nature portfolio

Corresponding author(s): Adam Auton

Last updated by author(s): Feb 19, 2026

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 (*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 *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 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 *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

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	Phenotype data was collected via the 23andMe Research platform. No additional software was used.
Data analysis	Standard GWAS analyses were performed using the 23andMe Research platform, as described in numerous peer-reviewed publications (https://research.23andme.com/publications/). Additional analyses were conducted in R version 4.4.0, python3, and statsmodels 0.14.1.

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

The full set of de-identified summary statistics can be made available to qualified investigators who enter into an agreement with 23andMe that protects participant confidentiality. Interested investigators should visit the 23andMe Dataset Access Program at https://research.23andme.com/dataset-access/. Individual-level data

from 23andMe participants used in the analyses are not publicly available due to participant confidentiality and in accordance with the IRB-approved protocol under which the study was conducted.

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	In the context of this study, biological sex was determined on the based on the number of X and Y chromosomes detected in the genetic sample.
Reporting on race, ethnicity, or other socially relevant groupings	Ancestry groups were determined by a genetic ancestry classification algorithm, as detailed in Durand, E. Y. et al. A scalable pipeline for local ancestry inference using tens of thousands of reference haplotypes. bioRxiv 2021.01.19.427308 (2021) doi:10.1101/2021.01.19.427308.
Population characteristics	Details of the population characteristics are described in Table 1.
Recruitment	Participants in this study were recruited from the customer base of 23andMe Research Institute, a nonprofit medical research organization. Participants provided informed consent and volunteered to participate in the research online, under a protocol approved by the external AAHRPP-accredited Salus IRB (https://www.versiticlinicaltrials.org/salusirb). Participants were included in the analysis on the basis of consent status verified at the time data analyses were initiated. Given this approach to recruitment, the participants represent a self-selected cohort which may induce the generalizability of the findings.
Ethics oversight	The research protocol is approved by the external AAHRPP-accredited Salus IRB (https://www.versiticlinicaltrials.org/salusirb)

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	Sample size was determined on the basis of the number of respondents to online surveys and was judged appropriate to adequately power genome-wide association studies. A freeze of the data collection was taken in August 2025, with all subsequent analyses derived from that data freeze.
Data exclusions	Only 23andMe Research participants that consented to participate in research and completed the online survey were included. Additional exlusion criteria for specific analyses are detailed in the manuscript for QC purposes.
Replication	Replication was performed in the All of Us and UK Biobank cohorts, as detailed in the manuscript. The All of Us replication successfully replicated the efficacy finding in the manuscript. The UK Biobank replication did not replicate the finding, but had limited power and differed substantially in terms of the medications under consideration.
Randomization	This is an observations population study for which randomization is not applicable.
Blinding	This is an observations population study for which blinding is not applicable.

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 and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Plants

Seed stocks	n/a
Novel plant genotypes	n/a
Authentication	n/a