

Package ‘SomatiCAData’

October 17, 2019

Version 1.22.0

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/SomatiCAData>

git_branch RELEASE_3_9

git_last_commit bb7beb1

git_last_commit_date 2019-05-02

Date/Publication 2019-10-17

R topics documented:

SomatiCAData-package	1
glio	2
Index	3

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)

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

*Topic **datasets**

glio, [2](#)

*Topic **package**

SomaticAData-package, [1](#)

glio, [2](#)

SomaticAData (SomaticAData-package), [1](#)

SomaticAData-package, [1](#)