

Reporting Summary

Nature Research 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 Research 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 HP chemstation used for GC data acquisition. GC-MS control and acquisition used Xcalibur Thermo Scientific. Isotope Data acquisition was carried out using Ion Vantage software (version 1.5.6.0, IsoPrime) and Isodat 3.0.

Data analysis HP chemstation used for GC data analysis GC-MS analysis used Xcalibur Thermo Scientific. Isotope data analysis was carried out using Ion Vantage software (version 1.5.6.0, IsoPrime) and Isodat 3.0. R code used for downstream data analysis available of public repositories.

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 Research [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 list of figures that have associated raw data
- A description of any restrictions on data availability

All data generated during this study are available on request or published in publicly accessible data bases. R Code for running the UK Biobank analyses are available from: <https://github.com/MRCIEU/lp-coevolution>. R and Python code for running the Ancient DNA analyses are available from: https://github.com/ydiekmann/Evershed_Nature_2022. R code for processing model variables, mapping and summary archaeological and isotopic data is available at <https://github.com/AdrianTimpson/2020-03-03523A>

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](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Ecological, evolutionary & environmental sciences study design

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

Study description	Analysis of human genetic selection using a large scale collation and analysis of novel and existing archaeological and modern data comprising organic residue composition and isotope values, demographic proxy data comprising radiocarbon and faunal remains, and ancient human DNA.
Research sample	UK Biobank cohort study of approximately 500,000 UK participants aged 37-73 years , containing wide-range of measures including demographics, health status, lifestyle, cognitive function, mental and physical health and molecular data such as genetic and biomarkers. BAM files from 674 ancient Eurasian individuals aligned to the GRCh37/hg19 human reference assembly. Demographic proxy data constructed using >110,000 radiocarbon dates compiled from over 1,000 published sources. Organic residue data for 6,610 animal fat residues derived from >12,700 potsherds from 527 archaeological sites.
Sampling strategy	Our objective was to include all available data across Europe.
Data collection	Novel and existing data was collated from published literature and databases, and where appropriate was aggregated into a MySQL Relational database
Timing and spatial scale	The study focuses on Europe. Archaeological data spans c.7kyrBCE to 1kyrCE, and ancient human DNA also extends into Asia.
Data exclusions	Beyond standard quality control, we took a fully inclusive approach to all relevant data.
Reproducibility	Results and analysis are fully reproducible using our publicly available methods and data.
Randomization	Randomization was not required, since we utilized all published and novel data to maximize sample sizes.
Blinding	Novel organic residue data acquisition was achieved through a largely automated pipeline. Any potential human influence from lab technicians remains blind to the archaeological contexts of samples.
Did the study involve field work?	☐ Yes ☒ No

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
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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