

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

[qqman](#)

RRID:SCR_024293

Type: Tool

Proper Citation

qqman (RRID:SCR_024293)

Resource Information

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

Proper Citation: qqman (RRID:SCR_024293)

Description: Software R package to create Q-Q and manhattan plots for GWAS data from PLINK output files.

Resource Type: software resource, software toolkit

Defining Citation: [DOI:10.1101/005165](https://doi.org/10.1101/005165)

Keywords: create Q-Q and manhattan plots, GWAS data, PLINK output files,

Availability: Free, Available for download, Freely available,

Resource Name: qqman

Resource ID: SCR_024293

Alternate IDs: OMICS_12451

Alternate URLs: <https://sources.debian.org/src/r-cran-qqman/>

License: GPL-3

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260801T190856+0000

Ratings and Alerts

No rating or validation information has been found for qqman.

No alerts have been found for qqman.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Zhou X, et al. (2025) Characterization of m6A-regulated targets and immune cells in dental caries: insights from multi-omics analysis. *European journal of medical research*, 30(1), 1258.

Bielski W, et al. (2025) Molecular dissection of the genetic architecture of phenology underlying *Lupinus hispanicus* early flowering and adaptation to winter- or spring sowing. *Scientific reports*, 15(1), 15324.

Cuenca-Guardiola J, et al. (2025) Advanced analysis of retrotransposon variation in the human genome with nanopore sequencing using RetroInspector. *Scientific reports*, 15(1), 14489.

Ibrahim A, et al. (2024) Genome sequencing of *Plasmodium malariae* identifies continental segregation and mutations associated with reduced pyrimethamine susceptibility. *Nature communications*, 15(1), 10779.

Yang JS, et al. (2024) Genome-wide association study and polygenic risk scores predict psoriasis and its shared phenotypes in Taiwan. *Molecular medicine reports*, 30(1).

Zhang S, et al. (2024) Exploring the influence of a single-nucleotide mutation in EIN4 on tomato fruit firmness diversity through fruit pericarp microstructure. *Plant biotechnology journal*, 22(9), 2379.

Tsukamoto M, et al. (2024) GWAS of Folate Metabolism With Gene-environment Interaction Analysis Revealed the Possible Role of Lifestyles in the Control of Blood Folate Metabolites in Japanese: The J-MICC Study. *Journal of epidemiology*, 34(5), 228.

Li T, et al. (2024) N6-methyladenosine-associated genetic variants in NECTIN2 and HPCAL1 are risk factors for abdominal aortic aneurysm. *iScience*, 27(4), 109419.

Kamitaki N, et al. (2024) A sequence of SVA retrotransposon insertions in ASIP shaped human pigmentation. *Nature genetics*, 56(8), 1583.

Salami M, et al. (2023) Integration of genome-wide association studies, metabolomics, and transcriptomics reveals phenolic acid- and flavonoid-associated genes and their regulatory elements under drought stress in rapeseed flowers. *Frontiers in plant science*, 14, 1249142.

Piccardi M, et al. (2023) Exploring the Neandertal legacy of pancreatic ductal adenocarcinoma risk in Eurasians. *Biological research*, 56(1), 46.

He Z, et al. (2023) Combined effect of microbially derived cecal SCFA and host genetics on feed efficiency in broiler chickens. *Microbiome*, 11(1), 198.