

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 2, 2026

HaploReg

RRID:SCR_006796

Type: Tool

Proper Citation

HaploReg (RRID:SCR_006796)

Resource Information

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

Proper Citation: HaploReg (RRID:SCR_006796)

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

Funding: NHGRI R01-HG004037;
NHGRI RC1-HG005334;
NSF 0644282

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: 20260829T182944+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 [SPARC SAWG](#) .

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.

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

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).

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

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

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).

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 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 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).

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).

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

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.

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).

Camarota F, et al. (2026) Molecular Basis of Adenomatous Gastrointestinal Polyposis Syndromes: Role of Pathogenic and Benign Variants in Disease Onset. *Biomedicines*, 14(2).

Wang Y, et al. (2026) Genetic associations of LXN polymorphisms with toxicities of platinum-based concurrent chemoradiotherapy of nasopharyngeal carcinoma. *Supportive care in cancer : official journal of the Multinational Association of Supportive Care in Cancer*, 34(3), 166.