Resource Summary Report

Generated by nidm-terms on Jul 28, 2026

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

Availability: Account required

Resource Name: ABSOLUTE

Resource ID: SCR_005198

Alternate IDs: OMICS_00217

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260725T190600+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 263 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Song Y, et al. (2026) Evaluating and Optimizing Mass Spectrometry Proteomics Data to Deconvolve Cell-Type-Specific Protein Expression in Tumors. Journal of proteome research, 25(1), 471.

Hu K, et al. (2025) Development and Application of MiMouse, a Comprehensive Genomic Profiling Panel for Credentialing Mouse Tumor Models. Cancer research communications, 5(10), 1910.

Bökenkamp JE, et al. (2025) Proteogenomic analysis reveals adaptive strategies for alleviating the consequences of aneuploidy in cancer. The EMBO journal, 44(6), 1829.

Heller EM, et al. (2025) Explainable Machine Learning Identifies Factors for Dosage Compensation in Aneuploid Human Cancer Cells. bioRxiv : the preprint server for biology.

Almeida-Lima K, et al. (2025) Heterogeneous expression of immunotherapy response markers in non-small cell lung cancer with hyperactive NRF2 pathway: PD-L1 and beyond. Redox biology, 87, 103889.

Merzliakov S, et al. (2025) Widespread Epistasis between Cancer Driver Mutations and Allele-Specific Copy Number Variations. bioRxiv : the preprint server for biology.

Liu F, et al. (2025) Integrated analysis of single-cell and bulk transcriptomics reveals cellular subtypes and molecular features associated with osteosarcoma prognosis. BMC cancer, 25(1), 280.

Sasagawa S, et al. (2025) Predicting chemotherapy responsiveness in gastric cancer through machine learning analysis of genome, immune, and neutrophil signatures. Gastric cancer : official journal of the International Gastric Cancer Association and the Japanese Gastric Cancer Association, 28(2), 228.

Wan H, et al. (2025) Tumor evolution and immune microenvironment dynamics in primary and relapsed mantle cell lymphoma. Cell reports. Medicine, 6(9), 102318.

Kübler K, et al. (2025) Tamoxifen induces PI3K activation in uterine cancer. Nature genetics, 57(9), 2192.

Li R, et al. (2025) Numbat-multiome: inferring copy number variations by combining RNA and chromatin accessibility information from single-cell data. Briefings in bioinformatics, 26(5).

Han J, et al. (2025) The Evolutionary Trajectory and Prognostic Value of GITR+ Tregs Reprogramed by Tumor-Intrinsic PD-1/c-MET Signaling in Pancreatic Cancer. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(36), e00806.

Dollar JJ, et al. (2025) Early Genetic Evolution of Driver Mutations in Uveal Melanoma. medRxiv : the preprint server for health sciences.

Disharoon AO, et al. (2025) Half the Chromosome It Used to Be: Identifying Cancer Treatments Targeting Aneuploid Losses. Genes, 16(6).

Hao W, et al. (2025) Multi-modal characterization of metabolic and immune gene clusters in adrenocortical carcinoma treatment. NPJ precision oncology, 9(1), 314.

Waks AG, et al. (2025) Efficacy, safety, and predictive biomarkers of neoadjuvant nab-paclitaxel and pembrolizumab in hormone receptor-positive breast cancer: A randomized pilot trial. Nature communications, 16(1), 10705.

Knight AD, et al. (2025) Melanoma to rhabdomyosarcoma plasticity in the setting of immunotherapy. medRxiv : the preprint server for health sciences.

Chida K, et al. (2025) DEPTH2 score was associated with cell proliferation and immune cell infiltrations but not with systemic treatment response in breast cancer. Scientific reports, 15(1), 42225.

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.

Antysheva Z, et al. (2025) Machine learning-based single-sample molecular classifier for cancer grading. Frontiers in oncology, 15, 1617898.