

Resource Summary Report

Generated by T1D on Jul 30, 2026

PredictHaplo

RRID:SCR_005207

Type: Tool

Proper Citation

PredictHaplo (RRID:SCR_005207)

Resource Information

URL: <http://bmda.cs.unibas.ch/HivHaploTyper/>

Proper Citation: PredictHaplo (RRID:SCR_005207)

Description: Software for reconstructing haplotypes from next-generation sequencing data., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: PredictHaplo

Resource Type: software resource

Keywords: haplotype, next-generation sequencing

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: PredictHaplo

Resource ID: SCR_005207

Alternate IDs: OMICS_00228

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260725T190603+0000

Ratings and Alerts

No rating or validation information has been found for PredictHaplo.

No alerts have been found for PredictHaplo.

Data and Source Information

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Fuhrmann L, et al. (2024) V-pipe 3.0: a sustainable pipeline for within-sample viral genetic diversity estimation. *GigaScience*, 13.

Fuhrmann L, et al. (2024) VILOCA: sequencing quality-aware viral haplotype reconstruction and mutation calling for short-read and long-read data. *NAR genomics and bioinformatics*, 6(4), lqae152.

Venturini C, et al. (2022) Haplotype assignment of longitudinal viral deep sequencing data using covariation of variant frequencies. *Virus evolution*, 8(2), veac093.

Deng ZL, et al. (2021) Evaluating assembly and variant calling software for strain-resolved analysis of large DNA viruses. *Briefings in bioinformatics*, 22(3).

Gibson KM, et al. (2020) A cross-sectional study to characterize local HIV-1 dynamics in Washington, DC using next-generation sequencing. *Scientific reports*, 10(1), 1989.

Brand??o PE, et al. (2020) Extinction and emergence of genomic haplotypes during the evolution of Avian coronavirus in chicken embryos. *Genetics and molecular biology*, 43(2), e20190064.

Gibson KM, et al. (2020) Validation of Variant Assembly Using HAPHPIPE with Next-Generation Sequence Data from Viruses. *Viruses*, 12(7).

Ahn S, et al. (2018) Viral quasispecies reconstruction via tensor factorization with successive read removal. *Bioinformatics (Oxford, England)*, 34(13), i23.

Baaijens JA, et al. (2017) De novo assembly of viral quasispecies using overlap graphs. *Genome research*, 27(5), 835.

Rose R, et al. (2016) Challenges in the analysis of viral metagenomes. *Virus evolution*, 2(2), vew022.

Liang M, et al. (2016) Distinguishing highly similar gene isoforms with a clustering-based bioinformatics analysis of PacBio single-molecule long reads. *BioData mining*, 9, 13.

Pulido-Tamayo S, et al. (2015) Frequency-based haplotype reconstruction from deep sequencing data of bacterial populations. *Nucleic acids research*, 43(16), e105.

Ogishi M, et al. (2015) Deconvoluting the composition of low-frequency hepatitis C viral quasispecies: comparison of genotypes and NS3 resistance-associated variants between HCV/HIV coinfecting hemophiliacs and HCV monoinfected patients in Japan. *PloS one*, 10(3), e0119145.

Giallonardo FD, et al. (2014) Full-length haplotype reconstruction to infer the structure of heterogeneous virus populations. *Nucleic acids research*, 42(14), e115.

Poh WT, et al. (2013) Viral quasispecies inference from 454 pyrosequencing. *BMC bioinformatics*, 14, 355.