

# Package ‘CopyNumber450kData’

October 7, 2015

**Version** 1.4.0

**Date** 2014-01-22

**Title** Example data for the Illumina Methylation 450k array

**Description** Data from 52 control samples from 450k methylation arrays

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**License** Artistic-2.0

**Depends** R (>= 2.13.0), minfi, IlluminaHumanMethylation450kmanifest,  
IlluminaHumanMethylation450kanno.ilmn12.hg19

**LazyData** yes

**biocViews** Tissue, Homo\_sapiens\_Data, MicroarrayData,  
MethylationArrayData, TissueMicroarrayData

**NeedsCompilation** no

## R topics documented:

RGcontrolSetEx . . . . . 1

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RGcontrolSetEx	<i>An example control dataset for Illumina’s Human Methylation 450k dataset.</i>
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## Description

This contains the raw data for 52 control samples from Illumina’s Human Methylation 450k dataset. The samples are from different tissue from control patient with nominally no copy number aberrations.

**Usage**

```
data(RGcontrolSetEx)
```

**Format**

An object of class "RGChannelSet"

**Details**

Scripts for creating the object is found in the scripts directory of the package and extdata contains the IDAT files.

**See Also**

[RGChannelSet](#) for the class definition,

**Examples**

```
data(RGcontrolSetEx)  
pData(RGcontrolSetEx)
```

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\*Topic **datasets**

RGcontrolSetEx, [1](#)

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