

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
<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. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P 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 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 no software was used in the data collection

Data analysis Data were analyzed using R v. 4.0 with the BayesFactor package v. 0.9.12-4.4. Genetic analyses were performed using plink v. 2.0, LDpred2, smartpca v. 16000, and ADMIXTURE v. 1.3.0. Code used in the analysis is available at https://github.com/mathilab/Neolithic_height

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](#)

Genetic data can be downloaded from the Allen Ancient DNA Resource (AADR; <https://reich.hms.harvard.edu/allen-ancient-dna-resource-aadr-downloadable-genotypes-present-day-and-ancient-dna-data>) or from their original publications: Antonio & Gao, et al 2019, Brunel et al 2020, Childebayeva et al 2022, Fernandes et al 2020, Fregel et al 2018, Fu et al 2016, Gamba et al 2014, Gonzalez et al 2017, Hofmanova et al 2016, Jones et al 2015, Lazaridis et al 2017, Lipson et al 2017,

Marcus et al 2020, Mathieson et al 2015, Mathieson et al 2018, Nikitin et al 2019, Olalde et al 2015, Olalde et al 2019, Rivollat et al 2020, Valdiosera et al 2018, Villalba et al 2019.

GWAS summary statistics from the Neale Lab (<http://www.nealelab.is>); sibling GWAS summary statistics published in Howe et al 2022 from OpenGWAS (<https://gwas.mrcieu.ac.uk/>).

Skeletal metrics originally published in this article and also taken from Hujic 2016, Nicklisch 2017, Ruff (ed) 2018 (data available: <https://www.hopkinsmedicine.org/fae/CBR.html>), Meyer et al 2018, Rosenstock et al 2019 (LiVES database doi: 10.17171/2-12-2-1), Rosenstock et al 2019 (doi: 10.1007/s12520-019-00850-3)

Isotopic data from Durrwachter et al 2006, Richards et al 2008, Oelze et al 2011, Bickle & Whittle (eds) 2013, Ash et al 2016, Hujic 2016, Scheibner 2016, Meyer et al 2018, Munster et al 2018, Knipper et al 2020

Paleopathology data from Lillie 2008, Bickle & Whittle (eds) 2013, Ash et al 2016, Hujic 2016, Nicklisch 2017

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender	Since we are analyzing archaeological data, it is not possible for us to assess gender identifications of the individuals. Sex was determined based on morphological characteristics or from DNA, as applicable.
Population characteristics	Exact ages unknown, individuals morphologically aged <3 removed. XX Males YY Females (see supplementary table 1). Dated between 6000 and 8000 BP, located in Europe (see supplementary table 1)
Recruitment	Individuals in the study were included based on their previous publication in the archaeological/anthropological literature or previous data collection by a co-author. We are limited by the excavation, preservation, and publication of archaeological sites which has biased our sample towards Central Europe. As a result, we have more statistical power in this region and can perform more nuanced analysis than is possible in Southern and Southeastern Europe.
Ethics oversight	All previously unpublished osteological data was collected and analyzed by co-authors in accordance with German laws and policies with permission from the necessary regulating organizations and the institutions housing the skeletal remains.

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](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	This study investigates the genetic and environmental components of height phenotypes in ancient Europeans using linear modeling and descriptive statistics. We used 1535 early Neolithic (6000-8000 years BP) skeletal and ancient DNA samples from North Central, South Central, Southern, and Southeastern Europe. Variables in our model include polygenic scores for height, maximum femur length, date (years BP), geographic group, sex, stable isotope values of delta-13C and delta-15N, and paleopathological stress markers (linear enamel hypoplasias, cribra orbitalia, porotic hyperostosis).
Research sample	The sample is comprised of 1535 individuals who have one or more of our study data types available (genetics, skeletal metrics, stable isotopes, or paleopathology). To be included, each individual must have at least one type of data, but was not required to have all 4. While there are a number of individuals with multiple data types, the overlaps in the data are small. We chose the Early Neolithic period because it is one of the most researched periods in Europe, with thousands of published settlements, cemeteries, and datasets.
Sampling strategy	We included all adult individuals that we could find in the literature from our study regions with either DNA, skeletal metrics, stable isotopes, or paleopathology data. Our sample size is driven by the amount of data available in the literature and from co-authors. While there is excellent archaeological coverage over the Northern and Southern Central European regions, there are many fewer published sites from Southern and Southeastern Europe in our time range. This gives us more power to detect relationships in Central Europe than in our other two populations; as a result, we include the other populations to provide comparisons and give context to our larger Central Europeans sample, but cannot accomplish the same level of nuanced analysis.
Data collection	Data were collected by going through published literature looking for data from our designated regions and time periods. Many of our co-authors have spent many years working in these regions and amassing large archaeological datasets. They were able to provide us with both their published and unpublished data as well as direct us towards relevant literature.
Timing and spatial scale	Data were collected beginning in October 2021 and continued up until August 2022 as new samples were located and added to the dataset.
Data exclusions	Isotope data were excluded completely if the individual was under the age of 3, as breast milk feeding considerably inflates nitrogen

Data exclusions	values. Individuals under the age of 18 were excluded from sex-specific diet analyses as sex cannot be accurately estimated in subadults. Genetic samples were excluded if coverage was less than 1%. Paleopathology samples were excluded from sex-specific analyses if there were conflicting morphological sex estimates from different publications which could not be resolved. Stature data was excluded if the publication did not report what estimation method was used to calculate it because we could not estimate the femur length without knowing the method.
Reproducibility	All data are provided in Supplementary Table 1; and the code is available at https://github.com/mathilab/Neolithic_height .
Randomization	No randomization was performed.
Blinding	Not applicable

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
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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

Palaeontology and Archaeology

Specimen provenance	Data in this study come from existing skeletal collections. Included samples have all been previously collected and analyzed by co-authors for other publications. Newly reported data come from samples that were either not included in the publications for which they were obtained or were not published as raw measurements in those publications. Previous studies were performed in accordance with German policies and laws and with permissions from the museums and institutions which house the skeletal collections.
Specimen deposition	Data which has been used in our analysis is available in Supplementary Table 1.
Dating methods	no new dating was performed
☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.	
Ethics oversight	All previously unpublished osteological data was collected and analyzed by co-authors with permission from the necessary regulating organizations and in accordance with German laws and policies with permissions from the museums and institutions which house the skeletal collections..

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