

Reporting Summary

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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
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
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 code was use for data collection

Data analysis

Oxcal computer program (v4.3)(Ramsey & Lee, 2013)
 bcl2Fastq v2.17.1
 SeqPrep v1.1(John JS, 2011)
 BWA 0.7. (Li & Durbin, 2010)
 SAMtools v1.9 (Li, 2011)
 Picard v1.141 (<http://broadinstitute.github.io/picard>)
 GATK v3.4.0 (McKenna et al., 2010)
 Geneious® v7.0.336 (Kearse et al., 2012)
 BLASTn (Altschul, Gish, Miller, Myers, & Lipman, 1990; Johnson et al., 2008)
 Mitobim v1.9.0 (Hahn, Bachmann, & Chevreur, 2013)
 BEAST2 v2.4.0 (Bouckaert et al., 2014)
 Tracer v.1.6 (Rambaut, Suchard, Xie, & Drummond, 2014)
 TreeAnnotator v.1.7.5 (Rambaut & Drummond, 2013)
 FigTree v.1.4.3 (Rambaut, 2007)

References

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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. 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 raw genomic data will be publicly available on ENA (study number: PRJEB35255)

Figures:

Figure 1. (a, b) Dorsal and ventral view of the c. 46 ka old bird carcass recovered from the Siberian permafrost. (c) Map indicating its sampling location (red dot).
 Figure 2. Bayesian phylogeny for the concatenated ND2 and cytb (2034 bp) for 31 horned lark from Ghorbani et al.20 and the ancient horned lark highlighted in grey. Nodes with <0.5 support should be considered collapsed.

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	<input type="text" value="This study uses ancient DNA techniques to identify the age, sex and species identity of a near-intact Pleistocene bird carcass"/>
Research sample	<input type="text" value="The feather and tissue sample used was taken from near-complete bird carcass found in Siberia"/>
Sampling strategy	<input type="text" value="The sample was obtained opportunistically from a permafrost tunnel"/>
Data collection	<input type="text" value="Boris Berezhnov and Spartak Khabrov found the bird remains"/>
Timing and spatial scale	<input type="text" value="only one sample alone dating back some 46 ka BP was obtained"/>
Data exclusions	<input type="text" value="NA"/>
Reproducibility	<input type="text" value="NA"/>
Randomization	<input type="text" value="NA"/>
Blinding	<input type="text" value="NA"/>
Did the study involve field work?	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> 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	Included in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
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<input type="checkbox"/>	<input checked="" type="checkbox"/> Palaeontology
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data

Methods

n/a	Included 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

Specimen deposition

Dating methods

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

Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals

Wild animals

Field-collected samples

Ethics oversight

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