Package ‘LungCancerLines’
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Type Package
Title Reads from Two Lung Cancer Cell Lines
Version 0.12.0
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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
NeedsCompilation no

R topics documented:

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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

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

Author(s)

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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.
LungCancerFastqFiles

Author(s)
Michael Lawrence

Examples
LungCancerBamFiles()

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
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