# Package ‘h5vcData’

May 7, 2026

**Type** Package

**Title** Example data for the h5vc package

**Version** 2.33.0

**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

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## Contents

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`h5vcData-package` *Example data for the* `h5vc` *package*

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### Description

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

## Details

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|---|---|
| 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