

# Package ‘GSE159526’

June 11, 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 `{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.

**License** MIT + file LICENSE

**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>

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GSE159526-package	<i>GEO accession GSE159526 available as raw data in a RGChannelSetExtended object, and as processed normalized data.</i>
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## 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)
```

# Index

\* **utilities**

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