

Resource Summary Report

Generated by [dkNET](#) on Aug 24, 2026

CNVtools

RRID:SCR_001250

Type: Tool

Proper Citation

CNVtools (RRID:SCR_001250)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/CNVtools.html>

Proper Citation: CNVtools (RRID:SCR_001250)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 23,2022. Software package to facilitate the testing of Copy Number Variant data for genetic association, typically in case-control studies.

Abbreviations: CNVtools

Synonyms: CNVtools - A package to test genetic association with CNV data

Resource Type: software resource

Defining Citation: [PMID:18776912](#)

Keywords: genetic variability, copy number variant, genetic association

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: CNVtools

Resource ID: SCR_001250

Alternate IDs: OMICS_02090

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260815T182154+0000

Ratings and Alerts

No rating or validation information has been found for CNVtools.

No alerts have been found for CNVtools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Wu J, et al. (2023) Genetic Association Analysis of Copy Number Variations for Meat Quality in Beef Cattle. *Foods* (Basel, Switzerland), 12(21).

Xu L, et al. (2019) Probe-based association analysis identifies several deletions associated with average daily gain in beef cattle. *BMC genomics*, 20(1), 31.

Liu M, et al. (2019) Array CGH-based detection of CNV regions and their potential association with reproduction and other economic traits in Holsteins. *BMC genomics*, 20(1), 181.

Kucukkilic E, et al. (2018) Complement receptor 1 gene (CR1) intragenic duplication and risk of Alzheimer's disease. *Human genetics*, 137(4), 305.

Rahbari R, et al. (2017) Understanding the Genomic Structure of Copy-Number Variation of the Low-Affinity Fc γ Receptor Region Allows Confirmation of the Association of FCGR3B Deletion with Rheumatoid Arthritis. *Human mutation*, 38(4), 390.

Bourgeois S, et al. (2016) A multi-factorial analysis of response to warfarin in a UK prospective cohort. *Genome medicine*, 8(1), 2.

Park TJ, et al. (2016) Identification of a Copy Number Variation on Chromosome 20q13.12 Associated with Osteoporotic Fractures in the Korean Population. *Genomics & informatics*, 14(4), 216.

Polley S, et al. (2016) Copy number variation of scavenger-receptor cysteine-rich domains within DMBT1 and Crohn's disease. *European journal of human genetics : EJHG*, 24(9), 1294.

Polley S, et al. (2016) Analysis of copy number variation at DMBT1 and age-related macular degeneration. *BMC medical genetics*, 17(1), 44.

Forni D, et al. (2015) Determining multiallelic complex copy number and sequence variation from high coverage exome sequencing data. *BMC genomics*, 16, 891.

Blackburn A, et al. (2015) Effects of copy number variable regions on local gene expression in white blood cells of Mexican Americans. *European journal of human genetics : EJHG*, 23(9), 1229.

Hwang MY, et al. (2015) Combinatorial approach to estimate copy number genotype using whole-exome sequencing data. *Genomics*, 105(3), 145.