# Resource Summary Report

Generated by RRID on Aug 15, 2026

## Canvas Copy Number Variant Caller

RRID:SCR_027970
Type: Tool

### Proper Citation

Canvas Copy Number Variant Caller (RRID:SCR_027970)

### Resource Information

**URL:** https://github.com/Illumina/canvas

**Proper Citation:** Canvas Copy Number Variant Caller (RRID:SCR_027970)

**Description:** Software tool for calling copy number variants (CNVs) from human DNA sequencing data. It can work either with germline data, or paired tumor/normal samples. Its primary input is aligned reads (in .bam format), and its primary output is a report (in a .vcf file) giving the copy number status of the genome.

**Abbreviations:** canvas

**Synonyms:** Illumina Canvas, Canvas

**Resource Type:** source code, software application, software resource

**Defining Citation:** PMID:27153601, PMID:29028893

**Keywords:** detection of copy number variants, copy number variants, human DNA sequencing data,

**Resource Name:** Canvas Copy Number Variant Caller

**Resource ID:** SCR_027970

**Record Creation Time:** 20260218T060348+0000

**Record Last Update:** 20260815T183312+0000

### Ratings and Alerts

No rating or validation information has been found for Canvas Copy Number Variant Caller.

No alerts have been found for Canvas Copy Number Variant Caller.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Sun D, et al. (2026) Analysis of familial exudative vitreoretinopathy (FEVR) cases in the UK 100 000 genomes project increases diagnostic rate and implicates heterozygous CTNND1 mutations in FEVR. Journal of medical genetics, 63(3), 187.