

## Life Sciences Reporting Summary

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### ▶ Experimental design

#### 1. Sample size

Describe how sample size was determined.

No statistical methods were used to predetermine sample sizes. Sample size in this study was limited by the fact that to date, USR1 is the only human skeleton from Terminal Pleistocene East Beringia that has allowed for high coverage genome sequencing.

#### 2. Data exclusions

Describe any data exclusions.

We sequenced libraries from both UDG- and non-UDG-treated extracts. Yet, in order to minimize the bias introduced by post-mortem DNA damage, genotype calls were based only on UDG-treated libraries. Note however, that all UDG-treated libraries come from extracts from which we were able to identify aDNA-characteristic damage patterns, by sequencing non-UDG-treated libraries (SI Section 3).

#### 3. Replication

Describe whether the experimental findings were reliably reproduced.

No specific attempts were made to replicate the experimental findings. While the USR1 remains represent the only Terminal Pleistocene East Beringia sample suited for whole genome sequence to date, the USR1 genome derives from different extracts and libraries, all of which carry similar population genetic signatures. Moreover, this study relies on genomic data which implies that each site in the genome represents an 'independent' realization of the USR1 evolutionary history. These provide 'internal' replicates.

#### 4. Randomization

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

Samples were not randomized for the experiments. Only one ancient genome (USR1) is presented in this study.

#### 5. Blinding

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

No blinding techniques were implemented. Group allocation is not relevant to population history studies of this kind.

Note: all studies involving animals and/or human research participants must disclose 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  |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> The <u>exact sample size</u> ( $n$ ) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)   |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly   |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> A statement indicating how many times each experiment was replicated   |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section) |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> A description of any assumptions or corrections, such as an adjustment for multiple comparisons  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> The test results (e.g. $P$ values) given as exact values whenever possible and with confidence intervals noted   |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> A clear description of statistics including <u>central tendency</u> (e.g. median, mean) and <u>variation</u> (e.g. standard deviation, interquartile range)  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> Clearly defined error bars   |

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.

Computer programs and software used in this work are publicly available and they are referred to their respective publications in the main text and supplementary material. List of software and respective versions:

CASAVA v1.8.2  
 AdapterRemoval v1.5.3  
 bwa v0.6.2-r126  
 picard tools v2.7.1  
 samtools v1.3.1  
 GATK v3.4-0-3.3  
 shapeit2-r727  
 bammds v20140402  
 ANGSD v0.915  
 contamMix v1.0-5  
 HAPLOFIND  
 DICE  
 NGSrelate  
 relate v0.9993  
 plink v1.90b3.42  
 ADMIXTURE v1.23  
 admixtools v4.1  
 TreeMix v. 1.12  
 R 3.2.3  
 python 2.7.12  
 perl v5.22.1  
 admixturegraph v1.0.2 (R package)  
 dical2  
 momi2

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 for-profit company.

No unique materials were used. Materials and Reagents are detailed in Supplementary Section 2. Laboratory Procedures

## 9. Antibodies

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

NA

## 10. Eukaryotic cell lines

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

NA

b. Describe the method of cell line authentication used.

NA

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

NA

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.

NA

## ► Animals and human research participants

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Policy information about [studies involving animals](#); when reporting animal research, follow the [ARRIVE guidelines](#)

### 11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.

NA

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.

NA