

Package ‘EatonEtAlChIPseq’

August 14, 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 0.46.0

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_21

git_last_commit 01a07b9

git_last_commit_date 2025-04-15

Repository Bioconductor 3.21

Date/Publication 2025-08-14

Contents

orcAligns	2
orcPeaks	3
Index	4

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)
```

Index

* **datasets**

orcAligns, [2](#)

orcPeaks, [3](#)

orcAligns, [2](#)

orcAlignsRep1 (orcAligns), [2](#)

orcAlignsRep2 (orcAligns), [2](#)

orcPeaks, [3](#)

orcPeaksRep1 (orcPeaks), [3](#)

orcPeaksRep2 (orcPeaks), [3](#)