

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 <i>P</i> 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	No software was used for data collection.
Data analysis	All software packages used for analysis are cited in the Methods section and all used packages are publicly available: mMass: https://github.com/chhh/mmass , version: 5.5.0 PEAKS Online: https://www.bioinfor.com/peaks-online , version: 12/11.5 deamidation: https://github.com/dblyon/deamidation , commit: c572dcf Mascot: https://www.matrixscience.com , version: 2.6 ClassiCOL: https://github.com/EngelsI/ClassiCOL , version: 1.0.2 pep2prot: https://api.unipept.ugent.be/api/v2/pept2prot , version: 2 BLAST: https://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/2.15.0 , version: 2.15.0 MaxQuant: https://maxquant.org , version: 2.6.0.0 pFind: https://pfind.ict.ac.cn , version: 3.2.1 Partition Finder: http://www.robertlanfear.com/partitionfinder , version: 2.1.1 MrBayes: https://nbisweden.github.io/MrBayes , version: 3.2.6 x64 Mimics: https://www.materialise.com , version: 17.0 VGSTUDIO MAX: https://volumegraphics.hexagon.com/en/products/vgstudio-max.html , version: 2023.1 Avizo: https://www.thermofisher.com/amira-avizo , version: 9.2 Deformetrica: https://gitlab.com/icm-institute/aramislab/deformetrica , version: 4.3 R: https://www.r-project.org/ version: 4.1.0

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 proteomic mass spectrometry data and search database have been deposited in the ProteomeXchange Consortium via the PRIDE partner repository⁸⁸ under the dataset identifier PXD073112. Protein consensus sequences for the Bianfu Cave hominin fossils used for phylogenetic analysis are available in Supplementary Data 6. The “Hominid Palaeoproteomic Reference Dataset” is available through the Zenodo repository (<https://doi.org/10.5281/zenodo.7728060> (ref.70)). All other reference protein sequences are available in the UniProt Knowledgebase (<https://www.uniprot.org/>). The 3D data of hominins fossils from the Bainfu Cave are available in MorphoSource (<https://www.morphosource.org>) under Media IDs 000891397, 000891405 and 000891392. And the comparative datasets were also obtained from MorphoSource under the following Media IDs: 000050419, 000091844, 000091928, 000095008, 000167806, 000725317, 000725398, 000725430, 000725455, 000085875, 000086646, 000090825, 000091645, 000468985, 000725268, 000725343, 000725374, 000725558, 000088099, 000093969, 000095247, 000095255, 000095420, 000160955, and 000735170. Details were provided in Supplementary Table 4. The worldwide base maps of land, ocean, and rivers are available in Natural Earth (<https://www.naturalearthdata.com/>).

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	NA
Reporting on race, ethnicity, or other socially relevant groupings	NA
Population characteristics	NA
Recruitment	NA
Ethics oversight	NA

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

Ecological, evolutionary & environmental sciences study design

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

Study description	Proteomic analysis of archaic hominin and mammalian remains from paleolithic site
Research sample	fragment bones, hominin teeth
Sampling strategy	protein extraction
Data collection	All the pretreatment of the sample were conducted by the technicians at the Key Laboratory of Vertebrate Evolution and Human Origins, Institute of Vertebrate Paleontology and Paleoanthropology (IVPP), Chinese Academy of Sciences (CAS). And the LC MS/MS analysis was conducted by technicians in Central Laboratory (Capital Medical University) and State Key Laboratory of Genetics and Development of Complex Phenotypes (Fudan University).
Timing and spatial scale	~190-70 ka, Yunan, China
Data exclusions	No data was excluded during the study.
Reproducibility	Replicate runs were conducted on MALDI TOF MS and LC MSMS analysis. These results can be cross-validated.

Randomization	Randomization was not relevant to this study.
Blinding	Blinding was not relevant to this study.
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
☒	☐ Plants

Methods

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

Palaeontology and Archaeology

Specimen provenance	Permission was granted to Qiaomei Fu of the IVPP, CAS for the sampling of the specimens for molecular analyses.
Specimen deposition	Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Sciences, Yunnan Provincial Institute of Cultural Relics and Archaeology
Dating methods	The specimens are dated by U-series
☒ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.	
Ethics oversight	The protein analyses on five hominin specimens were approved by Yunnan Provincial Institute of Cultural Relics and Archaeology and the researcher from the institute has been affiliated.

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

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.