# 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/

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**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.

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

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

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.