Package ‘LungCancerLines’

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Type Package
Title Reads from Two Lung Cancer Cell Lines
Version 0.12.0
Author Cory Barr, Michael Lawrence
Maintainer Cory Barr <barr.cory@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
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

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
- distantsplice_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()

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**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

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