

Resource Summary Report

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Sniffles

RRID:SCR_017619

Type: Tool

Proper Citation

Sniffles (RRID:SCR_017619)

Resource Information

URL: <https://github.com/fritzsedlazeck/Sniffles>

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Description: Software tool as structural variation caller using third generation sequencing (PacBio or Oxford Nanopore). It detects all types of SVs (10bp+) using evidence from split-read alignments, high-mismatch regions, and coverage analysis. Used to avoid single molecule long read sequencing high error rates.

Resource Type: software resource, software application, data processing software

Defining Citation: [PMID:29713083](#)

Keywords: Structural, variation, caller, third, generation, sequencing, SV, split, read, alignment, mismatch, region, analysis, error, bio.tools

Funding: NHGRI R01 HG006677;
NHGRI UM1 HG008898

Availability: Free, Available for download, Freely available

Resource Name: Sniffles

Resource ID: SCR_017619

Alternate IDs: biotools:sniffles

Alternate URLs: <https://bio.tools/sniffles>

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260801T190844+0000

Ratings and Alerts

No rating or validation information has been found for Sniffles.

No alerts have been found for Sniffles.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 59 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Schall PZ, et al. (2025) Integrative Genotyping and Analysis of Canine Structural Variation Using Long-read and Short-read Data. *Genome biology and evolution*, 17(10).

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.

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.

Padilla-García N, et al. (2025) The Demographic History of Populations and Genomic Imprinting have Shaped the Transposon Patterns in *Arabidopsis lyrata*. *Molecular biology and evolution*, 42(5).

Parida P, et al. (2025) Precise identification of viral-host integration events in HPV-positive cervical cancers by targeted long-read sequencing. *Tumour virus research*, 20, 200325.

Colombini L, et al. (2025) A 69.9-kb long inverted repeat increases genome instability in a strain of *Lactobacillus crispatus*. *NAR genomics and bioinformatics*, 7(2), lqaf085.

Izydorczyk MB, et al. (2025) Single cell long read whole genome sequencing reveals somatic transposon activity in human brain. *Communications biology*, 8(1), 1627.

Su X, et al. (2025) The promising role of nanopore sequencing in cancer diagnostics and treatment. *Cell insight*, 4(2), 100229.

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.

Khan N, et al. (2025) Human Papillomavirus Integration Induces Oncogenic Host Gene Fusions in Oropharyngeal Cancers. *Cancer discovery*, 15(9), 1927.

Peter CJ, et al. (2024) Single chromatin fiber profiling and nucleosome position mapping in the human brain. *Cell reports methods*, 4(12), 100911.

- Smolka M, et al. (2024) Detection of mosaic and population-level structural variants with Sniffles2. *Nature biotechnology*, 42(10), 1571.
- 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.
- Bivona D, et al. (2024) Generation and Characterization of Stable Small Colony Variants of USA300 *Staphylococcus aureus* in RAW 264.7 Murine Macrophages. *Antibiotics (Basel, Switzerland)*, 13(3).
- Ijaz J, et al. (2024) Haplotype-specific assembly of shattered chromosomes in esophageal adenocarcinomas. *Cell genomics*, 4(2), 100484.
- Alvarez Viar G, et al. (2024) Protofilament-specific nanopatterns of tubulin post-translational modifications regulate the mechanics of ciliary beating. *Current biology : CB*, 34(19), 4464.
- Yan X, et al. (2024) Molecular diagnosis, clinical evaluation and phenotypic spectrum of Townes-Brocks syndrome: insights from a large Chinese hearing loss cohort. *Journal of medical genetics*, 61(5), 459.
- Low EL, et al. (2024) Chromosome-scale *Elaeis guineensis* and *E. oleifera* assemblies: comparative genomics of oil palm and other Arecaceae. *G3 (Bethesda, Md.)*, 14(9).
- Grochowski CM, et al. (2024) Inverted triplications formed by iterative template switches generate structural variant diversity at genomic disorder loci. *Cell genomics*, 4(7), 100590.
- Kuznetsov N, et al. (2024) CNV-Finder: Streamlining Copy Number Variation Discovery. *bioRxiv : the preprint server for biology*.