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 resource, software application

Keywords: gene, genetic, genomic

Funding:

Resource Name: HAPLOTYPER

Resource ID: SCR_009232

Alternate IDs: nlx_154389

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250416T063540+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 18 mentions in open access literature.

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

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.

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

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.

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.

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

Ardelli BF, et al. (2006) Characterization of a half-size ATP-binding cassette transporter gene which may be a useful marker for ivermectin selection in Onchocerca volvulus. Molecular and biochemical parasitology, 145(1), 94.

Weale ME, et al. (2004) A survey of current software for haplotype phase inference. Human genomics, 1(2), 141.

Lötsch J, et al. (2003) Simultaneous screening for three mutations in the ABCB1 gene. Genomics, 82(5), 503.