

FDb.UCSC.snp135common.hg19

January 14, 2026

FDb.UCSC.snp135common.hg19

UCSC common SNPs track, dbSNP build 135, genome assembly hg19

Description

FDb.UCSC.snp135common.hg19 is a FeatureDb created from the UCSC common SNPs track for dbSNP build 135 and genome assembly hg19. The track is too large to automatically construct a FeatureDb using `makeFeatureDbFromUCSC`, so here it has been manually retrieved (see `inst/build/FDb.UCSC.snp135common.hg19.R`) and saved as a FeatureDb.

Author(s)

Tim Triche, Jr.

See Also

[features](#) [makeFeatureDbFromUCSC](#)

Examples

```
## load the library
library(FDb.UCSC.snp135common.hg19)

## list the contents that are loaded into memory
ls('package:FDb.UCSC.snp135common.hg19')

## show the db object that is loaded by calling it's name
FDb.UCSC.snp135common.hg19

## extract features for use in annotating data
snp135common <- features(FDb.UCSC.snp135common.hg19)
met <- metadata(FDb.UCSC.snp135common.hg19) ## need to fetch genome
genome(snp135common) <- met[which(met[, 'name'] == 'Genome'), 'value']
```

Index

* **data**

FDb.UCSC.snp135common.hg19, [1](#)

* **package**

FDb.UCSC.snp135common.hg19, [1](#)

FDb.UCSC.snp135common.hg19, [1](#)

FDb.UCSC.snp135common.hg19-package

(FDb.UCSC.snp135common.hg19), [1](#)

features, [1](#)

makeFeatureDbFromUCSC, [1](#)