

# Package ‘MMDiffBamSubset’

May 30, 2024

**Type** Package

**Title** Example ChIP-Seq data for the MMDiff package

**Version** 1.40.0

**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** RELEASE\_3\_19

**git\_last\_commit** 17d7b82

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

**Repository** Bioconductor 3.19

**Date/Publication** 2024-05-30

## Contents

MMDiffBamSubset-package . . . . .	2
<b>Index</b>	<b>4</b>

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](#)