Resource Summary Report

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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 resource, software application

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: Gerstner Family Foundation ;
Canadian Institutes for Health Research Postdoctoral Fellowship ;
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: 20260731T043200+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 21 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

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.

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.

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.

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

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.

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.

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.

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.

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

Garinet S, et al. (2025) Detection and monitoring of translocation renal cell carcinoma via plasma cell-free epigenomic profiling. bioRxiv : the preprint server for biology.

Chauhan PS, et al. (2025) Genomic and Epigenomic Analysis of Plasma Cell-Free DNA Identifies Stemness Features Associated with Worse Survival in Lethal Prostate Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(1), 151.

Pearlman AH, et al. (2025) Detection of human brain cancers using genomic and immune cell characterization of cerebrospinal fluid through CSF-BAM. Cancer discovery.

Wong D, et al. (2024) Early Cancer Detection in Li-Fraumeni Syndrome with Cell-Free DNA. Cancer discovery, 14(1), 104.

Stanley KE, et al. (2024) Cell type signatures in cell-free DNA fragmentation profiles reveal disease biology. Nature communications, 15(1), 2220.

Moldovan N, et al. (2024) Comparison of cell-free and small extracellular-vesicle-associated DNA by sequencing plasma of lung cancer patients. iScience, 27(9), 110742.

Lleshi E, et al. (2024) Prostate cancer detection through unbiased capture of methylated cell-free DNA. iScience, 27(7), 110330.

González-Medina A, et al. (2024) Clinical Value of Liquid Biopsy in Patients with FGFR2 Fusion-Positive Cholangiocarcinoma During Targeted Therapy. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(19), 4491.

Ak Ç, et al. (2024) Multiplex imaging of localized prostate tumors reveals altered spatial organization of AR-positive cells in the microenvironment. iScience, 27(9), 110668.

Ju J, et al. (2024) Cell-free DNA end characteristics enable accurate and sensitive cancer diagnosis. Cell reports methods, 4(10), 100877.