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

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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 168 mentions in open access literature.

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

Cross WCH, et al. (2026) Negative Selection Maintains Grossly Altered but Broadly Stable Karyotypes in Metastatic Colorectal Cancer. Cancer discovery, 16(2), 218.

Skrupskelyte G, et al. (2026) The dynamics of mutational selection in cutaneous squamous carcinogenesis. Communications biology, 9(1), 127.

Douville C, et al. (2026) Evidence that extra copies of chromosome 1q play a role in the early phases of pancreatic neoplasia. Science advances, 12(8), eadx7501.

Bhuwapathanapun M, et al. (2026) Rapid prenatal CNV detection using nanopore technology. BMC research notes, 19(1).

Kommoss FKF, et al. (2026) Spatial single cell transcriptomic analysis informs tumor developmental hierarchy of DICER1 syndrome related sarcoma. Nature communications, 17(1).

Hong J, et al. (2026) A novel 2-piperazino-pyrimidine compound exhibits asexual antimalarial activity by targeting Plasmodium falciparum plasmepsin X. International journal for parasitology. Drugs and drug resistance, 31, 100644.

Avolio M, et al. (2026) The Molecular and Functional Landscape of Resistance to FOLFIRI Chemotherapy in Metastatic Colorectal Cancer. Cancer discovery, 16(2), 270.

Weng J, et al. (2026) Copy number alteration fingerprint predicts the clinical response of oxaliplatin-based chemotherapy in metastatic colorectal cancer. NPJ precision oncology, 10(1).

Lourenço FC, et al. (2026) Decay of driver mutations shapes the landscape of intestinal transformation. Nature, 649(8097), 729.

Zhong Y, et al. (2026) Dynamics of circulating tumour DNA in relapsed/refractory diffuse large B-cell lymphoma patients. British journal of haematology, 208(3), 874.

Eriksson L, et al. (2026) Sensitive detection of copy number alterations in low-pass liquid biopsy sequencing data. Briefings in bioinformatics, 27(2).

Abuijlan E, et al. (2026) Targeted long-read genomic and epigenomic profiling enhances timely comprehensive variant discovery in hypotonia and muscle weakness. BMC medicine, 24(1).

Salmon M, et al. (2026) Long read nanopore DNA sequencing with adaptive sampling to identify tyrosine kinase fusion genes. Leukemia, 40(1), 37.

Zhou Z, et al. (2026) ctDNA monitoring using tumor-informed copy number analysis. EMBO molecular medicine, 18(4), 1429.

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.

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).

Su W, et al. (2025) Deconvolution of the On-Target Activity of Plasmepsin V Peptidomimetics in Plasmodium falciparum Parasites. ACS infectious diseases, 11(12), 3581.

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