

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 necrosis factor" ...
```

```
## $ 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/EDNRA" ...
```

```
## $ 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  "G0:0035631" "G0:0005677" "G0:0009898"
## $ Description: chr  "CD40 receptor complex" "chromatin silencing complex" "cytoplasmic side of plas
## $ 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
```

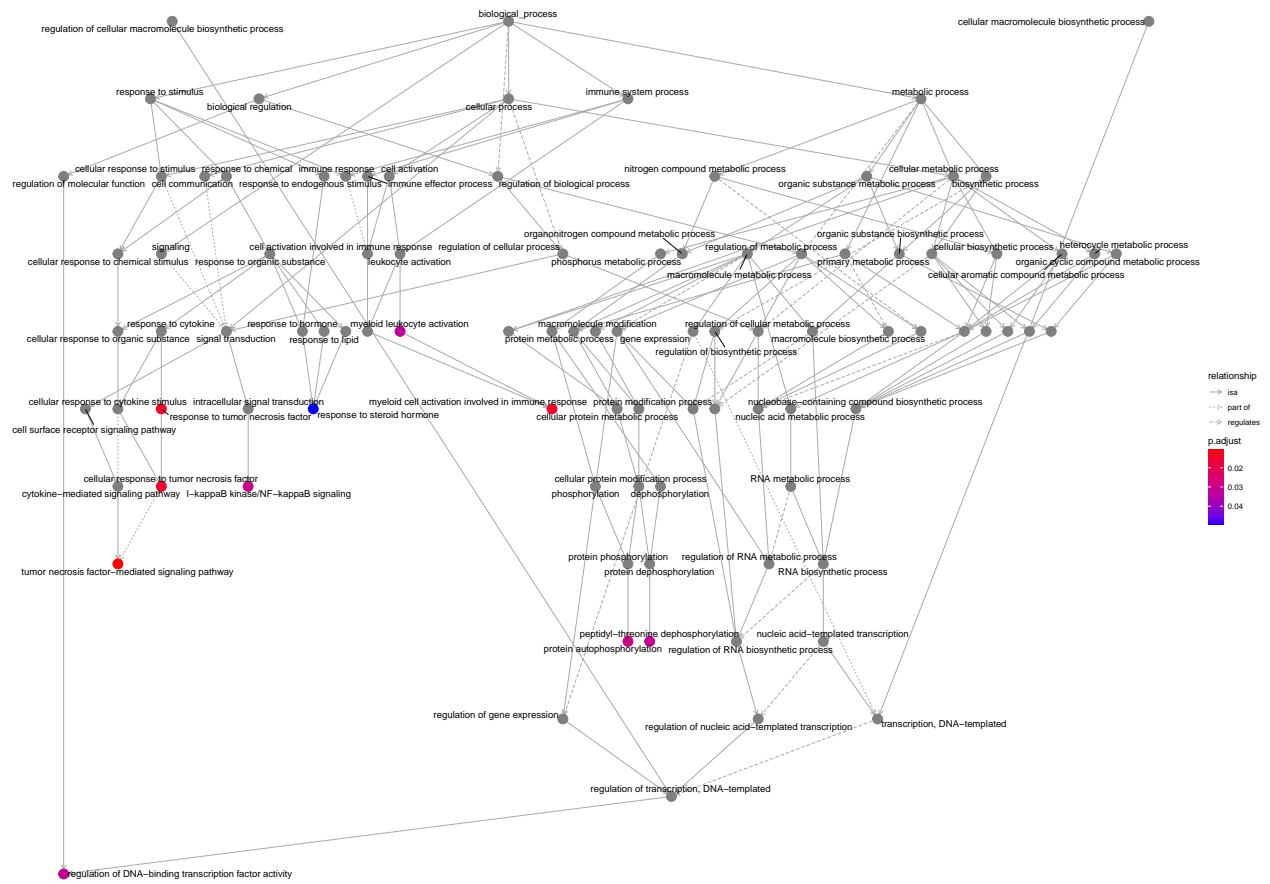
```
# ego3: enriched terms = 1
egoMF
```

```
## #
## # 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  "G0:0031996"
## $ 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

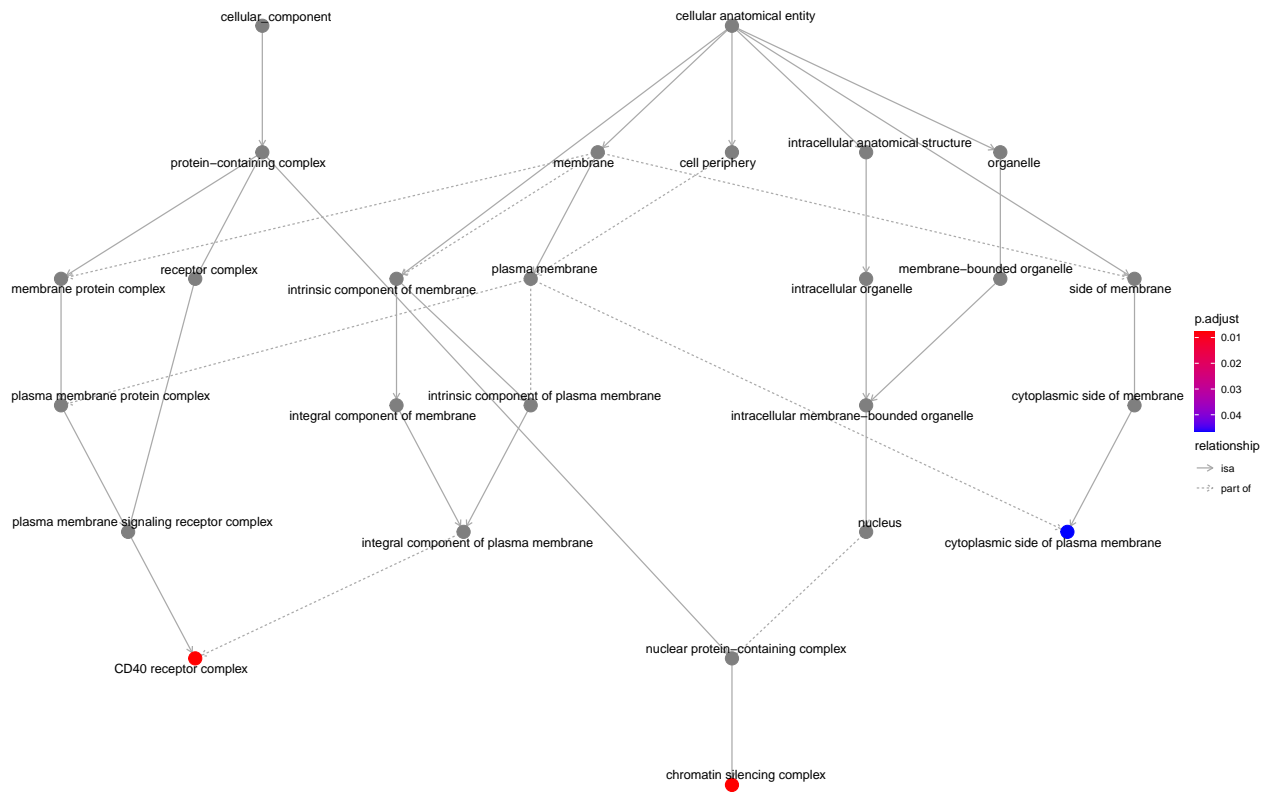
```
goplot(egoBP, showCategory = 17)
```

Warning: ggrepel: 16 unlabeled data points (too many overlaps). Consider
increasing max.overlaps



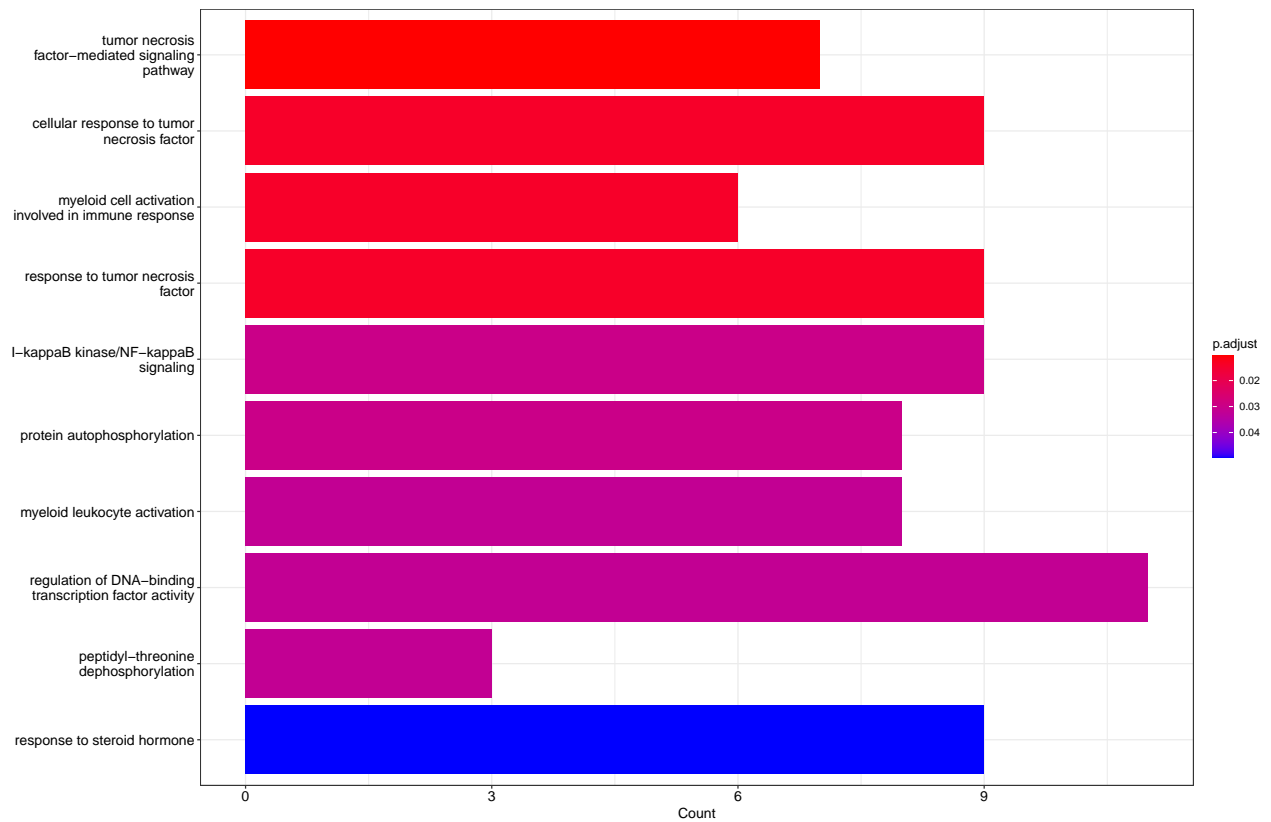
Go plot

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

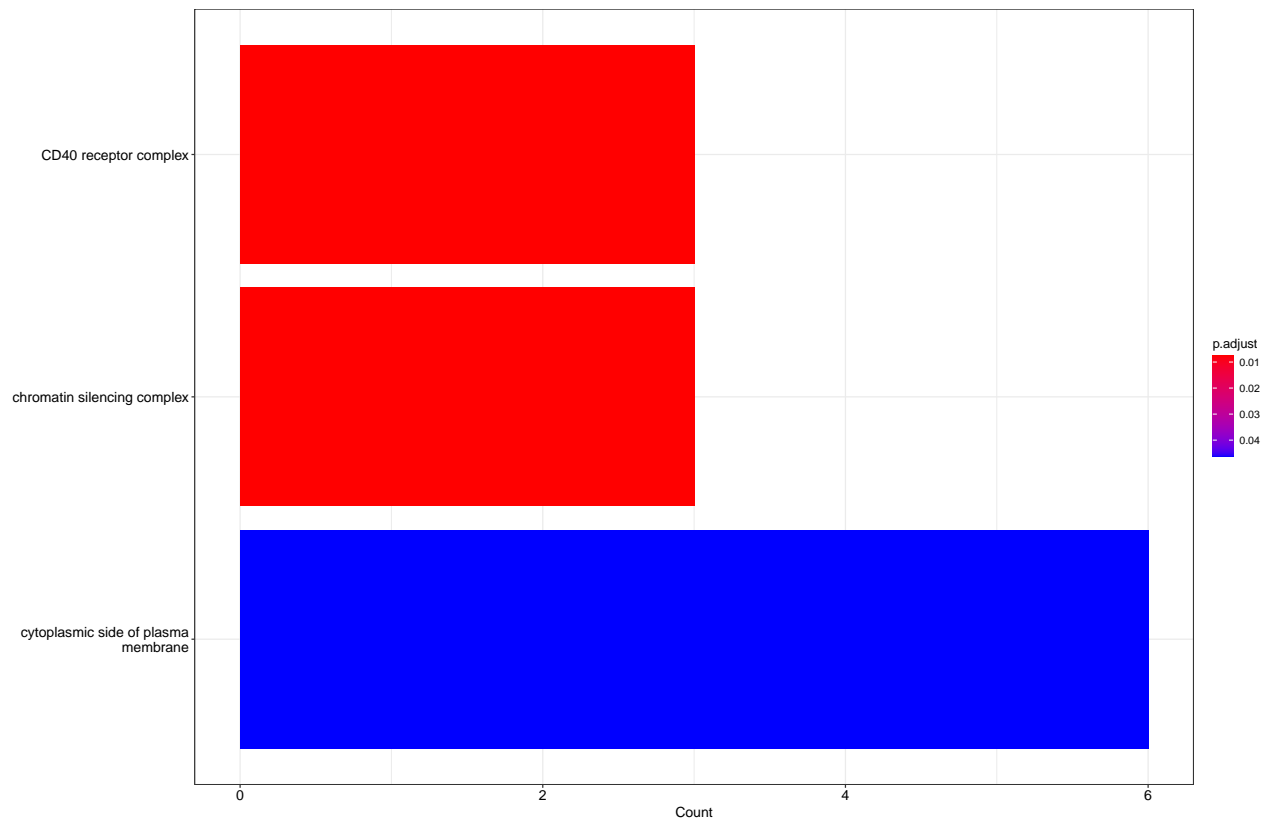


Bar plot

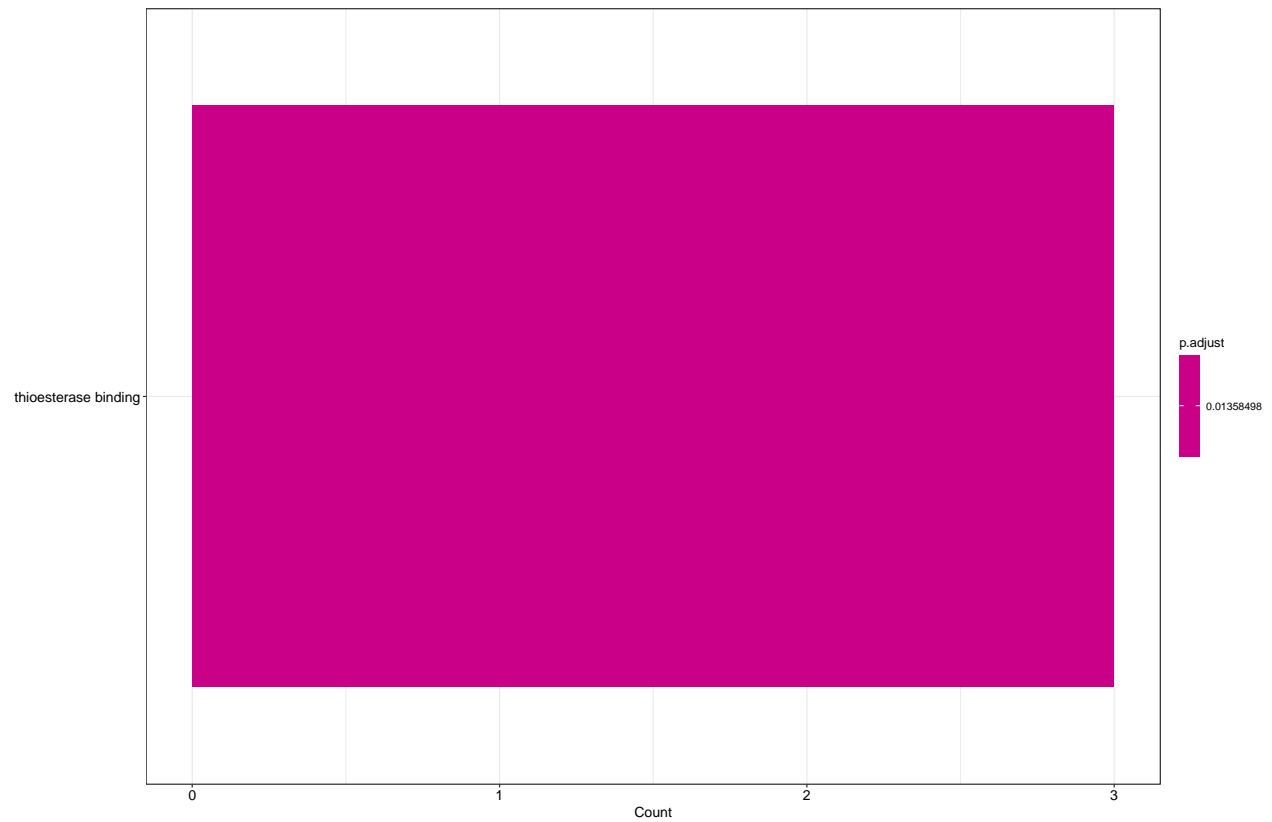
```
# Display all the enriched terms in BP, CC and MF
barplot(egoBP, showCategory = 17)
```



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

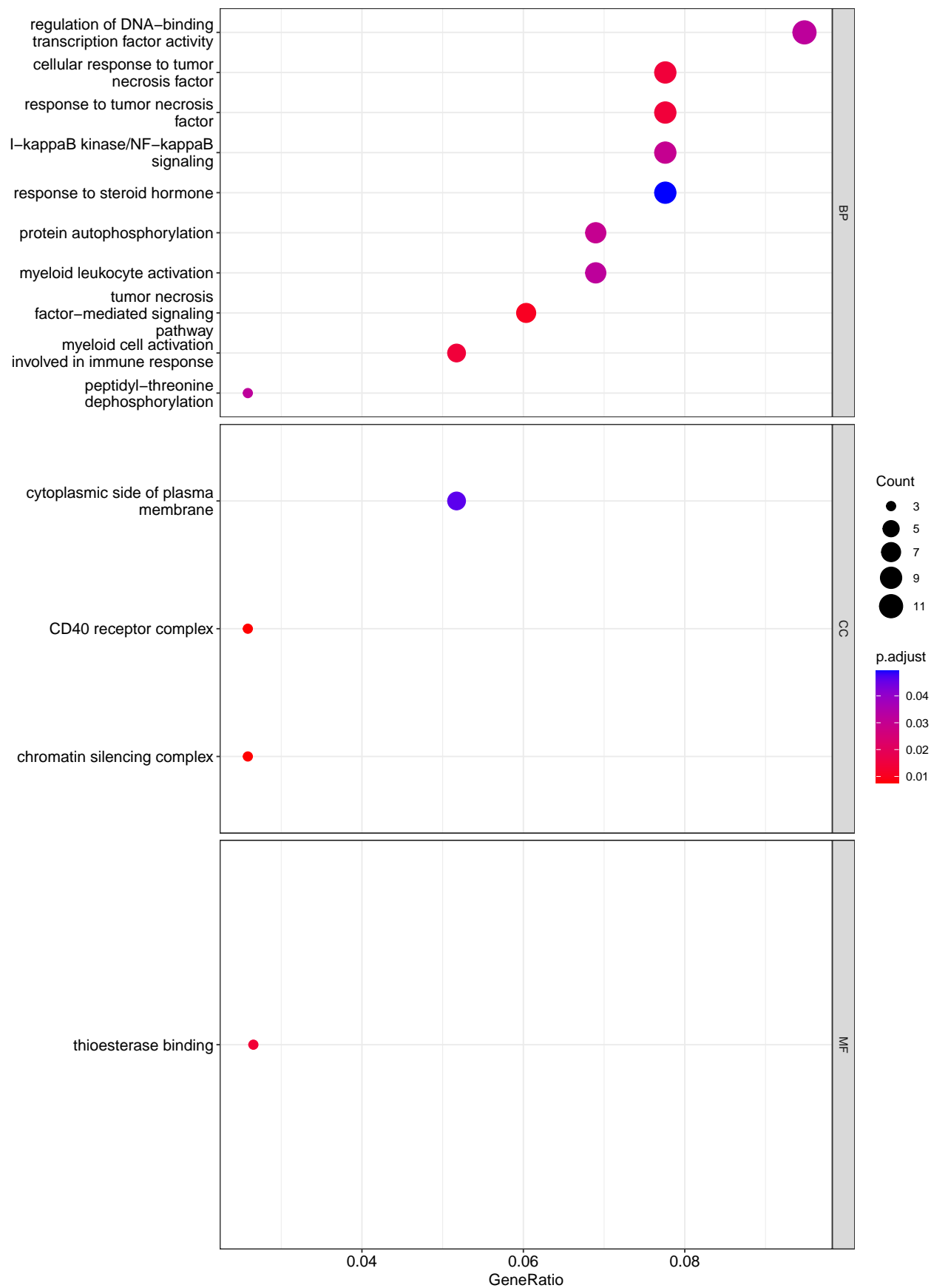


```
barplot(egoMF, showCategory = 1)
```



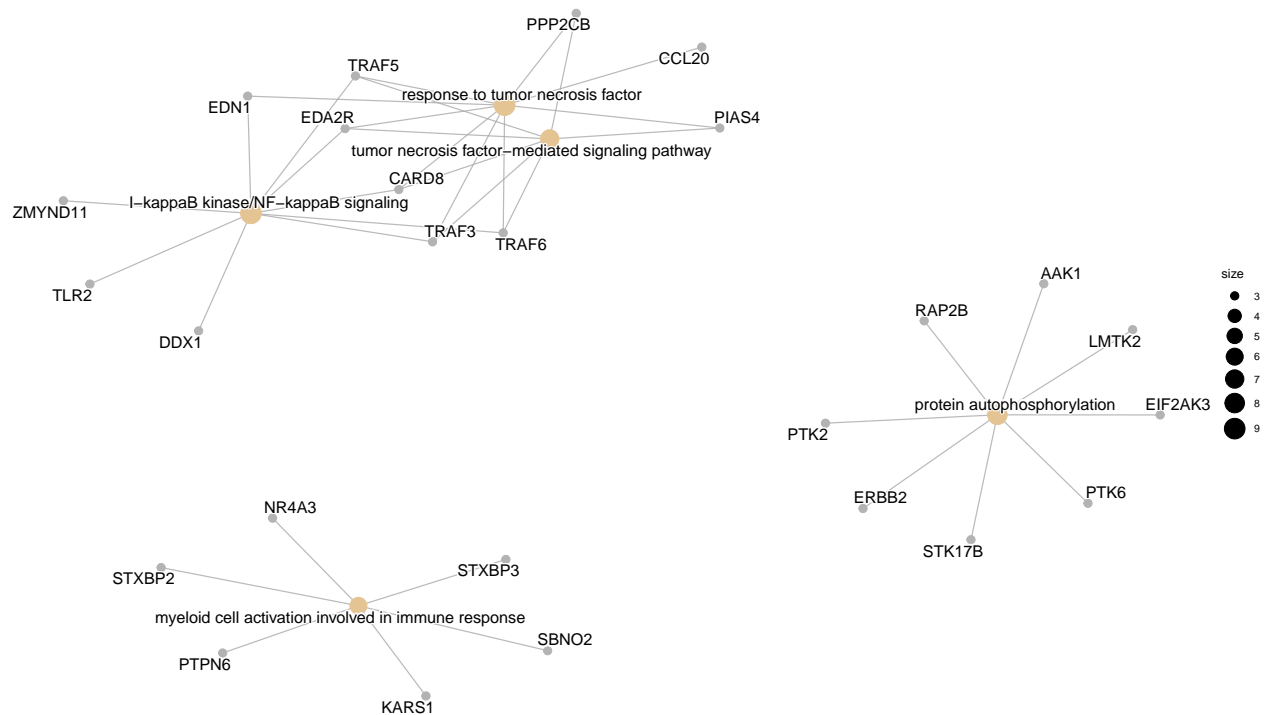
Dot plot

```
dotplot(go, split = "ONTOLOGY") + facet_grid(ONTOLOGY ~ ., scale = "free")
```

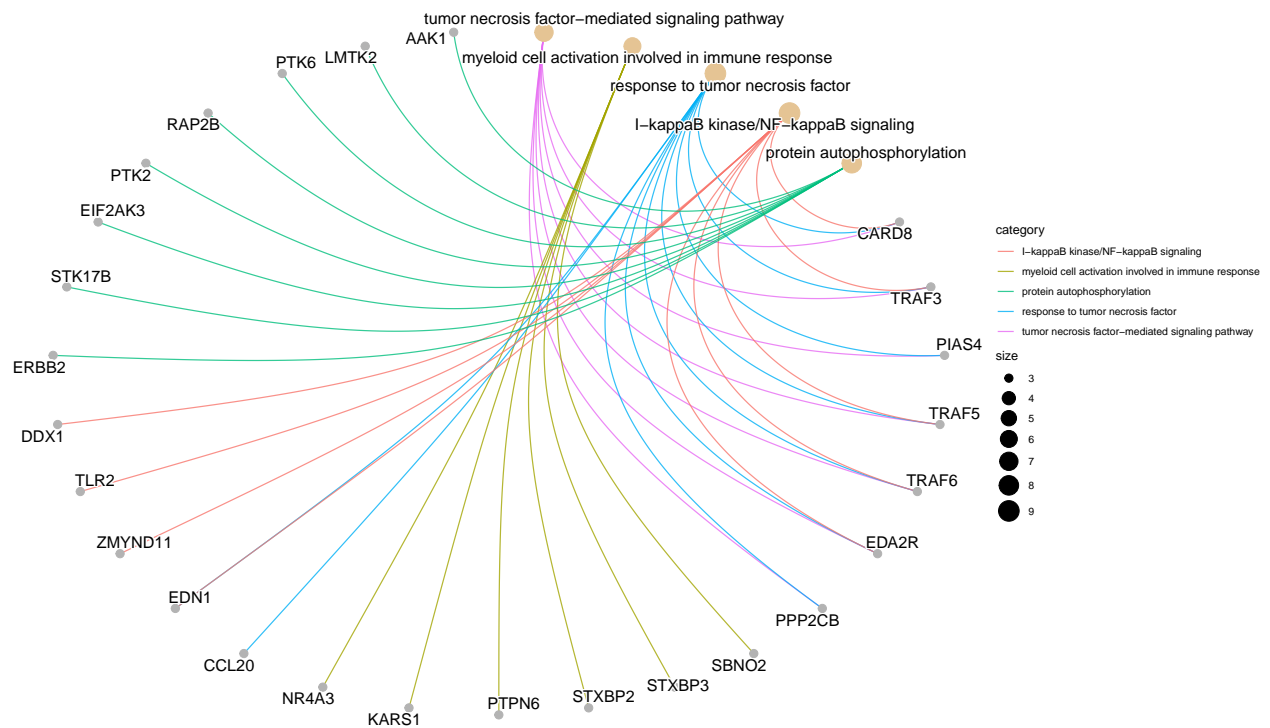


Gene-Concept Network plot

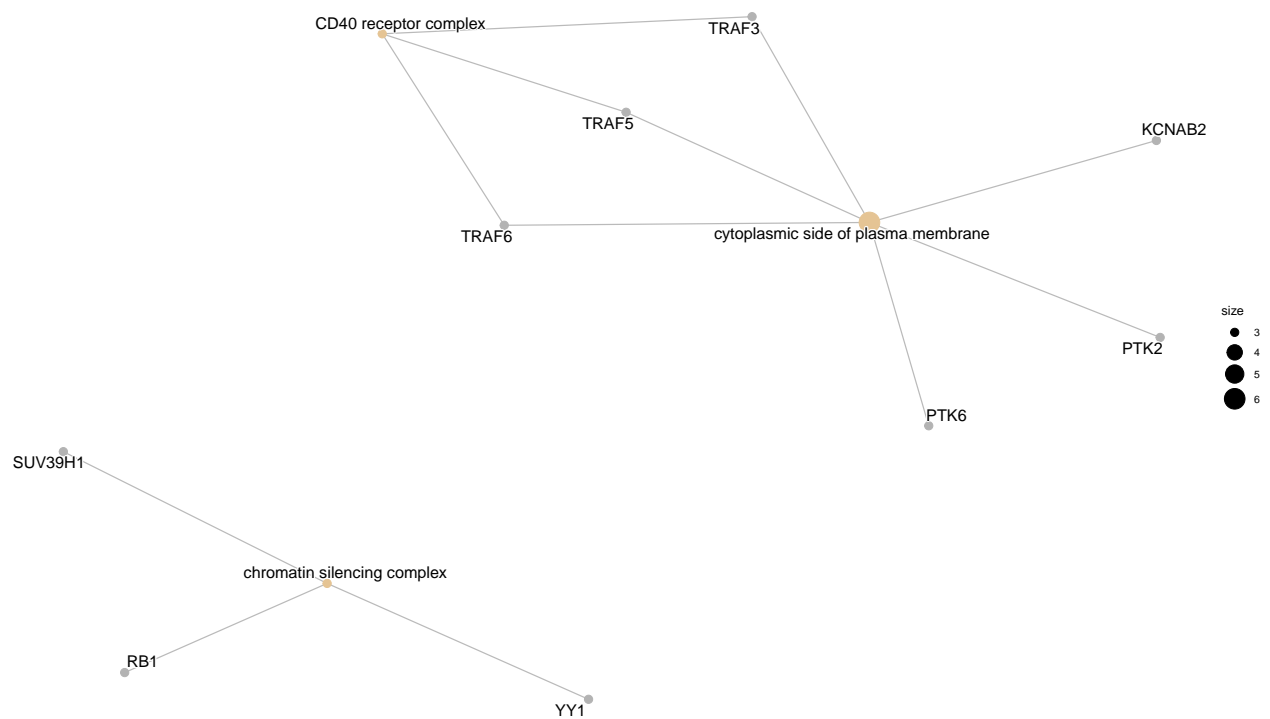
```
egoBP2 <- simplify(egoBP)
egoCC2 <- simplify(egoCC)
egoMF2 <- simplify(egoMF)
cnetplot(egoBP2)
```



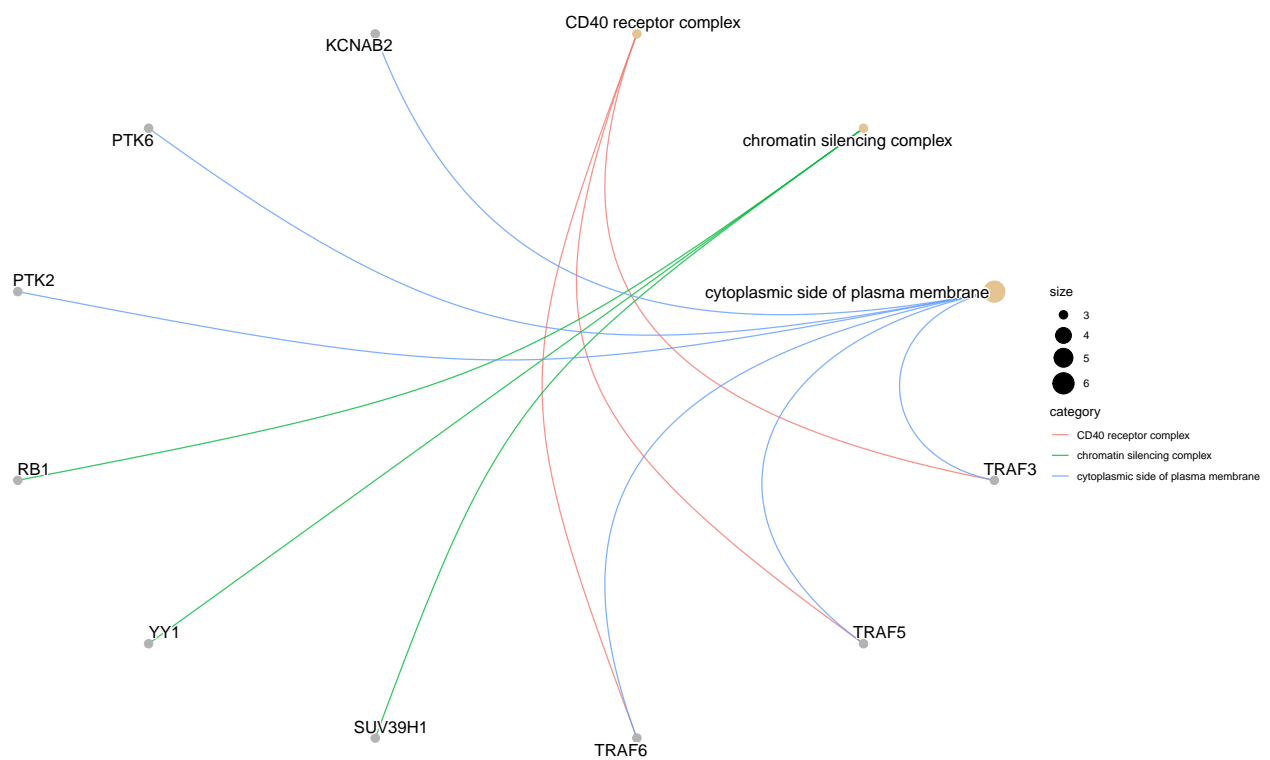
```
cnetplot(egoBP2, circular = TRUE, colorEdge = TRUE)
```



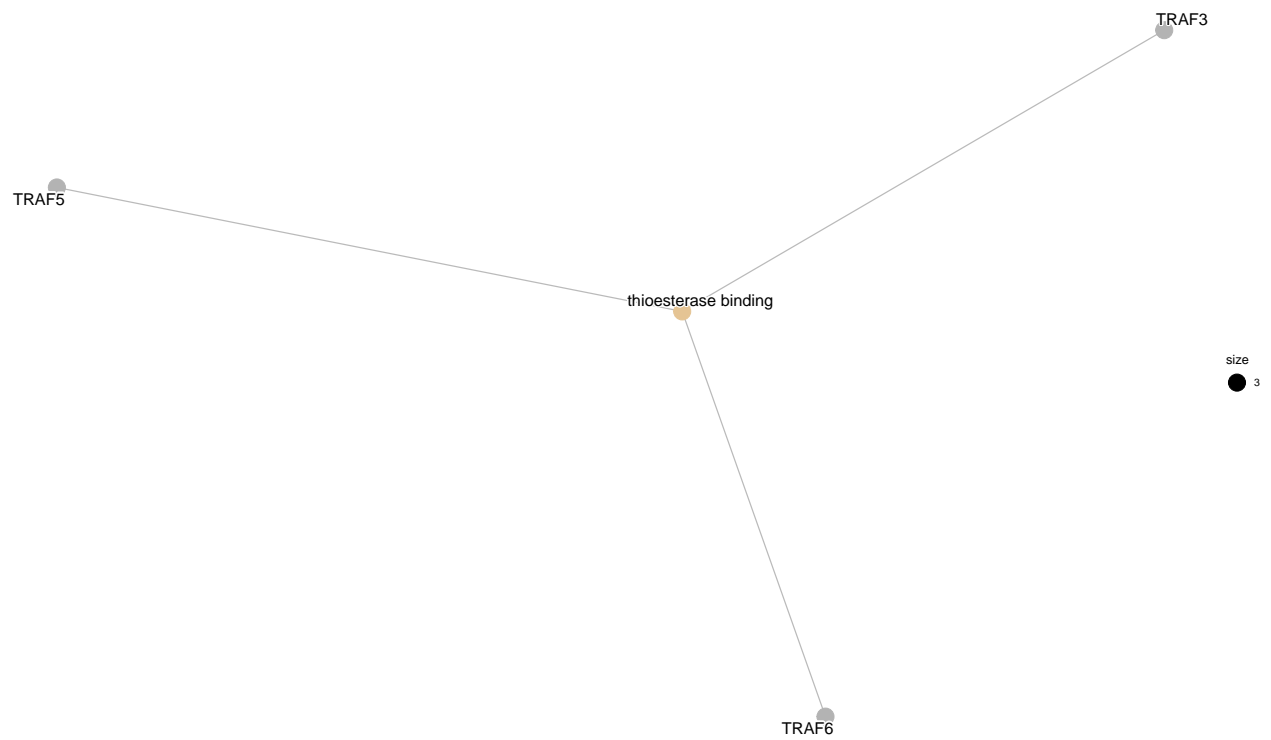

```
cnetplot(egoCC2)
```



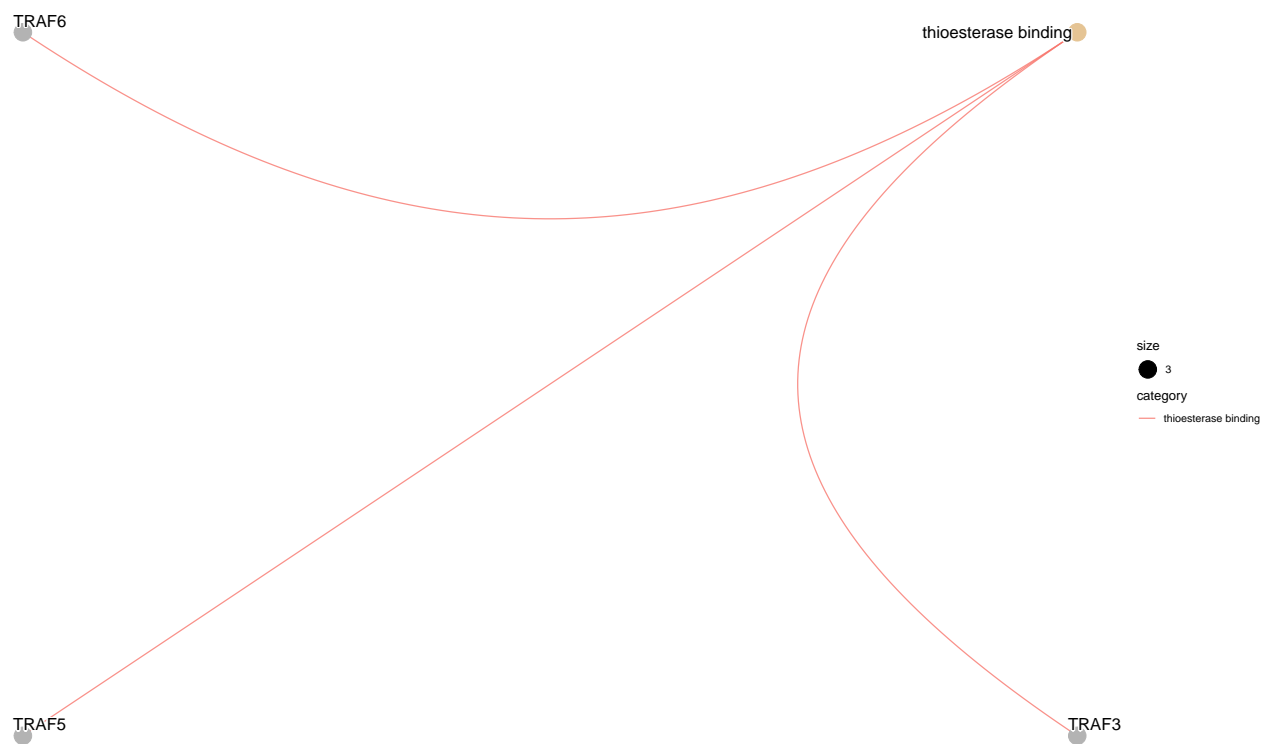
```
cnetplot(egoCC2, circular = TRUE, colorEdge = TRUE)
```



```
cnetplot(egoMF2)
```

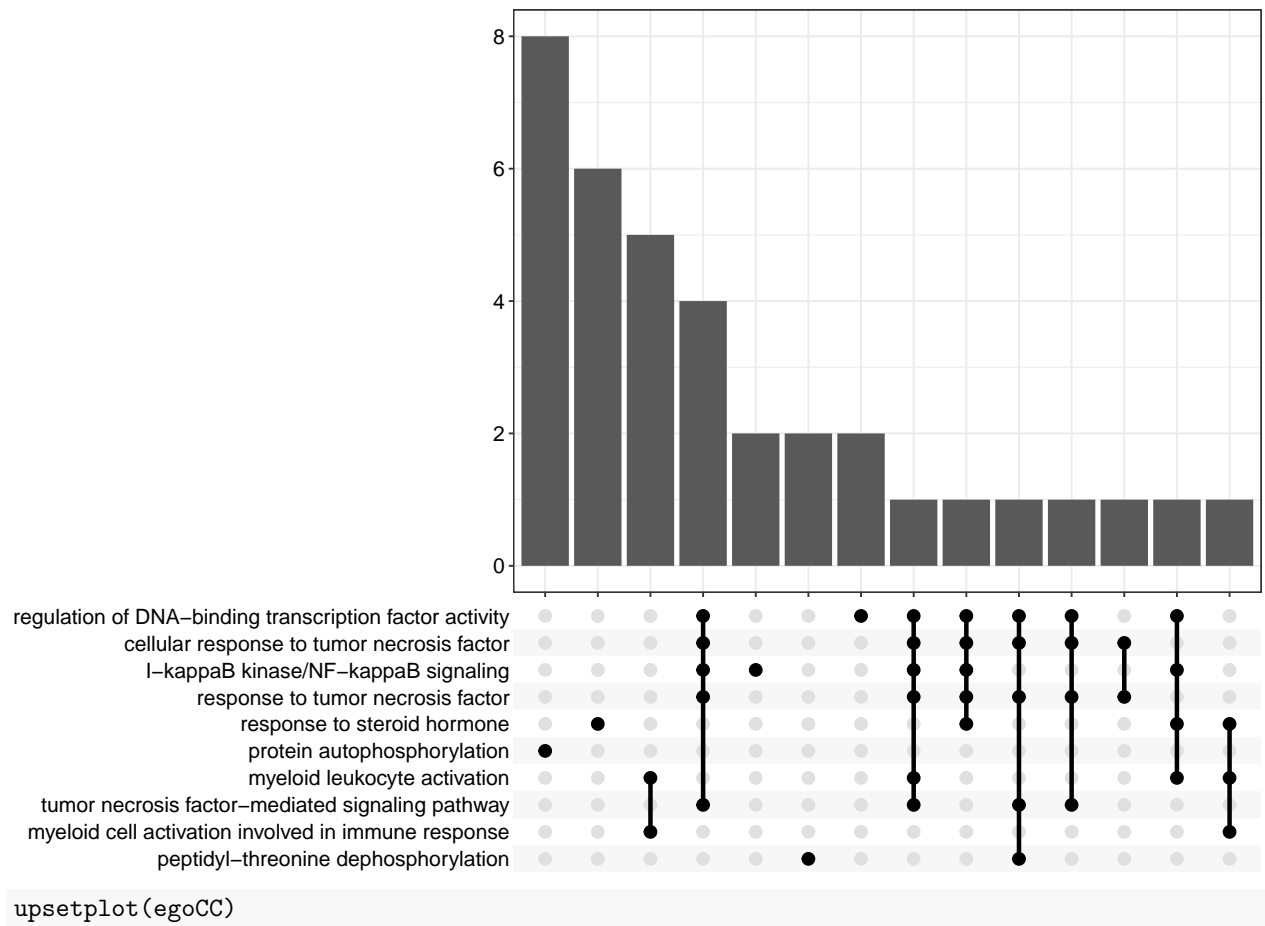


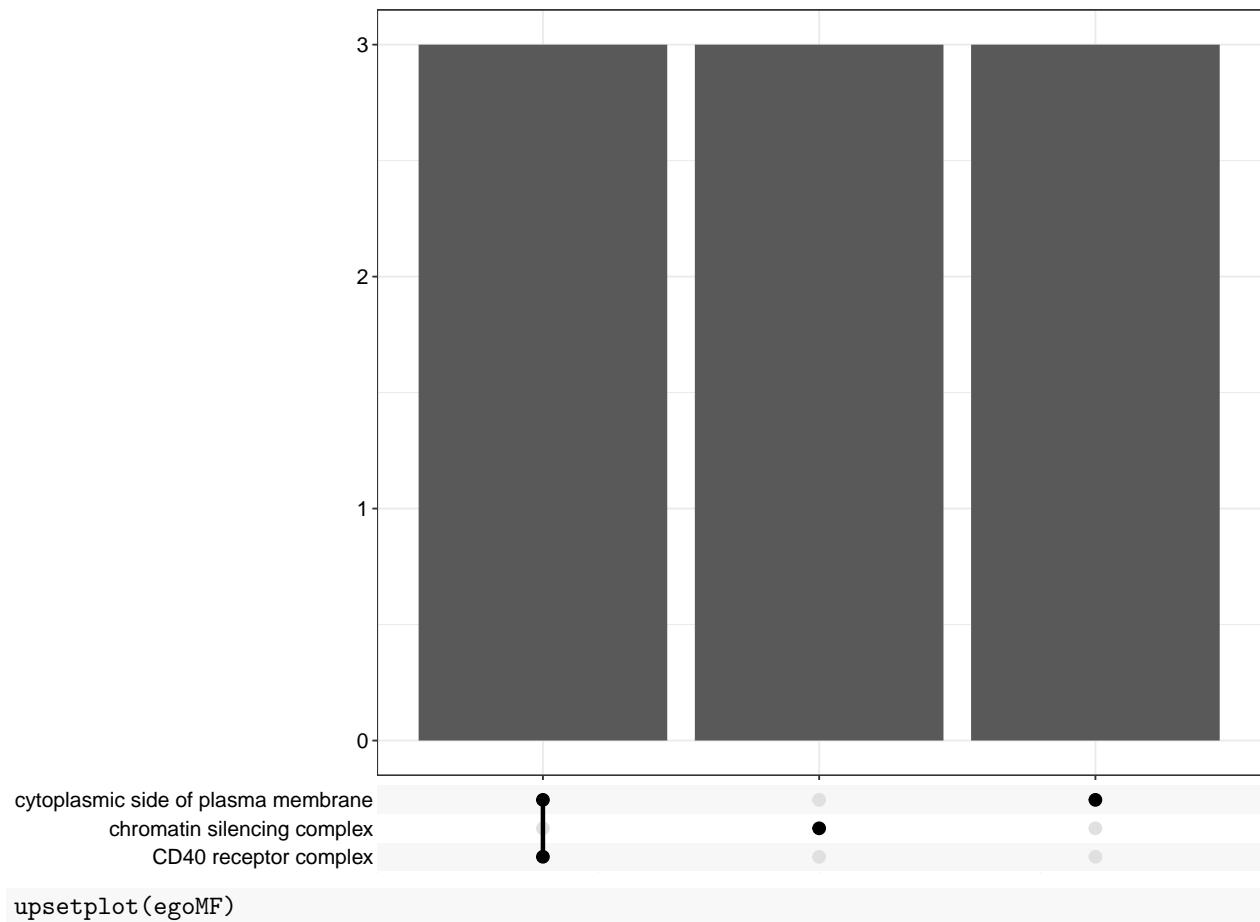
```
cnetplot(egoMF2, circular = TRUE, colorEdge = TRUE)
```



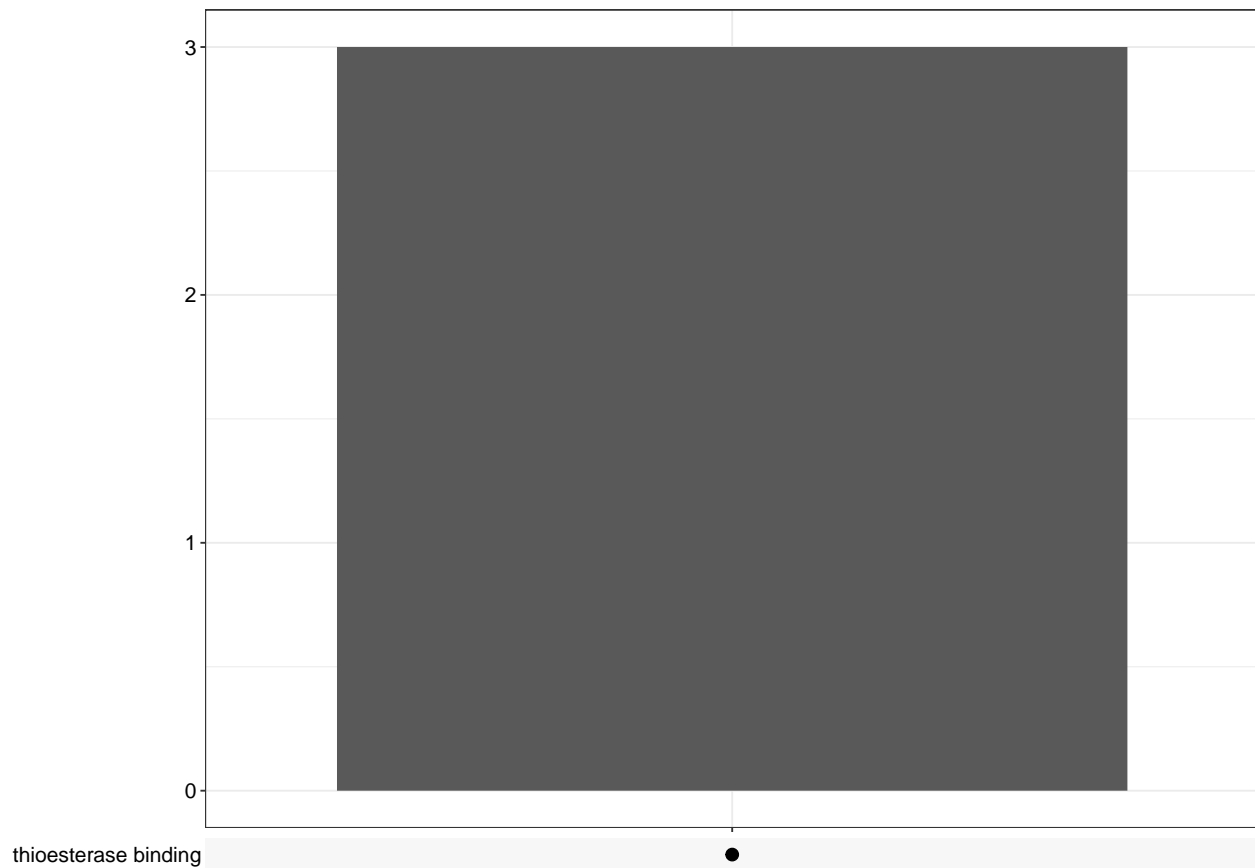
UpSet plot

```
upsetplot(egoBP)
```



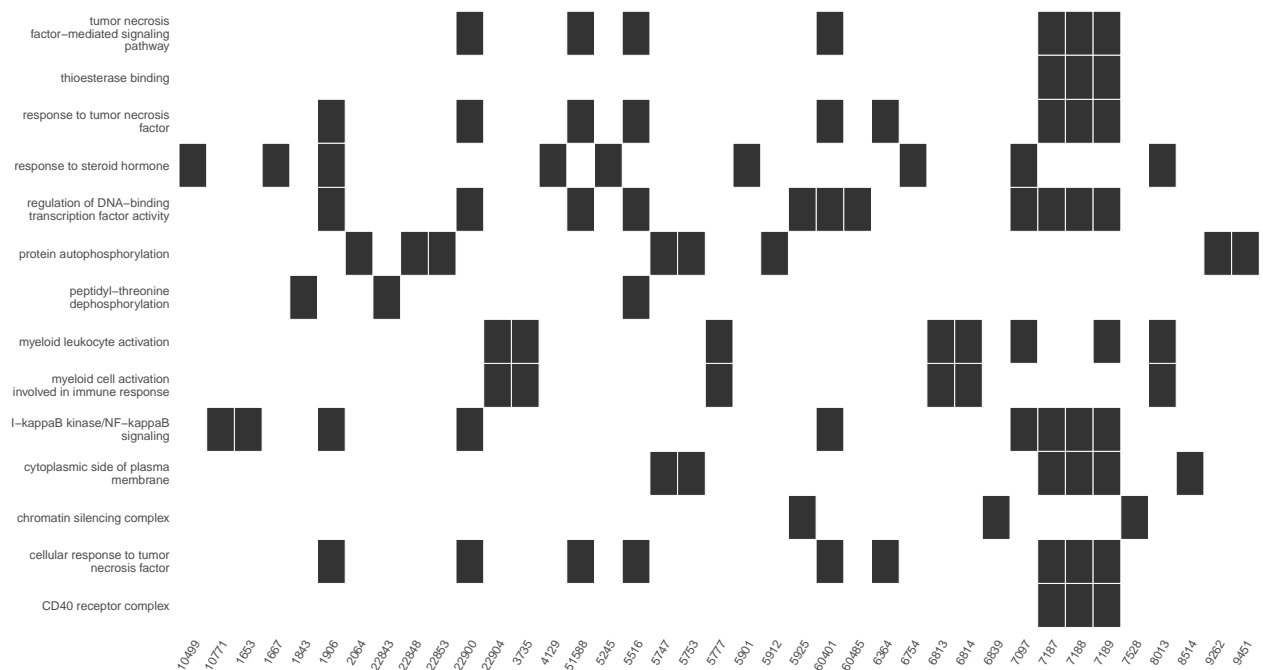


```
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
## geom_path: Each group consists of only one observation. Do you need to adjust
## the group aesthetic?
```



Heatmap-like functional classification

heatplot(go)



Enrichment map

```
emapplot(x)
```

