

# Package ‘TCGAbiolinksGUI.data’

November 6, 2025

**Title** Data for the TCGAbiolinksGUI package

**Version** 1.31.0

**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** e7aa3af

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.23

**Date/Publication** 2025-11-06

## Contents

|                                       |   |
|---------------------------------------|---|
| GDCdisease . . . . .                  | 2 |
| encode.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        |
| <b>Index</b>                   | <b>8</b> |

---

|            |                     |
|------------|---------------------|
| GDCdisease | <i>GDC projects</i> |
|------------|---------------------|

---

**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        |
| <i>GENCODE v36 gene information</i> |

---

**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](https://www.gencodegenes.org/human/release_36.html) Comprehensive gene annotation and filtered to genes

---

|                    |                                      |
|--------------------|--------------------------------------|
| gene.location.hg19 | <i>Biomart hg19 gene information</i> |
|--------------------|--------------------------------------|

---

### **Description**

Biomart hg19 gene information

### **Usage**

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

### **Format**

A table

### **Source**

Downloaded with biomaRt

---

|                    |                                      |
|--------------------|--------------------------------------|
| gene.location.hg38 | <i>Biomart hg38 gene information</i> |
|--------------------|--------------------------------------|

---

### **Description**

Biomart hg38 gene information

### **Usage**

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

### **Format**

A table

### **Source**

Downloaded with biomaRt

---

|                    |                       |
|--------------------|-----------------------|
| glioma.gcimp.model | <i>gcimp RF model</i> |
|--------------------|-----------------------|

---

**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 | <i>IDH RF model</i> |
|------------------|---------------------|

---

**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 | <i>IDHmut RF model</i> |
|---------------------|------------------------|

---

**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 | <i>IDHwt RF model</i> |
|--------------------|-----------------------|

---

**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](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](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](#)