

Package ‘LungCancerLines’

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Type Package
Title Reads from Two Lung Cancer Cell Lines
Version 0.46.0
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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.
License Artistic-2.0
biocViews ExperimentData, Genome, CancerData, LungCancerData, RNASeqData
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TP53Genome-package	<i>Genomic Sequence of the TP53 Gene Plus a 1-Megabase Region on Each Side of the Gene</i>
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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

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Examples

```
data(p53Genome)
```

LungCancerBamFiles	<i>Get the BAM paths</i>
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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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