Resource Summary Report

Generated by RRID on Aug 2, 2026

CNVPartition

RRID:SCR_010925
Type: Tool

Proper Citation

CNVPartition (RRID:SCR_010925)

Resource Information

URL: http://www.illumina.com/software/illumina_connect.ilmn

Proper Citation: CNVPartition (RRID:SCR_010925)

Description: Software that estimates copy number and annotates regions with copy number variants(CNV).

Abbreviations: CNVPartition

Resource Type: software resource

Resource Name: CNVPartition

Resource ID: SCR_010925

Alternate IDs: OMICS_00716

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260801T190418+0000

Ratings and Alerts

No rating or validation information has been found for CNVPartition.

No alerts have been found for CNVPartition.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 130 mentions in open access literature.

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

Hale EB, et al. (2025) The TECTB-C225Y Variant Causing Autosomal Dominant Deafness in a Nicaraguan Family Enhances Sensitivity to Noise-Induced Hearing Loss in Mice. medRxiv : the preprint server for health sciences.

Fan KH, et al. (2025) Genome-wide association of tau neuroimaging and plasma biomarkers in adults with Down syndrome. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(7), e70398.

Freitas-Castro F, et al. (2025) SLC25A11, a Novel Gene Associated With Carney-Stratakis Syndrome. Journal of the Endocrine Society, 9(5), bvaf052.

Zhang S, et al. (2025) Preimplantation genetic testing for structural rearrangements by genome-wide SNP genotyping and haplotype analysis: a prospective multicenter clinical study. EBioMedicine, 111, 105514.

Kazakou NL, et al. (2025) Metformin alters mitochondria-related metabolism and enhances human oligodendrocyte function. Nature communications, 16(1), 8126.

Haake J, et al. (2025) Chromosomal quality control in hPSCs: A practical guide to SNP array analysis with GenomeStudio. Frontiers in cell and developmental biology, 13, 1599923.

Khan H, et al. (2024) Biallelic variants identified in 36 Pakistani families and trios with autism spectrum disorder. Scientific reports, 14(1), 9230.

Chen Y, et al. (2024) Novel evidence of CNV deletion in KCTD13 related to the severity of isolated hypospadias in Chinese population. Frontiers in pediatrics, 12, 1409264.

Viggiano M, et al. (2024) Genomic analysis of 116 autism families strengthens known risk genes and highlights promising candidates. NPJ genomic medicine, 9(1), 21.

Dahawi M, et al. (2024) Genetic heterogeneity in familial forms of genetic generalized epilepsy: from mono- to oligogenism. Human genomics, 18(1), 130.

Yu K, et al. (2024) Genomic landscape of patients with germline RUNX1 variants and familial platelet disorder with myeloid malignancy. Blood advances, 8(2), 497.

Chan ER, et al. (2024) Importance of copy number variants in childhood apraxia of speech and other speech sound disorders. Communications biology, 7(1), 1273.

Wagstaff LJ, et al. (2024) CRISPR-edited human ES-derived oligodendrocyte progenitor cells improve remyelination in rodents. Nature communications, 15(1), 8570.

Jin Y, et al. (2024) Modeling Lewy body disease with SNCA triplication iPSC-derived cortical organoids and identifying therapeutic drugs. Science advances, 10(37), eadk3700.

De Angeli P, et al. (2024) Splicing defects and CRISPR-Cas9 correction in isogenic homozygous photoreceptor precursors harboring clustered deep-intronic ABCA4 variants.

Molecular therapy. Nucleic acids, 35(1), 102113.

Wesely J, et al. (2024) A repository of Ogden syndrome patient derived iPSC lines and isogenic pairs by X-chromosome screening and genome-editing. bioRxiv : the preprint server for biology.

Pommerenke C, et al. (2024) Molecular Characterization and Subtyping of Breast Cancer Cell Lines Provide Novel Insights into Cancer Relevant Genes. Cells, 13(4).

Carlisle SG, et al. (2023) Rare Genomic Copy Number Variants Implicate New Candidate Genes for Bicuspid Aortic Valve. medRxiv : the preprint server for health sciences.

Xu P, et al. (2023) OGM and WES identifies translocation breakpoints in PKD1 gene in an polycystic kidney patient and healthy baby delivered using PGT. BMC medical genomics, 16(1), 285.

Winden KD, et al. (2023) Increased degradation of FMRP contributes to neuronal hyperexcitability in tuberous sclerosis complex. Cell reports, 42(8), 112838.