Package 'GSE62944'

April 24, 2025

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 1.36.0

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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, 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=GSE
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

```
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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