

Resource Summary Report

Generated by [NIF](#) on Sep 5, 2026

R/SNP.PLOTTER

RRID:SCR_009376

Type: Tool

Proper Citation

R/SNP.PLOTTER (RRID:SCR_009376)

Resource Information

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

Proper Citation: R/SNP.PLOTTER (RRID:SCR_009376)

Description: An R package that creates publishable-quality plots of p-values using single SNP and/or haplotype data. Main features of the package include options to display a linkage disequilibrium (LD) plot and the ability to plot multiple sets of results simultaneously. Plots can be created using global and/or individual haplotype p-values along with single SNP p-values. Images are created as either Portable Document Format (PDF) or Encapsulated (EPS) files. (entry from Genetic Analysis Software)

Synonyms: SNP.PLOTTER

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, r

Resource Name: R/SNP.PLOTTER

Resource ID: SCR_009376

Alternate IDs: nlx_154599, SCR_009405, nlx_154649

Alternate URLs: https://github.com/cannin/snp_plotter

Old URLs: <http://cbdb.nimh.nih.gov/~kristin/snp.plotter.html>

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260904T000436+0000

Ratings and Alerts

No rating or validation information has been found for R/SNP.PLOTTER.

No alerts have been found for R/SNP.PLOTTER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Chung CC, et al. (2013) Meta-analysis identifies four new loci associated with testicular germ cell tumor. Nature genetics, 45(6), 680.

Savage SA, et al. (2013) Genome-wide association study identifies two susceptibility loci for osteosarcoma. Nature genetics, 45(7), 799.