

Resource Summary Report

Generated by T1D on Aug 3, 2026

CNAnorm

RRID:SCR_010816

Type: Tool

Proper Citation

CNAnorm (RRID:SCR_010816)

Resource Information

URL: <http://www.precancer.leeds.ac.uk/software-and-datasets/cnanorm/>

Proper Citation: CNAnorm (RRID:SCR_010816)

Description: A Bioconductor package to estimate Copy Number Aberrations (CNA) in cancer samples.

Abbreviations: CNAnorm

Resource Type: software resource

Resource Name: CNAnorm

Resource ID: SCR_010816

Alternate IDs: OMICS_00336

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260801T190416+0000

Ratings and Alerts

No rating or validation information has been found for CNAnorm.

No alerts have been found for CNAnorm.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Min Z, et al. (2024) Paromomycin targets HDAC1-mediated SUMOylation and IGF1R translocation in glioblastoma. *Frontiers in pharmacology*, 15, 1490878.

Hecht V, et al. (2023) Analyzing histone ChIP-seq data with a bin-based probability of being signal. *PLoS computational biology*, 19(10), e1011568.

Symer DE, et al. (2022) Diverse tumorigenic consequences of human papillomavirus integration in primary oropharyngeal cancers. *Genome research*, 32(1), 55.

Kashofer K, et al. (2022) Driver gene mutations in micro-invasive cervical squamous cancers have no prognostic significance. *Gynecologic oncology*, 165(1), 121.

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

Chu Y, et al. (2018) Modeling and correct the GC bias of tumor and normal WGS data for SCNA based tumor subclonal population inferring. *BMC bioinformatics*, 19(Suppl 5), 112.

Luo Z, et al. (2018) Accurity: accurate tumor purity and ploidy inference from tumor-normal WGS data by jointly modelling somatic copy number alterations and heterozygous germline single-nucleotide-variants. *Bioinformatics (Oxford, England)*, 34(12), 2004.

Lohberger B, et al. (2017) Establishment of a novel cellular model for myxofibrosarcoma heterogeneity. *Scientific reports*, 7, 44700.

Weil T, et al. (2017) Adaptive Mistranslation Accelerates the Evolution of Fluconazole Resistance and Induces Major Genomic and Gene Expression Alterations in *Candida albicans*. *mSphere*, 2(4).

Wood HM, et al. (2017) The genomic road to invasion-examining the similarities and differences in the genomes of associated oral pre-cancer and cancer samples. *Genome medicine*, 9(1), 53.

Zhang Z, et al. (2015) SAAS-CNV: A Joint Segmentation Approach on Aggregated and Allele Specific Signals for the Identification of Somatic Copy Number Alterations with Next-Generation Sequencing Data. *PLoS computational biology*, 11(11), e1004618.

Quenel-Tueux N, et al. (2015) Clinical and genomic analysis of a randomised phase II study evaluating anastrozole and fulvestrant in postmenopausal patients treated for large operable or locally advanced hormone-receptor-positive breast cancer. *British journal of cancer*, 113(4), 585.

De Faveri LE, et al. (2015) Polycomb Repressor Complex 1 Member, BMI1 Contributes to Urothelial Tumorigenesis through p16-Independent Mechanisms. *Translational oncology*, 8(5), 387.

Akagi K, et al. (2014) Genome-wide analysis of HPV integration in human cancers reveals recurrent, focal genomic instability. *Genome research*, 24(2), 185.

Belvedere O, et al. (2012) A computational index derived from whole-genome copy number analysis is a novel tool for prognosis in early stage lung squamous cell carcinoma. *Genomics*, 99(1), 18.