

# Package ‘chromstaRData’

October 16, 2021

**Type** Package

**Title** ChIP-seq data for Demonstration Purposes

**Version** 1.18.0

**Date** 2016-06

**Author** Aaron Taudt

**Maintainer** Aaron Taudt <aaron.taudt@gmail.com>

**Description** ChIP-seq data for demonstration purposes in the chromstaR package.

**Depends** R (>= 3.3)

**License** GPL-3

**biocViews** Mus\_musculus\_Data, StemCell, ChIPSeqData

**NeedsCompilation** no

**RoxygenNote** 5.0.1

**git\_url** <https://git.bioconductor.org/packages/chromstaRData>

**git\_branch** RELEASE\_3\_13

**git\_last\_commit** 46bfa44

**git\_last\_commit\_date** 2021-05-19

**Date/Publication** 2021-10-16

## R topics documented:

chromstaRData . . . . .	2
experiment_table . . . . .	2
experiment_table_H4K20me1 . . . . .	2
experiment_table_SHR . . . . .	3
expression_lv . . . . .	3
m4_chrominfo . . . . .	3

<b>Index</b>	<b>4</b>
--------------	----------

---

chromstaRData	<i>ChIP-seq data from the EURATRANS project</i>
---------------	---

---

### Description

ChIP-seq data from the EURATRANS project for left-ventricle (lv) heart tissue in brown normay (BN) and spontaneous hypertensive rat (SHR). The data was downsampled to chr12 to reduce the file size for demonstration purposes.

### Format

BED files with aligned reads.

### Source

[www.euratrans.eu](http://www.euratrans.eu)

---

experiment_table	<i>Experiment data table for EURATRANS example</i>
------------------	--

---

### Description

Experiment data table for the EURTRANS data sets of left-ventricle (lv) heart tissue for usage in vignette examples of package **chromstaR**.

### Format

A data.frame with columns 'file', 'mark', 'condition', 'replicate' and 'pairedEndReads'.

---

experiment_table_H4K20me1	<i>Experiment data table for EURATRANS H4K20me1-example</i>
---------------------------	---

---

### Description

Experiment data table for the EURTRANS H4K20me1 data sets of left-ventricle (lv) heart tissue for usage in vignette examples of package **chromstaR**.

### Format

A data.frame with columns 'file', 'mark', 'condition', 'replicate' and 'pairedEndReads'.

---

experiment\_table\_SHR *Experiment data table for EURATRANS SHR-example*

---

**Description**

Experiment data table for the EURATRANS data sets of left-ventricle (lv) heart tissue in spontaneous hypertensive rat (SHR) for usage in vignette examples of package **chromstaR**.

**Format**

A data.frame with columns 'file', 'mark', 'condition', 'replicate' and 'pairedEndReads'.

---

expression\_lv *Expression data for the EURATRANS project*

---

**Description**

Expression values for left-ventricle (lv) heart tissue in brown norway (BN) and spontaneous hypertensive rat (SHR).

**Format**

A data.frame with columns 'ensembl\_gene\_id', 'expression\_BN' and 'expression\_SHR'

---

rn4\_chrominfo *Chromosome length information for rn4*

---

**Description**

Chromosome length information for rat assembly rn4.

**Format**

A data.frame with chromosome and length information.

**See Also**

[fetchExtendedChromInfoFromUCSC](#)

# Index

[chromstaRData](#), [2](#)

[euratrans \(chromstaRData\)](#), [2](#)

[experiment\\_table](#), [2](#)

[experiment\\_table\\_H4K20me1](#), [2](#)

[experiment\\_table\\_SHR](#), [3](#)

[expression\\_lv](#), [3](#)

[fetchExtendedChromInfoFromUCSC](#), [3](#)

[rat \(chromstaRData\)](#), [2](#)

[rn4\\_chrominfo](#), [3](#)