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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 (*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 *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 *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	No code was used for data collection, only published raw data and newly measured/obtained raw data.
Data analysis	R v.4.1.3, R Studio v.2022.02.1-461, R packages: ggplot2, ggrepel, tidyr, SIBER, MixSIAR, dplyr, tidyverse, ggtern, scales, RColorBrewer, here

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 and analyzed in this paper are provided as raw values either in the main text, as Extended Data Figures, or can be found in the electronic Supplementary Information.

Human research participants

Policy information about studies involving human research participants and Sex and Gender in Research.

Reporting on sex and gender	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

Ecological, evolutionary & environmental sciences study design

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

Study description	We have analyzed stable carbon, nitrogen, and sulfur isotope abundances from the preserved bone collagen of archaeologically retrieved raven bones, and then dated a sub-sample of the same bones. With the data obtained, we were able to reconstruct the diet and geographic origin/relative mobility of these ravens, demonstrating human influence on their feeding behavior.
Research sample	17 archaeological bird bones (15 common raven, 1 griffon vulure, and 1 snowy owl) were initially sampled for isotope analysis. 7 of these bones were further subjected to AMS radiocarbon dating.
Sampling strategy	For collagen extraction and isotopic analysis, 0.7-1.1g of bone were sampled. Extraction of collagen and analysis of stable C, N and S isotopes were performed according to established protocols of the AG Biogeology in Tübingen. All samples were considered individually and the diet was calculated separately for each specimen. Sampling was guided by prior published taxonomic determinations of bird species and zooarchaeological studies, following a hypothesis-testing approach.
Data collection	Sampling of the bones, as well as photographic and contextual documentation, was performed by Chris Baumann, Shumon T. Hussain and Martina Roblíčková near Brno. The subsequent laboratory procedures and all statistical analyses as well as diet-composition and geographic origin/mobility analyses were performed by Chris Baumann.
Timing and spatial scale	Bone sampling took place In October 2021 in Brno, and laboratory work and statistical analysis from November 2021 to May 2022 in Tübingen. The sampled bones are about 30 000 years old and belong to the Gravettian complex ("Pavlovian" and were excavated in the 1970s. To independently confirm this archaeological age determination, 7 of the sampled raven bones were additionally radiocarbon dated.
Data exclusions	We excluded samples that showed poor preservation. This includes bones that yielded less than 0.4% nitrogen or carbon contents of less than 20% in the collagen. These criteria reduced the previous number of 17 bones sampled to 12 successful samples, meaning that 5 bird bones had to be discarded from the analysis, including the griffon vulture and snowy owl specimens.
Reproducibility	All measurements can in principle be repeated/replicated, as the original bones are still available/stored in the Moravian Museum in Brno. Furthermore, the extracted collagen, if not fully depleted in the course of analysis, is also available for further research (stored in Tübingen). Since all raw data are published in the paper or the Supplementary Information, the statistical estimates of raven diet and geographic origin can in principle also be reproduced.
Randomization	Grouping of specimens was based on either stable C and N isotopes (prey resources), stable S isotopes (local vs. non-local ravens), or based on calculated/inferred diets and dietary groups.
Blinding	Not applicable to our study design/context as bird bone specimens had to be collected based on bone preservation and security/reliability of taxonomic determinations, leaving little leeway for randomization, blinding or hyper-selectivity.

Did the study involve field work? ☐ Yes ☒ No

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

Methods

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