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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	Open source: SeqPrep v0.1, bwa v0.7.7, samtools v.0.1.19, RAxML v.8.2.10, RAxML-HPC2 v.8.2.3, MarkReadsByStartEnd.jar, GenomeAnalysisToolkit v.3.1, MUSCLE, ETE3 Commercial: Genious v.7.0 Custom: custom C scripts (haploidisation, D and f-hat statistics), custom perl scripts (phylogenetic admixture tests)

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

Raw nucleotide sequence data generated in this study have been deposited in the European Nucleotide Archive (ENA) with the run accession codes ERR2678614–ERR2678640. The haploidised fasta sequences have been deposited in the Dryad Digital Repository: https://doi.org/10.5061/dryad.cr1496b. The kudarensis (sample HV74) consensus mitochondrial sequence has been deposited in GenBank with the accession code MH605139.

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

Ecological, evolutionary & environmental sciences study design

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

Study description	Investigation of admixture between extinct and extant bears
Research sample	Low to medium coverage genome data from individual bears. 4 cave bear individuals were selected to provide sampling of the major Late Pleistocene lineages, based on mtDNA evidence. 8 brown bears were selected to sample the entire Holarctic distribution of the species, as well as providing geographically paired sampling with each investigated cave bear. Published datasets from 3 polar bears were included, as well as 4 outgroup taxa (Asiatic black bear, American black bear, spectacled bear, giant panda) for use in admixture tests
Sampling strategy	No sample size calculation was performed. Only a single individual per group is required for admixture tests. Multiple comparisons across sets of individuals allow more generalised conclusions with the potential to identify specific or localised patterns
Data collection	Shotgun sequencing using Illumina technology
Timing and spatial scale	Sequencing data collected in this project is insensitive to the timing of data collection
Data exclusions	No data were excluded
Reproducibility	Testing across multiple individuals provides a degree of experimental replication
Randomization	Genetic analyses performed in this study are sufficiently objective that randomisation is not required
Blinding	Genetic analyses performed in this study are sufficiently objective that investigator blinding is not required

Did the study involve field work? ☐ Yes ☒ No

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants

Methods

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