

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: 20260805T044219+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 23 mentions in open access literature.

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

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).

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.

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

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.

Babinsky VN, et al. (2015) Association studies of calcium-sensing receptor (CaSR) polymorphisms with serum concentrations of glucose and phosphate, and vascular calcification in renal transplant recipients. *PloS one*, 10(3), e0119459.

Sch??ler S, et al. (2014) Polymorphisms in the promoter region of ESR2 gene and susceptibility to ovarian cancer. *Gene*, 546(2), 283.