Resource Summary Report

Generated by NIF on Apr 20, 2025

SVDetect

RRID:SCR_010812
Type: Tool

Proper Citation

SVDetect (RRID:SCR_010812)

Resource Information

URL: http://svdetect.sourceforge.net/Site/Home.html

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Description: Software application for the isolation and the type prediction of intra- and inter-chromosomal rearrangements from paired-end/mate-pair sequencing data provided by the high-throughput sequencing technologies. This tool aims to identify structural variations with both clustering and sliding-window strategies, and helping in their visualization at the genome scale. It is compatible with SOLiD and Illumina (>=1.3) reads.

Abbreviations: SVDetect

Synonyms: SVDetect: a tool to detect genomic structural variations from paired-end and mate-pair sequencing data

Resource Type: software resource

Defining Citation: PMID:20639544

Keywords: structural variation, sequencing, chromosomal rearrangement, high-throughput sequencing, solid, illumina, genome, insertion, deletion, inversion, duplication, translocation, command-line, perl, bio.tools

Funding:

Availability: GNU General Public License, v3

Resource Name: SVDetect

Resource ID: SCR_010812

Alternate IDs: OMICS_00324, biotools:svdetect

Alternate URLs: https://bio.tools/svdetect

Record Creation Time: 20220129T080300+0000

Record Last Update: 20250420T014510+0000

Ratings and Alerts

No rating or validation information has been found for SVDetect.

No alerts have been found for SVDetect.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Yang M, et al. (2025) Molecular characterization of EBV-associated primary pulmonary lymphoepithelial carcinoma by multiomics analysis. BMC cancer, 25(1), 85.

Li X, et al. (2021) Genomic Feature Analysis of Betacoronavirus Provides Insights Into SARS and COVID-19 Pandemics. Frontiers in microbiology, 12, 614494.

Cline E, et al. (2020) Recalibration of mapping quality scores in Illumina short-read alignments improves SNP detection results in low-coverage sequencing data. PeerJ, 8, e10501.

Zhang X, et al. (2020) Osteogenesis imperfecta in a male holstein calf associated with a possible oligogenic origin. The veterinary quarterly, 40(1), 58.

Liu JJ, et al. (2020) Genomic, transcriptomic, and viral integration profiles associated with recurrent/metastatic progression in high-risk human papillomavirus cervical carcinomas. Cancer medicine, 9(21), 8243.

Al Abri MA, et al. (2020) Whole genome detection of sequence and structural polymorphism in six diverse horses. PloS one, 15(4), e0230899.

Bianchi JJ, et al. (2019) Breakage-Fusion-Bridge Events Trigger Complex Genome Rearrangements and Amplifications in Developmentally Arrested T Cell Lymphomas. Cell reports, 27(10), 2847.

Luukkonen TM, et al. (2018) Breakpoint mapping and haplotype analysis of translocation t(1;12)(q43;q21.1) in two apparently independent families with vascular phenotypes. Molecular genetics & genomic medicine, 6(1), 56.

Aristidou C, et al. (2018) Position effect, cryptic complexity, and direct gene disruption as disease mechanisms in de novo apparently balanced translocation cases. PloS one, 13(10), e0205298.

Fève K, et al. (2017) Identification of a t(3;4)(p1.3;q1.5) translocation breakpoint in pigs using somatic cell hybrid mapping and high-resolution mate-pair sequencing. PloS one, 12(11), e0187617.

Sivalingam J, et al. (2016) Multidimensional Genome-wide Analyses Show Accurate FVIII Integration by ZFN in Primary Human Cells. Molecular therapy : the journal of the American Society of Gene Therapy, 24(3), 607.

Lescale C, et al. (2016) RAG2 and XLF/Cernunnos interplay reveals a novel role for the RAG complex in DNA repair. Nature communications, 7, 10529.

Schütz E, et al. (2016) The Holstein Friesian Lethal Haplotype 5 (HH5) Results from a Complete Deletion of TBF1M and Cholesterol Deficiency (CDH) from an ERV-(LTR) Insertion into the Coding Region of APOB. PloS one, 11(4), e0154602.

Kang G, et al. (2016) Integrated genomic analyses identify frequent gene fusion events and VHL inactivation in gastrointestinal stromal tumors. Oncotarget, 7(6), 6538.

Gannon OM, et al. (2015) No association between HPV positive breast cancer and expression of human papilloma viral transcripts. Scientific reports, 5, 18081.

Pirooznia M, et al. (2015) Whole-genome CNV analysis: advances in computational approaches. Frontiers in genetics, 6, 138.

Wang Q, et al. (2015) VERSE: a novel approach to detect virus integration in host genomes through reference genome customization. Genome medicine, 7(1), 2.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.

Dorshorst B, et al. (2015) Dominant Red Coat Color in Holstein Cattle Is Associated with a Missense Mutation in the Coatomer Protein Complex, Subunit Alpha (COPA) Gene. PloS one, 10(6), e0128969.

Fonseca AC, et al. (2015) The segregation of different submicroscopic imbalances underlying the clinical variability associated with a familial karyotypically balanced translocation. Molecular cytogenetics, 8, 106.