Resource Summary Report

Generated by NIF on Apr 28, 2025

CNVrd2

RRID:SCR_001723
Type: Tool

Proper Citation

CNVrd2 (RRID:SCR_001723)

Resource Information

URL: http://www.bioconductor.org/packages/devel/bioc/html/CNVrd2.html

Proper Citation: CNVrd2 (RRID:SCR_001723)

Description: A software package that uses next-generation sequencing data to measure human gene copy number for multiple samples, indentify SNPs tagging copy number variants and detect copy number polymorphic genomic regions.

Synonyms: CNVrd2: a read depth-based method to detect and genotype complex common copy number variants from next generation sequencing data

Resource Type: software resource

Defining Citation: PMID:23646200

Keywords: standalone software, illumina, unix/linux, mac os x, windows, r, clustering., copy number variation, coverage, linkage disequilibrium, snp, sequencing

Funding:

Availability: GNU General Public License, v2

Resource Name: CNVrd2

Resource ID: SCR_001723

Alternate IDs: OMICS_03924

Alternate URLs: http://www.bioconductor.org/packages/release/bioc/html/CNVrd2.html, https://github.com/hoangtn/CNVrd2

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250420T014036+0000

Ratings and Alerts

No rating or validation information has been found for CNVrd2.

No alerts have been found for CNVrd2.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Shebanits K, et al. (2019) Copy number determination of the gene for the human pancreatic polypeptide receptor NPY4R using read depth analysis and droplet digital PCR. BMC biotechnology, 19(1), 31.

Dharanipragada P, et al. (2018) iCopyDAV: Integrated platform for copy number variations-Detection, annotation and visualization. PloS one, 13(4), e0195334.

Boocock J, et al. (2015) The distribution and impact of common copy-number variation in the genome of the domesticated apple, Malus x domestica Borkh. BMC genomics, 16, 848.

Pirooznia M, et al. (2015) Whole-genome CNV analysis: advances in computational approaches. Frontiers in genetics, 6, 138.

Nguyen HT, et al. (2014) The CNVrd2 package: measurement of copy number at complex loci using high-throughput sequencing data. Frontiers in genetics, 5, 248.