Resource Summary Report

Generated by T1D on Sep 5, 2026

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: 20260903T234559+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 7041 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Ennahoui SM, et al. (2026) Impact of TNF-? (- 308G>A and - 857 C>T) promoter variants on susceptibility to chronic hepatitis B virus infection in a cohort of Mauritanian patients: pilot study. BMC microbiology, 26(1).

Liu L, et al. (2026) The ATP7B c.3316 G > A variant is associated with mild subphenotype in Wilson disease: a single-center cohort study. Orphanet journal of rare diseases, 21(1).

Liu C, et al. (2026) Characterization of the genetic architecture of adult plant resistance to sharp eyespot in Chinese wheat germplasm. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 139(1), 38.

Pervaiz H, et al. (2026) Genetic analysis of key players in PI3K signaling cascade of colorectal carcinoma. Scientific reports, 16(1).

Liu S, et al. (2026) A bacterial ecocline in Klebsiella pneumoniae may explain its backboned phylogeny. PLoS biology, 24(3), e3003672.

Feng YJ, et al. (2026) A Genetic Risk Prediction Model for Coronary Artery Disease Integrating CYP17A1 Polymorphisms and Clinical Variables in a Chinese Population. International journal of general medicine, 19, 572183.

Wang K, et al. (2026) GGPS1 Promoter Variant (rs3806394) Is Associated With Larger Simple Renal Cysts via Reduced GGPPS Expression. Human mutation, 2026, 8347509.

Kang M, et al. (2026) MTHFR polymorphism is associated with increased adverse events and poor clinical outcomes in gastric cancer patients with adjuvant S-1 chemotherapy. Scientific reports, 16(1).

Li A, et al. (2026) Association analysis and in silico functional predictions of RMDN2 variants in chickens. Animal bioscience, 39(6), 250758.

Sun X, et al. (2026) Genome-Wide Association Study Reveals Genetic Loci, Candidate Genes and Favorable Haplotypes for Important Agronomic Traits in Auricularia cornea. Journal of fungi (Basel, Switzerland), 12(3).

Vince N, et al. (2026) HLA Class II Protein Expression Regulation Is Strongly Linked to Cis-Acting SNPs. HLA, 107(4), e70669.

Savassi BSAE, et al. (2026) Host genetic background influences the severity of disease in Schistosoma haematobium infections. Parasite (Paris, France), 33, 14.

Yang H, et al. (2026) Genetic architecture of two novel chicken breeds from Xinjiang: A whole-genome sequencing study on Ili gamecock and Yemili Chicken. Poultry science, 105(7), 106845.

Feng Y, et al. (2026) Genetic loci and key candidate genes associated with fatty acid composition in the breast muscle of Sansui ducks identified through GWAS. BMC genomics, 27(1).

Paradowska E, et al. (2026) TLR7 polymorphisms are associated with COVID-19 susceptibility and severity. Frontiers in immunology, 17, 1837208.

Cho H, et al. (2026) Genome-wide association study on soybean canopy wilting under drought stress conditions in a rainout-shelter greenhouse. Frontiers in plant science, 17, 1840313.

Kruger B, et al. (2026) Genetic Variation in CYP2B6, UGT1A4 and Sulfotransferases Is Associated with Disease-Free Survival in South African Breast Cancer Patients Treated with Tamoxifen. Journal of personalized medicine, 16(4).

Yang Y, et al. (2026) m6A-SNPs identified by integrating genomic data are associated with the occurrence and prognosis of HCC. Scientific reports, 16(1).

Sangiorgi G, et al. (2026) Genetic dissection of root traits in barley identifies major QTLs and domestication signature. Plant cell reports, 45(6).

Yin W, et al. (2026) Identification of SNPs Associated With mRNA Expression Differences of the Complement Receptor Type 1-Like Gene in Landrace Weaned Piglets. Veterinary medicine and science, 12(4), e70980.