

# Package ‘TBX20BamSubset’

June 27, 2024

**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** 1.40.0

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**Depends** Rsamtools (>= 1.9.8)

**Imports** xtable

**Collate** getBamFileList.R

**biocViews** ExperimentData, SequencingData, RNASeqData

**License** LGPL

**git\_url** <https://git.bioconductor.org/packages/TBX20BamSubset>

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TBX20BamSubset-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 regulate adult cardiac structure and function*

## Examples

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

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getBamFileList

*Retrieving file paths pointing to the BAM files.*

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## Description

Retrieves the file paths for accessing the data of the TBX20BamSubset package.

## Usage

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

## Arguments

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

## Details

Accessory function to the BAM files of the TBX20BamSubset package.

**Value**

Returns a named character vector pointing to the BAM files included in TBX20BamSubset package.

**Author(s)**

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**See Also**

[TBX20BamSubset](#)

**Examples**

```
bf1 <- getBamFileList()  
bf1
```

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