

# Package ‘knowYourCG’

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**Type** Package

**Title** Functional analysis of DNA methylome datasets

**Version** 1.3.15

**Description** KnowYourCG (KYCG) is a supervised learning framework designed for the functional analysis of DNA methylation data. Unlike existing tools that focus on genes or genomic intervals, KnowYourCG directly targets CpG dinucleotides, featuring automated supervised screenings of diverse biological and technical influences, including sequence motifs, transcription factor binding, histone modifications, replication timing, cell-type-specific methylation, and trait-epigenome associations. KnowYourCG addresses the challenges of data sparsity in various methylation datasets, including low-pass Nanopore sequencing, single-cell DNA methylomes, 5-hydroxymethylation profiles, spatial DNA methylation maps, and array-based datasets for epigenome-wide association studies and epigenetic clocks.

**Depends** R (>= 4.4.0)

**URL** <https://github.com/zhou-lab/knowYourCG>

**BugReports** <https://github.com/zhou-lab/knowYourCG/issues>

**License** MIT + file LICENSE

**VignetteBuilder** knitr

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aggregateTestEnrichments . . . . .	3
annoProbes . . . . .	3
buildGeneDBs . . . . .	4
dbStats . . . . .	5
getDBs . . . . .	6
KYCG_plotBar . . . . .	7
KYCG_plotDot . . . . .	8
KYCG_plotEnrichAll . . . . .	9
KYCG_plotLollipop . . . . .	10
KYCG_plotManhattan . . . . .	10
KYCG_plotMeta . . . . .	12
KYCG_plotMetaEnrichment . . . . .	12
KYCG_plotPointRange . . . . .	13
KYCG_plotSetEnrichment . . . . .	14
KYCG_plotVolcano . . . . .	14
KYCG_plotWaterfall . . . . .	15
listDBGroups . . . . .	16
testEnrichment . . . . .	17
testEnrichment2 . . . . .	18
testEnrichmentFisher . . . . .	19
testEnrichmentSEA . . . . .	19
testEnrichmentSpearman . . . . .	20
testGO . . . . .	21
testProbeProximity . . . . .	22

**Index****23**

---

aggregateTestEnrichments

*Aggregate test enrichment results*

---

### Description

Aggregate test enrichment results

### Usage

```
aggregateTestEnrichments(result_list, column = "estimate", return_df = FALSE)
```

### Arguments

result\_list      a list of results from testEnrichment  
column            the column name to aggregate (Default: estimate)  
return\_df        whether to return a merged data frame

### Value

a matrix for all results

### Examples

```
## pick some big TFBS-overlapping CpG groups  
sesameData::sesameDataCache(data_titles=  
c("KYCG.MM285.TFBSconsensus.20220116", "KYCG.MM285.chromHMM.20210210",  
"probeIDSignature", "MM285.address"))  
cg_lists <- getDBs("MM285.TFBS")  
queries <- cg_lists[(sapply(cg_lists, length) > 40000)]  
result_list <- lapply(queries, testEnrichment, "MM285.chromHMM")  
mtx <- aggregateTestEnrichments(result_list)
```

---

annoProbes

*Annotate Probe IDs using KYCG databases*

---

### Description

see sesameData\_annoProbes if you'd like to annotate by genomic coordinates (in GRanges)

**Usage**

```
annoProbes(
  probeIDs,
  databases,
  db_names = NULL,
  platform = NULL,
  sep = ",",
  indicator = FALSE,
  silent = FALSE
)
```

**Arguments**

probeIDs	probe IDs in a character vector
databases	character or actual database (i.e. list of probe IDs)
db_names	specific database (default to all databases)
platform	EPIC, MM285 etc. will infer from probe IDs if not given
sep	delimiter used in paste
indicator	return the indicator matrix instead of a concatenated annotation (in the case of have multiple annotations)
silent	suppress message

**Value**

named annotation vector, or indicator matrix

**Examples**

```
sesameData::sesameDataCache(data_titles=
c("MM285.address", "probeIDSignature", "KYCG.MM285.designGroup.20210210"))
probes <- names(sesameData::sesameData_getManifestGRanges("MM285"))
anno <- annoProbes(probeIDs=probes, "designGroup", silent = TRUE)
```

---

buildGeneDBs

*build gene-probe association database*

---

**Description**

build gene-probe association database

**Usage**

```
buildGeneDBs(
  probeIDs = NULL,
  platform = NULL,
  genome = NULL,
  max_distance = 10000,
  silent = FALSE
)
```

**Arguments**

probeIDs	the query probe list. If NULL, use all the probes on the platform
platform	HM450, EPIC, MM285, Mammal40, will infer from query if not given
genome	hg38, mm10, ..., will infer if not given.
max_distance	probe-gene distance for association
silent	suppress messages

**Value**

gene databases

**Examples**

```
sesameData::sesameDataCache(data_titles=
c("EPIC.address", "genomeInfo.hg38", "probeIDSignature"))
query <- c("cg04707299", "cg13380562", "cg00480749")
dbs <- buildGeneDBs(query, platform = "EPIC")
testEnrichment(query, dbs, platform = "EPIC")
```

---

dbStats	<i>dbStats aggregates methylation of a given betas matrix over specified database set features</i>
---------	--

---

**Description**

dbStats aggregates methylation of a given betas matrix over specified database set features

**Usage**

```
dbStats(
  betas,
  databases,
  fun = mean,
  na.rm = TRUE,
  n_min = NULL,
  f_min = 0.1,
  long = FALSE
)
```

**Arguments**

betas	matrix of beta values where probes are on the rows and samples are on the columns
databases	List of vectors corresponding to probe locations for which the features will be extracted
fun	aggregation function, default to mean
na.rm	whether to remove NA
n_min	min number of non-NA for aggregation function to apply, overrides f_min
f_min	min fraction of non-NA for aggregation function to apply
long	produce long-form result

**Value**

matrix with samples on the rows and database set on the columns

**Examples**

```
library(SummarizedExperiment)
sesameData::sesameDataCache(data_titles=
c("MM285.467.SE.tissue20Kprobes", "KYCG.MM285.probeType.20210630"))
se <- sesameData::sesameDataGet("MM285.467.SE.tissue20Kprobes")
head(dbStats(assay(se), "MM285.probeType")[,1:3])
sesameData::sesameDataGet_resetEnv()
```

---

getDBs

---

*Get databases by full or partial names of the database group(s)*


---

**Description**

Get databases by full or partial names of the database group(s)

**Usage**

```
getDBs(
  group_nms,
  db_names = NULL,
  platform = NULL,
  summary = FALSE,
  allow_multi = FALSE,
  type = NULL,
  silent = FALSE
)
```

**Arguments**

group_nms	database group names
db_names	name of the database, fetch only the given databases
platform	EPIC, HM450, MM285, ... If given, will restrict to that platform.
summary	return a summary of database instead of db itself
allow_multi	allow multiple groups to be returned for
type	numerical, categorical, default: all
silent	no messages each query.

**Value**

a list of databases, return NULL if no database is found

**Examples**

```
sesameData::sesameDataCache(data_titles=
c("KYCG.MM285.chromHMM.20210210", "KYCG.MM285.probeType.20210630"))
dbs <- getDBs("MM285.chromHMM")
dbs <- getDBs(c("MM285.chromHMM", "MM285.probeType"))
```

---

KYCG\_plotBar

*Bar plot to show most enriched CG groups from testEnrichment*


---

**Description**

The input data frame should have an "estimate" and a "FDR" columns.

**Usage**

```
KYCG_plotBar(df, y = "-log10(FDR)", n = 20, order_by = "FDR", label = FALSE)
```

**Arguments**

df	KYCG result data frame
y	the column to be plotted on y-axis
n	number of CG groups to plot
order_by	the column by which CG groups are ordered
label	whether to label significant bars

**Details**

Top CG groups are determined by estimate (descending order).

**Value**

grid plot object

**Examples**

```
KYCG_plotBar(data.frame(
  estimate=runif(10,0,10), FDR=runif(10,0,1), nD=10,
  overlap=as.integer(runif(10,0,30)), group="g", dbname=seq_len(10)))
```

---

 KYCG\_plotDot

*Dot plot to show most enriched CG groups from testEnrichment*


---

**Description**

The input data frame should have an "estimate" and a "FDR" columns.

**Usage**

```
KYCG_plotDot(
  df,
  y = "-log10(FDR)",
  n = 20,
  order_by = "FDR",
  title = "Enriched Knowledgebases",
  label_by = "dbname",
  size_by = "overlap",
  color_by = "estimate",
  short_label = FALSE
)
```

**Arguments**

df	KYCG result data frame
y	the column to be plotted on y-axis
n	number of CG groups to plot
order_by	the column by which CG groups are ordered
title	plot title
label_by	the column for label
size_by	the column by which CG group size plot
color_by	the column by which CG groups are colored
short_label	omit group in label

**Details**

Top CG groups are determined by estimate (descending order).



**Value**

grid plot object (by ggplot)

**Examples**

```
KYCG_plotDot(data.frame(
  estimate=runif(10,0,10), FDR=runif(10,0,1), nD=runif(10,10,20),
  overlap=as.integer(runif(10,0,30)), group="g", dbname=seq_len(10)))
```

---

KYCG\_plotEnrichAll      *plot enrichment test result*

---

**Description**

plot enrichment test result

**Usage**

```
KYCG_plotEnrichAll(
  df,
  fdr_max = 25,
  n_label = 15,
  min_estimate = 0,
  short_label = TRUE
)
```

**Arguments**

df	test enrichment result data frame
fdr_max	maximum fdr for capping
n_label	number of database to label
min_estimate	minimum estimate
short_label	use short label

**Value**

grid object

**Examples**

```
query <- getDBs("MM285.designGroup")["PGCMeth"]
res <- testEnrichment(query, platform="MM285")
KYCG_plotEnrichAll(res)
```

---

KYCG\_plotLollipop      *creates a lollipop plot of log(estimate) given data with fields estimate.*

---

### Description

creates a lollipop plot of log(estimate) given data with fields estimate.

### Usage

```
KYCG_plotLollipop(df, label_column = "dbname", n = 20)
```

### Arguments

df	DataFrame where each row is a database name with its estimate.
label_column	column in df to be used as the label (default: dbname)
n	Integer representing the number of top enrichments to report. Optional. (Default: 10)

### Value

ggplot lollipop plot

### Examples

```
KYCG_plotLollipop(data.frame(
  estimate=runif(10,0,10), FDR=runif(10,0,1), nD=runif(10,10,20),
  overlap=as.integer(runif(10,0,30)), group="g",
  dbname=as.character(seq_len(10))))
```

---

KYCG\_plotManhattan      *KYCG\_plotManhattan makes a manhattan plot to summarize EWAS results*

---

### Description

KYCG\_plotManhattan makes a manhattan plot to summarize EWAS results

**Usage**

```
KYCG_plotManhattan(
  vals,
  platform = NULL,
  genome = NULL,
  title = NULL,
  rasterize = FALSE,
  rasterize_thres = 3,
  label_min = 100,
  col = c("wheat1", "sienna3"),
  ylabel = "Value"
)
```

**Arguments**

<code>vals</code>	named vector of values (P,Q etc), vector name is Probe ID.
<code>platform</code>	String corresponding to the type of platform to use for retrieving GRanges coordinates of probes. Either MM285, EPIC, HM450, or HM27. If it is not provided, it will be inferred from the query set probeIDs (Default: NA).
<code>genome</code>	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.
<code>title</code>	title for plot
<code>rasterize</code>	if true use ggrastr to rasterize non-significant data.
<code>rasterize_thres</code>	the threshold of rasterize
<code>label_min</code>	Threshold above which data points will be labelled with Probe ID
<code>col</code>	color
<code>ylabel</code>	y-axis label

**Value**

a ggplot object

**Examples**

```
## see vignette for examples
```

---

KYCG\_plotMeta      *Plot meta gene or other meta genomic features*

---

**Description**

Plot meta gene or other meta genomic features

**Usage**

```
KYCG_plotMeta(betas, platform = NULL)
```

**Arguments**

betas              a named numeric vector or a matrix (row: probes; column: samples)  
platform          if not given and x is a SigDF, will be inferred the meta features

**Value**

a grid plot object

**Examples**

```
library(sesameData)  
library(sesame)  
sdf <- sesameDataGet("EPIC.1.SigDF")  
KYCG_plotMeta(getBetas(sdf))
```

---

KYCG\_plotMetaEnrichment      *Plot meta gene or other meta genomic features*

---

**Description**

Plot meta gene or other meta genomic features

**Usage**

```
KYCG_plotMetaEnrichment(result_list)
```

**Arguments**

result\_list      one or a list of testEnrichment

**Value**

a grid plot object

**Examples**

```
cg_lists <- getDBs("MM285.TFBS")
queries <- cg_lists[(sapply(cg_lists, length) > 40000)]
result_list <- lapply(queries, testEnrichment,
  "MM285.metagene", silent=TRUE, platform="MM285")

KYCG_plotMetaEnrichment(result_list)
```

---

KYCG_plotPointRange	<i>Plot point range for a list of enrichment testing results against the same set of databases</i>
---------------------	--

---

**Description**

Plot point range for a list of enrichment testing results against the same set of databases

**Usage**

```
KYCG_plotPointRange(result_list)
```

**Arguments**

result\_list     a list of testEnrichment resultsx

**Value**

grid plot object

**Examples**

```
## pick some big TFBS-overlapping CpG groups
cg_lists <- getDBs("MM285.TFBS")
queries <- cg_lists[(sapply(cg_lists, length) > 40000)]
result_list <- lapply(queries, testEnrichment,
  "MM285.chromHMM", platform="MM285")
KYCG_plotPointRange(result_list)
```

---

 KYCG\_plotSetEnrichment

*Plot Set Enrichment*


---

**Description**

Plot Set Enrichment

**Usage**

```
KYCG_plotSetEnrichment(result, n_sample = 1000, n_presence = 200)
```

**Arguments**

result	result object as returned from an element of the list of testEnrichmentSEA(..., prepPlot=TRUE)
n_sample	number of CpGs to sample
n_presence	number of overlap to sample for the plot

**Value**

grid object for plot

**Examples**

```
query <- getDBs("KYCG.MM285.designGroup")[[ "VMR" ]]
db <- getDBs("MM285.seqContextN", "distToTSS")
res <- testEnrichmentSEA(query, db, prepPlot = TRUE)
KYCG_plotSetEnrichment(res[[1]])
```

---

KYCG_plotVolcano	<i>creates a volcano plot of <math>-\log_2(p.value)</math> and <math>\log(estimate)</math> given data with fields estimate and p.value.</i>
------------------	---

---

**Description**

creates a volcano plot of  $-\log_2(p.value)$  and  $\log(estimate)$  given data with fields estimate and p.value.

**Usage**

```
KYCG_plotVolcano(df, label_by = "dbname", alpha = 0.05)
```

**Arguments**

df	DataFrame where each field is a database name with two fields for the estimate and p.value.
label_by	column in df to be used as the label (default: dbname)
alpha	Float representing the cut-off alpha value for the plot. Optional. (Default: 0.05)

**Value**

ggplot volcano plot

**Examples**

```
KYCG_plotVolcano(data.frame(
  estimate=runif(10,0,10), FDR=runif(10,0,1), nD=runif(10,10,20),
  overlap=as.integer(runif(10,0,30)), group="g", dbname=seq_len(10)))
```

---

KYCG\_plotWaterfall      *create a waterfall plot of log(estimate) given test enrichment*

---

**Description**

create a waterfall plot of log(estimate) given test enrichment

**Usage**

```
KYCG_plotWaterfall(
  df,
  order_by = "Log2(OR)",
  size_by = "-log10(FDR)",
  label_by = "dbname",
  n_label = 10
)
```

**Arguments**

df	data frame where each row is a database with test enrichment result
order_by	the column by which CG groups are ordered
size_by	the column by which CG group size plot
label_by	column in df to be used as the label (default: dbname)
n_label	number of datapoints to label

**Value**

grid

## Examples

```
library(SummarizedExperiment)
library(sesameData)
df <- rowData(sesameDataGet('MM285.tissueSignature'))
query <- df$Probe_ID[df$branch == "fetal_brain" & df$type == "Hypo"]
results <- testEnrichment(query, "TFBS", platform="MM285")
KYCG_plotWaterfall(results)
```

---

listDBGroups	<i>List database group names</i>
--------------	----------------------------------

---

## Description

List database group names

## Usage

```
listDBGroups(filter = NULL, path = NULL, type = NULL)
```

## Arguments

filter	keywords for filtering
path	file path to downloaded knowledgebase sets
type	categorical, numerical (default: all)

## Value

a list of db group names

## Examples

```
head(listDBGroups("chromHMM"))
## or listDBGroups(path = "~/Downloads")
```



---

testEnrichment	<i>testEnrichment tests for the enrichment of query in knowledgebase sets</i>
----------------	---

---

## Description

testEnrichment tests for the enrichment of query in knowledgebase sets

## Usage

```
testEnrichment(
  query,
  databases = NULL,
  universe = NULL,
  alternative = "greater",
  include_genes = FALSE,
  platform = NULL,
  silent = FALSE
)
```

## Arguments

query	For array input, it is a vector of probes of interest (e.g., significant differential methylated probes). For sequencing data input, it expect the file name for YAME-compressed CG sets.
databases	List of vectors corresponding to the database sets of interest with associated meta data as an attribute to each element. Optional. (Default: NA)
universe	Vector of probes in the universe set containing all of the probes to be considered in the test. If it is not provided, it will be inferred from the provided platform. (Default: NA).
alternative	"two.sided", "greater", or "less"
include_genes	include gene link enrichment testing
platform	String corresponding to the type of platform to use. Either MM285, EPIC, HM450, or HM27. If it is not provided, it will be inferred from the query set probeIDs (Default: NA).
silent	output message? (Default: FALSE)

## Value

A data frame containing features corresponding to the test estimate, p-value, and type of test.

## Examples

```
library(SummarizedExperiment)
sesameData::sesameDataCache(data_titles=
c("MM285.tissueSignature", "KYCG.MM285.chromHMM.20210210", "MM285.address"))
df <- rowData(sesameData::sesameDataGet("MM285.tissueSignature"))
```

```

probes <- df$Probe_ID[df$branch == "B_cell"]
res <- testEnrichment(probes, "chromHMM", platform="MM285")
sesameData::sesameDataGet_resetEnv()

## Not run:
# Define temporary directory and file URLs
temp_dir <- tempdir()
knowledgebase <- file.path(temp_dir, "ChromHMM.20220414.cm")
query <- file.path(temp_dir, "single_cell_10_samples.cg")
# URLs for the knowledgebase and query files
knowledgebase_url <- "https://github.com/zhou-lab/KYCGKB_mm10/raw/refs/heads/main/ChromHMM.20220414.cm"
query_url <- "https://github.com/zhou-lab/YAME/raw/refs/heads/main/test/input/single_cell_10_samples.cg"
# Download the files
download.file(knowledgebase_url, destfile = knowledgebase)
download.file(query_url, destfile = query)
# Confirm file download
list.files(temp_dir)
res = testEnrichment(query, knowledgebase)

## End(Not run)

```

---

testEnrichment2

*Test enrichment from YAME-compressed CG sets*


---

## Description

Test enrichment from YAME-compressed CG sets

## Usage

```

testEnrichment2(
  query_fn,
  knowledge_fn,
  universe_fn = NULL,
  alternative = "greater"
)

```

## Arguments

query_fn	File path to query
knowledge_fn	File path to knowledgebase
universe_fn	optional file path to universe
alternative	greater, less

## Value

A single concatenated string.

**Examples**

```

if (.Platform$OS.type!="windows") {
kfn = system.file("extdata", "chromhmm.cm", package = "knowYourCG")
qfn = system.file("extdata", "onecell.cg", package = "knowYourCG")
testEnrichment2(qfn, kfn)
}

```

---

testEnrichmentFisher    *testEnrichmentFisher uses Fisher's exact test to estimate the association between two categorical variables.*

---

**Description**

Estimates log2 Odds ratio

**Usage**

```
testEnrichmentFisher(query, database, universe, alternative = "greater")
```

**Arguments**

query	Vector of probes of interest (e.g., significant probes)
database	Vectors corresponding to the database set of interest with associated meta data as an attribute to each element.
universe	Vector of probes in the universe set containing all of
alternative	greater or two.sided (default: greater) the probes to be considered in the test. (Default: NULL)

**Value**

A DataFrame with the estimate/statistic, p-value, and name of test for the given results.

---

testEnrichmentSEA    *uses the GSEA-like test to estimate the association of a categorical variable against a continuous variable.*

---

**Description**

estimate represent enrichment score and negative estimate indicate a test for depletion

**Usage**

```
testEnrichmentSEA(
  query,
  databases,
  platform = NULL,
  silent = FALSE,
  precise = FALSE,
  prepPlot = FALSE
)
```

**Arguments**

query	query, if numerical, expect categorical database, if categorical expect numerical database
databases	database, numerical or categorical, but needs to be different from query
platform	EPIC, MM285, ..., infer if not given
silent	suppress message (default: FALSE)
precise	whether to compute precise p-value (up to numerical limit) of interest.
prepPlot	return the raw enrichment scores and presence vectors for plotting

**Value**

A DataFrame with the estimate/statistic, p-value, and name of test for the given results.

**Examples**

```
sesameData::sesameDataCache(data_titles=
c("KYCG.MM285.designGroup.20210210", "KYCG.MM285.seqContextN.20210630",
"probeIDSignature"))
query <- getDBs("KYCG.MM285.designGroup")[[ "TSS" ]]
res <- testEnrichmentSEA(query, "MM285.seqContextN")
```

---

testEnrichmentSpearman

*testEnrichmentSpearman uses the Spearman statistical test to estimate the association between two continuous variables.*

---

**Description**

testEnrichmentSpearman uses the Spearman statistical test to estimate the association between two continuous variables.

**Usage**

```
testEnrichmentSpearman(num_query, num_db)
```

**Arguments**

num_query	named numeric vector of probes of interest where names are probe IDs (e.g significant probes)
num_db	List of vectors corresponding to the database set of interest with associated meta data as an attribute to each element.

**Value**

A DataFrame with the estimate/statistic, p-value, and name of test for the given results.

---

testGO	<i>tests Gene Ontology of genes overlapping CpG query</i>
--------	---

---

**Description**

estimate represent enrichment score and negative estimate indicate a test for depletion

**Usage**

```
testGO(probeIDs, platform = NULL, organism = "hsapiens", gene_name = TRUE, ...)
```

**Arguments**

probeIDs	Vector of CpG probes IDs or a data frame with gene_name column, usually the output of testEnrichment() function
platform	EPIC, MM285, ..., infer if not given
organism	The organism corresponding to the CpG platform or genes in gene_name column
gene_name	If query is data frame from testEnrichment output, whether to use the gene_name column. If set to FALSE, TFBS will be used (default: FALSE)
...	Additional arguments to sesameData_getGenesByProbes and gost()

**Value**

A list of enriched terms and meta data from gprofiler2 output

**Examples**

```
library(SummarizedExperiment)
sesameData::sesameDataCache(data_titles=
c("MM285.tissueSignature", "probeIDSignature",
"MM285.address", "genomeInfo.mm10"))
df <- rowData(sesameData::sesameDataGet('MM285.tissueSignature'))
query <- df$Probe_ID[df$branch == "fetal_liver" & df$type == "Hypo"]
res <- testGO(query, platform="MM285")
```

---

testProbeProximity	<i>testProbeProximity tests if a query set of probes share closer genomic proximity than if randomly distributed</i>
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### Description

testProbeProximity tests if a query set of probes share closer genomic proximity than if randomly distributed

### Usage

```
testProbeProximity(
  probeIDs,
  gr = NULL,
  platform = NULL,
  iterations = 100,
  bin_size = 1500
)
```

### Arguments

probeIDs	Vector of probes of interest (e.g., significant probes)
gr	GRanges to draw samples and compute genomic distances
platform	String corresponding to the type of platform to use. Either MM285, EPIC, HM450, or HM27. If it is not provided, it will be inferred from the query set probeIDs (Default: NA).
iterations	Number of random samples to generate null distribution (Default: 100).
bin_size	the poisson interval size for computing neighboring hits

### Value

list containing a dataframe for the poisson statistics and a data frame for the probes in close proximity

### Examples

```
sesameData::sesameDataCache(data_titles=
c("MM285.tissueSignature", "MM285.address", "probeIDSignature"))
library(SummarizedExperiment)
df <- rowData(sesameData::sesameDataGet("MM285.tissueSignature"))
probes <- df$Probe_ID[df$branch == "B_cell"]
res <- testProbeProximity(probeIDs=probes, platform="MM285")
sesameData::sesameDataGet_resetEnv()
```

# Index

[aggregateTestEnrichments](#), 3  
[annoProbes](#), 3

[buildGeneDBs](#), 4

[dbStats](#), 5

[getDBs](#), 6

[KYCG\\_plotBar](#), 7

[KYCG\\_plotDot](#), 8

[KYCG\\_plotEnrichAll](#), 9

[KYCG\\_plotLollipop](#), 10

[KYCG\\_plotManhattan](#), 10

[KYCG\\_plotMeta](#), 12

[KYCG\\_plotMetaEnrichment](#), 12

[KYCG\\_plotPointRange](#), 13

[KYCG\\_plotSetEnrichment](#), 14

[KYCG\\_plotVolcano](#), 14

[KYCG\\_plotWaterfall](#), 15

[listDBGroups](#), 16

[testEnrichment](#), 17

[testEnrichment2](#), 18

[testEnrichmentFisher](#), 19

[testEnrichmentSEA](#), 19

[testEnrichmentSpearman](#), 20

[testGO](#), 21

[testProbeProximity](#), 22