

# Package ‘chipenrich.data’

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**Title** Companion package to chipenrich

**Version** 2.35.0

**Date** 2023-03-29

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

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

**Depends** R (>= 3.4.0)

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

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

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

**VignetteBuilder** knitr

**RoxygenNote** 6.1.1

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

---

## Description

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

---

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

---

## Description

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

## Usage

`enhancer.dnase_thurman.0`

## Format

A GRanges object with the following `mcols`:

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

**symbol** The gene symbol for the TSS

---

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

---

## Description

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

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

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

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

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

## Usage

```
gene.enh.desc
```

## Format

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

---

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

---

## Description

Class for storing sets of genes and their corresponding metadata.

## Objects from the Class

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

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

## Slots

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

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

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

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

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

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

**Note**

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

**Author(s)**

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**Examples**

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

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

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

---

geneset.biocarta\_pathway.hsa

*geneset.biocarta\_pathway.hsa genesets for BioCarta*

---

**Description**

BioCarta (biocarta\_pathway) genesets. All genesets are required to have  $\geq 10$  Entrez IDs. Built on Mon Oct 16 18:46:04 2017.

**Usage**

geneset.biocarta\_pathway.hsa

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

[https://cgap.nci.nih.gov/Pathways/BioCarta\\_Pathways](https://cgap.nci.nih.gov/Pathways/BioCarta_Pathways)

---

*geneset.biocarta\_pathway.mmu*  
*geneset.biocarta\_pathway.mmu*

---

## Description

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

## Usage

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

## Format

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

## See Also

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

---

*geneset.biocarta\_pathway.rno*  
*geneset.biocarta\_pathway.rno*

---

## Description

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

## Usage

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

## Format

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

## See Also

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

---

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

---

## Description

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

## Usage

`geneset.ctd.hsa`

## Format

A GeneSet object with the following slots:

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

## Source

<http://ctdbase.org>

---

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

---

## Description

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

## Usage

`geneset.ctd.mmu`

## Format

A GeneSet object with the following slots:

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

## Source

<http://ctdbase.org>

---

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

---

## Description

GeneSet object which stores information about sets of genes.

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

## Usage

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

## Format

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

## See Also

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

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

---

geneset.drug\_bank.hsa *geneset.drug\_bank.hsa genesets for DrugBank*

---

### Description

DrugBank (drug\_bank) genesets. All genesets are required to have  $\geq 10$  Entrez IDs. Built on Mon Oct 16 18:46:13 2017.

### Usage

`geneset.drug_bank.hsa`

### Format

A GeneSet object with the following slots:

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

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

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

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

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

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

### Source

<https://www.drugbank.ca>

---

geneset.drug\_bank.mmu *geneset.drug\_bank.mmu*

---

### Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

### Usage

`data(geneset.drug_bank.mmu)`

### Format

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

## See Also

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

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

---

`geneset.drug_bank.rno` *geneset.drug\_bank.rno*

---

## Description

GeneSet object which stores information about sets of genes.

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

## Usage

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

## Format

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

## See Also

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

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

---

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

---

## Description

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

## Usage

```
geneset.GOBP.dme
```

## Format

A GeneSet object with the following slots:

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

## Source

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

---

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

---

## Description

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

## Usage

geneset.GOBP.dre

## Format

A GeneSet object with the following slots:

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

## Source

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

---

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

---

## Description

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

## Usage

`geneset.GOBP.hsa`

## Format

A GeneSet object with the following slots:

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

## Source

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

---

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

---

## Description

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

## Usage

`geneset.GOBP.mmu`

**Format**

A GeneSet object with the following slots:

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

**Source**

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

---

`geneset.GOBP.rno`

*geneset.GOBP.rno genesets for Rattus norvegicus*

---

**Description**

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

**Usage**

`geneset.GOBP.rno`

**Format**

A GeneSet object with the following slots:

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

**Source**

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

---

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

---

## Description

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

## Usage

`geneset.GOCC.dme`

## Format

A GeneSet object with the following slots:

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

## Source

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

---

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

---

## Description

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

## Usage

`geneset.GOCC.dre`

**Format**

A GeneSet object with the following slots:

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

**Source**

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

---

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

---

**Description**

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

**Usage**

`geneset.GOCC.hsa`

**Format**

A GeneSet object with the following slots:

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

**Source**

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

geneset.GOCC.mmu

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

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

**Usage**

geneset.GOCC.mmu

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

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

geneset.GOCC.rno

*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 *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 *genesets for Homo sapiens*

---

## Description

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

## Usage

```
geneset.GOMF.hsa
```

**Format**

A GeneSet object with the following slots:

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

**Source**

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

---

*geneset.GOMF.mmu*

*geneset.GOMF.mmu genesets for Mus musculus*

---

**Description**

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

**Usage**

*geneset.GOMF.mmu*

**Format**

A GeneSet object with the following slots:

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

**Source**

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

---

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

---

## Description

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

## Usage

`geneset.GOMF.rno`

## Format

A GeneSet object with the following slots:

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

## Source

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

---

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

---

## Description

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

## Usage

`geneset.hallmark.hsa`

## Format

A GeneSet object with the following slots:

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

## Source

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

---

geneset.immunologic.hsa

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

---

## Description

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

## Usage

`geneset.immunologic.hsa`

## Format

A GeneSet object with the following slots:

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

**Source**

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

---

geneset.kegg\_pathway.hsa

*geneset.kegg\_pathway.hsa genesets for KEGG Pathways*

---

**Description**

KEGG Pathways (kegg\_pathway) genesets. All genesets are required to have  $\geq 10$  Entrez IDs.  
Built on Mon Oct 16 18:46:53 2017.

**Usage**

`geneset.kegg_pathway.hsa`

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

<http://kegg.jp>

---

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

---

## Description

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

## Usage

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

## Format

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

## See Also

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

---

---

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

---

## Description

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

## Usage

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

## Format

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

## See Also

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

---

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

---

### Description

GeneSet object which stores information about sets of genes.

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

### Usage

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

### Format

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

### See Also

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

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

---

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

---

### Description

GeneSet object which stores information about sets of genes.

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

### Usage

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

### Format

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

### See Also

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

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

---

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

---

### Description

GeneSet object which stores information about sets of genes.

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

### Usage

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

### Format

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

### See Also

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

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

---

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

---

### Description

GeneSet object which stores information about sets of genes.

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

### Usage

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

### Format

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

### See Also

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

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

---

`geneset.metabolite.mmu`

*geneset.metabolite.mmu*

---

## Description

GeneSet object which stores information about sets of genes.

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

## Usage

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

## Format

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

## See Also

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

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

---

---

`geneset.metabolite.rno`

*geneset.metabolite.rno*

---

## Description

GeneSet object which stores information about sets of genes.

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

## Usage

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

## Format

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

## See Also

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

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

---

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

---

## Description

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

## Usage

```
geneset.microrna.hsa
```

## Format

A GeneSet object with the following slots:

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

## Source

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

---

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

---

## Description

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

## Usage

```
geneset.oncogenic.hsa
```

## Format

A GeneSet object with the following slots:

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

## Source

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

---

geneset.panther\_pathway.hsa  
*geneset.panther\_pathway.hsa*

---

## Description

GeneSet object which stores information about sets of genes.

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

## Usage

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

## Format

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

## See Also

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

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

---

`geneset.panther_pathway.mmu`  
*geneset.panther\_pathway.mmu*

---

## Description

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

## Usage

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

## Format

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

## See Also

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

---

`geneset.panther_pathway.rno`  
*geneset.panther\_pathway.rno*

---

## Description

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

## Usage

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

## Format

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

## See Also

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

---

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

---

**Description**

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

**Usage**

```
geneset.pfam.hsa
```

**Format**

A GeneSet object with the following slots:

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

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

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

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

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

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

**Source**

<http://pfam.xfam.org>

---

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

---

**Description**

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

**Usage**

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

**Format**

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

## See Also

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

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

---

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

---

## Description

GeneSet object which stores information about sets of genes.

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

## Usage

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

## Format

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

## See Also

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

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

---

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

---

## Description

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

## Usage

```
geneset.protein_interaction_biogrid.hsa
```

## Format

A GeneSet object with the following slots:

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

## Source

<https://thebiogrid.org>

---

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

---

## Description

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

## Usage

`geneset.reactome.dme`

## Format

A GeneSet object with the following slots:

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

## Source

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

---

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

---

## Description

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

## Usage

```
geneset.reactome.dre
```

## Format

A GeneSet object with the following slots:

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

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

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

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

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

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

## Source

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

---

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

---

## Description

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

## Usage

```
geneset.reactome.hsa
```

## Format

A GeneSet object with the following slots:

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

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

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

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

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

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

## Source

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

---

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

---

## Description

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

## Usage

`geneset.reactome.mmu`

## Format

A GeneSet object with the following slots:

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

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

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

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

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

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

## Source

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

---

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

---

## Description

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

## Usage

geneset.reactome.rno

## Format

A GeneSet object with the following slots:

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

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

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

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

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

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

## Source

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

---

```
geneset.transcription_factors.hsa
```

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

---

## Description

Transcription Factor Targets (MSigDB) (transcription\_factors) genesets. All genesets are required to have >= 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.

---

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

---

**Description**

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

**Usage**

`locusdef.dm3.10kb`

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

```
locusdef_dm3.10kb_outside
```

*locusdef\_dm3.10kb\_outside locus definition*

---

## Description

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

## Usage

```
locusdef_dm3.10kb_outside
```

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

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

## Source

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

---

```
locusdef_dm3.10kb_outside_upstream
```

*locusdef\_dm3.10kb\_outside\_upstream locus definition*

---

## Description

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

**Usage**

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

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

*locusdef.dm3.1kb*

*locusdef.dm3.1kb locus definition*

---

**Description**

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

**Usage**

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

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

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

## Source

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

---

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

---

## Description

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

## Usage

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

## Format

A LocusDefinition object with the following slots:

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

## Details

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

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

## Source

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

---

locusdef.dm3.1kb\_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 `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

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

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

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

## Details

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

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

## Source

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

---

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

---

## Description

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

## Usage

locusdef.dm3.5kb

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

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

## Source

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

---

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

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

---

## Description

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

## Usage

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

## Format

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

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

---

**Description**

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

**Usage**

`locusdef.dm3.5kb_outside_upstream`

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

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

---

### Description

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

### Usage

```
locusdef.dm3.exon
```

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

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

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

### Source

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

---

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

---

### Description

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

### Usage

```
locusdef.dm3.intron
```

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

`locusdef.dm3.nearest_gene`

*locusdef.dm3.nearest\_gene locus definition*

**Description**

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

**Usage**

`locusdef.dm3.nearest_gene`

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

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

## Source

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

---

locusdef.dm3.nearest\_tss

*locusdef.dm3.nearest\_tss locus definition*

---

## Description

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

## Usage

locusdef.dm3.nearest\_tss

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

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

## Source

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

---

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

---

## Description

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

## Usage

`locusdef.dm6.10kb`

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

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

## Source

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

---

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

---

## Description

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

## Usage

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

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

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

## Source

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

---

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

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

---

## Description

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

## Usage

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

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

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

## Source

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

---

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

---

## Description

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

## Usage

`locusdef.dm6.1kb`

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

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

## Source

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

---

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

*locusdef.dm6.1kb\_outside locus definition*

---

## Description

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

## Usage

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

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

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

## Source

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

---

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

*locusdef.dm6.1kb\_outside\_upstream locus definition*

---

## Description

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

**Usage**

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

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

*locusdef.dm6.5kb*

*locusdef.dm6.5kb locus definition*

**Description**

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

**Usage**

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

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

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

## Source

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

---

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

---

## Description

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

## Usage

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

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

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

## Source

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

---

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

---

## Description

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

## Usage

locusdef.dm6.5kb\_outside\_upstream

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

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

## Source

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

---

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

---

## Description

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

## Usage

locusdef.dm6.exon

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

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

## Source

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

---

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

---

## Description

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

## Usage

locusdef.dm6.intron

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

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

**Source**

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

---

```
locusdef.dm6.nearest_gene
```

*locusdef.dm6.nearest\_gene locus definition*

---

**Description**

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

**Usage**

```
locusdef.dm6.nearest_gene
```

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

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

**Source**

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

---

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

---

## Description

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

## Usage

```
locusdef.dm6.nearest_tss
```

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

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

## Source

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

---

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

---

## Description

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

## Usage

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

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

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

---

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

---

**Description**

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

**Usage**

`locusdef.hg19.10kb_outside`

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

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](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.metadata](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata).EntrezGene

---

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

---

## Description

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

## Usage

locusdef.hg19.1kb

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

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

---

## Description

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

## Usage

locusdef.hg19.1kb\_outside

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

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

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

---

locusdef.hg19.nearest\_tss

*locusdef.hg19.nearest\_tss locus definition*

---

## Description

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

## Usage

locusdef.hg19.nearest\_tss

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.annotation](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](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](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/gencode.v25.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz)

---

locusdef.hg38.10kb\_outside

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

---

## Description

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

## Usage

locusdef.hg38.10kb\_outside

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

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

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

---

## Description

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

## Usage

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

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

R packages: `TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0` and `org.Hs.eg.db_3.5.0`. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/gencode.v25.annotation.gff3.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/gencode.v25.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz)

---

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

*locusdef.hg38.1kb locus definition*

---

## Description

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

## Usage

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

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

`locusdef.hg38.1kb_outside`

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

---

## Description

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

## Usage

`locusdef.hg38.1kb_outside`

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

locusdef.hg38.1kb\_outside\_upstream

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

---

## Description

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

## Usage

locusdef.hg38.1kb\_outside\_upstream

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

locusdef.hg38.5kb      *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](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/gencode.v25.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz)

---

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

---

### Description

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

### Usage

locusdef.hg38.5kb\_outside

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

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

---

## Description

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

## Usage

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

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

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

---

## Description

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

## Usage

locusdef.hg38.exon

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

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

---

### Description

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

### Usage

```
locusdef.hg38.intron
```

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

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

### Source

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

---

locusdef.mm10.10kb      *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](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz)

---

```
locusdef.mm10.10kb_outside
```

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

---

## Description

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

## Usage

```
locusdef.mm10.10kb_outside
```

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

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

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

---

## Description

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

**Usage**

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

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.annotation.gff3.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz)

---

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

*locusdef.mm10.1kb locus definition*

---

**Description**

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

**Usage**

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

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.annotation.gff3.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz)

---

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

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

---

**Description**

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

**Usage**

`locusdef.mm10.1kb_outside`

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.annotation.gff3.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz)

---

```
locusdef.mm10.1kb_outside_upstream
```

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

---

## Description

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

## Usage

```
locusdef.mm10.1kb_outside_upstream
```

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.annotation.gff3.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz)

---

```
locusdef.mm10.5kb
```

*locusdef.mm10.5kb locus definition*

---

## Description

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

## Usage

```
locusdef.mm10.5kb
```

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

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

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

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

**Description**

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

**Usage**

`locusdef.mm10.5kb_outside`

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.annotation.gff3.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz)

---

`locusdef.mm10.5kb_outside_upstream`

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

---

## Description

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

## Usage

`locusdef.mm10.5kb_outside_upstream`

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.annotation.gff3.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz)

---

locusdef.mm10.exon      *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](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.intron      *locusdef.mm10.intron locus definition*

---

## Description

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

## Usage

locusdef.mm10.intron

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.annotation.gff3.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz)

---

```
locusdef.mm10.nearest_gene
  locusdef.mm10.nearest_gene locus definition
```

---

## Description

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

## Usage

```
locusdef.mm10.nearest_gene
```

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.annotation.gff3.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz)

---

```
locusdef.mm10.nearest_tss
```

*locusdef.mm10.nearest\_tss locus definition*

---

## Description

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

## Usage

```
locusdef.mm10.nearest_tss
```

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.annotation.gff3.gz](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.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](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M9/gencode.vM9.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz)

---

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

---

## Description

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

## Usage

```
locusdef.mm9.10kb_outside
```

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

Built on Fri Apr 13 09:50:44 2018.

## Source

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

---

locusdef.mm9.10kb\_outside\_upstream  
*locusdef.mm9.10kb\_outside\_upstream locus definition*

---

## Description

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

## Usage

locusdef.mm9.10kb\_outside\_upstream

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

Built on Fri Apr 13 09:50:44 2018.

## Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene\_3.2.2 and org.Mm.eg.db\_3.5.0. GEN-CODE 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

*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. GEN-CODE 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**

*locusdef.mm9.1kb\_outside locus definition*

---

## Description

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

## Usage

`locusdef.mm9.1kb_outside`

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

Built on Fri Apr 13 09:50:42 2018.

## Source

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.5.0`. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M9/gencode.vM9.annotation.gff3.gz](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](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M9/gencode.vM9.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz)

---

**locusdef.mm9.5kb\_outside**

*locusdef.mm9.5kb\_outside locus definition*

---

**Description**

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

**Usage**

**locusdef.mm9.5kb\_outside**

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Fri Apr 13 09:50:43 2018.

**Source**

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

---

```
locusdef.mm9.5kb_outside_upstream
```

*locusdef.mm9.5kb\_outside\_upstream locus definition*

---

## Description

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

## Usage

```
locusdef.mm9.5kb_outside_upstream
```

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

Built on Fri Apr 13 09:50:43 2018.

## Source

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.5.0`. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M9/gencode.vM9.annotation.gff3.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M9/gencode.vM9.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz)

---

```
locusdef.mm9.exon
```

*locusdef.mm9.exon locus definition*

---

## Description

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

## Usage

```
locusdef.mm9.exon
```

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

**Source**

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene\_3.2.2 and org.Mm.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M9/gencode.vM9.annotation.gff3.gz](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.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 `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

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

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

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

## Details

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

## Source

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

---

`locusdef.mm9.nearest_tss`

*locusdef.mm9.nearest\_tss locus definition*

---

## Description

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

## Usage

`locusdef.mm9.nearest_tss`

## Format

A LocusDefinition object with the following slots:

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

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

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

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

## Details

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

## Source

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.5.0`. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M9/gencode.vM9.annotation.gff3.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M9/gencode.vM9.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz)

---

`locusdef.rn4.10kb`

*locusdef.rn4.10kb locus definition*

---

## Description

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

## Usage

`locusdef.rn4.10kb`

## Format

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn4`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

## Details

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

## Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

---

```
locusdef.rn4.10kb_outside
  locusdef.rn4.10kb_outside locus definition
```

---

## Description

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

## Usage

```
locusdef.rn4.10kb_outside
```

## Format

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn4`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:03 2018.

**Source**

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

---

```
locusdef.rn4.10kb_outside_upstream
```

*locusdef.rn4.10kb\_outside\_upstream locus definition*

---

**Description**

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

**Usage**

```
locusdef.rn4.10kb_outside_upstream
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, rn4.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

**Details**

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

**Source**

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

---

locusdef.rn4.1kb      *locusdef.rn4.1kb locus definition*

---

## Description

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

## Usage

locusdef.rn4.1kb

## Format

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, rn4.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

## Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

## Source

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

---

locusdef.rn4.1kb\_outside      *locusdef.rn4.1kb\_outside locus definition*

---

## Description

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

**Usage**

```
locusdef.rn4.1kb_outside
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn4`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

**Source**

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

*locusdef.rn4.1kb\_outside\_upstream*

*locusdef.rn4.1kb\_outside\_upstream locus definition*

**Description**

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

**Usage**

```
locusdef.rn4.1kb_outside_upstream
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn4`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

## Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

## Source

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

---

locusdef.rn4.5kb      *locusdef.rn4.5kb locus definition*

---

## Description

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

## Usage

locusdef.rn4.5kb

## Format

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, rn4.

**organism** A character indicating the organism name. In this case, *Rattus norvegicus*.

## Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

## Source

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

---

```
locusdef.rn4.5kb_outside
```

*locusdef.rn4.5kb\_outside locus definition*

---

## Description

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

## Usage

```
locusdef.rn4.5kb_outside
```

## Format

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn4`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

## Details

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

## Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

---

```
locusdef.rn4.5kb_outside_upstream
```

*locusdef.rn4.5kb\_outside\_upstream locus definition*

---

## Description

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

**Usage**

```
locusdef.rn4.5kb_outside_upstream
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, rn4.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

**Details**

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

**Source**

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

---

locusdef.rn4.exon      *locusdef.rn4.exon* locus definition

---

**Description**

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

**Usage**

```
locusdef.rn4.exon
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, rn4.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

**Details**

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:51:59 2018.

**Source**

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

---

`locusdef.rn4.intron`    *locusdef.rn4.intron* locus definition

---

**Description**

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

**Usage**

`locusdef.rn4.intron`

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, rn4.

**organism** A character indicating the organism name. In this case, *Rattus norvegicus*.

**Details**

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:00 2018.

**Source**

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

---

```
locusdef.rn4.nearest_gene
```

*locusdef.rn4.nearest\_gene locus definition*

---

## Description

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

## Usage

```
locusdef.rn4.nearest_gene
```

## Format

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn4`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

## Details

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:51:58 2018.

## Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

---

```
locusdef.rn4.nearest_tss
```

*locusdef.rn4.nearest\_tss locus definition*

---

## Description

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

**Usage**

```
locusdef.rn4.nearest_tss
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn4`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:51:58 2018.

**Source**

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

*locusdef.rn5.10kb*

*locusdef.rn5.10kb locus definition*

**Description**

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

**Usage**

```
locusdef.rn5.10kb
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn5`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

## Details

Built on Fri Apr 13 09:52:20 2018.

## Source

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

---

```
locusdef.rn5.10kb_outside
  locusdef.rn5.10kb_outside locus definition
```

---

## Description

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

## Usage

```
locusdef.rn5.10kb_outside
```

## Format

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, rn5.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:21 2018.

## Source

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

---

```
locusdef.rn5.10kb_outside_upstream
  locusdef.rn5.10kb_outside_upstream locus definition
```

---

## Description

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

## Usage

```
locusdef.rn5.10kb_outside_upstream
```

## Format

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, `rn5`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

## Details

Built on Fri Apr 13 09:52:21 2018.

## Source

R packages: `TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2` and `org.Rn.eg.db_3.5.0`.

---

```
locusdef.rn5.1kb      locusdef.rn5.1kb locus definition
```

---

## Description

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

## Usage

```
locusdef.rn5.1kb
```

## Format

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, rn5.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:19 2018.

## Source

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

---

locusdef.rn5.1kb\_outside

*locusdef.rn5.1kb\_outside locus definition*

---

## Description

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

## Usage

locusdef.rn5.1kb\_outside

## Format

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, rn5.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:19 2018.

**Source**

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

---

**locusdef.rn5.1kb\_outside\_upstream**

*locusdef.rn5.1kb\_outside\_upstream locus definition*

---

**Description**

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

**Usage**

`locusdef.rn5.1kb_outside_upstream`

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A character indicating the genome build. In this case, `rn5`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

**Details**

Built on Fri Apr 13 09:52:19 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.2 and org.Rn.eg.db\_3.5.0.

---

```
locusdef.rn5.5kb      locusdef.rn5.5kb locus definition
```

---

### Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

### Usage

```
locusdef.rn5.5kb
```

### Format

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn5.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

### Details

Built on Fri Apr 13 09:52:20 2018.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.2 and org.Rn.eg.db\_3.5.0.

---

```
locusdef.rn5.5kb_outside
locusdef.rn5.5kb_outside locus definition
```

---

### Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

### Usage

```
locusdef.rn5.5kb_outside
```

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn5.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

**Details**

Built on Fri Apr 13 09:52:20 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.2 and org.Rn.eg.db\_3.5.0.

---

`locusdef.rn5.5kb_outside_upstream`

*locusdef.rn5.5kb\_outside\_upstream locus definition*

---

**Description**

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

**Usage**

`locusdef.rn5.5kb_outside_upstream`

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn5.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

**Details**

Built on Fri Apr 13 09:52:20 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.2 and org.Rn.eg.db\_3.5.0.

---

locusdef.rn5.exon      *locusdef.rn5.exon locus definition*

---

**Description**

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

**Usage**

locusdef.rn5.exon

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn5.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

**Details**

Built on Fri Apr 13 09:52:17 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.2 and org.Rn.eg.db\_3.5.0.

---

locusdef.rn5.intron      *locusdef.rn5.intron locus definition*

---

**Description**

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

**Usage**

locusdef.rn5.intron

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn5.

**organism** A character indicating the organism name. In this case, *Rattus norvegicus*.

**Details**

Built on Fri Apr 13 09:52:19 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.2 and org.Rn.eg.db\_3.5.0.

---

**locusdef.rn5.nearest\_gene**  
*locusdef.rn5.nearest\_gene locus definition*

---

**Description**

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

**Usage**

**locusdef.rn5.nearest\_gene**

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn5.

**organism** A character indicating the organism name. In this case, *Rattus norvegicus*.

**Details**

Built on Fri Apr 13 09:52:16 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.2 and org.Rn.eg.db\_3.5.0.

---

**locusdef.rn5.nearest\_tss**  
*locusdef.rn5.nearest\_tss locus definition*

---

**Description**

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

**Usage**

```
locusdef.rn5.nearest_tss
```

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn5.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

**Details**

Built on Fri Apr 13 09:52:16 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.2 and org.Rn.eg.db\_3.5.0.

---

`locusdef.rn6.10kb` *locusdef.rn6.10kb locus definition*

---

### Description

A LocusDefinition where a gene locus is defined within 10kb upstream and downstream of the TSS.

### Usage

`locusdef.rn6.10kb`

### Format

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A character indicating the genome build. In this case, `rn6`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

### Details

Built on Fri Apr 13 09:52:39 2018.

### Source

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

---

`locusdef.rn6.10kb_outside`  
*locusdef.rn6.10kb\_outside locus definition*

---

### Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

### Usage

`locusdef.rn6.10kb_outside`

## Format

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn6.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:40 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.1 and org.Rn.eg.db\_3.5.0.

---

```
locusdef.rn6.10kb_outside_upstream
  locusdef.rn6.10kb_outside_upstream locus definition
```

---

## Description

A LocusDefinition where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

## Usage

```
locusdef.rn6.10kb_outside_upstream
```

## Format

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn6.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:39 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.1 and org.Rn.eg.db\_3.5.0.

---

**locusdef.rn6.1kb**      *locusdef.rn6.1kb locus definition*

---

**Description**

A LocusDefinition where a gene locus is defined within 1kb upstream and downstream of the TSS.

**Usage**

**locusdef.rn6.1kb**

**Format**

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn6.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

**Details**

Built on Fri Apr 13 09:52:38 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.1 and org.Rn.eg.db\_3.5.0.

---

```
locusdef.rn6.1kb_outside
```

*locusdef.rn6.1kb\_outside locus definition*

---

## Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

## Usage

```
locusdef.rn6.1kb_outside
```

## Format

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A character indicating the genome build. In this case, `rn6`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

## Details

Built on Fri Apr 13 09:52:38 2018.

## Source

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

---

```
locusdef.rn6.1kb_outside_upstream
```

*locusdef.rn6.1kb\_outside\_upstream locus definition*

---

## Description

A LocusDefinition where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

## Usage

```
locusdef.rn6.1kb_outside_upstream
```

## Format

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn6.

**organism** A character indicating the organism name. In this case, *Rattus norvegicus*.

## Details

Built on Fri Apr 13 09:52:38 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.1 and org.Rn.eg.db\_3.5.0.

---

**locusdef.rn6.5kb**      *locusdef.rn6.5kb locus definition*

---

## Description

A LocusDefinition where a gene locus is defined within 5kb upstream and downstream of the TSS.

## Usage

**locusdef.rn6.5kb**

## Format

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn6.

**organism** A character indicating the organism name. In this case, *Rattus norvegicus*.

## Details

Built on Fri Apr 13 09:52:38 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.1 and org.Rn.eg.db\_3.5.0.

---

```
locusdef.rn6.5kb_outside
  locusdef.rn6.5kb_outside locus definition
```

---

## Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

## Usage

```
locusdef.rn6.5kb_outside
```

## Format

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A character indicating the genome build. In this case, `rn6`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

## Details

Built on Fri Apr 13 09:52:39 2018.

## Source

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

---

```
locusdef.rn6.5kb_outside_upstream
  locusdef.rn6.5kb_outside_upstream locus definition
```

---

## Description

A LocusDefinition where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

## Usage

```
locusdef.rn6.5kb_outside_upstream
```

## Format

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn6.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:39 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.1 and org.Rn.eg.db\_3.5.0.

---

locusdef.rn6.exon      *locusdef.rn6.exon* locus definition

---

## Description

A LocusDefinition where a gene locus is defined as the exons belonging to genes.

## Usage

locusdef.rn6.exon

## Format

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn6.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:36 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.1 and org.Rn.eg.db\_3.5.0.

---

```
locusdef.rn6.intron      locusdef.rn6.intron locus definition
```

---

## Description

A LocusDefinition where a gene locus is defined as the introns belonging to genes.

## Usage

```
locusdef.rn6.intron
```

## Format

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with `ncols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A character indicating the genome build. In this case, `rn6`.

**organism** A character indicating the organism name. In this case, `Rattus norvegicus`.

## Details

Built on Fri Apr 13 09:52:37 2018.

## Source

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

---

```
locusdef.rn6.nearest_gene
      locusdef.rn6.nearest_gene locus definition
```

---

## Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

## Usage

```
locusdef.rn6.nearest_gene
```

## Format

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn6.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:35 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.1 and org.Rn.eg.db\_3.5.0.

---

locusdef.rn6.nearest\_tss

*locusdef.rn6.nearest\_tss locus definition*

---

## Description

A LocusDefinition where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

## Usage

locusdef.rn6.nearest\_tss

## Format

A LocusDefinition object with the following slots:

**granges** A GRanges of the locus definitions with mcols for Entrez Gene ID gene\_id and gene symbol symbol

**dframe** A data.frame of the locus definitions with columns for chr, start, end, gene\_id, and symbol

**genome.build** A character indicating the genome build. In this case, rn6.

**organism** A character indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:34 2018.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.1 and org.Rn.eg.db\_3.5.0.

---

LocusDefinition-class *Class "LocusDefinition"*

---

**Description**

A storage class representing gene locus definitions and their corresponding metadata.

**Objects from the Class**

Objects can be created by calls of the form `new("LocusDefinition")`. These objects are used internally by the `chipenrich` package and users will not likely need to create these.

**Slots**

**dframe:** Object of class `"data.frame"`. Each row represents a locus for a particular geneid.  
**granges:** Object of class `"GenomicRanges"`. Locus definitions stored as a `GenomicRanges` object.  
**genome.build:** Object of class `"character"`. Genome build these definitions were generated from.  
**organism:** Object of class `"character"`. Organism code.

**Note**

Not typically accessed by the user - this is used internally by the `chipenrich` package.

**Author(s)**

Ryan Welch <welchr@umich.edu>

**Examples**

```
# Show info about the class.
showClass("LocusDefinition");

# Example of what a locus definition object looks like.
data(locusdef.mm9.nearest_tss)
lapply(attributes(locusdef.mm9.nearest_tss), head)
```

---

**mappa.hg19.10kb.100mer**  
*mappa.hg19.10kb.100mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.10kb.100mer)
```

## Format

A data frame containing:

```
geneid Entrez Gene IDs  
mappa Gene locus mappability
```

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

**mappa.hg19.10kb.24mer** *mappa.hg19.10kb.24mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.10kb.24mer)
```

**Format**

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.10kb.36mer` *mappa.hg19.10kb.36mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.10kb.36mer)
```

**Format**

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.10kb.40mer` *mappa.hg19.10kb.40mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.10kb.40mer)
```

## Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.10kb.50mer` *mappa.hg19.10kb.50mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.10kb.50mer)
```

**Format**

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

*mappa.hg19.10kb.75mer mappa.hg19.10kb.75mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.10kb.75mer)
```

**Format**

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.1kb.100mer` *mappa.hg19.1kb.100mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.1kb.100mer)
```

## Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.1kb.24mer` *mappa.hg19.1kb.24mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.1kb.24mer)
```

**Format**

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.1kb.36mer`    *mappa.hg19.1kb.36mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.1kb.36mer)
```

**Format**

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.1kb.40mer` *mappa.hg19.1kb.40mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.1kb.40mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs  
`mappa` Gene locus mappability

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.1kb.50mer` *mappa.hg19.1kb.50mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.1kb.50mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.hg19.1kb.75mer mappa.hg19.1kb.75mer

---

**Description**

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.1kb.75mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.5kb.100mer` *mappa.hg19.5kb.100mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.5kb.100mer)
```

## Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.5kb.24mer` *mappa.hg19.5kb.24mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.5kb.24mer)
```

**Format**

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.5kb.36mer`    *mappa.hg19.5kb.36mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.5kb.36mer)
```

**Format**

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.5kb.40mer` *mappa.hg19.5kb.40mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.5kb.40mer)
```

## Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.5kb.50mer` *mappa.hg19.5kb.50mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.5kb.50mer)
```

**Format**

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.5kb.75mer` *mappa.hg19.5kb.75mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.5kb.75mer)
```

**Format**

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

**mappa.hg19.exon.100mer**  
*mappa.hg19.exon.100mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.exon.100mer)
```

## Format

A data frame containing:

```
geneid Entrez Gene IDs  
mappa Gene locus mappability
```

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

**mappa.hg19.exon.24mer** *mappa.hg19.exon.24mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.exon.24mer)
```

**Format**

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.exon.36mer` *mappa.hg19.exon.36mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.exon.36mer)
```

**Format**

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.exon.40mer` *mappa.hg19.exon.40mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.exon.40mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs  
`mappa` Gene locus mappability

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.exon.50mer` *mappa.hg19.exon.50mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.exon.50mer)
```

**Format**

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

*mappa.hg19.exon.75mer mappa.hg19.exon.75mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.exon.75mer)
```

**Format**

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.intron.100mer`  
*mappa.hg19.intron.100mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.intron.100mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs  
`mappa` Gene locus mappability

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.intron.24mer`  
*mappa.hg19.intron.24mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.intron.24mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.hg19.intron.36mer

*mappa.hg19.intron.36mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.intron.36mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.intron.40mer`  
*mappa.hg19.intron.40mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.intron.40mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs  
`mappa` Gene locus mappability

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.intron.50mer`  
*mappa.hg19.intron.50mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.intron.50mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.hg19.intron.75mer

*mappa.hg19.intron.75mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.intron.75mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.nearest_gene.100mer`  
*mappa.hg19.nearest\_gene.100mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest\_gene
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.nearest_gene.100mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs  
`mappa` Gene locus mappability

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.nearest_gene.24mer`  
*mappa.hg19.nearest\_gene.24mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest\_gene
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.nearest_gene.24mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

*mappa.hg19.nearest\_gene.36mer*

*mappa.hg19.nearest\_gene.36mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest\_gene
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.nearest_gene.36mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.nearest_gene.40mer`  
*mappa.hg19.nearest\_gene.40mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest\_gene
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.nearest_gene.40mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs  
`mappa` Gene locus mappability

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.nearest_gene.50mer`  
*mappa.hg19.nearest\_gene.50mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest\_gene
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.nearest_gene.50mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

*mappa.hg19.nearest\_gene.75mer*

*mappa.hg19.nearest\_gene.75mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest\_gene
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.nearest_gene.75mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.nearest_tss.100mer`  
*mappa.hg19.nearest\_tss.100mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest\_tss
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.nearest_tss.100mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs  
`mappa` Gene locus mappability

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.nearest_tss.24mer`  
*mappa.hg19.nearest\_tss.24mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest\_tss
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.nearest_tss.24mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.hg19.nearest\_tss.36mer

*mappa.hg19.nearest\_tss.36mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest\_tss
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.nearest_tss.36mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.nearest_tss.40mer`  
*mappa.hg19.nearest\_tss.40mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest\_tss
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.nearest_tss.40mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs  
`mappa` Gene locus mappability

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.hg19.nearest_tss.50mer`  
*mappa.hg19.nearest\_tss.50mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest\_tss
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.nearest_tss.50mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.hg19.nearest\_tss.75mer

*mappa.hg19.nearest\_tss.75mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest\_tss
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.hg19.nearest_tss.75mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.10kb.100mer` *mappa.mm9.10kb.100mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.mm9.10kb.100mer)
```

## Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.10kb.36mer` *mappa.mm9.10kb.36mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.10kb.36mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

*mappa.mm9.10kb.40mer*    *mappa.mm9.10kb.40mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.10kb.40mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.10kb.50mer` *mappa.mm9.10kb.50mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.mm9.10kb.50mer)
```

## Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.10kb.75mer` *mappa.mm9.10kb.75mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.10kb.75mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

*mappa.mm9.1kb.100mer*    *mappa.mm9.1kb.100mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.1kb.100mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.1kb.36mer`    *mappa.mm9.1kb.36mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.mm9.1kb.36mer)
```

## Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.1kb.40mer`    *mappa.mm9.1kb.40mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.1kb.40mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

*mappa.mm9.1kb.50mer*      *mappa.mm9.1kb.50mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.1kb.50mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.1kb.75mer`    *mappa.mm9.1kb.75mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.mm9.1kb.75mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs  
`mappa` Gene locus mappability

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.5kb.100mer`    *mappa.mm9.5kb.100mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.5kb.100mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

*mappa.mm9.5kb.36mer*      *mappa.mm9.5kb.36mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.5kb.36mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.5kb.40mer`      *mappa.mm9.5kb.40mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.5kb.40mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs  
`mappa` Gene locus mappability

### Author(s)

Ryan Welch <welchr@umich.edu>

### See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.5kb.50mer`      *mappa.mm9.5kb.50mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.5kb.50mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.5kb.75mer      *mappa.mm9.5kb.75mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.5kb.75mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.exon.100mer` *mappa.mm9.exon.100mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.mm9.exon.100mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs  
`mappa` Gene locus mappability

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.exon.36mer` *mappa.mm9.exon.36mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.exon.36mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

*mappa.mm9.exon.40mer*    *mappa.mm9.exon.40mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.exon.40mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.exon.50mer` *mappa.mm9.exon.50mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.mm9.exon.50mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs  
`mappa` Gene locus mappability

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.exon.75mer` *mappa.mm9.exon.75mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.exon.75mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs  
mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.intron.100mer

*mappa.mm9.intron.100mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.intron.100mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs  
mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.intron.36mer`  
*mappa.mm9.intron.36mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.intron.36mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs  
`mappa` Gene locus mappability

### Author(s)

Ryan Welch <welchr@umich.edu>

### See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.intron.40mer`  
*mappa.mm9.intron.40mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.intron.40mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs  
mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

mappa.mm9.intron.50mer

*mappa.mm9.intron.50mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.intron.50mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs  
mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.intron.75mer`  
*mappa.mm9.intron.75mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.intron.75mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs  
`mappa` Gene locus mappability

### Author(s)

Ryan Welch <welchr@umich.edu>

### See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.nearest_gene.100mer`  
*mappa.mm9.nearest\_gene.100mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_gene
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.nearest_gene.100mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.nearest_gene.36mer`

*mappa.mm9.nearest\_gene.36mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_gene
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.nearest_gene.36mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.nearest_gene.40mer`  
*mappa.mm9.nearest\_gene.40mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_gene
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.mm9.nearest_gene.40mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs  
`mappa` Gene locus mappability

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.nearest_gene.50mer`  
*mappa.mm9.nearest\_gene.50mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_gene
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.nearest_gene.50mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.nearest_gene.75mer`

*mappa.mm9.nearest\_gene.75mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_gene
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.nearest_gene.75mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.nearest_tss.100mer`  
*mappa.mm9.nearest\_tss.100mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_tss
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.mm9.nearest_tss.100mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs  
`mappa` Gene locus mappability

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

`mappa.mm9.nearest_tss.36mer`  
*mappa.mm9.nearest\_tss.36mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_tss
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.nearest_tss.36mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

*mappa.mm9.nearest\_tss.40mer*

*mappa.mm9.nearest\_tss.40mer*

---

**Description**

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_tss
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.nearest_tss.40mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

```
mappa.mm9.nearest_tss.50mer
mappa.mm9.nearest_tss.50mer
```

---

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_tss
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.mm9.nearest_tss.50mer)
```

## Format

A data frame containing:

```
geneid Entrez Gene IDs
mappa Gene locus mappability
```

## Author(s)

Ryan Welch <welchr@umich.edu>

## See Also

For more information about gene locus definitions: [chipenrich.data](#)

---

```
mappa.mm9.nearest_tss.75mer
mappa.mm9.nearest_tss.75mer
```

---

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest\_tss
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

**Usage**

```
data(mappa.mm9.nearest_tss.75mer)
```

**Format**

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

**Author(s)**

Ryan Welch <welchr@umich.edu>

**See Also**

For more information about gene locus definitions: [chipenrich.data](#)

---

peaks\_E2F4

*ChIP-seq Peaks for the E2F4 Transcription Factor*

---

**Description**

A dataset containing the binding locations (peaks) of the transcription factor E2F4 called from a ChIP-seq experiment

**Usage**

```
peaks_E2F4
```

**Format**

A data frame containing 16,245 peak binding locations. Each row is a peak location, and the 3 variables/columns are chromosome, start peak coordinate, and end peak coordinate. Peak coordinates are in hg19 (UCSC) coordinates.

**Source**

The data and information regarding the experiment can be found in the following publication:

Lee, B. K., A. A. Bhinge, et al. (2011). "Wide-ranging functions of E2F4 in transcriptional activation and repression revealed by genome-wide analysis." Nucleic Acids Res 39(9): 3558-3573.

**Examples**

```
# Load E2F4 peak data.  
data(peaks_E2F4)  
  
# Print the first 10 peaks in the dataset.  
print(head(peaks_E2F4))
```

---

**peaks\_H3K4me3\_GM12878** *ChIP-seq Peaks for the Histone Modification H3K4me3 in GM12878*

---

**Description**

A dataset containing the binding locations (peaks) of the histone modification H3K4me3 called from a ChIP-seq experiment in the GM12878 cell line

**Usage**

```
peaks_H3K4me3_GM12878
```

**Format**

A data frame containing 57,476 peak binding locations. Each row is a peak location, and the 3 variables/columns are chromosome, start peak coordinate, and end peak coordinate. Peak coordinates are in hg19 (UCSC) coordinates.

**Source**

The data and information regarding the experiment can be found at the following ENCODE URL:

<http://hgdownload.cse.ucsc.edu/goldenPath/hg19/encodeDCC/wgEncodeBroadHistone/wgEncodeBroadHistoneGm12878H3K4me3>

**Examples**

```
# Load H3K4me3 in GM12878 peak data.
data(peaks_H3K4me3_GM12878)

# Print the first 10 peaks in the dataset.
print(head(peaks_H3K4me3_GM12878))
```

---

**spline.log\_dtss.90ENCODE**

*DTSS Spline adjustment*

---

**Description**

A mgcv:::gam object on a combined data of 90 ENCODE ChIP-seq datasets that modeled the relationship between a gene's locus length the distance from a peak to the gene's transcription start site, using a cubic spline. This is used to adjust for the proximity to TSSes test.

**Usage**

```
spline.log_dtss.90ENCODE
```

**Format**

An object of class `gam` (inherits from `glm`, `lm`) of length 46.

---

`tss.danRer10`*tss.danRer10 TSS locations*

---

### Description

A GRanges with all the TSSs for danRer10. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

### Usage

`tss.danRer10`

### Format

A GRanges object with the following `mcols`:

**gene\_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

### Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.2 and org.Dr.eg.db\_3.5.0.

---

`tss.dm3`*tss.dm3 TSS locations*

---

### Description

A GRanges with all the TSSs for dm3. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

### Usage

`tss.dm3`

### Format

A GRanges object with the following `mcols`:

**gene\_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

### Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene\_3.2.2 and org.Dm.eg.db\_3.5.0.

---

tss.dm6	<i>tss.dm6 TSS locations</i>
---------	------------------------------

---

## Description

A GRanges with all the TSSs for dm6. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

## Usage

`tss.dm6`

## Format

A GRanges object with the following `mcols`:

- gene\_id** The Entrez ID for the TSS
- symbol** The gene symbol for the TSS

## Source

R packages: `TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1` and `org.Dm.eg.db_3.5.0`.

---

tss.hg19	<i>tss.hg19 TSS locations</i>
----------	-------------------------------

---

## Description

A GRanges with all the TSSs for hg19. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

## Usage

`tss.hg19`

## Format

A GRanges object with the following `mcols`:

- gene\_id** The Entrez ID for the TSS
- symbol** The gene symbol for the TSS

## Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.annotation.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.EntrezGene.gz)

---

---

tss.hg38

*tss.hg38 TSS locations*

---

## Description

A GRanges with all the TSSs for hg38. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

## Usage

`tss.hg38`

## Format

A GRanges object with the following `ncols`:

**gene\_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

## Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene\_3.4.0 and org.Hs.eg.db\_3.5.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/gencode.v25.annotation.gff3.gz](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)

---

---

tss.mm10

*tss.mm10 TSS locations*

---

## Description

A GRanges with all the TSSs for mm10. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

## Usage

`tss.mm10`

**Format**

A GRanges object with the following `mcols`:

**gene\_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

**Source**

R packages: `TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0` and `org.Mm.eg.db_3.5.0`. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.annotation.gff3.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M12/gencode.vM12.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz)

---

`tss.mm9`*tss.mm9 TSS locations*

---

**Description**

A GRanges with all the TSSs for mm9. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

**Usage**`tss.mm9`**Format**

A GRanges object with the following `mcols`:

**gene\_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

**Source**

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.5.0`. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M9/gencode.vM9.annotation.gff3.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M9/gencode.vM9.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz)

---

`tss.rn4`*tss.rn4 TSS locations*

---

### Description

A GRanges with all the TSSs for rn4. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

### Usage

`tss.rn4`

### Format

A GRanges object with the following `mcols`:

**gene\_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

### Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.5.0`.

---

`tss.rn5`*tss.rn5 TSS locations*

---

### Description

A GRanges with all the TSSs for rn5. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

### Usage

`tss.rn5`

### Format

A GRanges object with the following `mcols`:

**gene\_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

### Source

R packages: `TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2` and `org.Rn.eg.db_3.5.0`.

---

<code>tss.rn6</code>	<i>tss.rn6 TSS locations</i>
----------------------	------------------------------

---

### Description

A GRanges with all the TSSs for rn6. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

### Usage

```
tss.rn6
```

### Format

A GRanges object with the following `mcols`:

**gene\_id** The Entrez ID for the TSS  
**symbol** The gene symbol for the TSS

### Source

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1` and `org.Rn.eg.db_3.5.0`.

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