

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 <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	bcl2fastq v2.20.0.422
Data analysis	FastQC v0.11.8, leeHom v1.1.5, BWA v0.7.17, SAMtools v1.9, picard v2.20.0, mapDamage v2.2.1., BamUtil v1.0.14, Qualimap v2.2.2a, Haplogrep2, Haplocheck v1.3.3, Schmutzi v1.5.5.5, Geneious Prime 2022, MrBayes v3.2.6, JModelTest2 v.2.1.10, FigTree v1.4.4, Pathphynder v1.a, BEDTools v2.27.1, pileupcaller v1.4.0.5, Haplotypecaller in GenomeAnalysisTK v.4.1.9, bcftools v1.9, ADMIXTOOLS v5.0, ADMIXTOOLS2 v2.0.0, cmdscale function in R v4.3.1, OxCal v4.4

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](#)

Sequence data generated in this study are available through the EBI Sequence Read Archive PRJEB64496. The mitochondrial sequences are available through GenBank (accession number MK934322 and OR327029).

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender

NA

Population characteristics

NA

Recruitment

NA

Ethics oversight

NA

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)

Ecological, evolutionary & environmental sciences study design

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

Study description

Paleogenomics analysis was performed on two bone fragments

Research sample

Two cranial fragments from layers 6-1 and 6-2 from the site Buran Kaya III

Sampling strategy

A small part of each of the two cranial fragments was removed for genetic analysis

Data collection

Genetic data was collected at the Institut Jacques Monod, Paris, France

Timing and spatial scale

Timing and spatial scale are not relevant to this study.

Data exclusions

No data were excluded

Reproducibility

DNA Libraries were prepared from 5 different areas of sample BuKa3A and from one area of sample BuKa3C, and multiple libraries were prepared from each point. Libraries varied in endogenous DNA content, but all showed similar characteristics.

Randomization

Randomization was not possible with two samples studied.

Blinding

The use of negative controls was more appropriate than blinding for this study.

Did the study involve field work?

☒ Yes

☐ No

Field work, collection and transport

Field conditions	One half-square meter section was excavated incorporating precautions against contamination: a maximum of two excavators dug the square wearing masks and gloves, and when potential human remains were discovered, one excavator put on a new full body protection suit, including masks and gloves, to perform the removal of the material
Location	Buran-Kaya III rock shelter in Crimea, 45° 00' N. and 34° 00' E.
Access & import/export	Excavation at Buran-Kaya III was performed with the permission of the National Academy of Sciences of Ukraine under the direction of Alexandr Yanevich.
Disturbance	No disturbance reported.

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

Palaeontology and Archaeology

Specimen provenance	Excavation at Buran-Kaya III was performed with the permission of the National Academy of Sciences of Ukraine. The sample was transferred by the excavators directly from the site to the Institut Jacques Monod in Paris, France.
Specimen deposition	Institut Jacques Monod, Paris, France
Dating methods	All radiocarbon dates were recalibrated using the software OxCal v4.4 based on the IntCal20 calibration data set (Reimer et al., 2020)
☒	Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.
Ethics oversight	No ethic approval was required at the time of sample collection. The samples are 37,000-year-old samples collected in Crimea in 2009 under the supervision of an Ukrainian archaeologist of the National Academy of Sciences of Ukraine.

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