

Resource Summary Report

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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 application, software resource

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: 20260821T193746+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 169 mentions in open access literature.

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

Duan YW, et al. (2026) Module-level recombination drives DBLMSP polymorphism and functional conservation in *Plasmodium falciparum*. *Parasite* (Paris, France), 33, 24.

Naing NNZN, et al. (2026) Unraveling the Genetic Architecture of Photoperiod Sensitivity in Myanmar Rice Landraces Through Integrated GWAS and Transcriptome Analysis. *International journal of molecular sciences*, 27(4).

Babiye B, et al. (2026) Multi-locus genome-wide association mapping reveals loci underlying malt quality traits in heterogeneous Ethiopian Barley (*Hordeum vulgare* L.) germplasm. *Scientific reports*, 16(1).

Liu J, et al. (2026) A functional variant in the porcine APOA2 promoter alters hepatic gene expression via ROR α . *Scientific reports*, 16(1).

Ramirez-Gil JG, et al. (2026) GermVersity: A free and user-friendly interface to enhance the visualization and analysis of genebank data. *PloS one*, 21(1), e0340826.

Wang D, et al. (2026) Natural variation in PtoCPK3 governs drought tolerance by orchestrating xylem remodeling and lignin metabolism in *Populus*. *Science advances*, 12(23), eade2172.

Babiye B, et al. (2026) Genome-wide association study of pre-indicative agronomic traits affecting malt quality in Ethiopian barley (*Hordeum vulgare* L.) germplasm. *BMC genomics*, 27(1), 151.

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.

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.

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.

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.

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.

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

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).

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

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