

Resource Summary Report

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CNVcaller

RRID:SCR_015752

Type: Tool

Proper Citation

CNVcaller (RRID:SCR_015752)

Resource Information

URL: <https://github.com/JiangYuLab/CNVcaller>

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Description: Software for detecting the integrated copy number variation regions (CNVRs) using population sequencing data. The high-confidence CNVRs are discovered and refined by both individual and population criteria, and the result is a VCF format genotype file which can be used in GWAS/QLT research.

Abbreviations: CNVcaller

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource, source code

Keywords: copy number variation, cnv, next-generation sequencing, ngs, population genetic, segmental duplication, absolute copy number

Availability: Free, Available for download

Resource Name: CNVcaller

Resource ID: SCR_015752

License: GNU General Public License v 3.0

License URLs: <https://github.com/JiangYuLab/CNVcaller/blob/master/LICENSE>

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260829T182501+0000

Ratings and Alerts

No rating or validation information has been found for CNVcaller.

No alerts have been found for CNVcaller.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 40 mentions in open access literature.

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

Yuan Y, et al. (2026) Integrative multi-omics analysis identifies C-type lectin CNVs as functional targets for breeding mastitis-resistant dairy goats. *Animal microbiome*, 8(1).

Nikoghosyan M, et al. (2026) Population structure of wild and cultivated grapevines in Armenia. *BMC plant biology*, 26(1).

Ma Y, et al. (2026) Insights into lentil diversity, domestication, and the genetic basis of important agronomic traits through resequencing of 238 Lens accessions. *The Plant journal : for cell and molecular biology*, 126(3), e70908.

Li W, et al. (2026) Identification of the Genetic Characteristics of Copy Number Variation Regions in Diverse Goat Populations. *Genes*, 17(6).

Zhang X, et al. (2025) Genomic variation responding to artificial selection on different lines of Pekin duck. *Poultry science*, 104(2), 104785.

Wang Z, et al. (2025) A high-quality assembly revealing the PMEL gene for the unique plumage phenotype in Liancheng ducks. *GigaScience*, 14.

Guo J, et al. (2025) Whole-genome sequencing reveals complex structural variations at a major locus linked to pigmented spot sizes in Tianfu goats. *BMC genomics*, 26(1), 848.

Wu X, et al. (2025) Genome-wide scan for selection signatures reveals novel insights into the adaptive capacity characteristics in three Chinese cattle breeds. *BMC genomics*, 26(1), 206.

Dussex N, et al. (2025) The Genomic Basis of the Svalbard Reindeer's Adaptation to an Extreme Arctic Environment. *Genome biology and evolution*, 17(9).

Dauphin B, et al. (2025) Genetic variation among progeny shapes symbiosis in a basidiomycete with poplar. *The New phytologist*, 248(1), 157.

Wang G, et al. (2025) Genomic evidence for hybridization and introgression between blue peafowl and endangered green peafowl and molecular foundation of leucistic plumage of blue peafowl. *GigaScience*, 14.

Dang D, et al. (2024) Analysis of genomic copy number variations through whole-genome scan in Yunling cattle. *Frontiers in veterinary science*, 11, 1413504.

Zhang Y, et al. (2024) Genome-wide association study reveals 2 copy number variations associated with the variation of plumage color in the white duck hybrid population. *Poultry science*, 103(10), 104107.

Morales-Cruz A, et al. (2023) Multigenic resistance to *Xylella fastidiosa* in wild grapes (*Vitis* spp.) and its implications within a changing climate. *Communications biology*, 6(1), 580.

Song X, et al. (2023) InDel and CNV within the AKAP13 Gene Revealing Strong Associations with Growth Traits in Goat. *Animals : an open access journal from MDPI*, 13(17).

Yu S, et al. (2023) Resequencing of a Pekin duck breeding population provides insights into the genomic response to short-term artificial selection. *GigaScience*, 12.

Yuan Y, et al. (2023) A 1.1 Mb duplication CNV on chromosome 17 contributes to skeletal muscle development in Boer goats. *Zoological research*, 44(2), 303.

He X, et al. (2023) Identification of Candidate Genes for Min Pig Villi Hair Traits by Genome-Wide Association of Copy Number Variation. *Veterinary sciences*, 10(5).

Zhang X, et al. (2022) Comparative analyses of copy number variations between swamp and river buffalo. *Gene*, 830, 146509.

Guo J, et al. (2021) Genome-wide association study reveals 14 new SNPs and confirms two structural variants highly associated with the horned/polled phenotype in goats. *BMC genomics*, 22(1), 769.