

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: software resource, software application, data management software

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, biotools:vcftools, SCR_012092, 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: 20260801T190135+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 4095 mentions in open access literature.

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

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.

Yu J, et al. (2026) Unraveling the population genetic structure and identifying candidate genes for dorsal plumage color in Liangshan Yanying chickens. Poultry science, 105(1), 106180.

Singh G, et al. (2026) Genetic analysis of a quantitative trait locus associated with resistance to the root-lesion nematode *Pratylenchus neglectus* in triticale. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 139(1), 24.

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.

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.

Waesch C, et al. (2026) Population-wide single-pollen nuclei genotyping in rye sheds light on the genetic basis and environmental plasticity of meiotic recombination. The New phytologist, 249(1), 512.

Mohn RA, et al. (2026) Variant Calling in the Goldilocks Zone: How Reference Genome Choice and Read Mapping Stringency Impact Heterozygosity Estimates and Phylogenetic Analyses. Molecular ecology resources, 26(1), e70079.

Estand??a A, et al. (2026) The Genetic Consequences of Dispersal and Immigration in a Wild Great Tit Population. Molecular ecology, 35(1), e70206.

Teng CS, et al. (2026) Actomyosin contractility and a threshold of cadherin cell adhesion are required during tissue fusion. The Journal of cell biology, 225(1).

Nachtigall PG, et al. (2026) The Golden Lancehead Genome Reveals Distinct Selective Processes Acting on Venom Genes of an Island Endemic Snake. *Genome biology and evolution*, 18(1).

Jeon JY, et al. (2026) Short-Read Pangenomes and Their Potential Utility in Population and Conservation Genomics. *Molecular ecology resources*, 26(1), e70060.

Huang X, et al. (2026) PMEL governs autosomal dominant inheritance of white-tail independent of yellow body plumage in chickens (*Gallus gallus domesticus*). *Poultry science*, 105(1), 106127.

Taylor RS, et al. (2026) Accurate Runs of Homozygosity Estimation From Low Coverage Genome Sequences in Non-Model Species. *Molecular ecology resources*, 26(1), e70083.

Voisin C, et al. (2026) Spatiotemporal Diversification of Forest Understorey Species Reveals the Existence of Multiple Pleistocene Forest Refugia in Central Europe. *Molecular ecology*, 35(1), e70200.

Cao C, et al. (2025) A near telomere-to-telomere genome assembly of the Jinhua pig: enabling more accurate genetic research. *GigaScience*, 14.

Kershenbaum S, et al. (2025) Variation in phenotype, genotype, and somatic diversity among asexual *Schmidtea mediterranea* planarians. *iScience*, 28(8), 113035.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. *GigaScience*, 14.

Wang G, et al. (2025) Genomic evidence for hybridization and introgression between blue peafowl and endangered green peafowl and molecular foundation of leucistic plumage of blue peafowl. *GigaScience*, 14.

Chen H, et al. (2025) Chromosome-level genome assembly of *Pinus massoniana* provides insights into conifer adaptive evolution. *GigaScience*, 14.

Chase MA, et al. (2025) Evidence that genetic drift not adaptation drives fast-Z and large-Z effects in *Ficedula* flycatchers. *Molecular ecology*, 34(18), e17262.