Package ‘CopyhelpeR’

February 1, 2017

Type Package
Title Helper files for CopywriteR
Version 1.6.0
Date 2015-02-18
Author Thomas Kuilman
Maintainer Thomas Kuilman <t.kuilman@nki.nl>
Depends R(>= 2.10)
Suggests BiocStyle
Description This package contains the helper files that are required to run the Bioconductor package CopywriteR. It contains pre-assembled 1kb bin GC-content and mappability files for the reference genomes hg18, hg19, hg38, mm9 and mm10. In addition, it contains a blacklist filter to remove regions that display CNV. Files are stored as GRanges objects from the GenomicRanges Bioconductor package.
License GPL-2
biocViews Homo_sapiens, GenomicSequence
NeedsCompilation no

R topics documented:

getPathHelperFiles .................................................. 1

Index

getPathHelperFiles CopyhelpeR: Helper files for CopywriteR

Description

This package contains the helper files that are required to run the CopywriteR R package (see https://github.com/PeeperLab/CopywriteR/releases). It contains pre-assembled 1kb bin GC-content and mappability files for the reference genomes hg18, hg19, hg38, mm9 and mm10. In addition, it contains a blacklist filter to remove regions that display CNV. Files are stored as GRanges objects from the GenomicRanges Bioconductor package.
Usage

getPathHelperFiles(ref.genome)

Arguments

ref.genome the reference genome for which the helper files are required.

Details

The getPathHelperFiles() function returns the full path to the helper files folder for the relevant reference genomes ("hg18", "hg19", "hg38", "mm9" or "mm10").

Value

Returns the full path to the helper files folder for the relevant reference genomes ("hg18", "hg19", "hg38", "mm9" or "mm10").

Author(s)

Thomas Kuilman (t.kuilman@nki.nl)

Examples

getPathHelperFiles("hg19")
Index

Copyhelper(getPathHelperFiles), 1

getPathHelperFiles, 1