

# Package ‘chipenrich.data’

January 30, 2025

**Title** Companion package to chipenrich

**Version** 2.30.0

**Date** 2023-03-29

**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

**Maintainer** Kai Wang <wangdaha@umich.edu>

**git\_url** <https://git.bioconductor.org/packages/chipenrich.data>

**git\_branch** RELEASE\_3\_20

**git\_last\_commit** 4981ec3

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.20

**Date/Publication** 2025-01-30

**Author** Ryan P. Welch [aut, cph],  
 Chee Lee [aut],  
 Raymond G. Cavalcante [aut],  
 Kai Wang [cre],  
 Laura J. Scott [ths],  
 Maureen A. Sartor [ths]

## Contents

chipenrich.data . . . . .	7
enhancer.dnase_thurman.0 . . . . .	7
gene.enh.desc . . . . .	8
GeneSet-class . . . . .	8
geneset.biocarta_pathway.hsa . . . . .	9
geneset.biocarta_pathway.mmu . . . . .	10
geneset.biocarta_pathway.rno . . . . .	10
geneset.ctd.hsa . . . . .	11
geneset.ctd.mmu . . . . .	11
geneset.cytoband.hsa . . . . .	12
geneset.drug_bank.hsa . . . . .	13
geneset.drug_bank.mmu . . . . .	13
geneset.drug_bank.rno . . . . .	14
geneset.GOBP.dme . . . . .	14
geneset.GOBP.dre . . . . .	15
geneset.GOBP.hsa . . . . .	15
geneset.GOBP.mmu . . . . .	16
geneset.GOBP.rno . . . . .	17
geneset.GOCC.dme . . . . .	17
geneset.GOCC.dre . . . . .	18
geneset.GOCC.hsa . . . . .	19
geneset.GOCC.mmu . . . . .	19
geneset.GOCC.rno . . . . .	20
geneset.GOMF.dme . . . . .	21
geneset.GOMF.dre . . . . .	21
geneset.GOMF.hsa . . . . .	22
geneset.GOMF.mmu . . . . .	23
geneset.GOMF.rno . . . . .	23
geneset.hallmark.hsa . . . . .	24
geneset.immunologic.hsa . . . . .	25
geneset.kegg_pathway.hsa . . . . .	25
geneset.kegg_pathway.mmu . . . . .	26
geneset.kegg_pathway.rno . . . . .	27
geneset.mesh.hsa . . . . .	27
geneset.mesh.mmu . . . . .	28
geneset.mesh.rno . . . . .	28
geneset.metabolite.hsa . . . . .	29
geneset.metabolite.mmu . . . . .	29
geneset.metabolite.rno . . . . .	30
geneset.microrna.hsa . . . . .	30
geneset.oncogenic.hsa . . . . .	31
geneset.panther_pathway.hsa . . . . .	31
geneset.panther_pathway.mmu . . . . .	32

geneset.panther_pathway.rno . . . . .	32
geneset.pfam.hsa . . . . .	33
geneset.pfam.mmu . . . . .	33
geneset.pfam.rno . . . . .	34
geneset.protein_interaction_biogrid.hsa . . . . .	34
geneset.reactome.dme . . . . .	35
geneset.reactome.dre . . . . .	35
geneset.reactome.hsa . . . . .	36
geneset.reactome.mmu . . . . .	37
geneset.reactome.rno . . . . .	37
geneset.transcription_factors.hsa . . . . .	38
geneset.transcription_factors.mmu . . . . .	39
geneset.transcription_factors.rno . . . . .	39
locusdef.danRer10.10kb . . . . .	40
locusdef.danRer10.10kb_outside . . . . .	40
locusdef.danRer10.10kb_outside_upstream . . . . .	41
locusdef.danRer10.1kb . . . . .	42
locusdef.danRer10.1kb_outside . . . . .	42
locusdef.danRer10.1kb_outside_upstream . . . . .	43
locusdef.danRer10.5kb . . . . .	44
locusdef.danRer10.5kb_outside . . . . .	44
locusdef.danRer10.5kb_outside_upstream . . . . .	45
locusdef.danRer10.exon . . . . .	46
locusdef.danRer10.intron . . . . .	46
locusdef.danRer10.nearest_gene . . . . .	47
locusdef.danRer10.nearest_tss . . . . .	48
locusdef.dm3.10kb . . . . .	48
locusdef.dm3.10kb_outside . . . . .	49
locusdef.dm3.10kb_outside_upstream . . . . .	50
locusdef.dm3.1kb . . . . .	51
locusdef.dm3.1kb_outside . . . . .	51
locusdef.dm3.1kb_outside_upstream . . . . .	52
locusdef.dm3.5kb . . . . .	53
locusdef.dm3.5kb_outside . . . . .	53
locusdef.dm3.5kb_outside_upstream . . . . .	54
locusdef.dm3.exon . . . . .	55
locusdef.dm3.intron . . . . .	55
locusdef.dm3.nearest_gene . . . . .	56
locusdef.dm3.nearest_tss . . . . .	57
locusdef.dm6.10kb . . . . .	58
locusdef.dm6.10kb_outside . . . . .	58
locusdef.dm6.10kb_outside_upstream . . . . .	59
locusdef.dm6.1kb . . . . .	60
locusdef.dm6.1kb_outside . . . . .	60
locusdef.dm6.1kb_outside_upstream . . . . .	61
locusdef.dm6.5kb . . . . .	62
locusdef.dm6.5kb_outside . . . . .	62
locusdef.dm6.5kb_outside_upstream . . . . .	63
locusdef.dm6.exon . . . . .	64
locusdef.dm6.intron . . . . .	64
locusdef.dm6.nearest_gene . . . . .	65
locusdef.dm6.nearest_tss . . . . .	66

locusdef.hg19.10kb . . . . .	67
locusdef.hg19.10kb_outside . . . . .	67
locusdef.hg19.10kb_outside_upstream . . . . .	68
locusdef.hg19.1kb . . . . .	69
locusdef.hg19.1kb_outside . . . . .	70
locusdef.hg19.1kb_outside_upstream . . . . .	70
locusdef.hg19.5kb . . . . .	71
locusdef.hg19.5kb_outside . . . . .	72
locusdef.hg19.5kb_outside_upstream . . . . .	72
locusdef.hg19.exon . . . . .	73
locusdef.hg19.intron . . . . .	74
locusdef.hg19.nearest_gene . . . . .	74
locusdef.hg19.nearest_tss . . . . .	75
locusdef.hg38.10kb . . . . .	76
locusdef.hg38.10kb_outside . . . . .	77
locusdef.hg38.10kb_outside_upstream . . . . .	77
locusdef.hg38.1kb . . . . .	78
locusdef.hg38.1kb_outside . . . . .	79
locusdef.hg38.1kb_outside_upstream . . . . .	79
locusdef.hg38.5kb . . . . .	80
locusdef.hg38.5kb_outside . . . . .	81
locusdef.hg38.5kb_outside_upstream . . . . .	81
locusdef.hg38.exon . . . . .	82
locusdef.hg38.intron . . . . .	83
locusdef.hg38.nearest_gene . . . . .	83
locusdef.hg38.nearest_tss . . . . .	84
locusdef.mm10.10kb . . . . .	85
locusdef.mm10.10kb_outside . . . . .	86
locusdef.mm10.10kb_outside_upstream . . . . .	86
locusdef.mm10.1kb . . . . .	87
locusdef.mm10.1kb_outside . . . . .	88
locusdef.mm10.1kb_outside_upstream . . . . .	88
locusdef.mm10.5kb . . . . .	89
locusdef.mm10.5kb_outside . . . . .	90
locusdef.mm10.5kb_outside_upstream . . . . .	90
locusdef.mm10.exon . . . . .	91
locusdef.mm10.intron . . . . .	92
locusdef.mm10.nearest_gene . . . . .	92
locusdef.mm10.nearest_tss . . . . .	93
locusdef.mm9.10kb . . . . .	94
locusdef.mm9.10kb_outside . . . . .	95
locusdef.mm9.10kb_outside_upstream . . . . .	95
locusdef.mm9.1kb . . . . .	96
locusdef.mm9.1kb_outside . . . . .	97
locusdef.mm9.1kb_outside_upstream . . . . .	97
locusdef.mm9.5kb . . . . .	98
locusdef.mm9.5kb_outside . . . . .	99
locusdef.mm9.5kb_outside_upstream . . . . .	99
locusdef.mm9.exon . . . . .	100
locusdef.mm9.intron . . . . .	101
locusdef.mm9.nearest_gene . . . . .	101
locusdef.mm9.nearest_tss . . . . .	102

locusdef.rn4.10kb . . . . .	103
locusdef.rn4.10kb_outside . . . . .	104
locusdef.rn4.10kb_outside_upstream . . . . .	104
locusdef.rn4.1kb . . . . .	105
locusdef.rn4.1kb_outside . . . . .	106
locusdef.rn4.1kb_outside_upstream . . . . .	106
locusdef.rn4.5kb . . . . .	107
locusdef.rn4.5kb_outside . . . . .	108
locusdef.rn4.5kb_outside_upstream . . . . .	108
locusdef.rn4.exon . . . . .	109
locusdef.rn4.intron . . . . .	110
locusdef.rn4.nearest_gene . . . . .	110
locusdef.rn4.nearest_tss . . . . .	111
locusdef.rn5.10kb . . . . .	112
locusdef.rn5.10kb_outside . . . . .	112
locusdef.rn5.10kb_outside_upstream . . . . .	113
locusdef.rn5.1kb . . . . .	114
locusdef.rn5.1kb_outside . . . . .	114
locusdef.rn5.1kb_outside_upstream . . . . .	115
locusdef.rn5.5kb . . . . .	116
locusdef.rn5.5kb_outside . . . . .	116
locusdef.rn5.5kb_outside_upstream . . . . .	117
locusdef.rn5.exon . . . . .	118
locusdef.rn5.intron . . . . .	118
locusdef.rn5.nearest_gene . . . . .	119
locusdef.rn5.nearest_tss . . . . .	120
locusdef.rn6.10kb . . . . .	120
locusdef.rn6.10kb_outside . . . . .	121
locusdef.rn6.10kb_outside_upstream . . . . .	122
locusdef.rn6.1kb . . . . .	122
locusdef.rn6.1kb_outside . . . . .	123
locusdef.rn6.1kb_outside_upstream . . . . .	124
locusdef.rn6.5kb . . . . .	124
locusdef.rn6.5kb_outside . . . . .	125
locusdef.rn6.5kb_outside_upstream . . . . .	126
locusdef.rn6.exon . . . . .	126
locusdef.rn6.intron . . . . .	127
locusdef.rn6.nearest_gene . . . . .	128
locusdef.rn6.nearest_tss . . . . .	128
LocusDefinition-class . . . . .	129
mappa.hg19.10kb.100mer . . . . .	130
mappa.hg19.10kb.24mer . . . . .	131
mappa.hg19.10kb.36mer . . . . .	131
mappa.hg19.10kb.40mer . . . . .	132
mappa.hg19.10kb.50mer . . . . .	133
mappa.hg19.10kb.75mer . . . . .	133
mappa.hg19.1kb.100mer . . . . .	134
mappa.hg19.1kb.24mer . . . . .	135
mappa.hg19.1kb.36mer . . . . .	135
mappa.hg19.1kb.40mer . . . . .	136
mappa.hg19.1kb.50mer . . . . .	137
mappa.hg19.1kb.75mer . . . . .	137

mappa.hg19.5kb.100mer . . . . .	138
mappa.hg19.5kb.24mer . . . . .	139
mappa.hg19.5kb.36mer . . . . .	139
mappa.hg19.5kb.40mer . . . . .	140
mappa.hg19.5kb.50mer . . . . .	141
mappa.hg19.5kb.75mer . . . . .	141
mappa.hg19.exon.100mer . . . . .	142
mappa.hg19.exon.24mer . . . . .	143
mappa.hg19.exon.36mer . . . . .	143
mappa.hg19.exon.40mer . . . . .	144
mappa.hg19.exon.50mer . . . . .	145
mappa.hg19.exon.75mer . . . . .	145
mappa.hg19.intron.100mer . . . . .	146
mappa.hg19.intron.24mer . . . . .	147
mappa.hg19.intron.36mer . . . . .	147
mappa.hg19.intron.40mer . . . . .	148
mappa.hg19.intron.50mer . . . . .	149
mappa.hg19.intron.75mer . . . . .	149
mappa.hg19.nearest_gene.100mer . . . . .	150
mappa.hg19.nearest_gene.24mer . . . . .	151
mappa.hg19.nearest_gene.36mer . . . . .	151
mappa.hg19.nearest_gene.40mer . . . . .	152
mappa.hg19.nearest_gene.50mer . . . . .	153
mappa.hg19.nearest_gene.75mer . . . . .	153
mappa.hg19.nearest_tss.100mer . . . . .	154
mappa.hg19.nearest_tss.24mer . . . . .	155
mappa.hg19.nearest_tss.36mer . . . . .	155
mappa.hg19.nearest_tss.40mer . . . . .	156
mappa.hg19.nearest_tss.50mer . . . . .	157
mappa.hg19.nearest_tss.75mer . . . . .	157
mappa.mm9.10kb.100mer . . . . .	158
mappa.mm9.10kb.36mer . . . . .	159
mappa.mm9.10kb.40mer . . . . .	159
mappa.mm9.10kb.50mer . . . . .	160
mappa.mm9.10kb.75mer . . . . .	161
mappa.mm9.1kb.100mer . . . . .	161
mappa.mm9.1kb.36mer . . . . .	162
mappa.mm9.1kb.40mer . . . . .	163
mappa.mm9.1kb.50mer . . . . .	163
mappa.mm9.1kb.75mer . . . . .	164
mappa.mm9.5kb.100mer . . . . .	165
mappa.mm9.5kb.36mer . . . . .	165
mappa.mm9.5kb.40mer . . . . .	166
mappa.mm9.5kb.50mer . . . . .	167
mappa.mm9.5kb.75mer . . . . .	167
mappa.mm9.exon.100mer . . . . .	168
mappa.mm9.exon.36mer . . . . .	169
mappa.mm9.exon.40mer . . . . .	169
mappa.mm9.exon.50mer . . . . .	170
mappa.mm9.exon.75mer . . . . .	171
mappa.mm9.intron.100mer . . . . .	171
mappa.mm9.intron.36mer . . . . .	172

mappa.mm9.intron.40mer . . . . .	173
mappa.mm9.intron.50mer . . . . .	173
mappa.mm9.intron.75mer . . . . .	174
mappa.mm9.nearest_gene.100mer . . . . .	175
mappa.mm9.nearest_gene.36mer . . . . .	175
mappa.mm9.nearest_gene.40mer . . . . .	176
mappa.mm9.nearest_gene.50mer . . . . .	177
mappa.mm9.nearest_gene.75mer . . . . .	177
mappa.mm9.nearest_tss.100mer . . . . .	178
mappa.mm9.nearest_tss.36mer . . . . .	179
mappa.mm9.nearest_tss.40mer . . . . .	179
mappa.mm9.nearest_tss.50mer . . . . .	180
mappa.mm9.nearest_tss.75mer . . . . .	181
peaks_E2F4 . . . . .	181
peaks_H3K4me3_GM12878 . . . . .	182
spline.log_dtss.90ENCODE . . . . .	183
tss.danRer10 . . . . .	183
tss.dm3 . . . . .	184
tss.dm6 . . . . .	184
tss.hg19 . . . . .	185
tss.hg38 . . . . .	185
tss.mm10 . . . . .	186
tss.mm9 . . . . .	186
tss.rn4 . . . . .	187
tss.rn5 . . . . .	187
tss.rn6 . . . . .	188

## Index 189

---

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

---

### 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)**

Ryan Welch <welchr@umich.edu>

**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  $\geq 10$  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](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	<i>geneset.ctd.hsa genesets for Comparative Toxicogenomics Database</i>
-----------------	---

---

**Description**

Comparative Toxicogenomics Database (ctd) genesets. All genesets are required to have  $\geq 10$  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	<i>geneset.ctd.mmu genesets for Comparative Toxicogenomics Database</i>
-----------------	---

---

**Description**

Comparative Toxicogenomics Database (ctd) genesets. All genesets are required to have  $\geq 10$  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  $\geq 10$  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  $\geq 10$  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  $\geq 10$  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  $\geq 10$  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  $\geq 10$  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  $\geq 10$  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  $\geq 10$  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  $\geq 10$  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  $\geq 10$  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      *geneset.GOCC.mmu genesets for Mus musculus*

---

### Description

Gene Ontology Cellular Component (GOCC) genesets for Mus musculus. All genesets are required to have  $\geq 10$  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	<i>geneset.GOCC.rno genesets for Rattus norvegicus</i>
------------------	--

---

**Description**

Gene Ontology Cellular Component (GOCC) genesets for Rattus norvegicus. All genesets are required to have  $\geq 10$  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  $\geq 10$  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      *geneset.GOMF.dre genesets for Danio rerio*

---

### Description

Gene Ontology Molecular Function (GOMF) genesets for *Danio rerio*. All genesets are required to have  $\geq 10$  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	<i>geneset.GOMF.hsa genesets for Homo sapiens</i>
------------------	---

---

**Description**

Gene Ontology Molecular Function (GOMF) genesets for Homo sapiens. All genesets are required to have  $\geq 10$  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  $\geq 10$  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  $\geq 10$  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  $\geq 10$  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  $\geq$  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  $\geq$  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  $\geq 10$  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  $\geq 10$  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  $\geq 10$  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  $\geq 10$  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  $\geq 10$  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](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  $\geq 10$  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](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  $\geq 10$  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](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  $\geq 10$  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](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  $\geq 10$  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](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  $\geq 10$  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 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.danRer10.1kb\_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 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.danRer10.5kb *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.

---

locusdef.dm3.10kb

*locusdef.dm3.10kb locus definition*

---

### 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 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\_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 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\_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 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\_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 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      *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 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.dm6.1kb\_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 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.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 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.anno](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.anno) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.metadata.Ent](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.Ent)

---

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 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 09:45:59 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.annots and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.Ent

---

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.annots and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.Ent

---

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.annots and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.Ent

---

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](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](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata).Ent

---

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.annots and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.Ent

---

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.annots and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.Ent

---

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](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](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata).Ent

---

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.annota and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.Ent

---

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.annota and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.Ent

---

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.annots and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.Ent

---

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.annota and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.Ent

---

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.

**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.anno and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.Ent

---

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 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](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](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 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.hg38.1kb_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 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 09:49:40 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](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](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](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](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 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 09:49:37 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 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 09:49:38 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 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 09:51:41 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](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](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](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](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](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](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 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 09:51:38 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](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](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](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](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 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 09:51:38 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](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](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 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](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](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](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](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 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.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](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](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 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](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](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 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](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](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	<i>locusdef.mm9.exon locus definition</i>
-------------------	---

---

**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](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](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 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.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 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.rn4.10kb\_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 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 09:52:03 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 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\_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 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.rn4.5kb      *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 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.rn4.5kb\_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	<i>locusdef.rn4.exon locus definition</i>
-------------------	---

---

**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 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 09:52:00 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 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.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 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.rn6.10kb\_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 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 09:52:37 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. Bhingre, 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/wgEncodeBroadHistoneGm12878>

## 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`*tss.dm6 TSS locations*

---

**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`*tss.hg19 TSS locations*

---

**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](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](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata).EntrezGene

---

`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 mcols:

**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](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](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](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](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](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](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz)

---

tss.rn4	<i>tss.rn4 TSS locations</i>
---------	------------------------------

---

**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	<i>tss.rn5 TSS locations</i>
---------	------------------------------

---

**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, 8  
LocusDefinition-class, 129

## \* datasets

enhancer.dnase\_thurman.0, 7  
gene.enh.desc, 8  
geneset.biocarta\_pathway.hsa, 9  
geneset.biocarta\_pathway.mmu, 10  
geneset.biocarta\_pathway.rno, 10  
geneset.ctd.hsa, 11  
geneset.ctd.mmu, 11  
geneset.cytoband.hsa, 12  
geneset.drug\_bank.hsa, 13  
geneset.drug\_bank.mmu, 13  
geneset.drug\_bank.rno, 14  
geneset.GOBP.dme, 14  
geneset.GOBP.dre, 15  
geneset.GOBP.hsa, 15  
geneset.GOBP.mmu, 16  
geneset.GOBP.rno, 17  
geneset.GOCC.dme, 17  
geneset.GOCC.dre, 18  
geneset.GOCC.hsa, 19  
geneset.GOCC.mmu, 19  
geneset.GOCC.rno, 20  
geneset.GOMF.dme, 21  
geneset.GOMF.dre, 21  
geneset.GOMF.hsa, 22  
geneset.GOMF.mmu, 23  
geneset.GOMF.rno, 23  
geneset.hallmark.hsa, 24  
geneset.immunologic.hsa, 25  
geneset.kegg\_pathway.hsa, 25  
geneset.kegg\_pathway.mmu, 26  
geneset.kegg\_pathway.rno, 27  
geneset.mesh.hsa, 27  
geneset.mesh.mmu, 28  
geneset.mesh.rno, 28  
geneset.metabolite.hsa, 29  
geneset.metabolite.mmu, 29  
geneset.metabolite.rno, 30  
geneset.micrna.hsa, 30  
geneset.oncogenic.hsa, 31  
geneset.panther\_pathway.hsa, 31  
geneset.panther\_pathway.mmu, 32  
geneset.panther\_pathway.rno, 32  
geneset.pfam.hsa, 33  
geneset.pfam.mmu, 33  
geneset.pfam.rno, 34  
geneset.protein\_interaction\_biogrid.hsa, 34  
geneset.reactome.dme, 35  
geneset.reactome.dre, 35  
geneset.reactome.hsa, 36  
geneset.reactome.mmu, 37  
geneset.reactome.rno, 37  
geneset.transcription\_factors.hsa, 38  
geneset.transcription\_factors.mmu, 39  
geneset.transcription\_factors.rno, 39  
locusdef.danRer10.10kb, 40  
locusdef.danRer10.10kb\_outside, 40  
locusdef.danRer10.10kb\_outside\_upstream, 41  
locusdef.danRer10.1kb, 42  
locusdef.danRer10.1kb\_outside, 42  
locusdef.danRer10.1kb\_outside\_upstream, 43  
locusdef.danRer10.5kb, 44  
locusdef.danRer10.5kb\_outside, 44  
locusdef.danRer10.5kb\_outside\_upstream, 45  
locusdef.danRer10.exon, 46  
locusdef.danRer10.intron, 46  
locusdef.danRer10.nearest\_gene, 47  
locusdef.danRer10.nearest\_tss, 48  
locusdef.dm3.10kb, 48  
locusdef.dm3.10kb\_outside, 49  
locusdef.dm3.10kb\_outside\_upstream, 50  
locusdef.dm3.1kb, 51  
locusdef.dm3.1kb\_outside, 51  
locusdef.dm3.1kb\_outside\_upstream, 52

- locusdef.dm3.5kb, [53](#)
- locusdef.dm3.5kb\_outside, [53](#)
- locusdef.dm3.5kb\_outside\_upstream, [54](#)
- locusdef.dm3.exon, [55](#)
- locusdef.dm3.intron, [55](#)
- locusdef.dm3.nearest\_gene, [56](#)
- locusdef.dm3.nearest\_tss, [57](#)
- locusdef.dm6.10kb, [58](#)
- locusdef.dm6.10kb\_outside, [58](#)
- locusdef.dm6.10kb\_outside\_upstream, [59](#)
- locusdef.dm6.1kb, [60](#)
- locusdef.dm6.1kb\_outside, [60](#)
- locusdef.dm6.1kb\_outside\_upstream, [61](#)
- locusdef.dm6.5kb, [62](#)
- locusdef.dm6.5kb\_outside, [62](#)
- locusdef.dm6.5kb\_outside\_upstream, [63](#)
- locusdef.dm6.exon, [64](#)
- locusdef.dm6.intron, [64](#)
- locusdef.dm6.nearest\_gene, [65](#)
- locusdef.dm6.nearest\_tss, [66](#)
- locusdef.hg19.10kb, [67](#)
- locusdef.hg19.10kb\_outside, [67](#)
- locusdef.hg19.10kb\_outside\_upstream, [68](#)
- locusdef.hg19.1kb, [69](#)
- locusdef.hg19.1kb\_outside, [70](#)
- locusdef.hg19.1kb\_outside\_upstream, [70](#)
- locusdef.hg19.5kb, [71](#)
- locusdef.hg19.5kb\_outside, [72](#)
- locusdef.hg19.5kb\_outside\_upstream, [72](#)
- locusdef.hg19.exon, [73](#)
- locusdef.hg19.intron, [74](#)
- locusdef.hg19.nearest\_gene, [74](#)
- locusdef.hg19.nearest\_tss, [75](#)
- locusdef.hg38.10kb, [76](#)
- locusdef.hg38.10kb\_outside, [77](#)
- locusdef.hg38.10kb\_outside\_upstream, [77](#)
- locusdef.hg38.1kb, [78](#)
- locusdef.hg38.1kb\_outside, [79](#)
- locusdef.hg38.1kb\_outside\_upstream, [79](#)
- locusdef.hg38.5kb, [80](#)
- locusdef.hg38.5kb\_outside, [81](#)
- locusdef.hg38.5kb\_outside\_upstream, [81](#)
- locusdef.hg38.exon, [82](#)
- locusdef.hg38.intron, [83](#)
- locusdef.hg38.nearest\_gene, [83](#)
- locusdef.hg38.nearest\_tss, [84](#)
- locusdef.mm10.10kb, [85](#)
- locusdef.mm10.10kb\_outside, [86](#)
- locusdef.mm10.10kb\_outside\_upstream, [86](#)
- locusdef.mm10.1kb, [87](#)
- locusdef.mm10.1kb\_outside, [88](#)
- locusdef.mm10.1kb\_outside\_upstream, [88](#)
- locusdef.mm10.5kb, [89](#)
- locusdef.mm10.5kb\_outside, [90](#)
- locusdef.mm10.5kb\_outside\_upstream, [90](#)
- locusdef.mm10.exon, [91](#)
- locusdef.mm10.intron, [92](#)
- locusdef.mm10.nearest\_gene, [92](#)
- locusdef.mm10.nearest\_tss, [93](#)
- locusdef.mm9.10kb, [94](#)
- locusdef.mm9.10kb\_outside, [95](#)
- locusdef.mm9.10kb\_outside\_upstream, [95](#)
- locusdef.mm9.1kb, [96](#)
- locusdef.mm9.1kb\_outside, [97](#)
- locusdef.mm9.1kb\_outside\_upstream, [97](#)
- locusdef.mm9.5kb, [98](#)
- locusdef.mm9.5kb\_outside, [99](#)
- locusdef.mm9.5kb\_outside\_upstream, [99](#)
- locusdef.mm9.exon, [100](#)
- locusdef.mm9.intron, [101](#)
- locusdef.mm9.nearest\_gene, [101](#)
- locusdef.mm9.nearest\_tss, [102](#)
- locusdef.rn4.10kb, [103](#)
- locusdef.rn4.10kb\_outside, [104](#)
- locusdef.rn4.10kb\_outside\_upstream, [104](#)
- locusdef.rn4.1kb, [105](#)
- locusdef.rn4.1kb\_outside, [106](#)
- locusdef.rn4.1kb\_outside\_upstream, [106](#)
- locusdef.rn4.5kb, [107](#)
- locusdef.rn4.5kb\_outside, [108](#)
- locusdef.rn4.5kb\_outside\_upstream, [108](#)
- locusdef.rn4.exon, [109](#)
- locusdef.rn4.intron, [110](#)
- locusdef.rn4.nearest\_gene, [110](#)
- locusdef.rn4.nearest\_tss, [111](#)

- locusdef.rn5.10kb, [112](#)
- locusdef.rn5.10kb\_outside, [112](#)
- locusdef.rn5.10kb\_outside\_upstream, [113](#)
- locusdef.rn5.1kb, [114](#)
- locusdef.rn5.1kb\_outside, [114](#)
- locusdef.rn5.1kb\_outside\_upstream, [115](#)
- locusdef.rn5.5kb, [116](#)
- locusdef.rn5.5kb\_outside, [116](#)
- locusdef.rn5.5kb\_outside\_upstream, [117](#)
- locusdef.rn5.exon, [118](#)
- locusdef.rn5.intron, [118](#)
- locusdef.rn5.nearest\_gene, [119](#)
- locusdef.rn5.nearest\_tss, [120](#)
- locusdef.rn6.10kb, [120](#)
- locusdef.rn6.10kb\_outside, [121](#)
- locusdef.rn6.10kb\_outside\_upstream, [122](#)
- locusdef.rn6.1kb, [122](#)
- locusdef.rn6.1kb\_outside, [123](#)
- locusdef.rn6.1kb\_outside\_upstream, [124](#)
- locusdef.rn6.5kb, [124](#)
- locusdef.rn6.5kb\_outside, [125](#)
- locusdef.rn6.5kb\_outside\_upstream, [126](#)
- locusdef.rn6.exon, [126](#)
- locusdef.rn6.intron, [127](#)
- locusdef.rn6.nearest\_gene, [128](#)
- locusdef.rn6.nearest\_tss, [128](#)
- mappa.hg19.10kb.100mer, [130](#)
- mappa.hg19.10kb.24mer, [131](#)
- mappa.hg19.10kb.36mer, [131](#)
- mappa.hg19.10kb.40mer, [132](#)
- mappa.hg19.10kb.50mer, [133](#)
- mappa.hg19.10kb.75mer, [133](#)
- mappa.hg19.1kb.100mer, [134](#)
- mappa.hg19.1kb.24mer, [135](#)
- mappa.hg19.1kb.36mer, [135](#)
- mappa.hg19.1kb.40mer, [136](#)
- mappa.hg19.1kb.50mer, [137](#)
- mappa.hg19.1kb.75mer, [137](#)
- mappa.hg19.5kb.100mer, [138](#)
- mappa.hg19.5kb.24mer, [139](#)
- mappa.hg19.5kb.36mer, [139](#)
- mappa.hg19.5kb.40mer, [140](#)
- mappa.hg19.5kb.50mer, [141](#)
- mappa.hg19.5kb.75mer, [141](#)
- mappa.hg19.exon.100mer, [142](#)
- mappa.hg19.exon.24mer, [143](#)
- mappa.hg19.exon.36mer, [143](#)
- mappa.hg19.exon.40mer, [144](#)
- mappa.hg19.exon.50mer, [145](#)
- mappa.hg19.exon.75mer, [145](#)
- mappa.hg19.intron.100mer, [146](#)
- mappa.hg19.intron.24mer, [147](#)
- mappa.hg19.intron.36mer, [147](#)
- mappa.hg19.intron.40mer, [148](#)
- mappa.hg19.intron.50mer, [149](#)
- mappa.hg19.intron.75mer, [149](#)
- mappa.hg19.nearest\_gene.100mer, [150](#)
- mappa.hg19.nearest\_gene.24mer, [151](#)
- mappa.hg19.nearest\_gene.36mer, [151](#)
- mappa.hg19.nearest\_gene.40mer, [152](#)
- mappa.hg19.nearest\_gene.50mer, [153](#)
- mappa.hg19.nearest\_gene.75mer, [153](#)
- mappa.hg19.nearest\_tss.100mer, [154](#)
- mappa.hg19.nearest\_tss.24mer, [155](#)
- mappa.hg19.nearest\_tss.36mer, [155](#)
- mappa.hg19.nearest\_tss.40mer, [156](#)
- mappa.hg19.nearest\_tss.50mer, [157](#)
- mappa.hg19.nearest\_tss.75mer, [157](#)
- mappa.mm9.10kb.100mer, [158](#)
- mappa.mm9.10kb.36mer, [159](#)
- mappa.mm9.10kb.40mer, [159](#)
- mappa.mm9.10kb.50mer, [160](#)
- mappa.mm9.10kb.75mer, [161](#)
- mappa.mm9.1kb.100mer, [161](#)
- mappa.mm9.1kb.36mer, [162](#)
- mappa.mm9.1kb.40mer, [163](#)
- mappa.mm9.1kb.50mer, [163](#)
- mappa.mm9.1kb.75mer, [164](#)
- mappa.mm9.5kb.100mer, [165](#)
- mappa.mm9.5kb.36mer, [165](#)
- mappa.mm9.5kb.40mer, [166](#)
- mappa.mm9.5kb.50mer, [167](#)
- mappa.mm9.5kb.75mer, [167](#)
- mappa.mm9.exon.100mer, [168](#)
- mappa.mm9.exon.36mer, [169](#)
- mappa.mm9.exon.40mer, [169](#)
- mappa.mm9.exon.50mer, [170](#)
- mappa.mm9.exon.75mer, [171](#)
- mappa.mm9.intron.100mer, [171](#)
- mappa.mm9.intron.36mer, [172](#)
- mappa.mm9.intron.40mer, [173](#)
- mappa.mm9.intron.50mer, [173](#)
- mappa.mm9.intron.75mer, [174](#)
- mappa.mm9.nearest\_gene.100mer, [175](#)
- mappa.mm9.nearest\_gene.36mer, [175](#)
- mappa.mm9.nearest\_gene.40mer, [176](#)
- mappa.mm9.nearest\_gene.50mer, [177](#)

- mappa.mm9.nearest\_gene.75mer, [177](#)
- mappa.mm9.nearest\_tss.100mer, [178](#)
- mappa.mm9.nearest\_tss.36mer, [179](#)
- mappa.mm9.nearest\_tss.40mer, [179](#)
- mappa.mm9.nearest\_tss.50mer, [180](#)
- mappa.mm9.nearest\_tss.75mer, [181](#)
- peaks\_E2F4, [181](#)
- peaks\_H3K4me3\_GM12878, [182](#)
- spline.log\_dtss.90ENCODE, [183](#)
- tss.danRer10, [183](#)
- tss.dm3, [184](#)
- tss.dm6, [184](#)
- tss.hg19, [185](#)
- tss.hg38, [185](#)
- tss.mm10, [186](#)
- tss.mm9, [186](#)
- tss.rn4, [187](#)
- tss.rn5, [187](#)
- tss.rn6, [188](#)
  
- chipenrich.data, [7](#), [10](#), [12–14](#), [26–34](#), [39](#), [130–181](#)
- chipenrich.data-package  
(chipenrich.data), [7](#)
  
- enhancer.dnase\_thurman.0, [7](#)
  
- gene.enh.desc, [8](#)
- GeneSet-class, [8](#)
- geneset.biocarta\_pathway.hsa, [9](#)
- geneset.biocarta\_pathway.mmu, [10](#)
- geneset.biocarta\_pathway.rno, [10](#)
- geneset.ctd.hsa, [11](#)
- geneset.ctd.mmu, [11](#)
- geneset.cytoband.hsa, [12](#)
- geneset.drug\_bank.hsa, [13](#)
- geneset.drug\_bank.mmu, [13](#)
- geneset.drug\_bank.rno, [14](#)
- geneset.GOBP.dme, [14](#)
- geneset.GOBP.dre, [15](#)
- geneset.GOBP.hsa, [15](#)
- geneset.GOBP.mmu, [16](#)
- geneset.GOBP.rno, [17](#)
- geneset.GOCC.dme, [17](#)
- geneset.GOCC.dre, [18](#)
- geneset.GOCC.hsa, [19](#)
- geneset.GOCC.mmu, [19](#)
- geneset.GOCC.rno, [20](#)
- geneset.GOMF.dme, [21](#)
- geneset.GOMF.dre, [21](#)
- geneset.GOMF.hsa, [22](#)
- geneset.GOMF.mmu, [23](#)
- geneset.GOMF.rno, [23](#)
  
- geneset.hallmark.hsa, [24](#)
- geneset.immunologic.hsa, [25](#)
- geneset.kegg\_pathway.hsa, [25](#)
- geneset.kegg\_pathway.mmu, [26](#)
- geneset.kegg\_pathway.rno, [27](#)
- geneset.mesh.hsa, [27](#)
- geneset.mesh.mmu, [28](#)
- geneset.mesh.rno, [28](#)
- geneset.metabolite.hsa, [29](#)
- geneset.metabolite.mmu, [29](#)
- geneset.metabolite.rno, [30](#)
- geneset.microrna.hsa, [30](#)
- geneset.oncogenic.hsa, [31](#)
- geneset.panther\_pathway.hsa, [31](#)
- geneset.panther\_pathway.mmu, [32](#)
- geneset.panther\_pathway.rno, [32](#)
- geneset.pfam.hsa, [33](#)
- geneset.pfam.mmu, [33](#)
- geneset.pfam.rno, [34](#)
- geneset.protein\_interaction\_biogrid.hsa, [34](#)
- geneset.reactome.dme, [35](#)
- geneset.reactome.dre, [35](#)
- geneset.reactome.hsa, [36](#)
- geneset.reactome.mmu, [37](#)
- geneset.reactome.rno, [37](#)
- geneset.transcription\_factors.hsa, [38](#)
- geneset.transcription\_factors.mmu, [39](#)
- geneset.transcription\_factors.rno, [39](#)
  
- locusdef.danRer10.10kb, [40](#)
- locusdef.danRer10.10kb\_outside, [40](#)
- locusdef.danRer10.10kb\_outside\_upstream, [41](#)
- locusdef.danRer10.1kb, [42](#)
- locusdef.danRer10.1kb\_outside, [42](#)
- locusdef.danRer10.1kb\_outside\_upstream, [43](#)
- locusdef.danRer10.5kb, [44](#)
- locusdef.danRer10.5kb\_outside, [44](#)
- locusdef.danRer10.5kb\_outside\_upstream, [45](#)
- locusdef.danRer10.exon, [46](#)
- locusdef.danRer10.intron, [46](#)
- locusdef.danRer10.nearest\_gene, [47](#)
- locusdef.danRer10.nearest\_tss, [48](#)
- locusdef.dm3.10kb, [48](#)
- locusdef.dm3.10kb\_outside, [49](#)
- locusdef.dm3.10kb\_outside\_upstream, [50](#)
- locusdef.dm3.1kb, [51](#)
- locusdef.dm3.1kb\_outside, [51](#)
- locusdef.dm3.1kb\_outside\_upstream, [52](#)
- locusdef.dm3.5kb, [53](#)



- locusdef.dm3.5kb\_outside, 53
- locusdef.dm3.5kb\_outside\_upstream, 54
- locusdef.dm3.exon, 55
- locusdef.dm3.intron, 55
- locusdef.dm3.nearest\_gene, 56
- locusdef.dm3.nearest\_tss, 57
- locusdef.dm6.10kb, 58
- locusdef.dm6.10kb\_outside, 58
- locusdef.dm6.10kb\_outside\_upstream, 59
- locusdef.dm6.1kb, 60
- locusdef.dm6.1kb\_outside, 60
- locusdef.dm6.1kb\_outside\_upstream, 61
- locusdef.dm6.5kb, 62
- locusdef.dm6.5kb\_outside, 62
- locusdef.dm6.5kb\_outside\_upstream, 63
- locusdef.dm6.exon, 64
- locusdef.dm6.intron, 64
- locusdef.dm6.nearest\_gene, 65
- locusdef.dm6.nearest\_tss, 66
- locusdef.hg19.10kb, 67
- locusdef.hg19.10kb\_outside, 67
- locusdef.hg19.10kb\_outside\_upstream, 68
- locusdef.hg19.1kb, 69
- locusdef.hg19.1kb\_outside, 70
- locusdef.hg19.1kb\_outside\_upstream, 70
- locusdef.hg19.5kb, 71
- locusdef.hg19.5kb\_outside, 72
- locusdef.hg19.5kb\_outside\_upstream, 72
- locusdef.hg19.exon, 73
- locusdef.hg19.intron, 74
- locusdef.hg19.nearest\_gene, 74
- locusdef.hg19.nearest\_tss, 75
- locusdef.hg38.10kb, 76
- locusdef.hg38.10kb\_outside, 77
- locusdef.hg38.10kb\_outside\_upstream, 77
- locusdef.hg38.1kb, 78
- locusdef.hg38.1kb\_outside, 79
- locusdef.hg38.1kb\_outside\_upstream, 79
- locusdef.hg38.5kb, 80
- locusdef.hg38.5kb\_outside, 81
- locusdef.hg38.5kb\_outside\_upstream, 81
- locusdef.hg38.exon, 82
- locusdef.hg38.intron, 83
- locusdef.hg38.nearest\_gene, 83
- locusdef.hg38.nearest\_tss, 84
- locusdef.mm10.10kb, 85
- locusdef.mm10.10kb\_outside, 86
- locusdef.mm10.10kb\_outside\_upstream, 86
- locusdef.mm10.1kb, 87
- locusdef.mm10.1kb\_outside, 88
- locusdef.mm10.1kb\_outside\_upstream, 88
- locusdef.mm10.5kb, 89
- locusdef.mm10.5kb\_outside, 90
- locusdef.mm10.5kb\_outside\_upstream, 90
- locusdef.mm10.exon, 91
- locusdef.mm10.intron, 92
- locusdef.mm10.nearest\_gene, 92
- locusdef.mm10.nearest\_tss, 93
- locusdef.mm9.10kb, 94
- locusdef.mm9.10kb\_outside, 95
- locusdef.mm9.10kb\_outside\_upstream, 95
- locusdef.mm9.1kb, 96
- locusdef.mm9.1kb\_outside, 97
- locusdef.mm9.1kb\_outside\_upstream, 97
- locusdef.mm9.5kb, 98
- locusdef.mm9.5kb\_outside, 99
- locusdef.mm9.5kb\_outside\_upstream, 99
- locusdef.mm9.exon, 100
- locusdef.mm9.intron, 101
- locusdef.mm9.nearest\_gene, 101
- locusdef.mm9.nearest\_tss, 102
- locusdef.rn4.10kb, 103
- locusdef.rn4.10kb\_outside, 104
- locusdef.rn4.10kb\_outside\_upstream, 104
- locusdef.rn4.1kb, 105
- locusdef.rn4.1kb\_outside, 106
- locusdef.rn4.1kb\_outside\_upstream, 106
- locusdef.rn4.5kb, 107
- locusdef.rn4.5kb\_outside, 108
- locusdef.rn4.5kb\_outside\_upstream, 108
- locusdef.rn4.exon, 109
- locusdef.rn4.intron, 110
- locusdef.rn4.nearest\_gene, 110
- locusdef.rn4.nearest\_tss, 111
- locusdef.rn5.10kb, 112
- locusdef.rn5.10kb\_outside, 112
- locusdef.rn5.10kb\_outside\_upstream, 113
- locusdef.rn5.1kb, 114
- locusdef.rn5.1kb\_outside, 114
- locusdef.rn5.1kb\_outside\_upstream, 115
- locusdef.rn5.5kb, 116
- locusdef.rn5.5kb\_outside, 116
- locusdef.rn5.5kb\_outside\_upstream, 117
- locusdef.rn5.exon, 118
- locusdef.rn5.intron, 118
- locusdef.rn5.nearest\_gene, 119
- locusdef.rn5.nearest\_tss, 120
- locusdef.rn6.10kb, 120
- locusdef.rn6.10kb\_outside, 121

- locusdef.rn6.10kb\_outside\_upstream, [122](#)
- locusdef.rn6.1kb, [122](#)
- locusdef.rn6.1kb\_outside, [123](#)
- locusdef.rn6.1kb\_outside\_upstream, [124](#)
- locusdef.rn6.5kb, [124](#)
- locusdef.rn6.5kb\_outside, [125](#)
- locusdef.rn6.5kb\_outside\_upstream, [126](#)
- locusdef.rn6.exon, [126](#)
- locusdef.rn6.intron, [127](#)
- locusdef.rn6.nearest\_gene, [128](#)
- locusdef.rn6.nearest\_tss, [128](#)
- LocusDefinition-class, [129](#)
  
- mappa.hg19.10kb.100mer, [130](#)
- mappa.hg19.10kb.24mer, [131](#)
- mappa.hg19.10kb.36mer, [131](#)
- mappa.hg19.10kb.40mer, [132](#)
- mappa.hg19.10kb.50mer, [133](#)
- mappa.hg19.10kb.75mer, [133](#)
- mappa.hg19.1kb.100mer, [134](#)
- mappa.hg19.1kb.24mer, [135](#)
- mappa.hg19.1kb.36mer, [135](#)
- mappa.hg19.1kb.40mer, [136](#)
- mappa.hg19.1kb.50mer, [137](#)
- mappa.hg19.1kb.75mer, [137](#)
- mappa.hg19.5kb.100mer, [138](#)
- mappa.hg19.5kb.24mer, [139](#)
- mappa.hg19.5kb.36mer, [139](#)
- mappa.hg19.5kb.40mer, [140](#)
- mappa.hg19.5kb.50mer, [141](#)
- mappa.hg19.5kb.75mer, [141](#)
- mappa.hg19.exon.100mer, [142](#)
- mappa.hg19.exon.24mer, [143](#)
- mappa.hg19.exon.36mer, [143](#)
- mappa.hg19.exon.40mer, [144](#)
- mappa.hg19.exon.50mer, [145](#)
- mappa.hg19.exon.75mer, [145](#)
- mappa.hg19.intron.100mer, [146](#)
- mappa.hg19.intron.24mer, [147](#)
- mappa.hg19.intron.36mer, [147](#)
- mappa.hg19.intron.40mer, [148](#)
- mappa.hg19.intron.50mer, [149](#)
- mappa.hg19.intron.75mer, [149](#)
- mappa.hg19.nearest\_gene.100mer, [150](#)
- mappa.hg19.nearest\_gene.24mer, [151](#)
- mappa.hg19.nearest\_gene.36mer, [151](#)
- mappa.hg19.nearest\_gene.40mer, [152](#)
- mappa.hg19.nearest\_gene.50mer, [153](#)
- mappa.hg19.nearest\_gene.75mer, [153](#)
- mappa.hg19.nearest\_tss.100mer, [154](#)
- mappa.hg19.nearest\_tss.24mer, [155](#)
- mappa.hg19.nearest\_tss.36mer, [155](#)
- mappa.hg19.nearest\_tss.40mer, [156](#)
- mappa.hg19.nearest\_tss.50mer, [157](#)
- mappa.hg19.nearest\_tss.75mer, [157](#)
- mappa.mm9.10kb.100mer, [158](#)
- mappa.mm9.10kb.36mer, [159](#)
- mappa.mm9.10kb.40mer, [159](#)
- mappa.mm9.10kb.50mer, [160](#)
- mappa.mm9.10kb.75mer, [161](#)
- mappa.mm9.1kb.100mer, [161](#)
- mappa.mm9.1kb.36mer, [162](#)
- mappa.mm9.1kb.40mer, [163](#)
- mappa.mm9.1kb.50mer, [163](#)
- mappa.mm9.1kb.75mer, [164](#)
- mappa.mm9.5kb.100mer, [165](#)
- mappa.mm9.5kb.36mer, [165](#)
- mappa.mm9.5kb.40mer, [166](#)
- mappa.mm9.5kb.50mer, [167](#)
- mappa.mm9.5kb.75mer, [167](#)
- mappa.mm9.exon.100mer, [168](#)
- mappa.mm9.exon.36mer, [169](#)
- mappa.mm9.exon.40mer, [169](#)
- mappa.mm9.exon.50mer, [170](#)
- mappa.mm9.exon.75mer, [171](#)
- mappa.mm9.intron.100mer, [171](#)
- mappa.mm9.intron.36mer, [172](#)
- mappa.mm9.intron.40mer, [173](#)
- mappa.mm9.intron.50mer, [173](#)
- mappa.mm9.intron.75mer, [174](#)
- mappa.mm9.nearest\_gene.100mer, [175](#)
- mappa.mm9.nearest\_gene.36mer, [175](#)
- mappa.mm9.nearest\_gene.40mer, [176](#)
- mappa.mm9.nearest\_gene.50mer, [177](#)
- mappa.mm9.nearest\_gene.75mer, [177](#)
- mappa.mm9.nearest\_tss.100mer, [178](#)
- mappa.mm9.nearest\_tss.36mer, [179](#)
- mappa.mm9.nearest\_tss.40mer, [179](#)
- mappa.mm9.nearest\_tss.50mer, [180](#)
- mappa.mm9.nearest\_tss.75mer, [181](#)
  
- peaks\_E2F4, [181](#)
- peaks\_H3K4me3\_GM12878, [182](#)
  
- spline.log\_dtss.90ENCODE, [183](#)
  
- tss.danRer10, [183](#)
- tss.dm3, [184](#)
- tss.dm6, [184](#)
- tss.hg19, [185](#)
- tss.hg38, [185](#)
- tss.mm10, [186](#)
- tss.mm9, [186](#)
- tss.rn4, [187](#)
- tss.rn5, [187](#)
- tss.rn6, [188](#)