

Resource Summary Report

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HAPLOTYPER

RRID:SCR_009232

Type: Tool

Proper Citation

HAPLOTYPER (RRID:SCR_009232)

Resource Information

URL: <http://www.people.fas.harvard.edu/~junliu/Haplo/docMain.htm>

Proper Citation: HAPLOTYPER (RRID:SCR_009232)

Description: Software application (entry from Genetic Analysis Software)

Abbreviations: HAPLOTYPER

Resource Type: software application, software resource

Keywords: gene, genetic, genomic

Resource Name: HAPLOTYPER

Resource ID: SCR_009232

Alternate IDs: nlx_154389

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260905T133247+0000

Ratings and Alerts

No rating or validation information has been found for HAPLOTYPER.

No alerts have been found for HAPLOTYPER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 25 mentions in open access literature.

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

Churchman ML, et al. (2026) The Oncology Research Information Exchange Network (ORIEN) - Building a Real-World Collaborative, Patient-driven Infrastructure for Discovery Research and Precision Oncology. Research square.

Vanheer LN, et al. (2025) Preferential transmission of minority and drug-resistant clones in polyclonal infections in Mali. Malaria journal, 24(1), 111.

Patel SP, et al. (2025) Phase II basket trial of Dual Anti-CTLA-4 and anti-PD-1 blockade in Rare Tumors (DART) SWOG S1609: pancreatic neuroendocrine neoplasm (PNEN) cohort. Journal for immunotherapy of cancer, 13(6).

Chen W, et al. (2025) EPI-SauriCas9-based mouse ovarian cancer models recapitulating pten deletion in patients. Communications biology, 9(1), 159.

Lan T, et al. (2025) Enhancing inbreeding estimation and global conservation insights through chromosome-level assemblies of the Chinese and Malayan pangolin. GigaScience, 14.

Xia R, et al. (2025) Associations between RetNet gene polymorphisms and the efficacy of orthokeratology for myopia control: a retrospective clinical study. Eye and vision (London, England), 12(1), 13.

Zhang J, et al. (2025) Phenotypic adaptation and genomic variation of *Kandelia obovata* associated with its northern introduction along southeastern coast of China. Frontiers in plant science, 16, 1512620.

Hsu JS, et al. (2024) Complete genomic profiles of 1496 Taiwanese reveal curated medical insights. Journal of advanced research, 66, 197.

Qin S, et al. (2022) Identification of an SRY-negative 46,XX infertility male with a heterozygous deletion downstream of SOX3 gene. Molecular cytogenetics, 15(1), 2.

Pan B, et al. (2022) Assessing reproducibility of inherited variants detected with short-read whole genome sequencing. Genome biology, 23(1), 2.

Cutrer FM, et al. (2021) Genetic variants related to successful migraine prophylaxis with verapamil. Molecular genetics & genomic medicine, 9(6), e1680.

Ruan Y, et al. (2021) Conditional Mapping Identified Quantitative Trait Loci for Grain Protein Concentration Expressing Independently of Grain Yield in Canadian Durum Wheat. Frontiers in plant science, 12, 642955.

Ren Z, et al. (2020) Functional analysis of a novel C-glycosyltransferase in the orchid *Dendrobium catenatum*. Horticulture research, 7, 111.

Ahamed H, et al. (2020) Phenotypic expression and clinical outcomes in a South Asian PRKAG2 cardiomyopathy cohort. Scientific reports, 10(1), 20610.

Kendig KI, et al. (2019) Sentieon DNaseq Variant Calling Workflow Demonstrates Strong Computational Performance and Accuracy. *Frontiers in genetics*, 10, 736.

Zhao J, et al. (2019) Presence of recombination hotspots throughout SLC6A3. *PloS one*, 14(6), e0218129.

Zhang LJ, et al. (2017) Phylogeographic patterns of *Lygus pratensis* (Hemiptera: Miridae): Evidence for weak genetic structure and recent expansion in northwest China. *PloS one*, 12(4), e0174712.

Jaumdally SZ, et al. (2017) CCR5 expression, haplotype and immune activation in protection from infection in HIV-exposed uninfected individuals in HIV-serodiscordant relationships. *Immunology*, 151(4), 464.

Erson-Omay EZ, et al. (2017) Longitudinal analysis of treatment-induced genomic alterations in gliomas. *Genome medicine*, 9(1), 12.

Cuevas HE, et al. (2016) The Evolution of Photoperiod-Insensitive Flowering in Sorghum, A Genomic Model for Panicoid Grasses. *Molecular biology and evolution*, 33(9), 2417.