

# Package ‘ChIPexoQualExample’

May 9, 2024

**Type** Package

**Title** Example data for the ChIPexoQual package, which implements a quality control pipeline for ChIP-exo data

**Version** 1.28.0

**Depends** R (>= 3.3)

**Date** 2016-07-18

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**Description** Data for the ChIPexoQual package, consisting of (3) chromosome 1 aligned reads from a ChIP-exo experiment for FoxA1 in mouse liver cell lines aligned to the mm9 genome.

**License** GPL (>= 2)

**URL** <http://www.github.com/keleslab/ChIPexoQualExample>

**LazyLoad** yes

**VignetteBuilder** knitr

**Suggests** BiocStyle, knitr, rmarkdown

**Encoding** UTF-8

**biocViews** ExperimentData, Genome

**NeedsCompilation** no

**RoxygenNote** 7.1.1

**git\_url** <https://git.bioconductor.org/packages/ChIPexoQualExample>

**git\_branch** RELEASE\_3\_19

**git\_last\_commit** 1ea14b9

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.19

**Date/Publication** 2024-05-09

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|---------|----------------------------------|
| extdata | <i>FoxA1 ChIP-exo experiment</i> |
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### Description

bam file with the reads aligned to chr1 from FoxA1 in mm9 liver cell lines published by Serandour et al., 2013. This package contains the files

### Format

bam files (with their respective indexes)

### Details

- ChIPexo\_carroll\_FoxA1\_mouse\_rep1\_chr1.bam
- ChIPexo\_carroll\_FoxA1\_mouse\_rep2\_chr1.bam
- ChIPexo\_carroll\_FoxA1\_mouse\_rep3\_chr1.bam

and their respective index files.

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