Resource Summary Report

Generated by kravitz2 on Sep 5, 2026

aCGH

RRID:SCR_013232
Type: Tool

Proper Citation

aCGH (RRID:SCR_013232)

Resource Information

URL: http://www.bioconductor.org/packages//2.10/bioc/html/aCGH.html

Proper Citation: aCGH (RRID:SCR_013232)

Description: Software functions for reading aCGH data from image analysis output files and clone information files, creation of aCGH S3 objects for storing these data. Basic methods for accessing/replacing, subsetting, printing and plotting aCGH objects.

Abbreviations: aCGH

Resource Type: software resource

Resource Name: aCGH

Resource ID: SCR_013232

Alternate IDs: OMICS_00698

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260903T235231+0000

Ratings and Alerts

No rating or validation information has been found for aCGH.

No alerts have been found for aCGH.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 136 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Cappuccio G, et al. (2025) Computationally resolved neuroprogenitor cell biomarkers associate with human disorders. Stem cell reports, 20(9), 102606.

Du H, et al. (2025) An integrated platform for concurrent structural and single-nucleotide variants improves copy-number detection and reveals pathogenic alleles in undiagnosed Mendelian families. Genome medicine, 18(1), 16.

Kim JW, et al. (2024) Clinical outcomes of preimplantation genetic testing for aneuploidy in high-risk patients: a retrospective cohort study. Clinical and experimental reproductive medicine, 51(1), 75.

Madritsch S, et al. (2024) Aneuploidy detection in pooled polar bodies using rapid nanopore sequencing. Journal of assisted reproduction and genetics, 41(5), 1261.

Cuenca-Guardiola J, et al. (2023) Improvement of large copy number variant detection by whole genome nanopore sequencing. Journal of advanced research, 50, 145.

Sagath L, et al. (2022) A custom ddPCR method for the detection of copy number variations in the nebulin triplicate region. PloS one, 17(5), e0267793.

Wyrwoll MJ, et al. (2022) Analysis of copy number variation in men with non-obstructive azoospermia. Andrology, 10(8), 1593.

Fuke T, et al. (2021) Role of Imprinting Disorders in Short Children Born SGA and Silver-Russell Syndrome Spectrum. The Journal of clinical endocrinology and metabolism, 106(3), 802.

Konstantinidis M, et al. (2020) Aneuploidy and recombination in the human preimplantation embryo. Copy number variation analysis and genome-wide polymorphism genotyping. Reproductive biomedicine online, 40(4), 479.

Kahraman S, et al. (2020) High rates of aneuploidy, mosaicism and abnormal morphokinetic development in cases with low sperm concentration. Journal of assisted reproduction and genetics, 37(3), 629.

Vielh P, et al. (2020) DNA FISH Diagnostic Assay on Cytological Samples of Thyroid Follicular Neoplasms. Cancers, 12(9).

Chung CCY, et al. (2020) Cost-effectiveness analysis of chromosomal microarray as a primary test for prenatal diagnosis in Hong Kong. BMC pregnancy and childbirth, 20(1), 109.

Bartels CB, et al. (2020) In vitro fertilization outcomes after preimplantation genetic testing for chromosomal structural rearrangements comparing fluorescence in-situ hybridization, microarray comparative genomic hybridization, and next-generation sequencing. F&S reports, 1(3), 249.

Seifert M, et al. (2020) Molecular Characterization of Astrocytoma Progression Towards Secondary Glioblastomas Utilizing Patient-Matched Tumor Pairs. Cancers, 12(6).

Hong B, et al. (2020) The outcome of human mosaic aneuploid blastocysts after intrauterine transfer: A retrospective study. Medicine, 99(9), e18768.

Brasó-Vives M, et al. (2020) Copy number variants and fixed duplications among 198 rhesus macaques (Macaca mulatta). PLoS genetics, 16(5), e1008742.

Chai H, et al. (2019) Integrated FISH, Karyotyping and aCGH Analyses for Effective Prenatal Diagnosis of Common Aneuploidies and Other Cytogenomic Abnormalities. Medical sciences (Basel, Switzerland), 7(2).

Lemay MA, et al. (2019) Screening populations for copy number variation using genotyping-by-sequencing: a proof of concept using soybean fast neutron mutants. BMC genomics, 20(1), 634.

Wen J, et al. (2019) Analytical validation and chromosomal distribution of regions of homozygosity by oligonucleotide array comparative genomic hybridization from normal prenatal and postnatal case series. Molecular cytogenetics, 12, 12.

Mu W, et al. (2019) Detection of structural variation using target captured next-generation sequencing data for genetic diagnostic testing. Genetics in medicine : official journal of the American College of Medical Genetics, 21(7), 1603.