Resource Summary Report

Generated by kravitz2 on Jul 31, 2026

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 kravitz2 .

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).

Ordonez 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. Biomedicines, 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).