Package 'NGScopyData'

November 10, 2026

Type Package

Version 1.32.0

Date 2014-08-08 11:47:26 EDT

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.html

biocViews ExperimentData, CancerData, LungCancerData, SequencingData

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git_url https://git.bioconductor.org/packages/NGScopyData

git_branch RELEASE_3_23

git_last_commit 63b7ebe

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-10

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`NGScopyData-package` *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

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()
```

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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