

Package ‘OryzaProbe’

January 20, 2025

Type Package

Title Rice Microarray Probe ID Conversion, from Probe ID to RAP-DB ID

Version 0.1.0

Description

Microarray probe ID is not convenient for further enrichment analysis and target gene selection. The package is created for the rice microarray probe ID conversion.

This package can convert microarray probe ID from GPL6864 <<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL6864>>, GPL8852 <<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL8852>>, and GPL2025 <<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL2025>> platforms to RAP-DB ID. RAP-DB ``The Rice Annotation Project Database" <<https://rapdb.dna.affrc.go.jp>> is a well-known database for rice *Oryza sativa*, and the gene ID in this database is widely used in many areas related to rice research.

For multiple probes representing a single gene, This package can merge them by taking the mean, max, or min value of these probes.

Or we can keep multiple probes by appending sequence numbers to duplicate the RAP-DB ID.

License GPL-3

Encoding UTF-8

Imports stats

Depends R (>= 2.10)

RoxygenNote 7.2.1

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

Config/testthat/edition 3

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

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Description

Convert rice microarray probe ID to RAP-DB ID and merge multiple probes for one gene

Usage

```
probeConvert(exprMatrix, probeMerge = FALSE, mergeBy = "mean")
```

Arguments

exprMatrix	A expression matrix is required. Row names of the matrix should be the microarray probe ID.
probeMerge	A instruction is needed. If probeMerge = F, the multiple probes for one gene will not be merged. If probeMerge = T, the multiple probes for one gene will be merged. The default value is F.
mergeBy	A method for merging multiple probes for one gene if probeMerge = T. Mean, max and min value is available.

Value

A matrix.

Examples

```
expr <- system.file("test_file", header = TRUE, sep="\t", header=TRUE, stringsAsFactors = FALSE)
formatted_expr <- probeConvert(exprMatrix = expr)
formatted_expr1 <- probeConvert(exprMatrix = expr, probeMerge = TRUE)
```

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