

Resource Summary Report

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[maftools](#)

RRID:SCR_024519

Type: Tool

Proper Citation

maftools (RRID:SCR_024519)

Resource Information

URL: <https://github.com/PoisonAlien/Maftools>

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Description: Software R package offers multitude of analysis and visualization modules that are commonly used in cancer genomic studies, including driver gene identification, pathway, signature, enrichment, and association analyses. Maftools requires somatic variants in Mutation Annotation Format (MAF) and is independent of larger alignment files.

Resource Type: software toolkit, software resource

Defining Citation: [PMID:30341162](#)

Keywords: MAF summarize, MAF analyze, MAF visualize, Mutation Annotation Format files, driver gene identification, pathway, signature, enrichment, association analyses, somatic variants in Mutation Annotation Format, MAF

Availability: Free, Available for download, Freely available

Resource Name: maftools

Resource ID: SCR_024519

Alternate URLs: <https://bioconductor.org/packages/maftools/>

License: MIT license

Record Creation Time: 20231002T161337+0000

Record Last Update: 20260729T044607+0000

Ratings and Alerts

No rating or validation information has been found for maftools.

No alerts have been found for maftools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 195 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Yoshimura T, et al. (2025) High-Throughput Drug Screening of Clear Cell Ovarian Cancer Organoids Reveals Vulnerability to Proteasome Inhibitors and Dinaciclib and Identifies AGR2 as a Therapeutic Target. Cancer research communications, 5(6), 1018.

Zhou J, et al. (2025) Construction of enhanced MRI-based radiomics models using machine learning algorithms for non-invasive prediction of IL7R expression in high-grade gliomas and its prognostic value in clinical practice. Journal of translational medicine, 23(1), 383.

Renatino Canevarolo R, et al. (2025) Epigenetic Plasticity Drives Carcinogenesis and Multi-Therapy Resistance in Multiple Myeloma. Research square.

Zhang J, et al. (2025) Multi-omics analysis reveals the panoramic picture of TOP2A in pan-cancer. Scientific reports, 15(1), 6046.

Yang F, et al. (2025) Exploring the prognostic role of microbial and genetic markers in lung squamous cell carcinoma. Scientific reports, 15(1), 4499.

Zhou H, et al. (2025) A comprehensive prognostic and immune analysis of LAPTM4B in pan-cancer and Philadelphia chromosome-positive acute lymphoblastic leukemia. Frontiers in immunology, 16, 1522293.

Chen Y, et al. (2025) Understanding the cellular and molecular heterogeneity in colorectal cancer through the use of single-cell RNA sequencing. Translational oncology, 55, 102374.

Zhang M, et al. (2025) EZH2 loss promotes gastric squamous cell carcinoma. Nature communications, 16(1), 6032.

Yu H, et al. (2025) The Clinical and Molecular Characterization of Distinct Subtypes in Adult T Cell Acute Lymphoblastic Leukemia. Cancer science, 116(4), 1126.

Ishikawa R, et al. (2025) Immunohistochemical and molecular evolutionary features of jejunoileal adenocarcinoma unveiled through comparative analysis with colorectal adenocarcinoma. Neoplasia (New York, N.Y.), 66, 101180.

Huang ML, et al. (2025) An exploratory study on the potential of angiogenic genes in early HNSCC detection. *Discover oncology*, 16(1), 1854.

Hu J, et al. (2025) A prognostic signature of Glutathione metabolism-associated long non-coding RNAs for lung adenocarcinoma with immune microenvironment insights. *Frontiers in immunology*, 16, 1477437.

Zhu Q, et al. (2025) Development of a novel prognostic signature based on cytotoxic T lymphocyte-evasion genes for hepatocellular carcinoma patient management. *Discover oncology*, 16(1), 144.

Li Y, et al. (2025) Identification and multi-omics analysis of essential coding and long non-coding genes in colorectal cancer. *Biochemistry and biophysics reports*, 41, 101938.

Zeng Y, et al. (2025) Mapping the chromothripsis landscape in urothelial carcinoma unravels great intratumoral and intertumoral heterogeneity. *iScience*, 28(1), 111510.

Guo Y, et al. (2025) Oncogenic and immunological functions of USP35 in pan-cancer and its potential as a biomarker in kidney clear cell carcinoma. *BMC cancer*, 25(1), 617.

Ren J, et al. (2025) Characterization of the Genomic Landscape in HPV-positive Cervical and Head and Neck Squamous Cell Carcinomas by Whole Genome Next Generation Sequencing. *Cancer genomics & proteomics*, 22(2), 188.

Pecora G, et al. (2025) Genetic insight into lung neuroendocrine tumors: Notch and Wnt signaling pathways as potential targets. *Journal of translational medicine*, 23(1), 538.

Liu Y, et al. (2025) Integrated pan-cancer analysis of ADM's role in prognosis, immune modulation and resistance. *Frontiers in immunology*, 16, 1573250.

Li Y, et al. (2025) Spatial Transcriptomics and snRNA-seq Expose CAF Niches Orchestrating Dual Stromal-Immune Barriers in Hepatocellular Carcinoma. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(48), e14661.