nature portfolio

Corresponding author(s): Ali Akbari, David Reich

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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
☐	☒ 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	ADNA-Tools v2.1.0, BWA SAMSE v.0.7.15, Picard MarkDuplicates v.2.17.10
Data analysis	GLIMPSE vl.0.0, SAMTOOLS vl.15.1, BCFTOOLS vl.14, tabix vl.14, PLINK vl.90b6.24, PLINK2 v2.00a3LM, GEMMA v0.98.5, LDSC vl.0.1, S-LDXR v0.3-beta, CrossMap v0.5.2, SLiM v4.0.1, qpAdm v1700, PQLseqPy v0.1.2 (https://github.com/mokar2001/PQLseqPy)

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

Aligned sequences for the newly reported data from 10016 ancient individuals are available through the European Nucleotide Archive under an accession number PRJEB106907. This includes complete genetic data for all newly reported individuals alongside point estimates of their dates and geographic categorization into five regions of West Eurasia, which is the full data used in the present study (Supplementary Tables 1-3). Our release of these data without restrictions to enable studies

of natural selection has written approval from third-party sample custodians. Please contact corresponding author DR for any questions regarding metadata not used in this study—such as skeletal codes, latitudes and longitudes, site names, site descriptions, physical anthropology, and cultural context—which will be reported in future work that should be the references for studies of population history and archaeology (as a backup in case these studies are not published in reasonable time, we have deposited a version of the Supplementary Tables with the full archaeological metadata for all these individuals to Harvard Dataverse at https://doi.org/10.7910/DVN/7RVV9N with a 15 year embargo so it will go public in the year 2041). Imputed genomes for ancient individuals are also available at the Harvard Dataverse: https://doi.org/10.7910/DVN/7RVV9N. High-coverage (30x) Phase 3 sequences from the 1000 Genomes Project were downloaded from ftp.1000genomes.ebi.ac.uk/vol1/ftp/data_collections/1000G_2504_high_coverage/working/20201028_3202_phased. Genome coordinates were converted to GRCh37/hg19 using CrossMap v0.5.2. The processed 1000 Genomes data used as the imputation reference panel and for downstream analyses are publicly available at the Harvard Dataverse: https://doi.org/10.7910/DVN/7RVV9N. Individual-level data from the UK Biobank used in this study were obtained from the UK Biobank Resource and are available to eligible researchers upon application through the UK Biobank Access Management System, in accordance with UK Biobank policies.

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	The data reporting spreadsheets provide an indication of whether each analyzed individual is "M" (defined as having a 1:1 ratio of X to Y chromosomes) or "F" (defined as having a 2:0 ratio of X to Y chromosomes), or "U" (having an unclear ratio). Sex and gender are not in any way a focus of the study.
Reporting on race, ethnicity, or other socially relevant groupings	There is no categorization of people based on ethnicity. Because this analysis is focused on natural selection in West Eurasia over the last 18000 years, we use geography to restrict to 15836 ancient individuals of genetically West Eurasian-related ancestry living between longitude 50W and 120E and latitude greater than 24N. For modern comparators, we use UK Biobank and 1000 Genomes Project place-of-birth information to ensure a relative even distribution of modern individuals from different parts of West Eurasia.
Population characteristics	See above. We use geography to restrict to people living between longitude 50W and 120E and latitude greater than 24N; and UK Biobank and 1000 Genomes Project place-of-birth information to ensure a relative even distribution of modern individuals from different parts of West Eurasia. We do not have systematic information on the ages of ancient individuals, which come from archaeological excavations and in many cases lack standardized physical anthropological age estimates.
Recruitment	There is no new recruitment of individuals for this study.
Ethics oversight	There is no collection of new data from human subjects. All data from modern individuals is analyzed until approved analysis protocols (UK Biobank Resource under Application 16549).

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	Genetic analyses were conducted on genomic data from ancient human skeletons. Population genetics statistical models were applied to the data to gain insights into how natural selection forces shape human genome.
Research sample	For single-allele analysis, we studied 13936 unrelated ancient individuals from the last 18000 years, while for polygenic analyses we included relatives allowing us to study 15836 people. The data for 12900 individuals come from enriching ancient DNA libraries for more than one million single nucleotide polymorphisms (SNPs) where median coverage is 4.00-fold (at least 0.48-fold); the remaining 2936 are shotgun sequenced with median 1.24-fold coverage (at least 0.10-fold). For 5800 ancient individuals, the analyzed sequences are previously reported. For 468, we increased data quality on individuals with previously reported capture data: 287 through shotgun sequencing and 181 through more capture data. Adding entirely new individuals, we report 368 shotgun genomes with median 4.89-fold coverage (43 at >20-fold). For 9568 never-before-reported ancient individuals obtained by in-solution enrichment of sequencing 18007 libraries and shotgun sequencing of an additional 81 libraries, we make data available for studies of selection with the support of sample custodians; archaeological contextual information will be provided in future publications which should be the references for analyses of their population history. We co-analyzed with 6438 modern people: 503 from the 1000 Genomes Project, and 5935 from the UK Biobank20 (subsampled so their countries of origin were evenly spread over West Eurasia)
Sampling strategy	We restricted the study to individuals from West Eurasia and its neighbors in the Near East, as they have similar ancestral components and provide a considerable sample size suitable for studying natural selection.
Data collection	DNA from the ancient remains was extracted, sequenced, and processed into SNP genotype calls (final data overseen by S.M., N.R., R.P., and D.R.)

Timing and spatial scale	We analyzed 15836 ancient individuals from the past 18,000 years, alongside 6,438 contemporary individuals, all of whom lived between longitude 50W and 120E and latitude greater than 24N.
Data exclusions	We included only individuals who passed our quality control metrics in this study. To ensure broad representation across Western Eurasia, we subsampled the selection to a maximum of 300 people per country in contemporary populations, focusing on countries with ancient DNA in this study.
Reproducibility	All attempts to reproduce were successful.
Randomization	We used a mixed model approach to control for the genetic correlation among individuals, which leads to correlated residual error in the regression.
Blinding	Analyses were conducted based on the broad region and sample dates; other sample-specific features were not relevant to the results.

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
☒	☐ 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

Plants

Seed stocks	n/a
Novel plant genotypes	n/a
Authentication	n/a