

Reporting Summary

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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

No software was used for data collection.

Data analysis

We used the MCMCglmm package for R version 3.4.3 for data analysis.

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

Specimen-level data that support the findings of this study are provided in Supplementary Tables 1 and 2. Quantification data for skeletal elements are available from the corresponding author upon reasonable request. Source Data for Figures 2 and 3 and Extended Data Figures 1 and 2 are provided with the paper.

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	We did not determine or restrict sample size a priori but collected as many fossil specimens as possible from available published resources when the following criteria were met: (1) age-at-death > 12 years , (2) from a time period between ca. 80-20 ka BP, and (3) quantifiable, i.e. published with anatomical descriptions, or depictions like photos, scans, etc.
Data exclusions	We analyzed the full data set without any exclusions in models 1 and 5. Subsequently, in models 2 to 4 and 6 to 8, we used different data subsets enabling us to add more predictors into the models by excluding incompletely scored variables. We therefore excluded sex unknown, age indeterminate or female skeletal elements in different combinations in these model variants.
Replication	We did not perform experiments. Our data was collected from the literature and trauma diagnoses were adopted from the original specimens' examiners, i.e. all data analyzed in this study is publicly available. Results can be recalculated using our data and methods and are therefore replicable.
Randomization	Randomization is not relevant to our study because no experiments were performed. All biological categories used in our study (taxon, sex, age) are predetermined by assessments of the original specimens' examiners. We adopted those assessments to allocate fossil specimens into our sample groups. We assigned each skeletal element to one of four preservation categories based on its completeness. In this respect we considered a 25 % grading a good balance between detailed data recording and analytical applicability. We allocated sites providing fossil specimens to geographical locations based on conglomerates of sites and geographical barriers in Eurasia.
Blinding	Our analytical framework did not require blinding because we did not perform experiments but data was collected from the literature.

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