

Resource Summary Report

Generated by ASWG on Aug 9, 2026

vcfR

RRID:SCR_023453

Type: Tool

Proper Citation

vcfR (RRID:SCR_023453)

Resource Information

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

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Description: Software R package to read, write, manipulate and analyze variant call format data. Facilitates easy manipulation of variant call format (VCF) data.

Synonyms: variant call format in R

Resource Type: software resource, software toolkit

Keywords: Manipulate and visualize VCF data, variant call format data, VCF data, extract data matrices, genomic data visualization, VCF file, variant call format files,

Availability: Free, Available for download, Freely available

Resource Name: vcfR

Resource ID: SCR_023453

Alternate URLs: https://knausb.github.io/vcfR_documentation/, <https://github.com/knausb/vcfR>, https://cran.r-project.org/web/packages/vcfR/vignettes/intro_to_vcfR.html,

License: GPL v3

Record Creation Time: 20230411T050206+0000

Record Last Update: 20260808T190534+0000

Ratings and Alerts

No rating or validation information has been found for vcfR.

No alerts have been found for vcfr.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Brown N, et al. (2026) Replication stress increases de novo CNVs across the malaria parasite genome. *Nucleic acids research*, 54(1).

George SL, et al. (2025) Stratified Medicine Pediatrics: Cell-Free DNA and Serial Tumor Sequencing Identifies Subtype-Specific Cancer Evolution and Epigenetic States. *Cancer discovery*, 15(4), 717.

Curry E, et al. (2025) Surveillance of single nucleotide polymorphisms correlated to macrocyclic lactone resistance in *Dirofilaria immitis* from client-owned dogs across the United States. *International journal for parasitology. Drugs and drug resistance*, 29, 100604.

Brown N, et al. (2024) Replication stress increases de novo CNVs across the malaria parasite genome. *bioRxiv : the preprint server for biology*.

Aribi HB, et al. (2024) NeuroVar: an open-source tool for the visualization of gene expression and variation data for biomarkers of neurological diseases. *GigaByte (Hong Kong, China)*, 2024, gigabyte143.

Chen C, et al. (2024) GWAS reveals a rapidly evolving candidate avirulence effector in the *Cercospora* leaf spot pathogen. *Molecular plant pathology*, 25(1), e13407.

Howard-McCombe J, et al. (2023) Genetic swamping of the critically endangered Scottish wildcat was recent and accelerated by disease. *Current biology : CB*, 33(21), 4761.

Barbosa CFC, et al. (2023) Genome-Wide SNP and Indel Discovery in Abaca (*Musa textilis* N??e) and among Other *Musa* spp. for Abaca Genetic Resources Management. *Current issues in molecular biology*, 45(7), 5776.

Chakrabarty S, et al. (2022) Genetic and genomic diversity in the sorghum gene bank collection of Uganda. *BMC plant biology*, 22(1), 378.