Package 'yeastNagalakshmi'

April 20, 2016

Type Package

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

Version 1.6.0

Author Martin Morgan <mtmorgan@fhcrc.org>

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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.

biocViews ExperimentData, Genome, Saccharomyces_cerevisiae_Data, SequencingData, BiocViews, ChIPSeqData

License Artistic-2.0

NeedsCompilation no

R topics documented:

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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.

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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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