

Package ‘GSE62944’

January 26, 2022

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 1.22.0

Author Sonali Arora

Maintainer Bioconductor Package Maintainer <maintainer@bioconductor.org>

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, rmarkdown

License Artistic-2.0

VignetteBuilder knitr

NeedsCompilation no

git_url <https://git.bioconductor.org/packages/GSE62944>

git_branch RELEASE_3_14

git_last_commit b31a1d3

git_last_commit_date 2021-10-26

Date/Publication 2022-01-26

R topics documented:

GSE62944-package 2

Index 3

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 created 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)
```

Index

* **utilities**

GSE62944-package, [2](#)

GSE62944 (GSE62944-package), [2](#)

GSE62944-package, [2](#)