FDb.FANTOM4.promoters.hg19

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`hg18ToHg19` *UCSC liftOver chain for hg18 to hg19, used in build scripts*

Description

In the subdirectory inst/build/, there are several scripts that rebuild this FeatureDb from scratch. Since this is lifted from hg18, a chain is included.

Author(s)

Tim Triche, Jr.

Examples

```
data(hg18ToHg19)
hg18ToHg19
```

`FDb.FANTOM4.promoters.hg19`
Annotation package for FANTOM4 CAGE promoters from THP-1 cells

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Description

This package loads one or more FeatureDb objects. Such FeatureDb objects are an R interface to prefabricated databases contained by this package. In the case of the FANTOM4 promoter database, it is FDb.FANTOM4.promoters.hg19 (hg18 is available directly from unibas.ch).

Author(s)

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See Also

features makeFeatureDbFromUCSC import.bed

Examples

```
## load the library
library(FDb.FANTOM4.promoters.hg19)

## list the contents that are loaded into memory
ls('package:FDb.FANTOM4.promoters.hg19')

## show the db object that is loaded by calling it's name
FDb.FANTOM4.promoters.hg19

## extract features for use in annotating data
FANTOM4.hg19 <- features(FDb.FANTOM4.promoters.hg19)

## we'd prefer if R would stop us from comparing across assemblies:
met <- metadata(FDb.FANTOM4.promoters.hg19) ## need to fetch genome
genome(FANTOM4.hg19) <- met[which(met[,'name']=='Genome'),'value']

## Plot the observed/expected CpG ratio look like across promoters
## (computed as Pr(CG) / Pr(C)Pr(G)Pr(CG|G,C) within a 3kb window)
## Conversion back to numeric is due to an artifact of features()
values(FANTOM4.hg19)$oecg <- as.numeric(values(FANTOM4.hg19)$oecg)
hist(values(FANTOM4.hg19)$oecg, breaks=200,
     xlab='Observed/expected CpG content from hg19',
     main='FANTOM4 promoter CpG content, 3kb windows')

## The function used for this is FDb.FANTOM4.promoters.hg19:::oecg()
```

Index

∗ **data**
FDb.FANTOM4.promoters.hg19, 1
hg18ToHg19, 1
∗ **package**
FDb.FANTOM4.promoters.hg19, 1

FDb.FANTOM4.promoters.hg19, 1
FDb.FANTOM4.promoters.hg19-package
*(*FDb.FANTOM4.promoters.hg19*)*, 1
features, *2*

hg18ToHg19, 1

import.bed, *2*

makeFeatureDbFromUCSC, *2*