

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 statify bladder cancer patient prognosis.

Depends R (>= 4.0.1)

License GPL-3 + file LICENSE

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:

calIRGPI	1
Index	3

calIRGPI	<i>Calculate immune-related genes pair index (IRGPI) for bladder cancer</i>
----------	---

Description

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

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)

Xiaofan Lu

References

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

Index

calIRGPI, [1](#)