

Package ‘h5vcData’

July 31, 2025

Type Package

Title Example data for the h5vc package

Version 2.28.0

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_21

git_last_commit 6b82461

git_last_commit_date 2025-04-15

Repository Bioconductor 3.21

Date/Publication 2025-07-31

Contents

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)

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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)
```

Index

* **package**

h5vcData-package, [2](#)

h5vc, [2](#)

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

h5vcData-package, [2](#)

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