Resource Summary Report

Generated by RRID on Aug 4, 2026

SvABA

RRID:SCR_022998
Type: Tool

Proper Citation

SvABA (RRID:SCR_022998)

Resource Information

URL: https://github.com/walaj/svaba

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Description: Software tool for detecting structural variants in sequencing data using genome wide local assembly. Genome wide detection of structural variants and indels by local assembly. Used for detecting SVs from short read sequencing data using genome wide local assembly with low memory and computing requirements.

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

Defining Citation: PMID:29535149

Keywords: genome wide detection, structural variants, indels, local assembly

Funding: NHGRI T32 HG002295;
NCI U54CA143798;
NCI R01CA188228;
DFCI-Novartis Drug Discovery Program ;
Voices Against Brain Cancer ;
Pediatric Low-Grade Astrocytoma Foundation ;
Broad Institute ;
Wellcome Fund Career Award for Medical Scientists

Availability: Free, Available for download, Freely available

Resource Name: SvABA

Resource ID: SCR_022998

License: GPL v3.0

Record Creation Time: 20221124T050201+0000

Record Last Update: 20260804T043752+0000

Ratings and Alerts

No rating or validation information has been found for SvABA.

No alerts have been found for SvABA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Duan DM, et al. (2025) Comparisons of performances of structural variants detection algorithms in solitary or combination strategy. PloS one, 20(2), e0314982.

Zeng Y, et al. (2025) Mapping the chromothripsis landscape in urothelial carcinoma unravels great intratumoral and intertumoral heterogeneity. iScience, 28(1), 111510.

Sugo N, et al. (2025) DNA polymerase ?? suppresses somatic indels at CpG dinucleotides in developing cortical neurons. Proceedings of the National Academy of Sciences of the United States of America, 122(33), e2506846122.

Domenico D, et al. (2025) Enabling whole genome sequencing analysis from FFPE specimens in clinical oncology. Nature communications, 16(1), 10649.

Chukwu W, et al. (2025) A sequence context-based approach for classifying tumor structural variants without paired normal samples. Cell reports methods, 5(3), 100991.

Rekhtman N, et al. (2025) Chromothripsis-Mediated Small Cell Lung Carcinoma. Cancer discovery, 15(1), 83.

Persaud N, et al. (2025) Clinical Significance of TERT Promoter Mutations in Neuroblastoma. JCO precision oncology, 9, e2500074.

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.

Frank S, et al. (2024) Molecular consequences of acute versus chronic CDK12 loss in prostate carcinoma nominates distinct therapeutic strategies. bioRxiv : the preprint server for biology.

Nguyen DD, et al. (2024) The interplay of mutagenesis and ecDNA shapes urothelial cancer evolution. Nature, 635(8037), 219.

Schott CR, et al. (2024) Osteosarcoma PDX-Derived Cell Line Models for Preclinical Drug Evaluation Demonstrate Metastasis Inhibition by Dinaciclib through a Genome-Targeted Approach. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(4), 849.

Conway JR, et al. (2024) Somatic structural variants drive distinct modes of oncogenesis in melanoma. The Journal of clinical investigation, 134(13).

Khani F, et al. (2023) Evolution of structural rearrangements in prostate cancer intracranial metastases. NPJ precision oncology, 7(1), 91.

Di Genova A, et al. (2022) A molecular phenotypic map of malignant pleural mesothelioma. GigaScience, 12.