

# Resource Summary Report

Generated by [NIF](#) on Sep 2, 2026

## CNVnator

RRID:SCR\_010821

Type: Tool

### Proper Citation

CNVnator (RRID:SCR\_010821)

### Resource Information

**URL:** <http://sv.gersteinlab.org/cnvnator/>

**Proper Citation:** CNVnator (RRID:SCR\_010821)

**Description:** An approach to discover, genotype, and characterize typical and atypical CNVs from family and population genome sequencing.

**Abbreviations:** CNVnator

**Resource Type:** software resource

**Resource Name:** CNVnator

**Resource ID:** SCR\_010821

**Alternate IDs:** OMICS\_00343

**Record Creation Time:** 20220129T080300+0000

**Record Last Update:** 20260829T182347+0000

### Ratings and Alerts

No rating or validation information has been found for CNVnator.

No alerts have been found for CNVnator.

### Data and Source Information

**Source:** [SciCrunch Registry](#)

### Usage and Citation Metrics

We found 547 mentions in open access literature.

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

Chirmade S, et al. (2026) GWAS SVatalog: a visualization tool to aid fine-mapping of GWAS loci with structural variations. *Heredity*, 135(3), 199.

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

Tang Y, et al. (2026) Genomic variation analysis and discovery of stable heterozygous loci in Loquat (*Eriobotrya Japonica* Lindl.). *BMC plant biology*, 26(1).

Smolen C, et al. (2026) Protocol for identifying genetic modifiers of phenotypes in individuals with disease-associated variants. *STAR protocols*, 7(2), 104546.

de Araujo AT, et al. (2026) KitBase Expanded: An Integrated Genomic and Phenotypic Resource for 3,268 Fast-Neutron-Irradiated Rice Mutants. *Database : the journal of biological databases and curation*, 2026.

Bohner F, et al. (2026) Micafungin microevolution in *Candida auris* reveals resistance development without in vivo fitness compromise. *Virulence*, 17(1), 2664993.

Kusumoto-Matsuo R, et al. (2026) Genome instability is increased during DNA replication in the presence of the CPD UV photoproduct in transcriptionally active genes. *iScience*, 29(7), 116322.

Si YW, et al. (2026) Evolution of rhizobial siderophore utilization via accessory xeno-siderophore receptors and flexible intake machinery for self-produced siderophores. *The ISME journal*, 20(1).

Tasnawijitwong N, et al. (2026) Characterization of adaptive evolution strains for the development of triclosan resistance in *Agrobacterium tumefaciens* C58. *Applied and environmental microbiology*, 92(1), e0123225.

Wang W, et al. (2026) Whole-genome resequencing and genetic diversity of five indigenous cattle breeds from China. *Scientific data*, 13(1), 282.

Ahmed L, et al. (2026) A novel phenotype-guided genome analysis pipeline for variant discovery. *NPJ genomic medicine*, 11(1).

Zhang J, et al. (2026) Genomic resequencing provides new insights into ecological diversification of four *Saccharina Japonica* varieties. *BMC genomics*, 27(1).

Wang Y, et al. (2026) Detection and evaluation of copy number variation using both linked-read and short-read sequencing in New Zealand dairy cattle. *Frontiers in genetics*, 17, 1856199.

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

Hua R, et al. (2026) Genetic risk assessment of pregnancy-associated venous thromboembolism: dual utility of maternal peripheral blood in NIPT and VTE evaluation. BMC pregnancy and childbirth, 26(1), 123.

Wang J, et al. (2026) Genetic diagnosis in fetal hydronephrosis: assessment using chromosomal microarray analysis and whole-genome sequencing. Human genomics, 20(1).

Bircham PW, et al. (2026) Distinctive domestication of farmhouse beer yeasts preserved pre-industrial genetic and phenotypic diversity. Current biology : CB, 36(8), 2028.

Chai Y, et al. (2026) A Comprehensive Adenoid Cystic Carcinoma-Derived Organoid Platform for Disease Modeling and Drug Screening Captures Interpatient Heterogeneity. Cells, 15(4).

Marangoni S, et al. (2026) GeNePi: a graphics processing unit enhanced next-generation bioinformatics pipeline for whole-genome sequencing analysis. Briefings in bioinformatics, 27(1).

Zhou R, et al. (2026) Structural and mechanistic insights into the dual-nuclease defense protein Upx as an anti-phage system. Nature communications, 17(1).