Bipolar Disorder and Schizophrenia Working Group results – June 2018 release

This README corresponds to the results from the recent publication in *Cell* of the Bipolar Disorder and Schizophrenia Working Group of the Psychiatric Genomics Consortium.

Citation

Bipolar Disorder and Schizophrenia Working Group of the Psychiatric Genomics Consortium, 2018. Genomic Dissection of bipolcellar disorder and schizophrenia, including 28 subphenotypes. Cell 173. https://doi.org/10.1016/j.cell.2018.05.046

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Description of files

This directory contains 4 gzipped summary statistic files that correspond to the different GWAS performed in this manuscript. These files are filtered for allele frequency > 1%, INFO > 0.3 and for variants that were genotyped/imputed in all cohorts.

BDSCZvsCONT.sumstats.gz: Bipolar disorder cases (n=20,129) combined with schizophrenia cases (n=33,426) against controls (n=54,065):

BDvsCONT.sumstats.gz: Bipolar disorder cases (n=20,129) against an independent bipolar specific set of controls (n=21,524):

SCZvsCONT.sumstats.gz: Schizophrenia cases (n=33,426) against an independent schizophrenia specific set of controls (n=32,541)

SCZvsBD.sumstats.gz: A subset of schizophrenia cases (n=23,585) and bipolar disorder cases (n=15,270) matched for ancestry and genotyping array platform.

These files all have the same format and headers
CHR: Chromosome
SNP: Variant
BP: Genomic position
A1: Effect allele (used for frequency and OR)
A2: Non-effect allele
FRQ_A: Frequency in cases (header includes number of cases)
FRQ_U: Frequency in controls (header includes number of controls)
INFO : Information score representing quality of imputation
OR: Odds ratio based on A1
SE: Standard error
P: P-value
Direction: Direction of effect of each included cohort
HetPVa: Heterogeneity test p-value across included cohorts