

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 [Authors & Referees](#) 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 to collect data.

Data analysis

Aviso
Landmark Editor
Mathematica
Geomagic Studio
Agisoft
mMass (v. 5.5.0)
ProteoWizard (v.3)
PEAKS (v. 7.0)
Geneious (v. 5.4.4)
RAXML (v. 8.0)
MrBayes (v. 3.2.6)
R (v. 3.4.3) custom code based on packages ("ggplot2", "stringi", "stringr", "lattice" and "seqinr").

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/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 the proteomic mass spectrometry data have been deposited in the ProteomeXchange Consortium repository with the identifier PXD011377. Protein consensus sequences for the Xiahe hominin used for phylogenetic analysis are available in Supplementary File 2. A surface scan model of the Xiahe mandible is publicly available at: <https://www.eva.mpg.de/evolution/downloads/registration-form-xiahe.html>.

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)

Life sciences study design

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

Sample size	Sample size was not pre-determined, but based on the availability of a single mandible from the Baishiya Karst Cave.
Data exclusions	Data was not excluded during any part of the study.
Replication	Proteomic and U-Th dating were independently replicated several times, as indicated in the manuscript.
Randomization	Randomization was not relevant to this study, as only a single specimen was analyzed.
Blinding	Blinding was not relevant to this study, as only a single specimen was analyzed.

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
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

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

Palaeontology

Specimen provenance	The Xiahe mandible was handed by the Sixth Gung-Thang Living Buddha to Lanzhou University for further study in the 1980s, after the dedication by a local monk in Xiahe county, who had found it in 1980 in Baishiya Karst Cave, Ganjia Basin, Xiahe County, Gansu Province, China. Lanzhou University and Gansu Provincial Institute of Cultural Relics and Archaeological Research, which has the right and authority to manage and study all the cultural heritage found in Gansu Province, started to work on this specimen together in 2010. All research on the specimen was carried out in agreement with Lanzhou University and Gansu Provincial Institute of Cultural Relics and Archaeological Research, China (Prof. F. Chen and Dr. D. Zhang).
Specimen deposition	The Xiahe mandible is available for study upon contacting Prof. F. Chen and Dr. D. Zhang.
Dating methods	U-Th dating was performed on one bulk sample and two serial samples of carbonate crust adhering to the Xiahe mandible. One subsample, XH-SD-U01, 0.5 x 0.5 x 1.0 cm, was taken and gently crushed. Another relatively large segment, 2.5 x 1.5 x 1.5 cm, was also carefully separated from the mandible. Two subsamples, XH-SD-U04 and XH-SD-U06, roughly 0.2 g each, were then collected from the uppermost and lowermost portion of this segment. After an ultrasonic cleaning step with ultrapure water, U-

Th dating was applied to the three subsamples. Chemistry was conducted on class-100 laminar flow benches in a class-10,000 clean room at the High-Precision Mass Spectrometry and Environment Change Laboratory (HISPEC), Department of Geosciences, National Taiwan University. After being dissolved in 7 N HNO₃ and spiked with a ²³³U-²³⁶U-²²⁹Th tracer, the sample solution was added to 0.2 ml HClO₄ and refluxed at 90-100 °C overnight for over 10 hours to decompose organic material. Uranium and thorium were purified with chemical methods including Fe co-precipitation and anion-exchange chromatography. After the final column separation step the separated U and Th aliquots were further treated with 0.05-0.2 ml HClO₄, refluxed at 90-100 °C for over 5 hours, and dried to effectively remove organic material and reduce polyatomic interferences. U and Th fractions were then dissolved in 1% HNO₃ (+0.05% HF) for instrumental analysis. Determinations of all isotopic compositions and concentrations were made on a Thermo-Finnigan NEPTUNE multi-collector inductively coupled plasma mass spectrometer (MC-ICP-M). Together the ²³⁰Th dates provide a minimum age assessment of the mandible.

☒ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.