

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")

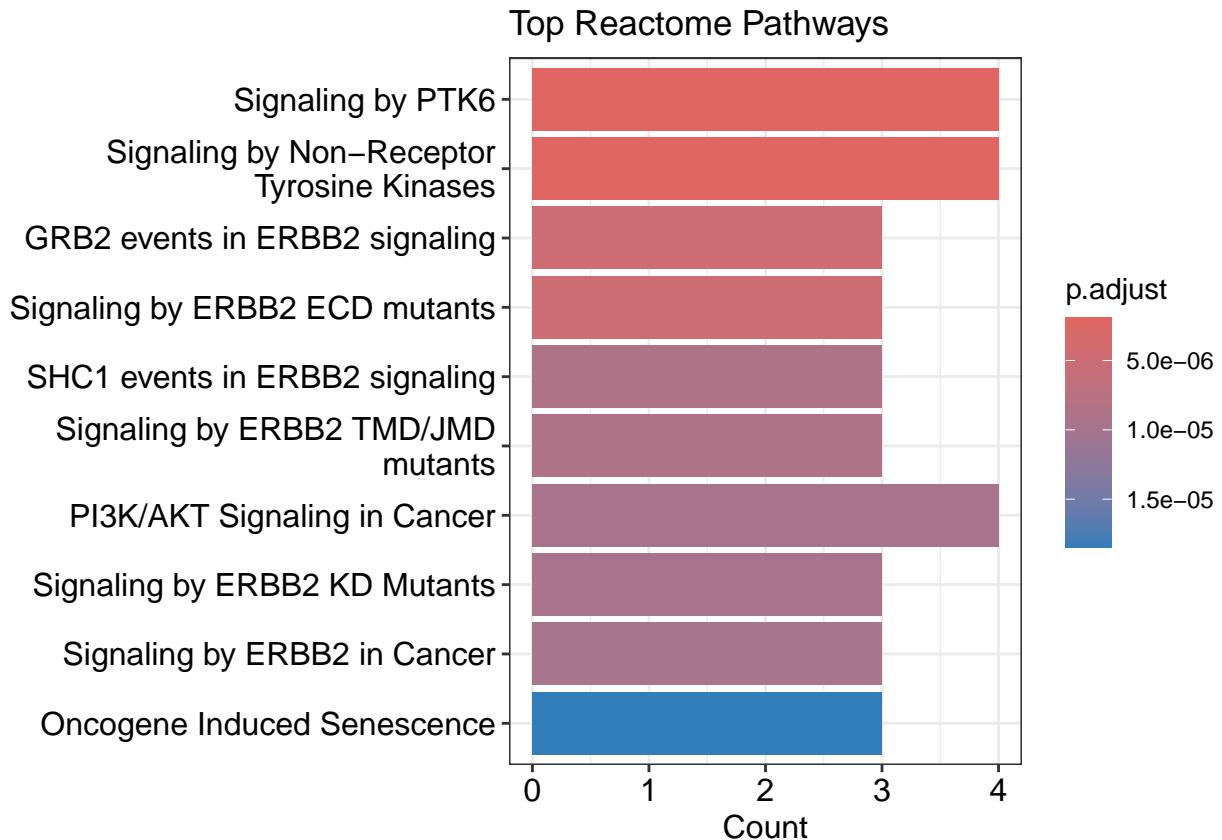
```

```

## 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.

```



```
dotplot(reactome_res,
        showCategory = 15,
        title = "Reactome Pathway Dotplot")
```

