

# Resource Summary Report

Generated by T1D on Sep 5, 2026

## cn.mops

RRID:SCR\_013036

Type: Tool

### Proper Citation

cn.mops (RRID:SCR\_013036)

### Resource Information

**URL:** <http://bioconductor.org/packages/2.12/bioc/html/cn.mops.html>

**Proper Citation:** cn.mops (RRID:SCR\_013036)

**Description:** A data processing pipeline for copy number variations and aberrations (CNVs and CNAs) from next generation sequencing (NGS) data.

**Abbreviations:** cn.mops

**Synonyms:** Copy Number estimation by a Mixture Of PoissonS

**Resource Type:** software resource

**Keywords:** bio.tools

**Resource Name:** cn.mops

**Resource ID:** SCR\_013036

**Alternate IDs:** biotools:cn.mops, OMICS\_00335

**Alternate URLs:** <https://bio.tools/cn.mops>

**Record Creation Time:** 20220129T080313+0000

**Record Last Update:** 20260903T235203+0000

### Ratings and Alerts

No rating or validation information has been found for cn.mops.

No alerts have been found for cn.mops.

### Data and Source Information

## Usage and Citation Metrics

We found 10 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

Louw N, et al. (2023) Incorporating CNV analysis improves the yield of exome sequencing for rare monogenic disorders-an important consideration for resource-constrained settings. *Frontiers in genetics*, 14, 1277784.

Bijarnia-Mahay S, et al. (2022) Growth and neurodevelopmental disorder with arthrogryposis, microcephaly and structural brain anomalies caused by Bi-allelic partial deletion of SMPD4 gene. *Journal of human genetics*, 67(3), 133.

Belyeu JR, et al. (2021) De novo structural mutation rates and gamete-of-origin biases revealed through genome sequencing of 2,396 families. *American journal of human genetics*, 108(4), 597.

Song L, et al. (2020) Integrated Analysis of Gene Expression, SNP, InDel, and CNV Identifies Candidate Avirulence Genes in Australian Isolates of the Wheat Leaf Rust Pathogen *Puccinia triticina*. *Genes*, 11(9).

Zhao L, et al. (2020) Comparative study of whole exome sequencing-based copy number variation detection tools. *BMC bioinformatics*, 21(1), 97.

Kommadath A, et al. (2019) A large interactive visual database of copy number variants discovered in taurine cattle. *GigaScience*, 8(6).

Raman L, et al. (2019) WisecondorX: improved copy number detection for routine shallow whole-genome sequencing. *Nucleic acids research*, 47(4), 1605.

Genova F, et al. (2018) First genome-wide CNV mapping in FELIS CATUS using next generation sequencing data. *BMC genomics*, 19(1), 895.

Krishnaprasad GN, et al. (2015) Variation in crossover frequencies perturb crossover assurance without affecting meiotic chromosome segregation in *Saccharomyces cerevisiae*. *Genetics*, 199(2), 399.

Petrovics G, et al. (2015) A novel genomic alteration of LSAMP associates with aggressive prostate cancer in African American men. *EBioMedicine*, 2(12), 1957.