Resource Summary Report

Generated by NIF on May 20, 2025

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

Funding:

Availability: GNU General Public License

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: 20250519T203235+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 126 mentions in open access literature.

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

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

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).

Ganguli P, et al. (2025) Context-dependent effects of CDKN2A and other 9p21 gene losses during the evolution of esophageal cancer. Nature cancer, 6(1), 158.

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

Lynch AR, et al. (2024) A survey of chromosomal instability measures across mechanistic models. Proceedings of the National Academy of Sciences of the United States of America, 121(16), e2309621121.

Hintzen DC, et al. (2024) Reduction of chromosomal instability and inflammation is a common aspect of adaptation to aneuploidy. EMBO reports, 25(11), 5169.

Zhang Y, et al. (2024) Permanent neonatal diabetes-causing insulin mutations have dominant negative effects on beta cell identity. Molecular metabolism, 80, 101879.

Pan JW, et al. (2024) Clustering of HR?+?/HER2- breast cancer in an Asian cohort is driven by immune phenotypes. Breast cancer research : BCR, 26(1), 67.

Pan JW, et al. (2024) Gene expression signature for predicting homologous recombination deficiency in triple-negative breast cancer. NPJ breast cancer, 10(1), 60.

Ciwinska M, et al. (2024) Mechanisms that clear mutations drive field cancerization in mammary tissue. Nature, 633(8028), 198.

Fortunato A, et al. (2024) Evolutionary Measures Show that Recurrence of DCIS is Distinct from Progression to Breast Cancer. medRxiv : the preprint server for health sciences.

Ambriz-Barrera F, et al. (2024) Mutational spectrum of breast cancer by shallow whole-genome sequencing of cfDNA and tumor gene panel analysis. PloS one, 19(9), e0308176.

Potente S, et al. (2024) SAMURAI: shallow analysis of copy number alterations using a reproducible and integrated bioinformatics pipeline. Briefings in bioinformatics, 26(1).

Wils LJ, et al. (2024) Genomic Engineering of Oral Keratinocytes to Establish In Vitro Oral Potentially Malignant Disease Models as a Platform for Treatment Investigation. Cells, 13(8).

Leto SM, et al. (2024) XENTURION is a population-level multidimensional resource of xenografts and tumoroids from metastatic colorectal cancer patients. Nature communications, 15(1), 7495.

Sadien ID, et al. (2024) Polyclonality overcomes fitness barriers in Apc-driven tumorigenesis. Nature, 634(8036), 1196.

Di Cosimo S, et al. (2024) Low-pass whole genome sequencing of circulating tumor cells to evaluate chromosomal instability in triple-negative breast cancer. Scientific reports, 14(1), 20479.

Ng AWT, et al. (2024) Disentangling oncogenic amplicons in esophageal adenocarcinoma. Nature communications, 15(1), 4074.

Al Bakir I, et al. (2024) Low coverage whole genome sequencing of low-grade dysplasia strongly predicts colorectal cancer risk in ulcerative colitis. medRxiv : the preprint server for health sciences.

Jamieson A, et al. (2024) Targeted and Shallow Whole-Genome Sequencing Identifies Therapeutic Opportunities in p53abn Endometrial Cancers. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(11), 2461.