Resource Summary Report

Generated by RRID on Sep 10, 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: 20260905T132725+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 349 mentions in open access literature.

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

Tao T, et al. (2026) Copy-Number Aberrations in Circulating Tumor DNA Enable Diagnosis and Risk Stratification of Pediatric Neuroblastic Tumors. Cancer research communications, 6(1), 36.

Shu D, et al. (2026) Haplotype Construction Using Embryos as Probands of the Pathogenic Variations in EXT1, CUL3, and HBA. Human mutation, 2026, 2768102.

Bellomo SE, et al. (2026) Genome-wide biomarker analysis across the full spectrum of HER2-expressing breast cancers to reveal a clonal chromosome 17 imbalance defining unfavourable HER2-low disease. Biomarker research, 14(1).

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

Loipfinger S, et al. (2026) Association of copy number alterations with the immune transcriptomic landscape in cancer. NPJ systems biology and applications, 12(1), 28.

Kim YM, et al. (2026) Targeting eIF4A-dependent translation in genetically complex sarcoma. JCI insight, 11(10).

Beernaert B, et al. (2026) Chromosomal instability shapes the tumor microenvironment of esophageal adenocarcinoma via a cGAS-chemokine-myeloid axis. Science advances, 12(11), eaeb1611.

Wang X, et al. (2026) PScnv: personalized self-normalizing CNV detection with a hierarchical multi-phase framework. Bioinformatics (Oxford, England), 42(3).

Oriowo TO, et al. (2026) Different sex determination systems in two closely related Eurasian minnow (Phoxinus) species. Heredity, 135(4), 259.

Zhang J, et al. (2026) Androgen activity in the male embryonic hindbrain drives lethal PFA ependymoma. Nature, 652(8110), 763.

Helle K, et al. (2026) De Novo Complex Genomic Rearrangement Spanning 2q31.1 in a Proband With Congenital Malformations: Genotype-Phenotype Correlation and Development of a CGR Detection Pipeline. American journal of medical genetics. Part A, 200(8), 1832.

Cheng S, et al. (2026) Cross-Strand Chimeric RNA Signature Predicts Prognosis and Identifies Tumor Immune Microenvironment Associations in Gastric Cancer. Human mutation, 2026, 4428673.

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.

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.

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

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.

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.

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

G??kbuget 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.