# Package 'TCGAbiolinksGUI.data'

April 24, 2025

**Title** Data for the TCGAbiolinksGUI package

**Version** 1.28.0

**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** RELEASE_3_21

**git_last_commit** 487076b

**git_last_commit_date** 2025-04-15

**Repository** Bioconductor 3.21

**Date/Publication** 2025-04-24

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`GDCdisease` *GDC projects*

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## Description

Contains all GDC projects with open data

## Usage

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

## Format

A named list with 39 projects

## Source

Retrivied from GDC API

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

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## Description

GENCODE v36 gene information

## Usage

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

## Format

A Granges object

## Source

Downloaded from GENCODE v36 https://www.gencodegenes.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

## 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

## 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

## 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

## linkedOmics.data *linkedOmics table*

### Description

linkedOmics table with links

### Usage

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

### Format

A table

### Source

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

## maf.tumor *GDC open MAF files*

### 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

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