

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	The FastBio study was advertised during Autumn 2017 to the local communities of Thessaloniki, Greece through various means, including the press, radio, social media, and word of mouth. Candidate participants expressed their interest via telephone, email or via the project's website (www.fastbio.gr). Following screening of over 1000 candidates from the greater area of Thessaloniki through two interviews, 411 apparently healthy unrelated individuals, who met FastBio selection criteria were included in the study. Participants belonged to one of two groups, specified by their diet: 200 individuals who followed a temporally structured dietary pattern of animal product restriction (periodically restricted, PR group) and 211 continuously omnivorous individuals who follow the diet of the general population and were not under any kind of special diet (non-restricted group, NR group).
Data analysis	Data analysis and statistical procedures have been described in the Methods Section of the current Manuscript. Code linked to the analyses of the current Manuscript is available at " https://github.com/AlexSimis/FastBio_pqtl_project ". For proteomic data QC, all steps were performed using R (v.4.4.1) and publicly available R packages. For genotype data QC, all steps were performed using plink (v2.00a3LM). Proteogenomic analysis, i.e. cis-pQTL mapping was performed using TensorQTL software (v. 1.0.8)(https://github.com/broadinstitute/tensorqtl) implemented by python (v. 3.8.10). Differential cis-pQTL mapping was performed using mashr R package (v. 0.2.79) (https://stephenslab.github.io/mashr/) Colocalization analyses were made using Coloc R package (v. 5.2.3). Regional plots for the colocalization results were produced using locuszoomr R package (v. 0.3.5). All figures were produced using ggplot2 R package (v. 0.6.0).

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](#)

All summary statistics and association results supporting the findings of this study are available in Zenodo (<https://doi.org/10.5281/zenodo.2113246769>) and in Supplementary Tables 1 to 6. The GWAS summary statistics used for colocalization analyses were retrieved from the OpenGWAS catalog (<https://opengwas.io/>). Publicly available cis-pQTL summary statistics from the UKB-PPP, which were used to assess cross-study overlap, were accessed via Synapse (<https://doi.org/10.7303/syn51364943>). Source data are provided with this paper. The informed consent provided by the FastBio study participants does not cover the public release of individual-level data. Individual-level data are available through collaboration under a data usage agreement. Data access requests will be considered by the FastBio core team and the BSRC Alexander Fleming Bioethics Committee and should be directed to dimas@fleming.gr. Access is subject to approval of the proposed research, compliance with ethical and data protection requirements, and execution of a data use agreement. Applicants will receive an initial response within 14 working days. Approved data may be used only for the agreed research purpose and may not be redistributed.

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	Sex information was self-reported at the time of recruitment and confirmed based on genotype data. All genetic association analyses have been adjusted for sex.
Reporting on race, ethnicity, or other socially relevant groupings	Study participants clustered clustered close to individuals of Tuscan, Cypriot, Bulgarian, and Turkish descent based on their genotype data. Downstream genetic analysis were adjusted for genetic ancestry using principal components.
Population characteristics	FastBio comprises of two groups specified by their diet. Periodically restricted individuals (N = 191) who alternate between omnivory and restriction of all animal products, and non-restricted individuals (N = 195) as a control group who are continuously omnivorous. Population characteristics have been described in previous publications of our group, Rouskas, K., Bocher, O., Simistiras, A. et al. Periodic dietary restriction of animal products induces metabolic reprogramming in humans with effects on cardiometabolic health. npj Metab Health Dis 3, 14 (2025). https://doi.org/10.1038/s44324-025-00057-2
Recruitment	Recruitment has been described in detail in Rouskas, K., Bocher, O., Simistiras, A. et al. Periodic dietary restriction of animal products induces metabolic reprogramming in humans with effects on cardiometabolic health. npj Metab Health Dis 3, 14 (2025). https://doi.org/10.1038/s44324-025-00057-2
Ethics oversight	All participants gave their written informed consent and the study was approved by the local ethics committee (BSRC Alexander Fleming Bioethics Committee Approval 17/02/2017)

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	FastBio cohort comprises of N = 411. The sample size of the current study, after QC, was N = 386 individuals, comprising of 191 periodically restricted and 195 non-restricted, control individuals. No statistical procedure was used to predetermine the sample size of the current study.
Data exclusions	For the proteomic data, Olink Assays from Olink 1536 Explore that had > 40% missing rate were excluded from downstream analyses. Additionally, Assays located on chromosome X were not tested resulting in 1,181 proteins. Based on the specific QC of genotype data, three first degree relatives were omitted from all analyses and a single individual was excluded due to low call rate and excess heterozygosity.
Replication	All steady state and differential cis-pQTLs were compared to publically available summary statistics from UKB-PPP Sun, B.B., Chiou, J., Traylor, M. et al. Plasma proteomic associations with genetics and health in the UK Biobank. Nature 622, 329–338 (2023). https://doi.org/10.1038/s41586-023-06592-6 .
Randomization	Not applicable. We performed targeted sampling.

Blinding

Not applicable no randomization was done.

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