# Package 'WGSmapp'

December 10, 2024

Type Package

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

Version 1.19.0

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 4daaa9f

git\_last\_commit\_date 2024-10-29

**Repository** Bioconductor 3.21

Date/Publication 2024-12-10

# Contents

mapp_hg19																				•			2	
mapp_hg38							•		•			•		•	•		•	•	•	•		•	2	

# Index

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

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

# 3

# Index

\* datasets

mapp\_hg19, 2
mapp\_hg38, 2

mapp\_hg19, 2
mapp\_hg38, 2