Package 'GSE159526'

July 25, 2024

Title Placental cell DNA methylation data from GEO accession GSE159526

Version 1.10.0

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

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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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