Resource Summary Report

Generated by RRID on May 25, 2025

ABSOLUTE

RRID:SCR_005198
Type: Tool

Proper Citation

ABSOLUTE (RRID:SCR_005198)

Resource Information

URL: http://www.broadinstitute.org/cancer/cga/absolute

Proper Citation: ABSOLUTE (RRID:SCR_005198)

Description: Software to estimate purity / ploidy, and from that compute absolute copy-number and mutation multiplicities. When DNA is extracted from an admixed population of cancer and normal cells, the information on absolute copy number per cancer cell is lost in the mixing. The purpose of ABSOLUTE is to re-extract these data from the mixed DNA population. This process begins by generation of segmented copy number data, which is input to the ABSOLUTE algorithm together with pre-computed models of recurrent cancer karyotypes and, optionally, allelic fraction values for somatic point mutations. The output of ABSOLUTE then provides re-extracted information on the absolute cellular copy number of local DNA segments and, for point mutations, the number of mutated alleles.

Abbreviations: ABSOLUTE

Resource Type: software resource

Defining Citation: PMID:22544022

Related Condition: Cancer, Normal

Funding:

Availability: Account required

Resource Name: ABSOLUTE

Resource ID: SCR_005198

Alternate IDs: OMICS_00217

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250525T030857+0000

Ratings and Alerts

No rating or validation information has been found for ABSOLUTE.

No alerts have been found for ABSOLUTE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 232 mentions in open access literature.

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

Dai J, et al. (2025) Atezolizumab plus bevacizumab in patients with unresectable or metastatic mucosal melanoma: 3-year survival update and multi-omics analysis. Clinical and translational medicine, 15(1), e70169.

Krull JE, et al. (2024) Follicular lymphoma B cells exhibit heterogeneous transcriptional states with associated somatic alterations and tumor microenvironments. Cell reports. Medicine, 5(3), 101443.

Antonello A, et al. (2024) Computational validation of clonal and subclonal copy number alterations from bulk tumor sequencing using CNAqc. Genome biology, 25(1), 38.

Morton LM, et al. (2024) Genomic characterization of cervical lymph node metastases in papillary thyroid carcinoma following the Chornobyl accident. Nature communications, 15(1), 5053.

Adams KM, et al. (2024) Cell-intrinsic platinum response and associated genetic and gene expression signatures in ovarian cancer cell lines and isogenic models. bioRxiv : the preprint server for biology.

Burr R, et al. (2024) Developmental mosaicism underlying EGFR-mutant lung cancer presenting with multiple primary tumors. Nature cancer, 5(11), 1681.

Li J, et al. (2024) Spatial whole exome sequencing reveals the genetic features of highly-aggressive components in lung adenocarcinoma. Neoplasia (New York, N.Y.), 54, 101013.

Yang B, et al. (2024) AI-powered genomic mutation signature for predicting immune checkpoint inhibitor therapy outcomes in gastroesophageal cancer: a multi-cohort analysis. Discover oncology, 15(1), 507.

Zerbib J, et al. (2024) Human aneuploid cells depend on the RAF/MEK/ERK pathway for overcoming increased DNA damage. Nature communications, 15(1), 7772.

Blanco-Heredia J, et al. (2024) Converging and evolving immuno-genomic routes toward immune escape in breast cancer. Nature communications, 15(1), 1302.

Voutsadakis IA, et al. (2024) CDX2-Suppressed Colorectal Cancers Possess Potentially Targetable Alterations in Receptor Tyrosine Kinases and Other Colorectal-Cancer-Associated Pathways. Diseases (Basel, Switzerland), 12(10).

Cai Q, et al. (2024) Identification of CNKSR1 as a biomarker for "cold" tumor microenvironment in lung adenocarcinoma: An integrative analysis based on a novel workflow. Heliyon, 10(8), e29126.

Dopeso H, et al. (2024) Genomic and epigenomic basis of breast invasive lobular carcinomas lacking CDH1 genetic alterations. NPJ precision oncology, 8(1), 33.

Yu X, et al. (2024) A pan-cancer gamma delta T cell repertoire. bioRxiv : the preprint server for biology.

Yu D, et al. (2024) Combination of MRI-based prediction and CRISPR/Cas12a-based detection for IDH genotyping in glioma. NPJ precision oncology, 8(1), 140.

Xie F, et al. (2024) Genomic and transcriptomic landscape of human gastrointestinal stromal tumors. Nature communications, 15(1), 9495.

Sasiain I, et al. (2024) Tumor purity estimated from bulk DNA methylation can be used for adjusting beta values of individual samples to better reflect tumor biology. NAR genomics and bioinformatics, 6(4), lqae146.

Wei H, et al. (2024) Mutational Landscape of Gastric Adenocarcinoma of the Fundic Gland Type Revealed by Whole Genome Sequencing. Cancer medicine, 13(19), e70290.

Choudhury AD, et al. (2024) Randomized Phase II Study Evaluating the Addition of Pembrolizumab to Radium-223 in Metastatic Castration-resistant Prostate Cancer. Cancer immunology research, 12(6), 704.

Yin G, et al. (2024) Genomic and transcriptomic analysis of breast cancer identifies novel signatures associated with response to neoadjuvant chemotherapy. Genome medicine, 16(1), 11.