

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](#).

Statistics

For all statistical analyses, confirm that the following items are present in the 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 |
| ☒ | ☐ A statement on 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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☐ | ☒ 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 statistical parameters 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
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ 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 |

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

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

Data collection

We used published summary statistics or performed GWAS based on data collected by UKBiobank

Data analysis

GWASs of UKB cohort was performed with PLINK v1.9, gene and gene-set analyses were performed with MAGMA v1.06, lead SNPs and trait-associated loci for each GWAS were defined using FUMA v1.3.3, colocalization was performed with coloc package in R, fine-mapping was performed with FINEMAP v1.3, functional consequence of SNPs were annotated with ANNOVAR, SNP heritability and genetic correlation were estimated using LD score regression and SumHer implemented in LDAK v5, polygenicity and discoverability was estimated using MiXeR, all other statistical analyses were performed with R v3.4.3.

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. 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

All publicly available GWAS summary statistics (original) files curated in this study are accessible from the original links provided at <http://atlas.ctglab.nl>. GWAS summary statistics for 600 traits from UK Biobank performed in this study are also provided at <http://atlas.ctglab.nl> and an archived file will be made available upon publication from https://ctg.cncr.nl/software/summary_statistics.

Field-specific reporting

Please select the one below that is 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/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Life sciences study design

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

Sample size	We used maximum number of samples for UKB GWASs with limiting the subjects to unrelated European ancestry and no-missing phenotype and covariates for each trait.
Data exclusions	For main analyses in the manuscript we selected 558 GWASs from 4155 GWASs curated in the ATLAS database, based on sample size. When there were multiple GWASs with the same trait, GWAS with the largest sample size was selected.
Replication	Replication is not applicable: we analyzed all available GWAS results to obtain a global overview of pleiotropy, genetic architectures and genetic correlations.
Randomization	N.A.
Blinding	N.A.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

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

Methods

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

Human research participants

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

Population characteristics	We utilized data collected previously by UK biobank. All individuals included in the study provided informed consent, and the study was approved by the concerned ethical committee.
Recruitment	See above (and in Methods section of the manuscript)
Ethics oversight	NHS Health Research Authority provided ethics approval for the UKB study

Note that full information on the approval of the study protocol must also be provided in the manuscript.