

# Package ‘SomatiCAData’

April 20, 2016

**Version** 1.8.0

**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

**NeedsCompilation** no

## R topics documented:

SomatiCAData-package	1
glio	2
<b>Index</b>	<b>3</b>

---

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**

SomaticData-package, [1](#)

glio, [2](#)

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

SomaticData-package, [1](#)