EatonEtAlChIPseq

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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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