

# Package ‘yeastNagalakshmi’

July 2, 2024

**Type** Package

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

**Version** 1.40.0

**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\_19

**git\_last\_commit** d6bf00c

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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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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)

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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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\* **package**

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