

# Package ‘chromstaRData’

July 3, 2025

**Type** Package

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

**Version** 1.34.0

**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\_21

**git\_last\_commit** 3fce415

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.21

**Date/Publication** 2025-07-03

## Contents

|                                     |   |
|-------------------------------------|---|
| chromstaRData . . . . .             | 2 |
| experiment_table . . . . .          | 2 |
| experiment_table_H4K20me1 . . . . . | 2 |
| experiment_table_SHR . . . . .      | 3 |
| expression_lv . . . . .             | 3 |
| rn4_chrominfo . . . . .             | 3 |

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

---

|              |                                                 |
|--------------|-------------------------------------------------|
| chromstaData | <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 | <i>Experiment data table for EURATRANS SHR-example</i> |
|----------------------|--------------------------------------------------------|

---

**Description**

Experiment data table for the EURTRANS 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 | <i>Expression data for the EURATRANS project</i> |
|---------------|--------------------------------------------------|

---

**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 | <i>Chromosome length information for rn4</i> |
|---------------|----------------------------------------------|

---

**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](#)