Package 'LungCancerLines'

October 7, 2021

Type Package

Title Reads from Two Lung Cancer Cell Lines

Version 0.30.0

Author Cory Barr, Michael Lawrence

Maintainer Cory Barr <barr.cory@gene.com>

Imports Rsamtools

Description Reads from an RNA-seq experiment between two lung cancer
cell lines: H1993 (met) and H2073 (primary).
The reads are stored as Fastq files and are meant for use with
the TP53Genome object in the gmapR package.

License Artistic-2.0

biocViews ExperimentData, Genome, CancerData, LungCancerData,
RNASeqData

git_url https://git.bioconductor.org/packages/LungCancerLines

git_branch RELEASE_3_13

git_last_commit 76a4666

git_last_commit_date 2021-05-19

Date/Publication 2021-10-07

R topics documented:

TP53Genome-package   *Genomic Sequence of the TP53 Gene Plus a 1-Megabase Region on Each Side of the Gene*

Description

This package was created to use in examples and test sets for the gmapR and VariationTools packages.

1

Details

Package:	TP53Genome
Type:	Package
Version:	1.0
Date:	2012-09-05
License:	Artistic-2.0

By calling data(p53Genome), users will have access to a GmapGenome object for the TP53 genome.

Author(s)

Cory Barr

Maintainer: Cory Barr <barr.cory@gene.com>

Examples

```
data(p53Genome)
```

LungCancerBamFiles   *Get the BAM paths*

Description

Gets a `BamFileList` pointing to BAM files containing read alignments for the H1993 and H2073 RNA-seq samples. The files are the "analyzed" BAM files as output by the `HTSeqGenie` package.

Usage

```
LungCancerBamFiles()
```

Details

The reads were aligned to genome TP53Genome, using the following parameters:

- `splicing`: knownGene
- `novelsplicing`: 1
- `indel_penalty`: 1
- `distant_splice_penalty`: 1
- `suboptimal_levels`: 2
- `npaths`: 10

Note that the BAM files contain only unique alignments.

Value

A `BamFileList` pointing to two BAM files, one for H1993, one for H2073.

Author(s)

Michael Lawrence

Examples

```
LungCancerBamFiles()
```

LungCancerFastqFiles   *Get the Fastq paths*

Description

Returns a character vector of file paths to the demo Fastq files.

Usage

```
LungCancerFastqFiles()
```

Value

A character vector, named according to "H[1993/2073].[first/last]".

Author(s)

Michael Lawrence

Examples

```
LungCancerFastqFiles()
```

Index