

# Package ‘SomatiCAData’

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**Version** 1.51.0

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

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

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**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>

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

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## Description

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

**Author(s)**

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**Examples**

```
data(glio)
```

---

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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