Resource Summary Report

Generated by RRID on Aug 12, 2026

SigProfilerMatrixGenerator

RRID:SCR_023122
Type: Tool

Proper Citation

SigProfilerMatrixGenerator (RRID:SCR_023122)

Resource Information

URL: https://github.com/AlexandrovLab/SigProfilerMatrixGenerator/

Proper Citation: SigProfilerMatrixGenerator (RRID:SCR_023122)

Description: Software tool to create mutational matrices for all types of somatic mutations. Used to generate mutational matrices for set of samples with associated mutational catalogues. Used for optimized exploration and visualization of mutational patterns for all types of small mutational events. In addition to extending classification of single base substitutions, provides support for classifying doublet base substitutions and small insertions and deletions.

Resource Type: software application, software resource

Defining Citation: PMID:31470794

Keywords: mutational patterns, small mutational events, create mutational matrices, somatic mutations, samples with associated mutational catalogues,

Funding: Cancer Research UK Grand Challenge Award ;
Singapore Ministry of Health ;
Singapore National Medical Research Council

Availability: Free, Available for download, Freely available

Resource Name: SigProfilerMatrixGenerator

Resource ID: SCR_023122

Alternate URLs: https://osf.io/s93d5/wiki/home

License: BSD 2-Clause "Simplified" License

Record Creation Time: 20230116T062750+0000

Record Last Update: 20260810T040831+0000

Ratings and Alerts

No rating or validation information has been found for SigProfilerMatrixGenerator .

No alerts have been found for SigProfilerMatrixGenerator .

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 35 mentions in open access literature.

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

Portasany-Rodríguez M, et al. (2026) PULPO: pipeline of understanding large-scale patterns of oncogenomic signatures. Bioinformatics (Oxford, England), 42(6).

Dong YP, et al. (2026) Early replication fragile sites are associated with cancer-related CNVs and SNVs in human embryonic stem cells. Stem cell reports, 21(7), 102968.

Bertoli R, et al. (2025) 5-Azacytidine and decitabine induce C > G transversions in both murine and human cells. Leukemia, 39(9), 2112.

Bergsma P, et al. (2025) Integration of Whole-Genome Sequencing Analysis with Unique Patient-Derived Models Reveals Clinically Relevant Drug Targets in TFCP2 Fusion-Defined Rhabdomyosarcoma. Molecular cancer therapeutics, 24(12), 1989.

Li YR, et al. (2025) Long-Term Latency of Highly Mutated Cells in Normal Mouse Skin Is Reversed by Exposure to Tumor Promoters and Chronic Tissue Damage. Cancer discovery, 15(6), 1115.

Zhou Z, et al. (2025) Recurrent patterns of widespread neuronal genomic damage shared by major neurodegenerative disorders. bioRxiv : the preprint server for biology.

Jiang Z, et al. (2025) The Impact of Variant Calling on Substitution Mutational Signature Inference. bioRxiv : the preprint server for biology.

Kinnersley B, et al. (2025) Genomic landscape of diffuse glioma revealed by whole genome sequencing. Nature communications, 16(1), 4233.

Torrens L, et al. (2025) The complexity of tobacco smoke-induced mutagenesis in head and neck cancer. Nature genetics, 57(4), 884.

Bose A, et al. (2025) APOBEC3A-Induced DNA Damage Drives Polymerase ? Dependency and Synthetic Lethality in Cancer. bioRxiv : the preprint server for biology.

Sasa N, et al. (2025) Intratumor heterogeneity of HPV integration in HPV-associated head and neck cancer. Nature communications, 16(1), 1052.

Asada S, et al. (2025) Disruption of Microhomology-mediated End-joining in Ewing Sarcoma. bioRxiv : the preprint server for biology.

Sugo N, et al. (2025) DNA polymerase ? suppresses somatic indels at CpG dinucleotides in developing cortical neurons. Proceedings of the National Academy of Sciences of the United States of America, 122(33), e2506846122.

Zhu G, et al. (2025) Defective Microhomology-Mediated End-joining in SMARCB1-Deficient Tumors. bioRxiv : the preprint server for biology.

Luzadder MM, et al. (2025) The Distinct Roles of NEIL1 and XPA in Limiting Aflatoxin B1-Induced Mutagenesis in Mice. Molecular cancer research : MCR, 23(1), 46.

Mitsiades IR, et al. (2024) ERBB2/HOXB13 co-amplification with interstitial loss of BRCA1 defines a unique subset of breast cancers. Breast cancer research : BCR, 26(1), 185.

Kundnani DL, et al. (2024) Distinct features of ribonucleotides within genomic DNA in Aicardi-Goutières syndrome ortholog mutants of Saccharomyces cerevisiae. iScience, 27(6), 110012.

Battuello P, et al. (2024) Mutational signatures of colorectal cancers according to distinct computational workflows. Briefings in bioinformatics, 25(4).

Jalan M, et al. (2024) RAD52 resolves transcription-replication conflicts to mitigate R-loop induced genome instability. Nature communications, 15(1), 7776.

Morton LM, et al. (2024) Genomic characterization of cervical lymph node metastases in papillary thyroid carcinoma following the Chornobyl accident. Nature communications, 15(1), 5053.