

# Package ‘h5vcData’

July 1, 2025

**Type** Package

**Title** Example data for the h5vc package

**Version** 2.29.0

**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** devel

**git\_last\_commit** 48435e6

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.22

**Date/Publication** 2025-07-01

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| h5vcData-package | <i>Example data for the h5vc package</i> |
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## 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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