

# Package ‘yeastNagalakshmi’

June 23, 2022

**Type** Package

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

**Version** 1.33.0

**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** master

**git\_last\_commit** c1a3074

**git\_last\_commit\_date** 2022-04-26

**Date/Publication** 2022-06-23

## R topics documented:

yeastNagalakshmi-package . . . . . 1

**Index** . . . . . 4

---

yeastNagalakshmi-package

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

---

## 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

**Index:**

yeastNagalakshmi-package

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)**

Martin Morgan <mtmorgan@fhcrc.org>

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)
```

# Index

\* **package**

[yeastNagalakshmi-package, 1](#)

yeastNagalakshmi

[\(yeastNagalakshmi-package\), 1](#)

[yeastNagalakshmi-package, 1](#)