erccdashboard Package Vignette

1 201

[illegible]

[illegible]

- [illegible]
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$m m n m m n$

m

m

[illegible]

```
> data(SEQC.Example)
```

[illegible]

- [illegible]
- [illegible]
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[illegible]

- [illegible]
- [illegible]

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```
> datType = "count" # "count" for RNA-Seq data, "array" for microarray data
> isNorm = FALSE # flag to indicate if input expression measures are already
>                     # normalized, default is FALSE
> exTable = MET.CTL.countDat # the expression measure table
> filenameRoot = "RatTox" # user defined filename prefix for results files
> sample1Name = "MET" # name for sample 1 in the experiment
> sample2Name = "CTL" # name for sample 2 in the experiment
> erccmix = "RatioPair" # name of ERCC mixture design, "RatioPair" is default
> erccdilution = 1/100 # dilution factor used for Ambion spike-in mixtures
> spikeVol = 1 # volume (in microliters) of diluted spike-in mixture added to
>                   #    total RNA mass
> totalRNAmass = 0.500 # mass (in micrograms) of total RNA
> choseFDR = 0.05 # user defined false discovery rate (FDR), default is 0.05
```

[illegible]

```
> head(MET.CTL.countDat)
            Feature MET_1 MET_2 MET_3 CTL_1 CTL_2 CTL_3
16499 ERCC-00002 16629 18798 26568 36600 45436 25163
16500 ERCC-00003  1347  1565  1983  3048  3447  2195
16501 ERCC-00004  4569  5570  6755  1240  1484   902
16502 ERCC-00009   811   869  1123   909  1073   537
16503 ERCC-00012     0     0     0     0     0     0
16504 ERCC-00013     3     1     2     1     5     1
```

[illegible]

```
[1] "Analyzing Gene # 2"
[1] "Analyzing Gene # 10"
[1] "Analyzing Gene # 2"
[1] "Analyzing Gene # 10"
Note: 'test.mat ' not provided. Comparing each model
from 'design.list  ' to first model in   'design.list  ', which must be the full model
[1] "Spline scaling factor: 0.933720469163937"
[1] "Finished DE testing"
[1] "Spline scaling factor: 0.933720469163937"

Finished examining dispersions

Threshold P-value
0.00775934

Generating ROC curve and AUC statistics...

Area Under the Curve (AUC) Results:
 Ratio   AUC Detected Spiked
   4:1 1.000       16     23
 1:1.5 0.950       16     23
   1:2 0.971       16     23

Estimating ERCC LODR
.............................................
 Ratio LODR Estimate 90% CI Lower Bound 90% CI Upper Bound
   4:1            26                 19                 32
 1:1.5           Inf               <NA>               <NA>
   1:2           270                140                390

LODR estimates are available to code ratio-abundance plot

Saving main dashboard plots to pdf file...

Saving exDat list to .RData file...
Analysis completed.
```

[illegible]
[illegible]
[illegible]

```
> summary(exDat)
            Length Class      Mode
sampleInfo  11     -none-     list
plotInfo     9     -none-     list
erccInfo     4     -none-     list
Transcripts  7     data.frame list
designMat    3     data.frame list
sampleNames  2     -none-     character
```