Package 'fission'

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Title RangedSummarizedExperiment for time course RNA-Seq of fission yeast in response to stress, by Leong et al., Nat Commun 2014.

Version 1.32.0

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Description This package provides a RangedSummarizedExperiment object of read counts in genes for a time course RNA-Seq experiment of fission yeast (Schizosaccharomyces pombe) in response to oxidative stress (1M sorbitol treatment) at 0, 15, 30, 60, 120 and 180 mins. The samples are further divided between a wild-type group and a group with deletion of atf21. The read count matrix was prepared and provided by the author of the study: Leong HS, Dawson K, Wirth C, Li Y, Connolly Y, Smith DL, Wilkinson CR, Miller CJ. ``A global non-coding RNA system modulates fission yeast protein levels in response to stress". Nat Commun 2014 May 23;5:3947. PMID: 24853205. GEO: GSE56761.

biocViews ExperimentData, Genome, Saccharomyces_cerevisiae_Data, SequencingData, RNASeqData, GEO

License LGPL

Depends R (>= 2.10), SummarizedExperiment

Suggests knitr, markdown

VignetteBuilder knitr

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`fission` *Fission yeast time course*

Description

Read counts per gene for fission yeast time course RNA-Seq experiment

Usage

```
data("fission")
```

Format

RangedSummarizedExperiment

Details

From the GEO series:

Global transcription profiles of fission yeast wild type (WT) and atf21del strains over an osmotic stress time course following treatment with 1M sorbitol at 0, 15, 30, 60, 120 and 180 mins. Strand-specific single end sequencing of total RNA was performed in biological triplicates on the Applied Biosystems SOLiD 5500xl Genetic Analyzer System.

Sequencing reads were aligned to the fission yeast genome (PomBase database release 11) using SHRiMP2 aligner with default parameters. Total number of reads that can be aligned to the genome at exactly one locus per sample range from 7.5 to 20.1 millions. These uniquely mapped reads were used to identify stretches of unambiguous transcription. Reads that aligned to more than one locus (generally paralogous regions in the genome) were discarded. Adjacent unambiguous transcription regions with minimum peak height of two and located within 50 bases of each other were merged to yield an extensive transcription map of S. pombe. These regions were then positioned relative to known annotation and labelled according to the gene(s) they overlapped with using the Bioconductor package annmap.

Source

Read count matrix prepared and provided by authors of the study

References

Leong HS, Dawson K, Wirth C, Li Y, Connolly Y, Smith DL, Wilkinson CR, Miller CJ. 'A global non-coding RNA system modulates fission yeast protein levels in response to stress'. Nat Commun 2014. PMID: 24853205. GEO: GSE56761.

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