

Package ‘MMAPPR2data’

March 29, 2021

Type Package

Title Sample Data for MMAPPR2

Version 1.4.0

Description Contains data for illustration purposes in the MMAPPR2 package, namely simulated BAM files containing RNA-Seq data for a mutation in the *slc24a5* gene, taken from the GRCz11 genome. Also contains reference sequence and annotation files for the region.

Depends R (>= 3.6.0)

VignetteBuilder knitr

Enhances MMAPPR2

Suggests knitr, rmarkdown, BiocStyle, roxygen2, seqinr, readr

Imports Rsamtools

License GPL-3

Encoding UTF-8

biocViews RNASeqData, Danio_rerio_Data, SequencingData, Genome

URL <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3613585/>,
<https://github.com/kjohnsen/MMAPPR2>

RoxygenNote 6.1.1

git_url <https://git.bioconductor.org/packages/MMAPPR2data>

git_branch RELEASE_3_12

git_last_commit f0ff55d

git_last_commit_date 2020-10-27

Date/Publication 2021-03-29

Author Kyle Johnsen [aut],
Jonathon Hill [cre]

Maintainer Jonathon Hill <jhill@byu.edu>

R topics documented:

| | |
|-----------------------|----------|
| MMAPPR2data | 2 |
| Index | 3 |

MMAPPR2data

MMAPPR2data: Example Data for MMAPPR2

Description

Contains BAM files and indices for example use in MMAPPR2. The data is artificial, meant to simulate sequencing of the zebrafish *slc24a5* gene in mutant and wild-type pools resulting from the cross of a novel mutant from a forward genetics screen with a wild-type line, as described in Hill et al. 2013.

Usage

`exampleMutBam()`

`exampleWTbam()`

`goldenFasta()`

`goldenGFF()`

Details

Besides BAM files and indices, the package also contains fasta and gtf files for just the region of the *slc24a5* gene, which are also used in demonstrating MMAPPR2's functionality. They are based on the GRCz11 assembly and were obtained from Ensembl version 95.

Value

A [BamFile](#) object referencing a BAM file and its index.

A [BamFile](#) object referencing a BAM file and its index.

A path to the bgzipped *slc24a5* fasta file

The path to the bgzipped GFF file

Functions

- `exampleMutBam`: Easy access to example mutant pool BAM file.
- `exampleWTbam`: Easy access to example wild-type pool BAM file.
- `goldenFasta`: Easy access to example fasta file for *slc24a5* gene.
- `goldenGFF`: Easy access to example GFF file for *slc24a5* gene.

Examples

```
mutFile <- exampleMutBam()
wtFile <- exampleWTbam()
goldenFasta <- goldenFasta()
goldenGFF <- goldenGFF()
```

Index

BamFile, [2](#)

exampleMutBam (MMAPPR2data), [2](#)

exampleWTbam (MMAPPR2data), [2](#)

goldenFasta (MMAPPR2data), [2](#)

goldenGFF (MMAPPR2data), [2](#)

MMAPPR2data, [2](#)

MMAPPR2data-package (MMAPPR2data), [2](#)