Package 'GSE62944'

October 18, 2017

Title GEO accession data GSE62944 as a SummarizedExperiment

Description TCGA processed RNA-Seq data for 9264 tumor and 741 normal
samples across 24 cancer types and made them available as GEO accession
[GSE62944](http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE62944).
GSE62944 data have been parsed into a SummarizedExperiment object available
in ExperimentHub.

Version 1.4.0

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URL http://bioconductor.org/packages/release/bioc/html/GSE62944.html

biocViews ExperimentData, Genome, DNASeqData, RNASeqData

Depends Biobase, GEOquery

Suggests ExperimentHub (>= 0.99.6), knitr, BiocStyle

License Artistic-2.0

VignetteBuilder knitr

NeedsCompilation no

R topics documented:

GSE62944-package   *GEO accession GSE62944 available as an* ExpressionSet *object.*

Description

TCGA re-processed RNA-Seq data from 9264 Tumor Samples and 741 normal samples across 24
cancer types and made it available as GEO accession [GSE62944](http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=G
These data have been parsed into a SummarizedExperiment objects and are available in ExperimentHub.

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Details

See the vignette for examples of using these data in differential gene expression analysis.

browseVignettes("GSE62944")

Details of how these data were creates are in the scripts/ directory of the source package.

Examples

```
library(ExperimentHub)
hub <- ExperimentHub()
x <- query(hub, c("GSE62944", "tumor"))
x
y <- query(hub, c("GSE62944", "normal"))
y
## Not run:
## download resource
se_tumor = x[[1]]
se_normal = y[[1]]

## End(Not run)
```

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