

# Package ‘SomatiCAData’

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**Version** 1.48.0

**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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**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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## Contents

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

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|                      |                                                                                |
|----------------------|--------------------------------------------------------------------------------|
| SomatiCAData-package | <i>An example cancer whole genome sequencing data for the SomatiCA package</i> |
|----------------------|--------------------------------------------------------------------------------|

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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)
```

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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

# Index

- \* **datasets**

- glio, [2](#)

- \* **package**

- SomaticADData-package, [1](#)

glio, [2](#)

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

SomaticADData-package, [1](#)