

go_networks_plus_trifid

2023-12-15

Figure 2F

```
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"))
specific = arrange(specific, desc(Count))
head(specific, n=10)[3:9]
```

```
##
## GOBP_MONOCARBOXYLIC_ACID_METABOLIC_PROCESS
## GOCC_MITOCHONDRIAL_MATRIX
## HALLMARK_ADIPOGENESIS
## GOBP_ADAPTIVE_THERMOGENESIS
## HALLMARK_FATTY_ACID_METABOLISM
## GOBP_POSITIVE_REGULATION_OF_COLD_INDUCED_THERMOGENESIS
## GOBP_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY
## REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_B
## WP_THERMOGENESIS
## WP_DIFFERENTIATION_OF_WHITE_AND_BROWN_ADIPOCYTE
##
## GOBP_MONOCARBOXYLIC_ACID_METABOLIC_PROCESS
## GOCC_MITOCHONDRIAL_MATRIX
## HALLMARK_ADIPOGENESIS
## GOBP_ADAPTIVE_THERMOGENESIS
## HALLMARK_FATTY_ACID_METABOLISM
## GOBP_POSITIVE_REGULATION_OF_COLD_INDUCED_THERMOGENESIS
## GOBP_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY
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## HALLMARK_FATTY_ACID_METABOLISM
## GOBP_POSITIVE_REGULATION_OF_COLD_INDUCED_THERMOGENESIS
```

```

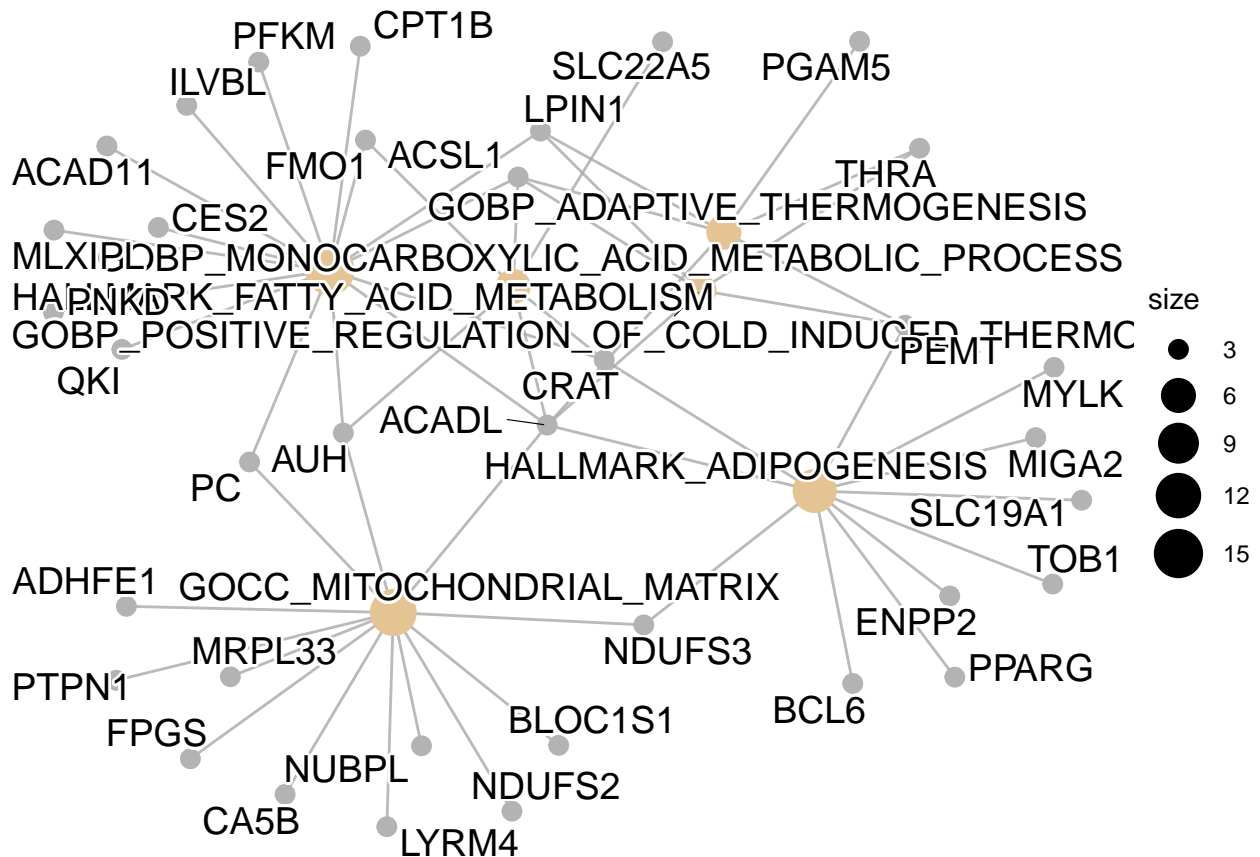
## GOBP_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY
## REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_B
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## HALLMARK_ADIPOGENESIS
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## HALLMARK_FATTY_ACID_METABOLISM
## GOBP_POSITIVE_REGULATION_OF_COLD_INDUCED_THERMOGENESIS
## GOBP_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY
## REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_SYNTHESIS_BY_CHEMIOSMOTIC_COUPLING_AND_HEAT_PRODUCTION_B
## WP_THERMOGENESIS
## WP_DIFFERENTIATION_OF_WHITE_AND_BROWN_ADIPOCYTE
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## GOBP_MONOCARBOXYLIC_ACID_METABOLIC_PROCESS
## GOCC_MITOCHONDRIAL_MATRIX
## HALLMARK_ADIPOGENESIS
## GOBP_ADAPTIVE_THERMOGENESIS
## HALLMARK_FATTY_ACID_METABOLISM
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## WP_THERMOGENESIS
## WP_DIFFERENTIATION_OF_WHITE_AND_BROWN_ADIPOCYTE

```

```

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_to_plot
diff = diff[order(diff, decreasing=T)]
summary(diff)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## -1.10000 -0.46190  0.00000 -0.02781  0.37770  1.10000
```

If multiple gene names choose

```
select_gene = function(gene_str){
  genel = stringr::str_split_1(gene_str, pattern = ",")
  unknown = grepl("^A[CP][0-9]{3,}", genel)
  if (!unknown[1]){
    return(genel[1])
  } else if (!unknown[2]){
    return(genel[2])
  } else if (!unknown[3]){
    return(genel[3])
  } else{
    return(genel[4])
  }
}
```

```

    print("unknown gene")
    return(gene1[1])}
}

sapply(grep(",", names(diff), value=T), select_gene)

```

```

##      AC010332.3,ZNF578      CPT1B,CHKB-CPT1B      DTD2,AL139353.1
##      "ZNF578"      "CPT1B"      "DTD2"
##      HILPDA,AC010655.2      BABAM2,MRPL33      FAM47E-STBD1,FAM47E
##      "HILPDA"      "BABAM2"      "FAM47E-STBD1"
##      AC129492.3,VAMP2      TARDBP,AL109811.3      AC020907.2,FXYP1
##      "VAMP2"      "TARDBP"      "FXYP1"
##      AP001458.2,C11orf98      PEX19,PEX19,AL139011.2      ALG9,AP001781.2
##      "C11orf98"      "PEX19"      "ALG9"
##      C11orf52,HSPB2-C11orf52      ZNF781,ZFP30      ELAC1,AC091551.1
##      "C11orf52"      "ZNF781"      "ELAC1"
##      AC016026.1,MICAL3      NDUFS3,PTPMT1
##      "MICAL3"      "NDUFS3"

```

```

names(diff)[grep(",", names(diff))] = sapply(grep(",", names(diff), value=T), select_gene, USE.NAMES=F)

```

```

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)

```

```

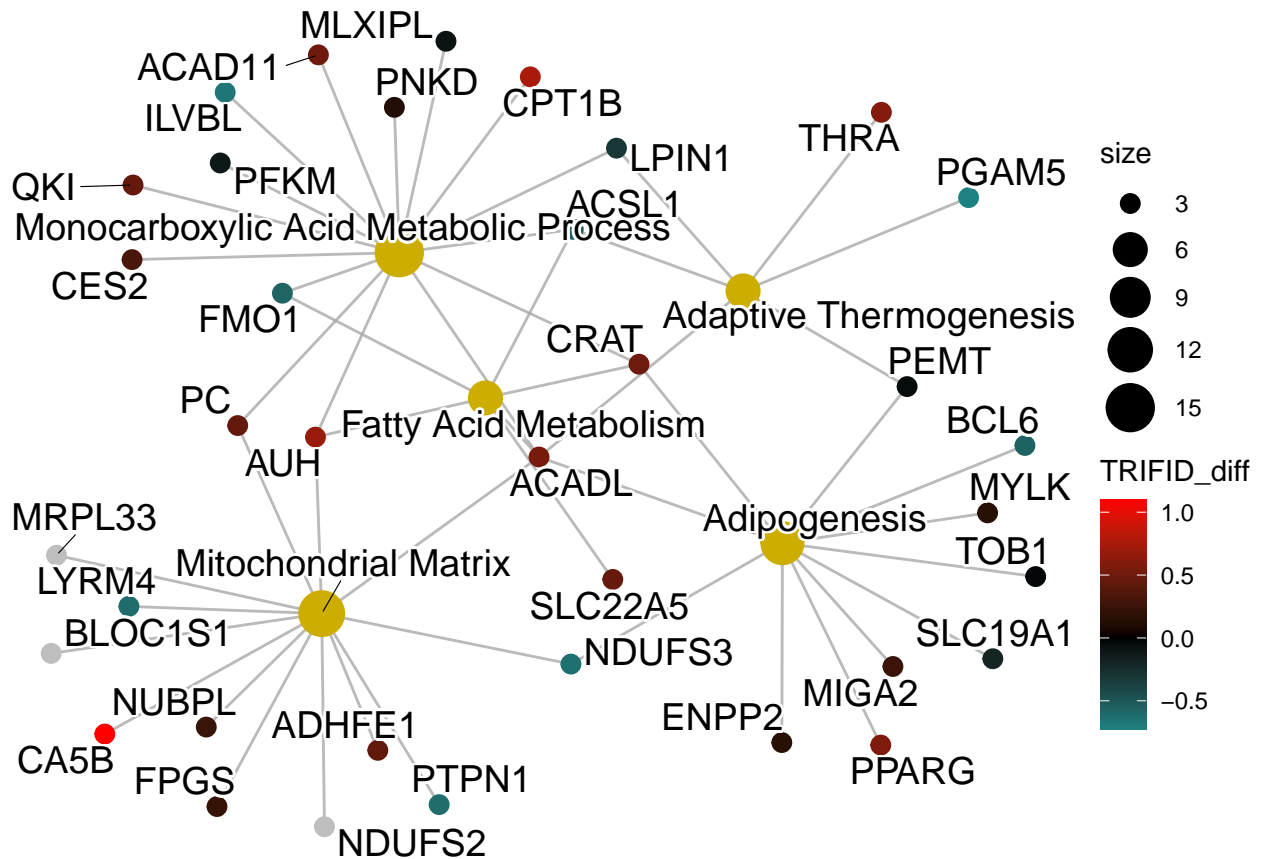
## Warning in cnetplot.enrichResult(x, ...): Use 'color.params = list(foldChange = your_value)' instead
## The foldChange parameter will be removed in the next version.

```

```

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

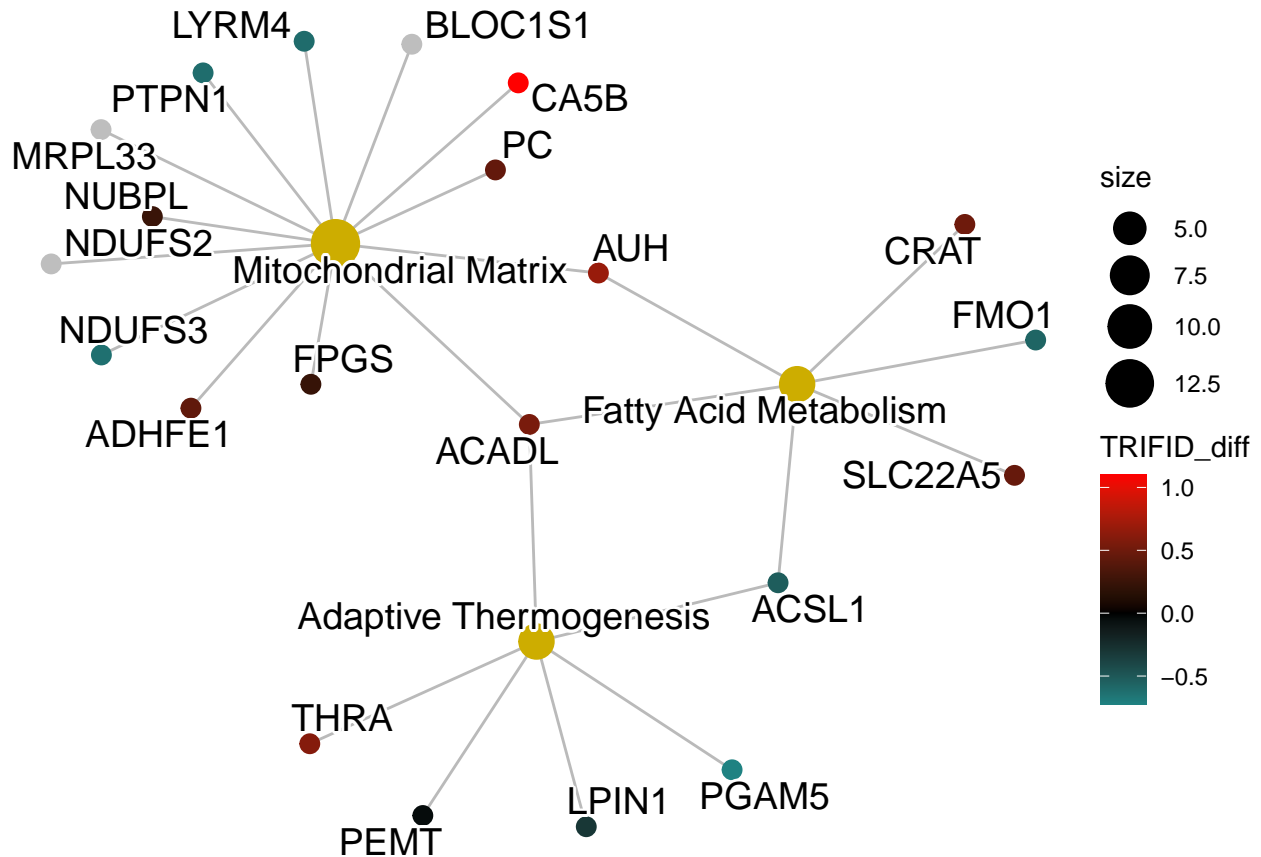
```

```
cnetplot(filter(specific,ID %in% c("GOCC_MITOCHONDRIAL_MATRIX","GOBP_ADAPTIVE_THERMOGENESIS","HALLMARK_1",
showCategory=5, categorySize="geneNum", color.params = list(foldChange = diff),
color_category='gold3' ) + scale_colour_gradient2(high="red", low="cyan3", mid="black", na.val
```

```
## 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.
```

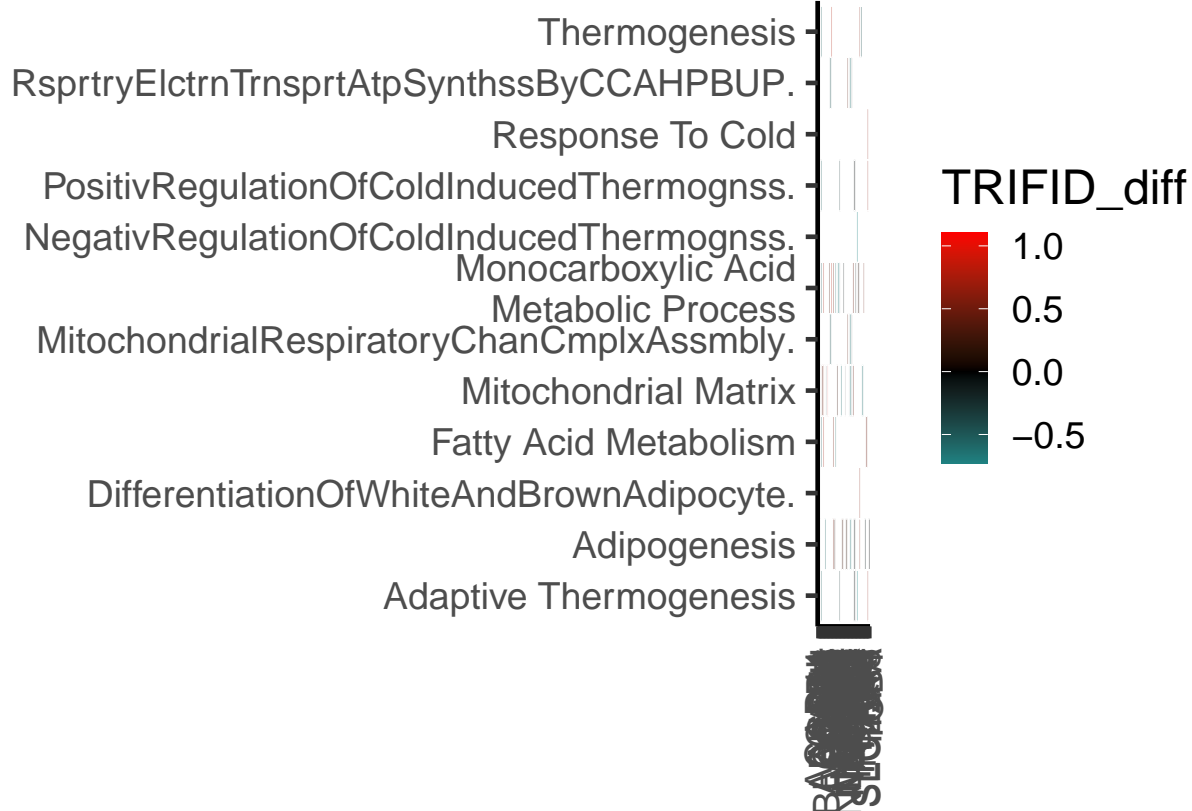


```
ggsave(file.path(figs, "thermogenesis_network_w_trifid.pdf"), width=9, height=7)
```

```
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
## GOCC_GOLGI_CIS_CISTERNA           GOCC_GOLGI_CIS_CISTERNA
## GOCC_CELL_CORTEX                   GOCC_CELL_CORTEX
## GOCC_CELL_PROJECTION_MEMBRANE      GOCC_CELL_PROJECTION_MEMBRANE
## GOCC_T_TUBULE                      GOCC_T_TUBULE
## GOCC_MAIN_AXON                     GOCC_MAIN_AXON
## GOCC_TRANSPORTER_COMPLEX           GOCC_TRANSPORTER_COMPLEX
##                                     Description GeneRatio BgRatio
## GOCC_GOLGI_CIS_CISTERNA           GOCC_GOLGI_CIS_CISTERNA    5/308 17/7873
## GOCC_CELL_CORTEX                   GOCC_CELL_CORTEX           17/308 184/7873
## GOCC_CELL_PROJECTION_MEMBRANE      GOCC_CELL_PROJECTION_MEMBRANE 16/308 175/7873
## GOCC_T_TUBULE                      GOCC_T_TUBULE              5/308 25/7873
## GOCC_MAIN_AXON                     GOCC_MAIN_AXON             5/308 26/7873
## GOCC_TRANSPORTER_COMPLEX           GOCC_TRANSPORTER_COMPLEX    14/308 158/7873
##                                     pvalue    p.adjust    qvalue
## GOCC_GOLGI_CIS_CISTERNA           0.0003722310 0.0003722310 0.1324359
## GOCC_CELL_CORTEX                   0.0008414744 0.0008414744 0.1496939
## GOCC_CELL_PROJECTION_MEMBRANE      0.0013281127 0.0013281127 0.1575095
## GOCC_T_TUBULE                      0.0024709528 0.0024709528 0.2060370
## GOCC_MAIN_AXON                     0.0029628746 0.0029628746 0.2060370
```



```

## GOCC_TRANSPORTER_COMPLEX      0.0034904584 0.0034904584 0.2060370
##
## GOCC_GOLGI_CIS_CISTERNA
## GOCC_CELL_CORTEX              ADD3/FGF1/MY01C/MY06/CLIP1/FMN2/NEDD4/MICAL3/EXOC6B/SPTBN1/CLASP2
## GOCC_CELL_PROJECTION_MEMBRANE CD44/PEX19/KANK1/MY01C/INPP5K/MY06/ARHGEF2/EPB41L3/SLC6A6/SLC7A8/SLC19
## GOCC_T_TUBULE
## GOCC_MAIN_AXON
## GOCC_TRANSPORTER_COMPLEX      FXYD1/LRRC8B/LRRC8C/ATP11C/PTPA/NDUFS2/CACNB3/CASQ2/ATP
##
## Count setSize
## GOCC_GOLGI_CIS_CISTERNA      5      308
## GOCC_CELL_CORTEX             17      308
## GOCC_CELL_PROJECTION_MEMBRANE 16      308
## GOCC_T_TUBULE                5      308
## GOCC_MAIN_AXON              5      308
## GOCC_TRANSPORTER_COMPLEX     14      308

```

```

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.val

```

```

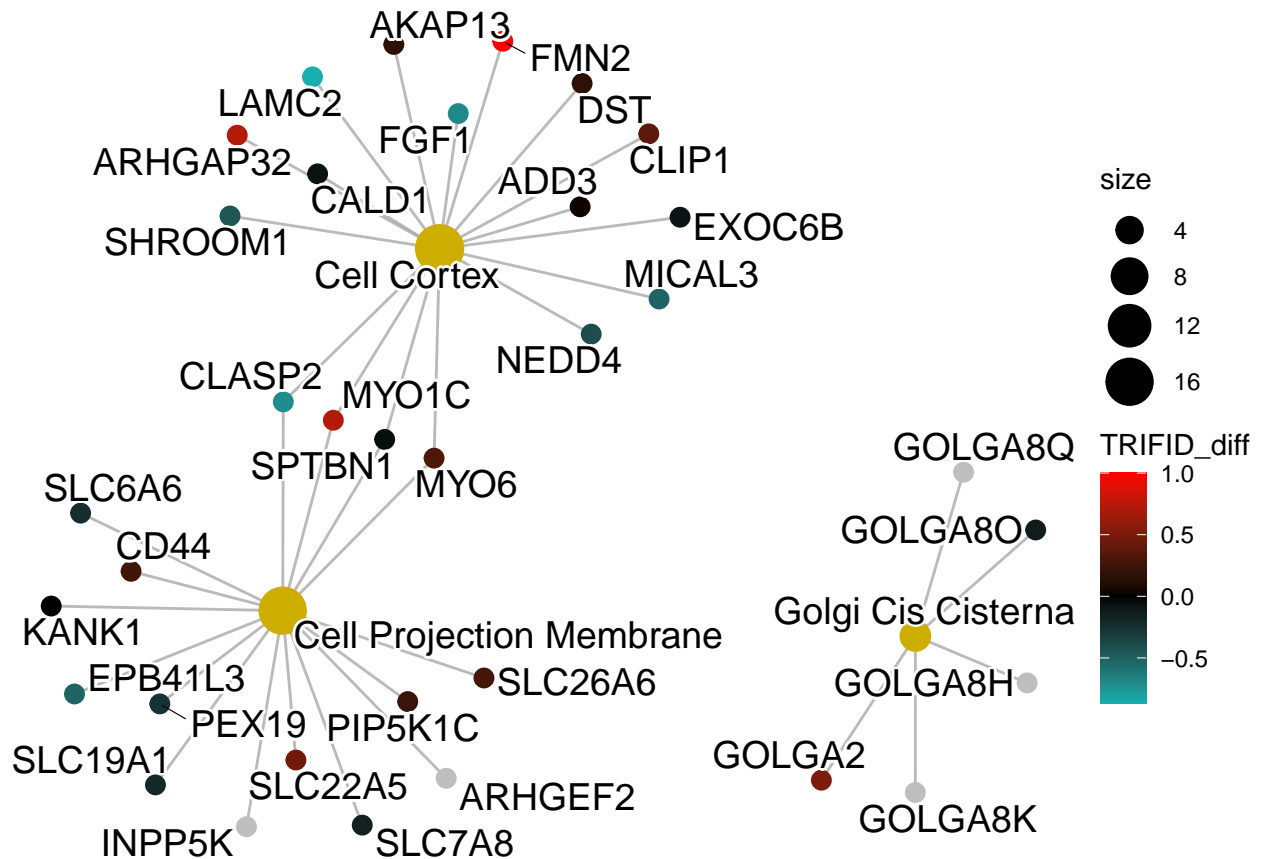
## Warning in cnetplot.enrichResult(x, ...): Use 'color.params = list(category = your_value)' instead of
## The color_category parameter will be removed in the next version.

```

```

## 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.
```

