Resource Summary Report

Generated by T1D on Aug 9, 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: 20260808T185739+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 T1D .

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?? 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.