Resource Summary Report

Generated by ASWG on May 6, 2025

deepSNV

RRID:SCR_006214
Type: Tool

Proper Citation

deepSNV (RRID:SCR_006214)

Resource Information

URL: http://www.bioconductor.org/packages/devel/bioc/html/deepSNV.html

Proper Citation: deepSNV (RRID:SCR_006214)

Description: Software package that provides quantitative variant callers for detecting subclonal mutations in ultra-deep (>=100x coverage) sequencing experiments. The algorithm is used for a comparative setup with a control experiment of the same loci and uses a beta-binomial model and a likelihood ratio test to discriminate sequencing errors and subclonal SNVs (single nucleotide variants).

Abbreviations: deepSNV

Synonyms: deepSNV - Detection of subclonal SNVs in deep sequencing experiments

Resource Type: software resource

Defining Citation: PMID:24443148

Keywords: data import, genetic variability, genetics, snp, sequencing, single nucleotide variant, bio.tools

Funding:

Availability: GNU General Public License, v3

Resource Name: deepSNV

Resource ID: SCR_006214

Alternate IDs: OMICS_02239, biotools:deepsnv

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

Record Creation Time: 20220129T080234+0000

Record Last Update: 20250420T014317+0000

Ratings and Alerts

No rating or validation information has been found for deepSNV.

No alerts have been found for deepSNV.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 33 mentions in open access literature.

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

Hobor S, et al. (2024) Mixed responses to targeted therapy driven by chromosomal instability through p53 dysfunction and genome doubling. Nature communications, 15(1), 4871.

Willett JDS, et al. (2024) SARS-CoV-2 rapidly evolves lineage-specific phenotypic differences when passaged repeatedly in immune-naïve mice. Communications biology, 7(1), 191.

Caswell DR, et al. (2024) The role of APOBEC3B in lung tumor evolution and targeted cancer therapy resistance. Nature genetics, 56(1), 60.

Herms A, et al. (2024) Organismal metabolism regulates the expansion of oncogenic PIK3CA mutant clones in normal esophagus. Nature genetics, 56(10), 2144.

Bartel A, et al. (2024) Timely Monitoring of SARS-CoV-2 RNA Fragments in Wastewater Shows the Emergence of JN.1 (BA.2.86.1.1, Clade 23I) in Berlin, Germany. Viruses, 16(1).

King C, et al. (2023) Somatic mutations in facial skin from countries of contrasting skin cancer risk. Nature genetics, 55(9), 1440.

Stankunaite R, et al. (2022) Circulating tumour DNA sequencing to determine therapeutic response and identify tumour heterogeneity in patients with paediatric solid tumours. European journal of cancer (Oxford, England : 1990), 162, 209.

Tornabene P, et al. (2022) Therapeutic homology-independent targeted integration in retina and liver. Nature communications, 13(1), 1963.

Kim KQ, et al. (2022) N1-methylpseudouridine found within COVID-19 mRNA vaccines produces faithful protein products. Cell reports, 40(9), 111300.

Cagan A, et al. (2022) Somatic mutation rates scale with lifespan across mammals. Nature, 604(7906), 517.

Neggers JE, et al. (2021) enAsCas12a Enables CRISPR-Directed Evolution to Screen for Functional Drug Resistance Mutations in Sequences Inaccessible to SpCas9. Molecular therapy : the journal of the American Society of Gene Therapy, 29(1), 208.

Li Z, et al. (2021) Profiling of hepatocellular carcinoma neoantigens reveals immune microenvironment and clonal evolution related patterns. Chinese journal of cancer research = Chung-kuo yen cheng yen chiu, 33(3), 364.

Lin PC, et al. (2020) Intratumor Heterogeneity of MYO18A and FBXW7 Variants Impact the Clinical Outcome of Stage III Colorectal Cancer. Frontiers in oncology, 10, 588557.

Patterson EI, et al. (2020) Measuring Alphavirus Fidelity Using Non-Infectious Virus Particles. Viruses, 12(5).

Kleftogiannis D, et al. (2019) Identification of single nucleotide variants using position-specific error estimation in deep sequencing data. BMC medical genomics, 12(1), 115.

Collins ND, et al. (2019) Inter- and intra-lineage genetic diversity of wild-type Zika viruses reveals both common and distinctive nucleotide variants and clusters of genomic diversity. Emerging microbes & infections, 8(1), 1126.

Gómez-González B, et al. (2019) Rpd3L Contributes to the DNA Damage Sensitivity of Saccharomyces cerevisiae Checkpoint Mutants. Genetics, 211(2), 503.

Meier B, et al. (2018) Mutational signatures of DNA mismatch repair deficiency in C. elegans and human cancers. Genome research, 28(5), 666.

McCrone JT, et al. (2018) Stochastic processes constrain the within and between host evolution of influenza virus. eLife, 7.

Collins ND, et al. (2018) Structural and Nonstructural Genes Contribute to the Genetic Diversity of RNA Viruses. mBio, 9(5).