

Resource Summary Report

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CGHcall

RRID:SCR_001578

Type: Tool

Proper Citation

CGHcall (RRID:SCR_001578)

Resource Information

URL: <http://www.bioconductor.org/packages/2.12/bioc/html/CGHcall.html>

Proper Citation: CGHcall (RRID:SCR_001578)

Description: Software that calls aberrations for array CGH data using a six state mixture model and several biological concepts. It is written in R.

Resource Type: software application, software resource, data analysis software, data processing software

Keywords: cgh data analysis, objective classification, data aberration

Availability: Free, Available for download, Freely available

Resource Name: CGHcall

Resource ID: SCR_001578

Alternate IDs: OMICS_00709

License: General Public License

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260729T044013+0000

Ratings and Alerts

No rating or validation information has been found for CGHcall.

No alerts have been found for CGHcall.

Data and Source Information

Usage and Citation Metrics

We found 30 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

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.

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.

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.

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

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*.

Garrido Ruiz PA, et al. (2024) Paired Primary and Recurrent Rhabdoid Meningiomas: Cytogenetic Alterations, BAP1 Gene Expression Profile and Patient Outcome. *Biology*, 13(5).

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.

Lu B, et al. (2023) CNETML: maximum likelihood inference of phylogeny from copy number profiles of multiple samples. *Genome biology*, 24(1), 144.

Schnöller LE, et al. (2023) Systematic in vitro analysis of therapy resistance in glioblastoma cell lines by integration of clonogenic survival data with multi-level molecular data. *Radiation oncology (London, England)*, 18(1), 51.

Vasquez Kuntz KL, et al. (2022) Inheritance of somatic mutations by animal offspring. *Science advances*, 8(35), eabn0707.

Deger T, et al. (2022) A pipeline for copy number profiling of single circulating tumour cells to assess intrapatient tumour heterogeneity. *Molecular oncology*, 16(16), 2981.

Martens-de Kemp SR, et al. (2022) Overexpression of the miR-17-92 cluster in colorectal adenoma organoids causes a carcinoma-like gene expression signature. *Neoplasia (New York, N.Y.)*, 32, 100820.

Chen X, et al. (2021) Patient-derived non-small cell lung cancer xenograft mirrors complex tumor heterogeneity. *Cancer biology & medicine*, 18(1), 184.

Pan JW, et al. (2020) The molecular landscape of Asian breast cancers reveals clinically relevant population-specific differences. *Nature communications*, 11(1), 6433.

Patmore DM, et al. (2020) DDX3X Suppresses the Susceptibility of Hindbrain Lineages to Medulloblastoma. *Developmental cell*, 54(4), 455.

Badhai J, et al. (2020) Combined deletion of Bap1, Nf2, and Cdkn2ab causes rapid onset of malignant mesothelioma in mice. *The Journal of experimental medicine*, 217(6).

Hoefsmit EP, et al. (2020) Comprehensive analysis of cutaneous and uveal melanoma liver metastases. *Journal for immunotherapy of cancer*, 8(2).

Swarts DRA, et al. (2018) Molecular heterogeneity in human papillomavirus-dependent and -independent vulvar carcinogenesis. *Cancer medicine*, 7(9), 4542.

Semeraro R, et al. (2018) Xome-Blender: A novel cancer genome simulator. *PloS one*, 13(4), e0194472.

Tokar T, et al. (2018) Differentially expressed microRNAs in lung adenocarcinoma invert effects of copy number aberrations of prognostic genes. *Oncotarget*, 9(10), 9137.