Allen Ancient DNA Resource (AADR): Downloadable genotypes of present-day and ancient DNA data

\*\*\* V54.1.p1: Data release: Mar 6 2023 (minor patch on v54.1) \*\*\*

On this page you can download a merged dataset consisting of genotypes for thousands of ancient and present-day individuals at up to 1.23 million positions in the genome (in hg19 coordinates).

The aim of Allen Ancient DNA Resource (AADR) is to provide a uniformly curated dataset that can be useful for scientists interested in carrying out analyses of population history and natural selection.

The genotypes in the AADR are not always a perfect match to those from the associated published papers. This is because to make it easier to coanalyze datasets we have started from bam or fastq files, trimmed the ends of sequences to reduce errors due to ancient DNA damage in a way that is largely uniform across datasets, which may be slightly different from that used in the individual publications, and determined genotypes anew by sampling a random sequence to cover each position.

Researchers who wish to use this compilation as the basis of their publications should cite this website and release version (e.g. "Allen Ancient DNA Resource https://reich.hms.harvard.edu/allen-ancient-dna-resource-aadr-downloadable-genotypes-present-day-and-ancient-dna-data", version 54.1.p1), while also citing the individual papers that report the data for each of the individuals they analyze (all references for the source data are listed below).

Going forward, we expect to be updating this resource every couple of months to keep it maximally useful to the community. Please let us know if you have recommendations for improvements or identify errors or other issues.

We thank the Paul G. Allen Foundation, the John Templeton Foundation, a grant from the U.S. National Institutes of Health, and the Howard Hughes Medical Institute, for providing the resources needed to create and update this dataset.

**Updated in this release:**

• No new data added; minor edits

All data released here:

(a) have already been published (some by our group and some by other groups - see full list of references below),

(b) have permissions appropriate for fully public data release,

(c) have data reported for a set of 1,233,013 sites in the genome (or 597,573 sites for present-day individuals genotyped on the Affymetrix Human Origins array). For most individuals, genetic data are represented by randomly sampled sequences at positions covered by at least one sequence.

There are two datasets:

"1240K”: *Ancient and present-day individuals (from either shotgun sequencing data or in-solution target capture, with a range of coverages) at 1,233,013 sites,*

"1240K+HO": *Data from the above set merged with present-day individuals typed on the Human Origins array with 597,573 sites.*

Each dataset consists of four files, in [eigenstrat](https://reich.hms.harvard.edu/software/InputFileFormats) format. For details, please see: [eigensoft](https://github.com/DReichLab/EIG/tree/master/EIGENSTRAT):

*.anno*: Rich meta-information for each individual.

*.ind* : Three columns: Individual ID, sex determination, and group label (population).

*.snp* : Information on each analyzed SNP position (SNP id, physical/genetic location and reference/variant alleles, where the reference allele matches hg19).

*.geno*: Genotypes (see note 2 below)

**Version v54.1.p1**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| *Description* | *.anno* | *.ind* | *.snp* | *.geno* | *Notes* |
| *1240k* | (6.1 Mb) | (666 Kb) | (75 Mb) | (4.8 Gb) | *16389 unique individuals*  *(9990 ancient, 6399 present-day)1* |
| *1240K+HO* | (7.1 Mb) | (718 Kb) | (36 Mb) | (2.9 Gb) | *20503 unique individuals*  *(9990 ancient, 10513 present-day)1* |

*1: includes one ancestral reference, and three present-day references: human, chimp, gorilla.*

*2: genotypes are in a binary form using the 'packedancestrymap' format described in in [eigensoft](https://github.com/DReichLab/EIG/tree/master/EIGENSTRAT); this may be converted to a (large) text file (i.e. 'eigenstrat' format, using the software 'convertf').*

*3: md5sums are available: in files.md5sum  These may be used to verify that files which are downloaded match this distribution, using the linux command: 'md5sum < file >'.*

**Please note**: The unique individual identifier is given in the 'Master ID' field. Multiple representatives of the same individual are thus indicated by a duplicated master ID. Some individuals are represented more than once to reflect different versions of processing or different publications. This may happen for example, when increased coverage has been generated after an initial publication. For many analyses it may be necessary to select only one version: for example the single sample Loschbour (master ID=I0001) is represented by two Version IDs, 'Loschbour\_snpAD.DG' and 'Loschbour\_published.DG'. It would be incorrect to consider these as two samples from the same population. If it is not important which version is used, we suggest choosing the master ID which has the highest number of SNPs hit on autosomal targets.

In addition, mitogenomes for samples generated at the Reich Lab are available (see: aadr\_v54.1.p1\_\_MT\_\_README.docx )

We would be grateful if users of this dataset could alert us to any errors they detect and help us to fill in missing data. This could include: (1) errors or missing information for location, latitude, longitude, archaeological context, date, and group label, (2) concerns about Y chromosome or mitochondrial DNA haplogroup determinations, and (3) evidence for other problems in the data or annotations for individuals. Please write to [Swapan 'Shop' Mallick](mailto:shop@genetics.med.harvard.edu) ([shop@genetics.med.harvard.edu](mailto:shop@genetics.med.harvard.edu)) and [David Reich](mailto:reich@genetics.med.harvard.edu) ([reich@genetics.med.harvard.edu](mailto:reich@genetics.med.harvard.edu)) with any suggestions. We would also be grateful if members of the community could suggest additional content that would be helpful to add to this page to make it maximally useful. Finally, please let us know if there are any published ancient or modern DNA datasets that are not included in this compendium and that should be. The following datasets are already processed for inclusion in the next release which will be v55. However, if you write to us to let us know of any missing datasets not on this list we will make a special effort to include them.

**Terminology and abbreviations used:**

*HG=hunter-gatherer, N=Neolithic, C=Chalcolithic/CopperAge, BA=BronzeAge, IA=IronAge*

*E=Early, M=Middle, L=Late, A=Antiquity*

*SG=samples with whole genome shotgun sequence data, randomly drawing a single read to represent each position in the genome*

*DG=samples shotgun sequenced with high enough coverage to call diploid genotypes, allowing for heterozygous calls*

*SDG=Sanger dipoid genotypes*

*WGC=Whole genome capture*

*WGA=Whole genome amplified*

*Individuals marked as 'Ignore\_' or 'outlier' have been identified as ones which may be filtered out from primary analyses for various reasons, such as being outliers from their main clusters or close relatives of others from the same group.*

**UDG treatments:**

Various UDG protocols are available to researchers, indicated in field 'Library type'.

• UDG-minus means that no UDG treatment is used. The typical deamination profile that results is then high towards the ends of the molecules and drops off slowly as one moves 5-10 bases towards the centre of the molecule; deamination still occurs throughout the molecule.

• UDG-plus means that UDG is used. With this, molecules are cleaved where a uracil exists prior to sequencing. This means that deamination (generally) does not exist (there are some situations where UDG treatment fails, for example at methylated sites).

• UDG-half is a specialised form of UDG treatment, where uracils are not completely removed, and left at the first one or two bases. The profile of deamination is then very high at the first base, drops fast and by the third base is very low. This continues throughout the molecule, until one or two bases at the other end. This is useful in that molecules which are clearly ancient from the deamination signature may be identified (using tools such as MapDamage, or pmdtools), but the number of bases which are 'damaged' and typically have to be removed prior to analysis is low - just one or two bases, whereas with UDG-minus, typically, five or even ten bases should be removed. Given how short ancient DNA molecules can be compared with modern DNA, because of degradation, losing five or ten bases can be a considerable loss of data for some samples (in the dataset provided here, we almost always ignore data derives from sites 1-2 nucleotides from either end for UDG-half, and 5-10 nucleotides from either end for UDG-minus).

• mixed treatments, eg:UDG-plus,half: For each sample, a number of libraries may be constructed, and of course different UDG treatments can be used for different libraries. The different libraries are useful because they capture different molecules and thus increase data quality for the individual. When these libraries are combined into a single bam (or aligned dataset) for an individual sample, these can be annotated according to the separate treatments, eg: "plus,half".

**Update history:**

[Wed Mar 29 20:12:11 EDT 2023]: V54.1.p1. migrate to dataverse (no data change)

[Mon Mar 6 22:35:44 EST 2023]: V54.1.p1 release (minor patch release)

[Wed Nov 16 14:37:52 EST 2022]: V54.1 release

[Thu Aug 22 22:46:15 EDT 2022]: V52.2 release

[Mon Aug 1 02:01:40 EDT 2022]: V50.0.p1 release (minor patch release)

[Sun Oct 10 02:13:04 EDT 2021]: V50.0 release

[Wed Jan 20 22:51:34 EST 2021]: V44.3 release

[Wed Jun 24 16:14:09 EDT 2020]: md5sums added

[Sun Mar 1 10:32:12 EDT 2020]: data release

[Sat Feb 29 15:44:38 EST 2020]: V42.4 update

[Tue Apr 2 18:07:09 EDT 2019]: edits

[Mon Apr 1 22:15:31 EDT 2019]: website integration edits

[Thu Mar 28 23:33:13 EDT 2019]: V37.2 minor edits.

[Tue Mar 26 11:59:31 EDT 2019]: V37.2 minor edits.

[Mon Mar 25 16:26:10 EDT 2019]: V37.2 tidy .anno.

[Fri Feb 22 12:25:37 EST 2019]: V37.2 new release.

**Previous versions:**

[V54.1](https://reichdata.hms.harvard.edu/pub/datasets/amh_repo/curated_releases/index_v54.1.html): released Nov 22 2022

[V52.2](https://reichdata.hms.harvard.edu/pub/datasets/amh_repo/curated_releases/index_v52.2.html): released Aug 22 2022

[V50.0.p1](https://reichdata.hms.harvard.edu/pub/datasets/amh_repo/curated_releases/index_v50.0.p1.html): released Aug 1 2022

[V50.0](https://reichdata.hms.harvard.edu/pub/datasets/amh_repo/curated_releases/index_v50.0.html): released Oct 2021

[V44.3](https://reichdata.hms.harvard.edu/pub/datasets/amh_repo/curated_releases/index_v44.3.html): released Jan 2021

[V42.4](https://reichdata.hms.harvard.edu/pub/datasets/amh_repo/curated_releases/index_v42.4.html): released Mar 2020

[V37.2](https://reichdata.hms.harvard.edu/pub/datasets/amh_repo/curated_releases/index_v37.2.html): released Feb 2019

**References:**

[1KGPhase3]:

**A global reference for human genetic variation.** 1000 Genomes Project Consortium, Auton A, Brooks LD, Durbin RM, Garrison EP, Kang HM, Korbel JO, Marchini JL, McCarthy S, McVean GA, Abecasis GR. Nature. 2015 Oct 1;526(7571):68-74. doi: 10.1038/nature15393. PMID: 26432245. <http://www.internationalgenome.org/data/> .

[AgranatTamirCell2020]:

**The Genomic History of the Bronze Age Southern Levant.** Agranat-Tamir L, Waldman S, Martin MAS, Gokhman D, Mishol N, Eshel T, Cheronet O, Rohland N, Mallick S, Adamski N, Lawson AM, Mah M, Michel M, Oppenheimer J, Stewardson K, Candilio F, Keating D, Gamarra B, Tzur S, Novak M, Kalisher R, Bechar S, Eshed V, Kennett DJ, Faerman M, Yahalom-Mack N, Monge JM, Govrin Y, Erel Y, Yakir B, Pinhasi R, Carmi S, Finkelstein I, Carmel L, Reich D.Cell. 2020 May 28;181(5):1146-1157.e11. doi: 10.1016/j.cell.2020.04.024. PMID: 32470400.

[AllentoftNature2015]:

**Population genomics of Bronze Age Eurasia.** Allentoft ME, Sikora M, Sjögren KG, Rasmussen S, Rasmussen M, Stenderup J, Damgaard PB, Schroeder H, Ahlström T, Vinner L, Malaspinas AS, Margaryan A, Higham T, Chivall D, Lynnerup N, Harvig L, Baron J, Della Casa P, Dąbrowski P, Duffy PR, Ebel AV, Epimakhov A, Frei K, Furmanek M, Gralak T, Gromov A, Gronkiewicz S, Grupe G, Hajdu T, Jarysz R, Khartanovich V, Khokhlov A, Kiss V, Kolář J, Kriiska A, Lasak I, Longhi C, McGlynn G, Merkevicius A, Merkyte I, Metspalu M, Mkrtchyan R, Moiseyev V, Paja L, Pálfi G, Pokutta D, Pospieszny Ł, Price TD, Saag L, Sablin M, Shishlina N, Smrčka V, Soenov VI, Szeverényi V, Tóth G, Trifanova SV, Varul L, Vicze M, Yepiskoposyan L, Zhitenev V, Orlando L, Sicheritz-Pontén T, Brunak S, Nielsen R, Kristiansen K, Willerslev E. Nature. 2015 Jun 11;522(7555):167-72. doi: 10.1038/nature14507.

[AmorimNatureCommunications2018]:

**Understanding 6th-century barbarian social organization and migration through paleogenomics.** Amorim CEG, Vai S, Posth C, Modi A, Koncz I, Hakenbeck S, La Rocca MC, Mende B, Bobo D, Pohl W, Baricco LP, Bedini E, Francalacci P, Giostra C, Vida T, Winger D, von Freeden U, Ghirotto S, Lari M, Barbujani G, Krause J, Caramelli D, Geary PJ, Veeramah KR. Nat Commun. 2018 Sep 11;9(1):3547. doi: 10.1038/s41467-018-06024-4.

[AneliPaganiMolBioEvol2022]:

**The Genetic Origin of Daunians and the Pan-Mediterranean Southern Italian Iron Age Context.** Aneli S, Saupe T, Montinaro F, Solnik A, Molinaro L, Scaggion C, Carrara N, Raveane A, Kivisild T, Metspalu M, Scheib CL, Pagani L. The Genetic Origin of Daunians and the Pan-Mediterranean Southern Italian Iron Age Context. Mol Biol Evol. 2022 Feb 3;39(2):msac014. doi: 10.1093/molbev/msac014. PMID: 35038748; PMCID: PMC8826970.

[AntoniobioRxiv2022]:

**Stable population structure in Europe since the Iron Age, despite high mobility.** Margaret L. Antonio, Clemens L. Weiß, Ziyue Gao, Susanna Sawyer, Victoria Oberreiter, Hannah M. Moots, Jeffrey P. Spence, Olivia Cheronet, Brina Zagorc, Elisa Praxmarer, Kadir Toykan Özdoğan, Lea Demetz, Michaela Lucci, Timka Alihodžić, Selma Amrani, Pavel Avetisyan, Christèle Baillif-Ducros, Željka Bedić, Audrey Bertrand, Maja Bilić, Luca Bondioli, Paulina Borówka, Emmanuel Botte, Josip Burmaz, Domagoj Bužanić, Francesca Candilio, Mirna Cvetko, Daniela De Angelis, Ivan Drnić, Kristián Elschek, Mounir Fantar, Andrej Gaspari, Gabriella Gasperetti, Francesco Genchi, Snežana Golubović, Zuzana Hukeľová, Rimantas Jankauskas, Kristina Jelinčić Vučković, Gordana Jeremić, Iva Kaić, Kevin Kazek, Hamazasp Khachatryan, Anahit Khudaverdyan, Sylvia Kirchengast, Miomir Korać, Valérie Kozlowski, Mária Krošláková, Dora Kušan Špalj, Francesco La Pastina, Marie Laguardia, Sandra Legrand, Tino Leleković, Tamara Leskovar, Wiesław Lorkiewicz, Dženi Los, Ana Maria Silva, Rene Masaryk, Vinka Matijević, Yahia Mehdi Seddik Cherifi, Nicholas Meyer, Ilija Mikić, Nataša Miladinović-Radmilović, Branka Milošević Zakić, Lina Nacouzi, Magdalena Natuniewicz-Sekuła, Alessia Nava, Christine Neugebauer-Maresch, Jan Nováček, Anna Osterholtz, Julianne Paige, Lujana Paraman, Dominique Pieri, Karol Pieta, Stefan Pop-Lazić, Matej Ruttkay, Mirjana Sanader, Arkadiusz Sołtysiak, Alessandra Sperduti, Tijana Stankovic Pesterac, Maria Teschler-Nicola, Iwona Teul, Domagoj Tončinić, Julien Trapp, Dragana Vulović, Tomasz Waliszewski, Diethard Walter, Milos Zivanovic, Mohamed el Mostefa Filah, Morana Čaušević-Bully, Mario Šlaus, Dusan Boric, Mario Novak, Alfredo Coppa, Ron Pinhasi, Jonathan K. Pritchard. bioRxiv 2022.05.15.491973; doi: https://doi.org/10.1101/2022.05.15.491973

[AntonioGaoMootsScience2019]:

**Ancient Rome: A genetic crossroads of Europe and the Mediterranean.** Antonio ML, Gao Z, Moots HM, Lucci M, Candilio F, Sawyer S, Oberreiter V, Calderon D, Devitofranceschi K, Aikens RC, Aneli S, Bartoli F, Bedini A, Cheronet O, Cotter DJ, Fernandes DM, Gasperetti G, Grifoni R, Guidi A, La Pastina F, Loreti E, Manacorda D, Matullo G, Morretta S, Nava A, Fiocchi Nicolai V, Nomi F, Pavolini C, Pentiricci M, Pergola P, Piranomonte M, Schmidt R, Spinola G, Sperduti A, Rubini M, Bondioli L, Coppa A, Pinhasi R, Pritchard JK. Science. 2019 Nov 8;366(6466):708-714. doi: 10.1126/science.aay6826. PMID: 31699931.

[BergstromScience2020]:

**Insights into human genetic variation and population history from 929 diverse genomes.** Bergström A, McCarthy SA, Hui R, Almarri MA, Ayub Q, Danecek P, Chen Y, Felkel S, Hallast P, Kamm J, Blanché H, Deleuze JF, Cann H, Mallick S, Reich D, Sandhu MS, Skoglund P, Scally A, Xue Y, Durbin R, Tyler-Smith C. Science. 2020 Mar 20;367(6484):eaay5012. doi: 10.1126/science.aay5012. PMID: 32193295; PMCID: PMC7115999.

[BiaginiEJHG2019]:

**People from Ibiza: an unexpected isolate in the Western Mediterranean.** Biagini SA, Solé-Morata N, Matisoo-Smith E, Zalloua P, Comas D, Calafell F. People from Ibiza: an unexpected isolate in the Western Mediterranean. Eur J Hum Genet. 2019 Jun;27(6):941-951. doi: 10.1038/s41431-019-0361-1. Epub 2019 Feb 14. PMID: 30765884; PMCID: PMC6777470.

[BongersPNAS2020]:

**Integration of ancient DNA with transdisciplinary dataset finds strong support for Inca resettlement in the south Peruvian coast.** Bongers JL, Nakatsuka N, O'Shea C, Harper TK, Tantaleán H, Stanish C, Fehren-Schmitz L. Proc Natl Acad Sci U S A. 2020 Aug 4;117(31):18359-18368. doi: 10.1073/pnas.2005965117. Epub 2020 Jul 13. PMID: 32661160; PMCID: PMC7414190.

[BortoliniBenazziCurBio2021]:

**Early Alpine occupation backdates westward human migration in Late Glacial Europe.** Bortolini E, Pagani L, Oxilia G, Posth C, Fontana F, Badino F, Saupe T, Montinaro F, Margaritora D, Romandini M, Lugli F, Papini A, Boggioni M, Perrini N, Oxilia A, Cigliano RA, Barcelona R, Visentin D, Fasser N, Arrighi S, Figus C, Marciani G, Silvestrini S, Bernardini F, Menghi Sartorio JC, Fiorenza L, Cecchi JM, Tuniz C, Kivisild T, Gianfrancesco F, Peresani M, Scheib CL, Talamo S, D'Esposito M, Benazzi S. Early Alpine occupation backdates westward human migration in Late Glacial Europe. Curr Biol. 2021 Jun 7;31(11):2484-2493.e7. doi: 10.1016/j.cub.2021.03.078. Epub 2021 Apr 21. PMID: 33887180.

[BroushakiScience2016]:

**Early Neolithic genomes from the eastern Fertile Crescent.** Broushaki F, Thomas MG, Link V, López S, van Dorp L, Kirsanow K, Hofmanová Z, Diekmann Y, Cassidy LM, Díez-Del-Molino D, Kousathanas A, Sell C, Robson HK, Martiniano R, Blöcher J, Scheu A, Kreutzer S, Bollongino R, Bobo D, Davudi H, Munoz O, Currat M, Abdi K, Biglari F, Craig OE, Bradley DG, Shennan S, Veeramah K, Mashkour M, Wegmann D, Hellenthal G, Burger J. Science. 2016 Jul 29;353(6298):499-503. doi: 10.1126/science.aaf7943. Epub 2016 Jul 14. PubMed PMID: 27417496; PubMed Central PMCID: PMC5113750.

[BrunelPNAS2020]:

**Ancient genomes from present-day France unveil 7,000 years of its demographic history.** Brunel S, Bennett EA, Cardin L, Garraud D, Barrand Emam H, Beylier A, Boulestin B, Chenal F, Ciesielski E, Convertini F, Dedet B, Desbrosse-Degobertiere S, Desenne S, Dubouloz J, Duday H, Escalon G, Fabre V, Gailledrat E, Gandelin M, Gleize Y, Goepfert S, Guilaine J, Hachem L, Ilett M, Lambach F, Maziere F, Perrin B, Plouin S, Pinard E, Praud I, Richard I, Riquier V, Roure R, Sendra B, Thevenet C, Thiol S, Vauquelin E, Vergnaud L, Grange T, Geigl EM, Pruvost M. Proc Natl Acad Sci U S A. 2020 Jun 9;117(23):12791-12798. doi: 10.1073/pnas.1918034117. Epub 2020 May 26. PMID: 32457149; PMCID: PMC7293694.

[CapodiferroAchilliCell2021]:

**Archaeogenomic distinctiveness of the Isthmo-Colombian area.** Capodiferro MR, Aram B, Raveane A, Rambaldi Migliore N, Colombo G, Ongaro L, Rivera J, Mendizábal T, Hernández-Mora I, Tribaldos M, Perego UA, Li H, Scheib CL, Modi A, Gòmez-Carballa A, Grugni V, Lombardo G, Hellenthal G, Pascale JM, Bertolini F, Grieco GS, Cereda C, Lari M, Caramelli D, Pagani L, Metspalu M, Friedrich R, Knipper C, Olivieri A, Salas A, Cooke R, Montinaro F, Motta J, Torroni A, Martín JG, Semino O, Malhi RS, Achilli A. Archaeogenomic distinctiveness of the Isthmo-Colombian area. Cell. 2021 Apr 1;184(7):1706-1723.e24. doi: 10.1016/j.cell.2021.02.040. Epub 2021 Mar 23. PMID: 33761327; PMCID: PMC8024902.

[CarlhoffBrummNature2021]:

**Genome of a middle Holocene hunter-gatherer from Wallacea.** Carlhoff S, Duli A, Nägele K, Nur M, Skov L, Sumantri I, Oktaviana AA, Hakim B, Burhan B, Syahdar FA, McGahan DP, Bulbeck D, Perston YL, Newman K, Saiful AM, Ririmasse M, Chia S, Hasanuddin, Pulubuhu DAT, Suryatman, Supriadi, Jeong C, Peter BM, Prüfer K, Powell A, Krause J, Posth C, Brumm A. Nature. 2021 Aug;596(7873):543-547. doi: 10.1038/s41586-021-03823-6. Epub 2021 Aug 25. PMID: 34433944; PMCID: PMC8387238.

[CassidyPNAS2016]:

**Neolithic and Bronze Age migration to Ireland and establishment of the insular Atlantic genome.** Cassidy LM, Martiniano R, Murphy EM, Teasdale MD, Mallory J, Hartwell B, Bradley DG. Proc Natl Acad Sci U S A. 2016 Jan 12;113(2):368-73. doi: 10.1073/pnas.1518445113. Epub 2015 Dec 28.

[CassidyNature2020]:

**A dynastic elite in monumental Neolithic society.** Cassidy LM, Maoldúin RÓ, Kador T, Lynch A, Jones C, Woodman PC, Murphy E, Ramsey G, Dowd M, Noonan A, Campbell C, Jones ER, Mattiangeli V, Bradley DG. Nature. 2020 Jun;582(7812):384-388. doi: 10.1038/s41586-020-2378-6. Epub 2020 Jun 17. PMID: 32555485.

[ChangmaiPLoSGenetics2022]:

**Indian genetic heritage in Southeast Asian populations.** Changmai P, Jaisamut K, Kampuansai J, Kutanan W, Altınışık NE, Flegontova O, Inta A, Yüncü E, Boonthai W, Pamjav H, Reich D, Flegontov P. PLoS Genet. 2022 Feb 17;18(2):e1010036. doi: 10.1371/journal.pgen.1010036. PMID: 35176016; PMCID: PMC8853555.

[ChildebayevaHaakMolBioEvo2022]:

**Population Genetics and Signatures of Selection in Early Neolithic European Farmers.** Childebayeva A, Rohrlach AB, Barquera R, Rivollat M, Aron F, Szolek A, Kohlbacher O, Nicklisch N, Alt KW, Gronenborn D, Meller H, Friederich S, Prüfer K, Deguilloux MF, Krause J, Haak W. Population Genetics and Signatures of Selection in Early Neolithic European Farmers. Mol Biol Evol. 2022 Jun 2;39(6):msac108. doi: 10.1093/molbev/msac108. PMID: 35578825; PMCID: PMC9171004.

[ClementeCell2021]:

**The genomic history of the Aegean palatial civilizations.** Clemente F, Unterländer M, Dolgova O, Amorim CEG, Coroado-Santos F, Neuenschwander S, Ganiatsou E, Cruz Dávalos DI, Anchieri L, Michaud F, Winkelbach L, Blöcher J, Arizmendi Cárdenas YO, Sousa da Mota B, Kalliga E, Souleles A, Kontopoulos I, Karamitrou-Mentessidi G, Philaniotou O, Sampson A, Theodorou D, Tsipopoulou M, Akamatis I, Halstead P, Kotsakis K, Urem-Kotsou D, Panagiotopoulos D, Ziota C, Triantaphyllou S, Delaneau O, Jensen JD, Moreno-Mayar JV, Burger J, Sousa VC, Lao O, Malaspinas AS, Papageorgopoulou C. The genomic history of the Aegean palatial civilizations. Cell. 2021 May 13;184(10):2565-2586.e21. doi: 10.1016/j.cell.2021.03.039. Epub 2021 Apr 29. PMID: 33930288; PMCID: PMC8127963.

[CookeNakagomeSciAdv2021]:

**Ancient genomics reveals tripartite origins of Japanese populations.** Cooke NP, Mattiangeli V, Cassidy LM, Okazaki K, Stokes CA, Onbe S, Hatakeyama S, Machida K, Kasai K, Tomioka N, Matsumoto A, Ito M, Kojima Y, Bradley DG, Gakuhari T, Nakagome S. Sci Adv. 2021 Sep 17;7(38):eabh2419. doi: 10.1126/sciadv.abh2419. Epub 2021 Sep 17. PMID: 34533991; PMCID: PMC8448447.

[CoutinhoJakobssonAJPA2020]:

**The Neolithic Pitted Ware culture foragers were culturally but not genetically influenced by the Battle Axe culture herders.** Coutinho A, Günther T, Munters AR, Svensson EM, Götherström A, Storå J, Malmström H, Jakobsson M. The Neolithic Pitted Ware culture foragers were culturally but not genetically influenced by the Battle Axe culture herders. Am J Phys Anthropol. 2020 Aug;172(4):638-649. doi: 10.1002/ajpa.24079. Epub 2020 Jun 4. PMID: 32497286.

[CsakySciRep2020]:

**Early medieval genetic data from Ural region evaluated in the light of archaeological evidence of ancient Hungarians.** Csáky V, Gerber D, Szeifert B, Egyed B, Stégmár B, Botalov SG, Grudochko IV, Matveeva NP, Zelenkov AS, Sleptsova AV, Goldina RD, Danich AV, Mende BG, Türk A, Szécsényi-Nagy A. Early medieval genetic data from Ural region evaluated in the light of archaeological evidence of ancient Hungarians. Sci Rep. 2020 Nov 5;10(1):19137. doi: 10.1038/s41598-020-75910-z. PMID: 33154399; PMCID: PMC7645724.

[DamgaardNature2018]:

**137 ancient human genomes from across the Eurasian steppes.** Damgaard PB, Marchi N, Rasmussen S, Peyrot M, Renaud G, Korneliussen T, Moreno-Mayar JV, Pedersen MW, Goldberg A, Usmanova E, Baimukhanov N, Loman V, Hedeager L, Pedersen AG, Nielsen K, Afanasiev G, Akmatov K, Aldashev A, Alpaslan A, Baimbetov G, Bazaliiskii VI, Beisenov A, Boldbaatar B, Boldgiv B, Dorzhu C, Ellingvag S, Erdenebaatar D, Dajani R, Dmitriev E, Evdokimov V, Frei KM, Gromov A, Goryachev A, Hakonarson H, Hegay T, Khachatryan Z, Khaskhanov R, Kitov E, Kolbina A, Kubatbek T, Kukushkin A, Kukushkin I, Lau N, Margaryan A, Merkyte I, Mertz IV, Mertz VK, Mijiddorj E, Moiyesev V, Mukhtarova G, Nurmukhanbetov B, Orozbekova Z, Panyushkina I, Pieta K, Smrčka V, Shevnina I, Logvin A, Sjögren KG, Štolcová T, Taravella AM, Tashbaeva K, Tkachev A, Tulegenov T, Voyakin D, Yepiskoposyan L, Undrakhbold S, Varfolomeev V, Weber A, Wilson Sayres MA, Kradin N, Allentoft ME, Orlando L, Nielsen R, Sikora M, Heyer E, Kristiansen K, Willerslev E. Nature. 2018 May;557(7705):369-374. doi: 10.1038/s41586-018-0094-2. Epub 2018 May 9.

[DamgaardScience2018]:

**The first horse herders and the impact of early Bronze Age steppe expansions into Asia.** de Barros Damgaard P, Martiniano R, Kamm J, Moreno-Mayar JV, Kroonen G, Peyrot M, Barjamovic G, Rasmussen S, Zacho C, Baimukhanov N, Zaibert V, Merz V, Biddanda A, Merz I, Loman V, Evdokimov V, Usmanova E, Hemphill B, Seguin-Orlando A, Yediay FE, Ullah I, Sjögren KG, Iversen KH, Choin J, de la Fuente C, Ilardo M, Schroeder H, Moiseyev V, Gromov A, Polyakov A, Omura S, Senyurt SY, Ahmad H, McKenzie C, Margaryan A, Hameed A, Samad A, Gul N, Khokhar MH, Goriunova OI, Bazaliiskii VI, Novembre J, Weber AW, Orlando L, Allentoft ME, Nielsen R, Kristiansen K, Sikora M, Outram AK, Durbin R, Willerslev E. Science. 2018 Jun 29;360(6396). pii: eaar7711. doi: 10.1126/science.aar7711. Epub 2018 May 9. PubMed PMID: 29743352.

[DeAngelisRickardsGenes2022]

**First Glimpse into the Genomic Characterization of People from the Imperial Roman Community of Casal Bertone (Rome, First–Third Centuries AD).** De Angelis F, Romboni M, Veltre V, Catalano P, Martínez-Labarga C, Gazzaniga V, Rickards O. First Glimpse into the Genomic Characterization of People from the Imperial Roman Community of Casal Bertone (Rome, First-Third Centuries AD). Genes (Basel). 2022 Jan 13;13(1):136. doi: 10.3390/genes13010136. PMID: 35052476; PMCID: PMC8774527.

[DuliasPNAS2022]

**Ancient DNA at the edge of the world: Continental immigration and the persistence of Neolithic male lineages in Bronze Age Orkney.** Dulias K, Foody MGB, Justeau P, Silva M, Martiniano R, Oteo-García G, Fichera A, Rodrigues S, Gandini F, Meynert A, Donnelly K, Aitman TJ; Scottish Genomes Partnership, Chamberlain A, Lelong O, Kozikowski G, Powlesland D, Waddington C, Mattiangeli V, Bradley DG, Bryk J, Soares P, Wilson JF, Wilson G, Moore H, Pala M, Edwards CJ, Richards MB. Ancient DNA at the edge of the world: Continental immigration and the persistence of Neolithic male lineages in Bronze Age Orkney. Proc Natl Acad Sci U S A. 2022 Feb 22;119(8):e2108001119. doi: 10.1073/pnas.2108001119. PMID: 35131896; PMCID: PMC8872714.

[EbenesersdottirScience2018]

**Ancient genomes from Iceland reveal the making of a human population.** Ebenesersdóttir SS, Sandoval-Velasco M, Gunnarsdóttir ED, Jagadeesan A, Guòmundsdóttir VB, Thordardóttir VB, Thordardóttir MS, Moore KHS, Siguròsson Á, Magnúsdóttir DN, Jónsson H, Snorradóttir S, Hovig E, Møller P, Kockum I, Olsson T, Alfredsson L, Hansen TF, Werge T, Cavalleri GL, Gilbert E, Lalueza-Fox C, Walser JW 3rd, Kristjánsdóttir S, Gopalakrishnan S, Árnadóttir L, Magnússon ÓP, Gilbert MTP, Stefánsson K, Helgason A. Science. 2018 Jun 1;360(6392):1028-1032. doi: 10.1126/science.aar2625. PMID: 29853688.

[EgfjordAllentoftPLOS2021]:

**Genomic Steppe ancestry in skeletons from the Neolithic Single Grave Culture in Denmark.** Egfjord AF, Margaryan A, Fischer A, Sjögren KG, Price TD, Johannsen NN, Nielsen PO, Sørensen L, Willerslev E, Iversen R, Sikora M, Kristiansen K, Allentoft ME. Genomic Steppe ancestry in skeletons from the Neolithic Single Grave Culture in Denmark. PLoS One. 2021 Jan 14;16(1):e0244872. doi: 10.1371/journal.pone.0244872. PMID: 33444387; PMCID: PMC7808695.

[FeldmanNatureCommunications2019]:

**Late Pleistocene human genome suggests a local origin for the first farmers of central Anatolia.** Feldman M, Fernández-Domínguez E, Reynolds L, Baird D, Pearson J, Hershkovitz I, May H, Goring-Morris N, Benz M, Gresky J, Bianco RA, Fairbairn A, Mustafaolu G, Stockhammer PW, Posth C, Haak W, Jeong C, Krause J. Nat Commun. 2019 Mar 19;10(1):1218. doi: 10.1038/s41467-019-09209-7. PMID: 30890703.

[FeldmanScienceAdvances2019]:

**Ancient DNA sheds light on the genetic origins of early Iron Age Philistines.** Feldman M, Master DM, Bianco RA, Burri M, Stockhammer PW, Mittnik A, Aja AJ, Jeong C, Krause J. Sci Adv. 2019 Jul 3;5(7):eaax0061. doi: 10.1126/sciadv.aax0061. eCollection 2019 Jul. PMID: 31281897.

[FernandesNatureEcologyEvolution2020]:

**The spread of steppe and Iranian-related ancestry in the islands of the western Mediterranean.** Fernandes DM, Mittnik A, Olalde I, Lazaridis I, Cheronet O, Rohland N, Mallick S, Bernardos R, Broomandkhoshbacht N, Carlsson J, Culleton BJ, Ferry M, Gamarra B, Lari M, Mah M, Michel M, Modi A, Novak M, Oppenheimer J, Sirak KA, Stewardson K, Mandl K, Schattke C, Özdoğan KT, Lucci M, Gasperetti G, Candilio F, Salis G, Vai S, Camarós E, Calò C, Catalano G, Cueto M, Forgia V, Lozano M, Marini E, Micheletti M, Miccichè RM, Palombo MR, Ramis D, Schimmenti V, Sureda P, Teira L, Teschler-Nicola M, Kennett DJ, Lalueza-Fox C, Patterson N, Sineo L, Coppa A, Caramelli D, Pinhasi R, Reich D. Nat Ecol Evol. 2020 Mar;4(3):334-345. doi: 10.1038/s41559-020-1102-0. Epub 2020 Feb 24. Erratum in: Nat Ecol Evol. 2020 May;4(5):764. PMID: 32094539; PMCID: PMC7080320.

[FernandesSirakNature2020]:

**A genetic history of the pre-contact Caribbean.** Fernandes DM, Sirak KA, Ringbauer H, Sedig J, Rohland N, Cheronet O, Mah M, Mallick S, Olalde I, Culleton BJ, Adamski N, Bernardos R, Bravo G, Broomandkhoshbacht N, Callan K, Candilio F, Demetz L, Carlson KSD, Eccles L, Freilich S, George RJ, Lawson AM, Mandl K, Marzaioli F, McCool WC, Oppenheimer J, Özdogan KT, Schattke C, Schmidt R, Stewardson K, Terrasi F, Zalzala F, Antúnez CA, Canosa EV, Colten R, Cucina A, Genchi F, Kraan C, La Pastina F, Lucci M, Maggiolo MV, Marcheco-Teruel B, Maria CT, Martínez C, París I, Pateman M, Simms TM, Sivoli CG, Vilar M, Kennett DJ, Keegan WF, Coppa A, Lipson M, Pinhasi R, Reich D. Nature. 2020 Dec 23. doi: 10.1038/s41586-020-03053-2. Epub ahead of print. PMID: 33361817.

[FowlerOlaldeNature2021]:

**A high-resolution picture of kinship practices in an Early Neolithic tomb..** Fowler C, Olalde I, Cummings V, Armit I, Büster L, Cuthbert S, Rohland N, Cheronet O, Pinhasi R, Reich D. Nature. 2022 Jan;601(7894):584-587. doi: 10.1038/s41586-021-04241-4. Epub 2021 Dec 22. PMID: 34937939; PMCID: PMC8896835.

[FreilichPinhasiScientificReports2021]:

**Reconstructing genetic histories and social organisation in Neolithic and Bronze Age Croatia. .** Freilich S, Ringbauer H, Los D, Novak M, Pavičić DT, Schiffels S, Pinhasi R. Sci Rep. 2021 Aug 18;11(1):16729. doi: 10.1038/s41598-021-94932-9. PMID: 34408163; PMCID: PMC8373892.

[delaFuentePNAS2018]:

**Genomic insights into the origin and diversification of late maritime hunter-gatherers from the Chilean Patagonia.** De la Fuente C, Ávila-Arcos MC, Galimany J, Carpenter ML, Homburger JR, Blanco A, Contreras P, Cruz Dávalos D, Reyes O, San Roman M, Moreno-Estrada A, Campos PF, Eng C, Huntsman S, Burchard EG, Malaspinas AS, Bustamante CD, Willerslev E, Llop E, Verdugo RA, Moraga M. Proc Natl Acad Sci U S A. 2018 Apr 24;115(17):E4006-E4012. doi: 10.1073/pnas.1715688115. Epub 2018 Apr 9. PubMed PMID: 29632188; PubMed Central PMCID: PMC5924884.

[FernandesScientificReports2018]:

**A genomic Neolithic time transect of hunter-farmer admixture in central Poland.** Fernandes DM, Strapagiel D, Borówka P, Marciniak B, Żądzińska E, Sirak K, Siska V, Grygiel R, Carlsson J, Manica A, Lorkiewicz W, Pinhasi R. Sci Rep. 2018 Oct 5;8(1):14879. doi: 10.1038/s41598-018-33067-w.

[FlegontovNature2019]:

**Palaeo-Eskimo genetic ancestry and the peopling of Chukotka and North America.** Flegontov P, Altinisik NE, Changmai P, Rohland N, Mallick S, Adamski N, Bolnick DA, Broomandkhoshbacht N, Candilio F, Culleton BJ, Flegontova O, Friesen TM, Jeong C, Harper TK, Keating D, Kennett DJ, Kim AM, Lamnidis TC, Lawson AM, Olalde I, Oppenheimer J, Potter BA, Raff J, Sattler RA, Skoglund P, Stewardson K, Vajda EJ, Vasilyev S, Veselovskaya E, Hayes MG, O'Rourke DH, Krause J, Pinhasi R, Reich D, Schiffels S. Nature. 2019 Jun;570(7760):236-240. doi: 10.1038/s41586-019-1251-y. Epub 2019 Jun 5. PMID: 31168094.

[FregelPNAS2018]:

**Ancient genomes from North Africa evidence prehistoric migrations to the Maghreb from both the Levant and Europe.** Fregel R, Méndez FL, Bokbot Y, Martín-Socas D, Camalich-Massieu MD, Santana J, Morales J, Ávila-Arcos MC, Underhill PA, Shapiro B, Wojcik G, Rasmussen M, Soares AER, Kapp J, Sockell A, Rodríguez-Santos FJ, Mikdad A, Trujillo-Mederos A, Bustamante CD. Proc Natl Acad Sci U S A. 2018 Jun 26;115(26):6774-6779. doi: 10.1073/pnas.1800851115. Epub 2018 Jun 12. Erratum in: Proc Natl Acad Sci U S A. 2018 Jul 24;115(30):E7231. PubMed PMID: 29895688; PubMed Central PMCID: PMC6042094.

[FuNature2014]:

**Genome sequence of a 45,000-year-old modern human from western Siberia.** Fu Q, Li H, Moorjani P, Jay F, Slepchenko SM, Bondarev AA, Johnson PL, Aximu-Petri A, Prüfer K, de Filippo C, Meyer M, Zwyns N, Salazar-García DC, Kuzmin YV, Keates SG, Kosintsev PA, Razhev DI, Richards MP, Peristov NV, Lachmann M, Douka K, Higham TF, Slatkin M, Hublin JJ, Reich D, Kelso J, Viola TB, Pääbo S. Nature. 2014 Oct 23;514(7523):445-9. doi: 10.1038/nature13810.

[FuNature2015]:

**An early modern human from Romania with a recent Neanderthal ancestor.** Fu Q, Hajdinjak M, Moldovan OT, Constantin S, Mallick S, Skoglund P, Patterson N, Rohland N, Lazaridis I, Nickel B, Viola B, Prüfer K, Meyer M, Kelso J, Reich D, Pääbo S. Nature. 2015 Aug 13;524(7564):216-9. doi: 10.1038/nature14558. Epub 2015 Jun 22.

[FuNature2016]:

**The genetic history of Ice Age Europe.** Fu Q, Posth C, Hajdinjak M, Petr M, Mallick S, Fernandes D, Furtwängler A, Haak W, Meyer M, Mittnik A, Nickel B, Peltzer A, Rohland N, Slon V, Talamo S, Lazaridis I, Lipson M, Mathieson I, Schiffels S, Skoglund P, Derevianko AP, Drozdov N, Slavinsky V, Tsybankov A, Cremonesi RG, Mallegni F, Gély B, Vacca E, Morales MR, Straus LG, Neugebauer-Maresch C, Teschler-Nicola M, Constantin S, Moldovan OT, Benazzi S, Peresani M, Coppola D, Lari M, Ricci S, Ronchitelli A, Valentin F, Thevenet C, Wehrberger K, Grigorescu D, Rougier H, Crevecoeur I, Flas D, Semal P, Mannino MA, Cupillard C, Bocherens H, Conard NJ, Harvati K, Moiseyev V, Drucker DG, Svoboda J, Richards MP, Caramelli D, Pinhasi R, Kelso J, Patterson N, Krause J, Pääbo S, Reich D. Nature. 2016 Jun 9;534(7606):200-5. doi: 10.1038/nature17993. Epub 2016 May 2.

[FurtwanglerNatureCommunications2020]:

**Comparison of target enrichment strategies for ancient pathogen DNA.** Furtwängler A, Neukamm J, Böhme L, Reiter E, Vollstedt M, Arora N, Singh P, Cole ST, Knauf S, Calvignac-Spencer S, Krause-Kyora B, Krause J, Schuenemann VJ, Herbig A. Biotechniques. 2020 Dec;69(6):455-459. doi: 10.2144/btn-2020-0100. Epub 2020 Nov 2. PMID: 33135465.

[GambaNatureCommunications2014]:

**Genome flux and stasis in a five millennium transect of European prehistory.** Gamba C, Jones ER, Teasdale MD, McLaughlin RL, Gonzalez-Fortes G, Mattiangeli V, Domboróczki L, Kővári I, Pap I, Anders A, Whittle A, Dani J, Raczky P, Higham TF, Hofreiter M, Bradley DG, Pinhasi R. Nat Commun. 2014 Oct 21;5:5257. doi: 10.1038/ncomms6257. PubMed PMID: 25334030; PubMed Central PMCID: PMC4218962.

[GelabertCurrBio2022]:

**Northeastern Asian and Jomon-related genetic structure in the Three Kingdoms period of Gimhae, Korea.** Gelabert P, Blazyte A, Chang Y, Fernandes DM, Jeon S, Hong JG, Yoon J, Ko Y, Oberreiter V, Cheronet O, Özdoğan KT, Sawyer S, Yang S, Greytak EM, Choi H, Kim J, Kim JI, Jeong C, Bae K, Bhak J, Pinhasi R. Northeastern Asian and Jomon-related genetic structure in the Three Kingdoms period of Gimhae, Korea. Curr Biol. 2022 Aug 8;32(15):3232-3244.e6. doi: 10.1016/j.cub.2022.06.004. Epub 2022 Jun 21. PMID: 35732180.

[GelabertSciRep2022]:

**Genomes from Verteba cave suggest diversity within the Trypillians in Ukraine.** Gelabert P, Schmidt RW, Fernandes DM, Karsten JK, Harper TK, Madden GD, Ledogar SH, Sokhatsky M, Oota H, Kennett DJ, Pinhasi R. Genomes from Verteba cave suggest diversity within the Trypillians in Ukraine. Sci Rep. 2022 May 4;12(1):7242. doi: 10.1038/s41598-022-11117-8. PMID: 35508651; PMCID: PMC9068698.

[GnecchiRusconeCell2022]:

**Ancient genomes reveal origin and rapid trans-Eurasian migration of 7th century Avar elites.** Gnecchi-Ruscone GA, Szécsényi-Nagy A, Koncz I, Csiky G, Rácz Z, Rohrlach AB, Brandt G, Rohland N, Csáky V, Cheronet O, Szeifert B, Rácz TÁ, Benedek A, Bernert Z, Berta N, Czifra S, Dani J, Farkas Z, Hága T, Hajdu T, Jászberényi M, Kisjuhász V, Kolozsi B, Major P, Marcsik A, Kovacsóczy BN, Balogh C, Lezsák GM, Ódor JG, Szelekovszky M, Szeniczey T, Tárnoki J, Tóth Z, Tutkovics EK, Mende BG, Geary P, Pohl W, Vida T, Pinhasi R, Reich D, Hofmanová Z, Jeong C, Krause J. Ancient genomes reveal origin and rapid trans-Eurasian migration of 7th century Avar elites. Cell. 2022 Apr 14;185(8):1402-1413.e21. doi: 10.1016/j.cell.2022.03.007. Epub 2022 Apr 1. PMID: 35366416; PMCID: PMC9042794.

[GnecchiRusconeScienceAdvances2021]:

**Ancient genomic time transect from the Central Asian Steppe unravels the history of the Scythians.** Gnecchi-Ruscone GA, Khussainova E, Kahbatkyzy N, Musralina L, Spyrou MA, Bianco RA, Radzeviciute R, Martins NFG, Freund C, Iksan O, Garshin A, Zhaniyazov Z, Bekmanov B, Kitov E, Samashev Z, Beisenov A, Berezina N, Berezin Y, Bíró AZ, Évinger S, Bissembaev A, Akhatov G, Mamedov A, Onggaruly A, Voyakin D, Chotbayev A, Kariyev Y, Buzhilova A, Djansugurova L, Jeong C, Krause J. Ancient genomic time transect from the Central Asian Steppe unravels the history of the Scythians. Sci Adv. 2021 Mar 26;7(13):eabe4414. doi: 10.1126/sciadv.abe4414. PMID: 33771866; PMCID: PMC7997506.

[GokhmanNatureCommunications2020]:

**Differential DNA methylation of vocal and facial anatomy genes in modern humans.** Gokhman D, Nissim-Rafinia M, Agranat-Tamir L, Housman G, García-Pérez R, Lizano E, Cheronet O, Mallick S, Nieves-Colón MA, Li H, Alpaslan-Roodenberg S, Novak M, Gu H, Osinski JM, Ferrando-Bernal M, Gelabert P, Lipende I, Mjungu D, Kondova I, Bontrop R, Kullmer O, Weber G, Shahar T, Dvir-Ginzberg M, Faerman M, Quillen EE, Meissner A, Lahav Y, Kandel L, Liebergall M, Prada ME, Vidal JM, Gronostajski RM, Stone AC, Yakir B, Lalueza-Fox C, Pinhasi R, Reich D, Marques-Bonet T, Meshorer E, Carmel L. Nat Commun. 2020 Mar 4;11(1):1189. doi: 10.1038/s41467-020-15020-6. PMID: 32132541; PMCID: PMC7055320.

[GonzalesFortesCurrentBiology2017]:

**Paleogenomic Evidence for Multi-generational Mixing between Neolithic Farmers and Mesolithic Hunter-Gatherers in the Lower Danube Basin.** González-Fortes G, Jones ER, Lightfoot E, Bonsall C, Lazar C, Grandal-d'Anglade A, Garralda MD, Drak L, Siska V, Simalcsik A, Boroneanţ A, Vidal Romaní JR, Vaqueiro Rodríguez M, Arias P, Pinhasi R, Manica A, Hofreiter M. Paleogenomic Evidence for Multi-generational Mixing between Neolithic Farmers and Mesolithic Hunter-Gatherers in the Lower Danube Basin. Curr Biol. 2017 Jun 19;27(12):1801-1810.e10. doi: 10.1016/j.cub.2017.05.023. Epub 2017 May 25. PubMed PMID: 28552360; PubMed Central PMCID: PMC5483232.

[GonzalesFortesProcRoyalSocB2019]:

**A western route of prehistoric human migration from Africa into the Iberian Peninsula.** González-Fortes G, Tassi F, Trucchi E, Henneberger K, Paijmans JLA, Díez-Del-Molino D, Schroeder H, Susca RR, Barroso-Ruíz C, Bermudez FJ, Barroso-Medina C, Bettencourt AMS, Sampaio HA, Grandal-d'Anglade A, Salas A, de Lombera-Hermida A, Fabregas Valcarce R, Vaquero M, Alonso S, Lozano M, Rodríguez-Alvarez XP, Fernández-Rodríguez C, Manica A, Hofreiter M, Barbujani G. Proc Biol Sci. 2019 Jan 30;286(1895):20182288. doi: 10.1098/rspb.2018.2288. PMID: 30963949.

[GretzingerNature2022]:

**The Anglo-Saxon migration and the formation of the early English gene pool.** Gretzinger J, Sayer D, Justeau P, Altena E, Pala M, Dulias K, Edwards CJ, Jodoin S, Lacher L, Sabin S, Vågene ÅJ, Haak W, Ebenesersdóttir SS, Moore KHS, Radzeviciute R, Schmidt K, Brace S, Bager MA, Patterson N, Papac L, Broomandkhoshbacht N, Callan K, Harney É, Iliev L, Lawson AM, Michel M, Stewardson K, Zalzala F, Rohland N, Kappelhoff-Beckmann S, Both F, Winger D, Neumann D, Saalow L, Krabath S, Beckett S, Van Twest M, Faulkner N, Read C, Barton T, Caruth J, Hines J, Krause-Kyora B, Warnke U, Schuenemann VJ, Barnes I, Dahlström H, Clausen JJ, Richardson A, Popescu E, Dodwell N, Ladd S, Phillips T, Mortimer R, Sayer F, Swales D, Stewart A, Powlesland D, Kenyon R, Ladle L, Peek C, Grefen-Peters S, Ponce P, Daniels R, Spall C, Woolcock J, Jones AM, Roberts AV, Symmons R, Rawden AC, Cooper A, Bos KI, Booth T, Schroeder H, Thomas MG, Helgason A, Richards MB, Reich D, Krause J, Schiffels S. The Anglo-Saxon migration and the formation of the early English gene pool. Nature. 2022 Oct;610(7930):112-119. doi: 10.1038/s41586-022-05247-2. Epub 2022 Sep 21. Erratum in: Nature. 2022 Nov;611(7934):E3. PMID: 36131019; PMCID: PMC9534755.

[GuntherPLoSBiology2018]:

**Population genomics of Mesolithic Scandinavia: Investigating early postglacial migration routes and high-latitude adaptation.** Günther T, Malmström H, Svensson EM, Omrak A, Sánchez-Quinto F, Kılınç GM, Krzewińska M, Eriksson G, Fraser M, Edlund H, Munters AR, Coutinho A, Simões LG, Vicente M, Sjölander A, Jansen Sellevold B, Jørgensen R, Claes P, Shriver MD, Valdiosera C, Netea MG, Apel J, Lidén K, Skar B, Storå J, Götherström A, Jakobsson M. PLoS Biol. 2018 Jan 9;16(1):e2003703. doi: 10.1371/journal.pbio.2003703. eCollection 2018 Jan.

[GuntherPNAS2015]:

**Ancient genomes link early farmers from Atapuerca in Spain to modern-day Basques.** Günther T, Valdiosera C, Malmström H, Ureña I, Rodriguez-Varela R, Sverrisdóttir ÓO, Daskalaki EA, Skoglund P, Naidoo T, Svensson EM, Bermúdez de Castro JM, Carbonell E, Dunn M, Storå J, Iriarte E, Arsuaga JL, Carretero JM, Götherström A, Jakobsson M. Proc Natl Acad Sci U S A. 2015 Sep 22;112(38):11917-22. doi: 10.1073/pnas.1509851112. Epub 2015 Sep 8.

[HaberAJHG2017]:

**Continuity and Admixture in the Last Five Millennia of Levantine History from Ancient Canaanite and Present-Day Lebanese Genome Sequences.** Haber M, Doumet-Serhal C, Scheib C, Xue Y, Danecek P, Mezzavilla M, Youhanna S, Martiniano R, Prado-Martinez J, Szpak M, Matisoo-Smith E, Schutkowski H, Mikulski R, Zalloua P, Kivisild T, Tyler-Smith C. Am J Hum Genet. 2017 Aug 3;101(2):274-282. doi: 10.1016/j.ajhg.2017.06.013. Epub 2017 Jul 27. PubMed PMID: 28757201; PubMed Central PMCID: PMC5544389.

[HaberAJHG2018]:

**A Transient Pulse of Genetic Admixture from the Crusaders in the Near East Identified from Ancient Genome Sequences.** Haber M, Doumet-Serhal C, Scheib CL, Xue Y, Mikulski R, Martiniano R, Fischer-Genz B, Schutkowski H, Kivisild T, Tyler-Smith C. Am J Hum Genet. 2019 May 2;104(5):977-984. doi: 10.1016/j.ajhg.2019.03.015. Epub 2019 Apr 18. PMID: 31006515.

[HaberAJHG2020]:

**A Genetic History of the Near East from an aDNA Time Course Sampling Eight Points in the Past 4,000 Years.** Haber M, Nassar J, Almarri MA, Saupe T, Saag L, Griffith SJ, Doumet-Serhal C, Chanteau J, Saghieh-Beydoun M, Xue Y, Scheib CL, Tyler-Smith C. Am J Hum Genet. 2020 Jul 2;107(1):149-157. doi: 10.1016/j.ajhg.2020.05.008. Epub 2020 May 28. PMID: 32470374; PMCID: PMC7332655.

[HajdinjakNature2018]:

**Reconstructing the genetic history of late Neanderthals.** Hajdinjak M, Fu Q, Hübner A, Petr M, Mafessoni F, Grote S, Skoglund P, Narasimham V, Rougier H, Crevecoeur I, Semal P, Soressi M, Talamo S, Hublin JJ, Gušić I, Kućan Ž, Rudan P, Golovanova LV, Doronichev VB, Posth C, Krause J, Korlević P, Nagel S, Nickel B, Slatkin M, Patterson N, Reich D, Prüfer K, Meyer M, Pääbo S, Kelso J. Nature. 2018 Mar 29;555(7698):652-656. doi: 10.1038/nature26151. Epub 2018 Mar 21.

[HajdinjakPaaboNature2021]:

**Initial Upper Palaeolithic humans in Europe had recent Neanderthal ancestry. .** Hajdinjak M, Mafessoni F, Skov L, Vernot B, Hübner A, Fu Q, Essel E, Nagel S, Nickel B, Richter J, Moldovan OT, Constantin S, Endarova E, Zahariev N, Spasov R, Welker F, Smith GM, Sinet-Mathiot V, Paskulin L, Fewlass H, Talamo S, Rezek Z, Sirakova S, Sirakov N, McPherron SP, Tsanova T, Hublin JJ, Peter BM, Meyer M, Skoglund P, Kelso J, Pääbo S. Nature. 2021 Apr;592(7853):253-257. doi: 10.1038/s41586-021-03335-3. Epub 2021 Apr 7. PMID: 33828320; PMCID: PMC8026394.

[HarneyCheronetGenomeResearch2021]:

**A minimally destructive protocol for DNA extraction from ancient teeth.** Harney É, Cheronet O, Fernandes DM, Sirak K, Mah M, Bernardos R, Adamski N, Broomandkhoshbacht N, Callan K, Lawson AM, Oppenheimer J, Stewardson K, Zalzala F, Anders A, Candilio F, Constantinescu M, Coppa A, Ciobanu I, Dani J, Gallina Z, Genchi F, Nagy EG, Hajdu T, Hellebrandt M, Horváth A, Király Á, Kiss K, Kolozsi B, Kovács P, Köhler K, Lucci M, Pap I, Popovici S, Raczky P, Simalcsik A, Szeniczey T, Vasilyev S, Virag C, Rohland N, Reich D, Pinhasi R. A minimally destructive protocol for DNA extraction from ancient teeth. Genome Res. 2021 Mar;31(3):472-483. doi: 10.1101/gr.267534.120. Epub 2021 Feb 12. PMID: 33579752; PMCID: PMC7919446.

[HarneyMayNatureCommunications2018]:

**Ancient DNA from Chalcolithic Israel reveals the role of population mixture in cultural transformation.** Harney É, May H, Shalem D, Rohland N, Mallick S, Lazaridis I, Sarig R, Stewardson K, Nordenfelt S, Patterson N, Hershkovitz I, Reich D. Nat Commun. 2018 Aug 20;9(1):3336. doi: 10.1038/s41467-018-05649-9. Erratum in: Nat Commun. 2018 Sep 20;9(1):3913.

[HarneyNatureCommunications2019]:

**Ancient DNA from the skeletons of Roopkund Lake reveals Mediterranean migrants in India.** Harney É, Nayak A, Patterson N, Joglekar P, Mushrif-Tripathy V, Mallick S, Rohland N, Sedig J, Adamski N, Bernardos R, Broomandkhoshbacht N, Culleton BJ, Ferry M, Harper TK, Michel M, Oppenheimer J, Stewardson K, Zhang Z, Harashawaradhana, Bartwal MS, Kumar S, Diyundi SC, Roberts P, Boivin N, Kennett DJ, Thangaraj K, Reich D, Rai N. Nat Commun. 2019 Aug 20;10(1):3670. doi: 10.1038/s41467-019-11357-9. PMID: 31431628.

[HofmanovaPNAS2016]:

**Early farmers from across Europe directly descended from Neolithic Aegeans.** Hofmanová Z, Kreutzer S, Hellenthal G, Sell C, Diekmann Y, Díez-Del-Molino D, van Dorp L, López S, Kousathanas A, Link V, Kirsanow K, Cassidy LM, Martiniano R, Strobel M, Scheu A, Kotsakis K, Halstead P, Triantaphyllou S, Kyparissi-Apostolika N, Urem-Kotsou D, Ziota C, Adaktylou F, Gopalan S, Bobo DM, Winkelbach L, Blöcher J, Unterländer M, Leuenberger C, Çilingiroğlu Ç, Horejs B, Gerritsen F, Shennan SJ, Bradley DG, Currat M, Veeramah KR, Wegmann D, Thomas MG, Papageorgopoulou C, Burger J. Proc Natl Acad Sci U S A. 2016 Jun 21;113(25):6886-91. doi: 10.1073/pnas.1523951113. Epub 2016 Jun 6.

[IngmanStockhammerPLoS2021]:

**Turkey during the 2nd millennium BC: Integration of isotopic and genomic evidence..** Ingman T, Eisenmann S, Skourtanioti E, Akar M, Ilgner J, Gnecchi Ruscone GA, le Roux P, Shafiq R, Neumann GU, Keller M, Freund C, Marzo S, Lucas M, Krause J, Roberts P, Yener KA, Stockhammer PW. Human mobility at Tell Atchana (Alalakh), Hatay, PLoS One. 2021 Jun 30;16(6):e0241883. doi: 10.1371/journal.pone.0241883. PMID: 34191795; PMCID: PMC8244877.

[JarveCurrentBiology2019]:

**Shifts in the Genetic Landscape of the Western Eurasian Steppe Associated with the Beginning and End of the Scythian Dominance.** Järve M, Saag L, Scheib CL, Pathak AK, Montinaro F, Pagani L, Flores R, Guellil M, Saag L, Tambets K, Kushniarevich A, Solnik A, Varul L, Zadnikov S, Petrauskas O, Avramenko M, Magomedov B, Didenko S, Toshev G, Bruyako I, Grechko D, Okatenko V, Gorbenko K, Smyrnov O, Heiko A, Reida R, Sapiehin S, Sirotin S, Tairov A, Beisenov A, Starodubtsev M, Vasilev V, Nechvaloda A, Atabiev B, Litvinov S, Ekomasova N, Dzhaubermezov M, Voroniatov S, Utevska O, Shramko I, Khusnutdinova E, Metspalu M, Savelev N, Kriiska A, Kivisild T, Villems R. Curr Biol. 2019 Jul 22;29(14):2430-2441.e10. doi: 10.1016/j.cub.2019.06.019. Epub 2019 Jul 11. PMID: 31303491.

[JensenSchroederNatureCommunications2019]:

**A 5700 year-old human genome and oral microbiome from chewed birch pitch. .** Jensen TZT, Niemann J, Iversen KH, Fotakis AK, Gopalakrishnan S, Vågene ÅJ, Pedersen MW, Sinding MS, Ellegaard MR, Allentoft ME, Lanigan LT, Taurozzi AJ, Nielsen SH, Dee MW, Mortensen MN, Christensen MC, Sørensen SA, Collins MJ, Gilbert MTP, Sikora M, Rasmussen S, Schroeder H. Nat Commun. 2019 Dec 17;10(1):5520. doi: 10.1038/s41467-019-13549-9. PMID: 31848342; PMCID: PMC6917805.

[JeongCell2020]:

**A Dynamic 6,000-Year Genetic History of Eurasia's Eastern Steppe.** Jeong C, Wang K, Wilkin S, Taylor WTT, Miller BK, Bemmann JH, Stahl R, Chiovelli C, Knolle F, Ulziibayar S, Khatanbaatar D, Erdenebaatar D, Erdenebat U, Ochir A, Ankhsanaa G, Vanchigdash C, Ochir B, Munkhbayar C, Tumen D, Kovalev A, Kradin N, Bazarov BA, Miyagashev DA, Konovalov PB, Zhambaltarova E, Miller AV, Haak W, Schiffels S, Krause J, Boivin N, Erdene M, Hendy J, Warinner C. A Dynamic 6,000-Year Genetic History of Eurasia's Eastern Steppe. Cell. 2020 Nov 12;183(4):890-904.e29. doi: 10.1016/j.cell.2020.10.015. Epub 2020 Nov 5. PMID: 33157037; PMCID: PMC7664836.

[JeongNatureEcologyEvolution2019]:

**The genetic history of admixture across inner Eurasia.** Jeong C, Balanovsky O, Lukianova E, Kahbatkyzy N, Flegontov P, Zaporozhchenko V, Immel A, Wang CC, Ixan O, Khussainova E, Bekmanov B, Zaibert V, Lavryashina M, Pocheshkhova E, Yusupov Y, Agdzhoyan A, Koshel S, Bukin A, Nymadawa P, Turdikulova S, Dalimova D, Churnosov M, Skhalyakho R, Daragan D, Bogunov Y, Bogunova A, Shtrunov A, Dubova N, Zhabagin M, Yepiskoposyan L, Churakov V, Pislegin N, Damba L, Saroyants L, Dibirova K, Atramentova L, Utevska O, Idrisov E, Kamenshchikova E, Evseeva I, Metspalu M, Outram AK, Robbeets M, Djansugurova L, Balanovska E, Schiffels S, Haak W, Reich D, Krause J. Nat Ecol Evol. 2019 Jun;3(6):966-976. doi: 10.1038/s41559-019-0878-2. Epub 2019 Apr 29. PMID: 31036896.

[JeongPNAS2016]:

**Long-term genetic stability and a high-altitude East Asian origin for the peoples of the high valleys of the Himalayan arc.** Jeong C, Ozga AT, Witonsky DB, Malmström H, Edlund H, Hofman CA, Hagan RW, Jakobsson M, Lewis CM, Aldenderfer MS, Di Rienzo A, Warinner C. Proc Natl Acad Sci U S A. 2016 Jul 5;113(27):7485-90. doi: 10.1073/pnas.1520844113. Epub 2016 Jun 20. PMID: 27325755.

[JeongPNAS2018]:

**Bronze Age population dynamics and the rise of dairy pastoralism on the eastern Eurasian steppe.** Jeong C, Wilkin S, Amgalantugs T, Bouwman AS, Taylor WTT, Hagan RW, Bromage S, Tsolmon S, Trachsel C, Grossmann J, Littleton J, Makarewicz CA, Krigbaum J, Burri M, Scott A, Davaasambuu G, Wright J, Irmer F, Myagmar E, Boivin N, Robbeets M, Rühli FJ, Krause J, Frohlich B, Hendy J, Warinner C. Proc Natl Acad Sci U S A. 2018 Nov 27;115(48):E11248-E11255. doi: 10.1073/pnas.1813608115. Epub 2018 Nov 5. PMID:30397125.

[JonesNatureCommunications2015]:

**Upper Palaeolithic genomes reveal deep roots of modern Eurasians.** Jones ER, Gonzalez-Fortes G, Connell S, Siska V, Eriksson A, Martiniano R, McLaughlin RL, Gallego Llorente M, Cassidy LM, Gamba C, Meshveliani T, Bar-Yosef O, Müller W, Belfer-Cohen A, Matskevich Z, Jakeli N, Higham TF, Currat M, Lordkipanidze D, Hofreiter M, Manica A, Pinhasi R, Bradley DG. Nat Commun. 2015 Nov 16;6:8912. doi: 10.1038/ncomms9912. PMID: 26567969.

[JonesCurrentBiology2017]:

**The Neolithic Transition in the Baltic Was Not Driven by Admixture with Early European Farmers.** Jones ER, Zarina G, Moiseyev V, Lightfoot E, Nigst PR, Manica A, Pinhasi R, Bradley DG. Curr Biol. 2017 Feb 20;27(4):576-582.

[KanzawaKiriyamaJHG2016:]

**A partial nuclear genome of the Jomons who lived 3000 years ago in Fukushima, Japan.** Kanzawa-Kiriyama H, Kryukov K, Jinam TA, Hosomichi K, Saso A, Suwa G, Ueda S, Yoneda M, Tajima A, Shinoda KI, Inoue I, Saitou N. J Hum Genet. 2017 Feb;62(2):213-221. doi: 10.1038/jhg.2016.110. Epub 2016 Sep 1.

[KellerNatureCommunications2012]:

**New insights into the Tyrolean Iceman's origin and phenotype as inferred by whole-genome sequencing.** Keller A1, Graefen A, Ball M, Matzas M, Boisguerin V, Maixner F, Leidinger P, Backes C, Khairat R, Forster M, Stade B, Franke A, Mayer J, Spangler J, McLaughlin S, Shah M, Lee C, Harkins TT, Sartori A, Moreno-Estrada A, Henn B, Sikora M, Semino O, Chiaroni J, Rootsi S, Myres NM, Cabrera VM, Underhill PA, Bustamante CD, Vigl EE, Samadelli M, Cipollini G, Haas J, Katus H, O'Connor BD, Carlson MR, Meder B, Blin N, Meese E, Pusch CM, Zink A. Nat Commun. 2012 Feb 28;3:698. doi: 10.1038/ncomms1701.Paperpile.

[KennettLipsonPruferNatureCommunications2022]:

**South-to-north migration preceded the advent of intensive farming in the Maya region.** Kennett DJ, Lipson M, Prufer KM, Mora-Marín D, George RJ, Rohland N, Robinson M, Trask WR, Edgar HHJ, Hill EC, Ray EE, Lynch P, Moes E, O'Donnell L, Harper TK, Kate EJ, Ramos J, Morris J, Gutierrez SM, Ryan TM, Culleton BJ, Awe JJ, Reich D. Nat Commun. 2022 Mar 22;13(1):1530. doi: 10.1038/s41467-022-29158-y. PMID: 35318319; PMCID: PMC8940966.

[KennettNatureCommunications2017]:

**Archaeogenomic evidence reveals prehistoric matrilineal dynasty.** Kennett DJ, Plog S, George RJ, Culleton BJ, Watson AS, Skoglund P, Rohland N, Mallick S, Stewardson K, Kistler L, LeBlanc SA, Whiteley PM, Reich D, Perry GH. Nat Commun. 2017 Feb 21;8:14115. doi: 10.1038/ncomms14115. PMID: 28221340.

[KilincCurrentBiology2016]:

**The Demographic Development of the First Farmers in Anatolia.**Kılınç GM, Omrak A, Özer F, Günther T, Büyükkarakaya AM, Bıçakçı E, Baird D, Dönertaş HM, Ghalichi A, Yaka R, Koptekin D, Açan SC, Parvizi P, Krzewińska M, Daskalaki EA, Yüncü E, Dağtaş ND, Fairbairn A, Pearson J, Mustafaoğlu G, Erdal YS, Çakan YG, Togan İ, Somel M, Storå J, Jakobsson M, Götherström A. Curr Biol. 2016 Oct 10;26(19):2659-2666. doi: 10.1016/j.cub.2016.07.057. Epub 2016 Aug 4. PMID: 27498567.

[KilincSciAdv2021]:

**Human population dynamics and Yersinia pestis in ancient northeast Asia.** Kılınç GM, Kashuba N, Koptekin D, Bergfeldt N, Dönertaş HM, Rodríguez-Varela R, Shergin D, Ivanov G, Kichigin D, Pestereva K, Volkov D, Mandryka P, Kharinskii A, Tishkin A, Ineshin E, Kovychev E, Stepanov A, Dalén L, Günther T, Kırdök E, Jakobsson M, Somel M, Krzewińska M, Storå J, Götherström A. Human population dynamics and Yersinia pestis in ancient northeast Asia. Sci Adv. 2021 Jan 6;7(2):eabc4587. doi: 10.1126/sciadv.abc4587. PMID: 33523963; PMCID: PMC7787494.

[KrzewinskaCurrentBiology2018]:

**Genomic and Strontium Isotope Variation Reveal Immigration Patterns in a Viking Age Town.** Krzewińska M, Kjellström A, Günther T, Hedenstierna-Jonson C, Zachrisson T, Omrak A, Yaka R, Kılınç GM, Somel M, Sobrado V, Evans J, Knipper C, Jakobsson M, Storå J, Götherström A. Curr Biol. 2018 Sep 10;28(17):2730-2738.e10. doi: 10.1016/j.cub.2018.06.053. Epub 2018 Aug 23. PMID: 30146150.

[KrzewinskaScienceAdvances2018]:

**Ancient genomes suggest the eastern Pontic-Caspian steppe as the source of western Iron Age nomads.** Krzewińska M, Kılınç GM, Juras A, Koptekin D, Chyleński M, Nikitin AG, Shcherbakov N, Shuteleva I, Leonova T, Kraeva L, Sungatov FA, Sultanova AN, Potekhina I, Łukasik S, Krenz-Niedbała M, Dalén L, Sinika V, Jakobsson M, Storå J, Götherström A. Sci Adv. 2018 Oct 3;4(10):eaat4457. doi: 10.1126/sciadv.aat4457. eCollection 2018 Oct. PMID: 30417088.

[KumarFuScience2022]:

**Bronze and Iron Age population movements underlie Xinjiang population history.** Kumar V, Wang W, Zhang J, Wang Y, Ruan Q, Yu J, Wu X, Hu X, Wu X, Guo W, Wang B, Niyazi A, Lv E, Tang Z, Cao P, Liu F, Dai Q, Yang R, Feng X, Ping W, Zhang L, Zhang M, Hou W, Liu Y, Bennett EA, Fu Q. Science. 2022 Apr;376(6588):62-69. doi: 10.1126/science.abk1534. Epub 2022 Mar 31. PMID: 35357918.

[LamnidisNatureCommunications2018]:

**Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe.** Lamnidis TC, Majander K, Jeong C, Salmela E, Wessman A, Moiseyev V, Khartanovich V, Balanovsky O, Ongyerth M, Weihmann A, Sajantila A, Kelso J, Pääbo S, Onkamo P, Haak W, Krause J, Schiffels S. Nat Commun. 2018 Nov 27;9(1):5018. doi: 10.1038/s41467-018-07483-5. PMID: 30479341.

[LarenaJakobbsonPNAS2021]:

**Multiple migrations to the Philippines during the last 50,000 years.** Larena M, Sanchez-Quinto F, Sjödin P, McKenna J, Ebeo C, Reyes R, Casel O, Huang JY, Hagada KP, Guilay D, Reyes J, Allian FP, Mori V, Azarcon LS, Manera A, Terando C, Jamero L Jr, Sireg G, Manginsay-Tremedal R, Labos MS, Vilar RD, Latiph A, Saway RL, Marte E, Magbanua P, Morales A, Java I, Reveche R, Barrios B, Burton E, Salon JC, Kels MJT, Albano A, Cruz-Angeles RB, Molanida E, Granehäll L, Vicente M, Edlund H, Loo JH, Trejaut J, Ho SYW, Reid L, Malmström H, Schlebusch C, Lambeck K, Endicott P, Jakobsson M. Multiple migrations to the Philippines during the last 50,000 years. Proc Natl Acad Sci U S A. 2021 Mar 30;118(13):e2026132118. doi: 10.1073/pnas.2026132118. PMID: 33753512; PMCID: PMC8020671.

[LazaridisAlpaslanRoodenbergScience2022]:

**The genetic history of the Southern Arc: A bridge between West Asia and Europe.**Lazaridis I, Alpaslan-Roodenberg S, Acar A, Açıkkol A, Agelarakis A, Aghikyan L, Akyüz U, Andreeva D, Andrijašević G, Antonović D, Armit I, Atmaca A, Avetisyan P, Aytek Aİ, Bacvarov K, Badalyan R, Bakardzhiev S, Balen J, Bejko L, Bernardos R, Bertsatos A, Biber H, Bilir A, Bodružić M, Bonogofsky M, Bonsall C, Borić D, Borovinić N, Bravo Morante G, Buttinger K, Callan K, Candilio F, Carić M, Cheronet O, Chohadzhiev S, Chovalopoulou ME, Chryssoulaki S, Ciobanu I, Čondić N, Constantinescu M, Cristiani E, Culleton BJ, Curtis E, Davis J, Demcenco TI, Dergachev V, Derin Z, Deskaj S, Devejyan S, Djordjević V, Duffett Carlson KS, Eccles LR, Elenski N, Engin A, Erdoğan N, Erir-Pazarcı S, Fernandes DM, Ferry M, Freilich S, Frînculeasa A, Galaty ML, Gamarra B, Gasparyan B, Gaydarska B, Genç E, Gültekin T, Gündüz S, Hajdu T, Heyd V, Hobosyan S, Hovhannisyan N, Iliev I, Iliev L, Iliev S, İvgin İ, Janković I, Jovanova L, Karkanas P, Kavaz-Kındığılı B, Kaya EH, Keating D, Kennett DJ, Deniz Kesici S, Khudaverdyan A, Kiss K, Kılıç S, Klostermann P, Kostak Boca Negra Valdes S, Kovačević S, Krenz-Niedbała M, Krznarić Škrivanko M, Kurti R, Kuzman P, Lawson AM, Lazar C, Leshtakov K, Levy TE, Liritzis I, Lorentz KO, Łukasik S, Mah M, Mallick S, Mandl K, Martirosyan-Olshansky K, Matthews R, Matthews W, McSweeney K, Melikyan V, Micco A, Michel M, Milašinović L, Mittnik A, Monge JM, Nekhrizov G, Nicholls R, Nikitin AG, Nikolov V, Novak M, Olalde I, Oppenheimer J, Osterholtz A, Özdemir C, Özdoğan KT, Öztürk N, Papadimitriou N, Papakonstantinou N, Papathanasiou A, Paraman L, Paskary EG, Patterson N, Petrakiev I, Petrosyan L, Petrova V, Philippa-Touchais A, Piliposyan A, Pocuca Kuzman N, Potrebica H, Preda-Bălănică B, Premužić Z, Price TD, Qiu L, Radović S, Raeuf Aziz K, Rajić Šikanjić P, Rasheed Raheem K, Razumov S, Richardson A, Roodenberg J, Ruka R, Russeva V, Şahin M, Şarbak A, Savaş E, Schattke C, Schepartz L, Selçuk T, Sevim-Erol A, Shamoon-Pour M, Shephard HM, Sideris A, Simalcsik A, Simonyan H, Sinika V, Sirak K, Sirbu G, Šlaus M, Soficaru A, Söğüt B, Sołtysiak A, Sönmez-Sözer Ç, Stathi M, Steskal M, Stewardson K, Stocker S, Suata-Alpaslan F, Suvorov A, Szécsényi-Nagy A, Szeniczey T, Telnov N, Temov S, Todorova N, Tota U, Touchais G, Triantaphyllou S, Türker A, Ugarković M, Valchev T, Veljanovska F, Videvski Z, Virag C, Wagner A, Walsh S, Włodarczak P, Workman JN, Yardumian A, Yarovoy E, Yavuz AY, Yılmaz H, Zalzala F, Zettl A, Zhang Z, Çavuşoğlu R, Rohland N, Pinhasi R, Reich D, Davtyan R. The genetic history of the Southern Arc: A bridge between West Asia and Europe. Science. 2022 Aug 26;377(6609):eabm4247. doi: 10.1126/science.abm4247. Epub 2022 Aug 26. PMID: 36007055.

[LazaridisNature2014]:

**Ancient human genomes suggest three ancestral populations for present-day Europeans.** Lazaridis I, Patterson N, Mittnik A, Renaud G, Mallick S, Kirsanow K, Sudmant PH, Schraiber JG, Castellano S, Lipson M, Berger B, Economou C, Bollongino R, Fu Q, Bos KI, Nordenfelt S, Li H, de Filippo C, Prüfer K, Sawyer S, Posth C, Haak W, Hallgren F, Fornander E, Rohland N, Delsate D, Francken M, Guinet JM, Wahl J, Ayodo G, Babiker HA, Bailliet G, Balanovska E, Balanovsky O, Barrantes R, Bedoya G, Ben-Ami H, Bene J, Berrada F, Bravi CM, Brisighelli F, Busby GB, Cali F, Churnosov M, Cole DE, Corach D, Damba L, van Driem G, Dryomov S, Dugoujon JM, Fedorova SA, Gallego Romero I, Gubina M, Hammer M, Henn BM, Hervig T, Hodoglugil U, Jha AR, Karachanak-Yankova S, Khusainova R, Khusnutdinova E, Kittles R, Kivisild T, Klitz W, Kučinskas V, Kushniarevich A, Laredj L, Litvinov S, Loukidis T, Mahley RW, Melegh B, Metspalu E, Molina J, Mountain J, Näkkäläjärvi K, Nesheva D, Nyambo T, Osipova L, Parik J, Platonov F, Posukh O, Romano V, Rothhammer F, Rudan I, Ruizbakiev R, Sahakyan H, Sajantila A, Salas A, Starikovskaya EB, Tarekegn A, Toncheva D, Turdikulova S, Uktveryte I, Utevska O, Vasquez R, Villena M, Voevoda M, Winkler CA, Yepiskoposyan L, Zalloua P, Zemunik T, Cooper A, Capelli C, Thomas MG, Ruiz-Linares A, Tishkoff SA, Singh L, Thangaraj K, Villems R, Comas D, Sukernik R, Metspalu M, Meyer M, Eichler EE, Burger J, Slatkin M, Pääbo S, Kelso J, Reich D, Krause J. Nature. 2014 Sep 18;513(7518):409-13. doi: 10.1038/nature13673. PMID: 25230663.

[LazaridisNature2016]:

**Genomic insights into the origin of farming in the ancient Near East.** Lazaridis I, Nadel D, Rollefson G, Merrett DC, Rohland N, Mallick S, Fernandes D, Novak M, Gamarra B, Sirak K, Connell S, Stewardson K, Harney E, Fu Q, Gonzalez-Fortes G, Jones ER, Roodenberg SA, Lengyel G, Bocquentin F, Gasparian B, Mongce JM, Gregg M, Eshed V, Mizrahi AS, Meiklejohn C, Gerritsen F, Bejenaru L, Blüher M, Campbell A, Cavalleri G, Comas D, Froguel P, Gilbert E, Kerr SM, Kovacs P, Krause J, McGettigan D, Merrigan M, Merriwether DA, O'Reilly S, Richards MB, Semino O, Shamoon-Pour M, Stefanescu G, Stumvoll M, Tönjes A, Torroni A, Wilson JF, Yengo L, Hovhannisyan NA, Patterson N, Pinhasi R, Reich D. Nature. 2016 Aug 25;536(7617):419-24. Epub 2016 Jul 25. PMID: 27459054.

[LazaridisNature2017]:

**Genetic origins of the Minoans and Mycenaeans.** Lazaridis I, Mittnik A, Patterson N, Mallick S, Rohland N, Pfrengle S, Furtwängler A, Peltzer A, Posth C, Vasilakis A, McGeorge PJP, Konsolaki-Yannopoulou E, Korres G, Martlew H, Michalodimitrakis M, Özsait M, Özsait N, Papathanasiou A, Richards M, Roodenberg SA, Tzedakis Y, Arnott R, Fernandes DM, Hughey JR, Lotakis DM, Navas PA, Maniatis Y, Stamatoyannopoulos JA, Stewardson K, Stockhammer P, Pinhasi R, Reich D, Krause J, Stamatoyannopoulos G. Nature. 2017 Aug 10;548(7666):214-218. doi: 10.1038/nature23310. Epub 2017 Aug 2. PMID: 28783727.

[LindoFigueiroPNASNexus2022]:

**The genomic prehistory of the Indigenous peoples of Uruguay.**John Lindo, Rosseirys De La Rosa, Andre L C d Santos, Mónica Sans, Michael DeGiorgio, Gonzalo Figueiro, The genomic prehistory of the Indigenous peoples of Uruguay, PNAS Nexus, Volume 1, Issue 2, May 2022, pgac047, https://doi.org/10.1093/pnasnexus/pgac047.

[LindoPNAS2017]:

**Ancient individuals from the North American Northwest Coast reveal 10,000 years of regional genetic continuity.** Lindo J, Achilli A, Perego UA, Archer D, Valdiosera C, Petzelt B, Mitchell J, Worl R, Dixon EJ, Fifield TE, Rasmussen M, Willerslev E, Cybulski JS, Kemp BM, DeGiorgio M, Malhi RS. Proc Natl Acad Sci U S A. 2017 Apr 18;114(16):4093-4098. doi: 10.1073/pnas.1620410114. Epub 2017 Apr 4. PMID: 28377518.

[LindoScienceAdvances2018]:

**The genetic prehistory of the Andean highlands 7000 years BP though European contact.** Lindo J, Haas R, Hofman C, Apata M, Moraga M, Verdugo RA, Watson JT, Viviano Llave C, Witonsky D, Beall C, Warinner C, Novembre J, Aldenderfer M, Di Rienzo A. Sci Adv. 2018 Nov 8;4(11):eaau4921. doi: 10.1126/sciadv.aau4921. eCollection 2018 Nov. PMID: 30417096.

[LinderholmNatureScientificReports2020]:

**Corded Ware cultural complexity uncovered using genomic and isotopic analysis from south-eastern Poland.** Linderholm A, Kılınç GM, Szczepanek A, Włodarczak P, Jarosz P, Belka Z, Dopieralska J, Werens K, Górski J, Mazurek M, Hozer M, Rybicka M, Ostrowski M, Bagińska J, Koman W, Rodríguez-Varela R, Storå J, Götherström A, Krzewińska M. Sci Rep. 2020 Apr 14;10(1):6885. doi: 10.1038/s41598-020-63138-w. PMID: 32303690; PMCID: PMC7165176.

[LipsonSawchukNature2022]:

**Ancient DNA and deep population structure in sub-Saharan African foragers.** Lipson M, Sawchuk EA, Thompson JC, Oppenheimer J, Tryon CA, Ranhorn KL, de Luna KM, Sirak KA, Olalde I, Ambrose SH, Arthur JW, Arthur KJW, Ayodo G, Bertacchi A, Cerezo-Román JI, Culleton BJ, Curtis MC, Davis J, Gidna AO, Hanson A, Kaliba P, Katongo M, Kwekason A, Laird MF, Lewis J, Mabulla AZP, Mapemba F, Morris A, Mudenda G, Mwafulirwa R, Mwangomba D, Ndiema E, Ogola C, Schilt F, Willoughby PR, Wright DK, Zipkin A, Pinhasi R, Kennett DJ, Manthi FK, Rohland N, Patterson N, Reich D, Prendergast ME. Nature. 2022 Mar;603(7900):290-296. doi: 10.1038/s41586-022-04430-9. Epub 2022 Feb 23. PMID: 35197631; PMCID: PMC8907066.

[LipsonCurrentBiology2018]:

**Population Turnover in Remote Oceania Shortly after Initial Settlement.** Lipson M, Skoglund P, Spriggs M, Valentin F, Bedford S, Shing R, Buckley H, Phillip I, Ward GK, Mallick S, Rohland N, Broomandkhoshbacht N, Cheronet O, Ferry M, Harper TK, Michel M, Oppenheimer J, Sirak K, Stewardson K, Auckland K, Hill AVS, Maitland K, Oppenheimer SJ, Parks T, Robson K, Williams TN, Kennett DJ, Mentzer AJ, Pinhasi R, Reich D. Curr Biol. 2018 Apr 2;28(7):1157-1165.e7. doi: 10.1016/j.cub.2018.02.051. Epub 2018 Feb 28. PMID:29501328.

[LipsonCurrentBiology2020]:

**Three Phases of Ancient Migration Shaped the Ancestry of Human Populations in Vanuatu.** Lipson M, Spriggs M, Valentin F, Bedford S, Shing R, Zinger W, Buckley H, Petchey F, Matanik R, Cheronet O, Rohland N, Pinhasi R, Reich D. Three Phases of Ancient Migration Shaped the Ancestry of Human Populations in Vanuatu. Curr Biol. 2020 Dec 21;30(24):4846-4856.e6. doi: 10.1016/j.cub.2020.09.035. Epub 2020 Oct 15. PMID: 33065004; PMCID: PMC7755836.

[LipsonNature2017]:

**Parallel palaeogenomic transects reveal complex genetic history of early European farmers.** Lipson M, Szécsényi-Nagy A, Mallick S, Pósa A, Stégmár B, Keerl V, Rohland N, Stewardson K, Ferry M, Michel M, Oppenheimer J, Broomandkhoshbacht N, Harney E, Nordenfelt S, Llamas B, Gusztáv Mende B, Köhler K, Oross K, Bondár M, Marton T, Osztás A, Jakucs J, Paluch T, Horváth F, Csengeri P, Koós J, Sebők K, Anders A, Raczky P, Regenye J, Barna JP, Fábián S, Serlegi G, Toldi Z, GyÖngyvér Nagy E, Dani J, Molnár E, Pálfi G, Márk L, Melegh B, Bánfai Z, Domboróczki L, Fernández-Eraso J, Antonio Mujika-Alustiza J, Alonso Fernández C, Jiménez Echevarría J, Bollongino R, Orschiedt J, Schierhold K, Meller H, Cooper A, Burger J, Bánffy E, Alt KW, Lalueza-Fox C, Haak W, Reich D. Nature. 2017 Nov 16;551(7680):368-372. doi: 10.1038/nature24476. Epub 2017 Nov 8. PMID: 29144465.

[LipsonNature2020]:

**Ancient West African foragers in the context of African population history.** Lipson M, Ribot I, Mallick S, Rohland N, Olalde I, Adamski N, Broomandkhoshbacht N, Lawson AM, López S, Oppenheimer J, Stewardson K, Asombang RN, Bocherens H, Bradman N, Culleton BJ, Cornelissen E, Crevecoeur I, de Maret P, Fomine FLM, Lavachery P, Mindzie CM, Orban R, Sawchuk E, Semal P, Thomas MG, Van Neer W, Veeramah KR, Kennett DJ, Patterson N, Hellenthal G, Lalueza-Fox C, MacEachern S, Prendergast ME, Reich D. Nature. 2020 Jan;577(7792):665-670. doi: 10.1038/s41586-020-1929-1. Epub 2020 Jan 22. PMID: 31969706.

[LipsonScience2018]:

**Ancient genomes document multiple waves of migration in Southeast Asian prehistory.** Lipson M, Cheronet O, Mallick S, Rohland N, Oxenham M, Pietrusewsky M, Pryce TO, Willis A, Matsumura H, Buckley H, Domett K, Nguyen GH, Trinh HH, Kyaw AA, Win TT, Pradier B, Broomandkhoshbacht N, Candilio F, Changmai P, Fernandes D, Ferry M, Gamarra B, Harney E, Kampuansai J, Kutanan W, Michel M, Novak M, Oppenheimer J, Sirak K, Stewardson K, Zhang Z, Flegontov P, Pinhasi R, Reich D. Science. 2018 Jul 6;361(6397):92-95. doi: 10.1126/science.aat3188. Epub 2018 May 17. PMID: 29773666.

[LiuJeongNatComm2022]:

**Ancient genomes from the Himalayas illuminate the genetic history of Tibetans and their Tibeto-Burman speaking neighbors.** Liu CC, Witonsky D, Gosling A, Lee JH, Ringbauer H, Hagan R, Patel N, Stahl R, Novembre J, Aldenderfer M, Warinner C, Di Rienzo A, Jeong C.Nat Commun. 2022 Mar 8;13(1):1203. doi: 10.1038/s41467-022-28827-2. PMID: 35260549; PMCID: PMC8904508.

[LiuScience2022]:

**Ancient DNA reveals five streams of migration into Micronesia and matrilocality in early Pacific seafarers.** Liu YC, Hunter-Anderson R, Cheronet O, Eakin J, Camacho F, Pietrusewsky M, Rohland N, Ioannidis A, Athens JS, Douglas MT, Ikehara-Quebral RM, Bernardos R, Culleton BJ, Mah M, Adamski N, Broomandkhoshbacht N, Callan K, Lawson AM, Mandl K, Michel M, Oppenheimer J, Stewardson K, Zalzala F, Kidd K, Kidd J, Schurr TG, Auckland K, Hill AVS, Mentzer AJ, Quinto-Cortés CD, Robson K, Kennett DJ, Patterson N, Bustamante CD, Moreno-Estrada A, Spriggs M, Vilar M, Lipson M, Pinhasi R, Reich D. Science. 2022 Jul;377(6601):72-79. doi: 10.1126/science.abm6536. Epub 2022 Jun 30. PMID: 35771911.

[LlorenteScience2015]:

**Ancient Ethiopian genome reveals extensive Eurasian admixture throughout the African continent.** Gallego Llorente M, Jones ER, Eriksson A, Siska V, Arthur KW, Arthur JW, Curtis MC, Stock JT, Coltorti M, Pieruccini P, Stretton S, Brock F, Higham T, Park Y, Hofreiter M, Bradley DG, Bhak J, Pinhasi R, Manica A. Science. 2015 Nov 13;350(6262):820-2. doi: 10.1126/science.aad2879. Epub 2015 Oct 8. Erratum in: Science. 2016 Feb 19;351(6275). pii: aaf3945. doi: 10.1126/science.aaf3945. PMID: 26449472.

[MafessoniPNAS2020]:

**A high-coverage Neandertal genome from Chagyrskaya Cave.** Mafessoni F, Grote S, de Filippo C, Slon V, Kolobova KA, Viola B, Markin SV, Chintalapati M, Peyrégne S, Skov L, Skoglund P, Krivoshapkin AI, Derevianko AP, Meyer M, Kelso J, Peter B, Prüfer K, Pääbo S. Proc Natl Acad Sci U S A. 2020 Jun 30;117(26):15132-15136. doi: 10.1073/pnas.2004944117. Epub 2020 Jun 16. PMID: 32546518; PMCID: PMC7334501.

[MalaspinasCurrentBiology2014]:

**Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil.** Malaspinas AS, Lao O, Schroeder H, Rasmussen M, Raghavan M, Moltke I, Campos PF, Sagredo FS, Rasmussen S, Gonçalves VF, Albrechtsen A, Allentoft ME, Johnson PL, Li M, Reis S, Bernardo DV, DeGiorgio M, Duggan AT, Bastos M, Wang Y, Stenderup J, Moreno-Mayar JV, Brunak S, Sicheritz-Ponten T, Hodges E, Hannon GJ, Orlando L, Price TD, Jensen JD, Nielsen R, Heinemeier J, Olsen J, Rodrigues-Carvalho C, Lahr MM, Neves WA, Kayser M, Higham T, Stoneking M, Pena SD, Willerslev E. Curr Biol. 2014 Nov 3;24(21):R1035-7. doi: 10.1016/j.cub.2014.09.078. Epub 2014 Oct 23. PMID: 25455029.

[MallickNature2016]:

**The Simons Genome Diversity Project: 300 genomes from 142 diverse populations.** Mallick S, Li H, Lipson M, Mathieson I, Gymrek M, Racimo F, Zhao M, Chennagiri N, Nordenfelt S, Tandon A, Skoglund P, Lazaridis I, Sankararaman S, Fu Q, Rohland N, Renaud G, Erlich Y, Willems T, Gallo C, Spence JP, Song YS, Poletti G, Balloux F, van Driem G, de Knijff P, Romero IG, Jha AR, Behar DM, Bravi CM, Capelli C, Hervig T, Moreno-Estrada A, Posukh OL, Balanovska E, Balanovsky O, Karachanak-Yankova S, Sahakyan H, Toncheva D, Yepiskoposyan L, Tyler-Smith C, Xue Y, Abdullah MS, Ruiz-Linares A, Beall CM, Di Rienzo A, Jeong C, Starikovskaya EB, Metspalu E, Parik J, Villems R, Henn BM, Hodoglugil U, Mahley R, Sajantila A, Stamatoyannopoulos G, Wee JT, Khusainova R, Khusnutdinova E, Litvinov S, Ayodo G, Comas D, Hammer MF, Kivisild T, Klitz W, Winkler CA, Labuda D, Bamshad M, Jorde LB, Tishkoff SA, Watkins WS, Metspalu M, Dryomov S, Sukernik R, Singh L, Thangaraj K, Pääbo S, Kelso J, Patterson N, Reich D. Nature. 2016 Oct 13;538(7624):201-206. doi: 10.1038/nature18964. Epub 2016 Sep 21. PMID: 27654912.

[MalmstromProcBiolSci2019]:

**The genomic ancestry of the Scandinavian Battle Axe Culture people and their relation to the broader Corded Ware horizon.** Malmström H, Günther T, Svensson EM, Juras A, Fraser M, Munters AR, Pospieszny L , Tõrv M, Lindström J, Götherström A, Storå J, Jakobsson M. Proc Biol Sci. 2019 Oct 9;286(1912):20191528. doi: 10.1098/rspb.2019.1528. Epub 2019 Oct 9. PMID: 31594508.

[MartinianoNatureCommunications2016]:

**Genomic signals of migration and continuity in Britain before the Anglo-Saxons.** Martiniano R, Caffell A, Holst M, Hunter-Mann K, Montgomery J, Müldner G, McLaughlin RL, Teasdale MD, van Rheenen W, Veldink JH, van den Berg LH, Hardiman O, Carroll M, Roskams S, Oxley J, Morgan C, Thomas MG, Barnes I, McDonnell C, Collins MJ, Bradley DG. Nat Commun. 2016 Jan 19;7:10326. doi: 10.1038/ncomms10326. PMID: 26783717.

[MaoFuCell2021]:

**The deep population history of northern East Asia from the Late Pleistocene to the Holocene.** Mao X, Zhang H, Qiao S, Liu Y, Chang F, Xie P, Zhang M, Wang T, Li M, Cao P, Yang R, Liu F, Dai Q, Feng X, Ping W, Lei C, Olsen JW, Bennett EA, Fu Q. The deep population history of northern East Asia from the Late Pleistocene to the Holocene. Cell. 2021 Jun 10;184(12):3256-3266.e13. doi: 10.1016/j.cell.2021.04.040. Epub 2021 May 27. PMID: 34048699.

[MarchExcoffierCell2022]:

**The genomic origins of the world's first farmers world.**Marchi N, Winkelbach L, Schulz I, Brami M, Hofmanová Z, Blöcher J, Reyna-Blanco CS, Diekmann Y, Thiéry A, Kapopoulou A, Link V, Piuz V, Kreutzer S, Figarska SM, Ganiatsou E, Pukaj A, Struck TJ, Gutenkunst RN, Karul N, Gerritsen F, Pechtl J, Peters J, Zeeb-Lanz A, Lenneis E, Teschler-Nicola M, Triantaphyllou S, Stefanović S, Papageorgopoulou C, Wegmann D, Burger J, Excoffier L. The genomic origins of the world's first farmers. Cell. 2022 May 26;185(11):1842-1859.e18. doi: 10.1016/j.cell.2022.04.008. Epub 2022 May 12. PMID: 35561686; PMCID: PMC9166250.

[MarcusNatureCommunications2020]:

**Genetic history from the Middle Neolithic to present on the Mediterranean island of Sardinia.** Marcus JH, Posth C, Ringbauer H, Lai L, Skeates R, Sidore C, Beckett J, Furtwängler A, Olivieri A, Chiang CWK, Al-Asadi H, Dey K, Joseph TA, Liu CC, Der Sarkissian C, Radzevičiūtė R, Michel M, Gradoli MG, Marongiu P, Rubino S, Mazzarello V, Rovina D, La Fragola A, Serra RM, Bandiera P, Bianucci R, Pompianu E, Murgia C, Guirguis M, Orquin RP, Tuross N, van Dommelen P, Haak W, Reich D, Schlessinger D, Cucca F, Krause J, Novembre J. Nat Commun. 2020 Feb 24;11(1):939. doi: 10.1038/s41467-020-14523-6. PMID: 32094358; PMCID: PMC7039977.

[MargaryanWillerslevNature2020]:

**Population genomics of the Viking world.** Margaryan A, Lawson DJ, Sikora M, Racimo F, Rasmussen S, Moltke I, Cassidy LM, Jørsboe E, Ingason A, Pedersen MW, Korneliussen T, Wilhelmson H, Buś MM, de Barros Damgaard P, Martiniano R, Renaud G, Bhérer C, Moreno-Mayar JV, Fotakis AK, Allen M, Allmäe R, Molak M, Cappellini E, Scorrano G, McColl H, Buzhilova A, Fox A, Albrechtsen A, Schütz B, Skar B, Arcini C, Falys C, Jonson CH, Błaszczyk D, Pezhemsky D, Turner-Walker G, Gestsdóttir H, Lundstrøm I, Gustin I, Mainland I, Potekhina I, Muntoni IM, Cheng J, Stenderup J, Ma J, Gibson J, Peets J, Gustafsson J, Iversen KH, Simpson L, Strand L, Loe L, Sikora M, Florek M, Vretemark M, Redknap M, Bajka M, Pushkina T, Søvsø M, Grigoreva N, Christensen T, Kastholm O, Uldum O, Favia P, Holck P, Sten S, Arge SV, Ellingvåg S, Moiseyev V, Bogdanowicz W, Magnusson Y, Orlando L, Pentz P, Jessen MD, Pedersen A, Collard M, Bradley DG, Jørkov ML, Arneborg J, Lynnerup N, Price N, Gilbert MTP, Allentoft ME, Bill J, Sindbæk SM, Hedeager L, Kristiansen K, Nielsen R, Werge T, Willerslev E. Nature. 2020 Sep;585(7825):390-396. doi: 10.1038/s41586-020-2688-8. Epub 2020 Sep 16. PMID: 32939067.

[MarotiTorokCurrBio2022]:

**The genetic origin of Huns, Avars, and conquering Hungarians.** Maróti Z, Neparáczki E, Schütz O, Maár K, Varga GIB, Kovács B, Kalmár T, Nyerki E, Nagy I, Latinovics D, Tihanyi B, Marcsik A, Pálfi G, Bernert Z, Gallina Z, Horváth C, Varga S, Költő L, Raskó I, Nagy PL, Balogh C, Zink A, Maixner F, Götherström A, George R, Szalontai C, Szenthe G, Gáll E, Kiss AP, Gulyás B, Kovacsóczy BN, Gál SS, Tomka P, Török T. The genetic origin of Huns, Avars, and conquering Hungarians. Curr Biol. 2022 Jul 11;32(13):2858-2870.e7. doi: 10.1016/j.cub.2022.04.093. Epub 2022 May 25. PMID: 35617951.

[MartinianoPLoSGenetics2017]:

**The population genomics of archaeological transition in west Iberia: Investigation of ancient substructure using imputation and haplotype-based methods.** Martiniano R, Cassidy LM, Ó'Maoldúin R, McLaughlin R, Silva NM, Manco L, Fidalgo D, Pereira T, Coelho MJ, Serra M, Burger J, Parreira R, Moran E, Valera AC, Porfirio E, Boaventura R, Silva AM, Bradley DG. PLoS Genet. 2017 Jul 27;13(7):e1006852. doi: 10.1371/journal.pgen.1006852. eCollection 2017 Jul. PMID: 28749934.

[MassilaniPaaboScience2020]:

**Denisovan ancestry and population history of early East Asians.** Massilani D, Skov L, Hajdinjak M, Gunchinsuren B, Tseveendorj D, Yi S, Lee J, Nagel S, Nickel B, Devièse T, Higham T, Meyer M, Kelso J, Peter BM, Pääbo S. Denisovan ancestry and population history of early East Asians. Science. 2020 Oct 30;370(6516):579-583. doi: 10.1126/science.abc1166. PMID: 33122380.

[MathiesonNature2015]:

**Genome-wide patterns of selection in 230 ancient Eurasians.** Mathieson I, Lazaridis I, Rohland N, Mallick S, Patterson N, Roodenberg SA, Harney E, Stewardson K, Fernandes D, Novak M, Sirak K, Gamba C, Jones ER, Llamas B, Dryomov S, Pickrell J, Arsuaga JL, de Castro JM, Carbonell E, Gerritsen F, Khokhlov A, Kuznetsov P, Lozano M, Meller H, Mochalov O, Moiseyev V, Guerra MA, Roodenberg J, Vergès JM, Krause J, Cooper A, Alt KW, Brown D, Anthony D, Lalueza-Fox C, Haak W, Pinhasi R, Reich D. Nature. 2015 Dec 24;528(7583):499-503. doi: 10.1038/nature16152. Epub 2015 Nov 23. PMID: 26595274.

[MathiesonNature2018]:

**The genomic history of southeastern Europe.** Mathieson I, Alpaslan-Roodenberg S, Posth C, Szécsényi-Nagy A, Rohland N, Mallick S, Olalde I, Broomandkhoshbacht N, Candilio F, Cheronet O, Fernandes D, Ferry M, Gamarra B, Fortes GG, Haak W, Harney E, Jones E, Keating D, Krause-Kyora B, Kucukkalipci I, Michel M, Mittnik A, Nägele K, Novak M, Oppenheimer J, Patterson N, Pfrengle S, Sirak K, Stewardson K, Vai S, Alexandrov S, Alt KW, Andreescu R, Antonović D, Ash A, Atanassova N, Bacvarov K, Gusztáv MB, Bocherens H, Bolus M, Boroneanţ A, Boyadzhiev Y, Budnik A, Burmaz J, Chohadzhiev S, Conard NJ, Cottiaux R, Čuka M, Cupillard C, Drucker DG, Elenski N, Francken M, Galabova B, Ganetsovski G, Gély B, Hajdu T, Handzhyiska V, Harvati K, Higham T, Iliev S, Janković I, Karavanić I, Kennett DJ, Komšo D, Kozak A, Labuda D, Lari M, Lazar C, Leppek M, Leshtakov K, Vetro DL, Los D, Lozanov I, Malina M, Martini F, McSweeney K, Meller H, Menđušić M, Mirea P, Moiseyev V, Petrova V, Price TD, Simalcsik A, Sineo L, Šlaus M, Slavchev V, Stanev P, Starović A, Szeniczey T, Talamo S, Teschler-Nicola M, Thevenet C, Valchev I, Valentin F, Vasilyev S, Veljanovska F, Venelinova S, Veselovskaya E, Viola B, Virag C, Zaninović J, Zäuner S, Stockhammer PW, Catalano G, Krauß R, Caramelli D, Zariņa G, Gaydarska B, Lillie M, Nikitin AG, Potekhina I, Papathanasiou A, Borić D, Bonsall C, Krause J, Pinhasi R, Reich D. Nature. 2018 Mar 8;555(7695):197-203. doi: 10.1038/nature25778. Epub 2018 Feb 21. PMID: 29466330.

[McCollScience2018]:

**The prehistoric peopling of Southeast Asia.** McColl H, Racimo F, Vinner L, Demeter F, Gakuhari T, Moreno-Mayar JV, van Driem G, Gram Wilken U, Seguin-Orlando A, de la Fuente Castro C, Wasef S, Shoocongdej R, Souksavatdy V, Sayavongkhamdy T, Saidin MM, Allentoft ME, Sato T, Malaspinas AS, Aghakhanian FA, Korneliussen T, Prohaska A, Margaryan A, de Barros Damgaard P, Kaewsutthi S, Lertrit P, Nguyen TMH, Hung HC, Minh Tran T, Nghia Truong H, Nguyen GH, Shahidan S, Wiradnyana K, Matsumae H, Shigehara N, Yoneda M, Ishida H, Masuyama T, Yamada Y, Tajima A, Shibata H, Toyoda A, Hanihara T, Nakagome S, Deviese T, Bacon AM, Duringer P, Ponche JL, Shackelford L, Patole-Edoumba E, Nguyen AT, Bellina-Pryce B, Galipaud JC, Kinaston R, Buckley H, Pottier C, Rasmussen S, Higham T, Foley RA, Lahr MM, Orlando L, Sikora M, Phipps ME, Oota H, Higham C, Lambert DM, Willerslev E. Science. 2018 Jul 6;361(6397):88-92. doi: 10.1126/science.aat3628. PMID: 29976827.

[MeyerScience2012]:

**A high-coverage genome sequence from an archaic Denisovan individual.** Meyer M, Kircher M, Gansauge MT, Li H, Racimo F, Mallick S, Schraiber JG, Jay F, Prüfer K, de Filippo C, Sudmant PH, Alkan C, Fu Q, Do R, Rohland N, Tandon A, Siebauer M, Green RE, Bryc K, Briggs AW, Stenzel U, Dabney J, Shendure J, Kitzman J, Hammer MF, Shunkov MV, Derevianko AP, Patterson N, Andrés AM, Eichler EE, Slatkin M, Reich D, Kelso J, Pääbo S. Science. 2012 Oct 12;338(6104):222-6. doi: 10.1126/science.1224344. Epub 2012 Aug 30. PMID: 22936568.

[MittnikNatureCommunications2018]:

**The genetic prehistory of the Baltic Sea region.** Mittnik A, Wang CC, Pfrengle S, Daubaras M, Zariņa G, Hallgren F, Allmäe R, Khartanovich V, Moiseyev V, Tõrv M, Furtwängler A, Andrades Valtueña A, Feldman M, Economou C, Oinonen M, Vasks A, Balanovska E, Reich D, Jankauskas R, Haak W, Schiffels S, Krause J. Nat Commun. 2018 Jan 30;9(1):442. doi: 10.1038/s41467-018-02825-9. Erratum in: Nat Commun. 2018 Apr 11;9(1):1494. PMID: 29382937.

[MittnikScience2019]:

**Kinship-based social inequality in Bronze Age Europe.** Mittnik A, Massy K, Knipper C, Wittenborn F, Friedrich R, Pfrengle S, Burri M, Carlichi-Witjes N, Deeg H, Furtwängler A, Harbeck M, von Heyking K, Kociumaka C, Kucukkalipci I, Lindauer S, Metz S, Staskiewicz A, Thiel A, Wahl J, Haak W, Pernicka E, Schiffels S, Stockhammer PW, Krause J. Science. 2019 Nov 8;366(6466):731-734. doi: 10.1126/science.aax6219. Epub 2019 Oct 10. PMID: 31601705.

[MondalNatureGenetics2016]:

**Genomic analysis of Andamanese provides insights into ancient human migration into Asia and adaptation.** Mondal M, Casals F, Xu T, Dall'Olio GM, Pybus M, Netea MG, Comas D, Laayouni H, Li Q, Majumder PP, Bertranpetit J. Nat Genet. 2016 Sep;48(9):1066-70. doi: 10.1038/ng.3621. Epub 2016 Jul 25. PMID: 27455350.

[MootsbioRxiv2022]:

**A Genetic History of Continuity and Mobility in the Iron Age Central Mediterranean.** Hannah M. Moots, Margaret Antonio, Susanna Sawyer, Jeffrey P. Spence, Victoria Oberreiter, Clemens L. Weiß, Michaela Lucci, Yahia Mehdi Seddik Cherifi, Francesco La Pastina, Francesco Genchi, Elisa Praxmeier, Brina Zagorc, Olivia Cheronot, Kadir T. Özdoğan, Lea Demetz, Selma Amrani, Francesca Candilio, Daniela De Angelis, Gabriella Gasperetti, Daniel Fernandes, Ziyue Gao, Mounir Fantar, Alfredo Coppa, Jonathan K. Pritchard, Ron Pinhasi.

bioRxiv 2022.03.13.483276; doi: https://doi.org/10.1101/2022.03.13.483276.

[MorenoMayarNature2017]:

**Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans.** Moreno-Mayar JV, Potter BA, Vinner L, Steinrücken M, Rasmussen S, Terhorst J, Kamm JA, Albrechtsen A, Malaspinas AS, Sikora M, Reuther JD, Irish JD, Malhi RS, Orlando L, Song YS, Nielsen R, Meltzer DJ, Willerslev E. Nature. 2018 Jan 11;553(7687):203-207. doi: 10.1038/nature25173. Epub 2018 Jan 3. PMID: 29323294.

[MorenoMayarScience2018]:

**Early human dispersals within the Americas.** Moreno-Mayar JV, Vinner L, de Barros Damgaard P, de la Fuente C, Chan J, Spence JP, Allentoft ME, Vimala T, Racimo F, Pinotti T, Rasmussen S, Margaryan A, Iraeta Orbegozo M, Mylopotamitaki D, Wooller M, Bataille C, Becerra-Valdivia L, Chivall D, Comeskey D, Devièse T, Grayson DK, George L, Harry H, Alexandersen V, Primeau C, Erlandson J, Rodrigues-Carvalho C, Reis S, Bastos MQR, Cybulski J, Vullo C, Morello F, Vilar M, Wells S, Gregersen K, Hansen KL, Lynnerup N, Mirazón Lahr M, Kjær K, Strauss A, Alfonso-Durruty M, Salas A, Schroeder H, Higham T, Malhi RS, Rasic JT, Souza L, Santos FR, Malaspinas AS, Sikora M, Nielsen R, Song YS, Meltzer DJ, Willerslev E. Science. 2018 Dec 7;362(6419). pii: eaav2621. doi: 10.1126/science.aav2621. Epub 2018 Nov 8. PMID: 30409807.

[NagelePosthScience2020]:

**Genomic insights into the early peopling of the Caribbean.** Nägele K, Posth C, Iraeta Orbegozo M, Chinique de Armas Y, Hernández Godoy ST, González Herrera UM, Nieves-Colón MA, Sandoval-Velasco M, Mylopotamitaki D, Radzeviciute R, Laffoon J, Pestle WJ, Ramos-Madrigal J, Lamnidis TC, Schaffer WC, Carr RS, Day JS, Arredondo Antúnez C, Rangel Rivero A, Martínez-Fuentes AJ, Crespo-Torres E, Roksandic I, Stone AC, Lalueza-Fox C, Hoogland M, Roksandic M, Hofman CL, Krause J, Schroeder H. Science. 2020 Jul 24;369(6502):456-460. doi: 10.1126/science.aba8697. Epub 2020 Jun 4. PMID: 32499399.

[NakatsukaLuisiNatureCommunications2020]:

**Ancient genomes in South Patagonia reveal population movements associated with technological shifts and geography.** Nakatsuka N, Luisi P, Motti JMB, Salemme M, Santiago F, D'Angelo Del Campo MD, Vecchi RJ, Espinosa-Parrilla Y, Prieto A, Adamski N, Lawson AM, Harper TK, Culleton BJ, Kennett DJ, Lalueza-Fox C, Mallick S, Rohland N, Guichón RA, Cabana GS, Nores R, Reich D. Ancient genomes in South Patagonia reveal population movements associated with technological shifts and geography. Nat Commun. 2020 Aug 3;11(1):3868. doi: 10.1038/s41467-020-17656-w. PMID: 32747648; PMCID: PMC7400565.

[NakatsukaCell2020]:

**A Paleogenomic Reconstruction of the Deep Population History of the Andes.** Nakatsuka N, Lazaridis I, Barbieri C, Skoglund P, Rohland N, Mallick S, Posth C, Harkins-Kinkaid K, Ferry M, Harney É, Michel M, Stewardson K, Novak-Forst J, Capriles JM, Durruty MA, Álvarez KA, Beresford-Jones D, Burger R, Cadwallader L, Fujita R, Isla J, Lau G, Aguirre CL, LeBlanc S, Maldonado SC, Meddens F, Messineo PG, Culleton BJ, Harper TK, Quilter J, Politis G, Rademaker K, Reindel M, Rivera M, Salazar L, Sandoval JR, Santoro CM, Scheifler N, Standen V, Barreto MI, Espinoza IF, Tomasto-Cagigao E, Valverde G, Kennett DJ, Cooper A, Krause J, Haak W, Llamas B, Reich D, Fehren-Schmitz L. Cell. 2020 May 28;181(5):1131-1145.e21. doi: 10.1016/j.cell.2020.04.015. Epub 2020 May 7. PMID: 32386546; PMCID: PMC7304944.

[NarasimhanPattersonScience2019]:

**The formation of human populations in South and Central Asia.** Narasimhan VM, Patterson N, Moorjani P, Rohland N, Bernardos R, Mallick S, Lazaridis I, Nakatsuka N, Olalde I, Lipson M, Kim AM, Olivieri LM, Coppa A, Vidale M, Mallory J, Moiseyev V, Kitov E, Monge J, Adamski N, Alex N, Broomandkhoshbacht N, Candilio F, Callan K, Cheronet O, Culleton BJ, Ferry M, Fernandes D, Freilich S, Gamarra B, Gaudio D, Hajdinjak M, Harney É, Harper TK, Keating D, Lawson AM, Mah M, Mandl K, Michel M, Novak M, Oppenheimer J, Rai N, Sirak K, Slon V, Stewardson K, Zalzala F, Zhang Z, Akhatov G, Bagashev AN, Bagnera A, Baitanayev B, Bendezu-Sarmiento J, Bissembaev AA, Bonora GL, Chargynov TT, Chikisheva T, Dashkovskiy PK, Derevianko A, Dobeš M, Douka K, Dubova N, Duisengali MN, Enshin D, Epimakhov A, Fribus AV, Fuller D, Goryachev A, Gromov A, Grushin SP, Hanks B, Judd M, Kazizov E, Khokhlov A, Krygin AP, Kupriyanova E, Kuznetsov P, Luiselli D, Maksudov F, Mamedov AM, Mamirov TB, Meiklejohn C, Merrett DC, Micheli R, Mochalov O, Mustafokulov S, Nayak A, Pettener D, Potts R, Razhev D, Rykun M, Sarno S, Savenkova TM, Sikhymbaeva K, Slepchenko SM, Soltobaev OA, Stepanova N, Svyatko S, Tabaldiev K, Teschler-Nicola M, Tishkin AA, Tkachev VV, Vasilyev S, Velemínský P, Voyakin D, Yermolayeva A, Zahir M, Zubkov VS, Zubova A, Shinde VS, Lalueza-Fox C, Meyer M, Anthony D, Boivin N, Thangaraj K, Kennett DJ, Frachetti M, Pinhasi R, Reich D. Science. 2019 Sep 6;365(6457). pii: eaat7487. doi: 10.1126/science.aat7487. PMID: 31488661.

[Nieves-ColónMolecularBiologyandEvolution2020]:

**Ancient DNA Reconstructs the Genetic Legacies of Precontact Puerto Rico Communities.** Nieves-Colón MA, Pestle WJ, Reynolds AW, Llamas B, de la Fuente C, Fowler K, Skerry KM, Crespo-Torres E, Bustamante CD, Stone AC. Mol Biol Evol. 2020 Mar 1;37(3):611-626. doi: 10.1093/molbev/msz267. PMID: 31710665.

[NikitinScientificReports2019]:

**Interactions between earliest Linearbandkeramik farmers and central European hunter gatherers at the dawn of European Neolithization.** Nikitin AG, Stadler P, Kotova N, Teschler-Nicola M, Price TD, Hoover J, Kennett DJ, Lazaridis I, Rohland N, Lipson M, Reich D. Sci Rep. 2019 Dec 20;9(1):19544. doi: 10.1038/s41598-019-56029-2. PMID: 31863024.

[NingCurrentBiology2019]:

**Ancient Genomes Reveal Yamnaya-Related Ancestry and a Potential Source of Indo-European Speakers in Iron Age Tianshan.** Ning C, Wang CC, Gao S, Yang Y, Zhang X, Wu X, Zhang F, Nie Z, Tang Y, Robbeets M, Ma J, Krause J, Cui Y. Curr Biol. 2019 Aug 5;29(15):2526-2532.e4. doi: 10.1016/j.cub.2019.06.044. Epub 2019 Jul 25. PMID: 31353181.

[NingNatureCommunications2020]:

**Ancient genomes from northern China suggest links between subsistence changes and human migration.** Ning C, Li T, Wang K, Zhang F, Li T, Wu X, Gao S, Zhang Q, Zhang H, Hudson MJ, Dong G, Wu S, Fang Y, Liu C, Feng C, Li W, Han T, Li R, Wei J, Zhu Y, Zhou Y, Wang CC, Fan S, Xiong Z, Sun Z, Ye M, Sun L, Wu X, Liang F, Cao Y, Wei X, Zhu H, Zhou H, Krause J, Robbeets M, Jeong C, Cui Y. Nat Commun. 2020 Jun 1;11(1):2700. doi: 10.1038/s41467-020-16557-2. PMID: 32483115; PMCID: PMC7264253.

[NovakPLoSOne2021]:

**Genome-wide analysis of nearly all the victims of a 6200 year old massacre.** Novak M, Olalde I, Ringbauer H, Rohland N, Ahern J, Balen J, Janković I, Potrebica H, Pinhasi R, Reich D. Genome-wide analysis of nearly all the victims of a 6200 year old massacre. PLoS One. 2021 Mar 10;16(3):e0247332. doi: 10.1371/journal.pone.0247332. PMID: 33690651; PMCID: PMC7946188.

[OlaldeMBE2015]:

**A Common Genetic Origin for Early Farmers from Mediterranean Cardial and Central European LBK Cultures.** Olalde I, Schroeder H, Sandoval-Velasco M, Vinner L, Lobón I, Ramirez O, Civit S, García Borja P, Salazar-García DC, Talamo S, María Fullola J, Xavier Oms F, Pedro M, Martínez P, Sanz M, Daura J, Zilhão J, Marquès-Bonet T, Gilbert MT, Lalueza-Fox C. Mol Biol Evol. 2015 Dec;32(12):3132-42. doi: 10.1093/molbev/msv181. Epub 2015 Sep 2. PMID: 26337550.

[OlaldeNature2014]:

**Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European.** Olalde I, Allentoft ME, Sánchez-Quinto F, Santpere G, Chiang CW, DeGiorgio M, Prado-Martinez J, Rodríguez JA, Rasmussen S, Quilez J, Ramírez O, Marigorta UM, Fernández-Callejo M, Prada ME, Encinas JM, Nielsen R, Netea MG, Novembre J, Sturm RA, Sabeti P, Marquès-Bonet T, Navarro A, Willerslev E, Lalueza-Fox C. Nature. 2014 Mar 13;507(7491):225-8. doi: 10.1038/nature12960. Epub 2014 Jan 26. PMID: 24463515.

[OlaldeNature2018]:

**The Beaker phenomenon and the genomic transformation of northwest Europe.** Olalde I, Brace S, Allentoft ME, Armit I, Kristiansen K, Booth T, Rohland N, Mallick S, Szécsényi-Nagy A, Mittnik A, Altena E, Lipson M, Lazaridis I, Harper TK, Patterson N, Broomandkhoshbacht N, Diekmann Y, Faltyskova Z, Fernandes D, Ferry M, Harney E, de Knijff P, Michel M, Oppenheimer J, Stewardson K, Barclay A, Alt KW, Liesau C, Ríos P, Blasco C, Miguel JV, García RM, Fernández AA, Bánffy E, Bernabò-Brea M, Billoin D, Bonsall C, Bonsall L, Allen T, Büster L, Carver S, Navarro LC, Craig OE, Cook GT, Cunliffe B, Denaire A, Dinwiddy KE, Dodwell N, Ernée M, Evans C, Kuchařík M, Farré JF, Fowler C, Gazenbeek M, Pena RG, Haber-Uriarte M, Haduch E, Hey G, Jowett N, Knowles T, Massy K, Pfrengle S, Lefranc P, Lemercier O, Lefebvre A, Martínez CH, Olmo VG, Ramírez AB, Maurandi JL, Majó T, McKinley JI, McSweeney K, Mende BG, Modi A, KulcsáR G, Kiss V, Czene A, Patay R, Endrődi A, Köhler K, Hajdu T, Szeniczey T, Dani J, Bernert Z, Hoole M, Cheronet O, Keating D, Velemínský P, Dobeš M, Candilio F, Brown F, Fernández RF, Herrero-Corral AM, Tusa S, Carnieri E, Lentini L, Valenti A, Zanini A, Waddington C, Delibes G, Guerra-Doce E, Neil B, Brittain M, Luke M, Mortimer R, Desideri J, Besse M, Brücken G, Furmanek M, Hałuszko A, Mackiewicz M, Rapiński A, Leach S, Soriano I, Lillios KT, Cardoso JL, Pearson MP, Włodarczak P, Price TD, Prieto P, Rey PJ, Risch R, Rojo Guerra MA, Schmitt A, Serralongue J, Silva AM, Smrčka V, Vergnaud L, Zilhão J, Caramelli D, Higham T, Thomas MG, Kennett DJ, Fokkens H, Heyd V, Sheridan A, Sjögren KG, Stockhammer PW, Krause J, Pinhasi R, Haak W, Barnes I, Lalueza-Fox C, Reich D. Nature. 2018 Mar 8;555(7695):190-196. doi: 10.1038/nature25738. Epub 2018 Feb 21. Erratum in: Nature. 2018 Mar 21;555(7697):543. PMID: 29466337.

[OlaldeScience2019]:

**The genomic history of the Iberian Peninsula over the past 8000 years.** Output encoded/decoded text Olalde I, Mallick S, Patterson N, Rohland N, Villalba-Mouco V, Silva M, Dulias K, Edwards CJ, Gandini F, Pala M, Soares P, Ferrando-Bernal M, Adamski N, Broomandkhoshbacht N, Cheronet O, Culleton BJ, Fernandes D, Lawson AM, Mah M, Oppenheimer J, Stewardson K, Zhang Z, Jiménez Arenas JM, Toro Moyano IJ, Salazar-García DC, Castanyer P, Santos M, Tremoleda J, Lozano M, García Borja P, Fernández-Eraso J, Mujika-Alustiza JA, Barroso C, Bermúdez FJ, Viguera Mínguez E, Burch J, Coromina N, Vivó D, Cebrià A, Fullola JM, García-Puchol O, Morales JI, Oms FX, Majó T, Vergès JM, Díaz-Carvajal A, Ollich-Castanyer I, López-Cachero FJ, Silva AM, Alonso-Fernández C, Delibes de Castro G, Jiménez Echevarría J, Moreno-Márquez A, Pascual Berlanga G, Ramos-García P, Ramos-Muñoz J, Vijande Vila E, Aguilella Arzo G, Esparza Arroyo Á, Lillios KT, Mack J, Velasco-Vázquez J, Waterman A, Benítez de Lugo Enrich L, Benito Sánchez M, Agustí B, Codina F, de Prado G, Estalrrich A, Fernández Flores Á, Finlayson C, Finlayson G, Finlayson S, Giles-Guzmán F, Rosas A, Barciela González V, García Atiénzar G, Hernández Pérez MS, Llanos A, Carrión Marco Y, Collado Beneyto I, López-Serrano D, Sanz Tormo M, Valera AC, Blasco C, Liesau C, Ríos P, Daura J, de Pedro Michó MJ, Diez-Castillo AA, Flores Fernández R, Francès Farré J, Garrido-Pena R, Gonçalves VS, Guerra-Doce E, Herrero-Corral AM, Juan-Cabanilles J, López-Reyes D, McClure SB, Merino Pérez M, Oliver Foix A, Sanz Borràs M, Sousa AC, Vidal Encinas JM, Kennett DJ, Richards MB, Werner Alt K, Haak W, Pinhasi R, Lalueza-Fox C, Reich D. Science. 2019 Mar 15;363(6432):1230-1234. doi: 10.1126/science.aav4040. PMID: 30872528.

[OliveiraNatureEcologyEvolution2022]:

**Ancient genomes from the last three millennia support multiple human dispersals into Wallacea.** Oliveira S, Nägele K, Carlhoff S, Pugach I, Koesbardiati T, Hübner A, Meyer M, Oktaviana AA, Takenaka M, Katagiri C, Murti DB, Putri RS, Mahirta, Petchey F, Higham T, Higham CFW, O'Connor S, Hawkins S, Kinaston R, Bellwood P, Ono R, Powell A, Krause J, Posth C, Stoneking M. Ancient genomes from the last three millennia support multiple human dispersals into Wallacea. Nat Ecol Evol. 2022 Jul;6(7):1024-1034. doi: 10.1038/s41559-022-01775-2. Epub 2022 Jun 9. PMID: 35681000; PMCID: PMC9262713.

[OmrakCurrentBiology2016]:

**Genomic Evidence Establishes Anatolia as the Source of the European Neolithic Gene Pool.** Omrak A, Günther T, Valdiosera C, Svensson EM, Malmström H, Kiesewetter H, Aylward W, Storå J, Jakobsson M, Götherström A. Curr Biol. 2016 Jan 25;26(2):270-275. doi: 10.1016/j.cub.2015.12.019. Epub 2015 Dec 31. PMID: 26748850.

[PapacScienceAdvances2021]:

**Dynamic changes in genomic and social structures in third millennium BCE central Europe.** Papac L, Ernée M, Dobeš M, Langová M, Rohrlach AB, Aron F, Neumann GU, Spyrou MA, Rohland N, Velemínský P, Kuna M, Brzobohatá H, Culleton B, Daněček D, Danielisová A, Dobisíková M, Hložek J, Kennett DJ, Klementová J, Kostka M, Krištuf P, Kuchařík M, Hlavová JK, Limburský P, Malyková D, Mattiello L, Pecinovská M, Petriščáková K, Průchová E, Stránská P, Smejtek L, Špaček J, Šumberová R, Švejcar O, Trefný M, Vávra M, Kolář J, Heyd V, Krause J, Pinhasi R, Reich D, Schiffels S, Haak W. Dynamic changes in genomic and social structures in third millennium BCE central Europe. Sci Adv. 2021 Aug 25;7(35):eabi6941. doi: 10.1126/sciadv.abi6941. PMID: 34433570; PMCID: PMC8386934.

[PattersonNature2021]:

**Large-scale migration into Britain during the Middle to Late Bronze Age.** Patterson N, Isakov M, Booth T, Büster L, Fischer CE, Olalde I, Ringbauer H, Akbari A, Cheronet O, Bleasdale M, Adamski N, Altena E, Bernardos R, Brace S, Broomandkhoshbacht N, Callan K, Candilio F, Culleton B, Curtis E, Demetz L, Carlson KSD, Edwards CJ, Fernandes DM, Foody MGB, Freilich S, Goodchild H, Kearns A, Lawson AM, Lazaridis I, Mah M, Mallick S, Mandl K, Micco A, Michel M, Morante GB, Oppenheimer J, Özdoğan KT, Qiu L, Schattke C, Stewardson K, Workman JN, Zalzala F, Zhang Z, Agustí B, Allen T, Almássy K, Amkreutz L, Ash A, Baillif-Ducros C, Barclay A, Bartosiewicz L, Baxter K, Bernert Z, Blažek J, Bodružić M, Boissinot P, Bonsall C, Bradley P, Brittain M, Brookes A, Brown F, Brown L, Brunning R, Budd C, Burmaz J, Canet S, Carnicero-Cáceres S, Čaušević-Bully M, Chamberlain A, Chauvin S, Clough S, Čondić N, Coppa A, Craig O, Črešnar M, Cummings V, Czifra S, Danielisová A, Daniels R, Davies A, de Jersey P, Deacon J, Deminger C, Ditchfield PW, Dizdar M, Dobeš M, Dobisíková M, Domboróczki L, Drinkall G, Đukić A, Ernée M, Evans C, Evans J, Fernández-Götz M, Filipović S, Fitzpatrick A, Fokkens H, Fowler C, Fox A, Gallina Z, Gamble M, González Morales MR, González-Rabanal B, Green A, Gyenesei K, Habermehl D, Hajdu T, Hamilton D, Harris J, Hayden C, Hendriks J, Hernu B, Hey G, Horňák M, Ilon G, Istvánovits E, Jones AM, Kavur MB, Kazek K, Kenyon RA, Khreisheh A, Kiss V, Kleijne J, Knight M, Kootker LM, Kovács PF, Kozubová A, Kulcsár G, Kulcsár V, Le Pennec C, Legge M, Leivers M, Loe L, López-Costas O, Lord T, Los D, Lyall J, Marín-Arroyo AB, Mason P, Matošević D, Maxted A, McIntyre L, McKinley J, McSweeney K, Meijlink B, Mende BG, Menđušić M, Metlička M, Meyer S, Mihovilić K, Milasinovic L, Minnitt S, Moore J, Morley G, Mullan G, Musilová M, Neil B, Nicholls R, Novak M, Pala M, Papworth M, Paresys C, Patten R, Perkić D, Pesti K, Petit A, Petriščáková K, Pichon C, Pickard C, Pilling Z, Price TD, Radović S, Redfern R, Resutík B, Rhodes DT, Richards MB, Roberts A, Roefstra J, Sankot P, Šefčáková A, Sheridan A, Skae S, Šmolíková M, Somogyi K, Somogyvári Á, Stephens M, Szabó G, Szécsényi-Nagy A, Szeniczey T, Tabor J, Tankó K, Maria CT, Terry R, Teržan B, Teschler-Nicola M, Torres-Martínez JF, Trapp J, Turle R, Ujvári F, van der Heiden M, Veleminsky P, Veselka B, Vytlačil Z, Waddington C, Ware P, Wilkinson P, Wilson L, Wiseman R, Young E, Zaninović J, Žitňan A, Lalueza-Fox C, de Knijff P, Barnes I, Halkon P, Thomas MG, Kennett DJ, Cunliffe B, Lillie M, Rohland N, Pinhasi R, Armit I, Reich D. Nature. 2022 Jan;601(7894):588-594. doi: 10.1038/s41586-021-04287-4. Epub 2021 Dec 22. PMID: 34937049; PMCID: PMC8889665.

[PattersonGenetics2012]:

**Ancient admixture in human history.** Patterson N, Moorjani P, Luo Y, Mallick S, Rohland N, Zhan Y, Genschoreck T, Webster T, Reich D. Genetics. 2012 Nov;192(3):1065-93. doi: 10.1534/genetics.112.145037. Epub 2012 Sep 7. PMID: 22960212.

[PickrellNatureCommunications2012]:

**The genetic prehistory of southern Africa.** Pickrell JK, Patterson N, Barbieri C, Berthold F, Gerlach L, Güldemann T, Kure B, Mpoloka SW, Nakagawa H, Naumann C, Lipson M, Loh PR, Lachance J, Mountain J, Bustamante CD, Berger B, Tishkoff SA, Henn BM, Stoneking M, Reich D, Pakendorf B. Nat Commun. 2012;3:1143. doi: 10.1038/ncomms2140. PMID: 23072811.

[PopovicBacaSciAdv2021]:

**Ancient genomes reveal long-range influence of the pre-Columbian culture and site of Tiwanaku.** Popović D, Molak M, Ziółkowski M, Vranich A, Sobczyk M, Vidaurre DU, Agresti G, Skrzypczak M, Ginalski K, Lamnidis TC, Nakatsuka N, Mallick S, Baca M. Sci Adv. 2021 Sep 24;7(39):eabg7261. doi: 10.1126/sciadv.abg7261. Epub 2021 Sep 24. PMID: 34559567; PMCID: PMC8462900.

[PosthScienceAdvances2021]:

**The origin and legacy of the Etruscans through a 2000-year archeogenomic time transect.** Posth C, Zaro V, Spyrou MA, Vai S, Gnecchi-Ruscone GA, Modi A, Peltzer A, Mötsch A, Nägele K, Vågene ÅJ, Nelson EA, Radzevičiūtė R, Freund C, Bondioli LM, Cappuccini L, Frenzel H, Pacciani E, Boschin F, Capecchi G, Martini I, Moroni A, Ricci S, Sperduti A, Turchetti MA, Riga A, Zavattaro M, Zifferero A, Heyne HO, Fernández-Domínguez E, Kroonen GJ, McCormick M, Haak W, Lari M, Barbujani G, Bondioli L, Bos KI, Caramelli D, Krause J. Sci Adv. 2021 Sep 24;7(39):eabi7673. doi: 10.1126/sciadv.abi7673. Epub 2021 Sep 24. PMID: 34559560; PMCID: PMC8462907.

[PosthNakatsukaCell2018]:

**Reconstructing the Deep Population History of Central and South America.** Posth C, Nakatsuka N, Lazaridis I, Skoglund P, Mallick S, Lamnidis TC, Rohland N, Nägele K, Adamski N, Bertolini E, Broomandkhoshbacht N, Cooper A, Culleton BJ, Ferraz T, Ferry M, Furtwängler A, Haak W, Harkins K, Harper TK, Hünemeier T, Lawson AM, Llamas B, Michel M, Nelson E, Oppenheimer J, Patterson N, Schiffels S, Sedig J, Stewardson K, Talamo S, Wang CC, Hublin JJ, Hubbe M, Harvati K, Nuevo Delaunay A, Beier J, Francken M, Kaulicke P, Reyes-Centeno H, Rademaker K, Trask WR, Robinson M, Gutierrez SM, Prufer KM, Salazar-García DC, Chim EN, Müller Plumm Gomes L, Alves ML, Liryo A, Inglez M, Oliveira RE, Bernardo DV, Barioni A, Wesolowski V, Scheifler NA, Rivera MA, Plens CR, Messineo PG, Figuti L, Corach D, Scabuzzo C, Eggers S, DeBlasis P, Reindel M, Méndez C, Politis G, Tomasto-Cagigao E, Kennett DJ, Strauss A, Fehren-Schmitz L, Krause J, Reich D. Cell. 2018 Nov 15;175(5):1185-1197.e22. doi: 10.1016/j.cell.2018.10.027. Epub 2018 Nov 8. PMID: 30415837.

[PosthNatureEcologyEvolution2018]:

**Language continuity despite population replacement in Remote Oceania.** Posth C, Nägele K, Colleran H, Valentin F, Bedford S, Kami KW, Shing R, Buckley H, Kinaston R, Walworth M, Clark GR, Reepmeyer C, Flexner J, Maric T, Moser J, Gresky J, Kiko L, Robson KJ, Auckland K, Oppenheimer SJ, Hill AVS, Mentzer AJ, Zech J, Petchey F, Roberts P, Jeong C, Gray RD, Krause J, Powell A. Nat Ecol Evol. 2018 Apr;2(4):731-740. doi: 10.1038/s41559-018-0498-2. Epub 2018 Feb 27. PMID: 29487365.

[PrendergastLipsonSawchukScience2019]:

**Ancient DNA reveals a multistep spread of the first herders into sub-Saharan Africa.** Prendergast ME, Lipson M, Sawchuk EA, Olalde I, Ogola CA, Rohland N, Sirak KA, Adamski N, Bernardos R, Broomandkhoshbacht N, Callan K, Culleton BJ, Eccles L, Harper TK, Lawson AM, Mah M, Oppenheimer J, Stewardson K, Zalzala F, Ambrose SH, Ayodo G, Gates HL Jr, Gidna AO, Katongo M, Kwekason A, Mabulla AZP, Mudenda GS, Ndiema EK, Nelson C, Robertshaw P, Kennett DJ, Manthi FK, Reich D. Science. 2019 Jul 5;365(6448). pii: eaaw6275. doi: 10.1126/science.aaw6275. Epub 2019 May 30. PMID: 31147405.

[PrueferNatureEcologyEvolution2021]:

**A genome sequence from a modern human skull over 45,000 years old from Zlatý kůň in Czechia.** Prüfer K, Posth C, Yu H, Stoessel A, Spyrou MA, Deviese T, Mattonai M, Ribechini E, Higham T, Velemínský P, Brůžek J, Krause J. Nat Ecol Evol. 2021 Jun;5(6):820-825. doi: 10.1038/s41559-021-01443-x. Epub 2021 Apr 7. PMID: 33828249; PMCID: PMC8175239.

[Pruefer2017]:

**A high-coverage Neandertal genome from Vindija Cave in Croatia.** Prüfer K, de Filippo C, Grote S, Mafessoni F, Korlević P, Hajdinjak M, Vernot B, Skov L, Hsieh P, Peyrégne S, Reher D, Hopfe C, Nagel S, Maricic T, Fu Q, Theunert C, Rogers R, Skoglund P, Chintalapati M, Dannemann M, Nelson BJ, Key FM, Rudan P, Kućan Ž, Gušić I, Golovanova LV, Doronichev VB, Patterson N, Reich D, Eichler EE, Slatkin M, Schierup MH, Andrés AM, Kelso J, Meyer M, Pääbo S. Science. 2017 Nov 3;358(6363):655-658. doi: 10.1126/science.aao1887. Epub 2017 Oct 5. PMID: 28982794.

[PrueferNature2013]:

**The complete genome sequence of a Neanderthal from the Altai Mountains.** Prüfer K, Racimo F, Patterson N, Jay F, Sankararaman S, Sawyer S, Heinze A, Renaud G, Sudmant PH, de Filippo C, Li H, Mallick S, Dannemann M, Fu Q, Kircher M, Kuhlwilm M, Lachmann M, Meyer M, Ongyerth M, Siebauer M, Theunert C, Tandon A, Moorjani P, Pickrell J, Mullikin JC, Vohr SH, Green RE, Hellmann I, Johnson PL, Blanche H, Cann H, Kitzman JO, Shendure J, Eichler EE, Lein ES, Bakken TE, Golovanova LV, Doronichev VB, Shunkov MV, Derevianko AP, Viola B, Slatkin M, Reich D, Kelso J, Pääbo S. Nature. 2014 Jan 2;505(7481):43-9. doi: 10.1038/nature12886. Epub 2013 Dec 18. PMID: 24352235.

[PugachPNAS2020]:

**Ancient DNA from Guam and the peopling of the Pacific.** Pugach I, Hübner A, Hung HC, Meyer M, Carson MT, Stoneking M. Ancient DNA from Guam and the peopling of the Pacific. Proc Natl Acad Sci U S A. 2021 Jan 5;118(1):e2022112118. doi: 10.1073/pnas.2022112118. PMID: 33443177; PMCID: PMC7817125.

[RaghavanNature2013]:

**Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans.** Raghavan M, Skoglund P, Graf KE, Metspalu M, Albrechtsen A, Moltke I, Rasmussen S, Stafford TW Jr, Orlando L, Metspalu E, Karmin M, Tambets K, Rootsi S, Mägi R, Campos PF, Balanovska E, Balanovsky O, Khusnutdinova E, Litvinov S, Osipova LP, Fedorova SA, Voevoda MI, DeGiorgio M, Sicheritz-Ponten T, Brunak S, Demeshchenko S, Kivisild T, Villems R, Nielsen R, Jakobsson M, Willerslev E.

[RaghavanNature2014]:

**Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans.** Raghavan M, Skoglund P, Graf KE, Metspalu M, Albrechtsen A, Moltke I, Rasmussen S, Stafford TW Jr, Orlando L, Metspalu E, Karmin M, Tambets K, Rootsi S, Mägi R, Campos PF, Balanovska E, Balanovsky O, Khusnutdinova E, Litvinov S, Osipova LP, Fedorova SA, Voevoda MI, DeGiorgio M, Sicheritz-Ponten T, Brunak S, Demeshchenko S, Kivisild T, Villems R, Nielsen R, Jakobsson M, Willerslev E. Nature. 2014 Jan 2;505(7481):87-91. doi: 10.1038/nature12736. Epub 2013 Nov 20. PMID: 24256729.

[RaghavanScience2014]:

**The genetic prehistory of the New World Arctic.** Raghavan M, DeGiorgio M, Albrechtsen A, Moltke I, Skoglund P, Korneliussen TS, Grønnow B, Appelt M, Gulløv HC, Friesen TM, Fitzhugh W, Malmström H, Rasmussen S, Olsen J, Melchior L, Fuller BT, Fahrni SM, Stafford T Jr, Grimes V, Renouf MA, Cybulski J, Lynnerup N, Lahr MM, Britton K, Knecht R, Arneborg J, Metspalu M, Cornejo OE, Malaspinas AS, Wang Y, Rasmussen M, Raghavan V, Hansen TV, Khusnutdinova E, Pierre T, Dneprovsky K, Andreasen C, Lange H, Hayes MG, Coltrain J, Spitsyn VA, Götherström A, Orlando L, Kivisild T, Villems R, Crawford MH, Nielsen FC, Dissing J, Heinemeier J, Meldgaard M, Bustamante C, O'Rourke DH, Jakobsson M, Gilbert MT, Nielsen R, Willerslev E. Science. 2014 Aug 29;345(6200):1255832. doi: 10.1126/science.1255832. PMID: 25170159.

[RaghavanScience2015]:

**POPULATION GENETICS. Genomic evidence for the Pleistocene and recent population history of Native Americans.** Raghavan M, Steinrücken M, Harris K, Schiffels S, Rasmussen S, DeGiorgio M, Albrechtsen A, Valdiosera C, Ávila-Arcos MC, Malaspinas AS, Eriksson A, Moltke I, Metspalu M, Homburger JR, Wall J, Cornejo OE, Moreno-Mayar JV, Korneliussen TS, Pierre T, Rasmussen M, Campos PF, de Barros Damgaard P, Allentoft ME, Lindo J, Metspalu E, Rodríguez-Varela R, Mansilla J, Henrickson C, Seguin-Orlando A, Malmström H, Stafford T Jr, Shringarpure SS, Moreno-Estrada A, Karmin M, Tambets K, Bergström A, Xue Y, Warmuth V, Friend AD, Singarayer J, Valdes P, Balloux F, Leboreiro I, Vera JL, Rangel-Villalobos H, Pettener D, Luiselli D, Davis LG, Heyer E, Zollikofer CPE, Ponce de León MS, Smith CI, Grimes V, Pike KA, Deal M, Fuller BT, Arriaza B, Standen V, Luz MF, Ricaut F, Guidon N, Osipova L, Voevoda MI, Posukh OL, Balanovsky O, Lavryashina M, Bogunov Y, Khusnutdinova E, Gubina M, Balanovska E, Fedorova S, Litvinov S, Malyarchuk B, Derenko M, Mosher MJ, Archer D, Cybulski J, Petzelt B, Mitchell J, Worl R, Norman PJ, Parham P, Kemp BM, Kivisild T, Tyler-Smith C, Sandhu MS, Crawford M, Villems R, Smith DG, Waters MR, Goebel T, Johnson JR, Malhi RS, Jakobsson M, Meltzer DJ, Manica A, Durbin R, Bustamante CD, Song YS, Nielsen R, Willerslev E. Science. 2015 Aug 21;349(6250):aab3884. doi: 10.1126/science.aab3884. Epub 2015 Jul 21. PMID: 26198033.

[RasmussenNature2010]:

**Ancient human genome sequence of an extinct Palaeo-Eskimo.** Rasmussen M, Li Y, Lindgreen S, Pedersen JS, Albrechtsen A, Moltke I, Metspalu M, Metspalu E, Kivisild T, Gupta R, Bertalan M, Nielsen K, Gilbert MT, Wang Y, Raghavan M, Campos PF, Kamp HM, Wilson AS, Gledhill A, Tridico S, Bunce M, Lorenzen ED, Binladen J, Guo X, Zhao J, Zhang X, Zhang H, Li Z, Chen M, Orlando L, Kristiansen K, Bak M, Tommerup N, Bendixen C, Pierre TL, Grønnow B, Meldgaard M, Andreasen C, Fedorova SA, Osipova LP, Higham TF, Ramsey CB, Hansen TV, Nielsen FC, Crawford MH, Brunak S, Sicheritz-Pontén T, Villems R, Nielsen R, Krogh A, Wang J, Willerslev E. Nature. 2010 Feb 11;463(7282):757-62. doi: 10.1038/nature08835. PMID: 20148029.

[RasmussenNature2014]:

**The genome of a Late Pleistocene human from a Clovis burial site in western Montana.** Rasmussen M, Anzick SL, Waters MR, Skoglund P, DeGiorgio M, Stafford TW Jr, Rasmussen S, Moltke I, Albrechtsen A, Doyle SM, Poznik GD, Gudmundsdottir V, Yadav R, Malaspinas AS, White SS 5th, Allentoft ME, Cornejo OE, Tambets K, Eriksson A, Heintzman PD, Karmin M, Korneliussen TS, Meltzer DJ, Pierre TL, Stenderup J, Saag L, Warmuth VM, Lopes MC, Malhi RS, Brunak S, Sicheritz-Ponten T, Barnes I, Collins M, Orlando L, Balloux F, Manica A, Gupta R, Metspalu M, Bustamante CD, Jakobsson M, Nielsen R, Willerslev E. Nature. 2014 Feb 13;506(7487):225-9. doi: 10.1038/nature13025. PMID: 24522598.

[RasmussenNature2015]:

**The ancestry and affiliations of Kennewick Man.** Rasmussen M, Sikora M, Albrechtsen A, Korneliussen TS, Moreno-Mayar JV, Poznik GD, Zollikofer CPE, de León MP, Allentoft ME, Moltke I, Jónsson H, Valdiosera C, Malhi RS, Orlando L, Bustamante CD, Stafford TW Jr, Meltzer DJ, Nielsen R, Willerslev E. Nature. 2015 Jul 23;523(7561):455-458. doi: 10.1038/nature14625.

[ReichNature2010]:

**Genetic history of an archaic hominin group from Denisova Cave in Siberia.** Reich D, Green RE, Kircher M, Krause J, Patterson N, Durand EY, Viola B, Briggs AW, Stenzel U, Johnson PL, Maricic T, Good JM, Marques-Bonet T, Alkan C, Fu Q, Mallick S, Li H, Meyer M, Eichler EE, Stoneking M, Richards M, Talamo S, Shunkov MV, Derevianko AP, Hublin JJ, Kelso J, Slatkin M, Pääbo S. Nature. 2010 Dec 23;468(7327):1053-60. doi: 10.1038/nature09710. PMID: 21179161; PMCID: PMC4306417.

[RivollatDeguillouxPNAS2022]:

**Ancient DNA gives new insights into a Norman Neolithic monumental cemetery dedicated to male elites.** Rivollat M, Thomas A, Ghesquière E, Rohrlach AB, Späth E, Pemonge MH, Haak W, Chambon P, Deguilloux MF. Ancient DNA gives new insights into a Norman Neolithic monumental cemetery dedicated to male elites. Proc Natl Acad Sci U S A. 2022 May 3;119(18):e2120786119. doi: 10.1073/pnas.2120786119. Epub 2022 Apr 21. PMID: 35446690; PMCID: PMC9170172.

[RobbeetsNingNature2021]:

**Triangulation supports agricultural spread of the Transeurasian languages.** Robbeets M, Bouckaert R, Conte M, Savelyev A, Li T, An DI, Shinoda KI, Cui Y, Kawashima T, Kim G, Uchiyama J, Dolińska J, Oskolskaya S, Yamano KY, Seguchi N, Tomita H, Takamiya H, Kanzawa-Kiriyama H, Oota H, Ishida H, Kimura R, Sato T, Kim JH, Deng B, Bjørn R, Rhee S, Ahn KD, Gruntov I, Mazo O, Bentley JR, Fernandes R, Roberts P, Bausch IR, Gilaizeau L, Yoneda M, Kugai M, Bianco RA, Zhang F, Himmel M, Hudson MJ, Ning C. TNature. 2021 Nov;599(7886):616-621. doi: 10.1038/s41586-021-04108-8. Epub 2021 Nov 10. PMID: 34759322; PMCID: PMC8612925.

[RodriguezVarelaCurrentBiology2017]:

**Genomic Analyses of Pre-European Conquest Human Remains from the Canary Islands Reveal Close Affinity to Modern North Africans.** Rodríguez-Varela R, Günther T, Krzewińska M, Storå J, Gillingwater TH, MacCallum M, Arsuaga JL, Dobney K, Valdiosera C, Jakobsson M, Götherström A, Girdland-Flink L. Curr Biol. 2017 Nov 6;27(21):3396-3402.e5. doi: 10.1016/j.cub.2017.09.059. Epub 2017 Oct 26. Erratum in: Curr Biol. 2018 May 21;28(10 ):1677-1679. PMID: 29107554.

[RivollatScienceAdvance2020]:

**Ancient genome-wide DNA from France highlights the complexity of interactions between Mesolithic hunter-gatherers and Neolithic farmers.** Rivollat M, Jeong C, Schiffels S, Küçükkalıpçı İ, Pemonge MH, Rohrlach AB, Alt KW, Binder D, Friederich S, Ghesquière E, Gronenborn D, Laporte L, Lefranc P, Meller H, Réveillas H, Rosenstock E, Rottier S, Scarre C, Soler L, Wahl J, Krause J, Deguilloux MF, Haak W. Sci Adv. 2020 May 29;6(22):eaaz5344. doi: 10.1126/sciadv.aaz5344. PMID: 32523989; PMCID: PMC7259947.

[SaagCurrentBiology2017]:

**Extensive Farming in Estonia Started through a Sex-Biased Migration from the Steppe.** Saag L, Varul L, Scheib CL, Stenderup J, Allentoft ME, Saag L, Pagani L, Reidla M, Tambets K, Metspalu E, Kriiska A, Willerslev E, Kivisild T, Metspalu M.Curr Biol. 2017 Jul 24;27(14):2185-2193.e6. doi: 10.1016/j.cub.2017.06.022. Epub 2017 Jul 14. PMID: 28712569.

[SaagCurrentBiology2019]:

**The Arrival of Siberian Ancestry Connecting the Eastern Baltic to Uralic Speakers further East.** Saag L, Laneman M, Varul L, Malve M, Valk H, Razzak MA, Shirobokov IG, Khartanovich VI, Mikhaylova ER, Kushniarevich A, Scheib CL, Solnik A, Reisberg T, Parik J, Saag L, Metspalu E, Rootsi S, Montinaro F, Remm M, Mägi R, D'Atanasio E, Crema ER, D'Atanasio E, Crema ER, Díez-Del-Molino D, Thomas MG, Kriiska A, Kivisild T, Villems R, Lang V, Metspalu M, Tambets K. Curr Biol. 2019 May 20;29(10):1701-1711.e16. doi: 10.1016/j.cub.2019.04.026. Epub 2019 May 9. PMID: 31080083.

[SaagMetspaluScience2021]:

**Genetic ancestry changes in Stone to Bronze Age transition in the East European plain.** Saag L, Vasilyev SV, Varul L, Kosorukova NV, Gerasimov DV, Oshibkina SV, Griffith SJ, Solnik A, Saag L, D'Atanasio E, Metspalu E, Reidla M, Rootsi S, Kivisild T, Scheib CL, Tambets K, Kriiska A, Metspalu M. Genetic ancestry changes in Stone to Bronze Age transition in the East European plain. Sci Adv. 2021 Jan 20;7(4):eabd6535. doi: 10.1126/sciadv.abd6535. PMID: 33523926; PMCID: PMC7817100.

[ScheibAnnHumBio2019]:

**East Anglian early Neolithic monument burial linked to contemporary Megaliths.** Scheib CL, Hui R, D'Atanasio E, Wohns AW, Inskip SA, Rose A, Cessford C, O'Connell TC, Robb JE, Evans C, Patten R, Kivisild T. East Anglian early Neolithic monument burial linked to contemporary Megaliths. Ann Hum Biol. 2019 Mar;46(2):145-149. doi: 10.1080/03014460.2019.1623912. PMID: 31184205; PMCID: PMC6816495.

[ScheibScience2018]:

**Ancient human parallel lineages within North America contributed to a coastal expansion.** Scheib CL, Li H, Desai T, Link V, Kendall C, Dewar G, Griffith PW, Mörseburg A, Johnson JR, Potter A, Kerr SL, Endicott P, Lindo J, Haber M, Xue Y, Tyler-Smith C, Sandhu MS, Lorenz JG, Randall TD, Faltyskova Z, Pagani L, Danecek P, O'Connell TC, Martz P, Boraas AS, Byrd BF, Leventhal A, Cambra R, Williamson R, Lesage L, Holguin B, Ygnacio-De Soto E, Rosas J, Metspalu M, Stock JT, Manica A, Scally A, Wegmann D, Malhi RS, Kivisild T. Science. 2018 Jun 1;360(6392):1024-1027. doi: 10.1126/science.aar6851. PMID: 29853687.

[SanchezQuintoPNAS2019]:

**Megalithic tombs in western and northern Neolithic Europe were linked to a kindred society.** Sánchez-Quinto F, Malmström H, Fraser M, Girdland-Flink L, Svensson EM, Simões LG, George R, Hollfelder N, Burenhult G, Noble G, Britton K, Talamo S, Curtis N, Brzobohata H, Sumberova R, Götherström A, Storå J, Jakobsson M. Proc Natl Acad Sci U S A. 2019 May 7;116(19):9469-9474. doi: 10.1073/pnas.1818037116. Epub 2019 Apr 15. PMID: 30988179.

[SaupeScheibCurrBio2021]:

**Ancient genomes reveal structural shifts after the arrival of Steppe-related ancestry in the Italian Peninsula.** Saupe T, Montinaro F, Scaggion C, Carrara N, Kivisild T, D'Atanasio E, Hui R, Solnik A, Lebrasseur O, Larson G, Alessandri L, Arienzo I, De Angelis F, Rolfo MF, Skeates R, Silvestri L, Beckett J, Talamo S, Dolfini A, Miari M, Metspalu M, Benazzi S, Capelli C, Pagani L, Scheib CL. Curr Biol. 2021 Jun 21;31(12):2576-2591.e12. doi: 10.1016/j.cub.2021.04.022. Epub 2021 May 10. PMID: 33974848.

[ScheunemannNatureCommunications2017]:

**Ancient Egyptian mummy genomes suggest an increase of Sub-Saharan African ancestry in post-Roman periods.** Schuenemann VJ, Peltzer A, Welte B, van Pelt WP, Molak M, Wang CC, Furtwängler A, Urban C, Reiter E, Nieselt K, Teßmann B, Francken M, Harvati K, Haak W, Schiffels S, Krause J. Nat Commun. 2017 May 30;8:15694. doi: 10.1038/ncomms15694. PMID: 28556824.

[SchiffelsNatureCommunications2016]:

**Iron Age and Anglo-Saxon genomes from East England reveal British migration history.** Schiffels S, Haak W, Paajanen P, Llamas B, Popescu E, Loe L, Clarke R, Lyons A, Mortimer R, Sayer D, Tyler-Smith C, Cooper A, Durbin R. Nat Commun. 2016 Jan 19;7:10408. doi: 10.1038/ncomms10408. PMID: 26783965.

[SchlebuschScience2017]:

**Southern African ancient genomes estimate modern human divergence to 350,000 to 260,000 years ago.** Schlebusch CM, Malmström H, Günther T, Sjödin P, Coutinho A, Edlund H, Munters AR, Vicente M, Steyn M, Soodyall H, Lombard M, Jakobsson M. Science. 2017 Nov 3;358(6363):652-655. doi: 10.1126/science.aao6266. Epub 2017 Sep 28. PMID: 28971970.

[SchroederPNAS2018]:

**Origins and genetic legacies of the Caribbean Taino.** Schroeder H, Sikora M, Gopalakrishnan S, Cassidy LM, Maisano Delser P, Sandoval Velasco M, Schraiber JG, Rasmussen S, Homburger JR, Ávila-Arcos MC, Allentoft ME, Moreno-Mayar JV, Renaud G, Gómez-Carballa A, Laffoon JE, Hopkins RJA, Higham TFG, Carr RS, Schaffer WC, Day JS, Hoogland M, Salas A, Bustamante CD, Nielsen R, Bradley DG, Hofman CL, Willerslev E. Proc Natl Acad Sci U S A. 2018 Mar 6;115(10):2341-2346. doi: 10.1073/pnas.1716839115. Epub 2018 Feb 20. PMID: 29463742.

[SchroederPNAS2019]:

**Unraveling ancestry, kinship, and violence in a Late Neolithic mass grave.** Schroeder H, Margaryan A, Szmyt M, Theulot B, Wlodarczak P, Rasmussen S, Gopalakrishnan S, Szczepanek A, Konopka T, Jensen TZT, Witkowska B, Wilk S, Przybyla MM, Pospieszny L, Sjögren KG, Belka Z, Olsen J, Kristiansen K, Willerslev E, Frei KM, Sikora M, Johannsen NN, Allentoft ME. Proc Natl Acad Sci U S A. 2019 May 28;116(22):10705-10710. doi: 10.1073/pnas.1820210116. Epub 2019 May 6. PMID: 31061125.

[ScorranoMacciardiSciRep2022]:

**Bioarchaeological and palaeogenomic portrait of two Pompeians that died during the eruption of Vesuvius in 79 AD.** Scorrano G, Viva S, Pinotti T, Fabbri PF, Rickards O, Macciardi F. Bioarchaeological and palaeogenomic portrait of two Pompeians that died during the eruption of Vesuvius in 79 AD. Sci Rep. 2022 May 26;12(1):6468. doi: 10.1038/s41598-022-10899-1. PMID: 35618734; PMCID: PMC9135728.

[SeguinOrlandoCurrBio2021]:

**Heterogeneous Hunter-Gatherer and Steppe-Related Ancestries in Late Neolithic and Bell Beaker Genomes from Present-Day France.** Seguin-Orlando A, Donat R, Der Sarkissian C, Southon J, Thèves C, Manen C, Tchérémissinoff Y, Crubézy E, Shapiro B, Deleuze JF, Dalén L, Guilaine J, Orlando L. Heterogeneous Hunter-Gatherer and Steppe-Related Ancestries in Late Neolithic and Bell Beaker Genomes from Present-Day France. Curr Biol. 2021 Mar 8;31(5):1072-1083.e10. doi: 10.1016/j.cub.2020.12.015. PMID: 33434506.

[Seguin-OrlandoScience2014]:odarczak P, Rasmussen S, Gopalakrishnan S, Szczepanek A, Konopka T, Jensen TZT, Witkowska B, Wilk S, Przybya MM, Pospieszny

**Paleogenomics. Genomic structure in Europeans dating back at least 36,200 years.** Seguin-Orlando A, Korneliussen TS, Sikora M, Malaspinas AS, Manica A, Moltke I, Albrechtsen A, Ko A, Margaryan A, Moiseyev V, Goebel T, Westaway M, Lambert D, Khartanovich V, Wall JD, Nigst PR, Foley RA, Lahr MM, Nielsen R, Orlando L, Willerslev E. Science. 2014 Nov 28;346(6213):1113-8. doi: 10.1126/science.aaa0114. Epub 2014 Nov 6. PMID: 25378462.

[ShindeNarasimhanCell2019]:

**An Ancient Harappan Genome Lacks Ancestry from Steppe Pastoralists or Iranian Farmers.** Shinde V, Narasimhan VM, Rohland N, Mallick S, Mah M, Lipson M, Nakatsuka N, Adamski N, Broomandkhoshbacht N, Ferry M, Lawson AM, Michel M, Oppenheimer J, Stewardson K, Jadhav N, Kim YJ, Chatterjee M, Munshi A, Panyam A, Waghmare P, Yadav Y, Patel H, Kaushik A, Thangaraj K, Meyer M, Patterson N, Rai N, Reich D. Cell. 2019 Oct 17;179(3):729-735.e10. doi: 10.1016/j.cell.2019.08.048. Epub 2019 Sep 5. PMID: 31495572.

[SikoraNature2019]:

**The population history of northeastern Siberia since the Pleistocene.** Sikora M, Pitulko VV, Sousa VC, Allentoft ME, Vinner L, Rasmussen S, Margaryan A, de Barros Damgaard P, de la Fuente C, Renaud G, Yang MA, Fu Q, Dupanloup I, Giampoudakis K, Nogués-Bravo D, Rahbek C, Kroonen G, Peyrot M, McColl H, Vasilyev SV, Veselovskaya E, Gerasimova M, Pavlova EY, Chasnyk VG, Nikolskiy PA, Gromov AV, Khartanovich VI, Moiseyev V, Grebenyuk PS, Fedorchenko AY, Lebedintsev AI, Slobodin SB, Malyarchuk BA, Martiniano R, Meldgaard M, Arppe L, Palo JU, Sundell T, Mannermaa K, Putkonen M, Alexandersen V, Primeau C, Baimukhanov N, Malhi RS, Sjögren KG, Kristiansen K, Wessman A, Sajantila A, Lahr MM, Durbin R, Nielsen R, Meltzer DJ, Excoffier L, Willerslev E. Nature. 2019 Jun;570(7760):182-188. doi: 10.1038/s41586-019-1279-z. Epub 2019 Jun 5. PMID: 31168093.

[SikoraScience2017]:

**Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers.** Sikora M, Seguin-Orlando A, Sousa VC, Albrechtsen A, Korneliussen T, Ko A, Rasmussen S, Dupanloup I, Nigst PR, Bosch MD, Renaud G, Allentoft ME, Margaryan A, Vasilyev SV, Veselovskaya EV, Borutskaya SB, Deviese T, Comeskey D, Higham T, Manica A, Foley R, Meltzer DJ, Nielsen R, Excoffier L, Mirazon Lahr M, Orlando L, Willerslev E. Science. 2017 Nov 3;358(6363):659-662. doi: 10.1126/science.aao1807. Epub 2017 Oct 5.

[SilvaRichardsSciRep2021]:

**Biomolecular insights into North African-related ancestry, mobility and diet in eleventh-century Al-Andalus.** Silva M, Oteo-García G, Martiniano R, Guimarães J, von Tersch M, Madour A, Shoeib T, Fichera A, Justeau P, Foody MGB, McGrath K, Barrachina A, Palomar V, Dulias K, Yau B, Gandini F, Clarke DJ, Rosa A, Brehm A, Flaquer A, Rito T, Olivieri A, Achilli A, Torroni A, Gómez-Carballa A, Salas A, Bryk J, Ditchfield PW, Alexander M, Pala M, Soares PA, Edwards CJ, Richards MB. Biomolecular insights into North African-related ancestry, mobility and diet in eleventh-century Al-Andalus. Sci Rep. 2021 Sep 13;11(1):18121. doi: 10.1038/s41598-021-95996-3. PMID: 34518562; PMCID: PMC8438022.

[SirakNatureCommunications2021]:

**Social stratification without genetic differentiation at the site of Kulubnarti in Christian Period Nubia.** Sirak KA, Fernandes DM, Lipson M, Mallick S, Mah M, Olalde I, Ringbauer H, Rohland N, Hadden CS, Harney É, Adamski N, Bernardos R, Broomandkhoshbacht N, Callan K, Ferry M, Lawson AM, Michel M, Oppenheimer J, Stewardson K, Zalzala F, Patterson N, Pinhasi R, Thompson JC, Van Gerven D, Reich D. Nat Commun. 2021 Dec 14;12(1):7283. doi: 10.1038/s41467-021-27356-8. PMID: 34907168; PMCID: PMC8671435.

[SiskaScienceAdvances2017]:

**Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers.** Sikora M, Seguin-Orlando A, Sousa VC, Albrechtsen A, Korneliussen T, Ko A, Rasmussen S, Dupanloup I, Nigst PR, Bosch MD, Renaud G, Allentoft ME, Margaryan A, Vasilyev SV, Veselovskaya EV, Borutskaya SB, Deviese T, Comeskey D, Higham T, Manica A, Foley R, Meltzer DJ, Nielsen R, Excoffier L, Mirazon Lahr M, Orlando L, Willerslev E. Science. 2017 Nov 3;358(6363):659-662. doi: 10.1126/science.aao1807. Epub 2017 Oct 5. PMID: 28982795.

[SkoglundCell2017]:

**Reconstructing Prehistoric African Population Structure.** Skoglund P, Thompson JC, Prendergast ME, Mittnik A, Sirak K, Hajdinjak M, Salie T, Rohland N, Mallick S, Peltzer A, Heinze A, Olalde I, Ferry M, Harney E, Michel M, Stewardson K, Cerezo-Román JI, Chiumia C, Crowther A, Gomani-Chindebvu E, Gidna AO, Grillo KM, Helenius IT, Hellenthal G, Helm R, Horton M, López S, Mabulla AZP, Parkington J, Shipton C, Thomas MG, Tibesasa R, Welling M, Hayes VM, Kennett DJ, Ramesar R, Meyer M, Pääbo S, Patterson N, Morris AG, Boivin N, Pinhasi R, Krause J, Reich D. Cell. 2017 Sep 21;171(1):59-71.e21. doi: 10.1016/j.cell.2017.08.049. PMID: 28938123.

[SkoglundNature2015]:

**Genetic evidence for two founding populations of the Americas.** Skoglund P, Mallick S, Bortolini MC, Chennagiri N, Hünemeier T, Petzl-Erler ML, Salzano FM, Patterson N, Reich D. Nature. 2015 Sep 3;525(7567):104-8. doi: 10.1038/nature14895. Epub 2015 Jul 21. PMID: 26196601.

[SkoglundNature2016]:

**Genomic insights into the peopling of the Southwest Pacific.** Skoglund P, Posth C, Sirak K, Spriggs M, Valentin F, Bedford S, Clark GR, Reepmeyer C, Petchey F, Fernandes D, Fu Q, Harney E, Lipson M, Mallick S, Novak M, Rohland N, Stewardson K, Abdullah S, Cox MP, Friedlaender FR, Friedlaender JS, Kivisild T, Koki G, Kusuma P, Merriwether DA, Ricaut FX, Wee JT, Patterson N, Krause J, Pinhasi R, Reich D. Nature. 2016 Oct 27;538(7626):510-513. doi: 10.1038/nature19844. Epub 2016 Oct 3. PMID: 27698418.

[SkoglundScience2014]:

**Genomic diversity and admixture differs for Stone-Age Scandinavian foragers and farmers.** Skoglund P, Malmström H, Omrak A, Raghavan M, Valdiosera C, Günther T, Hall P, Tambets K, Parik J, Sjögren KG, Apel J, Willerslev E, Storå J, Götherström A, Jakobsson M. Science. 2014 May 16;344(6185):747-50. doi: 10.1126/science.1253448. Epub 2014 Apr 24. PMID: 24762536.

[SkourtaniotiCell2020]:

**Genomic History of Neolithic to Bronze Age Anatolia, Northern Levant, and Southern Caucasus.** Skourtanioti E, Erdal YS, Frangipane M, Balossi Restelli F, Yener KA, Pinnock F, Matthiae P, Özbal R, Schoop UD, Guliyev F, Akhundov T, Lyonnet B, Hammer EL, Nugent SE, Burri M, Neumann GU, Penske S, Ingman T, Akar M, Shafiq R, Palumbi G, Eisenmann S, D'Andrea M, Rohrlach AB, Warinner C, Jeong C, Stockhammer PW, Haak W, Krause J. Cell. 2020 May 28;181(5):1158-1175.e28. doi: 10.1016/j.cell.2020.04.044. PMID: 32470401.

[SlonNature2018]:

**The genome of the offspring of a Neanderthal mother and a Denisovan father.** Slon V, Mafessoni F, Vernot B, de Filippo C, Grote S, Viola B, Hajdinjak M, Peyrégne S, Nagel S, Brown S, Douka K, Higham T, Kozlikin MB, Shunkov MV, Derevianko AP, Kelso J, Meyer M, Prüfer K, Pääbo S.Nature. 2018 Sep;561(7721):113-116. doi: 10.1038/s41586-018-0455-x. Epub 2018 Aug 22. PMID: 30135579.

[SpyrouNature2022]:

**The source of the Black Death in fourteenth-century central Eurasia.** Spyrou MA, Musralina L, Gnecchi Ruscone GA, Kocher A, Borbone PG, Khartanovich VI, Buzhilova A, Djansugurova L, Bos KI, Kühnert D, Haak W, Slavin P, Krause J. The source of the Black Death in fourteenth-century central Eurasia. Nature. 2022 Jun;606(7915):718-724. doi: 10.1038/s41586-022-04800-3. Epub 2022 Jun 15. PMID: 35705810; PMCID: PMC9217749.

[SrigyanValdioseraCommBio2022]:

**Bioarchaeological evidence of one of the earliest Islamic burials in the Levant.** Srigyan M, Bolívar H, Ureña I, Santana J, Petersen A, Iriarte E, Kırdök E, Bergfeldt N, Mora A, Jakobsson M, Abdo K, Braemer F, Smith C, Ibañez JJ, Götherström A, Günther T, Valdiosera C. Bioarchaeological evidence of one of the earliest Islamic burials in the Levant. Commun Biol. 2022 Jun 7;5(1):554. doi: 10.1038/s42003-022-03508-4. PMID: 35672445; PMCID: PMC9174286.

[SullivanScienceAdvances2018]:

**Ancient genome-wide analyses infer kinship structure in an Early Medieval Alemannic graveyard.** O'Sullivan N, Posth C, Coia V, Schuenemann VJ, Price TD, Wahl J, Pinhasi R, Zink A, Krause J, Maixner F. Sci Adv. 2018 Sep 5;4(9):eaao1262. doi: 10.1126/sciadv.aao1262. PMID: 30191172; PMCID: PMC6124919.

[SvenssonJakobssonCurrBio2021]:

**Genome of Peştera Muierii skull shows high diversity and low mutational load in pre-glacial Europe.** Svensson E, Günther T, Hoischen A, Hervella M, Munters AR, Ioana M, Ridiche F, Edlund H, van Deuren RC, Soficaru A, de-la-Rua C, Netea MG, Jakobsson M. Genome of Peştera Muierii skull shows high diversity and low mutational load in pre-glacial Europe. Curr Biol. 2021 Jul 26;31(14):2973-2983.e9. doi: 10.1016/j.cub.2021.04.045. Epub 2021 May 18. PMID: 34010592.

[TeschlerNicolaCommunicationsBiology2020]:

**Ancient DNA reveals monozygotic newborn twins from the Upper Palaeolithic.** Teschler-Nicola M, Fernandes D, Händel M, Einwögerer T, Simon U, Neugebauer-Maresch C, Tangl S, Heimel P, Dobsak T, Retzmann A, Prohaska T, Irrgeher J, Kennett DJ, Olalde I, Reich D, Pinhasi R. Commun Biol. 2020 Nov 6;3(1):650. doi: 10.1038/s42003-020-01372-8. PMID: 33159107; PMCID: PMC7648643.

[TieslerSedigAntiquity2022]:

**Life and death in early colonial Campeche: New insights from ancient DNA.** Tiesler, V., Sedig, J., Nakatsuka, N., Mallick, S., Lazaridis, I., Bernardos, R., Broomandkhoshbacht , N., Oppenheimer, J., Marie Lawson, A., Stewardson, K., Rohland, N., Kennett, D., Price, T., Reich, D. (2022). Antiquity, 96(388), 937-954. doi:10.15184/aqy.2022.79

[UllingerNearEasternArchaeology2022]:

**A Bioarchaeological Investigation of Fraternal Stillborn Twins from Tell el-Hesi.** Jaime Ullinger, Lesley Gregoricka, Rebecca Bernardos, David Reich, Amel Langston, Paige Ferreri, and Brittney Ingram (2022). Near Eastern Archaelogy 85:3, doi: https://doi.org/10.1086/720748.

[UnterlanderNatureCommunications2017]:

**Ancestry and demography and descendants of Iron Age nomads of the Eurasian Steppe.** Unterländer M, Palstra F, Lazaridis I, Pilipenko A, Hofmanová Z, Groß M, Sell C, Blöcher J, Kirsanow K, Rohland N, Rieger B, Kaiser E, Schier W, Pozdniakov D, Khokhlov A, Georges M, Wilde S, Powell A, Heyer E, Currat M, Reich D, Samashev Z, Parzinger H, Molodin VI, Burger J. Nat Commun. 2017 Mar 3;8:14615. doi: 10.1038/ncomms14615. PMID: 28256537.

[ValdioseraPNAS2018]:

**Four millennia of Iberian biomolecular prehistory illustrate the impact of prehistoric migrations at the far end of Eurasia.** Valdiosera C, Günther T, Vera-Rodríguez JC, Ureña I, Iriarte E, Rodríguez-Varela R, Simões LG, Martínez-Sánchez RM, Svensson EM, Malmström H, Rodríguez L, Bermúdez de Castro JM, Carbonell E, Alday A, Hernández Vera JA, Götherström A, Carretero JM, Arsuaga JL, Smith CI, Jakobsson M. Proc Natl Acad Sci U S A. 2018 Mar 27;115(13):3428-3433. doi: 10.1073/pnas.1717762115. Epub 2018 Mar 12. PMID: 29531053.

[vandeLoosdrechtScience2018]:

**Pleistocene North African genomes link Near Eastern and sub-Saharan African human populations.** van de Loosdrecht M, Bouzouggar A, Humphrey L, Posth C, Barton N, Aximu-Petri A, Nickel B, Nagel S, Talbi EH, El Hajraoui MA, Amzazi S, Hublin JJ, Pääbo S, Schiffels S, Meyer M, Haak W, Jeong C, Krause J. Science. 2018 May 4;360(6388):548-552. doi: 10.1126/science.aar8380. Epub 2018 Mar 15.

[VanDenBrink2017]:

**A Late Bronze Age II clay coffin from Tel Shaddudin the Central Jezreel Valley, Israel: context andhistorical implications.** Edwin C. M. van den Brink, Ron Beeri, Dan Kirzner, Enno Bron, Anat Cohen-Weinberger, Elisheva Kamaisky, Tamar Gonen, Lilly Gershuny, Yossi Nagar, Daphna Ben-Tor,Naama Sukenik, Orit Shamir, Edward F. Maher & David Reich Levant, 49:2, 105-135, DOI:10.1080/00758914.2017.1368204.

[VeeramahPNAS2018]:

**Population genomic analysis of elongated skulls reveals extensive female-biased immigration in Early Medieval Bavaria.** Veeramah KR, Rott A, Groß M, van Dorp L, López S, Kirsanow K, Sell C, Blöcher J, Wegmann D, Link V, Hofmanová Z, Peters J, Trautmann B, Gairhos A, Haberstroh J, Päffgen B, Hellenthal G, Haas-Gebhard B, Harbeck M, Burger J. Proc Natl Acad Sci U S A. 2018 Mar 27;115(13):3494-3499. doi: 10.1073/pnas.1719880115. Epub 2018 Mar 12. pPMID: 29531040.

[VillalbaMoucoSciAdv2021]:

**Genomic transformation and social organization during the Copper Age-Bronze Age transition in southern Iberia.** Villalba-Mouco V, Oliart C, Rihuete-Herrada C, Childebayeva A, Rohrlach AB, Fregeiro MI, Celdrán Beltrán E, Velasco-Felipe C, Aron F, Himmel M, Freund C, Alt KW, Salazar-García DC, García Atiénzar G, de Miguel Ibáñez MP, Hernández Pérez MS, Barciela V, Romero A, Ponce J, Martínez A, Lomba J, Soler J, Martínez AP, Avilés Fernández A, Haber-Uriarte M, Roca de Togores Muñoz C, Olalde I, Lalueza-Fox C, Reich D, Krause J, García Sanjuán L, Lull V, Micó R, Risch R, Haak W. Sci Adv. 2021 Nov 19;7(47):eabi7038. doi: 10.1126/sciadv.abi7038. Epub 2021 Nov 17. PMID: 34788096; PMCID: PMC8597998.

[VillalbaMoucoCurrentBiology2019]:

**Survival of Late Pleistocene Hunter-Gatherer Ancestry in the Iberian Peninsula.** Villalba-Mouco V, van de Loosdrecht MS, Posth C, Mora R, Martínez-Moreno J, Rojo-Guerra M, Salazar-García DC, Royo-Guillén JI, Kunst M, Rougier H, Crevecoeur I, Arcusa-Magallón H, Tejedor-Rodríguez C, García-Martínez de Lagrán I, Garrido-Pena R, Alt KW, Jeong C, Schiffels S, Utrilla P, Krause J, Haak W. Survival of Late Pleistocene Hunter-Gatherer Ancestry in the Iberian Peninsula. Curr Biol. 2019 Apr 1;29(7):1169-1177.e7. doi: 10.1016/j.cub.2019.02.006. Epub 2019 Mar 14. PMID: 30880015.

[VyasAJPA2017/VyasDryadDigitalRepository2017]:

**Testing support for the northern and southern dispersal routes out of Africa: an analysis of Levantine and southern Arabian populations.** Vyas DN, Al-Meeri A, Mulligan CJ. Am J Phys Anthropol. 2017 Dec;164(4):736-749. doi: 10.1002/ajpa.23312. Epub 2017 Sep 15. PMID: 28913852.

[WangCell2021]:

**Human population history at the crossroads of East and Southeast Asia since 11,000 years ago.** Wang T, Wang W, Xie G, Li Z, Fan X, Yang Q, Wu X, Cao P, Liu Y, Yang R, Liu F, Dai Q, Feng X, Wu X, Qin L, Li F, Ping W, Zhang L, Zhang M, Liu Y, Chen X, Zhang D, Zhou Z, Wu Y, Shafiey H, Gao X, Curnoe D, Mao X, Bennett EA, Ji X, Yang MA, Fu Q. Human population history at the crossroads of East and Southeast Asia since 11,000 years ago. Cell. 2021 Jul 8;184(14):3829-3841.e21. doi: 10.1016/j.cell.2021.05.018. Epub 2021 Jun 24. PMID: 34171307.

[WangNature2021]:

**Genomic insights into the formation of human populations in East Asia.** Wang CC, Yeh HY, Popov AN, Zhang HQ, Matsumura H, Sirak K, Cheronet O, Kovalev A, Rohland N, Kim AM, Mallick S, Bernardos R, Tumen D, Zhao J, Liu YC, Liu JY, Mah M, Wang K, Zhang Z, Adamski N, Broomandkhoshbacht N, Callan K, Candilio F, Carlson KSD, Culleton BJ, Eccles L, Freilich S, Keating D, Lawson AM, Mandl K, Michel M, Oppenheimer J, Özdoğan KT, Stewardson K, Wen S, Yan S, Zalzala F, Chuang R, Huang CJ, Looh H, Shiung CC, Nikitin YG, Tabarev AV, Tishkin AA, Lin S, Sun ZY, Wu XM, Yang TL, Hu X, Chen L, Du H, Bayarsaikhan J, Mijiddorj E, Erdenebaatar D, Iderkhangai TO, Myagmar E, Kanzawa-Kiriyama H, Nishino M, Shinoda KI, Shubina OA, Guo J, Cai W, Deng Q, Kang L, Li D, Li D, Lin R, Nini, Shrestha R, Wang LX, Wei L, Xie G, Yao H, Zhang M, He G, Yang X, Hu R, Robbeets M, Schiffels S, Kennett DJ, Jin L, Li H, Krause J, Pinhasi R, Reich D. Genomic insights into the formation of human populations in East Asia. Nature. 2021 Mar;591(7850):413-419. doi: 10.1038/s41586-021-03336-2. Epub 2021 Feb 22. PMID: 33618348; PMCID: PMC7993749.

[WangNatureCommunications2019]:

**Ancient human genome-wide data from a 3000-year interval in the Caucasus corresponds with eco-geographic regions.** Wang CC, Reinhold S, Kalmykov A, Wissgott A, Brandt G, Jeong C, Cheronet O, Ferry M, Harney E, Keating D, Mallick S, Rohland N, Stewardson K, Kantorovich AR, Maslov VE, Petrenko VG, Erlikh VR, Atabiev BC, Magomedov RG, Kohl PL, Alt KW, Pichler SL, Gerling C, Meller H, Vardanyan B, Yeganyan L, Rezepkin AD, Mariaschk D, Berezina N, Gresky J, Fuchs K, Knipper C, Schiffels S, Balanovska E, Balanovsky O, Mathieson I, Higham T, Berezin YB, Buzhilova A, Trifonov V, Pinhasi R, Belinskij AB, Reich D, Hansen S, Krause J, Haak W. Nat Commun. 2019 Feb 4;10(1):590. doi: 10.1038/s41467-018-08220-8. PMID: 30713341.

[WangbioRxiv2020]:

**The Genomic Formation of Human Populations in East Asia.** Chuan-Chao Wang, Hui-Yuan Yeh, Alexander N Popov, Hu-Qin Zhang, Hirofumi Matsumura, Kendra Sirak, Olivia Cheronet, Alexey Kovalev, Nadin Rohland, Alexander M. Kim, Rebecca Bernardos, Dashtseveg Tumen, Jing Zhao, Yi-Chang Liu, Jiun-Yu Liu, Matthew Mah, Swapan Mallick, Ke Wang, Zhao Zhang, Nicole Adamski, Nasreen Broomandkhoshbacht, Kimberly Callan, Brendan J. Culleton, Laurie Eccles, Ann Marie Lawson, Megan Michel, Jonas Oppenheimer, Kristin Stewardson, Shaoqing Wen, Shi Yan, Fatma Zalzala, Richard Chuang, Ching-Jung Huang, Chung-Ching Shiung, Yuri G. Nikitin, Andrei V. Tabarev, Alexey A. Tishkin, Song Lin, Zhou-Yong Sun, Xiao-Ming Wu, Tie-Lin Yang, Xi Hu, Liang Chen, Hua Du, Jamsranjav Bayarsaikhan, Enkhbayar Mijiddorj, Diimaajav Erdenebaatar, Tumur-Ochir Iderkhangai, Erdene Myagmar, Hideaki Kanzawa-Kiriyama, Msato Nishino, Ken-ichi Shinoda, Olga A. Shubina, Jianxin Guo, Qiongying Deng, Longli Kang, Dawei Li, Dongna Li, Rong Lin, Wangwei Cai, Rukesh Shrestha, Ling-Xiang Wang, Lanhai Wei, Guangmao Xie, Hongbing Yao, Manfei Zhang, Guanglin He, Xiaomin Yang, Rong Hu, Martine Robbeets, Stephan Schiffels, Douglas J. Kennett, Li Jin, Hui Li, Johannes Krause, Ron Pinhasi, David Reich bioRxiv 2020.03.25.004606; doi: https://doi.org/10.1101/2020.03.25.004606.

[WangSciAdv2020]:

**Ancient genomes reveal complex patterns of population movement, interaction, and replacement in sub-Saharan Africa.** Wang K, Goldstein S, Bleasdale M, Clist B, Bostoen K, Bakwa-Lufu P, Buck LT, Crowther A, Dème A, McIntosh RJ, Mercader J, Ogola C, Power RC, Sawchuk E, Robertshaw P, Wilmsen EN, Petraglia M, Ndiema E, Manthi FK, Krause J, Roberts P, Boivin N, Schiffels S. Sci Adv. 2020 Jun 12;6(24):eaaz0183. doi: 10.1126/sciadv.aaz0183. PMID: 32582847; PMCID: PMC7292641.

[WegmannCurBio2020]:

**Low Prevalence of Lactase Persistence in Bronze Age Europe Indicates Ongoing Strong Selection over the Last 3,000 Years.** Burger J, Link V, Blöcher J, Schulz A, Sell C, Pochon Z, Diekmann Y, Žegarac A, Hofmanová Z, Winkelbach L, Reyna-Blanco CS, Bieker V, Orschiedt J, Brinker U, Scheu A, Leuenberger C, Bertino TS, Bollongino R, Lidke G, Stefanović S, Jantzen D, Kaiser E, Terberger T, Thomas MG, Veeramah KR, Wegmann D. Low Prevalence of Lactase Persistence in Bronze Age Europe Indicates Ongoing Strong Selection over the Last 3,000 Years. Curr Biol. 2020 Nov 2;30(21):4307-4315.e13. doi: 10.1016/j.cub.2020.08.033. Epub 2020 Sep 3. PMID: 32888485.

[WohnsScience2022]:

**A unified genealogy of modern and ancient genomes.** Wohns AW, Wong Y, Jeffery B, Akbari A, Mallick S, Pinhasi R, Patterson N, Reich D, Kelleher J, McVean G. Science. 2022 Feb 25;375(6583):eabi8264. doi: 10.1126/science.abi8264. Epub 2022 Feb 25. PMID: 35201891.

[YakaSomelCurrBio2021]:

**Variable kinship patterns in Neolithic Anatolia revealed by ancient genomes.** Yaka R, Mapelli I, Kaptan D, Doğu A, Chyleński M, Erdal ÖD, Koptekin D, Vural KB, Bayliss A, Mazzucato C, Fer E, Çokoğlu SS, Lagerholm VK, Krzewińska M, Karamurat C, Gemici HC, Sevkar A, Dağtaş ND, Kılınç GM, Adams D, Munters AR, Sağlıcan E, Milella M, Schotsmans EMJ, Yurtman E, Çetin M, Yorulmaz S, Altınışık NE, Ghalichi A, Juras A, Bilgin CC, Günther T, Storå J, Jakobsson M, de Kleijn M, Mustafaoğlu G, Fairbairn A, Pearson J, Togan İ, Kayacan N, Marciniak A, Larsen CS, Hodder I, Atakuman Ç, Pilloud M, Sürer E, Gerritsen F, Özbal R, Baird D, Erdal YS, Duru G, Özbaşaran M, Haddow SD, Knüsel CJ, Götherström A, Özer F, Somel M. Variable kinship patterns in Neolithic Anatolia revealed by ancient genomes. Curr Biol. 2021 Jun 7;31(11):2455-2468.e18. doi: 10.1016/j.cub.2021.03.050. Epub 2021 Apr 14. PMID: 33857427; PMCID: PMC8210650.

[YangCurrentBiology2017]:

**40,000-Year-Old Individual from Asia Provides Insight into Early Population Structure in Eurasia.** Yang MA, Gao X, Theunert C, Tong H, Aximu-Petri A, Nickel B, Slatkin M, Meyer M, Pääbo S, Kelso J, Fu Q. Curr Biol. 2017 Oct 23;27(20):3202-3208.e9. doi: 10.1016/j.cub.2017.09.030. Epub 2017 Oct 12. PMID: 29033327.

[YangScience2020]:

**Ancient DNA indicates human population shifts and admixture in northern and southern China.** Yang MA, Fan X, Sun B, Chen C, Lang J, Ko YC, Tsang CH, Chiu H, Wang T, Bao Q, Wu X, Hajdinjak M, Ko AM, Ding M, Cao P, Yang R, Liu F, Nickel B, Dai Q, Feng X, Zhang L, Sun C, Ning C, Zeng W, Zhao Y, Zhang M, Gao X, Cui Y, Reich D, Stoneking M, Fu Q. Science. 2020 Jul 17;369(6501):282-288. doi: 10.1126/science.aba0909. Epub 2020 May 14. PMID: 32409524.

[YuCell2020]:

**Paleolithic to Bronze Age Siberians Reveal Connections with First Americans and across Eurasia.** Yu H, Spyrou MA, Karapetian M, Shnaider S, Radzevičiūtė R, Nägele K, Neumann GU, Penske S, Zech J, Lucas M, LeRoux P, Roberts P, Pavlenok G, Buzhilova A, Posth C, Jeong C, Krause J. Cell. 2020 Jun 11;181(6):1232-1245.e20. doi: 10.1016/j.cell.2020.04.037. Epub 2020 May 20. PMID: 32437661.

[YuvandeLoosdrechtiScience2022]:

**Genomic and dietary discontinuities during the Mesolithic and Neolithic in Sicily.** Yu H, van de Loosdrecht MS, Mannino MA, Talamo S, Rohrlach AB, Childebayeva A, Villalba-Mouco V, Aron F, Brandt G, Burri M, Freund C, Radzeviciute R, Stahl R, Wissgott A, Fewlass H, Tagliacozzo A, Piperno M, Tusa S, Collina C, Schimmenti V, Di Salvo R, Prüfer K, Posth C, Hublin JJ, Gronenborn D, Binder D, Jeong C, Haak W, Krause J. iScience. 2022 Apr 12;25(5):104244. doi: 10.1016/j.isci.2022.104244. PMID: 35494246; PMCID: PMC9051636.

[ZallouaScientificReports2018]:

**Ancient DNA of Phoenician remains indicates discontinuity in the settlement history of Ibiza.** Zalloua P, Collins CJ, Gosling A, Biagini SA, Costa B, Kardailsky O, Nigro L, Khalil W, Calafell F, Matisoo-Smith E. Sci Rep. 2018 Dec 4;8(1):17567. doi: 10.1038/s41598-018-35667-y. PMID: 30514893.

[ZegaracBurgerbioRxiv2021]:

**Kinship, acquired and inherited status, and population structure at the Early Bronze Age Mokrin necropolis in northern Serbia.** Aleksandra Žegarac, Laura Winkelbach, Jens Blöcher, Yoan Diekmann, Marija Krečković Gavrilović, Marko Porčić, Biljana Stojković, Lidija Milašinović, Mona Schreiber, Daniel Wegmann, Krishna R. Veeramah, Sofija Stefanović, Joachim Burger

bioRxiv 2020.05.18.101337; doi: https://doi.org/10.1101/2020.05.18.101337.

[ZhangNature2021]:

**The genomic origins of the Bronze Age Tarim Basin mummies.** Zhang F, Ning C, Scott A, Fu Q, Bjørn R, Li W, Wei D, Wang W, Fan L, Abuduresule I, Hu X, Ruan Q, Niyazi A, Dong G, Cao P, Liu F, Dai Q, Feng X, Yang R, Tang Z, Ma P, Li C, Gao S, Xu Y, Wu S, Wen S, Zhu H, Zhou H, Robbeets M, Kumar V, Krause J, Warinner C, Jeong C, Cui Y. The genomic origins of the Bronze Age Tarim Basin mummies. Nature. 2021 Nov;599(7884):256-261. doi: 10.1038/s41586-021-04052-7. Epub 2021 Oct 27. PMID: 34707286; PMCID: PMC8580821.