

Reporting Summary

Nature Portfolio 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 Portfolio policies, see our [Editorial Policies](#) 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 (<i>n</i>) 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> 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 <i>d</i> , Pearson's <i>r</i>), 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	N/A
Data analysis	Custom code written for executing experiments is available via GitHub (https://github.com/ArtomovLab/Cost-efficient-non-additive-GWAS). REGENIE, SUSIE, PLINK were used for manipulation and analysis of genetic data, and are mentioned in the Methods section of the manuscript.

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 and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [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 description of any restrictions on data availability
 - For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

Additive p-value thresholds for dominant and recessive analyses of binary and continuous traits generated by this study are available in Supplementary Data 1. Descriptions of traits are available in Supplementary Data 2. Summary statistics for 781 new associations generated by this study are available in Supplementary Data 3. The results of fine-mapping, colocalization, and replication generated by this study are available in Supplementary Data 4, 5, and 6, respectively. Full

summary statistics for additive, dominant, and recessive GWAS of 19 traits; all summary statistics generated by the dominant GWAS of 2,329 traits; and raw colocalization and fine-mapping outputs generated by this study have been deposited in Zenodo (zenodo.org/records/17449480)

Under national and European regulations (GDPR), access to individual-level sensitive health data requires approval by national authorities for specific projects and named researchers. The health data used here were generated by the National Health Register Authorities (Finnish Institute for Health and Welfare, Statistics Finland, KELA, and the Digital and Population Data Services Agency) and authorized – by the respective authorities or by the Finnish Health and Social Data Permit Authority (Findata) – for use within FinnGen. Accordingly, we are not able to grant access to individual-level data. Researchers may apply for health-register data via Findata (<https://findata.fi/en/permits/>) and for individual-level genotype data from Finnish biobanks through the Fingenious portal (<https://site.fingenious.fi/en/>) operated by the Finnish Biobank Cooperative (FINBB; <https://finbb.fi/en/>).

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender	All the analyses included sex as a covariate.
Reporting on race, ethnicity, or other socially relevant groupings	All analyses were adjusted for the genetic principal components to account for genetic ancestry diversity within the dataset.
Population characteristics	Details about the dataset and study population could be found in https://www.nature.com/articles/s41586-022-05473-8
Recruitment	N/A
Ethics oversight	Study subjects in FinnGen provided informed consent for biobank research, based on the Finnish Biobank Act. Alternatively, separate research cohorts, collected prior the Finnish Biobank Act came into effect (in September 2013) and start of FinnGen (August 2017), were collected based on study-specific consents and later transferred to the Finnish biobanks after approval by Fimea (Finnish Medicines Agency), the National Supervisory Authority for Welfare and Health. Recruitment protocols followed the biobank protocols approved by Fimea. The Coordinating Ethics Committee of the Hospital District of Helsinki and Uusimaa (HUS) statement number for the FinnGen study is Nr HUS/990/2017

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

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

Life sciences study design

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

Sample size	GWAS was conducted on data from 500,329 individuals The sample size was not predetermined but was instead defined by the availability of genotyped and phenotyped participants in the FinnGen biobank. Using all eligible individuals maximizes statistical power and reflects the full population represented in the resource.
Data exclusions	The rules for control exclusions were established by the FinnGen team in earlier analyses. Participants with comorbid or overlapping phenotypes were removed from the control cohorts. Details of phenotype-specific exclusions are provided in the Supplementary Data 2
Replication	Replication of the results was carried out in Million Veterans Program data, and 35% of the matched variants were replicated at FDR < 5%.
Randomization	This study is based on observational pre-existing biobank data rather than an experiment; therefore, there were no interventions that would require randomization
Blinding	This study is based on observational pre-existing biobank data rather than an experiment; therefore, there were no interventions that would require blinding

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	Involvement in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Plants

Seed stocks

Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.

Novel plant genotypes

Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.

Authentication

Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.