

# Package: GSE280465 (via r-universe)

October 10, 2026

**Type** Package

**Title** EPICv2 Methylation ExperimentHub Data from GEO

**Version** 0.99.1

**Description** Provides ExperimentHub access to a processed DNA methylation resource derived from GEO accession GSE280465. The resource contains adult Illumina Infinium MethylationEPIC version 2 data from 163 samples across four tissue types, represented as a RangedSummarizedExperiment with beta, M, and CN assays, hg38 genomic ranges, and sample phenotype metadata.

**URL** <https://github.com/paulYRP/GSE280465>

**BugReports** <https://github.com/paulYRP/GSE280465/issues>

**License** Artistic-2.0

**Depends** R (>= 4.4.0)

**Imports** ExperimentHub, utils

**Suggests** BiocStyle, ExperimentHubData, knitr, rmarkdown, SummarizedExperiment, testthat (>= 3.0.0)

**VignetteBuilder** knitr

**Config/testthat/edition** 3

**biocViews** ExperimentData, ExperimentHub, GEO, Homo\_sapiens\_Data, MethylationArrayData, MicroarrayData, Tissue

**Encoding** UTF-8

**NeedsCompilation** no

**Config/pak/sysreqs** libicu-dev libpng-dev libssl-dev zlib1g-dev

**Repository** <https://bioc.r-universe.dev>

**Date/Publication** 2026-08-07 01:11:20 UTC

**RemoteUrl** <https://github.com/bioc/GSE280465>

**RemoteRef** HEAD

**RemoteSha** acd0a41e56c08234910288ac98972c0c19b68798

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| GSE280465-package | <i>GSE280465 EPICv2 methylation data in ExperimentHub</i> |
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## Description

The **GSE280465** package provides ExperimentHub access to a processed adult DNA methylation resource derived from GEO accession GSE280465.

## Details

The hosted resource is a RangedSummarizedExperiment created from an Illumina Infinium MethylationEPIC version 2 GenomicRatioSet. It contains beta, M, and CN assays for 163 adult samples from 47 individuals across buccal, saliva, dried blood spot, and peripheral blood mononuclear cell tissues.

The resource is hosted on Zenodo at <https://zenodo.org/records/21200586> and is registered for access through **ExperimentHub**.

See `browseVignettes("GSE280465")` for a usage example.

## See Also

<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE280465>

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|           |                                                  |
|-----------|--------------------------------------------------|
| GSE280465 | <i>Load the GSE280465 ExperimentHub resource</i> |
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## Description

Convenience helper for loading the GSE280465 EPICv2 adult cross-tissue DNA methylation resource from **ExperimentHub**.

## Usage

```
GSE280465(metadata = FALSE, filterBy = "GSE280465_GPL33022_EPICv2")
```

```
GSE280465_GPL33022_EPICv2(metadata = FALSE)
```

## Arguments

|          |                                                                                                                     |
|----------|---------------------------------------------------------------------------------------------------------------------|
| metadata | logical(1). If TRUE, return ExperimentHub metadata for the matching resource. If FALSE, load the matching resource. |
| filterBy | character(1). Resource title used to filter the <b>ExperimentHub</b> entries for this package.                      |

## Details

The resource is registered as GSE280465\_GPL33022\_EPICv2 in **ExperimentHub**. It contains beta, M, and CN assays with hg38 genomic ranges and sample-level phenotype metadata.

The GSE280465\_GPL33022\_EPICv2() function is the resource-title accessor generated from ‘inst/extdata/metadata.csv’ when the package is loaded. It returns the same hosted resource as GSE280465().

## Value

When metadata = FALSE, a RangedSummarizedExperiment. When metadata = TRUE, the matching ExperimentHub metadata.

## See Also

[ExperimentHub](#), [listResources](#), [loadResources](#)

## Examples

```
metadata_file <- system.file("extdata", "metadata.csv", package = "GSE280465")
metadata <- utils::read.csv(metadata_file, stringsAsFactors = FALSE)
metadata[, c("Title", "Genome", "RDataClass")]

if (interactive()) {
  library(GSE280465)
  GSE280465(metadata = TRUE)
  se <- GSE280465()
  se
  se <- GSE280465_GPL33022_EPICv2()
}
```

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