Resource Summary Report

Generated by T1D on Sep 5, 2026

readDepth

RRID:SCR_010824
Type: Tool

Proper Citation

readDepth (RRID:SCR_010824)

Resource Information

URL: http://code.google.com/p/readdepth/

Proper Citation: readDepth (RRID:SCR_010824)

Description: This package for R can detect copy number aberrations by measuring the depth of coverage obtained by massively parallel sequencing of the genome.

Abbreviations: readDepth

Resource Type: software resource

Resource Name: readDepth

Resource ID: SCR_010824

Alternate IDs: OMICS_00350

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260903T235040+0000

Ratings and Alerts

No rating or validation information has been found for readDepth.

No alerts have been found for readDepth.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 23 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Sankar V, et al. (2026) Genetic elements promote retention of extrachromosomal DNA in cancer cells. Nature, 649(8095), 152.

Sankar V, et al. (2025) Genetic elements promote retention of extrachromosomal DNA in cancer cells. bioRxiv : the preprint server for biology.

Erickson A, et al. (2025) Clonal phylogenies inferred from bulk, single cell, and spatial transcriptomic analysis of epithelial cancers. PloS one, 20(1), e0316475.

Yang Q, et al. (2025) SVLearn: a dual-reference machine learning approach enables accurate cross-species genotyping of structural variants. Nature communications, 16(1), 2406.

Meng X, et al. (2023) Systematic evaluation of multiple NGS platforms for structural variants detection. The Journal of biological chemistry, 299(12), 105436.

Dharanipragada P, et al. (2023) Blocking Genomic Instability Prevents Acquired Resistance to MAPK Inhibitor Therapy in Melanoma. Cancer discovery, 13(4), 880.

Peng L, et al. (2022) eccDNAdb: a database of extrachromosomal circular DNA profiles in human cancers. Oncogene, 41(19), 2696.

Han Y, et al. (2021) An epigenomic landscape of cervical intraepithelial neoplasia and cervical cancer using single-base resolution methylome and hydroxymethylome. Clinical and translational medicine, 11(7), e498.

Kosugi S, et al. (2019) Comprehensive evaluation of structural variation detection algorithms for whole genome sequencing. Genome biology, 20(1), 117.

Zhang L, et al. (2019) Comprehensively benchmarking applications for detecting copy number variation. PLoS computational biology, 15(5), e1007069.

Luo F, et al. (2019) A systematic evaluation of copy number alterations detection methods on real SNP array and deep sequencing data. BMC bioinformatics, 20(Suppl 25), 692.

Kang M, et al. (2019) Genomic analysis of Korean patients with advanced prostate cancer by use of a comprehensive next-generation sequencing panel and low-coverage, whole-genome sequencing. Investigative and clinical urology, 60(4), 227.

Deshpande V, et al. (2019) Exploring the landscape of focal amplifications in cancer using AmpliconArchitect. Nature communications, 10(1), 392.

Duan J, et al. (2019) Detection of False-Positive Deletions from the Database of Genomic Variants. BioMed research international, 2019, 8420547.

Xu W, et al. (2019) Genomic analysis reveals rich genetic variation and potential targets of selection during domestication of castor bean from perennial woody tree to annual semi-woody crop. Plant direct, 3(10), e00173.

Dharanipragada P, et al. (2018) iCopyDAV: Integrated platform for copy number variations-Detection, annotation and visualization. PloS one, 13(4), e0195334.

Filiault DL, et al. (2018) The Aquilegia genome provides insight into adaptive radiation and reveals an extraordinarily polymorphic chromosome with a unique history. eLife, 7.

Turner KM, et al. (2017) Extrachromosomal oncogene amplification drives tumour evolution and genetic heterogeneity. Nature, 543(7643), 122.

Ni J, et al. (2016) Combination inhibition of PI3K and mTORC1 yields durable remissions in mice bearing orthotopic patient-derived xenografts of HER2-positive breast cancer brain metastases. Nature medicine, 22(7), 723.

Pirooznia M, et al. (2015) Whole-genome CNV analysis: advances in computational approaches. Frontiers in genetics, 6, 138.