Package 'MMDiffBamSubset'

November 10, 2026

Type Package

Title Example ChIP-Seq data for the MMDiff package

Version 1.49.1

Date 2016-10-12

Author Gabriele Schweikert

Maintainer Gabriele Schweikert <G.Schweikert@ed.ac.uk>

Description Subset of BAM files, including WT_2.bam, Null_2.bam, Resc_2.bam, Input.bam from the ``Cfp1" experiment (see Clouaire et al., Genes Dev. 2012). Data is available under ArrayExpress accession numbers E-ERAD-79.
Additionally, corresponding subset of peaks called by MACS

biocViews ExperimentData, Genome, StemCell, Mus_musculus_Data, DNASeqData, ChIPSeqData, ArrayExpress

Suggests MMDiff2

License LGPL

PackageStatus Deprecated

git_url https://git.bioconductor.org/packages/MMDiffBamSubset

git_branch devel

git_last_commit 87648ae

git_last_commit_date 2026-09-14

Repository Bioconductor 3.24

Date/Publication 2026-11-10

Contents

MMDiffBamSubset-package 2

Index 4

`MMDiffBamSubset-package`

Utilities returning the paths to the sample sheet Cfp1.csv, to the BAM files WT_2.bam, Null_2.bam, Resc_2.bam and Input.bam, as well as corresponding peak files WT_2_Macs_peaks.xls, Null_2_Macs_peaks.xls Resc_2_Macs_peaks.xls

Description

Cfp1.csv Sample Sheet containing meta information about the experiment.

BAM files each containing subsets of original files with reads mapping to region ch1:3000000...75000000. The data is available as part of ArrayExpress Experiment E-ERAD-79, which contains ChIP-Seq of mice cells to assess the link between histone modification states of H3K4me3 with respect to the mediator proteins Cfp1.

WT_2.bam: organism: Mus musculus; Cell type: ES cells, Immunoprecipitate: H3K4me3

Null_2.bam: organism: Mus musculus; Cell type: Cfp1 -/- ES cells, Immunoprecipitate: H3K4me3

Resc_2.bam: organism: Mus musculus; Cell type: Cfp1-/- ES cells and wtCfp1 rescue cDNA, Immunoprecipitate: H3K4me3

Input.bam: organism: Mus musculus; input_DNA (pooled from different cell types)

`WT.AB2`, `Null.AB2`, `Resc.AB2` and `Input` return the path to those files.

Additionally, subsets of peaks called by MACS[2] are provided.

`WT.AB2.Peaks`, `Null.AB2.Peaks` and `Resc.AB2.Peaks` return the path to the respective peak files.

Usage

```
Cfp1.Exp()
WT.AB2()
Null.AB2()
Resc.AB2()
Input()
WT.AB2.Peaks()
Null.AB2.Peaks()
Resc.AB2.Peaks()
```

Details

See the MMDiff package or [1] for details about the experiment (ChIP-seq, H3K4me3, Mus musculus). BAM files contain single-end reads aligned to reference genome *NBCI37/mm9*

References

[1] Clouaire T et al. (2012). Cfp1 integrates both CpG content and gene activity for accurate H3K4me3 deposition in embryonic stem cells. Genes Dev. August 1, 2012 26: 1714–1728

[2] Zhang Y et al. (20078). Model-based analysis of ChIP-Seq (MACS). Genome Biol 2008, 9(9):R137.

Examples

```
Cfp1.Exp()
WT.AB2()
Null.AB2()
Resc.AB2()
Input()
WT.AB2.Peaks()
Null.AB2.Peaks()
Resc.AB2.Peaks()
```

Index

∗ **utilities**
MMDiffBamSubset-package, 2

Cfp1.Exp *(*MMDiffBamSubset-package*)*, 2

Input *(*MMDiffBamSubset-package*)*, 2

MMDiffBamSubset
*(*MMDiffBamSubset-package*)*, 2
MMDiffBamSubset-package, 2

Null.AB2 *(*MMDiffBamSubset-package*)*, 2

Resc.AB2 *(*MMDiffBamSubset-package*)*, 2

WT.AB2 *(*MMDiffBamSubset-package*)*, 2