Package 'RNAseqData.HNRNPC.bam.chr14'

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Title Aligned reads from RNAseq experiment: Transcription profiling by high throughput sequencing of HNRNPC knockdown and control HeLa cells

Description The package contains 8 BAM files, 1 per sequencing run. Each BAM file was obtained by (1) aligning the reads (paired-end) to the full hg19 genome with TopHat2, and then (2) subsetting to keep only alignments on chr14. See accession number E-MTAB-1147 in the ArrayExpress database for details about the experiment, including links to the published study (by Zarnack et al., 2012) and to the FASTQ files.

URL http://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-1147/

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biocViews ExperimentData, Genome, Homo_sapiens_Data, SequencingData, GEO, NCI, RNASeqData, ArrayExpress

License LGPL

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Contents

RNAseqData.HNRNPC.bam.chr14-package 2

Index **4**

RNAseqData.HNRNPC.bam.chr14-package

Aligned reads from RNAseq experiment: Transcription profiling by high throughput sequencing of HNRNPC knockdown and control HeLa cells

Description

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`RNAseqData.HNRNPC.bam.chr14_RUNNAMES` is a predefined character vector containing the names of the 8 runs of the RNAseq experiment. The name of each run is its accession number on the European Nucleotide Archive (ENA).

`RNAseqData.HNRNPC.bam.chr14_BAMFILES` is a predefined named character vector of length 8 containing the paths to the 8 BAM files obtained by aligning the reads from each sequencing run. The reads were aligned to the full hg19 genome with TopHat2 and then the resulting BAM file was subset to keep only alignments located on chr14.

Usage

```
RNAseqData.HNRNPC.bam.chr14_RUNNAMES
RNAseqData.HNRNPC.bam.chr14_BAMFILES
```

Details

The scripts/ folder in the package contains the scripts that were used to generate the data contained in the package (note that all the data contained in the package is located in its extdata/ folder). The README.TXT file in the scripts/ folder describes how to use those scripts to re-generate the data.

References

Direct Competition between hnRNP C and U2AF65 Protects the Transcriptome from the Exonization of Alu Elements. Kathi Zarnack, Julian Konig, Mojca Tajnik, Inigo Martincorena, Sebastian Eustermann, Isabelle Stevant, Alejandro Reyes, Simon Anders, Nicholas M. Luscombe, Jernej Ule. *Cell* 2012, Europe PMC 23374342

TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions. Daehwan Kim, Geo Pertea, Cole Trapnell, Harold Pimentel, Ryan Kelley and Steven L Salzberg. *Genome biology* 2013, 14:R36

See Also

- http://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-1147/ for details about the experiment, including links to the published study (by Kathi Zarnack et al., 2012) and to the FASTQ files.

- http://www.ebi.ac.uk/ena/data/view/ERR127306, http://www.ebi.ac.uk/ena/data/view/ERR127307, http://www.ebi.ac.uk/ena/data/view/ERR127308, http://www.ebi.ac.uk/ena/data/view/ERR127309, http://www.ebi.ac.uk/ena/data/view/ERR127302, http://www.ebi.ac.uk/ena/data/view/ERR127303, http://www.ebi.ac.uk/ena/data/view/ERR127304, and http://www.ebi.ac.uk/ena/data/view/ERR127305, for direct access to individual runs on the European Nucleotide Archive (ENA).
- http://ccb.jhu.edu/software/tophat for the TopHat2 software.
- http://samtools.sourceforge.net/SAM1.pdf for the SAM Format Specification.
- The readGAlignmentPairs function in the **GenomicAlignments** package for more information about how to read paired-end reads from a BAM file into Bioconductor.
- The ScanBamParam function in the **Rsamtools** package for how to get control over what to import from a BAM file.

Examples

```
RNAseqData.HNRNPC.bam.chr14_RUNNAMES
RNAseqData.HNRNPC.bam.chr14_BAMFILES

if (require(GenomicAlignments)) {
    bamfiles <- RNAseqData.HNRNPC.bam.chr14_BAMFILES
    param <- ScanBamParam(tag="NM")
    galp <- readGAlignmentPairs(bamfiles[1L], use.names=TRUE, param=param)
    galp

    first(galp)  # 1st segment in each pair
    last(galp)  # 2nd segment in each pair

    ## The alignments contain insertions, deletions, and junctions (I, D,
    ## and N CIGAR operations, respectively):
    colSums(cigarOpTable(cigar(first(galp))))
    colSums(cigarOpTable(cigar(last(galp))))

    ## njunc() returns the nb of junctions for each alignment:
    table(njunc(first(galp)))
    table(njunc(last(galp)))
    table(njunc(first(galp)) + njunc(last(galp)))  # up to 5 junctions
                                                   # per pair!

    ## The NM tag gives the edit distance of each alignment to the
    ## reference (ignoring the junction gaps):
    table(mcols(first(galp))$NM)
    table(mcols(last(galp))$NM)
    table(mcols(first(galp))$NM + mcols(last(galp))$NM)
}

## See README.TXT in scripts/ folder:
README_file <- system.file("scripts", "README.TXT",
                           package="RNAseqData.HNRNPC.bam.chr14")
cat(readLines(README_file), sep="\n")
```

Index

∗ **package**
RNAseqData.HNRNPC.bam.chr14-package, 2

readGAlignmentPairs, *3*
RNAseqData.HNRNPC.bam.chr14 (RNAseqData.HNRNPC.bam.chr14-package), 2
RNAseqData.HNRNPC.bam.chr14-package, 2
RNAseqData.HNRNPC.bam.chr14_BAMFILES (RNAseqData.HNRNPC.bam.chr14-package), 2
RNAseqData.HNRNPC.bam.chr14_RUNNAMES (RNAseqData.HNRNPC.bam.chr14-package), 2

ScanBamParam, *3*