Package ‘LungCancerLines’

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Type Package

Title Reads from Two Lung Cancer Cell Lines

Version 0.49.0

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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.

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biocViews ExperimentData, Genome, CancerData, LungCancerData, RNASeqData

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Contents

`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.

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()
```

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