

Resource Summary Report

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CMplot

RRID:SCR_024514

Type: Tool

Proper Citation

CMplot (RRID:SCR_024514)

Resource Information

URL: <https://CRAN.R-project.org/package=CMplot>

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Description: Software drawing R package designed for Manhattan plot of genomic analysis.

Synonyms: Circle Manhattan Plot

Resource Type: software resource, software toolkit

Keywords: drawing tool, Manhattan plot of genomic analysis,

Availability: Free, Available for download, Freely available

Resource Name: CMplot

Resource ID: SCR_024514

Alternate URLs: <https://github.com/YinLiLin/CMplot>

License: GNU GPL v3.0

Record Creation Time: 20231002T161337+0000

Record Last Update: 20260821T194302+0000

Ratings and Alerts

No rating or validation information has been found for CMplot.

No alerts have been found for CMplot.

Data and Source Information

Usage and Citation Metrics

We found 96 mentions in open access literature.

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

Huang X, et al. (2026) PMEL governs autosomal dominant inheritance of white-tail independent of yellow body plumage in chickens (*Gallus gallus domesticus*). *Poultry science*, 105(1), 106127.

Rathore M, et al. (2026) Genetic dissection of cold stress tolerance and yield potential under cold stress in nested synthetic wheat (*Triticum aestivum* L.) introgression libraries using multi-locus genome-wide association and haplotype analysis. *Functional & integrative genomics*, 26(1).

Potapenko E, et al. (2026) Intraspecific genome size variation is attributed to adaptive silencing of transposable elements in *Hordeum* species. *Molecular biology and evolution*, 43(3).

Song Q, et al. (2026) Uncovering the Genetic Basis of Grain Protein Content and Wet Gluten Content in Common Wheat (*Triticum aestivum* L.). *Plants (Basel, Switzerland)*, 15(2).

Neto JBS, et al. (2026) Modeling genotype-by-environment interactions across climatic conditions reveals environment-specific genomic regions and candidate genes underlying feed efficiency traits in tropical beef cattle. *Scientific reports*, 16(1), 643.

Liu Q, et al. (2026) Genome-wide association study of myopia progression in Chinese adolescents and application of polygenic risk score prediction. *Frontiers in chemistry*, 14, 1778732.

Chen T, et al. (2026) Genomic and transcriptomic insights into color pigmentation variation in barred chickens. *Poultry science*, 105(10), 107245.

An D, et al. (2026) Sweet Potato Gene Clusters Control Anthocyanin Biosynthesis and Leaf Morphology. *Plant biotechnology journal*, 24(7), 4500.

Sun J, et al. (2026) An integrated QTL-GWAS approach fine-maps a major locus (qMWS3 - 2) for stable resistance to maize white spot in tropical germplasm. *BMC plant biology*, 26(1).

You Q, et al. (2026) Sub-pangenome analysis reveals structural variants associated with fruit color and bacterial wilt resistance in eggplant. *Nature communications*, 17(1).

Salek Ardestani S, et al. (2026) GENOVIS: a Python package for the visualization of population genetic analyses. *BMC genomics*, 27(1), 190.

Babu P, et al. (2026) Dissecting adult plant resistance to stripe and leaf rust in advanced Indian wheat breeding lines through a genome-wide association study. *BMC plant biology*,

26(1).

Jiang F, et al. (2026) Machine learning identifies a NETs-related four-gene diagnostic signature for abdominal aortic aneurysm. *Medicine*, 105(21), e48987.

Yang Y, et al. (2026) Identification of Body Color-Related QTLs in Leopard Coral Grouper (*Plectropomus leopardus*) Based on GWAS and the HSV Color System. *Animals : an open access journal from MDPI*, 16(11).

Tu Y, et al. (2026) Identification of molecular markers associated with comb traits through genome-wide association study on a specialized strain of yellow feathered broilers. *Poultry science*, 105(1), 106125.

Hsiao YW, et al. (2026) Whole-Genome Sequencing Reveals Genetic Diversity and Structure of Taiwan Commercial Red-Feathered Country Chickens. *Animals : an open access journal from MDPI*, 16(2).

Shango AJ, et al. (2026) Genetic diversity and population structure of jute mallow (*Corchorus olitorius* L.) global collection to guide conservation and breeding. *The plant genome*, 19(2), e70252.

Wang L, et al. (2025) Integrative GWAS and transcriptomics reveal GhAMT2 as a key regulator of cotton resistance to *Verticillium* wilt. *Frontiers in plant science*, 16, 1563466.

Silva Neto JB, et al. (2025) Genome-wide association study for feed efficiency indicator traits in Nellore cattle considering genotype-by-environment interactions. *Frontiers in genetics*, 16, 1539056.

Xiong Y, et al. (2025) Analysis of allohexaploid wheatgrass genome reveals its Y haplome origin in Triticeae and high-altitude adaptation. *Nature communications*, 16(1), 3104.