Package 'EatonEtAlChIPseq'

November 10, 2026

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 0.50.0

Author Patrick Aboyoun <paboyoun@fhcrc.org>

Maintainer Patrick Aboyoun <paboyoun@fhcrc.org>

Depends GenomicRanges (>= 1.5.42), ShortRead, rtracklayer

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biocViews ExperimentData, Saccharomyces_cerevisiae_Data, SequencingData, ChIPSeqData, GEO

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

git_branch RELEASE_3_23

git_last_commit 87df82d

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-10

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orcAligns *Alignments of ChIP-seq data to yeast chromosome XIV*

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)
```

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