# Package 'xcoredata'

October 27, 2026

**Type** Package

**Title** data package for xcore

**Version** 1.16.0

**Description** Provides data to use with xcore package.

**Depends** R (>= 4.2)

**Imports** ExperimentHub (>= 2.2.0), utils (>= 4.2.0)

**Suggests** BiocGenerics (>= 0.40.0), data.table (>= 1.14.2), GenomeInfoDb (>= 1.30.0), GenomicRanges (>= 1.46.1), IRanges (>= 2.28.0), knitr (>= 1.37), rmarkdown (>= 2.11), Matrix (>= 1.3.4), stringr (>= 1.4.0), S4Vectors (>= 0.32.3), TxDb.Hsapiens.UCSC.hg38.knownGene (>= 3.14.0), xcore

**License** GPL-2

**Encoding** UTF-8

**RoxygenNote** 7.1.2

**VignetteBuilder** knitr

**biocViews** ExperimentHub, ExperimentData, Homo_sapiens_Data

**git_url** https://git.bioconductor.org/packages/xcoredata

**git_branch** RELEASE_3_23

**git_last_commit** 7b335b4

**git_last_commit_date** 2026-04-28

**Repository** Bioconductor 3.23

**Date/Publication** 2026-10-27

**Author** Maciej Migdał [aut, cre] (ORCID: <https://orcid.org/0000-0002-8021-7263>), Bogumił Kaczkowski [aut] (ORCID: <https://orcid.org/0000-0001-6554-5608>)

**Maintainer** Maciej Migdał <mcjmigdal@gmail.com>

# Contents

chip_atlas_meta . . . . . 2
chip_atlas_promoters_f5 . . . . . 3
entrez2fantom . . . . . 3
promoters_f5 . . . . . 4
promoters_f5_core . . . . . 4
remap_meta . . . . . 5
remap_promoters_f5 . . . . . 6
symbol2fantom . . . . . 6

**Index** **7**

---

`chip_atlas_meta` *ChIP-Atlas metadata*

---

## Description

Metadata associated with `chip_atlas_promoters`.

## Usage

```
chip_atlas_meta
```

## Format

A `data.frame` with 13891 rows and 5 columns.

**id** Character giving internal experiment ID.

**tf** Character giving transcription factor name.

**tf_dbd** Character giving transcription factor DNA binding domain family, as per CIS BP database.

**biotype** Character giving experiment biological origin.

**study** Character giving study ID.

## Examples

```
chip_atlas_meta()
```

## chip_atlas_promoters_f5 *ChIP-Atlas FANTOM5 promoters intersection matrix*

### Description

An intersection matrix describing overlaps between ChIP-Atlas's ChIP-seq tracks and promoters_f5. To find overlapping regions promoters were extended by 500bp in both directions.

### Usage

```
chip_atlas_promoters_f5
```

### Format

A Matrix with 209911 rows and 13891 columns. Row names corresponds to promoters names, column names are formatted as TranscriptionFactor_Origin_Cell_ExperimentID (eg. PARK7_Neural_SH-SY5Y_DRX000550, MLL-AF6_Blood_ML-2_DRX001460).

### Examples

```
chip_atlas_promoters_f5()
```

## entrez2fantom *ENTREZ IDs to FANTOM5 core promoters names mappings*

### Description

Vector mapping ENTREZ IDs to FANTOM5 core promoters names.

### Usage

```
entrez2fantom
```

### Format

A named character vector of length 14214.

### Examples

```
entrez2fantom()
```

## promoters_f5 *Promoters GenomicRanges object*

### Description

FANTOM5's hg38 promoters annotated with nearest features in GENCODE ver. 38 annotation and UCSC hg38 knownGene annotation ver. 3.13.0.

### Usage

```
promoters_f5
```

### Format

A `GenomicRanges` object of length 209911, with 11 metadata columns:

**name** Promotor name.

**score** Numeric vector.

**gene_type_gencode** Gene type of associated gene as defined by GENCODE annotation.

**ENTREZID** ENTREZ ID of associated gene as defined by all three annotation sources. Prevalence of annotations: UCSC > GENCODE > FANTOM5.

**SYMBOL** Gene symbol of associated gene as defined by all three annotation sources. Prevalence of annotations: UCSC > GENCODE > FANTOM5.

### Examples

```
promoters_f5()
```

## promoters_f5_core *Core promoters GenomicRanges object*

### Description

Core promoters selected from promoters_f5. Selection criteria were GENCODE confirmation and ENCODE ROADMAP confirmation. Further for each gene single promoter with highest FANTOM5 score was selected.

### Usage

```
promoters_f5_core
```

## Format

A GenomicRanges object of length 14191, with 16 metadata columns:

**name** Promotor name.

**score** Numeric vector.

**gene_type_gencode** Gene type of associated gene as defined by GENCODE annotation.

**ENTREZID** ENTREZ ID of associated gene as defined by all three annotation sources. Prevalence of annotations: UCSC > GENCODE > FANTOM5.

**SYMBOL** Gene symbol of associated gene as defined by all three annotation sources. Prevalence of annotations: UCSC > GENCODE > FANTOM5.

## Examples

```
promoters_f5_core()
```

---

# remap_meta *ReMap2020 metadata*

---

## Description

Metadata associated with remap_promoters.

## Usage

```
remap_meta
```

## Format

A data.table with 5798 rows and 6 columns.

**id** Character giving internal experiment ID.

**tf** Character giving transcription factor name.

**tf_dbd** Character giving transcription factor DNA binding domain family, as per CIS BP database.

**biotype** Character giving experiment biological origin.

**study** Character giving study ID.

**condition** Character specifiying experiment conditions or treatment.

## Examples

```
remap_meta()
```

## remap_promoters_f5 *ReMap2020 and FANTOM5 promoters intersection matrix*

### Description

An intersection matrix describing overlaps between ReMap2020's ChIP-seq tracks and promoters_f5. To find overlapping regions promoters were extended by 500bp in both directions.

### Usage

```
remap_promoters_f5
```

### Format

A Matrix with 209911 rows and 5728 columns. Row names corresponds to promoters names, column names are formatted as ExperimentID.TranscriptionFactor.Biotype.

### Examples

```
remap_promoters_f5()
```

## symbol2fantom *Gene symbols to FANTOM5 core promoters names mappings*

### Description

Vector mapping gene symbols to FANTOM5 core promoters names.

### Usage

```
symbol2fantom
```

### Format

A named character vector of length 14222.

### Examples

```
symbol2fantom()
```

# Index

∗ **datasets**
chip_atlas_meta, 2
chip_atlas_promoters_f5, 3
entrez2fantom, 3
promoters_f5, 4
promoters_f5_core, 4
remap_meta, 5
remap_promoters_f5, 6
symbol2fantom, 6

chip_atlas_meta, 2
chip_atlas_promoters_f5, 3

entrez2fantom, 3

promoters_f5, *3*, 4, *6*
promoters_f5_core, 4

remap_meta, 5
remap_promoters_f5, 6

symbol2fantom, 6