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

NeedsCompilation no

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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

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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)

Additionally, subsets of peaks called by MACS[2] are provided.
WT.Ab2, Null.Ab2, Resc.Ab2 and Input return the path to those 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 NCBI37/mm9

References


Examples

Cfp1.Exp()
WT.Ab2()
Null.Ab2()
Resc.Ab2()
Input()
WT.Ab2.Peaks()
Null.Ab2.Peaks()
Resc.Ab2.Peaks()
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