

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

Defining Citation: [DOI:10.1101/2022.08.29.505534](https://doi.org/10.1101/2022.08.29.505534), [PMID:35751813](https://pubmed.ncbi.nlm.nih.gov/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: 20260821T043126+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),

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.