

# Package ‘chipenrich.data’

February 10, 2026

**Title** Companion package to chipenrich

**Version** 2.35.0

**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** devel

**git\_last\_commit** ab7960d

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.23

**Date/Publication** 2026-02-10

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

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

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

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

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

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

tss.rn5 . . . . .	197
tss.rn6 . . . . .	198

<b>Index</b>	<b>199</b>
--------------	------------

---

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

*geneset.ctd.hsa genesets for Comparative Toxicogenomics Database*

---

### 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

*geneset.ctd.mmu genesets for Comparative Toxicogenomics Database*

---

### 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	<i>geneset.GOBP.hsa</i> genesets for <i>Homo sapiens</i>
------------------	--

---

### 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	<i>geneset.GOBP.mmu</i> genesets for <i>Mus musculus</i>
------------------	--

---

### 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	<i>geneset.GOCC.dme</i> genesets for <i>Drosophila melanogaster</i>
------------------	---

---

### 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	<i>geneset.GOCC.dre</i> genesets for <i>Danio rerio</i>
------------------	---

---

### 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*geneset.GOCC.rno* genesets for *Rattus norvegicus*

---

**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	<i>geneset.GOMF.dre</i> genesets for <i>Danio rerio</i>
------------------	---

---

### 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</i> genesets for <i>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 >= 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	<i>geneset.GOMF.rno</i> genesets for <i>Rattus norvegicus</i>
------------------	---

---

### 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	<i>geneset.hallmark.hsa</i> 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	<i>geneset.mesh.hsa</i>
------------------	-------------------------

---

**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	<i>geneset.mesh.mmu</i>
------------------	-------------------------

---

**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	<i>geneset.mesh.rno</i>
------------------	-------------------------

---

**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	<i>geneset.metabolite.hsa</i>
------------------------	-------------------------------

---

**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	<i>geneset.pfam.rno</i>
------------------	-------------------------

---

**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	
<i>geneset.protein_interaction_biogrid.hsa</i>	<i>genesets for BioGRID Protein Interactions</i>

---

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

---

**Description**

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

**Usage**

```
locusdef.dm3.10kb
```

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene\_3.2.2 and org.Dm.eg.db\_3.5.0.

---

locusdef.dm3.10kb\_outside

*locusdef.dm3.10kb\_outside locus definition*


---

### Description

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

### Usage

```
locusdef.dm3.10kb_outside
```

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

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

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

### Source

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

---

locusdef.dm3.10kb\_outside\_upstream

*locusdef.dm3.10kb\_outside\_upstream locus definition*


---

### Description

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

**Usage**

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

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

<code>locusdef.dm3.1kb</code>	<i>locusdef.dm3.1kb locus definition</i>
-------------------------------	--

---

**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	<i>locusdef.dm3.exon locus definition</i>
-------------------	---

---

### 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	<i>locusdef.dm3.intron locus definition</i>
---------------------	---

---

### 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	<i>locusdef.dm6.10kb locus definition</i>
-------------------	---

---

### 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`

**dframe** A data.frame of 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	<i>locusdef.dm6.10kb_outside locus definition</i>
---------------------------	---

---

### 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	<i>locusdef.dm6.1kb locus definition</i>
------------------	--

---

**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`.

---

<code>locusdef.dm6.5kb</code>	<i>locusdef.dm6.5kb locus definition</i>
-------------------------------	--

---

**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	<i>locusdef.dm6.intron locus definition</i>
---------------------	---

---

**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.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). EntrezG

---

locusdef.hg19.10kb\_outside

*locusdef.hg19.10kb\_outside locus definition*

---

**Description**

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

**Usage**

locusdef.hg19.10kb\_outside

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with 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.annotation.  
and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.EntrezG

---

locusdef.hg19.10kb\_outside\_upstream

*locusdef.hg19.10kb\_outside\_upstream locus definition*

---

**Description**

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

**Usage**

locusdef.hg19.10kb\_outside\_upstream

**Format**

A LocusDefinition object with the following slots:

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

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

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

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

**Details**

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

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.5.0. GENCODE  
resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.annotation.  
and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.EntrezG

---

locusdef.hg19.1kb	<i>locusdef.hg19.1kb locus definition</i>
-------------------	---

---

### Description

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

### Usage

locusdef.hg19.1kb

### Format

A LocusDefinition object with the following slots:

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

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

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

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

### Details

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

### Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.annotation](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). EntrezG

---

locusdef.hg19.1kb_outside	<i>locusdef.hg19.1kb_outside locus definition</i>
---------------------------	---

---

### Description

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

### Usage

locusdef.hg19.1kb\_outside

**Format**

A LocusDefinition object with the following slots:

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

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

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

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

**Details**

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

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.annotation. and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.EntrezG

---

locusdef.hg19.1kb\_outside\_upstream

*locusdef.hg19.1kb\_outside\_upstream locus definition*

---

**Description**

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

**Usage**

locusdef.hg19.1kb\_outside\_upstream

**Format**

A LocusDefinition object with the following slots:

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

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

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

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

**Details**

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

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.5.0. GENCODE  
 resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.annotation.  
 and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.EntrezG

---

locusdef.hg19.5kb	<i>locusdef.hg19.5kb locus definition</i>
-------------------	---

---

**Description**

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

**Usage**

```
locusdef.hg19.5kb
```

**Format**

A LocusDefinition object with the following slots:

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

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

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

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

**Details**

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

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.5.0. GENCODE  
 resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.annotation.  
 and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.EntrezG

---

`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). EntrezG

---

`locusdef.hg19.5kb_outside_upstream`*locusdef.hg19.5kb\_outside\_upstream locus definition*

---

### Description

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

**Usage**

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

**Format**

A LocusDefinition object with the following slots:

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

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

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

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

**Details**

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

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.annotation](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). EntrezG

---

locusdef.hg19.exon	<i>locusdef.hg19.exon locus definition</i>
--------------------	--

---

**Description**

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

**Usage**

```
locusdef.hg19.exon
```

**Format**

A LocusDefinition object with the following slots:

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

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

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

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

**Details**

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

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.5.0. GENCODE  
resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.annotation.  
and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.EntrezG

---

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

---

**Description**

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

**Usage**

```
locusdef.hg19.intron
```

**Format**

A LocusDefinition object with the following slots:

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

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

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

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

**Details**

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

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.5.0. GENCODE  
resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.annotation.  
and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.EntrezG

---

```
locusdef.hg19.nearest_gene
      locusdef.hg19.nearest_gene locus definition
```

---

### Description

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

### Usage

```
locusdef.hg19.nearest_gene
```

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

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

### Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.annotation](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). EntrezG

---

```
locusdef.hg19.nearest_tss
      locusdef.hg19.nearest_tss locus definition
```

---

### Description

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

### Usage

```
locusdef.hg19.nearest_tss
```

**Format**

A LocusDefinition object with the following slots:

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

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

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

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

**Details**

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

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.annotation](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). EntrezG

---

locusdef.hg38.10kb	<i>locusdef.hg38.10kb locus definition</i>
--------------------	--

---

**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 and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/gencode.v25.metadata.EntrezGene.gz

---

```
locusdef.hg38.10kb_outside_upstream
    locusdef.hg38.10kb_outside_upstream locus definition
```

---

### Description

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

### Usage

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

### Format

A LocusDefinition object with the following slots:

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

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

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

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

### Details

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

### Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene\_3.4.0 and org.Hs.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/gencode.v25.annotation.gff3.gz](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    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](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

*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](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	<i>locusdef.hg38.5kb locus definition</i>
-------------------	---

---

### 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](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	<i>locusdef.hg38.5kb_outside locus definition</i>
---------------------------	---

---

### Description

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

### Usage

```
locusdef.hg38.5kb_outside
```

**Format**

A LocusDefinition object with the following slots:

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

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

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

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

**Details**

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

**Source**

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene\_3.4.0 and org.Hs.eg.db\_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/gencode.v25.metadata.EntrezGene.gz

---

locusdef.hg38.5kb\_outside\_upstream

*locusdef.hg38.5kb\_outside\_upstream locus definition*

---

**Description**

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

**Usage**

locusdef.hg38.5kb\_outside\_upstream

**Format**

A LocusDefinition object with the following slots:

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

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

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

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

**Details**

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

## Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene\_3.4.0 and org.Hs.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/gencode.v25.annotation.gff3.gz](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.exon	<i>locusdef.hg38.exon locus definition</i>
--------------------	--

---

## 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](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.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](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.mm10.10kb	<i>locusdef.mm10.10kb locus definition</i>
--------------------	--

---

**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](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

*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	<i>locusdef.mm10.1kb locus definition</i>
-------------------	---

---

**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 and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.metadata.EntrezGene.gz

---

locusdef.mm10.5kb\_outside

*locusdef.mm10.5kb\_outside locus definition*

---

**Description**

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

**Usage**

locusdef.mm10.5kb\_outside

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with 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](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.exon	<i>locusdef.mm10.exon locus definition</i>
--------------------	--

---

### 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	<i>locusdef.mm10.intron locus definition</i>
----------------------	--

---

### 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	<i>locusdef.mm9.10kb locus definition</i>
-------------------	---

---

**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	<i>locusdef.mm9.10kb_outside locus definition</i>
---------------------------	---

---

**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	<i>locusdef.mm9.1kb locus definition</i>
------------------	--

---

**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](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)

---

<code>locusdef.mm9.5kb</code>	<i>locusdef.mm9.5kb locus definition</i>
-------------------------------	--

---

**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](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

*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](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.exon

*locusdef.mm9.exon locus definition*


---

### Description

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

### Usage

```
locusdef.mm9.exon
```

**Format**

A LocusDefinition object with the following slots:

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

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, mm9.

**organism** A character indicating the organism name. In this case, Mus musculus.

**Details**

Built on Fri Apr 13 09:50:39 2018.

**Source**

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene\_3.2.2 and org.Mm.eg.db\_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.metadata.EntrezGene.gz

---

locusdef.mm9.intron      *locusdef.mm9.intron locus definition*

---

**Description**

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

**Usage**

```
locusdef.mm9.intron
```

**Format**

A LocusDefinition object with the following slots:

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

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, mm9.

**organism** A character indicating the organism name. In this case, Mus musculus.

**Details**

Built on Fri Apr 13 09:50:41 2018.

**Source**

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene\_3.2.2 and org.Mm.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M9/gencode.vM9.annotation.gff3.gz](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](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\_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](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.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	<i>locusdef.rn4.1kb locus definition</i>
------------------	--

---

### 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	<i>locusdef.rn4.1kb_outside locus definition</i>
--------------------------	--

---

### 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	<i>locusdef.rn4.5kb locus definition</i>
------------------	--

---

### 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	<i>locusdef.rn4.intron locus definition</i>
---------------------	---

---

**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	<i>locusdef.rn5.10kb locus definition</i>
-------------------	---

---

**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	<i>locusdef.rn5.5kb locus definition</i>
------------------	--

---

**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	<i>locusdef.rn5.5kb_outside locus definition</i>
--------------------------	--

---

**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	<i>locusdef.rn5.exon locus definition</i>
-------------------	---

---

**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	<i>locusdef.rn5.intron locus definition</i>
---------------------	---

---

**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 `symbol`

**dframe** A data.frame of 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	<i>locusdef.rn6.10kb locus definition</i>
-------------------	---

---

### 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	<i>locusdef.rn6.10kb_outside locus definition</i>
---------------------------	---

---

### 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	<i>locusdef.rn6.1kb locus definition</i>
------------------	--

---

**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	<i>locusdef.rn6.5kb locus definition</i>
------------------	--

---

**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	<i>locusdef.rn6.exon locus definition</i>
-------------------	---

---

**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	<i>locusdef.rn6.intron locus definition</i>
---------------------	---

---

### 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	<i>locusdef.rn6.nearest_gene locus definition</i>
---------------------------	---

---

### 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.mn6.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.mm9.1kb.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.mm9.1kb.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	<i>mappa.mm9.1kb.36mer</i>
---------------------	----------------------------

---

**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	<i>mappa.mm9.1kb.40mer</i>
---------------------	----------------------------

---

**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	<i>mappa.mm9.1kb.75mer</i>
---------------------	----------------------------

---

**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	<i>mappa.mm9.5kb.100mer</i>
----------------------	-----------------------------

---

**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	<i>mappa.mm9.5kb.36mer</i>
---------------------	----------------------------

---

**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	<i>mappa.mm9.5kb.40mer</i>
---------------------	----------------------------

---

**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	<i>mappa.mm9.5kb.50mer</i>
---------------------	----------------------------

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 50mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.5kb.50mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.5kb.75mer      *mappa.mm9.5kb.75mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 75mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.5kb.75mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.exon.100mer    *mappa.mm9.exon.100mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 100mer

These objects are used internally by the chipenrich package.

### Usage

```
data(mappa.mm9.exon.100mer)
```

### Format

A data frame containing:

geneid    Entrez Gene IDs

mappa    Gene locus mappability

### Author(s)

Ryan Welch <welchr@umich.edu>

### See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.exon.36mer    *mappa.mm9.exon.36mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 36mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.exon.36mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.exon.40mer    *mappa.mm9.exon.40mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 40mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.exon.40mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.exon.50mer    *mappa.mm9.exon.50mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 50mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.exon.50mer)
```

**Format**

A data frame containing:

geneid    Entrez Gene IDs

mappa    Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.exon.75mer    *mappa.mm9.exon.75mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 75mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.exon.75mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

```
mappa.mm9.intron.100mer
```

*mappa.mm9.intron.100mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 100mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.intron.100mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.intron.36mer`*mappa.mm9.intron.36mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 36mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.intron.36mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.intron.40mer`*mappa.mm9.intron.40mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 40mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.intron.40mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

```
mappa.mm9.intron.50mer
```

```
mappa.mm9.intron.50mer
```

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 50mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.intron.50mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.intron.75mer

*mappa.mm9.intron.75mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 75mer

These objects are used internally by the chipenrich package.

### Usage

```
data(mappa.mm9.intron.75mer)
```

### Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

### Author(s)

Ryan Welch <welchr@umich.edu>

### See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.nearest\_gene.100mer

*mappa.mm9.nearest\_gene.100mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_gene
- K-Mer Reads: 100mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.nearest_gene.100mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

```
mappa.mm9.nearest_gene.36mer
```

```
mappa.mm9.nearest_gene.36mer
```

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_gene
- K-Mer Reads: 36mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.nearest_gene.36mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

```
mappa.mm9.nearest_gene.40mer  
mappa.mm9.nearest_gene.40mer
```

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_gene
- K-Mer Reads: 40mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.nearest_gene.40mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

```
mappa.mm9.nearest_gene.50mer  
mappa.mm9.nearest_gene.50mer
```

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_gene
- K-Mer Reads: 50mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.nearest_gene.50mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

*mappa.mm9.nearest\_gene.75mer**mappa.mm9.nearest\_gene.75mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_gene
- K-Mer Reads: 75mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.nearest_gene.75mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

```
mappa.mm9.nearest_tss.100mer  
mappa.mm9.nearest_tss.100mer
```

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_tss
- K-Mer Reads: 100mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.nearest_tss.100mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

```
mappa.mm9.nearest_tss.36mer  
mappa.mm9.nearest_tss.36mer
```

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_tss
- K-Mer Reads: 36mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.nearest_tss.36mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

```
mappa.mm9.nearest_tss.40mer
```

```
mappa.mm9.nearest_tss.40mer
```

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_tss
- K-Mer Reads: 40mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.nearest_tss.40mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.nearest\_tss.50mer  
*mappa.mm9.nearest\_tss.50mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_tss
- K-Mer Reads: 50mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.nearest_tss.50mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.nearest\_tss.75mer  
*mappa.mm9.nearest\_tss.75mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_tss
- K-Mer Reads: 75mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.nearest_tss.75mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

peaks\_E2F4

*ChIP-seq Peaks for the E2F4 Transcription Factor*

---

**Description**

A dataset containing the binding locations (peaks) of the transcription factor E2F4 called from a ChIP-seq experiment

**Usage**

```
peaks_E2F4
```

**Format**

A data frame containing 16,245 peak binding locations. Each row is a peak location, and the 3 variables/columns are chromosome, start peak coordinate, and end peak coordinate. Peak coordinates are in hg19 (UCSC) coordinates.

**Source**

The data and information regarding the experiment can be found in the following publication:

Lee, B. K., A. A. Bhinge, et al. (2011). "Wide-ranging functions of E2F4 in transcriptional activation and repression revealed by genome-wide analysis." *Nucleic Acids Res* 39(9): 3558-3573.

**Examples**

```
# Load E2F4 peak data.
data(peaks_E2F4)

# Print the first 10 peaks in the dataset.
print(head(peaks_E2F4))
```

---

peaks\_H3K4me3\_GM12878 *ChIP-seq Peaks for the Histone Modification H3K4me3 in GM12878*

---

### Description

A dataset containing the binding locations (peaks) of the histone modification H3K4me3 called from a ChIP-seq experiment in the GM12878 cell line

### Usage

```
peaks_H3K4me3_GM12878
```

### Format

A data frame containing 57,476 peak binding locations. Each row is a peak location, and the 3 variables/columns are chromosome, start peak coordinate, and end peak coordinate. Peak coordinates are in hg19 (UCSC) coordinates.

### Source

The data and information regarding the experiment can be found at the following ENCODE URL:

<http://hgdownload.cse.ucsc.edu/goldenPath/hg19/encodeDCC/wgEncodeBroadHistone/wgEncodeBroadHistoneGm12878H>

### 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	<i>tss.danRer10 TSS locations</i>
--------------	-----------------------------------

---

**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	<i>tss.dm3 TSS locations</i>
---------	------------------------------

---

**Description**

A GRanges with all the TSSs for dm3. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

**Usage**

```
tss.dm3
```

**Format**

A GRanges object with the following mcols:

**gene\_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene\_3.2.2 and org.Dm.eg.db\_3.5.0.

---

tss.dm6	<i>tss.dm6 TSS locations</i>
---------	------------------------------

---

**Description**

A GRanges with all the TSSs for dm6. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

**Usage**

```
tss.dm6
```

**Format**

A GRanges object with the following mcols:

**gene\_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene\_3.4.1 and org.Dm.eg.db\_3.5.0.

---

tss.hg19	<i>tss.hg19 TSS locations</i>
----------	-------------------------------

---

**Description**

A GRanges with all the TSSs for hg19. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

**Usage**

```
tss.hg19
```

**Format**

A GRanges object with the following mcols:

**gene\_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.annotation](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 and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.metadata.EntrezGene.gz

---

tss.mm9	<i>tss.mm9 TSS locations</i>
---------	------------------------------

---

**Description**

A GRanges with all the TSSs for mm9. Primarily used in the assign\_peaks() function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

**Usage**

tss.mm9

**Format**

A GRanges object with the following mcols:

- gene\_id** The Entrez ID for the TSS
- symbol** The gene symbol for the TSS

**Source**

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene\_3.2.2 and org.Mm.eg.db\_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.metadata.EntrezGene.gz

---

tss.rn4	<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	<i>tss.rn6 TSS locations</i>
---------	------------------------------

---

**Description**

A GRanges with all the TSSs for rn6. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

**Usage**

tss.rn6

**Format**

A GRanges object with the following mcols:

**gene\_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.1 and org.Rn.eg.db\_3.5.0.

# Index

## \* classes

GeneSet-class, [9](#)

LocusDefinition-class, [139](#)

## \* datasets

enhancer.dnase\_thurman.0, [8](#)

gene.enh.desc, [9](#)

geneset.biocarta\_pathway.hsa, [10](#)

geneset.biocarta\_pathway.mmu, [11](#)

geneset.biocarta\_pathway.rno, [11](#)

geneset.ctd.hsa, [12](#)

geneset.ctd.mmu, [12](#)

geneset.cytoband.hsa, [13](#)

geneset.drug\_bank.hsa, [14](#)

geneset.drug\_bank.mmu, [14](#)

geneset.drug\_bank.rno, [15](#)

geneset.GOBP.dme, [15](#)

geneset.GOBP.dre, [16](#)

geneset.GOBP.hsa, [17](#)

geneset.GOBP.mmu, [17](#)

geneset.GOBP.rno, [18](#)

geneset.GOCC.dme, [19](#)

geneset.GOCC.dre, [19](#)

geneset.GOCC.hsa, [20](#)

geneset.GOCC.mmu, [21](#)

geneset.GOCC.rno, [21](#)

geneset.GOMF.dme, [22](#)

geneset.GOMF.dre, [23](#)

geneset.GOMF.hsa, [23](#)

geneset.GOMF.mmu, [24](#)

geneset.GOMF.rno, [25](#)

geneset.hallmark.hsa, [25](#)

geneset.immunologic.hsa, [26](#)

geneset.kegg\_pathway.hsa, [27](#)

geneset.kegg\_pathway.mmu, [28](#)

geneset.kegg\_pathway.rno, [28](#)

geneset.mesh.hsa, [29](#)

geneset.mesh.mmu, [29](#)

geneset.mesh.rno, [30](#)

geneset.metabolite.hsa, [30](#)

geneset.metabolite.mmu, [31](#)

geneset.metabolite.rno, [31](#)

geneset.micrna.hsa, [32](#)

geneset.oncogenic.hsa, [32](#)

geneset.panther\_pathway.hsa, [33](#)

geneset.panther\_pathway.mmu, [34](#)

geneset.panther\_pathway.rno, [34](#)

geneset.pfam.hsa, [35](#)

geneset.pfam.mmu, [35](#)

geneset.pfam.rno, [36](#)

geneset.protein\_interaction\_biogrid.hsa, [36](#)

geneset.reactome.dme, [37](#)

geneset.reactome.dre, [38](#)

geneset.reactome.hsa, [38](#)

geneset.reactome.mmu, [39](#)

geneset.reactome.rno, [40](#)

geneset.transcription\_factors.hsa, [41](#)

geneset.transcription\_factors.mmu, [41](#)

geneset.transcription\_factors.rno, [42](#)

locusdef.danRer10.10kb, [42](#)

locusdef.danRer10.10kb\_outside, [43](#)

locusdef.danRer10.10kb\_outside\_upstream, [44](#)

locusdef.danRer10.1kb, [45](#)

locusdef.danRer10.1kb\_outside, [45](#)

locusdef.danRer10.1kb\_outside\_upstream, [46](#)

locusdef.danRer10.5kb, [47](#)

locusdef.danRer10.5kb\_outside, [48](#)

locusdef.danRer10.5kb\_outside\_upstream, [48](#)

locusdef.danRer10.exon, [49](#)

locusdef.danRer10.intron, [50](#)

locusdef.danRer10.nearest\_gene, [50](#)

locusdef.danRer10.nearest\_tss, [51](#)

locusdef.dm3.10kb, [52](#)  
locusdef.dm3.10kb\_outside, [53](#)  
locusdef.dm3.10kb\_outside\_upstream,  
[53](#)  
locusdef.dm3.1kb, [54](#)  
locusdef.dm3.1kb\_outside, [55](#)  
locusdef.dm3.1kb\_outside\_upstream,  
[56](#)  
locusdef.dm3.5kb, [56](#)  
locusdef.dm3.5kb\_outside, [57](#)  
locusdef.dm3.5kb\_outside\_upstream,  
[58](#)  
locusdef.dm3.exon, [59](#)  
locusdef.dm3.intron, [59](#)  
locusdef.dm3.nearest\_gene, [60](#)  
locusdef.dm3.nearest\_tss, [61](#)  
locusdef.dm6.10kb, [62](#)  
locusdef.dm6.10kb\_outside, [62](#)  
locusdef.dm6.10kb\_outside\_upstream,  
[63](#)  
locusdef.dm6.1kb, [64](#)  
locusdef.dm6.1kb\_outside, [65](#)  
locusdef.dm6.1kb\_outside\_upstream,  
[65](#)  
locusdef.dm6.5kb, [66](#)  
locusdef.dm6.5kb\_outside, [67](#)  
locusdef.dm6.5kb\_outside\_upstream,  
[68](#)  
locusdef.dm6.exon, [68](#)  
locusdef.dm6.intron, [69](#)  
locusdef.dm6.nearest\_gene, [70](#)  
locusdef.dm6.nearest\_tss, [71](#)  
locusdef.hg19.10kb, [71](#)  
locusdef.hg19.10kb\_outside, [72](#)  
locusdef.hg19.10kb\_outside\_upstream,  
[73](#)  
locusdef.hg19.1kb, [74](#)  
locusdef.hg19.1kb\_outside, [74](#)  
locusdef.hg19.1kb\_outside\_upstream,  
[75](#)  
locusdef.hg19.5kb, [76](#)  
locusdef.hg19.5kb\_outside, [77](#)  
locusdef.hg19.5kb\_outside\_upstream,  
[77](#)  
locusdef.hg19.exon, [78](#)  
locusdef.hg19.intron, [79](#)  
locusdef.hg19.nearest\_gene, [80](#)  
locusdef.hg19.nearest\_tss, [80](#)  
locusdef.hg38.10kb, [81](#)  
locusdef.hg38.10kb\_outside, [82](#)  
locusdef.hg38.10kb\_outside\_upstream,  
[83](#)  
locusdef.hg38.1kb, [83](#)  
locusdef.hg38.1kb\_outside, [84](#)  
locusdef.hg38.1kb\_outside\_upstream,  
[85](#)  
locusdef.hg38.5kb, [86](#)  
locusdef.hg38.5kb\_outside, [86](#)  
locusdef.hg38.5kb\_outside\_upstream,  
[87](#)  
locusdef.hg38.exon, [88](#)  
locusdef.hg38.intron, [89](#)  
locusdef.hg38.nearest\_gene, [89](#)  
locusdef.hg38.nearest\_tss, [90](#)  
locusdef.mm10.10kb, [91](#)  
locusdef.mm10.10kb\_outside, [92](#)  
locusdef.mm10.10kb\_outside\_upstream,  
[92](#)  
locusdef.mm10.1kb, [93](#)  
locusdef.mm10.1kb\_outside, [94](#)  
locusdef.mm10.1kb\_outside\_upstream,  
[95](#)  
locusdef.mm10.5kb, [95](#)  
locusdef.mm10.5kb\_outside, [96](#)  
locusdef.mm10.5kb\_outside\_upstream,  
[97](#)  
locusdef.mm10.exon, [98](#)  
locusdef.mm10.intron, [98](#)  
locusdef.mm10.nearest\_gene, [99](#)  
locusdef.mm10.nearest\_tss, [100](#)  
locusdef.mm9.10kb, [101](#)  
locusdef.mm9.10kb\_outside, [101](#)  
locusdef.mm9.10kb\_outside\_upstream,  
[102](#)  
locusdef.mm9.1kb, [103](#)  
locusdef.mm9.1kb\_outside, [104](#)  
locusdef.mm9.1kb\_outside\_upstream,  
[104](#)  
locusdef.mm9.5kb, [105](#)  
locusdef.mm9.5kb\_outside, [106](#)  
locusdef.mm9.5kb\_outside\_upstream,  
[107](#)  
locusdef.mm9.exon, [107](#)  
locusdef.mm9.intron, [108](#)  
locusdef.mm9.nearest\_gene, [109](#)  
locusdef.mm9.nearest\_tss, [110](#)

- locusdef.rn4.10kb, [110](#)
- locusdef.rn4.10kb\_outside, [111](#)
- locusdef.rn4.10kb\_outside\_upstream, [112](#)
- locusdef.rn4.1kb, [113](#)
- locusdef.rn4.1kb\_outside, [113](#)
- locusdef.rn4.1kb\_outside\_upstream, [114](#)
- locusdef.rn4.5kb, [115](#)
- locusdef.rn4.5kb\_outside, [116](#)
- locusdef.rn4.5kb\_outside\_upstream, [116](#)
- locusdef.rn4.exon, [117](#)
- locusdef.rn4.intron, [118](#)
- locusdef.rn4.nearest\_gene, [119](#)
- locusdef.rn4.nearest\_tss, [119](#)
- locusdef.rn5.10kb, [120](#)
- locusdef.rn5.10kb\_outside, [121](#)
- locusdef.rn5.10kb\_outside\_upstream, [122](#)
- locusdef.rn5.1kb, [122](#)
- locusdef.rn5.1kb\_outside, [123](#)
- locusdef.rn5.1kb\_outside\_upstream, [124](#)
- locusdef.rn5.5kb, [125](#)
- locusdef.rn5.5kb\_outside, [125](#)
- locusdef.rn5.5kb\_outside\_upstream, [126](#)
- locusdef.rn5.exon, [127](#)
- locusdef.rn5.intron, [127](#)
- locusdef.rn5.nearest\_gene, [128](#)
- locusdef.rn5.nearest\_tss, [129](#)
- locusdef.rn6.10kb, [130](#)
- locusdef.rn6.10kb\_outside, [130](#)
- locusdef.rn6.10kb\_outside\_upstream, [131](#)
- locusdef.rn6.1kb, [132](#)
- locusdef.rn6.1kb\_outside, [133](#)
- locusdef.rn6.1kb\_outside\_upstream, [133](#)
- locusdef.rn6.5kb, [134](#)
- locusdef.rn6.5kb\_outside, [135](#)
- locusdef.rn6.5kb\_outside\_upstream, [135](#)
- locusdef.rn6.exon, [136](#)
- locusdef.rn6.intron, [137](#)
- locusdef.rn6.nearest\_gene, [137](#)
- locusdef.rn6.nearest\_tss, [138](#)
- mappa.hg19.10kb.100mer, [140](#)
- mappa.hg19.10kb.24mer, [140](#)
- mappa.hg19.10kb.36mer, [141](#)
- mappa.hg19.10kb.40mer, [142](#)
- mappa.hg19.10kb.50mer, [142](#)
- mappa.hg19.10kb.75mer, [143](#)
- mappa.hg19.1kb.100mer, [144](#)
- mappa.hg19.1kb.24mer, [144](#)
- mappa.hg19.1kb.36mer, [145](#)
- mappa.hg19.1kb.40mer, [146](#)
- mappa.hg19.1kb.50mer, [146](#)
- mappa.hg19.1kb.75mer, [147](#)
- mappa.hg19.5kb.100mer, [148](#)
- mappa.hg19.5kb.24mer, [148](#)
- mappa.hg19.5kb.36mer, [149](#)
- mappa.hg19.5kb.40mer, [150](#)
- mappa.hg19.5kb.50mer, [150](#)
- mappa.hg19.5kb.75mer, [151](#)
- mappa.hg19.exon.100mer, [152](#)
- mappa.hg19.exon.24mer, [152](#)
- mappa.hg19.exon.36mer, [153](#)
- mappa.hg19.exon.40mer, [154](#)
- mappa.hg19.exon.50mer, [154](#)
- mappa.hg19.exon.75mer, [155](#)
- mappa.hg19.intron.100mer, [156](#)
- mappa.hg19.intron.24mer, [156](#)
- mappa.hg19.intron.36mer, [157](#)
- mappa.hg19.intron.40mer, [158](#)
- mappa.hg19.intron.50mer, [158](#)
- mappa.hg19.intron.75mer, [159](#)
- mappa.hg19.nearest\_gene.100mer, [160](#)
- mappa.hg19.nearest\_gene.24mer, [160](#)
- mappa.hg19.nearest\_gene.36mer, [161](#)
- mappa.hg19.nearest\_gene.40mer, [162](#)
- mappa.hg19.nearest\_gene.50mer, [162](#)
- mappa.hg19.nearest\_gene.75mer, [163](#)
- mappa.hg19.nearest\_tss.100mer, [164](#)
- mappa.hg19.nearest\_tss.24mer, [164](#)
- mappa.hg19.nearest\_tss.36mer, [165](#)
- mappa.hg19.nearest\_tss.40mer, [166](#)
- mappa.hg19.nearest\_tss.50mer, [166](#)
- mappa.hg19.nearest\_tss.75mer, [167](#)
- mappa.mm9.10kb.100mer, [168](#)
- mappa.mm9.10kb.36mer, [168](#)
- mappa.mm9.10kb.40mer, [169](#)
- mappa.mm9.10kb.50mer, [170](#)
- mappa.mm9.10kb.75mer, [170](#)

- mappa.mm9.1kb.100mer, [171](#)
- mappa.mm9.1kb.36mer, [172](#)
- mappa.mm9.1kb.40mer, [172](#)
- mappa.mm9.1kb.50mer, [173](#)
- mappa.mm9.1kb.75mer, [174](#)
- mappa.mm9.5kb.100mer, [174](#)
- mappa.mm9.5kb.36mer, [175](#)
- mappa.mm9.5kb.40mer, [176](#)
- mappa.mm9.5kb.50mer, [176](#)
- mappa.mm9.5kb.75mer, [177](#)
- mappa.mm9.exon.100mer, [178](#)
- mappa.mm9.exon.36mer, [178](#)
- mappa.mm9.exon.40mer, [179](#)
- mappa.mm9.exon.50mer, [180](#)
- mappa.mm9.exon.75mer, [180](#)
- mappa.mm9.intron.100mer, [181](#)
- mappa.mm9.intron.36mer, [182](#)
- mappa.mm9.intron.40mer, [182](#)
- mappa.mm9.intron.50mer, [183](#)
- mappa.mm9.intron.75mer, [184](#)
- mappa.mm9.nearest\_gene.100mer, [184](#)
- mappa.mm9.nearest\_gene.36mer, [185](#)
- mappa.mm9.nearest\_gene.40mer, [186](#)
- mappa.mm9.nearest\_gene.50mer, [186](#)
- mappa.mm9.nearest\_gene.75mer, [187](#)
- mappa.mm9.nearest\_tss.100mer, [188](#)
- mappa.mm9.nearest\_tss.36mer, [188](#)
- mappa.mm9.nearest\_tss.40mer, [189](#)
- mappa.mm9.nearest\_tss.50mer, [190](#)
- mappa.mm9.nearest\_tss.75mer, [190](#)
- peaks\_E2F4, [191](#)
- peaks\_H3K4me3\_GM12878, [192](#)
- spline.log\_dtss.90ENCODE, [192](#)
- tss.danRer10, [193](#)
- tss.dm3, [193](#)
- tss.dm6, [194](#)
- tss.hg19, [194](#)
- tss.hg38, [195](#)
- tss.mm10, [195](#)
- tss.mm9, [196](#)
- tss.rn4, [197](#)
- tss.rn5, [197](#)
- tss.rn6, [198](#)
- chipenrich.data, [8](#), [11](#), [13](#), [15](#), [28–31](#), [33](#), [34](#), [36](#), [42](#), [140–191](#)
- chipenrich.data-package  
(chipenrich.data), [8](#)
- enhancer.dnase\_thurman.0, [8](#)
- gene.enh.desc, [9](#)
- GeneSet-class, [9](#)
- geneset.biocarta\_pathway.hsa, [10](#)
- geneset.biocarta\_pathway.mmu, [11](#)
- geneset.biocarta\_pathway.rno, [11](#)
- geneset.ctd.hsa, [12](#)
- geneset.ctd.mmu, [12](#)
- geneset.cytoband.hsa, [13](#)
- geneset.drug\_bank.hsa, [14](#)
- geneset.drug\_bank.mmu, [14](#)
- geneset.drug\_bank.rno, [15](#)
- geneset.GOBP.dme, [15](#)
- geneset.GOBP.dre, [16](#)
- geneset.GOBP.hsa, [17](#)
- geneset.GOBP.mmu, [17](#)
- geneset.GOBP.rno, [18](#)
- geneset.GOCC.dme, [19](#)
- geneset.GOCC.dre, [19](#)
- geneset.GOCC.hsa, [20](#)
- geneset.GOCC.mmu, [21](#)
- geneset.GOCC.rno, [21](#)
- geneset.GOMF.dme, [22](#)
- geneset.GOMF.dre, [23](#)
- geneset.GOMF.hsa, [23](#)
- geneset.GOMF.mmu, [24](#)
- geneset.GOMF.rno, [25](#)
- geneset.hallmark.hsa, [25](#)
- geneset.immunologic.hsa, [26](#)
- geneset.kegg\_pathway.hsa, [27](#)
- geneset.kegg\_pathway.mmu, [28](#)
- geneset.kegg\_pathway.rno, [28](#)
- geneset.mesh.hsa, [29](#)
- geneset.mesh.mmu, [29](#)
- geneset.mesh.rno, [30](#)
- geneset.metabolite.hsa, [30](#)
- geneset.metabolite.mmu, [31](#)
- geneset.metabolite.rno, [31](#)
- geneset.microrna.hsa, [32](#)
- geneset.oncogenic.hsa, [32](#)
- geneset.panther\_pathway.hsa, [33](#)
- geneset.panther\_pathway.mmu, [34](#)
- geneset.panther\_pathway.rno, [34](#)
- geneset.pfam.hsa, [35](#)
- geneset.pfam.mmu, [35](#)
- geneset.pfam.rno, [36](#)
- geneset.protein\_interaction\_biogrid.hsa, [36](#)

geneset.reactome.dme, [37](#)  
 geneset.reactome.dre, [38](#)  
 geneset.reactome.hsa, [38](#)  
 geneset.reactome.mmu, [39](#)  
 geneset.reactome.rno, [40](#)  
 geneset.transcription\_factors.hsa, [41](#)  
 geneset.transcription\_factors.mmu, [41](#)  
 geneset.transcription\_factors.rno, [42](#)

locusdef.danRer10.10kb, [42](#)  
 locusdef.danRer10.10kb\_outside, [43](#)  
 locusdef.danRer10.10kb\_outside\_upstream, [44](#)  
 locusdef.danRer10.1kb, [45](#)  
 locusdef.danRer10.1kb\_outside, [45](#)  
 locusdef.danRer10.1kb\_outside\_upstream, [46](#)  
 locusdef.danRer10.5kb, [47](#)  
 locusdef.danRer10.5kb\_outside, [48](#)  
 locusdef.danRer10.5kb\_outside\_upstream, [48](#)  
 locusdef.danRer10.exon, [49](#)  
 locusdef.danRer10.intron, [50](#)  
 locusdef.danRer10.nearest\_gene, [50](#)  
 locusdef.danRer10.nearest\_tss, [51](#)  
 locusdef.dm3.10kb, [52](#)  
 locusdef.dm3.10kb\_outside, [53](#)  
 locusdef.dm3.10kb\_outside\_upstream, [53](#)  
 locusdef.dm3.1kb, [54](#)  
 locusdef.dm3.1kb\_outside, [55](#)  
 locusdef.dm3.1kb\_outside\_upstream, [56](#)  
 locusdef.dm3.5kb, [56](#)  
 locusdef.dm3.5kb\_outside, [57](#)  
 locusdef.dm3.5kb\_outside\_upstream, [58](#)  
 locusdef.dm3.exon, [59](#)  
 locusdef.dm3.intron, [59](#)  
 locusdef.dm3.nearest\_gene, [60](#)  
 locusdef.dm3.nearest\_tss, [61](#)  
 locusdef.dm6.10kb, [62](#)  
 locusdef.dm6.10kb\_outside, [62](#)  
 locusdef.dm6.10kb\_outside\_upstream, [63](#)  
 locusdef.dm6.1kb, [64](#)  
 locusdef.dm6.1kb\_outside, [65](#)  
 locusdef.dm6.1kb\_outside\_upstream, [65](#)  
 locusdef.dm6.5kb, [66](#)  
 locusdef.dm6.5kb\_outside, [67](#)  
 locusdef.dm6.5kb\_outside\_upstream, [68](#)  
 locusdef.dm6.exon, [68](#)  
 locusdef.dm6.intron, [69](#)

locusdef.dm6.nearest\_gene, [70](#)  
 locusdef.dm6.nearest\_tss, [71](#)  
 locusdef.hg19.10kb, [71](#)  
 locusdef.hg19.10kb\_outside, [72](#)  
 locusdef.hg19.10kb\_outside\_upstream, [73](#)  
 locusdef.hg19.1kb, [74](#)  
 locusdef.hg19.1kb\_outside, [74](#)  
 locusdef.hg19.1kb\_outside\_upstream, [75](#)  
 locusdef.hg19.5kb, [76](#)  
 locusdef.hg19.5kb\_outside, [77](#)  
 locusdef.hg19.5kb\_outside\_upstream, [77](#)  
 locusdef.hg19.exon, [78](#)  
 locusdef.hg19.intron, [79](#)  
 locusdef.hg19.nearest\_gene, [80](#)  
 locusdef.hg19.nearest\_tss, [80](#)  
 locusdef.hg38.10kb, [81](#)  
 locusdef.hg38.10kb\_outside, [82](#)  
 locusdef.hg38.10kb\_outside\_upstream, [83](#)  
 locusdef.hg38.1kb, [83](#)  
 locusdef.hg38.1kb\_outside, [84](#)  
 locusdef.hg38.1kb\_outside\_upstream, [85](#)  
 locusdef.hg38.5kb, [86](#)  
 locusdef.hg38.5kb\_outside, [86](#)  
 locusdef.hg38.5kb\_outside\_upstream, [87](#)  
 locusdef.hg38.exon, [88](#)  
 locusdef.hg38.intron, [89](#)  
 locusdef.hg38.nearest\_gene, [89](#)  
 locusdef.hg38.nearest\_tss, [90](#)  
 locusdef.mm10.10kb, [91](#)  
 locusdef.mm10.10kb\_outside, [92](#)  
 locusdef.mm10.10kb\_outside\_upstream, [92](#)  
 locusdef.mm10.1kb, [93](#)  
 locusdef.mm10.1kb\_outside, [94](#)  
 locusdef.mm10.1kb\_outside\_upstream, [95](#)  
 locusdef.mm10.5kb, [95](#)  
 locusdef.mm10.5kb\_outside, [96](#)  
 locusdef.mm10.5kb\_outside\_upstream, [97](#)  
 locusdef.mm10.exon, [98](#)  
 locusdef.mm10.intron, [98](#)  
 locusdef.mm10.nearest\_gene, [99](#)  
 locusdef.mm10.nearest\_tss, [100](#)  
 locusdef.mm9.10kb, [101](#)  
 locusdef.mm9.10kb\_outside, [101](#)  
 locusdef.mm9.10kb\_outside\_upstream, [102](#)

- locusdef.mm9.1kb, [103](#)
- locusdef.mm9.1kb\_outside, [104](#)
- locusdef.mm9.1kb\_outside\_upstream, [104](#)
- locusdef.mm9.5kb, [105](#)
- locusdef.mm9.5kb\_outside, [106](#)
- locusdef.mm9.5kb\_outside\_upstream, [107](#)
- locusdef.mm9.exon, [107](#)
- locusdef.mm9.intron, [108](#)
- locusdef.mm9.nearest\_gene, [109](#)
- locusdef.mm9.nearest\_tss, [110](#)
- locusdef.rn4.10kb, [110](#)
- locusdef.rn4.10kb\_outside, [111](#)
- locusdef.rn4.10kb\_outside\_upstream, [112](#)
- locusdef.rn4.1kb, [113](#)
- locusdef.rn4.1kb\_outside, [113](#)
- locusdef.rn4.1kb\_outside\_upstream, [114](#)
- locusdef.rn4.5kb, [115](#)
- locusdef.rn4.5kb\_outside, [116](#)
- locusdef.rn4.5kb\_outside\_upstream, [116](#)
- locusdef.rn4.exon, [117](#)
- locusdef.rn4.intron, [118](#)
- locusdef.rn4.nearest\_gene, [119](#)
- locusdef.rn4.nearest\_tss, [119](#)
- locusdef.rn5.10kb, [120](#)
- locusdef.rn5.10kb\_outside, [121](#)
- locusdef.rn5.10kb\_outside\_upstream, [122](#)
- locusdef.rn5.1kb, [122](#)
- locusdef.rn5.1kb\_outside, [123](#)
- locusdef.rn5.1kb\_outside\_upstream, [124](#)
- locusdef.rn5.5kb, [125](#)
- locusdef.rn5.5kb\_outside, [125](#)
- locusdef.rn5.5kb\_outside\_upstream, [126](#)
- locusdef.rn5.exon, [127](#)
- locusdef.rn5.intron, [127](#)
- locusdef.rn5.nearest\_gene, [128](#)
- locusdef.rn5.nearest\_tss, [129](#)
- locusdef.rn6.10kb, [130](#)
- locusdef.rn6.10kb\_outside, [130](#)
- locusdef.rn6.10kb\_outside\_upstream, [131](#)
- locusdef.rn6.1kb, [132](#)
- locusdef.rn6.1kb\_outside, [133](#)
- locusdef.rn6.1kb\_outside\_upstream, [133](#)
- locusdef.rn6.5kb, [134](#)
- locusdef.rn6.5kb\_outside, [135](#)
- locusdef.rn6.5kb\_outside\_upstream, [135](#)
- locusdef.rn6.exon, [136](#)
- locusdef.rn6.intron, [137](#)
- locusdef.rn6.nearest\_gene, [137](#)
- locusdef.rn6.nearest\_tss, [138](#)
- LocusDefinition-class, [139](#)
- mappa.hg19.10kb.100mer, [140](#)
- mappa.hg19.10kb.24mer, [140](#)
- mappa.hg19.10kb.36mer, [141](#)
- mappa.hg19.10kb.40mer, [142](#)
- mappa.hg19.10kb.50mer, [142](#)
- mappa.hg19.10kb.75mer, [143](#)
- mappa.hg19.1kb.100mer, [144](#)
- mappa.hg19.1kb.24mer, [144](#)
- mappa.hg19.1kb.36mer, [145](#)
- mappa.hg19.1kb.40mer, [146](#)
- mappa.hg19.1kb.50mer, [146](#)
- mappa.hg19.1kb.75mer, [147](#)
- mappa.hg19.5kb.100mer, [148](#)
- mappa.hg19.5kb.24mer, [148](#)
- mappa.hg19.5kb.36mer, [149](#)
- mappa.hg19.5kb.40mer, [150](#)
- mappa.hg19.5kb.50mer, [150](#)
- mappa.hg19.5kb.75mer, [151](#)
- mappa.hg19.exon.100mer, [152](#)
- mappa.hg19.exon.24mer, [152](#)
- mappa.hg19.exon.36mer, [153](#)
- mappa.hg19.exon.40mer, [154](#)
- mappa.hg19.exon.50mer, [154](#)
- mappa.hg19.exon.75mer, [155](#)
- mappa.hg19.intron.100mer, [156](#)
- mappa.hg19.intron.24mer, [156](#)
- mappa.hg19.intron.36mer, [157](#)
- mappa.hg19.intron.40mer, [158](#)
- mappa.hg19.intron.50mer, [158](#)
- mappa.hg19.intron.75mer, [159](#)
- mappa.hg19.nearest\_gene.100mer, [160](#)
- mappa.hg19.nearest\_gene.24mer, [160](#)
- mappa.hg19.nearest\_gene.36mer, [161](#)
- mappa.hg19.nearest\_gene.40mer, [162](#)
- mappa.hg19.nearest\_gene.50mer, [162](#)
- mappa.hg19.nearest\_gene.75mer, [163](#)
- mappa.hg19.nearest\_tss.100mer, [164](#)
- mappa.hg19.nearest\_tss.24mer, [164](#)
- mappa.hg19.nearest\_tss.36mer, [165](#)
- mappa.hg19.nearest\_tss.40mer, [166](#)
- mappa.hg19.nearest\_tss.50mer, [166](#)
- mappa.hg19.nearest\_tss.75mer, [167](#)
- mappa.mm9.10kb.100mer, [168](#)

mappa.mm9.10kb.36mer, [168](#)  
mappa.mm9.10kb.40mer, [169](#)  
mappa.mm9.10kb.50mer, [170](#)  
mappa.mm9.10kb.75mer, [170](#)  
mappa.mm9.1kb.100mer, [171](#)  
mappa.mm9.1kb.36mer, [172](#)  
mappa.mm9.1kb.40mer, [172](#)  
mappa.mm9.1kb.50mer, [173](#)  
mappa.mm9.1kb.75mer, [174](#)  
mappa.mm9.5kb.100mer, [174](#)  
mappa.mm9.5kb.36mer, [175](#)  
mappa.mm9.5kb.40mer, [176](#)  
mappa.mm9.5kb.50mer, [176](#)  
mappa.mm9.5kb.75mer, [177](#)  
mappa.mm9.exon.100mer, [178](#)  
mappa.mm9.exon.36mer, [178](#)  
mappa.mm9.exon.40mer, [179](#)  
mappa.mm9.exon.50mer, [180](#)  
mappa.mm9.exon.75mer, [180](#)  
mappa.mm9.intron.100mer, [181](#)  
mappa.mm9.intron.36mer, [182](#)  
mappa.mm9.intron.40mer, [182](#)  
mappa.mm9.intron.50mer, [183](#)  
mappa.mm9.intron.75mer, [184](#)  
mappa.mm9.nearest\_gene.100mer, [184](#)  
mappa.mm9.nearest\_gene.36mer, [185](#)  
mappa.mm9.nearest\_gene.40mer, [186](#)  
mappa.mm9.nearest\_gene.50mer, [186](#)  
mappa.mm9.nearest\_gene.75mer, [187](#)  
mappa.mm9.nearest\_tss.100mer, [188](#)  
mappa.mm9.nearest\_tss.36mer, [188](#)  
mappa.mm9.nearest\_tss.40mer, [189](#)  
mappa.mm9.nearest\_tss.50mer, [190](#)  
mappa.mm9.nearest\_tss.75mer, [190](#)  
  
peaks\_E2F4, [191](#)  
peaks\_H3K4me3\_GM12878, [192](#)  
  
spline.log\_dtss.90ENCODE, [192](#)  
  
tss.danRer10, [193](#)  
tss.dm3, [193](#)  
tss.dm6, [194](#)  
tss.hg19, [194](#)  
tss.hg38, [195](#)  
tss.mm10, [195](#)  
tss.mm9, [196](#)  
tss.rn4, [197](#)  
tss.rn5, [197](#)  
tss.rn6, [198](#)