

# Package ‘HarmonizedTCGAData’

July 4, 2024

**Type** Package

**Title** Processed Harmonized TCGA Data of Five Selected Cancer Types

**Version** 1.27.0

**Author** Tianle Ma

**Maintainer** Tianle Ma <tianlema@buffalo.edu>

**Description** This package contains the processed harmonized TCGA data of five cancer types used in ``Tianle Ma and Aidong Zhang, Integrate Multi-omic Data Using Affinity Network Fusion (ANF) for Cancer Patient Clustering".

**License** GPL-3

**Imports** ExperimentHub

**Depends** R (>= 3.4.0)

**VignetteBuilder** knitr

**Suggests** AnnotationHub, knitr, rmarkdown, igraph, survival, ANF, stats, testthat

**biocViews** CancerData, ReproducibleResearch

**RoxygenNote** 6.0.1

**LazyData** true

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

**git\_branch** devel

**git\_last\_commit** f9ba285

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.20

**Date/Publication** 2024-07-04

## Contents

HarmonizedTCGAData . . . . .	2
project_ids . . . . .	2
surv.plot . . . . .	3
Wall . . . . .	3

**Index****5**

---

HarmonizedTCGAData	<i>HarmonizedTCGAData.</i>
--------------------	----------------------------

---

**Description**

HarmonizedTCGAData.

---

project_ids	<i>project_ids</i>
-------------	--------------------

---

**Description**

A named character vector: mapping case\_id (i.e., patient ID) to the TCGA project ID they belong to

**Usage**

```
project_ids
```

**Format**

An object of class character of length 14551.

**Examples**

```
library(ExperimentHub)
eh <- ExperimentHub()
myfiles <- query(eh, "HarmonizedTCGAData")
project_ids <- myfiles[[2]]
# project_ids <- myfiles[['EH1015']]
head(project_ids)
```

---

surv.plot	<i>surv.plot</i>
-----------	------------------

---

**Description**

Patient survival information (overall survival plot data) were downloaded from <https://portal.gdc.cancer.gov/exploration?search=overall%20survival>  
For detailed information: see section "Survival analysis" in [https://docs.gdc.cancer.gov/Data\\_Portal/PDF/Data\\_Portal\\_UG.pdf](https://docs.gdc.cancer.gov/Data_Portal/PDF/Data_Portal_UG.pdf)

**Usage**

```
surv.plot
```

**Format**

A data frame with four variables: survivalEstimate, id, censored, and time

**Examples**

```
library(ExperimentHub)
eh <- ExperimentHub()
myfiles <- query(eh, "HarmonizedTCGAData")
surv.plot <- myfiles[[3]]
# surv.plot <- myfiles[['EH1016']]
head(surv.plot)
```

---

Wall	<i>Wall</i>
------	-------------

---

**Description**

Wall contains a list of precomputed affinity (similarity) matrices of 2582 patients. These matrices were derived from 10382 gene expression, miRNA expression and DNA methylation data files downloaded from GDC data portal The file UUIDs can be found in `inst/extdata/fileUUIDs.csv` Using these file UUIDs, users can download the original data from <https://portal.gdc.cancer.gov/repository> ‘Wall’ is a complex list and contains lists inside list. Precisely, Wall is a list (five cancer types) of list (six feature normalization types: raw.all, raw.sel, log.all, log.sel, vst.sel, normalized) of list (three feature spaces or views: fpkm, mirna, and methy450) of matrices. (So Wall contains 90 matrices in total) The rownames of each matrix is the case\_id (i.e., patient id), and the column names of each matrix is the aliquot IDs (i.e., TCGA barcode, which contains the case\_id as prefix).

**Usage**

```
Wall
```

**Format**

An object of class `list` of length 5.

**Examples**

```
library(ExperimentHub)
eh <- ExperimentHub()
myfiles <- query(eh, "HarmonizedTCGAData")
Wall <- myfiles[[1]]
# Wall <- myfiles[['EH1014']]
names(Wall)
names(Wall[[1]])
names(Wall[[1]][[1]])
dim(Wall[[1]][[1]][[1]])
```

# Index

## \* datasets

project\_ids, [2](#)

surv.plot, [3](#)

Wall, [3](#)

HarmonizedTCGAData, [2](#)

HarmonizedTCGAData-package  
(HarmonizedTCGAData), [2](#)

project\_ids, [2](#)

surv.plot, [3](#)

Wall, [3](#)