Resource Summary Report

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Haploview

RRID:SCR_003076
Type: Tool

Proper Citation

Haploview (RRID:SCR_003076)

Resource Information

URL: http://www.broadinstitute.org/scientific-community/science/programs/medical-and-population-genetics/haploview/haploview

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Description: A Java based software tool designed to simplify and expedite the process of haplotype analysis by providing a common interface to several tasks relating to such analyses. Haploview currently allows users to examine block structures, generate haplotypes in these blocks, run association tests, and save the data in a number of formats. All functionalities are highly customizable. (entry from Genetic Analysis Software) * LD & haplotype block analysis * haplotype population frequency estimation * single SNP and haplotype association tests * permutation testing for association significance * implementation of Paul de Bakker's Tagger tag SNP selection algorithm. * automatic download of phased genotype data from HapMap * visualization and plotting of PLINK whole genome association results including advanced filtering options Haploview is fully compatible with data dumps from the HapMap project and the Perlegen Genotype Browser. It can analyze thousands of SNPs (tens of thousands in command line mode) in thousands of individuals. Note: Haploview is currently on a development and support freeze. The team is currently looking at a variety of options in order to provide support for the software. Haploview is an open source project hosted by SourceForge. The source can be downloaded at the SourceForge project site.

Abbreviations: Haploview

Resource Type: data processing software, source code, software resource, software application

Defining Citation: PMID:15297300, PMID:21356869, PMID:20147036

Keywords: linkage disequilibrium, haplotype, genotype, visualization, analysis, single nucleotide polymorphism, gene, genetic, genomic, java

Funding:

Availability: Open unspecified license, See license information, Http://www.broadinstitute.org/science/programs/medical-and-population-genetics/haploview/contact

Resource Name: Haploview

Resource ID: SCR_003076

Alternate IDs: nif-0000-30472

Alternate URLs: http://www.broad.mit.edu/personal/jcbarret/haploview/

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250416T063316+0000

Ratings and Alerts

No rating or validation information has been found for Haploview.

No alerts have been found for Haploview.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 6802 mentions in open access literature.

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

Liu Y, et al. (2025) Novel genetic variants in the NLRP3 inflammasome-related PANX1 and APP genes predict survival of patients with hepatitis B virus-related hepatocellular carcinoma. Clinical & translational oncology : official publication of the Federation of Spanish Oncology Societies and of the National Cancer Institute of Mexico, 27(2), 630.

Lan H, et al. (2025) PDIA3 rs2788: An Independent Risk Factor for Hypertension and Its Interaction With Antihypertensive Medications. Journal of clinical hypertension (Greenwich, Conn.), 27(1), e14959.

Ye M, et al. (2025) EGR1 mRNA expression levels and polymorphisms are associated with slaughter performance in chickens. Poultry science, 104(1), 104533.

Zhang Y, et al. (2025) Identification of superior haplotypes and candidate gene for seed size-related traits in soybean (Glycine max L.). Molecular breeding : new strategies in plant improvement, 45(1), 3.

Yang X, et al. (2025) Novel candidate genes and genetic basis analysis of kernel starch content in tropical maize. BMC plant biology, 25(1), 105.

Xu J, et al. (2025) Identification of genetic variants of the IL18R1 gene in association with COPD susceptibility. Annals of medicine, 57(1), 2446690.

Van K, et al. (2025) Network analysis combined with genome-wide association study helps identification of genes related to amino acid contents in soybean. BMC genomics, 26(1), 21.

Tough RH, et al. (2025) Functionally-informed fine-mapping identifies genetic variants linking increased CHD1L expression and HIV restriction in monocytes. Scientific reports, 15(1), 2325.

Djordjevic N, et al. (2025) ABCB1 Polymorphism Is Associated with Higher Carbamazepine Clearance in Children. Pediatric reports, 17(1).

Rolling WR, et al. (2025) Combining genome-wide association and genomic prediction to unravel the genetic architecture of carotenoid accumulation in carrot. The plant genome, 18(1), e20560.

Abuzahra M, et al. (2025) A novel p.127Val>Ile single nucleotide polymorphism in the MTNR1A gene and its relation to litter size in Thin-tailed Indonesian ewes. Animal bioscience, 38(2), 209.

Chen B, et al. (2025) Functional analysis of key members affecting egg production in the transglutaminase gene family in chickens. Poultry science, 104(2), 104794.

Knaga S, et al. (2025) Ovalbumin gene polymorphism: Implications for hatchability and egg quality changes during storage in Japanese quail. Poultry science, 104(2), 104788.

Britto GSG, et al. (2025) Genome-Wide Insights into Internalizing Symptoms in Admixed Latin American Children. Genes, 16(1).

Oh S, et al. (2025) Genome-wide association studies in lettuce reveal the interplay of seed age, color, and germination under high temperatures. Scientific reports, 15(1), 733.

Stegemiller MR, et al. (2025) Identifying Genetic Predisposition to Dozer Lamb Syndrome: A Semi-Lethal Muscle Weakness Disease in Sheep. Genes, 16(1).

Kami?ski A, et al. (2025) The VDR rs1544410 and rs11568820 Variants and the Risk of Osteoporosis in the Polish Population. International journal of molecular sciences, 26(2).

Kölz C, et al. (2024) In silico and biological analyses of missense variants of the human biliary efflux transporter ABCC2: effects of novel rare missense variants. British journal of pharmacology, 181(22), 4593.

Posadas-Sánchez R, et al. (2024) Increased carotid intima-media thickness and cardiometabolic risk factors are associated with IL-6 gene polymorphisms in Mexican individuals: The Genetics of Atherosclerotic Disease Mexican study. Biomolecules & biomedicine, 24(2), 315.

Sakrajda K, et al. (2024) Abelson Helper Integration Site 1 haplotypes and peripheral blood expression associates with lithium response and immunomodulation in bipolar patients. Psychopharmacology, 241(4), 727.