Resource Summary Report

Generated by NIF on Apr 22, 2025

DINDEL

RRID:SCR_001827
Type: Tool

Proper Citation

DINDEL (RRID:SCR_001827)

Resource Information

URL: http://www.sanger.ac.uk/science/tools/dindel

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on March 7,2024. Software program for calling small indels from short-read sequence data ("next generation sequence data"). It is currently designed to handle only Illumina data. Dindel takes BAM files with mapped Illumina read data and enables researchers to detect small indels and produce a VCF file of all the variant calls. It has been written in C++ and can be used on Linux-based and Mac computers (it has not been tested on Windows operating systems).

Abbreviations: Dindel

Synonyms: Dindel: Accurate indel calls from short-read data

Resource Type: software resource, software application

Defining Citation: PMID:20980555, DOI:10.1101/gr.112326.110

Keywords: indel, short-read, next generation sequence, illumina, gene, genetic, genomic, c++, linux, macos, bio.tools

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: DINDEL

Resource ID: SCR_001827

Alternate IDs: , nlx_154283, OMICS_00096, biotools:dindel

Alternate URLs: https://bio.tools/dindel, https://sources.debian.org/src/dindel/

Old URLs: http://www.sanger.ac.uk/resources/software/dindel/

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250421T053256+0000

Ratings and Alerts

No rating or validation information has been found for DINDEL.

No alerts have been found for DINDEL.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 44 mentions in open access literature.

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

Ziaei Jam H, et al. (2024) LongTR: genome-wide profiling of genetic variation at tandem repeats from long reads. Genome biology, 25(1), 176.

Brepoels P, et al. (2022) Antibiotic Cycling Affects Resistance Evolution Independently of Collateral Sensitivity. Molecular biology and evolution, 39(12).

Lewis MA, et al. (2022) Identification and characterisation of spontaneous mutations causing deafness from a targeted knockout programme. BMC biology, 20(1), 67.

Rymer K, et al. (2019) Expanding the phenotype for the recurrent p.Ala391Glu variant in FGFR3: Beyond crouzon syndrome and acanthosis nigricans. Molecular genetics & genomic medicine, 7(6), e656.

Jain A, et al. (2019) InDel markers: An extended marker resource for molecular breeding in chickpea. PloS one, 14(3), e0213999.

Maharaj A, et al. (2019) Predicted Benign and Synonymous Variants in CYP11A1 Cause Primary Adrenal Insufficiency Through Missplicing. Journal of the Endocrine Society, 3(1),

201.

Mun DG, et al. (2019) Proteogenomic Characterization of Human Early-Onset Gastric Cancer. Cancer cell, 35(1), 111.

Kim MS, et al. (2019) Genetic Mutation Profiles in Korean Patients with Inherited Retinal Diseases. Journal of Korean medical science, 34(21), e161.

Zhang B, et al. (2018) Genome-wide definition of selective sweeps reveals molecular evidence of trait-driven domestication among elite goat (Capra species) breeds for the production of dairy, cashmere, and meat. GigaScience, 7(12).

Arita JH, et al. (2018) Metabolic studies of a patient harbouring a novel S487L mutation in the catalytic subunit of AMPK. Biochimica et biophysica acta. Molecular basis of disease, 1864(5 Pt A), 1896.

Diaz Caballero J, et al. (2018) A genome-wide association analysis reveals a potential role for recombination in the evolution of antimicrobial resistance in Burkholderia multivorans. PLoS pathogens, 14(12), e1007453.

Van Nieuwenhuysen E, et al. (2018) The genetic landscape of 87 ovarian germ cell tumors. Gynecologic oncology, 151(1), 61.

Schütte M, et al. (2017) Molecular dissection of colorectal cancer in pre-clinical models identifies biomarkers predicting sensitivity to EGFR inhibitors. Nature communications, 8, 14262.

Schober T, et al. (2017) A human immunodeficiency syndrome caused by mutations in CARMIL2. Nature communications, 8, 14209.

Brown D, et al. (2017) Phylogenetic analysis of metastatic progression in breast cancer using somatic mutations and copy number aberrations. Nature communications, 8, 14944.

Hovelson DH, et al. (2017) Characterization of ADME gene variation in 21 populations by exome sequencing. Pharmacogenetics and genomics, 27(3), 89.

Kim BY, et al. (2017) Optimized detection of insertions/deletions (INDELs) in whole-exome sequencing data. PloS one, 12(8), e0182272.

Ziff JL, et al. (2016) Mutations and altered expression of SERPINF1 in patients with familial otosclerosis. Human molecular genetics, 25(12), 2393.

Hasan MS, et al. (2016) SPAI: an interactive platform for indel analysis. BMC genomics, 17 Suppl 5(Suppl 5), 496.

Wang Z, et al. (2016) Hyperlipidemia-associated gene variations and expression patterns revealed by whole-genome and transcriptome sequencing of rabbit models. Scientific reports, 6, 26942.