Package ‘RNASeqDataSubset’

March 25, 2013

Title Subset of BAM files from the ‘‘TBX20’’ experiment

Description Dual transcriptional activator and repressor roles of TBX20 regulate adult cardiac structure and function. A subset of the RNA-Seq data.

Version 0.99.1

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Depends Rsamtools (>= 1.9.8)

Imports xtable

Collate getBamFileList.R

biocViews ExperimentData, RNAseqData

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`RNASeqDataSubset-package`

Utilities returning the paths to BAM files of the data package

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Description

The package contains 6 subset of BAM files from the TBX20 RNA-Seq experiment.

Details

The TBX20 data set basically provides ChIP-Seq and RNA-Seq data. In here only the RNA-Seq part of the data is utilized. TBX20 (T-box 20) is a transcriptional regulator essential for cardiac development and maintenance of mouse heart tissue. In this study TXB20 was knocked out by using a Tamoxifen mediated conditional knock-out system. Transcriptional changes caused by the ablation of the second exon of TBX20 result in rapid onset of heart failures and the subsequent death of the mice. TBX20 knock-out adult heart tissue was compared to wild type adult heart tissue. The associated RNA-Seq raw data can be retrieved by the following code chunk.

References

Noboru J. Sakabe, Ivy Aneas, Tao Shen, Leila Shokri, Soo-Young Park, Martha L. Bulyk, Sylvia M. Evans and Marcelo A. Nobrega Human Molecular Genetics Date: Feb 2012 *Dual transcriptional activator and repressor roles of TBX20 regulateadult cardiac structure and function*

Examples

```
bfs <- getBamFileList()
```

`getBamFileList` *Retrieving file paths pointing to the BAM files.*

Description

Retrieves the file paths for accessing the data of the `RNASeqDataSubset` package.

Usage

```
getBamFileList(...)
```

Arguments

`...`	Arguments to be passed to or from methods.

Details

Accessory function to the BAM files of the `RNASeqDataSubset` package.

Value

Returns a named character vector pointing to the BAM files included in `RNASeqDataSubset` package.

Author(s)

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See Also

`RNASeqDataSubset`

Examples

```
bfl <- getBamFileList()
bfl
```

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