

Package ‘SomatiCData’

July 11, 2024

Version 1.43.0

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

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

Author Mengjie Chen

Maintainer Mengjie Chen <mengjie.chen@yale.edu>

Depends R (>= 2.14)

License Artistic-2.0

LazyData yes

biocViews ExperimentData, Genome, CancerData, SequencingData

InstallableEverywhere yes

git_url <https://git.bioconductor.org/packages/SomatiCData>

git_branch devel

git_last_commit 7239164

git_last_commit_date 2024-04-30

Repository Bioconductor 3.20

Date/Publication 2024-07-11

Contents

SomatiCData-package	2
glio	2

Index	3
--------------	----------

SomaticData-package *An example cancer whole genome sequencing data for the SomaticData package*

Description

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

Author(s)

Mengjie Chen <mengjie.chen@yale.edu>

Maintainer: Mengjie Chen <mengjie.chen@yale.edu>

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

Index

- * **datasets**

- [glio, 2](#)

- * **package**

- [SomatiCData-package, 2](#)

[glio, 2](#)

[SomatiCData \(SomatiCData-package\), 2](#)

[SomatiCData-package, 2](#)