

Resource Summary Report

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mutationalpatterns

RRID:SCR_024247

Type: Tool

Proper Citation

mutationalpatterns (RRID:SCR_024247)

Resource Information

URL: <https://bioconductor.org/packages/release/bioc/html/MutationalPatterns.html>

Proper Citation: mutationalpatterns (RRID:SCR_024247)

Description: Software R package provides set of flexible functions to evaluate and visualize multitude of mutational patterns in base substitution catalogues of e.g. healthy samples, tumour samples, or DNA-repair deficient cells.

Resource Type: software resource, software toolkit

Keywords: evaluate and visualize multitude of mutational patterns, base substitution catalogues patterns,

Funding:

Availability: Free, Available for download, Freely available,

Resource Name: mutationalpatterns

Resource ID: SCR_024247

Alternate URLs: <https://sources.debian.org/src/r-bioc-mutationalpatterns/>

Record Creation Time: 20230830T050217+0000

Record Last Update: 20250421T054522+0000

Ratings and Alerts

No rating or validation information has been found for mutational patterns.

No alerts have been found for mutational patterns.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 162 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

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

Nero C, et al. (2025) POLE mutations in endometrial carcinoma: Clinical and genomic landscape from a large prospective single-center cohort. *Cancer*, 131(3), e35731.

Kubitschek J, et al. (2025) Single-nucleotide-resolution genomic maps of O6-methylguanine from the glioblastoma drug temozolomide. *Nucleic acids research*, 53(2).

Liao R, et al. (2025) Characterization of the genomic landscape in liver oligometastatic NSCLC. *BMC cancer*, 25(1), 93.

Jing X, et al. (2024) DNA damage response alterations in clear cell renal cell carcinoma: clinical, molecular, and prognostic implications. *European journal of medical research*, 29(1), 107.

Yaacov A, et al. (2024) Cancer mutational signatures identification in clinical assays using neural embedding-based representations. *Cell reports. Medicine*, 5(6), 101608.

Liang YX, et al. (2024) Whole-Exome Sequencing and Experimental Validation Unveil the Roles of TMEM229A Q200del Mutation in Lung Adenocarcinoma. *The clinical respiratory journal*, 18(8), e70006.

Hariprakash JM, et al. (2024) Leveraging Tissue-Specific Enhancer-Target Gene Regulatory Networks Identifies Enhancer Somatic Mutations That Functionally Impact Lung Cancer. *Cancer research*, 84(1), 133.

Lim H, et al. (2024) Somatic mutations of esophageal adenocarcinoma: a comparison between Black and White patients. *Scientific reports*, 14(1), 8988.

Yu L, et al. (2024) A somatic genetic clock for clonal species. *Nature ecology & evolution*, 8(7), 1327.

Medo M, et al. (2024) A comprehensive comparison of tools for fitting mutational signatures. *Nature communications*, 15(1), 9467.

Poort VM, et al. (2024) Transient Differentiation-State Plasticity Occurs during Acute Lymphoblastic Leukemia Initiation. *Cancer research*, 84(16), 2720.

Butt Y, et al. (2024) Distinguishing preferences of human APOBEC3A and APOBEC3B for cytosines in hairpin loops, and reflection of these preferences in APOBEC-signature cancer genome mutations. *Nature communications*, 15(1), 2369.

Sveen A, et al. (2024) Evolutionary mode and timing of dissemination of high-grade serous carcinomas. *JCI insight*, 9(3).

Salgkamis D, et al. (2024) Systematic review and feasibility study on pre-analytical factors and genomic analyses on archival formalin-fixed paraffin-embedded breast cancer tissue. *Scientific reports*, 14(1), 18275.

Xu S, et al. (2024) Whole-exome sequencing reveals novel genomic signatures and potential therapeutic targets during the progression of rectal neuroendocrine neoplasm. *Cell death & disease*, 15(11), 833.

Derks LLM, et al. (2024) Protocol for genome-wide analysis of somatic variants at single-cell resolution using primary template-directed DNA amplification. *STAR protocols*, 6(1), 103499.

Koh GCC, et al. (2024) The chemotherapeutic drug CX-5461 is a potent mutagen in cultured human cells. *Nature genetics*, 56(1), 23.

Yang Q, et al. (2024) Image-guided metabolomics and transcriptomics reveal tumour heterogeneity in luminal A and B human breast cancer beyond glucose tracer uptake. *Clinical and translational medicine*, 14(2), e1550.

Nead KT, et al. (2024) Impact of cancer therapy on clonal hematopoiesis mutations and subsequent clinical outcomes. *Blood advances*, 8(19), 5215.