

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 (<i>n</i>) 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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☒	☐ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
☒	☐ 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 <i>d</i> , Pearson's <i>r</i>), 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 newly computer code published in this study.
Data analysis	All software packages used for analysis are cited in the Methods section and in the Supplementary Information and all used packages are publicly available: BWA 0.6.1: http://bio-bwa.sourceforge.net ContamMix 1.0-10: https://github.com/StanfordBioinformatics/DEFUNCT-env-modules/tree/master/contamMix/ READ: https://bitbucket.org/tguenther/read/src/master/ EIGENSOFT 6.1.4: https://github.com/DReichLab/EIG ADMIXTURE 1.3.0: http://dalexander.github.io/admixture/download.html PLINK v1.9: https://www.cog-genomics.org/plink/1.9 ADMIXTOOLS (qp3Pop, qpDstat, qpAdm, qpGraph): https://github.com/DReichLab/AdmixTools

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](#)

The raw sequence reads and aligned BAM files reported in this paper have been deposited in the Genome Sequence Archive (Genomics, Proteomics & Bioinformatics 2021) in the National Genomics Data Center, China National Center for Bioinformation / Beijing Institute of Genomics, Chinese Academy of Sciences that are publicly accessible at <https://ngdc.cncb.ac.cn/gsa-human>. The pseudo-diploid genotype calls (Eigenstrat format) reported in this paper have been deposited in OMIX, China National Center for Bioinformation / Beijing Institute of Genomics, Chinese Academy of Sciences (<https://ngdc.cncb.ac.cn/omix>). The BioProject accession number is PRJCA026441. All data needed to evaluate the conclusions in the paper are present in the paper and/or the Supplementary Materials.

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

(1) The results of this study are independent of the sex/gender of the samples; (2) Sex/gender were not considered in study design; (3) The biological sex of an ancient DNA sample is determined by the chromosome it was sequenced from and does not address the social gender of the sample. (4) The gender data has not been collected and provided. (5) The main purpose of this study is to investigate the genetic characteristics and genetic history of the northern populations of East Asia as a whole, so this study was lacked of sex- and gender-based analysis.

Reporting on race, ethnicity, or other socially relevant groupings

No socially constructed or socially relevant categorical variables were used in this study. The individuals involved in this study were ancient samples, so we used only (1) the sampling location (2) the archaeological culture of the samples (3) the radiocarbon dating information of the samples as a way to categorize the different populations. We hope to use this categorization to explore genetic links between populations from different cultures or eras, as well as different regions. No confounding variables were involved in this study.

Population characteristics

Covariates related to population characteristics were not involved in the analysis of this study.

Recruitment

The samples involved in this study were taken from sampling of archaeological excavation samples.

Ethics oversight

Key Laboratory of Vertebrate Evolution and Human Origins, Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Sciences.

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

Life sciences study design

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

Sample size

We are unable to artificially control the size of the sample size in ancient DNA study, and in order to obtain a more comprehensive set of data, we included all published data as well as our newly sequenced data in this study.

Data exclusions

Data were not excluded from this experiment, for the three individuals with high contamination (>5%), we restricted our analyses to fragments showing characteristic aDNA deamination when performing genotype calling for downstream analyses.

Replication

The results derived from this study can all be obtained with the same population genetics analysis method or software using the same dataset and the same grouping strategy illustrated in the SI. information.

Randomization

Unrelated to the present study. This study only analyzed genetic associations between populations of different cultural eras in different regions, and did not involve experimental design of the experimental and control groups.

Blinding

The current study was not blinded to group assignment during data collection and or analysis. At the time of data collection, the current study used all published data and the current newly sequenced data to ensure a more comprehensive resolution of the genetic characteristics of ancient populations. And during the analysis, this study objectively described the genetic links between each population.

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

Palaeontology and Archaeology

Specimen provenance	All specimens are deposited at the Shandong Provincial Institute of Cultural Relics and Archaeology and Shandong University. Permission was granted to Qiaomei Fu of the IVPP, CAS and for the sampling of those specimens for genetic analyses. Specimens were sampled in the clean room facility of the IVPP, CAS in Beijing, China in.
Specimen deposition	This study does not involve the analysis of ancient skeletal samples. The raw sequence reads and aligned BAM files reported in this paper have been deposited in the Genome Sequence Archive (Genomics, Proteomics & Bioinformatics 2021) in the National Genomics Data Center, China National Center for Bioinformation / Beijing Institute of Genomics, Chinese Academy of Sciences that are publicly accessible at https://ngdc.cncb.ac.cn/gsa-human . The pseudo-diploid genotype calls (Eigenstrat format) reported in this paper have been deposited in OMIX, China National Center for Bioinformation / Beijing Institute of Genomics, Chinese Academy of Sciences (https://ngdc.cncb.ac.cn/omix). The BioProject accession number is PRJCA026441. All data needed to evaluate the conclusions in the paper are present in the paper and/or the Supplementary Materials.
Dating methods	The newly results of radiocarbon dating were provide by Xi'an-AMS (lab code of radiocarbon dating were XA56246-XA56256, XA58594-XA58596) .
☒ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.	
Ethics oversight	Permission to test for ancient DNA in the human specimens from this study was obtained through discussions with local archaeologists who excavated them, with final approval granted by the institutes in Shandong where they are managed and cared for, the Shandong Provincial Institute of Cultural Relics and Archaeology and Shandong University. Additional oversight and approval were obtained from the Institutional Review Board at the Institute of Vertebrate Paleontology and Paleoanthropology of the Chinese Academy of Sciences to sample the genomes of the ancient humans included in this study (202310250014). Protocols used to sample the genomes follow the highest standards used in archaeogenomic research. The work was done in collaboration with several local archaeologists, who were included as co-authors for their contributions to collation of archaeological material, dating of specimens, and/or discussions that contributed to the connections made to archaeological research cited in this study.

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

Plants

Seed stocks	<i>Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.</i>
Novel plant genotypes	<i>Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.</i>
Authentication	<i>Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.</i>