

Resource Summary Report

Generated by [NIF](#) on Aug 6, 2026

[maps](#)

RRID:SCR_019296

Type: Tool

Proper Citation

maps (RRID:SCR_019296)

Resource Information

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

Proper Citation: maps (RRID:SCR_019296)

Description: Software R package to draw geographical maps.

Resource Type: data processing software, software application, data visualization software, software toolkit, software resource

Keywords: Maps display, geographical maps drawing

Availability: Free, Available for download, Freely available

Resource Name: maps

Resource ID: SCR_019296

License: GPL-2

Record Creation Time: 20220129T080344+0000

Record Last Update: 20260806T054713+0000

Ratings and Alerts

No rating or validation information has been found for maps.

No alerts have been found for maps.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 27 mentions in open access literature.

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

Guo Y, et al. (2025) A haplotype-based evolutionary history of barley domestication. *Nature*, 647(8090), 680.

Berger C, et al. (2025) In situ and in vitro cryo-EM reveal structures of mycobacterial encapsulin assembly intermediates. *Communications biology*, 8(1), 245.

Sadler MC, et al. (2025) Genetic determinants of zinc homeostasis and its role in cardiometabolic diseases. *PLoS genetics*, 21(12), e1011928.

Glemain B, et al. (2024) Estimating SARS-CoV-2 infection probabilities with serological data and a Bayesian mixture model. *Scientific reports*, 14(1), 9503.

Letcher B, et al. (2024) Role for gene conversion in the evolution of cell-surface antigens of the malaria parasite *Plasmodium falciparum*. *PLoS biology*, 22(3), e3002507.

Wright DJ, et al. (2024) An international estimate of the prevalence of differing visual imagery abilities. *Frontiers in psychology*, 15, 1454107.

Zhao D, et al. (2024) Members of the class *Candidatus Ordosarchaeia* imply an alternative evolutionary scenario from methanogens to haloarchaea. *The ISME journal*, 18(1).

Abhari N, et al. (2024) Measuring genetic diversity across populations. *PLoS computational biology*, 20(12), e1012651.

Stormo BM, et al. (2024) Intrinsically disordered sequences can tune fungal growth and the cell cycle for specific temperatures. *Current biology : CB*, 34(16), 3722.

Saha I, et al. (2023) The AAA+ chaperone VCP disaggregates Tau fibrils and generates aggregate seeds in a cellular system. *Nature communications*, 14(1), 560.

Kusmec A, et al. (2023) A genetic tradeoff for tolerance to moderate and severe heat stress in US hybrid maize. *PLoS genetics*, 19(7), e1010799.

Tamaki I, et al. (2023) Phylogenetic, population structure, and population demographic analyses reveal that *Vicia sepium* in Japan is native and not introduced. *Scientific reports*, 13(1), 20746.

Chong F, et al. (2023) High concentrations of floating neustonic life in the plastic-rich North Pacific Garbage Patch. *PLoS biology*, 21(5), e3001646.

Wu D, et al. (2022) Dual genome-wide coding and lncRNA screens in neural induction of induced pluripotent stem cells. *Cell genomics*, 2(11).

Kreiling AK, et al. (2022) Invertebrate communities in springs across a gradient in thermal regimes. *PloS one*, 17(5), e0264501.

Lenton TM, et al. (2022) Resilience of countries to COVID-19 correlated with trust. *Scientific reports*, 12(1), 75.

Fukunaga K, et al. (2022) Recombinant inbred lines and next-generation sequencing enable rapid identification of candidate genes involved in morphological and agronomic traits in foxtail millet. *Scientific reports*, 12(1), 218.

Parry R, et al. (2021) Uncovering the Worldwide Diversity and Evolution of the Virome of the Mosquitoes *Aedes aegypti* and *Aedes albopictus*. *Microorganisms*, 9(8).

, et al. (2021) From grassroots to global: A blueprint for building a reproducibility network. *PLoS biology*, 19(11), e3001461.

Wu H, et al. (2021) Identification of a novel interplay between intestinal bacteria and metabolites in Chinese patients with IgA nephropathy via integrated microbiome and metabolome approaches. *Annals of translational medicine*, 9(1), 32.