Package 'BCaller'

April 23, 2021

Title Calculate immune-related genes pair index (IRGPI) for bladder cancer

Version 0.99.1

Description This package calculates an IRGPI risk score from a single-sample perspective to statifiy bladder cancer patient prognosis.

Depends R (>= 4.0.1)

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Encoding UTF-8

LazyData true

Suggests testthat,
knitr,
rmarkdown,
kableExtra

VignetteBuilder knitr

RoxygenNote 7.1.1

biocViews Classification, Survival

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

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

Collate 'calIRGPI.R'

R topics documented:

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calIRGPI	*Calculate immune-related genes pair index (IRGPI) for bladder cancer*

Description

This function calculates an IRGPI risk score individually for bladder cancer only.

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Usage

```
calIRGPI(expr = NULL, res.path = getwd())
```

Arguments

expr   A numerical expression matrix or data frame with row for gene symbol name
            and column for sample ID. Note: In principle, the expression profile does not
            need any normalization, but since the amount of gene expression is affected by
            the gene length, the original count or the normalized count data may not be
            suitable for this analysis. It is recommended to provide FPKM or TPM value
            and log transformation is not necessary.

res.path   A string value to indicate the output path for storing the Estimated IRGPI.txt
            file.

Value

A data frame stored sample name and estimated IRGPI.

Author(s)

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References

Prognosis stratification and personalized treatment in bladder cancer through a robust immune gene-
pair based signature

Examples

```
library(BCaller)
load(system.file("extdata", "demo.RData", package = "BCaller", mustWork = TRUE)) # load example data
IRGPI  <- calIRGPI(expr = demo)
head(IRGPI)
```

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