# Package ‘chipenrich.data’

May 19, 2026

**Title** Companion package to chipenrich

**Version** 2.37.0

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

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

**Depends** R (>= 3.4.0)

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

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

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

**VignetteBuilder** knitr

**RoxygenNote** 6.1.1

**Maintainer** Kai Wang <`wangdaha@umich.edu`>

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# Contents

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## `chipenrich.data` *chipenrich.data: Data for chipenrich: gene set enrichment analysis for ChIP-seq data*

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### Description

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

---

## `enhancer.dnase_thurman.0` *Enhancer locations*

---

### Description

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

### Usage

```
enhancer.dnase_thurman.0
```

### Format

A `GRanges` object with the following `mcols`:

- **gene_id** The Entrez ID for the TSS
- **symbol** The gene symbol for the TSS

---

## `gene.enh.desc` *Gene-Enhancer descriptives*

### Description

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

- **gene_id** The Entrez ID for the a gene
- **avg_denh_emp** The empirical average distance to an enhancer from 90 ENCODE ChIP-seq datasets. This is used as the adjustment.
- **num_enh** The number of enhancers assigned to the gene, defined by closest gene TSS
- **avgdenh** The theoretical average distance to an enhancer assuming every base pair on the genome is equally likely to have a peak binding.

### Usage

```
gene.enh.desc
```

### Format

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

---

## `GeneSet-class` *Class* `"GeneSet"`

### Description

Class for storing sets of genes and their corresponding metadata.

### Objects from the Class

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

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

### Slots

- `set.gene`: Object of class `"environment"`. Maps from geneset IDs to lists of Entrez gene IDs.
- `type`: Object of class `"character"`. The formal name for this collection of genesets.
- `set.name`: Object of class `"environment"`. Maps from geneset IDs to their descriptions/names.
- `all.genes`: Object of class `"character"`. A set of all genes present across every geneset.
- `organism`: Object of class `"character"`. Organism code for gene IDs.
- `dburl`: Object of class `"character"`. Web URL for this collection of genesets.

## Note

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

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## Examples

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

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

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

---

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

## Description

BioCarta (biocarta_pathway) genesets. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 18:46:04 2017.

## Usage

```
geneset.biocarta_pathway.hsa
```

## Format

A `GeneSet` object with the following slots:

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

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

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

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

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

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

## Source

https://cgap.nci.nih.gov/Pathways/BioCarta_Pathways

---

`geneset.biocarta_pathway.mmu`

## *geneset.biocarta_pathway.mmu*

---

### Description

GeneSet object which stores information about sets of genes.

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

### Usage

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

### Format

See `GeneSet-class` for a description of the format.

### See Also

For more information about genesets: `chipenrich.data`

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

---

`geneset.biocarta_pathway.rno`

## *geneset.biocarta_pathway.rno*

---

### Description

GeneSet object which stores information about sets of genes.

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

### Usage

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

### Format

See `GeneSet-class` for a description of the format.

### See Also

For more information about genesets: `chipenrich.data`

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

---

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

---

### Description

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

### Usage

```
geneset.ctd.hsa
```

### Format

A `GeneSet` object with the following slots:

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

### Source

http://ctdbase.org

---

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

---

### Description

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

### Usage

```
geneset.ctd.mmu
```

## Format

A `GeneSet` object with the following slots:

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

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

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

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

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

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

## Source

http://ctdbase.org

---

# `geneset.cytoband.hsa` *geneset.cytoband.hsa*

## Description

GeneSet object which stores information about sets of genes.

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

## Usage

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

## Format

See `GeneSet-class` for a description of the format.

## See Also

For more information about genesets: `chipenrich.data`

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

---

## `geneset.drug_bank.hsa` *geneset.drug_bank.hsa genesets for DrugBank*

---

### Description

DrugBank (drug_bank) genesets. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 18:46:13 2017.

### Usage

```
geneset.drug_bank.hsa
```

### Format

A `GeneSet` object with the following slots:

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

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

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

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

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

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

### Source

https://www.drugbank.ca

---

## `geneset.drug_bank.mmu` *geneset.drug_bank.mmu*

---

### Description

GeneSet object which stores information about sets of genes.

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

### Usage

```
data(geneset.drug_bank.mmu)
```

### Format

See `GeneSet-class` for a description of the format.

### See Also

For more information about genesets: `chipenrich.data`

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

---

## `geneset.drug_bank.rno` *geneset.drug_bank.rno*

---

### Description

GeneSet object which stores information about sets of genes.

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

### Usage

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

### Format

See `GeneSet-class` for a description of the format.

### See Also

For more information about genesets: `chipenrich.data`

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

---

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

---

### Description

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

### Usage

```
geneset.GOBP.dme
```

### Format

A `GeneSet` object with the following slots:

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

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

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

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

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

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

### Source

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

---

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

---

### Description

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

### Usage

```
geneset.GOBP.dre
```

### Format

A `GeneSet` object with the following slots:

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

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

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

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

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

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

### Source

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

---

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

---

### Description

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

### Usage

```
geneset.GOBP.hsa
```

### Format

A `GeneSet` object with the following slots:

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

### Source

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

---

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

### Description

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

### Usage

```
geneset.GOBP.mmu
```

### Format

A `GeneSet` object with the following slots:

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

### Source

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

---

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

---

## Description

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

## Usage

```
geneset.GOBP.rno
```

## Format

A `GeneSet` object with the following slots:

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

## Source

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

---

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

---

## Description

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

## Usage

```
geneset.GOCC.dme
```

### Format

A `GeneSet` object with the following slots:

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

### Source

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

---

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

### Description

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

### Usage

```
geneset.GOCC.dre
```

### Format

A `GeneSet` object with the following slots:

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

### Source

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

---

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

---

### Description

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

### Usage

```
geneset.GOCC.hsa
```

### Format

A `GeneSet` object with the following slots:

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

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

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

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

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

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

### Source

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

---

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

---

### Description

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

### Usage

```
geneset.GOCC.mmu
```

## Format

A `GeneSet` object with the following slots:

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

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

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

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

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

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

## Source

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

---

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

## Description

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

## Usage

```
geneset.GOCC.rno
```

## Format

A `GeneSet` object with the following slots:

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

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

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

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

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

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

## Source

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

---

## `geneset.GOMF.dme` *geneset.GOMF.dme genesets for Drosophila melanogaster*

---

### Description

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

### Usage

```
geneset.GOMF.dme
```

### Format

A `GeneSet` object with the following slots:

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

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

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

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

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

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

### Source

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

---

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

---

### Description

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

### Usage

```
geneset.GOMF.dre
```

## Format

A `GeneSet` object with the following slots:

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

## Source

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

---

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

## Description

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

## Usage

```
geneset.GOMF.hsa
```

## Format

A `GeneSet` object with the following slots:

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

## Source

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

---

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

---

### Description

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

### Usage

```
geneset.GOMF.mmu
```

### Format

A `GeneSet` object with the following slots:

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

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

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

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

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

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

### Source

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

---

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

---

### Description

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

### Usage

```
geneset.GOMF.rno
```

## Format

A `GeneSet` object with the following slots:

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

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

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

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

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

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

## Source

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

---

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

## Description

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

## Usage

```
geneset.hallmark.hsa
```

## Format

A `GeneSet` object with the following slots:

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

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

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

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

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

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

## Source

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

---

`geneset.immunologic.hsa`

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

---

### Description

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

### Usage

```
geneset.immunologic.hsa
```

### Format

A `GeneSet` object with the following slots:

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

### Source

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

---

`geneset.kegg_pathway.hsa`

## *geneset.kegg_pathway.hsa genesets for KEGG Pathways*

---

### Description

KEGG Pathways (kegg_pathway) genesets. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 18:46:53 2017.

### Usage

```
geneset.kegg_pathway.hsa
```

## Format

A `GeneSet` object with the following slots:

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

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

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

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

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

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

## Source

http://kegg.jp

---

`geneset.kegg_pathway.mmu`

# *geneset.kegg_pathway.mmu*

## Description

GeneSet object which stores information about sets of genes.

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

## Usage

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

## Format

See `GeneSet-class` for a description of the format.

## See Also

For more information about genesets: `chipenrich.data`

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

---

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

---

### Description

GeneSet object which stores information about sets of genes.

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

### Usage

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

### Format

See `GeneSet-class` for a description of the format.

### See Also

For more information about genesets: `chipenrich.data`

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

---

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

---

### Description

GeneSet object which stores information about sets of genes.

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

### Usage

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

### Format

See `GeneSet-class` for a description of the format.

### See Also

For more information about genesets: `chipenrich.data`

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

---

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

---

### Description

GeneSet object which stores information about sets of genes.

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

### Usage

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

### Format

See `GeneSet-class` for a description of the format.

### See Also

For more information about genesets: `chipenrich.data`

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

---

## `geneset.mesh.rno` *geneset.mesh.rno*

---

### Description

GeneSet object which stores information about sets of genes.

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

### Usage

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

### Format

See `GeneSet-class` for a description of the format.

### See Also

For more information about genesets: `chipenrich.data`

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

---

`geneset.metabolite.hsa`

# *geneset.metabolite.hsa*

---

## Description

GeneSet object which stores information about sets of genes.

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

## Usage

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

## Format

See `GeneSet-class` for a description of the format.

## See Also

For more information about genesets: `chipenrich.data`

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

---

`geneset.metabolite.mmu`

# *geneset.metabolite.mmu*

---

## Description

GeneSet object which stores information about sets of genes.

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

## Usage

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

## Format

See `GeneSet-class` for a description of the format.

## See Also

For more information about genesets: `chipenrich.data`

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

---

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

---

### Description

GeneSet object which stores information about sets of genes.

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

### Usage

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

### Format

See `GeneSet-class` for a description of the format.

### See Also

For more information about genesets: `chipenrich.data`

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

---

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

---

### Description

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

### Usage

```
geneset.microrna.hsa
```

### Format

A `GeneSet` object with the following slots:

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

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

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

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

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

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

### Source

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

---

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

---

### Description

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

### Usage

```
geneset.oncogenic.hsa
```

### Format

A `GeneSet` object with the following slots:

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

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

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

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

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

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

### Source

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

---

`geneset.panther_pathway.hsa`
*geneset.panther_pathway.hsa*

---

### Description

GeneSet object which stores information about sets of genes.

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

### Usage

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

### Format

See `GeneSet-class` for a description of the format.

### See Also

For more information about genesets: `chipenrich.data`

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

---

`geneset.panther_pathway.mmu`

## *geneset.panther_pathway.mmu*

---

### Description

GeneSet object which stores information about sets of genes.

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

### Usage

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

### Format

See `GeneSet-class` for a description of the format.

### See Also

For more information about genesets: `chipenrich.data`

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

---

`geneset.panther_pathway.rno`

## *geneset.panther_pathway.rno*

---

### Description

GeneSet object which stores information about sets of genes.

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

### Usage

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

### Format

See `GeneSet-class` for a description of the format.

### See Also

For more information about genesets: `chipenrich.data`

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

---

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

---

### Description

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

### Usage

```
geneset.pfam.hsa
```

### Format

A `GeneSet` object with the following slots:

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

### Source

http://pfam.xfam.org

---

## `geneset.pfam.mmu` *geneset.pfam.mmu*

---

### Description

GeneSet object which stores information about sets of genes.

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

### Usage

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

### Format

See `GeneSet-class` for a description of the format.

### See Also

For more information about genesets: `chipenrich.data`

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

---

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

---

### Description

GeneSet object which stores information about sets of genes.

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

### Usage

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

### Format

See `GeneSet-class` for a description of the format.

### See Also

For more information about genesets: `chipenrich.data`

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

---

## `geneset.protein_interaction_biogrid.hsa` *geneset.protein_interaction_biogrid.hsa genesets for BioGRID Protein Interactions*

---

### Description

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

### Usage

```
geneset.protein_interaction_biogrid.hsa
```

### Format

A `GeneSet` object with the following slots:

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

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

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

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

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

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

### Source

https://thebiogrid.org

---

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

### Description

Reactome genesets for Drosophila melanogaster. All genesets are required to have >= 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 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 >= 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 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 >= 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 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 >= 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 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 >= 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 downloaded on 2017-03-19

---

`geneset.transcription_factors.hsa`

# *geneset.transcription_factors.hsa genesets for Transcription Factor Targets (MSigDB)*

---

## Description

Transcription Factor Targets (MSigDB) (transcription_factors) genesets. All genesets are required to have >= 10 Entrez IDs. Built on Mon Oct 16 18:47:33 2017.

## Usage

```
geneset.transcription_factors.hsa
```

## Format

A `GeneSet` object with the following slots:

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

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

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

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

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

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

## Source

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

---

`geneset.transcription_factors.mmu` *geneset.transcription_factors.mmu*

---

### Description

GeneSet object which stores information about sets of genes.

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

### Usage

```
data(geneset.transcription_factors.mmu)
```

### Format

See `GeneSet-class` for a description of the format.

### See Also

For more information about genesets: `chipenrich.data`

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

---

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

---

### Description

GeneSet object which stores information about sets of genes.

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

### Usage

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

### Format

See `GeneSet-class` for a description of the format.

### See Also

For more information about genesets: `chipenrich.data`

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

---

`locusdef.danRer10.10kb`

## *locusdef.danRer10.10kb locus definition*

---

### Description

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

### Usage

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

### Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, danRer10.
- **organism** A `character` indicating the organism name. In this case, Danio rerio.

### Details

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

### Source

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

---

`locusdef.danRer10.10kb_outside`

## *locusdef.danRer10.10kb_outside locus definition*

---

### Description

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

### Usage

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

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

# `locusdef.danRer10.10kb_outside_upstream` *locusdef.danRer10.10kb_outside_upstream locus definition*

## Description

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

## Usage

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

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

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

---

### Description

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

### Usage

```
locusdef.danRer10.1kb
```

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

### Source

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

---

## `locusdef.danRer10.1kb_outside` *locusdef.danRer10.1kb_outside locus definition*

---

### Description

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

### Usage

```
locusdef.danRer10.1kb_outside
```

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

# `locusdef.danRer10.1kb_outside_upstream` *locusdef.danRer10.1kb_outside_upstream locus definition*

## Description

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

## Usage

```
locusdef.danRer10.1kb_outside_upstream
```

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

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

---

### Description

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

### Usage

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

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

### Source

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

---

## `locusdef.danRer10.5kb_outside` *locusdef.danRer10.5kb_outside locus definition*

---

### Description

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

### Usage

```
locusdef.danRer10.5kb_outside
```

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

`locusdef.danRer10.5kb_outside_upstream`

# *locusdef.danRer10.5kb_outside_upstream locus definition*

## Description

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

## Usage

```
locusdef.danRer10.5kb_outside_upstream
```

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

`locusdef.danRer10.exon`

## *locusdef.danRer10.exon locus definition*

---

### Description

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

### Usage

```
locusdef.danRer10.exon
```

### Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, danRer10.
- **organism** A `character` indicating the organism name. In this case, Danio rerio.

### Details

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

### Source

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

---

`locusdef.danRer10.intron`

## *locusdef.danRer10.intron locus definition*

---

### Description

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

### Usage

```
locusdef.danRer10.intron
```

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

`locusdef.danRer10.nearest_gene`

# *locusdef.danRer10.nearest_gene locus definition*

## Description

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

## Usage

```
locusdef.danRer10.nearest_gene
```

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

## `locusdef.danRer10.nearest_tss` *locusdef.danRer10.nearest_tss locus definition*

---

### Description

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

### Usage

```
locusdef.danRer10.nearest_tss
```

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

### Source

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

---

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

---

### Description

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

### Usage

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

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

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

## Source

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

---

`locusdef.dm3.10kb_outside`

# *locusdef.dm3.10kb_outside locus definition*

## Description

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

## Usage

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

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

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

### Source

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

---

## `locusdef.dm3.10kb_outside_upstream` *locusdef.dm3.10kb_outside_upstream locus definition*

### Description

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

### Usage

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

### Format

A `LocusDefinition` object with the following slots:

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

### Details

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

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

### Source

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

---

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

---

### Description

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

### Usage

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

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

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

### Source

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

---

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

---

### Description

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

### Usage

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

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

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

## Source

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

---

# `locusdef.dm3.1kb_outside_upstream` *locusdef.dm3.1kb_outside_upstream locus definition*

## Description

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

## Usage

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

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

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

### Source

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

---

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

### Description

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

### Usage

```
locusdef.dm3.5kb
```

### Format

A `LocusDefinition` object with the following slots:

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

### Details

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

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

### Source

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

---

## `locusdef.dm3.5kb_outside` *locusdef.dm3.5kb_outside locus definition*

### Description

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

### Usage

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

### Format

A `LocusDefinition` object with the following slots:

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

### Details

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

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

### Source

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

---

`locusdef.dm3.5kb_outside_upstream`

## *locusdef.dm3.5kb_outside_upstream locus definition*

### Description

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

### Usage

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

### Format

A `LocusDefinition` object with the following slots:

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

### Details

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

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

## Source

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

---

## `locusdef.dm3.exon` *locusdef.dm3.exon locus definition*

### Description

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

### Usage

```
locusdef.dm3.exon
```

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

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

### Source

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

---

## `locusdef.dm3.intron` *locusdef.dm3.intron locus definition*

### Description

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

### Usage

```
locusdef.dm3.intron
```

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

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

### Source

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

---

`locusdef.dm3.nearest_gene`

## *locusdef.dm3.nearest_gene locus definition*

### Description

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

### Usage

```
locusdef.dm3.nearest_gene
```

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

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

## Source

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

---

`locusdef.dm3.nearest_tss`

# *locusdef.dm3.nearest_tss locus definition*

---

## Description

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

## Usage

```
locusdef.dm3.nearest_tss
```

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

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

## Source

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

---

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

---

### Description

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

### Usage

```
locusdef.dm6.10kb
```

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

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

### Source

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

---

## `locusdef.dm6.10kb_outside`
*locusdef.dm6.10kb_outside locus definition*

---

### Description

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

### Usage

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

### Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, dm6.
- **organism** A `character` indicating the organism name. In this case, Drosophila melanogaster.

### Details

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

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

### Source

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

---

## `locusdef.dm6.10kb_outside_upstream` *locusdef.dm6.10kb_outside_upstream locus definition*

### Description

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

### Usage

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

### Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, dm6.
- **organism** A `character` indicating the organism name. In this case, Drosophila melanogaster.

### Details

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

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

### Source

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

---

## `locusdef.dm6.1kb` *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 Fri Apr 13 09:53:34 2018.

### Source

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

---

## `locusdef.dm6.1kb_outside` *locusdef.dm6.1kb_outside locus definition*

### Description

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

### Usage

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

## Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, dm6.
- **organism** A `character` indicating the organism name. In this case, Drosophila melanogaster.

## Details

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

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

## Source

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

---

`locusdef.dm6.1kb_outside_upstream`

# *locusdef.dm6.1kb_outside_upstream locus definition*

---

## Description

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

## Usage

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

## Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, dm6.
- **organism** A `character` indicating the organism name. In this case, Drosophila melanogaster.

## Details

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

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

## Source

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

---

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

## Description

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

## Usage

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

## Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, dm6.
- **organism** A `character` indicating the organism name. In this case, Drosophila melanogaster.

## Details

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

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

## Source

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

---

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

## Description

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

## Usage

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

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

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

## Source

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

---

`locusdef.dm6.5kb_outside_upstream`

# *locusdef.dm6.5kb_outside_upstream locus definition*

---

## Description

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

## Usage

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

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

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

### Source

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

---

## `locusdef.dm6.exon` *locusdef.dm6.exon locus definition*

### Description

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

### Usage

```
locusdef.dm6.exon
```

### Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, dm6.
- **organism** A `character` indicating the organism name. In this case, Drosophila melanogaster.

### Details

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

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

### Source

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

---

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

### Description

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

### Usage

```
locusdef.dm6.intron
```

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

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

### Source

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

---

## `locusdef.dm6.nearest_gene` *locusdef.dm6.nearest_gene locus definition*

### Description

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

### Usage

```
locusdef.dm6.nearest_gene
```

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

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

### Source

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

---

`locusdef.dm6.nearest_tss`

## *locusdef.dm6.nearest_tss locus definition*

---

### Description

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

### Usage

```
locusdef.dm6.nearest_tss
```

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

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

### Source

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

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

### Description

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

### Usage

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

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

### Source

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

## `locusdef.hg19.10kb_outside` *locusdef.hg19.10kb_outside locus definition*

### Description

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

### Usage

```
locusdef.hg19.10kb_outside
```

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

### Source

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

---

## `locusdef.hg19.10kb_outside_upstream`
## *locusdef.hg19.10kb_outside_upstream locus definition*

### Description

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

### Usage

```
locusdef.hg19.10kb_outside_upstream
```

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

### Source

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

---

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

### Description

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

### Usage

```
locusdef.hg19.1kb
```

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

### Source

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

---

## `locusdef.hg19.1kb_outside`

### *locusdef.hg19.1kb_outside locus definition*

---

### Description

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

### Usage

```
locusdef.hg19.1kb_outside
```

### Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, hg19.
- **organism** A `character` indicating the organism name. In this case, Homo sapiens.

### Details

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

### Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annota
and 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 Fri Apr 13 09:45:56 2018.

## Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annota 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 Fri Apr 13 09:45:57 2018.

## Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annota 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 Fri Apr 13 09:45:58 2018.

### Source

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

---

## `locusdef.hg19.5kb_outside_upstream` *locusdef.hg19.5kb_outside_upstream locus definition*

---

### Description

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

### Usage

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

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

# `locusdef.hg19.exon` *locusdef.hg19.exon locus definition*

## Description

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

## Usage

```
locusdef.hg19.exon
```

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

## `locusdef.hg19.intron` *locusdef.hg19.intron locus definition*

---

### Description

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

### Usage

```
locusdef.hg19.intron
```

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

### Source

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

---

## `locusdef.hg19.nearest_gene` *locusdef.hg19.nearest_gene locus definition*

---

### Description

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

### Usage

```
locusdef.hg19.nearest_gene
```

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

`locusdef.hg19.nearest_tss`

# *locusdef.hg19.nearest_tss locus definition*

---

## Description

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

## Usage

```
locusdef.hg19.nearest_tss
```

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

### Source

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

---

## `locusdef.hg38.10kb` *locusdef.hg38.10kb locus definition*

### Description

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

### Usage

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

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

### Source

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

---

## `locusdef.hg38.10kb_outside`
### *locusdef.hg38.10kb_outside locus definition*

---

### Description

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

### Usage

```
locusdef.hg38.10kb_outside
```

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

### Source

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

---

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

---

### Description

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

### Usage

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

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

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

## Description

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

## Usage

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

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz 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 Fri Apr 13 09:49:40 2018.

### Source

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

---

`locusdef.hg38.1kb_outside_upstream`

## *locusdef.hg38.1kb_outside_upstream locus definition*

---

### Description

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

### Usage

```
locusdef.hg38.1kb_outside_upstream
```

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

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

## Description

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

## Usage

```
locusdef.hg38.5kb
```

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

## `locusdef.hg38.5kb_outside` *locusdef.hg38.5kb_outside locus definition*

---

### Description

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

### Usage

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

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

### Source

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

---

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

---

### Description

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

### Usage

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

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

# `locusdef.hg38.exon` *locusdef.hg38.exon locus definition*

## Description

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

## Usage

```
locusdef.hg38.exon
```

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

## `locusdef.hg38.intron` *locusdef.hg38.intron locus definition*

---

### Description

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

### Usage

```
locusdef.hg38.intron
```

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

### Source

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

---

## `locusdef.hg38.nearest_gene` *locusdef.hg38.nearest_gene locus definition*

---

### Description

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

### Usage

```
locusdef.hg38.nearest_gene
```

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

### Source

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

---

`locusdef.hg38.nearest_tss`

## *locusdef.hg38.nearest_tss locus definition*

### Description

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

### Usage

```
locusdef.hg38.nearest_tss
```

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

## Source

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

---

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

## Description

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

## Usage

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

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

## `locusdef.mm10.10kb_outside` *locusdef.mm10.10kb_outside locus definition*

---

### Description

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

### Usage

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

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

### Source

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

---

## `locusdef.mm10.10kb_outside_upstream` *locusdef.mm10.10kb_outside_upstream locus definition*

---

### Description

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

### Usage

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

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

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

## Description

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

## Usage

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

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

`locusdef.mm10.1kb_outside`

## *locusdef.mm10.1kb_outside locus definition*

---

### Description

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

### Usage

```
locusdef.mm10.1kb_outside
```

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

### Source

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

---

`locusdef.mm10.1kb_outside_upstream`

## *locusdef.mm10.1kb_outside_upstream locus definition*

---

### Description

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

### Usage

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

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

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

## Description

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

## Usage

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

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

`locusdef.mm10.5kb_outside` *locusdef.mm10.5kb_outside locus definition*

---

### Description

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

### Usage

```
locusdef.mm10.5kb_outside
```

### Format

A `LocusDefinition` object with the following slots:

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

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

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

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

### Details

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

### Source

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

---

`locusdef.mm10.5kb_outside_upstream` *locusdef.mm10.5kb_outside_upstream locus definition*

---

### Description

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

### Usage

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

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

# `locusdef.mm10.exon` *locusdef.mm10.exon locus definition*

## Description

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

## Usage

```
locusdef.mm10.exon
```

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

## `locusdef.mm10.intron` *locusdef.mm10.intron locus definition*

---

### Description

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

### Usage

```
locusdef.mm10.intron
```

### Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, mm10.
- **organism** A `character` indicating the organism name. In this case, Mus musculus.

### Details

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

### Source

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

---

## `locusdef.mm10.nearest_gene` *locusdef.mm10.nearest_gene locus definition*

---

### Description

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

### Usage

```
locusdef.mm10.nearest_gene
```

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

`locusdef.mm10.nearest_tss`

# *locusdef.mm10.nearest_tss locus definition*

## Description

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

## Usage

```
locusdef.mm10.nearest_tss
```

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

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

---

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

## Description

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

## Usage

```
locusdef.mm9.10kb
```

## Format

A `LocusDefinition` object with the following slots:

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

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

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

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

## Details

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

## Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

## `locusdef.mm9.10kb_outside` *locusdef.mm9.10kb_outside locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

### Usage

```
locusdef.mm9.10kb_outside
```

### Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, mm9.

**organism** A `character` indicating the organism name. In this case, Mus musculus.

### Details

Built on Fri Apr 13 09:50:44 2018.

### Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

## `locusdef.mm9.10kb_outside_upstream` *locusdef.mm9.10kb_outside_upstream locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

### Usage

```
locusdef.mm9.10kb_outside_upstream
```

### Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, mm9.

**organism** A `character` indicating the organism name. In this case, Mus musculus.

### Details

Built on Fri Apr 13 09:50:44 2018.

### Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

## `locusdef.mm9.1kb` *locusdef.mm9.1kb locus definition*

### Description

A `LocusDefinition` where a gene locus is defined within 1kb upstream and downstream of the TSS.

### Usage

```
locusdef.mm9.1kb
```

### Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, mm9.

**organism** A `character` indicating the organism name. In this case, Mus musculus.

### Details

Built on Fri Apr 13 09:50:41 2018.

### Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

`locusdef.mm9.1kb_outside`

## *locusdef.mm9.1kb_outside locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

### Usage

```
locusdef.mm9.1kb_outside
```

### Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, mm9.

**organism** A `character` indicating the organism name. In this case, Mus musculus.

### Details

Built on Fri Apr 13 09:50:42 2018.

### Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

`locusdef.mm9.1kb_outside_upstream`

## *locusdef.mm9.1kb_outside_upstream locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

### Usage

```
locusdef.mm9.1kb_outside_upstream
```

## Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, mm9.

**organism** A `character` indicating the organism name. In this case, Mus musculus.

## Details

Built on Fri Apr 13 09:50:41 2018.

## Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz 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 Fri Apr 13 09:50:42 2018.

## Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

`locusdef.mm9.5kb_outside`

## *locusdef.mm9.5kb_outside locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

### Usage

```
locusdef.mm9.5kb_outside
```

### Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, mm9.

**organism** A `character` indicating the organism name. In this case, Mus musculus.

### Details

Built on Fri Apr 13 09:50:43 2018.

### Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

`locusdef.mm9.5kb_outside_upstream`

## *locusdef.mm9.5kb_outside_upstream locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

### Usage

```
locusdef.mm9.5kb_outside_upstream
```

## Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, mm9.

**organism** A `character` indicating the organism name. In this case, Mus musculus.

## Details

Built on Fri Apr 13 09:50:43 2018.

## Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

# `locusdef.mm9.exon` *locusdef.mm9.exon locus definition*

## Description

A `LocusDefinition` where a gene locus is defined as the exons belonging to genes.

## Usage

```
locusdef.mm9.exon
```

## Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, mm9.

**organism** A `character` indicating the organism name. In this case, Mus musculus.

## Details

Built on Fri Apr 13 09:50:39 2018.

## Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

## `locusdef.mm9.intron` *locusdef.mm9.intron locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the introns belonging to genes.

### Usage

```
locusdef.mm9.intron
```

### Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, mm9.
- **organism** A `character` indicating the organism name. In this case, Mus musculus.

### Details

Built on Fri Apr 13 09:50:41 2018.

### Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

## `locusdef.mm9.nearest_gene` *locusdef.mm9.nearest_gene locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

### Usage

```
locusdef.mm9.nearest_gene
```

## Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, mm9.

**organism** A `character` indicating the organism name. In this case, Mus musculus.

## Details

Built on Fri Apr 13 09:50:37 2018.

## Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

`locusdef.mm9.nearest_tss`

# *locusdef.mm9.nearest_tss locus definition*

## Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

## Usage

```
locusdef.mm9.nearest_tss
```

## Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, mm9.

**organism** A `character` indicating the organism name. In this case, Mus musculus.

## Details

Built on Fri Apr 13 09:50:37 2018.

## Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

# `locusdef.rn4.10kb` *locusdef.rn4.10kb locus definition*

## Description

A `LocusDefinition` where a gene locus is defined within 10kb upstream and downstream of the TSS.

## Usage

```
locusdef.rn4.10kb
```

## Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn4.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

---

`locusdef.rn4.10kb_outside`

## *locusdef.rn4.10kb_outside locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

### Usage

```
locusdef.rn4.10kb_outside
```

### Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn4.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

### Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:03 2018.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

---

`locusdef.rn4.10kb_outside_upstream`

## *locusdef.rn4.10kb_outside_upstream locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

### Usage

```
locusdef.rn4.10kb_outside_upstream
```

### Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn4.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

### Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

---

## `locusdef.rn4.1kb` *locusdef.rn4.1kb locus definition*

### Description

A `LocusDefinition` where a gene locus is defined within 1kb upstream and downstream of the TSS.

### Usage

```
locusdef.rn4.1kb
```

### Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn4.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

### Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

---

`locusdef.rn4.1kb_outside`

## *locusdef.rn4.1kb_outside locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

### Usage

```
locusdef.rn4.1kb_outside
```

### Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn4.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

### Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

---

`locusdef.rn4.1kb_outside_upstream`

## *locusdef.rn4.1kb_outside_upstream locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

### Usage

```
locusdef.rn4.1kb_outside_upstream
```

## Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn4.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

---

# `locusdef.rn4.5kb` *locusdef.rn4.5kb locus definition*

## Description

A `LocusDefinition` where a gene locus is defined within 5kb upstream and downstream of the TSS.

## Usage

```
locusdef.rn4.5kb
```

## Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn4.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:01 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

---

`locusdef.rn4.5kb_outside`

## *locusdef.rn4.5kb_outside locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

### Usage

```
locusdef.rn4.5kb_outside
```

### Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn4.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

### Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

---

`locusdef.rn4.5kb_outside_upstream`

## *locusdef.rn4.5kb_outside_upstream locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

### Usage

```
locusdef.rn4.5kb_outside_upstream
```

## Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn4.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:02 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

---

# `locusdef.rn4.exon` *locusdef.rn4.exon locus definition*

## Description

A `LocusDefinition` where a gene locus is defined as the exons belonging to genes.

## Usage

```
locusdef.rn4.exon
```

## Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn4.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:51:59 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

---

`locusdef.rn4.intron` *locusdef.rn4.intron locus definition*

---

## Description

A `LocusDefinition` where a gene locus is defined as the introns belonging to genes.

## Usage

```
locusdef.rn4.intron
```

## Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn4.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:52:00 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

---

`locusdef.rn4.nearest_gene`
*locusdef.rn4.nearest_gene locus definition*

---

## Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

## Usage

```
locusdef.rn4.nearest_gene
```

## Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn4.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:51:58 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

---

`locusdef.rn4.nearest_tss`

# *locusdef.rn4.nearest_tss locus definition*

## Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

## Usage

```
locusdef.rn4.nearest_tss
```

## Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn4.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

For the rn4 genome, original gene IDs are from ENSEMBL and so an additional step of converting to Entrez IDs is done.

Built on Fri Apr 13 09:51:58 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

---

# `locusdef.rn5.10kb` *locusdef.rn5.10kb locus definition*

## Description

A `LocusDefinition` where a gene locus is defined within 10kb upstream and downstream of the TSS.

## Usage

```
locusdef.rn5.10kb
```

## Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn5.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:20 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

---

# `locusdef.rn5.10kb_outside` *locusdef.rn5.10kb_outside locus definition*

## Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

## Usage

```
locusdef.rn5.10kb_outside
```

## Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn5.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:21 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

---

`locusdef.rn5.10kb_outside_upstream`

# *locusdef.rn5.10kb_outside_upstream locus definition*

## Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

## Usage

```
locusdef.rn5.10kb_outside_upstream
```

## Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn5.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:21 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

---

## `locusdef.rn5.1kb` *locusdef.rn5.1kb locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined within 1kb upstream and downstream of the TSS.

### Usage

```
locusdef.rn5.1kb
```

### Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn5.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

### Details

Built on Fri Apr 13 09:52:19 2018.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

---

## `locusdef.rn5.1kb_outside` *locusdef.rn5.1kb_outside locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

### Usage

```
locusdef.rn5.1kb_outside
```

## Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn5.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:19 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

---

`locusdef.rn5.1kb_outside_upstream`

# *locusdef.rn5.1kb_outside_upstream locus definition*

## Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

## Usage

```
locusdef.rn5.1kb_outside_upstream
```

## Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn5.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:19 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

---

## `locusdef.rn5.5kb` *locusdef.rn5.5kb locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined within 5kb upstream and downstream of the TSS.

### Usage

```
locusdef.rn5.5kb
```

### Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn5.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

### Details

Built on Fri Apr 13 09:52:20 2018.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

---

## `locusdef.rn5.5kb_outside` *locusdef.rn5.5kb_outside locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

### Usage

```
locusdef.rn5.5kb_outside
```

## Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn5.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:20 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

---

`locusdef.rn5.5kb_outside_upstream`

# *locusdef.rn5.5kb_outside_upstream locus definition*

## Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

## Usage

```
locusdef.rn5.5kb_outside_upstream
```

## Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn5.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:20 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

---

## `locusdef.rn5.exon` *locusdef.rn5.exon locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the exons belonging to genes.

### Usage

```
locusdef.rn5.exon
```

### Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn5.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

### Details

Built on Fri Apr 13 09:52:17 2018.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

---

## `locusdef.rn5.intron` *locusdef.rn5.intron locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the introns belonging to genes.

### Usage

```
locusdef.rn5.intron
```

### Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn5.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:19 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

---

`locusdef.rn5.nearest_gene`

# *locusdef.rn5.nearest_gene locus definition*

---

## Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

## Usage

```
locusdef.rn5.nearest_gene
```

## Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn5.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:16 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

---

## `locusdef.rn5.nearest_tss` *locusdef.rn5.nearest_tss locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

### Usage

```
locusdef.rn5.nearest_tss
```

### Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn5.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

### Details

Built on Fri Apr 13 09:52:16 2018.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

---

## `locusdef.rn6.10kb` *locusdef.rn6.10kb locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined within 10kb upstream and downstream of the TSS.

### Usage

```
locusdef.rn6.10kb
```

## Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn6.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:39 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

---

# `locusdef.rn6.10kb_outside` *locusdef.rn6.10kb_outside locus definition*

## Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

## Usage

```
locusdef.rn6.10kb_outside
```

## Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn6.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:40 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

---

`locusdef.rn6.10kb_outside_upstream` *locusdef.rn6.10kb_outside_upstream locus definition*

---

## Description

A `LocusDefinition` where a gene locus is defined as the region beyond 10kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

## Usage

```
locusdef.rn6.10kb_outside_upstream
```

## Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn6.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:39 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

---

`locusdef.rn6.1kb` *locusdef.rn6.1kb locus definition*

---

## Description

A `LocusDefinition` where a gene locus is defined within 1kb upstream and downstream of the TSS.

## Usage

```
locusdef.rn6.1kb
```

## Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn6.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:38 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

---

`locusdef.rn6.1kb_outside`

# *locusdef.rn6.1kb_outside locus definition*

## Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

## Usage

```
locusdef.rn6.1kb_outside
```

## Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn6.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:38 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

---

## `locusdef.rn6.1kb_outside_upstream` *locusdef.rn6.1kb_outside_upstream locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the region beyond 1kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

### Usage

```
locusdef.rn6.1kb_outside_upstream
```

### Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn6.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

### Details

Built on Fri Apr 13 09:52:38 2018.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

---

## `locusdef.rn6.5kb` *locusdef.rn6.5kb locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined within 5kb upstream and downstream of the TSS.

### Usage

```
locusdef.rn6.5kb
```

## Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn6.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:38 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

---

`locusdef.rn6.5kb_outside`

# *locusdef.rn6.5kb_outside locus definition*

---

## Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream and downstream of the TSS and bounded by the midpoints between the TSS and the next upstream and downstream TSSs.

## Usage

```
locusdef.rn6.5kb_outside
```

## Format

A `LocusDefinition` object with the following slots:

- **granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`
- **dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`
- **genome.build** A `character` indicating the genome build. In this case, rn6.
- **organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:39 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

---

## `locusdef.rn6.5kb_outside_upstream` *locusdef.rn6.5kb_outside_upstream locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the region beyond 5kb upstream of the TSS and bounded by the midpoint between the TSS and the next upstream TSS.

### Usage

```
locusdef.rn6.5kb_outside_upstream
```

### Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn6.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

### Details

Built on Fri Apr 13 09:52:39 2018.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

---

## `locusdef.rn6.exon` *locusdef.rn6.exon locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the exons belonging to genes.

### Usage

```
locusdef.rn6.exon
```

### Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn6.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

### Details

Built on Fri Apr 13 09:52:36 2018.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

---

## `locusdef.rn6.intron` *locusdef.rn6.intron locus definition*

### Description

A `LocusDefinition` where a gene locus is defined as the introns belonging to genes.

### Usage

```
locusdef.rn6.intron
```

### Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn6.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

### Details

Built on Fri Apr 13 09:52:37 2018.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

---

`locusdef.rn6.nearest_gene`

## *locusdef.rn6.nearest_gene locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs and TESs.

### Usage

```
locusdef.rn6.nearest_gene
```

### Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn6.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

### Details

Built on Fri Apr 13 09:52:35 2018.

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

---

`locusdef.rn6.nearest_tss`

## *locusdef.rn6.nearest_tss locus definition*

---

### Description

A `LocusDefinition` where a gene locus is defined as the region spanning the midpoints between adjacent TSSs.

### Usage

```
locusdef.rn6.nearest_tss
```

## Format

A `LocusDefinition` object with the following slots:

**granges** A `GRanges` of the locus definitions with `mcols` for Entrez Gene ID `gene_id` and gene symbol `symbol`

**dframe** A `data.frame` of the locus definitions with columns for `chr`, `start`, `end`, `gene_id`, and `symbol`

**genome.build** A `character` indicating the genome build. In this case, rn6.

**organism** A `character` indicating the organism name. In this case, Rattus norvegicus.

## Details

Built on Fri Apr 13 09:52:34 2018.

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

---

# `LocusDefinition-class` *Class* `"LocusDefinition"`

## Description

A storage class representing gene locus definitions and their corresponding metadata.

## Objects from the Class

Objects can be created by calls of the form `new("LocusDefinition")`. These objects are used internally by the `chipenrich` package and users will not likely need to create these.

## Slots

`dframe`**:** Object of class `"data.frame"`. Each row represents a locus for a particular geneid.

`granges`**:** Object of class `"GenomicRanges"`. Locus definitions stored as a GenomicRanges object.

`genome.build`**:** Object of class `"character"`. Genome build these definitions were generated from.

`organism`**:** Object of class `"character"`. Organism code.

## Note

Not typically accessed by the user - this is used internally by the `chipenrich` package.

## Author(s)

Ryan Welch `<welchr@umich.edu>`

## Examples

```
# Show info about the class.
showClass("LocusDefinition");

# Example of what a locus definition object looks like.
data(locusdef.mm9.nearest_tss)
lapply(attributes(locusdef.mm9.nearest_tss), head)
```

---

# `mappa.hg19.10kb.100mer` *mappa.hg19.10kb.100mer*

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.10kb.100mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.hg19.10kb.24mer` *mappa.hg19.10kb.24mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.10kb.24mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.hg19.10kb.36mer` *mappa.hg19.10kb.36mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.10kb.36mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.hg19.10kb.40mer` *mappa.hg19.10kb.40mer*

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.10kb.40mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.hg19.10kb.50mer` *mappa.hg19.10kb.50mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.10kb.50mer)
```

### Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.hg19.10kb.75mer` *mappa.hg19.10kb.75mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.10kb.75mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

# `mappa.hg19.1kb.100mer` *mappa.hg19.1kb.100mer*

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.1kb.100mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.hg19.1kb.24mer` *mappa.hg19.1kb.24mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.1kb.24mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.hg19.1kb.36mer` *mappa.hg19.1kb.36mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.1kb.36mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.hg19.1kb.40mer` *mappa.hg19.1kb.40mer*

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.1kb.40mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.hg19.1kb.50mer` *mappa.hg19.1kb.50mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.1kb.50mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.hg19.1kb.75mer` *mappa.hg19.1kb.75mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 1kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.1kb.75mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch `<welchr@umich.edu>`

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

# `mappa.hg19.5kb.100mer` *mappa.hg19.5kb.100mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.5kb.100mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch `<welchr@umich.edu>`

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.5kb.24mer` *mappa.hg19.5kb.24mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.5kb.24mer)
```

### Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.5kb.36mer` *mappa.hg19.5kb.36mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.5kb.36mer)
```

### Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.hg19.5kb.40mer` *mappa.hg19.5kb.40mer*

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.5kb.40mer)
```

### Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.5kb.50mer` *mappa.hg19.5kb.50mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.5kb.50mer)
```

### Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.5kb.75mer` *mappa.hg19.5kb.75mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 5kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.5kb.75mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.exon.100mer`

## *mappa.hg19.exon.100mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.exon.100mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.hg19.exon.24mer` *mappa.hg19.exon.24mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.exon.24mer)
```

### Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.hg19.exon.36mer` *mappa.hg19.exon.36mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.exon.36mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.exon.40mer` *mappa.hg19.exon.40mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.exon.40mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.hg19.exon.50mer` *mappa.hg19.exon.50mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.exon.50mer)
```

### Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.hg19.exon.75mer` *mappa.hg19.exon.75mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: exon
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.exon.75mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.intron.100mer`

## *mappa.hg19.intron.100mer*

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.intron.100mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.intron.24mer`

## *mappa.hg19.intron.24mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.intron.24mer)
```

### Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.intron.36mer`

## *mappa.hg19.intron.36mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.intron.36mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.intron.40mer`

## *mappa.hg19.intron.40mer*

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.intron.40mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.hg19.intron.50mer` *mappa.hg19.intron.50mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.intron.50mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.hg19.intron.75mer` *mappa.hg19.intron.75mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: intron
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.intron.75mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.nearest_gene.100mer`

# *mappa.hg19.nearest_gene.100mer*

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.nearest_gene.100mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.nearest_gene.24mer`

## *mappa.hg19.nearest_gene.24mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.nearest_gene.24mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.nearest_gene.36mer`

## *mappa.hg19.nearest_gene.36mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.nearest_gene.36mer)
```

## Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

## Author(s)

Ryan Welch `<welchr@umich.edu>`

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.nearest_gene.40mer`

# *mappa.hg19.nearest_gene.40mer*

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.nearest_gene.40mer)
```

## Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

## Author(s)

Ryan Welch `<welchr@umich.edu>`

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.nearest_gene.50mer`

## *mappa.hg19.nearest_gene.50mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.nearest_gene.50mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.nearest_gene.75mer`

## *mappa.hg19.nearest_gene.75mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_gene
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.nearest_gene.75mer)
```

### Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.nearest_tss.100mer`

## *mappa.hg19.nearest_tss.100mer*

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.nearest_tss.100mer)
```

### Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.nearest_tss.24mer`

*mappa.hg19.nearest_tss.24mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 24mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.nearest_tss.24mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.nearest_tss.36mer`

*mappa.hg19.nearest_tss.36mer*

---

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.nearest_tss.36mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.nearest_tss.40mer`

# *mappa.hg19.nearest_tss.40mer*

## Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.hg19.nearest_tss.40mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.nearest_tss.50mer`
*mappa.hg19.nearest_tss.50mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.nearest_tss.50mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.hg19.nearest_tss.75mer`
*mappa.hg19.nearest_tss.75mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: nearest_tss
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.hg19.nearest_tss.75mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

# `mappa.mm9.10kb.100mer` *mappa.mm9.10kb.100mer*

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.mm9.10kb.100mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.mm9.10kb.36mer` *mappa.mm9.10kb.36mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.10kb.36mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.mm9.10kb.40mer` *mappa.mm9.10kb.40mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.10kb.40mer)
```

### Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.mm9.10kb.50mer` *mappa.mm9.10kb.50mer*

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.10kb.50mer)
```

### Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.mm9.10kb.75mer` *mappa.mm9.10kb.75mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.10kb.75mer)
```

### Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.mm9.1kb.100mer` *mappa.mm9.1kb.100mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.1kb.100mer)
```

### Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.mm9.1kb.36mer` *mappa.mm9.1kb.36mer*

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.1kb.36mer)
```

### Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.mm9.1kb.40mer` *mappa.mm9.1kb.40mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.1kb.40mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.mm9.1kb.50mer` *mappa.mm9.1kb.50mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.1kb.50mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.mm9.1kb.75mer` *mappa.mm9.1kb.75mer*

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.1kb.75mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.mm9.5kb.100mer` *mappa.mm9.5kb.100mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.5kb.100mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.mm9.5kb.36mer` *mappa.mm9.5kb.36mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.5kb.36mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

# `mappa.mm9.5kb.40mer` *mappa.mm9.5kb.40mer*

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.mm9.5kb.40mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.mm9.5kb.50mer` *mappa.mm9.5kb.50mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.5kb.50mer)
```

### Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.mm9.5kb.75mer` *mappa.mm9.5kb.75mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.5kb.75mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

# `mappa.mm9.exon.100mer` *mappa.mm9.exon.100mer*

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.mm9.exon.100mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.mm9.exon.36mer` *mappa.mm9.exon.36mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.exon.36mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.mm9.exon.40mer` *mappa.mm9.exon.40mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.exon.40mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.mm9.exon.50mer` *mappa.mm9.exon.50mer*

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.exon.50mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.mm9.exon.75mer` *mappa.mm9.exon.75mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.exon.75mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.mm9.intron.100mer` *mappa.mm9.intron.100mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.intron.100mer)
```

## Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.mm9.intron.36mer`

# *mappa.mm9.intron.36mer*

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.mm9.intron.36mer)
```

## Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.mm9.intron.40mer`

## *mappa.mm9.intron.40mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.intron.40mer)
```

### Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.mm9.intron.50mer`

## *mappa.mm9.intron.50mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.intron.50mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.mm9.intron.75mer`

## *mappa.mm9.intron.75mer*

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.intron.75mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.mm9.nearest_gene.100mer`

## *mappa.mm9.nearest_gene.100mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.nearest_gene.100mer)
```

### Format

A data frame containing:

| | |
|---|---|
| `geneid` | Entrez Gene IDs |
| `mappa` | Gene locus mappability |

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.mm9.nearest_gene.36mer`

## *mappa.mm9.nearest_gene.36mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.nearest_gene.36mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.mm9.nearest_gene.40mer`

# *mappa.mm9.nearest_gene.40mer*

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.mm9.nearest_gene.40mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.mm9.nearest_gene.50mer` *mappa.mm9.nearest_gene.50mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.nearest_gene.50mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

## `mappa.mm9.nearest_gene.75mer` *mappa.mm9.nearest_gene.75mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.nearest_gene.75mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.mm9.nearest_tss.100mer`

## *mappa.mm9.nearest_tss.100mer*

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 100mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.nearest_tss.100mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.mm9.nearest_tss.36mer`

*mappa.mm9.nearest_tss.36mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 36mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.nearest_tss.36mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.mm9.nearest_tss.40mer`

*mappa.mm9.nearest_tss.40mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 40mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.nearest_tss.40mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.mm9.nearest_tss.50mer`

# *mappa.mm9.nearest_tss.50mer*

## Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 50mer

These objects are used internally by the `chipenrich` package.

## Usage

```
data(mappa.mm9.nearest_tss.50mer)
```

## Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

## Author(s)

Ryan Welch <`welchr@umich.edu`>

## See Also

For more information about gene locus definitions: `chipenrich.data`

---

`mappa.mm9.nearest_tss.75mer`

## *mappa.mm9.nearest_tss.75mer*

---

### Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 75mer

These objects are used internally by the `chipenrich` package.

### Usage

```
data(mappa.mm9.nearest_tss.75mer)
```

### Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

### Author(s)

Ryan Welch <`welchr@umich.edu`>

### See Also

For more information about gene locus definitions: `chipenrich.data`

---

`peaks_E2F4`

## *ChIP-seq Peaks for the E2F4 Transcription Factor*

---

### Description

A dataset containing the binding locations (peaks) of the transcription factor E2F4 called from a ChIP-seq experiment

### Usage

```
peaks_E2F4
```

### Format

A data frame containing 16,245 peak binding locations. Each row is a peak location, and the 3 variables/columns are chromosome, start peak coordinate, and end peak coordinate. Peak coordinates are in hg19 (UCSC) coordinates.

### Source

The data and information regarding the experiment can be found in the following publication:

Lee, B. K., A. A. Bhinge, et al. (2011). "Wide-ranging functions of E2F4 in transcriptional activation and repression revealed by genome-wide analysis." Nucleic Acids Res 39(9): 3558-3573.

### Examples

```
# Load E2F4 peak data.
data(peaks_E2F4)

# Print the first 10 peaks in the dataset.
print(head(peaks_E2F4))
```

---

## `peaks_H3K4me3_GM12878` *ChIP-seq Peaks for the Histone Modification H3K4me3 in GM12878*

### Description

A dataset containing the binding locations (peaks) of the histone modification H3K4me3 called from a ChIP-seq experiment in the GM12878 cell line

### Usage

```
peaks_H3K4me3_GM12878
```

### Format

A data frame containing 57,476 peak binding locations. Each row is a peak location, and the 3 variables/columns are chromosome, start peak coordinate, and end peak coordinate. Peak coordinates are in hg19 (UCSC) coordinates.

### Source

The data and information regarding the experiment can be found at the following ENCODE URL:

http://hgdownload.cse.ucsc.edu/goldenPath/hg19/encodeDCC/wgEncodeBroadHistone/wgEncodeBroadHistoneGm128

### Examples

```
# Load H3K4me3 in GM12878 peak data.
data(peaks_H3K4me3_GM12878)

# Print the first 10 peaks in the dataset.
print(head(peaks_H3K4me3_GM12878))
```

---

## `spline.log_dtss.90ENCODE` *DTSS Spline adjustment*

---

### Description

A mgcv::gam object on a combined data of 90 ENCODE ChIP-seq datasets that modeled the relationship between a gene's locus length the distance from a peak to the gene's transcription start site, using a cubic spline. This is used to adjust for the proximity to TSSes test.

### Usage

```
spline.log_dtss.90ENCODE
```

### Format

An object of class `gam` (inherits from `glm`, `lm`) of length 46.

---

## `tss.danRer10` *tss.danRer10 TSS locations*

---

### Description

A `GRanges` with all the TSSs for danRer10. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

### Usage

```
tss.danRer10
```

### Format

A `GRanges` object with the following `mcols`:

**gene_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

### Source

R packages: TxDb.Drerio.UCSC.danRer10.refGene_3.4.2 and org.Dr.eg.db_3.5.0.

---

## `tss.dm3` *tss.dm3 TSS locations*

---

### Description

A `GRanges` with all the TSSs for dm3. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

### Usage

```
tss.dm3
```

### Format

A `GRanges` object with the following `mcols`:

**gene_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

### Source

R packages: TxDb.Dmelanogaster.UCSC.dm3.ensGene_3.2.2 and org.Dm.eg.db_3.5.0.

---

## `tss.dm6` *tss.dm6 TSS locations*

---

### Description

A `GRanges` with all the TSSs for dm6. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

### Usage

```
tss.dm6
```

### Format

A `GRanges` object with the following `mcols`:

**gene_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

### Source

R packages: TxDb.Dmelanogaster.UCSC.dm6.ensGene_3.4.1 and org.Dm.eg.db_3.5.0.

---

## `tss.hg19` *tss.hg19 TSS locations*

---

### Description

A `GRanges` with all the TSSs for hg19. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

### Usage

```
tss.hg19
```

### Format

A `GRanges` object with the following `mcols`:

**gene_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

### Source

R packages: TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.annota
and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/GRCh37_mapping/gencode.v25lift37.metadata.Entr

---

## `tss.hg38` *tss.hg38 TSS locations*

---

### Description

A `GRanges` with all the TSSs for hg38. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

### Usage

```
tss.hg38
```

### Format

A `GRanges` object with the following `mcols`:

**gene_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

### Source

R packages: TxDb.Hsapiens.UCSC.hg38.knownGene_3.4.0 and org.Hs.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_human/release_25/gencode.v25.metadata.EntrezGene.gz

---

`tss.mm10` *tss.mm10 TSS locations*

---

### Description

A `GRanges` with all the TSSs for mm10. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

### Usage

```
tss.mm10
```

### Format

A `GRanges` object with the following `mcols`:

**gene_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

### Source

R packages: TxDb.Mmusculus.UCSC.mm10.knownGene_3.4.0 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M12/gencode.vM12.metadata.EntrezGene.gz

---

`tss.mm9` *tss.mm9 TSS locations*

---

### Description

A `GRanges` with all the TSSs for mm9. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

### Usage

```
tss.mm9
```

### Format

A `GRanges` object with the following `mcols`:

**gene_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

### Source

R packages: TxDb.Mmusculus.UCSC.mm9.knownGene_3.2.2 and org.Mm.eg.db_3.5.0. GENCODE resources: ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.annotation.gff3.gz and ftp://ftp.sanger.ac.uk/pub/gencode/Gencode_mouse/release_M9/gencode.vM9.metadata.EntrezGene.gz

---

## `tss.rn4` *tss.rn4 TSS locations*

### Description

A `GRanges` with all the TSSs for rn4. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

### Usage

```
tss.rn4
```

### Format

A `GRanges` object with the following `mcols`:

**gene_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn4.ensGene_3.2.2 and org.Rn.eg.db_3.5.0.

---

## `tss.rn5` *tss.rn5 TSS locations*

### Description

A `GRanges` with all the TSSs for rn5. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

### Usage

```
tss.rn5
```

### Format

A `GRanges` object with the following `mcols`:

**gene_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

### Source

R packages: TxDb.Rnorvegicus.UCSC.rn5.refGene_3.4.2 and org.Rn.eg.db_3.5.0.

---

`tss.rn6` *tss.rn6 TSS locations*

---

## Description

A `GRanges` with all the TSSs for rn6. Primarily used in the `assign_peaks()` function to report distance of a peak to the nearest TSS. Also used to build the QC plot with distribution of peaks to TSSs.

## Usage

```
tss.rn6
```

## Format

A `GRanges` object with the following `mcols`:

**gene_id** The Entrez ID for the TSS

**symbol** The gene symbol for the TSS

## Source

R packages: TxDb.Rnorvegicus.UCSC.rn6.refGene_3.4.1 and org.Rn.eg.db_3.5.0.

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