Resource Summary Report

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cuteSV

RRID:SCR_025233
Type: Tool

Proper Citation

cuteSV (RRID:SCR_025233)

Resource Information

URL: https://github.com/tjiangHIT/cuteSV

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Description: Software tool for long read based human genomic structural variation detection. Collects signatures of various types of SVs and employs clustering-and-refinement method to analyze signatures to implement sensitive SV detection.cuteSV2 is upgraded version of cuteSV.

Synonyms: cuteSV2

Resource Type: source code, data processing software, data analysis software, software resource, software application

Defining Citation: DOI:10.1101/2022.08.29.505534, PMID:35751813

Keywords: long-read-based SV detection, structural variation, SV detection, structural variation detection, long read based human genomic structural variation detection,

Funding: NSF of China

Availability: Free, Available for download, Freely available

Resource Name: cuteSV

Resource ID: SCR_025233

License: MIT license

Record Creation Time: 20240409T053245+0000

Record Last Update: 20250429T060406+0000

Ratings and Alerts

No rating or validation information has been found for cuteSV.

No alerts have been found for cuteSV.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Li R, et al. (2025) SUMMER: an integrated nanopore sequencing pipeline for variants detection and clinical annotation on the human genome. Functional & integrative genomics, 25(1), 21.

Margalit S, et al. (2025) Long-read structural and epigenetic profiling of a kidney tumor-matched sample with nanopore sequencing and optical genome mapping. NAR genomics and bioinformatics, 7(1), lqae190.

O'Neill K, et al. (2024) Long-read sequencing of an advanced cancer cohort resolves rearrangements, unravels haplotypes, and reveals methylation landscapes. Cell genomics, 4(11), 100674.

Luo C, et al. (2024) VolcanoSV enables accurate and robust structural variant calling in diploid genomes from single-molecule long read sequencing. Nature communications, 15(1), 6956.

Yuan N, et al. (2024) Comprehensive assessment of long-read sequencing platforms and calling algorithms for detection of copy number variation. Briefings in bioinformatics, 25(5).

Cao S, et al. (2024) Gapless genome assembly and epigenetic profiles reveal gene regulation of whole-genome triplication in lettuce. GigaScience, 13.

Margalit S, et al. (2024) Long-Read Structural and Epigenetic Profiling of a Kidney Tumor-Matched Sample with Nanopore Sequencing and Optical Genome Mapping. bioRxiv : the preprint server for biology.

Mc Cartney AM, et al. (2021) An international virtual hackathon to build tools for the analysis of structural variants within species ranging from coronaviruses to vertebrates. F1000Research, 10, 246.

Schwarz JM, et al. (2021) Novel sequencing technologies and bioinformatic tools for deciphering the non-coding genome. Medizinische Genetik : Mitteilungsblatt des Berufsverbandes Medizinische Genetik e.V, 33(2), 133.