

# Package ‘chromstaRData’

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**Type** Package

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

**Version** 1.31.0

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**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** devel

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chromstaRData      *ChIP-seq data from the EURATRANS project*

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### 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)

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experiment\_table      *Experiment data table for EURATRANS example*

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### 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'.

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experiment\_table\_H4K20me1  
*Experiment data table for EURATRANS H4K20me1-example*

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### 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'.

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

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**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'.

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expression\_lv *Expression data for the EURATRANS project*

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**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'

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rn4\_chrominfo *Chromosome length information for rn4*

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**Description**

Chromosome length information for rat assembly rn4.

**Format**

A data.frame with chromosome and length information.

**See Also**

[fetchExtendedChromInfoFromUCSC](#)

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