

# Package ‘WGSmapp’

May 28, 2026

**Type** Package

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

**Version** 1.25.0

**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** 1f88691

**git\_last\_commit\_date** 2026-04-28

**Repository** Bioconductor 3.24

**Date/Publication** 2026-05-28

## Contents

mapp_hg19	2
mapp_hg38	2
<b>Index</b>	<b>3</b>

---

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](#)