

Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. figure legend, table legend, main text, or Methods section).

n/a Confirmed

- ☐ ☒ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- ☐ ☒ An indication of whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☐ ☒ The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- ☐ ☒ A description of all covariates tested
- ☐ ☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- ☐ ☒ A full description of the statistics including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- ☐ ☒ For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- ☒ ☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- ☐ ☒ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- ☐ ☒ Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated
- ☐ ☒ Clearly defined error bars
State explicitly what error bars represent (e.g. SD, SE, CI)

Our web collection on [statistics for biologists](#) may be useful.

Software and code

Policy information about [availability of computer code](#)

Data collection

Collection of genotypic information was done using SNP array genotyping and subsequent calling of genotypes were done using the softwares GenCall, Birdseed and GenomeStudio

Data analysis

Quality control and association analyses were done using the Ricopili pipeline: <https://github.com/Nealelab/ricopili>, which include the following software: Shapelt, IMPUTE2, Plink 1.9, Eigensoft 6.1.3, METAL 2011-03-25.
For gene-based and gene-set analyses we used MAGMA 1.06
Analyses of credible SNPs were done using <https://github.com/hailianghuang/FMsummary>
Functional annotation of credible SNPs was done using Ensemble Variant Effect Predictor (VEP).
SNPs associated with gene expression were annotated using FUMA (<http://fuma.ctglab.nl/>)
SNP heritability, partitioning of the heritability and genetic correlations were estimated using LD score regression (<https://github.com/bulik/ldsc>) and LD hub (<http://ldsc.broadinstitute.org/>).
Genetic correlation between PGC case-control and trio samples was calculated using GCTA v1.26.0
Meta analyses of continuous and dichotomous ADHD measures were calculated

using adjusted sample size weighted meta-analysis, described in details in the Supplementary Information.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

Availability of genotype data and summary statistics

For access to genotypes from the PGC cohorts and the iPSYCH sample interested researchers should contact the lead PIs (iPSYCH: lead PI Anders D. Børghlum; PGC: Benjamin Neale and Stephen Faraone). Summary statistics can be downloaded from:

<https://www.med.unc.edu/pgc/results-and-downloads>

<http://ipsych.au.dk/downloads/>

<http://www.wikigenes.org/e/art/e/348.html>

Field-specific reporting

Please select the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	No sample size calculation was made. Previous studies of polygenic psychiatric disorders (e.g. schizophrenia) have demonstrated that high numbers of cases and controls (in line with the sample size analysed in this study) yield enough power to detect common risk variants with low effect sizes.
Data exclusions	Within each analysed cohort we aimed at analysing genetically homogenous samples of unrelated individuals. Related individuals were excluded based on Identity by State analyses (pseudo controls were used for trios) and genetic outliers were excluded based on principal component analyses
Replication	The results from our primary GWAS of diagnosed ADHD were replicated using results from analyses of three studies: a GWAS meta-analysis of ADHD symptom scores in the general population (EAGLE and QIMR cohorts), GWAS of self-reported ADHD (the 23andMe sample) and a sample of diagnosed ADHD (deCODE). We evaluated our results in the three replication studies in three ways: 1) sign test 2) genetic correlation 3) meta-analysis of the combined samples. The results of these three replication approaches support the results from our primary GWAS meta-analysis.
Randomization	Allocation into groups was not random. Individuals were allocated into the case group based on having a diagnosis of ADHD. The controls in each cohort did not have a diagnosis of ADHD.
Blinding	No blinding was done in this study. The design was a case-control study and therefore it was fundamental for the analyses that researchers knew the case-control status of the included individuals

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☐	☒ Unique biological materials
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☐	☒ Human research participants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Unique biological materials

Policy information about [availability of materials](#)Obtaining unique materials

Human research participants

Policy information about [studies involving human research participants](#)

Population characteristics *Describe the covariate-relevant population characteristics of the human research participants (e.g. age, gender, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."*

Recruitment

In the meta-analysis we included 11 cohorts from the Psychiatric Genetics Consortium (PGC) and the iPSYCH cohort. In the separate GWASs we corrected for population stratification using relevant principal components from principal component analyses as covariates.

The iPSYCH cohort was processed in 23 genotyping waves (genotyping, qc and imputation were done separately for these batches) of approximately 3,500 individuals each. In order to control for potential batch effects we included "wave" as a covariate in the regression models of all downstream analyses when relevant.

Sex was not used as covariate, as we found no indication of sex being a confounder in our analyses (results not shown).