Import dataset

```
dfBP <- read.csv("Supplementary_2BP.csv")
dfCC <- read.csv("Supplementary_2CC.csv")
dfMF <- read.csv("Supplementary_2MF.csv")
```

Extract Gene ID from the dataset

```
gene_BP <- parse_number(dfBP$X.term.ID)
gene_CC <- parse_number(dfCC$X.term.ID)
gene_MF <- parse_number(dfMF$X.term.ID)
gene_id <- c(gene_BP, gene_CC, gene_MF)
```

Parse in ID to "org.Hs.eg.db" package for computation

```
go <- enrichGO(gene_id, OrgDb = "org.Hs.eg.db", ont = "all")
```

```
##
```

```
egoBP <- enrichGO(gene_id, OrgDb = "org.Hs.eg.db", ont = "BP", readable = TRUE)
egoCC <- enrichGO(gene_id, OrgDb = "org.Hs.eg.db", ont = "CC", readable = TRUE)
egoMF <- enrichGO(gene_id, OrgDb = "org.Hs.eg.db", ont = "MF", readable = TRUE)
x <- pairwise_termsim(go, method = "JC")

# ego1: enriched terms = 17
egoBP
```

```
## #
## # over-representation test
## #
## #...@organism      Homo sapiens
## #...@ontology      BP
## #...@keytype       ENTREZID
## #...@gene      chr [1:528] "6119" "2181" "33108" "22900" "42773" "50770" "21953" "42775" ...
## #...pvalues adjusted by 'BH' with cutoff <0.05
## #...10 enriched terms found
## 'data.frame':    10 obs. of  9 variables:
##  $ ID         : chr  "GO:0033209" "GO:0071356" "GO:0002275" "GO:0034612" ...
##  $ Description: chr  "tumor necrosis factor-mediated signaling pathway" "cellular response to tumor n
##  $ GeneRatio  : chr  "7/116" "9/116" "6/116" "9/116" ...
##  $ BgRatio    : chr  "107/18800" "229/18800" "93/18800" "249/18800" ...
##  $ pvalue     : num  4.45e-06 1.24e-05 2.39e-05 2.41e-05 7.47e-05 ...
##  $ p.adjust   : num  0.0105 0.0143 0.0143 0.0143 0.0299 ...
##  $ qvalue     : num  0.00954 0.01294 0.01294 0.01294 0.02699 ...
##  $ geneID     : chr  "CARD8/TRAF3/PIAS4/TRAF5/TRAF6/EDA2R/PPP2CB" "CARD8/TRAF3/PIAS4/TRAF5/CCL20/EDN
##  $ Count      : int  7 9 6 9 9 8 8 11 3 9
## #...Citation
##  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
```

```
# ego2: enriched terms = 3
egoCC
```

```
## #
## # over-representation test
## #
## #...@organism     Homo sapiens
## #...@ontology     CC
## #...@keytype      ENTREZID
## #...@gene         chr [1:528] "6119" "2181" "33108" "22900" "42773" "50770" "21953" "42775" ...
## #...pvalues adjusted by 'BH' with cutoff <0.05
## #...3 enriched terms found
## 'data.frame':     3 obs. of  9 variables:
##  $ ID         : chr  "GO:0035631" "GO:0005677" "GO:0009898"
##  $ Description: chr  "CD40 receptor complex" "chromatin silencing complex" "cytoplasmic side of plasm
##  $ GeneRatio  : chr  "3/116" "3/116" "6/116"
##  $ BgRatio    : chr  "11/19594" "13/19594" "169/19594"
##  $ pvalue     : num  3.22e-05 5.54e-05 5.11e-04
##  $ p.adjust   : num  0.00753 0.00753 0.04633
##  $ qvalue     : num  0.00665 0.00665 0.04088
##  $ geneID     : chr  "TRAF3/TRAF5/TRAF6" "SUV39H1/YY1/RB1" "TRAF3/TRAF5/TRAF6/PTK2/PTK6/KCNAB2"
##  $ Count      : int  3 3 6
## #...Citation
##  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
# ego3: enriched terms = 1
egoMF
```

```
## #
## # over-representation test
## #
## #...@organism     Homo sapiens
## #...@ontology     MF
## #...@keytype      ENTREZID
## #...@gene         chr [1:528] "6119" "2181" "33108" "22900" "42773" "50770" "21953" "42775" ...
## #...pvalues adjusted by 'BH' with cutoff <0.05
## #...1 enriched terms found
## 'data.frame':     1 obs. of  9 variables:
##  $ ID         : chr "GO:0031996"
##  $ Description: chr "thioesterase binding"
##  $ GeneRatio  : chr "3/113"
##  $ BgRatio    : chr "11/18410"
##  $ pvalue     : num 3.58e-05
##  $ p.adjust   : num 0.0136
##  $ qvalue     : num 0.0125
##  $ geneID     : chr "TRAF3/TRAF5/TRAF6"
##  $ Count      : int 3
## #...Citation
##  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
```

Go plot

```
goplot(egoBP, showCategory = 17)
```

```
## Warning: ggrepel: 7 unlabeled data points (too many overlaps). Consider
## increasing max.overlaps
```
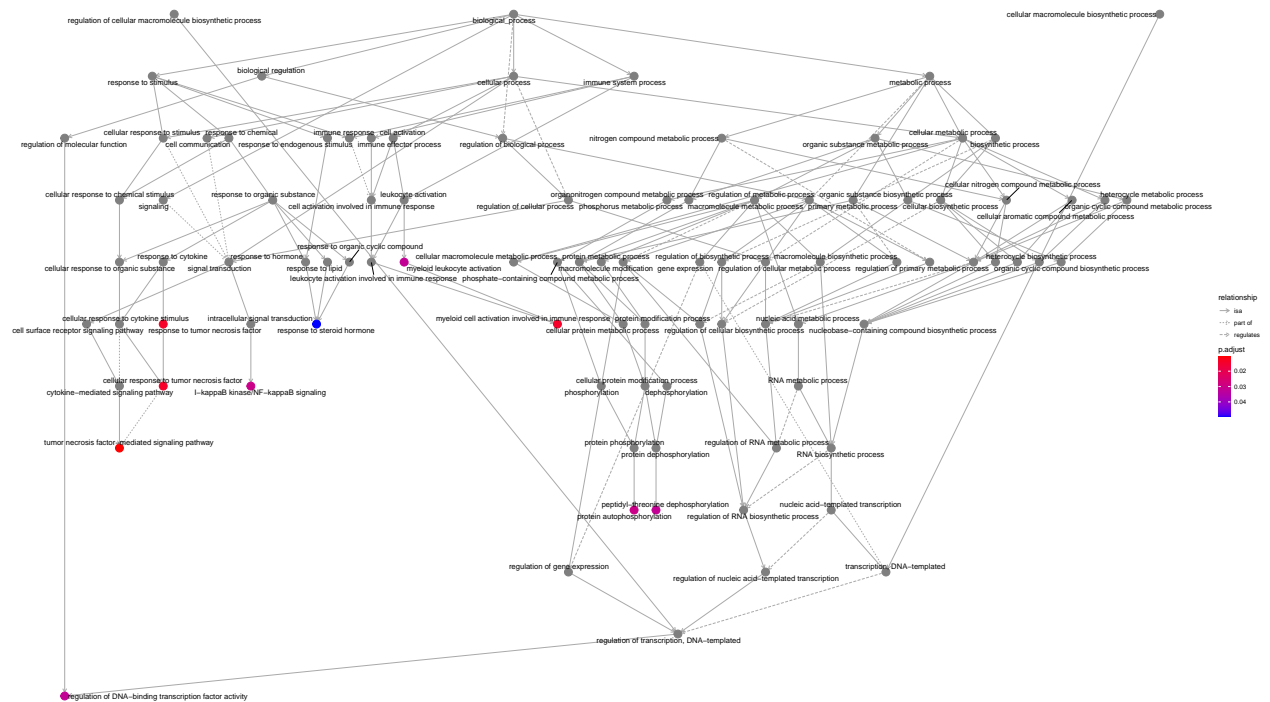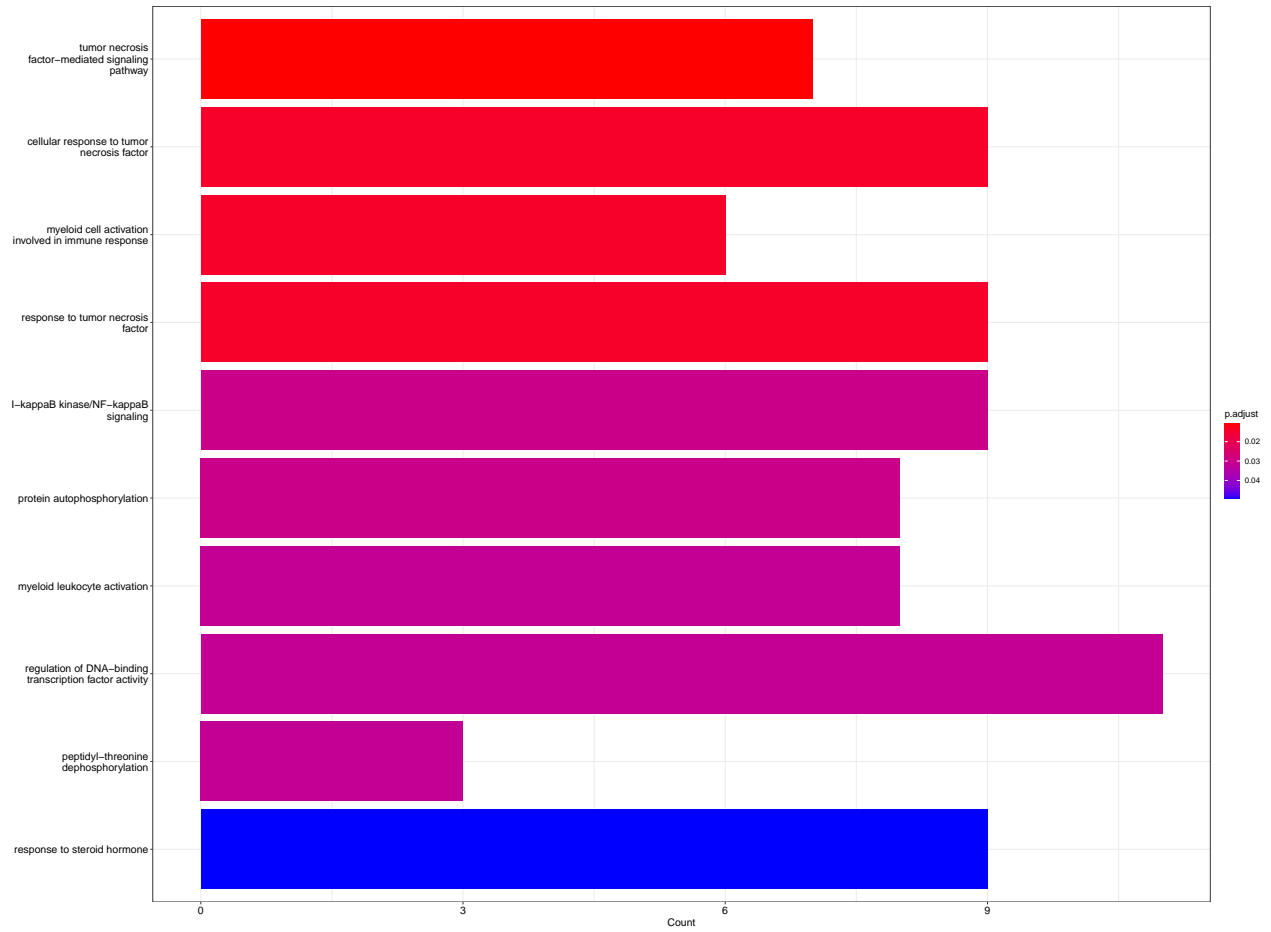


```
goplot(egoCC, showCategory = 3)
```
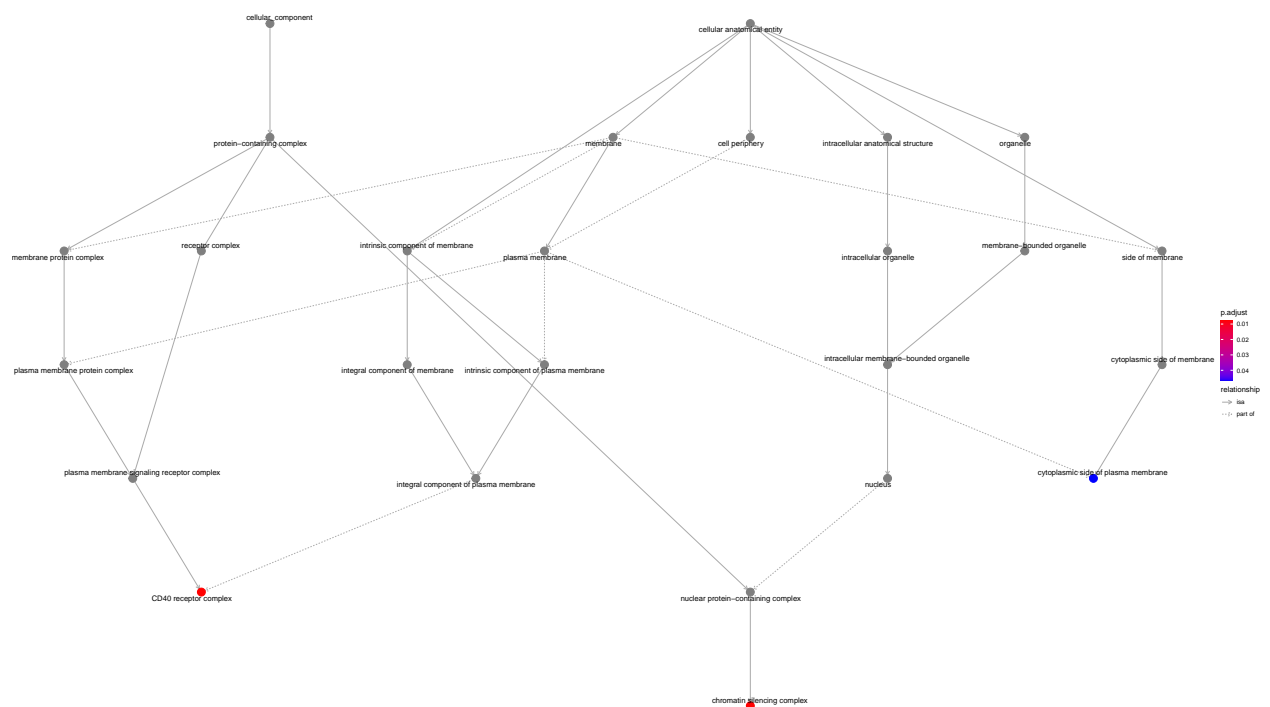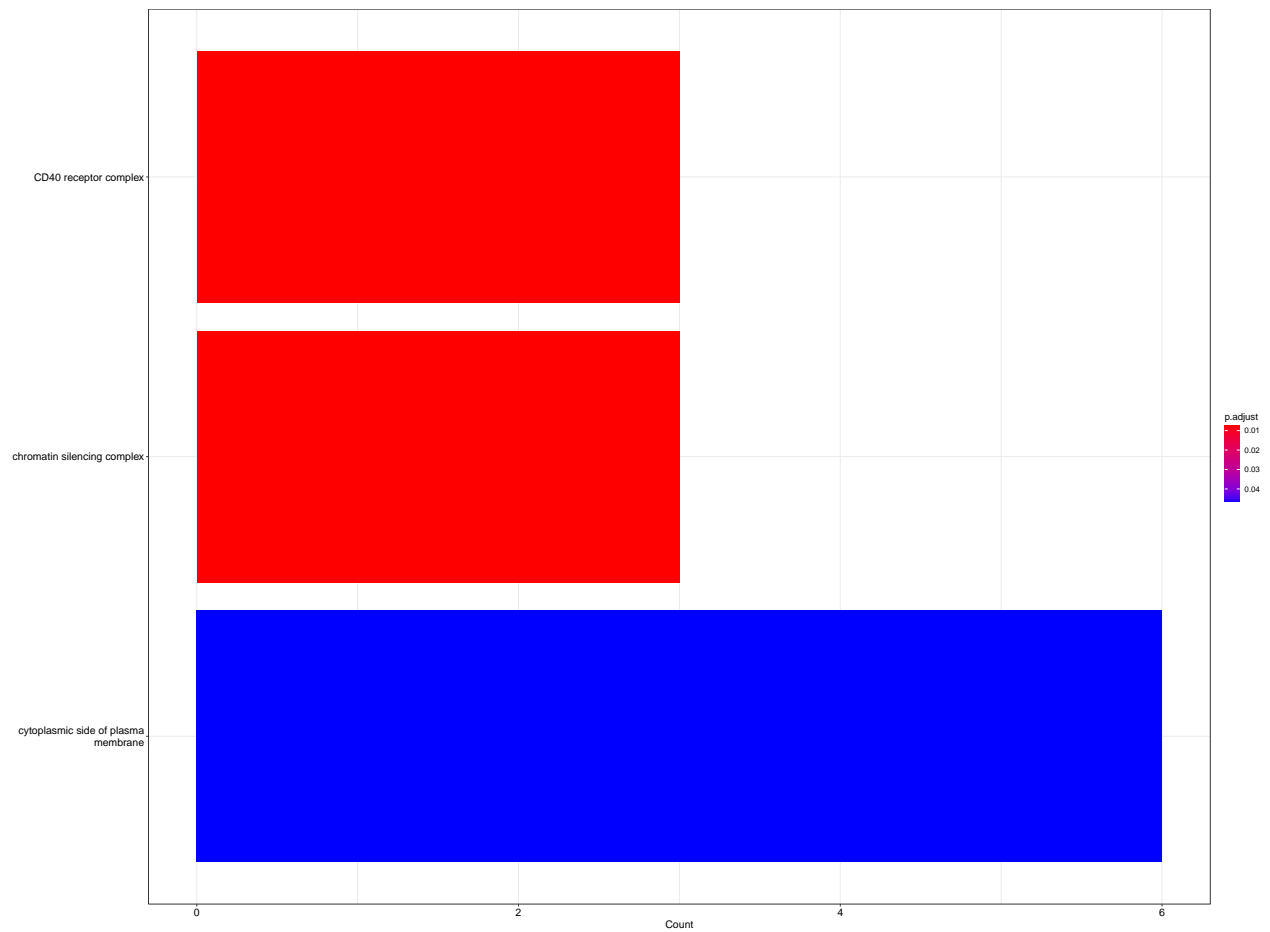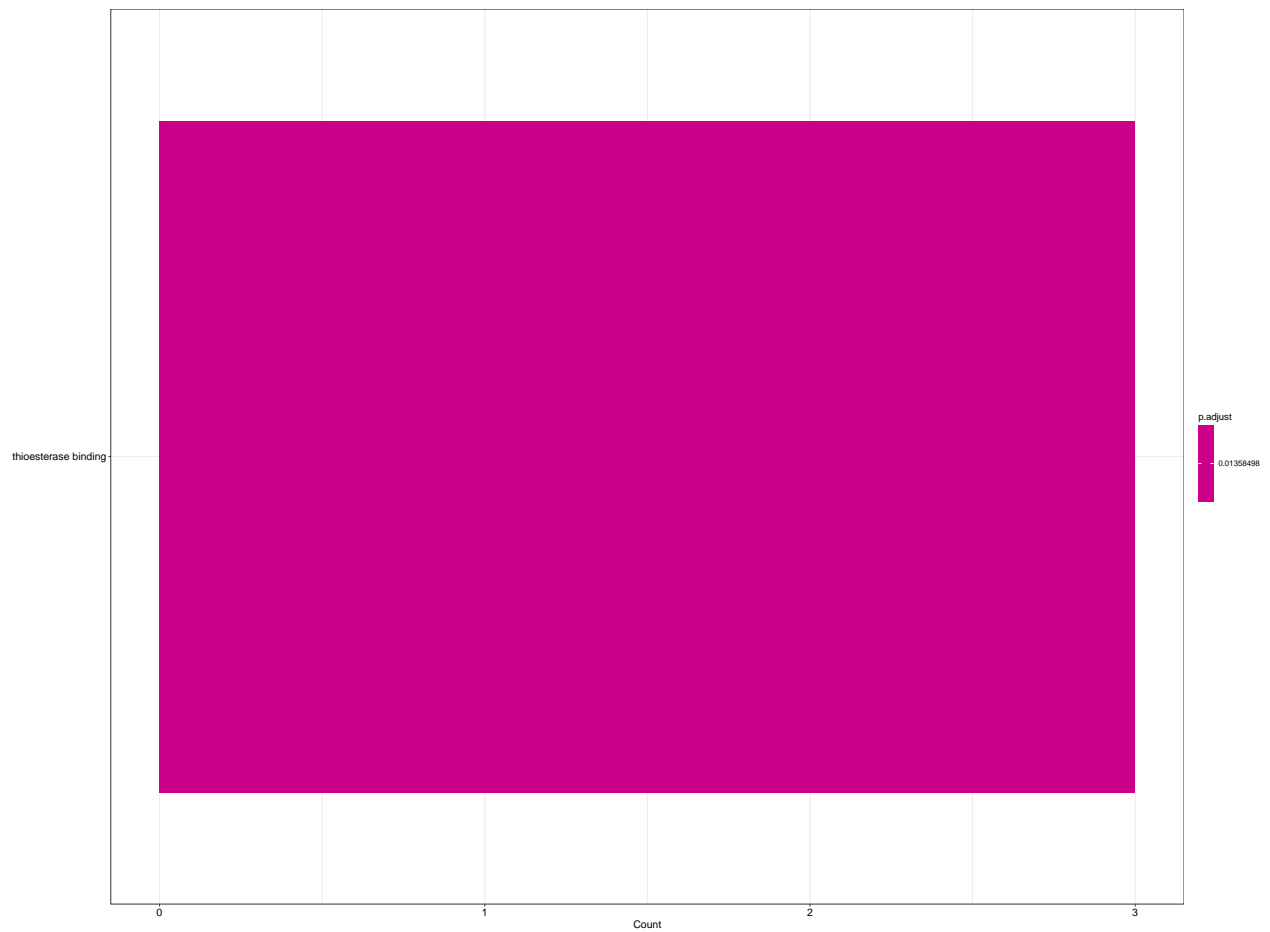

Bar plot

```
# Display all the enriched terms in BP, CC and MF
barplot(egoBP, showCategory = 17)
```
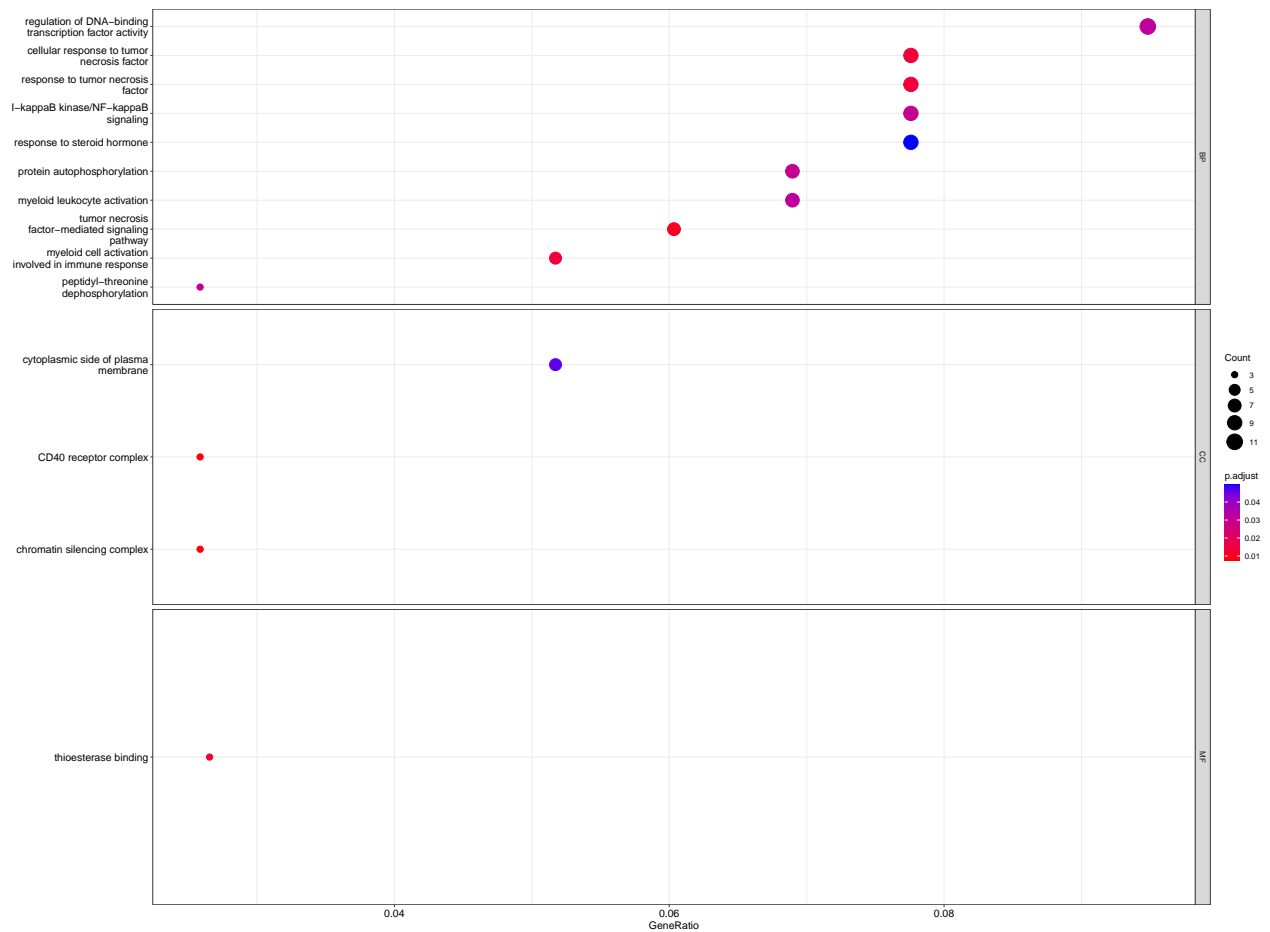
```
barplot(egoCC, showCategory = 3)
```
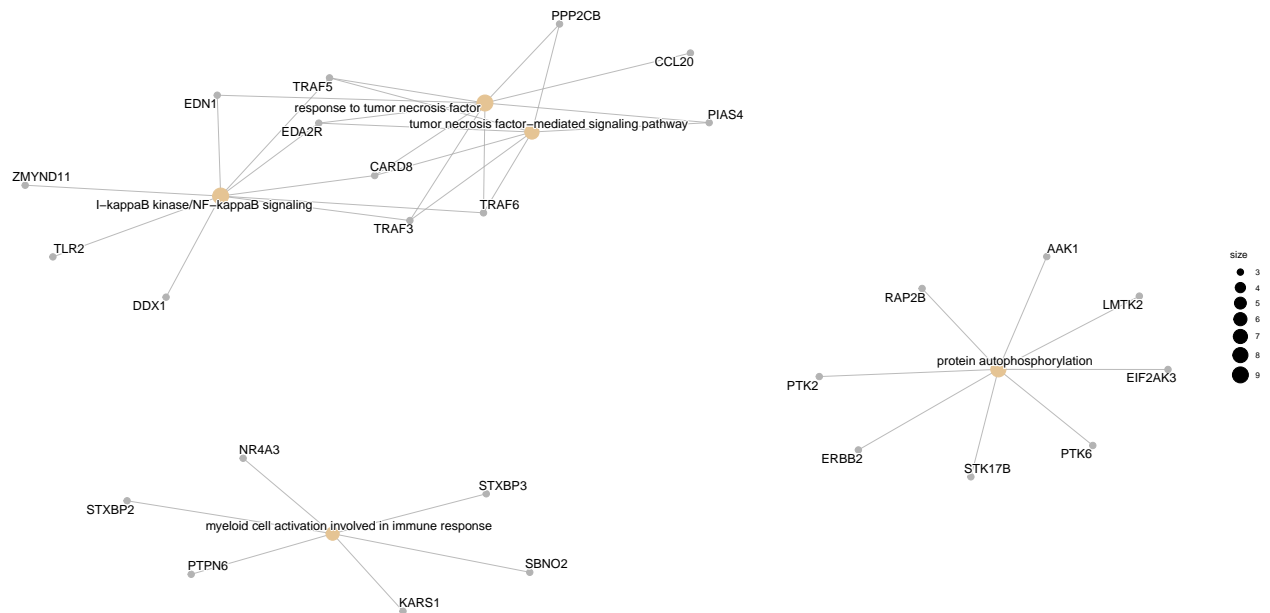
```
barplot(egoMF, showCategory = 1)
```

Dot plot

```
dotplot(go, split = "ONTOLOGY") + facet_grid(ONTOLOGY ~ ., scale = "free")
```
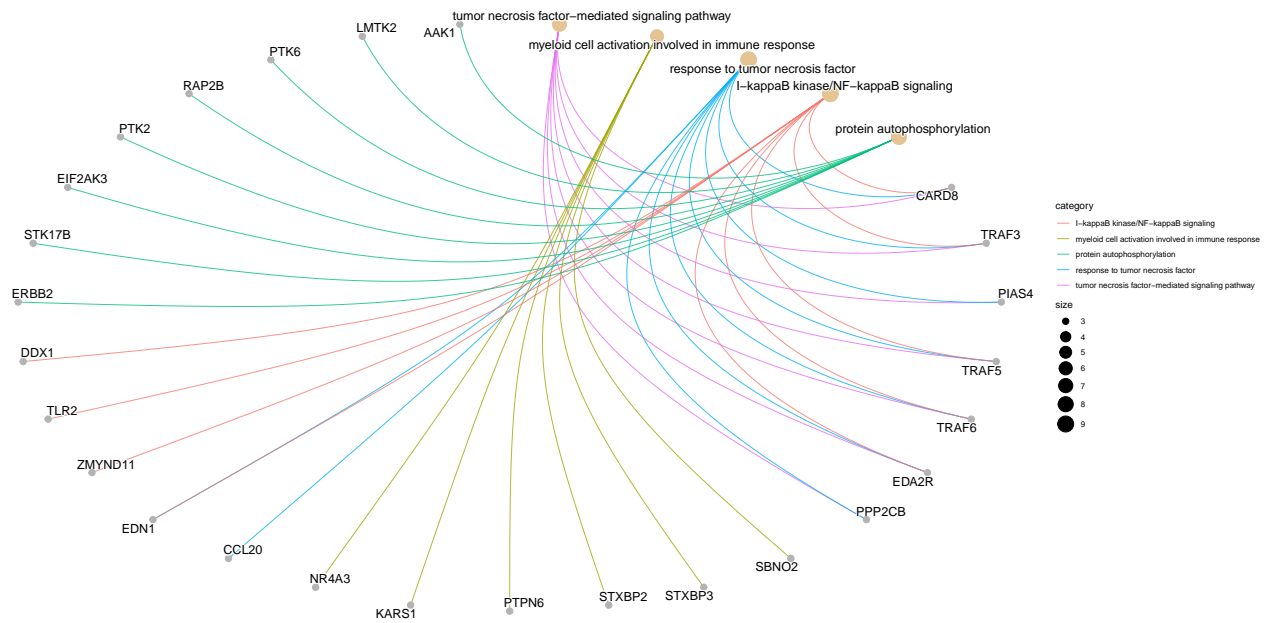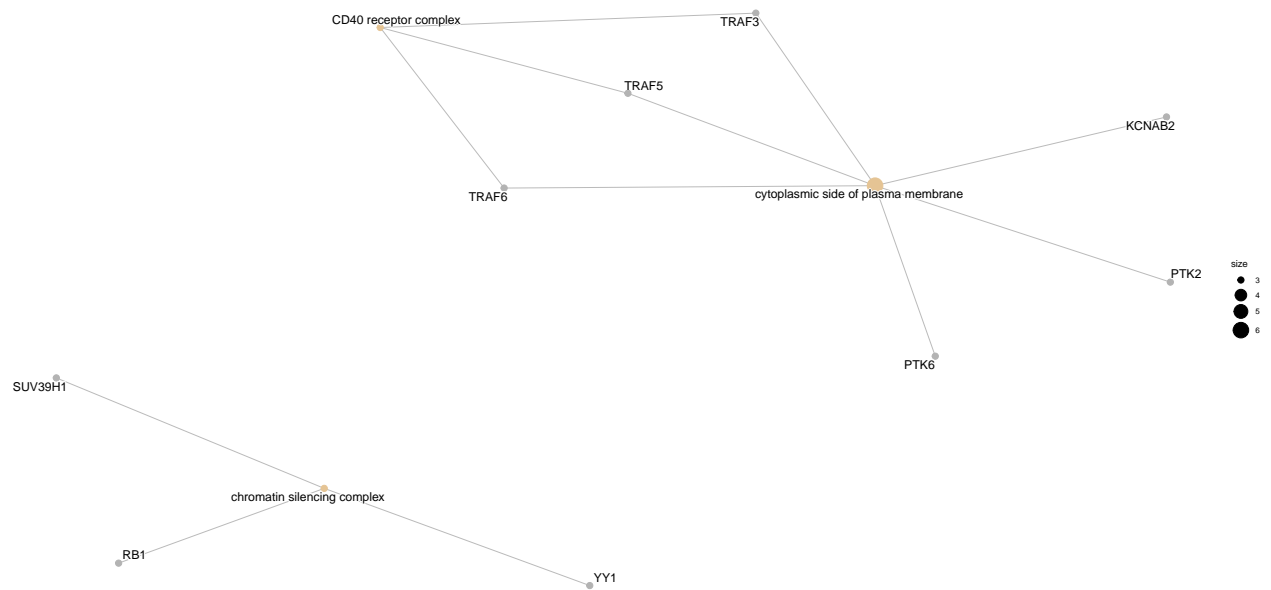
Gene-Concept Network plot

```
egoBP2 <- simplify(egoBP)
egoCC2 <- simplify(egoCC)
egoMF2 <- simplify(egoMF)
cnetplot(egoBP2)
```
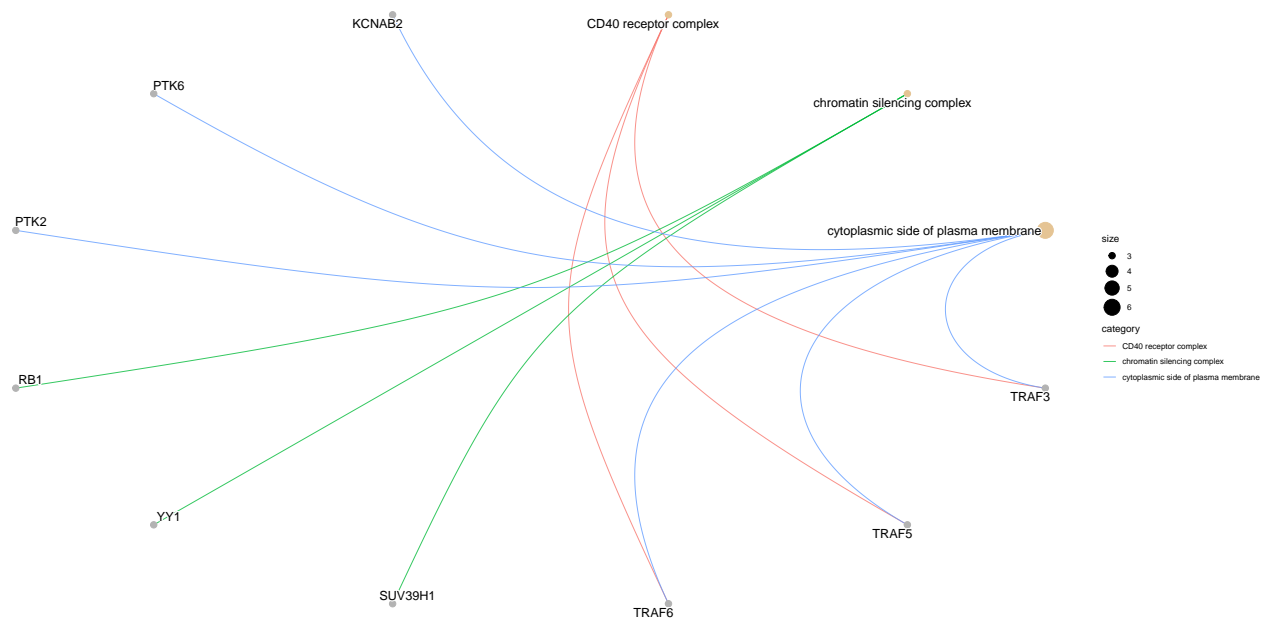
```
cnetplot(egoBP2, circular = TRUE, colorEdge = TRUE)
```
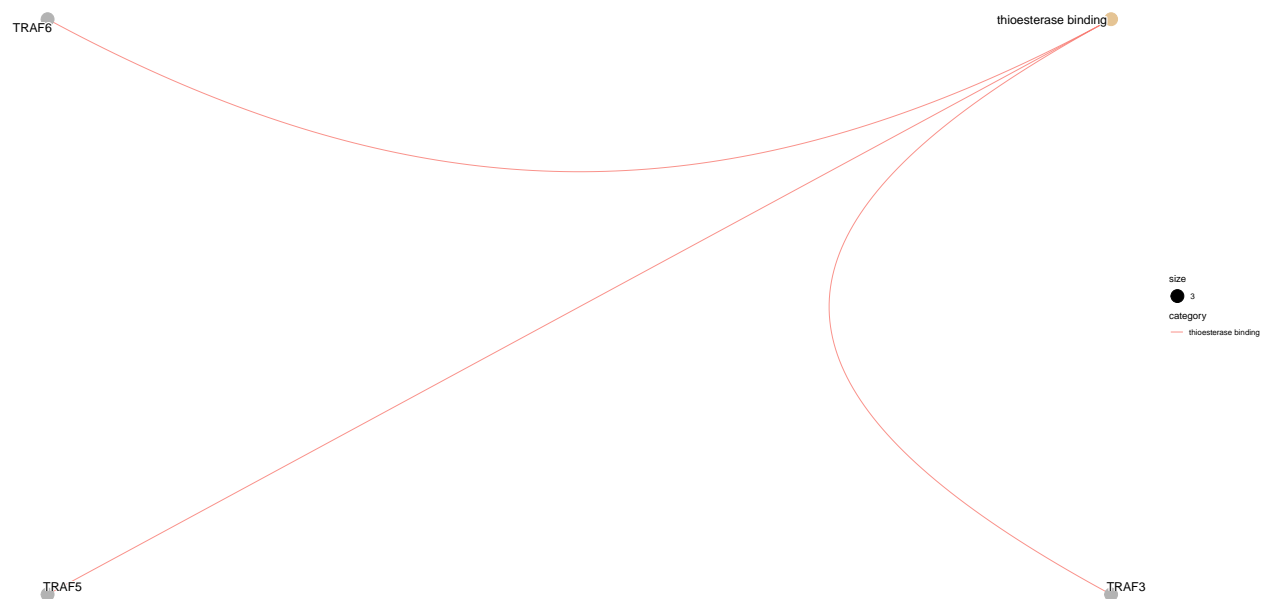


```
cnetplot(egoCC2)
```

```
cnetplot(egoCC2, circular = TRUE, colorEdge = TRUE)
```
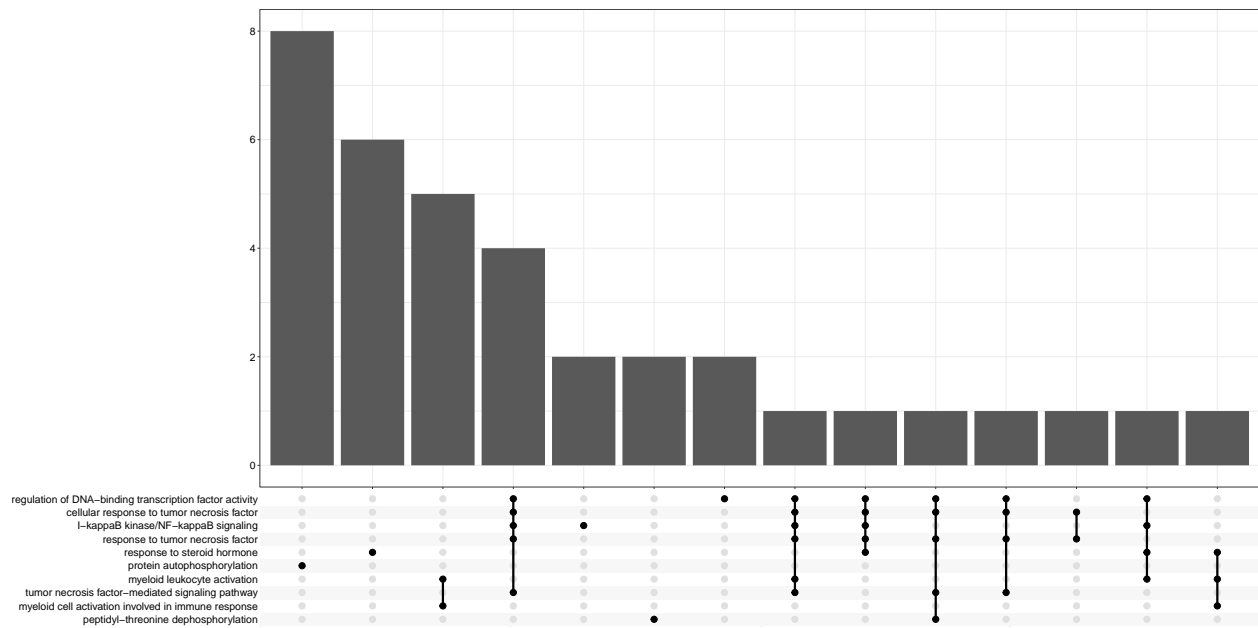


```
cnetplot(egoMF2)
```

```
cnetplot(egoMF2, circular = TRUE, colorEdge = TRUE)
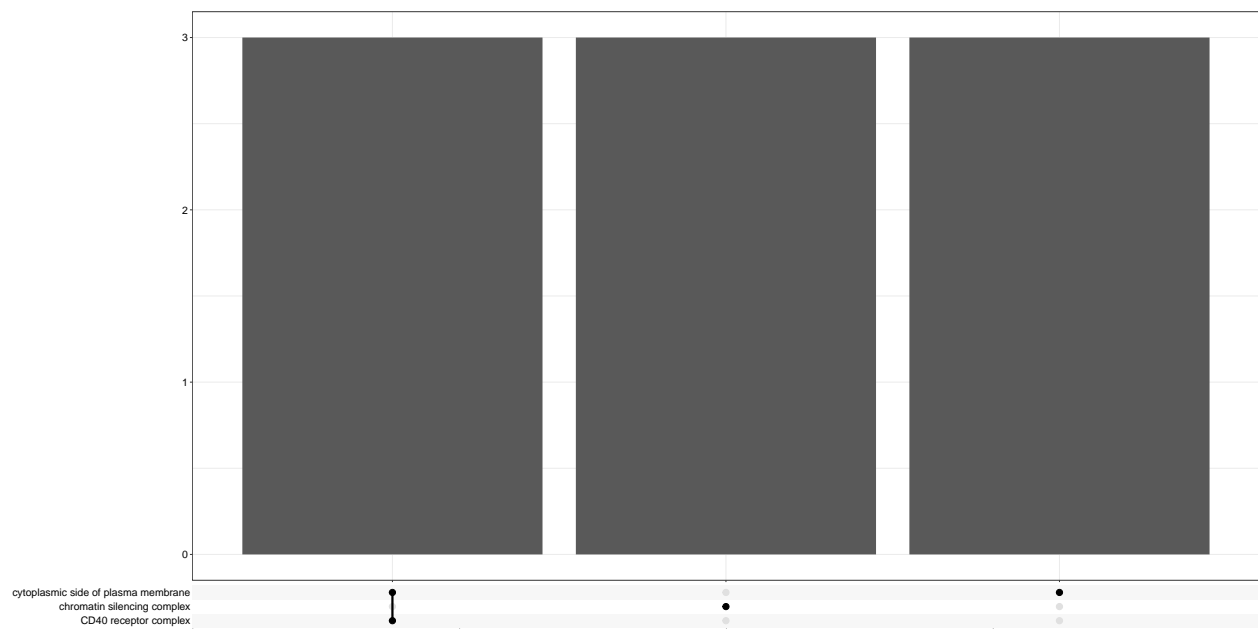```



## UpSet plot

```
upsetplot(egoBP)
```
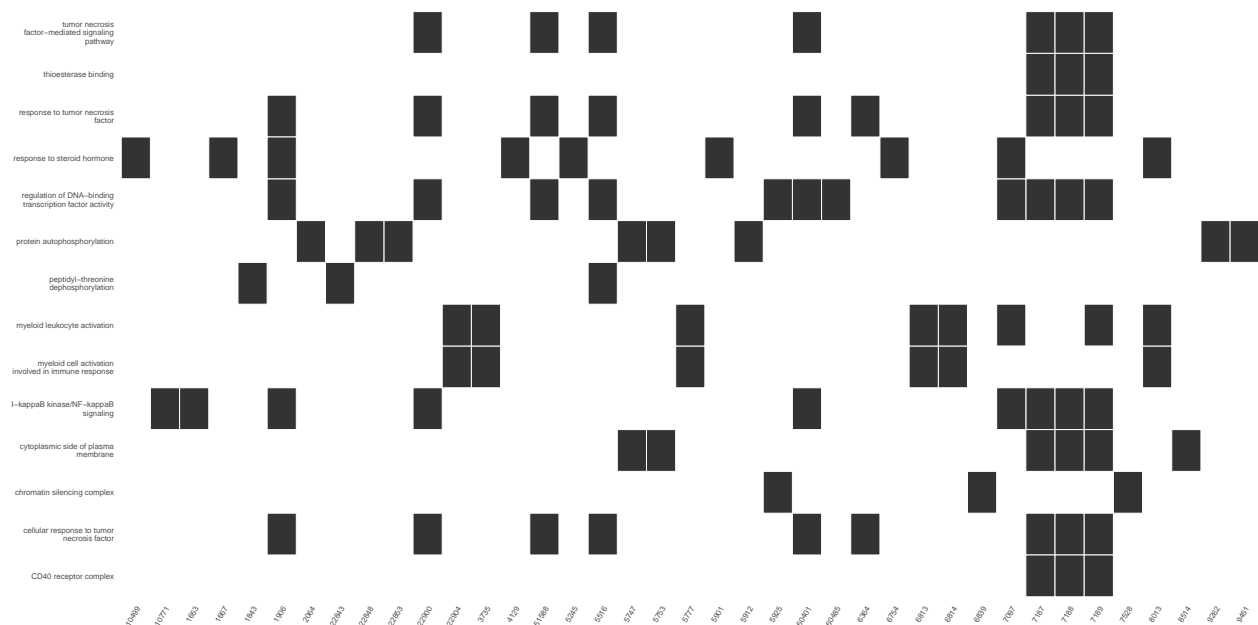
upsetplot(egoCC)



upsetplot(egoMF)

```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```

Heatmap-like functional classification

`heatplot(go)`

Enrichment map

`emapplot(x)`

response to steroid hormone

protein autophosphorylation

myeloid leukocyte activation

CD40 receptor complex

cytoplasmic side of plasma membrane

thioesterase binding

myeloid cell activation involved in immune response

tumor necrosis factor−mediated signaling pathway

I−kappaB kinase/NF−kappaB signaling

cellular response to tumor necrosis factor

response to tumor necrosis factor

regulation of DNA−binding transcription factor activity

chromatin silencing complex

peptidyl−threonine dephosphorylation

number of genes
○ 3
○ 5
○ 7
○ 9
○ 11

p.adjust
0.04
0.03
0.02
0.01