Resource Summary Report

Generated by NIF on Aug 6, 2026

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

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: 20260801T190238+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 557 mentions in open access literature.

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

Quarello P, et al. (2026) DNA Methylation Episignature as a Novel Diagnostic Tool for Diamond-Blackfan Anemia Syndrome. American journal of hematology, 101(2), 228.

Bergsma P, et al. (2025) Integration of Whole-Genome Sequencing Analysis with Unique Patient-Derived Models Reveals Clinically Relevant Drug Targets in TFCP2 Fusion-Defined Rhabdomyosarcoma. Molecular cancer therapeutics, 24(12), 1989.

Huo ??? X, et al. (2025) Genome-wide Genetic Mutations Accumulated in Pigs Genome-edited for Xenotransplantation and Their Filial Generation. Genomics, proteomics & bioinformatics, 23(4).

Marín-Garzón NA, et al. (2025) Detection and functional assessment of structural variants using whole-genome re-sequencing data in Nellore cattle. Scientific reports, 15(1), 30364.

Jiang K, et al. (2025) Evaluating sensitivity of NGS-based mutation detection across diverse sample types in prostate cancer. Diagnostic pathology, 20(1), 108.

Xiang X, et al. (2025) Whole genome sequencing and structural variations provide insights into the body size traits of Hu sheep. Scientific data, 12(1), 1373.

Chen X, et al. (2025) Identification of the putative regulatory regions and candidate genes associated with backfat thickness and intramuscular fat content traits in Xiang pigs. BMC genomics, 26(1), 733.

Rui G, et al. (2025) Genomic and transcriptomic analyses provide new insights into the complex impacts of bud mutation in peach. Scientific reports, 15(1), 22951.

Xiao H, et al. (2025) Impacts of reproductive systems on grapevine genome and breeding. Nature communications, 16(1), 2031.

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.

Luna MJ, et al. (2025) Frequently arising ESX-1-associated phase variants influence Mycobacterium tuberculosis fitness in the presence of host and antibiotic pressures. mBio, 16(3), e0376224.

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

Liu Y, et al. (2025) Case report: First report of metastatic esophageal squamous cell carcinoma with EGFR p.S768I mutation: remarkable response to third-generation EGFR-TKI. NPJ precision oncology, 9(1), 339.

Manko E, et al. (2025) Novel zoonotic cases of Plasmodium simium from São Paulo with a reference genome of the Brazilian strain. Scientific reports, 15(1), 43703.

Park H, et al. (2025) Cytokine and Whole-Genome Sequence Analysis in Korean Patients With Multisystem Inflammatory Syndrome in Children. Journal of Korean medical science, 40(48), e319.

Ahmad B, et al. (2025) Mango pangenome reveals dramatic impacts of reference bias on population genomic analyses. Horticulture research, 12(9), uhaf166.

Kim SR, et al. (2025) Molecular Classification of Endometrial Cancers Using an Integrative DNA Sequencing Panel. Journal of surgical oncology, 131(4), 734.

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.

Young JS, et al. (2025) IL-6 underlies microenvironment immunosuppression and resistance to therapy in glioblastoma. bioRxiv : the preprint server for biology.