

Package ‘yeastNagalakshmi’

November 30, 2023

Type Package

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

Version 1.38.0

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_18

git_last_commit 1687f8e

git_last_commit_date 2023-10-24

Repository Bioconductor 3.18

Date/Publication 2023-11-30

R topics documented:

yeastNagalakshmi-package 2

Index 3

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, 2](#)

yeastNagalakshmi

[\(yeastNagalakshmi-package\), 2](#)

[yeastNagalakshmi-package, 2](#)