Resource Summary Report

Generated by RRID on Aug 2, 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: 20260801T190848+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

Source: SciCrunch Registry

Usage and Citation Metrics

We found 220 mentions in open access literature.

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

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

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.

Lee S, et al. (2025) LocusMasterTE: integrating long-read RNA sequencing improves locus-specific quantification of transposable element expression. Genome biology, 26(1), 72.

Rebello RJ, et al. (2025) Whole genome sequencing improves tissue-of-origin diagnosis and treatment options for cancer of unknown primary. Nature communications, 16(1), 4422.

Corradi C, et al. (2025) Uncovering the Role of DNA Repair Impairment in UVA-Induced Mutagenesis in Human Xeroderma Pigmentosum Variant Cells. Molecular carcinogenesis, 64(11), 1823.

Helderman NC, et al. (2025) Clinical syndromes linked to biallelic germline variants in MCM8 and MCM9. HGG advances, 6(4), 100480.

Huo ??? X, et al. (2025) Genome-wide Genetic Mutations Accumulated in Pigs Genome-edited for Xenotransplantation and Their Filial Generation. Genomics, proteomics & bioinformatics, 23(4).

Firsanov D, et al. (2025) Evidence for improved DNA repair in the long-lived bowhead whale. Nature, 648(8094), 717.

Yoshizato T, et al. (2025) Stable clonal contribution of lineage-restricted stem cells to human hematopoiesis. Nature genetics, 57(12), 3088.

Zhang P, et al. (2025) Integrated pathway analysis identifies prognostically relevant subtypes of glioblastoma characterized by abnormalities in multi-omics. Clinical and translational medicine, 15(12), e70517.

Persaud N, et al. (2025) Clinical Significance of TERT Promoter Mutations in Neuroblastoma. JCO precision oncology, 9, e2500074.

Laplante P, et al. (2025) Effect of MisMatch repair deficiency on metastasis occurrence in a syngeneic mouse model. Neoplasia (New York, N.Y.), 62, 101145.

Yamamoto A, et al. (2025) A novel mouse model of upper tract urothelial carcinoma highlights the impact of dietary intervention on gut microbiota and carcinogenesis prevention despite carcinogen exposure. International journal of cancer, 156(7), 1439.

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

Dong G, et al. (2025) Diverse somatic genomic alterations in single neurons in chronic traumatic encephalopathy. bioRxiv : the preprint server for biology.

Weijers DD, et al. (2025) Unraveling mutagenic processes influencing the tumor mutational patterns of individuals with constitutional mismatch repair deficiency. Nature communications, 16(1), 4459.

Concetti L, et al. (2025) Multi-omic characterization of consensus molecular subtype 1 (CMS1) colorectal cancer with dampened immune response improves precision medicine. Molecular oncology, 19(12), 3486.

Talenti A, et al. (2025) The evolution and convergence of mutation spectra across mammals. Communications biology, 8(1), 763.

Dimitriou F, et al. (2025) Conjunctival melanoma genomic analysis reveals intermediate tumor mutation burden and genomic overlap with cutaneous melanoma. NPJ precision oncology, 9(1), 365.

Domenico D, et al. (2025) Enabling whole genome sequencing analysis from FFPE specimens in clinical oncology. Nature communications, 16(1), 10649.