Resource Summary Report

Generated by dkNET on May 20, 2025

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

Funding:

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: 20250519T203234+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 14 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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.

Özden 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.

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

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

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.

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

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.