

Package: GSE62944 (via r-universe)

October 13, 2026

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 1.40.0

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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

Config/pak/sysreqs libicu-dev libxml2-dev libssl-dev libx11-dev zlib1g-dev

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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 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)
```

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