Package 'hccPIRS'

September 3, 2021

Title Replication stress-related prognostic index in HCC

Version 0.99.1

Description This function calculates replication stress-related prognostic index (PIRS) for HBV-associated HCC patients, and estimates the enrichment of 21 replication stress signatures.

License GPL-3

Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.1

Depends R (>= 4.0.1)

Suggests testthat,
knitr,
rmarkdown

VignetteBuilder knitr

Imports GSVA,
ComplexHeatmap,
circlize,
gplots,
grid

biocViews Classification, CancerData

URL https://github.com/xlucpu/hccPIRS

BugReports https://github.com/xlucpu/hccPIRS/issues

Collate 'hccPIRS.R'
'dataset.R'
'global.R'

R topics documented:

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hccPIRS   *Replication stress-related prognostic index in HCC*

Description

This function calculates replication stress-related prognostic index (PIRS) for HBV-associated HCC patients, and estimates the enrichment of 21 replication stress signatures.

Usage

```
hccPIRS(
  expr = NULL,
  scaleFlag = FALSE,
  centerFlag = FALSE,
  doplot = TRUE,
  fig.path = getwd(),
  fig.name = "heatmap of replication stress",
  enrich = "gsva",
  width = 1,
  height = 4
)
```

Arguments

expr	A numeric expression matrix with row features and sample columns.
scaleFlag	A logic value to indicate if the expression data should be further scaled. FALSE by default.
centerFlag	A logic value to indicate if the expression data should be further centered. TRUE by default.
doplot	A logic value to indicate whether to generate heatmap of replication stress signatures and PIRS score; FALSE by default.
fig.path	A string value to indicate the output path for storing the heatmap.
fig.name	A string value to indicate the name of the heatmap.
enrich	A string value to indicate the method for single-sample enrichment analysis. Allowed values contain c('gsva', 'ssgsea', 'zscore', 'plage'); 'gsva' by default.
width	A numeric value to indicate the relative width for each cell in the heatmap; 1 by default.
height	A numeric value to indicate the relative height for each cell in the heatmap; 4 by default.

Author(s)

Xiaofan Lu

References

Dreyer, SB, Upstill-Goddard, R, Paulus-Hock, V, Paris, C, Lampraki, E-M, Dray, E, et al. (2021). Targeting DNA Damage Response and Replication Stress in Pancreatic Cancer. Gastroenterology 160: 362-377.e313.

Examples

```
library(hccPIRS)
load(system.file("extdata", "tpm.demo.RData", package = "hccPIRS", mustWork = TRUE)) # load example data
res <- hccPIRS(expr = tpm.demo,
               scaleFlag  = FALSE,
               centerFlag = FALSE,
               doplot = TRUE,
               fig.path = getwd(),
               fig.name   = "heatmap of replication stress",
               enrich = "gsva",
               width = 6,
               height = 4)
pirs <- res$pirs # extract normalized PIRS score for each sample
print(pirs)
rsMat <- res$RS.score # extract enrichment score for replication stress signatures
rsMat[1:21, 1:3]
res$hm # show the heatmap
```

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pirs.coeff	*Cox proportional hazards regression results of replication stress-related genes*

Description

A data frame storing feature coefficient for replication stress-related genes.

Usage

```
pirs.coeff
```

Format

A data frame with 9 rows (replication stress related genes) and 8 statistics
contains coefficient to calculate replication stress-related prognostic index.

RS.signature	*Replication stress signatures*

Description

A list storing 21 replication stress signatures.

Usage

```
RS.signature
```

Format

A list for 21 signatures
contains replication stress related genes in a total of 21 signatures for enrichment analysis.

Index