

Package ‘yriMulti’

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Title support for expression, methylation, DHS for YRI

Version 0.0.9

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Description expression, methylation, DHS for YRI

Suggests erma, BiocStyle, knitr, rmarkdown

Depends gQTLBase, SummarizedExperiment, GenomicRanges, Homo.sapiens,
dsQTL, geuvPack

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LazyLoad yes

VignetteBuilder knitr

NeedsCompilation no

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mexGR *combine expression data for a gene with nearby methylation data*

Description

combine expression data for a gene with nearby methylation data,

Usage

```
mexGR(methSE, exprSE, gradius = 0, symbol = "ORMDL3", etagname = "gene_name")
```

Arguments

methSE
exprSE
gradius
symbol
etaname

Value

GRanges instance with assay results in mcols

Examples

```
data(geuFPKM)  
data(banovichSE)  
m1 = mexGR(banovichSE, geuFPKM, gradius=5000)  
ii = bindelms(geuFPKM, banovichSE)
```

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*Topic **models**
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