

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, software application, software resource, source code

Defining Citation: [PMID:15297300](#), [PMID:21356869](#), [PMID:20147036](#)

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

Availability: Free, Available for download, Freely available

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: 20260805T044048+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 6933 mentions in open access literature.

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

Askari F, et al. (2026) Association of IL28B Polymorphisms With Hepatitis C Susceptibility in Southern Iran's α -Thalassemia Population: A Cross-Sectional Study. Health science reports, 9(1), e71648.

Yang R, et al. (2026) Population structure and genome-wide association study of body conformation traits of two native goat breeds in China. Animal bioscience, 39(1), 250334.

Mandle HB, et al. (2025) Inflammation and gut barrier function-related genes and colorectal cancer risk in western European populations. Mutagenesis, 40(1), 48.

Gupta D, et al. (2025) Association of Apolipoprotein E (APOE) Gene Polymorphism With Age-Related Macular Degeneration (AMD) in Indian Patients. Cureus, 17(6), e85441.

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.

Vargas-Alarcón G, et al. (2025) Cholesterol 7 α -hydroxylase (CYP7A1) gene polymorphisms are associated with increased LDL-cholesterol levels and the incidence of subclinical atherosclerosis. Biomolecules & biomedicine, 25(4), 822.

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.

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.

Vodnjov N, et al. (2025) TTN:c.12478del in proximal I-band of titin represents a common molecular cause of dilated cardiomyopathy in Slovenian patients. *Orphanet journal of rare diseases*, 20(1), 92.

Li X, et al. (2025) Do CRP gene variants and smoking elevate recurrent stroke risk in minor ischemic stroke patients? *European journal of medical research*, 30(1), 179.

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.

Akhiiarova K, et al. (2025) Molecular Pathogenesis of Joint Hypermobility: The Role of Intergenic Interactions. *Medical sciences (Basel, Switzerland)*, 13(4).

Chen YT, et al. (2025) Angiogenic Edge of ANGPT2: Genetic Variants Shape Prostate Cancer Prognosis on Androgen Deprivation Therapy. *Cancer genomics & proteomics*, 22(6), 991.

Saranyuk R, et al. (2025) Genetic Interactions of Phase II Xenobiotic-Metabolizing Enzymes GSTO1 and GCLC in Relation to Alcohol Abuse and Psoriasis Risk. *Journal of xenobiotics*, 15(2).

Oh S, et al. (2025) Association of APOC1 with cortical atrophy during conversion to Alzheimer's disease. *GeroScience*, 47(6), 6665.

Hu J, et al. (2025) Association Between KLF1, BCL11A and HBS1L-MYB Polymorphisms and Phenotypes With α -Thalassemia Patients in Hainan. *Molecular genetics & genomic medicine*, 13(9), e70142.

Chen G, et al. (2025) Polymorphism of NCAPG gene and its association with growth traits in Nanjiang Yellow goat. *Animal biotechnology*, 36(1), 2565161.

Ding J, et al. (2025) Integrative multi-omics analysis deciphers the regulatory mechanisms of egg weight traits in chickens. *Poultry science*, 104(11), 105813.

Niu H, et al. (2025) Association of polymorphisms and abnormal methylation of several autophagy genes with pulmonary tuberculosis susceptibility, clinical manifestations in a Chinese population. *BMC infectious diseases*, 25(1), 933.