

Resource Summary Report

Generated by [RRID](#) on Aug 2, 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 [RRID](#).

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.

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

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

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

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.

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.

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.

Zhou H, et al. (2023) Multi-ancestry study of the genetics of problematic alcohol use in over 1 million individuals. *Nature medicine*, 29(12), 3184.