Resource Summary Report

Generated by T1D on Sep 5, 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

Record Last Update: 20260903T234746+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 152 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Kuo HH, et al. (2026) Patient-derived organoids across cancers reveal conserved tumor heterogeneity and actionable therapeutic vulnerabilities. Science advances, 12(26), eadz3351.

Fleming AM, et al. (2026) Developmental reprogramming underlies chemotherapy resistance in favorable-histology Wilms tumor. Cell reports, 45(3), 117063.

Scimeca M, et al. (2026) Paired-Box (PAX) Gene Signatures as a Biomarker of Breast Cancer Progression. International journal of molecular sciences, 27(4).

Wang C, et al. (2026) A Deep Learning-Driven Framework Integrating Organoid-Based Functional Validation Identifies Universal Neoantigens from Recurrent Glioma Mutations. Cancer research, 86(12), 3074.

Aparicio B, et al. (2026) Immunogenicity of neoantigens from hepatocellular carcinoma patients treated with a combined radioimmunotherapy. Oncoimmunology, 15(1), 2645280.

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

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.

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.

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

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

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

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.

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.

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

Daniels CA, et al. (2025) Characterization of subclonal variants in HG002 Genome in a Bottle reference material as a resource for benchmarking variant callers. Cell genomics, 101104.

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.

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.