

# Package ‘epimutacionsData’

October 18, 2022

**Title** Data for epimutacions package

**Version** 1.0.0

**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.

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**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\_15

**git\_last\_commit** 939ec88

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R *topics documented:*

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