

# Package ‘yeastNagalakshmi’

October 16, 2018

**Type** Package

**Title** Yeast genome RNA sequencing data based on Nagalakshmi et. al.

**Version** 1.16.0

**Author** Martin Morgan <mtmorgan@fhcrc.org>

**Maintainer** Bioconductor Package Maintainer <maintainer@bioconductor.org>

**Description** The yeast genome data was retrieved from the sequence read archive, aligned with bwa, and converted to BAM format with samtools.

**biocViews** ExperimentData, Genome, Saccharomyces\_cerevisiae\_Data, SequencingData, BiocViews, ChIPSeqData

**License** Artistic-2.0

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

**git\_branch** RELEASE\_3\_7

**git\_last\_commit** 96c8c6c

**git\_last\_commit\_date** 2018-04-30

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yeastNagalakshmi-package

*Yeast genome RNA sequencing data based on Nagalakshmi et. al.*

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## Description

The yeast genome data was retrieved from the sequence read archive, aligned with bwa, and converted to BAM format with samtools.

**Details**

Package: yeastNagalakshmi  
Type: Package  
Version: 0.99.0  
biocViews: ExperimentData, yeast  
License: Artistic-2.0

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The package contains three files in extdata sub-directory. Two of them are pertained to RNA sequencing data in BAM format, and one is a TranscriptDb object of yeast from transcript annotations available at the UCSC Genome Browser.

**Author(s)**

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Maintainer: Biocore Team c/o BioC user list <bioconductor@stat.math.ethz.ch>

**References**

Nagalakshmi et. al., *The transcriptional landscape of the yeast genome defined by RNA sequencing*, Science, 320:1344:1349, June 2008.

**Examples**

```
y <- system.file("extdata", package="yeastNagalakshmi")  
dir(y)
```

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\*Topic **package**

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