

Package ‘LungCancerLines’

November 21, 2024

Type Package

Title Reads from Two Lung Cancer Cell Lines

Version 0.45.0

Author Cory Barr, Michael Lawrence

Maintainer Michael Lawrence <michafla@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 devel

git_last_commit b631993

git_last_commit_date 2024-10-29

Repository Bioconductor 3.21

Date/Publication 2024-11-21

Contents

TP53Genome-package	2
LungCancerBamFiles	2
LungCancerFastqFiles	3

Index	4
--------------	----------

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()
```

Index

LungCancerBamFiles, [2](#)

LungCancerFastqFiles, [3](#)

TP53Genome, [3](#)

TP53Genome (TP53Genome-package), [2](#)

TP53Genome-package, [2](#)