

Package ‘h5vcData’

April 16, 2024

Type Package

Title Example data for the h5vc package

Version 2.22.0

Date 2013-10-16

Author Paul Theodor Pyl

Maintainer Paul Theodor Pyl <pyl@embl.de>

Description This package contains the data used in the vignettes and examples of the 'h5vc' package

License GPL (>= 3)

Suggests h5vc

biocViews CancerData

git_url <https://git.bioconductor.org/packages/h5vcData>

git_branch RELEASE_3_18

git_last_commit 33c458b

git_last_commit_date 2023-10-24

Repository Bioconductor 3.18

Date/Publication 2024-04-16

R topics documented:

| | |
|----------------------------|----------|
| h5vcData-package | 2 |
| Index | 3 |

h5vcData-package

Example data for the h5vc package

Description

This package contains the example data needed for the vignettes and examples of the h5vc package.

Details

Package: h5vcData
Type: Package
Version: 1.0.0
Date: 2013-10-16
License: GPL (>= 3)

This package contains the following files in `inst/extdata`:

`example.tally.hfs5`: The example HDF5 tally file

`NRAS.AML.bam`: BAM file containig reads spanning the NRAS locus from an AML sample

`NRAS.AML.bam.bai`: BAM file index for `NRAS.AML.bam`

`NRAS.Control.bam`: BAM file containig reads spanning the NRAS locus from the matched control sample

`NRAS.Control.bam.bai`: BAM file index for `NRAS.Control.bam`

`Pt*bam`: BAM file containing reads spannign DNMT3A locus of cancer or control samples from a total of 6 pairs
`Pt*bam.bam`: Corresponding index files for the set of bam files overlapping the DNMT3A locus

This package contains the following data objects in `data`:

`variantCalls` is the `data.frame` containing a set of example variant calls on the example tally file

Author(s)

Paul Theodor Pyl Maintainer: Paul Theodor Pyl <pyl@embl.de>

See Also

[h5vc](#)

Examples

```
tallyFile <- system.file("extdata", "example.tally.hfs5", package = "h5vcData")
caseBamFile <- system.file("extdata", "NRAS.AML.bam", package = "h5vcData")
controlBamFile <- system.file("extdata", "NRAS.Control.bam", package = "h5vcData")
data( "example.variants", package = "h5vcData" )
head(variantCalls)
```

Index

* **package**

h5vcData-package, [2](#)

h5vc, [2](#)

h5vcData (h5vcData-package), [2](#)

h5vcData-package, [2](#)

variantCalls (h5vcData-package), [2](#)