

# Package ‘h5vcData’

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**Type** Package

**Title** Example data for the h5vc package

**Version** 2.28.0

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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>

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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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