Package `WGSmapp`

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Type Package

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

Version 1.14.0

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Description
This package provides whole-genome mappability tracks on human hg19/hg38 assembly. We employed the 100-mers mappability track from the ENCODE Project and computed weighted average of the mappability scores if multiple ENCODE regions overlap with the same bin. “Blacklist” bins, including segmental duplication regions and gaps in reference assembly from telomere, centromere, and/or heterochromatin regions are included. The dataset consists of three assembled .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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R topics documented:

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mapp_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

mapp_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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