Resource Summary Report

Generated by ASWG on Aug 4, 2026

epialleleR

RRID:SCR_023913
Type: Tool

Proper Citation

epialleleR (RRID:SCR_023913)

Resource Information

URL: http://bioconductor.org/packages/epialleleR/

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Description: Software R package for calling hypermethylated variant epiallele frequencies at level of genomic regions or individual cytosines in next-generation sequencing data using binary alignment map files as input. Used for sensitive allele specific methylation analysis in next generation sequencing data. Used for sensitive detection, quantification and visualisation of mosaic epimutations in methylation sequencing data.

Resource Type: software toolkit, software resource

Defining Citation: DOI:10.1101/2022.06.30.498213

Keywords: BAM files, binary alignment map files, allele specific methylation analysis, methylation sequencing data, next generation sequencing data, hypermethylated variant epiallele frequencies calling,

Funding: K.G.Jebsen Foundation ;
Norwegian Cancer Society ;
Norwegian Research Council

Availability: Free, Available for download, Freely available

Resource Name: epialleleR

Resource ID: SCR_023913

Alternate URLs: https://github.com/BBCG/epialleleR

License: Artistic 2.0

Record Creation Time: 20230804T050227+0000

Record Last Update: 20260803T040856+0000

Ratings and Alerts

No rating or validation information has been found for epialleleR.

No alerts have been found for epialleleR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Nikolaienko O, et al. (2022) epialleleR: an R/Bioconductor package for sensitive allele-specific methylation analysis in NGS data. GigaScience, 12.