Depression GWAS meta-analysis results excluding 23andMe, April 2023 release (iPSYCH2015i+UKB+PGC2(incl. iPSYCH2012)+FinnGen+MVP data)

The file 'daner_MDDwoBP_20201001_2015iR15iex_HRC_MDDwoBP_iPSYCH2015i_UKBtransformed_Wray_FinnGen_MVPaf_2_HRC_MAF01.gz' contains results from a GWAS meta-analysis of depression corresponding to the primary meta-analysis reported in the paper '*Depression pathophysiology, risk prediction of recurrence and comorbid psychiatric disorders using genome-wide analyses'* published in Nature Medicine, 2023 (DOI), but with the GWAS meta-analysis reported in Howard et al. 2019[1] (excluding all Danish samples) replaced by the UKB summary stats used in Howard et al. 2019[1], and PGC-MDD summary stats (including iPSYCH2012) from Wray et al. 2018[2], thus not including any 23andMe summary statistics. To access the summary statistics from the meta-analysis of all cohorts, including 23andMe, a data transfer agreement is required from 23andMe (dataset-request@23andMe.com) before a request is made to the corresponding authors. See https://research.23andme.com/collaborate/#dataset-access/ for more information and to apply for access to the data.

Citation for studies using these data

T. D. Als, M. Kurki, J. Grove, G. Voloudakis, K. Therrien, E. Tasanko, T. T. Nielsen, J. Naamanka, K. Veerapen, D. Levey, J. Bendl, J. Bybjerg-Grauholm, B. Zheng, D. Demontis, A. Rosengren, G. Athanasiadis, M. Bækved-Hansen, P. Qvist, G. B. Walters, T. Thorgeirsson, H. Stefánsson, K. L. Musliner, V. M. Rajagopal, L. Farajzadeh, J. Thirstrup, B. J. Vilhjálmsson, J. J. McGrath, M. Mattheisen, S. Meier, E. Agerbo, K. Stefánsson, M. Nordentoft, T. Werge, D. M. Hougaard, P. B. Mortensen, M. B. Stein, J. Gelernter, I. Hovatta, P. Roussos, M. J. Daly, O. Mors, A. Palotie, and A. D. Børglum (April 2023). *Depression pathophysiology, risk prediction of recurrence and comorbid psychiatric disorders using genome-wide analyses*. Nature Medicine (NMED-A120965C).

Disclaimer

These data are provided "as is", and without warranty, for scientific and educational use only. If you download these data, you acknowledge that these data will be used

only for non-commercial research purposes; that the investigator is in compliance with all applicable state, local, and federal laws or regulations and institutional policies regarding human subjects and genetics research; that secondary distribution of the data without registration by secondary parties is prohibited; and that the investigator will cite the publication in any communications or publications arising directly or indirectly from these data.

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5) Investigators will cite the appropriate publication in any communications or publications arising directly or indirectly from these data;
6) Investigators will never attempt to identify any participant who contributed to these data;
7) Investigators may not use these data to develop any type of risk or predictive test for an unborn individual;
8) For any risk or predictive test for a child or adult, investigators must acknowledge that this is an experimental use of these data and that essentially all psychiatric disorders have important non-genetic etiological components;
9) When these data are made available prior to publication, investigators agree to respect and not compete with the scientific priorities of the iPSYCH team according to the Fort Lauderdale principles.

Appropriate use of these data requires considerable attention to detail, prior experience, and technical skill. Errors are easy to make. If investigators use these data, any and all consequences are entirely their responsibility.

File Description

daner_MDDwoBP_20201001_2015iR15iex_HRC_MDDwoBP_iPSYCH2015i_UKBtransformed_Wray_FinnGen_MVPaf_2_HRC_MAF01.gz: A subset of the primary depression GWAS meta-analysis of samples of European ancestry, excluding 23andMe (cases and controls) but with the GWAS meta-analysis reported in Howard et al. 2019[1] (excluding all Danish samples) replaced by the UKB summary stats used in Howard et al. 2019[1] and PGC-MDD summary stats (including iPSYCH2012) from Wray et al. 2018[2].
CHR: Chromosome (hg19)
SNP: Marker name
BP: Base pair location (hg19)
A1: Reference allele for OR (may or may not be minor allele)
A2: Alternative allele
FRQ_A_294322: allele frequency in 294322 cases
FRQ_U_741438: allele frequency in 741438 controls
INFO: Imputation information score (the reported imputation INFO score is a weighted average across the cohorts, for which INFO score was available, contributing to the meta-analysis for that variant)
OR: Odds ratio for the effect of the A1 allele
SE: Standard error of the log(OR)
P: P-value for association test in the meta-analysis
Direction: direction of effect in the included cohorts

Additional Notes
MD5
(daner_MDDwoBP_20201001_2015iR15iex_HRC_MDDwoBP_iPSYCH2015i_UKBtransformed_Wray_FinnGen_MVPaf_2_HRC_MAF01.gz)
43a855b2d997a375a76c0da82351a70a

The reported imputation INFO score is a weighted average across the cohorts contributing to meta-analysis for that variant.

1 Howard, D. M. *et al.* Genome-wide meta-analysis of depression identifies 102 independent variants and highlights the importance of the prefrontal brain regions. *Nat Neurosci* **22**, 343-352 (2019). https://doi.org:10.1038/s41593-018-0326-7

2 Wray, N. R. *et al.* Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. *Nat Genet* **50**, 668-681 (2018). https://doi.org:10.1038/s41588-018-0090-3