

# Package ‘FunciSNP.data’

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**Type** Package

**Title** Various data sets for use with the FunciSNP package

**Version** 1.21.0

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**biocViews** SNPData, Project1000genomes, ENCODE

**Depends** R (>= 2.14.0), IRanges

**Imports** rtracklayer

## Description

Data sets needed for FunciSNP to integrate information from GWAS, 1000genomes and chromatin feature, in order to identify functional SNP in coding or non-coding regions.

**License** GPL-3

**URL** [http://coetzeeseq.usc.edu/publication/Coetzee\\_SG\\_et\\_al\\_2012/](http://coetzeeseq.usc.edu/publication/Coetzee_SG_et_al_2012/)

**LazyData** yes

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

**git\_branch** master

**git\_last\_commit** 097ba50

**git\_last\_commit\_date** 2019-05-02

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FunciSNP.builtin.features

*Builtin biological features used by FunciSNP package*

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## Description

These data were taken from the UCSC table browser and Encode website. Data retrieved on March of 2012. They include CTCF sites do not overlap a known Encode DNaseI site, Encode DNaseI site containing a CTCF site, Encode DNaseI not containing a CTCF site, ENCODE FAIRE clusters, promoters of known genes defined by -1000 and +100bp of a known transcription start site (TSS). These data were created to be used in the vignette for the **FunciSNP** package.

## Usage

```
ctcf_only
encode_dnase1_only
encode_dnase1_with_ctcf
encode_faire
known_gene_promoters
```

## Details

Each data set was extracted from the ENCODE and/or UCSC table browser on March of 2012. We retained only autosomal and sex linked chromosomes, removing unknown and random chromosomes. See reference for detail information on how these bed files were generated. Objects are stored as RangedData.

## References

SG. Coetzee, SK. Rhie, BP. Berman, GA. Coetzee and H. Noushmehr, FunciSNP: An R/Bioconductor Tool Integrating Functional Non-coding Datasets with Genetic Association Studies to Identify Candidate Regulatory SNPs., Nucleic Acids Research, In press, 2012 (doi:10.1093/nar/gks542).

## See Also

[FunciSNP.builtin.features lincRNA.hg19.rda refseqgenes.rda](#)

## Examples

```
dim(ctcf_only);
dim(encode_dnase1_only);
dim(encode_dnase1_with_ctcf);
dim(encode_faire);
dim(known_gene_promoters);
class(ctcf_only);
```

---

lincRNA.hg19.rda      *Known long intergenic non coding RNA*

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### Description

This data is taken from the UCSC table browser. Data retrieved on March of 2012. This data was created to be used in the vignette for the **FunciSNP** package.

### Usage

```
lincRNA
```

### References

SG. Coetzee, SK. Rhie, BP. Berman, GA. Coetzee and H. Noushmehr, FunciSNP: An R/Bioconductor Tool Integrating Functional Non-coding Datasets with Genetic Association Studies to Identify Candidate Regulatory SNPs., Nucleic Acids Research, In press, 2012 (doi:10.1093/nar/gks542).

### See Also

[FunciSNP.builtin.features refseqgenes.rda](#)

### Examples

```
lincRNA
dim(lincRNA)
head(lincRNA)
```

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refseqgenes.rda      *Known transcripts location*

---

### Description

This data is taken from the UCSC table browser. Data retrieved on March of 2012. This data was created to be used in the vignette for the **FunciSNP** package.

### Usage

```
refseqgenes.rda
```

### References

SG. Coetzee, SK. Rhie, BP. Berman, GA. Coetzee and H. Noushmehr, FunciSNP: An R/Bioconductor Tool Integrating Functional Non-coding Datasets with Genetic Association Studies to Identify Candidate Regulatory SNPs., Nucleic Acids Research, In press, 2012 (doi:10.1093/nar/gks542).

### See Also

[lincRNA.hg19.rda FunciSNP.builtin.features](#)

**Examples**

```
refseqgenes  
dim(refseqgenes)  
head(refseqgenes)
```

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