

Reporting Summary

Nature Research 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 Research 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 No software was used for data collection

Data analysis

```
SeqPrep 1.1
awk v4.0.2
BWA aln v0.7.8
Samtools 1.10
Python 2.7.15
R v.3.6.1
admixtograph (R package)
https://github.com/ekirving/qpbrute.git
github.com/stefaniehartmann/readLengthCutoff
github.com/pontusssk/PMDtools
mapDamage v.2.0.6
ANGSD v.0.921
RepeatMasker v.4.0.7
https://github.com/mpieva/mapping-iterative-assembler (MIA)
Muscle v3.8.31
jModelTest v2.1.10
BEAST v1.10.4
FASTME v.2.0
MEGAX v.10.1
Picard Toolkit v.2019
```

Admixtools v5
 TreeMix v.1.12
 github.com/LauritsSkov/Introgression-detection
 last v.1170
 maf-convert v.1170
 PAML v.1.3.1
 GOrilla v.2009

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 Research [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 list of figures that have associated raw data
- A description of any restrictions on data availability

All sequence data (in fastq format) for samples sequenced in this study are available through the European Nucleotide Archive under accession number PRJEB42269. Previously published data used in this study are available at PRJEB24361 and PRJEB7929.

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	Genetic analysis were performed on DNA data generated from over 1 million year old mammoth molars, as well as from two Late Pleistocene mammoths. Population genetic statistics and phylogenies, primarily focused on genetic relationships and admixture between the samples was assessed using single-nucleotide polymorphisms.
Research sample	Three Early Pleistocene mammoth samples from Siberia, and two Late Pleistocene mammoth samples from Siberia and Scotland respectively. In addition, previously published (Palkopoulou et al. 2015, 2018, Lynch et al. 2015) ancient and modern genomic data from elephants and mammoths was included in our analyses.
Sampling strategy	We sampled five Early to Late Pleistocene mammoth samples. We performed shotgun sequencing to obtain as complete genomes as possible for these samples.
Data collection	DNA from ancient samples was extracted, sequenced, and processed into SNP genotype calls or genotype likelihoods
Timing and spatial scale	Specimens originated from Siberia and Scotland, from mammoths that lived between ~1.2Ma and ~24Ka ago.
Data exclusions	The sequence data obtained was processed according to standard ancient DNA pipelines, excluding reads below 35 basepairs in length and unmerged reads. In addition, reads with low mapping quality (MQ<30) have been excluded. The exclusion of reads that have too low quality, and/or are too short to accurately map are standard practice in the field. We also applied a novel approach to identify how short reads that could be mapped accurately, as outlined in the Supplementary Information.
Reproducibility	All methods used are described in detail, so that the analyses can be reproduced by other researchers by accessing the raw data deposited in ENA (see above). All attempts to reproduce the results and analyses, done by separate co-authors, were successful
Randomization	No randomization was done. Samples were grouped by species for analysis of admixture (f4-stats and admixture graphs)
Blinding	Blinding was not relevant to this study. Analyses were performed either for all individuals separately or grouped by species. Other sample specific features were not relevant to the results.
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
☒	☐ Human research participants
☒	☐ 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

The provenance of the specimens is described in detail in the Supplementary information of the manuscript. The specimens are currently held at the Geological Institute at the Russian Academy of Sciences, The North-East Interdisciplinary Scientific Research Institute n. a. N. A. Shilo (Far East Branch, Russian Academy of Sciences), and the Hunterian Museum in the UK.

The specimens were sampled with the following permissions:

KRESTOVKA, ADYCHA and CHUKOCHYA

Sample ID: PIN-3491-3, 3723-511, PIN 3341-737

Issuing authority: Paleontological Institute n. a. A.A. Borissiak (Russian Academy of Sciences), Moscow, Russia

Sampled with permission from: E. N. Maschenko

Date: 13th October, 2016

SCOTLAND:

Sample ID: V5123

Issuing authority: The Hunterian museum, Glasgow, United Kingdom

Sampled with permission from: N. Clark

Date: 10th March, 2008

KANCHALAN:

Sample ID: 4-010

Issuing authority: Interdisciplinary Scientific Research Institute n. a. N. A. Shilo (Far East Branch, Russian Academy of Sciences).

Sampled with permission from: A.N. Kotov

Date: 28th November, 2004

Specimen deposition

The specimens are part of the collections of the Geological Institute at the Russian Academy of Sciences, The North-East Interdisciplinary Scientific Research Institute n. a. N. A. Shilo (Far East Branch, Russian Academy of Sciences), and the Hunterian Museum in the UK, and can be accessed following the same procedures as for other specimens in these collections.

Dating methods

Age estimates for the Late Pleistocene samples had previously been performed using radiocarbon dating (reported in Palkopoulou et al. 2013). The Early and Middle Pleistocene samples were dated using geological methods (see Supplementary Information), and genetic dating following Meyer et. al (2012) as well as using the software BEAST.

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

Ethics oversight

No ethical permits were needed for this study, since all analyses have been done on extinct species.

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