Package ‘SomatiCAData’

January 28, 2025

Version 1.45.0

Title An example cancer whole genome sequencing data for the SomatiCA package

Description An example cancer whole genome sequencing data for the SomatiCA package

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Depends R (>= 2.14)

License Artistic-2.0

LazyData yes

biocViews ExperimentData, Genome, CancerData, SequencingData

InstallableEverywhere yes

git_url https://git.bioconductor.org/packages/SomatiCAData

git_branch devel

git_last_commit 9292976

git_last_commit_date 2024-10-29

Repository Bioconductor 3.21

Date/Publication 2025-01-28

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`SomatiCAData-package` *An example cancer whole genome sequencing data for the SomatiCA package*

Description

A dataset of a paired tumor-normal sequencing sample from Complete Genomics.

Author(s)

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Examples

```
data(glio)
```

`glio` *Sequencing data for a tumor sample with control.*

Description

A dataset of a paired tumor-normal sequencing sample from Complete Genomics.

Usage

```
data(glio)
```

Format

A data frame with 3458745 rows on the following 7 variables.

`seqnames` a character vector

`start` a character vector

`zygosity` a character vector

`tCount` an integer vector

`LAF` a numeric vector

`tCountN` an integer vector

`germLAF` a numeric vector

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