

Resource Summary Report

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[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: 20260801T190446+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 [NIF](#) .

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.

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

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.

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.

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

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

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.