# Package 'HighlyReplicatedRNASeq'

December 10, 2024

Type Package

```
Title Collection of Bulk RNA-Seq Experiments With Many Replicates
Version 1.19.0
Description Gene-level count matrix data for bulk RNA-seq dataset with
     many replicates. The data are provided as easy to use SummarizedExperiment
     objects. The source data that is made accessible through this package comes
     from https://github.com/bartongroup/profDGE48.
URL https://github.com/const-ae/HighlyReplicatedRNASeq
BugReports https://github.com/const-ae/HighlyReplicatedRNASeq/issues
License MIT + file LICENSE
Encoding UTF-8
Depends SummarizedExperiment, ExperimentHub
Imports S4Vectors
Suggests BiocStyle, BiocFileCache, knitr, rmarkdown
biocViews ExperimentHub, ExperimentData, ExpressionData,
     SequencingData, RNASeqData
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Roxygen list(markdown = TRUE)
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HighlyReplicatedRNASeq

HighlyReplicatedRNASeq: Collection of Bulk RNA-Seq Experiments With Many Replicates

#### Description

The HighlyReplicatedRNASeq package provides access to the count matrix results from studies with many replicates. These datasets can be valuable for benchmarking tools designed to handle RNA-seq data.

#### **Details**

Available datasets:

- Schurch et al. (2016): 86 samples of S. cerevisiae in two conditions
  - Schurch16() / Schurch16\_metadata()

At the moment, this package contains only one dataset, but more datasets can be added in the future.

Schurch16

Get the RNA-seq counts from Schurch et al. (2016)

## Description

The data contains bulk RNA-seq count on 86 samples in two conditions. The first condition is wild type S. *cerevisiae* (taxonomic id: 1247190). The second condition is the same strain with a snf2 knockout.

### Usage

```
Schurch16(hub = ExperimentHub())
Schurch16_metadata(hub = ExperimentHub())
```

#### **Arguments**

hub

an ExperimentHub object that is used to load the resource "EH3315" and "EH3316". Default: ExperimentHub()

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#### **Details**

Schurch et al. originally generated this dataset to benchmark RNA-seq differential expression tools and find out how many replicates are necessary to detect most differentially expressed genes. The data that is returned by this packge comes from the GitHub repository that accompanied the study.

#### Value

Schurch16() returns a SummarizedExperiment with 7126 genes and 86 samples.

Schurch16\_metadata() returns a ExperimentHub object with the metadata on the Schurch16 dataset.

#### Author(s)

Constantin Ahlmann-Eltze

#### References

Schurch, N. J., Schofield, P., Gierliński, M., Cole, C., Sherstnev, A., Singh, V., ... Barton, G. J. (2016). How many biological replicates are needed in an RNA-seq experiment and which differential expression tool should you use? *RNA*, 22(6), 839–851. https://doi.org/10.1261/rna.053959.115

# Examples

```
Schurch16_metadata()
se <- Schurch16()
dim(se)
colData(se)
summary(c(assay(se, "counts")))</pre>
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