

# Package ‘ChIPexoQualExample’

December 2, 2025

**Type** Package

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

**Version** 1.35.0

**Depends** R (>= 3.3)

**Date** 2016-07-18

**Author** Rene Welch, Dongjun Chung, Sunduz Keles

**Maintainer** Rene Welch <welch@stat.wisc.edu>

**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** devel

**git\_last\_commit** b44ccfd

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.23

**Date/Publication** 2025-12-02

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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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