

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>

Proper Citation: CMplot (RRID:SCR_024514)

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: 20260725T191112+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 56 mentions in open access literature.

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

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.

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.

Wang R, et al. (2025) Evaluation and genome-wide association study of saline-alkali tolerance in high-latitude rice resource populations. *Frontiers in genetics*, 16, 1617034.

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.

Yang X, et al. (2025) Novel candidate genes and genetic basis analysis of kernel starch content in tropical maize. *BMC plant biology*, 25(1), 105.

Ramasamy R, et al. (2025) Genome-wide allele-specific expression in multi-tissue samples from healthy male baboons reveals the transcriptional complexity of mammals. *Cell genomics*, 5(5), 100823.

Zhang X, et al. (2025) Co-Selection of Low Cadmium Accumulation and High Yield During Tomato Improvement. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(39), e05138.

Liu F, et al. (2025) First development of a 100??K SNP array for small yellow croaker and its application in genomic selection for growth and disease resistance. *BMC genomics*, 26(1), 1139.

Lhamo D, et al. (2025) Genome-wide association studies on resistance to powdery mildew in cultivated emmer wheat. *The plant genome*, 18(1), e20493.

Jiang X, et al. (2025) A significant genomic region underlying growth traits in adult Beijing You chicken identified by genome-wide association analysis. *Poultry science*, 104(9), 105326.

Alahmad S, et al. (2025) Phenotyping the hidden half: combining UAV phenotyping and machine learning to predict barley root traits in the field. *Journal of experimental botany*, 76(17), 5161.

Agre PA, et al. (2025) Genome wide association studies in yam reveal the challenge of high heterozygosity. *Scientific reports*, 15(1), 26929.

Huang X, et al. (2025) Genome-wide association study reveals candidate genes associated with egg-laying performance in Wuhua yellow chicken. *Poultry science*, 104(11), 105739.

Weng J, et al. (2025) Identifying potential drug targets for sepsis-related adult respiratory distress syndrome through comprehensive genetic analysis and druggability assessment. *Journal of global health*, 15, 04117.

Lin L, et al. (2025) Multi-omics analysis unveiled fibroblast-mediated pathogenesis in male genital lichen sclerosis. *Cell & bioscience*, 15(1), 113.

Liu R, et al. (2025) A special short-wing petal faba genome and genetic dissection of floral and yield-related traits accelerate breeding and improvement of faba bean. *Genome biology*, 26(1), 62.

Ni A, et al. (2025) Identifying candidate genetic variants for egg number by analyzing over 1,000 fully sequenced layers. *GigaScience*, 14.

Chybowska AD, et al. (2025) A blood- and brain-based EWAS of smoking. *Nature communications*, 16(1), 3210.

Wang Y, et al. (2025) easyEWAS: a flexible and user-friendly R package for epigenome-wide association study. *Bioinformatics advances*, 5(1), vbaf026.