

# Package ‘chipenrich.data’

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**Title** Companion package to chipenrich

**Version** 2.0.0

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

**Depends** R (>= 3.3.0)

**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** 6.0.1

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**NeedsCompilation** no

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

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

---

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**

```
library(chipenrich.data)

# 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
```

---

**Description**

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

**Usage**

```
data(geneset.biocarta_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.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.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*

---

**Description**

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

**Usage**

```
data(geneset.drug_bank.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.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.ehmn\_pathway\_gene.hsa  
*geneset.ehmn\_pathway\_gene.hsa*

---

**Description**

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

**Usage**

```
data(geneset.ehmn_pathway_gene.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.ehmn\_pathway\_gene.mmu  
*geneset.ehmn\_pathway\_gene.mmu*

---

**Description**

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

**Usage**

```
data(geneset.ehmn_pathway_gene.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.ehmn_pathway_gene.rno`  
*geneset.ehmn\_pathway\_gene.rno*

---

### **Description**

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

### **Usage**

```
data(geneset.ehmn_pathway_gene.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.gene_expression.hsa`  
*geneset.gene\_expression.hsa*

---

### **Description**

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

### **Usage**

```
data(geneset.gene_expression.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.gene_expression.mmu
      geneset.gene_expression.mmu
```

---

**Description**

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

**Usage**

```
data(geneset.gene_expression.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.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 Mar 20 13:46:51 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_3.4.0 and GO.db_3.4.0
```

---

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 Tue Mar 28 12:58:30 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\_3.4.0 and GO.db\_3.4.0

---

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  $\geq 10$  Entrez IDs. Built on Sat Mar 18 13:14:28 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\_3.4.0 and GO.db\_3.4.0

---

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 Mar 20 13:45:24 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\_3.4.0 and GO.db\_3.4.0



---

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 Mar 20 13:46:20 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\_3.4.0 and GO.db\_3.4.0

---

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 Mar 20 13:46:51 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\_3.4.0 and GO.db\_3.4.0

---

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

---

**Description**

Gene Ontology Cellular Component (GOCC) genesets for Danio rerio. All genesets are required to have  $\geq 10$  Entrez IDs. Built on Tue Mar 28 12:58:30 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\_3.4.0 and GO.db\_3.4.0

---

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 Mar 20 13:44:28 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\_3.4.0 and GO.db\_3.4.0

---

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 Mar 20 13:45:24 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\_3.4.0 and GO.db\_3.4.0

---

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 Mar 20 13:46:20 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\_3.4.0 and GO.db\_3.4.0

---

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 Mar 20 13:46:51 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\_3.4.0 and GO.db\_3.4.0

---

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

---

### Description

Gene Ontology Molecular Function (GOMF) genesets for *Danio rerio*. All genesets are required to have  $\geq 10$  Entrez IDs. Built on Tue Mar 28 12:58:30 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\_3.4.0 and GO.db\_3.4.0

---

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

---

**Description**

Gene Ontology Molecular Function (GOMF) genesets for Homo sapiens. All genesets are required to have  $\geq 10$  Entrez IDs. Built on Mon Mar 20 13:44:28 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\_3.4.0 and GO.db\_3.4.0

---

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 Mar 20 13:45:24 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\_3.4.0 and GO.db\_3.4.0

---

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 Mar 20 13:46:20 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\_3.4.0 and GO.db\_3.4.0

---

geneset.kegg\_pathway.hsa

*geneset.kegg\_pathway.hsa*

---

**Description**

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

**Usage**

```
data(geneset.kegg_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.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.mirbase.hsa     *geneset.mirbase.hsa*

---

**Description**

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

**Usage**

```
data(geneset.mirbase.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.mirbase.mmu     *geneset.mirbase.mmu*

---

**Description**

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

**Usage**

```
data(geneset.mirbase.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.mirbase.rno`     *geneset.mirbase.rno*

---

**Description**

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

**Usage**

```
data(geneset.mirbase.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.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*

---

**Description**

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

**Usage**

```
data(geneset.pfam.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.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\_mimi.hsa  
*geneset.protein\_interaction\_mimi.hsa*

---

**Description**

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

**Usage**

```
data(geneset.protein_interaction_mimi.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.protein_interaction_mimi.mmu  
geneset.protein_interaction_mimi.mmu
```

---

**Description**

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

**Usage**

```
data(geneset.protein_interaction_mimi.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.protein_interaction_mimi.rno  
geneset.protein_interaction_mimi.rno
```

---

**Description**

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

**Usage**

```
data(geneset.protein_interaction_mimi.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.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*

---

**Description**

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

**Usage**

```
data(geneset.transcription_factors.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.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 Tue Mar 28 12:56:08 2017.

### Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.0 and org.Dr.eg.db\_3.4.0.

---

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 Tue Mar 28 12:56:09 2017.

**Source**

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.0 and org.Dr.eg.db\_3.4.0.

---

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 Tue Mar 28 12:56:08 2017.

**Source**

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.0 and org.Dr.eg.db\_3.4.0.

---

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 Tue Mar 28 12:56:06 2017.

### Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.0 and org.Dr.eg.db\_3.4.0.

---

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 Tue Mar 28 12:56:07 2017.

**Source**

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.0 and org.Dr.eg.db\_3.4.0.

---

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 Tue Mar 28 12:56:06 2017.

**Source**

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.0 and org.Dr.eg.db\_3.4.0.

---

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 Tue Mar 28 12:56:07 2017.

### Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.0 and org.Dr.eg.db\_3.4.0.

---

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 Tue Mar 28 12:56:08 2017.

**Source**

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.0 and org.Dr.eg.db\_3.4.0.

---

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 Tue Mar 28 12:56:07 2017.

**Source**

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.0 and org.Dr.eg.db\_3.4.0.

---

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 Tue Mar 28 12:56:04 2017.

### Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.0 and org.Dr.eg.db\_3.4.0.

---

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 Tue Mar 28 12:56:06 2017.

**Source**

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.0 and org.Dr.eg.db\_3.4.0.

---

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 Tue Mar 28 12:56:02 2017.

**Source**

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.0 and org.Dr.eg.db\_3.4.0.

---

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 Tue Mar 28 12:56:02 2017.

### Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.0 and org.Dr.eg.db\_3.4.0.

---

locusdef.dm3.10kb

*locusdef.dm3.10kb locus definition*

---

### Description

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

### Usage

locusdef.dm3.10kb



**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

Built on Sat Mar 18 13:08:03 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene\_3.2.2 and org.Dm.eg.db\_3.4.0.

---

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 Sat Mar 18 13:08:03 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene\_3.2.2 and org.Dm.eg.db\_3.4.0.

---

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 Sat Mar 18 13:08:03 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene\_3.2.2 and org.Dm.eg.db\_3.4.0.

---

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 Sat Mar 18 13:08:01 2017.

### Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene\_3.2.2 and org.Dm.eg.db\_3.4.0.

---

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

---

### Description

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

### Usage

locusdef.dm3.1kb\_outside

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

Built on Sat Mar 18 13:08:02 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene\_3.2.2 and org.Dm.eg.db\_3.4.0.

---

locusdef.dm3.1kb\_outside\_upstream

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

---

**Description**

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

**Usage**

```
locusdef.dm3.1kb_outside_upstream
```

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

Built on Sat Mar 18 13:08:02 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene\_3.2.2 and org.Dm.eg.db\_3.4.0.

---

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

---

**Description**

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

**Usage**

locusdef.dm3.5kb

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

Built on Sat Mar 18 13:08:02 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene\_3.2.2 and org.Dm.eg.db\_3.4.0.

---

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

---

**Description**

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

**Usage**

locusdef.dm3.5kb\_outside

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

Built on Sat Mar 18 13:08:02 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene\_3.2.2 and org.Dm.eg.db\_3.4.0.

---

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 Sat Mar 18 13:08:02 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene\_3.2.2 and org.Dm.eg.db\_3.4.0.

---

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 Sat Mar 18 13:08:00 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene\_3.2.2 and org.Dm.eg.db\_3.4.0.

---

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 Sat Mar 18 13:08:01 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene\_3.2.2 and org.Dm.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:59 2017.



**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene\_3.2.2 and org.Dm.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:59 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene\_3.2.2 and org.Dm.eg.db\_3.4.0.

---

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 Sat Mar 18 13:08:40 2017.

### Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene\_3.3.0 and org.Dm.eg.db\_3.4.0.

---

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

---

### Description

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

### Usage

locusdef.dm6.10kb\_outside

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

Built on Sat Mar 18 13:08:40 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene\_3.3.0 and org.Dm.eg.db\_3.4.0.

---

locusdef.dm6.10kb\_outside\_upstream

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

---

**Description**

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

**Usage**

locusdef.dm6.10kb\_outside\_upstream

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

Built on Sat Mar 18 13:08:40 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene\_3.3.0 and org.Dm.eg.db\_3.4.0.

---

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

---

**Description**

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

**Usage**

locusdef.dm6.1kb

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

Built on Sat Mar 18 13:08:39 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene\_3.3.0 and org.Dm.eg.db\_3.4.0.

---

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 Sat Mar 18 13:08:39 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene\_3.3.0 and org.Dm.eg.db\_3.4.0.

---

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 Sat Mar 18 13:08:39 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene\_3.3.0 and org.Dm.eg.db\_3.4.0.

---

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 Sat Mar 18 13:08:40 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene\_3.3.0 and org.Dm.eg.db\_3.4.0.

---

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

---

**Description**

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

**Usage**

locusdef.dm6.5kb\_outside

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

Built on Sat Mar 18 13:08:40 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene\_3.3.0 and org.Dm.eg.db\_3.4.0.

---

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 Sat Mar 18 13:08:40 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene\_3.3.0 and org.Dm.eg.db\_3.4.0.

---

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 Sat Mar 18 13:08:38 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene\_3.3.0 and org.Dm.eg.db\_3.4.0.

---

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 Sat Mar 18 13:08:39 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene\_3.3.0 and org.Dm.eg.db\_3.4.0.

---

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 Sat Mar 18 13:08:37 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene\_3.3.0 and org.Dm.eg.db\_3.4.0.

---

locusdef.dm6.nearest\_tss

*locusdef.dm6.nearest\_tss locus definition*

---

**Description**

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

**Usage**

locusdef.dm6.nearest\_tss

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

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

Built on Sat Mar 18 13:08:37 2017.

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene\_3.3.0 and org.Dm.eg.db\_3.4.0.

---

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

---

### Description

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

### Usage

locusdef.hg19.10kb

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

Built on Sat Mar 18 12:52:19 2017.

### Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.4.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.annota and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.Ent

---

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

---

### Description

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

### Usage

locusdef.hg19.10kb\_outside

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:52:20 2017.

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.4.0. GENCODE

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

---

locusdef.hg19.10kb\_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 Sat Mar 18 12:52:19 2017.

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.4.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.annots and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.Ent

---

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

---

**Description**

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

**Usage**

locusdef.hg19.1kb

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:52:15 2017.

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.4.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.annots and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.Ent

---

locusdef.hg19.1kb\_outside

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

---

### Description

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

### Usage

locusdef.hg19.1kb\_outside

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

Built on Sat Mar 18 12:52:16 2017.

### Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.4.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.annotation](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.metadata](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata).Ent

---

locusdef.hg19.1kb\_outside\_upstream

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

---

### Description

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

### Usage

locusdef.hg19.1kb\_outside\_upstream

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:52:15 2017.

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.4.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.annots and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.Ent

---

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

---

**Description**

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

**Usage**

locusdef.hg19.5kb

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:52:17 2017.

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.4.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.annots and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.Ent

---

locusdef.hg19.5kb\_outside

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

---

### Description

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

### Usage

locusdef.hg19.5kb\_outside

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

Built on Sat Mar 18 12:52:18 2017.

### Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.4.0. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.annotation](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annotation) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.metadata](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata).Ent

---

locusdef.hg19.5kb\_outside\_upstream

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

---

### Description

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

### Usage

locusdef.hg19.5kb\_outside\_upstream



**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:52:17 2017.

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.4.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.annota and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.Ent

---

locusdef.hg19.exon      *locusdef.hg19.exon locus definition*

---

**Description**

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

**Usage**

locusdef.hg19.exon

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:52:12 2017.

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.4.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.annota and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.Ent

---

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

---

### Description

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

### Usage

locusdef.hg19.intron

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

Built on Sat Mar 18 12:52:14 2017.

### Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.4.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.annota and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.Ent

---

locusdef.hg19.nearest\_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 Sat Mar 18 12:52:10 2017.

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.4.0. GENCODE

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

---

locusdef.hg19.nearest\_tss

*locusdef.hg19.nearest\_tss locus definition*

---

**Description**

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

**Usage**

locusdef.hg19.nearest\_tss

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:52:09 2017.

**Source**

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene\_3.2.2 and org.Hs.eg.db\_3.4.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_human/release\_25/GRCh37\_mapping/gencode.v25lift37.metadata.EntrezGene.gz

---

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 Sat Mar 18 12:56:36 2017.

**Source**

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

---

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

---

**Description**

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

**Usage**`locusdef.hg38.10kb_outside`**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:56:37 2017.

**Source**

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene\_3.4.0 and org.Hs.eg.db\_3.4.0. 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 Sat Mar 18 12:56:36 2017.

**Source**

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

---

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

---

**Description**

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

**Usage**

locusdef.hg38.1kb

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:56:32 2017.

**Source**

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

---

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

---

**Description**

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

**Usage**`locusdef.hg38.1kb_outside`**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:56:34 2017.

**Source**

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene\_3.4.0 and org.Hs.eg.db\_3.4.0. 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 Sat Mar 18 12:56:33 2017.

**Source**

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

---

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

---

**Description**

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

**Usage**

locusdef.hg38.5kb

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:56:34 2017.

**Source**

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



---

locusdef.hg38.5kb\_outside

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


---

### Description

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

### Usage

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

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

Built on Sat Mar 18 12:56:36 2017.

### Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene\_3.4.0 and org.Hs.eg.db\_3.4.0. 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 Sat Mar 18 12:56:35 2017.

**Source**

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

---

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

---

**Description**

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

**Usage**

locusdef.hg38.exon

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:56:29 2017.

**Source**

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

---

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

---

### Description

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

### Usage

locusdef.hg38.intron

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

Built on Sat Mar 18 12:56:31 2017.

### Source

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

---

locusdef.hg38.nearest\_gene  
*locusdef.hg38.nearest\_gene locus definition*

---

### Description

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

### Usage

locusdef.hg38.nearest\_gene

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:56:27 2017.

**Source**

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

---

locusdef.hg38.nearest\_tss

*locusdef.hg38.nearest\_tss locus definition*

---

**Description**

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

**Usage**

locusdef.hg38.nearest\_tss

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:56:26 2017.

**Source**

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

---

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

---

**Description**

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

**Usage**

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

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 13:06:22 2017.

**Source**

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

---

locusdef.mm10.10kb\_outside

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

---

### Description

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

### Usage

locusdef.mm10.10kb\_outside

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

Built on Sat Mar 18 13:06:23 2017.

### Source

R packages: `TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0` and `org.Mm.eg.db_3.4.0`. 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 Sat Mar 18 13:06:22 2017.

**Source**

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

---

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

---

**Description**

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

**Usage**

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

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:58:42 2017.

**Source**

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

---

locusdef.mm10.1kb\_outside

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

---

### Description

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

### Usage

locusdef.mm10.1kb\_outside

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

Built on Sat Mar 18 13:06:19 2017.

### Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.4.0. 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 Sat Mar 18 12:58:42 2017.

**Source**

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

---

locusdef.mm10.5kb	<i>locusdef.mm10.5kb locus definition</i>
-------------------	---

---

**Description**

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

**Usage**

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

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 13:06:20 2017.

**Source**

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

---

locusdef.mm10.5kb\_outside

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

---

### Description

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

### Usage

locusdef.mm10.5kb\_outside

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

Built on Sat Mar 18 13:06:21 2017.

### Source

R packages: `TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0` and `org.Mm.eg.db_3.4.0`. 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 Sat Mar 18 13:06:20 2017.

**Source**

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

---

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

---

**Description**

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

**Usage**

locusdef.mm10.exon

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:58:40 2017.

**Source**

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

---

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

---

### Description

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

### Usage

locusdef.mm10.intron

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

Built on Sat Mar 18 12:58:41 2017.

### Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene\_3.4.0 and org.Mm.eg.db\_3.4.0. 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 Sat Mar 18 12:58:37 2017.

**Source**

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

---

locusdef.mm10.nearest\_tss

*locusdef.mm10.nearest\_tss locus definition*

---

**Description**

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

**Usage**

locusdef.mm10.nearest\_tss

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:58:37 2017.

**Source**

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

---

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

---

**Description**

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

**Usage**

locusdef.mm9.10kb

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:57:38 2017.

**Source**

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene\_3.2.2 and org.Mm.eg.db\_3.4.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.metadata.EntrezGene.gz

---

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

---

**Description**

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

**Usage**`locusdef.mm9.10kb_outside`**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:57:38 2017.

**Source**

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.4.0`. 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 Sat Mar 18 12:57:38 2017.

**Source**

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene\_3.2.2 and org.Mm.eg.db\_3.4.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.metadata.EntrezGene.gz

---

locusdef.mm9.1kb

*locusdef.mm9.1kb locus definition*

---

**Description**

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

**Usage**

locusdef.mm9.1kb

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:57:35 2017.

**Source**

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene\_3.2.2 and org.Mm.eg.db\_3.4.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.metadata.EntrezGene.gz



---

locusdef.mm9.1kb\_outside

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


---

### Description

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

### Usage

```
locusdef.mm9.1kb_outside
```

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

Built on Sat Mar 18 12:57:36 2017.

### Source

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.4.0`. 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 Sat Mar 18 12:57:35 2017.

**Source**

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene\_3.2.2 and org.Mm.eg.db\_3.4.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.metadata.EntrezGene.gz

---

locusdef.mm9.5kb

*locusdef.mm9.5kb locus definition*

---

**Description**

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

**Usage**

locusdef.mm9.5kb

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:57:36 2017.

**Source**

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene\_3.2.2 and org.Mm.eg.db\_3.4.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.metadata.EntrezGene.gz

---

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

---

**Description**

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

**Usage**`locusdef.mm9.5kb_outside`**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:57:37 2017.

**Source**

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.4.0`. 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 Sat Mar 18 12:57:37 2017.

**Source**

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene\_3.2.2 and org.Mm.eg.db\_3.4.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.metadata.EntrezGene.gz

---

locusdef.mm9.exon	<i>locusdef.mm9.exon locus definition</i>
-------------------	---

---

**Description**

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

**Usage**

```
locusdef.mm9.exon
```

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:57:32 2017.

**Source**

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene\_3.2.2 and org.Mm.eg.db\_3.4.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.metadata.EntrezGene.gz

---

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

---

### Description

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

### Usage

locusdef.mm9.intron

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

Built on Sat Mar 18 12:57:34 2017.

### Source

R packages: `TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2` and `org.Mm.eg.db_3.4.0`. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M9/gencode.vM9.annotation.gff3.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz) and [ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\\_mouse/release\\_M9/gencode.vM9.metadata.EntrezGene.gz](ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz)

---

locusdef.mm9.nearest\_gene  
                                   *locusdef.mm9.nearest\_gene locus definition*

---

### Description

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

### Usage

locusdef.mm9.nearest\_gene

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:57:30 2017.

**Source**

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene\_3.2.2 and org.Mm.eg.db\_3.4.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.metadata.EntrezGene.gz

---

locusdef.mm9.nearest\_tss

*locusdef.mm9.nearest\_tss locus definition*

---

**Description**

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

**Usage**

locusdef.mm9.nearest\_tss

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

Built on Sat Mar 18 12:57:30 2017.

**Source**

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene\_3.2.2 and org.Mm.eg.db\_3.4.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode\_mouse/release\_M9/gencode.vM9.metadata.EntrezGene.gz

---

locusdef.rn4.10kb      *locusdef.rn4.10kb locus definition*

---

**Description**

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

**Usage**

locusdef.rn4.10kb

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Sat Mar 18 13:06:49 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene\_3.2.2 and org.Rn.eg.db\_3.4.0.

---

locusdef.rn4.10kb\_outside

*locusdef.rn4.10kb\_outside locus definition*


---

### Description

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

### Usage

```
locusdef.rn4.10kb_outside
```

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Sat Mar 18 13:06:50 2017.

### Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.4.0`.

---

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 Sat Mar 18 13:06:50 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene\_3.2.2 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:06:47 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene\_3.2.2 and org.Rn.eg.db\_3.4.0.

---

locusdef.rn4.1kb\_outside

*locusdef.rn4.1kb\_outside locus definition*

---

### Description

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

### Usage

locusdef.rn4.1kb\_outside

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

For the `rn4` genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Sat Mar 18 13:06:48 2017.

### Source

R packages: `TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2` and `org.Rn.eg.db_3.4.0`.

---

locusdef.rn4.1kb\_outside\_upstream

*locusdef.rn4.1kb\_outside\_upstream locus definition*

---

### Description

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

### Usage

locusdef.rn4.1kb\_outside\_upstream

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Sat Mar 18 13:06:48 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene\_3.2.2 and org.Rn.eg.db\_3.4.0.

---

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

---

**Description**

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

**Usage**

locusdef.rn4.5kb

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Sat Mar 18 13:06:48 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene\_3.2.2 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:06:49 2017.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene\_3.2.2 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:06:49 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene\_3.2.2 and org.Rn.eg.db\_3.4.0.

---

locusdef.rn4.exon	<i>locusdef.rn4.exon locus definition</i>
-------------------	---

---

**Description**

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

**Usage**

```
locusdef.rn4.exon
```

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Sat Mar 18 13:06:46 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene\_3.2.2 and org.Rn.eg.db\_3.4.0.

---

locusdef.rn4.intron     *locusdef.rn4.intron locus definition*

---

### Description

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

### Usage

locusdef.rn4.intron

### Format

A LocusDefinition object with the following slots:

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

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

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

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

### Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Sat Mar 18 13:06:47 2017.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene\_3.2.2 and org.Rn.eg.db\_3.4.0.

---

locusdef.rn4.nearest\_gene  
                                   *locusdef.rn4.nearest\_gene locus definition*

---

### Description

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

### Usage

locusdef.rn4.nearest\_gene

**Format**

A LocusDefinition object with the following slots:

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

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

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

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

**Details**

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Sat Mar 18 13:06:44 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene\_3.2.2 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:06:44 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene\_3.2.2 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:12 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:13 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:12 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:10 2017.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:11 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:10 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:11 2017.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:12 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:11 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:08 2017.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:09 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:06 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:06 2017.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

locusdef.rn6.10kb

*locusdef.rn6.10kb locus definition*


---

### Description

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

### Usage

```
locusdef.rn6.10kb
```



**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, rn6.

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

**Details**

Built on Sat Mar 18 13:07:32 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:33 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:32 2017.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:30 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:31 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:30 2017.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:31 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:32 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:31 2017.

### Source

R packages: `TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.0` and `org.Rn.eg.db_3.4.0`.

---

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 Sat Mar 18 13:07:28 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

locusdef.rn6.intron    *locusdef.rn6.intron locus definition*

---

**Description**

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

**Usage**

```
locusdef.rn6.intron
```

**Format**

A LocusDefinition object with the following slots:

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

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

**genome.build** A character indicating the genome build. In this case, rn6.

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

**Details**

Built on Sat Mar 18 13:07:30 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:26 2017.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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 Sat Mar 18 13:07:26 2017.

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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**

```
library(chipenrich.data)

# Show info about the class.
showClass("LocusDefinition");

# Example of what a locus definition object looks like.
data(locusdef.mm9.nearest_tss);
str(locusdef.mm9.nearest_tss);
```

---

```
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

```
library(chipenrich.data)

# Load E2F4 peak data.
data(peaks_E2F4)

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

---

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

---

## Description

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

## Usage

```
peaks_H3K4me3_GM12878
```

## Format

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

## Source

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

<http://hgdownload.cse.ucsc.edu/goldenPath/hg19/encodeDCC/wgEncodeBroadHistone/wgEncodeBroadHistoneGm12878>

## Examples

```
library(chipenrich.data)

# Load H3K4me3 in GM12878 peak data.
data(peaks_H3K4me3_GM12878)

# Print the first 10 peaks in the dataset.
print(head(peaks_H3K4me3_GM12878))
```

---

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

---

**Description**

A GRanges with all the TSSs for danRer10. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

**Usage**

```
tss.danRer10
```

**Format**

A GRanges object with the following mcols:

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

**symbol** The gene symbol for the TSS

**Source**

R packages: TxDb.Drerio.UCSC.danRer10.refGene\_3.4.0 and org.Dr.eg.db\_3.4.0.

---

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

---

**Description**

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

**Usage**

```
tss.dm3
```

**Format**

A GRanges object with the following mcols:

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

**symbol** The gene symbol for the TSS

**Source**

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene\_3.2.2 and org.Dm.eg.db\_3.4.0.

---

`tss.dm6`*tss.dm6 TSS locations*

---

**Description**

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

**Usage**`tss.dm6`**Format**

A GRanges object with the following mcols:

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

**symbol** The gene symbol for the TSS

**Source**

R packages: `TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.3.0` and `org.Dm.eg.db_3.4.0`.

---

`tss.hg19`*tss.hg19 TSS locations*

---

**Description**

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

**Usage**`tss.hg19`**Format**

A GRanges object with the following mcols:

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

**symbol** The gene symbol for the TSS

**Source**

R packages: `TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2` and `org.Hs.eg.db_3.4.0`. GENCODE resources: [ftp://ftp.sanger.ac.uk/pub/genCODE/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.anno](ftp://ftp.sanger.ac.uk/pub/genCODE/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.anno) and [ftp://ftp.sanger.ac.uk/pub/genCODE/Gencode\\_human/release\\_25/GRCh37\\_mapping/gencode.v25lift37.metadata.Ent](ftp://ftp.sanger.ac.uk/pub/genCODE/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.Ent)



---

`tss.hg38`*tss.hg38 TSS locations*

---

**Description**

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

**Usage**`tss.hg38`**Format**

A GRanges object with the following mcols:

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

**symbol** The gene symbol for the TSS

**Source**

R packages: `TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0` and `org.Hs.eg.db_3.4.0`. 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_3.4.0`. 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_3.4.0`. 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_3.4.0`.

---

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

---

**Description**

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

**Usage**

```
tss.rn5
```

**Format**

A GRanges object with the following mcols:

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

**symbol** The gene symbol for the TSS

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

---

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

---

**Description**

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

**Usage**

```
tss.rn6
```

**Format**

A GRanges object with the following mcols:

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

**symbol** The gene symbol for the TSS

**Source**

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene\_3.4.0 and org.Rn.eg.db\_3.4.0.

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