Package 'parathyroidSE'

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Title RangedSummarizedExperiment for RNA-Seq of primary cultures of parathyroid tumors by Haglund et al., J Clin Endocrinol Metab 2012.

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Description

This package provides RangedSummarizedExperiment objects of read counts in genes and exonic parts for paired-end RNA-Seq data from experiments on primary cultures of parathyroid tumors. The data were presented in the article ``Evidence of a Functional Estrogen Receptor in Parathyroid Adenomas'' by Haglund F, Ma R, Huss M, Sulaiman L, Lu M, Nilsson IL, Hoog A, Juhlin CC, Hartman J, Larsson C, J Clin Endocrinol Metab. jc.2012-2484, Epub 2012 Sep 28, PMID: 23024189. The sequencing was performed on tumor cultures from 4 patients at 2 time points over 3 conditions (DPN, OHT and control). One control sample was omitted by the paper authors due to low quality. The package vignette describes the creation of the object from raw sequencing data provided by NCBI Gene Expression Omnibus under accession number GSE37211. The gene and exon features are the GRCh37 Ensembl annotations.

biocViews ExperimentData, SequencingData, RNASeqData

License LGPL

Depends SummarizedExperiment, R (>= 2.10)

Suggests Rsamtools, GenomicAlignments, GEOquery, SRAdb, GenomicFeatures, BiocStyle

NeedsCompilation no

R topics documented:

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exonsByGene   *Subset of exons/exonic parts for Ensembl genes*

Description

exonsByGene is a GRangesList object with a subset of genes/transcripts from the GRCh37 Ensembl annotations. For complete details on the creation of this object, please see the vignette. exonicParts is a GRanges object with a subset of the exonic parts produced by the disjointExons function of the GenomicFeatures package.

Usage

```
data("exonsByGene")
data("exonicParts")
```

Format

GRangesList

Source

Ensembl

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parathyroidGenesSE   *Read counts per gene/exonic part from paired-end RNA-seq samples*

Description

parathyroidGenesSE is a [RangedSummarizedExperiment](#) object with gene level counts for each of the samples from Haglund et al.'s RNA-seq data.

parathyroidExonsSE is a [RangedSummarizedExperiment](#) object with exonic part counts.

The genes and exons are from the GRCh37 Ensembl annotations.

For complete details on the creation of this object, please see the vignette.

Usage

```
data("parathyroidGenesSE")
data("parathyroidExonsSE")
```

Format

RangedSummarizedExperiment

Source

Processed data from NCBI Gene Expression Omnibus under accession number GSE37211

References

Haglund F, Ma R, Huss M, Sulaiman L, Lu M, Nilsson IL, Höög A, Juhlin CC, Hartman J, Larsson C., Evidence of a Functional Estrogen Receptor in Parathyroid Adenomas. The Journal of Clinical Endocrinology & Metabolism, 2012

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