

Resource Summary Report

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RepEnrich

RRID:SCR_021733

Type: Tool

Proper Citation

RepEnrich (RRID:SCR_021733)

Resource Information

URL: <https://github.com/nskvir/RepEnrich>

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Description: Software tool to profile enrichment of next generation sequencing reads at transposable elements. Method to estimate repetitive element enrichment using high throughput sequencing data. Used to study genome wide transcriptional regulation of repetitive elements. RepEnrich2 is updated method to estimate repetitive element enrichment using high-throughput sequencing data.

Synonyms: RepEnrich2

Resource Type: software application, software resource, data processing software, data analysis software

Defining Citation: [PMID:25012247](#)

Keywords: profile enrichment, next generation sequencing reads, transposable elements, estimate repetitive element enrichment, genome wide transcriptional regulation, sequencing data

Funding: NIA K25 AG028753;
NIGMS T32 GM007601;
NIA R37 AG016694

Availability: Free, Available for download, Freely available

Resource Name: RepEnrich

Resource ID: SCR_021733

Alternate URLs: <https://github.com/nerettilab/RepEnrich2>

Record Creation Time: 20220129T080357+0000

Ratings and Alerts

No rating or validation information has been found for RepEnrich.

No alerts have been found for RepEnrich.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Leismann J, et al. (2025) DNA methylation at retrotransposons protects the germline by preventing NRF1-mediated activation. EMBO reports, 26(17), 4312.

Grillo G, et al. (2025) ZBTB24 is a conserved multifaceted transcription factor at genes and centromeres that governs the DNA methylation state and expression of satellite repeats. Human molecular genetics, 34(2), 161.

Wilkens M, et al. (2025) Unraveling developmental gene regulation in holometabolous insects through comparative transcriptomics and proteomics. Communications biology, 8(1), 980.

Fracassi C, et al. (2024) PML is a constitutive component of chromatin domains enriched in repetitive elements and duplicated gene clusters in cancer cells. Heliyon, 10(17), e36499.

Xie J, et al. (2024) Heterochromatin formation and remodeling by IRTKS condensates counteract cellular senescence. The EMBO journal, 43(20), 4542.

Trovato M, et al. (2024) Histone H3.3 lysine 9 and 27 control repressive chromatin at cryptic enhancers and bivalent promoters. Nature communications, 15(1), 7557.

Bedi K, et al. (2024) Isoform and pathway-specific regulation of post-transcriptional RNA processing in human cells. bioRxiv : the preprint server for biology.

Yuan Z, et al. (2021) Human Endogenous Retroviruses in Glioblastoma Multiforme. Microorganisms, 9(4).

McCarthy RL, et al. (2021) Diverse heterochromatin-associated proteins repress distinct classes of genes and repetitive elements. Nature cell biology, 23(8), 905.

Diao Z, et al. (2021) SIRT3 consolidates heterochromatin and counteracts senescence. Nucleic acids research, 49(8), 4203.

Page NF, et al. (2021) Alterations in Retrotransposition, Synaptic Connectivity, and Myelination Implicated by Transcriptomic Changes Following Maternal Immune Activation in Nonhuman Primates. *Biological psychiatry*, 89(9), 896.

Lester E, et al. (2021) Tau aggregates are RNA-protein assemblies that mislocalize multiple nuclear speckle components. *Neuron*, 109(10), 1675.

Kanne J, et al. (2021) Pericentromeric Satellite III transcripts induce etoposide resistance. *Cell death & disease*, 12(6), 530.

Costello KR, et al. (2021) Sequence features of retrotransposons allow for epigenetic variability. *eLife*, 10.

D'Anna F, et al. (2020) DNA methylation repels binding of hypoxia-inducible transcription factors to maintain tumor immunotolerance. *Genome biology*, 21(1), 182.

Hu H, et al. (2020) ZKSCAN3 counteracts cellular senescence by stabilizing heterochromatin. *Nucleic acids research*, 48(11), 6001.

Dhanwani R, et al. (2020) Cellular sensing of extracellular purine nucleosides triggers an innate IFN- γ response. *Science advances*, 6(30), eaba3688.

Fu X, et al. (2020) A transcriptional roadmap for 2C-like-to-pluripotent state transition. *Science advances*, 6(22), eaay5181.

Cruz-Tapias P, et al. (2019) The H3K9 Methylation Writer SETDB1 and its Reader MPP8 Cooperate to Silence Satellite DNA Repeats in Mouse Embryonic Stem Cells. *Genes*, 10(10).

Luense LJ, et al. (2019) Gcn5-Mediated Histone Acetylation Governs Nucleosome Dynamics in Spermiogenesis. *Developmental cell*, 51(6), 745.