go_networks_plus_trifid

2023-12-15

Figure 2 G, H

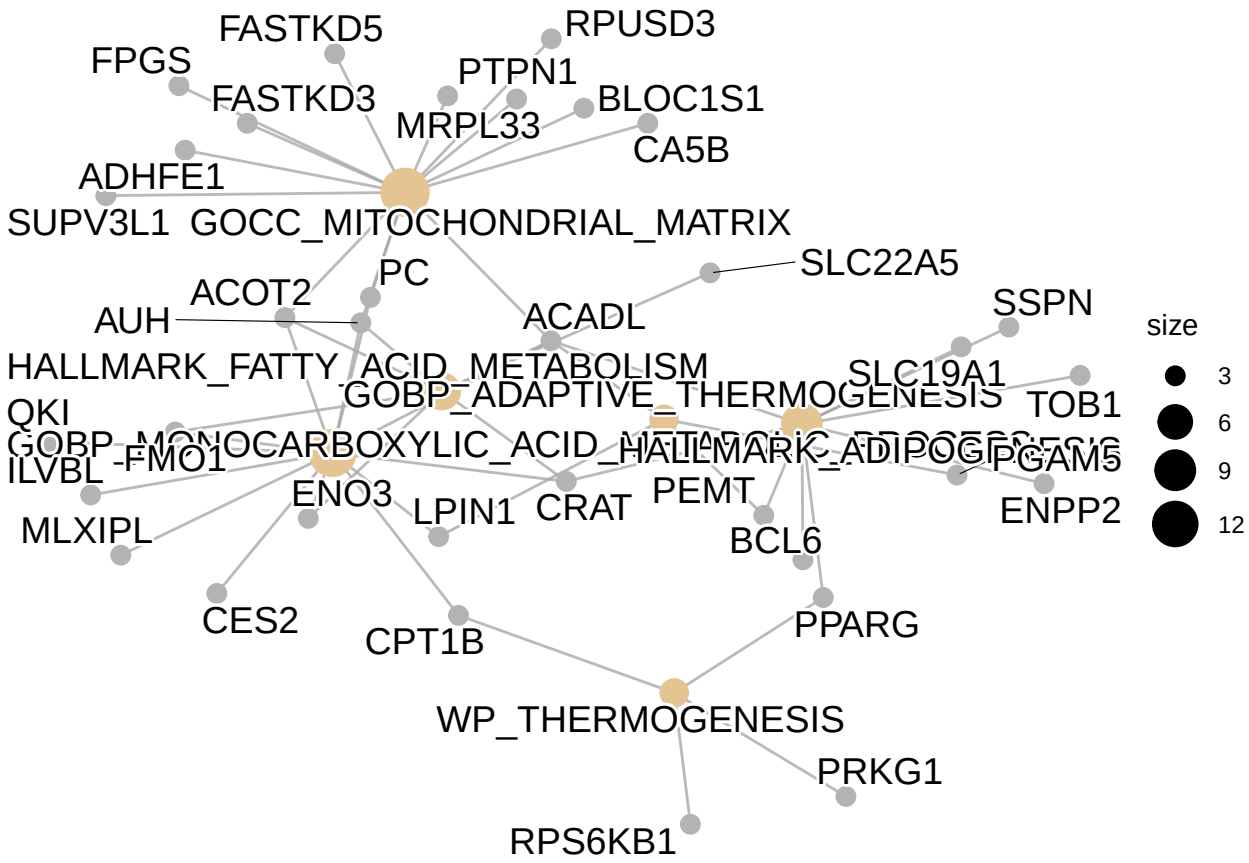
```
library(dplyr)
library(tidyr)
library(ggplot2)
library(enrichplot)
library(clusterProfiler)
library(here); i_am("R/17_go_networks_plus_trifid.Rmd")
```

```
figs =  here("R/plots")
load(file.path(figs, "Themogenesis_object.RData"))
head(specific)
```

```
##
## HALLMARK_ADIPOGENESIS                                                                  HALLMARK_ADI
## HALLMARK_FATTY_ACID_METABOLISM                                                HALLMARK_FATTY_ACID_M
## WP_THERMOGENESIS                                                                        WP_THERM
## GOBP_POSITIVE_REGULATION_OF_COLD_INDUCED_THERMOGENESIS GOBP_POSITIVE_REGULATION_OF_COLD_INDUCED_THERM
## WP_DIFFERENTIATION_OF_WHITE_AND_BROWN_ADIPOCYTE               WP_DIFFERENTIATION_OF_WHITE_AND_BROWN_A
## GOBP_ADAPTIVE_THERMOGENESIS                                                    GOBP_ADAPTIVE_THERM
##                                                                                                  Des
## HALLMARK_ADIPOGENESIS                                                                  HALLMARK_ADI
## HALLMARK_FATTY_ACID_METABOLISM                                                HALLMARK_FATTY_ACID_M
## WP_THERMOGENESIS                                                                        WP_THERM
## GOBP_POSITIVE_REGULATION_OF_COLD_INDUCED_THERMOGENESIS GOBP_POSITIVE_REGULATION_OF_COLD_INDUCED_THERM
## WP_DIFFERENTIATION_OF_WHITE_AND_BROWN_ADIPOCYTE               WP_DIFFERENTIATION_OF_WHITE_AND_BROWN_A
## GOBP_ADAPTIVE_THERMOGENESIS                                                    GOBP_ADAPTIVE_THERM
##                                                      GeneRatio  BgRatio
## HALLMARK_ADIPOGENESIS                                     9/35 181/1124
## HALLMARK_FATTY_ACID_METABOLISM                            7/35 129/1124
## WP_THERMOGENESIS                                          4/35  80/1124
## GOBP_POSITIVE_REGULATION_OF_COLD_INDUCED_THERMOGENESIS    3/35  58/1124
## WP_DIFFERENTIATION_OF_WHITE_AND_BROWN_ADIPOCYTE           1/35  13/1124
## GOBP_ADAPTIVE_THERMOGENESIS                               4/35 100/1124
##                                                         pvalue  p.adjust
## HALLMARK_ADIPOGENESIS                                0.09506160 0.4806583
## HALLMARK_FATTY_ACID_METABOLISM                       0.09613165 0.4806583
## WP_THERMOGENESIS                                     0.23428577 0.5027113
## GOBP_POSITIVE_REGULATION_OF_COLD_INDUCED_THERMOGENESIS 0.26843887 0.5027113
## WP_DIFFERENTIATION_OF_WHITE_AND_BROWN_ADIPOCYTE      0.33866058 0.5027113
## GOBP_ADAPTIVE_THERMOGENESIS                          0.37939955 0.5027113
##                                                        qvalue
## HALLMARK_ADIPOGENESIS                                0.4806583
```

```
## HALLMARK_FATTY_ACID_METABOLISM                          0.4806583
## WP_THERMOGENESIS                                        0.5027113
## GOBP_POSITIVE_REGULATION_OF_COLD_INDUCED_THERMOGENESIS 0.5027113
## WP_DIFFERENTIATION_OF_WHITE_AND_BROWN_ADIPOCYTE         0.5027113
## GOBP_ADAPTIVE_THERMOGENESIS                             0.5027113
##                                                                                                g
## HALLMARK_ADIPOGENESIS                                  PEMT/PPARG/ENPP2/TOB1/BCL6/ACADL/CRAT/SLC19A1/
## HALLMARK_FATTY_ACID_METABOLISM                                    FMO1/ACADL/CRAT/SLC22A5/AUH/ACOT2/
## WP_THERMOGENESIS                                                                PPARG/PRKG1/CPT1B/RPS
## GOBP_POSITIVE_REGULATION_OF_COLD_INDUCED_THERMOGENESIS                                  PEMT/LPIN1/A
## WP_DIFFERENTIATION_OF_WHITE_AND_BROWN_ADIPOCYTE                                                 I
## GOBP_ADAPTIVE_THERMOGENESIS                                                    PEMT/LPIN1/PGAM5/A
##                                                        Count
## HALLMARK_ADIPOGENESIS                                      9
## HALLMARK_FATTY_ACID_METABOLISM                             7
## WP_THERMOGENESIS                                           4
## GOBP_POSITIVE_REGULATION_OF_COLD_INDUCED_THERMOGENESIS     3
## WP_DIFFERENTIATION_OF_WHITE_AND_BROWN_ADIPOCYTE            1
## GOBP_ADAPTIVE_THERMOGENESIS                                4
```

```
specific = arrange(specific, desc(Count))

cnetplot(specific, showCategory=6, categorySize="geneNum")
```



depicts the linkages of genes and biological concepts (e.g. GO terms or KEGG pathways) as a network.

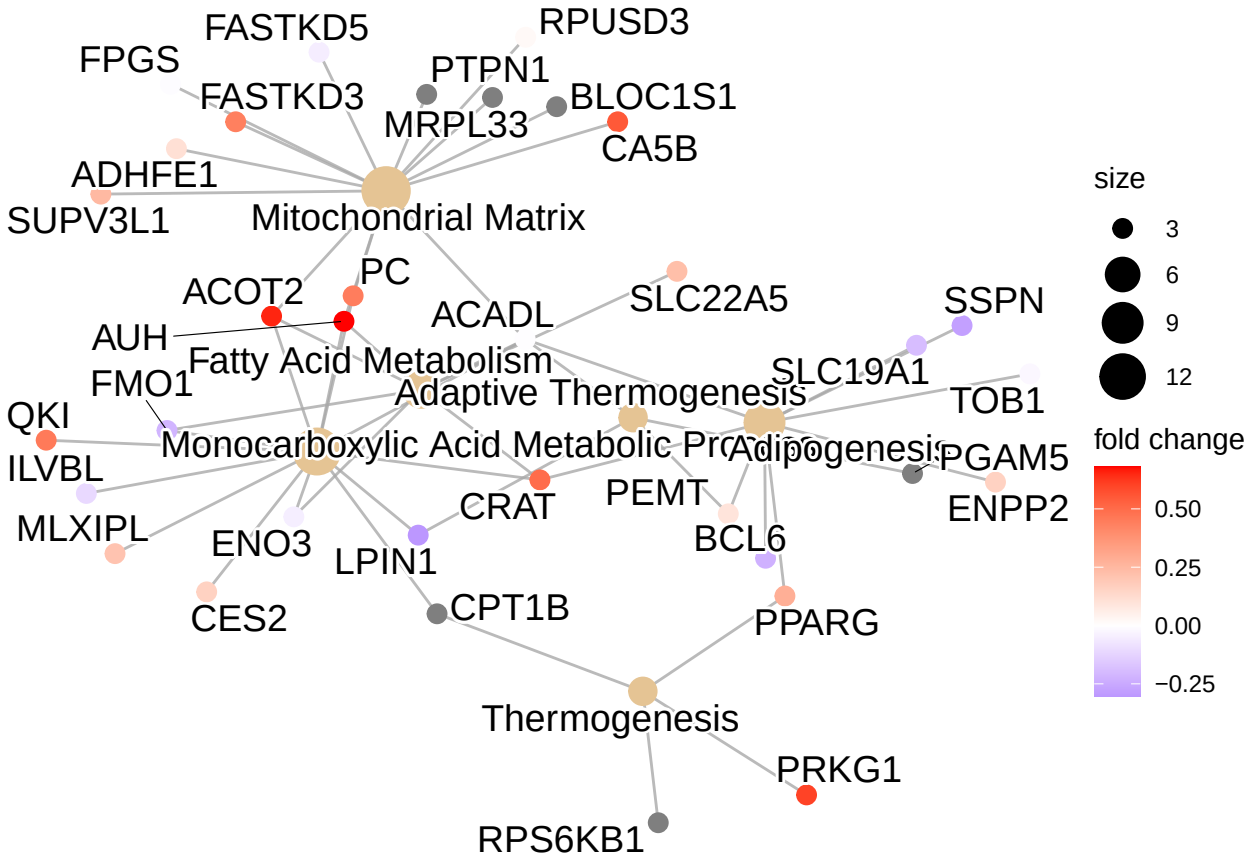
to plot the trifid score, we just need a sorted list of these with names of genes

```
trifid = read.delim(here("31_leafcutter", "trifid_DIFFERENCE_with_Alt_introns.tsv"))
diff = trifid$trifid_diff
names(diff) = trifid$gene_beige
diff = diff[order(diff, decreasing=T)]
summary(diff)
```

```
##      Min.   1st Qu.    Median      Mean   3rd Qu.      Max.      NA's
## -1.10000 -0.30421   0.00000 -0.01699   0.30189   1.10000         2
```

```
shorten = function(ont) {
  no_beg = gsub("^(GO..|HALLMARK|WP|REACTOME)_", "" ,ont)
  abb = abbreviate(stringr::str_to_title(gsub("_"," ", no_beg)),minlength=40, dot=T, named = F)
  return(abb)
}

specific = mutate(specific, Description = shorten(ID) )

cnetplot(specific, showCategory=6, categorySize="geneNum", foldChange=diff)
```

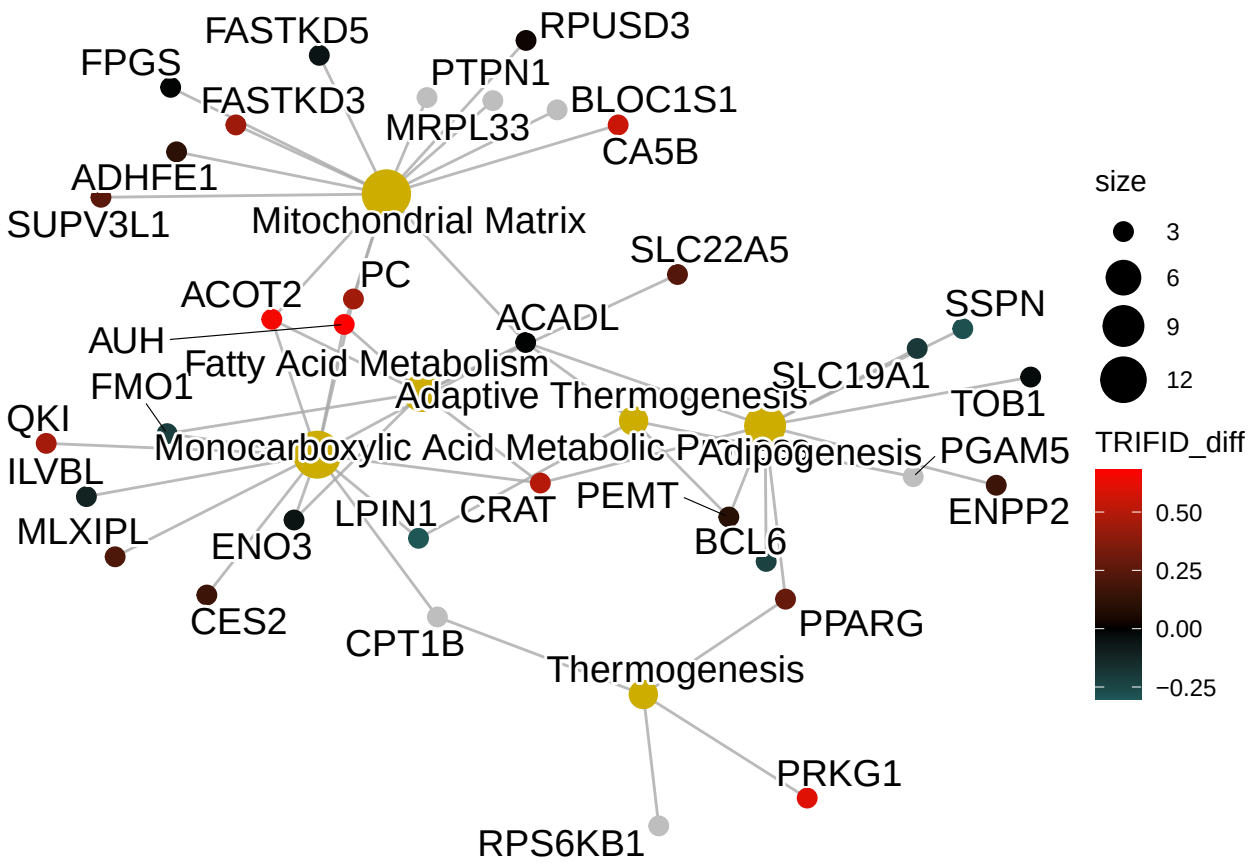
```
## Warning in cnetplot.enrichResult(x, ...): Use 'color.params = list(foldChange = your_value)' instead
##  The foldChange parameter will be removed in the next version.

## Scale for size is already present.
## Adding another scale for size, which will replace the existing scale.
```



```
cnetplot(specific, showCategory=6, categorySize="geneNum", color.params = list(foldChange = diff),
         color_category='gold3' ) + scale_colour_gradient2(high="red", low="cyan3", mid="black", na.valu
```

```
## Warning in cnetplot.enrichResult(x, ...): Use 'color.params = list(category = your_value)' instead o
##  The color_category parameter will be removed in the next version.
```

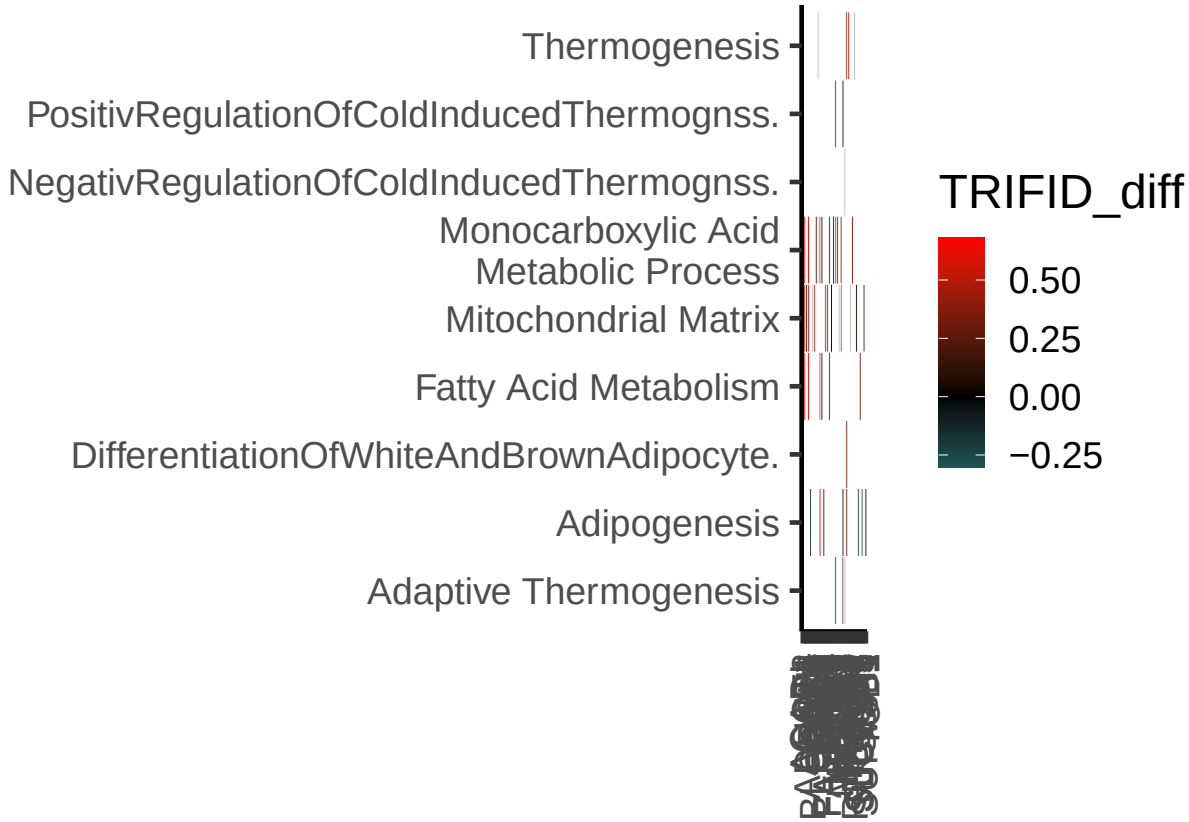
```
## Scale for size is already present.
## Adding another scale for size, which will replace the existing scale.
## Scale for colour is already present.
## Adding another scale for colour, which will replace the existing scale.
```




```
ggsave(file.path(figs, "thermogenesis_network_w_trifid.pdf"), width=9, height=7)
```

```
heatplot(specific, foldChange = diff) + theme_classic(base_size=18) +
  theme(axis.text.x = element_text(angle=90, vjust = 0.5, hjust=1))  +
  scale_fill_gradient2(high="red", low="cyan3", mid="black", na.value="grey", name="TRIFID_diff")
```

```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```




```
ggsave(file.path(figs, "thermogenesis_nheatplot_w_trifid.pdf"), width=15, height=4)
```

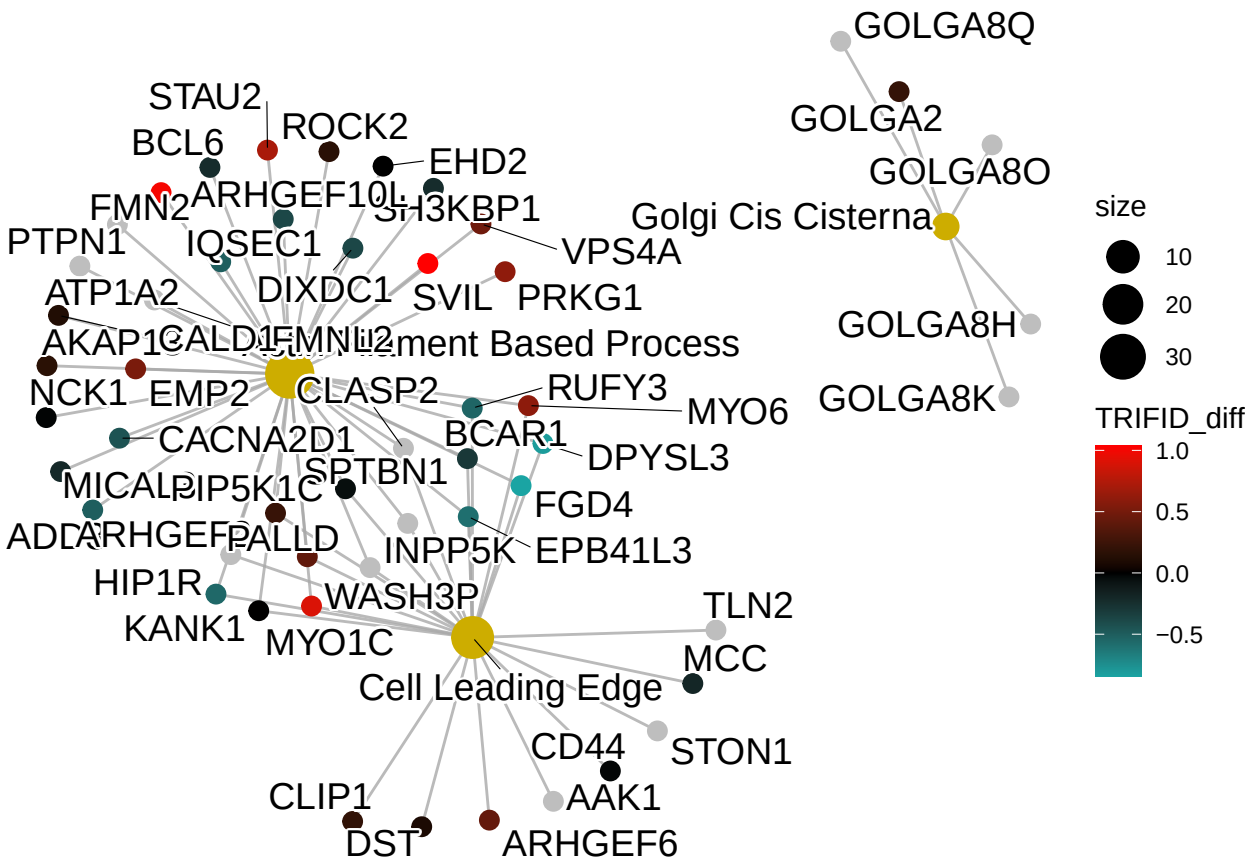
```
load(file.path(figs, "GO_object.RData"))
head(sig_ob)
```

```
##                                                                 ID
## GOBP_ACTIN_FILAMENT_BASED_PROCESS GOBP_ACTIN_FILAMENT_BASED_PROCESS
## GOCC_CELL_LEADING_EDGE                       GOCC_CELL_LEADING_EDGE
## GOCC_GOLGI_CIS_CISTERNA                     GOCC_GOLGI_CIS_CISTERNA
## GOCC_CELL_CORTEX                                   GOCC_CELL_CORTEX
## GOCC_CELL_PROJECTION_MEMBRANE         GOCC_CELL_PROJECTION_MEMBRANE
## GOCC_RUFFLE                                             GOCC_RUFFLE
##                                                         Description GeneRatio
## GOBP_ACTIN_FILAMENT_BASED_PROCESS GOBP_ACTIN_FILAMENT_BASED_PROCESS    38/344
## GOCC_CELL_LEADING_EDGE                       GOCC_CELL_LEADING_EDGE    24/292
## GOCC_GOLGI_CIS_CISTERNA                     GOCC_GOLGI_CIS_CISTERNA     5/292
## GOCC_CELL_CORTEX                                   GOCC_CELL_CORTEX    17/292
## GOCC_CELL_PROJECTION_MEMBRANE         GOCC_CELL_PROJECTION_MEMBRANE    16/292
## GOCC_RUFFLE                                             GOCC_RUFFLE    13/292
##                                     BgRatio       pvalue     p.adjust     qvalue
## GOBP_ACTIN_FILAMENT_BASED_PROCESS 484/9243 9.306001e-06 9.306001e-06 0.03123878
## GOCC_CELL_LEADING_EDGE            286/7873 1.465656e-04 1.465656e-04 0.04969881
## GOCC_GOLGI_CIS_CISTERNA            17/7873 2.905469e-04 2.905469e-04 0.04969881
## GOCC_CELL_CORTEX                  184/7873 4.595973e-04 4.595973e-04 0.05241022
## GOCC_CELL_PROJECTION_MEMBRANE     175/7873 7.541362e-04 7.541362e-04 0.05946280
```

```
## GOCC_RUFFLE                         128/7873 8.858972e-04 8.858972e-04 0.05946280
##
## GOBP_ACTIN_FILAMENT_BASED_PROCESS ADD3/KANK1/DIXDC1/SVIL/PRKG1/MYO1C/INPP5K/MYO6/DPYSL3/SH3KBP1/ARHGE
## GOCC_CELL_LEADING_EDGE
## GOCC_GOLGI_CIS_CISTERNA
## GOCC_CELL_CORTEX
## GOCC_CELL_PROJECTION_MEMBRANE
## GOCC_RUFFLE
##                                    Count setSize
## GOBP_ACTIN_FILAMENT_BASED_PROCESS    38     344
## GOCC_CELL_LEADING_EDGE               24     292
## GOCC_GOLGI_CIS_CISTERNA               5     292
## GOCC_CELL_CORTEX                     17     292
## GOCC_CELL_PROJECTION_MEMBRANE        16     292
## GOCC_RUFFLE                          13     292
```

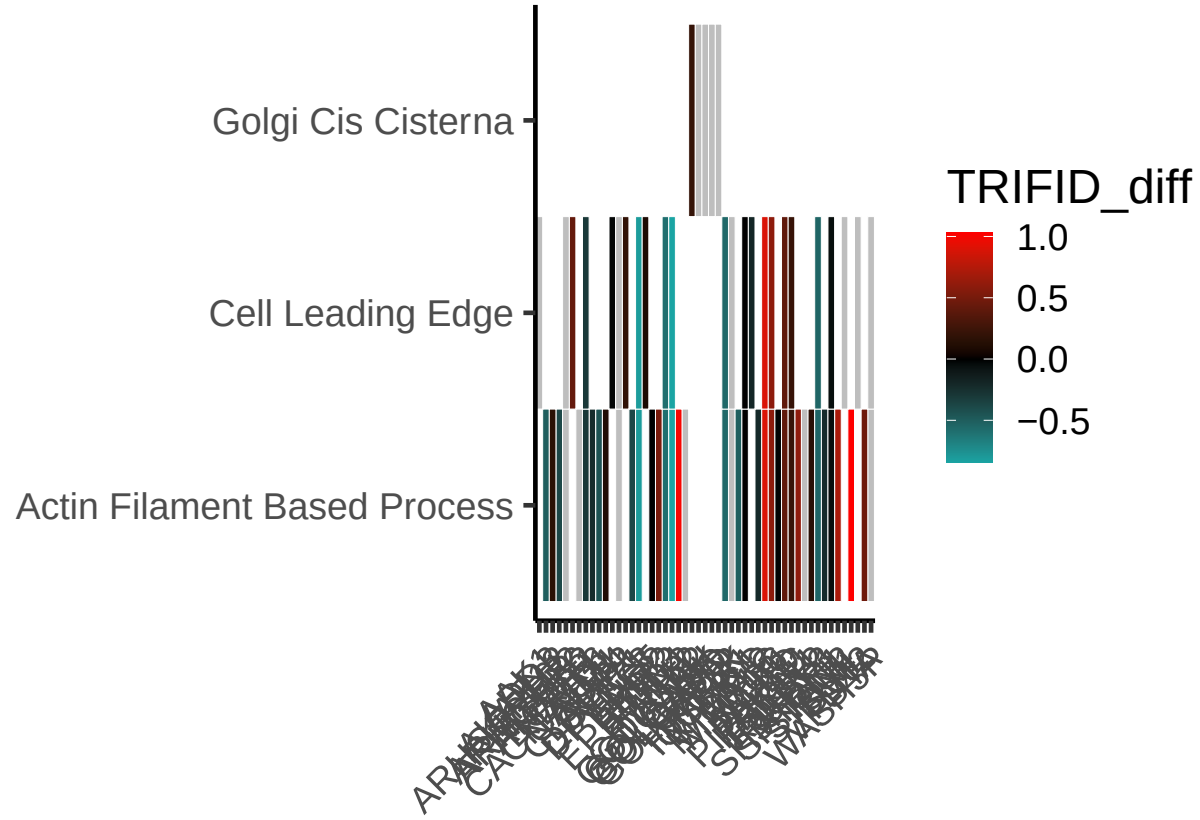
```
sig_ob = mutate(sig_ob, Description = shorten(ID) )

cnetplot(sig_ob, showCategory=3, categorySize="geneNum", color.params = list(foldChange = diff),
         color_category='gold3' ) + scale_colour_gradient2(high="red", low="cyan3", mid="black", na.valu
```

```
## Warning in cnetplot.enrichResult(x, ...): Use 'color.params = list(category = your_value)' instead of
##  The color_category parameter will be removed in the next version.

## Scale for size is already present.
## Adding another scale for size, which will replace the existing scale.
## Scale for colour is already present.
## Adding another scale for colour, which will replace the existing scale.
```




```
heatplot(sig_ob, foldChange = diff, showCategory = 3) + theme_classic(base_size=18) +
  theme(axis.text.x = element_text(angle=45, hjust=1)) + guides(fill = guide_colourbar(reverse=F)) +
  scale_fill_gradient2(high="red", low="cyan3", mid="black", na.value="grey", name="TRIFID_diff")
```

```
## Scale for fill is already present.
## Adding another scale for fill, which will replace the existing scale.
```




```
ggsave(file.path(figs, "go_heatplot_w_trifid.pdf"), width=15, height=3)
```

Average TRIFID scores per GO term

```
actin_genes = sig_ob@result$geneID[1]
actin_genes = stringr::str_split_1(actin_genes, "/")

mean = filter(trifid, gene_beige %in% actin_genes) %>% summarise(mean(trifid_diff))
head(mean)
```

```
##   mean(trifid_diff)
## 1       0.007550428
```

```
as.numeric(mean)
```

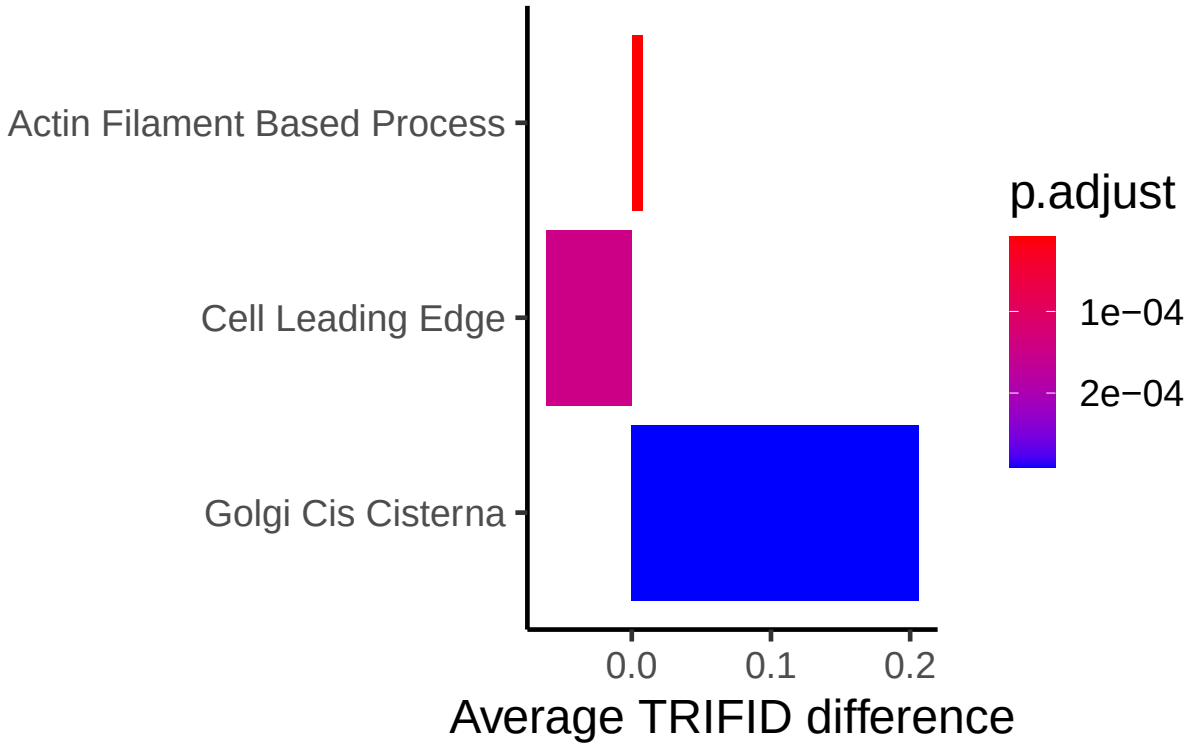
```
## [1] 0.007550428
```

```
average_trifid = function(geneID){
  score = c()
  for (i in 1:length(geneID)){
    genes = stringr::str_split_1(geneID[i], "/")
    trifid_score = filter(trifid, gene_beige %in% genes) %>% summarise(mean(trifid_diff))
```

```
    score = c(score, as.numeric(trifid_score))
  }
  return (score)
}

with_trifid = mutate(filter(sig_ob,qvalue < 0.05), trifid = average_trifid(geneID))
head(with_trifid)
```

```
##                                                                 ID
## GOBP_ACTIN_FILAMENT_BASED_PROCESS GOBP_ACTIN_FILAMENT_BASED_PROCESS
## GOCC_CELL_LEADING_EDGE                       GOCC_CELL_LEADING_EDGE
## GOCC_GOLGI_CIS_CISTERNA                     GOCC_GOLGI_CIS_CISTERNA
##                                                       Description GeneRatio
## GOBP_ACTIN_FILAMENT_BASED_PROCESS Actin Filament Based Process    38/344
## GOCC_CELL_LEADING_EDGE                       Cell Leading Edge    24/292
## GOCC_GOLGI_CIS_CISTERNA                     Golgi Cis Cisterna     5/292
##                                    BgRatio       pvalue     p.adjust     qvalue
## GOBP_ACTIN_FILAMENT_BASED_PROCESS 484/9243 9.306001e-06 9.306001e-06 0.03123878
## GOCC_CELL_LEADING_EDGE            286/7873 1.465656e-04 1.465656e-04 0.04969881
## GOCC_GOLGI_CIS_CISTERNA            17/7873 2.905469e-04 2.905469e-04 0.04969881
##
## GOBP_ACTIN_FILAMENT_BASED_PROCESS ADD3/KANK1/DIXDC1/SVIL/PRKG1/MYO1C/INPP5K/MYO6/DPYSL3/SH3KBP1/ARHG
## GOCC_CELL_LEADING_EDGE
## GOCC_GOLGI_CIS_CISTERNA
##                                   Count setSize       trifid
## GOBP_ACTIN_FILAMENT_BASED_PROCESS    38     344  0.007550428
## GOCC_CELL_LEADING_EDGE               24     292 -0.061614454
## GOCC_GOLGI_CIS_CISTERNA               5     292  0.206333333
```

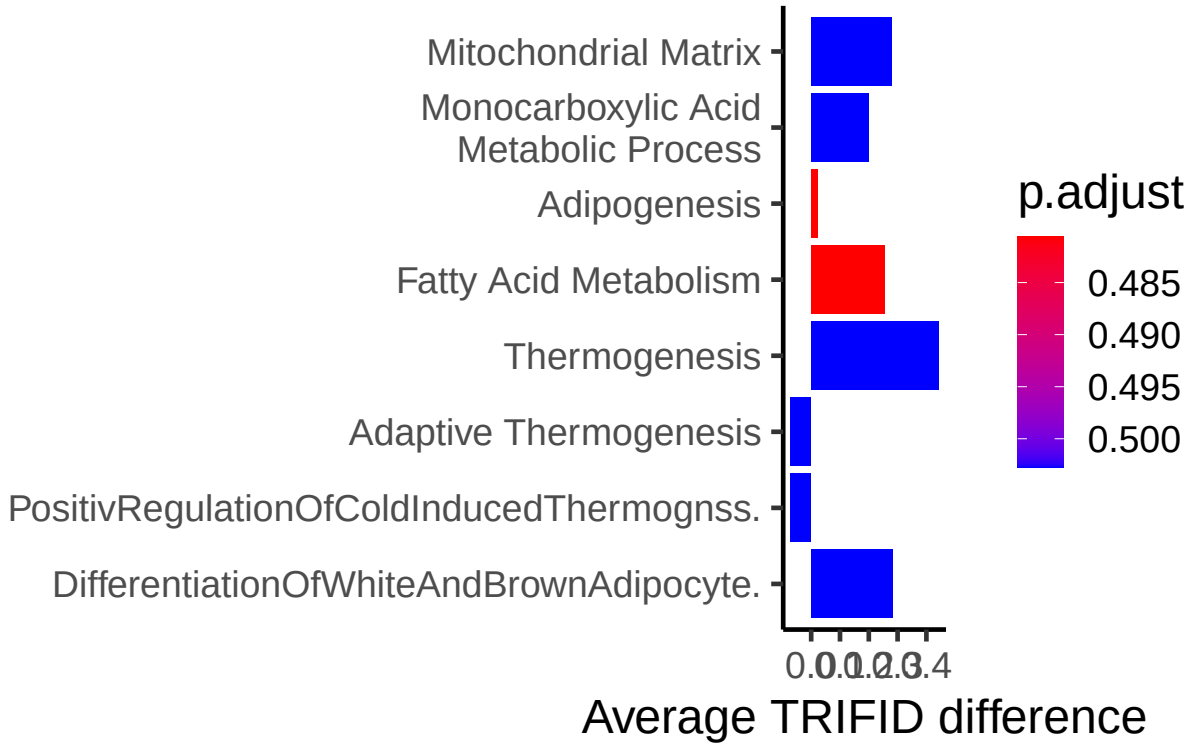
```
barplot(with_trifid, x="trifid") + labs(x="Average TRIFID difference")+ theme_classic(base_size=18)
```




```
#dotplot(with_trifid, x="trifid") + labs(x="Average TRIFID difference")
ggsave(file.path(figs, "actin_trifid_average.pdf"))
```

```
## Saving 6.5 x 4.5 in image
```

```
thermo_trifid = mutate(specific, trifid = average_trifid(geneID))
barplot(thermo_trifid, x="trifid") + labs(x="Average TRIFID difference") + theme_classic(base_size=18)
```




```
ggsave(file.path(figs, "thermogenesis_trifid_average.pdf"), width=9)
```

```
## Saving 9 x 4.5 in image
```