Resource Summary Report

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HaploReg

RRID:SCR_006796
Type: Tool

Proper Citation

HaploReg (RRID:SCR_006796)

Resource Information

URL: http://www.broadinstitute.org/mammals/haploreg/haploreg.php

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Description: HaploReg is a tool for exploring annotations of the noncoding genome at variants on haplotype blocks, such as candidate regulatory SNPs at disease-associated loci. Using linkage disequilibrium (LD) information from the 1000 Genomes Project, linked SNPs and small indels can be visualized along with their predicted chromatin state in nine cell types, conservation across mammals, and their effect on regulatory motifs. HaploReg is designed for researchers developing mechanistic hypotheses of the impact of non-coding variants on clinical phenotypes and normal variation.

Abbreviations: HaploReg

Resource Type: data or information resource, database

Defining Citation: PMID:22064851

Keywords: chromatin state, conservation, regulatory motif, alteration, variant, chromatin, motif, annotation, genome, variation, genome-wide association study, refsnp, refseq gene, snp, bio.tools, FASEB list

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Resource Name: HaploReg

Resource ID: SCR_006796

Alternate IDs: biotools:HaploReg, nlx_151407

Alternate URLs: http://compbio.mit.edu/HaploReg, https://bio.tools/HaploReg

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260919T195700+0000

Ratings and Alerts

No rating or validation information has been found for HaploReg.

No alerts have been found for HaploReg.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1048 mentions in open access literature.

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

Alorjani M, et al. (2026) Genotype-phenotype correlations in breast cancer susceptibility: evaluating MMP-2, TYMS, and eNOS variants in the Jordanian population. Scientific reports, 16(1), 4391.

Wang H, et al. (2026) NFKB1 genetic variation and allergic rhinitis susceptibility: a study in the Chinese Han population. Scientific reports, 16(1).

Hu N, et al. (2026) Genetic variations interact with polybrominated diphenyl ether exposure to alter lipid homeostasis. Nature communications, 17(1).

Sánchez-Maldonado JM, et al. (2026) ULK4 and CDKN2A polymorphisms influence the risk of developing monoclonal gammopathy of undetermined significance. International journal of cancer, 159(2), 410.

Zhang J, et al. (2026) Association of the FTO gene polymorphism with the features of the clinical course of tuberculosis infection. BMC infectious diseases, 26(1).

Yu EY, et al. (2026) Trans-ethnic estimation and implications of genetic impact on continuous glycemic profiles. Cell discovery, 12(1).

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).

Djuric T, et al. (2026) Association Between Multiple Sclerosis Severity and Functional Variants in Key Antioxidant Defense and Ferroptosis-Related Genes. Biology, 15(10).

Wang X, et al. (2026) Mapping Genetic Regulation of Transcription to Identify Functional Variants and Genes Associated with Pancreatic Cancer Risk. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(29), e17184.

Heumann P, et al. (2026) Genetic determinants of fatigue up to 2 years after radiotherapy in prostate cancer patients. Nature communications, 17(1).

Hwang LD, et al. (2026) A biologically informed framework for instrument selection in dietary Mendelian randomization using chemosensory genetics. BMC medicine, 24(1).

De Marco R, et al. (2026) Novel Potential Risk Loci for Migraine in the Portuguese Population. International journal of molecular sciences, 27(12).

Tiwari HK, et al. (2026) Exploration of Regulatory Elements, MicroRNAs, and Copy Number Variation in Urogenital Chlamydia Reinfection in African American Women. International journal of molecular sciences, 27(12).

de Magalhães Filho MF, et al. (2026) BCL11A and HBS1L-MYB polymorphisms, in association with hydroxyurea and sex, modulate fetal hemoglobin levels in individuals with sickle cell anemia in the western region of Bahia, Brazil. Molecular biology reports, 53(1).

Timasheva Y, et al. (2026) Integrative Analysis of Oxidative Stress and Cellular Senescence Pathways in Chronic Obstructive Pulmonary Disease. Genes, 17(6).

Srb N, et al. (2026) Hypoxia-Inducible Factor 1-? in Autoimmune Diseases-Insights from the Paradigm of Hashimoto's Thyroiditis: A Narrative Review. Medical sciences (Basel, Switzerland), 14(1).

Contreras AG, et al. (2026) Genetic modifiers of APOE-?4-associated cognitive decline. Nature communications, 17(1).

Fang X, et al. (2026) The AGPS regulatory variant rs113671272 confers esophageal squamous cell carcinoma susceptibility through allele-specific MEIS3 binding and NF-?B activation in Chinese populations. EBioMedicine, 127, 106249.

Cabrera-Serrano AJ, et al. (2026) Identification of new overlapping and disease-specific genetic risk factors for rheumatoid arthritis and radiographic axial spondyloarthritis: a meta-analysis of three large European populations and functional characterization. Frontiers in immunology, 17, 1637735.

Li Q, et al. (2026) Influence of MTHFD1L variants on the susceptibility to hypertension in the Chinese Han population. Annals of medicine, 58(1), 2553213.