nature portfolio

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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<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 | No software was used for data collection. |
| Data analysis | cutadapt 3.5, AdapterRemoval v2.3.0, BWA 0.7.5a-r405, samtools v1.13, Picard (version 2.22.1), GATK (v2.4), mapDamage v.2.0.6, github.com/pontussk/PMDtools, Qualimap v2.1.3, Trimmomatic v0.39, bcftools v1.12, ANGSD (version: 0.941-11-g7a5e0db), BEAST v2.6.6, bModelTest 1.2.1, Tracer v1.7.2, vcftools 0.1.17, GLIMPSE v1.1.1, PLINK v1.9, MSMC2 (2.1.3), ape v5.6.2, ADMIXTOOLS2, Clumpak v1.1, Treemix (v1.13), Python (2.7 & 3.5), R (version 4.1.2), PCAngsd (1.01), Integrative Genomics Viewer (1.13.11), NGSadmix (v32), Beagle 5.2, OxCal 4.4,**SeaView (5.05)** |

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 reads and alignment files of new data are available through the European Nucleotide Archive under accession number PRJEB75467. Previously published ancient data used in this study are available under accession numbers PRJEB31621, PRJNA379859, PRJNA803479 and PRJEB74338, and detailed in Supplementary Table 2. Sources for previously published modern genomic data analysed here are listed in Supplementary Data Table 3. The ARS-UCD1.2 reference genome is available under NCBI assembly accession GCF_002263795.1. The *Bos taurus* mitochondrial reference genome is available under NCBI accession number V00654.1.**

## 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 | Not applicable |
| Reporting on race, ethnicity, or other socially relevant groupings | Not applicable |
| Population characteristics | Not applicable |
| Recruitment | Not applicable |
| Ethics oversight | Not applicable |

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 | DNA was extracted from ancient bovine material. Shotgun sequencing data were generated and aligned to the cattle genome to produce whole genome data and analysed with previously published ancient and modern bovine genomes. |
| Research sample | 50 ancient samples were sequenced in this study, first presented here. These samples range across Eurasia (from Britain to Lake Baikal in Siberia) across a wide temporal range (47+ kya - 3.8 kya). The details of the samples are listed in Supplementary Data 1. These samples were contextualised with other published ancient samples (detailed in Supplementary Data 2) and modern bovinis (detailed in Supplementary Data 3). |
| Sampling strategy | We sampled 50 new samples from Late Pleistocene to the Holocene, producing 41 whole genomes suitable for phylogenetic analyses (mitochondrial sequences were produced for the remaining 9). The sample size was restricted by the availability of ancient material and the extent of DNA preservation. |
| Data collection | Ancient genomic data was collected according to laboratory protocols designed to maximise ancient DNA recovery while minimising contamination and destruction of ancient material, detailed in the Methods Section. DNA libraries were sequenced via shotgun sequencing. |
| Timing and spatial scale | Samples range across Eurasia (from Britain to Lake Baikal in Siberia) across a wide temporal range (47+ kya - 3.8 kya). Sample provenance and radiocarbon age (where available) are reported in Supplementary Data 1. |
| Data exclusions | All genomes collected for this study were analysed. Thresholds of coverages and subsetting of samples were applied for certain analyses, as detailed in the Methods Section. |
| Reproducibility | As ancient material finds are rare and unique, it was not possible to reproduce sampling. All bioinformatic analyses were described in detail and all data has been made available, therefore allowing reproduction of analyses by independent groups. |

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| Randomization | Randomisation was not applicable in this study. Samples were grouped into temporal and geographical groups which were relevant to the analysis as detailed in the Methods Section and Supplementary Data 1-3. |
| Blinding | Blinding of ancient samples was not applicable in this study as all data come from unique archaeological material. |

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 |
| ☒ | ☐ Plants |

## Methods

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

## Palaeontology and Archaeology

| | |
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| Specimen provenance | No new excavations were performed for this study. The age and provenance of the specimens is described in Supplementary Data 1. This table lists the steward institution which was responsible for the storage and curation of each sample. Ancient DNA sampling for each sample is supported with a letter of permission from the steward institution, most of whom are authors on the paper. Where relevant, a Material Transfer Agreement has been made under the The Nagoya Protocol. |
| Specimen deposition | Supplementary Table 1 lists each sample and its collection identifier. The steward institution that provided access and is responsible for long-term storage and curation of the specimens. Request for access for these specimens may be directed to its respective steward. |
| Dating methods | New radiocarbon dates were calibrated using the IntCal20 calibration curve using the OxCal v4.4 software. Radiocarbon dating labs are listed in Supplementary Data 1. |

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

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| Ethics oversight | Sampling was done with the ethical approval of the steward institution. |

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

## Plants

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|---|---|
| Seed stocks | not applicable |
| Novel plant genotypes | not applicable |
| Authentication | not applicable |