

Package ‘EatonEtAlChIPseq’

March 13, 2025

Title ChIP-seq data of ORC-binding sites in Yeast excerpted from Eaton et al. 2010

Description ChIP-seq analysis subset from ``Conserved nucleosome positioning defines replication origins" (PMID 20351051)

Version 0.44.0

Author Patrick Aboyoun <paboyoun@fhcrc.org>

Maintainer Patrick Aboyoun <paboyoun@fhcrc.org>

Depends GenomicRanges (>= 1.5.42), ShortRead, rtracklayer

License Artistic 2.0

biocViews ExperimentData, Saccharomyces_cerevisiae_Data, SequencingData, ChIPSeqData, GEO

git_url <https://git.bioconductor.org/packages/EatonEtAlChIPseq>

git_branch RELEASE_3_20

git_last_commit 04defe9

git_last_commit_date 2024-10-29

Repository Bioconductor 3.20

Date/Publication 2025-03-13

Contents

orcAligns	1
orcPeaks	2

Index	4
--------------	----------

orcAligns	<i>Alignments of ChIP-seq data to yeast chromosome XIV</i>
-----------	--

Description

MAQ alignments to yeast chromosome XIV of ChIP-seq data of ORC-binding sites in yeast from Eaton et al. 2010

Usage

```
data(orcAlignsRep1)
data(orcAlignsRep2)
```

Details

This is the subset of alignments from two ChIP-seq replicates of origin recognition complex (ORC) binding to chromosome XIV of *Saccharomyces cerevisiae*. The alignments were created using MAQ (Li et al. 2008) alignment software with a maximum mismatch of 3 bases and a minimum Phred quality score of 35.

Source

MAQ alignments extracted from ftp://ftp.ncbi.nih.gov/pub/geo/DATA/supplementary/samples/GSM424nnn/GSM424494/GSM424494_wt_G2_orc_chip_rep1.mapview.txt.gz and ftp://ftp.ncbi.nih.gov/pub/geo/DATA/supplementary/samples/GSM424nnn/GSM424494/GSM424494_wt_G2_orc_chip_rep2.mapview.txt.gz

References

Conserved nucleosome positioning defines replication origins. Eaton ML, Galani K, Kang S, Bell SP, MacAlpine DM. *Genes Dev.* 2010 Apr 15;24(8):748-53.

Examples

```
data(orcAlignsRep1)
data(orcAlignsRep2)

orcAlignsRep1
orcAlignsRep2
```

orcPeaks

Peaks from ChIP-seq alignments to yeast chromosome XIV

Description

Peaks on yeast chromosome XIV of ChIP-seq data of ORC-binding sites in yeast from Eaton et al. 2010

Usage

```
data(orcPeaksRep1)
data(orcPeaksRep2)
```

Details

This is the subset of *Saccharomyces cerevisiae* chromosome XIV peaks from two ChIP-seq replicates of a origin recognition complex (ORC) binding experiment.

Source

ChIP-seq peaks extracted from ftp://ftp.ncbi.nih.gov/pub/geo/DATA/supplementary/samples/GSM424nnn/GSM424494/GSM424494_wt_G2_orc_chip_rep1.bed.gz and ftp://ftp.ncbi.nih.gov/pub/geo/DATA/supplementary/samples/GSM424nnn/GSM424494/GSM424494_wt_G2_orc_chip_rep2.bed.gz

References

Conserved nucleosome positioning defines replication origins. Eaton ML, Galani K, Kang S, Bell SP, MacAlpine DM. *Genes Dev.* 2010 Apr 15;24(8):748-53.

Examples

```
data(orcPeaksRep1)
data(orcPeaksRep2)
```

Index

* datasets

orcAligns, [1](#)

orcPeaks, [2](#)

orcAligns, [1](#)

orcAlignsRep1 (orcAligns), [1](#)

orcAlignsRep2 (orcAligns), [1](#)

orcPeaks, [2](#)

orcPeaksRep1 (orcPeaks), [2](#)

orcPeaksRep2 (orcPeaks), [2](#)