

Resource Summary Report

Generated by T1D on Sep 5, 2026

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,

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: 20260904T000032+0000

Ratings and Alerts

No rating or validation information has been found for mutationalpatterns.

No alerts have been found for mutationalpatterns.

Data and Source Information

Usage and Citation Metrics

We found 247 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Schwartz I, et al. (2026) Guardian ubiquitin E3 ligases target cancer-associated APOBEC3 deaminases for degradation to promote human genome integrity. *Nature communications*, 17(1), 1723.

Zhang C, et al. (2026) R-loop editing by DNA cytosine deaminase APOBEC3B modulates the activity of oestrogen receptor enhancers. *Nature communications*, 17(1).

Jung S, et al. (2026) Microbiome-Genome Crosstalk in Colorectal Cancer: Colibactin Signatures and *Fusobacterium nucleatum* in Epidemiology, Driver Selection, and Translation. *International journal of molecular sciences*, 27(4).

Shao Y, et al. (2026) An AI-integrated organoid platform enables high-throughput functional evaluation of bioactive metal ions. *Bioactive materials*, 65, 556.

Tselikas L, et al. (2026) Safety and efficacy of intratumoural anti-CTLA4 with intravenous anti-PD1. *Nature*, 655(8121), 219.

Sauty SM, et al. (2026) Comparative whole-genome analyses of articular chondrocytes and skin fibroblasts reveal distinct genome instability landscapes in mesenchymal cell types. *PLoS genetics*, 22(5), e1012156.

Huang Z, et al. (2026) Non-invasive radiogenomic mapping of the SMARCA1-driven ferroptotic niche is associated with longitudinal MRD-negative surveillance in early-stage NSCLC. *Frontiers in immunology*, 17, 1835413.

Bilardi RA, et al. (2026) Mbd4 and MutS γ protect cells from spontaneous deamination of 5-methylcytosine. *Nucleic acids research*, 54(2).

Zhang X, et al. (2026) Benzo[b]fluoranthene Induces Mutation Accumulation and Cancer-Relevant Mutational Signatures in Mouse Lung Alongside Steady State Levels of Chromosome Damage in Blood. *Environmental and molecular mutagenesis*, 67(5-7), e70063.

Gurjao C, et al. (2026) Germline Predisposition to Oncogenic Alkylating Damage in Colorectal Cancer. *Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology*, 35(3), 420.

Odintsov I, et al. (2026) Clinical Utility of Next-Generation Sequencing in Tumors Diagnosed as Lung Squamous Cell Carcinoma: Real-World Data of Diagnostic and Therapeutic Implications. *Modern pathology : an official journal of the United States and Canadian Academy of Pathology, Inc*, 39(5), 100985.

Zhang J, et al. (2026) Biomimetic hydrogel for the construction of patient-derived bladder cancer organoids with aggressive growth. *iScience*, 29(2), 114786.

Zhong L, et al. (2026) Loss of FAT1 drives cyclophosphamide resistance in breast cancer via the Wnt/ β -Catenin pathway. *International journal of biological sciences*, 22(1), 447.

Sauty SM, et al. (2026) Comparative whole-genome analyses of articular chondrocytes and skin fibroblasts reveal distinct genome instability landscapes in mesenchymal cell types. *bioRxiv : the preprint server for biology*.

Vlachos G, et al. (2026) Functional footprints of homologous recombination deficiency in prostate cancer revealed by ctDNA fragmentation and transcription factor accessibility. *British journal of cancer*.

Stojkova O, et al. (2026) Identification of an ERCC2 mutation associated mutational signature of nucleotide excision repair deficiency in targeted panel sequencing data. *bioRxiv : the preprint server for biology*.

Nakamura Y, et al. (2026) Mutational profiles of spontaneous and radiation-related mammary carcinomas in a rat model of Brca1 haploinsufficiency. *Scientific reports*, 16(1).

Halperin R, et al. (2026) The GAPP Aggressivity Score Correlates with Total Enriched Somatic Variant Burden in Sporadic Pheochromocytoma-A Pilot Study. *Cancers*, 18(12).

Mao Y, et al. (2026) Prospective tumour mutation burden and neoantigen profiling predicts immunotherapy response in metastatic melanoma. *NPJ precision oncology*, 10(1), 55.

Song F, et al. (2026) Patient-derived organotypic tumor spheroids as a functional platform for predicting immunotherapeutic responses and guiding precision treatment for hepatocellular carcinoma. *Journal for immunotherapy of cancer*, 14(5).