

# Package ‘SomatiCData’

February 29, 2024

**Version** 1.40.0

**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** RELEASE\_3\_18

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

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**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)
```

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

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**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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