

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

PALEOMIX

RRID:SCR_015057

Type: Tool

Proper Citation

PALEOMIX (RRID:SCR_015057)

Resource Information

URL: <https://github.com/MikkelSchubert/paleomix>

Proper Citation: PALEOMIX (RRID:SCR_015057)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 28,2023. Software toolkit for the processing of ancient and modern HTS data. PALEOMIX also aids in metagenomic analysis of the extracts from the HTS processing.

Resource Type: data processing software, software application, software resource, software toolkit

Defining Citation: [PMID:24722405](https://pubmed.ncbi.nlm.nih.gov/24722405/), [DOI:10.1038/nprot.2014.063](https://doi.org/10.1038/nprot.2014.063)

Keywords: hts data, high-throughput sequencing, ancient dna, adna, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: PALEOMIX

Resource ID: SCR_015057

Alternate IDs: biotools:paleomix, OMICS_03749

Alternate URLs: <https://bio.tools/paleomix>, <https://sources.debian.org/src/paleomix/>

Record Creation Time: 20220129T080323+0000

Record Last Update: 20260905T133050+0000

Ratings and Alerts

No rating or validation information has been found for PALEOMIX .

No alerts have been found for PALEOMIX .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 66 mentions in open access literature.

Listed below are recent publications. The full list is available at [Kravitz](#) .

Peñerová P, et al. (2026) The genomic impact of population connectivity and decline in Africa's elephants. *Nature communications*, 17(1).

Smith TA, et al. (2024) Comparative Population Genomics of Arctic Sled Dogs Reveals a Deep and Complex History. *Genome biology and evolution*, 16(9).

Ruiz-Puerta EJ, et al. (2024) Greenland Norse walrus exploitation deep into the Arctic. *Science advances*, 10(39), eadq4127.

Sun Y, et al. (2024) Late Pleistocene polar bear genomes reveal the timing of allele fixation in key genes associated with Arctic adaptation. *BMC genomics*, 25(1), 826.

Skovrind M, et al. (2024) Elucidating the sustainability of 700 y of Inuvialuit beluga whale hunting in the Mackenzie River Delta, Northwest Territories, Canada. *Proceedings of the National Academy of Sciences of the United States of America*, 121(34), e2405993121.

Liu X, et al. (2024) Introgression and disruption of migration routes have shaped the genetic integrity of wildebeest populations. *Nature communications*, 15(1), 2921.

Przelomska NAS, et al. (2024) Morphometrics and Phylogenomics of Coca (*Erythroxylum* spp.) Illuminate Its Reticulate Evolution, With Implications for Taxonomy. *Molecular biology and evolution*, 41(7).

Martin-Roy R, et al. (2024) Advancing responsible genomic analyses of ancient mollusc shells. *PloS one*, 19(5), e0302646.

Gavriil M, et al. (2024) 2-Hydroxyglutarate modulates histone methylation at specific loci and alters gene expression via Rph1 inhibition. *Life science alliance*, 7(2).

Furness LH, et al. (2024) Population structure of Dugong dugon across the Indo-Pacific revealed by historical mitogenomes. *Royal Society open science*, 11(8), 240599.

Cobb L, et al. (2024) High-throughput sequencing of insect specimens with sub-optimal DNA preservation using a practical, plate-based Illumina-compatible Tn5 transposase library preparation method. *PloS one*, 19(3), e0300865.

Balboa RF, et al. (2024) African bushpigs exhibit porous species boundaries and appeared in Madagascar concurrently with human arrival. *Nature communications*, 15(1), 172.

Zhur KV, et al. (2024) Human DNA from the oldest Eneolithic cemetery in Nalchik points the spread of farming from the Caucasus to the Eastern European steppes. *iScience*, 27(11), 110963.

Oosting T, et al. (2023) Mitochondrial genomes reveal mid-Pleistocene population divergence, and post-glacial expansion, in Australasian snapper (*Chrysophrys auratus*). *Heredity*, 130(1), 30.

Ruiz-Puerta EJ, et al. (2023) Holocene deglaciation drove rapid genetic diversification of Atlantic walrus. *Proceedings. Biological sciences*, 290(2007), 20231349.

Sánchez-Barreiro F, et al. (2023) Historic Sampling of a Vanishing Beast: Population Structure and Diversity in the Black Rhinoceros. *Molecular biology and evolution*, 40(9).

Breglia F, et al. (2023) Disentangling the origins of viticulture in the western Mediterranean. *Scientific reports*, 13(1), 17284.

Hussin N, et al. (2022) Characterization of the first mitogenomes of the smallest fish in the world, *Paedocypris progenetica*, from peat swamp of Peninsular Malaysia, Selangor, and Perak. *Genomics & informatics*, 20(1), e12.

Jensen EL, et al. (2022) A new lineage of Galapagos giant tortoises identified from museum samples. *Heredity*, 128(4), 261.

Pérez-Escobar OA, et al. (2022) Genome Sequencing of up to 6,000-Year-Old *Citrullus* Seeds Reveals Use of a Bitter-Fleshed Species Prior to Watermelon Domestication. *Molecular biology and evolution*, 39(8).