# Package 'MMDiffBamSubset'

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**Type** Package

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

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**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

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`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()
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