Package 'NGScopyData'

October 17, 2019

LazyData yes URL http: //www.bioconductor.org/packages/release/data/experiment/html/NGScopyData.htm Repository Bioconductor biocViews ExperimentData, CancerData, LungCancerData, SequencingData Author Xiaobei Zhao [aut, cre, cph] Maintainer Xiaobei Zhao <xiaobei@binf.ku.dk> git_url https://git.bioconductor.org/packages/NGScopyData git_branch RELEASE_3_9 git_last_commit_ebba550 git_last_commit_date 2019-05-02 Date/Publication 2019-10-17</xiaobei@binf.ku.dk>	Type	Package
Title Subset of BAM files of human tumor and pooled normal sequencing data (Zhao et al. 2014) for the NGScopy package Description Subset of BAM files of human lung tumor and pooled normal samples by targeted panel sequencing. [Zhao et al 2014. Targeted Sequencing in Non-Small Cell Lung Cancer (NSCLC) Using the University of North Carolina (UNC) Sequencing Assay Captures Most Previously Described Genetic Aberrations in NSCLC. In preparation.] Each sample is a 10 percent random subsample drawn from the original sequencing data. The pooled normal sample has been rescaled accroding to the total number of normal samples in the "pool". Here provided is the subsampled data on chr6 (hg19). License GPL (>=2) LazyData yes URL http: //www.bioconductor.org/packages/release/data/experiment/html/NGScopyData.htm Repository Bioconductor biocViews ExperimentData, CancerData, LungCancerData, SequencingData Author Xiaobei Zhao [aut, cre, cph] Maintainer Xiaobei Zhao (xiaobei@binf.ku.dk> git_url https://git.bioconductor.org/packages/NGScopyData git_branch RELEASE_3_9 git_last_commit_date 2019-05-02 Date/Publication 2019-10-17 R topics documented: NGScopyData-package tps_27.chr6 tps_90.chr6	Versio	on 1.4.0
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Subset of BAM files of human tumor and pooled normal sequencing data (Zhao et al. 2014) for the NGScopy package

Description

Subset of BAM files of human tumor and pooled normal samples by targeted panel sequencing (Zhao et al. 2014). Each sample is a 10 percent random subsample drawn from the original sequencing data. The pooled normal sample has been rescaled accroding to the total number of normal samples in the "pool". Here provided is the subsampled data on chr6 (hg19).

Usage

```
tps_90.chr6()
tps_27.chr6()
tps_N8.chr6()
```

Author(s)

Xiaobei Zhao

References

Zhao et al (2014), Targeted Sequencing in Non-Small Cell Lung Cancer (NSCLC) Using the University of North Carolina (UNC) Sequencing Assay Captures Most Previously Described Genetic Aberrations in NSCLC. *In preparation*

See Also

NGScopy

tps_27.chr6

A subset of tumor sample (ID: 27) by targeted panel sequencing

Description

A subset of tumor sample (ID: 27) by targeted panel sequencing, a 10 percent random subsample drawn from chr6, hg19 (Zhao et al. 2014).

Usage

```
tps_27.chr6()
```

Value

character, the path of the (sorted) bam file and its index file

Author(s)

Xiaobei Zhao

tps_90.chr6 3

See Also

NGScopyData NGScopy

Examples

```
require(NGScopyData)
tps_27.chr6()
```

tps_90.chr6

A subset of tumor sample (ID: 90) by targeted panel sequencing

Description

A subset of tumor sample (ID: 90) by targeted panel sequencing, a 10 percent random subsample drawn from chr6, hg19 (Zhao et al. 2014).

Usage

```
tps_90.chr6()
```

Value

character, the path of the (sorted) bam file and its index file

Author(s)

Xiaobei Zhao

See Also

NGScopyData NGScopy

Examples

```
require(NGScopyData)
tps_90.chr6()
```

tps_N8.chr6

A subset of pooled normal sample (ID: N8) by targeted panel sequencing

Description

A subset of pooled normal sample (ID: N8) by targeted panel sequencing, a 10 percent random subsample, rescaled by the total number of normal samples in the "pool", drawn from chr6, hg19 (Zhao et al. 2014).

Usage

```
tps_N8.chr6()
```

tps_N8.chr6

Value

character, the path of the (sorted) bam file and its index file

Author(s)

Xiaobei Zhao

See Also

NGScopyData NGScopy

Examples

require(NGScopyData)
tps_N8.chr6()

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