

# Package ‘ChIPexoQualExample’

November 14, 2024

**Type** Package

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

**Version** 1.30.0

**Depends** R (>= 3.3)

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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\_20

**git\_last\_commit** 4b8f5c9

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.20

**Date/Publication** 2024-11-14

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extdata

*FoxA1 ChIP-exo experiment*

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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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