Resource Summary Report

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DELLY

RRID:SCR_004603
Type: Tool

Proper Citation

DELLY (RRID:SCR_004603)

Resource Information

URL: https://tobiasrausch.com/delly/

Proper Citation: DELLY (RRID:SCR_004603)

Description: Integrated structural variant prediction software that can detect deletions, tandem duplications, inversions and translocations at single-nucleotide resolution in short-read massively parallel sequencing data. It uses paired-ends and split-reads to sensitively and accurately delineate genomic rearrangements throughout genome.

Abbreviations: DELLY

Synonyms: DELLY, Structural variant discovery by integrated paired-end and split-read analysis

Resource Type: software resource

Defining Citation: PMID:22962449, DOI:10.1093/bioinformatics/bts378

Keywords: structural variant, genomic rearrangement, deletion, tandem duplication, inversion, translocation, bio.tools

Funding:

Resource Name: DELLY

Resource ID: SCR_004603

Alternate IDs: OMICS_00313, biotools:delly2

Alternate URLs: https://bio.tools/delly2, https://github.com/dellytools/delly/,

https://sources.debian.org/src/delly/

License: BSD 3-Clause

Record Creation Time: 20220129T080225+0000

Record Last Update: 20250214T183019+0000

Ratings and Alerts

No rating or validation information has been found for DELLY.

No alerts have been found for DELLY.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 470 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Kokuryo T, et al. (2025) Whole-genome Sequencing Analysis of Bile Tract Cancer Reveals Mutation Characteristics and Potential Biomarkers. Cancer genomics & proteomics, 22(1), 34.

Wang F, et al. (2025) Deciphering the complex molecular architecture of the genetically modified soybean FG72 through paired-end whole genome sequencing. Food chemistry. Molecular sciences, 10, 100238.

Llargués-Sistac G, et al. (2025) Germline structural variant as the cause of Lynch Syndrome in a family from Ecuador. NPJ genomic medicine, 10(1), 3.

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

Zhang X, et al. (2025) Genomic variation responding to artificial selection on different lines of Pekin duck. Poultry science, 104(2), 104785.

Fay CX, et al. (2025) Global proteomics and affinity mass spectrometry analysis of human Schwann cells indicates that variation in and loss of neurofibromin (NF1) alters protein expression and cellular and mitochondrial metabolism. Scientific reports, 15(1), 3883.

Chojnacka M, et al. (2024) Impact of Rare Structural Variant Events in Newly Diagnosed Multiple Myeloma. Clinical cancer research : an official journal of the American Association

for Cancer Research, 30(3), 575.

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.

Yang Y, et al. (2024) Large tandem duplications in cancer result from transcription and DNA replication collisions. medRxiv : the preprint server for health sciences.

Baek B, et al. (2024) Integrated drug response prediction models pinpoint repurposed drugs with effectiveness against rhabdomyosarcoma. PloS one, 19(1), e0295629.

Liang X, et al. (2024) Genomic structural variation contributes to evolved changes in gene expression in high-altitude Tibetan sheep. Proceedings of the National Academy of Sciences of the United States of America, 121(27), e2322291121.

Zheng D, et al. (2024) Brd4::Nutm1 fusion gene initiates NUT carcinoma in vivo. Life science alliance, 7(7).

Nguyen HTL, et al. (2024) A platform for rapid patient-derived cutaneous neurofibroma organoid establishment and screening. Cell reports methods, 4(5), 100772.

Poikela N, et al. (2024) Chromosomal Inversions and the Demography of Speciation in Drosophila montana and Drosophila flavomontana. Genome biology and evolution, 16(3).

Kim R, et al. (2024) Clinical application of whole-genome sequencing of solid tumors for precision oncology. Experimental & molecular medicine, 56(8), 1856.

Yum SY, et al. (2024) Long-term (10-year) monitoring of transposon-mediated transgenic cattle. Transgenic research, 33(5), 503.

Huang Y, et al. (2024) Identification of structural variation related to spawn capability of Penaeus vannamei. BMC genomics, 25(1), 934.

Yuan N, et al. (2024) Comprehensive assessment of long-read sequencing platforms and calling algorithms for detection of copy number variation. Briefings in bioinformatics, 25(5).

Rajaby R, et al. (2024) SurVIndel2: improving copy number variant calling from next-generation sequencing using hidden split reads. Nature communications, 15(1), 10473.

Lee Y, et al. (2024) Prediction of the 3D cancer genome from whole-genome sequencing using InfoHiC. Molecular systems biology, 20(11), 1156.