

Resource Summary Report

Generated by [ASWG](#) on Aug 3, 2026

[shapeit4](#)

RRID:SCR_024335

Type: Tool

Proper Citation

shapeit4 (RRID:SCR_024335)

Resource Information

URL: <https://odelaneau.github.io/shapeit4/>

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Description: Software tool for estimation of haplotypes aka phasing for SNP array and high coverage sequencing data. The version 4 is refactored and improved version of SHAPEIT algorithm with multiple key additional features.

Synonyms: SHAPEIT, SHAPEIT4

Resource Type: software resource, software application

Defining Citation: [PMID:31780650](#)

Keywords: estimation of haplotypes, phasing, SNP array data, high coverage sequencing data,

Availability: Free, Available for download, Freely available,

Resource Name: shapeit4

Resource ID: SCR_024335

Alternate URLs: <https://sources.debian.org/src/shapeit4/>

License: MIT license

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260801T191123+0000

Ratings and Alerts

No rating or validation information has been found for shapeit4.

No alerts have been found for shapeit4.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Thorgeirsson TE, et al. (2025) Rare loss-of-function variants in HECTD2 and AKAP11 confer risk of bipolar disorder. *Nature genetics*, 57(4), 851.

Odero JO, et al. (2025) Genomic evidence of spatially structured gene flow and divergent insecticide resistance backgrounds of the malaria vector *Anopheles funestus* in Tanzania. *Genetics*, 230(4).

De-Kayne R, et al. (2025) Incomplete recombination suppression fuels extensive haplotype diversity in a butterfly colour pattern supergene. *PLoS biology*, 23(2), e3003043.

Zhang X, et al. (2025) Protocol for reconstructing ancestral genomes from present-day samples by applying local ancestry inference. *STAR protocols*, 6(1), 103580.

Wang H, et al. (2025) Copy Number Variation and Haplotype Analysis of 17q21.31 Reveals Increased Risk Associated with Progressive Supranuclear Palsy and Gene Expression Changes in Neuronal Cells. *Movement disorders : official journal of the Movement Disorder Society*, 40(5), 950.

Shi S, et al. (2024) A Genomics England haplotype reference panel and imputation of UK Biobank. *Nature genetics*, 56(9), 1800.

Skuladottir AT, et al. (2024) GWAS meta-analysis reveals key risk loci in essential tremor pathogenesis. *Communications biology*, 7(1), 504.

Ferguson S, et al. (2024) Exploring the role of polymorphic interspecies structural variants in reproductive isolation and adaptive divergence in *Eucalyptus*. *GigaScience*, 13.

Nagi SC, et al. (2024) Parallel Evolution in Mosquito Vectors-A Duplicated Esterase Locus is Associated With Resistance to Pirmiphos-methyl in *Anopheles gambiae*. *Molecular biology and evolution*, 41(7).

Lin W, et al. (2024) Genetic regulatory effects in response to a high-cholesterol, high-fat diet in baboons. *Cell genomics*, 4(3), 100509.

Odero JO, et al. (2024) Discovery of Knock-Down Resistance in the Major African Malaria Vector *Anopheles funestus*. *Molecular ecology*, 33(22), e17542.

Bigdeli TB, et al. (2024) Biological Insights from Schizophrenia-associated Loci in Ancestral Populations. medRxiv : the preprint server for health sciences.

Honorato-Mauer J, et al. (2024) Characterizing features affecting local ancestry inference performance in admixed populations. bioRxiv : the preprint server for biology.

Borda V, et al. (2024) Genetics of Latin American Diversity Project: Insights into population genetics and association studies in admixed groups in the Americas. Cell genomics, 4(11), 100692.

Odero JO, et al. (2024) Discovery of knock-down resistance in the major African malaria vector *Anopheles funestus*. bioRxiv : the preprint server for biology.

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

Chou WC, et al. (2024) Genetic insights into carbohydrate sulfotransferase 8 and its impact on the immunotherapy efficacy of cancer. Cell reports, 43(1), 113641.

Tong X, et al. (2023) Accurate haplotype construction and detection of selection signatures enabled by high quality pig genome sequences. Nature communications, 14(1), 5126.

Bjornsdottir G, et al. (2023) Rare variants with large effects provide functional insights into the pathology of migraine subtypes, with and without aura. Nature genetics, 55(11), 1843.

Ziyatdinov A, et al. (2023) Genotyping, sequencing and analysis of 140,000 adults from Mexico City. Nature, 622(7984), 784.