

# Package ‘TCGAbiolinksGUI.data’

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**Title** Data for the TCGAbiolinksGUI package

**Version** 1.25.0

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

**License** GPL-3

**LazyData** false

**Depends** R (>= 3.5.0)

**Suggests** BiocStyle, knitr, 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** d5092e9

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GDCdisease	<i>GDC projects</i>
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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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gencode.v36.annotation.genes	<i>GENCODE v36 gene information</i>
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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.genecodegenes.org/human/release\\_36.html](https://www.genecodegenes.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)

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`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)

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`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)

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`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)

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linkedOmics.data	<i>linkedOmics table</i>
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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	<i>GDC open MAF files</i>
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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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