Package ‘h5vcData’

April 30, 2026

Type Package

Title Example data for the h5vc package

Version 2.32.0

Date 2013-10-16

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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_23

git_last_commit 3bb9448

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-04-30

Contents

`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)

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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)
```

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