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;
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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: 20260731T043012+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 kravitz2 .

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.

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.

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

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

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.

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

Ijaz J, et al. (2024) Haplotype-specific assembly of shattered chromosomes in esophageal adenocarcinomas. Cell genomics, 4(2), 100484.

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).

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.