

Package ‘SomatiCADATA’

February 3, 2026

Version 1.49.0

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 devel

git_last_commit ae5f18c

git_last_commit_date 2025-10-29

Repository Bioconductor 3.23

Date/Publication 2026-02-03

Contents

SomatiCADATA-package	2
glio	2
Index	3

SomaticData-package	<i>An example cancer whole genome sequencing data for the SomaticData package</i>
---------------------	---

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	<i>Sequencing data for a tumor sample with control.</i>
------	---

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**

- SomaticADData-package, [2](#)

glio, [2](#)

SomaticADData (SomaticADData-package), [2](#)

SomaticADData-package, [2](#)