

Package: qPCRhelper (via r-universe)

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Type Package

Title qPCR Ct Values to Expression Values

Version 0.1.0

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Description Computes normalized cycle threshold (Ct) values (delta Ct) from raw quantitative polymerase chain reaction (qPCR) Ct values and conducts test of significance using `t.test()`. Plots expression values based from $\log_2(2^{(-1 \cdot \text{delta Ct})})$ across groups per gene of interest. Methods for calculation of delta Ct and relative expression ($2^{(-1 \cdot \text{delta Ct})}$) values are described in: Livak & Schmittgen, (2001) <[doi:10.1006/meth.2001.1262](https://doi.org/10.1006/meth.2001.1262)>.

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Encoding UTF-8

Imports dplyr (>= 1.0.0), rstatix (>= 0.7.2), ggpubr (>= 0.5.0), ggplot2 (>= 3.4.0), magrittr (>= 2.0.3)

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Repository CRAN

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Contents

qPCRhelper	2
Index	4

qPCRhelper

qPCRhelper

Description

Computes normalized Ct values (delta Ct) from raw qPCR Ct values and conducts test of significance using t.test. Plots expression values based from $\log_2(2^{-1 \cdot \text{delta Ct}})$ across groups per gene of interest.

Usage

```
qPCRhelper(data.dir = NULL, ref.gene = NULL, ref.group = NULL,  
plot.ref.group = NULL, plot.nrow = 1,  
plot.title = NULL)
```

Arguments

<code>data.dir</code>	file path.
<code>ref.gene</code>	string: value should be one of column names in input table. Used for delta Ct computation.
<code>ref.group</code>	string: value should be one of 'Group' values in input table. Used for delta delta Ct computation.
<code>plot.ref.group</code>	string: value should be one of 'Group' values in input table. Used to set reference in plotting.
<code>plot.nrow</code>	numeric: optional. Number of rows for plotting n number of plots corresponding to n number of genes.
<code>plot.title</code>	plot title: optional.

Value

A dataframe with columns for normalized Ct values (dCt), and gene expression ($\log_2\text{RelExp}$).

Note

If gene names start with a number, e.g. 18S, please precede the gene name with 'X' without space, e.g.: 18S -> X18S

Author(s)

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Examples

```
## Create sample table with expected 'Sample', 'Group', and gene Ct columns
Sample <- c("C1", "C2", "T1", "T2") #required column
Group <- c("C", "C", "T", "T") #required column
# Gene Ct values, at least two columns: one reporter, one target gene
GAPDH <- c(18.1,18.2,18.1,18.2) #reporter, ref.gene
IL4 <- c(30.1,30.5,20.1,20.2) #target
a <- data.frame(Sample,Group,GAPDH,IL4) #export using write.table(a,...)

## Write the data frame to a file in a temporary directory
temp_file <- file.path(tempdir(), "a.txt")
write.table(a, file = temp_file, sep = "\t")

## Run qPCRhelper directly on the file
library(qPCRhelper)
b <- qPCRhelper(data.dir=temp_file,
                ref.gene="GAPDH",
                ref.group="C",
                plot.ref.group="C",
                plot.nrow=1,
                plot.title="My cool qPCR data")
```

Index

qPCRhelper, 2