nature portfolio

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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 <u>Editorial Policies</u> and the <u>Editorial Policy Checklist</u>.

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| For al | I statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section. |
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| n/a | Confirmed |
| | \times 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> 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 |
| | \boxtimes Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated |
| | Our web collection on <u>statistics for biologists</u> contains articles on many of the points above. |
| Sof | tware and code |

Delign information object quallability of company

Policy information about availability of computer code

Data collection No specific software used for data collection

Data analysis Python version 3.9, R 4.0.0

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

UK Biobank data are available upon application (http://www.ukbiobank.ac.uk/). The BIDMC dataset is restricted due to ethical limitations. Researchers affiliated to educational, or research institutions may make requests to access the datasets. Requests should be made to the corresponding author of this paper. They will be forwarded to the relevant steering committee.

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

Analyses were adjusted for self-reported sex, excluding GWAS, which used genetically determined sex. Sample sizes are provided in the manuscript.

Reporting on race, ethnicity, or other socially relevant groupings

Supplementary Table 1 provides a summary of the ethnicities of the participants. Relevant analyses were conducted for each ethnic group.

Population characteristics

Population characteristics are summarised in Supplementary Table 1.

Recruitment

The BIDMC cohort is a dataset comprised of routinely collected data from Beth Israel Deaconess Medical Center, Boston, USA. Subject over 16 years old with a valid ECG performed from 2000 to 2023 were included. ECGs were linked to clinical records. In total, 512950 ECGs from 114415 subjects were available for analysis.

UK Biobank

The BIDMC cohort

The UK Biobank is longitudinal study of over 500,000 volunteers aged 40-69 at the time of enrolment in 2006-2010 (1). At baseline assessment, participants provided information on health and lifestyle via questionnaire, had physical measures taken (including height, weight, and blood pressure), and donated samples of blood urine and saliva. A subgroup of participants was invited back for subsequent visits for additional investigations, including cardiac magnetic resonance imaging (MRI), brain MRI, and digital ECGs. 42,386 subjects with digital ECGs taken at the instance 2 visit were available for analysis. There is evidence of healthy volunteer selection bias (2). Outcomes were linked to cancer and death registry data, hospital admissions, and primary care records. Detailed phenotyping using the cardiac MRI data has been previously described (3, 4).

Ethics oversight

X Life sciences

For the Beth Israel Deaconess Medical Center (BIDMC) cohort ethics review and approval were provided by the Beth Israel Deaconess Medical Center Committee on Clinical Investigations, IRB protocol # 2023P000042.

Ecological, evolutionary & environmental sciences

The UK Biobank has approval from the North West Multi-Centre Research Ethics Committee as a Research Tissue Bank (application IDs 48666, 47602).

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

Field-specific reporting

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Behavioural & social sciences For a reference copy of the document with all sections, see <u>nature.com/documents/nr-reporting-summary-flat.pdf</u>

Life sciences study design

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

| Sample size | All participants meeting inclusion criteria |
|-----------------|--|
| Data exclusions | Participants excluded if no ECG or Body Mass Index available |
| Replication | External validation performed in the UK Biobank |
| Randomization | Observational study - no randomisation |
| Blinding | Observational study - no randomisation/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 & experime n/a Involved in the study Antibodies Eukaryotic cell lines Palaeontology and a Animals and other of Clinical data Dual use research of Plants | n/a Involved in the study ChIP-seq Flow cytometry MRI-based neuroimaging organisms |
|--|--|
| Clinical data Policy information about cl | inical studies |
| | with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions. |
| Clinical trial registration | Not a clinical trial |
| Study protocol | Not a clinical trial |
| Data collection | The BIDMC cohort The BIDMC cohort is a dataset comprised of routinely collected data from Beth Israel Deaconess Medical Center, Boston, USA. Subject over 16 years old with a valid ECG performed from 2000 to 2023 were included. ECGs were linked to clinical records. In total, 512950 ECGs from 114415 subjects were available for analysis. UK Biobank |
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| Outcomes | Cardiometabolic disease, Type 2 Diabetes Mellitus, Hypertension, Lipid disorders |
| 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

was applied.

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, mosiacism, off-target gene editing) were examined.