Package ‘SomatiCAData’

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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

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Contents

`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)

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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

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