

reactome_pa_top_mutated_genes

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```
library(ReactomePA)
```

```
##
```

```
## ReactomePA v1.52.0 Learn more at https://yulab-smu.top/contribution-knowledge-mining/
##
## Please cite:
##
## Guangchuang Yu, Qing-Yu He. ReactomePA: an R/Bioconductor package for
## reactome pathway analysis and visualization. Molecular BioSystems.
## 2016, 12(2):477-479
```

```
library(clusterProfiler)
```

```
## clusterProfiler v4.16.0 Learn more at https://yulab-smu.top/contribution-knowledge-mining/
##
## Please cite:
##
## S Xu, E Hu, Y Cai, Z Xie, X Luo, L Zhan, W Tang, Q Wang, B Liu, R Wang,
## W Xie, T Wu, L Xie, G Yu. Using clusterProfiler to characterize
## multiomics data. Nature Protocols. 2024, 19(11):3292-3320
```

```
##
```

```
## Attaching package: 'clusterProfiler'
```

```
## The following object is masked from 'package:stats':
```

```
##
```

```
## filter
```

```
library(org.Hs.eg.db)
```

```
## Loading required package: AnnotationDbi
```

```
## Loading required package: stats4
```

```
## Loading required package: BiocGenerics
```

```
## Loading required package: generics
```

```

##
## Attaching package: 'generics'

## The following objects are masked from 'package:base':
##
##      as.difftime, as.factor, as.ordered, intersect, is.element, setdiff,
##      setequal, union

##
## Attaching package: 'BiocGenerics'

## The following objects are masked from 'package:stats':
##
##      IQR, mad, sd, var, xtabs

## The following objects are masked from 'package:base':
##
##      anyDuplicated, aperm, append, as.data.frame, basename, cbind,
##      colnames, dirname, do.call, duplicated, eval, evalq, Filter, Find,
##      get, grep, grepl, is.unsorted, lapply, Map, mapply, match, mget,
##      order, paste, pmax, pmax.int, pmin, pmin.int, Position, rank,
##      rbind, Reduce, rownames, sapply, saveRDS, table, tapply, unique,
##      unsplit, which.max, which.min

## Loading required package: Biobase

## Welcome to Bioconductor
##
##      Vignettes contain introductory material; view with
##      'browseVignettes()'. To cite Bioconductor, see
##      'citation("Biobase")', and for packages 'citation("pkgname)".

## Loading required package: IRanges

## Loading required package: S4Vectors

##
## Attaching package: 'S4Vectors'

## The following object is masked from 'package:clusterProfiler':
##
##      rename

## The following object is masked from 'package:utils':
##
##      findMatches

## The following objects are masked from 'package:base':
##
##      expand.grid, I, unname

```

```
##
## Attaching package: 'IRanges'

## The following object is masked from 'package:clusterProfiler':
##
## slice

## The following object is masked from 'package:grDevices':
##
## windows

##
## Attaching package: 'AnnotationDbi'

## The following object is masked from 'package:clusterProfiler':
##
## select

##

library(enrichplot)

## enrichplot v1.28.4 Learn more at https://yulab-smu.top/contribution-knowledge-mining/
##
## Please cite:
##
## Guangchuang Yu. Gene Ontology Semantic Similarity Analysis Using
## GOSemSim. In: Kidder B. (eds) Stem Cell Transcriptional Networks.
## Methods in Molecular Biology. 2020, 2117:207-215. Humana, New York, NY.

library(ggplot2)

# Your genes
genes <- c("CDKN2A", "EGFR", "MDM2", "CDK4", "MET", "ERBB2", "KRAS")

# Convert to Entrez IDs
entrez_ids <- bitr(genes, fromType = "SYMBOL",
                  toType = "ENTREZID",
                  OrgDb = org.Hs.eg.db)

## 'select()' returned 1:1 mapping between keys and columns

entrez_ids

## SYMBOL ENTREZID
## 1 CDKN2A 1029
## 2 EGFR 1956
## 3 MDM2 4193
## 4 CDK4 1019
## 5 MET 4233
## 6 ERBB2 2064
## 7 KRAS 3845
```

```

reactome_res <- enrichPathway(gene = entrez_ids$ENTREZID,
                              organism = "human",
                              pvalueCutoff = 0.05,
                              qvalueCutoff = 0.2,
                              readable = TRUE)

# View top pathways
head(reactome_res)

```

##	ID	Description			
## R-HSA-8848021	R-HSA-8848021	Signaling by PTK6			
## R-HSA-9006927	R-HSA-9006927	Signaling by Non-Receptor Tyrosine Kinases			
## R-HSA-1963640	R-HSA-1963640	GRB2 events in ERBB2 signaling			
## R-HSA-9665348	R-HSA-9665348	Signaling by ERBB2 ECD mutants			
## R-HSA-1250196	R-HSA-1250196	SHC1 events in ERBB2 signaling			
## R-HSA-9665686	R-HSA-9665686	Signaling by ERBB2 TMD/JMD mutants			
##	GeneRatio	BgRatio	RichFactor	FoldEnrichment	zScore
## R-HSA-8848021	4/7	54/11214	0.07407407	118.6667	21.66125
## R-HSA-9006927	4/7	54/11214	0.07407407	118.6667	21.66125
## R-HSA-1963640	3/7	16/11214	0.18750000	300.3750	29.94819
## R-HSA-9665348	3/7	16/11214	0.18750000	300.3750	29.94819
## R-HSA-1250196	3/7	22/11214	0.13636364	218.4545	25.51474
## R-HSA-9665686	3/7	22/11214	0.13636364	218.4545	25.51474
##	pvalue	p.adjust	qvalue	geneID	Count
## R-HSA-8848021	1.662817e-08	1.903925e-06	3.763217e-07	EGFR/CDK4/ERBB2/KRAS	4
## R-HSA-9006927	1.662817e-08	1.903925e-06	3.763217e-07	EGFR/CDK4/ERBB2/KRAS	4
## R-HSA-1963640	8.312476e-08	4.758892e-06	9.406222e-07	EGFR/ERBB2/KRAS	3
## R-HSA-9665348	8.312476e-08	4.758892e-06	9.406222e-07	EGFR/ERBB2/KRAS	3
## R-HSA-1250196	2.282260e-07	8.710626e-06	1.721705e-06	EGFR/ERBB2/KRAS	3
## R-HSA-9665686	2.282260e-07	8.710626e-06	1.721705e-06	EGFR/ERBB2/KRAS	3

```

barplot(reactome_res,
        showCategory = 10,
        title = "Top Reactome Pathways")

```

```

## Warning in fortify(object, showCategory = showCategory, by = x, ...): Arguments in '...' must be used
## x Problematic argument:
## * by = x
## i Did you misspell an argument name?

## Warning: 'aes_string()' was deprecated in ggplot2 3.0.0.
## i Please use tidy evaluation idioms with 'aes()'.
## i See also 'vignette("ggplot2-in-packages")' for more information.
## i The deprecated feature was likely used in the enrichplot package.
## Please report the issue at
## <https://github.com/GuangchuangYu/enrichplot/issues>.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.

```



