

# Package ‘encoDnaseI’

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**Title** data provided by UCSC for Cd4 raw measures of DnaseI hypersensitivity

**Description** data provided by UCSC for Cd4 raw measures of DnaseI hypersensitivity

**Version** 0.8.0

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**Depends** R (>= 2.15.0), methods, Biobase (>= 2.5.5), lattice, GGtools, GGBase

**Suggests** GGdata

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**License** Artistic-2.0

**biocViews** ExperimentData, Genome, Homo\_sapiens\_Data, SNPData, ENCODE

**NeedsCompilation** no

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hg18track-class	<i>Class "hg18track" container for hg18 annotation found in genome browser track files; class "chrnum" extends numeric for an indexing application on hg18track objects.</i>
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## Description

container for hg18 annotation found in genome browser track files

### Objects from the Class

Objects can be created by calls of the form `new("hg18track", assayData, featureData, experimentData, annotation)`. These are single-sample eSet instances.

Note that `demoTrk19` is a restriction of the `rawCD4` structure to the interval of chromosome 19 that was assayed in the ENCODE project for DnaseI hypersensitivity.

### Slots

`assayData`: Object of class "AssayData" ~~  
`phenoData`: Object of class "AnnotatedDataFrame" ~~  
`featureData`: Object of class "AnnotatedDataFrame" ~~  
`experimentData`: Object of class "MIAME" ~~  
`annotation`: Object of class "character" ~~  
`._.classVersion_.`: Object of class "Versions" ~~

### Extends

Class "eSet", directly. Class "VersionedBiobase", by class "eSet", distance 2. Class "Versioned", by class "eSet", distance 3.

### Methods

[ signature(x = "hg18track"): select using numeric, logical, or chrnum indices.

**chrnum** signature(object = "hg18track"): extract numeric tokens for chromosome number at which data values are obtained; note that chrnum is also used as name of a class.

**dataVals** signature(object = "hg18track"): actual data values

**getTrkXY** signature(object = "hg18track", type = "character"): obtain a list with components x, y indicating location and data value respectively; location is within chromosome; default type is 'midpoint' of locations given as intervals

**getTrkXY** signature(object = "hg18track", type = "missing"): take default midpoint x values corresponding to data values

**rangeLocs** signature(object = "hg18track"): if measures from only one chromosome are present, this returns low and high values of chromStart and chromEnd respectively, otherwise error.

**clipTrk** signature(obj = "hg18track", low="numeric", hi="numeric", attr="ANY"): create a restriction of the track using an interval specification. by default the chromStart featureData component is used for coordinates to clip; if attr is non-missing, the featureData component named by attr will be used.

**initialize** signature(.Object = "hg18track"): create a new instance

### Author(s)

VJ Carey <stvjc@channing.harvard.edu>

**Examples**

```
showClass("hg18track")
data(rawCD4)
rawCD4
rawCD4.chr1 = rawCD4[ chrnum(1), ]
rangeLocs(rawCD4.chr1)
plot(getTrkXY(rawCD4.chr1), ylab="data value", xlab="interval midpt on chr 1" )
c52 = clipTrk(rawCD4[ chrnum(5), ], 1.30e8, 1.33e8 )
plot(getTrkXY(c52))
```

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juxtaPlot

*two-panel plot with track info and snp screen t-values*

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**Description**

two-panel plot with track info and snp screen t-values

**Usage**

```
juxtaPlot(trk, ssr, locstr)
```

**Arguments**

trk	instance of <a href="#">hg18track</a>
ssr	instance of GGtools snpScreenResult
locstr	matrix with 2 rows: rsid (numeric component of dbSNP id) and loc

**Details**

xyplot of lattice package is used.

**Value**

xyplot output; use print in Sweave.

**Author(s)**

VJ Carey <stvjc@channing.harvard.edu>

**Examples**

```
## Not run:
# see vignette
data(sOSR2)
data(c19g) # track excerpt
juxtaPlot(c19g, sOSR2)

## End(Not run)
```

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rawCd4DnaseI	<i>A data frame with information on the UCSC browser track related to DNaseI hypersensitivity</i>
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### Description

A data frame with information on the UCSC browser track related to DNaseI hypersensitivity; the rawCD4 object is an eSet extension representing the same information; rawHelaDnaseI is like rawCD4 but results on HeLa cells.

### Usage

```
data(rawCd4DnaseI)
data(rawHelaDnaseI)
data(rawCD4)
```

### Details

Obtained from a MySQL representation of the data distributed at the Genome Browser FTP site

### Value

a data.frame

### Author(s)

Vince Carey <stvjc@channing.harvard.edu>

### References

[hgdownload.cse.ucsc.edu](http://hgdownload.cse.ucsc.edu) ... it appears that they do not offer the MYD/MYI representations, just the txt.gz and sql files now. So if you obtain the encodeNhgriDnaseHsChipRawCd4.txt and .sql files at goldenPath/currentGenomes/Homo\_Sapiens/encode/database, you can reconstruct the underlying data for this data.frame (hg18, Nov 2007).

### Examples

```
data(rawCd4DnaseI)
dim(rawCd4DnaseI)
rawCd4DnaseI[1:5,]
library(lattice)
xyplot(dataValue~chromStart|chrom, data=rawCd4DnaseI, subset=chrom %in%
  c("chr1", "chr10", "chr19", "chr20"), scales=list(x=list(relation="free")))
```

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