

# Package ‘sesameData’

April 7, 2026

**Type** Package

**Title** Supporting Data for SeSAmE Package

**Description** Provides supporting annotation and test data for SeSAmE package. This includes chip tango addresses, mapping information, performance annotation, and trained predictor for Infinium array data. This package provides user access to essential annotation data for working with many generations of the Infinium DNA methylation array. Currently we support human array (HM27, HM450, EPIC), mouse array (MM285) and the Horvath-MethylChip40 (Mammal40) array.

**Version** 1.29.10

**License** Artistic-2.0

**Depends** R (>= 4.3.0), ExperimentHub, AnnotationHub

**Imports** utils, readr, stringr, GenomicRanges (>= 1.61.1), S4Vectors, IRanges, Seqinfo

**Suggests** BiocGenerics, GenomeInfoDb, sesame, testthat, knitr, rmarkdown

**biocViews** ExperimentData, MicroarrayData, Genome, ExperimentHub, MethylationArrayData

**URL** <https://github.com/zwdzwd/sesame>

**BugReports** <https://github.com/zwdzwd/sesame/issues>

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build_GENCODE_gtf	<i>build GENCODE gtf</i>
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### Description

build GENCODE gtf

### Usage

build\_GENCODE\_gtf(x)

### Arguments

x	GENCODE ftp url
---	-----------------

**Value**

GRangesList

df\_master

*Master data frame for all object to cache***Description**

This is an internal object which will be updated on every new release library(ExperimentHub) eh <- query(ExperimentHub(localHub=FALSE), c("sesameData", "v1.13.1")) data.frame(name=eh\$title, eh=names(eh))

**Format**

A data frame with 22 columns:

**Comments** Additional comments

**EHID** ExperimentHub ID

**VERSION** sesameData version

**IN\_USE** Logical indicating if the resource is in use

**Title** Title of the data resource

**Description** Description of the data resource

**BiocVersion** Bioconductor version

**Genome** Genome build (e.g., hg38, mm10)

**SourceType** Source file type

**SourceUrl** URL to source

**SourceVersion** Version of source data

**Species** Species name

**TaxonomyId** NCBI Taxonomy ID

**Coordinate\_1\_based** Logical indicating if coordinates are 1-based

**DataProvider** Data provider name

**Maintainer** Maintainer contact information

**RDataClass** R data class

**DispatchClass** Dispatch class for ExperimentHub

**RDataPath** Path to RData file

**Location\_Prefix** URL prefix for data location

**Tags** Tags for categorization

**Notes** Additional notes

**Details**

Cache location is default to /Users/zhouw3/Library/Caches/org.R-project.R/R/ExperimentHub/

**Value**

master sheet of sesameData objects

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extend	<i>Extend a GRanges</i>
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---

**Description**

source: <https://support.bioconductor.org/p/78652/>

**Usage**

```
extend(gr, upstream = 0, downstream = 0)
```

**Arguments**

gr	a GenomicRanges::GRanges
upstream	distance to expand upstream
downstream	distance to expand downstream

**Value**

a GenomicRanges::GRanges

---

inferPlatformFromProbeIDs	<i>infer platform from Probe_IDs</i>
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---

**Description**

infer platform from Probe\_IDs

**Usage**

```
inferPlatformFromProbeIDs(Probe_IDs, silent = FALSE)
```

**Arguments**

Probe_IDs	probe IDs
silent	suppress message

**Value**

a platform code

**Examples**

```
sesameDataCache("probeIDSignature")
inferPlatformFromProbeIDs(c("cg14620903", "cg22464003"))
```

---

sesameDataCache	<i>Cache SeSAmE data</i>
-----------------	--------------------------

---

**Description**

Cache SeSAmE data

**Usage**

```
sesameDataCache(data_titles = NULL)
```

**Arguments**

data\_titles      data to cache, if not given will cache all

**Value**

TRUE

**Examples**

```
sesameDataCache("genomeInfo.hg38")
```

---

sesameDataCacheAll	<i>Cache all SeSAmE data</i>
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---

**Description**

Cache all SeSAmE data

**Usage**

```
sesameDataCacheAll(data_titles = NULL)
```

**Arguments**

data\_titles      data to cache, if not given will cache all

**Value**

TRUE

**Examples**

```
sesameDataCache("genomeInfo.hg38")
```

---

sesameDataGet	<i>Get SeSAmE data</i>
---------------	------------------------

---

**Description**

Get SeSAmE data

**Usage**

```
sesameDataGet(title, verbose = FALSE)
```

**Arguments**

title	title of the data
verbose	whether to output ExperimentHub message

**Value**

data object

**Examples**

```
sesameDataCache("EPIC.1.SigDF")  
EPIC.1.SigDF <- sesameDataGet('EPIC.1.SigDF')
```

---

sesameDataGet_checkEnv	<i>Check whether the title exists in cacheEnv</i>
------------------------	---

---

**Description**

Check whether the title exists in cacheEnv

**Usage**

```
sesameDataGet_checkEnv(title)
```

**Arguments**

title	the title to check
-------	--------------------

**Value**

the data associated with the title or NULL if title doesn't exist

---

```
sesameDataGet_resetEnv
```

*Empty cache environment to free memory*

---

**Description**

When this function is called sesameDataGet will retrieve all data from disk again instead of using the in-memory cache, i.e., sesameData:::cacheEnv.

**Usage**

```
sesameDataGet_resetEnv()
```

**Details**

Note this is different from sesameDataClearHub which empties the ExperimentHub on disk.

**Value**

gc() output

**Examples**

```
sesameDataGet_resetEnv()
```

---

```
sesameDataHas
```

*Whether sesameData has*

---

**Description**

Whether sesameData has

**Usage**

```
sesameDataHas(data_titles)
```

**Arguments**

data\_titles      data titles to check

**Value**

a boolean vector the same length as data\_titles

**Examples**

```
sesameDataHas(c("EPIC.address", "EPIC.address.Nonexist"))
```

---

```
sesameDataList      List all SeSAmE data
```

---

**Description**

List all SeSAmE data

**Usage**

```
sesameDataList(filter = NULL, full = FALSE)
```

**Arguments**

`filter` keyword to filter title, optional  
`full` whether to display all columns

**Value**

all titles from SeSAmE Data

**Examples**

```
sesameDataList("KYCG")
```

---

```
sesameData_annoProbes Annotate Probes by Probe ID
```

---

**Description**

This function annotates probes based on genomic coordinate overlaps with provided genomic regions (GRanges). Columns in the manifests will be added to the annotation. Please note that if unfound, the annotation will be NA. The probe will always be kept in the output.

**Usage**

```

sesameData_annoProbes(
  Probe_IDs,
  regs = NULL,
  collapse = TRUE,
  chooseOne = FALSE,
  column = NULL,
  sep = ", ",
  return_ov_probes = FALSE,
  return_ov_features = FALSE,
  out_name = NULL,
  platform = NULL,
  genome = NULL,
  silent = FALSE
)

```

**Arguments**

Probe_IDs	a character vector of probe IDs
regs	a GenomicRanges::GRanges object against which probes will be annotated, default to genes if not given
collapse	whether to collapse multiple regs into one
chooseOne	choose an arbitrary annotation if multiple exist default to FALSE. which concatenates all with ", "
column	which column in regs to annotate, if not given return all overlapping probes
sep	the delimiter for collapsing
return_ov_probes	if TRUE will return overlapping probes in a GRanges object.
return_ov_features	if TRUE will return overlapping features in a GRanges object.
out_name	column header of the annotation, use column if not given
platform	EPIC, MM285 etc. will infer from Probe_IDs if not given
genome	hg38, mm10, ... will infer if not given. For additional mapping, download the GRanges object from <a href="http://zwdzwd.github.io/InfiniumAnnotation">http://zwdzwd.github.io/InfiniumAnnotation</a> and provide the following argument ..., genome = sesameAnno_buildManifestGRanges("downloaded_file"),... to this function.
silent	suppress messages

**Details**

For annotation by probe ID using KYCG databases (rather than by genomic coordinates), see `knowYourCG::annoProbes()`

**Value**

a GRanges with annotated column If a probe has no overlap with regs, it will be included in the results with NA. But if a probe is not included in the manifest (due to mappability), it won't be included in the results.

**Examples**

```
library(GenomicRanges)
sesameDataCache(c(
  "genomeInfo.mm10", "MM285.address",
  "genomeInfo.hg38", "Mammal40.address"))

## Example 1: Basic usage - annotate with gene names (default)
## When regs=NULL, function defaults to gene annotation
probes <- c("cg14620903", "cg22464003")
anno <- sesameData_annoProbes(probes)
## Returns GRanges with gene_name column

## Example 2: Annotate mouse probes with promoter regions
regs <- sesameData_getTxnGRanges("mm10")
Probe_IDs <- names(sesameData_getManifestGRanges("MM285"))[1:100]
anno <- sesameData_annoProbes(Probe_IDs, promoters(regs), column="gene_name")
## Probes overlapping promoters are annotated with gene names

## Example 3: Get features that overlap with probes
## return_ov_features=TRUE returns the overlapping genomic features
genes <- sesameData_getTxnGRanges("hg38", merge2gene = TRUE)
ov_genes <- sesameData_annoProbes(
  c("cg14620903", "cg22464003"), genes, return_ov_features=TRUE)
## Returns GRanges of genes overlapping the probes

## Example 4: Get probes that overlap with features
## return_ov_probes=TRUE returns only overlapping probes
ov_probes <- sesameData_annoProbes(
  c("cg14620903", "cg22464003"), genes, return_ov_probes=TRUE)
## Returns GRanges of probes that overlap genes

## Example 5: Control annotation collapsing behavior
## collapse=TRUE (default): multiple annotations concatenated with separator
anno_collapsed <- sesameData_annoProbes(
  c("cg14620903", "cg22464003"), genes, column="gene_name",
  collapse=TRUE, sep=";")
## Multiple overlapping genes listed as "GENE1;GENE2;GENE3"

## collapse=FALSE: each probe-feature overlap gets separate entry
anno_expanded <- sesameData_annoProbes(
  c("cg14620903", "cg22464003"), genes, column="gene_name",
  collapse=FALSE)
## Probes with multiple overlaps appear multiple times

## Example 6: Choose only first annotation when multiple exist
anno_one <- sesameData_annoProbes(
```

```

      c("cg14620903","cg22464003"), genes, column="gene_name",
      chooseOne=TRUE)
## Each probe gets only the first overlapping gene

## Example 7: Annotate with custom genomic regions
custom_regs <- GRanges(
  seqnames = c("chr5", "chr5"),
  ranges = IRanges(start = c(10000, 135350870),
                    end = c(135350866, 145369531)),
  feature_type = c("enhancer", "silencer"))
anno_custom <- sesameData_annoProbes(
  c("cg14620903","cg22464003"), custom_regs,
  column="feature_type", genome="hg38")

## Note: For annotation by probe ID using KYCG databases
## (rather than genomic coordinates), see knowYourCG::annoProbes()

```

---

```
sesameData_check_genome
```

*Find genome assembly version(s) supported for a platform*

---

## Description

Find genome assembly version(s) supported for a platform

## Usage

```
sesameData_check_genome(genome, platform)
```

## Arguments

genome	mm10, hg38, ..., or NULL
platform	HM27, HM450, EPIC, EPICv2, MSA, ...

## Value

genome as string

## Examples

```
sesameData_check_genome(NULL, "Mamma140")
```

---

`sesameData_check_platform`*Check platform code*

---

**Description**

Note: custome platforms lead to error here.

**Usage**

```
sesameData_check_platform(platform = NULL, probes = NULL, silent = TRUE)
```

**Arguments**

<code>platform</code>	input platform
<code>probes</code>	probes by which the platform may be guessed
<code>silent</code>	suppress message

**Value**

platform code

**Examples**

```
sesameData_check_platform("HM450")
```

---

`sesameData_getGenomeInfo`*Get genome info files*

---

**Description**

Get genome info files

**Usage**

```
sesameData_getGenomeInfo(genome)
```

**Arguments**

<code>genome</code>	hg38, mm10, or GRanges with a metadata(genome)[["genome"]]
---------------------	--

**Value**

a list of genome info files

### Examples

```
sesameDataCache("genomeInfo.hg38")
res <- sesameData_getGenomeInfo("hg38")
```

---

```
sesameData_getManifestGRanges
  get Infinium manifest GRanges
```

---

### Description

Note that some unaligned probes are not included. For full manifest, please visit <http://zwdzwd.github.io/InfiniumAnnotation>

### Usage

```
sesameData_getManifestGRanges(platform, genome = NULL)
```

### Arguments

platform	Mammal40, MM285, EPIC, and HM450
genome	hg38, mm10, ... will infer if not given. For additional mapping, download the GRanges object from <a href="http://zwdzwd.github.io/InfiniumAnnotation">http://zwdzwd.github.io/InfiniumAnnotation</a> and provide the following argument ..., genome = sesameAnno_buildManifestGRanges("downloaded_file"),... to this function.

### Value

GRanges

### Examples

```
sesameDataCache("Mammal40.address")
res <- sesameData_getManifestGRanges("Mammal40")
```

---

```
sesameData_getProbesByGene
  Get Probes by Genes or Gene Promoters
```

---

### Description

Get probes mapped to a gene. All transcripts for the gene are considered. The function takes a gene name as appears in UCSC RefGene database. The platform and reference genome build can be changed with 'platform' and 'genome' options. The function returns a vector of probes that falls into the given gene.

**Usage**

```
sesameData_getProbesByGene(
  gene_name = NULL,
  platform = NULL,
  promoter = FALSE,
  upstream = 1500,
  downstream = 1500,
  genome = NULL
)
```

**Arguments**

gene_name	gene name, if NULL return all genes
platform	EPIC or HM450
promoter	if TRUE, use TSS instead of the whole gene
upstream	number of bases to expand upstream of target gene
downstream	number of bases to expand downstream of target gene
genome	hg38 or hg19

**Value**

GRanges containing probes that fall into the given gene

**Examples**

```
## download needed data
sesameDataCache(c("Mammal40.address", "genomeInfo.hg38"))

## get all probes overlapping with DNMT3A
probes <- sesameData_getProbesByGene(
  'DNMT3A', "Mammal40", upstream=500, downstream=500)

## get the promoter-associated probes
probes <- sesameData_getProbesByGene('DNMT3A', "Mammal40", promoter = TRUE)
```

---

sesameData\_getProbesByRegion

*Get probes by genomic region*

---

**Description**

The function takes a genomic coordinate and output the a vector of probes on the specified platform that falls in the given genomic region.

**Usage**

```
sesameData_getProbesByRegion(
  regs,
  chrm = NULL,
  beg = 1,
  end = -1,
  platform = NULL,
  chrm_to_exclude = NULL,
  genome = NULL
)
```

**Arguments**

regs	GRanges
chrm	chromosome, when given regs are ignored
beg	begin, 1 if omitted
end	end, chromosome end if omitted
platform	EPICv2, EPIC, HM450, ...
chrm_to_exclude	chromosome to exclude.
genome	hg38, mm10, ... will infer if not given. For additional mapping, download the GRanges object from <a href="http://zwdzwd.github.io/InfiniumAnnotation">http://zwdzwd.github.io/InfiniumAnnotation</a> and provide the following argument ..., genome = sesameAnno_buildManifestGRanges("downloaded_file"),... to this function.

**Value**

GRanges of selected probes

**Examples**

```
## download needed data
sesameDataCache(c("Mammal40.address", "genomeInfo.hg38"))

## get probes in a region
library(GenomicRanges)
probes = sesameData_getProbesByRegion(
  GRanges('chr5', IRanges(135313937, 135419936)), platform = 'Mammal40')

## get all probes on chromosome 5
probes = sesameData_getProbesByRegion(chrm = "chr5", platform = "Mammal40")

## get all probes on chromosome X
probes = sesameData_getProbesByRegion(chrm = 'chrX', platform = "Mammal40")

## get all probes on both chromosome X and Y
probes = sesameData_getProbesByRegion(
  chrm = c('chrX', 'chrY'), platform = "Mammal40")
```

```
## get all autosomal probes
probes = sesameData_getProbesByRegion(
  chrm_to_exclude = c("chrX", "chrY"), platform = "Mammal40")
```

---

sesameData\_getTxnGRanges

*convert GRangesList to transcript GRanges*

---

## Description

convert GRangesList to transcript GRanges

## Usage

```
sesameData_getTxnGRanges(genome = NULL, gr1 = NULL, merge2gene = FALSE)
```

## Arguments

genome	hg38, mm10, ...
gr1	GRangesList object
merge2gene	merge transcript to genes

## Value

a GRanges object

## Examples

```
## all mm10 transcripts
txns <- sesameData_getTxnGRanges("mm10")

## verified protein-coding transcripts
txns[(txns$transcript_type == "protein_coding" & txns$level <= 2)]

## merged to genes
sesameData_getTxnGRanges("mm10", merge2gene = TRUE)
```

---

```
sesameData_txnToGeneGRanges
      convert transcript GRanges to gene GRanges
```

---

**Description**

convert transcript GRanges to gene GRanges

**Usage**

```
sesameData_txnToGeneGRanges(txns)
```

**Arguments**

txns                    GRanges object

**Value**

a GRanges object

**Examples**

```
txns <- sesameData_getTxnGRanges("mm10")
genes <- sesameData_txnToGeneGRanges(txns)
```

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