

Package ‘MMDiffBamSubset’

November 30, 2023

Type Package

Title Example ChIP-Seq data for the MMDiff package

Version 1.39.0

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

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

git_branch devel

git_last_commit f2f881e

git_last_commit_date 2023-10-24

Repository Bioconductor 3.19

Date/Publication 2023-11-30

Table of 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 *NBC137/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. (2007). 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](#)