Resource Summary Report

Generated by RRID on Aug 12, 2026

WhatsHap

RRID:SCR_025319
Type: Tool

Proper Citation

WhatsHap (RRID:SCR_025319)

Resource Information

URL: https://whatshap.readthedocs.io/en/latest/

Proper Citation: WhatsHap (RRID:SCR_025319)

Description: Software for phasing genomic variants using DNA sequencing reads, also called read-based phasing or haplotype assembly. Used for long reads, but works also well with short reads.

Resource Type: source code, software resource

Defining Citation: DOI:10.1101/085050

Keywords: Read-based phasing, genomic variants, haplotype assembly,

Funding: Swedish Knut and Alice Wallenberg Foundation

Availability: Free, Available for download, Freely available

Resource Name: WhatsHap

Resource ID: SCR_025319

License: MIT license

Record Creation Time: 20240511T053259+0000

Record Last Update: 20260810T040842+0000

Ratings and Alerts

No rating or validation information has been found for WhatsHap.

No alerts have been found for WhatsHap.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 97 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID .

Fakoya AO, et al. (2026) HapAsmbl: A reference-aided pipeline for assembling haplotypes in Nanopore amplicon sequence data of polymorphic populations. Applications in plant sciences, 14(3), e70062.

Jana U, et al. (2026) The human IG heavy chain constant gene locus is enriched for large structural variants and coding polymorphisms that vary among human populations. Cell genomics, 6(1), 101058.

Tengstedt ANB, et al. (2026) Evaluating inbreeding and assessing the risk of outbreeding depression in genetic rescue using whole-genome sequence data. Proceedings of the National Academy of Sciences of the United States of America, 123(1), e2526216122.

Wang S, et al. (2026) A Scalable Framework for Comprehensive Typing of Polymorphic Immune Genes from Long-Read Data. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(22), e21531.

Fry J, et al. (2026) Severe Thiopurine-Induced Myelosuppression in a Pediatric Acute Lymphoblastic Leukemia Patient With the NUDT15 *1/*6 Genotype: A Brief Report. Clinical and translational science, 19(6), e70639.

Satokangas I, et al. (2026) Introgression and Divergence in a Young Species Group. Molecular ecology, 35(12), e70448.

Lin Z, et al. (2026) RMPore: a comprehensive database of single-molecule RNA modifications detected by Nanopore direct RNA sequencing. Nucleic acids research, 54(D1), D291.

Eura N, et al. (2026) Pathogenic CGG expansions in oculopharyngodistal myopathy exhibit distinct characteristics of each causative gene on the flanking sequences as well as methylation status. Genome medicine, 18(1).

Devaney JM, et al. (2026) Sensitivity of HiFi long-read genome sequencing for difficult-to-detect pathogenic variants when applied to real-world clinical laboratory samples. American journal of human genetics, 113(5), 1036.

Bazzicalupo E, et al. (2026) Deep learning reveals genomic regions introgressed between two recurrently hybridizing lynx species. Molecular biology and evolution, 43(4).

Miranda I, et al. (2026) Balanced polymorphism underlies long-standing adaptation for seasonal camouflage in the least weasel. Communications biology, 9(1).

Amoako EK, et al. (2026) Genomic population structure and insecticide resistance mechanisms in the malaria vector An. coluzzii across contrasting bioclimatic zones in West Africa. BMC genomics, 27(1), 140.

Chamchoy K, et al. (2026) Resolving haplotypes of the glucose-6-phosphate dehydrogenase gene using long-range polymerase chain reaction and Oxford Nanopore sequencing. Biology methods & protocols, 11(1), bpag008.

Wang Y, et al. (2026) The 1000 Chinese Pangenome empowers medical and population genetics. Nature, 654(8117), 121.

Mortazavi M, et al. (2026) Long-read genome sequencing improves detection and functional interpretation of structural and repeat variants in autism. Cell genomics, 6(5), 101186.

Jamshidi J, et al. (2025) Long-range PCR and Nanopore sequencing for localisation and phasing variants: an end-to-end clinical application workflow. BMC medical genomics, 18(1), 186.

Ferrer Obiol J, et al. (2025) Evolutionarily distinct lineages of a migratory bird of prey show divergent responses to climate change. Nature communications, 16(1), 3503.

Jana U, et al. (2025) The human immunoglobulin heavy chain constant gene locus is enriched for large complex structural variants and coding polymorphisms that vary in frequency among human populations. bioRxiv : the preprint server for biology.

Kunigo K, et al. (2025) Targeted long-read methylation analysis using hybridization capture suitable for clinical specimens. Cell reports methods, 5(11), 101215.

Kersten O, et al. (2025) Single Nucleotide Polymorphisms, Structural Variants, and Short Tandem Repeats Capture Distinct Signals of Adaptive Divergence in the Atlantic Puffin. Genome biology and evolution, 17(9).