

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

SomaticSniper

RRID:SCR_005108

Type: Tool

Proper Citation

SomaticSniper (RRID:SCR_005108)

Resource Information

URL: <http://gmt.genome.wustl.edu/somatic-sniper/current/>

Proper Citation: SomaticSniper (RRID:SCR_005108)

Description: Software program to identify single nucleotide positions that are different between tumor and normal (or, in theory, any two bam files). It takes a tumor bam and a normal bam and compares the two to determine the differences. It outputs a file in a format very similar to Samtools consensus format. It uses the genotype likelihood model of MAQ (as implemented in Samtools) and then calculates the probability that the tumor and normal genotypes are different. This probability is reported as a somatic score. The somatic score is the Phred-scaled probability (between 0 to 255) that the Tumor and Normal genotypes are not different where 0 means there is no probability that the genotypes are different and 255 means there is a probability of $1 - 10^{-(255/-10)}$ that the genotypes are different between tumor and normal. This is consistent with how the SAM format reports such probabilities. It is currently available as source code via github or as a Debian APT package.

Abbreviations: SomaticSniper

Resource Type: software resource

Defining Citation: [PMID:22155872](#)

Related Condition: Cancer, Tumor, Normal

Availability: Acknowledgement requested

Resource Name: SomaticSniper

Resource ID: SCR_005108

Alternate IDs: OMICS_00092

Record Creation Time: 20220129T080228+0000

Ratings and Alerts

No rating or validation information has been found for SomaticSniper.

No alerts have been found for SomaticSniper.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 146 mentions in open access literature.

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

Cheng Y, et al. (2025) Stromal architecture and fibroblast subpopulations with opposing effects on outcomes in hepatocellular carcinoma. *Cell discovery*, 11(1), 1.

Ren W, et al. (2025) Whole-genome sequencing reveals three follicular lymphoma subtypes with distinct cell of origin and patient outcomes. *Cell reports. Medicine*, 6(8), 102278.

Zenga J, et al. (2025) Radiation therapy results in preferential tumor antigen-specific lymphodepletion in head and neck cancer. *Nature communications*, 16(1), 5660.

Karasozen Y, et al. (2025) Low-Allele-Frequency Somatic Variants in a Cohort of Sporadic Saccular "Berry" Cerebral Aneurysms. *Journal of the American Heart Association*, 14(18), e032483.

Morote-Faubel M, et al. (2025) Unveiling splicing disruptions due to common somatic variants in acute myeloid leukemia. *Human genomics*, 19(1), 129.

Wang S, et al. (2025) TMBquant: an explainable AI-powered caller advancing tumor mutation burden quantification across heterogeneous samples. *Briefings in bioinformatics*, 26(5).

Yamaguchi TN, et al. (2025) The Germline and Somatic Origins of Prostate Cancer Heterogeneity. *Cancer discovery*, 15(5), 988.

Ertürk RA, et al. (2025) From ideal to practical: Heterogeneity of student-generated variant lists highlights hidden reproducibility gaps. *PLoS computational biology*, 21(10), e1013552.

Xu X, et al. (2025) The landscape of N6-methyladenosine in localized primary prostate cancer. *Nature genetics*, 57(4), 934.

He S, et al. (2025) Comprehensive assessment of computational methods for cancer immunoediting. *Cell reports methods*, 5(3), 101006.

Zhao F, et al. (2025) Mono-ubiquitination of TopBP1 by PHRF1 enhances ATR activation and genomic stability. *Nucleic acids research*, 53(5).

Ye L, et al. (2025) Neoantigen load as a predictor of relapse in early-stage NSCLC: features that agonise and antagonise prognosis. *Cancer immunology, immunotherapy : CII*, 74(9), 285.

Wan H, et al. (2025) Tumor evolution and immune microenvironment dynamics in primary and relapsed mantle cell lymphoma. *Cell reports. Medicine*, 6(9), 102318.

Ahlgren L, et al. (2025) The genomic landscape of relapsed infant and childhood KMT2A-rearranged acute leukemia. *Nature communications*, 16(1), 8964.

Juric I, et al. (2025) Single-cell RNA-sequencing of BCG naïve and recurrent non-muscle invasive bladder cancer reveals a CD6/ALCAM-mediated immune-suppressive pathway. *NPJ precision oncology*, 9(1), 318.

Park J, et al. (2024) DeepSomatic: Accurate somatic small variant discovery for multiple sequencing technologies. *bioRxiv : the preprint server for biology*.

Guille A, et al. (2024) A benchmarking study of individual somatic variant callers and voting-based ensembles for whole-exome sequencing. *Briefings in bioinformatics*, 26(1).

Wang NK, et al. (2024) StableLift: Optimized Germline and Somatic Variant Detection Across Genome Builds. *bioRxiv : the preprint server for biology*.

Larkin J, et al. (2024) Nilotinib in KIT-driven advanced melanoma: Results from the phase II single-arm NICAM trial. *Cell reports. Medicine*, 5(3), 101435.

Ramakrishnan S, et al. (2024) Race-specific coregulatory and transcriptomic profiles associated with DNA methylation and androgen receptor in prostate cancer. *Genome medicine*, 16(1), 52.