

## 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 type="checkbox"/>            | <input checked="" 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<br><i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>                                                               |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A description of all covariates tested                                                                                                                                                                                                                                |
| <input checked="" type="checkbox"/> | <input 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 checked="" type="checkbox"/> | <input 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<br><i>Give <math>P</math> values as exact values whenever suitable.</i>                                       |
| <input type="checkbox"/>            | <input checked="" 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 checked="" type="checkbox"/> | <input 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 Newly reported data was generated on the Illumina NovaSeq 6000 and co-analysed alongside publicly available sequence data.

Data analysis

```

trimmomatic 0.36
bwa 0.7.17-r1188
SAMtools 1.13
sambamba 0.6.8
GATK 3.8
contamMix 1.0.9
ATLAS commit [647daf792df01c4aa8e686de0e462ddd8f91e6c6]
glimpse2
HaploGrep3
Yleaf2
BCFtools 1.13
plink 1.9
EIGENSOFT (smartpca) v8.0.0
ADMIXTOOLS 2.0.8
filia commit [2fa4117fc22597a106769e8d12758f7c33c51f75]
Chronograph commit
[affa83ffb04c6083d6fdf71a506b09ac0300fe74]
scikit-allele v1.3.1
statsmodels v.0.14.4
    
```

SLiM 4  
 pixy 1.2.7  
 hapROH 0.64  
 anclBD 0.5  
 twigstats 1.0.2  
 Relate 1.2.2  
 finestructure4  
 ChromoPainter2  
 SourceFind2  
 PANE 0.0.1  
 Additional code used in the analyses: <https://doi.org/10.5281/zenodo.17192653>

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](#)

Raw and aligned sequence reads are available at the European Nucleotide Archive under accession number PRJEB87112. The human reference genome (hg19) used during alignment is available via the 1000 genomes project repository ([https://ftp.1000genomes.ebi.ac.uk/vol1/ftp/technical/reference/phase2\\_reference\\_assembly\\_sequence/](https://ftp.1000genomes.ebi.ac.uk/vol1/ftp/technical/reference/phase2_reference_assembly_sequence/)). Genome sequences for the 379 modern day individuals from Germany are available upon request at the DZHK (<https://dzhk.de/en/dzhk-heart-bank/data-and-biospecimens/dzhkomics-resource>). The 1000GP phase 3 reference panel used for imputation and Relate can be downloaded from <https://ftp.1000genomes.ebi.ac.uk/vol1/ftp/release/20130502/>. Previously published genotype data for present-day and ancient individuals is available through the Allen Ancient DNA Resource at the Harvard dataverse (<https://dataverse.harvard.edu/dataset.xhtml?persistentId=doi:10.7910/DVN/FFIDCW>).

## 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                                        | Assignments of male/female were based on the distribution of reads aligned to the sex chromosomes. Genomes were grouped based on these assignments to draw conclusions about residence, marriage and kinship practices.                                                                                                                      |
| Reporting on race, ethnicity, or other socially relevant groupings | We did not categorize individuals by socially constructed categories such as ethnicity or race. Samples were grouped by geography, dating as well as funerary context. We furthermore used genomic ancestry and affinities to other geographic and temporally defined groups of individuals to assess demographic processes at local scales. |
| Population characteristics                                         | Osteological assessments of age-at-death, pathologies and potential trauma was carried out for some of the individuals in this study. We determined individual ancestry, shared genomic segments and affinities to other spatiotemporally defined groups.                                                                                    |
| 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](https://nature.com/documents/nr-reporting-summary-flat.pdf)

## Life sciences study design

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

|                 |    |
|-----------------|----|
| Sample size     | NA |
| Data exclusions | NA |
| Replication     | NA |

|               |    |
|---------------|----|
| Randomization | NA |
| Blinding      | NA |

## Behavioural & social sciences study design

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

|                   |    |
|-------------------|----|
| Study description | NA |
| Research sample   | NA |
| Sampling strategy | NA |
| Data collection   | NA |
| Timing            | NA |
| Data exclusions   | NA |
| Non-participation | NA |
| Randomization     | NA |

## Ecological, evolutionary & environmental sciences study design

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

|                          |                                                                                                                                                                                                                                                                                                                                                                                                        |
|--------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Study description        | We generated 258 genomes with a main focus on early medieval row-gravefields from southern Germany, with the intend to characterize the populations that started these customs and their social and kinship practices. Additionally we generated data from key sites dating to late Antiquity and the Iron Age for contextualization.                                                                  |
| Research sample          | Sequence data generated from human remains from different archaeological contexts                                                                                                                                                                                                                                                                                                                      |
| Sampling strategy        | For the four main sites we intended to generate a sample large enough to be able to capture temporal trends and identify potential kinship systems. Additional individuals from archaeological sites in the same regions were chosen for contextualization.                                                                                                                                            |
| Data collection          | The majority of newly reported data (239) was generated from individuals found during archaeological excavations in southern Germany, with additional data from individuals from northern Italy (2), Austria (3), Romania (3) Serbia (10) and Turkey(1). Bone samples were collected and transferred to the clean-room facilities of the Palaeogenetics Group of the JGU Mainz for further processing. |
| Timing and spatial scale | NA                                                                                                                                                                                                                                                                                                                                                                                                     |
| Data exclusions          | We created a subset of the data that excluded close-kin pairs for population genetic analyses. Data was excluded from certain analyses based on ancestry, geographical or temporal range. Specific data used and rationale for exclusion are given in the respective sections of the manuscript and the Supplementary Information.                                                                     |
| Reproducibility          | All data will be published alongside this study to ensure reproducibility                                                                                                                                                                                                                                                                                                                              |
| Randomization            | NA                                                                                                                                                                                                                                                                                                                                                                                                     |
| Blinding                 | NA                                                                                                                                                                                                                                                                                                                                                                                                     |

Did the study involve field work? ☐ Yes ☒ No

## Field work, collection and transport

|                        |    |
|------------------------|----|
| Field conditions       | NA |
| Location               | NA |
| Access & import/export | NA |

Disturbance

NA

## 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
- ☒ ☐ Antibodies
- ☒ ☐ Eukaryotic cell lines
- ☐ ☒ Palaeontology and archaeology
- ☒ ☐ Animals and other organisms
- ☒ ☐ Clinical data
- ☒ ☐ Dual use research of concern
- ☒ ☐ Plants

### Methods

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

### Antibodies

Antibodies used

NA

Validation

NA

### Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)

NA

Authentication

NA

Mycoplasma contamination

NA

Commonly misidentified lines  
(See [ICLAC](#) register)

NA

### Palaeontology and Archaeology

Specimen provenance

All samples were provided by co-authors/collaborators of this study who held the necessary permissions to sample those specimen for the analyses reported here.

Specimen deposition

Bone residuals from DNA sampling are stored in the clean room facilities of the Palaeogenetics Group, JGU Mainz

Dating methods

New radiocarbon dates were generated at the Curt-Engelhorn-Center for Archaeometry, Mannheim, Germany, the AMS laboratory Erlangen, Friedrich-Alexander Universität Erlangen-Nürnberg, Germany and Mass Spectrometry Laboratory, Center for Physical Sciences and Technology, in Vilnius, Lithuania. Laboratory protocols and further details can be found at each laboratories website.

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

Ethics oversight

All genomes published alongside this study originate from archaeological contexts and have no identifiable relationships to living persons.

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

### Animals and other research organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research, and [Sex and Gender in Research](#)

Laboratory animals

NA

Wild animals

NA

|                         |    |
|-------------------------|----|
| Reporting on sex        | NA |
| Field-collected samples | NA |
| Ethics oversight        | NA |

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

## Clinical data

Policy information about [clinical studies](#)

All manuscripts should comply with the ICMJE [guidelines for publication of clinical research](#) and a completed [CONSORT checklist](#) must be included with all submissions.

|                             |    |
|-----------------------------|----|
| Clinical trial registration | NA |
| Study protocol              | NA |
| Data collection             | NA |
| Outcomes                    | NA |

## Dual use research of concern

Policy information about [dual use research of concern](#)

### Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

| No                                  | Yes                      |                            |
|-------------------------------------|--------------------------|----------------------------|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Public health              |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | National security          |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Crops and/or livestock     |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Ecosystems                 |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Any other significant area |

### Experiments of concern

Does the work involve any of these experiments of concern:

| No                                  | Yes                      |                                                                             |
|-------------------------------------|--------------------------|-----------------------------------------------------------------------------|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Demonstrate how to render a vaccine ineffective                             |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Confer resistance to therapeutically useful antibiotics or antiviral agents |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Enhance the virulence of a pathogen or render a nonpathogen virulent        |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Increase transmissibility of a pathogen                                     |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Alter the host range of a pathogen                                          |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Enable evasion of diagnostic/detection modalities                           |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Enable the weaponization of a biological agent or toxin                     |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | Any other potentially harmful combination of experiments and agents         |

## Plants

|                       |    |
|-----------------------|----|
| Seed stocks           | NA |
| Novel plant genotypes | NA |
| Authentication        | NA |

## ChIP-seq

### Data deposition

- ☐ Confirm that both raw and final processed data have been deposited in a public database such as [GEO](#).
- ☐ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

|                                                                    |    |
|--------------------------------------------------------------------|----|
| Data access links<br><i>May remain private before publication.</i> | NA |
| Files in database submission                                       | NA |
| Genome browser session<br>(e.g. <a href="#">UCSC</a> )             | NA |

### Methodology

|                         |    |
|-------------------------|----|
| Replicates              | NA |
| Sequencing depth        | NA |
| Antibodies              | NA |
| Peak calling parameters | NA |
| Data quality            | NA |
| Software                | NA |

## Flow Cytometry

### Plots

Confirm that:

- ☐ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).
- ☐ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).
- ☐ All plots are contour plots with outliers or pseudocolor plots.
- ☐ A numerical value for number of cells or percentage (with statistics) is provided.

### Methodology

|                           |    |
|---------------------------|----|
| Sample preparation        | NA |
| Instrument                | NA |
| Software                  | NA |
| Cell population abundance | NA |

Gating strategy

NA

☐ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.

## Magnetic resonance imaging

### Experimental design

Design type

NA

Design specifications

NA

Behavioral performance measures

NA

### Acquisition

Imaging type(s)

NA

Field strength

NA

Sequence &amp; imaging parameters

NA

Area of acquisition

NA

Diffusion MRI

☐

Used

☐

Not used

### Preprocessing

Preprocessing software

NA

Normalization

NA

Normalization template

NA

Noise and artifact removal

NA

Volume censoring

NA

### Statistical modeling & inference

Model type and settings

NA

Effect(s) tested

NA

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference

NA

(See [Eklund et al. 2016](#))

Correction

NA

### Models & analysis

n/a | Involved in the study

☐

Functional and/or effective connectivity

☐

Graph analysis

☐

Multivariate modeling or predictive analysis

Functional and/or effective connectivity

NA

Graph analysis

NA

Multivariate modeling and predictive analysis

NA