

# Package ‘h5vcData’

April 4, 2014

**Type** Package

**Title** Example data for the h5vc package

**Version** 1.0.0

**Date** 2013-10-16

**Author** Paul Theodor Pyl

**Maintainer** Paul Theodor Pyl <pyl@embl.de>

**Description** This package contains the data used in the vignettes and examples of the 'h5vc' package

**License** GPL (>= 3)

**Suggests** h5vc

**biocViews** HighThroughputSequencingData

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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`

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)**

Paul Theodor Pyl Maintainer: Paul Theodor Pyl <pyl@embl.de>

### **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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