

Introduction:

These are the GWAS results files from the cross-disorder mega-analysis from the Lundbeck Foundation Initiative for Integrative Psychiatric Research (iPSYCH) released in November 2018.

Citation for studies using these data:

Andrew J. Schork, Hyejung Won, Vivek Appadurai, Ron Nudel, Mike Gandal, Olivier Delaneau, Malene Revsbech Christiansen, David M. Hougaard, Marie Bækved-Hansen, Jonas Bybjerg-Grauholm, Marianne Giørtz Pedersen, Esben Agerbo, Carsten Bøcker Pedersen, Benjamin M. Neale, Mark J. Daly, Naomi R. Wray, Merete Nordentoft, Ole Mors, Anders D. Børghlum, Preben Bo Mortensen, Alfonso Buil, Wesley K. Thompson, Daniel Geschwind, Thomas Werge. A genome-wide association study of shared risk across psychiatric disorders implicates gene regulation during fetal neurodevelopment. *Nature Neuroscience*. (In Press).

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 above manuscript in any communications or publications arising directly or indirectly from these data. A user also agrees that under no circumstances will any attempt to identify any participant be made.

Methods:

See the in-text *Methods* and *Supplementary Note 2* for the above manuscript for detailed information.

GWAS summary statistics were computed for imputed dosages of 8,008,973 variants (SNPs or indels) using logistic regression. Age, gender and 10 PCs were included as covariates. The total sample size included 65,534 individuals with 46,008 cases and 19,526 controls. There were no missing genotypes due to the imputation procedure, so each SNP test was performed on an identical set of subjects, in one mega-analysis.

File Description

iPSYCH_xDx_sumStats.txt.gz is a gzipped, space delimited file with the following data columns

SNP	Marker name
CHR	Chromosome (hg19)
BP	Base pair location (hg19)

A1	Reference allele for OR (may or may not be minor allele)
A2	Alternative allele
INFO	Imputation information score
OR	Odds ratio for the effect of the A1 allele
SElnOR	Standard error of the natural log of the odds ratio [$\ln(\text{OR})$]
STAT	test statistic for association test
P	P-value for association test in the meta-analysis