Resource Summary Report

Generated by RRID on May 25, 2025

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: software resource, simulation software, 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: 20250525T032957+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 8 mentions in open access literature.

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

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

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

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.

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.

Jiao Z, et al. (2024) Leveraging cfDNA fragmentomic features in a stacked ensemble model for early detection of esophageal squamous cell carcinoma. Cell reports. Medicine, 5(8), 101664.

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.