

# Package ‘HighlyReplicatedRNASeq’

October 12, 2020

**Type** Package

**Title** Collection of Bulk RNA-Seq Experiments With Many Replicates

**Version** 1.0.0

**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

**RoxygenNote** 7.1.0

**Roxygen** list(markdown = TRUE)

**VignetteBuilder** knitr

**git\_url** <https://git.bioconductor.org/packages/HighlyReplicatedRNASeq>

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**Author** Constantin Ahlmann-Eltze [aut, cre]  
(<<https://orcid.org/0000-0002-3762-068X>>)

**Maintainer** Constantin Ahlmann-Eltze <[artjom31415@gmail.com](mailto:artjom31415@gmail.com)>

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HighlyReplicatedRNASeq

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

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### 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.

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Schurch16

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

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### 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\(\)](#)

### 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 package 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")))
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