Resource Summary Report

Generated by NIF on Sep 17, 2026

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

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: 20260912T200440+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 20 mentions in open access literature.

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

Bimbocci A, et al. (2026) SnakeBITE: A SNAKEmake-Based Interface for Third-Generation Sequencing Data Analysis. Biomolecules, 16(2).

Wu SX, et al. (2026) Dynamic regulation of spermatogenesis and hybrid sterility revealed by single-cell analysis in yak and cattle. Molecular biology and evolution, 43(2).

Meng Q, et al. (2025) Pangenome analysis reveals yield- and fiber-related diversity and interspecific gene flow in Gossypium barbadense L. Nature communications, 16(1), 4995.

Munro R, et al. (2025) Enhancing nanopore adaptive sampling for PromethION using readfish at scale. Genome research, 35(4), 877.

Cuenca-Guardiola J, et al. (2025) Advanced analysis of retrotransposon variation in the human genome with nanopore sequencing using RetroInspector. Scientific reports, 15(1), 14489.

Gedamu AM, et al. (2025) Research evolution of flat peach (Prunus persica (L.) Batsch): a decadal bibliometric analysis. Frontiers in plant science, 16, 1710142.

Wold JR, et al. (2025) The promise and challenges of characterizing genome-wide structural variants: A case study in a critically endangered parrot. Molecular ecology resources, 25(5), e13783.

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.

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.

Nair S, et al. (2025) Pooled, Long-read Sequencing for Structural Variant Characterization in Schistosome Populations. Genome biology and evolution, 17(7).

Aydin SK, et al. (2025) Benchmarking long-read structural variant calling tools and combinations for detecting somatic variants in cancer genomes. Scientific reports, 15(1),

8707.

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

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).

English AC, et al. (2024) K-mer analysis of long-read alignment pileups for structural variant genotyping. bioRxiv : the preprint server for biology.

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.

Kaplun L, et al. (2023) ONT long-read WGS for variant discovery and orthogonal confirmation of short read WGS derived genetic variants in clinical genetic testing. Frontiers in genetics, 14, 1145285.

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.