Resource Summary Report

Generated by dkNET on May 18, 2025

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

Funding:

Availability: Open source, Available for download

Resource Name: CGHcall

Resource ID: SCR_001578

Alternate IDs: OMICS_00709

Record Creation Time: 20220129T080208+0000

Record Last Update: 20250517T055504+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

Source: SciCrunch Registry

Usage and Citation Metrics

We found 27 mentions in open access literature.

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

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

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.

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

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.

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.

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).

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

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.

Steeghs EMP, et al. (2018) High STAP1 expression in DUX4-rearranged cases is not suitable as therapeutic target in pediatric B-cell precursor acute lymphoblastic leukemia. Scientific reports, 8(1), 693.

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

Oikonomaki M, et al. (2017) Ubiquitin Specific Peptidase 15 (USP15) suppresses glioblastoma cell growth via stabilization of HECTD1 E3 ligase attenuating WNT pathway activity. Oncotarget, 8(66), 110490.

Yuan D, et al. (2017) Kupffer Cell-Derived Tnf Triggers Cholangiocellular Tumorigenesis through JNK due to Chronic Mitochondrial Dysfunction and ROS. Cancer cell, 31(6), 771.