

Package ‘chipenrich.data’

January 29, 2026

Title Companion package to chipenrich

Version 2.35.0

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Description Supporting data for the chipenrich package. Includes pre-defined gene sets, gene locus definitions, and mappability estimates.

biocViews ChIPSeq, Epigenetics, FunctionalGenomics, GeneSetEnrichment, HistoneModification, Regression

Depends R (>= 3.4.0)

Imports AnnotationDbi, BiocGenerics, methods, GenomicRanges, GenomeInfoDb, IRanges, readr, rtracklayer, S4Vectors, utils

License GPL-3

Encoding UTF-8

LazyData true

Suggests BiocStyle, devtools, knitr, rmarkdown, roxygen2, testthat, GO.db, org.Dm.eg.db, org.Dr.eg.db, org.Hs.eg.db, org.Mm.eg.db, org.Rn.eg.db, TxDb.Dmelanogaster.UCSC.dm3.ensGene, TxDb.Dmelanogaster.UCSC.dm6.ensGene, TxDb.Drerio.UCSC.danRer10.refGene, TxDb.Hsapiens.UCSC.hg19.knownGene, TxDb.Hsapiens.UCSC.hg38.knownGene, TxDb.Mmusculus.UCSC.mm9.knownGene, TxDb.Mmusculus.UCSC.mm10.knownGene, TxDb.Rnorvegicus.UCSC.rn4.ensGene, TxDb.Rnorvegicus.UCSC.rn5.refGene, TxDb.Rnorvegicus.UCSC.rn6.refGene

VignetteBuilder knitr

RoxygenNote 6.1.1

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Contents

chipenrich.data	8
enhancer.dnase_thurman.0	8
gene.enh.desc	9
GeneSet-class	9
geneset.biocarta_pathway.hsa	10
geneset.biocarta_pathway.mmu	11
geneset.biocarta_pathway.rno	11
geneset.ctd.hsa	12
geneset.ctd.mmu	12
geneset.cytoband.hsa	13
geneset.drug_bank.hsa	14
geneset.drug_bank.mmu	14
geneset.drug_bank.rno	15
geneset.GOBP.dme	15
geneset.GOBP.dre	16
geneset.GOBP.hsa	17
geneset.GOBP.mmu	17
geneset.GOBP.rno	18
geneset.GOCC.dme	19
geneset.GOCC.dre	19
geneset.GOCC.hsa	20
geneset.GOCC.mmu	21
geneset.GOCC.rno	21
geneset.GOMF.dme	22
geneset.GOMF.dre	23
geneset.GOMF.hsa	23
geneset.GOMF.mmu	24
geneset.GOMF.rno	25
geneset.hallmark.hsa	25
geneset.immunologic.hsa	26
geneset.kegg_pathway.hsa	27
geneset.kegg_pathway.mmu	28
geneset.kegg_pathway.rno	28
geneset.mesh.hsa	29
geneset.mesh.mmu	29

geneset.mesh.rno	30
geneset.metabolite.hsa	30
geneset.metabolite.mmu	31
geneset.metabolite.rno	31
geneset.microrna.hsa	32
geneset.oncogenic.hsa	32
geneset.panther_pathway.hsa	33
geneset.panther_pathway.mmu	34
geneset.panther_pathway.rno	34
geneset(pfam.hsa	35
geneset(pfam.mmu	35
geneset(pfam.rno	36
geneset.protein_interaction_biogrid.hsa	36
geneset.reactome.dme	37
geneset.reactome.dre	38
geneset.reactome.hsa	38
geneset.reactome.mmu	39
geneset.reactome.rno	40
geneset.transcription_factors.hsa	41
geneset.transcription_factors.mmu	41
geneset.transcription_factors.rno	42
locusdef.danRer10.10kb	42
locusdef.danRer10.10kb_outside	43
locusdef.danRer10.10kb_outside_upstream	44
locusdef.danRer10.1kb	45
locusdef.danRer10.1kb_outside	45
locusdef.danRer10.1kb_outside_upstream	46
locusdef.danRer10.5kb	47
locusdef.danRer10.5kb_outside	48
locusdef.danRer10.5kb_outside_upstream	48
locusdef.danRer10.exon	49
locusdef.danRer10.intron	50
locusdef.danRer10.nearest_gene	50
locusdef.danRer10.nearest_tss	51
locusdef.dm3.10kb	52
locusdef.dm3.10kb_outside	53
locusdef.dm3.10kb_outside_upstream	53
locusdef.dm3.1kb	54
locusdef.dm3.1kb_outside	55
locusdef.dm3.1kb_outside_upstream	56
locusdef.dm3.5kb	56
locusdef.dm3.5kb_outside	57
locusdef.dm3.5kb_outside_upstream	58
locusdef.dm3.exon	59
locusdef.dm3.intron	59
locusdef.dm3.nearest_gene	60
locusdef.dm3.nearest_tss	61
locusdef.dm6.10kb	62

locusdef.dm6.10kb_outside	62
locusdef.dm6.10kb_outside_upstream	63
locusdef.dm6.1kb	64
locusdef.dm6.1kb_outside	65
locusdef.dm6.1kb_outside_upstream	65
locusdef.dm6.5kb	66
locusdef.dm6.5kb_outside	67
locusdef.dm6.5kb_outside_upstream	68
locusdef.dm6.exon	68
locusdef.dm6.intron	69
locusdef.dm6.nearest_gene	70
locusdef.dm6.nearest_tss	71
locusdef.hg19.10kb	71
locusdef.hg19.10kb_outside	72
locusdef.hg19.10kb_outside_upstream	73
locusdef.hg19.1kb	74
locusdef.hg19.1kb_outside	74
locusdef.hg19.1kb_outside_upstream	75
locusdef.hg19.5kb	76
locusdef.hg19.5kb_outside	77
locusdef.hg19.5kb_outside_upstream	77
locusdef.hg19.exon	78
locusdef.hg19.intron	79
locusdef.hg19.nearest_gene	80
locusdef.hg19.nearest_tss	80
locusdef.hg38.10kb	81
locusdef.hg38.10kb_outside	82
locusdef.hg38.10kb_outside_upstream	83
locusdef.hg38.1kb	83
locusdef.hg38.1kb_outside	84
locusdef.hg38.1kb_outside_upstream	85
locusdef.hg38.5kb	86
locusdef.hg38.5kb_outside	86
locusdef.hg38.5kb_outside_upstream	87
locusdef.hg38.exon	88
locusdef.hg38.intron	89
locusdef.hg38.nearest_gene	89
locusdef.hg38.nearest_tss	90
locusdef.mm10.10kb	91
locusdef.mm10.10kb_outside	92
locusdef.mm10.10kb_outside_upstream	92
locusdef.mm10.1kb	93
locusdef.mm10.1kb_outside	94
locusdef.mm10.1kb_outside_upstream	95
locusdef.mm10.5kb	95
locusdef.mm10.5kb_outside	96
locusdef.mm10.5kb_outside_upstream	97
locusdef.mm10.exon	98

locusdef.mm10.intron	98
locusdef.mm10.nearest_gene	99
locusdef.mm10.nearest_tss	100
locusdef.mm9.10kb	101
locusdef.mm9.10kb_outside	101
locusdef.mm9.10kb_outside_upstream	102
locusdef.mm9.1kb	103
locusdef.mm9.1kb_outside	104
locusdef.mm9.1kb_outside_upstream	104
locusdef.mm9.5kb	105
locusdef.mm9.5kb_outside	106
locusdef.mm9.5kb_outside_upstream	107
locusdef.mm9.exon	107
locusdef.mm9.intron	108
locusdef.mm9.nearest_gene	109
locusdef.mm9.nearest_tss	110
locusdef.rn4.10kb	110
locusdef.rn4.10kb_outside	111
locusdef.rn4.10kb_outside_upstream	112
locusdef.rn4.1kb	113
locusdef.rn4.1kb_outside	113
locusdef.rn4.1kb_outside_upstream	114
locusdef.rn4.5kb	115
locusdef.rn4.5kb_outside	116
locusdef.rn4.5kb_outside_upstream	116
locusdef.rn4.exon	117
locusdef.rn4.intron	118
locusdef.rn4.nearest_gene	119
locusdef.rn4.nearest_tss	119
locusdef.rn5.10kb	120
locusdef.rn5.10kb_outside	121
locusdef.rn5.10kb_outside_upstream	122
locusdef.rn5.1kb	122
locusdef.rn5.1kb_outside	123
locusdef.rn5.1kb_outside_upstream	124
locusdef.rn5.5kb	125
locusdef.rn5.5kb_outside	125
locusdef.rn5.5kb_outside_upstream	126
locusdef.rn5.exon	127
locusdef.rn5.intron	127
locusdef.rn5.nearest_gene	128
locusdef.rn5.nearest_tss	129
locusdef.rn6.10kb	130
locusdef.rn6.10kb_outside	130
locusdef.rn6.10kb_outside_upstream	131
locusdef.rn6.1kb	132
locusdef.rn6.1kb_outside	133
locusdef.rn6.1kb_outside_upstream	133

locusdef.rn6.5kb	134
locusdef.rn6.5kb_outside	135
locusdef.rn6.5kb_outside_upstream	135
locusdef.rn6.exon	136
locusdef.rn6.intron	137
locusdef.rn6.nearest_gene	137
locusdef.rn6.nearest_tss	138
LocusDefinition-class	139
mappa.hg19.10kb.100mer	140
mappa.hg19.10kb.24mer	140
mappa.hg19.10kb.36mer	141
mappa.hg19.10kb.40mer	142
mappa.hg19.10kb.50mer	142
mappa.hg19.10kb.75mer	143
mappa.hg19.1kb.100mer	144
mappa.hg19.1kb.24mer	144
mappa.hg19.1kb.36mer	145
mappa.hg19.1kb.40mer	146
mappa.hg19.1kb.50mer	146
mappa.hg19.1kb.75mer	147
mappa.hg19.5kb.100mer	148
mappa.hg19.5kb.24mer	148
mappa.hg19.5kb.36mer	149
mappa.hg19.5kb.40mer	150
mappa.hg19.5kb.50mer	150
mappa.hg19.5kb.75mer	151
mappa.hg19.exon.100mer	152
mappa.hg19.exon.24mer	152
mappa.hg19.exon.36mer	153
mappa.hg19.exon.40mer	154
mappa.hg19.exon.50mer	154
mappa.hg19.exon.75mer	155
mappa.hg19.intron.100mer	156
mappa.hg19.intron.24mer	156
mappa.hg19.intron.36mer	157
mappa.hg19.intron.40mer	158
mappa.hg19.intron.50mer	158
mappa.hg19.intron.75mer	159
mappa.hg19.nearest_gene.100mer	160
mappa.hg19.nearest_gene.24mer	160
mappa.hg19.nearest_gene.36mer	161
mappa.hg19.nearest_gene.40mer	162
mappa.hg19.nearest_gene.50mer	162
mappa.hg19.nearest_gene.75mer	163
mappa.hg19.nearest_tss.100mer	164
mappa.hg19.nearest_tss.24mer	164
mappa.hg19.nearest_tss.36mer	165
mappa.hg19.nearest_tss.40mer	166

mappa.hg19.nearest_tss.50mer	166
mappa.hg19.nearest_tss.75mer	167
mappa.mm9.10kb.100mer	168
mappa.mm9.10kb.36mer	168
mappa.mm9.10kb.40mer	169
mappa.mm9.10kb.50mer	170
mappa.mm9.10kb.75mer	170
mappa.mm9.1kb.100mer	171
mappa.mm9.1kb.36mer	172
mappa.mm9.1kb.40mer	172
mappa.mm9.1kb.50mer	173
mappa.mm9.1kb.75mer	174
mappa.mm9.5kb.100mer	174
mappa.mm9.5kb.36mer	175
mappa.mm9.5kb.40mer	176
mappa.mm9.5kb.50mer	176
mappa.mm9.5kb.75mer	177
mappa.mm9.exon.100mer	178
mappa.mm9.exon.36mer	178
mappa.mm9.exon.40mer	179
mappa.mm9.exon.50mer	180
mappa.mm9.exon.75mer	180
mappa.mm9.intron.100mer	181
mappa.mm9.intron.36mer	182
mappa.mm9.intron.40mer	182
mappa.mm9.intron.50mer	183
mappa.mm9.intron.75mer	184
mappa.mm9.nearest_gene.100mer	184
mappa.mm9.nearest_gene.36mer	185
mappa.mm9.nearest_gene.40mer	186
mappa.mm9.nearest_gene.50mer	186
mappa.mm9.nearest_gene.75mer	187
mappa.mm9.nearest_tss.100mer	188
mappa.mm9.nearest_tss.36mer	188
mappa.mm9.nearest_tss.40mer	189
mappa.mm9.nearest_tss.50mer	190
mappa.mm9.nearest_tss.75mer	190
peaks_E2F4	191
peaks_H3K4me3_GM12878	192
spline.log_dtss.90ENCODE	192
tss.danRer10	193
tss.dm3	193
tss.dm6	194
tss.hg19	194
tss.hg38	195
tss.mm10	195
tss.mm9	196
tss.rn4	197

tss.rn5	197
tss.rn6	198

Index	199
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chipenrich.data	<i>chipenrich.data: Data for chipenrich: gene set enrichment analysis for ChIP-seq data</i>
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Description

Supporting data for the chipenrich package. Includes pre-defined gene sets, gene locus definitions, and mappability estimates.

enhancer.dnase_thurman.0	<i>Enhancer locations</i>
--------------------------	---------------------------

Description

A GRanges with all the enhancer locations for hg19. The locations were found using a combination of DNase data and from Thurman et al (PMID: 22955617)

Usage

`enhancer.dnase_thurman.0`

Format

A GRanges object with the following `mcols`:

gene_id The Entrez ID for the TSS

symbol The gene symbol for the TSS

gene.enh.desc	<i>Gene-Enhancer descriptives</i>
---------------	-----------------------------------

Description

A data frame with gene-level descriptions of enhancer properties using enhancers.dnase_thurman.0. Used in the adjustment of proximity test to enhancers.

gene_id The Entrez ID for the a gene

avg_denh_emp The empirical average distance to an enhancer from 90 ENCODE ChIP-seq datasets. This is used as the adjustment.

num_enh The number of enhancers assigned to the gene, defined by closest gene TSS

avgdenh The theoretical average distance to an enhancer assuming every base pair on the genome is equally likely to have a peak binding.

Usage

```
gene.enh.desc
```

Format

An object of class `data.frame` with 21600 rows and 4 columns.

GeneSet-class	<i>Class "GeneSet"</i>
---------------	------------------------

Description

Class for storing sets of genes and their corresponding metadata.

Objects from the Class

Objects can be created by calls of the form `new("GeneSet")`.

These objects are used internally by the `chipenrich` package and users will not likely need to create these.

Slots

set.gene: Object of class "environment". Maps from geneset IDs to lists of Entrez gene IDs.

type: Object of class "character". The formal name for this collection of genesets.

set.name: Object of class "environment". Maps from geneset IDs to their descriptions/names.

all.genes: Object of class "character". A set of all genes present across every geneset.

organism: Object of class "character". Organism code for gene IDs.

dburl: Object of class "character". Web URL for this collection of genesets.

Note

Not typically accessed by the user - this is used internally by the chipenrich package.

Author(s)

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Examples

```
# Show information about class.
showClass("GeneSet")

# What is stored inside a geneset object?
data("geneset.metabolite.hsa");
str(geneset.metabolite.hsa);

# How are the mappings from geneset IDs to gene IDs stored?
ls.str(geneset.metabolite.hsa@set.gene);
```

geneset.biocarta_pathway.hsa

geneset.biocarta_pathway.hsa genesets for BioCarta

Description

BioCarta (biocarta_pathway) genesets. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 18:46:04 2017.

Usage

geneset.biocarta_pathway.hsa

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

https://cgap.nci.nih.gov/Pathways/BioCarta_Pathways

geneset.biocarta_pathway.mmu
geneset.biocarta_pathway.mmu

Description

GeneSet object which stores information about sets of genes.
These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.biocarta_pathway.mmu)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)
For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.biocarta_pathway.rno
geneset.biocarta_pathway.rno

Description

GeneSet object which stores information about sets of genes.
These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.biocarta_pathway.rno)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)
For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.ctd.hsa

geneset.ctd.hsa genesets for Comparative Toxicogenomics Database

Description

Comparative Toxicogenomics Database (ctd) genesets. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 18:46:11 2017.

Usage

geneset.ctd.hsa

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<http://ctdbase.org>

geneset.ctd.mmu

geneset.ctd.mmu genesets for Comparative Toxicogenomics Database

Description

Comparative Toxicogenomics Database (ctd) genesets. All genesets are required to have ≥ 10 Entrez IDs. Built on Sat Nov 10 15:56:37 2018.

Usage

geneset.ctd.mmu

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<http://ctdbase.org>

geneset.cytoband.hsa *geneset.cytoband.hsa*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.cytoband.hsa)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.drug_bank.hsa *geneset.drug_bank.hsa genesets for DrugBank*

Description

DrugBank (drug_bank) genesets. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 18:46:13 2017.

Usage

`geneset.drug_bank.hsa`

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<https://www.drugbank.ca>

geneset.drug_bank.mmu *geneset.drug_bank.mmu*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

`data(geneset.drug_bank.mmu)`

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.drug_bank.rno` *geneset.drug_bank.rno*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.drug_bank.rno)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.GOBP.dme` *geneset.GOBP.dme genesets for Drosophila melanogaster*

Description

Gene Ontology Biological Process (GOBP) genesets for *Drosophila melanogaster*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:24:38 2017.

Usage

```
geneset.GOBP.dme
```

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Dm.eg.db_3.4.2 and GO.db_3.4.2

geneset.GOBP.dre *geneset.GOBP.dre genesets for Danio rerio*

Description

Gene Ontology Biological Process (GOBP) genesets for *Danio rerio*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:25:08 2017.

Usage

geneset.GOBP.dre

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Dr.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOBP.hsa`*geneset.GOBP.hsa genesets for Homo sapiens*

Description

Gene Ontology Biological Process (GOBP) genesets for *Homo sapiens*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:22:22 2017.

Usage

`geneset.GOBP.hsa`

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. *Homo sapiens*.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

`org.Hs.eg.db_3.4.2` and `GO.db_3.4.2`

`geneset.GOBP.mmu`*geneset.GOBP.mmu genesets for *Mus musculus**

Description

Gene Ontology Biological Process (GOBP) genesets for *Mus musculus*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:23:23 2017.

Usage

`geneset.GOBP.mmu`

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

`org.Mm.eg.db_3.4.2` and `GO.db_3.4.2`

`geneset.GOBP.rno`

geneset.GOBP.rno genesets for Rattus norvegicus

Description

Gene Ontology Biological Process (GOBP) genesets for *Rattus norvegicus*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:24:10 2017.

Usage

`geneset.GOBP.rno`

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

`org.Rn.eg.db_3.4.2` and `GO.db_3.4.2`

`geneset.GOCC.dme`*geneset.GOCC.dme genesets for Drosophila melanogaster*

Description

Gene Ontology Cellular Component (GOCC) genesets for *Drosophila melanogaster*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:24:38 2017.

Usage

`geneset.GOCC.dme`

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. *Homo sapiens*.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

`org.Dm.eg.db_3.4.2` and `GO.db_3.4.2`

`geneset.GOCC.dre`*geneset.GOCC.dre genesets for Danio rerio*

Description

Gene Ontology Cellular Component (GOCC) genesets for *Danio rerio*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:25:08 2017.

Usage

`geneset.GOCC.dre`

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

`org.Dr.eg.db_3.4.2` and `GO.db_3.4.2`

`geneset.GOCC.hsa` *geneset.GOCC.hsa genesets for Homo sapiens*

Description

Gene Ontology Cellular Component (GOCC) genesets for *Homo sapiens*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:22:22 2017.

Usage

`geneset.GOCC.hsa`

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

`org.Hs.eg.db_3.4.2` and `GO.db_3.4.2`

geneset.GOCC.mmu *genesets for Mus musculus*

Description

Gene Ontology Cellular Component (GOCC) genesets for *Mus musculus*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:23:23 2017.

Usage

geneset.GOCC.mmu

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. *Homo sapiens*.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Mm.eg.db_3.4.2 and GO.db_3.4.2

geneset.GOCC.rno *genesets for Rattus norvegicus*

Description

Gene Ontology Cellular Component (GOCC) genesets for *Rattus norvegicus*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:24:10 2017.

Usage

geneset.GOCC.rno

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Rn.eg.db_3.4.2 and GO.db_3.4.2

geneset.GOMF.dme

geneset.GOMF.dme genesets for Drosophila melanogaster

Description

Gene Ontology Molecular Function (GOMF) genesets for *Drosophila melanogaster*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:24:38 2017.

Usage

geneset.GOMF.dme

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Dm.eg.db_3.4.2 and GO.db_3.4.2

geneset.GOMF.dre *genesets for Danio rerio*

Description

Gene Ontology Molecular Function (GOMF) genesets for *Danio rerio*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:25:08 2017.

Usage

```
geneset.GOMF.dre
```

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. *Homo sapiens*.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Dr eg.db_3.4.2 and GO.db_3.4.2

geneset.GOMF.hsa *genesets for Homo sapiens*

Description

Gene Ontology Molecular Function (GOMF) genesets for *Homo sapiens*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:22:22 2017.

Usage

```
geneset.GOMF.hsa
```

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Hs.eg.db_3.4.2 and GO.db_3.4.2

geneset.GOMF.mmu *geneset.GOMF.mmu genesets for Mus musculus*

Description

Gene Ontology Molecular Function (GOMF) genesets for *Mus musculus*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:23:23 2017.

Usage

geneset.GOMF.mmu

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

org.Mm.eg.db_3.4.2 and GO.db_3.4.2

`geneset.GOMF.rno`*geneset.GOMF.rno genesets for Rattus norvegicus*

Description

Gene Ontology Molecular Function (GOMF) genesets for *Rattus norvegicus*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 16:24:10 2017.

Usage

`geneset.GOMF.rno`

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. *Homo sapiens*.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

`org.Rn.eg.db_3.4.2` and `GO.db_3.4.2`

`geneset.hallmark.hsa`*geneset.hallmark.hsa genesets for Hallmark (MSigDB)*

Description

Hallmark (MSigDB) (hallmark) genesets. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 18:46:15 2017.

Usage

`geneset.hallmark.hsa`

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<http://software.broadinstitute.org/gsea/msigdb/collections.jsp#H>

geneset.immunologic.hsa

geneset.immunologic.hsa genesets for Immunologic Signatures (MSigDB)

Description

Immunologic Signatures (MSigDB) (immunologic) genesets. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 18:46:45 2017.

Usage

`geneset.immunologic.hsa`

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<http://software.broadinstitute.org/gsea/msigdb/collections.jsp#C7>

geneset.kegg_pathway.hsa

geneset.kegg_pathway.hsa genesets for KEGG Pathways

Description

KEGG Pathways (kegg_pathway) genesets. All genesets are required to have ≥ 10 Entrez IDs.
Built on Mon Oct 16 18:46:53 2017.

Usage

`geneset.kegg_pathway.hsa`

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<http://kegg.jp>

```
geneset.kegg_pathway.mmu
geneset.kegg_pathway.mmu
```

Description

GeneSet object which stores information about sets of genes.
These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.kegg_pathway.mmu)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)
For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

```
geneset.kegg_pathway.rno
geneset.kegg_pathway.rno
```

Description

GeneSet object which stores information about sets of genes.
These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.kegg_pathway.rno)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)
For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.mesh.hsa` *geneset.mesh.hsa*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.mesh.hsa)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.mesh.mmu` *geneset.mesh.mmu*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.mesh.mmu)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.mesh.rno *geneset.mesh.rno*

Description

GeneSet object which stores information about sets of genes.
These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.mesh.rno)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)
For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.metabolite.hsa
 geneset.metabolite.hsa

Description

GeneSet object which stores information about sets of genes.
These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.metabolite.hsa)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)
For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.metabolite.mmu`

geneset.metabolite.mmu

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.metabolite.mmu)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.metabolite.rno`

geneset.metabolite.rno

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.metabolite.rno)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.microrna.hsa *geneset.microrna.hsa genesets for MicroRNA Targets (MSigDB)*

Description

MicroRNA Targets (MSigDB) (microrna) genesets. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 18:46:56 2017.

Usage

```
geneset.microrna.hsa
```

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<http://software.broadinstitute.org/gsea/msigdb/collections.jsp#C3>

geneset.oncogenic.hsa *geneset.oncogenic.hsa genesets for Oncogenic Signatures (MSigDB)*

Description

Oncogenic Signatures (MSigDB) (oncogenic) genesets. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 18:47:23 2017.

Usage

```
geneset.oncogenic.hsa
```

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<http://software.broadinstitute.org/gsea/msigdb/collections.jsp#C6>

geneset.panther_pathway.hsa
geneset.panther_pathway.hsa

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.panther_pathway.hsa)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

```
geneset.panther_pathway.mmu
geneset.panther_pathway.mmu
```

Description

GeneSet object which stores information about sets of genes.
These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.panther_pathway.mmu)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)
For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

```
geneset.panther_pathway.rno
geneset.panther_pathway.rno
```

Description

GeneSet object which stores information about sets of genes.
These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.panther_pathway.rno)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)
For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

geneset.pfam.hsa*geneset.pfam.hsa genesets for Pfam*

Description

Pfam (pfam) genesets. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Oct 16 18:47:28 2017.

Usage

```
geneset.pfam.hsa
```

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. GOBP.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. Homo sapiens.

set.gene An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<http://pfam.xfam.org>

geneset.pfam.mmu*geneset.pfam.mmu*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.pfam.mmu)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.pfam.rno` *geneset.pfam.rno*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.pfam.rno)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: `browseVignettes("chipenrich.data")`

`geneset.protein_interaction_biogrid.hsa`
geneset.protein_interaction_biogrid.hsa genesets for BioGRID Protein Interactions

Description

BioGRID Protein Interactions (`protein_interaction_biogrid`) genesets. All genesets are required to have ≥ 10 Entrez IDs. Built on Tue Oct 24 16:05:53 2017.

Usage

```
geneset.protein_interaction_biogrid.hsa
```

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<https://thebiogrid.org>

geneset.reactome.dme geneset.reactome.dme genesets for *Drosophila melanogaster*

Description

Reactome genesets for *Drosophila melanogaster*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Mar 20 15:14:03 2017.

Usage

geneset.reactome.dme

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. Reactome.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. R-HSA-109688), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://www.reactome.org/download/current/NCBI2Reactome_All_Levels.txt downloaded on 2017-03-19

geneset.reactome.dre *geneset.reactome.dre genesets for Danio rerio*

Description

Reactome genesets for *Danio rerio*. All genesets are required to have ≥ 10 Entrez IDs. Built on Tue Mar 28 13:03:21 2017.

Usage

```
geneset.reactome.dre
```

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. Reactome.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. *Homo sapiens*.

set.gene An environment containing a list whose keys are database specific accessions (e.g. R-HSA-109688), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://www.reactome.org/download/current/NCBI2Reactome_All_Levels.txt downloaded on 2017-03-19

geneset.reactome.hsa *geneset.reactome.hsa genesets for Homo sapiens*

Description

Reactome genesets for *Homo sapiens*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Mar 20 15:13:45 2017.

Usage

```
geneset.reactome.hsa
```

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. Reactome.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. R-HSA-109688), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://www.reactome.org/download/current/NCBI2Reactome_All_Levels.txt downloaded on 2017-03-19

geneset.reactome.mmu *geneset.reactome.mmu genesets for Mus musculus*

Description

Reactome genesets for *Mus musculus*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Mar 20 15:13:55 2017.

Usage

`geneset.reactome.mmu`

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. Reactome.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. R-HSA-109688), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://www.reactome.org/download/current/NCBI2Reactome_All_Levels.txt downloaded on 2017-03-19

geneset.reactome.rno *geneset.reactome.rno genesets for Rattus norvegicus*

Description

Reactome genesets for *Rattus norvegicus*. All genesets are required to have ≥ 10 Entrez IDs. Built on Mon Mar 20 15:13:59 2017.

Usage

geneset.reactome.rno

Format

A GeneSet object with the following slots:

type A character indicating the type of genesets, e.g. Reactome.

dburl A character of the URL of the database underlying the genesets.

organism A character of the organism, e.g. *Homo sapiens*.

set.gene An environment containing a list whose keys are database specific accessions (e.g. R-HSA-109688), and whose elements are character vectors of Entrez Gene IDs.

all.genes A character vector of all the Entrez Gene IDs contained over all the genesets in this type.

set.name An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

http://www.reactome.org/download/current/NCBI2Reactome_All_Levels.txt downloaded on 2017-03-19

```
geneset.transcription_factors.hsa
```

geneset.transcription_factors.hsa genesets for Transcription Factor Targets (MSigDB)

Description

Transcription Factor Targets (MSigDB) (transcription_factors) genesets. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 18:47:33 2017.

Usage

```
geneset.transcription_factors.hsa
```

Format

A GeneSet object with the following slots:

- type** A character indicating the type of genesets, e.g. GOBP.
- dburl** A character of the URL of the database underlying the genesets.
- organism** A character of the organism, e.g. Homo sapiens.
- set.gene** An environment containing a list whose keys are database specific accessions (e.g. GO IDs for GO terms), and whose elements are character vectors of Entrez Gene IDs.
- all.genes** A character vector of all the Entrez Gene IDs contained over all the genesets in this type.
- set.name** An environment containing a list whose keys are database specific accessions, and whose elements are human readable geneset names.

Source

<http://software.broadinstitute.org/gsea/msigdb/collections.jsp#C3>

```
geneset.transcription_factors.mmu
```

geneset.transcription_factors.mmu

Description

GeneSet object which stores information about sets of genes.
These objects are used internally by the chipenrich package.

Usage

```
data(geneset.transcription_factors.mmu)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: [browseVignettes\("chipenrich.data"\)](#)

`geneset.transcription_factors.rno`
geneset.transcription_factors.rno

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the `chipenrich` package.

Usage

```
data(geneset.transcription_factors.rno)
```

Format

See [GeneSet-class](#) for a description of the format.

See Also

For more information about genesets: [chipenrich.data](#)

For information regarding how the genesets were created: [browseVignettes\("chipenrich.data"\)](#)

`locusdef.danRer10.10kb`
locusdef.danRer10.10kb locus definition

Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

```
locusdef.danRer10.10kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, danRer10.

organism A character indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:27 2018.

Source

R packages: TxDb.DrERIO.UCSC.danRer10.refGene_3.4.2 and org.DR.eg.db_3.5.0.

```
locusdef.danRer10.10kb_outside
  locusdef.danRer10.10kb_outside locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.danRer10.10kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, danRer10.

organism A character indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:27 2018.

Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

locusdef.danRer10.10kb_outside_upstream
locusdef.danRer10.10kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

locusdef.danRer10.10kb_outside_upstream

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, danRer10.

organism A character indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:27 2018.

Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

locusdef.danRer10.1kb *locusdef.danRer10.1kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

```
locusdef.danRer10.1kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, danRer10.

organism A character indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:25 2018.

Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

locusdef.danRer10.1kb_outside
locusdef.danRer10.1kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.danRer10.1kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `danRer10`.

organism A character indicating the organism name. In this case, `Danio rerio`.

Details

Built on Fri Apr 13 09:54:26 2018.

Source

R packages: `TxDb.Drerio.UCSC.danRer10.refGene_3.4.2` and `org.Dr.eg.db_3.5.0`.

`locusdef.danRer10.1kb_outside_upstream`
locusdef.danRer10.1kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

`locusdef.danRer10.1kb_outside_upstream`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `danRer10`.

organism A character indicating the organism name. In this case, `Danio rerio`.

Details

Built on Fri Apr 13 09:54:25 2018.

Source

R packages: TxDb.DrERio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

locusdef.danRer10.5kb *locusdef.danRer10.5kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

locusdef.danRer10.5kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, danRer10.

organism A character indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:26 2018.

Source

R packages: TxDb.DrERio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

```
locusdef.danRer10.5kb_outside
  locusdef.danRer10.5kb_outside locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.danRer10.5kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, danRer10.

organism A character indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:27 2018.

Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

```
locusdef.danRer10.5kb_outside_upstream
  locusdef.danRer10.5kb_outside_upstream locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.danRer10.5kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol
- dframe** A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol
- genome.build** A character indicating the genome build. In this case, danRer10.
- organism** A character indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:26 2018.

Source

R packages: TxDb.DrERIO.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

locusdef.danRer10.exon

locusdef.danRer10.exon locus definition

Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

Usage

locusdef.danRer10.exon

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol
- dframe** A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol
- genome.build** A character indicating the genome build. In this case, danRer10.
- organism** A character indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:24 2018.

Source

R packages: TxDb.DrERIO.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

locusdef.danRer10.intron

locusdef.danRer10.intron locus definition

Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

Usage

locusdef.danRer10.intron

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, danRer10.

organism A character indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:25 2018.

Source

R packages: TxDb.DrERIO.UCSC.danRer10.refGene_3.4.2 and org.DR.eg.db_3.5.0.

locusdef.danRer10.nearest_gene

locusdef.danRer10.nearest_gene locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

locusdef.danRer10.nearest_gene

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, danRer10.

organism A character indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:23 2018.

Source

R packages: TxDb.DrERIO.UCSC.danRer10.refGene_3.4.2 and org.DR.eg.db_3.5.0.

```
locusdef.danRer10.nearest_tss
  locusdef.danRer10.nearest_tss locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

```
locusdef.danRer10.nearest_tss
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, danRer10.

organism A character indicating the organism name. In this case, Danio rerio.

Details

Built on Fri Apr 13 09:54:22 2018.

Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

<code>locusdef.dm3.10kb</code>	<i>locusdef.dm3.10kb locus definition</i>
--------------------------------	---

Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

`locusdef.dm3.10kb`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `dm3`.

organism A character indicating the organism name. In this case, `Drosophila melanogaster`.

Details

For the `dm3` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

```
locusdef_dm3.10kb_outside
```

locusdef_dm3.10kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef_dm3.10kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `dm3`.

organism A character indicating the organism name. In this case, `Drosophila melanogaster`.

Details

For the `dm3` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:06 2018.

Source

R packages: `TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2` and `org.Dm.eg.db_3.5.0`.

```
locusdef_dm3.10kb_outside_upstream
```

locusdef_dm3.10kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.dm3.10kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `dm3`.

organism A character indicating the organism name. In this case, `Drosophila melanogaster`.

Details

For the `dm3` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: `TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2` and `org.Dm.eg.db_3.5.0`.

locusdef.dm3.1kb

locusdef.dm3.1kb locus definition

Description

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

```
locusdef.dm3.1kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `dm3`.

organism A character indicating the organism name. In this case, `Drosophila melanogaster`.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

```
locusdef.dm3.1kb_outside
  locusdef.dm3.1kb_outside locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.dm3.1kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
genome.build A character indicating the genome build. In this case, dm3.
organism A character indicating the organism name. In this case, *Drosophila melanogaster*.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

locusdef.dm3.1kb_outside_upstream
locusdef.dm3.1kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

locusdef.dm3.1kb_outside_upstream

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `dm3`.

organism A character indicating the organism name. In this case, `Drosophila melanogaster`.

Details

For the `dm3` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: `TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2` and `org.Dm.eg.db_3.5.0`.

locusdef.dm3.5kb *locusdef.dm3.5kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

locusdef.dm3.5kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `dm3`.

organism A character indicating the organism name. In this case, `Drosophila melanogaster`.

Details

For the `dm3` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: `TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2` and `org.Dm.eg.db_3.5.0`.

```
locusdef.dm3.5kb_outside
```

locusdef.dm3.5kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.dm3.5kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `dm3`.

organism A character indicating the organism name. In this case, `Drosophila melanogaster`.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

locusdef.dm3.5kb_outside_upstream
locusdef.dm3.5kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

`locusdef.dm3.5kb_outside_upstream`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, dm3.

organism A character indicating the organism name. In this case, *Drosophila melanogaster*.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:05 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

locusdef.dm3.exon *locusdef.dm3.exon locus definition*

Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

Usage

```
locusdef.dm3.exon
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm3.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:04 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

locusdef.dm3.intron *locusdef.dm3.intron locus definition*

Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.dm3.intron
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `dm3`.

organism A character indicating the organism name. In this case, `Drosophila melanogaster`.

Details

For the `dm3` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:04 2018.

Source

R packages: `TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2` and `org.Dm.eg.db_3.5.0`.

`locusdef.dm3.nearest_gene`

locusdef.dm3.nearest_gene locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

`locusdef.dm3.nearest_gene`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `dm3`.

organism A character indicating the organism name. In this case, `Drosophila melanogaster`.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:03 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

```
locusdef.dm3.nearest_tss
```

locusdef.dm3.nearest_tss locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

```
locusdef.dm3.nearest_tss
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, dm3.

organism A character indicating the organism name. In this case, *Drosophila melanogaster*.

Details

For the dm3 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:03 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

`locusdef.dm6.10kb` *locusdef.dm6.10kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

`locusdef.dm6.10kb`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `dm6`.

organism A character indicating the organism name. In this case, `Drosophila melanogaster`.

Details

For the `dm6` genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: `TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1` and `org.Dm.eg.db_3.5.0`.

`locusdef.dm6.10kb_outside` *locusdef.dm6.10kb_outside locus definition*

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.dm6.10kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `dm6`.

organism A character indicating the organism name. In this case, `Drosophila melanogaster`.

Details

For the `dm6` genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: `TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1` and `org.Dm.eg.db_3.5.0`.

```
locusdef.dm6.10kb_outside_upstream
```

locusdef.dm6.10kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.dm6.10kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `dm6`.

organism A character indicating the organism name. In this case, `Drosophila melanogaster`.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

`locusdef.dm6.1kb` *locusdef.dm6.1kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

`locusdef.dm6.1kb`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `dm6`.

organism A character indicating the organism name. In this case, `Drosophila melanogaster`.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:34 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

```
locusdef.dm6.1kb_outside
```

locusdef.dm6.1kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.dm6.1kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `dm6`.

organism A character indicating the organism name. In this case, `Drosophila melanogaster`.

Details

For the `dm6` genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: `TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1` and `org.Dm.eg.db_3.5.0`.

```
locusdef.dm6.1kb_outside_upstream
```

locusdef.dm6.1kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.dm6.1kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm6.

organism A character indicating the organism name. In this case, *Drosophila melanogaster*.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:34 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

locusdef.dm6.5kb *locusdef.dm6.5kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

```
locusdef.dm6.5kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm6.

organism A character indicating the organism name. In this case, *Drosophila melanogaster*.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

```
locusdef.dm6.5kb_outside
  locusdef.dm6.5kb_outside locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.dm6.5kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `dm6`.

organism A character indicating the organism name. In this case, `Drosophila melanogaster`.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

locusdef.dm6.5kb_outside_upstream
locusdef.dm6.5kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

locusdef.dm6.5kb_outside_upstream

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm6.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:35 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

locusdef.dm6.exon *locusdef.dm6.exon locus definition*

Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

Usage

locusdef.dm6.exon

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol
- dframe** A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol
- genome.build** A character indicating the genome build. In this case, dm6.
- organism** A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:33 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

locusdef.dm6.intron *locusdef.dm6.intron locus definition*

Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

Usage

locusdef.dm6.intron

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol
- dframe** A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol
- genome.build** A character indicating the genome build. In this case, dm6.
- organism** A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:34 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

```
locusdef.dm6.nearest_gene
```

locusdef.dm6.nearest_gene locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.dm6.nearest_gene
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, dm6.

organism A character indicating the organism name. In this case, Drosophila melanogaster.

Details

For the dm6 genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:33 2018.

Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

```
locusdef.dm6.nearest_tss
  locusdef.dm6.nearest_tss locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

```
locusdef.dm6.nearest_tss
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `dm6`.

organism A character indicating the organism name. In this case, `Drosophila melanogaster`.

Details

For the `dm6` genome, original gene IDs are from FLYBASE and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:53:33 2018.

Source

R packages: `TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1` and `org.Dm.eg.db_3.5.0`.

```
locusdef.hg19.10kb      locusdef.hg19.10kb locus definition
```

Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

```
locusdef.hg19.10kb
```

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- genome.build** A character indicating the genome build. In this case, `hg19`.
- organism** A character indicating the organism name. In this case, `Homo sapiens`.

Details

Built on Fri Apr 13 09:45:58 2018.

Source

R packages: `TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2` and `org.Hs.eg.db_3.5.0`. GENCODE resources: `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation` and `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG`

locusdef.hg19.10kb_outside
locusdef.hg19.10kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

`locusdef.hg19.10kb_outside`

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- genome.build** A character indicating the genome build. In this case, `hg19`.
- organism** A character indicating the organism name. In this case, `Homo sapiens`.

Details

Built on Fri Apr 13 09:45:59 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezGene

locusdef.hg19.10kb_outside_upstream

locusdef.hg19.10kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

locusdef.hg19.10kb_outside_upstream

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg19.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:58 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezGene

locusdef.hg19.1kb *locusdef.hg19.1kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

locusdef.hg19.1kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg19.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:55 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG

locusdef.hg19.1kb_outside *locusdef.hg19.1kb_outside locus definition*

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

locusdef.hg19.1kb_outside

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol
- dframe** A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol
- genome.build** A character indicating the genome build. In this case, hg19.
- organism** A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:56 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG

```
locusdef.hg19.1kb_outside_upstream
      locusdef.hg19.1kb_outside_upstream locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.hg19.1kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol
- dframe** A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol
- genome.build** A character indicating the genome build. In this case, hg19.
- organism** A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:56 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezGene

locusdef.hg19.5kb *locusdef.hg19.5kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

locusdef.hg19.5kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg19.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:57 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezGene

```
locusdef.hg19.5kb_outside
```

locusdef.hg19.5kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.hg19.5kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `hg19`.

organism A character indicating the organism name. In this case, `Homo sapiens`.

Details

Built on Fri Apr 13 09:45:58 2018.

Source

R packages: `TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2` and `org.Hs.eg.db_3.5.0`. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation. and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezGene

```
locusdef.hg19.5kb_outside_upstream
```

locusdef.hg19.5kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.hg19.5kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg19.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:57 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation. and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG

locusdef.hg19.exon *locusdef.hg19.exon locus definition*

Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

Usage

```
locusdef.hg19.exon
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg19.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:53 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation. and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG

locusdef.hg19.intron *locusdef.hg19.intron locus definition*

Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

Usage

locusdef.hg19.intron

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg19.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:55 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation. and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG

locusdef.hg19.nearest_gene

locusdef.hg19.nearest_gene locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

locusdef.hg19.nearest_gene

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg19.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:51 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE

resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezG

locusdef.hg19.nearest_tss

locusdef.hg19.nearest_tss locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

locusdef.hg19.nearest_tss

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg19.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:45:51 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezGene

locusdef.hg38.10kb

locusdef.hg38.10kb locus definition

Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

locusdef.hg38.10kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg38.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:42 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

locusdef.hg38.10kb_outside

locusdef.hg38.10kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

locusdef.hg38.10kb_outside

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, hg38.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:43 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

```
locusdef.hg38.10kb_outside_upstream
```

locusdef.hg38.10kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.hg38.10kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `hg38`.

organism A character indicating the organism name. In this case, `Homo sapiens`.

Details

Built on Fri Apr 13 09:49:43 2018.

Source

R packages: `TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0` and `org.Hs.eg.db_3.5.0`. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

```
locusdef.hg38.1kb
```

locusdef.hg38.1kb locus definition

Description

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

```
locusdef.hg38.1kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `hg38`.

organism A character indicating the organism name. In this case, `Homo sapiens`.

Details

Built on Fri Apr 13 09:49:39 2018.

Source

R packages: `TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0` and `org.Hs.eg.db_3.5.0`. GENCODE resources: `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz` and `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz`

`locusdef.hg38.1kb_outside`

locusdef.hg38.1kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

`locusdef.hg38.1kb_outside`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `hg38`.

organism A character indicating the organism name. In this case, `Homo sapiens`.

Details

Built on Fri Apr 13 09:49:40 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

locusdef.hg38.1kb_outside_upstream

locusdef.hg38.1kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

locusdef.hg38.1kb_outside_upstream

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg38.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:39 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

locusdef.hg38.5kb *locusdef.hg38.5kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

locusdef.hg38.5kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, hg38.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:41 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

locusdef.hg38.5kb_outside *locusdef.hg38.5kb_outside locus definition*

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

locusdef.hg38.5kb_outside

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol
- dframe** A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol
- genome.build** A character indicating the genome build. In this case, hg38.
- organism** A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:42 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

```
locusdef.hg38.5kb_outside_upstream
      locusdef.hg38.5kb_outside_upstream locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.hg38.5kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol
- dframe** A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol
- genome.build** A character indicating the genome build. In this case, hg38.
- organism** A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:41 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

locusdef.hg38.exon *locusdef.hg38.exon* *locus definition*

Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

Usage

locusdef.hg38.exon

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, hg38.

organism A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:37 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

locusdef.hg38.intron *locusdef.hg38.intron locus definition*

Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.hg38.intron
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `hg38`.

organism A character indicating the organism name. In this case, `Homo sapiens`.

Details

Built on Fri Apr 13 09:49:38 2018.

Source

R packages: `TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0` and `org.Hs.eg.db_3.5.0`. GENCODE resources: `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz` and `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz`

locusdef.hg38.nearest_gene
locusdef.hg38.nearest_gene locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.hg38.nearest_gene
```

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol
- dframe** A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol
- genome.build** A character indicating the genome build. In this case, hg38.
- organism** A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:34 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

locusdef.hg38.nearest_tss
locusdef.hg38.nearest_tss locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

locusdef.hg38.nearest_tss

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol
- dframe** A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol
- genome.build** A character indicating the genome build. In this case, hg38.
- organism** A character indicating the organism name. In this case, Homo sapiens.

Details

Built on Fri Apr 13 09:49:34 2018.

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

locusdef.mm10.10kb *locusdef.mm10.10kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

```
locusdef.mm10.10kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm10.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:40 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

```
locusdef.mm10.10kb_outside
```

locusdef.mm10.10kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.mm10.10kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `mm10`.

organism A character indicating the organism name. In this case, `Mus musculus`.

Details

Built on Fri Apr 13 09:51:41 2018.

Source

R packages: `TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0` and `org.Mm.eg.db_3.5.0`. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

```
locusdef.mm10.10kb_outside_upstream
```

locusdef.mm10.10kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.mm10.10kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm10.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:40 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

```
locusdef.mm10.1kb
```

locusdef.mm10.1kb locus definition

Description

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

```
locusdef.mm10.1kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm10.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:37 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

locusdef.mm10.1kb_outside

locusdef.mm10.1kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

locusdef.mm10.1kb_outside

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `mm10`.

organism A character indicating the organism name. In this case, `Mus musculus`.

Details

Built on Fri Apr 13 09:51:38 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

```
locusdef.mm10.1kb_outside_upstream
```

locusdef.mm10.1kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.mm10.1kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `mm10`.

organism A character indicating the organism name. In this case, `Mus musculus`.

Details

Built on Fri Apr 13 09:51:37 2018.

Source

R packages: `TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0` and `org.Mm.eg.db_3.5.0`. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

```
locusdef.mm10.5kb
```

locusdef.mm10.5kb locus definition

Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

```
locusdef.mm10.5kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `mm10`.

organism A character indicating the organism name. In this case, `Mus musculus`.

Details

Built on Fri Apr 13 09:51:38 2018.

Source

R packages: `TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0` and `org.Mm.eg.db_3.5.0`. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

`locusdef.mm10.5kb_outside`

locusdef.mm10.5kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

`locusdef.mm10.5kb_outside`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `mm10`.

organism A character indicating the organism name. In this case, `Mus musculus`.

Details

Built on Fri Apr 13 09:51:39 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

`locusdef.mm10.5kb_outside_upstream`

locusdef.mm10.5kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

`locusdef.mm10.5kb_outside_upstream`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `mm10`.

organism A character indicating the organism name. In this case, `Mus musculus`.

Details

Built on Fri Apr 13 09:51:39 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

locusdef.mm10.exon *locusdef.mm10.exon locus definition*

Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

Usage

locusdef.mm10.exon

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm10.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:51:35 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

locusdef.mm10.intron *locusdef.mm10.intron locus definition*

Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

Usage

locusdef.mm10.intron

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol
- dframe** A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol
- genome.build** A character indicating the genome build. In this case, mm10.
- organism** A character indicating the organism name. In this case, *Mus musculus*.

Details

Built on Fri Apr 13 09:51:36 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

```
locusdef.mm10.nearest_gene
  locusdef.mm10.nearest_gene locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.mm10.nearest_gene
```

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol
- dframe** A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol
- genome.build** A character indicating the genome build. In this case, mm10.
- organism** A character indicating the organism name. In this case, *Mus musculus*.

Details

Built on Fri Apr 13 09:51:33 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

locusdef.mm10.nearest_tss

locusdef.mm10.nearest_tss locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

locusdef.mm10.nearest_tss

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `mm10`.

organism A character indicating the organism name. In this case, `Mus musculus`.

Details

Built on Fri Apr 13 09:51:33 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

locusdef.mm9.10kb *locusdef.mm9.10kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

```
locusdef.mm9.10kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm9.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:44 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

locusdef.mm9.10kb_outside *locusdef.mm9.10kb_outside locus definition*

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.mm9.10kb_outside
```

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol
- dframe** A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol
- genome.build** A character indicating the genome build. In this case, mm9.
- organism** A character indicating the organism name. In this case, *Mus musculus*.

Details

Built on Fri Apr 13 09:50:44 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

locusdef.mm9.10kb_outside_upstream
locusdef.mm9.10kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

locusdef.mm9.10kb_outside_upstream

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol
- dframe** A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol
- genome.build** A character indicating the genome build. In this case, mm9.
- organism** A character indicating the organism name. In this case, *Mus musculus*.

Details

Built on Fri Apr 13 09:50:44 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

locusdef.mm9.1kb

locusdef.mm9.1kb locus definition

Description

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

locusdef.mm9.1kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm9.

organism A character indicating the organism name. In this case, Mus musculus.

Details

Built on Fri Apr 13 09:50:41 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

locusdef.mm9.1kb_outside

locusdef.mm9.1kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

`locusdef.mm9.1kb_outside`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `mm9`.

organism A character indicating the organism name. In this case, `Mus musculus`.

Details

Built on Fri Apr 13 09:50:42 2018.

Source

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.5.0`. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

locusdef.mm9.1kb_outside_upstream

locusdef.mm9.1kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.mm9.1kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm9.

organism A character indicating the organism name. In this case, *Mus musculus*.

Details

Built on Fri Apr 13 09:50:41 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

locusdef.mm9.5kb *locusdef.mm9.5kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

```
locusdef.mm9.5kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm9.

organism A character indicating the organism name. In this case, *Mus musculus*.

Details

Built on Fri Apr 13 09:50:42 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

locusdef.mm9.5kb_outside

locusdef.mm9.5kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

locusdef.mm9.5kb_outside

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `mm9`.

organism A character indicating the organism name. In this case, `Mus musculus`.

Details

Built on Fri Apr 13 09:50:43 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

```
locusdef.mm9.5kb_outside_upstream
```

locusdef.mm9.5kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.mm9.5kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `mm9`.

organism A character indicating the organism name. In this case, `Mus musculus`.

Details

Built on Fri Apr 13 09:50:43 2018.

Source

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.5.0`. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

```
locusdef.mm9.exon
```

locusdef.mm9.exon locus definition

Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

Usage

```
locusdef.mm9.exon
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm9.

organism A character indicating the organism name. In this case, *Mus musculus*.

Details

Built on Fri Apr 13 09:50:39 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

locusdef.mm9.intron *locusdef.mm9.intron locus definition*

Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

Usage

locusdef.mm9.intron

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, mm9.

organism A character indicating the organism name. In this case, *Mus musculus*.

Details

Built on Fri Apr 13 09:50:41 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

`locusdef.mm9.nearest_gene`

locusdef.mm9.nearest_gene locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

`locusdef.mm9.nearest_gene`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `mm9`.

organism A character indicating the organism name. In this case, `Mus musculus`.

Details

Built on Fri Apr 13 09:50:37 2018.

Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

`locusdef.mm9.nearest_tss`

locusdef.mm9.nearest_tss locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

`locusdef.mm9.nearest_tss`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `mm9`.

organism A character indicating the organism name. In this case, `Mus musculus`.

Details

Built on Fri Apr 13 09:50:37 2018.

Source

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.5.0`. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

`locusdef.rn4.10kb`

locusdef.rn4.10kb locus definition

Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

`locusdef.rn4.10kb`

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- genome.build** A character indicating the genome build. In this case, `rn4`.
- organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn4.10kb_outside
  locusdef.rn4.10kb_outside locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn4.10kb_outside
```

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- genome.build** A character indicating the genome build. In this case, `rn4`.
- organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:03 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn4.10kb_outside_upstream`

locusdef.rn4.10kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

`locusdef.rn4.10kb_outside_upstream`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, rn4.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

locusdef.rn4.1kb *locusdef.rn4.1kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

locusdef.rn4.1kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn4.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

locusdef.rn4.1kb_outside *locusdef.rn4.1kb_outside locus definition*

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn4.1kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn4`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

locusdef.rn4.1kb_outside_upstream

locusdef.rn4.1kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn4.1kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn4`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

locusdef.rn4.5kb *locusdef.rn4.5kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

locusdef.rn4.5kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, rn4.

organism A character indicating the organism name. In this case, *Rattus norvegicus*.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

```
locusdef.rn4.5kb_outside
```

locusdef.rn4.5kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn4.5kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn4`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn4.5kb_outside_upstream
```

locusdef.rn4.5kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn4.5kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn4`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

locusdef.rn4.exon *locusdef.rn4.exon* locus definition

Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

Usage

```
locusdef.rn4.exon
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn4`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:51:59 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn4.intron` *locusdef.rn4.intron* locus definition

Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

Usage

`locusdef.rn4.intron`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, rn4.

organism A character indicating the organism name. In this case, *Rattus norvegicus*.

Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:00 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

```
locusdef.rn4.nearest_gene
```

locusdef.rn4.nearest_gene locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.rn4.nearest_gene
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn4`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:51:58 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn4.nearest_tss
```

locusdef.rn4.nearest_tss locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

```
locusdef.rn4.nearest_tss
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn4`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:51:58 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

locusdef.rn5.10kb

locusdef.rn5.10kb locus definition

Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

```
locusdef.rn5.10kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn5`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:20 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

```
locusdef.rn5.10kb_outside
  locusdef.rn5.10kb_outside locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn5.10kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn5.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:21 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

```
locusdef.rn5.10kb_outside_upstream
  locusdef.rn5.10kb_outside_upstream locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn5.10kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn5`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:21 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn5.1kb      locusdef.rn5.1kb locus definition
```

Description

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

```
locusdef.rn5.1kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn5.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:19 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

locusdef.rn5.1kb_outside

locusdef.rn5.1kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

locusdef.rn5.1kb_outside

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn5.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:19 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

locusdef.rn5.1kb_outside_upstream

locusdef.rn5.1kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

`locusdef.rn5.1kb_outside_upstream`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn5`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:19 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

```
locusdef.rn5.5kb      locusdef.rn5.5kb locus definition
```

Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

```
locusdef.rn5.5kb
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn5.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:20 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

```
locusdef.rn5.5kb_outside
locusdef.rn5.5kb_outside locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn5.5kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn5.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:20 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn5.5kb_outside_upstream`

locusdef.rn5.5kb_outside_upstream locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

`locusdef.rn5.5kb_outside_upstream`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn5.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:20 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

locusdef.rn5.exon *locusdef.rn5.exon locus definition*

Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

Usage

locusdef.rn5.exon

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn5`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:17 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

locusdef.rn5.intron *locusdef.rn5.intron locus definition*

Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

Usage

locusdef.rn5.intron

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn5.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:19 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

locusdef.rn5.nearest_gene
locusdef.rn5.nearest_gene locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

locusdef.rn5.nearest_gene

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn5.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:16 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

locusdef.rn5.nearest_tss
locusdef.rn5.nearest_tss locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

```
locusdef.rn5.nearest_tss
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn5.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:16 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

`locusdef.rn6.10kb` *locusdef.rn6.10kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

Usage

`locusdef.rn6.10kb`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn6`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:39 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

`locusdef.rn6.10kb_outside`
locusdef.rn6.10kb_outside locus definition

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

`locusdef.rn6.10kb_outside`

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn6.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:40 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

```
locusdef.rn6.10kb_outside_upstream
  locusdef.rn6.10kb_outside_upstream locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn6.10kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn6.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:39 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

locusdef.rn6.1kb *locusdef.rn6.1kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

Usage

locusdef.rn6.1kb

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn6.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:38 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

```
locusdef.rn6.1kb_outside
  locusdef.rn6.1kb_outside locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn6.1kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn6`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:38 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn6.1kb_outside_upstream
  locusdef.rn6.1kb_outside_upstream locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn6.1kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol
- dframe** A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol
- genome.build** A character indicating the genome build. In this case, rn6.
- organism** A character indicating the organism name. In this case, *Rattus norvegicus*.

Details

Built on Fri Apr 13 09:52:38 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

locusdef.rn6.5kb *locusdef.rn6.5kb locus definition*

Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

Usage

locusdef.rn6.5kb

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol
- dframe** A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol
- genome.build** A character indicating the genome build. In this case, rn6.
- organism** A character indicating the organism name. In this case, *Rattus norvegicus*.

Details

Built on Fri Apr 13 09:52:38 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

```
locusdef.rn6.5kb_outside
  locusdef.rn6.5kb_outside locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

Usage

```
locusdef.rn6.5kb_outside
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn6`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:39 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn6.5kb_outside_upstream
  locusdef.rn6.5kb_outside_upstream locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

Usage

```
locusdef.rn6.5kb_outside_upstream
```

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol
- dframe** A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol
- genome.build** A character indicating the genome build. In this case, rn6.
- organism** A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:39 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

locusdef.rn6.exon *locusdef.rn6.exon* locus definition

Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

Usage

locusdef.rn6.exon

Format

A LocusDefinition object with the following slots:

- granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol
- dframe** A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol
- genome.build** A character indicating the genome build. In this case, rn6.
- organism** A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:36 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

```
locusdef.rn6.intron      locusdef.rn6.intron locus definition
```

Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

Usage

```
locusdef.rn6.intron
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

dframe A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

genome.build A character indicating the genome build. In this case, `rn6`.

organism A character indicating the organism name. In this case, `Rattus norvegicus`.

Details

Built on Fri Apr 13 09:52:37 2018.

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

```
locusdef.rn6.nearest_gene
      locusdef.rn6.nearest_gene locus definition
```

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

Usage

```
locusdef.rn6.nearest_gene
```

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn6.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:35 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

locusdef.rn6.nearest_tss

locusdef.rn6.nearest_tss locus definition

Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

Usage

locusdef.rn6.nearest_tss

Format

A LocusDefinition object with the following slots:

granges A GRanges of the locus definitions with mcols for Entrez Gene ID gene_id and gene symbol symbol

dframe A data.frame of the locus definitions with columns for chr, start, end, gene_id, and symbol

genome.build A character indicating the genome build. In this case, rn6.

organism A character indicating the organism name. In this case, Rattus norvegicus.

Details

Built on Fri Apr 13 09:52:34 2018.

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

LocusDefinition-class *Class "LocusDefinition"*

Description

A storage class representing gene locus definitions and their corresponding metadata.

Objects from the Class

Objects can be created by calls of the form `new("LocusDefinition")`. These objects are used internally by the `chipenrich` package and users will not likely need to create these.

Slots

dframe: Object of class `"data.frame"`. Each row represents a locus for a particular geneid.
granges: Object of class `"GenomicRanges"`. Locus definitions stored as a `GenomicRanges` object.
genome.build: Object of class `"character"`. Genome build these definitions were generated from.
organism: Object of class `"character"`. Organism code.

Note

Not typically accessed by the user - this is used internally by the `chipenrich` package.

Author(s)

Ryan Welch <welchr@umich.edu>

Examples

```
# Show info about the class.
showClass("LocusDefinition");

# Example of what a locus definition object looks like.
data(locusdef.mm9.nearest_tss)
lapply(attributes(locusdef.mm9.nearest_tss), head)
```

mappa.hg19.10kb.100mer
mappa.hg19.10kb.100mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.10kb.100mer)
```

Format

A data frame containing:

```
geneid Entrez Gene IDs  
mappa Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.hg19.10kb.24mer *mappa.hg19.10kb.24mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.10kb.24mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.10kb.36mer` *mappa.hg19.10kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.10kb.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.10kb.40mer` *mappa.hg19.10kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.10kb.40mer)
```

Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.10kb.50mer` *mappa.hg19.10kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.10kb.50mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.10kb.75mer` *mappa.hg19.10kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.10kb.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.1kb.100mer` *mappa.hg19.1kb.100mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.1kb.100mer)
```

Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.1kb.24mer` *mappa.hg19.1kb.24mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.1kb.24mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.1kb.36mer` *mappa.hg19.1kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.1kb.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.1kb.40mer` *mappa.hg19.1kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.1kb.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.1kb.50mer` *mappa.hg19.1kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.1kb.50mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.hg19.1kb.75mer *mappa.hg19.1kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.1kb.75mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.5kb.100mer` *mappa.hg19.5kb.100mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.5kb.100mer)
```

Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.5kb.24mer` *mappa.hg19.5kb.24mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.5kb.24mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.5kb.36mer` *mappa.hg19.5kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.5kb.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.5kb.40mer` *mappa.hg19.5kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.5kb.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.5kb.50mer` *mappa.hg19.5kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.5kb.50mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.5kb.75mer` *mappa.hg19.5kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.5kb.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.hg19.exon.100mer
mappa.hg19.exon.100mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.exon.100mer)
```

Format

A data frame containing:

```
geneid Entrez Gene IDs  
mappa Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.hg19.exon.24mer *mappa.hg19.exon.24mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.exon.24mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.exon.36mer` *mappa.hg19.exon.36mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.exon.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.exon.40mer` *mappa.hg19.exon.40mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.exon.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.exon.50mer` *mappa.hg19.exon.50mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.exon.50mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.hg19.exon.75mer mappa.hg19.exon.75mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.exon.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.hg19.intron.100mer
mappa.hg19.intron.100mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.intron.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.hg19.intron.24mer
mappa.hg19.intron.24mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.intron.24mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.hg19.intron.36mer

mappa.hg19.intron.36mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.intron.36mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.intron.40mer`
mappa.hg19.intron.40mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.intron.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.intron.50mer`
mappa.hg19.intron.50mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.intron.50mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.hg19.intron.75mer

mappa.hg19.intron.75mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.intron.75mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.nearest_gene.100mer`
mappa.hg19.nearest_gene.100mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_gene.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.nearest_gene.24mer`
mappa.hg19.nearest_gene.24mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_gene.24mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.hg19.nearest_gene.36mer

mappa.hg19.nearest_gene.36mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_gene.36mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.nearest_gene.40mer`
mappa.hg19.nearest_gene.40mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_gene.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.nearest_gene.50mer`
mappa.hg19.nearest_gene.50mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_gene.50mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.hg19.nearest_gene.75mer

mappa.hg19.nearest_gene.75mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_gene.75mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.nearest_tss.100mer`
mappa.hg19.nearest_tss.100mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_tss.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.nearest_tss.24mer`
mappa.hg19.nearest_tss.24mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_tss.24mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.hg19.nearest_tss.36mer

mappa.hg19.nearest_tss.36mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_tss.36mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.nearest_tss.40mer`
mappa.hg19.nearest_tss.40mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_tss.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.hg19.nearest_tss.50mer`
mappa.hg19.nearest_tss.50mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_tss.50mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.hg19.nearest_tss.75mer

mappa.hg19.nearest_tss.75mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.hg19.nearest_tss.75mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.10kb.100mer` *mappa.mm9.10kb.100mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.10kb.100mer)
```

Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.10kb.36mer` *mappa.mm9.10kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.10kb.36mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.10kb.40mer *mappa.mm9.10kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.10kb.40mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.10kb.50mer` *mappa.mm9.10kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.10kb.50mer)
```

Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.10kb.75mer` *mappa.mm9.10kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.10kb.75mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.1kb.100mer *mappa.mm9.1kb.100mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.1kb.100mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.1kb.36mer` *mappa.mm9.1kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.1kb.36mer)
```

Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.1kb.40mer` *mappa.mm9.1kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.1kb.40mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.1kb.50mer *mappa.mm9.1kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.1kb.50mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.1kb.75mer` *mappa.mm9.1kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.1kb.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.5kb.100mer` *mappa.mm9.5kb.100mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.5kb.100mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.5kb.36mer *mappa.mm9.5kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.5kb.36mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.5kb.40mer` *mappa.mm9.5kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.5kb.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.5kb.50mer` *mappa.mm9.5kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.5kb.50mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.5kb.75mer *mappa.mm9.5kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.5kb.75mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.exon.100mer` *mappa.mm9.exon.100mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.exon.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.exon.36mer` *mappa.mm9.exon.36mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.exon.36mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.exon.40mer *mappa.mm9.exon.40mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.exon.40mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.exon.50mer` *mappa.mm9.exon.50mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.exon.50mer)
```

Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.exon.75mer` *mappa.mm9.exon.75mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.exon.75mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs
mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.intron.100mer

mappa.mm9.intron.100mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.intron.100mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs
mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.intron.36mer`
mappa.mm9.intron.36mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.intron.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.intron.40mer`
mappa.mm9.intron.40mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.intron.40mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs
mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.intron.50mer

mappa.mm9.intron.50mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.intron.50mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs
mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.intron.75mer`
mappa.mm9.intron.75mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.intron.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.nearest_gene.100mer`
mappa.mm9.nearest_gene.100mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_gene.100mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.nearest_gene.36mer`

mappa.mm9.nearest_gene.36mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_gene.36mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.nearest_gene.40mer`
mappa.mm9.nearest_gene.40mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_gene.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.nearest_gene.50mer`
mappa.mm9.nearest_gene.50mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_gene.50mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.nearest_gene.75mer`

mappa.mm9.nearest_gene.75mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_gene.75mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.nearest_tss.100mer`
mappa.mm9.nearest_tss.100mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_tss.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs
`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.nearest_tss.36mer`
mappa.mm9.nearest_tss.36mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_tss.36mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

`mappa.mm9.nearest_tss.40mer`
mappa.mm9.nearest_tss.40mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_tss.40mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

```
mappa.mm9.nearest_tss.50mer
mappa.mm9.nearest_tss.50mer
```

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_tss.50mer)
```

Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

```
mappa.mm9.nearest_tss.75mer
mappa.mm9.nearest_tss.75mer
```

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

Usage

```
data(mappa.mm9.nearest_tss.75mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: [chipenrich.data](#)

peaks_E2F4

ChIP-seq Peaks for the E2F4 Transcription Factor

Description

A dataset containing the binding locations (peaks) of the transcription factor E2F4 called from a ChIP-seq experiment

Usage

```
peaks_E2F4
```

Format

A data frame containing 16,245 peak binding locations. Each row is a peak location, and the 3 variables/columns are chromosome, start peak coordinate, and end peak coordinate. Peak coordinates are in hg19 (UCSC) coordinates.

Source

The data and information regarding the experiment can be found in the following publication:

Lee, B. K., A. A. Bhinge, et al. (2011). "Wide-ranging functions of E2F4 in transcriptional activation and repression revealed by genome-wide analysis." *Nucleic Acids Res* 39(9): 3558-3573.

Examples

```
# Load E2F4 peak data.  
data(peaks_E2F4)  
  
# Print the first 10 peaks in the dataset.  
print(head(peaks_E2F4))
```

peaks_H3K4me3_GM12878 *ChIP-seq Peaks for the Histone Modification H3K4me3 in GM12878*

Description

A dataset containing the binding locations (peaks) of the histone modification H3K4me3 called from a ChIP-seq experiment in the GM12878 cell line

Usage

```
peaks_H3K4me3_GM12878
```

Format

A data frame containing 57,476 peak binding locations. Each row is a peak location, and the 3 variables/columns are chromosome, start peak coordinate, and end peak coordinate. Peak coordinates are in hg19 (UCSC) coordinates.

Source

The data and information regarding the experiment can be found at the following ENCODE URL:

<http://hgdownload.cse.ucsc.edu/goldenPath/hg19/encodeDCC/wgEncodeBroadHistone/wgEncodeBroadHistoneGm12878H3K4me3>

Examples

```
# Load H3K4me3 in GM12878 peak data.
data(peaks_H3K4me3_GM12878)

# Print the first 10 peaks in the dataset.
print(head(peaks_H3K4me3_GM12878))
```

spline.log_dtss.90ENCODE

DTSS Spline adjustment

Description

A mgcv:::gam object on a combined data of 90 ENCODE ChIP-seq datasets that modeled the relationship between a gene's locus length the distance from a peak to the gene's transcription start site, using a cubic spline. This is used to adjust for the proximity to TSSes test.

Usage

```
spline.log_dtss.90ENCODE
```

Format

An object of class `gam` (inherits from `glm`, `lm`) of length 46.

`tss.danRer10`*tss.danRer10 TSS locations*

Description

A GRanges with all the TSSs for danRer10. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

`tss.danRer10`

Format

A GRanges object with the following `mcols`:

gene_id The Entrez ID for the TSS

symbol The gene symbol for the TSS

Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

`tss.dm3`*tss.dm3 TSS locations*

Description

A GRanges with all the TSSs for dm3. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

`tss.dm3`

Format

A GRanges object with the following `mcols`:

gene_id The Entrez ID for the TSS

symbol The gene symbol for the TSS

Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

tss.dm6	<i>tss.dm6 TSS locations</i>
---------	------------------------------

Description

A GRanges with all the TSSs for dm6. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

`tss.dm6`

Format

A GRanges object with the following `mcols`:

- gene_id** The Entrez ID for the TSS
- symbol** The gene symbol for the TSS

Source

R packages: `TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1` and `org.Dm.eg.db_3.5.0`.

tss.hg19	<i>tss.hg19 TSS locations</i>
----------	-------------------------------

Description

A GRanges with all the TSSs for hg19. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

`tss.hg19`

Format

A GRanges object with the following `mcols`:

- gene_id** The Entrez ID for the TSS
- symbol** The gene symbol for the TSS

Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezGene.gz

tss.hg38

tss.hg38 TSS locations

Description

A GRanges with all the TSSs for hg38. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

`tss.hg38`

Format

A GRanges object with the following `ncols`:

gene_id The Entrez ID for the TSS

symbol The gene symbol for the TSS

Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

tss.mm10

tss.mm10 TSS locations

Description

A GRanges with all the TSSs for mm10. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

`tss.mm10`

Format

A GRanges object with the following `mcols`:

gene_id The Entrez ID for the TSS

symbol The gene symbol for the TSS

Source

R packages: `TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0` and `org.Mm.eg.db_3.5.0`. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

`tss.mm9`*tss.mm9 TSS locations*

Description

A GRanges with all the TSSs for mm9. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

`tss.mm9`

Format

A GRanges object with the following `mcols`:

gene_id The Entrez ID for the TSS

symbol The gene symbol for the TSS

Source

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.5.0`. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

`tss.rn4`*tss.rn4 TSS locations*

Description

A GRanges with all the TSSs for rn4. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

`tss.rn4`

Format

A GRanges object with the following `mcols`:

gene_id The Entrez ID for the TSS

symbol The gene symbol for the TSS

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

`tss.rn5`*tss.rn5 TSS locations*

Description

A GRanges with all the TSSs for rn5. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

`tss.rn5`

Format

A GRanges object with the following `mcols`:

gene_id The Entrez ID for the TSS

symbol The gene symbol for the TSS

Source

R packages: `TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2` and `org.Rn.eg.db_3.5.0`.

tss.rn6*tss.rn6 TSS locations*

Description

A GRanges with all the TSSs for rn6. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

Usage

```
tss.rn6
```

Format

A GRanges object with the following `mcols`:

- gene_id** The Entrez ID for the TSS
- symbol** The gene symbol for the TSS

Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

Index

- * **classes**
 - GeneSet-class, 9
 - LocusDefinition-class, 139
- * **datasets**
 - enhancer.dnase_thurman.0, 8
 - gene.enh.desc, 9
 - geneset.biocarta_pathway.hsa, 10
 - geneset.biocarta_pathway.mmu, 11
 - geneset.biocarta_pathway.rno, 11
 - geneset.ctd.hsa, 12
 - geneset.ctd.mmu, 12
 - geneset.cytoband.hsa, 13
 - geneset.drug_bank.hsa, 14
 - geneset.drug_bank.mmu, 14
 - geneset.drug_bank.rno, 15
 - geneset.GOBP.dme, 15
 - geneset.GOBP.dre, 16
 - geneset.GOBP.hsa, 17
 - geneset.GOBP.mmu, 17
 - geneset.GOBP.rno, 18
 - geneset.GOCC.dme, 19
 - geneset.GOCC.dre, 19
 - geneset.GOCC.hsa, 20
 - geneset.GOCC.mmu, 21
 - geneset.GOCC.rno, 21
 - geneset.GOMF.dme, 22
 - geneset.GOMF.dre, 23
 - geneset.GOMF.hsa, 23
 - geneset.GOMF.mmu, 24
 - geneset.GOMF.rno, 25
 - geneset.hallmark.hsa, 25
 - geneset.immunologic.hsa, 26
 - geneset.kegg_pathway.hsa, 27
 - geneset.kegg_pathway.mmu, 28
 - geneset.kegg_pathway.rno, 28
 - geneset.mesh.hsa, 29
 - geneset.mesh.mmu, 29
 - geneset.mesh.rno, 30
 - geneset.metabolite.hsa, 30
 - geneset.metabolite.mmu, 31
 - geneset.metabolite.rno, 31
 - geneset.microrna.hsa, 32
 - geneset.oncogenic.hsa, 32
 - geneset.panther_pathway.hsa, 33
 - geneset.panther_pathway.mmu, 34
 - geneset.panther_pathway.rno, 34
 - geneset.pfam.hsa, 35
 - geneset.pfam.mmu, 35
 - geneset.pfam.rno, 36
 - geneset.protein_interaction_biogrid.hsa, 36
 - geneset.reactome.dme, 37
 - geneset.reactome.dre, 38
 - geneset.reactome.hsa, 38
 - geneset.reactome.mmu, 39
 - geneset.reactome.rno, 40
 - geneset.transcription_factors.hsa, 41
 - geneset.transcription_factors.mmu, 41
 - geneset.transcription_factors.rno, 42
 - locusdef.danRer10.10kb, 42
 - locusdef.danRer10.10kb_outside, 43
 - locusdef.danRer10.10kb_outside_upstream, 44
 - locusdef.danRer10.1kb, 45
 - locusdef.danRer10.1kb_outside, 45
 - locusdef.danRer10.1kb_outside_upstream, 46
 - locusdef.danRer10.5kb, 47
 - locusdef.danRer10.5kb_outside, 48
 - locusdef.danRer10.5kb_outside_upstream, 48
 - locusdef.danRer10.exon, 49
 - locusdef.danRer10.intron, 50
 - locusdef.danRer10.nearest_gene, 50
 - locusdef.danRer10.nearest_tss, 51

locusdef.dm3.10kb, 52
 locusdef.dm3.10kb_outside, 53
 locusdef.dm3.10kb_outside_upstream,
 53
 locusdef.dm3.1kb, 54
 locusdef.dm3.1kb_outside, 55
 locusdef.dm3.1kb_outside_upstream,
 56
 locusdef.dm3.5kb, 56
 locusdef.dm3.5kb_outside, 57
 locusdef.dm3.5kb_outside_upstream,
 58
 locusdef.dm3.exon, 59
 locusdef.dm3.intron, 59
 locusdef.dm3.nearest_gene, 60
 locusdef.dm3.nearest_tss, 61
 locusdef.dm6.10kb, 62
 locusdef.dm6.10kb_outside, 62
 locusdef.dm6.10kb_outside_upstream,
 63
 locusdef.dm6.1kb, 64
 locusdef.dm6.1kb_outside, 65
 locusdef.dm6.1kb_outside_upstream,
 65
 locusdef.dm6.5kb, 66
 locusdef.dm6.5kb_outside, 67
 locusdef.dm6.5kb_outside_upstream,
 68
 locusdef.dm6.exon, 68
 locusdef.dm6.intron, 69
 locusdef.dm6.nearest_gene, 70
 locusdef.dm6.nearest_tss, 71
 locusdef.hg19.10kb, 71
 locusdef.hg19.10kb_outside, 72
 locusdef.hg19.10kb_outside_upstream,
 73
 locusdef.hg19.1kb, 74
 locusdef.hg19.1kb_outside, 74
 locusdef.hg19.1kb_outside_upstream,
 75
 locusdef.hg19.5kb, 76
 locusdef.hg19.5kb_outside, 77
 locusdef.hg19.5kb_outside_upstream,
 77
 locusdef.hg19.exon, 78
 locusdef.hg19.intron, 79
 locusdef.hg19.nearest_gene, 80
 locusdef.hg19.nearest_tss, 80
 locusdef.hg38.10kb, 81
 locusdef.hg38.10kb_outside, 82
 locusdef.hg38.10kb_outside_upstream,
 83
 locusdef.hg38.1kb, 83
 locusdef.hg38.1kb_outside, 84
 locusdef.hg38.1kb_outside_upstream,
 85
 locusdef.hg38.5kb, 86
 locusdef.hg38.5kb_outside, 86
 locusdef.hg38.5kb_outside_upstream,
 87
 locusdef.hg38.exon, 88
 locusdef.hg38.intron, 89
 locusdef.hg38.nearest_gene, 89
 locusdef.hg38.nearest_tss, 90
 locusdef.mm10.10kb, 91
 locusdef.mm10.10kb_outside, 92
 locusdef.mm10.10kb_outside_upstream,
 92
 locusdef.mm10.1kb, 93
 locusdef.mm10.1kb_outside, 94
 locusdef.mm10.1kb_outside_upstream,
 95
 locusdef.mm10.5kb, 95
 locusdef.mm10.5kb_outside, 96
 locusdef.mm10.5kb_outside_upstream,
 97
 locusdef.mm10.exon, 98
 locusdef.mm10.intron, 98
 locusdef.mm10.nearest_gene, 99
 locusdef.mm10.nearest_tss, 100
 locusdef.mm9.10kb, 101
 locusdef.mm9.10kb_outside, 101
 locusdef.mm9.10kb_outside_upstream,
 102
 locusdef.mm9.1kb, 103
 locusdef.mm9.1kb_outside, 104
 locusdef.mm9.1kb_outside_upstream,
 104
 locusdef.mm9.5kb, 105
 locusdef.mm9.5kb_outside, 106
 locusdef.mm9.5kb_outside_upstream,
 107
 locusdef.mm9.exon, 107
 locusdef.mm9.intron, 108
 locusdef.mm9.nearest_gene, 109
 locusdef.mm9.nearest_tss, 110

- locusdef.rn4.10kb, 110
locusdef.rn4.10kb_outside, 111
locusdef.rn4.10kb_outside_upstream,
112
locusdef.rn4.1kb, 113
locusdef.rn4.1kb_outside, 113
locusdef.rn4.1kb_outside_upstream,
114
locusdef.rn4.5kb, 115
locusdef.rn4.5kb_outside, 116
locusdef.rn4.5kb_outside_upstream,
116
locusdef.rn4.exon, 117
locusdef.rn4.intron, 118
locusdef.rn4.nearest_gene, 119
locusdef.rn4.nearest_tss, 119
locusdef.rn5.10kb, 120
locusdef.rn5.10kb_outside, 121
locusdef.rn5.10kb_outside_upstream,
122
locusdef.rn5.1kb, 122
locusdef.rn5.1kb_outside, 123
locusdef.rn5.1kb_outside_upstream,
124
locusdef.rn5.5kb, 125
locusdef.rn5.5kb_outside, 125
locusdef.rn5.5kb_outside_upstream,
126
locusdef.rn5.exon, 127
locusdef.rn5.intron, 127
locusdef.rn5.nearest_gene, 128
locusdef.rn5.nearest_tss, 129
locusdef.rn6.10kb, 130
locusdef.rn6.10kb_outside, 130
locusdef.rn6.10kb_outside_upstream,
131
locusdef.rn6.1kb, 132
locusdef.rn6.1kb_outside, 133
locusdef.rn6.1kb_outside_upstream,
133
locusdef.rn6.5kb, 134
locusdef.rn6.5kb_outside, 135
locusdef.rn6.5kb_outside_upstream,
135
locusdef.rn6.exon, 136
locusdef.rn6.intron, 137
locusdef.rn6.nearest_gene, 137
locusdef.rn6.nearest_tss, 138
mappa.hg19.10kb.100mer, 140
mappa.hg19.10kb.24mer, 140
mappa.hg19.10kb.36mer, 141
mappa.hg19.10kb.40mer, 142
mappa.hg19.10kb.50mer, 142
mappa.hg19.10kb.75mer, 143
mappa.hg19.1kb.100mer, 144
mappa.hg19.1kb.24mer, 144
mappa.hg19.1kb.36mer, 145
mappa.hg19.1kb.40mer, 146
mappa.hg19.1kb.50mer, 146
mappa.hg19.1kb.75mer, 147
mappa.hg19.5kb.100mer, 148
mappa.hg19.5kb.24mer, 148
mappa.hg19.5kb.36mer, 149
mappa.hg19.5kb.40mer, 150
mappa.hg19.5kb.50mer, 150
mappa.hg19.5kb.75mer, 151
mappa.hg19.exon.100mer, 152
mappa.hg19.exon.24mer, 152
mappa.hg19.exon.36mer, 153
mappa.hg19.exon.40mer, 154
mappa.hg19.exon.50mer, 154
mappa.hg19.exon.75mer, 155
mappa.hg19.intron.100mer, 156
mappa.hg19.intron.24mer, 156
mappa.hg19.intron.36mer, 157
mappa.hg19.intron.40mer, 158
mappa.hg19.intron.50mer, 158
mappa.hg19.intron.75mer, 159
mappa.hg19.nearest_gene.100mer,
160
mappa.hg19.nearest_gene.24mer, 160
mappa.hg19.nearest_gene.36mer, 161
mappa.hg19.nearest_gene.40mer, 162
mappa.hg19.nearest_gene.50mer, 162
mappa.hg19.nearest_gene.75mer, 163
mappa.hg19.nearest_tss.100mer, 164
mappa.hg19.nearest_tss.24mer, 164
mappa.hg19.nearest_tss.36mer, 165
mappa.hg19.nearest_tss.40mer, 166
mappa.hg19.nearest_tss.50mer, 166
mappa.hg19.nearest_tss.75mer, 167
mappa.mm9.10kb.100mer, 168
mappa.mm9.10kb.36mer, 168
mappa.mm9.10kb.40mer, 169
mappa.mm9.10kb.50mer, 170
mappa.mm9.10kb.75mer, 170

- mappa.mm9.1kb.100mer, 171
- mappa.mm9.1kb.36mer, 172
- mappa.mm9.1kb.40mer, 172
- mappa.mm9.1kb.50mer, 173
- mappa.mm9.1kb.75mer, 174
- mappa.mm9.5kb.100mer, 174
- mappa.mm9.5kb.36mer, 175
- mappa.mm9.5kb.40mer, 176
- mappa.mm9.5kb.50mer, 176
- mappa.mm9.5kb.75mer, 177
- mappa.mm9.exon.100mer, 178
- mappa.mm9.exon.36mer, 178
- mappa.mm9.exon.40mer, 179
- mappa.mm9.exon.50mer, 180
- mappa.mm9.exon.75mer, 180
- mappa.mm9.intron.100mer, 181
- mappa.mm9.intron.36mer, 182
- mappa.mm9.intron.40mer, 182
- mappa.mm9.intron.50mer, 183
- mappa.mm9.intron.75mer, 184
- mappa.mm9.nearest_gene.100mer, 184
- mappa.mm9.nearest_gene.36mer, 185
- mappa.mm9.nearest_gene.40mer, 186
- mappa.mm9.nearest_gene.50mer, 186
- mappa.mm9.nearest_gene.75mer, 187
- mappa.mm9.nearest_tss.100mer, 188
- mappa.mm9.nearest_tss.36mer, 188
- mappa.mm9.nearest_tss.40mer, 189
- mappa.mm9.nearest_tss.50mer, 190
- mappa.mm9.nearest_tss.75mer, 190
- peaks_E2F4, 191
- peaks_H3K4me3_GM12878, 192
- spline.log_dtss.90ENCODE, 192
- tss.danRer10, 193
- tss.dm3, 193
- tss.dm6, 194
- tss.hg19, 194
- tss.hg38, 195
- tss.mm10, 195
- tss.mm9, 196
- tss.rn4, 197
- tss.rn5, 197
- tss.rn6, 198
- chipenrich.data, 8, 11, 13, 15, 28–31, 33, 34, 36, 42, 140–191
- chipenrich.data-package
(chipenrich.data), 8
- enhancer.dnase_thurman.0, 8
- gene.enh.desc, 9
- GeneSet-class, 9
- geneset.biocarta_pathway.hsa, 10
- geneset.biocarta_pathway.mmu, 11
- geneset.biocarta_pathway.rno, 11
- geneset.ctd.hsa, 12
- geneset.ctd.mmu, 12
- geneset.cytoband.hsa, 13
- geneset.drug_bank.hsa, 14
- geneset.drug_bank.mmu, 14
- geneset.drug_bank.rno, 15
- geneset.GOBP.dme, 15
- geneset.GOBP.dre, 16
- geneset.GOBP.hsa, 17
- geneset.GOBP.mmu, 17
- geneset.GOBP.rno, 18
- geneset.GOCC.dme, 19
- geneset.GOCC.dre, 19
- geneset.GOCC.hsa, 20
- geneset.GOCC.mmu, 21
- geneset.GOCC.rno, 21
- geneset.GOMF.dme, 22
- geneset.GOMF.dre, 23
- geneset.GOMF.hsa, 23
- geneset.GOMF.mmu, 24
- geneset.GOMF.rno, 25
- geneset.hallmark.hsa, 25
- geneset.immunologic.hsa, 26
- geneset.kegg_pathway.hsa, 27
- geneset.kegg_pathway.mmu, 28
- geneset.kegg_pathway.rno, 28
- geneset.mesh.hsa, 29
- geneset.mesh.mmu, 29
- geneset.mesh.rno, 30
- geneset.metabolite.hsa, 30
- geneset.metabolite.mmu, 31
- geneset.metabolite.rno, 31
- geneset.microrna.hsa, 32
- geneset.oncogenic.hsa, 32
- geneset.panther_pathway.hsa, 33
- geneset.panther_pathway.mmu, 34
- geneset.panther_pathway.rno, 34
- geneset.pfam.hsa, 35
- geneset.pfam.mmu, 35
- geneset.pfam.rno, 36
- geneset.protein_interaction_biogrid.hsa, 36

- geneset.reactome.dme, 37
geneset.reactome.dre, 38
geneset.reactome.hsa, 38
geneset.reactome.mmu, 39
geneset.reactome.rno, 40
geneset.transcription_factors.hsa, 41
geneset.transcription_factors.mmu, 41
geneset.transcription_factors.rno, 42
- locusdef.danRer10.10kb, 42
locusdef.danRer10.10kb_outside, 43
locusdef.danRer10.10kb_outside_upstream,
 44
locusdef.danRer10.1kb, 45
locusdef.danRer10.1kb_outside, 45
locusdef.danRer10.1kb_outside_upstream,
 46
locusdef.danRer10.5kb, 47
locusdef.danRer10.5kb_outside, 48
locusdef.danRer10.5kb_outside_upstream,
 48
locusdef.danRer10.exon, 49
locusdef.danRer10.intron, 50
locusdef.danRer10.nearest_gene, 50
locusdef.danRer10.nearest_tss, 51
locusdef.dm3.10kb, 52
locusdef.dm3.10kb_outside, 53
locusdef.dm3.10kb_outside_upstream, 53
locusdef.dm3.1kb, 54
locusdef.dm3.1kb_outside, 55
locusdef.dm3.1kb_outside_upstream, 56
locusdef.dm3.5kb, 56
locusdef.dm3.5kb_outside, 57
locusdef.dm3.5kb_outside_upstream, 58
locusdef.dm3.exon, 59
locusdef.dm3.intron, 59
locusdef.dm3.nearest_gene, 60
locusdef.dm3.nearest_tss, 61
locusdef.dm6.10kb, 62
locusdef.dm6.10kb_outside, 62
locusdef.dm6.10kb_outside_upstream, 63
locusdef.dm6.1kb, 64
locusdef.dm6.1kb_outside, 65
locusdef.dm6.1kb_outside_upstream, 65
locusdef.dm6.5kb, 66
locusdef.dm6.5kb_outside, 67
locusdef.dm6.5kb_outside_upstream, 68
locusdef.dm6.exon, 68
locusdef.dm6.intron, 69
- locusdef.dm6.nearest_gene, 70
locusdef.dm6.nearest_tss, 71
locusdef.hg19.10kb, 71
locusdef.hg19.10kb_outside, 72
locusdef.hg19.10kb_outside_upstream,
 73
locusdef.hg19.1kb, 74
locusdef.hg19.1kb_outside, 74
locusdef.hg19.1kb_outside_upstream, 75
locusdef.hg19.5kb, 76
locusdef.hg19.5kb_outside, 77
locusdef.hg19.5kb_outside_upstream, 77
locusdef.hg19.exon, 78
locusdef.hg19.intron, 79
locusdef.hg19.nearest_gene, 80
locusdef.hg19.nearest_tss, 80
locusdef.hg38.10kb, 81
locusdef.hg38.10kb_outside, 82
locusdef.hg38.10kb_outside_upstream,
 83
locusdef.hg38.1kb, 83
locusdef.hg38.1kb_outside, 84
locusdef.hg38.1kb_outside_upstream, 85
locusdef.hg38.5kb, 86
locusdef.hg38.5kb_outside, 86
locusdef.hg38.5kb_outside_upstream, 87
locusdef.hg38.exon, 88
locusdef.hg38.intron, 89
locusdef.hg38.nearest_gene, 89
locusdef.hg38.nearest_tss, 90
locusdef.mm10.10kb, 91
locusdef.mm10.10kb_outside, 92
locusdef.mm10.10kb_outside_upstream,
 92
locusdef.mm10.1kb, 93
locusdef.mm10.1kb_outside, 94
locusdef.mm10.1kb_outside_upstream, 95
locusdef.mm10.5kb, 95
locusdef.mm10.5kb_outside, 96
locusdef.mm10.5kb_outside_upstream, 97
locusdef.mm10.exon, 98
locusdef.mm10.intron, 98
locusdef.mm10.nearest_gene, 99
locusdef.mm10.nearest_tss, 100
locusdef.mm9.10kb, 101
locusdef.mm9.10kb_outside, 101
locusdef.mm9.10kb_outside_upstream,
 102

- locusdef.mm9.1kb, 103
- locusdef.mm9.1kb_outside, 104
- locusdef.mm9.1kb_outside_upstream, 104
- locusdef.mm9.5kb, 105
- locusdef.mm9.5kb_outside, 106
- locusdef.mm9.5kb_outside_upstream, 107
- locusdef.mm9.exon, 107
- locusdef.mm9.intron, 108
- locusdef.mm9.nearest_gene, 109
- locusdef.mm9.nearest_tss, 110
- locusdef.rn4.10kb, 110
- locusdef.rn4.10kb_outside, 111
- locusdef.rn4.10kb_outside_upstream, 112
- locusdef.rn4.1kb, 113
- locusdef.rn4.1kb_outside, 113
- locusdef.rn4.1kb_outside_upstream, 114
- locusdef.rn4.5kb, 115
- locusdef.rn4.5kb_outside, 116
- locusdef.rn4.5kb_outside_upstream, 116
- locusdef.rn4.exon, 117
- locusdef.rn4.intron, 118
- locusdef.rn4.nearest_gene, 119
- locusdef.rn4.nearest_tss, 119
- locusdef.rn5.10kb, 120
- locusdef.rn5.10kb_outside, 121
- locusdef.rn5.10kb_outside_upstream, 122
- locusdef.rn5.1kb, 122
- locusdef.rn5.1kb_outside, 123
- locusdef.rn5.1kb_outside_upstream, 124
- locusdef.rn5.5kb, 125
- locusdef.rn5.5kb_outside, 125
- locusdef.rn5.5kb_outside_upstream, 126
- locusdef.rn5.exon, 127
- locusdef.rn5.intron, 127
- locusdef.rn5.nearest_gene, 128
- locusdef.rn5.nearest_tss, 129
- locusdef.rn6.10kb, 130
- locusdef.rn6.10kb_outside, 130
- locusdef.rn6.10kb_outside_upstream, 131
- locusdef.rn6.1kb, 132
- locusdef.rn6.1kb_outside, 133
- locusdef.rn6.1kb_outside_upstream, 133
- locusdef.rn6.5kb, 134
- locusdef.rn6.5kb_outside, 135
- locusdef.rn6.5kb_outside_upstream, 135
- locusdef.rn6.exon, 136
- locusdef.rn6.intron, 137
- locusdef.rn6.nearest_gene, 137
- locusdef.rn6.nearest_tss, 138
- LocusDefinition-class, 139
- mappa.hg19.10kb.100mer, 140
- mappa.hg19.10kb.24mer, 140
- mappa.hg19.10kb.36mer, 141
- mappa.hg19.10kb.40mer, 142
- mappa.hg19.10kb.50mer, 142
- mappa.hg19.10kb.75mer, 143
- mappa.hg19.1kb.100mer, 144
- mappa.hg19.1kb.24mer, 144
- mappa.hg19.1kb.36mer, 145
- mappa.hg19.1kb.40mer, 146
- mappa.hg19.1kb.50mer, 146
- mappa.hg19.1kb.75mer, 147
- mappa.hg19.5kb.100mer, 148
- mappa.hg19.5kb.24mer, 148
- mappa.hg19.5kb.36mer, 149
- mappa.hg19.5kb.40mer, 150
- mappa.hg19.5kb.50mer, 150
- mappa.hg19.5kb.75mer, 151
- mappa.hg19.exon.100mer, 152
- mappa.hg19.exon.24mer, 152
- mappa.hg19.exon.36mer, 153
- mappa.hg19.exon.40mer, 154
- mappa.hg19.exon.50mer, 154
- mappa.hg19.exon.75mer, 155
- mappa.hg19.intron.100mer, 156
- mappa.hg19.intron.24mer, 156
- mappa.hg19.intron.36mer, 157
- mappa.hg19.intron.40mer, 158
- mappa.hg19.intron.50mer, 158
- mappa.hg19.intron.75mer, 159
- mappa.hg19.nearest_gene.100mer, 160
- mappa.hg19.nearest_gene.24mer, 160
- mappa.hg19.nearest_gene.36mer, 161
- mappa.hg19.nearest_gene.40mer, 162
- mappa.hg19.nearest_gene.50mer, 162
- mappa.hg19.nearest_gene.75mer, 163
- mappa.hg19.nearest_tss.100mer, 164
- mappa.hg19.nearest_tss.24mer, 164
- mappa.hg19.nearest_tss.36mer, 165
- mappa.hg19.nearest_tss.40mer, 166
- mappa.hg19.nearest_tss.50mer, 166
- mappa.hg19.nearest_tss.75mer, 167
- mappa.mm9.10kb.100mer, 168

mappa.mm9.10kb.36mer, 168
mappa.mm9.10kb.40mer, 169
mappa.mm9.10kb.50mer, 170
mappa.mm9.10kb.75mer, 170
mappa.mm9.1kb.100mer, 171
mappa.mm9.1kb.36mer, 172
mappa.mm9.1kb.40mer, 172
mappa.mm9.1kb.50mer, 173
mappa.mm9.1kb.75mer, 174
mappa.mm9.5kb.100mer, 174
mappa.mm9.5kb.36mer, 175
mappa.mm9.5kb.40mer, 176
mappa.mm9.5kb.50mer, 176
mappa.mm9.5kb.75mer, 177
mappa.mm9.exon.100mer, 178
mappa.mm9.exon.36mer, 178
mappa.mm9.exon.40mer, 179
mappa.mm9.exon.50mer, 180
mappa.mm9.exon.75mer, 180
mappa.mm9.intron.100mer, 181
mappa.mm9.intron.36mer, 182
mappa.mm9.intron.40mer, 182
mappa.mm9.intron.50mer, 183
mappa.mm9.intron.75mer, 184
mappa.mm9.nearest_gene.100mer, 184
mappa.mm9.nearest_gene.36mer, 185
mappa.mm9.nearest_gene.40mer, 186
mappa.mm9.nearest_gene.50mer, 186
mappa.mm9.nearest_gene.75mer, 187
mappa.mm9.nearest_tss.100mer, 188
mappa.mm9.nearest_tss.36mer, 188
mappa.mm9.nearest_tss.40mer, 189
mappa.mm9.nearest_tss.50mer, 190
mappa.mm9.nearest_tss.75mer, 190
peaks_E2F4, 191
peaks_H3K4me3_GM12878, 192
spline.log_dtss.90ENCODE, 192
tss.danRer10, 193
tss.dm3, 193
tss.dm6, 194
tss.hg19, 194
tss.hg38, 195
tss.mm10, 195
tss.mm9, 196
tss.rn4, 197
tss.rn5, 197
tss.rn6, 198