Resource Summary Report

Generated by ASWG on Aug 2, 2026

DNAcopy

RRID:SCR_012560
Type: Tool

Proper Citation

DNAcopy (RRID:SCR_012560)

Resource Information

URL: http://www.bioconductor.org/packages/2.12/bioc/html/DNAcopy.html

Proper Citation: DNAcopy (RRID:SCR_012560)

Description: Software that segments DNA copy number data using circular binary segmentation to detect regions with abnormal copy number.

Abbreviations: DNAcopy

Resource Type: software resource

Keywords: bio.tools

Resource Name: DNAcopy

Resource ID: SCR_012560

Alternate IDs: OMICS_00720, biotools:dnacopy

Alternate URLs: https://bio.tools/dnacopy, https://sources.debian.org/src/r-bioc-dnacopy/

Record Creation Time: 20220129T080311+0000

Record Last Update: 20260801T190446+0000

Ratings and Alerts

No rating or validation information has been found for DNAcopy.

No alerts have been found for DNAcopy.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 334 mentions in open access literature.

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

Lim KHJ, et al. (2026) Cross-presentation of dead cell-associated antigens shapes the neoantigenic landscape of tumor immunity. Nature immunology, 27(1), 72.

Hu K, et al. (2025) Development and Application of MiMouse, a Comprehensive Genomic Profiling Panel for Credentialing Mouse Tumor Models. Cancer research communications, 5(10), 1910.

Umeda M, et al. (2025) Fusion oncoproteins and cooperating mutations define disease phenotypes in NUP98-rearranged leukemia. medRxiv : the preprint server for health sciences.

Yu X, et al. (2025) HapCNV: A Comprehensive Framework for CNV Detection in Low-input DNA Sequencing Data. bioRxiv : the preprint server for biology.

Wang X, et al. (2025) ChromoPattern: characterizing chromosomal rearrangement patterns of copy number alteration in heterogeneous tumor cell populations at single-cell resolution. Briefings in bioinformatics, 26(5).

Beernaert B, et al. (2025) Chromosomal instability shapes the tumor microenvironment of esophageal adenocarcinoma via a cGAS-chemokine-myeloid axis. bioRxiv : the preprint server for biology.

Shu Z, et al. (2025) Preoperative plasma cell-free DNA chromosomal instability predicts microvascular invasion in hepatocellular carcinoma: a prospective study. BMC cancer, 25(1), 867.

Dimitriou F, et al. (2025) Conjunctival melanoma genomic analysis reveals intermediate tumor mutation burden and genomic overlap with cutaneous melanoma. NPJ precision oncology, 9(1), 365.

Vavoulis DV, et al. (2025) Multimodal cell-free DNA whole-genome TAPS is sensitive and reveals specific cancer signals. Nature communications, 16(1), 430.

Gökbuget D, et al. (2025) KMT2C/KMT2D-dependent H3K4me1 mediates changes in DNA replication timing and origin activity during a cell fate transition. Cell reports, 44(2), 115272.

Bouzid A, et al. (2025) Whole exome sequencing identifies ABHD14A and MRNIP as novel candidate genes for developmental language disorder. Scientific reports, 15(1), 367.

Tan B, et al. (2025) Single-cell analysis reveals transcriptomic features and therapeutic targets in primary pulmonary lymphoepithelioma-like carcinoma. Communications biology, 8(1), 394.

Nie R, et al. (2025) Mitigating Cell Cycle Effects in Multi-Omics Data: Solutions and Analytical Frameworks. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(29), e05823.

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.

Blouin T, et al. (2025) Translesion polymerases and DNA-protein crosslink repair shapes the cellular response to formaldehyde-induced DNA damage in ssDNA. Nucleic acids research, 53(17).

Zhu X, et al. (2025) Identification of maternal G?(A???)0 thalassemia through retrospective reanalysis of prenatal cfDNA sequencing data. Annals of medicine, 57(1), 2596498.

Cosenza MR, et al. (2025) Origins of chromosome instability unveiled by coupled imaging and genomics. Nature, 648(8093), 383.

Bökenkamp JE, et al. (2025) Proteogenomic analysis reveals adaptive strategies for alleviating the consequences of aneuploidy in cancer. The EMBO journal, 44(6), 1829.

Lehtonen J, et al. (2025) Genome sequencing reveals CCDC88A variants in malformations of cortical development and immune dysfunction. Human molecular genetics, 34(15), 1294.

Sharma S, et al. (2025) Functional genomics and tumor microenvironment analysis reveal prognostic biological subtypes in Mantle cell lymphoma. Nature communications, 16(1), 9762.