

# Package ‘WGSmapp’

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**Type** Package

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

**Version** 1.16.0

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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. “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>

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`mapp_hg19`*GRanges with mappability scores for hg19*

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**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

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`mapp_hg38`*GRanges with mappability scores for hg38*

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**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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