

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

biocViews Classification, CancerData

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

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

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

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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)

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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.

pirs.coeff	<i>Cox proportional hazards regression results of replication stress-related genes</i>
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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	<i>Replication stress signatures</i>
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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.

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