Resource Summary Report

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QDNAseq

RRID:SCR_003174
Type: Tool

Proper Citation

QDNAseq (RRID:SCR_003174)

Resource Information

URL: http://www.bioconductor.org/packages/release/bioc/html/QDNAseq.html

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Description: Software package for quantitative DNA sequencing for chromosomal aberrations providing a robust, cost-effective WGS method for DNA copy number analysis. The genome is divided into non-overlapping fixed-sized bins, number of sequence reads in each counted, adjusted with a simultaneous two-dimensional loess correction for sequence mappability and GC content, and filtered to remove spurious regions in the genome. Downstream steps of segmentation and calling are also implemented via packages DNAcopy and CGHcall, respectively.

Synonyms: QDNAseq - Quantitative DNA sequencing for chromosomal aberrations

Resource Type: software resource

Defining Citation: PMID:25236618

Keywords: software package, unix/linux, mac os x, windows, r, copy number variation, dna-seq, genetics, genome annotation, preprocessing, quality control, sequencing, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: QDNAseq

Resource ID: SCR_003174

Alternate IDs: OMICS_05902, biotools:qdnaseq

Alternate URLs: https://github.com/ccagc/QDNAseq, https://bio.tools/qdnaseq

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260725T190538+0000

Ratings and Alerts

No rating or validation information has been found for QDNAseq.

No alerts have been found for QDNAseq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 150 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Ahting S, et al. (2025) Incorporating Nanopore Sequencing Into a Diverse Diagnostic Toolkit for Incontinentia Pigmenti. Human mutation, 2025, 6657400.

Handoko , et al. (2025) Feasibility of long-read sequencing to identify molecular alterations in an Indonesian cohort of locally advanced to advanced nasopharyngeal cancer. Scientific reports, 15(1), 21087.

Rath P, et al. (2025) Optimizing approaches for targeted integration of transgenic cassettes by integrase-mediated cassette exchange in mouse and human stem cells. Stem cells (Dayton, Ohio), 43(1).

Stojanovi? Gužvi? N, et al. (2025) Cellular liquid biopsy provides unique chances for disease monitoring, preclinical model generation and therapy adjustment in rare salivary gland cancer patients. Molecular oncology, 19(7), 2056.

Pradella D, et al. (2025) Engineered extrachromosomal oncogene amplifications promote tumorigenesis. Nature, 637(8047), 955.

Qin X, et al. (2025) Single-Cell Expression Analysis of Ductal Carcinoma In Situ Identifies Complex Genotypic-Phenotypic Relationships Altering Epithelial Composition. Cancer research, 85(12), 2302.

Oliveira EA, et al. (2025) Epigenetic Heritability of Cell Plasticity Drives Cancer Drug Resistance through a One-to-Many Genotype-to-Phenotype Paradigm. Cancer research, 85(15), 2921.

Lin AY, et al. (2025) CfDNA-based copy-number dynamics during anti-PD1 treatment in metastatic triple negative breast cancer. Cell reports. Medicine, 6(12), 102512.

Subrini J, et al. (2025) Systematic identification of Y-chromosome gene functions in mouse spermatogenesis. Science (New York, N.Y.), 387(6732), 393.

Özkan A, et al. (2025) Human Organ Chips Reveal New Inflammatory Bowel Disease Drivers. Research square.

DeCarlo A, et al. (2025) Targeting synthetic lethality between non-homologous end joining and radiation in very-high-risk medulloblastoma. Cell reports. Medicine, 6(7), 102202.

Van TTV, et al. (2025) Multimodal analysis of cell-free DNA enhances differentiation of early-stage breast cancer from benign lesions and healthy individuals. BMC biology, 23(1), 259.

Fortunato A, et al. (2025) Evolutionary measures show that recurrence of DCIS is distinct from progression to breast cancer. Breast cancer research : BCR, 27(1), 43.

Zhao Y, et al. (2025) Origin and development of uniparental and polyploid blastomeres. iScience, 28(5), 112337.

Wang H, et al. (2025) A standardized framework for robust fragmentomic feature extraction from cell-free DNA sequencing data. Genome biology, 26(1), 141.

Beddowes EJ, et al. (2025) A large-scale retrospective study in metastatic breast cancer patients using circulating tumour DNA and machine learning to predict treatment outcome and progression-free survival. Molecular oncology, 19(12), 3518.

Sedaghatkish A, et al. (2025) The first single-cell sequencing of Plasmodiophora brassicae reveals genetic diversity and clonal dynamics. Frontiers in microbiology, 16, 1581233.

Chislock EM, et al. (2025) DTC-Flow: a flow cytometry-based detection platform for characterizing bone marrow disseminated tumor cells in breast cancer. NPJ breast cancer, 11(1), 139.

Geysens M, et al. (2025) Clinical evaluation of long-read sequencing-based episignature detection in developmental disorders. Genome medicine, 17(1), 1.

Al Bakir I, et al. (2025) Low-coverage whole genome sequencing of low-grade dysplasia strongly predicts advanced neoplasia risk in ulcerative colitis. Gut, 74(5), 740.