

Resource Summary Report

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Hapmix

RRID:SCR_004203

Type: Tool

Proper Citation

Hapmix (RRID:SCR_004203)

Resource Information

URL: <https://www.hsph.harvard.edu/alkes-price/software/>

Proper Citation: Hapmix (RRID:SCR_004203)

Description: Software application that uses genotyping data from SNP arrays for accurately inferring chromosomal segments of distinct continental ancestry in admixed populations, using dense genetic data. (entry from Genetic Analysis Software)

Abbreviations: HAPMIX

Resource Type: software application, software resource, source code

Defining Citation: [PMID:19543370](#)

Keywords: gene, genetic, genomic, admixed, population, genotype, single nucleotide polymorphism, ancestry, chromosomal segment, snp array

Funding: NHGRI U01-HG004168;
NHLBI R01-HL087699

Availability: Restricted

Resource Name: Hapmix

Resource ID: SCR_004203

Alternate IDs: nlx_22768, OMICS_02082

Alternate URLs: <http://www.hsph.harvard.edu/faculty/alkes-price/software/>,
<http://www.stats.ox.ac.uk/~myers/software.html>, <https://reich.hms.harvard.edu/software>

Old URLs: http://genetics.med.harvard.edu/reich/Reich_Lab/Software.html

Record Creation Time: 20220129T080223+0000

Ratings and Alerts

No rating or validation information has been found for Hapmix.

No alerts have been found for Hapmix.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 52 mentions in open access literature.

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

Ding W, et al. (2026) Genome-wide association analysis identifies the genetic basis of body size traits in Tan sheep (*Ovis aries*). *BMC genomics*, 27(1).

Zeng W, et al. (2026) Ancient Yellow River ancestry and divergent admixture histories in the Qiang people. *Science advances*, 12(3), eady6667.

Strom NI, et al. (2026) Genome-wide association study of major anxiety disorders in 122,341 European-ancestry cases identifies 58 loci and highlights GABAergic signaling. *Nature genetics*, 58(2), 275.

Chen S, et al. (2025) Tracing the Genetic Heritage of the Kirgiz People: Dual-Wave Admixture and Ancestry-Biased Adaptation. *Molecular biology and evolution*, 42(8).

Farnitano MC, et al. (2025) Fluctuating reproductive isolation and stable ancestry structure in a fine-scaled mosaic of hybridizing *Mimulus* monkeyflowers. *PLoS genetics*, 21(3), e1011624.

Hu S, et al. (2025) Fine-scale population structure and widespread conservation of genetic effect sizes between human groups across traits. *Nature genetics*, 57(2), 379.

Wen J, et al. (2025) Sex-Biased Admixture Followed by Isolation and Adaptive Evolution Shaped the Genomic and Blood Pressure Diversity of the LopNur People. *Molecular biology and evolution*, 42(4).

Strom NI, et al. (2025) Genome-wide analyses identify 30 loci associated with obsessive-compulsive disorder. *Nature genetics*, 57(6), 1389.

Wang Y, et al. (2024) NRDE2 deficiency impairs homologous recombination repair and sensitizes hepatocellular carcinoma to PARP inhibitors. *Cell genomics*, 4(5), 100550.

Fang S, et al. (2024) Phylogenetic Relations and High-Altitude Adaptation in Wild Boar (*Sus scrofa*), Identified Using Genome-Wide Data. *Animals : an open access journal from*

MDPI, 14(20).

Li J, et al. (2024) Genome-wide association research on the reproductive traits of Qianhua Mutton Merino sheep. *Animal bioscience*, 37(9), 1535.

Suzuki K, et al. (2024) Genetic drivers of heterogeneity in type 2 diabetes pathophysiology. *Nature*, 627(8003), 347.

Xu W, et al. (2024) Multiple-Wave Admixture and Adaptive Evolution of the Pamirian Wakhi People. *Molecular biology and evolution*, 41(12).

Strom NI, et al. (2024) Genome-wide association study identifies 30 obsessive-compulsive disorder associated loci. *medRxiv : the preprint server for health sciences*.

Lei C, et al. (2024) Ancestral Origins and Admixture History of Kazakhs. *Molecular biology and evolution*, 41(7).

Furuta Y, et al. (2024) Common protein-altering variant in GFAP is associated with white matter lesions in the older Japanese population. *NPJ genomic medicine*, 9(1), 59.

Wen J, et al. (2024) Ancestral origins and post-admixture adaptive evolution of highland Tajiks. *National science review*, 11(9), nwae284.

Jing Y, et al. (2023) Genetic diversity and structure of the 4th cycle breeding population of Chinese fir (*Cunninghamia lanceolata* (Lamb.) Hook). *Frontiers in plant science*, 14, 1106615.

Pan Y, et al. (2023) Comparative Genomic and Transcriptomic Analyses Reveal the Impacts of Genetic Admixture in Kazaks, Uyghurs, and Huis. *Molecular biology and evolution*, 40(3).

Wei Y, et al. (2023) Fast and accurate local ancestry inference with Recomb-Mix. *bioRxiv : the preprint server for biology*.