

# Package ‘TCGAbiolinksGUI.data’

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**Title** Data for the TCGAbiolinksGUI package

**Version** 1.8.0

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**Description** Supporting data for the TCGAbiolinksGUI package.

**License** GPL-3

**LazyData** false

**Depends** R (>= 3.5.0)

**Suggests** BiocStyle, knitr, readr, readxl, dplyr, caret, randomForest,  
doMC, e1071, DT, htmltab

**biocViews** AssayDomainData, TechnologyData, OrganismData

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

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

**VignetteBuilder** knitr

**RoxygenNote** 7.0.2

**git\_url** <https://git.bioconductor.org/packages/TCGAbiolinksGUI.data>

**git\_branch** RELEASE\_3\_11

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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**

Retrieved from GDC API

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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)

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`glioma.idh.model`      *IDH RF model*

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**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)

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

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**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*

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**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)

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linkedOmics.data     *linkedOmics table*

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**Description**

linkedOmics table with links

**Usage**

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

**Format**

A table

**Source**

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

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`maf.tumor`*GDC open MAF files*

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**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](https://gdc-docs.nci.nih.gov/Data/Release_Notes/Manifests/GDC_open_MAFs_manifest.txt)

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`probes2rm`*EPIC probes removed from newer versions*

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**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>

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TCGAbiolinksGUI.data *Auxiliary data for TCGAbiolinksGUI package.*

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## 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](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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