

Package ‘TCGAbiolinksGUI.data’

May 12, 2026

Title Data for the TCGAbiolinksGUI package

Version 1.33.0

Author Tiago Chedraoui Silva

Maintainer Tiago Chedraoui Silva <tiagochst@gmail.com>

Description Supporting data for the TCGAbiolinksGUI package.

License GPL-3

LazyData false

Depends R (>= 3.5.0)

Suggests BiocStyle, knitr, rmarkdown, readr, DT

biocViews AssayDomainData, TechnologyData, OrganismData

URL <https://github.com/BioinformaticsFMRP/TCGAbiolinksGUI.data>

BugReports <https://github.com/BioinformaticsFMRP/TCGAbiolinksGUI.data/issues>

VignetteBuilder knitr

RoxygenNote 7.1.2

git_url <https://git.bioconductor.org/packages/TCGAbiolinksGUI.data>

git_branch devel

git_last_commit a2c4747

git_last_commit_date 2026-04-28

Repository Bioconductor 3.24

Date/Publication 2026-05-12

Contents

GDCdisease	2
gencode.v36.annotation.genes	2
gene.location.hg19	3
gene.location.hg38	3
glioma.gcimp.model	4
glioma.idh.model	4
glioma.idhmut.model	5
glioma.idhwt.model	5
linkedOmics.data	6
maf.tumor	6
probes2rm	7
TCGAbiolinksGUI.data	7

Index**8**

`GDCdisease`*GDC projects*

Description

Contains all GDC projects with open data

Usage

```
data("GDCdisease")
```

Format

A named list with 39 projects

Source

Retrieved from GDC API

`gencode.v36.annotation.genes`*GENCODE v36 gene information*

Description

GENCODE v36 gene information

Usage

```
data("gencode.v36.annotation.genes")
```

Format

A Granges object

Source

Downloaded from GENCODE v36 https://www.encodegenes.org/human/release_36.html Comprehensive gene annotation and filtered to genes

gene.location.hg19 *Biomart hg19 gene information*

Description

Biomart hg19 gene information

Usage

```
data("gene.location.hg19")
```

Format

A table

Source

Downloaded with biomart

gene.location.hg38 *Biomart hg38 gene information*

Description

Biomart hg38 gene information

Usage

```
data("gene.location.hg38")
```

Format

A table

Source

Downloaded with biomart

glioma.gcimp.model *gcimp RF model*

Description

A RF model able to classify DNA methylation samples in to GCIMP groups

Usage

```
data("glioma.gcimp.model")
```

Format

A random forest model with 276 samples and 145 predictors classifying into 3 classes

Source

RF model created from DNA methylation signatures retrieved from [www.cell.com/cell/abstract/S0092-8674\(15\)01692-X](http://www.cell.com/cell/abstract/S0092-8674(15)01692-X)

glioma.idh.model *IDH RF model*

Description

A RF model able to classify DNA methylation samples in to IDH groups

Usage

```
data("glioma.idh.model")
```

Format

A random forest model with 880 samples and 1205 predictors classifying into 6 classes

Source

RF model created from DNA methylation signatures retrieved from [www.cell.com/cell/abstract/S0092-8674\(15\)01692-X](http://www.cell.com/cell/abstract/S0092-8674(15)01692-X)

`glioma.idhmut.model` *IDHmut RF model*

Description

A RF model able to classify DNA methylation samples in to IDHmut groups

Usage

```
data("glioma.idhmut.model")
```

Format

A random forest model with 450 samples and 1216 predictors classifying into 3 classes

Source

RF model created from DNA methylation signatures retrieved from [www.cell.com/cell/abstract/S0092-8674\(15\)01692-X](http://www.cell.com/cell/abstract/S0092-8674(15)01692-X)

`glioma.idhwt.model` *IDHwt RF model*

Description

A RF model able to classify DNA methylation samples in to IDHwt groups

Usage

```
data("glioma.idhwt.model")
```

Format

A random forest model with 430 samples and 843 predictors classifying into 3 classes

Source

RF model created from DNA methylation signatures retrieved from [www.cell.com/cell/abstract/S0092-8674\(15\)01692-X](http://www.cell.com/cell/abstract/S0092-8674(15)01692-X)

linkedOmics.data	<i>linkedOmics table</i>
------------------	--------------------------

Description

linkedOmics table with links

Usage

```
data("linkedOmics.data")
```

Format

A table

Source

Parsed from <http://linkedomics.org/login.php#dataSource>

maf.tumor	<i>GDC open MAF files</i>
-----------	---------------------------

Description

Contains the list of GDC project with open MAF files available

Usage

```
data(maf.tumor)
```

Format

A named list with 33 tumors

Source

https://gdc-docs.nci.nih.gov/Data/Release_Notes/Manifests/GDC_open_MAFs_manifest.txt

probes2rm

EPIC probes removed from newer versions

Description

EPIC probes removed from newer versions that should not be used in the analysis

Usage

```
data("probes2rm")
```

Format

A list with 977 probes

Source

<https://support.illumina.com/downloads/infinium-methylationepic-v1-0-product-files.html>

TCGAbiolinksGUI.data

Auxiliary data for TCGAbiolinksGUI package.

Description

Package: TCGAbiolinksGUI.data provide the necessary data for TCGAbiolinksGUI glioma classifier menu. It includes the following objects:

glioma.gcimp.model A train model for GCIMP DNA methylation signatures.

glioma.idhwt.model A train model for IDHwt DNA methylation signatures

glioma.idhmut.model A train model for IDHmut DNA methylation signatures

glioma.idh.model A train model for IDH DNA methylation signatures

probes2rm List of probes that should be removed from EPIC array due to different versions of the platform.

Source: <https://support.illumina.com/downloads/infinium-methylationepic-v1-0-product-files.html>

maf.tumor TCGA projects with open MAF files retrieved from the NCI's Genomic Data Commons (GDC).

Source: https://gdc-docs.nci.nih.gov/Data/Release_Notes/Manifests/GDC_open_MAFs_manifest.txt

GDCdisease The NCI's Genomic Data Commons (GDC) projects list

Index

* datasets

- GDCdisease, [2](#)
- gencode.v36.annotation.genes, [2](#)
- gene.location.hg19, [3](#)
- gene.location.hg38, [3](#)
- glioma.gcimp.model, [4](#)
- glioma.idh.model, [4](#)
- glioma.idhmut.model, [5](#)
- glioma.idhwt.model, [5](#)
- linkedOmics.data, [6](#)
- maf.tumor, [6](#)
- probes2rm, [7](#)

* utilities

- TCGAbiolinksGUI.data, [7](#)

- GDCdisease, [2](#), [7](#)
- gencode.v36.annotation.genes, [2](#)
- gene.location.hg19, [3](#)
- gene.location.hg38, [3](#)
- glioma.gcimp.model, [4](#), [7](#)
- glioma.idh.model, [4](#), [7](#)
- glioma.idhmut.model, [5](#), [7](#)
- glioma.idhwt.model, [5](#), [7](#)

- linkedOmics.data, [6](#)

- maf.tumor, [6](#), [7](#)

- probes2rm, [7](#), [7](#)

- TCGAbiolinksGUI.data, [7](#)