Package ‘GSE62944’

January 23, 2024

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  1.30.0

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biocViews  ExperimentData, Genome, DNASeqData, RNASeqData

Depends  Biobase, GEOquery

Suggests  ExperimentHub (>= 0.99.6), knitr, BiocStyle, rmarkdown, DESeq2

License  Artistic-2.0

VignetteBuilder  knitr

NeedsCompilation  no

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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=GSE62944). These data have been parsed into a SummarizedExperiment objects and are available in ExperimentHub.

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

```r
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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