

Resource Summary Report

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CNVpytor

RRID:SCR_021627

Type: Tool

Proper Citation

CNVpytor (RRID:SCR_021627)

Resource Information

URL: <https://github.com/abyzovlab/CNVpytor>

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Description: Software Python package and command line tool for CNV/CNA analysis from depth of coverage by mapped reads. Software tool for CNV/CNA detection and analysis from read depth and allele imbalance in whole genome sequencing.

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource

Defining Citation: [DOI:10.1101/2021.01.27.428472](https://doi.org/10.1101/2021.01.27.428472)

Keywords: Copy number variations, copy number alternations, whole genome sequencing, Python

Funding: NCI U24 CA220242

Availability: Free, Available for download, Freely available

Resource Name: CNVpytor

Resource ID: SCR_021627

License: MIT License

Record Creation Time: 20220129T080356+0000

Record Last Update: 20260821T194212+0000

Ratings and Alerts

No rating or validation information has been found for CNVpytor.

No alerts have been found for CNVpytor.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

Zhang Z, et al. (2026) Persistence and spread of fluconazole-resistant *Candida parapsilosis* clinical isolates associated with increased ERG11 copies in Qatar. *Microbial genomics*, 12(2).

Nguyen TT, et al. (2026) Genome-Wide Analysis of Copy Number Variation in Vietnamese Local Chickens. *Animals : an open access journal from MDPI*, 16(7).

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 H, et al. (2026) Long-term outcomes by clinical and molecular risk stratification in patients with medulloblastoma receiving risk-adapted therapy. *Med (New York, N.Y.)*, 7(5), 101076.

Onetto CA, et al. (2025) Genetic and phenotypic diversity of wine-associated *Hanseniaspora* species. *FEMS yeast research*, 25.

Maron B, et al. (2025) Uncovering the genetic basis of *Staphylococcus aureus* resistance to single antimicrobial peptides and their combinations. *iScience*, 28(6), 112671.

Lei X, et al. (2025) Adaptive laboratory evolution of *Lachancea thermotolerans* for enhanced production of 2-Phenylethanol and 2-Phenylethyl acetate in wine. *Food chemistry: X*, 27, 102483.

Wallander K, et al. (2025) Optical Genome Mapping versus Whole-Genome Sequencing in the Clinical Diagnosis of Gynecologic Mesenchymal Tumors. *The Journal of molecular diagnostics : JMD*.

Wang H, et al. (2025) Copy Number Variation and Haplotype Analysis of 17q21.31 Reveals Increased Risk Associated with Progressive Supranuclear Palsy and Gene Expression Changes in Neuronal Cells. *Movement disorders : official journal of the Movement Disorder Society*, 40(5), 950.

Jain K, et al. (2025) Genomic analyses reveal high diversity and rapid evolution of *Pichia kudriavzevii* within a neonatal intensive care unit in Delhi, India. *Antimicrobial agents and chemotherapy*, 69(3), e0170924.

Taylor AM, et al. (2025) A feasibility study of enzymatic methylation sequencing of cell-free DNA from cerebrospinal fluid of pediatric central nervous system tumor patients for molecular classification. *Neuro-oncology advances*, 7(1), vdaf159.

Mirahmadi M, et al. (2025) Genetic Heterogeneity of Autism Spectrum Disorder: Identification of Five Novel Mutations (RIMS2, FOXP1, AUTS2, ZCCHC17, and SPTBN5) in Iranian Families via Whole-Exome and Whole-Genome Sequencing. *Biochemical genetics*.

Boehler NA, et al. (2024) A novel copy number variant in the murine *Cdh23* gene gives rise to profound deafness and vestibular dysfunction. *Human molecular genetics*, 33(19), 1648.

Xie X, et al. (2024) Genome wide detection of CNV and their association with body size in Danzhou chickens. *Poultry science*, 103(12), 104266.

Wang C, et al. (2024) High-depth whole-genome sequencing identifies structure variants, copy number variants and short tandem repeats associated with Parkinson's disease. *NPJ Parkinson's disease*, 10(1), 134.

Panda A, et al. (2024) Genome-wide analysis and visualization of copy number with CNVpytor in igv.js. *Bioinformatics (Oxford, England)*, 40(8).

Liu YF, et al. (2024) Genetic architecture of long-distance migration and population genomics of the endangered Japanese eel. *iScience*, 27(8), 110563.

Garrison MA, et al. (2023) Genomic data resources of the Brain Somatic Mosaicism Network for neuropsychiatric diseases. *Scientific data*, 10(1), 813.

Reis ALM, et al. (2023) The landscape of genomic structural variation in Indigenous Australians. *Nature*, 624(7992), 602.

Sun Z, et al. (2023) Performance comparisons of methylation and structural variants from low-input whole-genome methylation sequencing. *Epigenomics*, 15(1), 11.