

## 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 [Authors & Referees](#) and the [Editorial Policy Checklist](#).

### Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
- An indication of 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 statistics 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
- Clearly defined error bars  
*State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on [statistics for biologists](#) may be useful.

### Software and code

Policy information about [availability of computer code](#)

Data collection

No software was used

Data analysis

AdapterRemoval v2  
bwa 0.7.10-r789  
picard-tools 1.127  
AdmixTools 4.1  
Eigensoft 6.1.3  
samtools 1.7  
bcftools 1.7  
plink v1.90b3w  
GATK 3.7  
mapDamage 2.0.8  
schmutzi 1.5.1  
HaploGrep 2  
RAxML 8.2.11  
BEDTools 2.33.0  
snakemake 4.3.0  
angsd 0.917  
Arlequin 3.5.2.2

```
fastsimcoal2 2.6.0.3
ibdseq r1206
shapeit v2.r790
Chromopainter v2
admixr 0.1.0
OxCal v4.3
Calib 7.0.0
```

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/reviewers upon request. 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

Sequence data were deposited in the European Nucleotide Archive (ENA) under accessions PRJEB29700 and PRJEB26336.

## Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf](https://www.nature.com/authors/policies/ReportingSummary-flat.pdf)

## Life sciences study design

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

Sample size	The number of genomes included in this study was determined by the availability of ancient remains with sufficient preservation for genome sequencing. The sample size is sufficient for the study, as even a single genome provides information from thousands of independent loci.
Data exclusions	Related individuals were removed for all population genetic analyses, according to pre-established relatedness cutoffs (1st and 2nd degree relatives)
Replication	Replication was not attempted
Randomization	No randomization was carried out. Individuals were assigned to groups based on genetic similarity as described
Blinding	Blinding was not relevant to this study. Individuals were assigned to groups based on genetic similarity as described

## Reporting for specific materials, systems and methods

### Materials & experimental systems

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Unique biological materials
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input type="checkbox"/>	<input checked="" type="checkbox"/> Palaeontology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants

### Methods

n/a	Involvement in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

## Palaeontology

Specimen provenance

Sample provenance: Institute for the History of Material Culture, Russian Academy of Sciences, 18 Dvortsovaya nab., St. Petersburg 191186, Russia.

Issuing authority: Institute for the History of Material Culture, Russian Academy of Sciences, 18 Dvortsovaya nab., St. Petersburg 191186, Russia.

Permit by: Director V.A. Lapshin

Date: 24.11.2017.

Based on: AGREEMENT FOR JOINT SCIENTIFIC RESEARCH between Institute for the History of Material Culture, Russian Academy of Science (St. Petersburg, Russia) and Centre for Geogenetics of Natural History Museum University of Copenhagen (Copenhagen, Denmark).

Samples from Uelen, Ekven, Ust'Belaya and Devil's Gate cave

Sample provenance: Centre of Physical Anthropology, Institute of Ethnology and Anthropology Russian Academy of Science, Vavilova street, 37a, Moscow, 119991, Russia.

Issuing authority: Centre of Physical Anthropology, Institute of Ethnology and Anthropology Russian Academy of Science, Vavilova street, 37a, Moscow, 119991, Russia.

Permit by: Director of Centre S.V. Vasilyev

Date: 24.11.2016 r.

Based on: AGREEMENT FOR JOINT SCIENTIFIC RESEARCH between Centre of Physical Anthropology, Institute of Ethnology and Anthropology Russian Academy of Science (Moscow, Russia) and Centre for Geogenetics of Natural History Museum University of Copenhagen (Copenhagen, Denmark).

Samples from Magadan

Sample provenance: North-East Interdisciplinary Scientific Research Institute, Far East Branch, Russian Academy of Sciences, 16 Portovaya street, Magadan, 685000, Russia.

Issuing authority: North-East Interdisciplinary Scientific Research Institute, Far East Branch, Russian Academy of Sciences, 16 Portovaya street, Magadan, 685000, Russia.

Permit by: Director V.V. Akinin

Date: 24.11.2016 r.

Based on: AGREEMENT FOR JOINT SCIENTIFIC RESEARCH between North-East interdisciplinary research institute (Magadan, Russia) and Centre for Geogenetics of Natural History Museum University of Copenhagen (Copenhagen, Denmark).

Specimen deposition

All specimens are in deposition at the respective institutions providing access for this study

Dating methods

New datings for this project were made in at the Chrono laboratory, Queens University, Belfast, UK; Aarhus AMS Centre, Aarhus, Denmark; KCCAMS Facility at UC Irvine, Irvine, USA; and the Oxford Radiocarbon Accelerator Unit, Oxford, UK. using their standard protocols. Lab numbers and raw and calibrated dates are available in Supplementary Data Table SD1. Calibrations were made in Oxcal 4.3 using the Intcal13 calibration curve.

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