

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

mrCaNaVaR

RRID:SCR_003135

Type: Tool

Proper Citation

mrCaNaVaR (RRID:SCR_003135)

Resource Information

URL: <http://mrcanavar.sourceforge.net/>

Proper Citation: mrCaNaVaR (RRID:SCR_003135)

Description: Copy number caller that analyzes the whole-genome next-generation sequence mapping read depth to discover large segmental duplications and deletions. It also has the capability of predicting absolute copy numbers of genomic intervals.

Abbreviations: mrCaNaVaR

Synonyms: mrCaNaVaR - micro-read Copy Number Variant Regions, micro-read Copy Number Variant Regions

Resource Type: software resource

Keywords: genome, next-generation sequence, duplication, deletion, copy number variant, bio.tools

Availability: Free, Freely available

Resource Name: mrCaNaVaR

Resource ID: SCR_003135

Alternate IDs: OMICS_02138, nlx_156790, biotools:mrcanavar

Alternate URLs: <https://bio.tools/mrcanavar>

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260808T185800+0000

Ratings and Alerts

No rating or validation information has been found for mrCaNaVaR.

No alerts have been found for mrCaNaVaR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Scheer K, et al. (2026) Rapid adaptive increase of amylase gene copy number in Indigenous Andeans. *Nature communications*, 17(1).

Brown N, et al. (2026) SVCROWS: a user-defined tool for interpreting significant structural variants in heterogeneous datasets. *Nucleic acids research*, 54(1).

Aversano R, et al. (2024) Distinct structural variants and repeat landscape shape the genomes of the ancient grapes Aglianico and Falanghina. *BMC plant biology*, 24(1), 88.

??zden F, et al. (2022) Polishing copy number variant calls on exome sequencing data via deep learning. *Genome research*, 32(6), 1170.

Catacchio CR, et al. (2019) Transcriptomic and genomic structural variation analyses on grape cultivars reveal new insights into the genotype-dependent responses to water stress. *Scientific reports*, 9(1), 2809.

Kuderna LFK, et al. (2019) Selective single molecule sequencing and assembly of a human Y chromosome of African origin. *Nature communications*, 10(1), 4.

Zhang L, et al. (2019) Comprehensively benchmarking applications for detecting copy number variation. *PLoS computational biology*, 15(5), e1007069.

Komissarov A, et al. (2018) B Chromosomes of the Asian Seabass (*Lates calcarifer*) Contribute to Genome Variations at the Level of Individuals and Populations. *Genes*, 9(10).

Zhernakova DV, et al. (2018) Analytical "bake-off" of whole genome sequencing quality for the Genome Russia project using a small cohort for autoimmune hepatitis. *PloS one*, 13(7), e0200423.

Mak SST, et al. (2017) Comparative performance of the BGISEQ-500 vs Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. *GigaScience*, 6(8), 1.

Rubin BE, et al. (2016) Comparative genomics reveals convergent rates of evolution in ant-plant mutualisms. *Nature communications*, 7, 12679.

Usher CL, et al. (2015) Structural forms of the human amylase locus and their relationships to SNPs, haplotypes and obesity. *Nature genetics*, 47(8), 921.

Dobrynin P, et al. (2015) Genomic legacy of the African cheetah, *Acinonyx jubatus*. *Genome biology*, 16, 277.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. *Database : the journal of biological databases and curation*, 2015.

Zhao M, et al. (2013) Computational tools for copy number variation (CNV) detection using next-generation sequencing data: features and perspectives. *BMC bioinformatics*, 14 Suppl 11(Suppl 11), S1.

Miyake K, et al. (2013) Comparison of Genomic and Epigenomic Expression in Monozygotic Twins Discordant for Rett Syndrome. *PloS one*, 8(6), e66729.