Package 'depmap'

May 12, 2026

Type Package

Title Cancer Dependency Map Data Package

Version 1.27.0

Description The depmap package is a data package that accesses datsets from the Broad Institute DepMap cancer dependency study using ExperimentHub. Datasets from the most current release are available, including RNAI and CRISPR-Cas9 gene knockout screens quantifying the genetic dependency for select cancer cell lines. Additional datasets are also available pertaining to the log copy number of genes for select cell lines, protein expression of cell lines as measured by reverse phase protein lysate microarray (RPPA), 'Transcript Per Million' (TPM) data, as well as supplementary datasets which contain metadata and mutation calls for the other datasets found in the current release. The 19Q3 release adds the drug_dependency dataset, that contains cancer cell line dependency data with respect to drug and drug-candidate compounds. The 20Q2 release adds the proteomic dataset that contains quantitative profiling of proteins via mass spectrometry. This package will be updated on a quarterly basis to incorporate the latest Broad Institute DepMap Public cancer dependency datasets. All data made available in this package was generated by the Broad Institute DepMap for research purposes and not intended for clinical use. This data is distributed under the Creative Commons license (Attribution 4.0 International (CC BY 4.0)).

Depends R (>= 3.6), methods, dplyr

Imports utils, ExperimentHub, AnnotationHub, BiocFileCache, httr2, curl, tibble

License Artistic-2.0

Encoding UTF-8

RoxygenNote 7.3.1

Suggests knitr, rmarkdown, BiocStyle, viridis, gridExtra, ggplot2, readr, stringr, tidyverse, magick

VignetteBuilder knitr

biocViews ExperimentHub, ExperimentData, ReproducibleResearch, RepositoryData, AssayDomainData, CopyNumberVariationData, DiseaseModel, CancerData, BreastCancerData, ColonCancerData, KidneyCancerData, LeukemiaCancerData, LungCancerData, OvarianCancerData, ProstateCancerData, OrganismData, Homo_sapiens_Data, PackageTypeData, SpecimenSource, CellCulture, Genome, Proteome, StemCell, Tissue

git_url https://git.bioconductor.org/packages/depmap

git_branch devel

git_last_commit c9de6f9

git_last_commit_date 2026-04-28

Repository Bioconductor 3.24

Date/Publication 2026-05-12

Author Laurent Gatto [cre, aut] (ORCID:
<https://orcid.org/0000-0002-1520-2268>),
Theo Killian [aut],
Alexander Peltzer [ctb] (ORCID:
<https://orcid.org/0000-0002-6503-2180>)

Maintainer Laurent Gatto <laurent.gatto@uclouvain.be>

Contents

`achilles` *achilles_22Q2*

Description

The 'achilles' dataset contains the metadata for DepMap's cancer models/cell lines, specific to Project Achilles' 22Q2 CRISPR screens. This dataset can be loaded into the R environment with the 'depmap_achilles' function.

Usage

```
achilles
```

Format

A data frame with 1036 rows and 6 variables:

depmap_id cancer cancer cell line foreign key (i.e. "ACH-00001")

cell_line CCLE name of cancer cell line (i.e. "184A1_BREAST")

achilles_n_replicates Number of replicates used in Achilles CRISPR screen passing QC

cell_line_NNMD Difference in the means of positive and negative controls normalized by the standard deviation of the negative control distribution

culture_medium Medium used to grow cell line

cas9_activity Percentage of cells remaining GFP negative on days 12-14 of cas9 activity assay as measured by FACs

Details

This data represents the 'Achilles_metadata.csv' file taken from the 22Q2 [Broad Institute](https://depmap.org/portal/dow
release.

Change log

- 22Q1: Initial dataset

- 22Q2: "culture_type" column was removed

Source

DepMap, Broad Institute: https://depmap.org/portal/download/

References

Tsherniak, A., Vazquez, F., Montgomery, P. G., Weir, B. A., Kryukov, G., Cowley, G. S., ... & Meyers, R. M. (2017). Defining a cancer dependency map. Cell, 170(3), 564-576.

James M. McFarland, Zandra V. Ho, Guillaume Kugener, Joshua M. Dempster, Phillip G. Montgomery, Jordan G. Bryan, John M. Krill-Burger, Thomas M. Green, Francisca Vazquez, Jesse S. Boehm, Todd R. Golub, William C. Hahn, David E. Root, Aviad Tsherniak. (2018). Improved estimation of cancer dependencies from large-scale RNAi screens using model-based normalization and data integration. Nature Communications 9, 1.

Examples

```
## Not run:
depmap_achilles()

## End(Not run)
```

copyNumber *copyNumber_22Q2*

Description

The ‘copyNumber‘ dataset contains the 22Q2 inferred copy number data for genes and cancer cell lines. This dataset includes data from 25368 genes, 1754 cell lines, 35 primary diseases and 38 lineages. The columns of ‘copyNumber‘ are: ‘depmap_id‘, a foreign key corresponding to the cancer cell lineage, ‘cell_line‘ containing the common CCLE name of the cancer cell lines, ‘gene‘ containing both the HUGO gene name of the knockdown gene along with entrez ID#, ‘gene_name‘ containing only the HUGO gene name, ‘entrez_id‘ containing only the entrez ID#, and ‘log_copy_number‘ containing the numerical dependency score values for each pair of genes and cell lines. This dataset can be loaded into the R environment with the ‘depmap_copyNumber‘ function.

Usage

```
copyNumber
```

Format

A data frame with 44799888 rows (cell lines) and 6 variables.

depmap_id Cancer cell line foreign key (i.e. "ACH-00001")

gene HUGO symbol (e.g. "SAP25") and Entrez ID# (e.g. 100316904)

gene_name HUGO symbol (e.g. "SAP25")

entrez_id Entrez ID# (e.g. 100316904)

log_copy_number numerical log fold change in copy number for a given gene and cell line

cell_line CCLE name of cancer cell line (i.e. "184A1_BREAST")

Details

This data represents the ‘CCLE_gene_cn.csv‘ file taken from the 22Q2 [Broad Institute](https://depmap.org/portal/downl cancer depenedency study. The derived dataset found in the ‘depmap‘ package features the addition of a foreign key ‘depmap_id‘ found in the first column of this dataset, which was added from the ‘metadata‘ dataset. This dataset has been converted to a long format tibble. Variables names from the original dataset were converted to lower case, put in snake case, and abbreviated where feasible.

Change log

- 19Q1: Initial dataset consisted of a data frame with 37907473 rows (cell lines) and 6 variables representing 23299 genes, 1604 cell lines, 38 primary diseases and 33 lineages.

- 19Q2: adds 23 cell lines and 1 lineage

- 19Q3: adds 3263 genes, 30 cell lines and removes 2 primary diseases. Now a dataframe with 45670234 rows and 6 variables

- 19Q4: adds 77 genes, 25 cell lines, 0 primary diseases and 2 lineages

- 20Q1: adds 31 cell lines

- 20Q2: adds 32 cell lines

- 20Q3: no change

- 20Q4: removes 77 genes, adds 8 cell lines and 1 lineage
- 21Q1: removes 13 cell lines
- 21Q2: adds 2 cell lines
- 21Q3: removes 1 cell line and 1 lineage
- 21Q4: removes 194 genes and adds 9 cell lines
- 22Q1: removes 2000 genes, adds 4 cell lines and 1 lineage
- 22Q2: adds 12 cell lines and removes 2 primary diseases and 8 lineages

Source

DepMap, Broad Institute: https://depmap.org/portal/download/

References

Tsherniak, A., Vazquez, F., Montgomery, P. G., Weir, B. A., Kryukov, G., Cowley, G. S., ... & Meyers, R. M. (2017). Defining a cancer dependency map. Cell, 170(3), 564-576.

DepMap, Broad (2019): DepMap Achilles 19Q1 Public. https://figshare.com/articles/DepMap_Achilles_19Q1_Public/7

Robin M. Meyers, Jordan G. Bryan, James M. McFarland, Barbara A. Weir, ... David E. Root, William C. Hahn, Aviad Tsherniak. Computational correction of copy number effect improves specificity of CRISPR-Cas9 essentiality screens in cancer cells. Nature Genetics 2017 October 49:1779–1784.

Mahmoud Ghandi, Franklin W. Huang, Judit Jané-Valbuena, Gregory V. Kryukov, ... Todd R. Golub, Levi A. Garraway & William R. Sellers. 2019. Next- generation characterization of the Cancer Cell Line Encyclopedia. Nature 569, 503–508 (2019).

Examples

```
## Not run:
depmap_copyNumber()

## End(Not run)
```

`crispr` *crispr_22Q2*

Description

The ‘crispr‘ dataset contains the 22Q2 genetic effect of CRISPR-Cas9 gene knockout of select genes in various cancer cell lines. This dataset includes data from 17386 genes, 1086 cell lines, 31 primary diseases and 28 lineages. The columns of ‘crispr‘ are: ‘depmap_id‘ a foreign key corresponding to the cancer cell lineage, ‘cell_line‘ containing the common CCLE name of the cancer cell lines, ‘gene‘ containing both the HUGO gene name of the knockout gene along with entrez ID#, ‘gene_name‘ containing only the HUGO gene name, ‘entrez_id‘ containing only the entrez ID# and ‘dependency‘ which contains the numerical dependency score values for each pair of genes and cell lines. This dataset can be loaded into R environment with the ‘depmap_crispr‘ function. NOTE: the ‘crispr‘ dataset has replaced the ‘rnai‘ dataset as the primary supported measurement of cancer dependency data as of the 19Q4 release.

Usage

```
crispr
```

Format

A data frame with 18881196 rows (cell lines) and 6 variables:

depmap_id Cancer cell line foreign key (i.e. "ACH-00001")

gene HUGO symbol (e.g. "SAP25") and Entrez ID# (e.g. 100316904)

gene_name HUGO symbol (e.g. "SAP25")

entrez_id Entrez ID# (e.g. 100316904)

dependency numerical depenency score of given gene and cell line

cell_line CCLE name of cancer cell line (i.e. "184A1_BREAST")

Details

This data represents the ‘Achilles_gene_effect.csv‘ file taken from the 22Q2 [Broad Institute](https://depmap.org/portal/d cancer depenedency study. The derived dataset found in the ‘depmap‘ package features the addition of a foreign key ‘depmap_id‘ found in the first column of this dataset, which was added from the ‘metadata‘ dataset. This dataset has been converted to a long format tibble. Variables names from the original dataset were converted to lower case, put in snake case, and abbreviated where feasible.

Change log

- 19Q1: Initial dataset consisted of a data frame with 9839772 rows (cell lines) and 6 variables representing 17634 genes, 558 cell lines, 26 primary diseases and 28 lineages.

- 19Q2: adds 5 cell lines, 1 primary disease and 1 lineage

- 19Q3: adds 699 genes, 62 cell lines and 1 primary disease. Now a dataset with 11458125 rows and 6 variables.

- 19Q4: adds 0 genes, 64 cell lines, 1 primary disease and 0 lineages.

- 20Q1: adds 50 cell lines.

- 20Q2: adds 30 cell lines.

- 20Q3: adds 20 cell lines, 1 primary disease and 1 lineages.

- 20Q4: adds 19 cell lines, 1 primary disease and 2 lineages

- 21Q1: no change

- 21Q2: removes 474 genes and adds 182 cell lines 1 primary disease and 1 lineage

- 21Q3: removes 252 genes and adds 42 cell lines

- 21Q4: removes 7 genes and 22 cell lines

- 22Q1: adds 16 cell lines and 1 lineage

- 22Q2: adds 16 cell lines and removes 1 primary diseases and 3 lineages.

Source

DepMap, Broad Institute: https://depmap.org/portal/download/

References

Tsherniak, A., Vazquez, F., Montgomery, P. G., Weir, B. A., Kryukov, G., Cowley, G. S., ... & Meyers, R. M. (2017). Defining a cancer dependency map. Cell, 170(3), 564-576.

DepMap, Broad (2019): DepMap Achilles 19Q1 Public. https://figshare.com/articles/DepMap_Achilles_19Q1_Public/7
Fileset.

Robin M. Meyers, Jordan G. Bryan, James M. McFarland, Barbara A. Weir, ... David E. Root, William C. Hahn, Aviad Tsherniak. Computational correction of copy number effect improves specificity of CRISPR-Cas9 essentiality screens in cancer cells. Nature Genetics 2017 October 49:1779–1784.

Mahmoud Ghandi, Franklin W. Huang, Judit Jané-Valbuena, Gregory V. Kryukov, ... Todd R. Golub, Levi A. Garraway & William R. Sellers. 2019. Next- generation characterization of the Cancer Cell Line Encyclopedia. Nature 569, 503–508 (2019).

Examples

```
## Not run:
depmap_crispr()

## End(Not run)
```

`depmap` *depmap: Cancer Dependency Map Data Package*

Description

The depmap package is a data package that accesses datsets from the Broad Institute DepMap cancer dependency study using ExperimentHub. Datasets from the most current release are available, including RNAI and CRISPR-Cas9 gene knockout screens quantifying the genetic dependency for select cancer cell lines. Additional datasets are also available pertaining to the log copy number of genes for select cell lines, protein expression of cell lines as measured by reverse phase protein lysate microarray (RPPA), 'Transcript Per Million' (TPM) data, chemical dependecy (drug_sensativity), mass spectrometry proteomic quantification (proteomic) as well as supplementary datasets which contain metadata and mutation calls for the other datasets found in the current release. This package will be updated on a quarterly basis to incorporate the latest Broad Institute DepMap Public cancer dependency datasets. All data made available in this package was generated by the Broad Institute DepMap for research purposes and not intended for clinical use. This data is distributed under the Creative Commons license (Attribution 4.0 International (CC BY 4.0)).

Details

See the package vignettes and respective man pages for details.

Author(s)

Maintainer: Laurent Gatto <laurent.gatto@uclouvain.be> (ORCID)

Authors:

- Theo Killian

DepMapFiles *DepMap Dataset and Files*

Description

Two tibbles are provided that give access to DepMap data, as shared by the Broad Institute's DepMap project on Figshare (https://figshare.com/authors/Broad_DepMap/5514062).

- The [dmsets()] function returns a tibble with DepMap datasets. Each dataset is described by its title, its unique identifier, the number of files it contains, the Figshare URL, and a 'DepMapDataset' object that contains further details of the dataset.

- The [dmfiles()] function returns a tibble with DepMap files. Each file is described by its dataset identifier, its own unique identifier, its name, size (in bytes), a download URL, md5 hash and mime type.

- Depmap data files can be downloaded with the [dmget()] function, that takes as input a tibble or data.frame of depmap files such as 'dmfiles'. Files are downloaded and automatically in the package's central cache. See [dmCache()].

Usage

```
DepMapDataset(id)

DepMapFiles(x)

dmFileNames(object)

dmTitle(object)

dmNumFiles(object)

dmget(dmtab, cache = dmCache())

dmfiles()

dmsets()
```

Arguments

id	'numeric()' with one or multiple DepMap dataset identifier(s). Note that 'id' is converted to an integer. Missing values are not permitted.
x	either an 'numeric()' that will be passed to 'DepMapDataset' or an instance (or list of) 'DepMapDataset'.
object	an instance of class 'DepMapDataset'.
dmtab	A 'tibble' or 'data.frame' containing the file to be downloaded, such as [dmfiles()], or created by [DepMapFiles()]. If is expected to contain the '"name"', '"id"' and '"dowload_url"' variables.
cache	Object of class [BiocFileCache()]. Default is to use the central 'depmap' cache returned by [dmCache()], but users can use their own cache.

Details

The 'DepMapDataset' class stores the informtion describing a depmap dataset, as stored on Figshare (articles, as it's called there). The [DepMapDataset()] constructor requires one or multiple dataset identifiers and returns one or a list of instances.

The following accessors are available: - [dmFileNames()] returns the dataset's filenames. - [dmTitle()] returns the dataset's title. - [dmNumFiles()] returns the number of files in the dataset.

(These are used to construct the main depmap dataset tibble.)

A tibble describing the files in depmap dataset can be cretated with the [DepMapFiles()] function. It either takes one or multiple dataset idenifiers, or one or a list of 'DepMapDataset' instances

The [DepMapDataset()] and [DepMapFiles()] functions are mostly used internally, to create the 'dmsets' and 'dmfiles' tibbles. If a more recent dataset is available on Figshare and not (yet) in the 'depmap' package, a user might create the depmap files table to download the files, and/or open a [GitHub issue](https://github.com/UCLouvain-CBIO/depmap) for the new data to be added by the maintainer(s).

All the information is retrieved from Figshare using their API, as described at https://docs.figshare.com.

Adding new datasets

Adding new datasets is simple. Once a new dataset (or Article, as called on Figshare) has been identified on the Broad Institute's [DepMap project on Figshare](https://figshare.com/authors/Broad_DepMap/5514062), one needs to add the dataset's URL to the 'depmapURLs' vector in ['inst/extdata/make-dmfiles.R'](https://github.com/UCLouvain-CBIO/depmap/blob/master/inst/scripts/make-dmfiles.R), and re-run the script to update the 'dmsets.rds.' and 'dmfiles.rds' files in 'inst/extdata'.

Feel free to send a GitHub pull request or open a [GitHub issue](https://github.com/UCLouvain-CBIO/depmap) for the new data to be added by the maintainer(s).

Author(s)

Laurent Gatto

Examples

```
## The depmap datasets
dmsets

## The depmap files
dmfiles

############################################################
## Mostly for internal use, or to update/generate the depmap
## dataset and files tables.

## One dataset identifier: 24667905
my_dmset <- DepMapDataset(24667905)
my_dmset

## Multiple dataset identifiers
my_dmsets <- DepMapDataset(c(24667905, 22765112))
my_dmsets

## Create the files table from one or dataset multiple dataset
## identifiers
```

```
DepMapFiles(24667905)
DepMapFiles(my_dmset)

DepMapFiles(c(24667905, 22765112))
DepMapFiles(my_dmsets)
```

`depmap_release` *Returns the depmap release*

Description

Returns the depmap release

Usage

```
depmap_release()
```

Value

`character(1)` with the depmap release

`dmCache` *Depmap Package Cache*

Description

Function to access (and manage) the depmap package cache. ‘dmCache()‘ returns the central ‘depmap‘ cache.

Usage

```
dmCache()
```

Details

The cache is an object of class ‘BiocFileCache‘, and created with [BiocFileCache::BiocFileCache()]. It can be either the package-wide cache as defined by ‘dmCache()‘ or an instaned provided by the user.

When projects are cached, they are given a resource name (‘rname‘), that is set to the file’s identifier.

Value

The ‘dmCache()‘ function returns an instance of class ‘BiocFileCache‘.

Author(s)

Laurent Gatto

Examples

```
## Default depmap cache
dmCache()
```

`drug_sensitivity` *drug_sensitivity_21Q2*

Description

The ‘drug_sensitivity‘ dataset contains the 19Q3 replicate collapsed logfold change values relative to DMSO, corrected for experimental confounders using ComBat. This dataset contains information refering to 4686 compounds, 578 cell lines, 23 primary diseases and 25 lineages. This dataset is part of the SIGMA Re-purposing release which contains small molecule viability datasets generated using the Broad Re-purposing Library and the PRISM multiplexed cell-line viability assay. The columns of ‘drug_sensitivity‘ are: ‘depmap_id‘ a foreign key corresponding to the cancer cell lineage, ‘cell_line‘ the common CCLE name of the cancer cell lines, ‘compound‘ the synonym for the drug compound, and ‘dependency‘ which contains the numerical dependency score values for each pair of genes and cell lines. Compounded metadata has also been added.

Usage

```
drug_sensitivity
```

Format

A data frame with 2708508 rows (cell lines) and 14 variables:

depmap_id Cell line foreign key (i.e. "ACH-000956")

cell_line Name of cancer cell line (i.e. "22RV1_PROSTATE")

compound Drug compound name (i.e. BRD-A00077618-236-07-6::2.5::HTS)

dependency numerical depenency score of a compound on a cell line

broad_id Broad ID for compound (i.e. BRD-A00077618-236-07-6)

name Standard chemical name (i.e. 8-bromo-cGMP)

dose Dose of compound

screen_id Broad ID for compound (i.e. HTS)

moa Mechanism of action (i.e. PKA activator)

target Molecular target of compount (i.e. PRKG1)

disease_area Anatomical target (i.e. hematologic malignancy)

indication Prescribed for disease (i.e. acute myeloid leukemia (AML))

smiles Simplified molecular-input line-entry specification

phase Clincal phase

Details

This data originates from the ‘primary_replicate_collapsed_logfold_change.csv‘ file taken from the 19Q3 [Broad Institute](https://depmap.org/portal/download/) cancer depenedency study. The derived dataset found in the ‘depmap‘ package features the addition of a foreign key ‘depmap_id‘ found in the first column of this dataset, which was added from the ‘metadata‘ dataset. This dataset has been converted to a long format tibble. Variables names from the original dataset were converted to lower case, put in snake case, and abbreviated where feasible. Note: compound metadata was added to this dataset, consisting of 10 new features derived from the file ‘primary-screen-replicate-collapsed-treatment-info.csv‘ from the [Broad Institute](https://depmap.org/portal/download/) website. The Drug sensitivity data remains from 19Q3, however the version was bumped to 21Q2 to distinguish between the different datasets.

Change log

- 19Q3: Initial dataset consisted of a data frame with 2708508 rows (cell lines) and 6 variables representing 686 compounds, 578 cell lines, 23 primary diseases and 25 lineages.

- 19Q4: no change, no further releases are scheduled at this time.

- 20Q1: no change, no further releases are scheduled at this time.

- 20Q2: no change, no further releases are scheduled at this time.

- 20Q3: no change, no further releases are scheduled at this time.

- 20Q4: no change, no further releases are scheduled at this time.

- 21Q1: no change, no further releases are scheduled at this time.

- 21Q2: Drug sensitivity data combined with compound metadata, added 10 new features from the file primary-screen-replicate-collapsed-treatment-info.csv

- 21Q3: no change, no further releases are scheduled at this time.

- 21Q4: no change, no further releases are scheduled at this time.

- 22Q1: no change, no further releases are scheduled at this time.

- 22Q2: no change, no further releases are scheduled at this time.

Source

DepMap, Broad Institute: https://depmap.org/portal/download/

References

Tsherniak, A., Vazquez, F., Montgomery, P. G., Weir, B. A., Kryukov, G., Cowley, G. S., ... & Meyers, R. M. (2017). Defining a cancer dependency map. Cell, 170(3), 564-576.

Steven M Corsello, Rohith T Nagari, Ryan D Spangler, Jordan Rossen, Mustafa Kocak, Jordan G Bryan, Ranad Humeidi, David Peck, Xiaoyun Wu, Andrew A Tang, Vickie MWang, Samantha A Bender, Evan Lemire, Rajiv Narayan, Philip Montgomery, Uri Ben-David, Yejia Chen, Matthew G Rees, Nicholas J Lyons, James M McFarland, Bang TWong, Li Wang, Nancy Dumont, Patrick J O'Hearn, Eric Stefan, John G Doench, HeidiGreulich, Matthew Meyerson, Francisca Vazquez, Aravind Subramanian, Jennifer A Roth, Joshua A Bittker, Jesse S Boehm, Christopher C Mader, Aviad Tsherniak, Todd R Golub. 2019. Non-oncology drugs are a source of previously unappreciated anti-cancer activity. bioRXiv. https://www.biorxiv.org/content/10.1101/730119v1

`gene_summary` *gene_summary_22Q1*

Description

The 'gene_summary' dataset contains the 22Q1 gene essentiality probabilities for select genes. This dataset can be loaded into the R environment with the 'depmap_gene_summary' function.

Usage

```
gene_summary
```

Format

A data frame with 69746 rows (cell lines) and 7 variables:

entrez_id Entrez ID# (e.g. 100316904)

gene_name HUGO symbol (e.g. "SAP25")

dataset which dataset this probability derives

dependent_cell_lines number of dependent cell lines

cell_lines_with_data number of cell lines with relevant dependency data

strongly_selective Gene knockout is selective (not pan-lethal)

common_essential common essential gene dependency

Details

This data represents the 'Gene Dependency Profile Summary.csv' file taken from the 22Q1 [Broad Institute](https://depmap.org/portal/api/download/gene_dep_summary) release.

Change log

- 22Q1: Initial dataset

- 22Q2: no change, no further releases are scheduled at this time.

Source

DepMap, Broad Institute: https://depmap.org/portal/download/

References

Tsherniak, A., Vazquez, F., Montgomery, P. G., Weir, B. A., Kryukov, G., Cowley, G. S., ... & Meyers, R. M. (2017). Defining a cancer dependency map. Cell, 170(3), 564-576.

James M. McFarland, Zandra V. Ho, Guillaume Kugener, Joshua M. Dempster, Phillip G. Montgomery, Jordan G. Bryan, John M. Krill-Burger, Thomas M. Green, Francisca Vazquez, Jesse S. Boehm, Todd R. Golub, William C. Hahn, David E. Root, Aviad Tsherniak. (2018). Improved estimation of cancer dependencies from large-scale RNAi screens using model-based normalization and data integration. Nature Communications 9, 1.

Examples

```
## Not run:
depmap_gene_summary()

## End(Not run)
```

`metadata` *metadata_22Q2*

Description

The ‘metadata‘ dataset contains the metadata about cell lines in the 22Q2 Broad Institute DepMap release, which includes mapping between ‘depmap_id‘ and ‘cell_line‘ name for cancer cell lines. This dataset does not contain any data from the Achilles screen nor dependency data, but contains the metadata from the other datasets pertaining to the 22Q1 DepMap release, for 1840 cell lines, 0 genes, 33 primary diseases and 30 lineages. The columns of ‘metadata‘ are: ‘depmap_id‘, ‘stripped_cell_line_name‘, ‘cell_line‘, ‘aliases‘, ‘cosmic_id‘, ‘sanger_id‘, ‘WTSI_master_cell_ID‘, ‘primary_disease‘, ‘subtype_disease‘, ‘sub_subtype_disease‘, ‘gender‘, ‘source‘ . This dataset can be loaded into the R environment with the ‘depmap_metadata‘ function.

Usage

```
metadata
```

Format

A data frame with 1829 rows (cell lines) and 22 variables:

depmap_id Cancer cell line primary key (i.e. "ACH-00001")

stripped_cell_line_name Name of stripped cell line

cell_line CCLE name of cancer cell line (i.e. "184A1_BREAST")

cell_line_name Abbreviated name of cancer cell line (i.e. "NIH:OVCAR-3")

aliases Aliases of cancer cell line

cosmic_id Catalogue Of Somatic Mutations In Cancer ID number (e.g. 905933)

sex Sex of tissue sample)

source Source of tissue sample)

culture_type Culture type of tissue sample)

RRID Resource Identification Portal ID

sample_collection_site Site of sample collection (AML), M3 (Promyelocytic))

primary_or_metastasis Primary cancer cell line or metastatic

primary_disease Primary Disease (e.g. cancer type)

subtype_disease Subtype Disease (e.g. Acute Myelogenous Leukemia)

age Age of individual sample of cell line was derived

sanger_id Sanger ID (eg. 2201)

WTSI_master_cell_ID Wellcome Trust Sanger Institute ID (eg. 1369)

additional_info Additional information about samples

lineage Lineage of cancer cell line

lineage_subtype Subtype of lineage of cancer cell line

lineage_sub_subtype Subtype of subtype of Lineage of cancer cell line

lineage_molecular_subtype Molecular type of Lineage of cancer cell line

model_manipulation Culture model manipulation details

model_manipulation_details Culture model manipulation details

patient_id Patient id

parent_patient_id Parent patient id

Cellosaurus_NCIt_disease Cellosaurus NCIt disease

Cellosaurus_NCIt_id Cellosaurus NCIt_id

Cellosaurus_NCIt_id Cellosaurus NCIt_id

Details

This data represents the ‘sample_info.csv‘ file taken from the 22Q2 [Broad Institute](https://depmap.org/portal/download cancer depenedency study. This dataset features the a primary key ‘depmap_id‘ which is a unique ID given to each cell line and is found in the first column of this dataset. The ‘depmap_id‘ attribute is used as a foreign key in all other datasets in the package. This dataset has been converted to a long format tibble. This dataset does not contain any expression or dependency data but rather contains the metadata for all cancer cell lines used in the depmap project. Variables names were converted to lower case, put in snake case, and abbreviated where feasible (e.g. "Sanger ID" was changed to "sanger_id").

Change log

- 19Q1: Initial dataset consisted of data frame with 1677 rows (cell lines) and 9 variables, representing 0 genes, 1677 cell lines, 38 primary diseases and 33 lineages

- 19Q2: adds 37 new cell lines, 1 primary disease and 1 lineage. This version of the metadata dataset contains 6 variables not found in previous versions, relating the the Achilles metadata: ‘Achilles_n_replicates‘, ‘cell_line_NNMD‘, ‘culture_type‘, ‘culture_medium‘, and ‘cas9_activity‘.

- 19Q3: adds 30 cell lines, 2 primary diseases and 2 lineages

- 19Q4: adds 42 cell lines, 0 primary diseases and 3 lineages

- 20Q1: adds 19 cell lines, ‘gender‘ was changed to ‘sex‘, ‘age‘, ‘primary_or_metastasis‘ and ‘sample_collection_site“ were added

- 20Q2: adds 30 cell lines and 1 lineage

- 20Q3: adds new column ‘WTSI_master_cell_ID‘

- 20Q4: adds 6 cell lines and 1 lineage. Adds column ‘cell_line_name‘

- 21Q1: removes 1 cell line

- 21Q2: adds 3 cell lines

- 21Q3: adds 1130 cell lines, 8 primary diseases and 8 lineages

- 21Q4: removes 1119 cell lines, 8 primary diseases and 8 lineages

- 22Q1: adds 4 cell lines. The features relating to Achilles metadata have been removed and put into their own dataset: ‘Achilles_n_replicates‘, ‘cell_line_NNMD‘, ‘culture_type‘, ‘culture_medium‘, and ‘cas9_activity‘.

- 22Q2: adds 11 cell lines and removes 2 primary diseases and 30 lineages. The feature ‘culture_type‘ has been removed and columns "model_manipulation", "model_manipulation_details", "patient_id", "parent_depmap_id", "Cellosaurus_NCIt_disease", "Cellosaurus_NCIt_id" and "Cellosaurus_issues" have been added.

Source

DepMap, Broad Institute: https://depmap.org/portal/download/

References

Tsherniak, A., Vazquez, F., Montgomery, P. G., Weir, B. A., Kryukov, G., Cowley, G. S., ... & Meyers, R. M. (2017). Defining a cancer dependency map. Cell, 170(3), 564-576.

DepMap, Broad (2019): DepMap Achilles 19Q1 Public. https://figshare.com/articles/DepMap_Achilles_19Q1_Public/7

Robin M. Meyers, Jordan G. Bryan, James M. McFarland, Barbara A. Weir, ... David E. Root, William C. Hahn, Aviad Tsherniak. Computational correction of copy number effect improves specificity of CRISPR-Cas9 essentiality screens in cancer cells. Nature Genetics 2017 October 49:1779–1784.

Mahmoud Ghandi, Franklin W. Huang, Judit Jané-Valbuena, Gregory V. Kryukov, ... Todd R. Golub, Levi A. Garraway & William R. Sellers. 2019. Next- generation characterization of the Cancer Cell Line Encyclopedia. Nature 569, 503–508 (2019).

Examples

```
## Not run:
depmap_metadata()

## End(Not run)
```

`mutationCalls` *mutationCalls_22Q2*

Description

The 'mutationCalls' dataset contains merged the 22Q2 mutation calls (for coding region, germline filtered) and includes data from 18784 genes, 1771 cell lines, 33 primary diseases and 30 lineages. This dataset can be considered the metadata data set for mutations and does not contain any dependency data. This dataset can be loaded into the R environment with the 'depmap_mutationCalls' function.

Usage

```
mutationCalls
```

Format

A data frame with 1235466 rows and 32 variables:

depmap_id depmap_id

gene_name Hugo Symbol denotes a unique and meaningful name for each gene (e.g. SAP25)

entrez_id Gene ID for NCBI Entrez gene database, (e.g. 100316904)

ncbi_build NCBI Build (i.e. reference genome)

chromosome Chromosome

start_pos Gene start position

end_pos Gene end position

strand Strand location of gene

var_class Variant Classification

var_type Variant Type

ref_allele Reference Allele

alt_allele Tumor Seq Allele1

dbSNP_RS Single Nucleotide Polymorphism Database (dbSNP) reference cluster

dbSNP_val_status dbSNP Val Status

genome_change Genome Change

annotation_transcript Annotation Transcript

cDNA_change change in cDNA

codon_change Codon_Change

protein_change Protein_Change

is_deleterious Status of gene knockout on cell lineage

is_tcga_hotspot isTCGAhotspot

tcga_hsCnt TCGAhsCnt

is_cosmic_hotspot isCOSMIChotspot

cosmic_hsCnt COSMIChsCnt

ExAC_AF ExAC_AF

CGA_WES_AC CGA_WES_AC

sanger_WES_AC SangerWES_AC

RNAseq_AC RNAseq_AC

HC_AC HC_AC

RD_AC RD_AC

WGS_AC WGS_AC

var_annotation Variant_annotation

Details

This data represents the ‘CCLE_mutations.csv‘ file taken from the 22Q2 [Broad Institute](https://depmap.org/portal/dow
cancer depenedency study. The derived dataset found in the ‘depmap‘ package features the addition of a foreign key ‘depmap_id‘ found in the first column of this dataset, which was added from the ‘metadata‘ dataset. This dataset has been converted to a long format tibble. Variables names from the original dataset were converted to lower case, put in snake case, and abbreviated where feasible.

Change log

- 19Q1: Initial dataset for package consisted of dataframe with 1243145 rows and 35 variables representing 18755 genes, 1601 cell lines, 37 primary diseases and 33 lineages.

- 19Q2: adds 30 cell lines, 1 primary disease and 1 lineage. This version has different columns than the previous version: the variable "VA_WES_AC" is no longer present in this dataset. Some minor alterations to the original file were made. The first column of the original dataset, (ID, Sample number) was removed, as this column was only the row number and did not serve any unique identifying purpose.

- 19Q3: adds 1 gene, 25 cell lines and removes 1 primary disease.

- 19Q4: adds 1 gene, 10 cell lines, 0 primary diseases and 2 lineages.

- 20Q1: adds 4 genes, 31 cell lines, 1 lineage.

- 20Q2: adds 44 cell lines, 1 lineage.

- 20Q3: no change.

- 20Q4: removes 13 genes, adds 8 cell lines and 1 lineage. Columns ‘tumor_sample_barcode‘ and ‘sanger_recalib_WES_AC‘ were removed.

- 21Q1: removes 11 genes and 2 cell lines.

- 21Q2: removes 1 genes and adds 3 cell lines.

- 21Q3: removes 3 genes, 4 cell lines and 1 lineage.

- 21Q3: removes 3 genes, 4 cell lines and 1 lineage.

- 21Q4: adds 9 cell lines.

- 22Q1: adds 4 cell lines and 1 lineage. The variable ‘tumor_seq_allele1‘ was renamed ‘alt_allele‘.

- 22Q2: adds 12 cell lines and removes 2 primary diseases and 8 lineages.

Source

DepMap, Broad Institute: https://depmap.org/portal/download/

References

Tsherniak, A., Vazquez, F., Montgomery, P. G., Weir, B. A., Kryukov, G., Cowley, G. S., ... & Meyers, R. M. (2017). Defining a cancer dependency map. Cell, 170(3), 564-576.

DepMap, Broad (2019): DepMap Achilles 19Q1 Public. https://figshare.com/articles/DepMap_Achilles_19Q1_Public/7

Robin M. Meyers, Jordan G. Bryan, James M. McFarland, Barbara A. Weir, ... David E. Root, William C. Hahn, Aviad Tsherniak. Computational correction of copy number effect improves specificity of CRISPR-Cas9 essentiality screens in cancer cells. Nature Genetics 2017 October 49:1779–1784.

Mahmoud Ghandi, Franklin W. Huang, Judit Jané-Valbuena, Gregory V. Kryukov, ... Todd R. Golub, Levi A. Garraway & William R. Sellers. 2019. Next- generation characterization of the Cancer Cell Line Encyclopedia. Nature 569, 503–508 (2019).

Examples

```
## Not run:
depmap_mutationCalls()

## End(Not run)
```

`proteomic` *proteomic_20Q2*

Description

The ‘proteomic‘ dataset contains the 20Q2 quantitative profiling of proteins via mass spectrometry from the Gygi lab. This dataset contains 12399 proteins tested in 375 cell lines, including 24 primary diseases and 27 lineages. The columns of this dataset are: ‘depmap_id‘, a foreign key corresponding to the cancer cell lineage, ‘cell_line‘ the common CCLE name of the cancer cell lines, ‘gene_name‘ containing the HUGO gene name and ‘entrez_id‘ containing only the entrez ID# and ‘protein_expression‘ which contains the normalized protein expression for cancer cell lines. This dataset can be loaded into R environment with the ‘depmap_proteomic‘ function.

Usage

```
proteomic
```

Format

A data frame with 24963776 rows (cell lines) and 12 variables:

depmap_id Cell line foreign key (i.e. "ACH-000956")

cell_line Name of cancer cell line (i.e. "22RV1_PROSTATE")

gene_name HUGO symbol (e.g. "TSPAN6")

entrez_id Ensembl ID (e.g. ENSG00000044574)

protein_expression normalized protein expression

protein protein name with TenPx (e.g. MDAMB468_BREAST_TenPx01)

protein_id Protein ID (e.g. sp|P55011|S12A2_HUMAN)

desc Description (e.g. S12A2_HUMAN Solute carrier family 12 member 2)

group_id Group ID

uniprot Uniprot ID (e.g. S12A2_HUMAN)

uniprot_acc Uniprot accession ID (e.g. P55011)

TenPx TenPx number (e.g. TenPx01)

Details

This data originates from the ‘protein_quant_current_normalized.csv‘ file taken from the 20Q2 [Broad Institute](https://depmap.org/portal/download/) cancer depenedency study. The derived dataset found in the ‘depmap‘ package features the addition of a foreign key ‘depmap_id‘ found in the first column of this dataset, which was added from the ‘metadata‘ dataset. This dataset has been converted to a long format tibble. Variables names from the original dataset were converted to lower case, put in snake case, and abbreviated where feasible.

Change log

- 20Q2: Initial dataset consisted of a data frame with 24963776 rows (cell lines) and 12 variables

- 20Q3: no change, no further releases are scheduled at this time.

- 20Q4: no change, no further releases are scheduled at this time.

- 21Q1: no change, no further releases are scheduled at this time.

- 21Q2: no change, no further releases are scheduled at this time.

- 21Q3: no change, no further releases are scheduled at this time.

- 21Q4: no change, no further releases are scheduled at this time.

- 22Q1: no change, no further releases are scheduled at this time.

- 22Q2: no change, no further releases are scheduled at this time.

Source

DepMap, Broad Institute: https://depmap.org/portal/download/

References

David P. Nusinow, John Szpyt, Mahmoud Ghandi, Christopher M. Rose, E. Robert McDonald III, Marian Kalocsay, Judit Jané-Valbuena, Ellen Gelfand, Devin K. Schweppe, Mark Jedrychowski, Javad Golji, Dale A. Porter, Tomas Rejtar, Y. Karen Wang, Gregory V. Kryukov, Frank Stegmeier, Brian K. Erickson, Levi A. Garraway, William R. Sellers, Steven P. Gygi (2020). Quantitative Proteomics of the Cancer Cell Line Encyclopedia. Cell 180, 2.

Examples

```
## Not run:
depmap_proteomic()

## End(Not run)
```

---

rnai *rnai_19Q3*

Description

The ‘rnai‘ dataset contains the 19Q3 cancer dependency of select cancer cell lines for genes found by RNAi gene knockdown. This dataset includes data from 17309 genes, 712 cancer cell lines, 31 primary diseases and 31 lineages. The columns of ‘rnai‘ are: ‘depmap_id‘, a foreign key corresponding to the cancer cell lineage, ‘cell_line‘ containing the common CCLE name of the cancer cell lines, ‘gene‘ containing both the HUGO gene name of the knockdown gene along with entrez ID#, ‘gene_name‘ which only contains HUGO gene name, ‘entrez_id‘ which contains only the entrez ID# and ‘dependency‘ which contains the numerical dependency score values for each pair of genes and cell lines. This dataset can be loaded into the R environment with the ‘depmap_rnai‘ function.

Usage

```
rnai
```

Format

A data frame with 12324008 rows (cell lines) and 6 variables:

depmap_id cancer cancer cell line foreign key (i.e. "ACH-00001")

cell_line CCLE name of cancer cell line (i.e. "184A1_BREAST")

gene HUGO symbol (e.g. "SAP25") and Entrez ID# (e.g. 100316904)

gene_name HUGO symbol (e.g. "SAP25")

entrez_id Entrez ID# (e.g. 100316904)

dependency numerical depenency score of a gene for a cell line

Details

This data represents the ‘D2_combined_genetic_dependency_scores‘ file taken from the 19Q3 [Broad Institute](https://depmap.org/portal/download/) cancer depenedency study. The derived dataset found in the ‘depmap‘ package features the addition of a foreign key ‘depmap_id‘ found in the first column of this dataset, which was added from the ‘metadata‘ dataset. This dataset has been converted to a long format tibble. Variables names from the original dataset were converted to lower case, put in snake case, and abbreviated where feasible.

Change log

- 19Q1: Initial dataset consisted of a data frame with 12324008 rows (cell lines) and 6 variables representing 17309 genes, 711 cancer cell lines, 30 primary diseases and 31 lineages.

- 19Q2: adds 1 cell line

- 19Q3: adds 1 primary disease

- 19Q4: no change, no further releases are scheduled at this time. NOTE: as of this release, the crispr dataset replaces the rnai dataset for dependency measurements in all future releases.

- 20Q1: no change, this dataset is superceded by the CRISPR dependency screens and no further releases are scheduled.

Source

DepMap, Broad Institute: https://depmap.org/portal/download/

References

Tsherniak, A., Vazquez, F., Montgomery, P. G., Weir, B. A., Kryukov, G., Cowley, G. S., ... & Meyers, R. M. (2017). Defining a cancer dependency map. Cell, 170(3), 564-576.

James M. McFarland, Zandra V. Ho, Guillaume Kugener, Joshua M. Dempster, Phillip G. Montgomery, Jordan G. Bryan, John M. Krill-Burger, Thomas M. Green, Francisca Vazquez, Jesse S. Boehm, Todd R. Golub, William C. Hahn, David E. Root, Aviad Tsherniak. (2018). Improved estimation of cancer dependencies from large-scale RNAi screens using model-based normalization and data integration. Nature Communications 9, 1.

Examples

```
## Not run:
depmap_rnai()

## End(Not run)
```

RPPA *RPPA_19Q3*

Description

The ‘RPPA‘ dataset contains the 19Q3 CCLE Reverse Phase Protein Array (RPPA) cellular model expression data. This dataset includes data from 214 genes, 899 cancer cell lines, 28 primary diseases and 28 lineages. The columns of ‘RPPA‘ are: ‘depmap_id‘, a foreign key corresponding to the cancer cell lineage, ‘cell_line‘ which contains the common CCLE name of the cancer cell lines, ‘gene‘ which contains the knockdown gene expression, ‘antibody‘ containing the name of knocked down gene and ‘expression‘ containing numerical protein expression data. This dataset can be loaded into R environment with the ‘depmap_RPPA‘ function.

Usage

```
RPPA
```

Format

A data frame with 192386 rows and 4 variables:

depmap_id cancer cell line foreign key (i.e. "ACH-000001")

cell_line CCLE name of cancer cell line (i.e. "NIHOVCAR3_OVARY")

antibody Name of antibody targeting protein (i.e. "14-3-3_beta")

expression Observed expression via RPPA of protein coding genes

Details

This data represents the ‘CCLE_RPPA_20181003.csv‘ file taken from the 19Q3 [Broad Institute](https://depmap.org/port
cancer depenedency study. The derived dataset found in the ‘depmap‘ package features the addition of a foreign key ‘depmap_id‘ found in the first column of this dataset, which was added from the ‘metadata‘ dataset. This dataset has been converted to a long format tibble. Variables names from the original dataset were converted to lower case, put in snake case, and abbreviated where feasible.

Change log

- 19Q1: Initial dataset consisted of a data frame with 192386 rows and 4 variables representing 214 genes, 899 cancer cell lines, 28 primary diseases and 28 lineages.

- 19Q2: no change

- 19Q3: no change, no further releases are scheduled at this time.

- 19Q4: no change, no further releases are scheduled at this time.

- 20Q1: no change, no further releases are scheduled at this time.

- 20Q2: no change, no further releases are scheduled at this time.

- 20Q3: no change, no further releases are scheduled at this time.

- 20Q4: no change, no further releases are scheduled at this time.

- 21Q1: no change, no further releases are scheduled at this time.

- 21Q2: no change, no further releases are scheduled at this time.

- 21Q3: no change, no further releases are scheduled at this time.

- 21Q4: no change, no further releases are scheduled at this time.

- 22Q1: no change, no further releases are scheduled at this time.

- 22Q2: no change, no further releases are scheduled at this time.

Source

DepMap, Broad Institute: https://depmap.org/portal/download/

References

Tsherniak, A., Vazquez, F., Montgomery, P. G., Weir, B. A., Kryukov, G., Cowley, G. S., ... & Meyers, R. M. (2017). Defining a cancer dependency map. Cell, 170(3), 564-576.

Mahmoud Ghandi, Franklin W. Huang, Judit Jané-Valbuena, Gregory V. Kryukov, ... Todd R. Golub, Levi A. Garraway & William R. Sellers. 2019. Next- generation characterization of the Cancer Cell Line Encyclopedia. Nature 569, 503–508 (2019).

Haoxin Li, Shaoyang Ning, Mahmoud Ghandi, Gregory V. Kryukov, Shuba Gopal, ... Levi A. Garraway & William R. Sellers. The landscape of cancer cell line metabolism. Nature Medicine 25, 850-860 (2019).

Examples

```
## Not run:
depmap_RPPA()

## End(Not run)
```

TPM *TPM_22Q2*

Description

The ‘TPM‘ dataset contains the 22Q2 CCLE "Transcript Per Million" RNAseq gene expression data for protein coding genes. This dataset includes data from 19221 genes, 1406 cell lines, 33 primary diseases and 30 lineages. The columns of ‘TPM‘ are: ‘depmap_id‘, a foreign key corresponding to the cancer cell lineage, ‘cell_line‘ the common CCLE name of the cancer cell lines, ‘gene‘ containing both the HUGO gene name of the knockdown gene along with ensembl ID#, ‘gene_name‘ containing the HUGO gene name and ‘ensembl_id‘ containing only the ensembl ID# and ‘rna_expression‘ which contains the numerical protein coding gene expression change at scale (log2(TPM+1)). This dataset can be loaded into R environment with the ‘depmap_TPM‘ function.

Usage

```
TPM
```

Format

A data frame with 27024726 rows (cell lines) and 6 variables:

depmap_id Cell line foreign key (i.e. "ACH-000956")

cell_line Name of cancer cell line (i.e. "22RV1_PROSTATE")

gene HUGO symbol and Ensembl ID (e.g. TSPAN6 (ENSG00000000003))

gene_name HUGO symbol (e.g. "TSPAN6")

ensembl_id Ensembl ID (e.g. ENSG00000044574)

rna_expression Log fold (log2(TPM+1)) protein expression change

Details

This data originates from the ‘CCLE_expression.csv‘ file taken from the 22Q2 [Broad Institute](https://depmap.org/porta
cancer depenedency study. The derived dataset found in the ‘depmap‘ package features the addition of a foreign key ‘depmap_id‘ found in the first column of this dataset, which was added from the ‘metadata‘ dataset. This dataset has been converted to a long format tibble. Variables names from the original dataset were converted to lower case, put in snake case, and abbreviated where feasible.

Change log

- 19Q1: Initial dataset consisted of a data frame with 67360300 rows (cell lines) and 6 variables representing 57820 genes, 1165 cell lines, 33 primary diseases, 32 lineages.

- 19Q2: removes 1618 genes, adds 36 cell lines, removes one primary disease and adds 1 lineage

- 19Q3: removes 37058 genes, adds 9 cell lines, removes 2 primary diseases. Now a 23164240 by 6 dataframe.

- 19Q4: 0 genes, 39 cancer cell lines, 0 primary diseases and 1 lineage

- 20Q1: adds 31 cell lines

- 20Q2: adds 34 cell lines. ‘expression‘ changed to ‘rna_expression‘

- 20Q3: adds 1 cell line

- 20Q4: removes 38 genes and 71 cell lines, addes 1 primary disease and 3 lineages

- 21Q1: removes 5 genes

- 21Q2: adds 3 cell lines. Additionally, a bug was fixed where the Entrez ID appeared as Ensembl_ID. This was changed for all previous versions of this dataset from 19Q3 to 21Q2

- 21Q3: removes 2 cell lines

- 21Q4: adds 12 cell lines

- 22Q1: adds 4 cell lines and 1 lineage

- 22Q2: adds 44 genes, 13 cell lines and removes 8 lineages

Source

DepMap, Broad Institute: https://depmap.org/portal/download/

References

Tsherniak, A., Vazquez, F., Montgomery, P. G., Weir, B. A., Kryukov, G., Cowley, G. S., ... & Meyers, R. M. (2017). Defining a cancer dependency map. Cell, 170(3), 564-576.

DepMap, Broad (2019): DepMap Achilles 19Q1 Public. https://figshare.com/articles/DepMap_Achilles_19Q1_Public/7
Fileset.

Robin M. Meyers, Jordan G. Bryan, James M. McFarland, Barbara A. Weir, ... David E. Root, William C. Hahn, Aviad Tsherniak. Computational correction of copy number effect improves specificity of CRISPR-Cas9 essentiality screens in cancer cells. Nature Genetics 2017 October 49:1779–1784.

Mahmoud Ghandi, Franklin W. Huang, Judit Jané-Valbuena, Gregory V. Kryukov, ... Todd R. Golub, Levi A. Garraway & William R. Sellers. 2019. Next- generation characterization of the Cancer Cell Line Encyclopedia. Nature 569, 503–508 (2019).

Examples

```
## Not run:
depmap_TPM()

## End(Not run)
```

Index