

# Package ‘epimutacionsData’

November 12, 2024

**Title** Data for epimutacions package

**Version** 1.10.0

**Description** This package includes the data necessary to run functions and examples in epimutacions package.

Collection of DNA methylation data.

The package contains 2 datasets:

(1) Control ( GEO: GSE104812), (GEO: GSE97362) case samples; and  
(2) reference panel (GEO: GSE127824).

It also contains candidate regions to  
be epimutations in 450k methylation arrays.

**License** MIT + file LICENSE

**biocViews** ExperimentHub, Homo\_sapiens\_Data, MethylationArrayData,  
MicroarrayData

**Suggests** rmarkdown, BiocStyle, knitr, ExperimentHub, minfi

**VignetteBuilder** knitr

**Encoding** UTF-8

**Depends** R (>= 4.2.0)

**URL** <https://github.com/LeireAbarrategui/epimutacionsData>

**BugReports** <https://github.com/LeireAbarrategui/epimutacionsData/issues>

**NeedsCompilation** no

**RoxygenNote** 7.1.2

**git\_url** <https://git.bioconductor.org/packages/epimutacionsData>

**git\_branch** RELEASE\_3\_20

**git\_last\_commit** 4d9e9ff

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.20

**Date/Publication** 2024-11-12

**Author** Leire Abarrategui [aut, cre],

Juan R. Gonzalez [aut],

Carlos Ruiz-Arenas [aut],

Carles Hernandez-Ferrer [aut]

**Maintainer** Leire Abarrategui <[abarrategui.leire@gmail.com](mailto:abarrategui.leire@gmail.com)>

## Contents