Resource Summary Report

Generated by NIF on May 6, 2025

CNV-seq

RRID:SCR_013357
Type: Tool

Proper Citation

CNV-seq (RRID:SCR_013357)

Resource Information

URL: http://tiger.dbs.nus.edu.sg/cnv-seq/

Proper Citation: CNV-seq (RRID:SCR_013357)

Description: A method for detecting DNA copy number variation (CNV) using high-throughput sequencing.

Abbreviations: CNV-seq

Resource Type: software resource

Keywords: bio.tools

Funding:

Resource Name: CNV-seq

Resource ID: SCR_013357

Alternate IDs: biotools:cnv-seq, OMICS_00339

Alternate URLs: https://bio.tools/cnv-seq

Record Creation Time: 20220129T080315+0000

Record Last Update: 20250420T014642+0000

Ratings and Alerts

No rating or validation information has been found for CNV-seq.

No alerts have been found for CNV-seq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 151 mentions in open access literature.

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

Zeng Y, et al. (2025) Prenatal genetic detection in foetus with gallbladder size anomalies: cohort study and systematic review of the literature. Annals of medicine, 57(1), 2440638.

Mao B, et al. (2025) Congenital muscular dystrophies and myopathies: the leading cause of genetic muscular disorders in eleven Chinese families. BMC musculoskeletal disorders, 26(1), 51.

Yang S, et al. (2025) Expanded non-invasive prenatal testing offers better detection of fetal copy number variations but not chromosomal aneuploidies. PloS one, 20(1), e0312184.

Tao H, et al. (2024) Genetic etiology and pregnancy outcomes of fetuses with central nervous system anomalies. Archives of gynecology and obstetrics, 309(6), 2567.

Xiao B, et al. (2024) Combining optical genome mapping and RNA-seq for structural variants detection and interpretation in unsolved neurodevelopmental disorders. Genome medicine, 16(1), 113.

Zhang H, et al. (2024) Simultaneous CNV-seq and WES: An effective strategy for molecular diagnosis of unexplained fetal structural anomalies. Heliyon, 10(20), e39392.

Vo TM, et al. (2024) Chromosomal Anomalies in Fetuses With Increased Nuchal Translucency: A Vietnamese Retrospective Study. Cureus, 16(10), e72235.

Wang Y, et al. (2024) Detection of genomic variants by genome sequencing in foetuses with central nervous system abnormalities. Annals of medicine, 56(1), 2399317.

Zeng Y, et al. (2024) High positive predictive value of CNVs detected by clinical exome sequencing in suspected genetic diseases. Journal of translational medicine, 22(1), 644.

Guo C, et al. (2024) Role of copy number variation analysis in prenatally diagnosed Blake's pouch cyst. BMC pregnancy and childbirth, 24(1), 842.

Yang L, et al. (2024) Efficiency of Non-Invasive Prenatal Testing in Detecting Fetal Copy

Number Variation: A Retrospective Cohort Study. International journal of women's health, 16, 1661.

Shao Y, et al. (2024) Identification of chromosomal abnormalities in miscarriages by CNV-Seq. Molecular cytogenetics, 17(1), 4.

Shirasawa K, et al. (2024) Propagation path of a flowering cherry (Cerasus × yedoensis) cultivar 'Somei-Yoshino' traced by somatic mutations. DNA research : an international journal for rapid publication of reports on genes and genomes, 31(5).

Liu A, et al. (2024) Analysis of copy number variants detected by sequencing in spontaneous abortion. Molecular cytogenetics, 17(1), 13.

Zhang X, et al. (2024) Pathogenic relationship between phenotypes of ARPKD and novel compound heterozygous mutations of PKHD1. Frontiers in genetics, 15, 1429336.

Dai YF, et al. (2024) Experience of copy number variation sequencing applied in spontaneous abortion. BMC medical genomics, 17(1), 15.

Wang F, et al. (2024) Prenatal ultrasound phenotype of fetuses with recurrent 1q21.1 deletion and duplication syndrome. Frontiers in pediatrics, 12, 1504122.

Liu JP, et al. (2024) Improving prenatal diagnosis with combined karyotyping, CNV-seq and QF-PCR: a comprehensive analysis of chromosomal abnormalities in high-risk pregnancies. Frontiers in genetics, 15, 1517270.

Van Den Berghe T, et al. (2024) Predicting cytogenetic risk in multiple myeloma using conventional whole-body MRI, spinal dynamic contrast-enhanced MRI, and spinal diffusion-weighted imaging. Insights into imaging, 15(1), 106.

Zhang J, et al. (2024) Genetic Testing for Global Developmental Delay in Early Childhood. JAMA network open, 7(6), e2415084.