

# Package ‘SCLCBam’

April 14, 2020

**Type** Package

**Title** Sequence data from chromosome 4 of a small-cell lung tumor

**Version** 1.18.0

**Date** 2015-02-18

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**Depends** R(>= 2.10)

**Suggests** BiocStyle

**Description** Whole-exome sequencing data from a murine small-cell lung tumor; only contains data of chromosome 4.

**License** GPL-2

**biocViews** SequencingData, LungCancerData

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

**git\_branch** RELEASE\_3\_10

**git\_last\_commit** 8fceb27

**git\_last\_commit\_date** 2019-10-29

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## R topics documented:

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## Description

Sequence reads from chromosome 4 of a whole-exome sequencing approach on a small-cell lung tumor.

**Usage**

```
getPathBamFolder()
```

**Details**

The `getPathBamFolder()` function returns the full path name to the folder containing the `.bam` file.

**Value**

Returns the full path name of the folder containing the `.bam` file.

**Author(s)**

Thomas Kuilman (t.kuilman@nki.nl)

**References**

The dataset was downloaded from the European Nucleotide Archive using the accession number PRJEB6954 using sample accession number SAMEA2697779, and reads on chromosome 4 were extracted. The full `.bam` file containing data for all chromosomes can be downloaded from here <http://www.ebi.ac.uk/ena/data/view/SAMEA2697779>

**Examples**

```
getPathBamFolder()
```

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