Package ‘FunciSNP.data’

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Type Package
Title Various data sets for use with the FunciSNP package
Version 1.10.0
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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/
LazyData yes
NeedsCompilation no

R topics documented:

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FunciSNP.builtin.features

Built-in 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 DNAaseI 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


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

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.
refseqgenes.rda

Usage

lincRNA

References


See Also

FunciSNP.builtin.features refseqgenes.rda

Examples

lincRNA
dim(lincRNA)
head(lincRNA)

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


See Also

lincRNA.hg19.rda FunciSNP.builtin.features

Examples

refseqgenes
dim(refseqgenes)
head(refseqgenes)
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