Package ‘GSE159526’

July 16, 2024

Title Placental cell DNA methylation data from GEO accession GSE159526

Version 1.11.0

Description 19 term and 9 first trimester placental chorionic villi and matched cell-sorted samples ran on Illumina HumanMethylationEPIC DNA methylation microarrays. This data was made available on GEO accession [GSE159526](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE159526). Both the raw and processed data has been made available on \code{ExperimentHub}. Raw unprocessed data formatted as an RGChannelSet object for integration and normalization using minfi and other existing Bioconductor packages. Processed normalized data is also available as a DNA methylation \code{matrix}, with a corresponding phenotype information as a \code{data.frame} object.

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Encoding UTF-8

LazyData false

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.1

URL https://github.com/wvictor14/GSE159526

BugReports https://github.com/wvictor14/GSE159526/issues

biocViews ExperimentData, ExperimentHub, GEO, Genome, Tissue, MethylationArrayData, Homo_sapiens_Data

Date 2021-06-10

Suggests ExperimentHub, BiocStyle, RefManageR, knitr, rmarkdown, testthat, minfi, tibble, sessioninfo

VignetteBuilder knitr

git_url https://git.bioconductor.org/packages/GSE159526

git_branch devel

git_last_commit 8fc7918

git_last_commit_date 2024-04-30

Repository Bioconductor 3.20

Date/Publication 2024-07-16

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Contents

`GSE159526-package` *GEO accession GSE159526 available as raw data in a* `RGChannelSetExtended` *object, and as processed normalized data.*

Description

19 term and 9 first trimester placental chorionic villi and matched cell-sorted samples ran on Illumina HumanMethylationEPIC DNA methylation microarrays. This data was made available on GEO accession [GSE159526](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE159526). Both the raw and processed data has been made available on `ExperimentHub`. Raw unprocessed data formatted as an RGChannelSet object for integration and normalization using minfi and other existing Bioconductor packages. Processed normalized data is also available as a DNA methylation `matrix`, with a corresponding phenotype information as a `data.frame` object.

Details

dd 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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