Resource Summary Report

Generated by Kravitz on Sep 10, 2026

ichorCNA

RRID:SCR_024768
Type: Tool

Proper Citation

ichorCNA (RRID:SCR_024768)

Resource Information

URL: https://github.com/broadinstitute/ichorCNA

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Description: Software tool that quantifies tumor content in cfDNA from 0.1× coverage whole-genome sequencing data without prior knowledge of tumor mutations. Used to simultaneously segment genome, predict large scale copy number alterations, and estimate tumor fraction of ultra low pass whole genome sequencing sample.

Resource Type: simulation software, software application, software resource

Defining Citation: PMID:29109393

Keywords: quantify tumor content, simultaneously segment genome, predict large scale copy number alterations, estimate tumor fraction, ultra low pass whole genome sequencing sample,

Funding: Canadian Institutes for Health Research Postdoctoral Fellowship ;
Gerstner Family Foundation ;
NCI P30 CA14051

Availability: Free, Available for download, Freely available

Resource Name: ichorCNA

Resource ID: SCR_024768

License: GNU GPL v3.0

Record Creation Time: 20231208T050229+0000

Record Last Update: 20260905T133441+0000

Ratings and Alerts

No rating or validation information has been found for ichorCNA.

No alerts have been found for ichorCNA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

Nteliopoulos G, et al. (2026) Identification of actionable targets using DEPArray-based sorting of pure carcinoma and stromal populations from formalin-fixed paraffin-embedded tissues followed by shallow whole-genome sequencing. The Journal of pathology, 268(1), 13.

Amghar M, et al. (2026) Genomic analysis in chemotherapy-naïve prostate cancer prior to PSMA-targeted treatment. Frontiers in oncology, 16, 1741080.

Amghar M, et al. (2026) Exploratory case series of circulating tumor DNA dynamics during tandem therapy in metastatic castration-resistant prostate cancer. EJNMMI research, 16(1).

Valentín López JC, et al. (2026) Evolution of AR and Non-AR Alterations in ctDNA of Patients with Metastatic Prostate Cancer Treated in the Phase III Alliance A031201 Trial. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(12), 2413.

Garinet S, et al. (2026) Cell-free DNA epigenomic profiling enables noninvasive detection and monitoring of translocation renal cell carcinoma. The Journal of clinical investigation, 136(3).

Tarantino P, et al. (2026) Quantitative HER2 tissue and plasma profiling predicts the activity of trastuzumab deruxtecan for breast cancer. NPJ precision oncology, 10(1).

Matchett CL, et al. (2026) Discovery and Validation of Molecular Biomarkers for Differentiation of Nondysplastic Barrett's Esophagus from High-grade Dysplasia and Esophageal Adenocarcinoma. Cancer prevention research (Philadelphia, Pa.), 19(1), 49.

Fang J, et al. (2026) Comprehensive molecular characterization of cfDNA as predictive and monitoring biomarkers in advanced gastric cancer receiving immunotherapy. Journal for immunotherapy of cancer, 14(4).

Wang X, et al. (2026) Development and Prospective Validation of a Cell-free DNA-Based Model for the Early Detection of Pancreatic Cancer. Cancer discovery, 16(1), 66.

De Paolis E, et al. (2025) Genomics and Epigenomics Approaches for the Quantification of Circulating Tumor DNA in Liquid Biopsy: Relevance of a Multimodal Strategy. International journal of molecular sciences, 26(22).

Xue Y, et al. (2025) 5-hydroxymethylcytosine analysis reveals stable epigenomic changes in tumor tissue that enable cancer detection in cell-free DNA. Communications biology, 8(1), 1613.

Curtis SD, et al. (2025) Minimizing and quantifying uncertainty in AI-informed decisions: Applications in medicine. Proceedings of the National Academy of Sciences of the United States of America, 122(34), e2424203122.

Allsopp RC, et al. (2025) Concurrent genomic assessment of circulating tumour cells and ctDNA to guide therapy in metastatic breast cancer. BMC cancer, 25(1), 1858.

Jones PA, et al. (2025) Integrated Multiclass Driver ctDNA Profiling Enables MPNST Detection and Monitoring in NF1 Patients. Research square.

George SL, et al. (2025) Stratified Medicine Pediatrics: Cell-Free DNA and Serial Tumor Sequencing Identifies Subtype-Specific Cancer Evolution and Epigenetic States. Cancer discovery, 15(4), 717.

Curtis SD, et al. (2025) Fragmentation signatures in cancer patients resemble those of patients with vascular or autoimmune diseases. Proceedings of the National Academy of Sciences of the United States of America, 122(34), e2426890122.

Semaan K, et al. (2025) Plasma epigenomic profiling reveals treatment-emergent squamous transformation in prostate cancer. NPJ precision oncology, 9(1), 233.

Lin AY, et al. (2025) CfDNA-based copy-number dynamics during anti-PD1 treatment in metastatic triple negative breast cancer. Cell reports. Medicine, 6(12), 102512.

Wang N, et al. (2025) Benchmarking copy number variation detection with low-coverage whole-genome sequencing. Briefings in bioinformatics, 26(5).

Virga A, et al. (2025) Mutational and low-coverage whole genome sequencing identifies actionable DNA repair alterations in prostate cancer plasma DNA. Scientific reports, 15(1), 21296.