

# 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

**git\_url** <https://git.bioconductor.org/packages/LungCancerLines>

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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

Maintainer: Cory Barr <barr.cory@gene.com>

## Examples

```
data(p53Genome)
```

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|                    |                          |
|--------------------|--------------------------|
| 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
- 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*

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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**

```
LungCancerFastqFiles()
```

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