

# Package ‘EatonEtAlChIPseq’

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**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** 0.22.0

**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>

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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](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](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
```

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 orcPeaks

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*Peaks from ChIP-seq alignments to yeast chromosome XIV*


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**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](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](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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