Package ‘CopyhelpeR’

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Type Package

Title Helper files for CopywriteR

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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.

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biocViews Homo_sapiens, GenomicSequence

NeedsCompilation no

R topics documented:

`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")
```

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