Package 'WGSmapp'

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Title Mappability tracks of Whole-genome Sequencing from the ENCODE

Type Package

Project **Version** 1.6.0

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mapp_hg38	Maintainer Rujin Wang <rujin@email.unc.edu></rujin@email.unc.edu>
License GPL-2 biocViews ExperimentData, SequencingData, DNASeqData, SingleCellData, Homo_sapiens_Data, Genome, ENCODE Encoding UTF-8 LazyData true RoxygenNote 6.1.1 git_url https://git.bioconductor.org/packages/WGSmapp git_branch RELEASE_3_14 git_last_commit_82f9c66 git_last_commit_date 2021-10-26 Date/Publication 2022-04-13 R topics documented: mapp_hg19 mapp_hg38 2 mapp_hg38 2	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.
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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

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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