

Reporting Summary

Nature Portfolio 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 Portfolio 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

- | | | |
|-------------------------------------|-------------------------------------|--|
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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> |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A description of all covariates tested |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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) |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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 in this study.

Data analysis OxCal 4.4, nf-core/eager v2, AdapterRemoval v2, bwa aln v0.7.17, samtools v1.8, bcftools v1.19, Picard Tools v2.1.1, htsbox pileup r345, ADMIXTURE v1.3.0, EIGENSOFT v7.2.1, ADMIXTOOLS2 v2.0.0

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 and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

Genomic data generated in this project is available at the European Nucleotide Archive under project accession number PRJEB90148. We archive all genomic data generated, regardless of endogenous content or other data properties. This includes different combinations of shotgun screening, genome-wide capture, and deep

shotgun data for different samples. We make the data available in two forms: all reads in FASTQ format, and analysis-ready BAM files containing the reads as mapped and filtered for our analyses.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender	NA
Reporting on race, ethnicity, or other socially relevant groupings	NA
Population characteristics	NA
Recruitment	NA
Ethics oversight	NA

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

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

Ecological, evolutionary & environmental sciences study design

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

Study description	We sequenced DNA from ancient canid remains, to learn about the evolutionary history of dogs, with a particular focus on Europe and the Upper Paleolithic and Mesolithic periods. We combined this with previously published ancient genomic data from dogs and wolves, as well data from present-day individuals.
Research sample	The research sample was 215 canid remains, in some cases of known or suspected wolf or dog ancestry, in other cases of unknown ancestry. The aim for this to as much as possible provide data that would be representative of the dogs that lived in Europe prior to the advent of agriculture. The level of DNA preservation can not be known prior to sampling, so in some cases we did not retrieve enough DNA to be able to say anything about the ancestry of a specimen. However, we report all remains sampled for the study, regardless of whether we obtained any usable data or not.
Sampling strategy	We aimed to sample canid remains broadly from Europe and from the Upper Paleolithic, Mesolithic, and to some extent also Neolithic periods. We contacted museum curators, zooarchaeologists and others with access to such remains. Due to the stochastic and uneven nature of the archaeological record, sampling for ancient DNA studies like this is necessarily never as comprehensive across space and time as one would ideally like, rather we are restricted by what remains have been excavated and are available for study.
Data collection	Data was generated in the laboratories of the Francis Crick Institute, London and the Max Planck Institute for Evolutionary Anthropology, Leipzig. Metadata on the sampled remains was obtained from the contributing museum curators or zooarchaeologists, and recorded in internal databases.
Timing and spatial scale	Data generation for this project started in 2020, and finished in 2024. Samples were processed continuously as they were obtained from contributors. The spatial scale of data generated primarily covers western and northern Europe, but there are also a few samples from the Caucasus and the Americas.
Data exclusions	Data from all remains sampled is reported in this paper, regardless of the amount of quality of that data. Even samples that produced no apparent endogenous, ancient DNA are still reported.
Reproducibility	This study was retrospective, aiming to understand an evolutionary history that occurred only once. The concept of reproducibility does thus not apply to the high-level conclusions of this study.
Randomization	This study was retrospective, aiming to understand an evolutionary history that occurred only once. Randomization is not a tool that can be applied to study such a history.
Blinding	No blinding was applied, as meaningful conclusions about a genome sequence can only be drawn when connected to its spatial and temporal metadata.

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
<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 and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern
<input checked="" type="checkbox"/>	<input type="checkbox"/> Plants

Methods

n/a	Involved 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 and Archaeology

Specimen provenance	The metadata for the canid remains from which genome sequencing data is reported is described in the Supplementary Data 1 table. For each specimen, this table lists the name and geographical coordinates of the site of excavation, the steward institution that provided access to and is responsible for the long-term storage of the specimen, the excavation or museum collection identifier, and what skeletal element was sampled for this study. As no new excavations were performed in this study, no excavation permits were necessary. Sampling for DNA extraction was performed with the permission of the specimen stewards, all of which are listed in Supplementary Data 1, and most of which are authors on the paper.
Specimen deposition	The metadata table in Supplementary Data 1 lists, for each of the canid remains from which novel genome sequencing data is reported, the steward institution that provided access to and is responsible for the long-term storage of the specimen, and the excavation or museum identifier if applicable. Requests for access to the specimens should be directed to these host institutions.
Dating methods	New radiocarbon dates were obtained from commercial radiocarbon dating laboratories, and calibrated using the IntCal20 calibration curve in the OxCal v4.4 software. The details of the obtained data is provided in the table in Supplementary Data 2. We refer to the dating laboratories for details on their experimental protocols.
<input checked="" type="checkbox"/> Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.	
Ethics oversight	No ethical oversight was required as this study comprises only zooarchaeological material, previously collected and curated by individual institutions and researchers following local regulations. Sampling for DNA was performed aiming to minimize the destructive impact on the zooarchaeological material.

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

Plants

Seed stocks	NA
Novel plant genotypes	NA
Authentication	NA