

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: data processing software, software application, software resource

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: 20260905T133054+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 76 mentions in open access literature.

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

Marcuzzo C, et al. (2026) High-quality chromosome-scale genome assemblies of 29 maize inbred lines of European breeding relevance. *Scientific data*, 13(1).

Pradhan B, et al. (2026) Dynamic and Ongoing De Novo L1 Retrotransposition Contributes to Genome Plasticity and Intrapatient Heterogeneity in Ovarian Cancer. *Cancer research*, 86(4), 1073.

Wen J, et al. (2026) De Novo Assembly of Eight Commercial Crossbred Pig Genomes Provides Insights into the Potential Functional Impact of Structural Variation Hotspots. *Biomolecules*, 16(2).

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

Gao S, et al. (2026) Optimal Preservation Method for Long-term Preservation in ddH₂O and Starvation Adaptive Mechanisms of *Flavobacterium columnare* Revealed by Multi-omic Analysis. *Microbial ecology*, 89(1).

Modlin SJ, et al. (2026) Pervasive genome structure heterogeneity in *Mycobacterium tuberculosis* constitutively generates subpopulations with distinct clinical phenotypes. *iScience*, 29(5), 115045.

Mortazavi M, et al. (2026) Long-read genome sequencing improves detection and functional interpretation of structural and repeat variants in autism. *Cell genomics*, 6(5), 101186.

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.

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.

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).

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).

Zhang Z, et al. (2025) Cost-effective and flexible preimplantation genetic testing (PGT) by nanopore adaptive sampling. *Journal of nanobiotechnology*, 24(1), 35.

Wang Y, et al. (2025) Long-read sequencing reveals HBV integration patterns and oncogenic impact on early-onset hepatocellular carcinoma. *Genome research*, 35(11), 2389.

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 W, et al. (2025) Deconvolution of the On-Target Activity of Plasmepsin V Peptidomimetics in *Plasmodium falciparum* Parasites. *ACS infectious diseases*, 11(12), 3581.

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

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.