# Package 'geneLenDataBase'

October 16, 2021

**Version** 1.28.0

<b>Date</b> 2019/04/26
Title Lengths of mRNA transcripts for a number of genomes
Author Matthew Young
Maintainer Matthew Young <my4@sanger.ac.uk>, Nadia Davidson <nadia.davidson@mcri.edu.au></nadia.davidson@mcri.edu.au></my4@sanger.ac.uk>
<b>Depends</b> R (>= $2.11.0$ )
Imports utils, rtracklayer, GenomicFeatures (>= 1.3.15)
LazyLoad yes
<b>Description</b> Length of mRNA transcripts for a number of genomes and gene ID formats, largely based on UCSC table browser
biocViews ExperimentData, Genome
License LGPL (>= 2)
NeedsCompilation no
git_url https://git.bioconductor.org/packages/geneLenDataBase git_branch RELEASE_3_13 git_last_commit 7f14bbc
git_last_commit_date 2021-05-19
Date/Publication 2021-10-16
R topics documented:
anoCar1.ensGene.LENGTH       8         anoCar1.genscan.LENGTH       9         anoCar1.xenoRefGene.LENGTH       9         anoGam1.ensGene.LENGTH       10         anoGam1.geneid.LENGTH       11         anoGam1.genscan.LENGTH       11         apiMel1.genscan.LENGTH       11         apiMel2.ensGene.LENGTH       12         apiMel2.geneid.LENGTH       12         apiMel2.genscan.LENGTH       13         aplCal1.xenoRefGene.LENGTH       13         bosTau2.geneid.LENGTH       14

bosTau2.geneSymbol.LENGTH	 14
bosTau2.genscan.LENGTH	 15
bosTau2.refGene.LENGTH	 15
bosTau2.sgpGene.LENGTH	 16
bosTau3.ensGene.LENGTH	16
bosTau3.geneid.LENGTH	17
bosTau3.geneSymbol.LENGTH	 17
bosTau3.genscan.LENGTH	 18
bosTau3.refGene.LENGTH	 18
bosTau3.sgpGene.LENGTH	19
bosTau4.ensGene.LENGTH	 19
bosTau4.geneSymbol.LENGTH	 20
bosTau4.genscan.LENGTH	 20
bosTau4.nscanGene.LENGTH	 21
bosTau4.refGene.LENGTH	 21
braFlo1.xenoRefGene.LENGTH	 22
caeJap1.xenoRefGene.LENGTH	
caePb1.xenoRefGene.LENGTH	 23
caePb2.xenoRefGene.LENGTH	 23
caeRem2.xenoRefGene.LENGTH	
caeRem3.xenoRefGene.LENGTH	
calJac1.genscan.LENGTH	
calJac1.nscanGene.LENGTH	
calJac1.xenoRefGene.LENGTH	 26
canFam1.ensGene.LENGTH	
canFam1.geneSymbol.LENGTH	
canFam1.genscan.LENGTH	
canFam1.nscanGene.LENGTH	
canFam1.refGene.LENGTH	
canFam1.xenoRefGene.LENGTH	
canFam2.ensGene.LENGTH	
canFam2.geneSymbol.LENGTH	
canFam2.genscan.LENGTH	
canFam2.nscanGene.LENGTH	
canFam2.refGene.LENGTH	
canFam2.xenoRefGene.LENGTH	
cavPor3.ensGene.LENGTH	32
cavPor3.genscan.LENGTH	33
cavPor3.nscanGene.LENGTH	33
cavPor3.xenoRefGene.LENGTH	34
	 34
	 35
ce2.geneid.LENGTH	35
ce2.geneSymbol.LENGTH	36
ce2.refGene.LENGTH	36
ce4.geneSymbol.LENGTH	37
•	 37
	 38
ce6.ensGene.LENGTH	38
ce6.geneSymbol.LENGTH	39
ce6.refGene.LENGTH	39
ce6.xenoRefGene.LENGTH	40

ci1.geneSymbol.LENGTH
cil.refGene.LENGTH
cil.xenoRefGene.LENGTH
ci2.ensGene.LENGTH
ci2.geneSymbol.LENGTH
ci2.refGene.LENGTH
ci2.xenoRefGene.LENGTH 43
danRer3.ensGene.LENGTH
danRer3.geneSymbol.LENGTH
danRer3.refGene.LENGTH
danRer4.ensGene.LENGTH
danRer4.geneSymbol.LENGTH
danRer4.genscan.LENGTH
danRer4.nscanGene.LENGTH
danRer4.refGene.LENGTH
danRer5.ensGene.LENGTH
danRer5.geneSymbol.LENGTH
danRer5.refGene.LENGTH
danRer5.vegaGene.LENGTH
danRer5.vegaPseudoGene.LENGTH
danRer6.ensGene.LENGTH
danRer6.geneSymbol.LENGTH
danRer6.refGene.LENGTH
danRer6.xenoRefGene.LENGTH
dm1.geneSymbol.LENGTH
dm1.genscan.LENGTH
dm1.refGene.LENGTH
dm2.geneid.LENGTH
dm2.geneSymbol.LENGTH
dm2.genscan.LENGTH
dm2.nscanGene.LENGTH
dm2.refGene.LENGTH
dm3.geneSymbol.LENGTH
dm3.nscanPasaGene.LENGTH
dm3.refGene.LENGTH
dp2.genscan.LENGTH
dp2.xenoRefGene.LENGTH
dp3.geneid.LENGTH
dp3.genscan.LENGTH
dp3.xenoRefGene.LENGTH
droAna1.geneid.LENGTH
droAna1.genscan.LENGTH
droAna1.xenoRefGene.LENGTH
droAna2.genscan.LENGTH
droAna2.xenoRefGene.LENGTH
droEre1.genscan.LENGTH
droEre1.xenoRefGene.LENGTH
droGri1.genscan.LENGTH
droGri1.xenoRefGene.LENGTH
droMoj1.geneid.LENGTH
droMoj1.genscan.LENGTH
droMoj1.xenoRefGene.LENGTH

droMoj2.genscan.LENGTH	 	 	 	 		 		66
droMoj2.xenoRefGene.LENGTH	 	 	 	 		 		67
droPer1.genscan.LENGTH	 	 	 	 		 		67
droPer1.xenoRefGene.LENGTH .	 	 	 	 		 		68
droSec1.genscan.LENGTH	 	 	 	 		 		68
droSec1.xenoRefGene.LENGTH .	 	 	 	 		 		69
droSim1.geneid.LENGTH	 	 	 	 		 		69
droSim1.genscan.LENGTH	 	 	 	 		 		70
droSim1.xenoRefGene.LENGTH.								70
droVir1.geneid.LENGTH	 	 	 	 		 		71
droVir1.genscan.LENGTH	 	 	 	 	 	 		71
droVir1.xenoRefGene.LENGTH .								72
droVir2.genscan.LENGTH								72
droVir2.xenoRefGene.LENGTH .								73
droYak1.geneid.LENGTH								73
droYak1.genscan.LENGTH								74
droYak1.xenoRefGene.LENGTH .	 	 	 	 	 	 		74
droYak2.genscan.LENGTH								75
droYak2.xenoRefGene.LENGTH .								75
equCab1.geneid.LENGTH								76
equCab1.geneSymbol.LENGTH .								76
equCab1.nscanGene.LENGTH								77
equCab1.refGene.LENGTH								77
equCab1.sgpGene.LENGTH								78
equCab2.ensGene.LENGTH								78
equCab2.geneSymbol.LENGTH .								79
equCab2.nscanGene.LENGTH								79
equCab2.refGene.LENGTH								
equCab2.xenoRefGene.LENGTH								
felCat3.ensGene.LENGTH								
felCat3.geneid.LENGTH								
felCat3.geneSymbol.LENGTH								
felCat3.genscan.LENGTH								
felCat3.nscanGene.LENGTH								
felCat3.refGene.LENGTH								
felCat3.sgpGene.LENGTH								
felCat3.xenoRefGene.LENGTH								
fr1.ensGene.LENGTH								85
fr1.genscan.LENGTH								85
fr2.ensGene.LENGTH								86
galGal2.ensGene.LENGTH								86
galGal2.geneid.LENGTH								87
galGal2.geneSymbol.LENGTH								87
galGal2.genscan.LENGTH								88
galGal2.refGene.LENGTH								88
E								89
galGal2.sgpGene.LENGTH galGal3.ensGene.LENGTH								89
galGal3.geneSymbol.LENGTH								
								90
galGal3.genscan.LENGTH								90
e								91
galGal3.refGene.LENGTH								91
galGal3.xenoRefGene.LENGTH .	 	 	 	 		 		92

<b>8</b>	92
D	93
	93
	94
$\mathcal{E}$	94
	95
	95
	96
	96
	97
	97
hg17.acembly.LENGTH	98
hg17.acescan.LENGTH	98
hg17.ccdsGene.LENGTH	99
hg17.ensGene.LENGTH	99
hg17.exoniphy.LENGTH	00
hg17.geneid.LENGTH	
hg17.geneSymbol.LENGTH	01
hg17.genscan.LENGTH	01
hg17.knownGene.LENGTH	02
hg17.refGene.LENGTH	02
hg17.sgpGene.LENGTH	
hg17.vegaGene.LENGTH	
hg17.vegaPseudoGene.LENGTH	
hg17.xenoRefGene.LENGTH	04
hg18.acembly.LENGTH	
hg18.acescan.LENGTH	
hg18.ccdsGene.LENGTH	
hg18.ensGene.LENGTH	
hg18.exoniphy.LENGTH	
hg18.geneid.LENGTH	
hg18.geneSymbol.LENGTH	
hg18.genscan.LENGTH	08
hg18.knownGene.LENGTH	
hg18.knownGeneOld3.LENGTH	
hg18.refGene.LENGTH	
hg18.sgpGene.LENGTH	
hg18.sibGene.LENGTH	
hg18.xenoRefGene.LENGTH	
hg19.ccdsGene.LENGTH	
hg19.ensGene.LENGTH	
hg19.exoniphy.LENGTH	
hg19.geneSymbol.LENGTH	
hg19.knownGene.LENGTH	
hg19.nscanGene.LENGTH	
hg19.refGene.LENGTH	
hg19.xenoRefGene.LENGTH	
loxAfr3.xenoRefGene.LENGTH	
mm7.ensGene.LENGTH	
mm7.geneid.LENGTH	
mm7.geneSymbol.LENGTH	
mm7.genscan.LENGTH	
	- 0

nm7.knownGene.LENGTH	. 118
nm7.refGene.LENGTH	. 119
nm7.sgpGene.LENGTH	
nm7.xenoRefGene.LENGTH	
nm8.ccdsGene.LENGTH	. 120
nm8.ensGene.LENGTH	. 121
nm8.geneid.LENGTH	. 121
nm8.geneSymbol.LENGTH	. 122
nm8.genscan.LENGTH	. 122
nm8.knownGene.LENGTH	. 123
nm8.nscanGene.LENGTH	. 123
nm8.refGene.LENGTH	
nm8.sgpGene.LENGTH	. 124
nm8.sibGene.LENGTH	
nm8.xenoRefGene.LENGTH	. 125
nm9.acembly.LENGTH	
nm9.ccdsGene.LENGTH	
nm9.ensGene.LENGTH	
nm9.exoniphy.LENGTH	
nm9.geneid.LENGTH	
nm9.geneSymbol.LENGTH	
nm9.genscan.LENGTH	
nm9.knownGene.LENGTH	
nm9.nscanGene.LENGTH	
nm9.refGene.LENGTH	
nm9.sgpGene.LENGTH	
nm9.xenoRefGene.LENGTH	
nonDom1.genscan.LENGTH	
nonDom4.ensGene.LENGTH	
nonDom4.geneSymbol.LENGTH	
nonDom4.genscan.LENGTH	
nonDom4.nscanGene.LENGTH	
nonDom4.refGene.LENGTH	
nonDom4.xenoRefGene.LENGTH	
nonDom5.ensGene.LENGTH	
nonDom5.geneSymbol.LENGTH	
nonDom5.genscan.LENGTH	
nonDom5.nscanGene.LENGTH	
nonDom5.refGene.LENGTH	
nonDom5.xenoRefGene.LENGTH	
ornAna1.ensGene.LENGTH	
ornAna1.geneSymbol.LENGTH	
ornAnal.refGene.LENGTH	
ornAna1.xenoRefGene.LENGTH	
oryLat2.ensGene.LENGTH	
pryLat2.geneSymbol.LENGTH	
bryLat2.refGene.LENGTH	
bryLat2.xenoRefGene.LENGTH	
panTro1.ensGene.LENGTH	
panTro1.geneid.LENGTH	
panTro1.genscan.LENGTH	
panTro1.xenoRefGene.LENGTH	

panTro2.ensGene.LENGTH		 			 					144
pan Tro 2. gene Symbol. LENG TH  .										
$pan Tro 2. gens can. LENG TH \ . \ . \ . \ .$										
pan Tro 2. ns can Gene. LENG TH  .  .										
$pan Tro 2. ref Gene. LENG TH \ . \ . \ . \ .$										
$pan Tro 2. xeno Ref Gene. LENG TH \ .$										
$pet Mar 1. xeno Ref Gene. LENG TH \ . \\$										
ponAbe2.ensGene.LENGTH		 			 					148
$pon Abe 2. gene Symbol. LENG TH \ .$		 			 					148
ponAbe2.genscan.LENGTH										
$pon Abe 2. ns can Gene. LENG TH\ .\ .$										
ponAbe2.refGene.LENGTH										
ponAbe2.xenoRefGene.LENGTH										
priPac1.xenoRefGene.LENGTH .		 			 					151
rheMac2.ensGene.LENGTH		 			 					151
rheMac2.geneid.LENGTH		 			 					152
$rhe Mac 2. gene Symbol. LENGTH \ .$		 			 					152
rheMac2.nscanGene.LENGTH		 			 					153
rheMac2.refGene.LENGTH		 			 					153
rheMac2.sgpGene.LENGTH										
rheMac2.xenoRefGene.LENGTH		 			 					154
rn3.ensGene.LENGTH		 			 					155
rn3.geneid.LENGTH										
rn3.geneSymbol.LENGTH										
rn3.genscan.LENGTH										
rn3.knownGene.LENGTH										
rn3.nscanGene.LENGTH		 			 					157
rn3.refGene.LENGTH										
rn3.sgpGene.LENGTH										
rn3.xenoRefGene.LENGTH										
rn4.ensGene.LENGTH										
rn4.geneid.LENGTH		 			 					160
rn4.geneSymbol.LENGTH										
rn4.genscan.LENGTH										
rn4.knownGene.LENGTH										
rn4.nscanGene.LENGTH										
rn4.refGene.LENGTH										
rn4.sgpGene.LENGTH		 			 					163
rn4.xenoRefGene.LENGTH										
sacCer1.ensGene.LENGTH										
sacCer2.ensGene.LENGTH										
strPur1.geneSymbol.LENGTH										
strPur1.genscan.LENGTH										
strPur1.refGene.LENGTH										
strPur1.xenoRefGene.LENGTH .										
strPur2.geneSymbol.LENGTH										
strPur2.genscan.LENGTH										
strPur2.refGene.LENGTH										
strPur2.xenoRefGene.LENGTH										
supportedGeneIDs										
supportedGenomes										
taeGut1.ensGene.LENGTH										

Index		179
	xenTro2.refGene.LENGTH	178
	xenTro2.genscan.LENGTH	
	xenTro2.geneSymbol.LENGTH	
	xenTro2.ensGene.LENGTH	
	xenTro1.genscan.LENGTH	
	unfactor	175
	tetNig2.ensGene.LENGTH	
	tetNig1.nscanGene.LENGTH	174
	tetNig1.genscan.LENGTH	174
	tetNig1.geneid.LENGTH	173
	tetNig1.ensGene.LENGTH	173
	taeGut1.xenoRefGene.LENGTH	172
	taeGut1.refGene.LENGTH	172
	taeGut1.nscanGene.LENGTH	171
	taeGut1.genscan.LENGTH	171
	taeGut1.geneSymbol.LENGTH	170

anoCar1.ensGene.LENGTH

Transcript length data for the organism anoCar

# Description

anoCar1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(anoCar1, ensGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(anoCar1.ensGene.LENGTH)
head(anoCar1.ensGene.LENGTH)
```

anoCar1.genscan.LENGTH

Transcript length data for the organism anoCar

## **Description**

anoCar1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(anoCar1, genscan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(anoCar1.genscan.LENGTH)
head(anoCar1.genscan.LENGTH)
```

anoCar1.xenoRefGene.LENGTH

Transcript length data for the organism anoCar

#### **Description**

anoCar1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(anoCar1, xenoRefGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(anoCar1.xenoRefGene.LENGTH)
head(anoCar1.xenoRefGene.LENGTH)
```

anoGam1.ensGene.LENGTH

Transcript length data for the organism anoGam

## **Description**

anoGam1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(anoGam1, ensGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(anoGam1.ensGene.LENGTH)
head(anoGam1.ensGene.LENGTH)
```

anoGam1.geneid.LENGTH Transcript length data for the organism anoGam

# Description

anoGam1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(anoGam1, geneid) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(anoGam1.geneid.LENGTH)
head(anoGam1.geneid.LENGTH)
```

anoGam1.genscan.LENGTH

Transcript length data for the organism anoGam

## **Description**

anoGam1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(anoGam1, genscan) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

#### **Examples**

```
data(anoGam1.genscan.LENGTH)
head(anoGam1.genscan.LENGTH)
```

apiMel1.genscan.LENGTH

Transcript length data for the organism apiMel

## **Description**

apiMel1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(apiMel1, genscan) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

```
data(apiMel1.genscan.LENGTH)
head(apiMel1.genscan.LENGTH)
```

apiMel2.ensGene.LENGTH

Transcript length data for the organism apiMel

## **Description**

apiMel2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(apiMel2, ensGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

# **Examples**

data(apiMel2.ensGene.LENGTH)
head(apiMel2.ensGene.LENGTH)

apiMel2.geneid.LENGTH Transcript length data for the organism apiMel

# Description

apiMel2.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(apiMel2, geneid) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(apiMel2.geneid.LENGTH)
head(apiMel2.geneid.LENGTH)
```

```
apiMel2.genscan.LENGTH
```

Transcript length data for the organism apiMel

## **Description**

apiMel2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(apiMel2, genscan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(apiMel2.genscan.LENGTH)
head(apiMel2.genscan.LENGTH)
```

```
aplCal1.xenoRefGene.LENGTH
```

Transcript length data for the organism aplCal

#### **Description**

aplCal1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(aplCal1, xenoRefGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

```
data(aplCal1.xenoRefGene.LENGTH)
head(aplCal1.xenoRefGene.LENGTH)
```

bosTau2.geneid.LENGTH Transcript length data for the organism bosTau

#### **Description**

bosTau2.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(bosTau2, geneid) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

#### **Examples**

data(bosTau2.geneid.LENGTH)
head(bosTau2.geneid.LENGTH)

bosTau2.geneSymbol.LENGTH

Transcript length data for the organism bosTau

# Description

bosTau2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(bosTau2, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(bosTau2.geneSymbol.LENGTH)
head(bosTau2.geneSymbol.LENGTH)
```

bosTau2.genscan.LENGTH

Transcript length data for the organism bosTau

## **Description**

bosTau2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(bosTau2, genscan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(bosTau2.genscan.LENGTH)
head(bosTau2.genscan.LENGTH)
```

bosTau2.refGene.LENGTH

Transcript length data for the organism bosTau

#### **Description**

bosTau2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(bosTau2, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(bosTau2.refGene.LENGTH)
head(bosTau2.refGene.LENGTH)
```

bosTau2.sgpGene.LENGTH

Transcript length data for the organism bosTau

## **Description**

bosTau2.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(bosTau2, sgpGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(bosTau2.sgpGene.LENGTH)
head(bosTau2.sgpGene.LENGTH)
```

bosTau3.ensGene.LENGTH

Transcript length data for the organism bosTau

## **Description**

bosTau3.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(bosTau3, ensGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

```
data(bosTau3.ensGene.LENGTH)
head(bosTau3.ensGene.LENGTH)
```

bosTau3.geneid.LENGTH Transcript length data for the organism bosTau

#### **Description**

bosTau3.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(bosTau3, geneid) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

#### **Examples**

```
data(bosTau3.geneid.LENGTH)
head(bosTau3.geneid.LENGTH)
```

bosTau3.geneSymbol.LENGTH

Transcript length data for the organism bosTau

# Description

bosTau3.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(bosTau3, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(bosTau3.geneSymbol.LENGTH)
head(bosTau3.geneSymbol.LENGTH)
```

bosTau3.genscan.LENGTH

Transcript length data for the organism bosTau

## **Description**

bosTau3.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(bosTau3, genscan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(bosTau3.genscan.LENGTH)
head(bosTau3.genscan.LENGTH)
```

bosTau3.refGene.LENGTH

Transcript length data for the organism bosTau

## **Description**

bosTau3.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(bosTau3, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(bosTau3.refGene.LENGTH)
head(bosTau3.refGene.LENGTH)
```

bosTau3.sgpGene.LENGTH

Transcript length data for the organism bosTau

## **Description**

bosTau3.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(bosTau3, sgpGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(bosTau3.sgpGene.LENGTH)
head(bosTau3.sgpGene.LENGTH)
```

bosTau4.ensGene.LENGTH

Transcript length data for the organism bosTau

#### **Description**

bosTau4.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(bosTau4, ensGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(bosTau4.ensGene.LENGTH)
head(bosTau4.ensGene.LENGTH)
```

bosTau4.geneSymbol.LENGTH

Transcript length data for the organism bosTau

## **Description**

bosTau4.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(bosTau4, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(bosTau4.geneSymbol.LENGTH)
head(bosTau4.geneSymbol.LENGTH)
```

bosTau4.genscan.LENGTH

Transcript length data for the organism bosTau

#### **Description**

bosTau4.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(bosTau4, genscan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(bosTau4.genscan.LENGTH)
head(bosTau4.genscan.LENGTH)
```

bosTau4.nscanGene.LENGTH

Transcript length data for the organism bosTau

## **Description**

bosTau4.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(bosTau4, nscanGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(bosTau4.nscanGene.LENGTH)
head(bosTau4.nscanGene.LENGTH)
```

bosTau4.refGene.LENGTH

Transcript length data for the organism bosTau

## **Description**

bosTau4.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(bosTau4, refGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

```
data(bosTau4.refGene.LENGTH)
head(bosTau4.refGene.LENGTH)
```

braFlo1.xenoRefGene.LENGTH

Transcript length data for the organism braFlo

## **Description**

braFlo1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(braFlo1, xenoRefGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(braFlo1.xenoRefGene.LENGTH)
head(braFlo1.xenoRefGene.LENGTH)
```

caeJap1.xenoRefGene.LENGTH

Transcript length data for the organism caeJap

## **Description**

caeJap1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(caeJap1, xenoRefGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(caeJap1.xenoRefGene.LENGTH)
head(caeJap1.xenoRefGene.LENGTH)
```

caePb1.xenoRefGene.LENGTH

Transcript length data for the organism caePb

## **Description**

caePb1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(caePb1, xenoRefGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(caePb1.xenoRefGene.LENGTH)
head(caePb1.xenoRefGene.LENGTH)
```

caePb2.xenoRefGene.LENGTH

Transcript length data for the organism caePb

## **Description**

caePb2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(caePb2, xenoRefGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(caePb2.xenoRefGene.LENGTH)
head(caePb2.xenoRefGene.LENGTH)
```

caeRem2.xenoRefGene.LENGTH

Transcript length data for the organism caeRem

## **Description**

caeRem2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(caeRem2, xenoRefGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(caeRem2.xenoRefGene.LENGTH)
head(caeRem2.xenoRefGene.LENGTH)
```

caeRem3.xenoRefGene.LENGTH

Transcript length data for the organism caeRem

## **Description**

caeRem3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(caeRem3, xenoRefGene) on the date on which the package was last updated.

# See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(caeRem3.xenoRefGene.LENGTH)
head(caeRem3.xenoRefGene.LENGTH)
```

calJac1.genscan.LENGTH

Transcript length data for the organism calJac

## **Description**

calJac1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(calJac1, genscan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(calJac1.genscan.LENGTH)
head(calJac1.genscan.LENGTH)
```

calJac1.nscanGene.LENGTH

Transcript length data for the organism calJac

#### **Description**

calJac1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(calJac1, nscanGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

```
data(calJac1.nscanGene.LENGTH)
head(calJac1.nscanGene.LENGTH)
```

calJac1.xenoRefGene.LENGTH

Transcript length data for the organism calJac

#### **Description**

calJac1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(calJac1, xenoRefGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(calJac1.xenoRefGene.LENGTH)
head(calJac1.xenoRefGene.LENGTH)
```

canFam1.ensGene.LENGTH

Transcript length data for the organism canFam

## **Description**

canFam1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(canFam1, ensGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(canFam1.ensGene.LENGTH)
head(canFam1.ensGene.LENGTH)
```

canFam1.geneSymbol.LENGTH

Transcript length data for the organism canFam

#### **Description**

canFam1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(canFam1, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(canFam1.geneSymbol.LENGTH)
head(canFam1.geneSymbol.LENGTH)
```

canFam1.genscan.LENGTH

Transcript length data for the organism canFam

## **Description**

canFam1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(canFam1, genscan) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

```
data(canFam1.genscan.LENGTH)
head(canFam1.genscan.LENGTH)
```

canFam1.nscanGene.LENGTH

Transcript length data for the organism canFam

# **Description**

canFam1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(canFam1, nscanGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(canFam1.nscanGene.LENGTH)
head(canFam1.nscanGene.LENGTH)
```

canFam1.refGene.LENGTH

Transcript length data for the organism canFam

## **Description**

canFam1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(canFam1, refGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(canFam1.refGene.LENGTH)
head(canFam1.refGene.LENGTH)
```

canFam1.xenoRefGene.LENGTH

Transcript length data for the organism canFam

#### **Description**

canFam1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(canFam1, xenoRefGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(canFam1.xenoRefGene.LENGTH)
head(canFam1.xenoRefGene.LENGTH)
```

canFam2.ensGene.LENGTH

Transcript length data for the organism canFam

## **Description**

canFam2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(canFam2, ensGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(canFam2.ensGene.LENGTH)
head(canFam2.ensGene.LENGTH)
```

canFam2.geneSymbol.LENGTH

Transcript length data for the organism canFam

## **Description**

canFam2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(canFam2, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(canFam2.geneSymbol.LENGTH)
head(canFam2.geneSymbol.LENGTH)
```

canFam2.genscan.LENGTH

Transcript length data for the organism canFam

## **Description**

canFam2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(canFam2, genscan) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(canFam2.genscan.LENGTH)
head(canFam2.genscan.LENGTH)
```

canFam2.nscanGene.LENGTH

Transcript length data for the organism canFam

# **Description**

canFam2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(canFam2, nscanGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

#### **Examples**

```
data(canFam2.nscanGene.LENGTH)
head(canFam2.nscanGene.LENGTH)
```

canFam2.refGene.LENGTH

Transcript length data for the organism canFam

## **Description**

canFam2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(canFam2, refGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(canFam2.refGene.LENGTH)
head(canFam2.refGene.LENGTH)
```

canFam2.xenoRefGene.LENGTH

Transcript length data for the organism canFam

#### **Description**

canFam2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(canFam2, xenoRefGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(canFam2.xenoRefGene.LENGTH)
head(canFam2.xenoRefGene.LENGTH)
```

cavPor3.ensGene.LENGTH

Transcript length data for the organism cavPor

## **Description**

cavPor3.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(cavPor3, ensGene) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

```
data(cavPor3.ensGene.LENGTH)
head(cavPor3.ensGene.LENGTH)
```

cavPor3.genscan.LENGTH

Transcript length data for the organism cavPor

#### **Description**

cavPor3.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(cavPor3, genscan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(cavPor3.genscan.LENGTH)
head(cavPor3.genscan.LENGTH)
```

cavPor3.nscanGene.LENGTH

Transcript length data for the organism cavPor

## **Description**

cavPor3.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(cavPor3, nscanGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(cavPor3.nscanGene.LENGTH)
head(cavPor3.nscanGene.LENGTH)
```

cavPor3.xenoRefGene.LENGTH

Transcript length data for the organism cavPor

## **Description**

cavPor3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(cavPor3, xenoRefGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(cavPor3.xenoRefGene.LENGTH)
head(cavPor3.xenoRefGene.LENGTH)
```

cb1.xenoRefGene.LENGTH

Transcript length data for the organism cb

## **Description**

cb1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(cb1, xenoRefGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(cb1.xenoRefGene.LENGTH)
head(cb1.xenoRefGene.LENGTH)
```

cb3.xenoRefGene.LENGTH

Transcript length data for the organism cb

# Description

cb3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(cb3, xenoRefGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

## **Examples**

```
data(cb3.xenoRefGene.LENGTH)
head(cb3.xenoRefGene.LENGTH)
```

ce2.geneid.LENGTH

Transcript length data for the organism ce

# Description

ce2.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(ce2, geneid) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(ce2.geneid.LENGTH)
head(ce2.geneid.LENGTH)
```

36 ce2.refGene.LENGTH

ce2.geneSymbol.LENGTH Transcript length data for the organism ce

## **Description**

ce2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(ce2, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(ce2.geneSymbol.LENGTH)
head(ce2.geneSymbol.LENGTH)
```

ce2.refGene.LENGTH

Transcript length data for the organism ce

# Description

ce2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(ce2, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(ce2.refGene.LENGTH)
head(ce2.refGene.LENGTH)
```

ce4.geneSymbol.LENGTH Transcript length data for the organism ce

# **Description**

ce4.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(ce4, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

# **Examples**

```
data(ce4.geneSymbol.LENGTH)
head(ce4.geneSymbol.LENGTH)
```

ce4.refGene.LENGTH

Transcript length data for the organism ce

# Description

ce4.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(ce4, refGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(ce4.refGene.LENGTH)
head(ce4.refGene.LENGTH)
```

38 ce6.ensGene.LENGTH

```
ce4.xenoRefGene.LENGTH
```

Transcript length data for the organism ce

# **Description**

ce4.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(ce4, xenoRefGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

# **Examples**

```
data(ce4.xenoRefGene.LENGTH)
head(ce4.xenoRefGene.LENGTH)
```

ce6.ensGene.LENGTH

Transcript length data for the organism ce

# Description

ce6.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(ce6, ensGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(ce6.ensGene.LENGTH)
head(ce6.ensGene.LENGTH)
```

ce6.geneSymbol.LENGTH Transcript length data for the organism ce

# **Description**

ce6.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(ce6, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

# **Examples**

```
data(ce6.geneSymbol.LENGTH)
head(ce6.geneSymbol.LENGTH)
```

ce6.refGene.LENGTH

Transcript length data for the organism ce

# Description

ce6.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(ce6, refGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(ce6.refGene.LENGTH)
head(ce6.refGene.LENGTH)
```

ce6.xenoRefGene.LENGTH

Transcript length data for the organism ce

# Description

ce6.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(ce6, xenoRefGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

# **Examples**

```
data(ce6.xenoRefGene.LENGTH)
head(ce6.xenoRefGene.LENGTH)
```

ci1.geneSymbol.LENGTH Transcript length data for the organism ci

# Description

ci1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(ci1, geneSymbol) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(ci1.geneSymbol.LENGTH)
head(ci1.geneSymbol.LENGTH)
```

ci1.refGene.LENGTH 41

ci1.refGene.LENGTH

Transcript length data for the organism ci

#### **Description**

ci1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(ci1, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

# **Examples**

```
data(ci1.refGene.LENGTH)
head(ci1.refGene.LENGTH)
```

ci1.xenoRefGene.LENGTH

Transcript length data for the organism ci

# Description

ci1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(ci1, xenoRefGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(ci1.xenoRefGene.LENGTH)
head(ci1.xenoRefGene.LENGTH)
```

ci2.ensGene.LENGTH

Transcript length data for the organism ci

# **Description**

ci2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(ci2, ensGene) on the date on which the package was last updated.

# See Also

 ${\tt downloadLengthFromUCSC}$ 

# **Examples**

```
data(ci2.ensGene.LENGTH)
head(ci2.ensGene.LENGTH)
```

ci2.geneSymbol.LENGTH Transcript length data for the organism ci

# Description

ci2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(ci2, geneSymbol) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(ci2.geneSymbol.LENGTH)
head(ci2.geneSymbol.LENGTH)
```

ci2.refGene.LENGTH 43

ci2.refGene.LENGTH

Transcript length data for the organism ci

#### **Description**

ci2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(ci2, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

# **Examples**

```
data(ci2.refGene.LENGTH)
head(ci2.refGene.LENGTH)
```

ci2.xenoRefGene.LENGTH

Transcript length data for the organism ci

# Description

ci2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(ci2, xenoRefGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(ci2.xenoRefGene.LENGTH)
head(ci2.xenoRefGene.LENGTH)
```

danRer3.ensGene.LENGTH

Transcript length data for the organism danRer

# **Description**

danRer3.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(danRer3, ensGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(danRer3.ensGene.LENGTH)
head(danRer3.ensGene.LENGTH)
```

danRer3.geneSymbol.LENGTH

Transcript length data for the organism danRer

#### **Description**

danRer3.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(danRer3, geneSymbol) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

```
data(danRer3.geneSymbol.LENGTH)
head(danRer3.geneSymbol.LENGTH)
```

danRer3.refGene.LENGTH

Transcript length data for the organism danRer

# **Description**

danRer3.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(danRer3, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(danRer3.refGene.LENGTH)
head(danRer3.refGene.LENGTH)
```

danRer4.ensGene.LENGTH

Transcript length data for the organism danRer

# **Description**

danRer4.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(danRer4, ensGene) on the date on which the package was last updated.

# See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(danRer4.ensGene.LENGTH)
head(danRer4.ensGene.LENGTH)
```

danRer4.geneSymbol.LENGTH

Transcript length data for the organism danRer

# **Description**

danRer4.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(danRer4, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(danRer4.geneSymbol.LENGTH)
head(danRer4.geneSymbol.LENGTH)
```

danRer4.genscan.LENGTH

Transcript length data for the organism danRer

#### **Description**

danRer4.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(danRer4, genscan) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(danRer4.genscan.LENGTH)
head(danRer4.genscan.LENGTH)
```

danRer4.nscanGene.LENGTH

Transcript length data for the organism danRer

# **Description**

danRer4.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(danRer4, nscanGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(danRer4.nscanGene.LENGTH)
head(danRer4.nscanGene.LENGTH)
```

danRer4.refGene.LENGTH

Transcript length data for the organism danRer

# **Description**

danRer4.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(danRer4, refGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

```
data(danRer4.refGene.LENGTH)
head(danRer4.refGene.LENGTH)
```

danRer5.ensGene.LENGTH

Transcript length data for the organism danRer

# **Description**

danRer5.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(danRer5, ensGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(danRer5.ensGene.LENGTH)
head(danRer5.ensGene.LENGTH)
```

danRer5.geneSymbol.LENGTH

Transcript length data for the organism danRer

#### **Description**

danRer5.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(danRer5, geneSymbol) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

```
data(danRer5.geneSymbol.LENGTH)
head(danRer5.geneSymbol.LENGTH)
```

danRer5.refGene.LENGTH

Transcript length data for the organism danRer

# **Description**

danRer5.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(danRer5, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(danRer5.refGene.LENGTH)
head(danRer5.refGene.LENGTH)
```

danRer5.vegaGene.LENGTH

Transcript length data for the organism danRer

# **Description**

danRer5.vegaGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the vegaGene table.

The data file was made by calling downloadLengthFromUCSC(danRer5, vegaGene) on the date on which the package was last updated.

# See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(danRer5.vegaGene.LENGTH)
head(danRer5.vegaGene.LENGTH)
```

danRer5.vegaPseudoGene.LENGTH

Transcript length data for the organism danRer

# **Description**

danRer5.vegaPseudoGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the vegaPseudoGene table.

The data file was made by calling downloadLengthFromUCSC(danRer5, vegaPseudoGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(danRer5.vegaPseudoGene.LENGTH)
head(danRer5.vegaPseudoGene.LENGTH)
```

danRer6.ensGene.LENGTH

Transcript length data for the organism danRer

#### **Description**

danRer6.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(danRer6, ensGene) on the date on which the package was last updated.

# See Also

downloadLengthFromUCSC

```
data(danRer6.ensGene.LENGTH)
head(danRer6.ensGene.LENGTH)
```

danRer6.geneSymbol.LENGTH

Transcript length data for the organism danRer

# **Description**

danRer6.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(danRer6, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(danRer6.geneSymbol.LENGTH)
head(danRer6.geneSymbol.LENGTH)
```

danRer6.refGene.LENGTH

Transcript length data for the organism danRer

#### **Description**

danRer6.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(danRer6, refGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

```
data(danRer6.refGene.LENGTH)
head(danRer6.refGene.LENGTH)
```

danRer6.xenoRefGene.LENGTH

Transcript length data for the organism danRer

# Description

danRer6.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(danRer6, xenoRefGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

# **Examples**

```
data(danRer6.xenoRefGene.LENGTH)
head(danRer6.xenoRefGene.LENGTH)
```

dm1.geneSymbol.LENGTH Transcript length data for the organism dm

# Description

dm1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(dm1, geneSymbol) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(dm1.geneSymbol.LENGTH)
head(dm1.geneSymbol.LENGTH)
```

dm1.genscan.LENGTH

Transcript length data for the organism dm

# **Description**

dm1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(dm1, genscan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

# **Examples**

```
data(dm1.genscan.LENGTH)
head(dm1.genscan.LENGTH)
```

dm1.refGene.LENGTH

Transcript length data for the organism dm

# Description

dm1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(dm1, refGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(dm1.refGene.LENGTH)
head(dm1.refGene.LENGTH)
```

dm2.geneid.LENGTH

Transcript length data for the organism dm

# **Description**

dm2.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(dm2, geneid) on the date on which the package was last updated.

# See Also

 ${\tt downloadLengthFromUCSC}$ 

# **Examples**

```
data(dm2.geneid.LENGTH)
head(dm2.geneid.LENGTH)
```

dm2.geneSymbol.LENGTH Transcript length data for the organism dm

# Description

dm2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(dm2, geneSymbol) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(dm2.geneSymbol.LENGTH)
head(dm2.geneSymbol.LENGTH)
```

dm2.genscan.LENGTH

Transcript length data for the organism dm

# **Description**

dm2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(dm2, genscan) on the date on which the package was last updated.

# See Also

 ${\tt downloadLengthFromUCSC}$ 

# **Examples**

```
data(dm2.genscan.LENGTH)
head(dm2.genscan.LENGTH)
```

dm2.nscanGene.LENGTH

Transcript length data for the organism dm

# Description

dm2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(dm2, nscanGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(dm2.nscanGene.LENGTH)
head(dm2.nscanGene.LENGTH)
```

dm2.refGene.LENGTH

Transcript length data for the organism dm

# Description

dm2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(dm2, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

# **Examples**

```
data(dm2.refGene.LENGTH)
head(dm2.refGene.LENGTH)
```

dm3.geneSymbol.LENGTH Transcript length data for the organism dm

# Description

dm3.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(dm3, geneSymbol) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(dm3.geneSymbol.LENGTH)
head(dm3.geneSymbol.LENGTH)
```

dm3.nscanPasaGene.LENGTH

Transcript length data for the organism dm

# Description

dm3.nscanPasaGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the nscanPasaGene table.

The data file was made by calling downloadLengthFromUCSC(dm3, nscanPasaGene) on the date on which the package was last updated.

# See Also

 ${\tt downloadLengthFromUCSC}$ 

# **Examples**

```
data(dm3.nscanPasaGene.LENGTH)
head(dm3.nscanPasaGene.LENGTH)
```

dm3.refGene.LENGTH

Transcript length data for the organism dm

# **Description**

dm3.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(dm3, refGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(dm3.refGene.LENGTH)
head(dm3.refGene.LENGTH)
```

dp2.genscan.LENGTH

Transcript length data for the organism dp

### **Description**

dp2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(dp2, genscan) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

# **Examples**

```
data(dp2.genscan.LENGTH)
head(dp2.genscan.LENGTH)
```

```
dp2.xenoRefGene.LENGTH
```

Transcript length data for the organism dp

# Description

dp2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(dp2, xenoRefGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(dp2.xenoRefGene.LENGTH)
head(dp2.xenoRefGene.LENGTH)
```

dp3.geneid.LENGTH 59

dp3.geneid.LENGTH

Transcript length data for the organism dp

# **Description**

dp3.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(dp3, geneid) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

# **Examples**

```
data(dp3.geneid.LENGTH)
head(dp3.geneid.LENGTH)
```

dp3.genscan.LENGTH

Transcript length data for the organism dp

# Description

dp3.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(dp3, genscan) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(dp3.genscan.LENGTH)
head(dp3.genscan.LENGTH)
```

```
dp3.xenoRefGene.LENGTH
```

Transcript length data for the organism dp

# Description

dp3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(dp3, xenoRefGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

# **Examples**

```
data(dp3.xenoRefGene.LENGTH)
head(dp3.xenoRefGene.LENGTH)
```

droAna1.geneid.LENGTH Transcript length data for the organism droAna

# Description

droAna1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(droAna1, geneid) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(droAna1.geneid.LENGTH)
head(droAna1.geneid.LENGTH)
```

droAna1.genscan.LENGTH

Transcript length data for the organism droAna

# **Description**

droAna1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(droAna1, genscan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(droAna1.genscan.LENGTH)
head(droAna1.genscan.LENGTH)
```

droAna1.xenoRefGene.LENGTH

Transcript length data for the organism droAna

#### **Description**

droAna1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(droAna1, xenoRefGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

```
data(droAna1.xenoRefGene.LENGTH)
head(droAna1.xenoRefGene.LENGTH)
```

droAna2.genscan.LENGTH

Transcript length data for the organism droAna

# **Description**

droAna2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(droAna2, genscan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(droAna2.genscan.LENGTH)
head(droAna2.genscan.LENGTH)
```

droAna2.xenoRefGene.LENGTH

Transcript length data for the organism droAna

# **Description**

droAna2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(droAna2, xenoRefGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

```
data(droAna2.xenoRefGene.LENGTH)
head(droAna2.xenoRefGene.LENGTH)
```

droEre1.genscan.LENGTH

Transcript length data for the organism droEre

# **Description**

droEre1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(droEre1, genscan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(droEre1.genscan.LENGTH)
head(droEre1.genscan.LENGTH)
```

droEre1.xenoRefGene.LENGTH

Transcript length data for the organism droEre

#### **Description**

droEre1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(droEre1, xenoRefGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

```
data(droEre1.xenoRefGene.LENGTH)
head(droEre1.xenoRefGene.LENGTH)
```

droGri1.genscan.LENGTH

Transcript length data for the organism droGri

# **Description**

droGri1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(droGri1, genscan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(droGri1.genscan.LENGTH)
head(droGri1.genscan.LENGTH)
```

droGri1.xenoRefGene.LENGTH

Transcript length data for the organism droGri

# **Description**

droGri1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(droGri1, xenoRefGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

```
data(droGri1.xenoRefGene.LENGTH)
head(droGri1.xenoRefGene.LENGTH)
```

droMoj1.geneid.LENGTH Transcript length data for the organism droMoj

#### **Description**

droMoj1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(droMoj1, geneid) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

### **Examples**

```
data(droMoj1.geneid.LENGTH)
head(droMoj1.geneid.LENGTH)
```

droMoj1.genscan.LENGTH

Transcript length data for the organism droMoj

# Description

droMoj1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(droMoj1, genscan) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(droMoj1.genscan.LENGTH)
head(droMoj1.genscan.LENGTH)
```

droMoj1.xenoRefGene.LENGTH

Transcript length data for the organism droMoj

# **Description**

droMoj1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(droMoj1, xenoRefGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

### **Examples**

```
data(droMoj1.xenoRefGene.LENGTH)
head(droMoj1.xenoRefGene.LENGTH)
```

droMoj2.genscan.LENGTH

Transcript length data for the organism droMoj

# **Description**

droMoj2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(droMoj2, genscan) on the date on which the package was last updated.

# See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(droMoj2.genscan.LENGTH)
head(droMoj2.genscan.LENGTH)
```

droMoj2.xenoRefGene.LENGTH

Transcript length data for the organism droMoj

# **Description**

droMoj2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(droMoj2, xenoRefGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(droMoj2.xenoRefGene.LENGTH)
head(droMoj2.xenoRefGene.LENGTH)
```

droPer1.genscan.LENGTH

Transcript length data for the organism droPer

# **Description**

droPer1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(droPer1, genscan) on the date on which the package was last updated.

# See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(droPer1.genscan.LENGTH)
head(droPer1.genscan.LENGTH)
```

droPer1.xenoRefGene.LENGTH

Transcript length data for the organism droPer

# **Description**

droPer1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(droPer1, xenoRefGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(droPer1.xenoRefGene.LENGTH)
head(droPer1.xenoRefGene.LENGTH)
```

 ${\tt droSec1.genscan.LENGTH}$ 

Transcript length data for the organism droSec

# **Description**

droSec1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(droSec1, genscan) on the date on which the package was last updated.

# See Also

downloadLengthFromUCSC

```
data(droSec1.genscan.LENGTH)
head(droSec1.genscan.LENGTH)
```

droSec1.xenoRefGene.LENGTH

Transcript length data for the organism droSec

# Description

droSec1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(droSec1, xenoRefGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

# **Examples**

```
data(droSec1.xenoRefGene.LENGTH)
head(droSec1.xenoRefGene.LENGTH)
```

droSim1.geneid.LENGTH Transcript length data for the organism droSim

# Description

droSim1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(droSim1, geneid) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(droSim1.geneid.LENGTH)
head(droSim1.geneid.LENGTH)
```

droSim1.genscan.LENGTH

Transcript length data for the organism droSim

# **Description**

droSim1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(droSim1, genscan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(droSim1.genscan.LENGTH)
head(droSim1.genscan.LENGTH)
```

droSim1.xenoRefGene.LENGTH

Transcript length data for the organism droSim

# **Description**

droSim1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(droSim1, xenoRefGene) on the date on which the package was last updated.

# See Also

downloadLengthFromUCSC

```
data(droSim1.xenoRefGene.LENGTH)
head(droSim1.xenoRefGene.LENGTH)
```

droVir1.geneid.LENGTH Transcript length data for the organism droVir

#### **Description**

droVir1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(droVir1, geneid) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

# **Examples**

```
data(droVir1.geneid.LENGTH)
head(droVir1.geneid.LENGTH)
```

droVir1.genscan.LENGTH

Transcript length data for the organism droVir

# Description

droVir1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(droVir1, genscan) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(droVir1.genscan.LENGTH)
head(droVir1.genscan.LENGTH)
```

droVir1.xenoRefGene.LENGTH

Transcript length data for the organism droVir

# **Description**

droVir1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(droVir1, xenoRefGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(droVir1.xenoRefGene.LENGTH)
head(droVir1.xenoRefGene.LENGTH)
```

droVir2.genscan.LENGTH

Transcript length data for the organism droVir

# **Description**

droVir2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(droVir2, genscan) on the date on which the package was last updated.

# See Also

downloadLengthFromUCSC

```
data(droVir2.genscan.LENGTH)
head(droVir2.genscan.LENGTH)
```

droVir2.xenoRefGene.LENGTH

Transcript length data for the organism droVir

## **Description**

droVir2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(droVir2, xenoRefGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

## **Examples**

```
data(droVir2.xenoRefGene.LENGTH)
head(droVir2.xenoRefGene.LENGTH)
```

droYak1.geneid.LENGTH Transcript length data for the organism droYak

# Description

dro Yak 1. geneid. LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(droYak1, geneid) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(droYak1.geneid.LENGTH)
head(droYak1.geneid.LENGTH)
```

droYak1.genscan.LENGTH

Transcript length data for the organism droYak

## **Description**

droYak1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(droYak1, genscan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(droYak1.genscan.LENGTH)
head(droYak1.genscan.LENGTH)
```

droYak1.xenoRefGene.LENGTH

Transcript length data for the organism droYak

## **Description**

droYak1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(droYak1, xenoRefGene) on the date on which the package was last updated.

# See Also

downloadLengthFromUCSC

```
data(droYak1.xenoRefGene.LENGTH)
head(droYak1.xenoRefGene.LENGTH)
```

droYak2.genscan.LENGTH

Transcript length data for the organism droYak

## **Description**

droYak2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(droYak2, genscan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(droYak2.genscan.LENGTH)
head(droYak2.genscan.LENGTH)
```

droYak2.xenoRefGene.LENGTH

Transcript length data for the organism droYak

## **Description**

dro Yak2.xeno Ref Gene. LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xeno Ref Gene table.

The data file was made by calling downloadLengthFromUCSC(droYak2, xenoRefGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

```
data(droYak2.xenoRefGene.LENGTH)
head(droYak2.xenoRefGene.LENGTH)
```

equCab1.geneid.LENGTH Transcript length data for the organism equCab

#### **Description**

equCab1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(equCab1, geneid) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

#### **Examples**

```
data(equCab1.geneid.LENGTH)
head(equCab1.geneid.LENGTH)
```

equCab1.geneSymbol.LENGTH

Transcript length data for the organism equCab

# Description

equCab1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(equCab1, geneSymbol) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(equCab1.geneSymbol.LENGTH)
head(equCab1.geneSymbol.LENGTH)
```

```
equCab1.nscanGene.LENGTH
```

Transcript length data for the organism equCab

## **Description**

equCab1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(equCab1, nscanGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(equCab1.nscanGene.LENGTH)
head(equCab1.nscanGene.LENGTH)
```

equCab1.refGene.LENGTH

Transcript length data for the organism equCab

#### **Description**

equCab1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(equCab1, refGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

```
data(equCab1.refGene.LENGTH)
head(equCab1.refGene.LENGTH)
```

```
equCab1.sgpGene.LENGTH
```

Transcript length data for the organism equCab

## **Description**

equCab1.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(equCab1, sgpGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(equCab1.sgpGene.LENGTH)
head(equCab1.sgpGene.LENGTH)
```

equCab2.ensGene.LENGTH

Transcript length data for the organism equCab

#### **Description**

equCab2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(equCab2, ensGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

```
data(equCab2.ensGene.LENGTH)
head(equCab2.ensGene.LENGTH)
```

equCab2.geneSymbol.LENGTH

Transcript length data for the organism equCab

## **Description**

equCab2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(equCab2, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(equCab2.geneSymbol.LENGTH)
head(equCab2.geneSymbol.LENGTH)
```

equCab2.nscanGene.LENGTH

Transcript length data for the organism equCab

#### **Description**

equCab2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(equCab2, nscanGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(equCab2.nscanGene.LENGTH)
head(equCab2.nscanGene.LENGTH)
```

equCab2.refGene.LENGTH

Transcript length data for the organism equCab

## **Description**

equCab2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(equCab2, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(equCab2.refGene.LENGTH)
head(equCab2.refGene.LENGTH)
```

equCab2.xenoRefGene.LENGTH

Transcript length data for the organism equCab

## **Description**

equCab2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(equCab2, xenoRefGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(equCab2.xenoRefGene.LENGTH)
head(equCab2.xenoRefGene.LENGTH)
```

felCat3.ensGene.LENGTH

Transcript length data for the organism felCat

## **Description**

felCat3.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(felCat3, ensGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

# **Examples**

data(felCat3.ensGene.LENGTH)
head(felCat3.ensGene.LENGTH)

felCat3.geneid.LENGTH Transcript length data for the organism felCat

# Description

felCat3.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(felCat3, geneid) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(felCat3.geneid.LENGTH)
head(felCat3.geneid.LENGTH)
```

felCat3.geneSymbol.LENGTH

Transcript length data for the organism felCat

## **Description**

felCat3.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(felCat3, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(felCat3.geneSymbol.LENGTH)
head(felCat3.geneSymbol.LENGTH)
```

felCat3.genscan.LENGTH

Transcript length data for the organism felCat

## **Description**

felCat3.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(felCat3, genscan) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(felCat3.genscan.LENGTH)
head(felCat3.genscan.LENGTH)
```

felCat3.nscanGene.LENGTH

Transcript length data for the organism felCat

## **Description**

felCat3.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(felCat3, nscanGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(felCat3.nscanGene.LENGTH)
head(felCat3.nscanGene.LENGTH)
```

felCat3.refGene.LENGTH

Transcript length data for the organism felCat

## **Description**

felCat3.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(felCat3, refGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(felCat3.refGene.LENGTH)
head(felCat3.refGene.LENGTH)
```

felCat3.sgpGene.LENGTH

Transcript length data for the organism felCat

## **Description**

felCat3.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(felCat3, sgpGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(felCat3.sgpGene.LENGTH)
head(felCat3.sgpGene.LENGTH)
```

felCat3.xenoRefGene.LENGTH

Transcript length data for the organism felCat

## **Description**

felCat3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(felCat3, xenoRefGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(felCat3.xenoRefGene.LENGTH)
head(felCat3.xenoRefGene.LENGTH)
```

fr1.ensGene.LENGTH 85

fr1.ensGene.LENGTH

Transcript length data for the organism fr

# **Description**

fr1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(fr1, ensGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(fr1.ensGene.LENGTH)
head(fr1.ensGene.LENGTH)
```

fr1.genscan.LENGTH

Transcript length data for the organism fr

# Description

fr1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(fr1, genscan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(fr1.genscan.LENGTH)
head(fr1.genscan.LENGTH)
```

fr2.ensGene.LENGTH

Transcript length data for the organism fr

#### **Description**

fr2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(fr2, ensGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

### **Examples**

```
data(fr2.ensGene.LENGTH)
head(fr2.ensGene.LENGTH)
```

galGal2.ensGene.LENGTH

Transcript length data for the organism galGal

# Description

galGal2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(galGal2, ensGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(galGal2.ensGene.LENGTH)
head(galGal2.ensGene.LENGTH)
```

galGal2.geneid.LENGTH Transcript length data for the organism galGal

#### **Description**

galGal2.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(galGal2, geneid) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

### **Examples**

```
data(galGal2.geneid.LENGTH)
head(galGal2.geneid.LENGTH)
```

```
galGal2.geneSymbol.LENGTH
```

Transcript length data for the organism galGal

# Description

galGal2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(galGal2, geneSymbol) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(galGal2.geneSymbol.LENGTH)
head(galGal2.geneSymbol.LENGTH)
```

galGal2.genscan.LENGTH

Transcript length data for the organism galGal

## **Description**

galGal2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(galGal2, genscan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(galGal2.genscan.LENGTH)
head(galGal2.genscan.LENGTH)
```

galGal2.refGene.LENGTH

Transcript length data for the organism galGal

#### **Description**

galGal2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(galGal2, refGene) on the date on which the package was last updated.

# See Also

downloadLengthFromUCSC

```
data(galGal2.refGene.LENGTH)
head(galGal2.refGene.LENGTH)
```

```
galGal2.sgpGene.LENGTH
```

## **Description**

galGal2.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(galGal2, sgpGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

#### **Examples**

```
data(galGal2.sgpGene.LENGTH)
head(galGal2.sgpGene.LENGTH)
```

```
galGal3.ensGene.LENGTH
```

Transcript length data for the organism galGal

#### **Description**

galGal3.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(galGal3, ensGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

```
data(galGal3.ensGene.LENGTH)
head(galGal3.ensGene.LENGTH)
```

```
galGal3.geneSymbol.LENGTH
```

## **Description**

galGal3.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(galGal3, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(galGal3.geneSymbol.LENGTH)
head(galGal3.geneSymbol.LENGTH)
```

galGal3.genscan.LENGTH

Transcript length data for the organism galGal

#### **Description**

galGal3.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(galGal3, genscan) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

```
data(galGal3.genscan.LENGTH)
head(galGal3.genscan.LENGTH)
```

```
galGal3.nscanGene.LENGTH
```

## **Description**

galGal3.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(galGal3, nscanGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(galGal3.nscanGene.LENGTH)
head(galGal3.nscanGene.LENGTH)
```

```
galGal3.refGene.LENGTH
```

Transcript length data for the organism galGal

#### **Description**

galGal3.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(galGal3, refGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

```
data(galGal3.refGene.LENGTH)
head(galGal3.refGene.LENGTH)
```

```
galGal3.xenoRefGene.LENGTH
```

#### **Description**

galGal3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(galGal3, xenoRefGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(galGal3.xenoRefGene.LENGTH)
head(galGal3.xenoRefGene.LENGTH)
```

gasAcu1.ensGene.LENGTH

Transcript length data for the organism gasAcu

#### **Description**

gasAcu1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(gasAcu1, ensGene) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

```
data(gasAcu1.ensGene.LENGTH)
head(gasAcu1.ensGene.LENGTH)
```

```
gasAcu1.nscanGene.LENGTH
```

## **Description**

gasAcu1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(gasAcu1, nscanGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

#### **Examples**

```
data(gasAcu1.nscanGene.LENGTH)
head(gasAcu1.nscanGene.LENGTH)
```

hg16.acembly.LENGTH

Transcript length data for the organism hg

## **Description**

hg16.acembly.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the acembly table.

The data file was made by calling downloadLengthFromUCSC(hg16, acembly) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(hg16.acembly.LENGTH)
head(hg16.acembly.LENGTH)
```

hg16.ensGene.LENGTH

Transcript length data for the organism hg

## **Description**

hg16.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(hg16, ensGene) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## **Examples**

```
data(hg16.ensGene.LENGTH)
head(hg16.ensGene.LENGTH)
```

hg16.exoniphy.LENGTH Transcript length data for the organism hg

# Description

hg16.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the exoniphy table.

The data file was made by calling downloadLengthFromUCSC(hg16, exoniphy) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(hg16.exoniphy.LENGTH)
head(hg16.exoniphy.LENGTH)
```

hg16.geneid.LENGTH

Transcript length data for the organism hg

#### **Description**

hg16.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(hg16, geneid) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(hg16.geneid.LENGTH)
head(hg16.geneid.LENGTH)
```

hg16.geneSymbol.LENGTH

Transcript length data for the organism hg

# Description

hg16.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(hg16, geneSymbol) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(hg16.geneSymbol.LENGTH)
head(hg16.geneSymbol.LENGTH)
```

hg16.genscan.LENGTH Transcript length data for the organism hg

## **Description**

hg16.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(hg16, genscan) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

data(hg16.genscan.LENGTH)
head(hg16.genscan.LENGTH)

hg16.knownGene.LENGTH Transcript length data for the organism hg

# Description

hg16.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the knownGene table.

The data file was made by calling downloadLengthFromUCSC(hg16, knownGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

data(hg16.knownGene.LENGTH)
head(hg16.knownGene.LENGTH)

hg16.refGene.LENGTH

Transcript length data for the organism hg

# Description

hg16.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(hg16, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(hg16.refGene.LENGTH)
head(hg16.refGene.LENGTH)
```

hg16.sgpGene.LENGTH

Transcript length data for the organism hg

# Description

hg16.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(hg16, sgpGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(hg16.sgpGene.LENGTH)
head(hg16.sgpGene.LENGTH)
```

hg17.acembly.LENGTH Transcript length data for the organism hg

## **Description**

hg17.acembly.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the acembly table.

The data file was made by calling downloadLengthFromUCSC(hg17, acembly) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## **Examples**

```
data(hg17.acembly.LENGTH)
head(hg17.acembly.LENGTH)
```

hg17.acescan.LENGTH

Transcript length data for the organism hg

# Description

hg17.acescan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the acescan table.

The data file was made by calling downloadLengthFromUCSC(hg17, acescan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(hg17.acescan.LENGTH)
head(hg17.acescan.LENGTH)
```

hg17.ccdsGene.LENGTH Transcript length data for the organism hg

## **Description**

hg17.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ccdsGene table.

The data file was made by calling downloadLengthFromUCSC(hg17, ccdsGene) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## **Examples**

```
data(hg17.ccdsGene.LENGTH)
head(hg17.ccdsGene.LENGTH)
```

hg17.ensGene.LENGTH

Transcript length data for the organism hg

# Description

hg17.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(hg17, ensGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(hg17.ensGene.LENGTH)
head(hg17.ensGene.LENGTH)
```

hg17.exoniphy.LENGTH Transcript length data for the organism hg

# Description

hg17.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the exoniphy table.

The data file was made by calling downloadLengthFromUCSC(hg17, exoniphy) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(hg17.exoniphy.LENGTH)
head(hg17.exoniphy.LENGTH)
```

hg17.geneid.LENGTH

Transcript length data for the organism hg

# Description

hg17.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(hg17, geneid) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(hg17.geneid.LENGTH)
head(hg17.geneid.LENGTH)
```

hg17.geneSymbol.LENGTH

Transcript length data for the organism hg

## **Description**

hg17.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(hg17, geneSymbol) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## **Examples**

```
data(hg17.geneSymbol.LENGTH)
head(hg17.geneSymbol.LENGTH)
```

hg17.genscan.LENGTH

Transcript length data for the organism hg

## **Description**

hg17.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(hg17, genscan) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(hg17.genscan.LENGTH)
head(hg17.genscan.LENGTH)
```

hg17.knownGene.LENGTH Transcript length data for the organism hg

## **Description**

hg17.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the knownGene table.

The data file was made by calling downloadLengthFromUCSC(hg17, knownGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(hg17.knownGene.LENGTH)
head(hg17.knownGene.LENGTH)
```

hg17.refGene.LENGTH

Transcript length data for the organism hg

# Description

hg17.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(hg17, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(hg17.refGene.LENGTH)
head(hg17.refGene.LENGTH)
```

hg17.sgpGene.LENGTH

Transcript length data for the organism hg

## **Description**

hg17.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(hg17, sgpGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(hg17.sgpGene.LENGTH)
head(hg17.sgpGene.LENGTH)
```

hg17.vegaGene.LENGTH Transcript length data for the organism hg

# Description

hg17.vegaGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the vegaGene table.

The data file was made by calling downloadLengthFromUCSC(hg17, vegaGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(hg17.vegaGene.LENGTH)
head(hg17.vegaGene.LENGTH)
```

hg17.vegaPseudoGene.LENGTH

Transcript length data for the organism hg

## **Description**

hg17.vegaPseudoGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the vegaPseudoGene table.

The data file was made by calling downloadLengthFromUCSC(hg17, vegaPseudoGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(hg17.vegaPseudoGene.LENGTH)
head(hg17.vegaPseudoGene.LENGTH)
```

hg17.xenoRefGene.LENGTH

Transcript length data for the organism hg

#### **Description**

hg17.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(hg17, xenoRefGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

```
data(hg17.xenoRefGene.LENGTH)
head(hg17.xenoRefGene.LENGTH)
```

hg18.acembly.LENGTH

Transcript length data for the organism hg

## **Description**

hg18.acembly.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the acembly table.

The data file was made by calling downloadLengthFromUCSC(hg18, acembly) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(hg18.acembly.LENGTH)
head(hg18.acembly.LENGTH)
```

hg18.acescan.LENGTH

Transcript length data for the organism hg

# Description

hg18.acescan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the acescan table.

The data file was made by calling downloadLengthFromUCSC(hg18, acescan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(hg18.acescan.LENGTH)
head(hg18.acescan.LENGTH)
```

hg18.ccdsGene.LENGTH Transcript length data for the organism hg

## **Description**

hg18.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ccdsGene table.

The data file was made by calling downloadLengthFromUCSC(hg18, ccdsGene) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## **Examples**

```
data(hg18.ccdsGene.LENGTH)
head(hg18.ccdsGene.LENGTH)
```

hg18.ensGene.LENGTH

Transcript length data for the organism hg

# Description

hg18.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(hg18, ensGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(hg18.ensGene.LENGTH)
head(hg18.ensGene.LENGTH)
```

hg18.exoniphy.LENGTH Transcript length data for the organism hg

## **Description**

hg18.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the exoniphy table.

The data file was made by calling downloadLengthFromUCSC(hg18, exoniphy) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(hg18.exoniphy.LENGTH)
head(hg18.exoniphy.LENGTH)
```

hg18.geneid.LENGTH

Transcript length data for the organism hg

# Description

hg18.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(hg18, geneid) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(hg18.geneid.LENGTH)
head(hg18.geneid.LENGTH)
```

```
hg18.geneSymbol.LENGTH
```

## **Description**

hg18.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(hg18, geneSymbol) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## **Examples**

```
data(hg18.geneSymbol.LENGTH)
head(hg18.geneSymbol.LENGTH)
```

hg18.genscan.LENGTH

Transcript length data for the organism hg

## **Description**

hg18.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(hg18, genscan) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(hg18.genscan.LENGTH)
head(hg18.genscan.LENGTH)
```

hg18.knownGene.LENGTH Transcript length data for the organism hg

#### **Description**

hg18.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the knownGene table.

The data file was made by calling downloadLengthFromUCSC(hg18, knownGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

### **Examples**

```
data(hg18.knownGene.LENGTH)
head(hg18.knownGene.LENGTH)
```

hg18.knownGeneOld3.LENGTH

Transcript length data for the organism hg

# Description

hg18.knownGeneOld3.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the knownGeneOld3 table.

The data file was made by calling downloadLengthFromUCSC(hg18, knownGeneOld3) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(hg18.knownGeneOld3.LENGTH)
head(hg18.knownGeneOld3.LENGTH)
```

hg18.refGene.LENGTH Transcript length data for the organism hg

## **Description**

hg18.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(hg18, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(hg18.refGene.LENGTH)
head(hg18.refGene.LENGTH)
```

hg18.sgpGene.LENGTH

Transcript length data for the organism hg

# Description

hg18.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(hg18, sgpGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(hg18.sgpGene.LENGTH)
head(hg18.sgpGene.LENGTH)
```

hg18.sibGene.LENGTH

Transcript length data for the organism hg

#### **Description**

hg18.sibGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sibGene table.

The data file was made by calling downloadLengthFromUCSC(hg18, sibGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

### **Examples**

```
data(hg18.sibGene.LENGTH)
head(hg18.sibGene.LENGTH)
```

hg18.xenoRefGene.LENGTH

Transcript length data for the organism hg

# Description

hg18.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(hg18, xenoRefGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(hg18.xenoRefGene.LENGTH)
head(hg18.xenoRefGene.LENGTH)
```

hg19.ccdsGene.LENGTH Transcript length data for the organism hg

## **Description**

hg19.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ccdsGene table.

The data file was made by calling downloadLengthFromUCSC(hg19, ccdsGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(hg19.ccdsGene.LENGTH)
head(hg19.ccdsGene.LENGTH)
```

hg19.ensGene.LENGTH

Transcript length data for the organism hg

# Description

hg19.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(hg19, ensGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(hg19.ensGene.LENGTH)
head(hg19.ensGene.LENGTH)
```

hg19.exoniphy.LENGTH Transcript length data for the organism hg

#### **Description**

hg19.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the exoniphy table.

The data file was made by calling downloadLengthFromUCSC(hg19, exoniphy) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

## **Examples**

```
data(hg19.exoniphy.LENGTH)
head(hg19.exoniphy.LENGTH)
```

hg19.geneSymbol.LENGTH

Transcript length data for the organism hg

# Description

hg19.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(hg19, geneSymbol) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(hg19.geneSymbol.LENGTH)
head(hg19.geneSymbol.LENGTH)
```

hg19.knownGene.LENGTH Transcript length data for the organism hg

## **Description**

hg19.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the knownGene table.

The data file was made by calling downloadLengthFromUCSC(hg19, knownGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

data(hg19.knownGene.LENGTH)
head(hg19.knownGene.LENGTH)

hg19.nscanGene.LENGTH Transcript length data for the organism hg

# Description

hg19.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(hg19, nscanGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

data(hg19.nscanGene.LENGTH)
head(hg19.nscanGene.LENGTH)

hg19.refGene.LENGTH

Transcript length data for the organism hg

#### **Description**

hg19.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(hg19, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(hg19.refGene.LENGTH)
head(hg19.refGene.LENGTH)
```

hg19.xenoRefGene.LENGTH

Transcript length data for the organism hg

# Description

hg19.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(hg19, xenoRefGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(hg19.xenoRefGene.LENGTH)
head(hg19.xenoRefGene.LENGTH)
```

116 mm7.ensGene.LENGTH

loxAfr3.xenoRefGene.LENGTH

Transcript length data for the organism loxAfr

## **Description**

loxAfr3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(loxAfr3, xenoRefGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

## **Examples**

```
data(loxAfr3.xenoRefGene.LENGTH)
head(loxAfr3.xenoRefGene.LENGTH)
```

mm7.ensGene.LENGTH

Transcript length data for the organism mm

# Description

mm7.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(mm7, ensGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(mm7.ensGene.LENGTH)
head(mm7.ensGene.LENGTH)
```

mm7.geneid.LENGTH

mm7.geneid.LENGTH

Transcript length data for the organism mm

## Description

mm7.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(mm7, geneid) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(mm7.geneid.LENGTH)
head(mm7.geneid.LENGTH)
```

mm7.geneSymbol.LENGTH Transcript length data for the organism mm

# Description

mm7.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(mm7, geneSymbol) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(mm7.geneSymbol.LENGTH)
head(mm7.geneSymbol.LENGTH)
```

mm7.genscan.LENGTH

Transcript length data for the organism mm

## **Description**

mm7.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(mm7, genscan) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(mm7.genscan.LENGTH)
head(mm7.genscan.LENGTH)
```

mm7.knownGene.LENGTH

Transcript length data for the organism mm

# Description

mm7.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the knownGene table.

The data file was made by calling downloadLengthFromUCSC(mm7, knownGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(mm7.knownGene.LENGTH)
head(mm7.knownGene.LENGTH)
```

mm7.refGene.LENGTH 119

mm7.refGene.LENGTH

Transcript length data for the organism mm

## **Description**

mm7.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(mm7, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(mm7.refGene.LENGTH)
head(mm7.refGene.LENGTH)
```

mm7.sgpGene.LENGTH

Transcript length data for the organism mm

# Description

mm7.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(mm7, sgpGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(mm7.sgpGene.LENGTH)
head(mm7.sgpGene.LENGTH)
```

mm7.xenoRefGene.LENGTH

Transcript length data for the organism mm

## **Description**

mm7.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(mm7, xenoRefGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

## **Examples**

```
data(mm7.xenoRefGene.LENGTH)
head(mm7.xenoRefGene.LENGTH)
```

mm8.ccdsGene.LENGTH

Transcript length data for the organism mm

# Description

mm8.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ccdsGene table.

The data file was made by calling downloadLengthFromUCSC(mm8, ccdsGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(mm8.ccdsGene.LENGTH)
head(mm8.ccdsGene.LENGTH)
```

mm8.ensGene.LENGTH 121

mm8.ensGene.LENGTH

Transcript length data for the organism mm

## Description

mm8.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(mm8, ensGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(mm8.ensGene.LENGTH)
head(mm8.ensGene.LENGTH)
```

mm8.geneid.LENGTH

Transcript length data for the organism mm

# Description

mm8.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(mm8, geneid) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(mm8.geneid.LENGTH)
head(mm8.geneid.LENGTH)
```

mm8.geneSymbol.LENGTH Transcript length data for the organism mm

## **Description**

mm8.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(mm8, geneSymbol) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(mm8.geneSymbol.LENGTH)
head(mm8.geneSymbol.LENGTH)
```

mm8.genscan.LENGTH

Transcript length data for the organism mm

# Description

mm8.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(mm8, genscan) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(mm8.genscan.LENGTH)
head(mm8.genscan.LENGTH)
```

## **Description**

mm8.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the knownGene table.

The data file was made by calling downloadLengthFromUCSC(mm8, knownGene) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## **Examples**

```
data(mm8.knownGene.LENGTH)
head(mm8.knownGene.LENGTH)
```

mm8.nscanGene.LENGTH Transcript length data for the organism mm

# Description

mm8.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(mm8, nscanGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(mm8.nscanGene.LENGTH)
head(mm8.nscanGene.LENGTH)
```

mm8.refGene.LENGTH

Transcript length data for the organism mm

## **Description**

mm8.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(mm8, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(mm8.refGene.LENGTH)
head(mm8.refGene.LENGTH)
```

mm8.sgpGene.LENGTH

Transcript length data for the organism mm

# Description

mm8.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(mm8, sgpGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(mm8.sgpGene.LENGTH)
head(mm8.sgpGene.LENGTH)
```

mm8.sibGene.LENGTH 125

mm8.sibGene.LENGTH

Transcript length data for the organism mm

#### **Description**

mm8.sibGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sibGene table.

The data file was made by calling downloadLengthFromUCSC(mm8, sibGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

## **Examples**

```
data(mm8.sibGene.LENGTH)
head(mm8.sibGene.LENGTH)
```

mm8.xenoRefGene.LENGTH

Transcript length data for the organism mm

# Description

mm8.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(mm8, xenoRefGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(mm8.xenoRefGene.LENGTH)
head(mm8.xenoRefGene.LENGTH)
```

mm9.acembly.LENGTH

Transcript length data for the organism mm

## **Description**

mm9.acembly.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the acembly table.

The data file was made by calling downloadLengthFromUCSC(mm9, acembly) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(mm9.acembly.LENGTH)
head(mm9.acembly.LENGTH)
```

mm9.ccdsGene.LENGTH

Transcript length data for the organism mm

# Description

mm9.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ccdsGene table.

The data file was made by calling downloadLengthFromUCSC(mm9, ccdsGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(mm9.ccdsGene.LENGTH)
head(mm9.ccdsGene.LENGTH)
```

mm9.ensGene.LENGTH 127

mm9.ensGene.LENGTH

Transcript length data for the organism mm

## **Description**

mm9.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(mm9, ensGene) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## **Examples**

```
data(mm9.ensGene.LENGTH)
head(mm9.ensGene.LENGTH)
```

mm9.exoniphy.LENGTH

Transcript length data for the organism mm

# Description

mm9.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the exoniphy table.

The data file was made by calling downloadLengthFromUCSC(mm9, exoniphy) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(mm9.exoniphy.LENGTH)
head(mm9.exoniphy.LENGTH)
```

mm9.geneid.LENGTH

Transcript length data for the organism mm

## **Description**

mm9.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(mm9, geneid) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(mm9.geneid.LENGTH)
head(mm9.geneid.LENGTH)
```

mm9.geneSymbol.LENGTH Transcript length data for the organism mm

# Description

mm9.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(mm9, geneSymbol) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(mm9.geneSymbol.LENGTH)
head(mm9.geneSymbol.LENGTH)
```

mm9.genscan.LENGTH

Transcript length data for the organism mm

## **Description**

mm9.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(mm9, genscan) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(mm9.genscan.LENGTH)
head(mm9.genscan.LENGTH)
```

mm9.knownGene.LENGTH

Transcript length data for the organism mm

# Description

mm9.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the knownGene table.

The data file was made by calling downloadLengthFromUCSC(mm9, knownGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(mm9.knownGene.LENGTH)
head(mm9.knownGene.LENGTH)
```

mm9.refGene.LENGTH

## **Description**

mm9.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(mm9, nscanGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(mm9.nscanGene.LENGTH)
head(mm9.nscanGene.LENGTH)
```

mm9.refGene.LENGTH

Transcript length data for the organism mm

# Description

mm9.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(mm9, refGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(mm9.refGene.LENGTH)
head(mm9.refGene.LENGTH)
```

mm9.sgpGene.LENGTH

Transcript length data for the organism mm

### **Description**

mm9.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(mm9, sgpGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

## **Examples**

```
data(mm9.sgpGene.LENGTH)
head(mm9.sgpGene.LENGTH)
```

mm9.xenoRefGene.LENGTH

Transcript length data for the organism mm

# Description

mm9.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(mm9, xenoRefGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(mm9.xenoRefGene.LENGTH)
head(mm9.xenoRefGene.LENGTH)
```

monDom1.genscan.LENGTH

Transcript length data for the organism monDom

### **Description**

monDom1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(monDom1, genscan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(monDom1.genscan.LENGTH)
head(monDom1.genscan.LENGTH)
```

monDom4.ensGene.LENGTH

Transcript length data for the organism monDom

## **Description**

monDom4.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(monDom4, ensGene) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

```
data(monDom4.ensGene.LENGTH)
head(monDom4.ensGene.LENGTH)
```

monDom4.geneSymbol.LENGTH

Transcript length data for the organism monDom

## **Description**

monDom4.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(monDom4, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(monDom4.geneSymbol.LENGTH)
head(monDom4.geneSymbol.LENGTH)
```

monDom4.genscan.LENGTH

Transcript length data for the organism monDom

## **Description**

monDom4.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(monDom4, genscan) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

```
data(monDom4.genscan.LENGTH)
head(monDom4.genscan.LENGTH)
```

monDom4.nscanGene.LENGTH

Transcript length data for the organism monDom

## **Description**

monDom4.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(monDom4, nscanGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

#### **Examples**

```
data(monDom4.nscanGene.LENGTH)
head(monDom4.nscanGene.LENGTH)
```

monDom4.refGene.LENGTH

Transcript length data for the organism monDom

## **Description**

monDom4.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(monDom4, refGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(monDom4.refGene.LENGTH)
head(monDom4.refGene.LENGTH)
```

monDom4.xenoRefGene.LENGTH

Transcript length data for the organism monDom

#### **Description**

monDom4.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(monDom4, xenoRefGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(monDom4.xenoRefGene.LENGTH)
head(monDom4.xenoRefGene.LENGTH)
```

monDom5.ensGene.LENGTH

Transcript length data for the organism monDom

## **Description**

monDom5.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(monDom5, ensGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(monDom5.ensGene.LENGTH)
head(monDom5.ensGene.LENGTH)
```

monDom5.geneSymbol.LENGTH

Transcript length data for the organism monDom

## **Description**

monDom5.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(monDom5, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(monDom5.geneSymbol.LENGTH)
head(monDom5.geneSymbol.LENGTH)
```

monDom5.genscan.LENGTH

Transcript length data for the organism monDom

## **Description**

monDom5.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(monDom5, genscan) on the date on which the package was last updated.

# See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(monDom5.genscan.LENGTH)
head(monDom5.genscan.LENGTH)
```

monDom5.nscanGene.LENGTH

Transcript length data for the organism monDom

## **Description**

monDom5.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(monDom5, nscanGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(monDom5.nscanGene.LENGTH)
head(monDom5.nscanGene.LENGTH)
```

monDom5.refGene.LENGTH

Transcript length data for the organism monDom

## **Description**

monDom5.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(monDom5, refGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(monDom5.refGene.LENGTH)
head(monDom5.refGene.LENGTH)
```

monDom5.xenoRefGene.LENGTH

Transcript length data for the organism monDom

#### **Description**

monDom5.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(monDom5, xenoRefGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(monDom5.xenoRefGene.LENGTH)
head(monDom5.xenoRefGene.LENGTH)
```

ornAna1.ensGene.LENGTH

Transcript length data for the organism ornAna

#### **Description**

ornAna1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(ornAna1, ensGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(ornAna1.ensGene.LENGTH)
head(ornAna1.ensGene.LENGTH)
```

ornAna1.geneSymbol.LENGTH

Transcript length data for the organism ornAna

## **Description**

ornAna1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(ornAna1, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(ornAna1.geneSymbol.LENGTH)
head(ornAna1.geneSymbol.LENGTH)
```

ornAna1.refGene.LENGTH

Transcript length data for the organism ornAna

#### **Description**

ornAna1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(ornAna1, refGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

```
data(ornAna1.refGene.LENGTH)
head(ornAna1.refGene.LENGTH)
```

ornAna1.xenoRefGene.LENGTH

Transcript length data for the organism ornAna

#### **Description**

ornAna1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(ornAna1, xenoRefGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(ornAna1.xenoRefGene.LENGTH)
head(ornAna1.xenoRefGene.LENGTH)
```

oryLat2.ensGene.LENGTH

Transcript length data for the organism oryLat

#### **Description**

oryLat2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(oryLat2, ensGene) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

```
data(oryLat2.ensGene.LENGTH)
head(oryLat2.ensGene.LENGTH)
```

oryLat2.geneSymbol.LENGTH

Transcript length data for the organism oryLat

## **Description**

oryLat2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(oryLat2, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(oryLat2.geneSymbol.LENGTH)
head(oryLat2.geneSymbol.LENGTH)
```

oryLat2.refGene.LENGTH

Transcript length data for the organism oryLat

#### **Description**

oryLat2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(oryLat2, refGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

```
data(oryLat2.refGene.LENGTH)
head(oryLat2.refGene.LENGTH)
```

oryLat2.xenoRefGene.LENGTH

Transcript length data for the organism oryLat

## **Description**

oryLat2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(oryLat2, xenoRefGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(oryLat2.xenoRefGene.LENGTH)
head(oryLat2.xenoRefGene.LENGTH)
```

panTro1.ensGene.LENGTH

Transcript length data for the organism panTro

## **Description**

panTro1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(panTro1, ensGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(panTro1.ensGene.LENGTH)
head(panTro1.ensGene.LENGTH)
```

panTro1.geneid.LENGTH Transcript length data for the organism panTro

#### **Description**

panTro1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(panTro1, geneid) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

### **Examples**

```
data(panTro1.geneid.LENGTH)
head(panTro1.geneid.LENGTH)
```

panTro1.genscan.LENGTH

Transcript length data for the organism panTro

# Description

panTro1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(panTro1, genscan) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(panTro1.genscan.LENGTH)
head(panTro1.genscan.LENGTH)
```

panTro1.xenoRefGene.LENGTH

Transcript length data for the organism panTro

#### **Description**

panTro1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(panTro1, xenoRefGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(panTro1.xenoRefGene.LENGTH)
head(panTro1.xenoRefGene.LENGTH)
```

panTro2.ensGene.LENGTH

Transcript length data for the organism panTro

## **Description**

panTro2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(panTro2, ensGene) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

```
data(panTro2.ensGene.LENGTH)
head(panTro2.ensGene.LENGTH)
```

panTro2.geneSymbol.LENGTH

Transcript length data for the organism panTro

## **Description**

panTro2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(panTro2, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(panTro2.geneSymbol.LENGTH)
head(panTro2.geneSymbol.LENGTH)
```

panTro2.genscan.LENGTH

Transcript length data for the organism panTro

## **Description**

panTro2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(panTro2, genscan) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

```
data(panTro2.genscan.LENGTH)
head(panTro2.genscan.LENGTH)
```

panTro2.nscanGene.LENGTH

Transcript length data for the organism panTro

## **Description**

panTro2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(panTro2, nscanGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(panTro2.nscanGene.LENGTH)
head(panTro2.nscanGene.LENGTH)
```

panTro2.refGene.LENGTH

Transcript length data for the organism panTro

## **Description**

panTro2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(panTro2, refGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(panTro2.refGene.LENGTH)
head(panTro2.refGene.LENGTH)
```

panTro2.xenoRefGene.LENGTH

Transcript length data for the organism panTro

## **Description**

panTro2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(panTro2, xenoRefGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(panTro2.xenoRefGene.LENGTH)
head(panTro2.xenoRefGene.LENGTH)
```

petMar1.xenoRefGene.LENGTH

Transcript length data for the organism petMar

## **Description**

petMar1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(petMar1, xenoRefGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(petMar1.xenoRefGene.LENGTH)
head(petMar1.xenoRefGene.LENGTH)
```

ponAbe2.ensGene.LENGTH

Transcript length data for the organism ponAbe

## **Description**

ponAbe2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, ensGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(ponAbe2.ensGene.LENGTH)
head(ponAbe2.ensGene.LENGTH)
```

ponAbe2.geneSymbol.LENGTH

Transcript length data for the organism ponAbe

#### **Description**

ponAbe2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, geneSymbol) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

```
data(ponAbe2.geneSymbol.LENGTH)
head(ponAbe2.geneSymbol.LENGTH)
```

ponAbe2.genscan.LENGTH

Transcript length data for the organism ponAbe

## **Description**

ponAbe2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, genscan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(ponAbe2.genscan.LENGTH)
head(ponAbe2.genscan.LENGTH)
```

ponAbe2.nscanGene.LENGTH

Transcript length data for the organism ponAbe

#### **Description**

ponAbe2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, nscanGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(ponAbe2.nscanGene.LENGTH)
head(ponAbe2.nscanGene.LENGTH)
```

ponAbe2.refGene.LENGTH

Transcript length data for the organism ponAbe

## **Description**

ponAbe2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

# Examples

```
data(ponAbe2.refGene.LENGTH)
head(ponAbe2.refGene.LENGTH)
```

ponAbe2.xenoRefGene.LENGTH

Transcript length data for the organism ponAbe

## **Description**

ponAbe2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, xenoRefGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(ponAbe2.xenoRefGene.LENGTH)
head(ponAbe2.xenoRefGene.LENGTH)
```

priPac1.xenoRefGene.LENGTH

Transcript length data for the organism priPac

## **Description**

priPac1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(priPac1, xenoRefGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(priPac1.xenoRefGene.LENGTH)
head(priPac1.xenoRefGene.LENGTH)
```

rheMac2.ensGene.LENGTH

Transcript length data for the organism rheMac

## **Description**

rheMac2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, ensGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(rheMac2.ensGene.LENGTH)
head(rheMac2.ensGene.LENGTH)
```

rheMac2.geneid.LENGTH Transcript length data for the organism rheMac

#### **Description**

rheMac2.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, geneid) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(rheMac2.geneid.LENGTH)
head(rheMac2.geneid.LENGTH)
```

rheMac2.geneSymbol.LENGTH

Transcript length data for the organism rheMac

# Description

rheMac2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, geneSymbol) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(rheMac2.geneSymbol.LENGTH)
head(rheMac2.geneSymbol.LENGTH)
```

rheMac2.nscanGene.LENGTH

Transcript length data for the organism rheMac

## **Description**

rheMac2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, nscanGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(rheMac2.nscanGene.LENGTH)
head(rheMac2.nscanGene.LENGTH)
```

rheMac2.refGene.LENGTH

Transcript length data for the organism rheMac

## **Description**

rheMac2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(rheMac2.refGene.LENGTH)
head(rheMac2.refGene.LENGTH)
```

rheMac2.sgpGene.LENGTH

Transcript length data for the organism rheMac

## **Description**

rheMac2.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, sgpGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(rheMac2.sgpGene.LENGTH)
head(rheMac2.sgpGene.LENGTH)
```

rheMac2.xenoRefGene.LENGTH

Transcript length data for the organism rheMac

## **Description**

rheMac2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, xenoRefGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(rheMac2.xenoRefGene.LENGTH)
head(rheMac2.xenoRefGene.LENGTH)
```

rn3.ensGene.LENGTH 155

rn3.ensGene.LENGTH

Transcript length data for the organism rn

# Description

rn3.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, ensGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(rn3.ensGene.LENGTH)
head(rn3.ensGene.LENGTH)
```

rn3.geneid.LENGTH

Transcript length data for the organism rn

# Description

rn3.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(rn3, geneid) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(rn3.geneid.LENGTH)
head(rn3.geneid.LENGTH)
```

rn3.geneSymbol.LENGTH Transcript length data for the organism rn

## Description

rn3.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(rn3, geneSymbol) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(rn3.geneSymbol.LENGTH)
head(rn3.geneSymbol.LENGTH)
```

rn3.genscan.LENGTH

Transcript length data for the organism rn

# Description

rn3.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(rn3, genscan) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(rn3.genscan.LENGTH)
head(rn3.genscan.LENGTH)
```

rn3.knownGene.LENGTH 157

rn3.knownGene.LENGTH Transcript length data for the organism rn

## Description

rn3.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the knownGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, knownGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(rn3.knownGene.LENGTH)
head(rn3.knownGene.LENGTH)
```

rn3.nscanGene.LENGTH Transcript length data for the organism rn

# Description

rn3.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, nscanGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(rn3.nscanGene.LENGTH)
head(rn3.nscanGene.LENGTH)
```

rn3.refGene.LENGTH

Transcript length data for the organism rn

# Description

rn3.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(rn3.refGene.LENGTH)
head(rn3.refGene.LENGTH)
```

rn3.sgpGene.LENGTH

Transcript length data for the organism rn

# Description

rn3.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, sgpGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(rn3.sgpGene.LENGTH)
head(rn3.sgpGene.LENGTH)
```

rn3.xenoRefGene.LENGTH

Transcript length data for the organism rn

# Description

rn3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, xenoRefGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

## **Examples**

```
data(rn3.xenoRefGene.LENGTH)
head(rn3.xenoRefGene.LENGTH)
```

rn4.ensGene.LENGTH

Transcript length data for the organism rn

# Description

rn4.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, ensGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(rn4.ensGene.LENGTH)
head(rn4.ensGene.LENGTH)
```

rn4.geneid.LENGTH

Transcript length data for the organism rn

## **Description**

rn4.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(rn4, geneid) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(rn4.geneid.LENGTH)
head(rn4.geneid.LENGTH)
```

rn4.geneSymbol.LENGTH Transcript length data for the organism rn

# Description

rn4.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(rn4, geneSymbol) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(rn4.geneSymbol.LENGTH)
head(rn4.geneSymbol.LENGTH)
```

rn4.genscan.LENGTH

Transcript length data for the organism rn

## **Description**

rn4.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(rn4, genscan) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(rn4.genscan.LENGTH)
head(rn4.genscan.LENGTH)
```

rn4.knownGene.LENGTH

Transcript length data for the organism rn

# Description

rn4.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the knownGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, knownGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(rn4.knownGene.LENGTH)
head(rn4.knownGene.LENGTH)
```

162 rn4.refGene.LENGTH

rn4.nscanGene.LENGTH Transcript length data for the organism rn

# Description

rn4.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, nscanGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(rn4.nscanGene.LENGTH)
head(rn4.nscanGene.LENGTH)
```

rn4.refGene.LENGTH

Transcript length data for the organism rn

# Description

rn4.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, refGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(rn4.refGene.LENGTH)
head(rn4.refGene.LENGTH)
```

rn4.sgpGene.LENGTH

Transcript length data for the organism rn

# Description

rn4.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, sgpGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(rn4.sgpGene.LENGTH)
head(rn4.sgpGene.LENGTH)
```

rn4.xenoRefGene.LENGTH

Transcript length data for the organism rn

# Description

rn4.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, xenoRefGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(rn4.xenoRefGene.LENGTH)
head(rn4.xenoRefGene.LENGTH)
```

sacCer1.ensGene.LENGTH

Transcript length data for the organism sacCer

## **Description**

sacCer1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(sacCer1, ensGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(sacCer1.ensGene.LENGTH)
head(sacCer1.ensGene.LENGTH)
```

sacCer2.ensGene.LENGTH

Transcript length data for the organism sacCer

## **Description**

sacCer2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(sacCer2, ensGene) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

```
data(sacCer2.ensGene.LENGTH)
head(sacCer2.ensGene.LENGTH)
```

strPur1.geneSymbol.LENGTH

Transcript length data for the organism strPur

## **Description**

strPur1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(strPur1, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(strPur1.geneSymbol.LENGTH)
head(strPur1.geneSymbol.LENGTH)
```

strPur1.genscan.LENGTH

Transcript length data for the organism strPur

## **Description**

strPur1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(strPur1, genscan) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(strPur1.genscan.LENGTH)
head(strPur1.genscan.LENGTH)
```

```
strPur1.refGene.LENGTH
```

Transcript length data for the organism strPur

## **Description**

strPur1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(strPur1, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(strPur1.refGene.LENGTH)
head(strPur1.refGene.LENGTH)
```

strPur1.xenoRefGene.LENGTH

Transcript length data for the organism strPur

## **Description**

strPur1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(strPur1, xenoRefGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(strPur1.xenoRefGene.LENGTH)
head(strPur1.xenoRefGene.LENGTH)
```

strPur2.geneSymbol.LENGTH

Transcript length data for the organism strPur

## **Description**

strPur2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(strPur2, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(strPur2.geneSymbol.LENGTH)
head(strPur2.geneSymbol.LENGTH)
```

strPur2.genscan.LENGTH

Transcript length data for the organism strPur

## **Description**

strPur2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(strPur2, genscan) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

```
data(strPur2.genscan.LENGTH)
head(strPur2.genscan.LENGTH)
```

strPur2.refGene.LENGTH

Transcript length data for the organism strPur

## **Description**

strPur2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(strPur2, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(strPur2.refGene.LENGTH)
head(strPur2.refGene.LENGTH)
```

strPur2.xenoRefGene.LENGTH

Transcript length data for the organism strPur

## **Description**

strPur2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(strPur2, xenoRefGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(strPur2.xenoRefGene.LENGTH)
head(strPur2.xenoRefGene.LENGTH)
```

supportedGeneIDs 169

supportedGeneIDs

Supported Gene IDs

#### **Description**

Lists supported gene ID formats

## Usage

supportedGeneIDs()

#### **Details**

Uses the supportedUCSCtables function from the GenomicFeatures package to obtain a list of gene ID formats available from the UCSC genome browser. The db column gives the gene ID formats which are provided to the id arguement of various functions. The track and subtrack columns are the names of the UCSC track/subtrack from which information is fetched.

The GeneID column lists the "full name" of the gene ID format where available.

The final column, headed AvailableGenomes lists the genomes for which there is a local copy of the length information avaible for the gene ID format listed in the geneLenDataBase package.

#### Value

A data.frame containing supported gene ID formats.

#### Author(s)

Matthew D. Young <myoung@wehi.edu.au>

## **Examples**

supportedGeneIDs()

 $supported {\tt Genomes}$ 

Supported Genomes

#### **Description**

Lists supported genomes

## Usage

supportedGenomes()

#### **Details**

Uses the ucscGenomes() function from the rtracklayer package to obtain a list of genomes available from the UCSC genome browser. The db column lists genomes as they are provided to the genome arguement of various functions.

The final column, headed AvailableGeneIDs lists the gene ID formats for which there is a local copy of the length information avaible for the genome listed in the geneLenDataBase package.

#### Value

A data.frame containing supported genomes.

#### Author(s)

Matthew D. Young <myoung@wehi.edu.au>

#### **Examples**

supportedGenomes()

taeGut1.ensGene.LENGTH

Transcript length data for the organism taeGut

# Description

taeGut1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(taeGut1, ensGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

# Examples

```
data(taeGut1.ensGene.LENGTH)
head(taeGut1.ensGene.LENGTH)
```

tae Gut 1.gene Symbol. LENG TH

Transcript length data for the organism taeGut

## **Description**

taeGut1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(taeGut1, geneSymbol) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(taeGut1.geneSymbol.LENGTH)
head(taeGut1.geneSymbol.LENGTH)
```

taeGut1.genscan.LENGTH

Transcript length data for the organism taeGut

#### **Description**

taeGut1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(taeGut1, genscan) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

## **Examples**

```
data(taeGut1.genscan.LENGTH)
head(taeGut1.genscan.LENGTH)
```

taeGut1.nscanGene.LENGTH

Transcript length data for the organism taeGut

# Description

taeGut1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(taeGut1, nscanGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(taeGut1.nscanGene.LENGTH)
head(taeGut1.nscanGene.LENGTH)
```

taeGut1.refGene.LENGTH

Transcript length data for the organism taeGut

## **Description**

taeGut1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(taeGut1, refGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(taeGut1.refGene.LENGTH)
head(taeGut1.refGene.LENGTH)
```

taeGut1.xenoRefGene.LENGTH

Transcript length data for the organism taeGut

## **Description**

taeGut1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(taeGut1, xenoRefGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(taeGut1.xenoRefGene.LENGTH)
head(taeGut1.xenoRefGene.LENGTH)
```

tetNig1.ensGene.LENGTH

Transcript length data for the organism tetNig

# Description

tetNig1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(tetNig1, ensGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(tetNig1.ensGene.LENGTH)
head(tetNig1.ensGene.LENGTH)
```

tetNig1.geneid.LENGTH Transcript length data for the organism tetNig

## **Description**

tetNig1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(tetNig1, geneid) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(tetNig1.geneid.LENGTH)
head(tetNig1.geneid.LENGTH)
```

tetNig1.genscan.LENGTH

Transcript length data for the organism tetNig

## **Description**

tetNig1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(tetNig1, genscan) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(tetNig1.genscan.LENGTH)
head(tetNig1.genscan.LENGTH)
```

tetNig1.nscanGene.LENGTH

Transcript length data for the organism tetNig

#### **Description**

tetNig1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(tetNig1, nscanGene) on the date on which the package was last updated.

## See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(tetNig1.nscanGene.LENGTH)
head(tetNig1.nscanGene.LENGTH)
```

tetNig2.ensGene.LENGTH

Transcript length data for the organism tetNig

## **Description**

tetNig2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(tetNig2, ensGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

#### **Examples**

```
data(tetNig2.ensGene.LENGTH)
head(tetNig2.ensGene.LENGTH)
```

unfactor

Purge factors

## **Description**

Removes all factors from a variable in a sensible way.

## Usage

unfactor(var)

#### **Arguments**

var

The variable from which you want the factors removed.

## **Details**

As factors are their own type, to remove factors we must convert each level into another type. This is currently done using "typeless" behaviour: a factor is converted to a numeric vector if this can be done without inducing NAs, otherwise it is coerced using as.character. Currently supported types are: /codefactor, /codedata.frame and /codelist.

## Value

The variable with all factors converted to characters or numbers (see details).

#### Author(s)

Matthew D. Young <myoung@wehi.edu.au>

#### **Examples**

```
#A named factor
x <- factor(sample(1:6, 100, replace=TRUE))
names(x) <- paste("Roll.No", 1:100, sep='.')
x
unfactor(x)

#A data.frame
x <- data.frame(player <- c("Alice", "Bob", "Mary", "Fred"), score <- factor(c(9, 7, 8, 9)), stringsAsFactors=T
x$player
x$score
y <- unfactor(x)
y$player
y$score</pre>
```

xenTro1.genscan.LENGTH

Transcript length data for the organism xenTro

## **Description**

xenTro1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(xenTro1, genscan) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## **Examples**

```
data(xenTro1.genscan.LENGTH)
head(xenTro1.genscan.LENGTH)
```

xenTro2.ensGene.LENGTH

Transcript length data for the organism xenTro

## **Description**

xenTro2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(xenTro2, ensGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

```
data(xenTro2.ensGene.LENGTH)
head(xenTro2.ensGene.LENGTH)
```

xenTro2.geneSymbol.LENGTH

Transcript length data for the organism xenTro

# Description

xenTro2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(xenTro2, geneSymbol) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

## **Examples**

```
data(xenTro2.geneSymbol.LENGTH)
head(xenTro2.geneSymbol.LENGTH)
```

xenTro2.genscan.LENGTH

Transcript length data for the organism xenTro

## **Description**

xenTro2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(xenTro2, genscan) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

```
data(xenTro2.genscan.LENGTH)
head(xenTro2.genscan.LENGTH)
```

xenTro2.refGene.LENGTH

Transcript length data for the organism xenTro

# Description

xenTro2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(xenTro2, refGene) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

# **Examples**

data(xenTro2.refGene.LENGTH)
head(xenTro2.refGene.LENGTH)

# Index

datasets	canFam2.ensGene.LENGTH, 29
anoCar1.ensGene.LENGTH, 8	canFam2.geneSymbol.LENGTH, 30
anoCar1.genscan.LENGTH, 9	canFam2.genscan.LENGTH, 30
anoCar1.xenoRefGene.LENGTH, 9	canFam2.nscanGene.LENGTH, 31
anoGam1.ensGene.LENGTH, 10	canFam2.refGene.LENGTH, 31
anoGam1.geneid.LENGTH, 10	canFam2.xenoRefGene.LENGTH, 32
anoGam1.genscan.LENGTH, 11	cavPor3.ensGene.LENGTH, 32
apiMel1.genscan.LENGTH, 11	cavPor3.genscan.LENGTH, 33
apiMel2.ensGene.LENGTH, 12	cavPor3.nscanGene.LENGTH, 33
apiMel2.geneid.LENGTH, 12	cavPor3.xenoRefGene.LENGTH, 34
apiMel2.genscan.LENGTH, 13	cb1.xenoRefGene.LENGTH, 34
aplCall.xenoRefGene.LENGTH, 13	cb3.xenoRefGene.LENGTH, 35
bosTau2.geneid.LENGTH, 14	ce2.geneid.LENGTH, 35
bosTau2.geneSymbol.LENGTH, 14	ce2.geneSymbol.LENGTH, 36
bosTau2.genscan.LENGTH, 15	ce2.refGene.LENGTH, 36
bosTau2.refGene.LENGTH, 15	ce4.geneSymbol.LENGTH, 37
bosTau2.sgpGene.LENGTH, 16	ce4.refGene.LENGTH, 37
bosTau3.ensGene.LENGTH, 16	ce4.xenoRefGene.LENGTH, 38
bosTau3.geneid.LENGTH, 17	ce6.ensGene.LENGTH, 38
bosTau3.geneSymbol.LENGTH, 17	ce6.geneSymbol.LENGTH, 39
bosTau3.genscan.LENGTH, 18	ce6.refGene.LENGTH, 39
bosTau3.refGene.LENGTH, 18	ce6.xenoRefGene.LENGTH, 40
bosTau3.sgpGene.LENGTH, 19	ci1.geneSymbol.LENGTH, 40
bosTau4.ensGene.LENGTH, 19	ci1.refGene.LENGTH,41
bosTau4.geneSymbol.LENGTH, 20	ci1.xenoRefGene.LENGTH,41
bosTau4.genscan.LENGTH, 20	ci2.ensGene.LENGTH,42
bosTau4.nscanGene.LENGTH, 21	ci2.geneSymbol.LENGTH,42
bosTau4.refGene.LENGTH, 21	ci2.refGene.LENGTH,43
braFlo1.xenoRefGene.LENGTH, 22	ci2.xenoRefGene.LENGTH, 43
caeJap1.xenoRefGene.LENGTH, 22	danRer3.ensGene.LENGTH, 44
caePb1.xenoRefGene.LENGTH, 23	danRer3.geneSymbol.LENGTH,44
caePb2.xenoRefGene.LENGTH, 23	danRer3.refGene.LENGTH,45
caeRem2.xenoRefGene.LENGTH, 24	danRer4.ensGene.LENGTH, 45
caeRem3.xenoRefGene.LENGTH, 24	danRer4.geneSymbol.LENGTH, $46$
calJac1.genscan.LENGTH, 25	danRer4.genscan.LENGTH,46
calJac1.nscanGene.LENGTH, 25	danRer4.nscanGene.LENGTH, 47
calJac1.xenoRefGene.LENGTH, 26	danRer4.refGene.LENGTH,47
canFam1.ensGene.LENGTH, 26	danRer5.ensGene.LENGTH, 48
canFam1.geneSymbol.LENGTH, 27	${\sf danRer5.geneSymbol.LENGTH,48}$
canFam1.genscan.LENGTH, 27	danRer5.refGene.LENGTH, 49
canFam1.nscanGene.LENGTH, 28	danRer5.vegaGene.LENGTH, 49
canFam1.refGene.LENGTH, 28	danRer5.vegaPseudoGene.LENGTH, 50
canFam1.xenoRefGene.LENGTH, 29	danRer6.ensGene.LENGTH, 50

danRer6.geneSymbol.LENGTH, 51	equCab1.nscanGene.LENGTH, 77
danRer6.refGene.LENGTH, 51	equCab1.refGene.LENGTH,77
danRer6.xenoRefGene.LENGTH, 52	equCab1.sgpGene.LENGTH, 78
dm1.geneSymbol.LENGTH, 52	equCab2.ensGene.LENGTH, 78
dm1.genscan.LENGTH, 53	equCab2.geneSymbol.LENGTH, 79
dm1.refGene.LENGTH, 53	equCab2.nscanGene.LENGTH, 79
dm2.geneid.LENGTH, 54	equCab2.refGene.LENGTH, $80$
dm2.geneSymbol.LENGTH, 54	equCab2.xenoRefGene.LENGTH, 80
dm2.genscan.LENGTH, 55	felCat3.ensGene.LENGTH, 81
dm2.nscanGene.LENGTH, 55	felCat3.geneid.LENGTH, 81
dm2.refGene.LENGTH, 56	felCat3.geneSymbol.LENGTH, 82
dm3.geneSymbol.LENGTH, 56	felCat3.genscan.LENGTH, 82
dm3.nscanPasaGene.LENGTH, 57	felCat3.nscanGene.LENGTH, 83
dm3.refGene.LENGTH, 57	felCat3.refGene.LENGTH,83
dp2.genscan.LENGTH, 58	felCat3.sgpGene.LENGTH,84
dp2.xenoRefGene.LENGTH, 58	felCat3.xenoRefGene.LENGTH, 84
dp3.geneid.LENGTH, 59	fr1.ensGene.LENGTH,85
dp3.genscan.LENGTH, 59	fr1.genscan.LENGTH, 85
dp3.xenoRefGene.LENGTH, 60	fr2.ensGene.LENGTH,86
droAna1.geneid.LENGTH, 60	galGal2.ensGene.LENGTH, 86
droAna1.genscan.LENGTH, 61	galGal2.geneid.LENGTH, 87
droAna1.xenoRefGene.LENGTH, 61	galGal2.geneSymbol.LENGTH, 87
droAna2.genscan.LENGTH, 62	galGal2.genscan.LENGTH, 88
droAna2.xenoRefGene.LENGTH, 62	galGal2.refGene.LENGTH,88
droEre1.genscan.LENGTH, 63	galGal2.sgpGene.LENGTH, 89
droEre1.xenoRefGene.LENGTH, 63	galGal3.ensGene.LENGTH, 89
droGri1.genscan.LENGTH, 64	galGal3.geneSymbol.LENGTH, 90
droGri1.xenoRefGene.LENGTH,64	galGal3.genscan.LENGTH, 90
droMoj1.geneid.LENGTH,65	galGal3.nscanGene.LENGTH, 91
droMoj1.genscan.LENGTH,65	galGal3.refGene.LENGTH, 91
droMoj1.xenoRefGene.LENGTH,66	galGal3.xenoRefGene.LENGTH, 92
droMoj2.genscan.LENGTH,66	gasAcu1.ensGene.LENGTH, 92
droMoj2.xenoRefGene.LENGTH,67	gasAcu1.nscanGene.LENGTH, 93
droPer1.genscan.LENGTH, 67	hg16.acembly.LENGTH, 93
droPer1.xenoRefGene.LENGTH, 68	hg16.ensGene.LENGTH, 94
droSec1.genscan.LENGTH, 68	hg16.exoniphy.LENGTH,94
droSec1.xenoRefGene.LENGTH, 69	hg16.geneid.LENGTH, 95
droSim1.geneid.LENGTH, 69	hg16.geneSymbol.LENGTH, 95
droSim1.genscan.LENGTH, 70	hg16.genscan.LENGTH, 96
droSim1.xenoRefGene.LENGTH, 70	hg16.knownGene.LENGTH, 96
droVir1.geneid.LENGTH,71	hg16.refGene.LENGTH,97
droVir1.genscan.LENGTH, 71	hg16.sgpGene.LENGTH, 97
droVir1.xenoRefGene.LENGTH,72	hg17.acembly.LENGTH, 98
droVir2.genscan.LENGTH, 72	hg17.acescan.LENGTH, 98
droVir2.xenoRefGene.LENGTH, 73	hg17.ccdsGene.LENGTH, 99
droYak1.geneid.LENGTH, 73	hg17.ensGene.LENGTH, 99
droYak1.genscan.LENGTH, 74	hg17.exoniphy.LENGTH, 100
droYak1.xenoRefGene.LENGTH, 74	hg17.geneid.LENGTH, 100
droYak2.genscan.LENGTH, 75	hg17.geneSymbol.LENGTH, 101
droYak2.xenoRefGene.LENGTH, 75	hg17.genscan.LENGTH, 101
equCab1.geneid.LENGTH, 76	hg17.knownGene.LENGTH, 102
equCab1.geneSymbol.LENGTH, 76	hg17.refGene.LENGTH, 102

hg17.sgpGene.LENGTH, 103	mm9.genscan.LENGTH, 129
hg17.vegaGene.LENGTH, 103	mm9.knownGene.LENGTH, 129
hg17.vegaPseudoGene.LENGTH, 104	mm9.nscanGene.LENGTH, 130
hg17.xenoRefGene.LENGTH, 104	mm9.refGene.LENGTH, 130
hg18.acembly.LENGTH, 105	mm9.sgpGene.LENGTH, 131
hg18.acescan.LENGTH, 105	mm9.xenoRefGene.LENGTH, 131
hg18.ccdsGene.LENGTH, 106	monDom1.genscan.LENGTH, 132
hg18.ensGene.LENGTH, 106	monDom4.ensGene.LENGTH, 132
hg18.exoniphy.LENGTH, 107	monDom4.geneSymbol.LENGTH, 133
hg18.geneid.LENGTH, 107	monDom4.genscan.LENGTH, 133
hg18.geneSymbol.LENGTH, 108	monDom4.nscanGene.LENGTH, 134
hg18.genscan.LENGTH, 108	monDom4.refGene.LENGTH, 134
hg18.knownGene.LENGTH, 109	monDom4.xenoRefGene.LENGTH, 135
hg18.knownGeneOld3.LENGTH, 109	monDom5.ensGene.LENGTH, 135
hg18.refGene.LENGTH, 110	monDom5.geneSymbol.LENGTH, 136
hg18.sgpGene.LENGTH, 110	monDom5.genscan.LENGTH, 136
hg18.sibGene.LENGTH, 111	monDom5.nscanGene.LENGTH, 137
hg18.xenoRefGene.LENGTH, 111	monDom5.refGene.LENGTH, 137
hg19.ccdsGene.LENGTH, 112	monDom5.xenoRefGene.LENGTH, 138
hg19.ensGene.LENGTH, 112	ornAna1.ensGene.LENGTH, 138
hg19.exoniphy.LENGTH, 113	ornAna1.geneSymbol.LENGTH, 139
hg19.geneSymbol.LENGTH, 113	ornAna1.refGene.LENGTH, 139
hg19.knownGene.LENGTH, 114	ornAna1.xenoRefGene.LENGTH, 140
hg19.nscanGene.LENGTH, 114	oryLat2.ensGene.LENGTH, 140
hg19.refGene.LENGTH, 115	oryLat2.geneSymbol.LENGTH, 141
hg19.xenoRefGene.LENGTH, 115	oryLat2.refGene.LENGTH, 141
loxAfr3.xenoRefGene.LENGTH, 116	oryLat2.xenoRefGene.LENGTH, 142
mm7.ensGene.LENGTH, 116	panTro1.ensGene.LENGTH, 142
mm7.geneid.LENGTH, 117	panTro1.geneid.LENGTH, 143
mm7.geneSymbol.LENGTH, 117	panTro1.genscan.LENGTH, 143
mm7.genscan.LENGTH, 118	panTro1.xenoRefGene.LENGTH, 144
mm7.knownGene.LENGTH, 118	panTro2.ensGene.LENGTH, 144
mm7.refGene.LENGTH, 119	panTro2.geneSymbol.LENGTH, 145
mm7.sgpGene.LENGTH, 119	panTro2.genscan.LENGTH, 145
mm7.xenoRefGene.LENGTH, 120	panTro2.nscanGene.LENGTH, 146
mm8.ccdsGene.LENGTH, 120	panTro2.refGene.LENGTH, 146
mm8.ensGene.LENGTH, 121	panTro2.xenoRefGene.LENGTH, 147
mm8.geneid.LENGTH, 121	petMar1.xenoRefGene.LENGTH, 147
mm8.geneSymbol.LENGTH, 122	ponAbe2.ensGene.LENGTH, 148
mm8.genscan.LENGTH, 122	ponAbe2.geneSymbol.LENGTH, 148
mm8.knownGene.LENGTH, 123	ponAbe2.genscan.LENGTH, 149
mm8.nscanGene.LENGTH, 123	ponAbe2.nscanGene.LENGTH, 149
mm8.refGene.LENGTH, 124	ponAbe2.refGene.LENGTH, 150
mm8.sgpGene.LENGTH, 124	ponAbe2.xenoRefGene.LENGTH, 150
mm8.sibGene.LENGTH, 125	priPac1.xenoRefGene.LENGTH, 151
mm8.xenoRefGene.LENGTH, 125	rheMac2.ensGene.LENGTH, 151
mm9.acembly.LENGTH, 126	rheMac2.geneid.LENGTH, 152
mm9.ccdsGene.LENGTH, 126	rheMac2.geneSymbol.LENGTH, 152
mm9.ensGene.LENGTH, 127	rheMac2.nscanGene.LENGTH, 153
mm9.exoniphy.LENGTH, 127	rheMac2.refGene.LENGTH, 153
mm9.geneid.LENGTH, 128	rheMac2.sgpGene.LENGTH, 154
_	i nenacz. sgpoene. Lenoin, 134
mm9.geneSymbol.LENGTH, 128	rheMac2.xenoRefGene.LENGTH, 154

rn3.ensGene.LENGTH, 155	apiMel2.geneid.LENGTH, 12
rn3.geneid.LENGTH, 155	apiMel2.genscan.LENGTH, 13
rn3.geneSymbol.LENGTH, 156	aplCal1.xenoRefGene.LENGTH, 13
rn3.genscan.LENGTH, 156	
rn3.knownGene.LENGTH, 157	bosTau2.geneid.LENGTH, 14
rn3.nscanGene.LENGTH, 157	bosTau2.geneSymbol.LENGTH, 14
rn3.refGene.LENGTH, 158	bosTau2.genscan.LENGTH, 15
rn3.sgpGene.LENGTH, 158	bosTau2.refGene.LENGTH, 15
rn3.xenoRefGene.LENGTH, 159	bosTau2.sgpGene.LENGTH, 16
rn4.ensGene.LENGTH, 159	bosTau3.ensGene.LENGTH, 16
rn4.geneid.LENGTH, 160	bosTau3.geneid.LENGTH, 17
rn4.geneSymbol.LENGTH, 160	bosTau3.geneSymbol.LENGTH, 17
rn4.genscan.LENGTH, 161	bosTau3.genscan.LENGTH, 18
rn4.knownGene.LENGTH, 161	bosTau3.refGene.LENGTH, 18
rn4.nscanGene.LENGTH, 162	bosTau3.sgpGene.LENGTH, 19
rn4.refGene.LENGTH, 162	bosTau4.ensGene.LENGTH, 19
rn4.sgpGene.LENGTH, 163	bosTau4.geneSymbol.LENGTH, 20
rn4.xenoRefGene.LENGTH, 163	bosTau4.genscan.LENGTH, 20
sacCer1.ensGene.LENGTH, 164	bosTau4.nscanGene.LENGTH, 21
sacCer2.ensGene.LENGTH, 164	bosTau4.refGene.LENGTH, 21
strPur1.geneSymbol.LENGTH, 165	braFlo1.xenoRefGene.LENGTH, 22
strPur1.genscan.LENGTH, 165	,
strPur1.refGene.LENGTH, 166	caeJap1.xenoRefGene.LENGTH, 22
strPur1.xenoRefGene.LENGTH, 166	caePb1.xenoRefGene.LENGTH, 23
strPur2.geneSymbol.LENGTH, 167	caePb2.xenoRefGene.LENGTH, 23
strPur2.genscan.LENGTH, 167	caeRem2.xenoRefGene.LENGTH, 24
strPur2.refGene.LENGTH, 168	caeRem3.xenoRefGene.LENGTH, 24
strPur2.xenoRefGene.LENGTH, 168	calJac1.genscan.LENGTH, 25
taeGut1.ensGene.LENGTH, 170	calJac1.nscanGene.LENGTH, 25
taeGut1.geneSymbol.LENGTH, 170	calJac1.xenoRefGene.LENGTH, 26
taeGut1.genscan.LENGTH, 171	canFam1.ensGene.LENGTH, 26
taeGut1.nscanGene.LENGTH, 171	canFam1.geneSymbol.LENGTH, 27
taeGut1.refGene.LENGTH, 172	canFam1.genscan.LENGTH, 27
taeGut1.xenoRefGene.LENGTH, 172	canFam1.nscanGene.LENGTH, 28
tetNig1.ensGene.LENGTH, 173	canFam1.refGene.LENGTH, 28
tetNig1.geneid.LENGTH, 173	canFam1.xenoRefGene.LENGTH, 29
tetNig1.genscan.LENGTH, 174	canFam2.ensGene.LENGTH, 29
tetNig1.nscanGene.LENGTH, 174	canFam2.geneSymbol.LENGTH, 30
tetNig2.ensGene.LENGTH, 175	canFam2.genscan.LENGTH, 30
xenTro1.genscan.LENGTH, 176	canFam2.nscanGene.LENGTH, 31
xenTro2.ensGene.LENGTH, 176	canFam2.refGene.LENGTH, 31
xenTro2.geneSymbol.LENGTH, 177	canFam2.xenoRefGene.LENGTH, 32
xenTro2.genscan.LENGTH, 177	cavPor3.ensGene.LENGTH, 32
xenTro2.refGene.LENGTH, 178	cavPor3.genscan.LENGTH, 33
XCIIII 02.1 CT OCHC. LENGTH, 170	cavPor3.nscanGene.LENGTH, 33
anoCar1.ensGene.LENGTH,8	cavPor3.xenoRefGene.LENGTH, 34
anoCar1.genscan.LENGTH, 9	cb1.xenoRefGene.LENGTH, 34
anoCar1.xenoRefGene.LENGTH, 9	cb3.xenoRefGene.LENGTH, 35
anoGam1.ensGene.LENGTH, 10	ce2.geneid.LENGTH, 35
anoGam1.geneid.LENGTH, 10	ce2.geneSymbol.LENGTH, 36
anoGam1.genscan.LENGTH, 11	ce2.refGene.LENGTH, 36
apiMel1.genscan.LENGTH, 11	ce4.geneSymbol.LENGTH, 37
apiMel2.ensGene.LENGTH, 12	ce4.refGene.LENGTH, 37
-p	33111 31 331131111, 37

ce4.xenoRefGene.LENGTH, 38	droEre1.xenoRefGene.LENGTH, 63
ce6.ensGene.LENGTH, 38	droGri1.genscan.LENGTH,64
ce6.geneSymbol.LENGTH, 39	droGri1.xenoRefGene.LENGTH, 64
ce6.refGene.LENGTH,39	droMoj1.geneid.LENGTH,65
ce6.xenoRefGene.LENGTH, 40	droMoj1.genscan.LENGTH,65
ci1.geneSymbol.LENGTH, 40	droMoj1.xenoRefGene.LENGTH, 66
ci1.refGene.LENGTH,41	droMoj2.genscan.LENGTH,66
ci1.xenoRefGene.LENGTH, 41	droMoj2.xenoRefGene.LENGTH, 67
ci2.ensGene.LENGTH, 42	droPer1.genscan.LENGTH,67
ci2.geneSymbol.LENGTH, 42	droPer1.xenoRefGene.LENGTH, 68
ci2.refGene.LENGTH,43	droSec1.genscan.LENGTH,68
ci2.xenoRefGene.LENGTH, 43	droSec1.xenoRefGene.LENGTH, 69
	droSim1.geneid.LENGTH, 69
danRer3.ensGene.LENGTH, 44	droSim1.genscan.LENGTH, 70
danRer3.geneSymbol.LENGTH, 44	droSim1.xenoRefGene.LENGTH, 70
danRer3.refGene.LENGTH, 45	droVir1.geneid.LENGTH,71
danRer4.ensGene.LENGTH, 45	droVir1.genscan.LENGTH, 71
danRer4.geneSymbol.LENGTH, 46	droVir1.xenoRefGene.LENGTH, 72
danRer4.genscan.LENGTH, 46	droVir2.genscan.LENGTH, 72
danRer4.nscanGene.LENGTH, 47	droVir2.xenoRefGene.LENGTH, 73
danRer4.refGene.LENGTH, 47	droYak1.geneid.LENGTH, 73
danRer5.ensGene.LENGTH, 48	droYak1.genscan.LENGTH, 74
danRer5.geneSymbol.LENGTH, 48	droYak1.xenoRefGene.LENGTH, 74
danRer5.refGene.LENGTH, 49	droYak2.genscan.LENGTH, 75
danRer5.vegaGene.LENGTH, 49	droYak2.xenoRefGene.LENGTH, 75
danRer5.vegaPseudoGene.LENGTH, 50	
danRer6.ensGene.LENGTH, 50	equCab1.geneid.LENGTH, 76
danRer6.geneSymbol.LENGTH, 51	equCab1.geneSymbol.LENGTH, 76
danRer6.refGene.LENGTH, 51	equCab1.nscanGene.LENGTH, 77
danRer6.xenoRefGene.LENGTH, 52	equCab1.refGene.LENGTH,77
dm1.geneSymbol.LENGTH, 52	equCab1.sgpGene.LENGTH, 78
dm1.genscan.LENGTH, 53	equCab2.ensGene.LENGTH, 78
dm1.refGene.LENGTH, 53	equCab2.geneSymbol.LENGTH, 79
dm2.geneid.LENGTH, 54	equCab2.nscanGene.LENGTH, 79
dm2.geneSymbol.LENGTH, 54	equCab2.refGene.LENGTH, 80
dm2.genscan.LENGTH, 55	equCab2.xenoRefGene.LENGTH, 80
dm2.nscanGene.LENGTH, 55	
dm2.refGene.LENGTH, 56	felCat3.ensGene.LENGTH, 81
dm3.geneSymbol.LENGTH, 56	felCat3.geneid.LENGTH, 81
dm3.nscanPasaGene.LENGTH, 57	felCat3.geneSymbol.LENGTH, 82
dm3.refGene.LENGTH, 57	felCat3.genscan.LENGTH, 82
downloadLengthFromUCSC, 8–168, 170–178	felCat3.nscanGene.LENGTH, 83
dp2.genscan.LENGTH, 58	felCat3.refGene.LENGTH, 83
dp2.xenoRefGene.LENGTH, 58	felCat3.sgpGene.LENGTH, 84
dp3.geneid.LENGTH, 59	felCat3.xenoRefGene.LENGTH, 84
dp3.genscan.LENGTH, 59	fr1.ensGene.LENGTH, 85
dp3.xenoRefGene.LENGTH, 60	fr1.genscan.LENGTH, 85
droAna1.geneid.LENGTH, 60	fr2.ensGene.LENGTH, 86
droAna1.genscan.LENGTH, 61	10-120 LENGTH 96
droAna1.xenoRefGene.LENGTH, 61	galGal2.ensGene.LENGTH, 86
droAna2.genscan.LENGTH, 62	galGal2.geneid.LENGTH, 87
droAna2.xenoRefGene.LENGTH, 62	galGal2.geneSymbol.LENGTH, 87
droEre1.genscan.LENGTH, 63	galGal2.genscan.LENGTH, 88

galGal2.refGene.LENGTH, 88	hg19.nscanGene.LENGTH, 114
galGal2.sgpGene.LENGTH, 89	hg19.refGene.LENGTH, 115
galGal3.ensGene.LENGTH, 89	hg19.xenoRefGene.LENGTH, 115
galGal3.geneSymbol.LENGTH, 90	
galGal3.genscan.LENGTH, 90	loxAfr3.xenoRefGene.LENGTH, 116
galGal3.nscanGene.LENGTH, 91	
galGal3.refGene.LENGTH, 91	mm7.ensGene.LENGTH, 116
galGal3.xenoRefGene.LENGTH, 92	mm7.geneid.LENGTH, 117
gasAcu1.ensGene.LENGTH, 92	mm7.geneSymbol.LENGTH, 117
gasAcu1.nscanGene.LENGTH, 93	mm7.genscan.LENGTH, 118
,	mm7.knownGene.LENGTH, 118
hg16.acembly.LENGTH, 93	mm7.refGene.LENGTH, 119
hg16.ensGene.LENGTH, 94	mm7.sgpGene.LENGTH, 119
hg16.exoniphy.LENGTH, 94	mm7.xenoRefGene.LENGTH, 120
hg16.geneid.LENGTH, 95	mm8.ccdsGene.LENGTH, 120
hg16.geneSymbol.LENGTH, 95	mm8.ensGene.LENGTH, 121
hg16.genscan.LENGTH, 96	mm8.geneid.LENGTH, 121
hg16.knownGene.LENGTH, 96	mm8.geneSymbol.LENGTH, 122
hg16.refGene.LENGTH, 97	mm8.genscan.LENGTH, 122
hg16.sgpGene.LENGTH, 97	mm8.knownGene.LENGTH, 123
hg17.acembly.LENGTH, 98	mm8.nscanGene.LENGTH, 123
hg17.acescan.LENGTH, 98	mm8.refGene.LENGTH, 124
hg17.ccdsGene.LENGTH, 99	mm8.sgpGene.LENGTH, 124
hg17.ensGene.LENGTH, 99	mm8.sibGene.LENGTH, 125
hg17.exoniphy.LENGTH, 100	mm8.xenoRefGene.LENGTH, 125
hg17.geneid.LENGTH, 100	mm9.acembly.LENGTH, 126
hg17.geneSymbol.LENGTH, 101	mm9.ccdsGene.LENGTH, 126
hg17.genscan.LENGTH, 101	mm9.ensGene.LENGTH, 127
hg17.knownGene.LENGTH, 102	mm9.exoniphy.LENGTH, 127
hg17.refGene.LENGTH, 102	mm9.geneid.LENGTH, 128
hg17.sgpGene.LENGTH, 103	mm9.geneSymbol.LENGTH, 128
hg17.vegaGene.LENGTH, 103	mm9.genscan.LENGTH, 129
hg17.vegaPseudoGene.LENGTH, 104	mm9.knownGene.LENGTH, 129
hg17.xenoRefGene.LENGTH, 104	mm9.nscanGene.LENGTH, 130
hg18.acembly.LENGTH, 105	mm9.refGene.LENGTH, 130
hg18.acescan.LENGTH, 105	mm9.sgpGene.LENGTH, 131
hg18.ccdsGene.LENGTH, 106	mm9.xenoRefGene.LENGTH, 131
hg18.ensGene.LENGTH, 106	monDom1.genscan.LENGTH, 132
hg18.exoniphy.LENGTH, 107	monDom4.ensGene.LENGTH, 132
hg18.geneid.LENGTH, 107	monDom4.geneSymbol.LENGTH, 133
hg18.geneSymbol.LENGTH, 108	monDom4.genscan.LENGTH, 133
hg18.genscan.LENGTH, 108	monDom4.nscanGene.LENGTH, 134
hg18.knownGene.LENGTH, 109	monDom4.refGene.LENGTH, 134
hg18.knownGeneOld3.LENGTH, 109	monDom4.xenoRefGene.LENGTH, 135
hg18.refGene.LENGTH, 110	monDom5.ensGene.LENGTH, 135
hg18.sgpGene.LENGTH, 110	monDom5.geneSymbol.LENGTH, 136
hg18.sibGene.LENGTH, 111	monDom5.genscan.LENGTH, 136
hg18.xenoRefGene.LENGTH, 111	monDom5.nscanGene.LENGTH, 137
hg19.ccdsGene.LENGTH, 112	monDom5.refGene.LENGTH, 137
hg19.ensGene.LENGTH, 112	monDom5.xenoRefGene.LENGTH, 138
hg19.exoniphy.LENGTH, 113	monbonio. Actioner delle. LENOTTI, 150
hg19.geneSymbol.LENGTH, 113	ornAna1.ensGene.LENGTH, 138
hg19.knownGene.LENGTH, 114	ornAna1.geneSymbol.LENGTH, 139
	The state of the s

ornAna1.refGene.LENGTH, 139	sacCer2.ensGene.LENGTH, 164
ornAna1.xenoRefGene.LENGTH, 140	strPur1.geneSymbol.LENGTH, 165
oryLat2.ensGene.LENGTH, 140	strPur1.genscan.LENGTH, 165
oryLat2.geneSymbol.LENGTH, 141	strPur1.refGene.LENGTH, 166
oryLat2.refGene.LENGTH, 141	strPur1.xenoRefGene.LENGTH, 166
oryLat2.xenoRefGene.LENGTH, 142	strPur2.geneSymbol.LENGTH, 167
	strPur2.genscan.LENGTH, 167
panTro1.ensGene.LENGTH, 142	strPur2.refGene.LENGTH, 168
panTro1.geneid.LENGTH, 143	strPur2.xenoRefGene.LENGTH, 168
panTro1.genscan.LENGTH, 143	supportedGeneIDs, 169
panTro1.xenoRefGene.LENGTH, 144	supportedGenomes, 169
panTro2.ensGene.LENGTH, 144	
panTro2.geneSymbol.LENGTH, 145	taeGut1.ensGene.LENGTH, 170
panTro2.genscan.LENGTH, 145	taeGut1.geneSymbol.LENGTH, 170
panTro2.nscanGene.LENGTH, 146	taeGut1.genscan.LENGTH, 171
panTro2.refGene.LENGTH, 146	taeGut1.nscanGene.LENGTH, 171
panTro2.xenoRefGene.LENGTH, 147	taeGut1.refGene.LENGTH, 172
petMar1.xenoRefGene.LENGTH, 147	taeGut1.xenoRefGene.LENGTH, 172
ponAbe2.ensGene.LENGTH, 148	tetNig1.ensGene.LENGTH, 173
ponAbe2.geneSymbol.LENGTH, 148	tetNig1.geneid.LENGTH, 173
ponAbe2.genscan.LENGTH, 149	tetNig1.genscan.LENGTH, 174
ponAbe2.nscanGene.LENGTH, 149	tetNig1.nscanGene.LENGTH, 174
ponAbe2.refGene.LENGTH, 150	tetNig2.ensGene.LENGTH, 175
ponAbe2.xenoRefGene.LENGTH, 150	<b>3</b>
priPac1.xenoRefGene.LENGTH, 151	unfactor, 175
pi ii aci . xenoker dene . LENdin, 131	
rheMac2.ensGene.LENGTH, 151	xenTro1.genscan.LENGTH, 176
rheMac2.geneid.LENGTH, 152	xenTro2.ensGene.LENGTH, 176
rheMac2.geneSymbol.LENGTH, 152	xenTro2.geneSymbol.LENGTH, 177
rheMac2.nscanGene.LENGTH, 153	xenTro2.genscan.LENGTH, 177
rheMac2.refGene.LENGTH, 153	xenTro2.refGene.LENGTH, 178
rheMac2.sgpGene.LENGTH, 154	
rheMac2.xenoRefGene.LENGTH, 154	
rn3.ensGene.LENGTH, 155	
rn3.geneid.LENGTH, 155	
rn3.geneSymbol.LENGTH, 156	
rn3.genscan.LENGTH, 156	
rn3.knownGene.LENGTH, 157	
rn3.nscanGene.LENGTH, 157	
rn3.refGene.LENGTH, 158	
rn3.sgpGene.LENGTH, 158	
rn3.xenoRefGene.LENGTH, 159	
rn4.ensGene.LENGTH, 159	
rn4.geneid.LENGTH, 160	
rn4.geneSymbol.LENGTH, 160	
rn4.genscan.LENGTH, 161	
rn4.knownGene.LENGTH, 161	
rn4.nscanGene.LENGTH, 162	
rn4.refGene.LENGTH, 162	
rn4.sgpGene.LENGTH, 163	
rn4.xenoRefGene.LENGTH, 163	
sacCer1.ensGene.LENGTH, 164	