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Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form is intended for publication with all accepted life science papers and provides structure for consistency and transparency in reporting. Every life science submission will use this form; some list items might not apply to an individual manuscript, but all fields must be completed for clarity.

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Please do not complete any field with "not applicable" or n/a. Refer to the help text for what text to use if an item is not relevant to your study.
For final submission: please carefully check your responses for accuracy; you will not be able to make changes later.

Experimental design

1. Sample size

   Describe how sample size was determined.

   The sample size is 1, as we are determining the genome of a single individual. For comparisons with other archaic genomes, all available high-coverage Neandertal and Denisovan genomes (n=3) were used.

2. Data exclusions

   Describe any data exclusions.

   Sequencing data excluded based on pre-established criteria: sequences that did not map to the human genome, sequences that were shorter than 35 bases, sequences mapping with a low mapping quality or within regions of low mappability - all of which were excluded to avoid using sequences that were not endogenous to the individual sequenced.

3. Replication

   Describe the measures taken to verify the reproducibility of the experimental findings.

   The bone fragment was sampled on three different occasions, on different areas of the specimen (total of six samples of bone powder). Six DNA extracts were prepared on three occasions, and ten DNA libraries were generated in three different experiments. We show in SI 3 that the results are stable across all different libraries.
   To allow the reproducibility of the analyses, all filtering steps and the comparative data used are detailed in the Methods section and the supplementary information; and the sequencing data generated here has been deposited in the European Nucleotide Archive.

4. Randomization

   Describe how samples/organisms/participants were allocated into experimental groups.

   This is not relevant for our study as we determined the genome of a single individual, therefore there were no experimental groups.

5. Blinding

   Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

   Blinding was not relevant for our study, as this is the genome of a single individual.

Note: all in vivo studies must report how sample size was determined and whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a	Confirmed
☐	☒ The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
☒	☐ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☒	☐ A statement indicating how many times each experiment was replicated
☐	☒ 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 any assumptions or corrections, such as an adjustment for multiple comparisons
☒	☐ Test values indicating whether an effect is present *Provide confidence intervals or give results of significance tests (e.g. P values) as exact values whenever appropriate and with effect sizes noted.*
☐	☒ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
☐	☒ Clearly defined error bars in all relevant figure captions (with explicit mention of central tendency and variation)

See the web collection on statistics for biologists for further resources and guidance.

Software

Policy information about availability of computer code

7. Software

Describe the software used to analyze the data in this study.

Basecalling: Bustard; Adapter trimming: leeHom; Demultiplexing: jivebunny; Mapping: BWA; Handling bam files: SAMtools; PCR duplicates removal: bam-rmdup; F3- and F4-statistics: Admixtools; Identification of variable sites: heffalump; Heterozygosity estimates: snpAD; Demography simulations: scrm; HMM: pomegranate; Statistics: R.

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* guidance for providing algorithms and software for publication provides further information on this topic.

Materials and reagents

Policy information about availability of materials

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a third party.

The sequencing data generated from the Denisova 11 bone fragment and the CT scans of the specimen are publicly available. Requests for further sampling of the bone fragment should be addressed to the Institute of Archaeology and Ethnography of the Russian Academy of Sciences.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

No antibodies were used.

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

No eukaryotic cell lines were used.

b. Describe the method of cell line authentication used.

No eukaryotic cell lines were used.

c. Report whether the cell lines were tested for mycoplasma contamination.

No eukaryotic cell lines were used.

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.

No eukaryotic cell lines were used.

Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals

Provide all relevant details on animals and/or animal-derived materials used in the study.	No animals were used.

Policy information about studies involving human research participants

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.	The research did not involve human participants.