

Reporting Summary

Nature Portfolio 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 Portfolio 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 (<i>n</i>) 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> 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 <i>d</i> , Pearson's <i>r</i>), 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	ArcGIS Pro v. 3.3, R-Cran v. 4.4.1, Oriana v. 3.13
Data analysis	ArcGIS Pro 3.3, R-Cran v. 4.4.1, Oriana v. 3.13

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 Portfolio [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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

All data generated or analysed during this study are included in this published article and its supplementary information files.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

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

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 bone tool assemblage reported here contains 27 artefacts, derived from an archaeological horizon excavated across 295 square meters. This archaeological horizon also yielded abundant fossils (over 22,800 remains) from mammals, reptiles and fish, as well as over 10,900 stone tools larger than 2 cm. Mammal bones ≥ 2 cm ($n = 8,930$) were sampled for full zooarchaeological analysis. The sample selected for full zooarchaeological analysis ($n = 2,075$) included all items identified as bone tools, all proboscidean fossils (as these are particularly significant among the bone assemblage), and a sample from all other ≥ 2 cm mammal bone specimens. The archaeological bone tools were compared to: 1- Dimensions of a control sample ($n = 4,507$) of long bone fragments from the same archaeological excavation. 2- Features of flake removals in a sample ($n = 250$) of long bone fragments. 3-Published experimental samples of horse (Doyon et al., ref 9) and elephant (Backwell and d'Errico, ref. 4) long bones fractured to expose marrow.
Data exclusions	Due to the large size of the mammal assemblage, full zooarchaeological analysis was conducted in a sample of the determinable mammal fossils. This selection included all items identified as bone tools plus all proboscidean fossils, as well as a sample from all other determinable specimens. For the comparison of dimensions and flaking patterns between bone tools and the rest of the mammal assemblage from the T69 Complex, a control sample of the latter was selected (see details in Methods).
Replication	All bones tools were first-hand analysed by two pairs of co-authors (IdIT-JKN and LD-Fd'E), and then each artefact was discussed in group meetings during two separate sessions of several days each, approximately 1 year apart. Results are available in Supplementary Information Dataset 2, which contains all data collected from each item interpreted as a bone tool. Each item is labelled with a unique ID that will enable reproducibility of data collection for any researcher re-studying the assemblage.
Randomization	Horizontal spatial distribution of all archaeological was tested through an Average Nearest Neighbour Analysis that compared the actual distance between items to a hypothetical random sample, following Ebdon (ref. 57).
Blinding	Bone tools were independently analysed by IdIT and LD-Fd'E, after which specimen features were discussed as a group and recorded in Supplementary Information Dataset 2.

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
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Palaeontology and Archaeology

Specimen provenance	All specimens are derived from excavations directed by at the FLK West T69 Complex in Olduvai Gorge. Fieldwork permits were renewed annually by the Tanzanian Commission for Science and Technology (COSTECH), the Ngorongoro Conservation Authority Area (NCAA), and the Department of Antiquities, Tanzanian Ministry of Natural Resources and Tourism, and an export permit for analysis was granted by the Department of Antiquities.
Specimen deposition	The specimens will be permanently housed at the Olduvai Research Laboratory in the Leakey Camp, a research and storage facility managed by the Tanzanian Ministry of Natural Resources and Tourism.
Dating methods	No new dates are provided
☐	Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.
Ethics oversight	Fieldwork and analysis protocols abided by guidance provided by COSTECH, NCAA, and the Department of Antiquities, Tanzanian Ministry of Natural Resources and Tourism.

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

Plants

Seed stocks	<i>Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.</i>
Novel plant genotypes	<i>Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.</i>
Authentication	<i>Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.</i>