# **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**

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| --- | --- | --- | --- | --- | --- |
| *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 file.md5sums. 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.  
  
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) and [David Reich](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:**   
[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: released Nov 22 2022   
V52.2: released Aug 22 2022   
V50.0.p1: released Aug 1 2022   
V50.0: released Oct 2021   
V44.3: released Jan 2021   
V42.4: released Mar 2020   
V37.2: released Feb 2019

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