

Package ‘parathyroid’

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

Version 1.1.1

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Description This package provides a CountDataSet and ExonCountSet of read counts 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 objects from raw sequencing data provided by NCBI Gene Expression Omnibus under accession number GSE37211. The gene and exon features are the GRCh37 Ensembl annotations, release 66.

biocViews ExperimentData, RNAseqData

License LGPL

Depends DEXSeq, DESeq, R (>= 2.10)

Suggests GEOquery, SRADB

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parathyroidGenes *Read counts per gene and per exon from paired-end RNA-seq samples*

Description

parathyroidGenes is an CountDataSet object with gene level counts. parathyroidExons is an ExonCountSet object containing exon counts for each of the samples from Haglund et al.'s RNA-seq data.

The genes and exons are from the GRCh37 Ensembl annotations, release 66 downloaded 9 March 2012.

For complete details on the creation of these objects, please see the vignette.

Usage

```
data("parathyroidGenes")  
data("parathyroidExons")
```

Format

CountDataSet, ExonCountSet

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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