

Resource Summary Report

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

NGSadmix

RRID:SCR_003208

Type: Tool

Proper Citation

NGSadmix (RRID:SCR_003208)

Resource Information

URL: <http://www.popgen.dk/software/index.php/NgsAdmix>

Proper Citation: NGSadmix (RRID:SCR_003208)

Description: A tool for finding admixture proportions from next generation sequencing (NGS) data that is based on genotype likelihoods. It is a multithreaded c/c++ program.

Abbreviations: NGSadmix

Resource Type: software resource

Defining Citation: [PMID:24026093](#)

Keywords: next generation sequencing, admixture proportion, admixture, genotype, c, c++, admixture, association study, population structure, resequencing

Availability: Acknowledgement requested

Resource Name: NGSadmix

Resource ID: SCR_003208

Alternate IDs: OMICS_01553

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260905T132459+0000

Ratings and Alerts

No rating or validation information has been found for NGSadmix.

No alerts have been found for NGSadmix.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 144 mentions in open access literature.

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

Crego-Walters M, et al. (2026) Targeted Chromosomal Sequencing of Wild Bonobos Identifies a Genetically Distinct Subpopulation East of the Lomami River. bioRxiv : the preprint server for biology.

Westbury MV, et al. (2026) Tracing the Drivers of Range-Wide Bowhead Whale Genomic Structure and Diversity. Molecular ecology, 35(10), e70378.

Feinauer IS, et al. (2026) Whole genomes reveal subpopulations and isolation-by-distance patterns in the Norwegian lemming. BMC biology, 24(1).

Szmato?a T, et al. (2026) Genomic diversity and structure in arabian horses revealed by whole-genome sequencing: establishment of an allele frequency database of common genetic variation. BMC genomics, 27(1).

Wang X, et al. (2026) Population structure and domestication history of the Javan banteng. Current biology : CB, 36(2), 458.

Witonsky D, et al. (2026) Genomic profiling of active vitamin D colonic responses in African- and European-Americans identifies an ancestry-related regulatory variant of POLB. PLoS genetics, 22(1), e1011983.

Tensen L, et al. (2026) Reduced Genetic Load and Inbreeding in Reintroduced African Wild Dogs Reflect the Benefits of Admixture. Molecular ecology, 35(12), e70424.

Brand JN, et al. (2026) Stepwise emergence of recombination suppression precedes fissiparous asexuality in the planarian Schmidtea mediterranea. Nature communications, 17(1).

Tensen L, et al. (2026) Genomic divergence of leopards in the Cape Floristic Region of South Africa: potential drivers for local adaptation. Heredity, 135(2), 86.

Ketchum RN, et al. (2026) Genomic signatures of speciation and adaptation in the ctenophore Mnemiopsis. BMC biology, 24(1).

Reeves IM, et al. (2025) Admixture Increases Genetic Diversity and Adaptive Potential in Australasian Killer Whales. Molecular ecology, 34(23), e17689.

Blom MPK, et al. (2025) Museomics unravels cryptic diversity in an endemic group of New Guinean songbirds. Biology letters, 21(7), 20240611.

Csapó HK, et al. (2025) Genome sequence analysis provides evidence that a boreal crustacean colonised Svalbard well before the ongoing Atlantification of the Arctic. *Heredity*, 134(9), 558.

Battlay P, et al. (2025) Haploblocks contribute to parallel climate adaptation following global invasion of a cosmopolitan plant. *Nature ecology & evolution*, 9(8), 1441.

McCarthy ML, et al. (2025) Range-Wide Genomic Analysis Reveals Regional and Meta-Population Dynamics of Decline and Recovery in the Grey Seal. *Molecular ecology*, 34(14), e17824.

Thörn F, et al. (2025) Frequent Hybridisation Between Parapatric Lekking Bird-of-Paradise Species. *Molecular ecology*, 34(11), e17780.

De Cahsan B, et al. (2025) Road to Extinction? Past and Present Population Structure and Genomic Diversity in the Koala. *Molecular biology and evolution*, 42(4).

Sotka EE, et al. (2025) The genetic legacy of a global marine invader. *Proceedings of the National Academy of Sciences of the United States of America*, 122(15), e2418730122.

Dallaire X, et al. (2025) Leveraging Whole Genomes, Mitochondrial DNA and Haploblocks to Decipher Complex Demographic Histories: An Example From a Broadly Admixed Arctic Fish. *Molecular ecology*, 34(10), e17772.

Kurta K, et al. (2025) Whole Genome Sequencing Reveals How Plasticity and Genetic Differentiation Underlie Sympatric Morphs of Arctic Charr. *Molecular ecology*, 34(19), e70085.