

GO Enrichment Analysis ABCB1

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Contents

```
library(clusterProfiler)
```

```
##
```

```
## clusterProfiler v4.16.0 Learn more at https://yulab-smu.top/contribution-knowledge-mining/
##
## Please cite:
##
## T Wu, E Hu, S Xu, M Chen, P Guo, Z Dai, T Feng, L Zhou, W Tang, L Zhan,
## X Fu, S Liu, X Bo, and G Yu. clusterProfiler 4.0: A universal
## enrichment tool for interpreting omics data. The Innovation. 2021,
## 2(3):100141
```

```
##
```

```
## 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:
##
## G Yu. Thirteen years of clusterProfiler. The Innovation. 2024,
## 5(6):100722
```

```
abcb1_gene <- c("ABCB1")
```

```
# Biological Process
```

```
go_bp <- enrichGO(
  gene = abcb1_gene,
  OrgDb = org.Hs.eg.db,
  keyType = "SYMBOL",
  ont = "BP",
  pAdjustMethod = "BH",
  pvalueCutoff = 0.05,
  qvalueCutoff = 0.2
)
```

```
# Molecular Function
```

```
go_mf <- enrichGO(
  gene = abcb1_gene,
  OrgDb = org.Hs.eg.db,
  keyType = "SYMBOL",
  ont = "MF",
  pAdjustMethod = "BH",
  pvalueCutoff = 0.05,
  qvalueCutoff = 0.2
)
```

```
# Cellular Component
```

```
go_cc <- enrichGO(
  gene = abcb1_gene,
```

```

OrgDb = org.Hs.eg.db,
keyType = "SYMBOL",
ont = "CC",
pAdjustMethod = "BH",
pvalueCutoff = 0.05,
qvalueCutoff = 0.2
)

library(ggplot2)

# Function to make readable plots

plot_readable <- function(result, title) {
  if (nrow(as.data.frame(result)) == 0) {
    ggplot() +
      annotate("text", x = 0.5, y = 0.5, label = "No significant GO terms found", size = 6) +
      ggtitle(title) +
      theme_void()
  } else {
    barplot(result, showCategory = 10, title = title) +
      theme(
        axis.text.y = element_text(size = 8),
        plot.title = element_text(size = 14, face = "bold"),
        legend.position = "bottom"
      )
  }
}

plot_readable(go_bp, "GO: Biological Process")

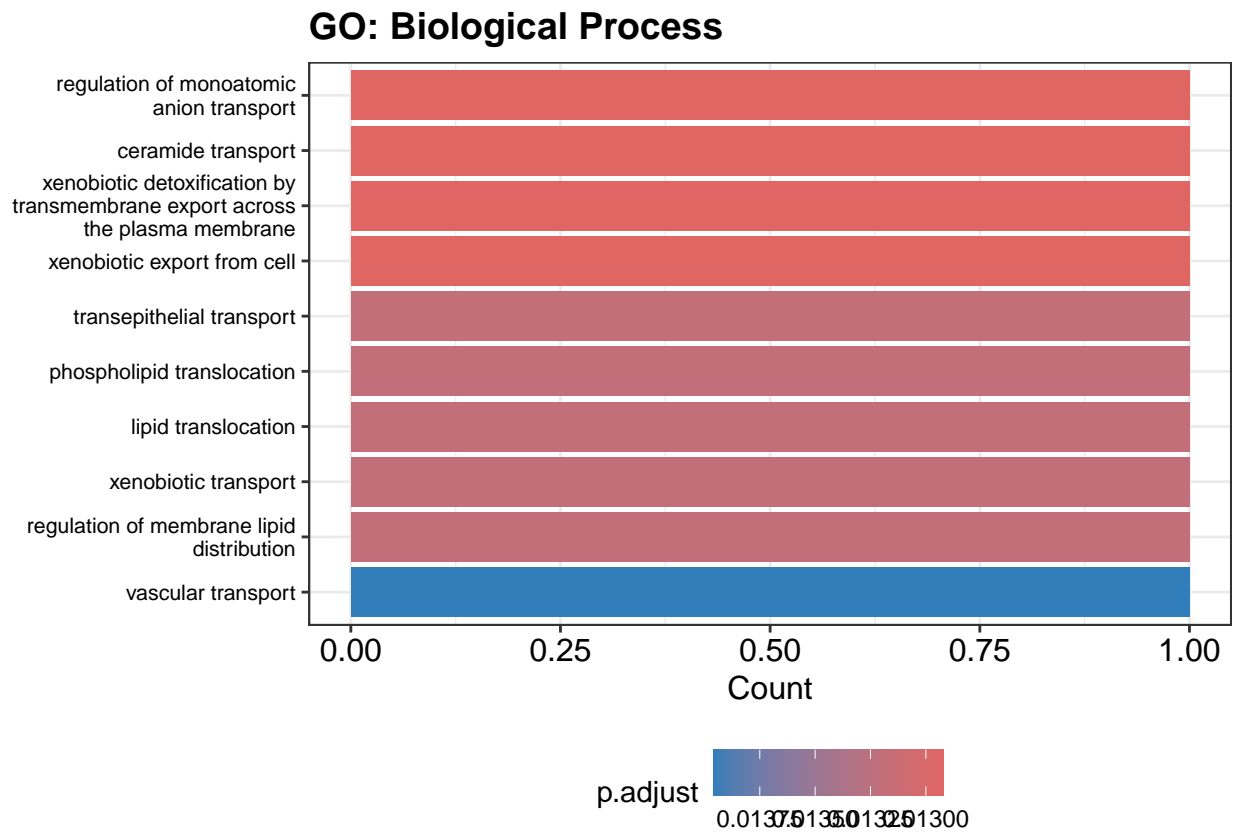
```

```

## 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.

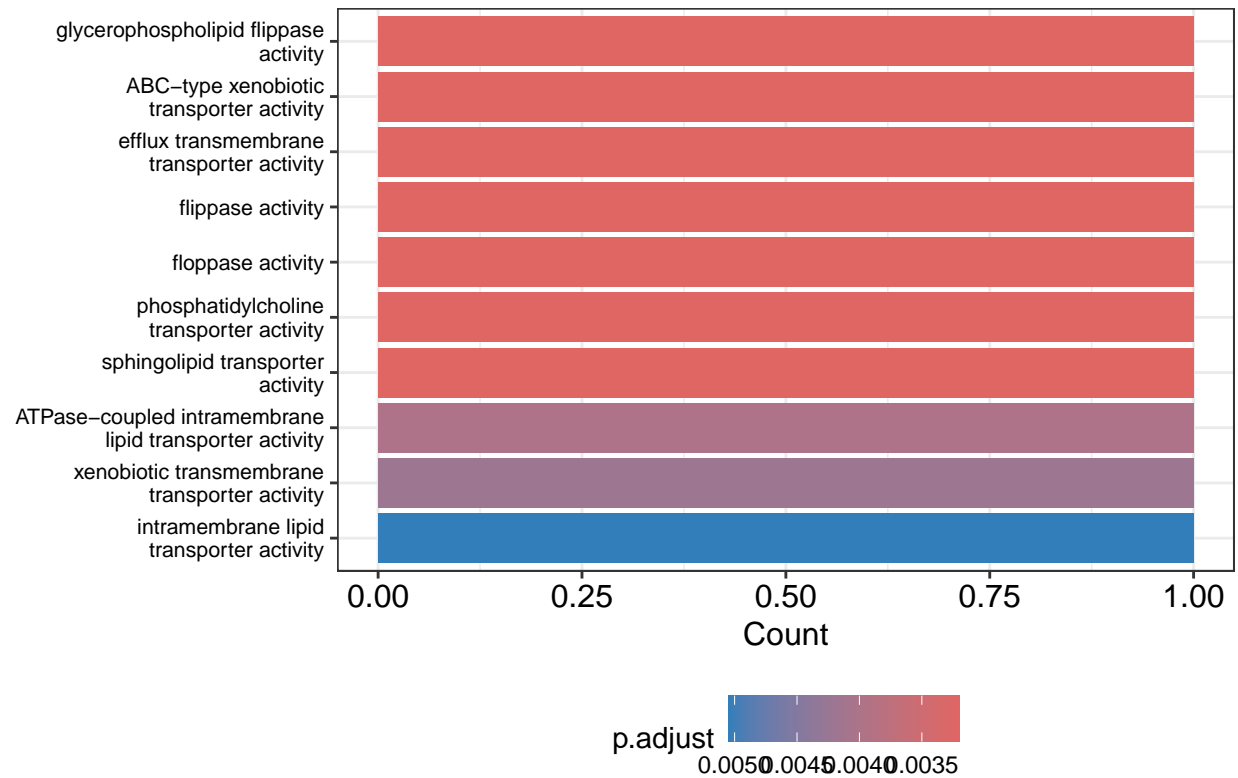
```



```
plot_readable(go_mf, "GO: Molecular Function")
```

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

GO: Molecular Function



```
plot_readable(go_cc, "GO: Cellular Component")
```

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

GO: Cellular Component

