

Resource Summary Report

Generated by [ASWG](#) on Aug 4, 2026

CNVnator

RRID:SCR_010821

Type: Tool

Proper Citation

CNVnator (RRID:SCR_010821)

Resource Information

URL: <http://sv.gersteinlab.org/cnvator/>

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: 20260801T190358+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 510 mentions in open access literature.

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

Garcia GL, et al. (2025) Aged and BRCA-Mutated Stromal Cells Drive Epithelial Cell Transformation. *Cancer discovery*, 15(6), 1203.

Hemara LM, et al. (2025) Genomic Biosurveillance of the Kiwifruit Pathogen *Pseudomonas syringae* pv. *actinidiae* Biovar 3 Reveals Adaptation to Selective Pressures in New Zealand Orchards. *Molecular plant pathology*, 26(2), e70056.

Hu L, et al. (2025) Regulating cellular metabolism and morphology to achieve high-yield synthesis of hyaluronan with controllable molecular weights. *Nature communications*, 16(1), 2076.

Ma W, et al. (2025) Whole-genome and whole-exome sequencing of Mayer-Rokitansky-Küster-Hauser syndrome-discordant monozygotic twins. *Journal of assisted reproduction and genetics*, 42(5), 1577.

Zhao M, et al. (2025) RNA sequencing and genome-wide association analysis reveal key genes responsible for different feather colors in Youjiang goose. *Poultry science*, 104(8), 105305.

Lindelöf H, et al. (2025) Genome sequencing in a cohort of 32 fetuses with genetic skeletal disorders. *European journal of human genetics : EJHG*, 33(11), 1474.

Marín-Garzón NA, et al. (2025) Detection and functional assessment of structural variants using whole-genome re-sequencing data in Nellore cattle. *Scientific reports*, 15(1), 30364.

Zhang Y, et al. (2025) Liquid crystal-guided DNA information storage: Nondestructive recovery and long-term preservation. *Science advances*, 11(39), eadu3957.

Xu J, et al. (2025) Clinical use of whole-genome sequencing in children with developmental delay or intellectual disability. *BMC medical genomics*, 18(1), 188.

Ye H, et al. (2025) Integrated chloroplast genomics and whole-genome resequencing reveals demographic history and selection signatures of black walnuts. *The plant genome*, 18(4), e70172.

Vani S, et al. (2025) Genome-wide copy number variation regions in indigenous (*Bos indicus*) cattle breeds of Tamil Nadu, India. *Animal bioscience*, 38(3), 395.

Mouton A, et al. (2025) Genetic and Anatomical Determinants of Olfaction in Dogs and Wild Canids. *Molecular biology and evolution*, 42(3).

Yang Y, et al. (2025) A De Novo Frameshift Variant in *SMC1A* Causes Non-Classic Cornelia de Lange Syndrome With Epilepsy: A Case Report and Literature Review. *Molecular genetics & genomic medicine*, 13(1), e70058.

De La Vega FM, et al. (2025) Benchmarking of germline copy number variant callers from whole genome sequencing data for clinical applications. *Bioinformatics advances*, 5(1), vbaf071.

Sugawara R, et al. (2025) A Pleiotropic and Functionally Divergent RAC3 Variant Disrupts Neurodevelopment and Impacts Organogenesis. *Cells*, 14(19).

Samano A, et al. (2025) Genome Structural Variants Shape Adaptive Success of an Invasive Urban Malaria Vector *Anopheles stephensi*. *Molecular biology and evolution*, 42(6).

Khor SS, et al. (2025) LILR genotype imputation with attribute bagging (LIBAG): leukocyte immunoglobulin-like receptor copy number imputation system. *Frontiers in immunology*, 16, 1559301.

Ehn E, et al. (2025) A de novo, mosaic and complex chromosome 21 rearrangement causes APP triplication and familial autosomal dominant early onset Alzheimer disease. *Scientific reports*, 15(1), 2912.

Behera S, et al. (2025) Comprehensive genome analysis and variant detection at scale using DRAGEN. *Nature biotechnology*, 43(7), 1177.

Zhang DF, et al. (2025) Prediction of mild cognitive impairment using blood multi-omics data. *Frontiers in genetics*, 16, 1552063.