

Resource Summary Report

Generated by PRECISE-TBI on Aug 1, 2026

LDHEATMAP

RRID:SCR_006312

Type: Tool

Proper Citation

LDHEATMAP (RRID:SCR_006312)

Resource Information

URL: <https://cran.r-project.org/web/packages/LDheatmap/index.html>

Proper Citation: LDHEATMAP (RRID:SCR_006312)

Description: Software application that plots measures of pairwise linkage disequilibria for SNPs (entry from Genetic Analysis Software)

Synonyms: R/LDHEATMAP

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, r

Resource Name: LDHEATMAP

Resource ID: SCR_006312

Alternate IDs: nlx_154424, SCR_009347, nlx_154561

Old URLs: <http://stat-db.stat.sfu.ca:8080/statgen/research/LDheatmap>

Record Creation Time: 20220129T080235+0000

Record Last Update: 20260731T042721+0000

Ratings and Alerts

No rating or validation information has been found for LDHEATMAP.

No alerts have been found for LDHEATMAP.

Data and Source Information

Usage and Citation Metrics

We found 160 mentions in open access literature.

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

Gardner KA, et al. (2025) Genome-wide association analysis identifies seven loci conferring resistance to multiple wheat foliar diseases, including brown and yellow rust resistance originating from *Aegilops ventricosa*. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 138(6), 133.

Lynch RC, et al. (2025) Domesticated cannabinoid synthases amid a wild mosaic cannabis pangenome. Nature, 643(8073), 1001.

Sun H, et al. (2025) Elite Alleles of EPE1 Identified via Genome-wide Association Studies Increase Panicle Elongation Length in Rice. Rice (New York, N.Y.), 18(1), 4.

Liu P, et al. (2025) SNP variation landscape of BMP15 gene from 75 global sheep breeds and their genetic effect on lambing traits. Frontiers in veterinary science, 12, 1612263.

Wang R, et al. (2025) Integration of GWAS and transcriptome analysis to identify temperature-dependent genes involved in germination of rapeseed (*Brassica napus* L.). Frontiers in plant science, 16, 1551317.

Lesturgie P, et al. (2025) Short-term evolutionary implications of an introgressed size-determining supergene in a vulnerable population. Nature communications, 16(1), 1096.

Liu H, et al. (2025) A single-base mutation in promoter of CsTPR enhances the negative regulation on mechanical-related leaf drooping in tea plants. Horticulture research, 12(7), uhaf098.

Meade RK, et al. (2025) Cathepsin Z is a conserved susceptibility factor underlying tuberculosis severity. PLoS biology, 23(9), e3003377.

Zhong Y, et al. (2025) ZmCCD8 regulates sugar and amino acid accumulation in maize kernels via strigolactone signalling. Plant biotechnology journal, 23(2), 492.

Yang X, et al. (2025) BR signalling haplotypes contribute to indica-japonica differentiation for grain yield and quality in rice. Plant biotechnology journal, 23(5), 1618.

Hartmann FE, et al. (2025) An Inversion Polymorphism Under Balancing Selection, Involving Giant Mobile Elements, in an Invasive Fungal Pathogen. Molecular biology and evolution, 42(2).

Lee BS, et al. (2025) NXPE1 alters the sialoglycome by acetylating sialic acids in the human colon. Nature communications, 16(1), 4912.

De-Kayne R, et al. (2025) Incomplete recombination suppression fuels extensive haplotype diversity in a butterfly colour pattern supergene. PLoS biology, 23(2), e3003043.

Hori K, et al. (2025) QTN detection and candidate gene identification for improved eating and cooking quality in rice using GWAS and PLS regression analysis. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 138(3), 58.

Jaegle B, et al. (2025) k-mer-based GWAS in a wheat collection reveals novel and diverse sources of powdery mildew resistance. Genome biology, 26(1), 172.

Augustinsson A, et al. (2025) Interplay between AHR genotypes, lifestyle factors and adjuvant breast cancer treatments significantly impacts clinical outcome in a population-based cohort. BJC reports, 3(1), 51.

Guo F, et al. (2025) Antagonistic effects of selection on alleles associated with seed size and seed dormancy in wheat. Genome biology, 26(1), 304.

Domínguez-Rondón A, et al. (2025) Integrating host-pathogen interaction genomics to boost wheat defense against septoria tritici blotch. BMC genomics, 26(1), 1066.

Mulim HA, et al. (2024) Detection and evaluation of parameters influencing the identification of heterozygous-enriched regions in Holstein cattle based on SNP chip or whole-genome sequence data. BMC genomics, 25(1), 726.

Wright TIC, et al. (2024) A new winter wheat genetic resource harbors untapped diversity from synthetic hexaploid wheat. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 137(3), 73.