

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.

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> |
|--------------------|--|

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
- novel_splicing: 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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