# Package 'WGSmapp'

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**Type** Package

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

**Version** 1.0.0

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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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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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