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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bioViews 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

Builtin biological features used by FunciSNP package
lincRNA.hg19.rda

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
decode_dnase1_only
decode_dnase1_with_ctcf
decode_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(decode_dnase1_only);
dim(decode_dnase1_with_ctcf);
dim(decode_faire);
dim(know gene_promoters);
class(ctcf_only);

lincRNA.hg19.rda  Known long intergenic non coding RNA

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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