

# Package ‘chipenrich.data’

April 10, 2025

**Title** Companion package to chipenrich

**Version** 2.31.0

**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

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

**git\_branch** devel

**git\_last\_commit** 955d144

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

**Repository** Bioconductor 3.21

**Date/Publication** 2025-04-10

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## Contents

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

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

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

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

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

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

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

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

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

---

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

---

### Description

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

### Usage

```
enhancer.dnase_thurman.0
```

### Format

A GRanges object with the following mcols:

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

**symbol** The gene symbol for the TSS



---

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

---

### Description

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

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

**avg\_denh\_emp** The empirical average distance to an enhancer from 90 ENCODE CHIP-seq datasets. This is used as the adjustment.

**num\_enh** The number of enhancers assigned to the gene, defined by closest gene TSS

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

### Usage

```
gene.enh.desc
```

### Format

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

---

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

---

### Description

Class for storing sets of genes and their corresponding metadata.

### Objects from the Class

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

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

### Slots

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

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

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

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

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

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

**Note**

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

**Author(s)**

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**Examples**

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

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

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

---

```
geneset.biocarta_pathway.hsa
      geneset.biocarta_pathway.hsa genesets for BioCarta
```

---

**Description**

BioCarta (biocarta\_pathway) genesets. All genesets are required to have  $\geq 10$  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      *geneset.GOBP.hsa genesets for Homo sapiens*

---

### Description

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

### Usage

geneset.GOBP.hsa

### Format

A GeneSet object with the following slots:

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

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

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

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

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

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

### Source

org.Hs.eg.db\_3.4.2 and GO.db\_3.4.2

---

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

---

### Description

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

### Usage

geneset.GOBP.mmu

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

org.Mm.eg.db\_3.4.2 and GO.db\_3.4.2

---

geneset.GOBP.rno

*geneset.GOBP.rno genesets for Rattus norvegicus*

---

**Description**

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

**Usage**

geneset.GOBP.rno

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

org.Rn.eg.db\_3.4.2 and GO.db\_3.4.2

---

geneset.GOCC.dme	<i>geneset.GOCC.dme genesets for 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 genesets for 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

---

<code>geneset.GOCC.hsa</code>	<i>geneset.GOCC.hsa genesets for Homo sapiens</i>
-------------------------------	---

---

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

---

### Description

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

### Usage

geneset.GOMF.dre

### Format

A GeneSet object with the following slots:

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

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

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

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

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

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

### Source

org.Dr.eg.db\_3.4.2 and GO.db\_3.4.2

---

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

---

### Description

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

### Usage

geneset.GOMF.hsa

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

org.Hs.eg.db\_3.4.2 and GO.db\_3.4.2

---

geneset.GOMF.mmu

*geneset.GOMF.mmu genesets for Mus musculus*

---

**Description**

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

**Usage**

geneset.GOMF.mmu

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

org.Mm.eg.db\_3.4.2 and GO.db\_3.4.2



---

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

---

### Description

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

### Usage

geneset.GOMF.rno

### Format

A GeneSet object with the following slots:

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

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

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

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

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

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

### Source

org.Rn.eg.db\_3.4.2 and GO.db\_3.4.2

---

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

---

### Description

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

### Usage

geneset.hallmark.hsa

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

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

---

geneset.immunologic.hsa

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

---

**Description**

Immunologic Signatures (MSigDB) (immunologic) genesets. All genesets are required to have >= 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`      *geneset.mesh.rno*

---

**Description**

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

**Usage**

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

**Format**

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

**See Also**

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

---

`geneset.metabolite.hsa`  
*geneset.metabolite.hsa*

---

**Description**

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

**Usage**

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

**Format**

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

**See Also**

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

---

geneset.metabolite.mmu  
*geneset.metabolite.mmu*

---

**Description**

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

**Usage**

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

**Format**

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

**See Also**

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

---

geneset.metabolite.rno  
*geneset.metabolite.rno*

---

**Description**

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

**Usage**

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

**Format**

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

**See Also**

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

---

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

---

**Description**

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

**Usage**

geneset.microrna.hsa

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

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

---

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

---

**Description**

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

**Usage**

geneset.oncogenic.hsa



**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

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

---

geneset.panther\_pathway.hsa

*geneset.panther\_pathway.hsa*

---

**Description**

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

**Usage**

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

**Format**

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

**See Also**

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

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

---

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

---

**Description**

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

**Usage**

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

**Format**

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

**See Also**

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

---

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

---

**Description**

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

**Usage**

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

**Format**

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

**See Also**

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

---

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

---

**Description**

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

**Usage**

```
geneset.pfam.hsa
```

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

<http://pfam.xfam.org>

---

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

---

**Description**

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

**Usage**

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

**Format**

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

**See Also**

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

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

---

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

---

**Description**

GeneSet object which stores information about sets of genes.

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

**Usage**

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

**Format**

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

**See Also**

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

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

---

`geneset.protein_interaction_biogrid.hsa`  
*geneset.protein\_interaction\_biogrid.hsa* *genesets for BioGRID Protein Interactions*

---

**Description**

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

**Usage**

```
geneset.protein_interaction_biogrid.hsa
```

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

<https://thebiogrid.org>

---

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

---

**Description**

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

**Usage**

geneset.reactome.dme

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

[http://www.reactome.org/download/current/NCBI2Reactome\\_All\\_Levels.txt](http://www.reactome.org/download/current/NCBI2Reactome_All_Levels.txt) downloaded on 2017-03-19

---

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

---

### Description

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

### Usage

geneset.reactome.dre

### Format

A GeneSet object with the following slots:

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

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

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

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

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

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

### Source

[http://www.reactome.org/download/current/NCBI2Reactome\\_All\\_Levels.txt](http://www.reactome.org/download/current/NCBI2Reactome_All_Levels.txt) downloaded on 2017-03-19

---

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

---

### Description

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

### Usage

geneset.reactome.hsa

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

[http://www.reactome.org/download/current/NCBI2Reactome\\_All\\_Levels.txt](http://www.reactome.org/download/current/NCBI2Reactome_All_Levels.txt) downloaded on 2017-03-19

---

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

---

**Description**

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

**Usage**

```
geneset.reactome.mmu
```

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

[http://www.reactome.org/download/current/NCBI2Reactome\\_All\\_Levels.txt](http://www.reactome.org/download/current/NCBI2Reactome_All_Levels.txt) downloaded on 2017-03-19

---

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

---

**Description**

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

**Usage**

geneset.reactome.rno

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

[http://www.reactome.org/download/current/NCBI2Reactome\\_All\\_Levels.txt](http://www.reactome.org/download/current/NCBI2Reactome_All_Levels.txt) downloaded on 2017-03-19



---

geneset.transcription\_factors.hsa

*geneset.transcription\_factors.hsa* genesets for Transcription Factor Targets (MSigDB)

---

### Description

Transcription Factor Targets (MSigDB) (transcription\_factors) genesets. All genesets are required to have  $\geq 10$  Entrez IDs. Built on Mon Oct 16 18:47:33 2017.

### Usage

geneset.transcription\_factors.hsa

### Format

A GeneSet object with the following slots:

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

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

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

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

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

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

### Source

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

---

geneset.transcription\_factors.mmu

*geneset.transcription\_factors.mmu*

---

### Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

### Usage

data(geneset.transcription\_factors.mmu)

**Format**

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

**See Also**

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

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

---

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

---

**Description**

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

**Usage**

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

**Format**

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

**See Also**

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

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

---

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

---

**Description**

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

**Usage**

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

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.2 and org.Dr.eg.db\_3.5.0.

---

locusdef.danRer10.10kb\_outside

*locusdef.danRer10.10kb\_outside locus definition*

---

**Description**

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

**Usage**

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

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.2 and org.Dr.eg.db\_3.5.0.

---

locusdef.danRer10.10kb\_outside\_upstream  
*locusdef.danRer10.10kb\_outside\_upstream locus definition*

---

**Description**

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

**Usage**

```
locusdef.danRer10.10kb_outside_upstream
```

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.2 and org.Dr.eg.db\_3.5.0.

---

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

---

### Description

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

### Usage

locusdef.danRer10.1kb

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

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

### Source

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

---

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

---

### Description

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

### Usage

locusdef.danRer10.1kb\_outside

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.2 and org.Dr.eg.db\_3.5.0.

---

locusdef.danRer10.1kb\_outside\_upstream

*locusdef.danRer10.1kb\_outside\_upstream locus definition*

---

**Description**

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

**Usage**

locusdef.danRer10.1kb\_outside\_upstream

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

## Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.2 and org.Dr.eg.db\_3.5.0.

---

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

---

## Description

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

## Usage

```
locusdef.danRer10.5kb
```

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.2 and org.Dr.eg.db\_3.5.0.

---

locusdef.danRer10.5kb\_outside

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

---

### Description

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

### Usage

locusdef.danRer10.5kb\_outside

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

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

### Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.2 and org.Dr.eg.db\_3.5.0.

---

locusdef.danRer10.5kb\_outside\_upstream

*locusdef.danRer10.5kb\_outside\_upstream locus definition*

---

### Description

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

### Usage

locusdef.danRer10.5kb\_outside\_upstream



**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.2 and org.Dr.eg.db\_3.5.0.

---

locusdef.danRer10.exon

*locusdef.danRer10.exon locus definition*

---

**Description**

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

**Usage**

locusdef.danRer10.exon

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.2 and org.Dr.eg.db\_3.5.0.

locusdef.danRer10.intron

*locusdef.danRer10.intron locus definition*

---

### Description

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

### Usage

locusdef.danRer10.intron

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

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

### Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.2 and org.Dr.eg.db\_3.5.0.

---

locusdef.danRer10.nearest\_gene

*locusdef.danRer10.nearest\_gene locus definition*

---

### Description

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

### Usage

locusdef.danRer10.nearest\_gene

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

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

---

locusdef.danRer10.nearest\_tss

*locusdef.danRer10.nearest\_tss locus definition*

---

**Description**

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

**Usage**

```
locusdef.danRer10.nearest_tss
```

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.2 and org.Dr.eg.db\_3.5.0.

---

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

---

**Description**

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

**Usage**

locusdef.dm3.10kb

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

locusdef.dm3.10kb\_outside

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

---

### Description

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

### Usage

locusdef.dm3.10kb\_outside

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

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

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

### Source

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

---

locusdef.dm3.10kb\_outside\_upstream

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

---

### Description

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

**Usage**

locusdef.dm3.10kb\_outside\_upstream

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

locusdef.dm3.1kb      *locusdef.dm3.1kb locus definition*

---

**Description**

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

**Usage**

locusdef.dm3.1kb

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

locusdef.dm3.1kb\_outside

*locusdef.dm3.1kb\_outside locus definition*

---

**Description**

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

**Usage**

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

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

locusdef.dm3.1kb\_outside\_upstream

*locusdef.dm3.1kb\_outside\_upstream locus definition*

---

### Description

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

### Usage

locusdef.dm3.1kb\_outside\_upstream

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

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

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

### Source

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

---

locusdef.dm3.5kb

*locusdef.dm3.5kb locus definition*

---

### Description

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

### Usage

locusdef.dm3.5kb



**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

locusdef.dm3.5kb\_outside

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

---

**Description**

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

**Usage**

`locusdef.dm3.5kb_outside`

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

### Details

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

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

### Source

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

---

locusdef.dm3.5kb\_outside\_upstream

*locusdef.dm3.5kb\_outside\_upstream locus definition*

---

### Description

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

### Usage

```
locusdef.dm3.5kb_outside_upstream
```

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

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

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

### Source

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

---

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

---

### Description

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

### Usage

locusdef.dm3.exon

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

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

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

### Source

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

---

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

---

### Description

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

### Usage

locusdef.dm3.intron

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

`locusdef.dm3.nearest_gene`

*locusdef.dm3.nearest\_gene locus definition*

---

**Description**

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

**Usage**

`locusdef.dm3.nearest_gene`

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

locusdef.dm3.nearest\_tss

*locusdef.dm3.nearest\_tss locus definition*

---

**Description**

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

**Usage**

```
locusdef.dm3.nearest_tss
```

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

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

---

### Description

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

### Usage

locusdef.dm6.10kb

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

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

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

### Source

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

---

locusdef.dm6.10kb\_outside  
*locusdef.dm6.10kb\_outside locus definition*

---

### Description

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

**Usage**

locusdef.dm6.10kb\_outside

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

locusdef.dm6.10kb\_outside\_upstream

*locusdef.dm6.10kb\_outside\_upstream locus definition*

---

**Description**

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

**Usage**

locusdef.dm6.10kb\_outside\_upstream

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

locusdef.dm6.1kb	<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`.

---

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

---

**Description**

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

**Usage**

locusdef.dm6.5kb

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

locusdef.dm6.5kb\_outside

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

---

**Description**

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

**Usage**

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

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

locusdef.dm6.5kb\_outside\_upstream

*locusdef.dm6.5kb\_outside\_upstream locus definition*


---

### Description

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

### Usage

```
locusdef.dm6.5kb_outside_upstream
```

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

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

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

### Source

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

---

locusdef.dm6.exon

*locusdef.dm6.exon locus definition*


---

### Description

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

### Usage

```
locusdef.dm6.exon
```

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

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

---

**Description**

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

**Usage**

```
locusdef.dm6.intron
```

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

locusdef.dm6.nearest\_gene

*locusdef.dm6.nearest\_gene locus definition*

---

**Description**

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

**Usage**

locusdef.dm6.nearest\_gene

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

locusdef.dm6.nearest\_tss  
*locusdef.dm6.nearest\_tss locus definition*

---

### Description

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

### Usage

locusdef.dm6.nearest\_tss

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

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

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

### Source

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

---

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

---

### Description

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

### Usage

locusdef.hg19.10kb

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.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      *locusdef.hg19.1kb locus definition*

---

### Description

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

### Usage

locusdef.hg19.1kb

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

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

### Source

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

---

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

---

### Description

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

### Usage

locusdef.hg19.1kb\_outside

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

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

---

locusdef.hg19.1kb\_outside\_upstream

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

---

**Description**

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

**Usage**

locusdef.hg19.1kb\_outside\_upstream

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

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

---

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

---

**Description**

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

**Usage**

locusdef.hg19.5kb

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

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

---

**Description**

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

**Usage**

locusdef.hg19.exon

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

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

---

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

---

**Description**

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

**Usage**

```
locusdef.hg19.intron
```

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

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

---

locusdef.hg19.nearest\_gene

*locusdef.hg19.nearest\_gene locus definition*

---

### Description

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

### Usage

locusdef.hg19.nearest\_gene

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

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

### Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.annotation](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      *locusdef.hg38.10kb locus definition*

---

**Description**

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

**Usage**

```
locusdef.hg38.10kb
```

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

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

---

locusdef.hg38.10kb\_outside

*locusdef.hg38.10kb\_outside locus definition*

---

**Description**

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

**Usage**

locusdef.hg38.10kb\_outside

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

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

---

locusdef.hg38.10kb\_outside\_upstream  
*locusdef.hg38.10kb\_outside\_upstream locus definition*

---

### Description

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

### Usage

locusdef.hg38.10kb\_outside\_upstream

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

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

### Source

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

---

locusdef.hg38.1kb      *locusdef.hg38.1kb locus definition*

---

### Description

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

### Usage

locusdef.hg38.1kb

**Format**

A LocusDefinition object with the following slots:

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

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

---

locusdef.hg38.1kb\_outside\_upstream

*locusdef.hg38.1kb\_outside\_upstream locus definition*

---

**Description**

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

**Usage**

locusdef.hg38.1kb\_outside\_upstream

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

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

---

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

---

### Description

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

### Usage

locusdef.hg38.5kb

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

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

### Source

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

---

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

---

### Description

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

### Usage

locusdef.hg38.5kb\_outside

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

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

---

locusdef.hg38.5kb\_outside\_upstream

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

---

**Description**

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

**Usage**

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

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

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

---

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

---

**Description**

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

**Usage**

```
locusdef.hg38.exon
```

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

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



---

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

---

### Description

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

### Usage

locusdef.hg38.intron

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

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

### Source

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

*locusdef.hg38.nearest\_tss locus definition*

---

**Description**

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

**Usage**

locusdef.hg38.nearest\_tss

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

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

---

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

---

**Description**

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

**Usage**

```
locusdef.mm10.10kb
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, mm10.

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

**Details**

Built on Fri Apr 13 09:51:40 2018.

**Source**

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.metadata.EntrezGene.gz

---

locusdef.mm10.10kb\_outside

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

---

### Description

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

### Usage

locusdef.mm10.10kb\_outside

### Format

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `mm10`.

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

### Details

Built on Fri Apr 13 09:51:41 2018.

### Source

R packages: `TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0` and `org.Mm.eg.db_3.5.0`. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.annotation.gff3.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz)

---

locusdef.mm10.10kb\_outside\_upstream

*locusdef.mm10.10kb\_outside\_upstream locus definition*

---

### Description

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

**Usage**

```
locusdef.mm10.10kb_outside_upstream
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `mm10`.

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

**Details**

Built on Fri Apr 13 09:51:40 2018.

**Source**

R packages: `TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0` and `org.Mm.eg.db_3.5.0`. GENCODE resources: `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz` and `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz`

---

`locusdef.mm10.1kb`      *locusdef.mm10.1kb locus definition*

---

**Description**

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

**Usage**

```
locusdef.mm10.1kb
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `mm10`.

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

**Details**

Built on Fri Apr 13 09:51:37 2018.

**Source**

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.metadata.EntrezGene.gz

---

locusdef.mm10.1kb\_outside

*locusdef.mm10.1kb\_outside locus definition*

---

**Description**

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

**Usage**

locusdef.mm10.1kb\_outside

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, mm10.

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

**Details**

Built on Fri Apr 13 09:51:38 2018.

**Source**

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.metadata.EntrezGene.gz

---

locusdef.mm10.1kb\_outside\_upstream  
*locusdef.mm10.1kb\_outside\_upstream locus definition*

---

### Description

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

### Usage

locusdef.mm10.1kb\_outside\_upstream

### Format

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, mm10.

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

### Details

Built on Fri Apr 13 09:51:37 2018.

### Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.metadata.EntrezGene.gz

---

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

---

### Description

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

### Usage

locusdef.mm10.5kb

**Format**

A LocusDefinition object with the following slots:

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

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

---

locusdef.mm10.5kb\_outside\_upstream

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

---

**Description**

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

**Usage**

```
locusdef.mm10.5kb_outside_upstream
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, mm10.

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

**Details**

Built on Fri Apr 13 09:51:39 2018.

**Source**

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.metadata.EntrezGene.gz

---

locusdef.mm10.exon     *locusdef.mm10.exon locus definition*

---

### Description

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

### Usage

locusdef.mm10.exon

### Format

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, mm10.

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

### Details

Built on Fri Apr 13 09:51:35 2018.

### Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.metadata.EntrezGene.gz

---

locusdef.mm10.intron     *locusdef.mm10.intron locus definition*

---

### Description

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

### Usage

locusdef.mm10.intron

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, mm10.

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

**Details**

Built on Fri Apr 13 09:51:36 2018.

**Source**

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.metadata.EntrezGene.gz

---

locusdef.mm10.nearest\_gene

*locusdef.mm10.nearest\_gene locus definition*

---

**Description**

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

**Usage**

locusdef.mm10.nearest\_gene

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, mm10.

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

**Details**

Built on Fri Apr 13 09:51:33 2018.

**Source**

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.metadata.EntrezGene.gz

---

locusdef.mm10.nearest\_tss

*locusdef.mm10.nearest\_tss locus definition*

---

**Description**

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

**Usage**

locusdef.mm10.nearest\_tss

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, mm10.

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

**Details**

Built on Fri Apr 13 09:51:33 2018.

**Source**

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.metadata.EntrezGene.gz

---

locusdef.mm9.10kb      *locusdef.mm9.10kb locus definition*

---

### Description

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

### Usage

locusdef.mm9.10kb

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

Built on Fri Apr 13 09:50:44 2018.

### Source

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.5.0`. GENCODE resources: `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz` and `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz`

---

locusdef.mm9.10kb\_outside  
*locusdef.mm9.10kb\_outside locus definition*

---

### Description

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

### Usage

locusdef.mm9.10kb\_outside

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Fri Apr 13 09:50:44 2018.

**Source**

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

---

locusdef.mm9.10kb\_outside\_upstream

*locusdef.mm9.10kb\_outside\_upstream locus definition*

---

**Description**

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

**Usage**

locusdef.mm9.10kb\_outside\_upstream

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Fri Apr 13 09:50:44 2018.

**Source**

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

---

locusdef.mm9.1kb      *locusdef.mm9.1kb locus definition*

---

**Description**

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

**Usage**

locusdef.mm9.1kb

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

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

---

locusdef.mm9.1kb\_outside

*locusdef.mm9.1kb\_outside locus definition*

---

### Description

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

### Usage

locusdef.mm9.1kb\_outside

### Format

A LocusDefinition object with the following slots:

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

**dframe** A data.frame of 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)

---

`locusdef.mm9.5kb`      *locusdef.mm9.5kb locus definition*

---

**Description**

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

**Usage**

```
locusdef.mm9.5kb
```

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

## Details

Built on Fri Apr 13 09:50:42 2018.

## Source

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

---

locusdef.mm9.5kb\_outside

*locusdef.mm9.5kb\_outside locus definition*

---

## Description

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

## Usage

```
locusdef.mm9.5kb_outside
```

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

Built on Fri Apr 13 09:50:43 2018.

## Source

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

---

locusdef.mm9.5kb\_outside\_upstream  
*locusdef.mm9.5kb\_outside\_upstream locus definition*

---

### Description

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

### Usage

locusdef.mm9.5kb\_outside\_upstream

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

Built on Fri Apr 13 09:50:43 2018.

### Source

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.5.0`. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M9/gencode.vM9.annotation.gff3.gz](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 and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.metadata.EntrezGene.gz

---

locusdef.mm9.nearest\_gene

*locusdef.mm9.nearest\_gene locus definition*

---

**Description**

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

**Usage**

locusdef.mm9.nearest\_gene

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Fri Apr 13 09:50:37 2018.

**Source**

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

---

locusdef.mm9.nearest\_tss

*locusdef.mm9.nearest\_tss locus definition*


---

### Description

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

### Usage

```
locusdef.mm9.nearest_tss
```

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

Built on Fri Apr 13 09:50:37 2018.

### Source

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.5.0`. GENCODE resources: `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz` and `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz`

---

locusdef.rn4.10kb

*locusdef.rn4.10kb locus definition*


---

### Description

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

### Usage

```
locusdef.rn4.10kb
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn4`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

**Source**

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

---

locusdef.rn4.10kb\_outside

*locusdef.rn4.10kb\_outside locus definition*

---

**Description**

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

**Usage**

```
locusdef.rn4.10kb_outside
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn4`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:03 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene\_3.2.2 and org.Rn.eg.db\_3.5.0.

---

locusdef.rn4.10kb\_outside\_upstream

*locusdef.rn4.10kb\_outside\_upstream locus definition*

---

**Description**

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

**Usage**

locusdef.rn4.10kb\_outside\_upstream

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, rn4.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

**Details**

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene\_3.2.2 and org.Rn.eg.db\_3.5.0.



---

locusdef.rn4.1kb      *locusdef.rn4.1kb locus definition*

---

### Description

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

### Usage

locusdef.rn4.1kb

### Format

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn4`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

### Details

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

### Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

---

locusdef.rn4.1kb\_outside      *locusdef.rn4.1kb\_outside locus definition*

---

### Description

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

**Usage**

```
locusdef.rn4.1kb_outside
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn4`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

**Source**

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

---

```
locusdef.rn4.1kb_outside_upstream
```

```
locusdef.rn4.1kb_outside_upstream locus definition
```

---

**Description**

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

**Usage**

```
locusdef.rn4.1kb_outside_upstream
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn4`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene\_3.2.2 and org.Rn.eg.db\_3.5.0.

---

locusdef.rn4.5kb	<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`.

---

<code>locusdef.rn4.exon</code>	<i>locusdef.rn4.exon locus definition</i>
--------------------------------	---

---

**Description**

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

**Usage**

```
locusdef.rn4.exon
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn4`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:51:59 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene\_3.2.2 and org.Rn.eg.db\_3.5.0.

---

locusdef.rn4.intron    *locusdef.rn4.intron locus definition*

---

**Description**

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

**Usage**

```
locusdef.rn4.intron
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, rn4.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

**Details**

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:00 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene\_3.2.2 and org.Rn.eg.db\_3.5.0.

---

`locusdef.rn4.nearest_gene`*locusdef.rn4.nearest\_gene locus definition*

---

**Description**

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

**Usage**`locusdef.rn4.nearest_gene`**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn4`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:51:58 2018.

**Source**

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

---

`locusdef.rn4.nearest_tss`*locusdef.rn4.nearest\_tss locus definition*

---

**Description**

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

**Usage**

```
locusdef.rn4.nearest_tss
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn4`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:51:58 2018.

**Source**

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

---

```
locusdef.rn5.10kb      locusdef.rn5.10kb locus definition
```

---

**Description**

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

**Usage**

```
locusdef.rn5.10kb
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn5`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.



**Details**

Built on Fri Apr 13 09:52:20 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.2 and org.Rn.eg.db\_3.5.0.

---

locusdef.rn5.10kb\_outside

*locusdef.rn5.10kb\_outside locus definition*

---

**Description**

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

**Usage**

locusdef.rn5.10kb\_outside

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, rn5.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

**Details**

Built on Fri Apr 13 09:52:21 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.2 and org.Rn.eg.db\_3.5.0.

---

locusdef.rn5.10kb\_outside\_upstream

*locusdef.rn5.10kb\_outside\_upstream locus definition*


---

### Description

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

### Usage

```
locusdef.rn5.10kb_outside_upstream
```

### Format

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn5`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

### Details

Built on Fri Apr 13 09:52:21 2018.

### Source

R packages: `TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2` and `org.Rn.eg.db_3.5.0`.

---

locusdef.rn5.1kb

*locusdef.rn5.1kb locus definition*


---

### Description

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

### Usage

```
locusdef.rn5.1kb
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn5`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

Built on Fri Apr 13 09:52:19 2018.

**Source**

R packages: `TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2` and `org.Rn.eg.db_3.5.0`.

---

locusdef.rn5.1kb\_outside

*locusdef.rn5.1kb\_outside locus definition*

---

**Description**

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

**Usage**

```
locusdef.rn5.1kb_outside
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn5`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

Built on Fri Apr 13 09:52:19 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.2 and org.Rn.eg.db\_3.5.0.

---

locusdef.rn5.1kb\_outside\_upstream  
*locusdef.rn5.1kb\_outside\_upstream locus definition*

---

**Description**

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

**Usage**

```
locusdef.rn5.1kb_outside_upstream
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn5`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

Built on Fri Apr 13 09:52:19 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.2 and org.Rn.eg.db\_3.5.0.

---

locusdef.rn5.5kb      *locusdef.rn5.5kb locus definition*

---

### Description

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

### Usage

locusdef.rn5.5kb

### Format

A LocusDefinition object with the following slots:

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

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn5.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

### Details

Built on Fri Apr 13 09:52:20 2018.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.2 and org.Rn.eg.db\_3.5.0.

---

locusdef.rn5.5kb\_outside  
*locusdef.rn5.5kb\_outside locus definition*

---

### Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

### Usage

locusdef.rn5.5kb\_outside

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A data.frame of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A character indicating the genome build. In this case, `rn5`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

Built on Fri Apr 13 09:52:20 2018.

**Source**

R packages: `TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2` and `org.Rn.eg.db_3.5.0`.

---

locusdef.rn5.5kb\_outside\_upstream

*locusdef.rn5.5kb\_outside\_upstream locus definition*

---

**Description**

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

**Usage**

```
locusdef.rn5.5kb_outside_upstream
```

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A data.frame of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A character indicating the genome build. In this case, `rn5`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

Built on Fri Apr 13 09:52:20 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.2 and org.Rn.eg.db\_3.5.0.

---

locusdef.rn5.exon      *locusdef.rn5.exon locus definition*

---

**Description**

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

**Usage**

locusdef.rn5.exon

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn5.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

**Details**

Built on Fri Apr 13 09:52:17 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.2 and org.Rn.eg.db\_3.5.0.

---

locusdef.rn5.intron      *locusdef.rn5.intron locus definition*

---

**Description**

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

**Usage**

locusdef.rn5.intron

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A data.frame of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A character indicating the genome build. In this case, `rn5`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

Built on Fri Apr 13 09:52:19 2018.

**Source**

R packages: `TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2` and `org.Rn.eg.db_3.5.0`.

---

`locusdef.rn5.nearest_gene`

*locusdef.rn5.nearest\_gene locus definition*

---

**Description**

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

**Usage**

```
locusdef.rn5.nearest_gene
```

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A data.frame of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A character indicating the genome build. In this case, `rn5`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

Built on Fri Apr 13 09:52:16 2018.



**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.2 and org.Rn.eg.db\_3.5.0.

---

locusdef.rn5.nearest\_tss

*locusdef.rn5.nearest\_tss locus definition*

---

**Description**

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

**Usage**

```
locusdef.rn5.nearest_tss
```

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A data.frame of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A character indicating the genome build. In this case, `rn5`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

Built on Fri Apr 13 09:52:16 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.2 and org.Rn.eg.db\_3.5.0.

---

locusdef.rn6.10kb      *locusdef.rn6.10kb locus definition*

---

### Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

### Usage

locusdef.rn6.10kb

### Format

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn6.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

### Details

Built on Fri Apr 13 09:52:39 2018.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.1 and org.Rn.eg.db\_3.5.0.

---

locusdef.rn6.10kb\_outside  
*locusdef.rn6.10kb\_outside locus definition*

---

### Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

### Usage

locusdef.rn6.10kb\_outside

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A data.frame of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A character indicating the genome build. In this case, `rn6`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

Built on Fri Apr 13 09:52:40 2018.

**Source**

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

---

locusdef.rn6.10kb\_outside\_upstream

*locusdef.rn6.10kb\_outside\_upstream locus definition*

---

**Description**

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

**Usage**

```
locusdef.rn6.10kb_outside_upstream
```

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A data.frame of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A character indicating the genome build. In this case, `rn6`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

Built on Fri Apr 13 09:52:39 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.1 and org.Rn.eg.db\_3.5.0.

---

locusdef.rn6.1kb      *locusdef.rn6.1kb locus definition*

---

**Description**

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

**Usage**

```
locusdef.rn6.1kb
```

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A data.frame of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A character indicating the genome build. In this case, `rn6`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

Built on Fri Apr 13 09:52:38 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.1 and org.Rn.eg.db\_3.5.0.

---

`locusdef.rn6.1kb_outside`*locusdef.rn6.1kb\_outside locus definition*

---

**Description**

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

**Usage**`locusdef.rn6.1kb_outside`**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A data.frame of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A character indicating the genome build. In this case, `rn6`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

Built on Fri Apr 13 09:52:38 2018.

**Source**

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

---

`locusdef.rn6.1kb_outside_upstream`*locusdef.rn6.1kb\_outside\_upstream locus definition*

---

**Description**

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

**Usage**`locusdef.rn6.1kb_outside_upstream`

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn6.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

**Details**

Built on Fri Apr 13 09:52:38 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.1 and org.Rn.eg.db\_3.5.0.

---

locusdef.rn6.5kb      *locusdef.rn6.5kb locus definition*

---

**Description**

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

**Usage**

locusdef.rn6.5kb

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn6.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

**Details**

Built on Fri Apr 13 09:52:38 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.1 and org.Rn.eg.db\_3.5.0.

---

`locusdef.rn6.5kb_outside`*locusdef.rn6.5kb\_outside locus definition*

---

**Description**

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

**Usage**`locusdef.rn6.5kb_outside`**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A data.frame of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A character indicating the genome build. In this case, `rn6`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

Built on Fri Apr 13 09:52:39 2018.

**Source**

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

---

`locusdef.rn6.5kb_outside_upstream`*locusdef.rn6.5kb\_outside\_upstream locus definition*

---

**Description**

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

**Usage**`locusdef.rn6.5kb_outside_upstream`

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A data.frame of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A character indicating the genome build. In this case, `rn6`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

Built on Fri Apr 13 09:52:39 2018.

**Source**

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

---

locusdef.rn6.exon	<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    *locusdef.rn6.intron locus definition*

---

### Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

### Usage

locusdef.rn6.intron

### Format

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn6.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

### Details

Built on Fri Apr 13 09:52:37 2018.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.1 and org.Rn.eg.db\_3.5.0.

---

locusdef.rn6.nearest\_gene  
*locusdef.rn6.nearest\_gene locus definition*

---

### Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

### Usage

locusdef.rn6.nearest\_gene

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A data.frame of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A character indicating the genome build. In this case, `rn6`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

Built on Fri Apr 13 09:52:35 2018.

**Source**

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

---

locusdef.rn6.nearest\_tss

*locusdef.rn6.nearest\_tss locus definition*

---

**Description**

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

**Usage**

`locusdef.rn6.nearest_tss`

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A data.frame of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A character indicating the genome build. In this case, `rn6`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

Built on Fri Apr 13 09:52:34 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.m6.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    *mappa.mm9.1kb.36mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 36mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.1kb.36mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.1kb.40mer    *mappa.mm9.1kb.40mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 40mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.1kb.40mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.1kb.50mer`     *mappa.mm9.1kb.50mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 50mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.1kb.50mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.1kb.75mer    *mappa.mm9.1kb.75mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 75mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.1kb.75mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.5kb.100mer    *mappa.mm9.5kb.100mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 100mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.5kb.100mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.5kb.36mer`     *mappa.mm9.5kb.36mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 36mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.5kb.36mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.5kb.40mer     *mappa.mm9.5kb.40mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 40mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.5kb.40mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.5kb.50mer     *mappa.mm9.5kb.50mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 50mer

These objects are used internally by the chipenrich package.



**Usage**

```
data(mappa.mm9.5kb.50mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

*mappa.mm9.5kb.75mer*     *mappa.mm9.5kb.75mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 75mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.5kb.75mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.exon.100mer *mappa.mm9.exon.100mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 100mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.exon.100mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.exon.36mer *mappa.mm9.exon.36mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 36mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.exon.36mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

*mappa.mm9.exon.40mer*    *mappa.mm9.exon.40mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 40mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.exon.40mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.exon.50mer    *mappa.mm9.exon.50mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 50mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.exon.50mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.exon.75mer    *mappa.mm9.exon.75mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 75mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.exon.75mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.intron.100mer

*mappa.mm9.intron.100mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 100mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.intron.100mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.intron.36mer

*mappa.mm9.intron.36mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 36mer

These objects are used internally by the chipenrich package.

### Usage

```
data(mappa.mm9.intron.36mer)
```

### Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

### Author(s)

Ryan Welch <welchr@umich.edu>

### See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.intron.40mer

*mappa.mm9.intron.40mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 40mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.intron.40mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.intron.50mer

*mappa.mm9.intron.50mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 50mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.intron.50mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.intron.75mer

*mappa.mm9.intron.75mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 75mer

These objects are used internally by the chipenrich package.

### Usage

```
data(mappa.mm9.intron.75mer)
```

### Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

### Author(s)

Ryan Welch <welchr@umich.edu>

### See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.nearest\_gene.100mer

*mappa.mm9.nearest\_gene.100mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_gene
- K-Mer Reads: 100mer

These objects are used internally by the chipenrich package.



**Usage**

```
data(mappa.mm9.nearest_gene.100mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

*mappa.mm9.nearest\_gene.36mer*

*mappa.mm9.nearest\_gene.36mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_gene
- K-Mer Reads: 36mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.nearest_gene.36mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.nearest\_gene.40mer  
*mappa.mm9.nearest\_gene.40mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_gene
- K-Mer Reads: 40mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.nearest_gene.40mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs  
mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.nearest\_gene.50mer  
*mappa.mm9.nearest\_gene.50mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_gene
- K-Mer Reads: 50mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.nearest_gene.50mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

*mappa.mm9.nearest\_gene.75mer*

*mappa.mm9.nearest\_gene.75mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_gene
- K-Mer Reads: 75mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.nearest_gene.75mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.nearest\_tss.100mer  
*mappa.mm9.nearest\_tss.100mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_tss
- K-Mer Reads: 100mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.nearest_tss.100mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs  
mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.nearest\_tss.36mer  
*mappa.mm9.nearest\_tss.36mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_tss
- K-Mer Reads: 36mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.nearest_tss.36mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

*mappa.mm9.nearest\_tss.40mer*

*mappa.mm9.nearest\_tss.40mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_tss
- K-Mer Reads: 40mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.nearest_tss.40mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

mappa.mm9.nearest\_tss.50mer  
*mappa.mm9.nearest\_tss.50mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_tss
- K-Mer Reads: 50mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.nearest_tss.50mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs  
mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.nearest\_tss.75mer  
*mappa.mm9.nearest\_tss.75mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_tss
- K-Mer Reads: 75mer

These objects are used internally by the chipenrich package.

**Usage**

```
data(mappa.mm9.nearest_tss.75mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

peaks\_E2F4

*ChIP-seq Peaks for the E2F4 Transcription Factor*

---

**Description**

A dataset containing the binding locations (peaks) of the transcription factor E2F4 called from a ChIP-seq experiment

**Usage**

```
peaks_E2F4
```

**Format**

A data frame containing 16,245 peak binding locations. Each row is a peak location, and the 3 variables/columns are chromosome, start peak coordinate, and end peak coordinate. Peak coordinates are in hg19 (UCSC) coordinates.

**Source**

The data and information regarding the experiment can be found in the following publication:

Lee, B. K., A. A. Bhinge, et al. (2011). "Wide-ranging functions of E2F4 in transcriptional activation and repression revealed by genome-wide analysis." *Nucleic Acids Res* 39(9): 3558-3573.

**Examples**

```
# Load E2F4 peak data.
data(peaks_E2F4)

# Print the first 10 peaks in the dataset.
print(head(peaks_E2F4))
```

---

peaks\_H3K4me3\_GM12878 *ChIP-seq Peaks for the Histone Modification H3K4me3 in GM12878*

---

### Description

A dataset containing the binding locations (peaks) of the histone modification H3K4me3 called from a ChIP-seq experiment in the GM12878 cell line

### Usage

```
peaks_H3K4me3_GM12878
```

### Format

A data frame containing 57,476 peak binding locations. Each row is a peak location, and the 3 variables/columns are chromosome, start peak coordinate, and end peak coordinate. Peak coordinates are in hg19 (UCSC) coordinates.

### Source

The data and information regarding the experiment can be found at the following ENCODE URL:

<http://hgdownload.cse.ucsc.edu/goldenPath/hg19/encodeDCC/wgEncodeBroadHistone/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`*tss.dm6 TSS locations*

---

**Description**

A GRanges with all the TSSs for dm6. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

**Usage**`tss.dm6`**Format**

A GRanges object with the following mcols:

**gene\_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene\_3.4.1 and org.Dm.eg.db\_3.5.0.

---

`tss.hg19`*tss.hg19 TSS locations*

---

**Description**

A GRanges with all the TSSs for hg19. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

**Usage**`tss.hg19`**Format**

A GRanges object with the following mcols:

**gene\_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.annotation](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.metadata](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata). EntrezGene

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tss.hg38	<i>tss.hg38 TSS locations</i>
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---

**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	<i>tss.mm10 TSS locations</i>
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---

**Description**

A GRanges with all the TSSs for mm10. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

**Usage**

```
tss.mm10
```

**Format**

A GRanges object with the following mcols:

**gene\_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

**Source**

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M12/gencode.vM12.metadata.EntrezGene.gz

---

tss.mm9

*tss.mm9 TSS locations*

---

**Description**

A GRanges with all the TSSs for mm9. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

**Usage**

tss.mm9

**Format**

A GRanges object with the following mcols:

**gene\_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

**Source**

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene\_3.2.2 and org.Mm.eg.db\_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.metadata.EntrezGene.gz

---

tss.rn4	<i>tss.rn4 TSS locations</i>
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---

**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.

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tss.rn5	<i>tss.rn5 TSS locations</i>
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---

**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>
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**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