

Resource Summary Report

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ExomeCNV

RRID:SCR_010815

Type: Tool

Proper Citation

ExomeCNV (RRID:SCR_010815)

Resource Information

URL: <http://cran.r-project.org/web/packages/ExomeCNV/index.html>

Proper Citation: ExomeCNV (RRID:SCR_010815)

Description: A statistical method to detect CNV and LOH using depth-of-coverage and B-allele frequencies from mapped short sequence reads in exome sequencing data.

Abbreviations: ExomeCNV

Resource Type: software resource

Resource Name: ExomeCNV

Resource ID: SCR_010815

Alternate IDs: OMICS_00333

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260725T190705+0000

Ratings and Alerts

No rating or validation information has been found for ExomeCNV.

No alerts have been found for ExomeCNV.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 59 mentions in open access literature.

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

Sholler GLS, et al. (2024) Molecular-guided therapy for the treatment of patients with relapsed and refractory childhood cancers: a Beat Childhood Cancer Research Consortium trial. *Genome medicine*, 16(1), 28.

Youngblood MW, et al. (2023) Super-enhancer hijacking drives ectopic expression of hedgehog pathway ligands in meningiomas. *Nature communications*, 14(1), 6279.

Kim SC, et al. (2023) Patient-derived glioblastoma cell lines with conserved genome profiles of the original tissue. *Scientific data*, 10(1), 448.

Park YH, et al. (2023) Longitudinal multi-omics study of palbociclib resistance in HR-positive/HER2-negative metastatic breast cancer. *Genome medicine*, 15(1), 55.

Kim SC, et al. (2022) Multifocal Organoid Capturing of Colon Cancer Reveals Pervasive Intratumoral Heterogenous Drug Responses. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 9(5), e2103360.

Migliaccio I, et al. (2022) PIK3CA co-occurring mutations and copy-number gain in hormone receptor positive and HER2 negative breast cancer. *NPJ breast cancer*, 8(1), 24.

Ülgen E, et al. (2021) Sequential filtering for clinically relevant variants as a method for clinical interpretation of whole exome sequencing findings in glioma. *BMC medical genomics*, 14(1), 54.

Chen M, et al. (2021) Cold and heterogeneous T cell repertoire is associated with copy number aberrations and loss of immune genes in small-cell lung cancer. *Nature communications*, 12(1), 6655.

Strom SP, et al. (2021) A Streamlined Approach to Prader-Willi and Angelman Syndrome Molecular Diagnostics. *Frontiers in genetics*, 12, 608889.

Edwards DM, et al. (2021) Mitotic Errors Promote Genomic Instability and Leukemia in a Novel Mouse Model of Fanconi Anemia. *Frontiers in oncology*, 11, 752933.

Schubert M, et al. (2021) AID Contributes to Accelerated Disease Progression in the TCL1 Mouse Transplant Model for CLL. *Cancers*, 13(11).

Ordóñez LD, et al. (2021) Reproductive history determines Erbb2 locus amplification, WNT signalling and tumour phenotype in a murine breast cancer model. *Disease models & mechanisms*, 14(5).

Byron SA, et al. (2021) Genomic and Transcriptomic Analysis of Relapsed and Refractory Childhood Solid Tumors Reveals a Diverse Molecular Landscape and Mechanisms of Immune Evasion. *Cancer research*, 81(23), 5818.

Ülgen E, et al. (2020) Mutations and Copy Number Alterations in IDH Wild-Type Glioblastomas Are Shaped by Different Oncogenic Mechanisms. *Biomedicine*, 8(12).

Zhu Z, et al. (2020) Whole-exome sequencing identifies prognostic mutational signatures in gastric cancer. *Annals of translational medicine*, 8(22), 1484.

Mitra A, et al. (2020) Spatially resolved analyses link genomic and immune diversity and reveal unfavorable neutrophil activation in melanoma. *Nature communications*, 11(1), 1839.

Sandmann S, et al. (2020) CopyDetective: Detection threshold-aware copy number variant calling in whole-exome sequencing data. *GigaScience*, 9(11).

Ramesh N, et al. (2020) Decoding the evolutionary response to prostate cancer therapy by plasma genome sequencing. *Genome biology*, 21(1), 162.

Chanwigoon S, et al. (2020) inCNV: An Integrated Analysis Tool for Copy Number Variation on Whole Exome Sequencing. *Evolutionary bioinformatics online*, 16, 1176934320956577.

Anderson AN, et al. (2020) Functional genomic analysis identifies drug targetable pathways in invasive and metastatic cutaneous squamous cell carcinoma. *Cold Spring Harbor molecular case studies*, 6(4).