Package 'chipenrich.data'

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

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LazyLoad yes

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`chipenrich.data-package`

Datasets required for the chipenrich package

Description

This package includes genesets (KEGG, GO, etc.), gene locus definitions, gene locus mappabilities, and other required data for the chipenrich package. It also includes example ChIP-seq peak datasets for use with chipenrich.

Details

Almost all of the datasets within this package, with the exception of the example ChIP-seq peak datasets, are not intended for direct use by the user. They are automatically used by the `chipenrich` package itself. This help file attempts to document each data source should a user wish to understand how each is computed, where it came from, etc.

Genesets are exactly that - sets of genes - as defined in various databases such as KEGG, Gene Ontology, and others.

Each geneset is stored per genome in the format "geneset.<name of geneset>.<genome build>", use `data(package="chipenrich.data")` for a full list.

Each geneset and the description for how it was generated can be found at:

http://sartorlab.ccmb.med.umich.edu/sites/default/files/pdf/geneset_information.pdf.

Gene locus definitions define regions in which peaks are assigned to genes. If a peak falls into a particular gene locus, it is assigned to that gene. Within the package, locus definitions are stored per genome and per definition in the format "locusdef.<genome>.<definition code>". We support multiple definitions currently:

- `nearest_tss`: assigns peaks to the gene with the closest transcription start site (TSS). Each gene locus stretches from the midpoint upstream between TSSs, and the midpoint downstream between TSSs.
- `nearest_gene`: assigns peaks to the nearest gene. Each gene locus stretches from the upstream midpoint between genes and the downstream midpoint between genes.
- `1kb`: each gene locus is defined as the region 1KB up- and down-stream of the TSS.
- `5kb`: each gene locus is defined as the region 5KB up- and down-stream of the TSS.
- `10kb`: each gene locus is defined as the region 10KB up- and down-stream of the TSS.
- `10kb_and_more_upstream`: each gene locus is defined as the region greater than 10KB upstream of the TSS.
- `exon`: each gene locus is defined as the exonic regions of each gene. In the case where exons from multiple transcripts of the same gene may overlap, the region was reduced to one non-overlapping region.
- `intron`: each gene locus is defined as the intronic regions of each gene, that is, the region between two non-overlapping exons of transcripts belonging to the same gene.

The mappability datasets stored within this package represent the average mappability per locus definition (above.) They are stored in the following format: "mappa.<genome build>.<locus definition code>.<read length>". Each dataset is simply an entrez ID, and the mappability score computed for the gene under the given locus definition and read length. For more information regarding how mappability is included, please see (Welch & Lee, 2014.)

Example ChIP-seq peak datasets are also included, and can be used for running `chipenrich`. Each dataset is stored as "peaks_<name of protein/transcription factor>". Use `example_datasets` or `data(package="chipenrich.data")` for a list.

Author(s)

Ryan Welch <welchr@umich.edu>

References

R.P. Welch*, C. Lee*, R.A. Smith, P. Imbriano, S. Patil, T. Weymouth, L.J. Scott, M.A. Sartor. "ChIP-Enrich: gene set enrichment testing for ChIP-seq data." Nucl. Acids Res. (2014) 42(13):e105. doi:10.1093/nar/gku463

Examples

```
# Get a list of all ChIP-seq peak example datasets.
example_datasets();

# Inspect an example geneset.
data("geneset.kegg_pathway.hsa");
str(geneset.kegg_pathway.hsa);

# Get the mappings from geneset ID to genes for KEGG (loaded above)
kegg_to_genes = as.list(geneset.kegg_pathway.hsa@set.gene);
```

```
# Get the mappings from geneset ID to geneset descriptions for KEGG
kegg_to_names = as.list(geneset.kegg_pathway.hsa@set.name);

# List all genes within KEGG pathways (as Entrez IDs.)
kegg_genes = geneset.kegg_pathway.hsa@all.genes;

# Inspect an example locus definition.
data(locusdef.hg19.nearest_tss);
str(locusdef.hg19.nearest_tss);

# Get a data frame specifying each gene locus, its chromosome, and start/end positions.
ldef = locusdef.hg19.nearest_tss@dframe;

# Get a GRanges object containing each locus definition for fast lookups.
granges = locusdef.hg19.nearest_tss@granges;
```

`example_datasets` *List ChIP-seq peak example datasets*

Description

Convenience function to list the example ChIP-seq peak datasets available for use with `chipenrich`.

Usage

```
example_datasets()
```

Details

Prints a list of all example datasets, and a tip on how to load them.

Author(s)

Ryan Welch <welchr@umich.edu>

Examples

```
library(chipenrich.data)
example_datasets()
```

`genes.dme` *genes.dme*

Description

Entrez Gene IDs for D. melanogaster and their corresponding gene symbols.

This is used internally by the `chipenrich` package.

Usage

```
data(genes.hsa)
```

Format

A data frame with 6790 observations on the following 2 variables.

`GENEID` Entrez Gene IDs

`SYMBOL` Official gene symbols

Author(s)

Chee Lee <cheelee@umich.edu>

See Also

chipenrich.data

`genes.hsa` *genes.hsa*

Description

Entrez Gene IDs for H. sapiens and their corresponding gene symbols.

This is used internally by the `chipenrich` package.

Usage

```
data(genes.hsa)
```

Format

A data frame with 19781 observations on the following 2 variables.

`GENEID` Entrez Gene IDs

`SYMBOL` Official gene symbols

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

chipenrich.data

genes.mmu *genes.mmu*

Description

Entrez Gene IDs for M. musculus and their corresponding gene symbols.
This is used internally by the chipenrich package.

Usage

```
data(genes.mmu)
```

Format

A data frame with 21388 observations on the following 2 variables.

GENEID Entrez Gene IDs
SYMBOL Official gene symbols

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

chipenrich.data

genes.rno *genes.rno*

Description

Entrez Gene IDs for R. norvegicus and their corresponding gene symbols.
This is used internally by the chipenrich package.

Usage

```
data(genes.rno)
```

Format

A data frame with 19746 observations on the following 2 variables.

GENEID Entrez Gene IDs
SYMBOL Official gene symbols

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

chipenrich.data

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

```
library(chipenrich.data)

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

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

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

`geneset.biocarta_pathway.hsa` *geneset.biocarta_pathway.hsa*

Description

GeneSet object which stores information about sets of genes.

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

Usage

```
data(geneset.biocarta_pathway.hsa)
```

Format

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

See Also

For more information about genesets: `chipenrich.data`

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

`geneset.biocarta_pathway.mmu` *geneset.biocarta_pathway.mmu*

Description

GeneSet object which stores information about sets of genes.

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

Usage

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

Format

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

See Also

For more information about genesets: `chipenrich.data`

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

`geneset.biocarta_pathway.rno` *geneset.biocarta_pathway.rno*

Description

GeneSet object which stores information about sets of genes.

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

Usage

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

Format

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

See Also

For more information about genesets: `chipenrich.data`

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

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

Description

GeneSet object which stores information about sets of genes.

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

Usage

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

Format

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

See Also

For more information about genesets: `chipenrich.data`

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

geneset.drug_bank.hsa *geneset.drug_bank.hsa*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.drug_bank.hsa)
```

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

geneset.drug_bank.mmu *geneset.drug_bank.mmu*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

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

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

geneset.drug_bank.rno *geneset.drug_bank.rno*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

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

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

geneset.ehmn_pathway_gene.hsa *geneset.ehmn_pathway_gene.hsa*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.ehmn_pathway_gene.hsa)
```

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

geneset.ehmn_pathway_gene.mmu *geneset.ehmn_pathway_gene.mmu*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.ehmn_pathway_gene.mmu)
```

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

geneset.ehmn_pathway_gene.rno *geneset.ehmn_pathway_gene.rno*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.ehmn_pathway_gene.rno)
```

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

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geneset.gene_expression.hsa *geneset.gene_expression.hsa*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.gene_expression.hsa)
```

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

---

geneset.gene_expression.mmu *geneset.gene_expression.mmu*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

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

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

geneset.GOBP.dme *geneset.GOBP.dme*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.GOBP.dme)
```

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.hsa *geneset.GOBP.hsa*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.GOBP.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.GOBP.mmu *geneset.GOBP.mmu*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.GOBP.mmu)
```

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

geneset.GOBP.rno *geneset.GOBP.rno*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.GOBP.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.GOCC.dme *geneset.GOCC.dme*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.GOCC.dme)
```

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.GOCC.hsa *geneset.GOCC.hsa*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.GOCC.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.GOCC.mmu *geneset.GOCC.mmu*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.GOCC.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.GOCC.rno *geneset.GOCC.rno*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.GOCC.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.GOMF.dme *geneset.GOMF.dme*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.GOMF.dme)
```

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.GOMF.hsa *geneset.GOMF.hsa*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.GOMF.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.GOMF.mmu *geneset.GOMF.mmu*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.GOMF.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.GOMF.rno *geneset.GOMF.rno*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.GOMF.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.kegg_pathway.hsa *geneset.kegg_pathway.hsa*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.kegg_pathway.hsa)
```

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

geneset.kegg_pathway.mmu *geneset.kegg_pathway.mmu*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

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

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

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

Description

GeneSet object which stores information about sets of genes.

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

Usage

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

Format

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

See Also

For more information about genesets: `chipenrich.data`

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

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

Description

GeneSet object which stores information about sets of genes.

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

Usage

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

Format

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

See Also

For more information about genesets: `chipenrich.data`

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

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

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

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

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

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

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

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

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

---

geneset.metabolite.hsa

geneset.metabolite.hsa

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

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

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

---

geneset.metabolite.mmu

geneset.metabolite.mmu

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

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

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

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

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

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

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

geneset.mirbase.hsa *geneset.mirbase.hsa*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.mirbase.hsa)
```

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

geneset.mirbase.mmu *geneset.mirbase.mmu*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.mirbase.mmu)
```

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

geneset.mirbase.rno *geneset.mirbase.rno*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.mirbase.rno)
```

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

geneset.panther_pathway.hsa
geneset.panther_pathway.hsa

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

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

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

geneset.panther_pathway.mmu
geneset.panther_pathway.mmu

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

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

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

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

Description

GeneSet object which stores information about sets of genes.

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

Usage

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

Format

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

See Also

For more information about genesets: `chipenrich.data`

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

`geneset.pfam.hsa` *geneset.pfam.hsa*

Description

GeneSet object which stores information about sets of genes.

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

Usage

```
data(geneset.pfam.hsa)
```

Format

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

See Also

For more information about genesets: `chipenrich.data`

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

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

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

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

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

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

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

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

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

`geneset.protein_interaction_mimi.hsa`
geneset.protein_interaction_mimi.hsa

Description

GeneSet object which stores information about sets of genes.

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

Usage

```
data(geneset.protein_interaction_mimi.hsa)
```

Format

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

See Also

For more information about genesets: `chipenrich.data`

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

`geneset.protein_interaction_mimi.mmu`
geneset.protein_interaction_mimi.mmu

Description

GeneSet object which stores information about sets of genes.

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

Usage

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

Format

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

See Also

For more information about genesets: `chipenrich.data`

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

geneset.protein_interaction_mimi.rno *geneset.protein_interaction_mimi.rno*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

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

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

geneset.reactome.hsa *geneset.reactome.hsa*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.reactome.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.reactome.mmu *geneset.reactome.mmu*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.reactome.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.reactome.rno *geneset.reactome.rno*

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

```
data(geneset.reactome.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.transcription_factors.hsa`
geneset.transcription_factors.hsa

Description

GeneSet object which stores information about sets of genes.

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

Usage

```
data(geneset.transcription_factors.hsa)
```

Format

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

See Also

For more information about genesets: `chipenrich.data`

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

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

Description

GeneSet object which stores information about sets of genes.

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

Usage

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

Format

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

See Also

For more information about genesets: `chipenrich.data`

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

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

Description

GeneSet object which stores information about sets of genes.

These objects are used internally by the chipenrich package.

Usage

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

Format

See GeneSet-class for a description of the format.

See Also

For more information about genesets: chipenrich.data

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

locusdef.dm3.10kb *locusdef.dm3.10kb*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.dm3.10kb)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

locusdef.dm3.10kb_and_more_upstream *locusdef.dm3.10kb_and_more_upstream*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.dm3.10kb_and_more_upstream)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

locusdef.dm3.1kb *locusdef.dm3.1kb*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.dm3.1kb)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

locusdef.dm3.5kb *locusdef.dm3.5kb*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.dm3.5kb)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

locusdef.dm3.exon *locusdef.dm3.exon*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.dm3.exon)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

`locusdef.dm3.intron` *locusdef.dm3.intron*

Description

LocusDefinition object which stores information about gene locus definitions.

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

Usage

```
data(locusdef.dm3.intron)
```

Format

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

See Also

For more information about gene locus definitions: `chipenrich.data`

`locusdef.dm3.nearest_gene` *locusdef.dm3.nearest_gene*

Description

LocusDefinition object which stores information about gene locus definitions.

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

Usage

```
data(locusdef.dm3.nearest_gene)
```

Format

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

See Also

For more information about gene locus definitions: `chipenrich.data`

`locusdef.dm3.nearest_tss` *locusdef.dm3.nearest_tss*

Description

LocusDefinition object which stores information about gene locus definitions.

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

Usage

```
data(locusdef.dm3.nearest_tss)
```

Format

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

See Also

For more information about gene locus definitions: `chipenrich.data`

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

Description

LocusDefinition object which stores information about gene locus definitions.

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

Usage

```
data(locusdef.hg19.10kb)
```

Format

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

See Also

For more information about gene locus definitions: `chipenrich.data`

locusdef.hg19.10kb_and_more_upstream *locusdef.hg19.10kb_and_more_upstream*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.hg19.10kb_and_more_upstream)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

locusdef.hg19.1kb *locusdef.hg19.1kb*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.hg19.1kb)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

locusdef.hg19.5kb *locusdef.hg19.5kb*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.hg19.5kb)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

locusdef.hg19.exon *locusdef.hg19.exon*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.hg19.exon)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

`locusdef.hg19.intron` *locusdef.hg19.intron*

Description

LocusDefinition object which stores information about gene locus definitions.

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

Usage

```
data(locusdef.hg19.intron)
```

Format

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

See Also

For more information about gene locus definitions: `chipenrich.data`

`locusdef.hg19.nearest_gene` *locusdef.hg19.nearest_gene*

Description

LocusDefinition object which stores information about gene locus definitions.

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

Usage

```
data(locusdef.hg19.nearest_gene)
```

Format

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

See Also

For more information about gene locus definitions: `chipenrich.data`

locusdef.hg19.nearest_tss *locusdef.hg19.nearest_tss*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.hg19.nearest_tss)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

locusdef.mm10.10kb *locusdef.mm10.10kb*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.mm10.10kb)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

locusdef.mm10.10kb_and_more_upstream *locusdef.mm10.10kb_and_more_upstream*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.mm10.10kb_and_more_upstream)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

locusdef.mm10.1kb *locusdef.mm10.1kb*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.mm10.1kb)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

locusdef.mm10.5kb *locusdef.mm10.5kb*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.mm10.5kb)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

locusdef.mm10.exon *locusdef.mm10.exon*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.mm10.exon)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

`locusdef.mm10.intron` *locusdef.mm10.intron*

Description

LocusDefinition object which stores information about gene locus definitions.

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

Usage

```
data(locusdef.mm10.intron)
```

Format

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

See Also

For more information about gene locus definitions: `chipenrich.data`

`locusdef.mm10.nearest_gene` *locusdef.mm10.nearest_gene*

Description

LocusDefinition object which stores information about gene locus definitions.

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

Usage

```
data(locusdef.mm10.nearest_gene)
```

Format

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

See Also

For more information about gene locus definitions: `chipenrich.data`

`locusdef.mm10.nearest_tss` *locusdef.mm10.nearest_tss*

Description

LocusDefinition object which stores information about gene locus definitions.

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

Usage

```
data(locusdef.mm10.nearest_tss)
```

Format

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

See Also

For more information about gene locus definitions: `chipenrich.data`

`locusdef.mm9.10kb` *locusdef.mm9.10kb*

Description

LocusDefinition object which stores information about gene locus definitions.

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

Usage

```
data(locusdef.mm9.10kb)
```

Format

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

See Also

For more information about gene locus definitions: `chipenrich.data`

locusdef.mm9.10kb_and_more_upstream *locusdef.mm9.10kb_and_more_upstream*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.mm9.10kb_and_more_upstream)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

locusdef.mm9.1kb *locusdef.mm9.1kb*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.mm9.1kb)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

locusdef.mm9.5kb *locusdef.mm9.5kb*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.mm9.5kb)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

locusdef.mm9.exon *locusdef.mm9.exon*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.mm9.exon)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

`locusdef.mm9.intron` *locusdef.mm9.intron*

Description

LocusDefinition object which stores information about gene locus definitions.

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

Usage

```
data(locusdef.mm9.intron)
```

Format

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

See Also

For more information about gene locus definitions: `chipenrich.data`

`locusdef.mm9.nearest_gene` *locusdef.mm9.nearest_gene*

Description

LocusDefinition object which stores information about gene locus definitions.

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

Usage

```
data(locusdef.mm9.nearest_gene)
```

Format

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

See Also

For more information about gene locus definitions: `chipenrich.data`

`locusdef.mm9.nearest_tss` *locusdef.mm9.nearest_tss*

Description

LocusDefinition object which stores information about gene locus definitions.

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

Usage

```
data(locusdef.mm9.nearest_tss)
```

Format

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

See Also

For more information about gene locus definitions: `chipenrich.data`

`locusdef.rn4.10kb` *locusdef.rn4.10kb*

Description

LocusDefinition object which stores information about gene locus definitions.

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

Usage

```
data(locusdef.rn4.10kb)
```

Format

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

See Also

For more information about gene locus definitions: `chipenrich.data`

locusdef.rn4.10kb_and_more_upstream *locusdef.rn4.10kb_and_more_upstream*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.rn4.10kb_and_more_upstream)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

locusdef.rn4.1kb *locusdef.rn4.1kb*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.rn4.1kb)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

locusdef.rn4.5kb *locusdef.rn4.5kb*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.rn4.5kb)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

locusdef.rn4.exon *locusdef.rn4.exon*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.rn4.exon)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

`locusdef.rn4.intron` *locusdef.rn4.intron*

Description

LocusDefinition object which stores information about gene locus definitions.

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

Usage

```
data(locusdef.rn4.intron)
```

Format

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

See Also

For more information about gene locus definitions: `chipenrich.data`

`locusdef.rn4.nearest_gene` *locusdef.rn4.nearest_gene*

Description

LocusDefinition object which stores information about gene locus definitions.

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

Usage

```
data(locusdef.rn4.nearest_gene)
```

Format

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

See Also

For more information about gene locus definitions: `chipenrich.data`

locusdef.rn4.nearest_tss *locusdef.rn4.nearest_tss*

Description

LocusDefinition object which stores information about gene locus definitions.

These objects are used internally by the chipenrich package.

Usage

```
data(locusdef.rn4.nearest_tss)
```

Format

See LocusDefinition-class for a description of the format.

See Also

For more information about gene locus definitions: chipenrich.data

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.

chrom2iranges: Object of class "list". List mapping chromosomes to IRanges objects.

genome.build: Object of class "character". Genome build these definitions were generated from.

organism: Object of class "character". Organism code.

Note

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

Author(s)

Ryan Welch <welchr@umich.edu>

Examples

```
library(chipenrich.data)

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

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

`mappa.hg19.10kb.100mer`

mappa.hg19.10kb.100mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 100mer

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

Usage

```
data(mappa.hg19.10kb.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.10kb.24mer` *mappa.hg19.10kb.24mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 24mer

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

Usage

```
data(mappa.hg19.10kb.24mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.10kb.36mer` *mappa.hg19.10kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 36mer

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

Usage

```
data(mappa.hg19.10kb.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.10kb.40mer` *mappa.hg19.10kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 40mer

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

Usage

```
data(mappa.hg19.10kb.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.10kb.50mer` *mappa.hg19.10kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 50mer

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

Usage

```
data(mappa.hg19.10kb.50mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.hg19.10kb.75mer` *mappa.hg19.10kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb
- K-Mer Reads: 75mer

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

Usage

```
data(mappa.hg19.10kb.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: chipenrich.data

---

`mappa.hg19.10kb_and_more_upstream.100mer`
mappa.hg19.10kb_and_more_upstream.100mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb_and_more_upstream
- K-Mer Reads: 100mer

These objects are used internally by the chipenrich package.

Usage

```
data(mappa.hg19.10kb_and_more_upstream.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_and_more_upstream.24mer`
mappa.hg19.10kb_and_more_upstream.24mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb_and_more_upstream
- K-Mer Reads: 24mer

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

Usage

```
data(mappa.hg19.10kb_and_more_upstream.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_and_more_upstream.36mer`
mappa.hg19.10kb_and_more_upstream.36mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb_and_more_upstream
- K-Mer Reads: 36mer

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

Usage

```
data(mappa.hg19.10kb_and_more_upstream.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_and_more_upstream.40mer`
mappa.hg19.10kb_and_more_upstream.40mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb_and_more_upstream
- K-Mer Reads: 40mer

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

Usage

```
data(mappa.hg19.10kb_and_more_upstream.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_and_more_upstream.50mer`
mappa.hg19.10kb_and_more_upstream.50mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb_and_more_upstream
- K-Mer Reads: 50mer

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

Usage

```
data(mappa.hg19.10kb_and_more_upstream.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_and_more_upstream.75mer`
mappa.hg19.10kb_and_more_upstream.75mer

Description

Gene locus mappability data, calculated for:

- Build: hg19
- Locus definition: 10kb_and_more_upstream
- K-Mer Reads: 75mer

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

Usage

```
data(mappa.hg19.10kb_and_more_upstream.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.mm9.10kb_and_more_upstream.100mer`
mappa.mm9.10kb_and_more_upstream.100mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb_and_more_upstream
- K-Mer Reads: 100mer

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

Usage

```
data(mappa.mm9.10kb_and_more_upstream.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_and_more_upstream.36mer`
mappa.mm9.10kb_and_more_upstream.36mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb_and_more_upstream
- K-Mer Reads: 36mer

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

Usage

```
data(mappa.mm9.10kb_and_more_upstream.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_and_more_upstream.40mer`
mappa.mm9.10kb_and_more_upstream.40mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb_and_more_upstream
- K-Mer Reads: 40mer

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

Usage

```
data(mappa.mm9.10kb_and_more_upstream.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_and_more_upstream.50mer`
mappa.mm9.10kb_and_more_upstream.50mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb_and_more_upstream
- K-Mer Reads: 50mer

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

Usage

```
data(mappa.mm9.10kb_and_more_upstream.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_and_more_upstream.75mer`
mappa.mm9.10kb_and_more_upstream.75mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 10kb_and_more_upstream
- K-Mer Reads: 75mer

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

Usage

```
data(mappa.mm9.10kb_and_more_upstream.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: chipenrich.data

---

`mappa.mm9.1kb.100mer` *mappa.mm9.1kb.100mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 100mer

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

Usage

```
data(mappa.mm9.1kb.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.1kb.36mer` *mappa.mm9.1kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 36mer

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

Usage

```
data(mappa.mm9.1kb.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.1kb.40mer` *mappa.mm9.1kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 40mer

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

Usage

```
data(mappa.mm9.1kb.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: `chipenrich.data`

mappa.mm9.1kb.50mer *mappa.mm9.1kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 50mer

These objects are used internally by the chipenrich package.

Usage

```
data(mappa.mm9.1kb.50mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: chipenrich.data

mappa.mm9.1kb.75mer *mappa.mm9.1kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 1kb
- K-Mer Reads: 75mer

These objects are used internally by the chipenrich package.

Usage

```
data(mappa.mm9.1kb.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.5kb.100mer` *mappa.mm9.5kb.100mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 100mer

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

Usage

```
data(mappa.mm9.5kb.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: `chipenrich.data`

mappa.mm9.5kb.36mer *mappa.mm9.5kb.36mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 36mer

These objects are used internally by the chipenrich package.

Usage

```
data(mappa.mm9.5kb.36mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: chipenrich.data

mappa.mm9.5kb.40mer *mappa.mm9.5kb.40mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 40mer

These objects are used internally by the chipenrich package.

Usage

```
data(mappa.mm9.5kb.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.5kb.50mer` *mappa.mm9.5kb.50mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 50mer

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

Usage

```
data(mappa.mm9.5kb.50mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.5kb.75mer` *mappa.mm9.5kb.75mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: 5kb
- K-Mer Reads: 75mer

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

Usage

```
data(mappa.mm9.5kb.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.exon.100mer` *mappa.mm9.exon.100mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 100mer

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

Usage

```
data(mappa.mm9.exon.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.exon.36mer` *mappa.mm9.exon.36mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 36mer

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

Usage

```
data(mappa.mm9.exon.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: `chipenrich.data`

mappa.mm9.exon.40mer *mappa.mm9.exon.40mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 40mer

These objects are used internally by the chipenrich package.

Usage

```
data(mappa.mm9.exon.40mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: chipenrich.data

mappa.mm9.exon.50mer *mappa.mm9.exon.50mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 50mer

These objects are used internally by the chipenrich package.

Usage

```
data(mappa.mm9.exon.50mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.exon.75mer` *mappa.mm9.exon.75mer*

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: exon
- K-Mer Reads: 75mer

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

Usage

```
data(mappa.mm9.exon.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: `chipenrich.data`

---

mappa.mm9.intron.100mer

mappa.mm9.intron.100mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 100mer

These objects are used internally by the chipenrich package.

Usage

```
data(mappa.mm9.intron.100mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: chipenrich.data

---

mappa.mm9.intron.36mer

mappa.mm9.intron.36mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 36mer

These objects are used internally by the chipenrich package.

Usage

```
data(mappa.mm9.intron.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: chipenrich.data

---

`mappa.mm9.intron.40mer`

mappa.mm9.intron.40mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 40mer

These objects are used internally by the chipenrich package.

Usage

```
data(mappa.mm9.intron.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: chipenrich.data

---

mappa.mm9.intron.50mer

mappa.mm9.intron.50mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 50mer

These objects are used internally by the chipenrich package.

Usage

```
data(mappa.mm9.intron.50mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: chipenrich.data

---

mappa.mm9.intron.75mer

mappa.mm9.intron.75mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: intron
- K-Mer Reads: 75mer

These objects are used internally by the chipenrich package.

Usage

```
data(mappa.mm9.intron.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: chipenrich.data

---

`mappa.mm9.nearest_gene.100mer`
mappa.mm9.nearest_gene.100mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 100mer

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

Usage

```
data(mappa.mm9.nearest_gene.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: chipenrich.data

---

`mappa.mm9.nearest_gene.36mer`
mappa.mm9.nearest_gene.36mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 36mer

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

Usage

```
data(mappa.mm9.nearest_gene.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.nearest_gene.40mer`
mappa.mm9.nearest_gene.40mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 40mer

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

Usage

```
data(mappa.mm9.nearest_gene.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: chipenrich.data

---

`mappa.mm9.nearest_gene.50mer`

mappa.mm9.nearest_gene.50mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 50mer

These objects are used internally by the chipenrich package.

Usage

```
data(mappa.mm9.nearest_gene.50mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: chipenrich.data

---

mappa.mm9.nearest_gene.75mer

mappa.mm9.nearest_gene.75mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_gene
- K-Mer Reads: 75mer

These objects are used internally by the chipenrich package.

Usage

```
data(mappa.mm9.nearest_gene.75mer)
```

Format

A data frame containing:

geneid Entrez Gene IDs

mappa Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: chipenrich.data

---

mappa.mm9.nearest_tss.100mer

mappa.mm9.nearest_tss.100mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 100mer

These objects are used internally by the chipenrich package.

Usage

```
data(mappa.mm9.nearest_tss.100mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: chipenrich.data

---

`mappa.mm9.nearest_tss.36mer`
mappa.mm9.nearest_tss.36mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 36mer

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

Usage

```
data(mappa.mm9.nearest_tss.36mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: chipenrich.data

---

`mappa.mm9.nearest_tss.40mer`
mappa.mm9.nearest_tss.40mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 40mer

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

Usage

```
data(mappa.mm9.nearest_tss.40mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: `chipenrich.data`

`mappa.mm9.nearest_tss.50mer`
mappa.mm9.nearest_tss.50mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 50mer

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

Usage

```
data(mappa.mm9.nearest_tss.50mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: chipenrich.data

---

`mappa.mm9.nearest_tss.75mer`

mappa.mm9.nearest_tss.75mer

Description

Gene locus mappability data, calculated for:

- Build: mm9
- Locus definition: nearest_tss
- K-Mer Reads: 75mer

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

Usage

```
data(mappa.mm9.nearest_tss.75mer)
```

Format

A data frame containing:

`geneid` Entrez Gene IDs

`mappa` Gene locus mappability

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

For more information about gene locus definitions: chipenrich.data

peaks_E2F4 *ChIP-seq Peaks for the E2F4 Transcription Factor*

Description

A dataset containing the binding locations (peaks) of the transcription factor E2F4 called from a ChIP-seq experiment

Usage

```
peaks_E2F4
```

Format

A data frame containing 16,245 peak binding locations. Each row is a peak location, and the 3 variables/columns are chromosome, start peak coordinate, and end peak coordinate. Peak coordinates are in hg19 (UCSC) coordinates.

Source

The data and information regarding the experiment can be found in the following publication:

Lee, B. K., A. A. Bhinge, et al. (2011). "Wide-ranging functions of E2F4 in transcriptional activation and repression revealed by genome-wide analysis." Nucleic Acids Res 39(9): 3558-3573.

Examples

```
library(chipenrich.data)

# Load E2F4 peak data.
data(peaks_E2F4)

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

peaks_H3K4me3_GM12878 *ChIP-seq Peaks for the Histone Modification H3K4me3 in GM12878*

Description

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

Usage

```
peaks_H3K4me3_GM12878
```

Format

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

Source

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

http://hgdownload.cse.ucsc.edu/goldenPath/hg19/encodeDCC/wgEncodeBroadHistone/wgEncodeBroadHistoneGm128

Examples

```
library(chipenrich.data)

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

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

`tss.dm3` *tss.dm3*

Description

Transcription start site information for dm3.

This is used internally by the `chipenrich` package.

Usage

```
data(tss.dm3)
```

Format

A list containing:

`data` A data frame containing TSSs for each gene.

`ranges` A list mapping chromosomes to IRanges objects.

`granges` TSSs stored as a GenomicRanges object, including strand info.

Author(s)

Chee Lee <cheelee@umich.edu>

See Also

`chipenrich.data`

tss.hg19 *tss.hg19*

Description

Transcription start site information for hg19.

This is used internally by the chipenrich package.

Usage

```
data(tss.hg19)
```

Format

A list containing:

data A data frame containing TSSs for each gene.

ranges A list mapping chromosomes to IRanges objects.

granges TSSs stored as a GenomicRanges object, including strand info.

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

chipenrich.data

tss.mm10 *tss.mm10*

Description

Transcription start site information for mm10.

This is used internally by the chipenrich package.

Usage

```
data(tss.mm10)
```

Format

A list containing:

data A data frame containing TSSs for each gene.

ranges A list mapping chromosomes to IRanges objects.

granges TSSs stored as a GenomicRanges object, including strand info.

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

chipenrich.data

---

tss.mm9 *tss.mm9*

Description

Transcription start site information for mm9.

This is used internally by the chipenrich package.

Usage

```
data(tss.mm9)
```

Format

A list containing:

data A data frame containing TSSs for each gene.

ranges A list mapping chromosomes to IRanges objects.

granges TSSs stored as a GenomicRanges object, including strand info.

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

chipenrich.data

---

tss.rn4 *tss.rn4*

Description

Transcription start site information for rn4.

This is used internally by the chipenrich package.

Usage

```
data(tss.rn4)
```

Format

A list containing:

`data` A data frame containing TSSs for each gene.

`ranges` A list mapping chromosomes to IRanges objects.

`granges` TSSs stored as a GenomicRanges object, including strand info.

Author(s)

Ryan Welch <welchr@umich.edu>

See Also

chipenrich.data

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