

Package ‘MMAPPR2data’

April 18, 2024

Type Package

Title Sample Data for MMAPPR2

Version 1.17.1

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

PackageStatus Deprecated

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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()
```

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