

Package ‘EatonEtAlChIPseq’

October 8, 2016

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 0.10.0

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Depends GenomicRanges (>= 1.5.42), ShortRead, rtracklayer

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biocViews ExperimentData, Saccharomyces_cerevisiae_Data, SequencingData, ChIPSeqData, GEO

NeedsCompilation no

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