

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](#).

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
- ☐ ☒ An indication of 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 statistics 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
- ☐ ☒ Clearly defined error bars
State explicitly what error bars represent (e.g. SD, SE, CI)

Our web collection on [statistics for biologists](#) may be useful.

Software and code

Policy information about [availability of computer code](#)

Data collection

Mass spectrometric data were acquired using the Xcalibur™ Software, controlling the Thermo Scientific™ LC-MS systems.

Data analysis

Xcalibur™ (version 4.1)
MaxQuant (version 1.5.3.30)
PEAKS (version 7.5)
Geneious (version 5.4.4)
Python (version 3.5.4)
Keras (version 2.0.8)
Tensorflow (version 1.3.0)
samtools (version 0.1.18)
ANGSD (version 0.913)
mafft (version 7.205)
Phangorn (version 2.4.0, R version 3.4.2)
BWA-MEM (version 0.7.7)
PICARD (version 1.91)
GATK UnifiedGenotyper (version 3.4-46)
blastall (version 2.2.26)
PHyML (version 3.1)

MrBayes (version 3.2.6)
 R (version 3.4.3)
 R, package vioplot (version 0.2)
 R, package ggplot2 (version 3.1.0 and version 3.1.1)
 R, package stringr (version 1.4.0)
 R, package stringi (version 1.2.4)
 Tracer (version 1.7.0)
 BEAST (version 2.5)
<https://github.com/cox-labs/wiNNer.git>

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 upon request. 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 mass spectrometry proteomics data have been deposited in the ProteomeXchange Consortium (<http://proteomecentral.proteomexchange.org>) via the PRIDE partner repository with the data set identifier PXD014342. Protein sequences generated as part of this study are provided as supplementary files.

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf](https://www.nature.com/authors/policies/ReportingSummary-flat.pdf)

Life sciences study design

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

Sample size	No sample size calculation was required. All available hominin specimens available to us (n=2) were analyzed, one from each hominin population of interest (Homo antecessor and Homo erectus).
Data exclusions	No data was excluded from the study.
Replication	Phylogenetic trees were reproduced using three different algorithms, and found consistent results (see Methods and SI). Proteomic results were replicated using repeated LC-MS/MS runs of different extracts for enamel of the same teeth, sometimes based on alternative extraction protocols, with extractions performed on different days in different laboratory sessions. Protein extracts were analyzed by LC-MS/MS on separate instruments in Copenhagen and Barcelona, with similar results obtained.
Randomization	Samples were injected in the LC-MS/MS system in randomised order.
Blinding	Blinding was not relevant to this study, with only two specimens analyzed

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☐	☒ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants

Methods

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

Palaeontology

Specimen provenance

Studied specimens derive from Gran Dolina, Atapuerca (Spain) and Dmanisi (Georgia). Export of specimens to the Globe Institute, University of Copenhagen was regulated by approval of Prof. J.M Bermudez de Castro (Atapuerca) and Prof. D. Lordkipanidze (Dmanisi) who are both co-authors of the current study.

Specimen deposition

Specimens are available upon request to E. Cappellini (Globe Institute, University of Copenhagen, Denmark), Prof. Bermudez de Castro (CENIEH, Burgos, Spain), or Prof. Lordkipanidze (Georgian National Museum, Georgia).

Dating methods

No new dates obtained.

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