

Resource Summary Report

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SURVIVOR

RRID:SCR_022995

Type: Tool

Proper Citation

SURVIVOR (RRID:SCR_022995)

Resource Information

URL: <https://github.com/fritzsedlazeck/SURVIVOR>

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Description: Software tool set for simulating and evaluating SVs, merging and comparing SVs within and among samples, and includes various methods to reformat or summarize SVs. Used for for SV simulation, comparison and filtering.

Abbreviations: SURVIVOR

Synonyms: StructURal Variant majorlty VOTE

Resource Type: software toolkit, software resource

Defining Citation: [PMID:28117401](#)

Keywords: Structural Variant, simulating and evaluating SVs, merging and comparing SVs, reformat or summarize SVs,

Funding: Swiss National Science Foundation ;
National Science Foundation DBI-1350041;
NHGRI R01-HG006677;
Wellcome Trust Senior Investigator Award ;
Royal Society Wolfson Research Merit Award ;
EPSRC Centre for Doctoral Training studentship at UCL CoMPLEX

Availability: Free, Available for download, Freely available

Resource Name: SURVIVOR

Resource ID: SCR_022995

License: MIT license

Record Creation Time: 20221124T050201+0000

Record Last Update: 20260810T040830+0000

Ratings and Alerts

No rating or validation information has been found for SURVIVOR.

No alerts have been found for SURVIVOR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Wu SX, et al. (2026) Dynamic regulation of spermatogenesis and hybrid sterility revealed by single-cell analysis in yak and cattle. *Molecular biology and evolution*, 43(2).

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

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.

Garcia GL, et al. (2025) Aged and BRCA-Mutated Stromal Cells Drive Epithelial Cell Transformation. *Cancer discovery*, 15(6), 1203.

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).

Gali KK, et al. (2025) Little millet genome reveals evolutionary insights into tetraploid structure and genetic basis of micronutrient density. *Nature communications*, 17(1), 74.

Cheng Y, et al. (2024) *Gossypium purpurascens* genome provides insight into the origin and domestication of upland cotton. *Journal of advanced research*, 56, 15.

Wang Y, et al. (2024) Mapping crossover events of mouse meiotic recombination by restriction fragment ligation-based Refresh-seq. *Cell discovery*, 10(1), 26.

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

Collins KM, et al. (2024) *Drosophila* Toxicogenomics: genetic variation and sexual dimorphism in susceptibility to 4-Methylimidazole. *Human genomics*, 18(1), 119.

Zhou BW, et al. (2023) Germline gene fusions across species reveal the chromosomal instability regions and cancer susceptibility. *iScience*, 26(12), 108431.

Shiraishi Y, et al. (2023) Precise characterization of somatic complex structural variations from tumor/control paired long-read sequencing data with nanomonsv. *Nucleic acids research*, 51(14), e74.

Xie H, et al. (2023) Long-read-based single sperm genome sequencing for chromosome-wide haplotype phasing of both SNPs and SVs. *Nucleic acids research*, 51(15), 8020.

Magi A, et al. (2023) GASOLINE: detecting germline and somatic structural variants from long-reads data. *Scientific reports*, 13(1), 20817.

Liu T, et al. (2023) Enhancer Coamplification and Hijacking Promote Oncogene Expression in Liposarcoma. *Cancer research*, 83(9), 1517.

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