

# Package ‘chipenrich.data’

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**Title** Companion package to chipenrich

**Version** 2.31.0

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

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

**Depends** R (>= 3.4.0)

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

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

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

**VignetteBuilder** knitr

**RoxygenNote** 6.1.1

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

---

**Description**

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

**Usage**

```
geneset.GOBP.hsa
```

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

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

---

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

---

**Description**

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

**Usage**

```
geneset.GOBP.mmu
```

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

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

---

geneset.GOBP.rno

*geneset.GOBP.rno genesets for Rattus norvegicus*

---

**Description**

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

**Usage**

geneset.GOBP.rno

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

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

---

geneset.GOCC.dme	<i>geneset.GOCC.dme 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

---

geneset.GOCC.hsa

*geneset.GOCC.hsa genesets for Homo sapiens*

---

**Description**

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

**Usage**

geneset.GOCC.hsa

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

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

---

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

---

### Description

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

### Usage

geneset.GOCC.mmu

### Format

A GeneSet object with the following slots:

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

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

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

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

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

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

### Source

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

---

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

---

### Description

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

### Usage

geneset.GOCC.rno

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

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

---

geneset.GOMF.dme

*geneset.GOMF.dme genesets for Drosophila melanogaster*

---

**Description**

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

**Usage**

geneset.GOMF.dme

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

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

---

geneset.GOMF.dre      *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	<i>geneset.GOMF.mmu genesets for Mus musculus</i>
------------------	---------------------------------------------------

---

**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/genocode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.annotation and ftp://ftp.sanger.ac.uk/pub/genocode/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` and `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz`

---

locusdef.mm9.exon      *locusdef.mm9.exon locus definition*

---

### Description

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

### Usage

locusdef.mm9.exon

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.5.0`. GENCODE resources: `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz` and `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz`

---

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

---

**Description**

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

**Usage**

```
locusdef.mm9.intron
```

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

## Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene\_3.2.2 and org.Mm.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M9/gencode.vM9.annotation.gff3.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M9/gencode.vM9.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz)

---

locusdef.mm9.nearest\_gene

*locusdef.mm9.nearest\_gene locus definition*

---

## Description

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

## Usage

locusdef.mm9.nearest\_gene

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

Built on Fri Apr 13 09:50:37 2018.

## Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene\_3.2.2 and org.Mm.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M9/gencode.vM9.annotation.gff3.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M9/gencode.vM9.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz)

---

locusdef.mm9.nearest\_tss

*locusdef.mm9.nearest\_tss locus definition*


---

### Description

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

### Usage

```
locusdef.mm9.nearest_tss
```

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

Built on Fri Apr 13 09:50:37 2018.

### Source

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.5.0`. GENCODE resources: `ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz` 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	<i>tss.dm6 TSS locations</i>
---------	------------------------------

---

**Description**

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

**Usage**

```
tss.dm6
```

**Format**

A GRanges object with the following mcols:

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

**symbol** The gene symbol for the TSS

**Source**

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

---

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

---

**Description**

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

**Usage**

```
tss.hg19
```

**Format**

A GRanges object with the following mcols:

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

**symbol** The gene symbol for the TSS

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.annotation](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.metadata](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata). EntrezG

---

tss.hg38

*tss.hg38 TSS locations*


---

**Description**

A GRanges with all the TSSs for hg38. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

**Usage**

```
tss.hg38
```

**Format**

A GRanges object with the following mcols:

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

**symbol** The gene symbol for the TSS

**Source**

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene\_3.4.0 and org.Hs.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/gencode.v25.annotation.gff3.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/gencode.v25.metadata](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata). EntrezGene.gz

---

tss.mm10

*tss.mm10 TSS locations*


---

**Description**

A GRanges with all the TSSs for mm10. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

**Usage**

```
tss.mm10
```

**Format**

A GRanges object with the following mcols:

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

**symbol** The gene symbol for the TSS

**Source**

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

---

tss.mm9

*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>
---------	------------------------------

---

**Description**

A GRanges with all the TSSs for rn4. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

**Usage**

```
tss.rn4
```

**Format**

A GRanges object with the following mcols:

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

**symbol** The gene symbol for the TSS

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene\_3.2.2 and org.Rn.eg.db\_3.5.0.

---

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

---

**Description**

A GRanges with all the TSSs for rn5. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

**Usage**

```
tss.rn5
```

**Format**

A GRanges object with the following mcols:

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

**symbol** The gene symbol for the TSS

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.2 and org.Rn.eg.db\_3.5.0.

---

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

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