

# Package ‘LungCancerLines’

April 8, 2015

**Type** Package

**Title** Reads from Two Lung Cancer Cell Lines

**Version** 0.3.1

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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

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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)
```

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LungCancerBamFiles     *Get the BAM paths*

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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()

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LungCancerFastqFiles *Get the Fastq paths*

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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

**Examples**

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