

Resource Summary Report

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VCFtools

RRID:SCR_001235

Type: Tool

Proper Citation

VCFtools (RRID:SCR_001235)

Resource Information

URL: <https://vcftools.github.io/index.html>

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Description: Software package for working with VCF files. Used to provide easily accessible methods for working with complex genetic variation data in the form of VCF files. Implements various utilities for processing Variant Call Format files, including validation, merging, comparing. Provides general Perl API.

Synonyms: Variant Call Format Tools

Resource Type: data management software, software application, software resource

Defining Citation: [PMID:21653522](#), [DOI:10.1093/bioinformatics/btr330](#)

Keywords: perl, genetic variation, variant call format, software, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: VCFtools

Resource ID: SCR_001235

Alternate IDs: OMICS_02105, SCR_012092, biotools:vcftools, OMICS_05112

Alternate URLs: <https://bio.tools/vcftools>, <https://sources.debian.org/src/vcftools/>

Old URLs: <http://vcftools.sourceforge.net/>

License: GNU Lesser General Public License v3

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260821T193629+0000

Ratings and Alerts

No rating or validation information has been found for VCFtools.

No alerts have been found for VCFtools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4555 mentions in open access literature.

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

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing Cobitis. *GigaScience*, 15.

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Lu Q, et al. (2026) Genomic characterization and pathogenicity validation of *Mycoplasma ovipneumoniae* strains from diseased sheep: insights into potential pathogenic mechanisms of GSWW364. *Veterinary research*, 57(1).

Yu K, et al. (2026) Phase II Trial of Ixazomib Combined with Gemcitabine and Doxorubicin in Patients with SMARCB1-Deficient Renal Medullary Carcinoma. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(10), 1946.

McFarland LN, et al. (2026) The dilution effect of stocking and the loss of wildness among North American mallards. *Current biology : CB*.

Liu Q, et al. (2026) Structural variation drives praziquantel response and host adaptation in *Schistosoma japonicum*. *iScience*, 29(6), 116118.

Denis H, et al. (2026) Contrasting population structures of reef-building corals and their algal symbionts inform adaptive potential across the western Pacific. *Current biology : CB*, 36(11), 2808.

Cappadona C, et al. (2026) Multi-omics identifies oxidative stress, prothrombotic pathways, and lactoperoxidase variants as key factors in COVID-19 severity. *EBioMedicine*, 123, 106111.

Ma Y, et al. (2026) Gene-culture coevolution shapes olfactory receptor gene diversity in Orang Asli populations. *Cell reports*, 117181.

Zhu C, et al. (2026) Identification of non-canonical peptides with moPepGen. *Nature biotechnology*, 44(4), 568.

Navarro D, et al. (2026) Development of High-Throughput Genomic Resources to Inform White-Tailed Deer Population and Disease Management. *Molecular ecology resources*, 26(1), e70085.

Hu H, et al. (2026) Structural variation drives rhizome innovation and adaptive divergence in sister *Medicago* species. *Journal of integrative plant biology*, 68(2), 406.

Liu J, et al. (2026) Genomic signatures of selection reveal genetic mechanisms underlying economic traits in Licha black pigs. *Animal bioscience*, 39(5), 250712.

Crego-Walters M, et al. (2026) Targeted Chromosomal Sequencing of Wild Bonobos Identifies a Genetically Distinct Subpopulation East of the Lomami River. *bioRxiv : the preprint server for biology*.

Xiao H, et al. (2026) Gene Flow and Habitat Heterogeneity Shape Coexistence Dynamics of Arctic Charr Morphs in Connected Lakes. *Molecular ecology*, 35(2), e70225.

Hagen IJ, et al. (2026) Genetic Markers for Tracing Introgression of Farmed Atlantic Salmon (*Salmo salar*) in Wild Conspecifics. *Molecular ecology resources*, 26(1), e70065.

Bai X, et al. (2026) Genome Variation Map: a platform for the analysis and integration of genomic variation. *Nucleic acids research*, 54(D1), D1208.

Rattanawong K, et al. (2026) Autonomous development and regeneration of isolated rice egg cells in vitro in a fertilization-independent manner. *Journal of experimental botany*, 77(2), 463.

Brown N, et al. (2026) SVCROWS: a user-defined tool for interpreting significant structural variants in heterogeneous datasets. *Nucleic acids research*, 54(1).

Koster S, et al. (2026) Five Hidden Species in a Widespread European Vertebrate: Disentangling the Alpine Newt Cryptic Species Complex Through Genomic Phylogeography. *Molecular ecology*, 35(5), e70300.