

Package: WGSmapp (via r-universe)

October 10, 2026

Type Package

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

Version 1.24.0

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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

Repository Bioconductor 3.23

Date/Publication 2026-04-28 12:33:51 UTC

RemoteUrl <https://github.com/bioc/WGSmapp>

RemoteRef RELEASE_3_23

RemoteSha cfa0b3ad3080c79f121326f1b3aa1fdd311bdcef

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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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