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 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	All code written for this project was deposited on GitHub: https://github.com/jcnicholas/SomaScan7k_OlinkExplore3072_MESA_Platform_Comparison/
Data analysis	tensorQTL v1.0.8 R Studio v 4.1.0 /4.3.1/4.4.0 plink 1.90b3 WGSA 0.95 MendelianRandomization R package (0.10.0) Pymol 2.6

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 cis- and trans-pQTL association statistics generated in this study have been deposited in a Zenodo site under accession code 10.5281/zenodo.17642644 (https://zenodo.org/records/17642645). Only trans-pQTL results for variants associated with p<1x10-8 are available in summary files. The individual level proteomics measures, whole genome sequences, and participant covariates are available under restricted access to ensure participant privacy; access can be obtained through dbGaP (phs001416 (https://dbgap.ncbi.nlm.nih.gov/beta/study/phs001416.v4.p1/#study); phs000209.v13.p3 (https://dbgap.ncbi.nlm.nih.gov/beta/study/phs000209.v13.p3/#study)) or upon request from the MESA coordinating center (chsccweb@u.washington.edu). Individual level data for variants, proteins, and phenotypes are protected and are not available publicly due to cohort consent and data privacy restrictions. The protein measure correlations, pQTL credible sets, protein and pQTL annotations, and protein-phenotype associations generated in this study are provided in the Supplementary Information.

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	Here, biological sex as determined through whole genome sequencing data was used as a covariate.
Reporting on race, ethnicity, or other socially relevant groupings	A central focus of this paper is to assess genetic variation that may vary in frequency between different ancestry groups. Here, participants were assigned to genetic ancestry group by Admixture analyses comparing to 1000G genetic ancestry reference panels.
Population characteristics	The mean age of the 1,930 participants included in this study was 58.2 years (+/- 8.8), with mean body mass index (BMI) of 28.1 kg/m2 and mean eGFR of 80.7 mL/min/1.73m^2.
Recruitment	Participants were recruited from six centers throughout the continental U.S. in North Carolina, New York, Maryland, Minnesota, Illinois, and California, with the first examination occurring between 2000-2002.
Ethics oversight	The Multi-Ethnic Study of Atherosclerosis (MESA) has been approved by the institutional review boards of each field center, the data coordinating center, and the genetic analysis center. The Institutional Review Board (IRB) at the Lundquist Institute for Biomedical Innovation also reviewed and approved this project. All participants provided written informed consent, including for genetic study, and participant compensation was approved by local IRBs at all MESA sites. All study activities were conducted in accordance with the criteria set by the Declaration of Helsinki.

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	Here, the 1,930 Multi-Ethnic Study of Atherosclerosis (MESA) participants with exam 1 plasma samples measured on both SomaScan 7k and Olink Explore 3072 were included in the study. For pQTL mapping the 1,889 unrelated participants with whole genome sequences (WGS) available were included in analysis.
Data exclusions	Direct relatives within study cohort were excluded from genetic analyses.
Replication	Protein measure correlations observed here were compared to existing platform comparisons in single-ancestry cohorts. Additionally, pQTL identified in MESA were compared to pQTL identified in deCODE (n=35,559, Ferkingstad et al., 2021) with SomaScan v4 and UK BioBank (n=54,219, Sun et al., 2023) with Olink Explore 3072.
Randomization	The present study is not a randomized trial and groups were not assigned, therefore randomization is not applicable.
Blinding	The present study is not a randomized trial and random groups were not assigned, therefore 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

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