

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 for data collection.
Data analysis	Protein data analysis was performed using Proteowizard MS Convert and Mascot (Matrix Science). Radiocarbon dates were analyzed using OxCal v4.3.262. MS-MARGE, an R script used to estimate the validity of peptide identifications and summarize the findings is available for use via Bitbucket: https://bitbucket.org/rwhagan/ms-marge/src/master/ . The custom dairy database used to analyze the data in this study is available as to download via the York Research Database.

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

Raw and processed MS/MS data from blanks, instrument washes and samples are available to download via the PRIDE partner repository (<https://www.ebi.ac.uk/pride/archive/>) under accession code PXD014730 and 10.6019/PXD014730.

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	The number of individuals analyzed was selected based on the presence of dental calculus deposits.
Data exclusions	Some protein results demonstrated inhibition during the extraction and were excluded from any further analysis due to their poor protein yield.
Replication	No replication was performed due to small quantities of starting material.
Randomization	Batches of extractions were performed in sets of 11 archaeological samples with 1 extraction blank. The order of samples run on the LC-MS/MS was randomized.
Blinding	Blinding is not relevant to the study.

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	Sample provenance is described in the main text of the article. Samples were exported to the Max Planck Institute for the Science of Human History under permission from the Ministry of Culture, Education, Science and Sports (Export number 10/413 (7b/52) was received on 2nd February, 2017 #A0109258, MN DE 7 643).
Specimen deposition	Osteological collections remains at the Department of Anthropology and Archaeology at the National University of Mongolia. Dental calculus collected from teeth for this study are housed at the Max Planck Institute for the Science of Human History. Interested researchers should contact the corresponding authors.
Dating methods	New radiocarbon dates were generated and are described in the manuscript. Briefly, a total of 26 bones and teeth from 24 individuals were radiocarbon dated at two research facilities, the Oxford Radiocarbon Accelerator Unit (ORAU, lab code OxA) and the Groningen Radiocarbon Laboratory (lab code GrM). Both sets of dates were calibrated using OxCal v4.3.2 and an IntCal13 atmospheric curve.

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