

Package ‘WGSmapp’

December 4, 2025

Type Package
Title Mappability tracks of Whole-genome Sequencing from the ENCODE Project
Version 1.23.0
Author Rujin Wang
Maintainer Rujin Wang <rujin@email.unc.edu>

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. “Black-list” 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
git_url <https://git.bioconductor.org/packages/WGSmapp>
git_branch devel
git_last_commit 7dcf161
git_last_commit_date 2025-10-29
Repository Bioconductor 3.23
Date/Publication 2025-12-04

Contents

mapp_hg19	2
mapp_hg38	2

Index**3**

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

Index

* **datasets**

mapp_hg19, [2](#)

mapp_hg38, [2](#)

mapp_hg19, [2](#)

mapp_hg38, [2](#)