Package 'WGSmapp'

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Type Package

Title Mappability tracks of Whole-genome Sequencing from the ENCODE
Project

Version 1.17.0

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Description
This package provides whole-genome mappability tracks on human hg19/hg38 assembly. We em-
ployed the 100-mers mappability track from the ENCODE Project and computed weighted aver-
age of the mappability scores if multiple ENCODE regions overlap with the same bin. "Black-
list" bins, including segmental duplication regions and gaps in reference assembly from telom-
ere, centromere, and/or heterochromatin regions are included. The dataset consists of three as-
sembled .bam files of single-cell whole genome sequencing from 10X for illustration purposes.

Depends R (>= 3.6.0), GenomicRanges

License GPL-2

biocViews ExperimentData, SequencingData, DNASeqData, SingleCellData,
Homo_sapiens_Data, Genome, ENCODE

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

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Contents

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mapp_hg19	*GRanges with mappability scores for hg19*

Description

GRanges of mappability track for 100-mers on the GRCh37/hg19 human reference genome from ENCODE.

Usage

```
mapp_hg19
```

Format

A GRanges object with 21591667 ranges and mappability scores

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mapp_hg38	*GRanges with mappability scores for hg38*

Description

Use liftOver utility to convert hg19 coordinates to hg38

Usage

```
mapp_hg38
```

Format

A GRanges object with 21584930 ranges and mappability scores

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