Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

CNVpytor

RRID:SCR_021627
Type: Tool

Proper Citation

CNVpytor (RRID:SCR_021627)

Resource Information

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

Proper Citation: CNVpytor (RRID:SCR_021627)

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

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: 20260905T132943+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 PRECISE-TBI .

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.

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.

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

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, FOXG1, 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.