

Resource Summary Report

Generated by [kravitz2](#) on Aug 8, 2026

EnrichedHeatmap

RRID:SCR_023082

Type: Tool

Proper Citation

EnrichedHeatmap (RRID:SCR_023082)

Resource Information

URL: <https://github.com/jokergoo/EnrichedHeatmap>

Proper Citation: EnrichedHeatmap (RRID:SCR_023082)

Description: Software R package for comprehensive visualization of genomic signal associations. Visualizes enrichment of genomic signals on specific target regions. Used to visualize e.g. how histone marks are enriched to specific sites.

Resource Type: software resource, software toolkit

Defining Citation: [PMID:29618320](#)

Keywords: visualization of genomic signal associations, enrichment of genomic signals, specific target regions,

Funding: German Cancer Research Center-Heidelberg Center for Personalized Oncology

Availability: Free, Available for download, Freely available

Resource Name: EnrichedHeatmap

Resource ID: SCR_023082

Alternate URLs: <https://bioconductor.org/packages/EnrichedHeatmap/>

Record Creation Time: 20221229T050156+0000

Record Last Update: 20260808T190529+0000

Ratings and Alerts

No rating or validation information has been found for EnrichedHeatmap.

No alerts have been found for EnrichedHeatmap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 78 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Xu K, et al. (2026) An intricate functional relationship between NuA4 and Sfp1 regulates ribosome biogenesis in response to nutrient availability. *The Journal of biological chemistry*, 302(6), 113107.

Barlier C, et al. (2026) The impact of fulvestrant on estrogen receptor-driven chromatin dynamics in breast cancer cells. *Epigenetics & chromatin*, 19(1).

Huang TC, et al. (2026) Global reorganization of genome architecture at the transition to gametogenesis. *Nature structural & molecular biology*, 33(3), 433.

Li W, et al. (2026) Multi-omics and low-input proteomics profiling reveals dynamic regulation driving pluripotency initiation in early mouse embryos. *FEBS open bio*, 16(6), 1102.

Manduchi E, et al. (2026) Epigenetic adaptation of beta cells across lifespan and disease. *Nature metabolism*, 8(4), 941.

Sankar V, et al. (2026) Genetic elements promote retention of extrachromosomal DNA in cancer cells. *Nature*, 649(8095), 152.

Aktary Z, et al. (2026) Archaeal G-quadruplexes: a novel model for understanding unusual DNA/RNA structures across the tree of life. *Nucleic acids research*, 54(4).

Mononen J, et al. (2026) Genetic variation shapes the chromatin accessibility landscape and transcriptional responses in mouse adipose tissue. *PLoS genetics*, 22(1), e1011716.

Abdelfattah N, et al. (2026) Male-biased Yap1-Cd276/B7-H3 axis for immune evasion in medulloblastoma. *Cancer cell*, 44(4), 760.

Li C, et al. (2026) ARID1A deficiency unleashes centromeric RNA transcription to drive chromosomal instability and boosts PKMYT1 inhibitor efficacy via RNA sensing. *bioRxiv* : the preprint server for biology.

Gehrs S, et al. (2025) DNMT3A-dependent DNA methylation shapes the endothelial enhancer landscape. *Nucleic acids research*, 53(10).

Lane KA, et al. (2025) PBRM1 directs PBAF to pericentromeres and protects centromere integrity. *Nature communications*, 16(1), 1980.

Petroll R, et al. (2025) The Expansion and Diversification of Epigenetic Regulatory Networks Underpins Major Transitions in the Evolution of Land Plants. *Molecular biology*

and evolution, 42(4).

Shoeb MR, et al. (2025) A stem cell differentiation model reveals two alternative fates in CBFA2T3::GLIS2-driven acute megakaryoblastic leukemia initiation. *Communications biology*, 8(1), 1289.

Ziegler FMR, et al. (2025) A full genome assembly reveals drought stress effects on gene expression and metabolite profiles in blackcurrant (*Ribes nigrum* L.). *Horticulture research*, 12(2), uhae313.

Palma LG, et al. (2025) Chromatin activity of I?B? mediates the exit from naïve pluripotency. *eLife*, 14.

Warburton A, et al. (2025) Human papillomavirus genomes associate with active host chromatin during persistent viral infection. *PLoS pathogens*, 21(9), e1013454.

Manduchi E, et al. (2025) Epigenetic adaptation of beta cells across lifespan and disease: age-related demethylation is advanced in type 2 diabetes. *bioRxiv : the preprint server for biology*.

Wang Z, et al. (2025) KDM6B inhibition enhances chemotherapeutic response in small cell lung cancer via epigenetic regulation of apoptosis and ferroptosis. *Cell & bioscience*, 15(1), 162.

Oak MS, et al. (2025) Pre-marking chromatin with H3K4 methylation is required for accurate zygotic genome activation and development. *Nature communications*, 16(1), 11334.