medical Genetics, University of British Columbia, Vancouver, BC, CA
80, Statistics, University of British Columbia, Vancouver, BC, CA
81, DZHK (German Centre for Cardiovascular Research), Partner Site Greifswald, University Medicine, University Medicine Greifswald, Greifswald, Mecklenburg-Vorpommern, DE
82, Institute of Clinical Chemistry and Laboratory Medicine, University Medicine Greifswald, Greifswald, Mecklenburg-Vorpommern, DE
83, Institute of Health and Biomedical Innovation, Queensland University of Technology, Brisbane, QLD, AU
84, Humus, Reykjavik, IS
85, Virginia Institute for Psychiatric & Behavioral Genetics, Virginia Commonwealth University, Richmond, VA, US
86, Clinical Genetics, Vrije Universiteit Medical Center, Amsterdam, NL
87, Complex Trait Genetics, Vrije Universiteit Amsterdam, Amsterdam, NL
88, Solid Biosciences, Boston, MA, US
89, Department of Psychiatry, Washington University in Saint Louis School of Medicine, Saint Louis, MO, US
90, Department of Biochemistry and Molecular Biology II, Institute of Neurosciences, Center for Biomedical Research, University of Granada, Granada, ES
91, Department of Psychiatry, University of Groningen, University Medical Center Groningen, Groningen, NL

92, Department of Psychiatry and Psychotherapy, Medical Center of the University of Munich, Campus Innenstadt, Munich, DE
93, Institute of Psychiatric Phenomics and Genomics (IPPG), Medical Center of the University of Munich, Campus Innenstadt, Munich, DE
94, Division of Cancer Epidemiology and Genetics, National Cancer Institute, Bethesda, MD, US
95, Behavioral Health Services, Kaiser Permanente Washington, Seattle, WA, US
96, Faculty of Medicine, Department of Psychiatry, University of Iceland, Reykjavik, IS
97, School of Medicine and Dentistry, James Cook University, Townsville, QLD, AU
98, Institute of Health and Wellbeing, University of Glasgow, Glasgow, GB
99, deCODE Genetics / Amgen, Reykjavik, IS
100, College of Biomedical and Life Sciences, Cardiff University, Cardiff, GB
101, Institute of Epidemiology and Social Medicine, University of Münster, Münster, Nordrhein-Westfalen, DE
102, Institute for Community Medicine, University Medicine Greifswald, Greifswald, Mecklenburg-Vorpommern, DE
103, Department of Psychiatry, University of California, San Diego, San Diego, CA, US
104, KG Jebsen Centre for Psychosis Research, Norway Division of Mental Health and Addiction, Oslo University Hospital, Oslo, NO
105, Medical Genetics Section, CGEM, IGMM, University of Edinburgh, Edinburgh, GB
106, Clinical Neurosciences, University of Cambridge, Cambridge, GB
107, Internal Medicine, Erasmus MC, Rotterdam, Zuid-Holland, NL
108, Roche Pharmaceutical Research and Early Development, Neuroscience, Ophthalmology and Rare Diseases Discovery & Translational Medicine Area, Roche Innovation Center Basel, F. Hoffmann-La Roche Ltd, Basel, CH
109, Department of Psychiatry and Psychotherapy, University Medicine Greifswald, Greifswald, Mecklenburg-Vorpommern, DE
110, Department of Psychiatry, Leiden University Medical Center, Leiden, NL
111, Virginia Institute for Psychiatric & Behavioral Genetics, Virginia Commonwealth University, Richmond, VA, US
112, Computational Sciences Center of Emphasis, Pfizer Global Research and Development, Cambridge, MA, US
113, Institute for Molecular Bioscience; Queensland Brain Institute, The University of Queensland, Brisbane, QLD, AU
114, Department of Psychiatry, University of Münster, Münster, Nordrhein-Westfalen, DE
115, Department of Psychiatry, Melbourne Medical School, University of Melbourne, Melbourne, AU
116, Institute of Medical Genetics and Pathology, University Hospital Basel, University of Basel, Basel, CH
117, Institute of Neuroscience and Medicine (INM-1), Research Center Juelich, Juelich, DE
118, Amsterdam Public Health Institute, Vrije Universiteit Medical Center, Amsterdam, NL
119, Centre for Integrative Biology, Università degli Studi di Trento, Trento, Trentino-Alto Adige, IT
120, Department of Psychiatry and Psychotherapy, Medical Center, University of Freiburg, Faculty of Medicine, University of Freiburg, Freiburg, DE
121, Psychiatry, Kaiser Permanente Northern California, San Francisco, CA, US
122, Medical Research Council Human Genetics Unit, Institute of Genetics and Molecular Medicine, University of Edinburgh, Edinburgh, GB
123, Department of Psychiatry, University of Toronto, Toronto, ON, CA
124, Centre for Addiction and Mental Health, Toronto, ON, CA
125, Division of Psychiatry, University College London, London, GB
126, Neuroscience Therapeutic Area, Janssen Research and Development, LLC, Titusville, NJ, US
127, Institute of Molecular and Cell Biology, University of Tartu, Tartu, EE
128, Psychosis Research Unit, Aarhus University Hospital, Risskov, Aarhus, DK
129, University of Liverpool, Liverpool, GB
130, Mental Health Center Copenhagen, Copenhagen Universtity Hospital, Copenhagen, DK
131, Human Genetics and Computational Biomedicine, Pfizer Global Research and Development, Groton, CT, US
132, Psychiatry, Harvard Medical School, Boston, MA, US

133, Psychiatry, University of Iowa, Iowa City, IA, US
134, Department of Psychiatry and Behavioral Sciences, Johns Hopkins University, Baltimore, MD, US
135, Department of Psychiatry and Psychotherapy, University Medical Center Göttingen, Goettingen, Niedersachsen, DE
136, Human Genetics Branch, NIMH Division of Intramural Research Programs, Bethesda, MD, US
137, Faculty of Medicine, University of Iceland, Reykjavik, IS
138, Child and Adolescent Psychiatry, Erasmus MC, Rotterdam, Zuid-Holland, NL
139, Psychiatry, Erasmus MC, Rotterdam, Zuid-Holland, NL
140, Psychiatry, Dalhousie University, Halifax, NS, CA
141, Division of Epidemiology, New York State Psychiatric Institute, New York, NY, US
142, Department of Clinical Medicine, University of Copenhagen, Copenhagen, DK
143, Department of Medical & Molecular Genetics, King's College London, London, GB
144, Psychiatry & Behavioral Sciences, Stanford University, Stanford, CA, US
145, NIHR Maudsley Biomedical Research Centre, King's College London, London, GB
146, Genetics, University of North Carolina at Chapel Hill, Chapel Hill, NC, US
147, Psychiatry, University of North Carolina at Chapel Hill, Chapel Hill, NC, US

Version 5. 2018-07-17