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# 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 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 (*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<br>*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 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<br>*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 |

*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 | Leica TS06-ultra2 V.4.4.4 - in-field 3D-coordiantes; micro-CT scans by Waygate Technologies GmbH using a phoenix 322 V\|tome\|xm micro CT scanner; 3D digital microscopy with Keyence VHXKeyence VHX-5000 with VHX-ZS20 zoom lens |
| Data analysis | QGIS 3.82 - GIS software, Oxcal V4.2.2 - C14 calibration; VGSTUDIO MAX 3.3.4 - CT imagery processing; VHXKeyence VHX-5000 in-builts software - 3D digital microscopy |

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 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

A 3D Video of the engraved giant deer bone is available online. It is free to view and can be download in .mp4 file format under the CC-BY-SA 3.0 license.
View: https://denkmalpflege.niedersachsen.de/live/institution/mediadb/mand_45/psfile/bild/57/CC_BY_SA_3606c7d7aad00b.mp4
Download: https://denkmalpflege.niedersachsen.de/download/167053/CC-BY-SA_3.0.mp4

A 3D model of the engraved giant deer bone can be download in .stl data format under the CC-BY-SA 3.0 license.
https://denkmalpflege.niedersachsen.de/download/166881/CC-BY-SA_3.0.stl

Further datasets generated during and/or analysed during the current study are available from the corresponding authors upon reasonable request.
List of figures with available raw data
Figure 2 – 3D-coordinate data of finds (.xlsx)
Figure 3 – micro CT-scan raw model data (.stl)
Figures 4 & 5– 3D digital microscopy images (.jpg, .tiff, and the like)
Supplementary Figure 5 – 3D-coordinates of individual samples (A); data spreadsheet for the sample contents (e.g. clay %, Dolomite cps, etc.) (B, C) as .xlsx.
Supplementary Figure 7 – 3D-coordinate data of finds (.xlsx)
Supplementary Figure 10 – micro CT-scan raw model data (.stl)
Supplementary Figure 11 – micro CT-scan raw model data (.stl; further photographs of experimental bone traces).
Supplementary Figures 12– 3D digital microscopy images (.jpg, .tiff, and the like)dinate data of finds
Supplementary Figure 10-11 – micro CT-scan raw model data (.stl)
Supplementary Figure 14 – micro CT-scan raw model data (.stl); Further photographs of experimental bone traces.

# 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 | The study deals with an engraved giant deer toe bone bearing systematic engravings. Radiometric data shows its association with Neanderthals some 51,000 years ago. Micro CT-scans and 3D digital microscopy illustrate the properties of individual engravings. Experimental studies suggest that the bone was carved in a two-step approach and that planning depth was prerequisite. We discuss the meaning of the object in connection with Neanderthals cognitive abilities and its independence form Homo sapiens. |
| Research sample | The bone item is a single find. However, comparisons are made with further known finds across Eurasia that imply symbolic expressions in Neanderthals. |
| Sampling strategy | Bone item: The bone item is a single find.<br>Radiocarbon dates: The sampling strategy is described in the main text and the supplement, especially for the engraved bone.<br>Sediment samples: These were taken from the main inplaces profile where no rocks were visible. The aim was to obtain two samples per layer to ensure within-layer consistency |
| Data collection | On-site data was collected using a total station. Finds and features were recorded in writing, by photographs, drawings and SfM imagery. The microCT-Scans were performed by Waygate Technologies GmbH, a commercial lab. 3D digital microscopy was performed by Tim Koddenberg. Bones and charcoals were selected by Thomas Terberger and Dirk Leder and then submitted to the various labs for radiocarbon sampling and dating. Sediment samples were collected by Dirk Leder during the final week of excavation and processed by Philipp Hoelzmann. The carving experiment was performed by Raphael Hermann and Dirk Leder and empirical data was collected based on observations and discussion. |
| Timing and spatial scale | The relevant samples were taken from a small area measuring about 1.5 x 1.5 x 1.0 metres. The duration of the excavation was 8 weeks in August/September 2019 and five weeks in 2020. Post-excavation processing commenced thereafter. Samples for radiometric dating were submitted between November 2019 and May 2020. Sediment samples were submitted in November 2019. Delays in processing are due to the Covid-19 pandemic and its effects. |
| Data exclusions | No data was exluded. |
| Reproducibility | We conducted an experiment on cattle bones to better understand the procedure involved in creating the engravings observed on the original find. Applying a cut-and groove technique, we were able to create about eight engravings on differently pretreated bones. The protocol for radiocarbon dating is outlined in the methods secition of the manuscript and detailed in the supplement. A comparative study can be found in Hüls et al. 2017 |
| Randomization | not applicable |
| Blinding | Blinding was not applied when carving the bones as the experimentators aimed to create engravings that appear similar to those observed on the original piece. |

Did the study involve field work? ☒ Yes ☐ No

## Field work, collection and transport

| | |
|---|---|
| Field conditions | The excavtion took place in a mid-latitude broad-leafed forest during summer in front of a former cave entrance that was partially eroded. Weather was mostly sunny, but there were some rainy days. The excavation area was complety sheltered by a white plastic foil roof. |

| | |
|---|---|
| Location | UTM 32N - E: 597097.067 N: 5721298.883 Elev: 381.145 m asl |
| Access & import/export | Niedersächsisches Landesamt für Denkmalpflege and Gesellschaft Unicornu fossile e.V. signed a collaboration contract in 2014. The Untere Denkmalschutzbehörde Landkreis Göttingen (formely Landkreis Osterode) and the Naturschutzbehörde Landkreis Göttingen (formely Landkreis Osterode) approved the excavation. Samples were 3D-recorded and photographed in the field and carefully placed in plastic bags and containers. Plan and section drawings were made and photographs taken. Individual finds and sample bags were collected in transport boxes and exported by car and van. |
| Disturbance | The trench left behind by the excavation was partially backfilled and fenced in. Excavations continue annually. |

# 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 |
| ☐ | ☐ Human research participants |
| ☐ | ☐ Clinical data |
| ☐ | ☐ Dual use research of concern |

## Methods

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

## Antibodies

| | |
|---|---|
| Antibodies used | *Describe all antibodies used in the study; as applicable, provide supplier name, catalog number, clone name, and lot number.* |
| Validation | *Describe the validation of each primary antibody for the species and application, noting any validation statements on the manufacturer's website, relevant citations, antibody profiles in online databases, or data provided in the manuscript.* |

## Eukaryotic cell lines

Policy information about cell lines

| | |
|---|---|
| Cell line source(s) | *State the source of each cell line used.* |
| Authentication | *Describe the authentication procedures for each cell line used OR declare that none of the cell lines used were authenticated.* |
| Mycoplasma contamination | *Confirm that all cell lines tested negative for mycoplasma contamination OR describe the results of the testing for mycoplasma contamination OR declare that the cell lines were not tested for mycoplasma contamination.* |
| Commonly misidentified lines (See ICLAC register) | *Name any commonly misidentified cell lines used in the study and provide a rationale for their use.* |

## Palaeontology and Archaeology

| | |
|---|---|
| Specimen provenance | The finds and sample come from a former cave entrance that by 2014 was completely covered by sediments. The finds and samples reported in the article were obtained through excavation in August/September 2019 and 2020. The necessary permits and collaborations are listed under the section, "Field work, collection and transport". |
| Specimen deposition | The samples have been deposited with the various specialists for analyses:<br>1. Gesellschaft Unicornu fossile e.V. – microfauna<br>2. Institute of Archaeological Sciences, Eberhard Karls University Tübingen – macrofauna<br>3. Institute of Geographical Sciences, Freie Universität Berlin – sediment samples<br>4. Various radiocarbon labs – charcoal and bone samples (whenever possible, remaining material was returned)<br>5. All other materials (including the decorated bone) and documentation are with the Niedersächsisches Landesamt für Denkmalpflege |
| Dating methods | All necessary information are provided in the main text or the supplementary material. |

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

| | |
|---|---|
| Ethics oversight | No ethical approval or guidance was neccessary as no human remains were invloved in the study. |

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

## Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

| | |
|---|---|
| Laboratory animals | *For laboratory animals, report species, strain, sex and age OR state that the study did not involve laboratory animals.* |
| Wild animals | *Provide details on animals observed in or captured in the field; report species, sex and age where possible. Describe how animals were caught and transported and what happened to captive animals after the study (if killed, explain why and describe method; if released, say where and when) OR state that the study did not involve wild animals.* |
| Field-collected samples | *For laboratory work with field-collected samples, describe all relevant parameters such as housing, maintenance, temperature, photoperiod and end-of-experiment protocol OR state that the study did not involve samples collected from the field.* |
| Ethics oversight | *Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.* |

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

## Human research participants

Policy information about studies involving human research participants

| | |
|---|---|
| Population characteristics | *Describe the covariate-relevant population characteristics of the human research participants (e.g. age, gender, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."* |
| Recruitment | *Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.* |
| Ethics oversight | *Identify the organization(s) that approved the study protocol.* |

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

## Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

| | |
|---|---|
| Clinical trial registration | *Provide the trial registration number from ClinicalTrials.gov or an equivalent agency.* |
| Study protocol | *Note where the full trial protocol can be accessed OR if not available, explain why.* |
| Data collection | *Describe the settings and locales of data collection, noting the time periods of recruitment and data collection.* |
| Outcomes | *Describe how you pre-defined primary and secondary outcome measures and how you assessed these measures.* |

## Dual use research of concern

Policy information about dual use research of concern

### Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

| No | Yes | |
|---|---|---|
| ☒ | ☐ | Public health |
| ☒ | ☐ | National security |
| ☒ | ☐ | Crops and/or livestock |
| ☒ | ☐ | Ecosystems |
| ☒ | ☐ | Any other significant area |

## Experiments of concern

Does the work involve any of these experiments of concern:

| No | Yes | |
|---|---|---|
| ☒ | ☐ | Demonstrate how to render a vaccine ineffective |
| ☒ | ☐ | Confer resistance to therapeutically useful antibiotics or antiviral agents |
| ☒ | ☐ | Enhance the virulence of a pathogen or render a nonpathogen virulent |
| ☒ | ☐ | Increase transmissibility of a pathogen |
| ☒ | ☐ | Alter the host range of a pathogen |
| ☒ | ☐ | Enable evasion of diagnostic/detection modalities |
| ☒ | ☐ | Enable the weaponization of a biological agent or toxin |
| ☒ | ☐ | Any other potentially harmful combination of experiments and agents |

# ChIP-seq

## Data deposition

☐ Confirm that both raw and final processed data have been deposited in a public database such as GEO.

☐ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

| | |
|---|---|
| Data access links<br>*May remain private before publication.* | *For "Initial submission" or "Revised version" documents, provide reviewer access links. For your "Final submission" document, provide a link to the deposited data.* |
| Files in database submission | *Provide a list of all files available in the database submission.* |
| Genome browser session<br>(e.g. UCSC) | *Provide a link to an anonymized genome browser session for "Initial submission" and "Revised version" documents only, to enable peer review. Write "no longer applicable" for "Final submission" documents.* |

## Methodology

| | |
|---|---|
| Replicates | *Describe the experimental replicates, specifying number, type and replicate agreement.* |
| Sequencing depth | *Describe the sequencing depth for each experiment, providing the total number of reads, uniquely mapped reads, length of reads and whether they were paired- or single-end.* |
| Antibodies | *Describe the antibodies used for the ChIP-seq experiments; as applicable, provide supplier name, catalog number, clone name, and lot number.* |
| Peak calling parameters | *Specify the command line program and parameters used for read mapping and peak calling, including the ChIP, control and index files used.* |
| Data quality | *Describe the methods used to ensure data quality in full detail, including how many peaks are at FDR 5% and above 5-fold enrichment.* |
| Software | *Describe the software used to collect and analyze the ChIP-seq data. For custom code that has been deposited into a community repository, provide accession details.* |

# Flow Cytometry

## Plots

Confirm that:

☐ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☐ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☐ All plots are contour plots with outliers or pseudocolor plots.

☐ A numerical value for number of cells or percentage (with statistics) is provided.

## Methodology

| | |
|---|---|
| Sample preparation | *Describe the sample preparation, detailing the biological source of the cells and any tissue processing steps used.* |
| Instrument | *Identify the instrument used for data collection, specifying make and model number.* |

| | |
|---|---|
| Software | *Describe the software used to collect and analyze the flow cytometry data. For custom code that has been deposited into a community repository, provide accession details.* |
| Cell population abundance | *Describe the abundance of the relevant cell populations within post-sort fractions, providing details on the purity of the samples and how it was determined.* |
| Gating strategy | *Describe the gating strategy used for all relevant experiments, specifying the preliminary FSC/SSC gates of the starting cell population, indicating where boundaries between "positive" and "negative" staining cell populations are defined.* |

☐ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.

## Magnetic resonance imaging

### Experimental design

| | |
|---|---|
| Design type | *Indicate task or resting state; event-related or block design.* |
| Design specifications | *Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.* |
| Behavioral performance measures | *State number and/or type of variables recorded (e.g. correct button press, response time) and what statistics were used to establish that the subjects were performing the task as expected (e.g. mean, range, and/or standard deviation across subjects).* |

### Acquisition

| | |
|---|---|
| Imaging type(s) | *Specify: functional, structural, diffusion, perfusion.* |
| Field strength | *Specify in Tesla* |
| Sequence & imaging parameters | *Specify the pulse sequence type (gradient echo, spin echo, etc.), imaging type (EPI, spiral, etc.), field of view, matrix size, slice thickness, orientation and TE/TR/flip angle.* |
| Area of acquisition | *State whether a whole brain scan was used OR define the area of acquisition, describing how the region was determined.* |

Diffusion MRI ☐ Used ☐ Not used

### Preprocessing

| | |
|---|---|
| Preprocessing software | *Provide detail on software version and revision number and on specific parameters (model/functions, brain extraction, segmentation, smoothing kernel size, etc.).* |
| Normalization | *If data were normalized/standardized, describe the approach(es): specify linear or non-linear and define image types used for transformation OR indicate that data were not normalized and explain rationale for lack of normalization.* |
| Normalization template | *Describe the template used for normalization/transformation, specifying subject space or group standardized space (e.g. original Talairach, MNI305, ICBM152) OR indicate that the data were not normalized.* |
| Noise and artifact removal | *Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and physiological signals (heart rate, respiration).* |
| Volume censoring | *Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.* |

### Statistical modeling & inference

| | |
|---|---|
| Model type and settings | *Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and second levels (e.g. fixed, random or mixed effects; drift or auto-correlation).* |
| Effect(s) tested | *Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.* |

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both

| | |
|---|---|
| Statistic type for inference (See Eklund et al. 2016) | *Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.* |
| Correction | *Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).* |

## Models & analysis

| n/a | Involved in the study |
|---|---|
| ☐ | ☐ Functional and/or effective connectivity |
| ☐ | ☐ Graph analysis |
| ☐ | ☐ Multivariate modeling or predictive analysis |

Functional and/or effective connectivity

*Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation, mutual information).*

Graph analysis

*Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph, subject- or group-level, and the global and/or node summaries used (e.g. clustering coefficient, efficiency, etc.).*

Multivariate modeling and predictive analysis

*Specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.*