

## ADHD GWAS meta-analysis results, January 2022 Release (iPSYCH+deCODE+PGC data)

The file “daner\_ADHD\_meta\_iPSYCH1\_iPSYCH2\_deCODE\_PGC\_v10\_filtered2.meta.gz” contains results from the updated GWAS meta-analysis of ADHD reported in the preprint below. Detailed information about generation of the data can be found in the preprint.

Ditte Demontis, G. Bragi Walters, Georgios Athanasiadis, Raymond Walters, Karen Therrien, Leila Farajzadeh, Georgios Voloudakis, Jaroslav Bendl, Biao Zeng, Wen Zhang, Jakob Grove, Thomas D. Als, Jinjie Duan, F. Kyle Satterstrom, Jonas Bybjerg-Grauholm, Marie Bækved-Hansen, Olafur O. Gudmundsson, Sigurdur H. Magnusson, Gisli Baldursson, Katrin Davidsdottir, Gyda S. Haraldsdottir, Trine Tollerup Nielsen, Esben Agerbo, Gabriel E. Hoffman, Søren Dalsgaard, Joanna Martin, Marta Ribasés, Dorret I. Boomsma, Maria Soler Artigas, Nina Roth Mota, Daniel Howrigan, Sarah E. Medland, Tetyana Zayats, Veera Manikandan, ADHD Working Group of the Psychiatric Genomics Consortium, iPSYCH-Broad Consortium, Merete Nordentoft, Ole Mors, David M. Hougaard, Preben Bo Mortensen, Mark J. Daly, Stephen V. Faraone, Hreinn Stefansson, Panos Roussos, Barbara Franke, Thomas Werge, Benjamin M. Neale, Kari Stefansson, Anders D. Børglum. **Genome-wide analyses of ADHD identify 27 risk loci, refine the genetic architecture and implicate several cognitive domains.** Under revision in Nature Genetics (**medRxiv**: doi: <https://doi.org/10.1101/2022.02.14.22270780>)

### File Description

MD5 (daner\_ADHD\_meta\_iPSYCH1\_iPSYCH2\_deCODE\_PGC\_v10\_filtered2.meta.gz) = 9a515c69ae3f36163ad83f674e5a5755

**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\_38691** allele frequency of A1 in 38,691 ADHD cases

**FRQ\_U\_186,843** allele frequency of A1 in 38,691 controls

**INFO** Imputation information score (the reported imputation INFO score is a weighted average across the cohorts 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

We are sharing the data on a collaborative basis, which means that key authors from iPSYCH and deCODE should be included as authors on the publication of your project.

Please note that the summary statistics cannot be shared outside your group and that the data can only be used for the approved project.