Resource Summary Report

Generated by kravitz2 on Aug 1, 2026

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., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: CNV-seq

Resource Type: software resource

Keywords: bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

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: 20260725T190750+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 167 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Chen S, et al. (2025) Noninvasive preimplantation genetic testing for aneuploidy using blastocyst spent culture medium may serve as a backup of trophectoderm biopsy in conventional preimplantation genetic testing. BMC medical genomics, 18(1), 34.

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.

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.

De Cock L, et al. (2025) Cracking rare disorders: a new minimally invasive RNA-seq protocol. NPJ genomic medicine, 10(1), 45.

Luo W, et al. (2025) Improved contingent screening strategy increased trisomy 21 detection rate in the second trimester. Archives of gynecology and obstetrics, 311(4), 1029.

Pang N, et al. (2025) The genetic spectrum features of 2261 Chinese children with epilepsy and intellectual disability. BMC medicine, 23(1), 388.

Peng H, et al. (2025) Prenatal diagnosis of imprinted associated chromosome abnormalities identified by noninvasive prenatal testing (NIPT). Scientific reports, 15(1), 12830.

Yang S, et al. (2025) The evolution of cell-free fetal DNA testing: expanded non-invasive prenatal testing and its effect on target populations. Frontiers in medicine, 12, 1522680.

Chang J, et al. (2025) Prenatal diagnosis and pregnancy outcomes of mosaicism detected by CMA-seq. BMC pregnancy and childbirth, 25(1), 912.

Yang H, et al. (2025) Genetic analysis of congenital unilateral renal agenesis in children based on next-generation sequencing. Pediatric research, 97(1), 273.

Zeng Z, et al. (2025) Clinical utility of trio whole exome sequencing in fetuses with ultrasound anomalies. Human genomics, 19(1), 37.

Zhu Y, et al. (2025) Lessons from a phenotypically normal infant with uniparental isodisomy of chromosome 21: a Case Report and review. Frontiers in genetics, 16, 1544565.

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.

Shi P, et al. (2025) The hidden causes of pregnancy loss: a closer look. Journal of translational medicine, 23(1), 656.

Huang Y, et al. (2025) Comprehensive chromosomal abnormality detection: integrating CNV-Seq with traditional karyotyping in prenatal diagnostics. BMC medical genomics, 18(1), 81.

Chenyue Z, et al. (2025) Genetic etiology of ventriculomegaly in 73 fetuses identified by High-Throughput sequencing. Scientific reports, 15(1), 23622.

Zhang F, et al. (2025) A rare HCN4 variant combined with sick sinus syndrome, left ventricular noncompaction, and complex congenital heart disease. Channels (Austin, Tex.), 19(1), 2517851.

Zhang F, et al. (2025) Prenatal diagnosis and molecular cytogenetic analyses of a rare 15q21.3 and 16p11.2 microduplication family. Molecular cytogenetics, 18(1), 8.

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

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