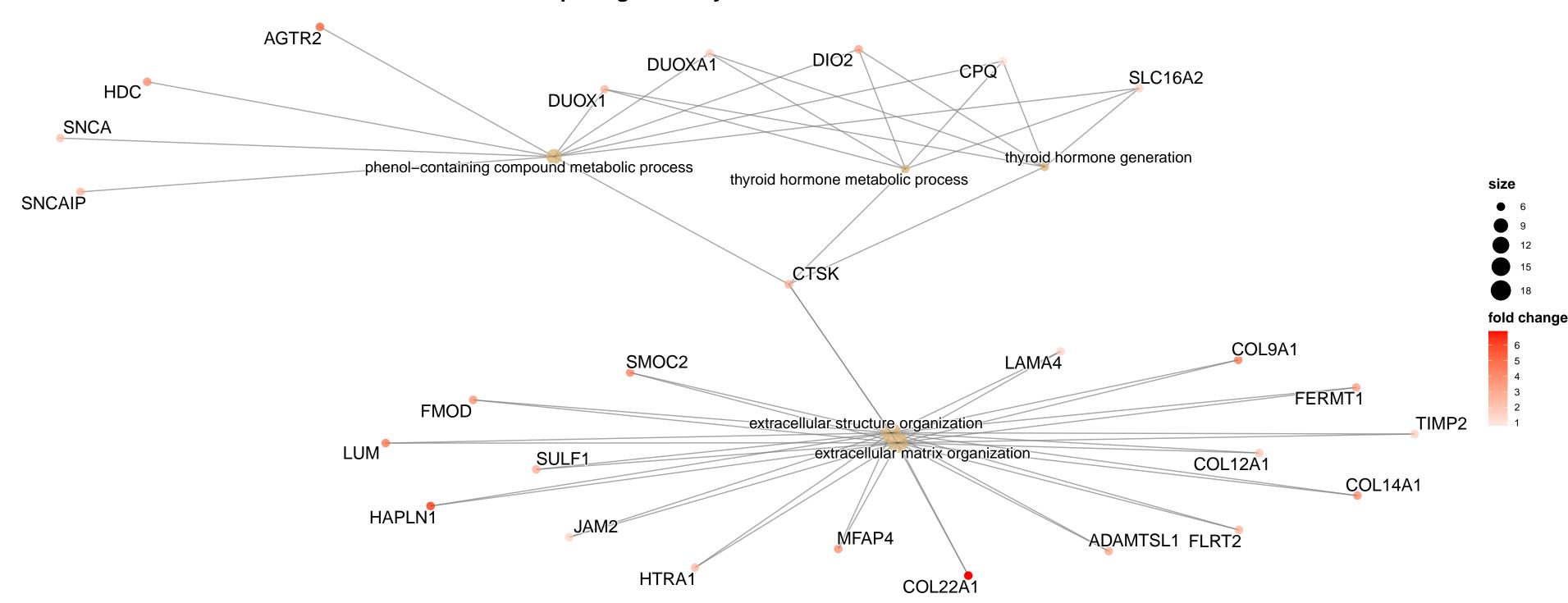
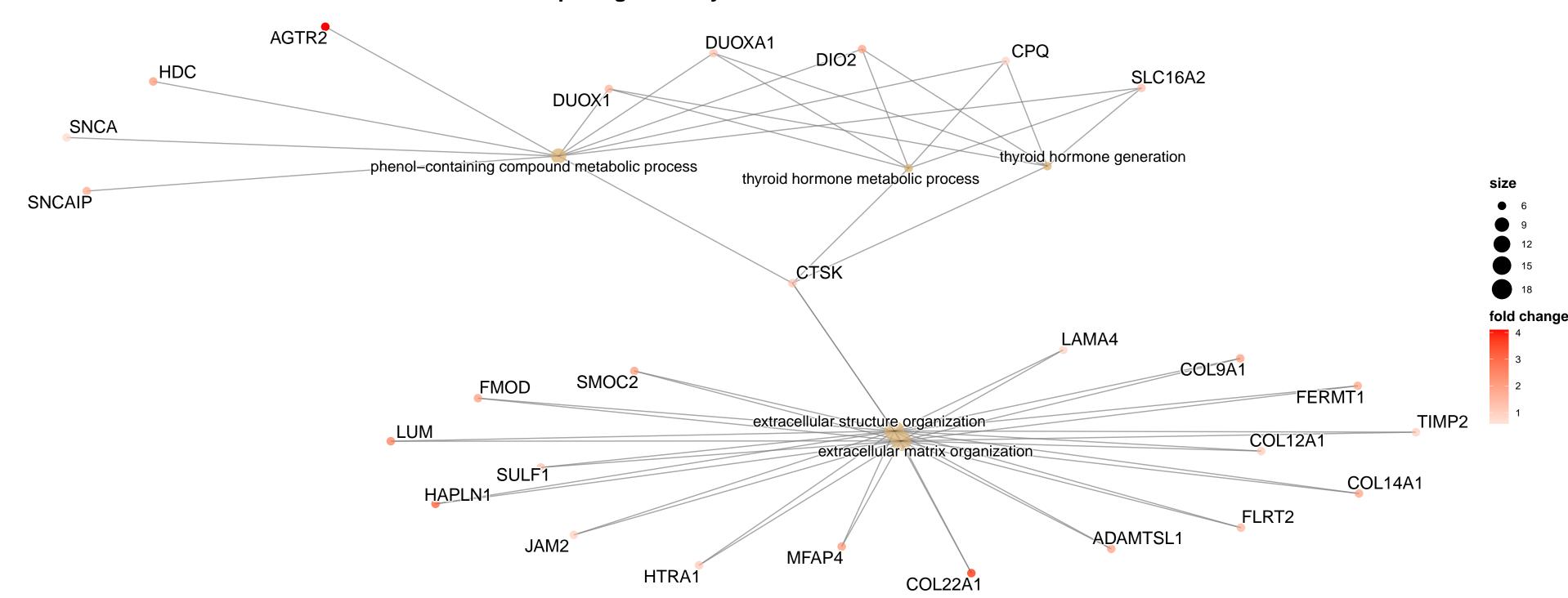
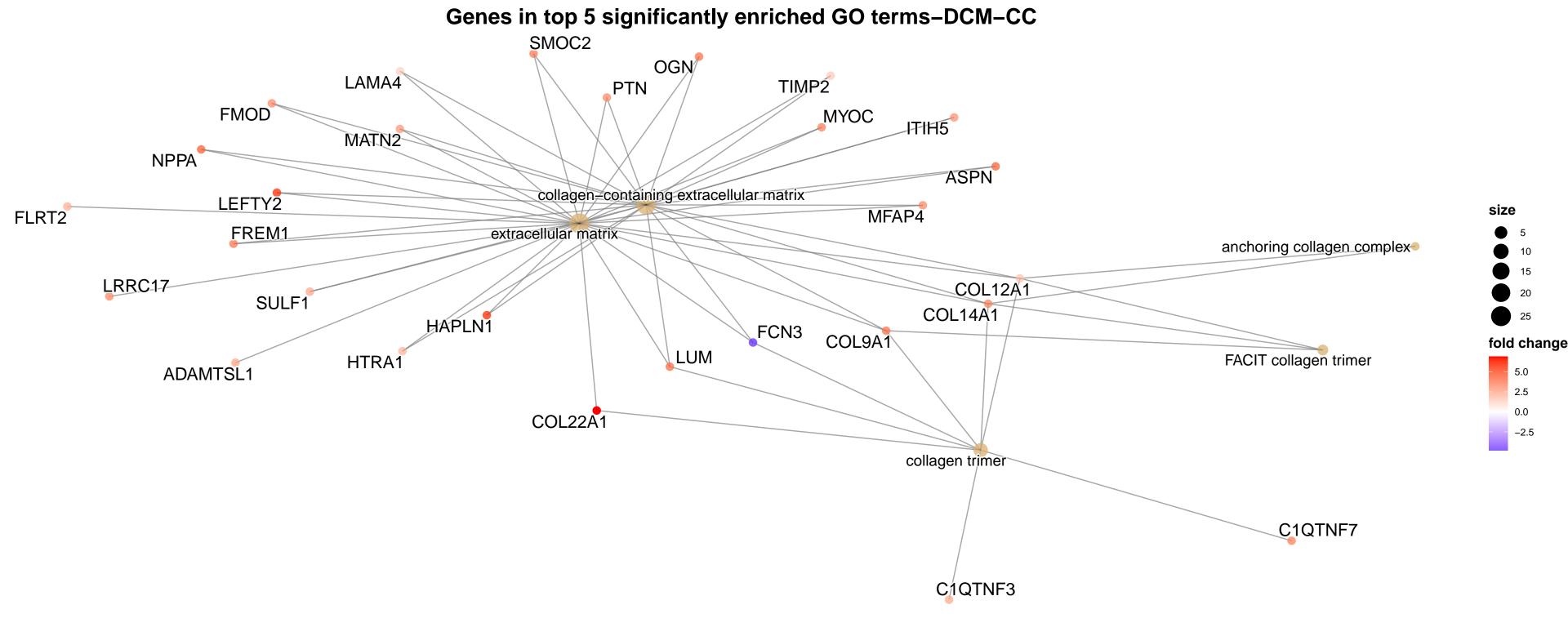
# Genes in top 5 significantly enriched GO terms-DCM-BP



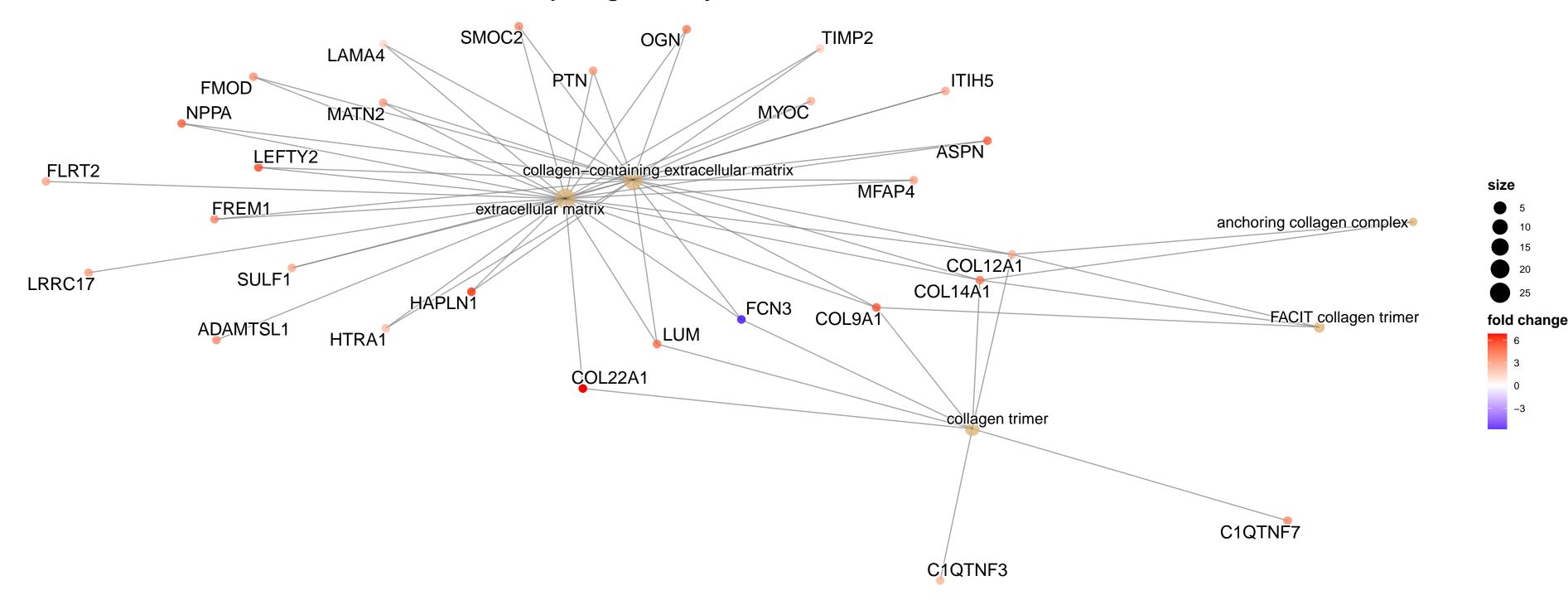
#### Genes in top 5 significantly enriched GO terms-HCM-BP AGTR2 DI02 DUOXA1 CPQ HDC DUOX1 SLC16A2 phenol-containing compound metabolic process SNCA thyroid hormone generation thyroid hormone metabolic process fold change SNCAIP CTSK size LAMA4 SMOC2 COL9A1 FMOD FERMT1 extracellular structure organization LUM COL12A1 TIMP2 extracellular matrix organization SULF1 HAPLN1 COL14A1 JAM2 MFAP4 FLRT2 HTRA1 COL22A1 ADAMTSL1

# Genes in top 5 significantly enriched GO terms-PPCM-BP



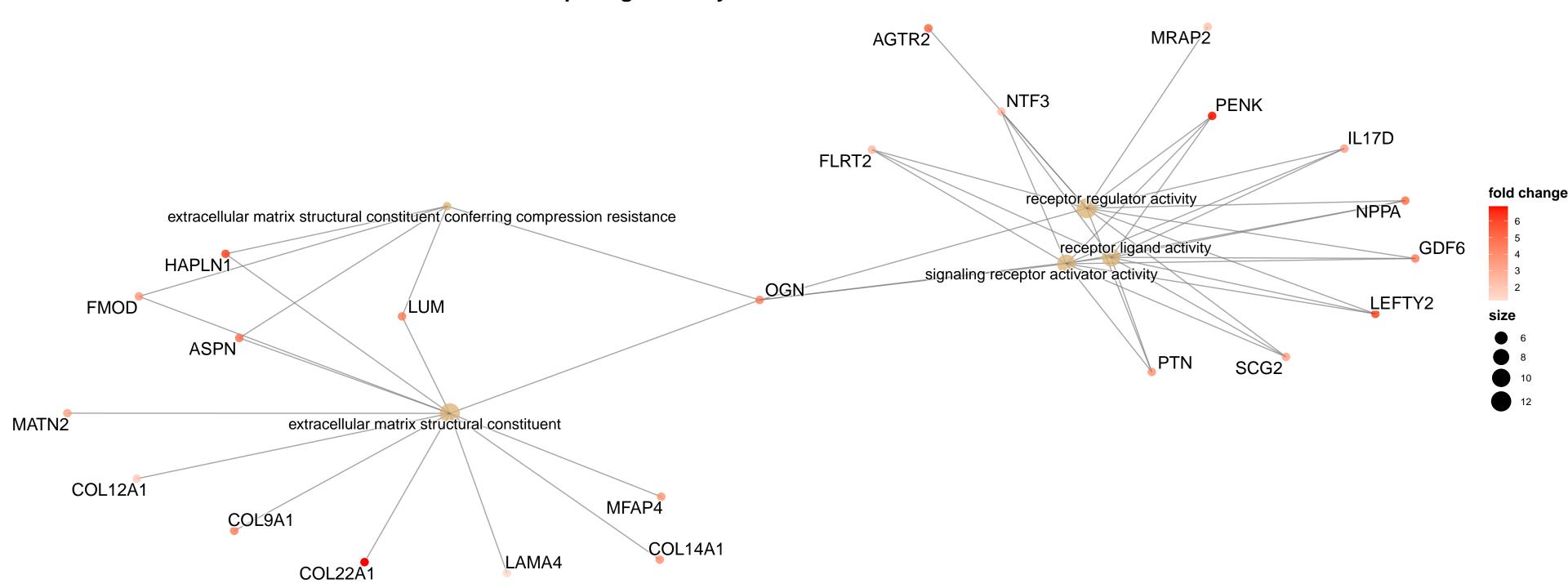


# Genes in top 5 significantly enriched GO terms-HCM-CC

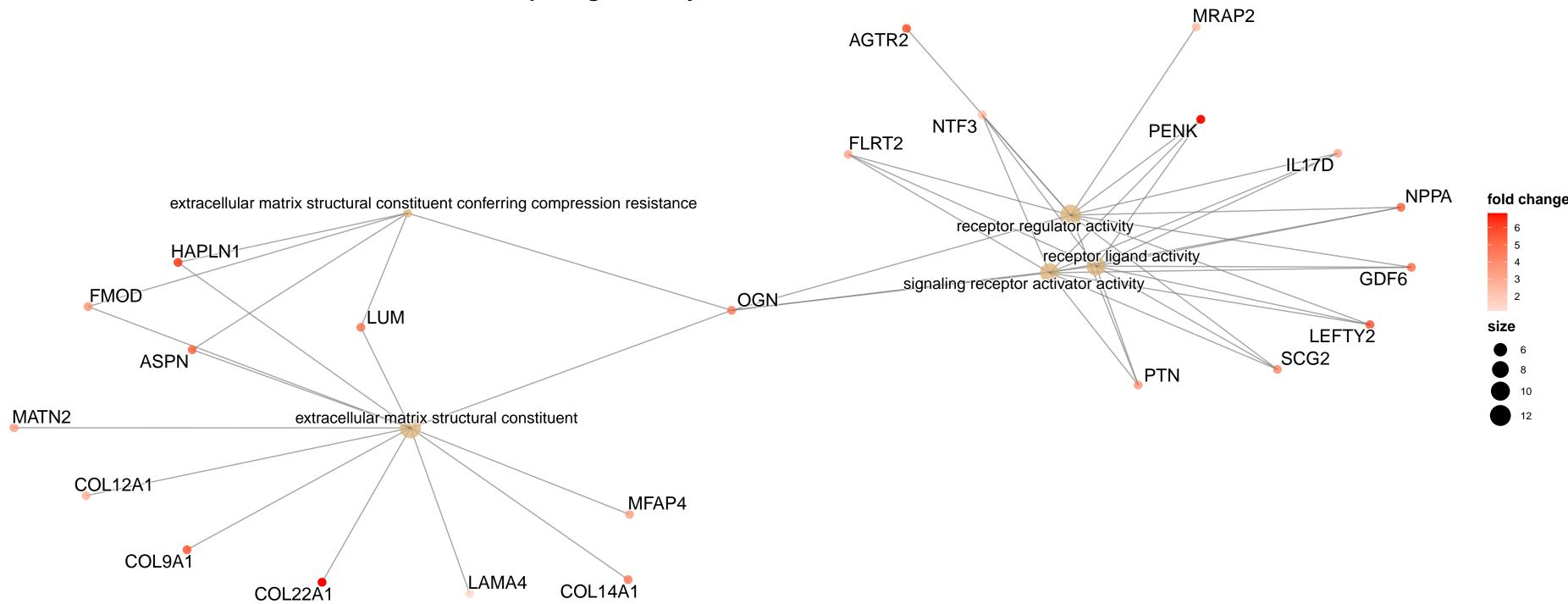


#### Genes in top 5 significantly enriched GO terms-PPCM-CC SMOC2 LAMA4 OGN TIMP2 PTN FMOD MYOC MATN2 JTH5 NPPA ASPN collagen-containing extracellular matrix MFAP4 LEFTY2 size FLRT2 extracellular matrix anchoring collagen complex• FREM1 LRRC17 COL12A1 SULF1 COL14A1 HAPLN1 COL9A1 FACIT collagen trimer fold change ADAMTSL1 FCN3 HTRA1 LUM COL22A1 collagen trimer C1QTNF7 C1QTNF3

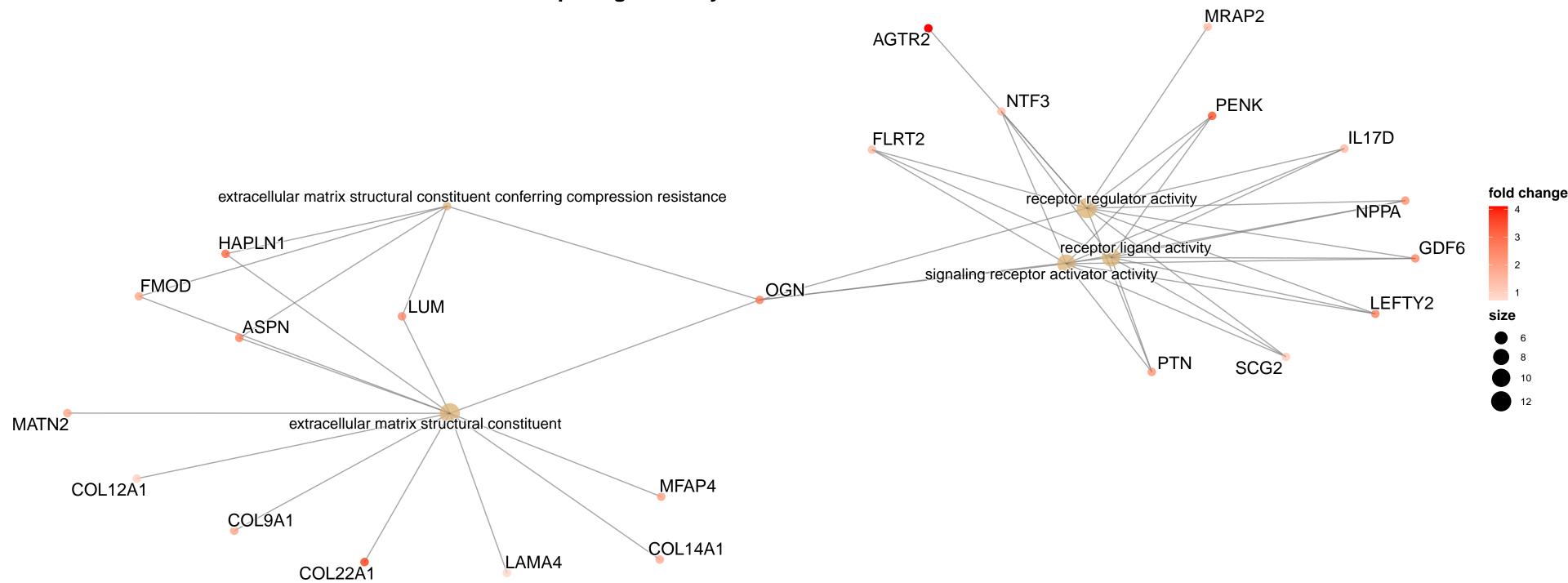
# Genes in top 5 significantly enriched GO terms-DCM-MF



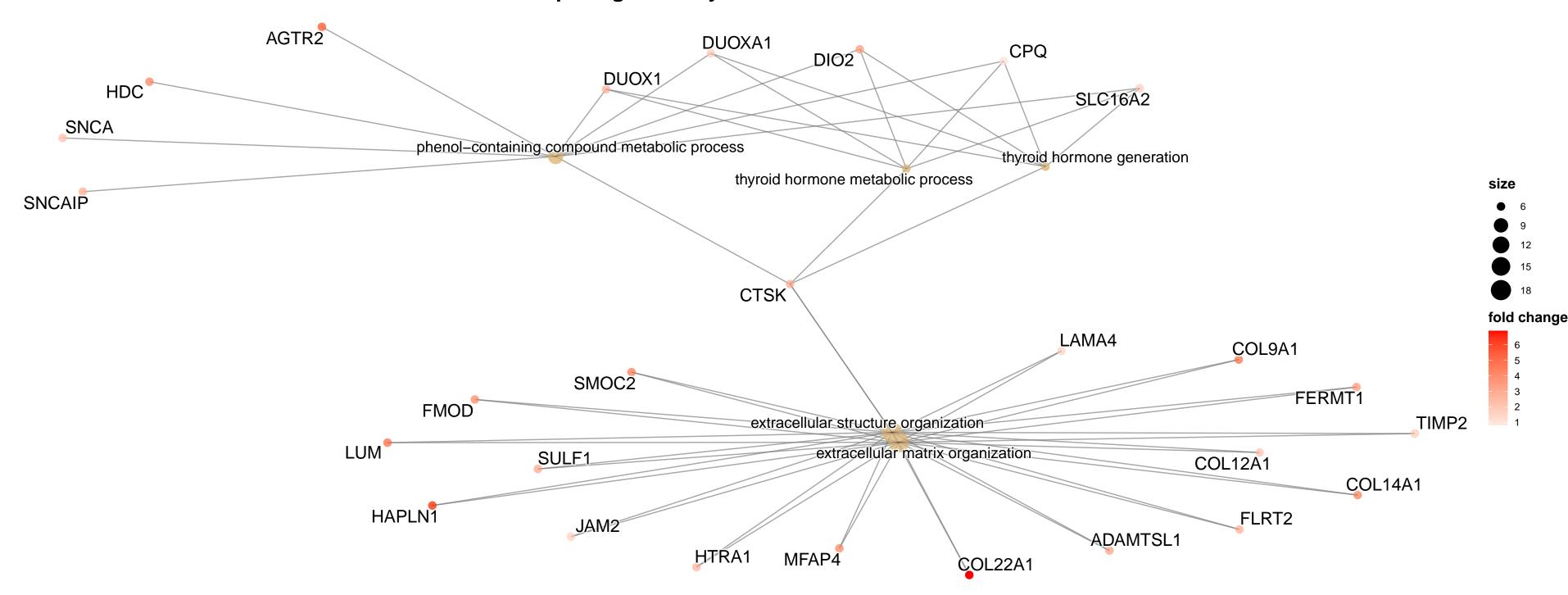
# Genes in top 5 significantly enriched GO terms-HCM-MF



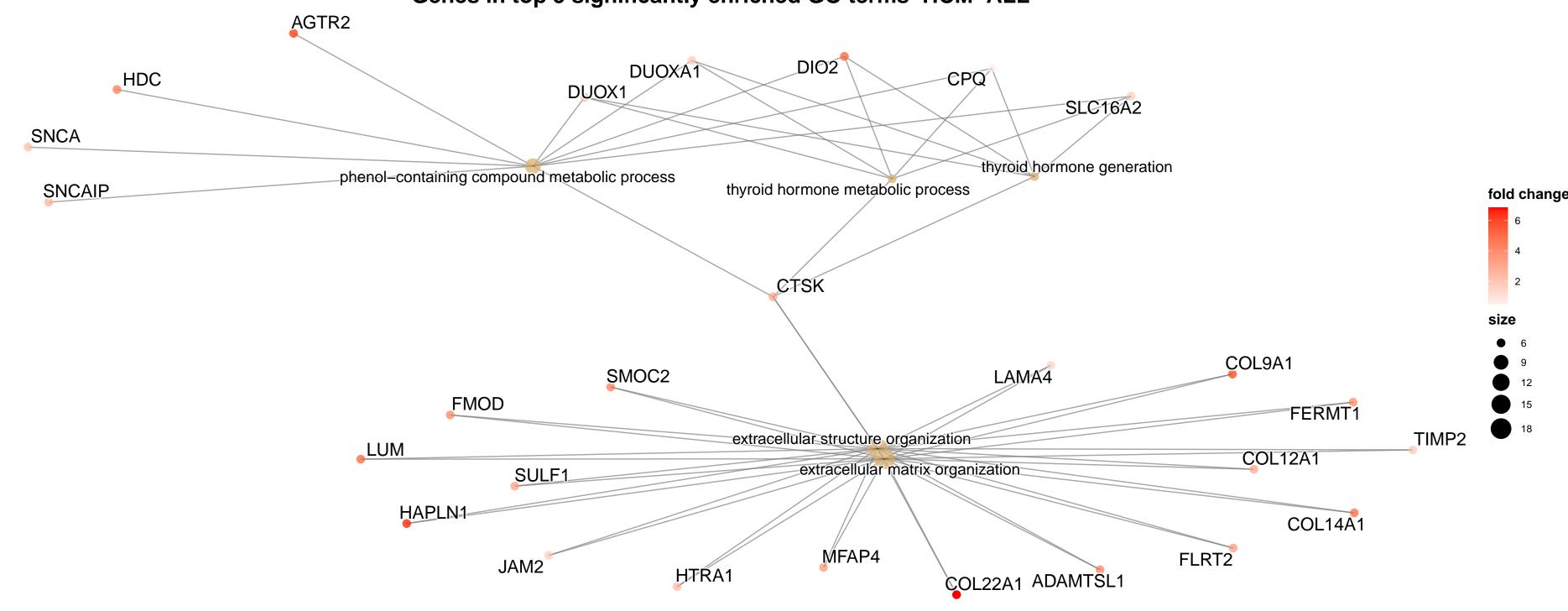
# Genes in top 5 significantly enriched GO terms-PPCM-MF



# Genes in top 5 significantly enriched GO terms-DCM-ALL

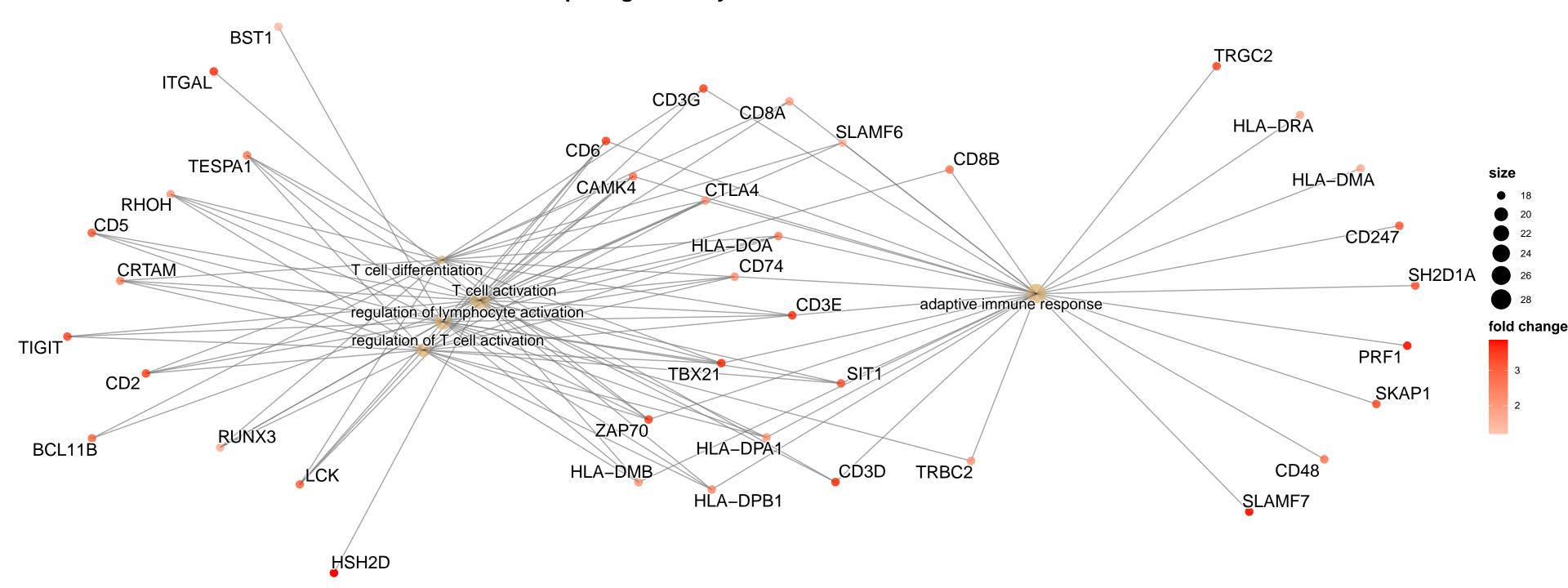


# Genes in top 5 significantly enriched GO terms-HCM-ALL

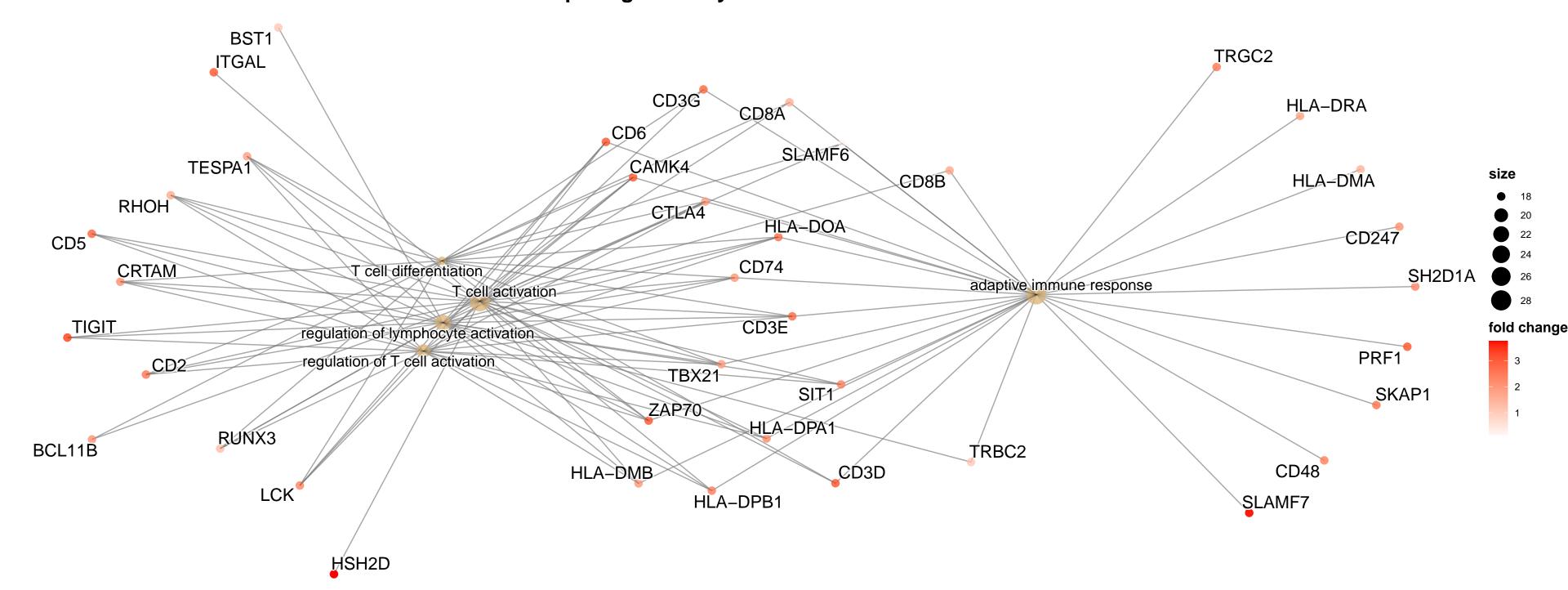


#### Genes in top 5 significantly enriched GO terms-PPCM-ALL AGTR2 **DUOXA1** CPQ DI02 HDC SLC16A2 DUOX1 phenol-containing compound metabolic process SNCA thyroid hormone generation thyroid hormone metabolic process size SNCAIP CTSK fold change COL9A1 LAMA4 SMOC2 FERMT1 FMOD TIMP2 extracellular structure organization COL12A1 LUM extracellular matrix organization SULF1 COL14A1 HAPLN1 FLRT2 JAM2 ADAMTSL1 HTRA1 MFAP4 COL22A1

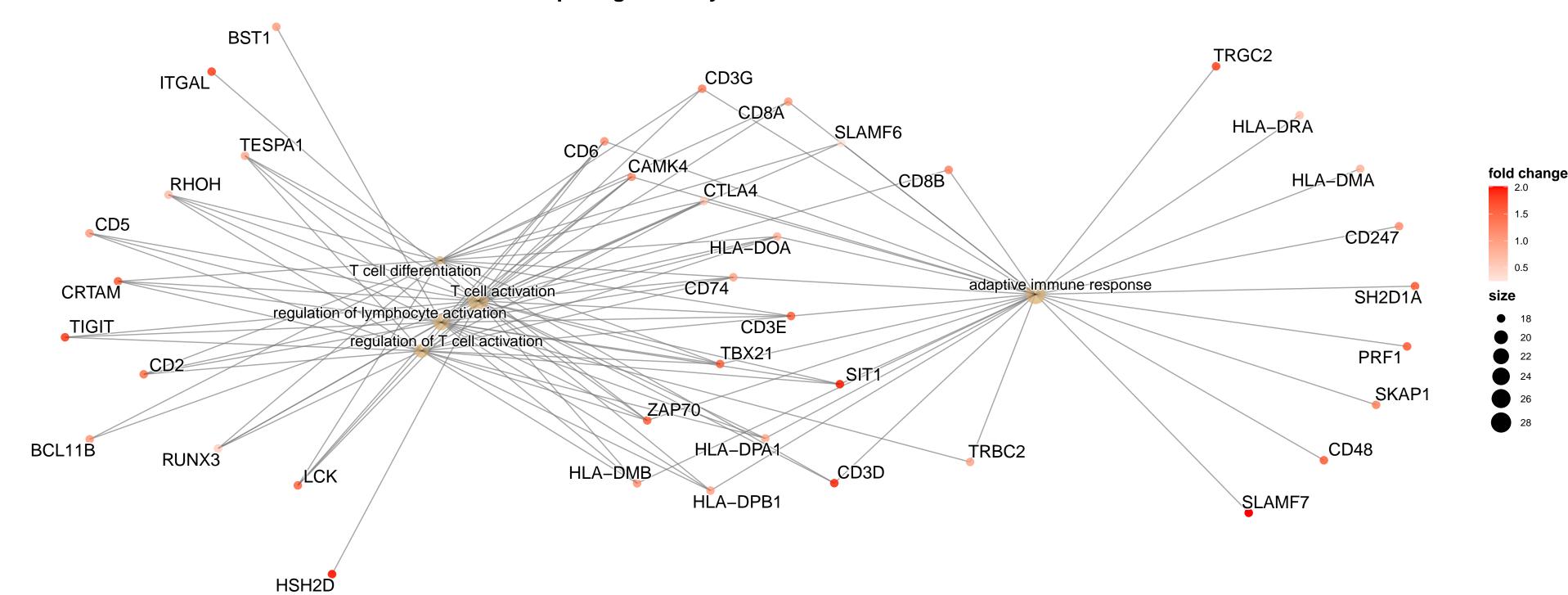
#### Genes in top 5 significantly enriched GO terms-DCM-BP



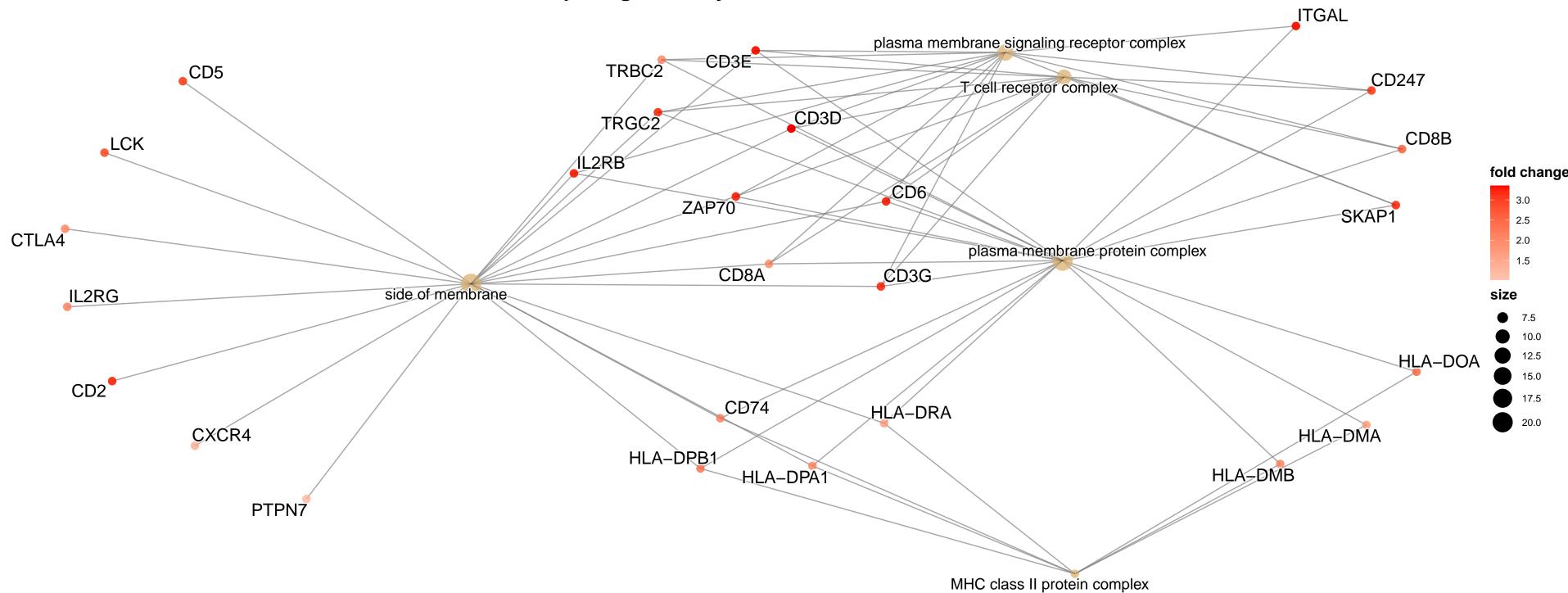
# Genes in top 5 significantly enriched GO terms-HCM-BP



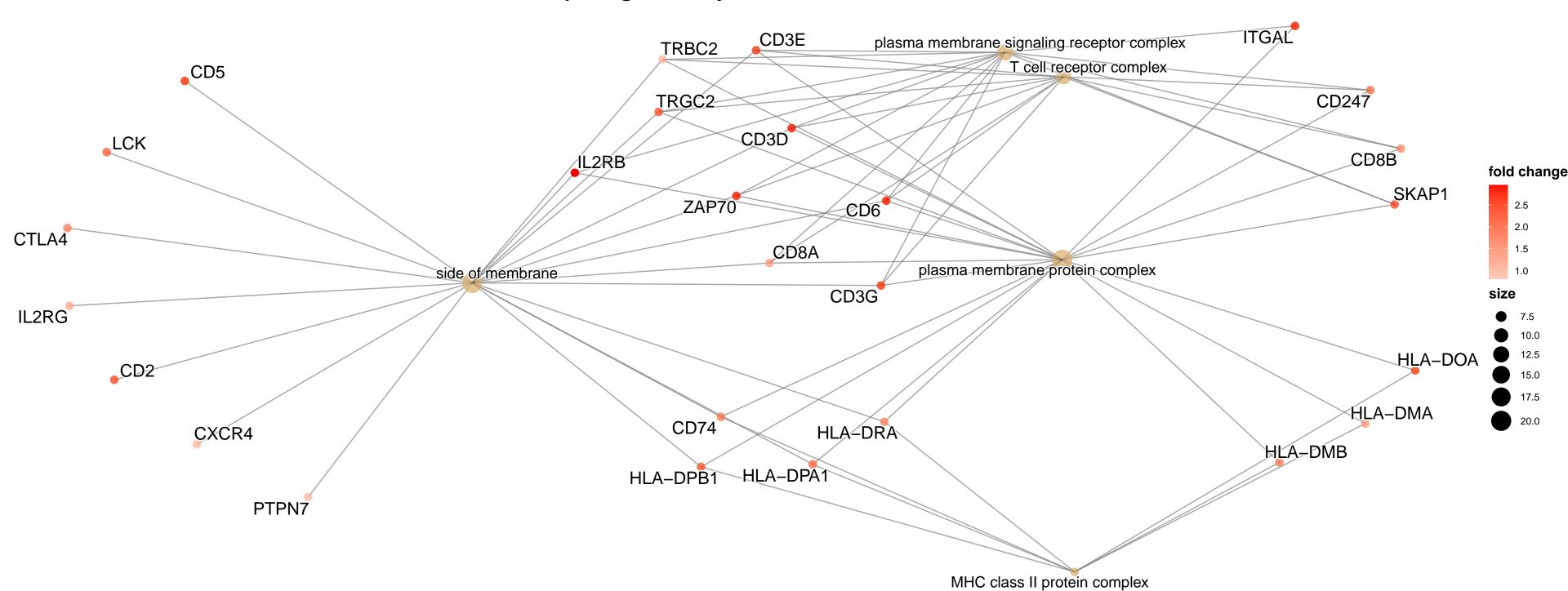
# Genes in top 5 significantly enriched GO terms-PPCM-BP



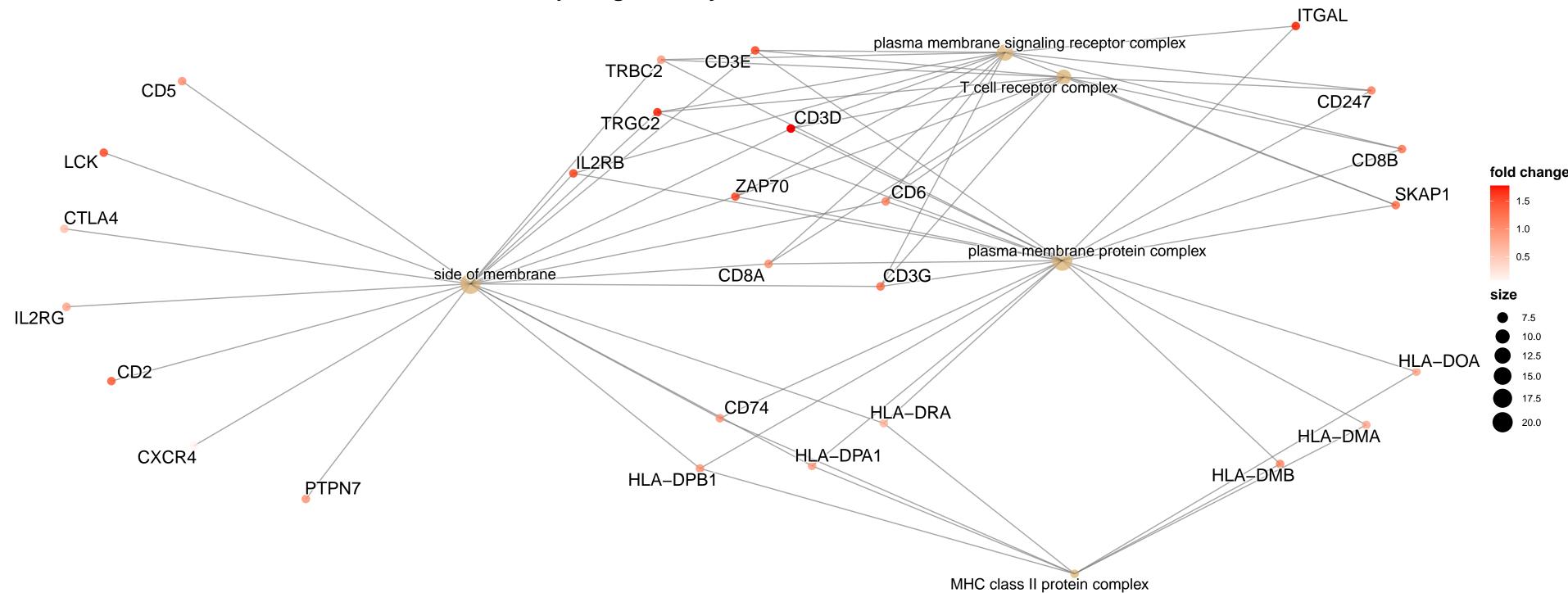
# Genes in top 5 significantly enriched GO terms-DCM-CC



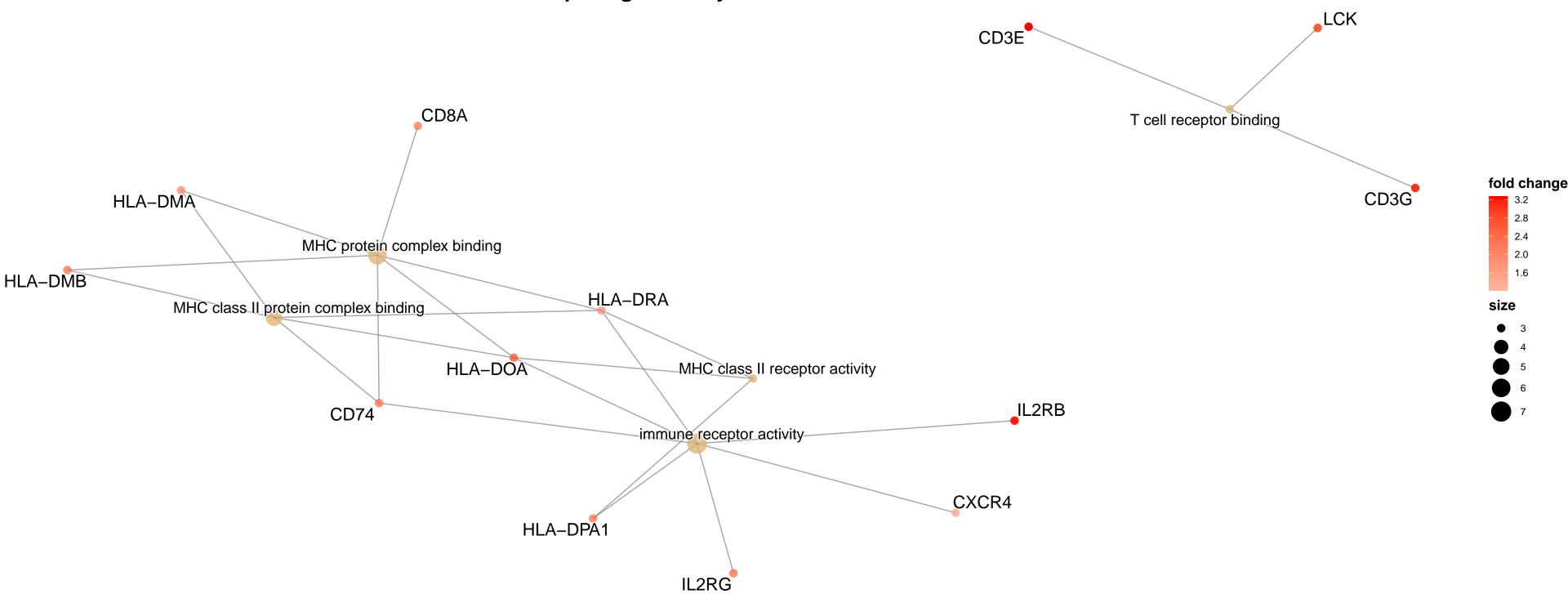
# Genes in top 5 significantly enriched GO terms-HCM-CC



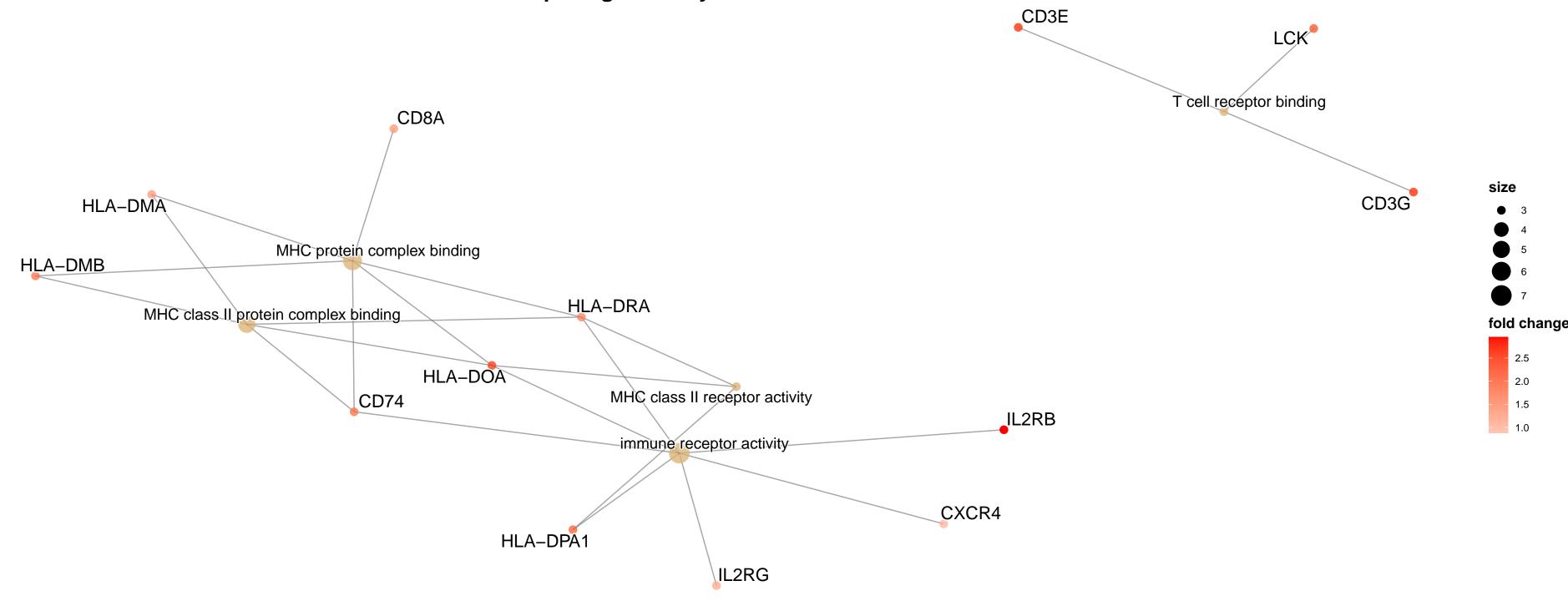
# Genes in top 5 significantly enriched GO terms-PPCM-CC



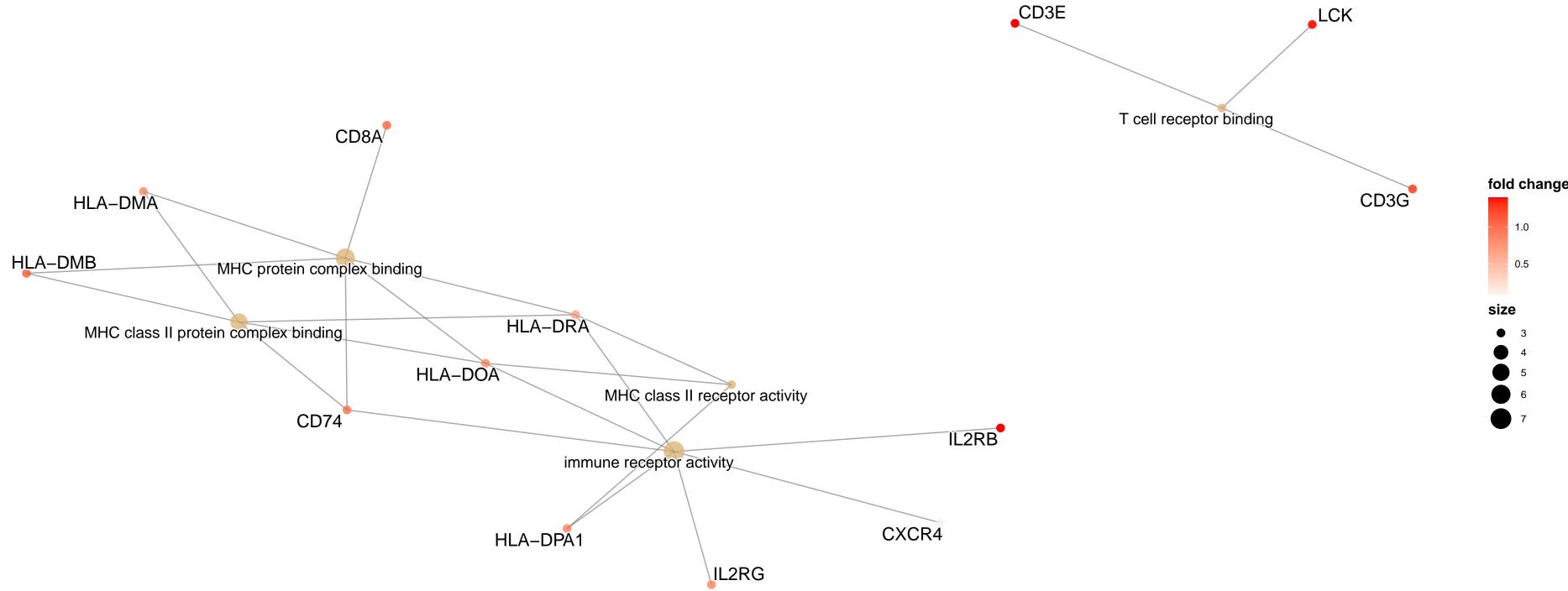
# Genes in top 5 significantly enriched GO terms-DCM-MF



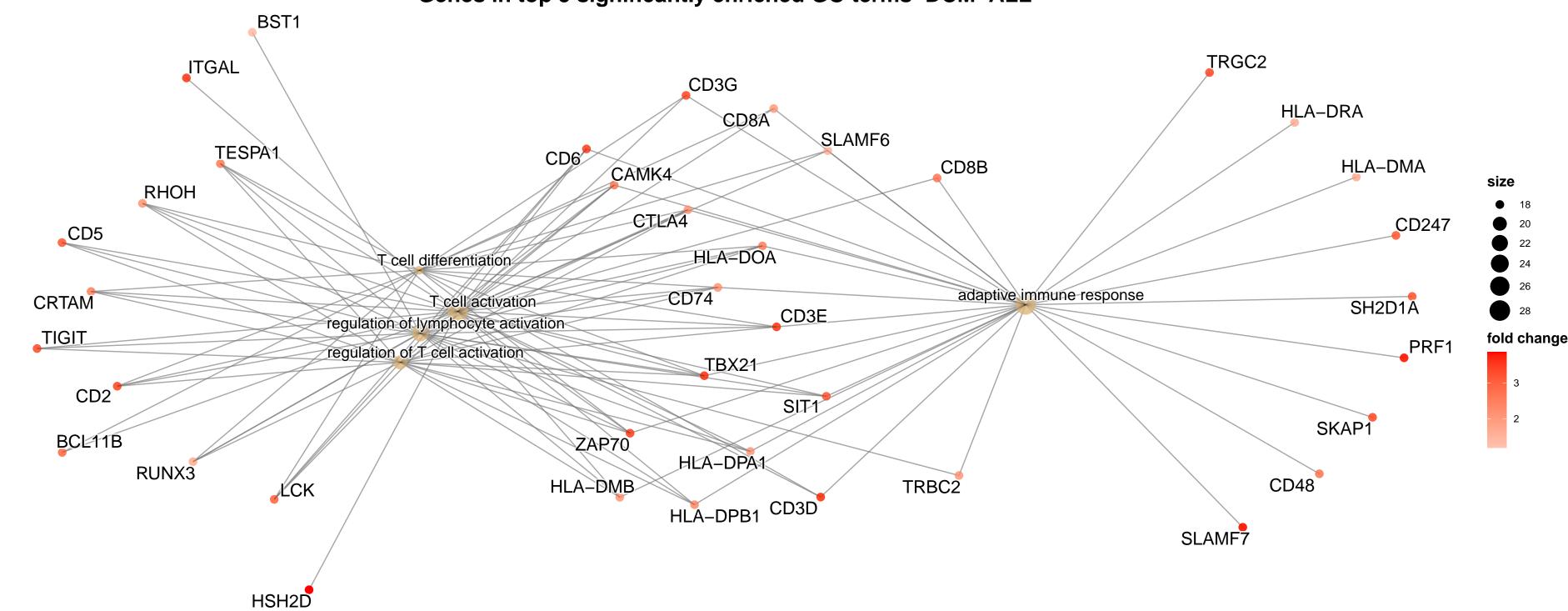
# Genes in top 5 significantly enriched GO terms-HCM-MF



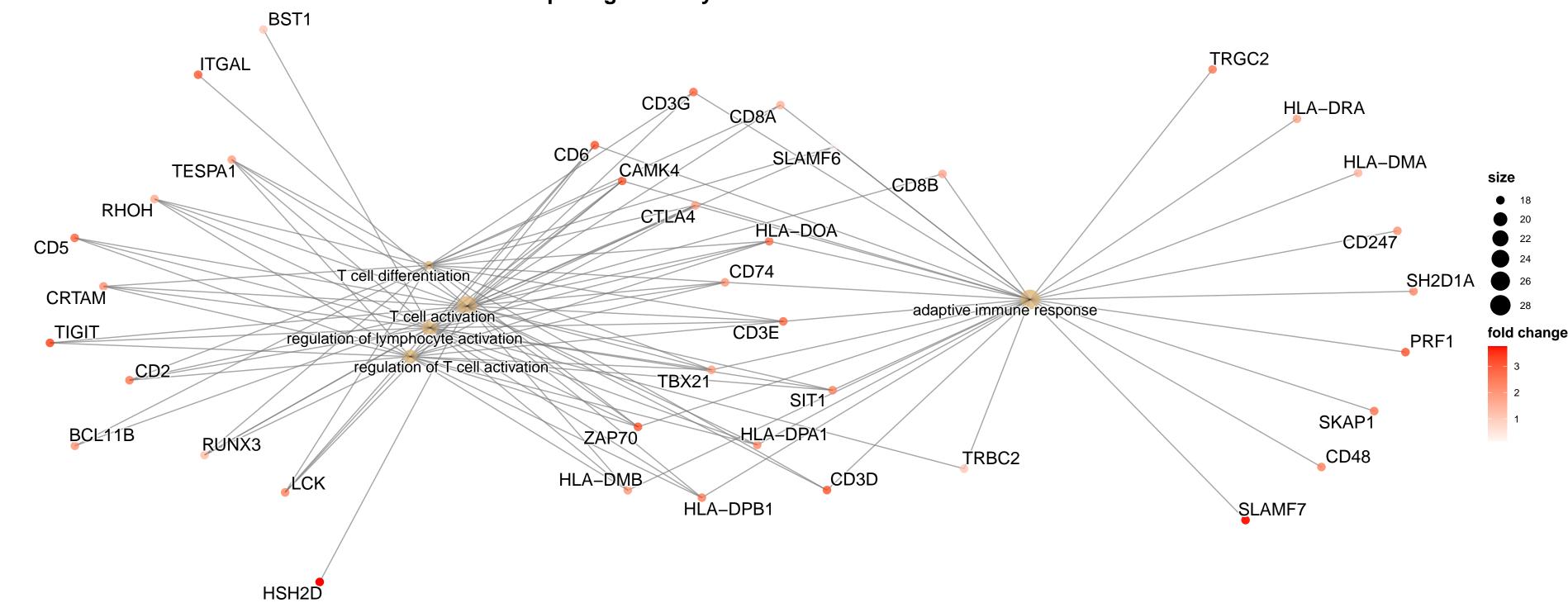
# Genes in top 5 significantly enriched GO terms-PPCM-MF



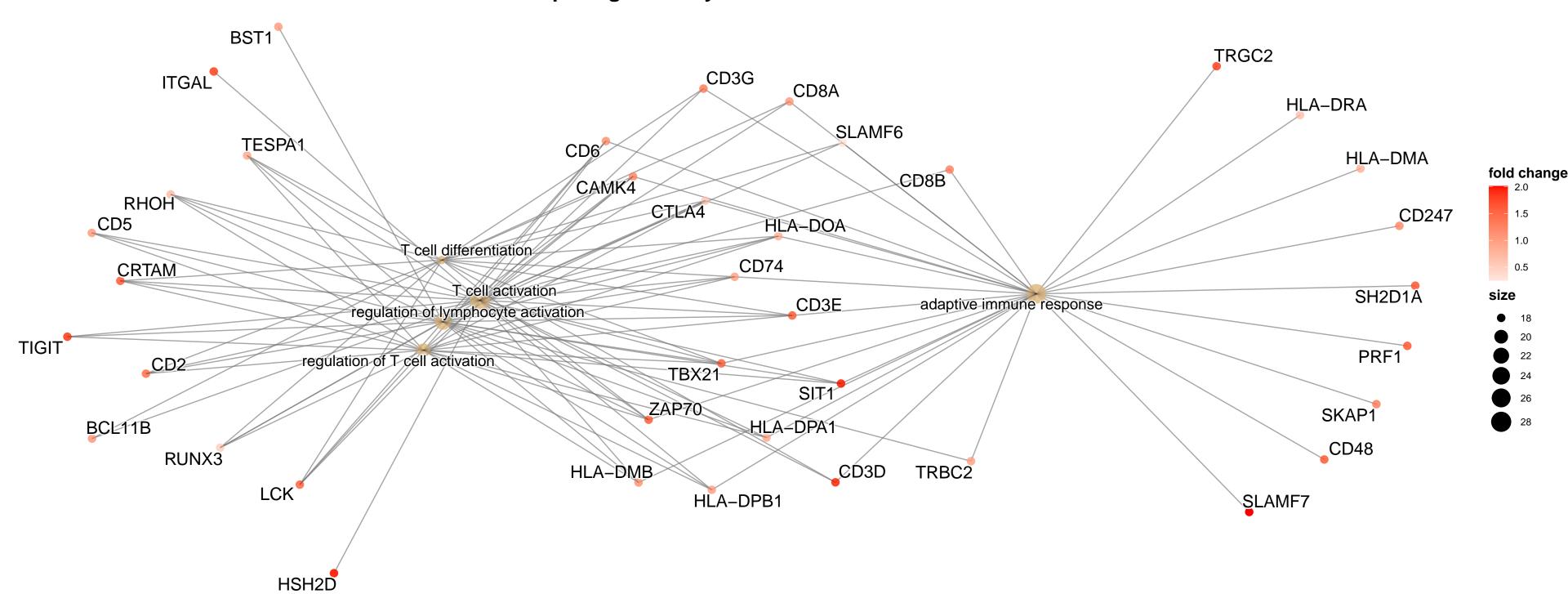
# Genes in top 5 significantly enriched GO terms-DCM-ALL

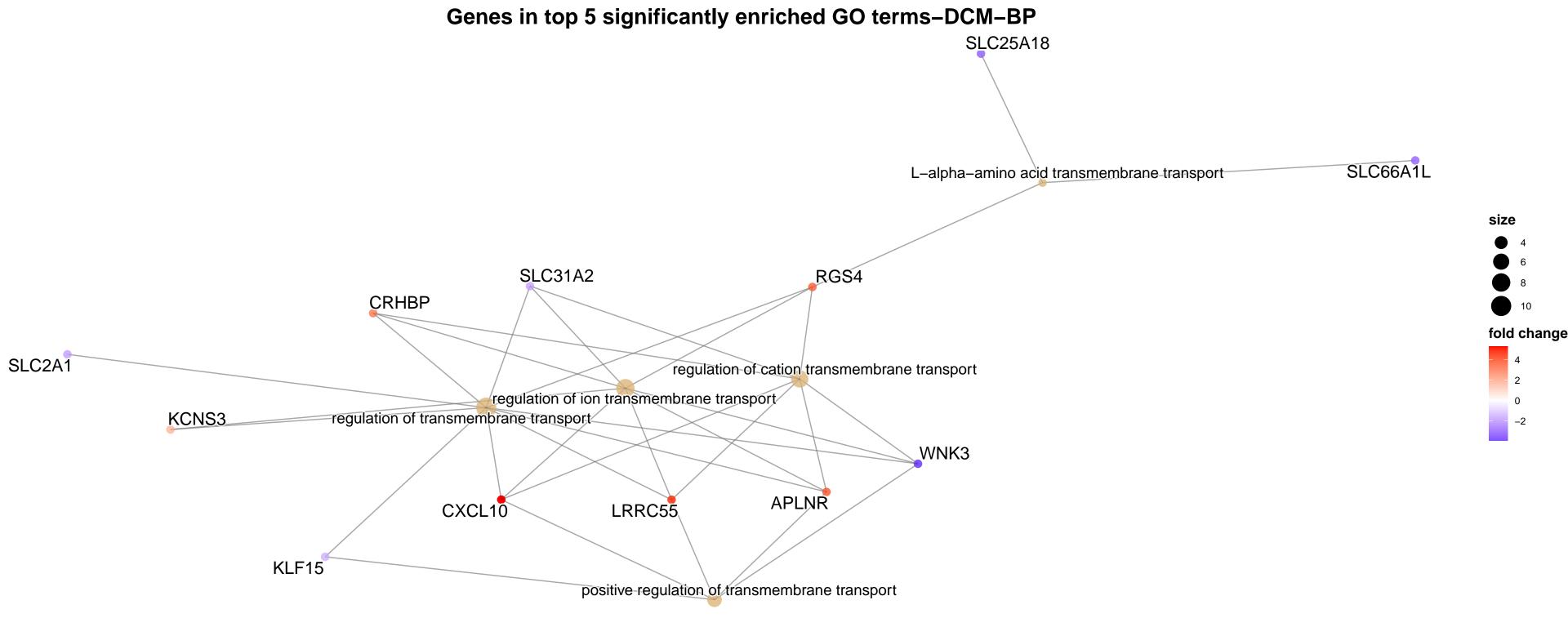


#### Genes in top 5 significantly enriched GO terms-HCM-ALL

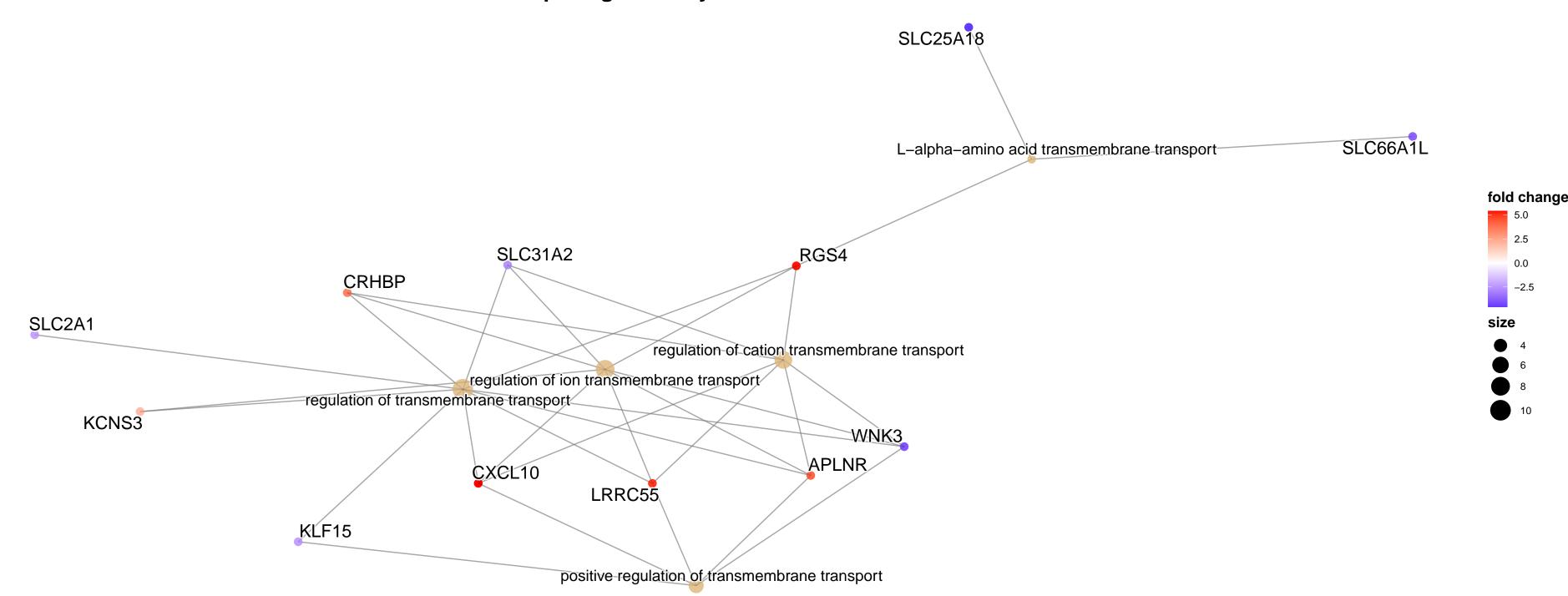


# Genes in top 5 significantly enriched GO terms-PPCM-ALL

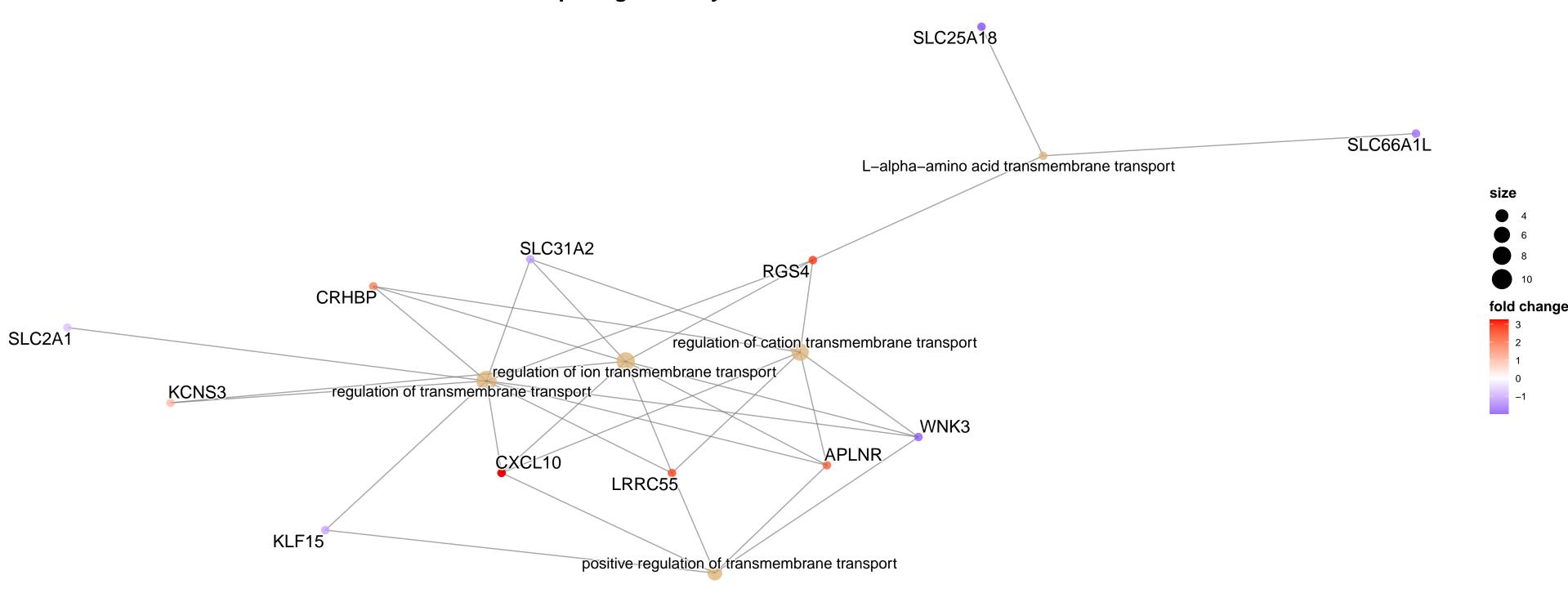




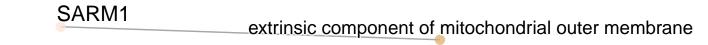
# Genes in top 5 significantly enriched GO terms-HCM-BP

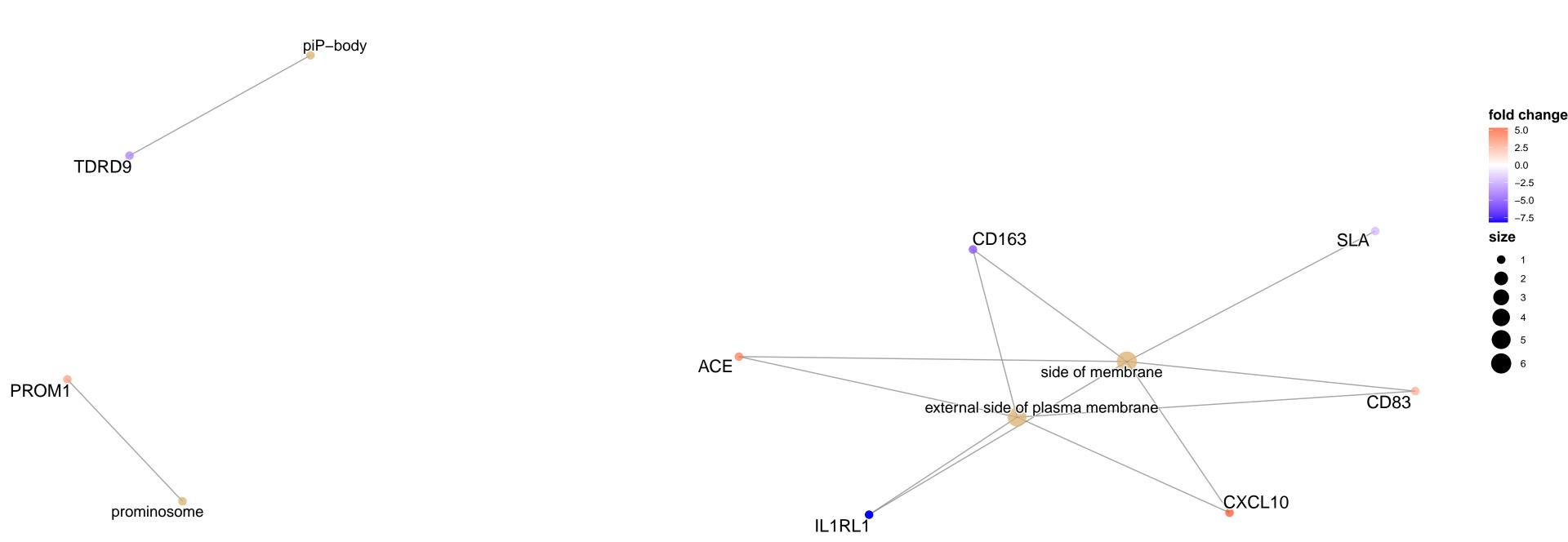


# Genes in top 5 significantly enriched GO terms-PPCM-BP

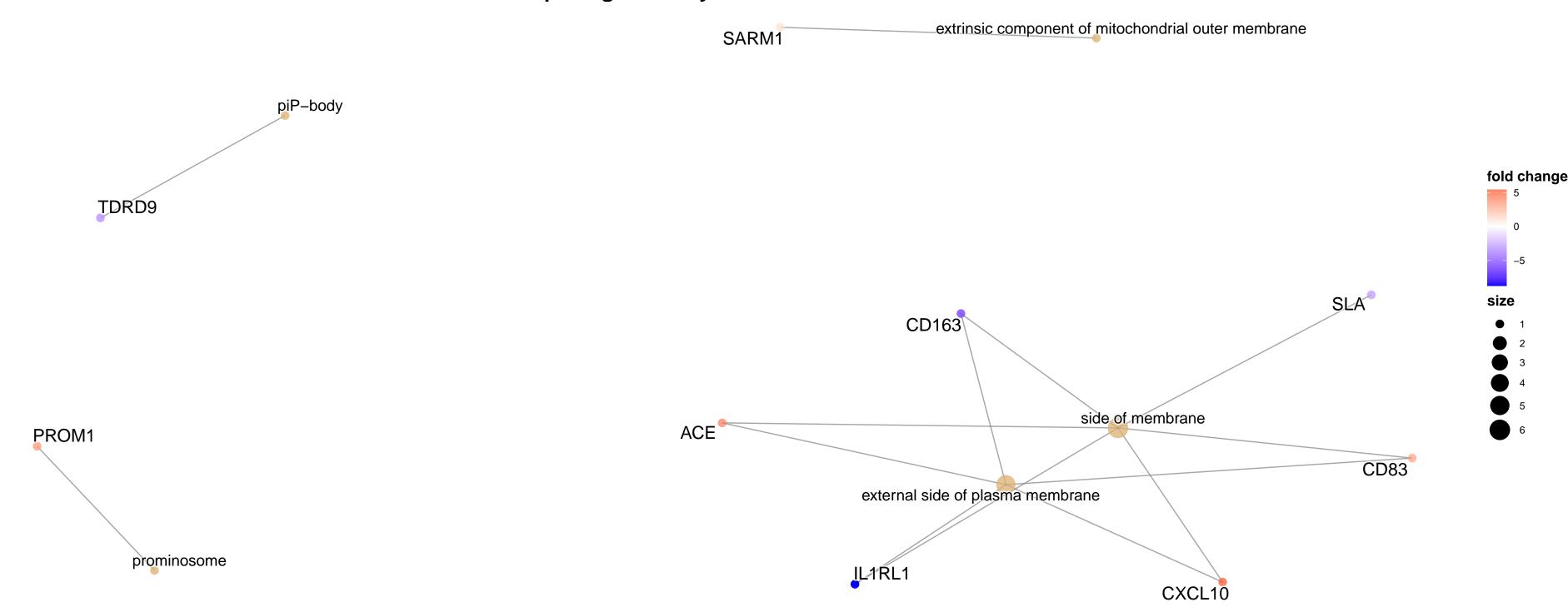


# Genes in top 5 significantly enriched GO terms-DCM-CC

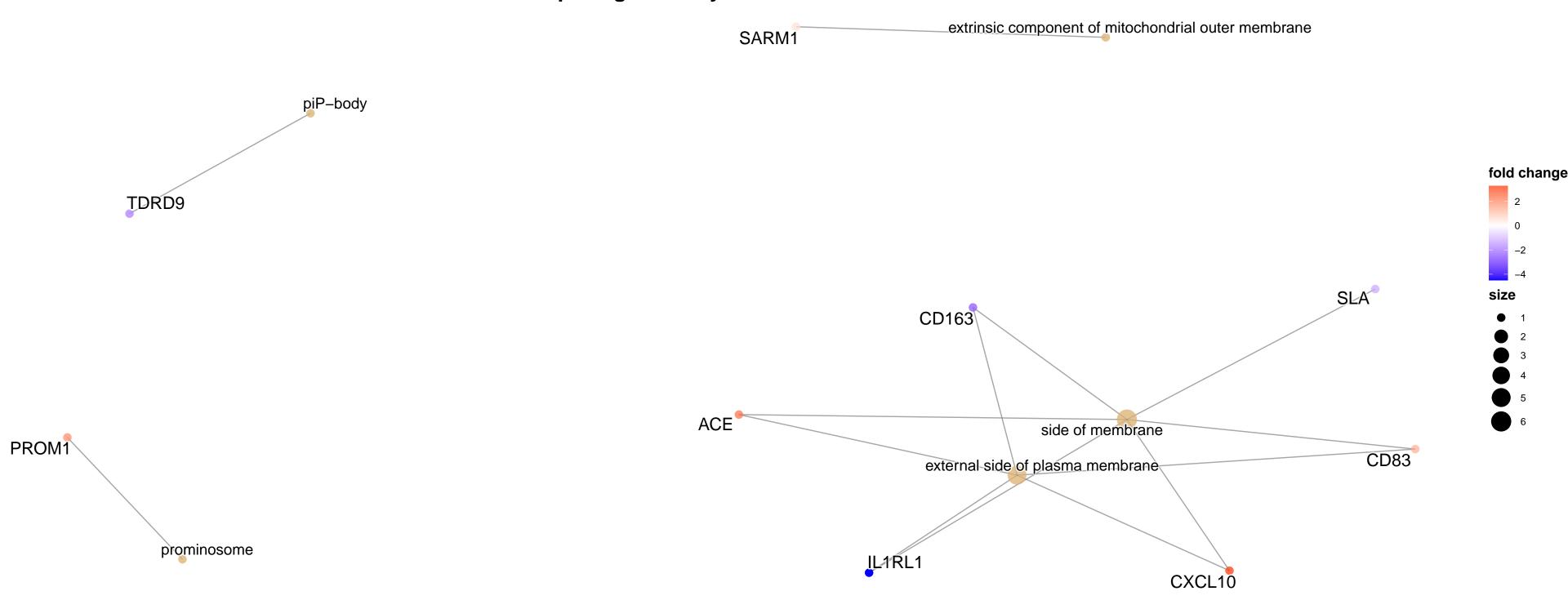




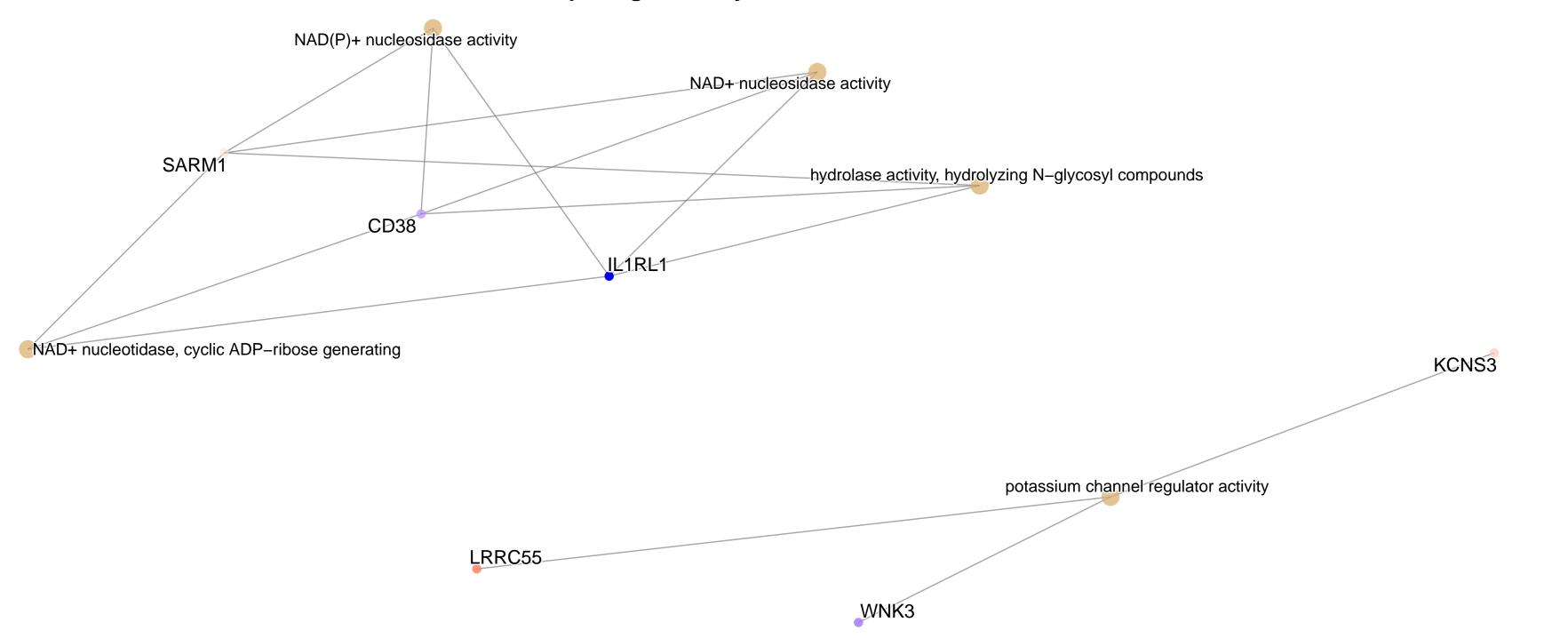
# Genes in top 5 significantly enriched GO terms-HCM-CC



# Genes in top 5 significantly enriched GO terms-PPCM-CC



# Genes in top 5 significantly enriched GO terms-DCM-MF



size

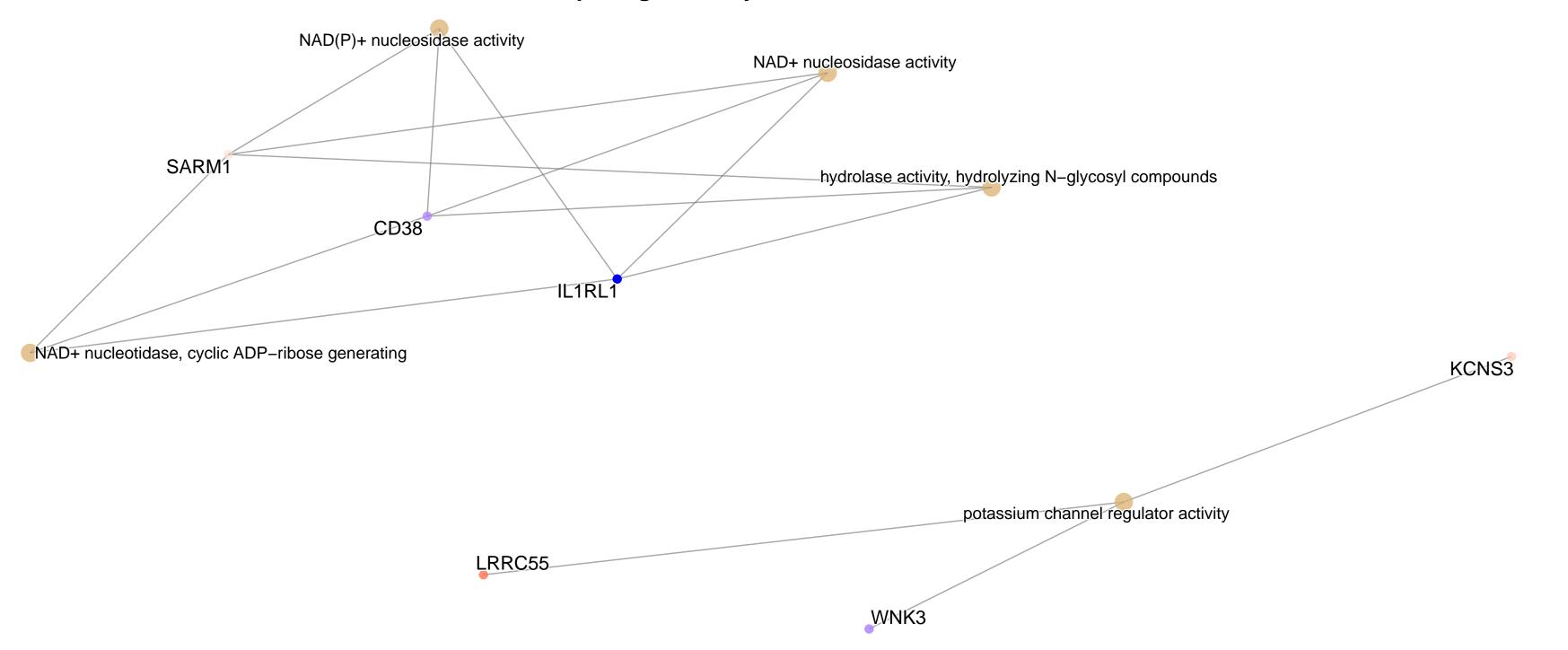
fold change

2.5

0.0

-2.5 -5.0

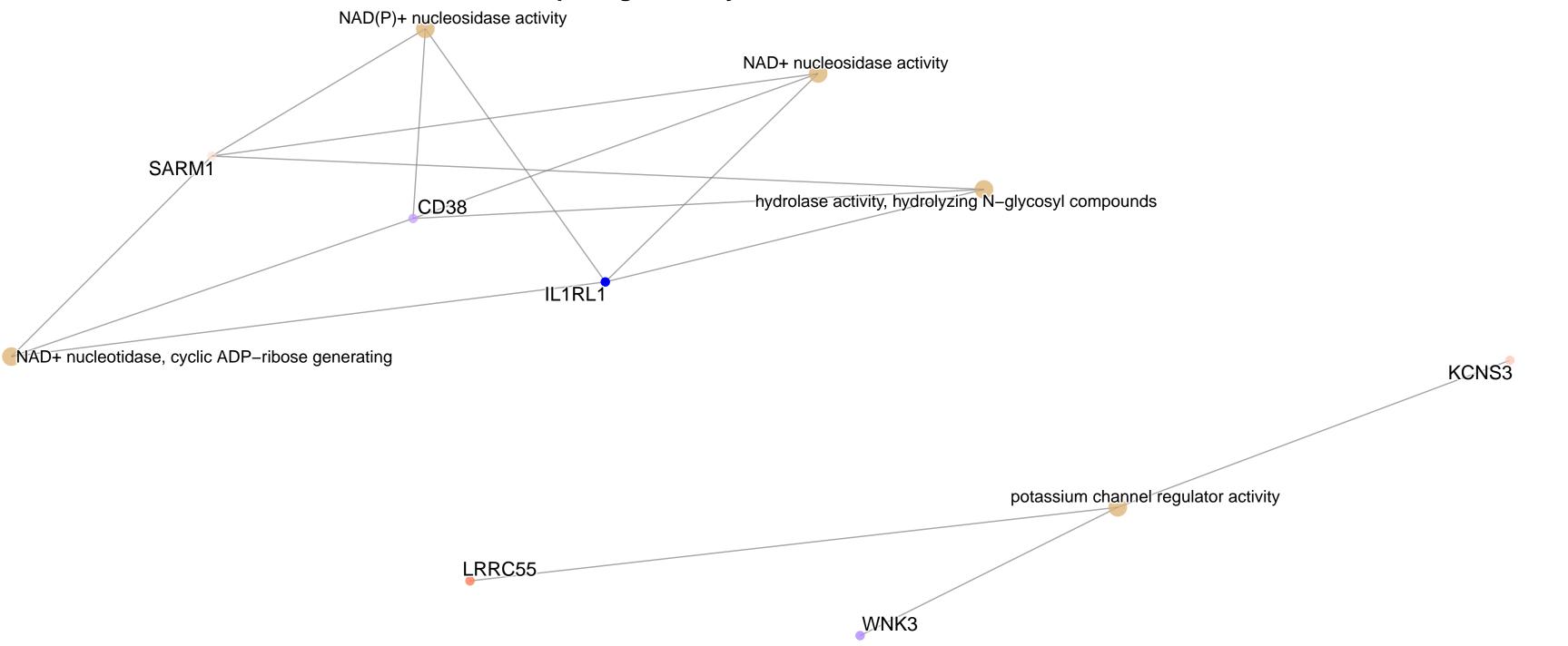
# Genes in top 5 significantly enriched GO terms-HCM-MF



size

fold change

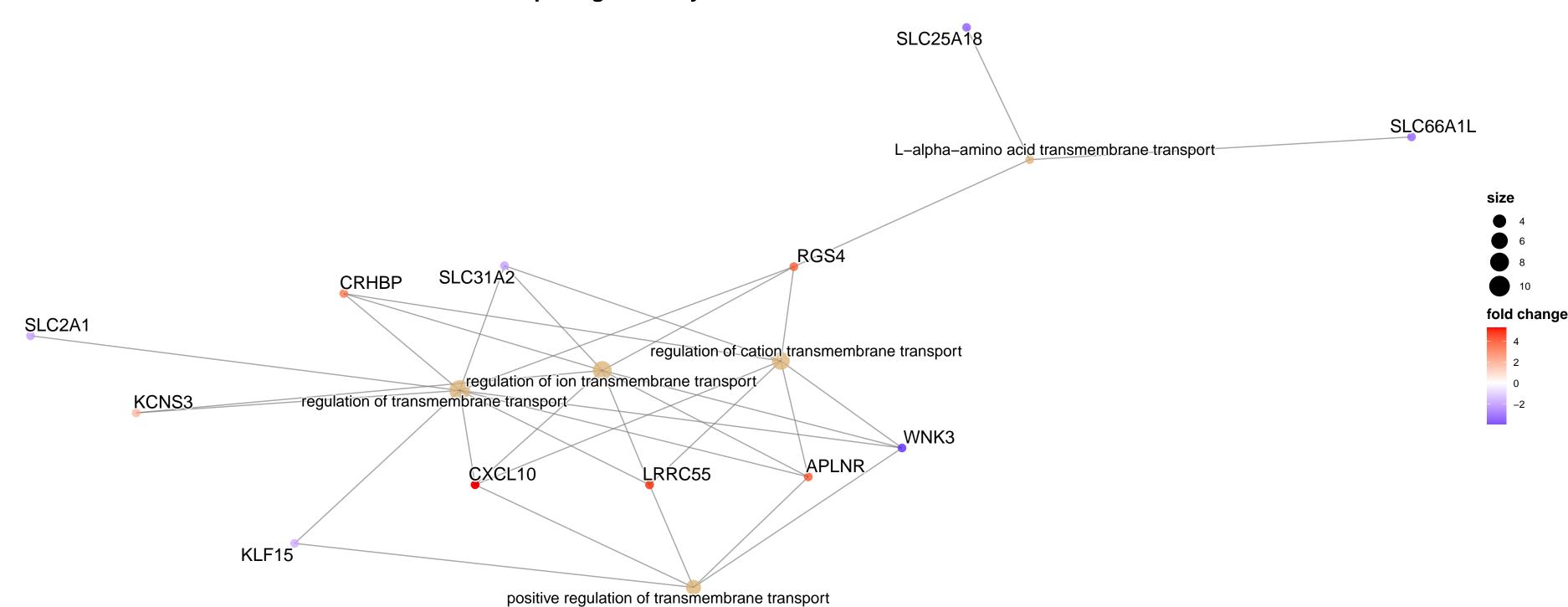
# Genes in top 5 significantly enriched GO terms-PPCM-MF

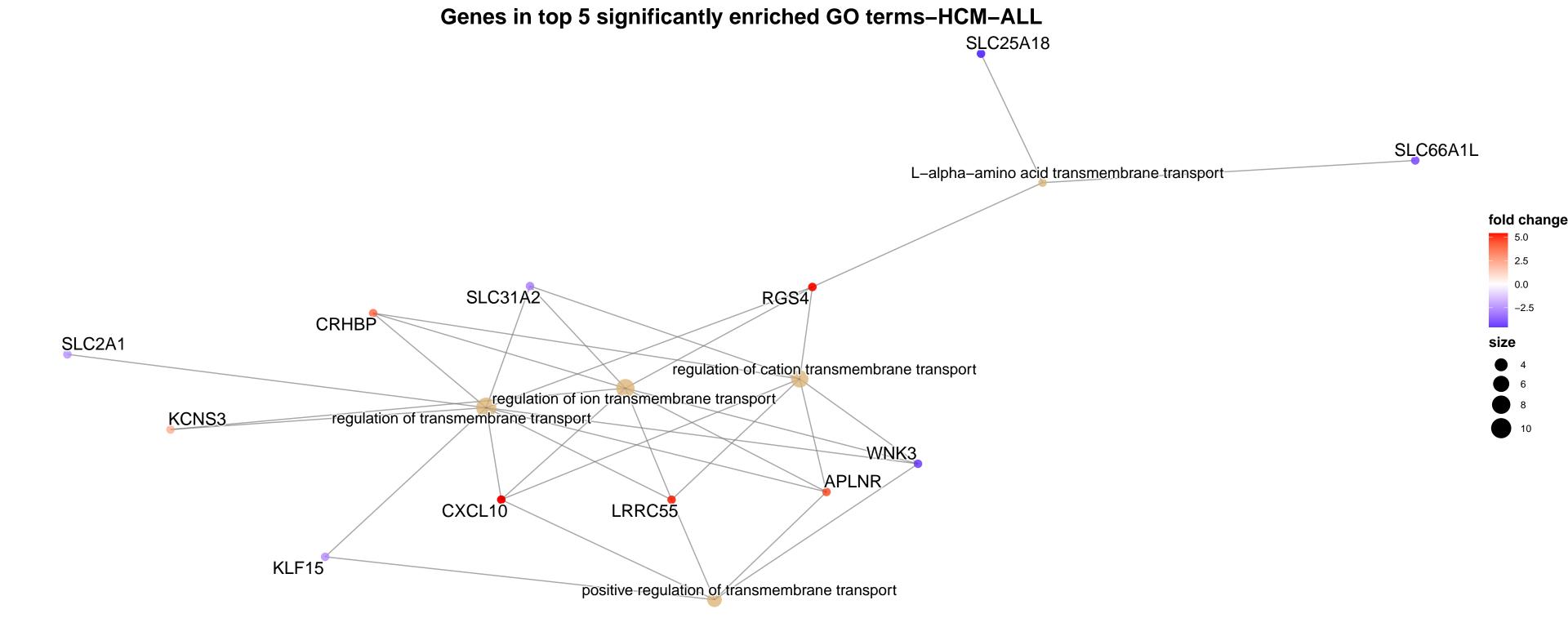


size

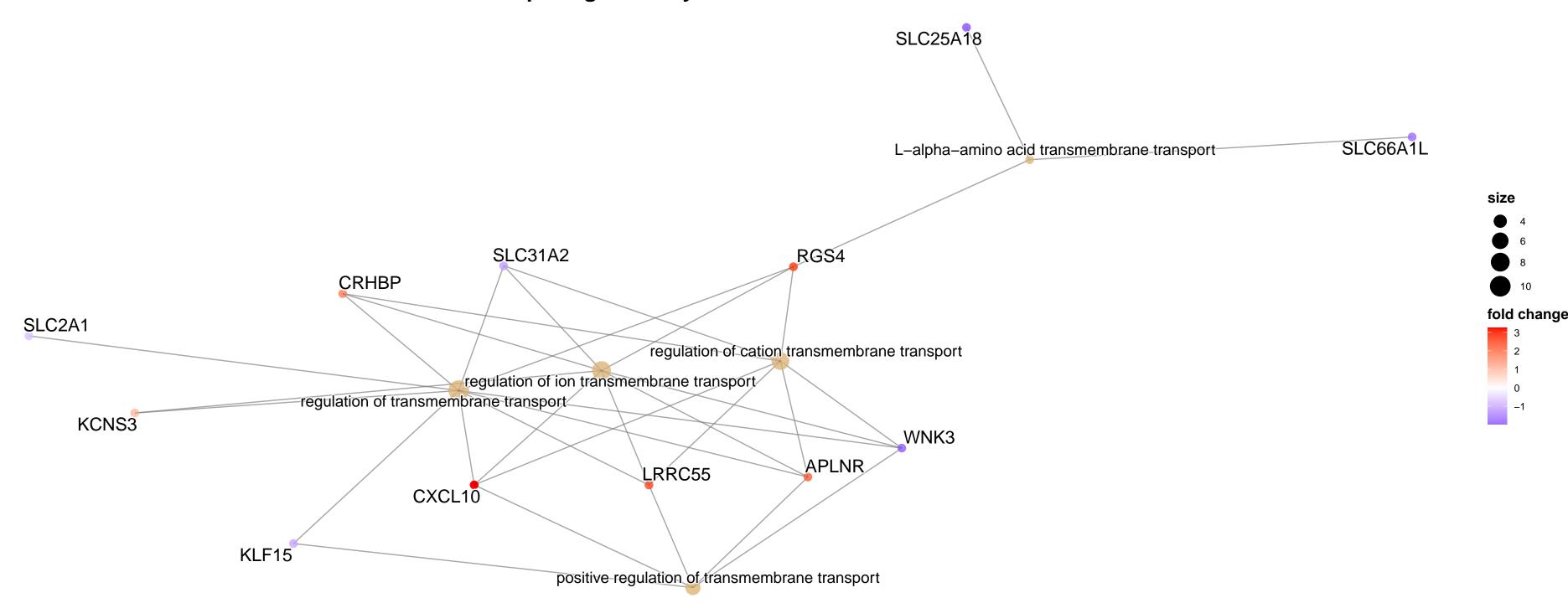
fold change

# Genes in top 5 significantly enriched GO terms-DCM-ALL

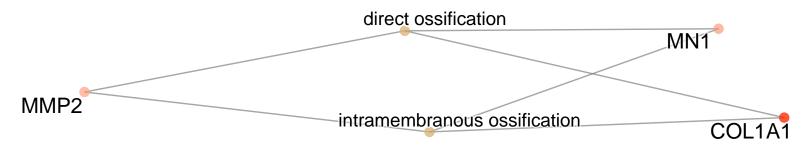


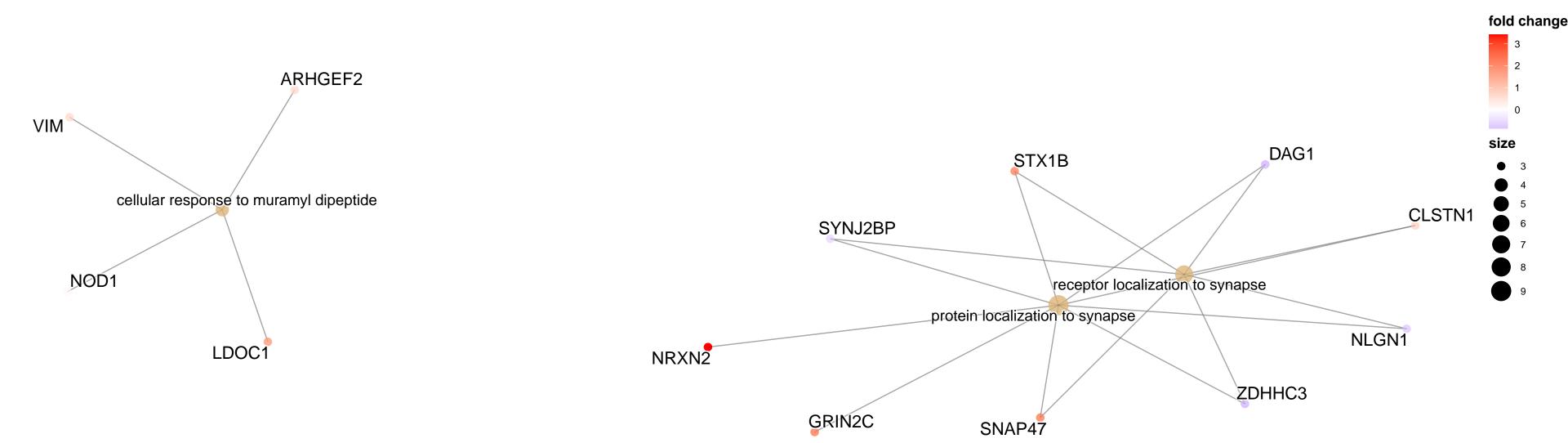


# Genes in top 5 significantly enriched GO terms-PPCM-ALL

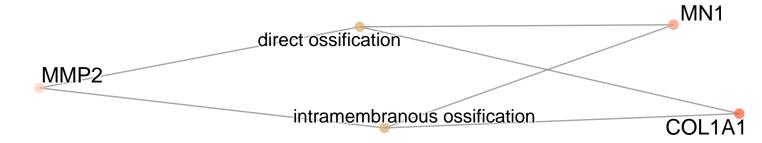


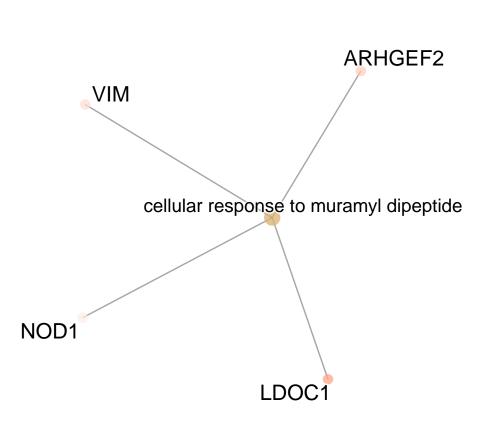
#### Genes in top 5 significantly enriched GO terms-DCM-BP

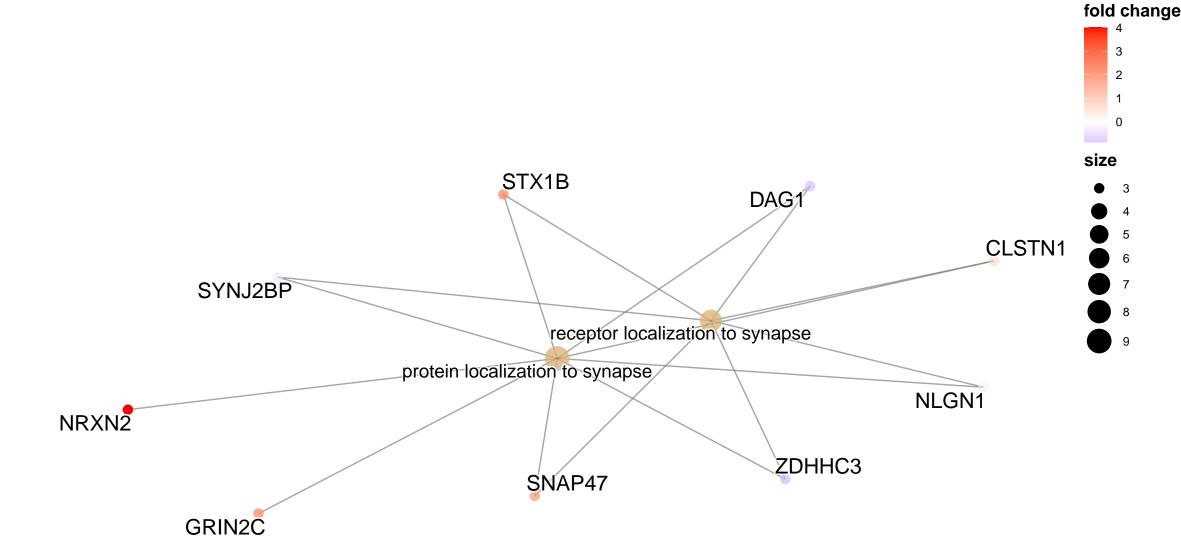




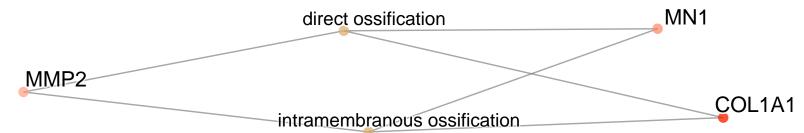
#### Genes in top 5 significantly enriched GO terms-HCM-BP

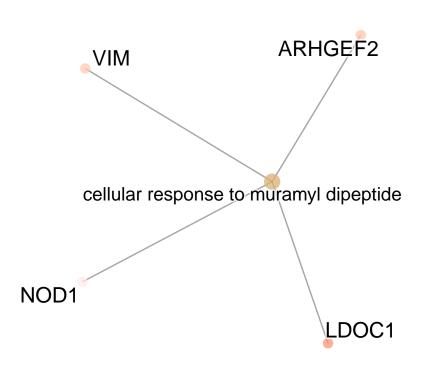


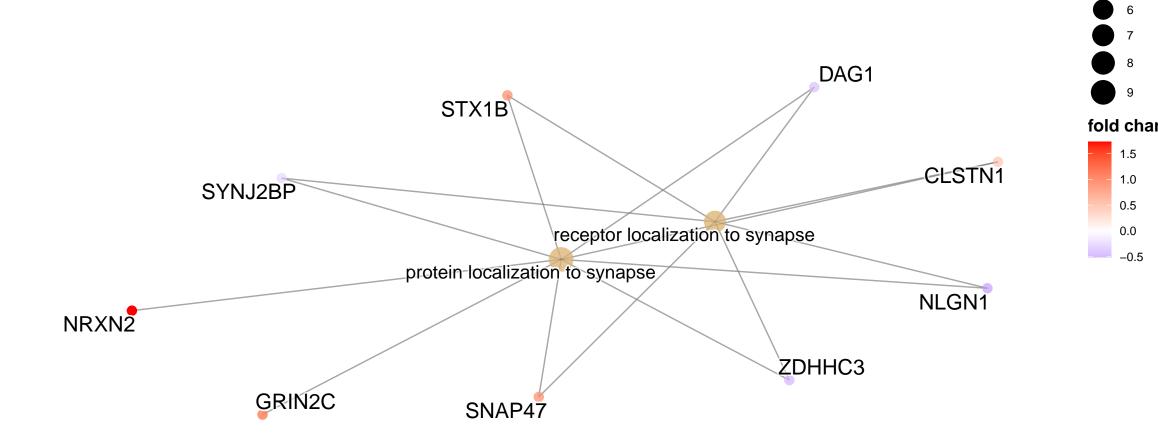




#### Genes in top 5 significantly enriched GO terms-PPCM-BP







size

fold change

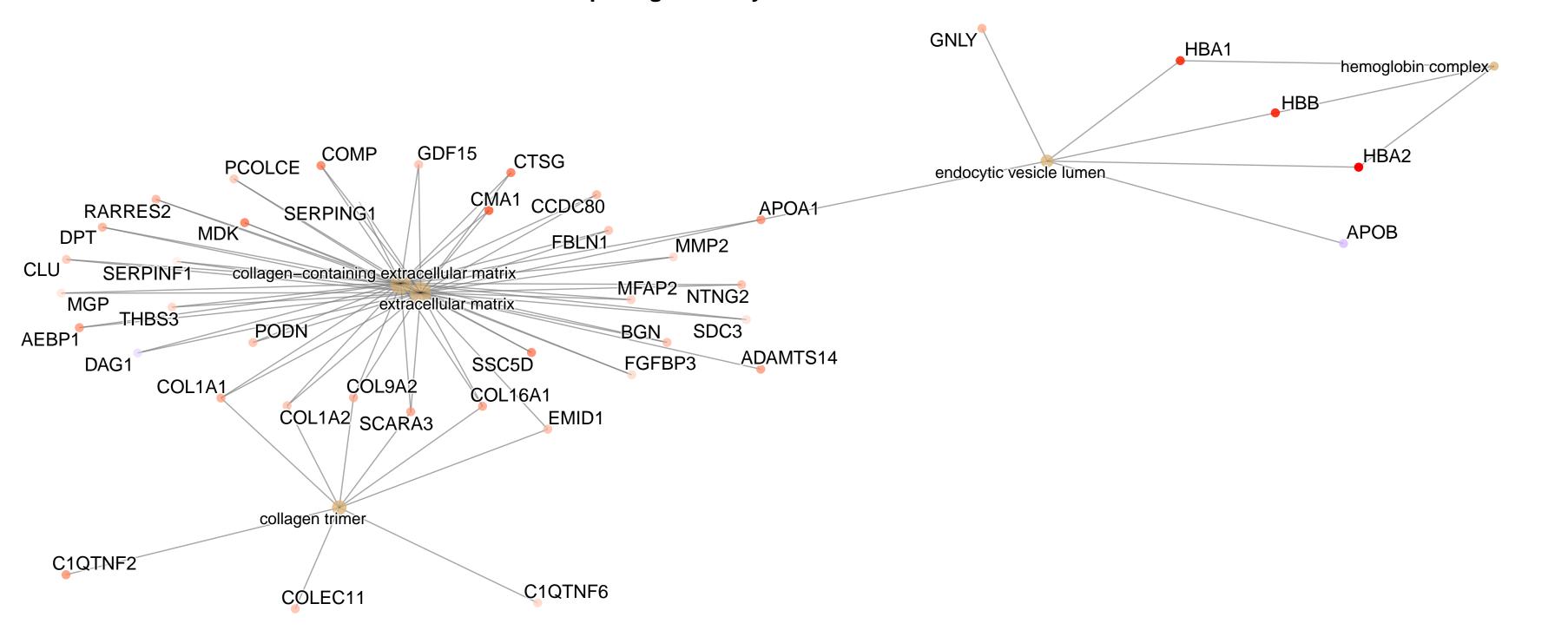
1.5

1.0

0.5

0.0

#### Genes in top 5 significantly enriched GO terms-DCM-CC



size

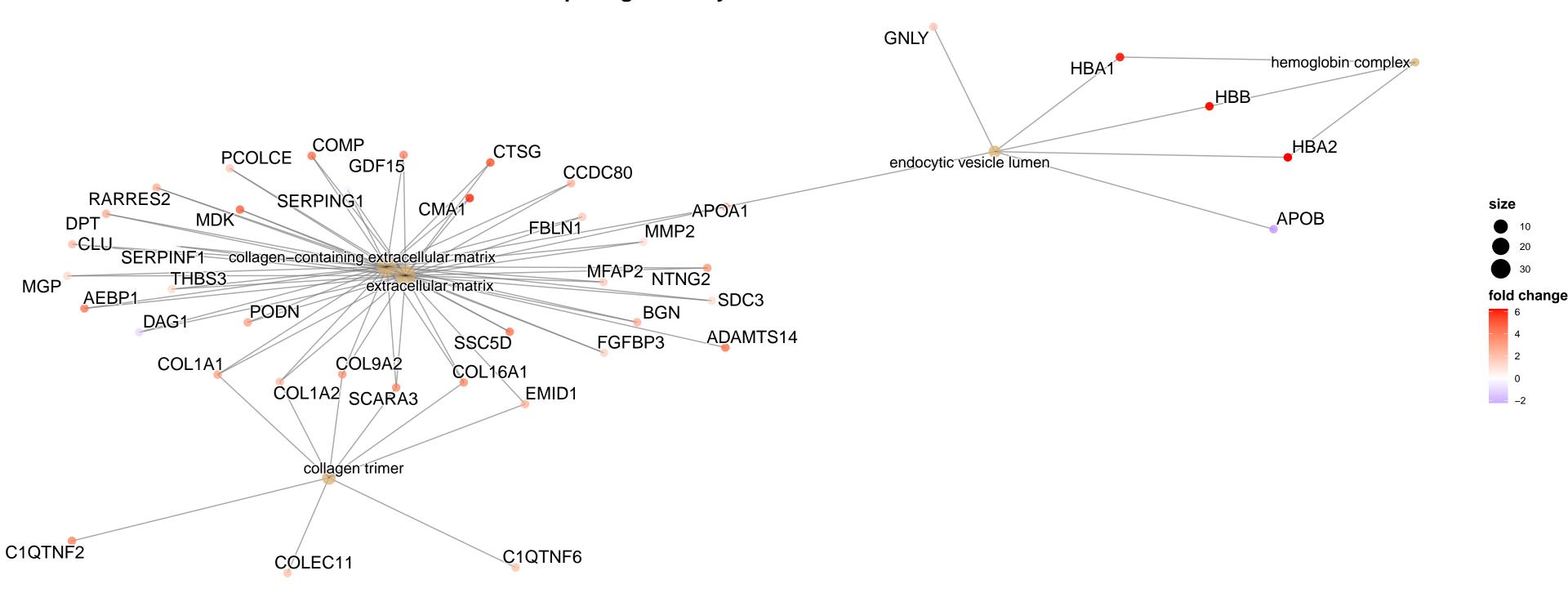
fold change

5.0

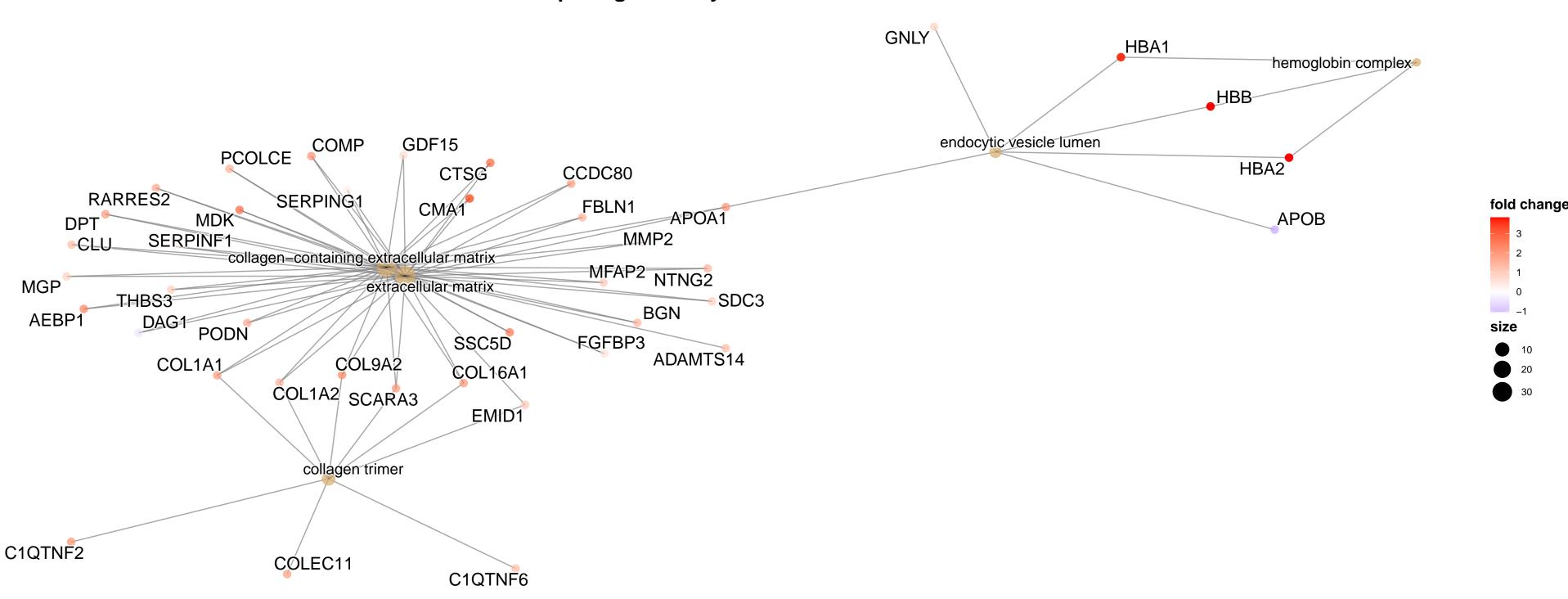
2.5

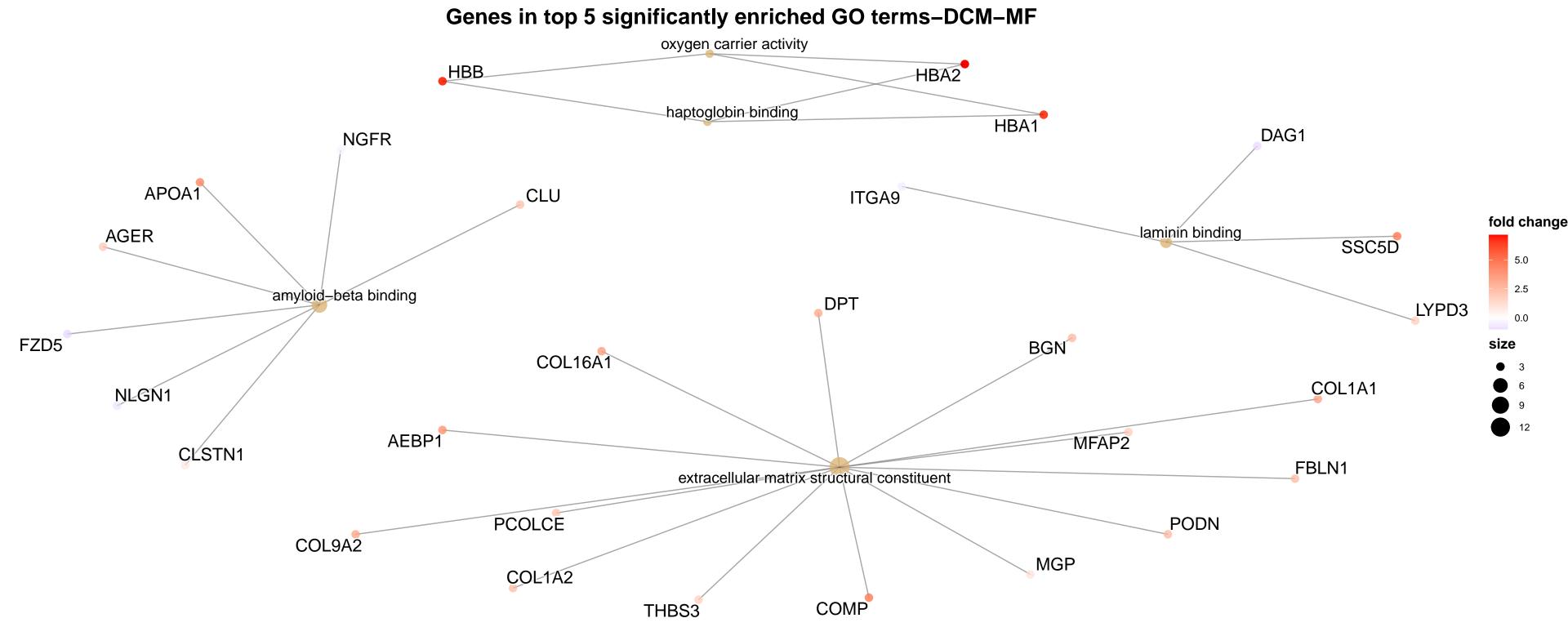
0.0

#### Genes in top 5 significantly enriched GO terms-HCM-CC

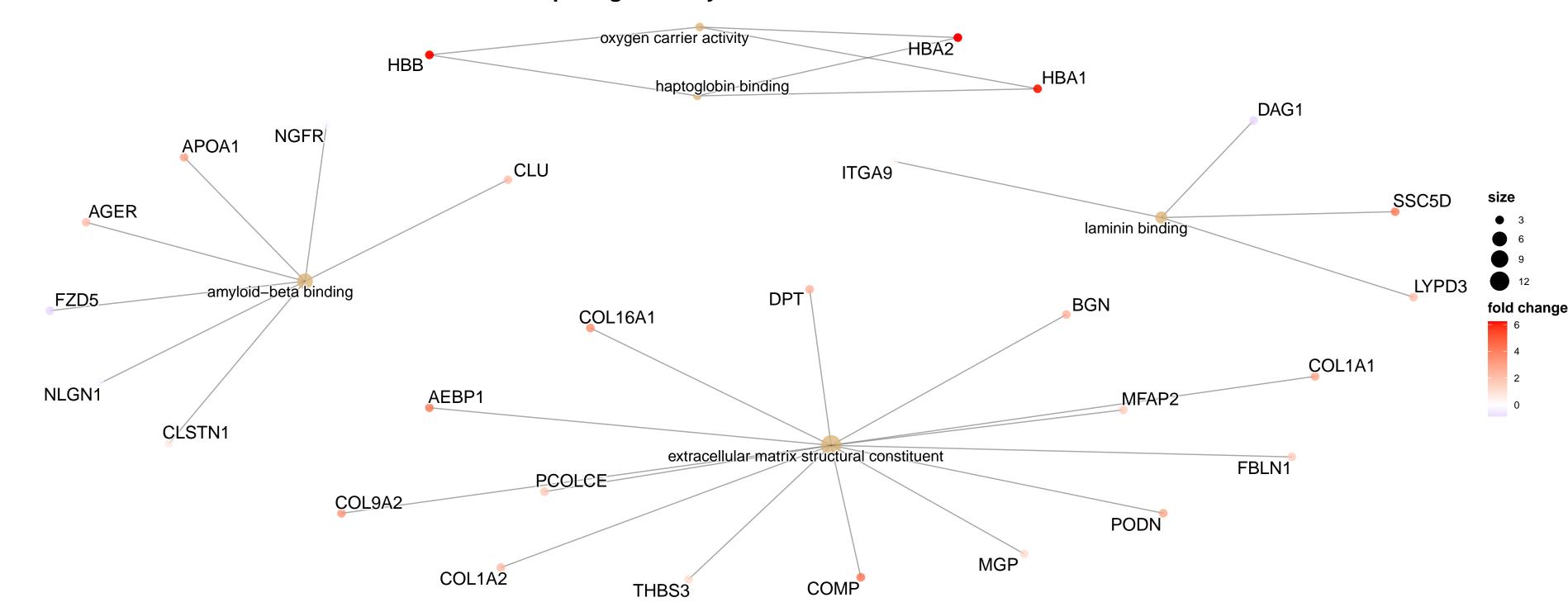


#### Genes in top 5 significantly enriched GO terms-PPCM-CC

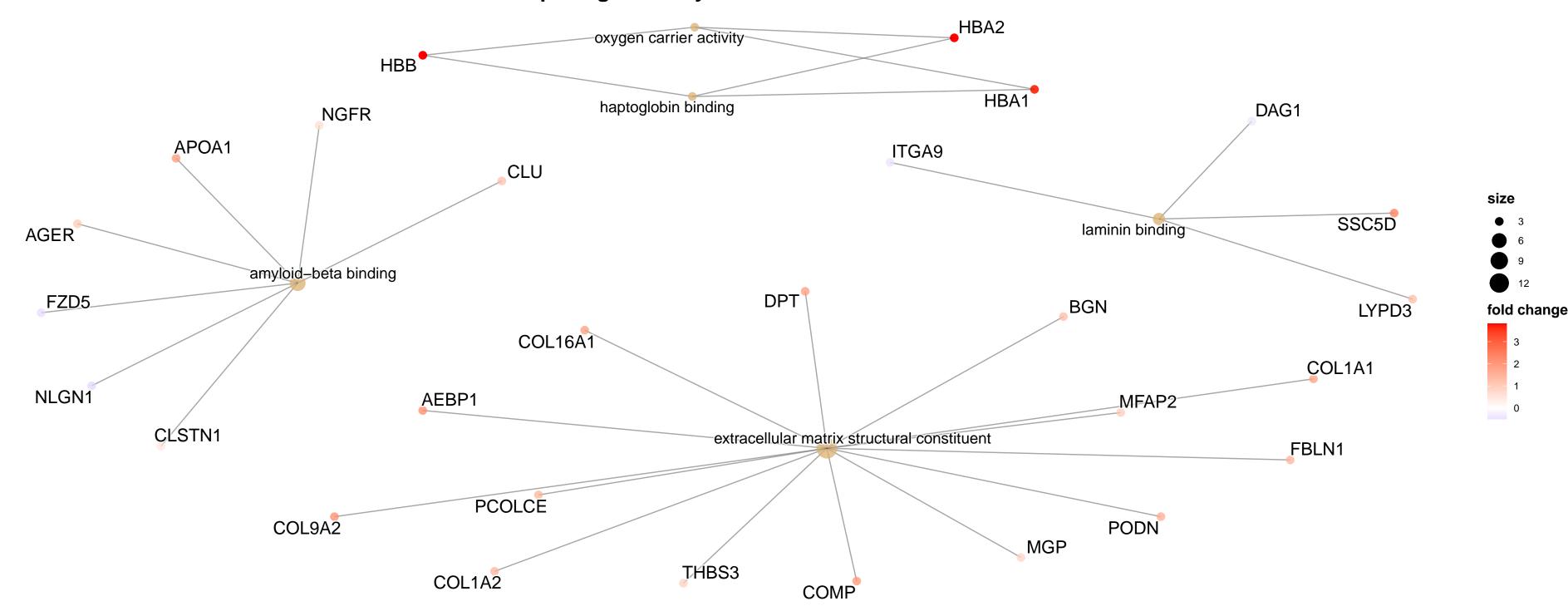




#### Genes in top 5 significantly enriched GO terms-HCM-MF



#### Genes in top 5 significantly enriched GO terms-PPCM-MF



#### Genes in top 5 significantly enriched GO terms-DCM-ALL

GRIN2C

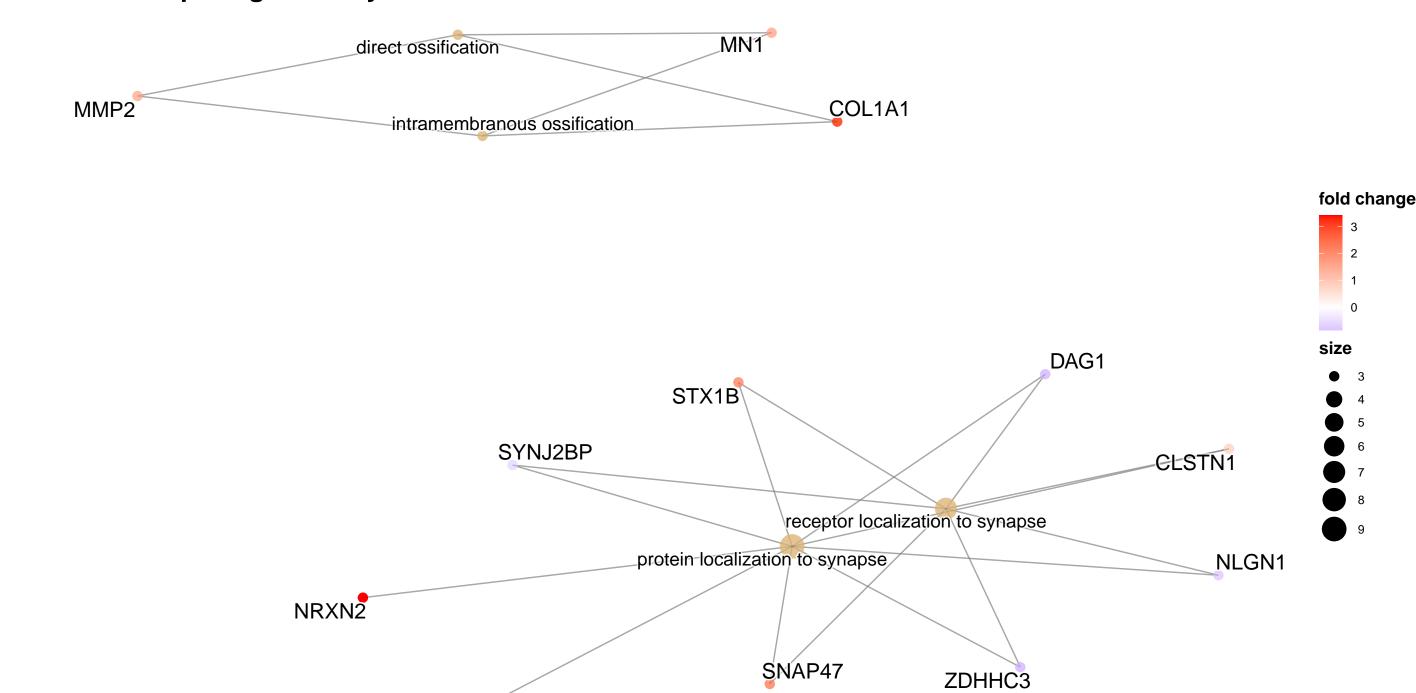
ARHGEF2

cellular response to muramyl dipeptide

LDOC1

VIM

NOD1



#### Genes in top 5 significantly enriched GO terms-HCM-ALL

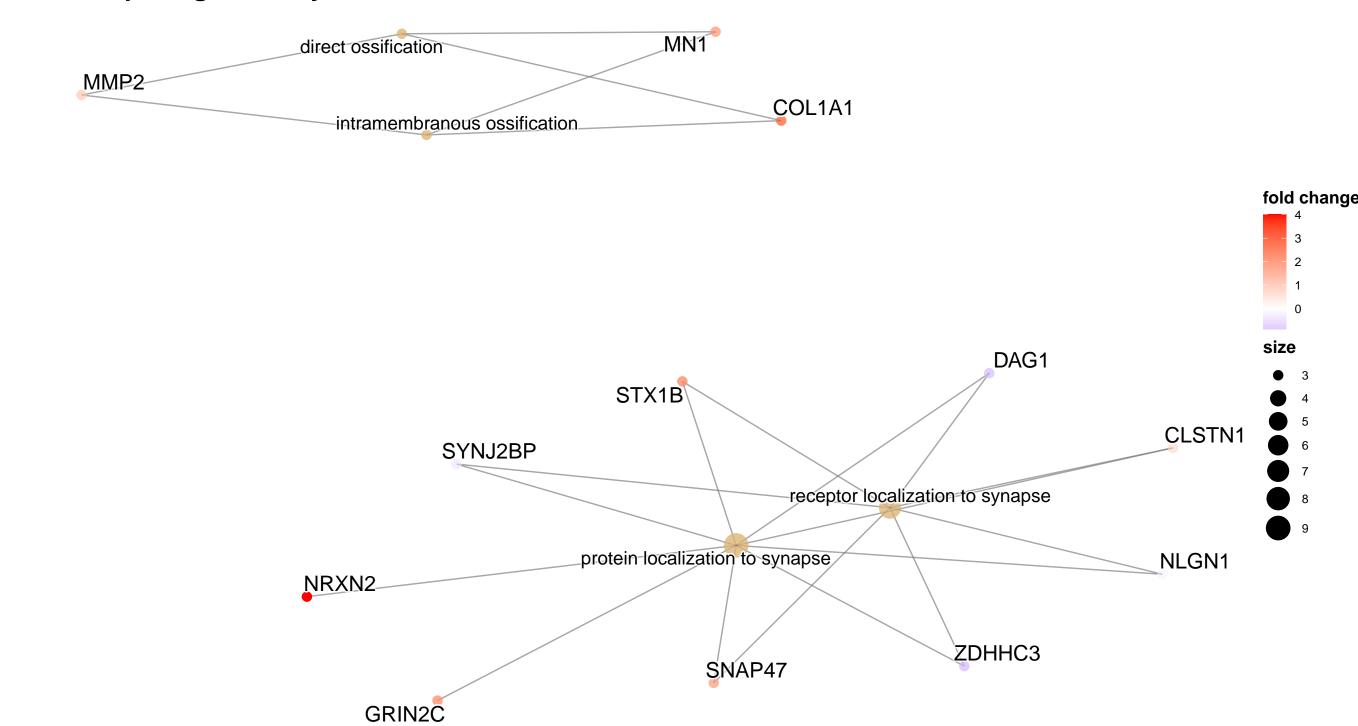
ARHGEF2

cellular response to muramyl dipeptide

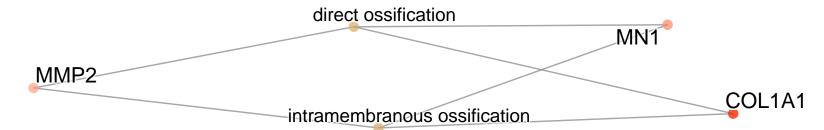
LDOC1

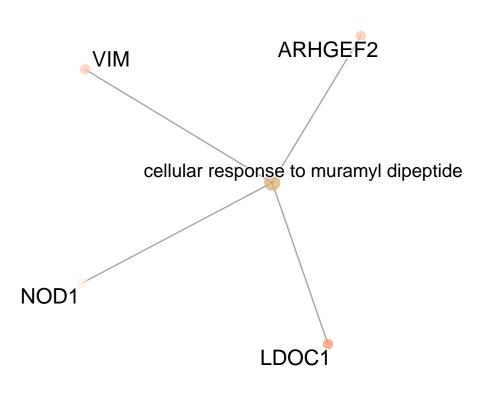
VIM

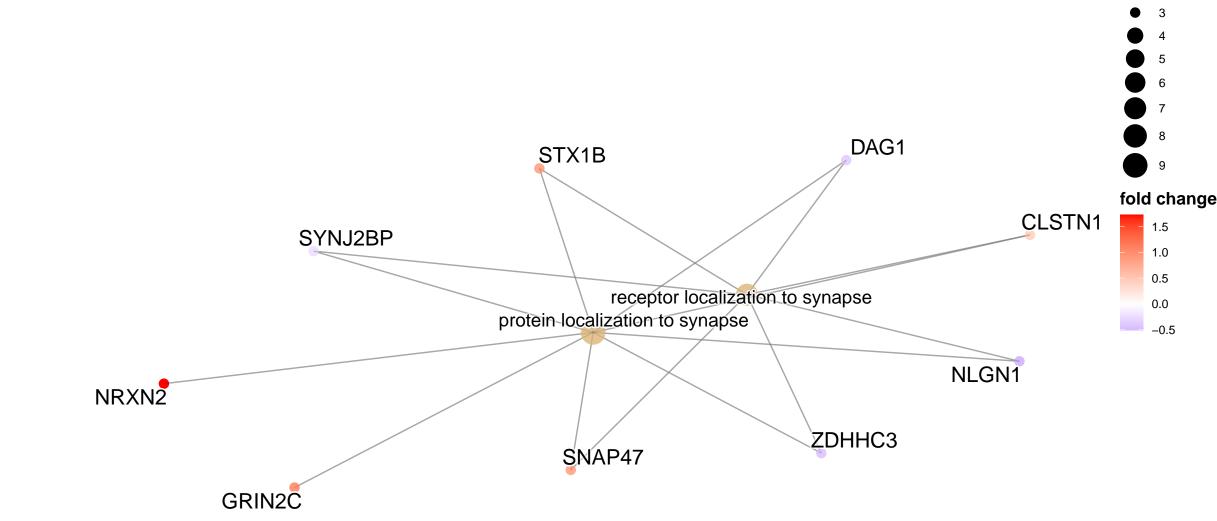
NOD1



#### Genes in top 5 significantly enriched GO terms-PPCM-ALL

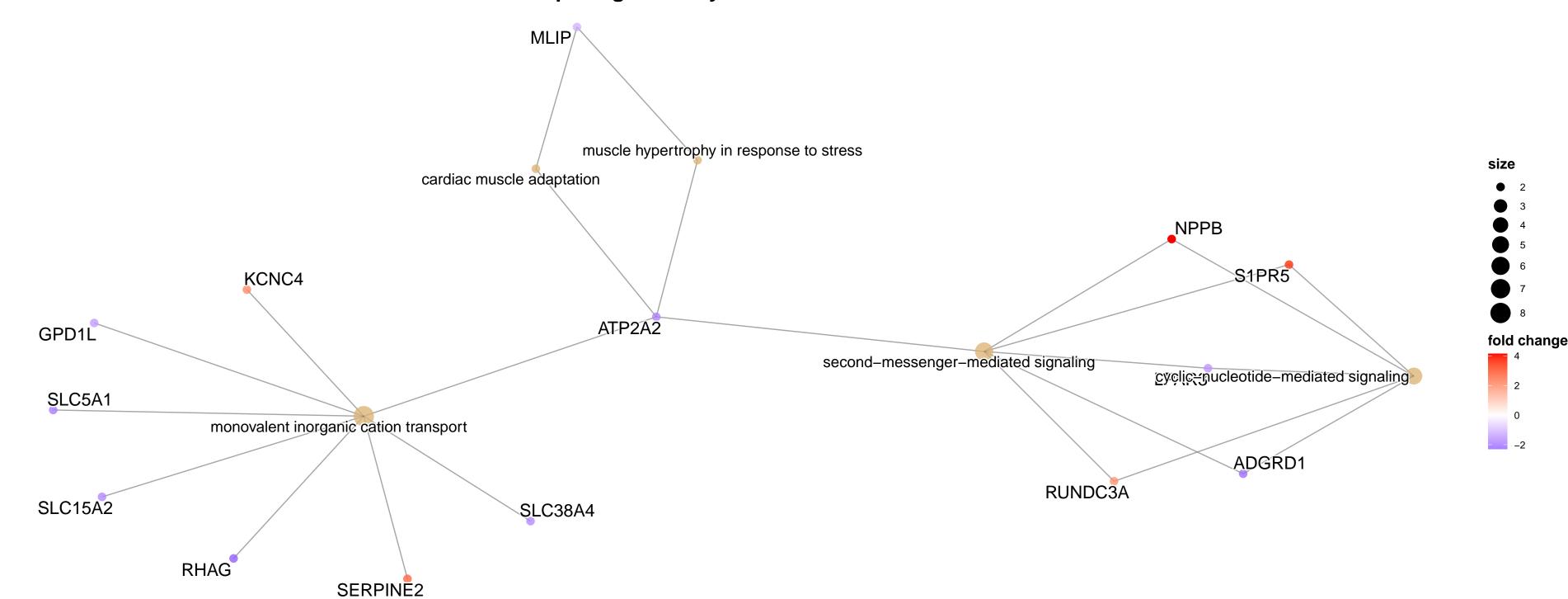




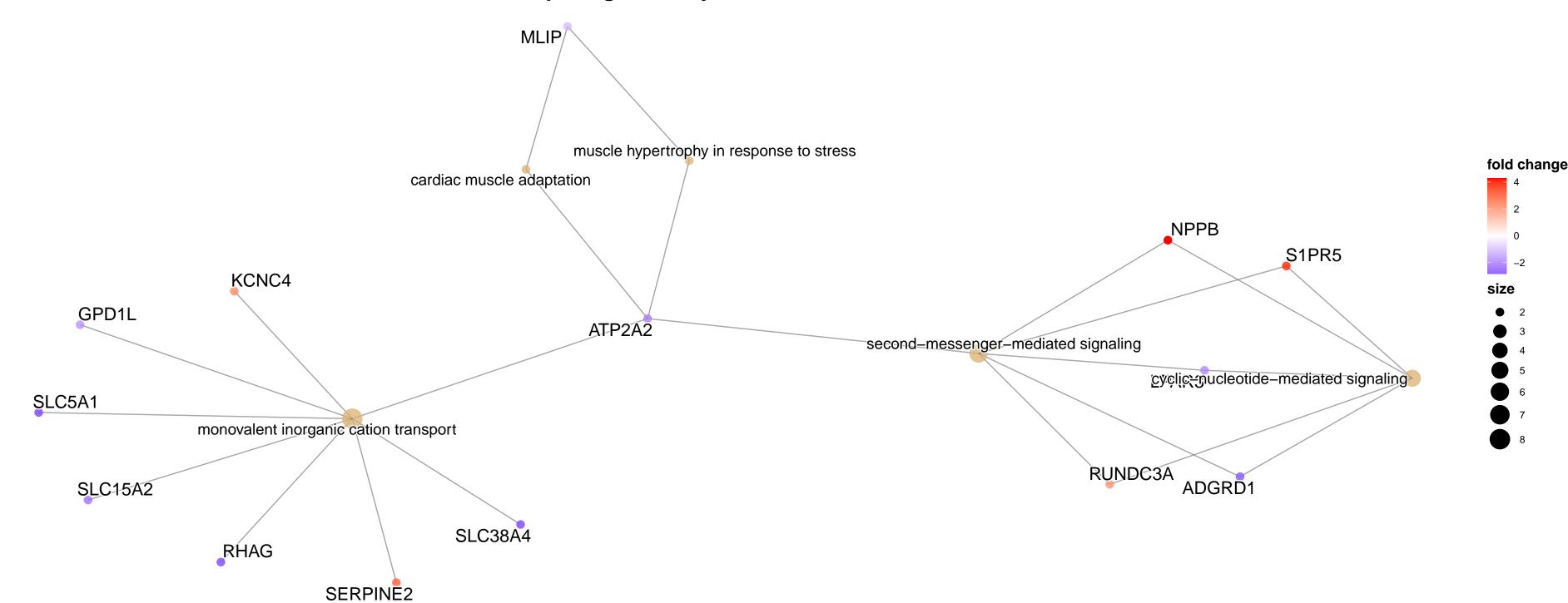


size

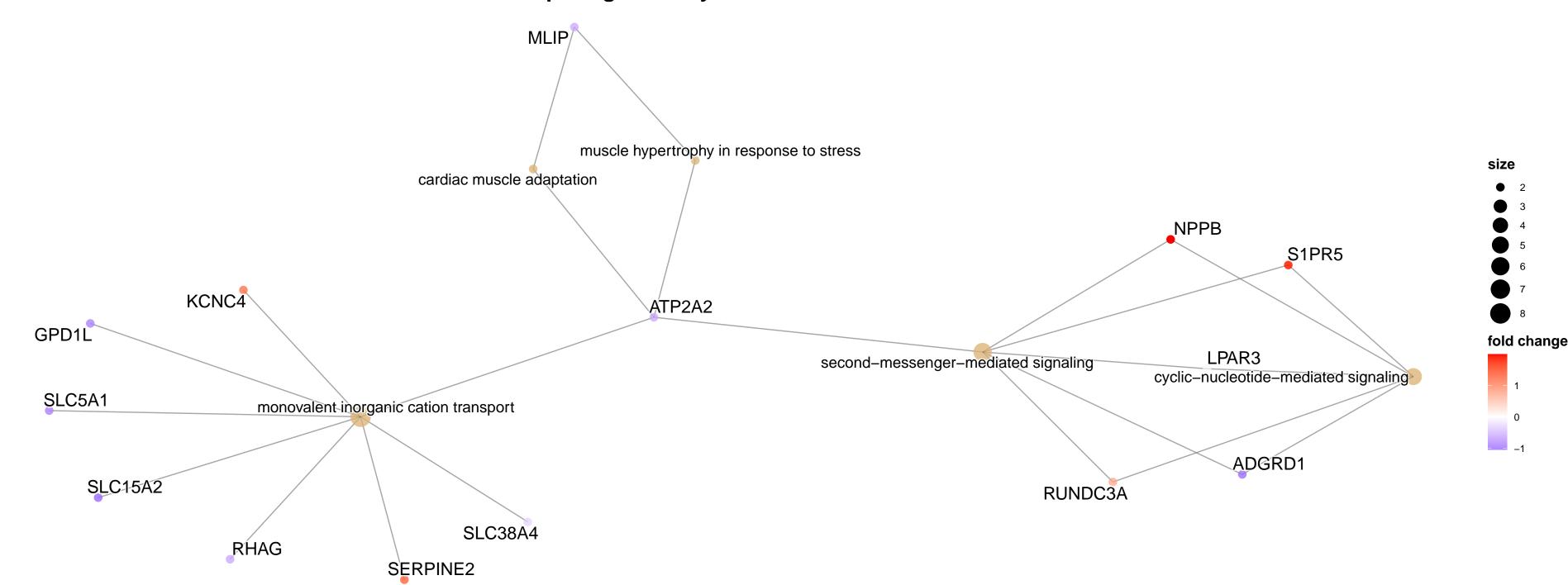
#### Genes in top 5 significantly enriched GO terms-DCM-BP



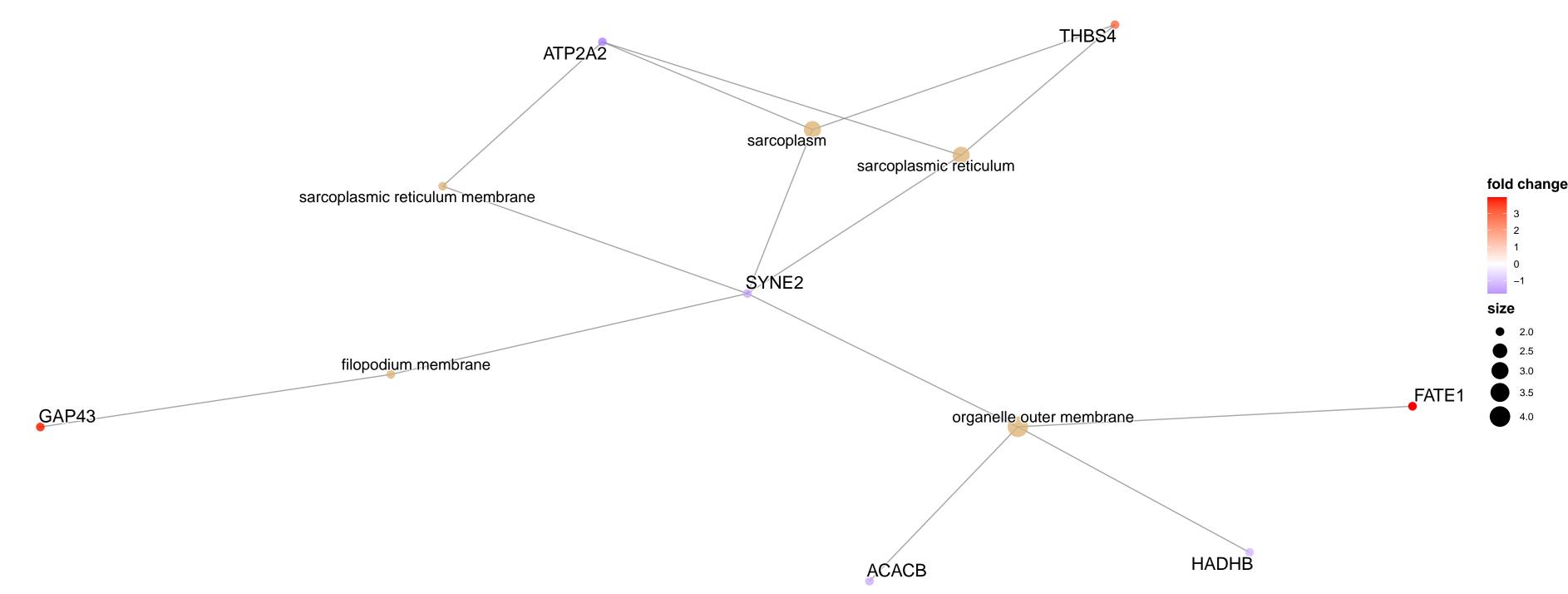
# Genes in top 5 significantly enriched GO terms-HCM-BP



#### Genes in top 5 significantly enriched GO terms-PPCM-BP

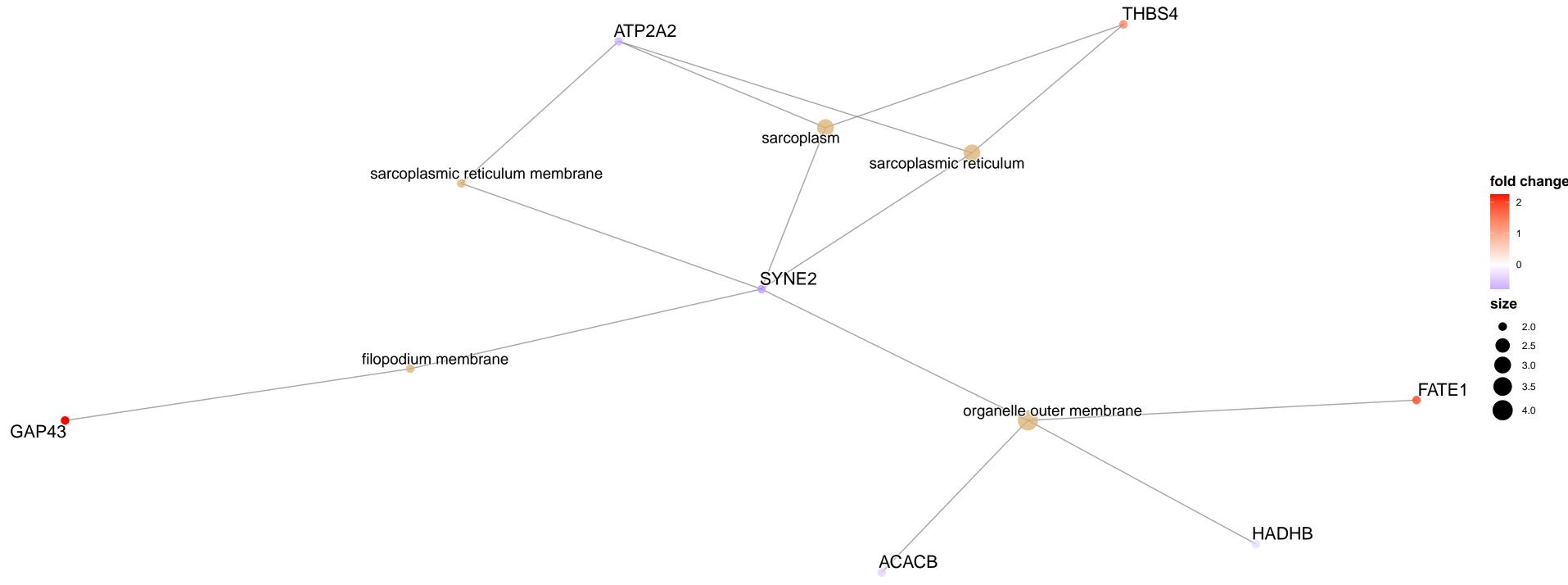


# Genes in top 5 significantly enriched GO terms-DCM-CC



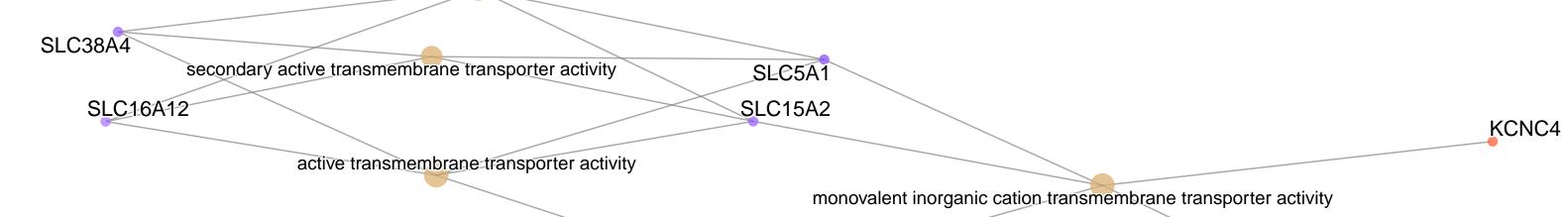
# Genes in top 5 significantly enriched GO terms-HCM-CC THBS4 ATP2A2 sarcoplasm sarcoplasmic reticulum fold change sarcoplasmic reticulum membrane SYNE2 filopodium membrane FATE1 organelle outer membrane GAP43 HADHB ACACB

# Genes in top 5 significantly enriched GO terms-PPCM-CC



#### Genes in top 5 significantly enriched GO terms-DCM-MF

symporter activity



ATP2A2

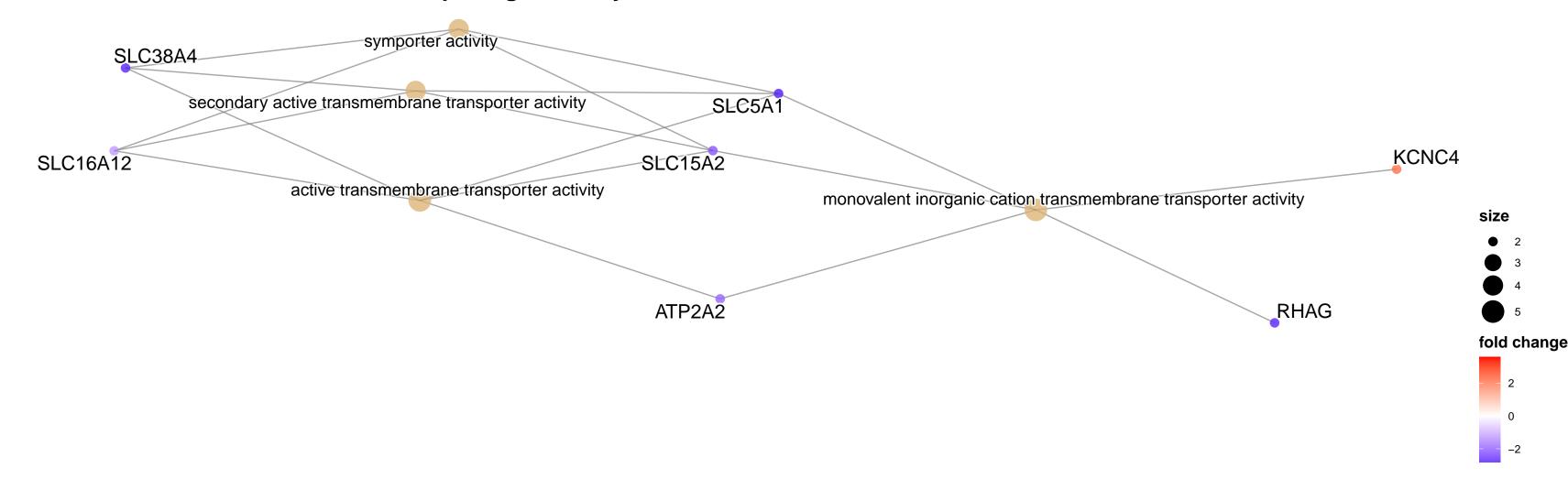
RHAG

fold change

size

LPAR3

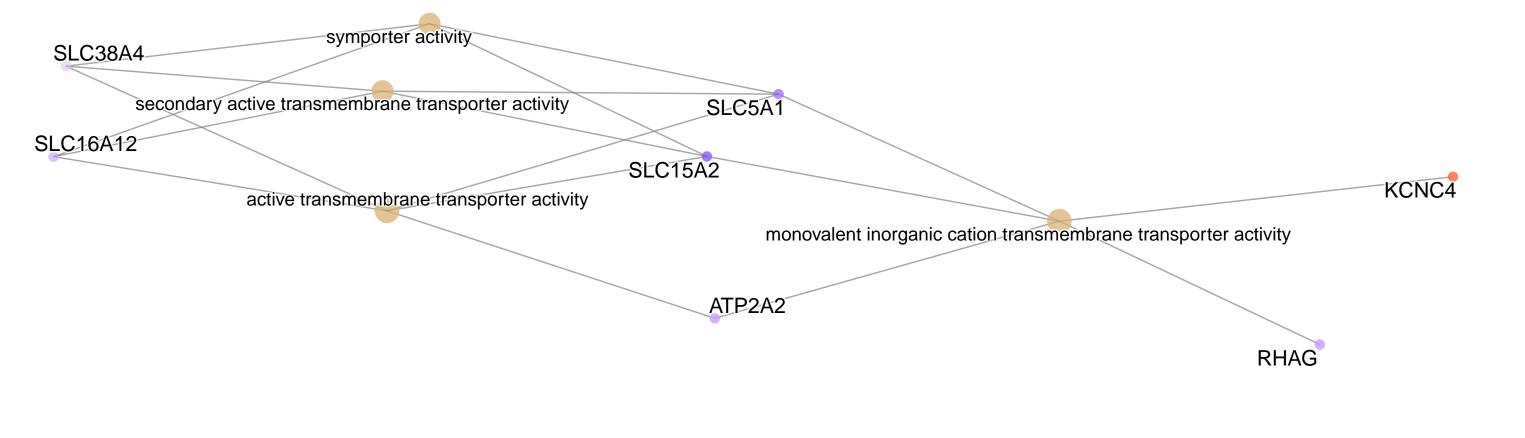
#### Genes in top 5 significantly enriched GO terms-HCM-MF



LPAR3

bioactive lipid receptor activity

#### Genes in top 5 significantly enriched GO terms-PPCM-MF

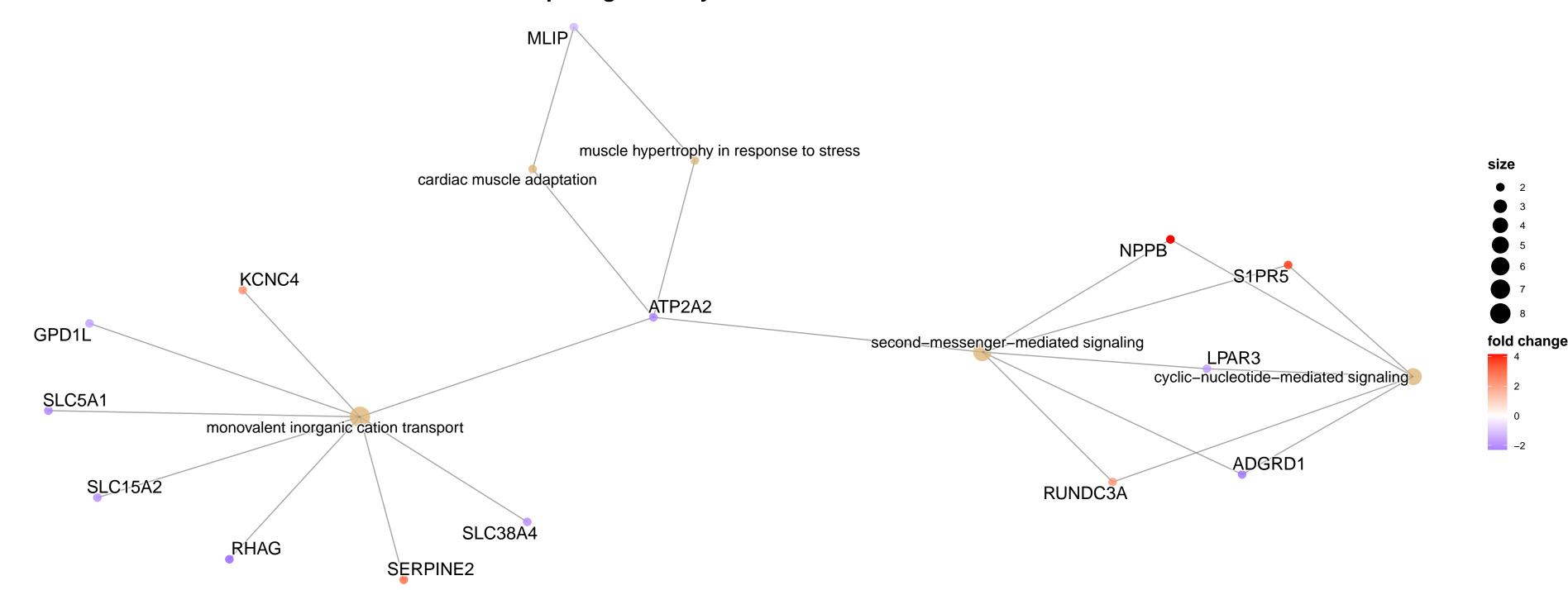


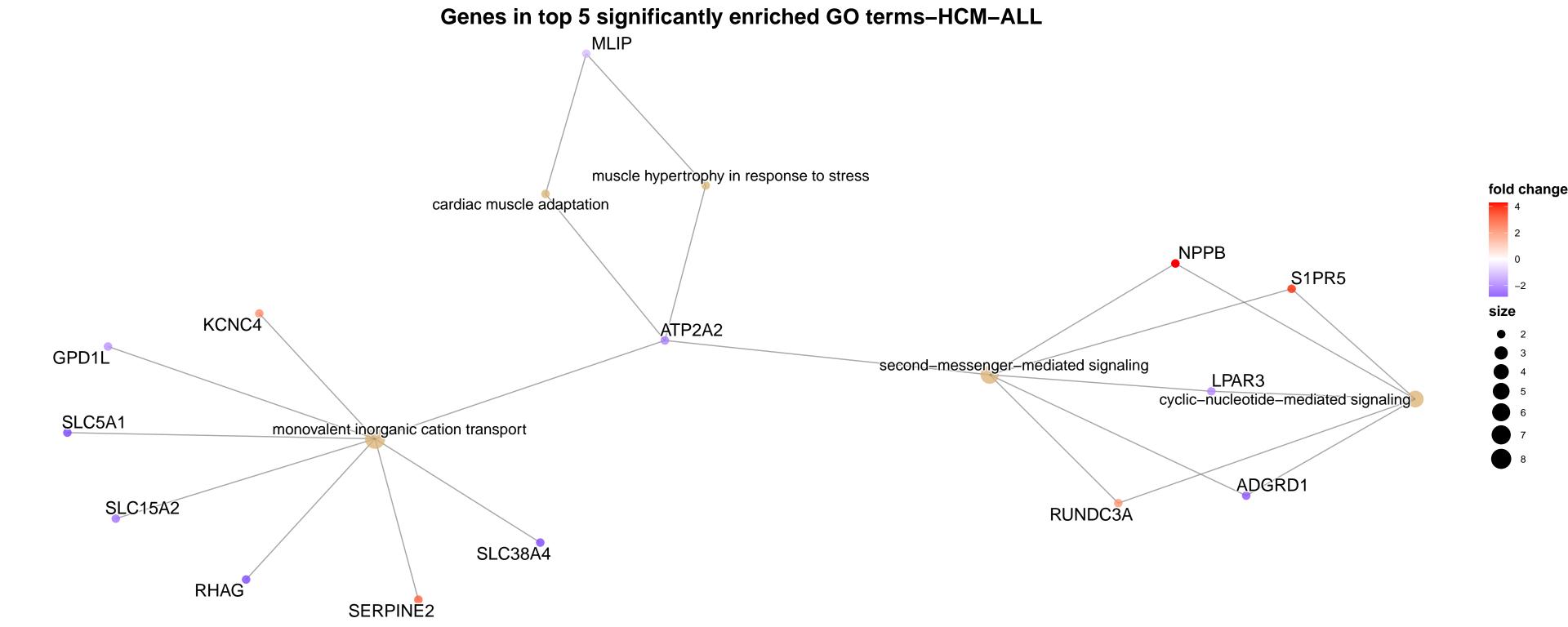
size

fold change

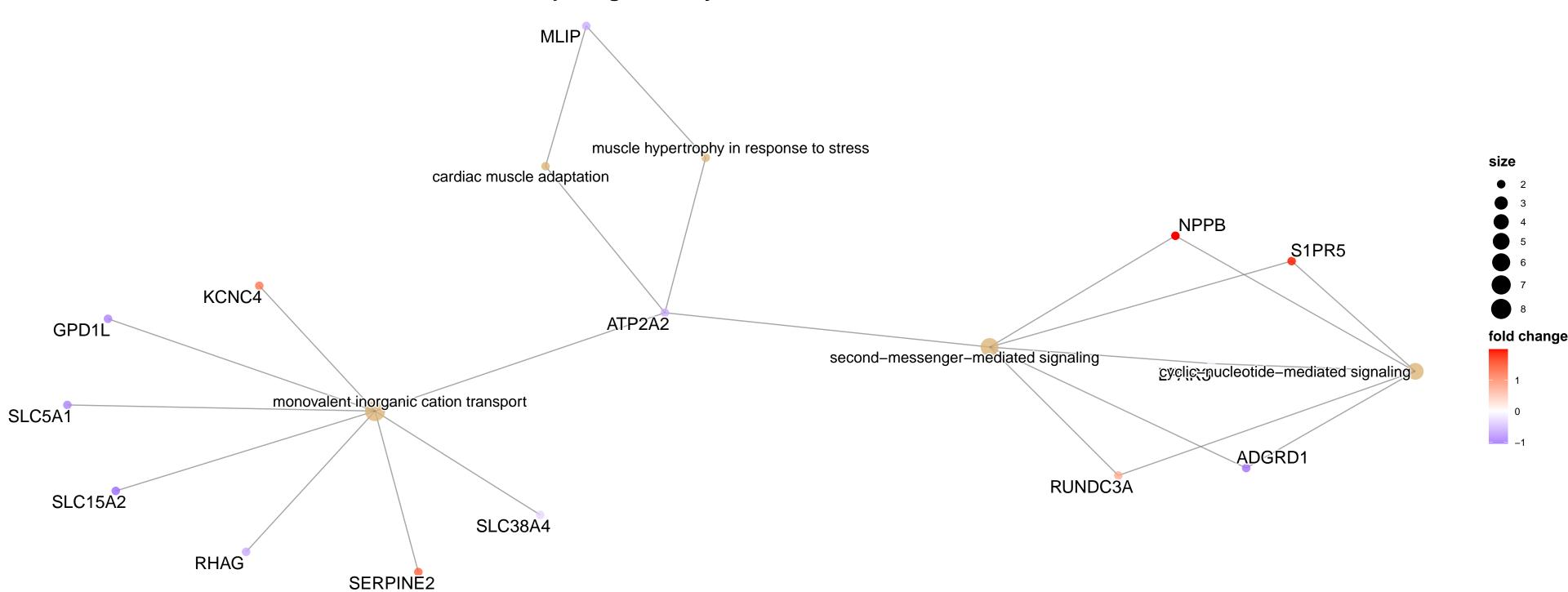
LPAR3

# Genes in top 5 significantly enriched GO terms-DCM-ALL

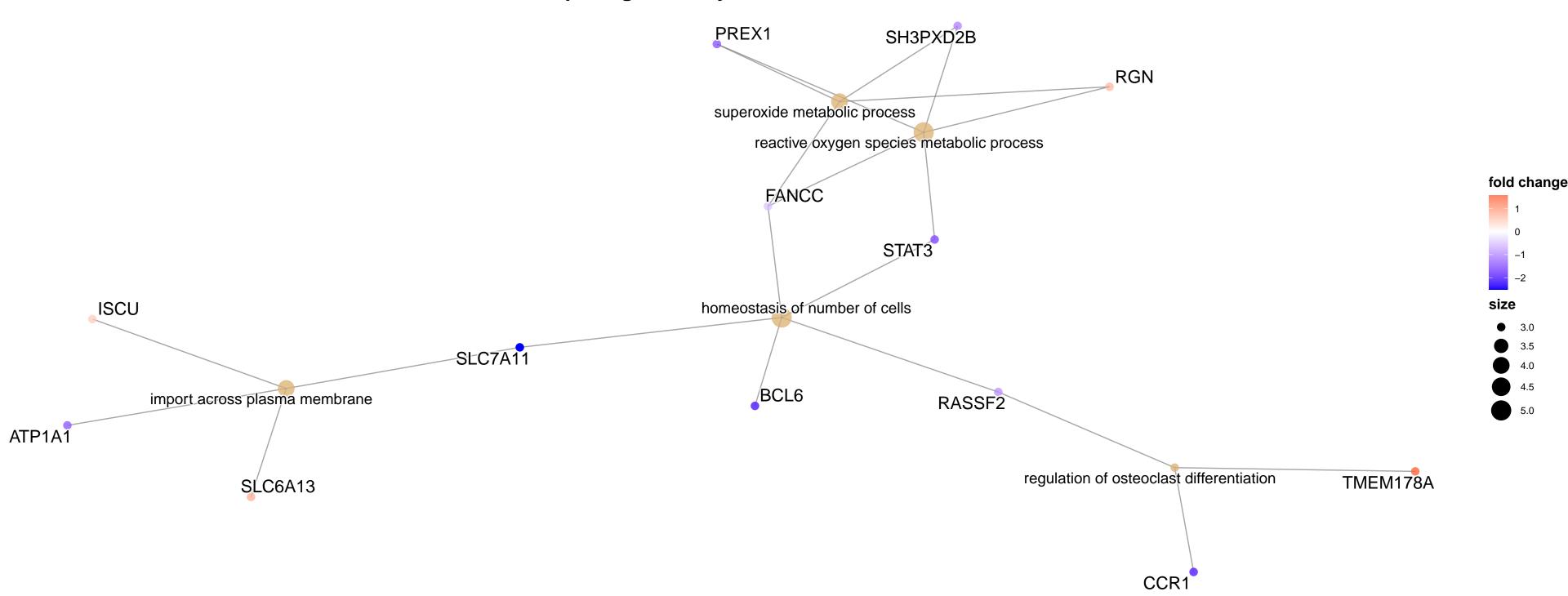




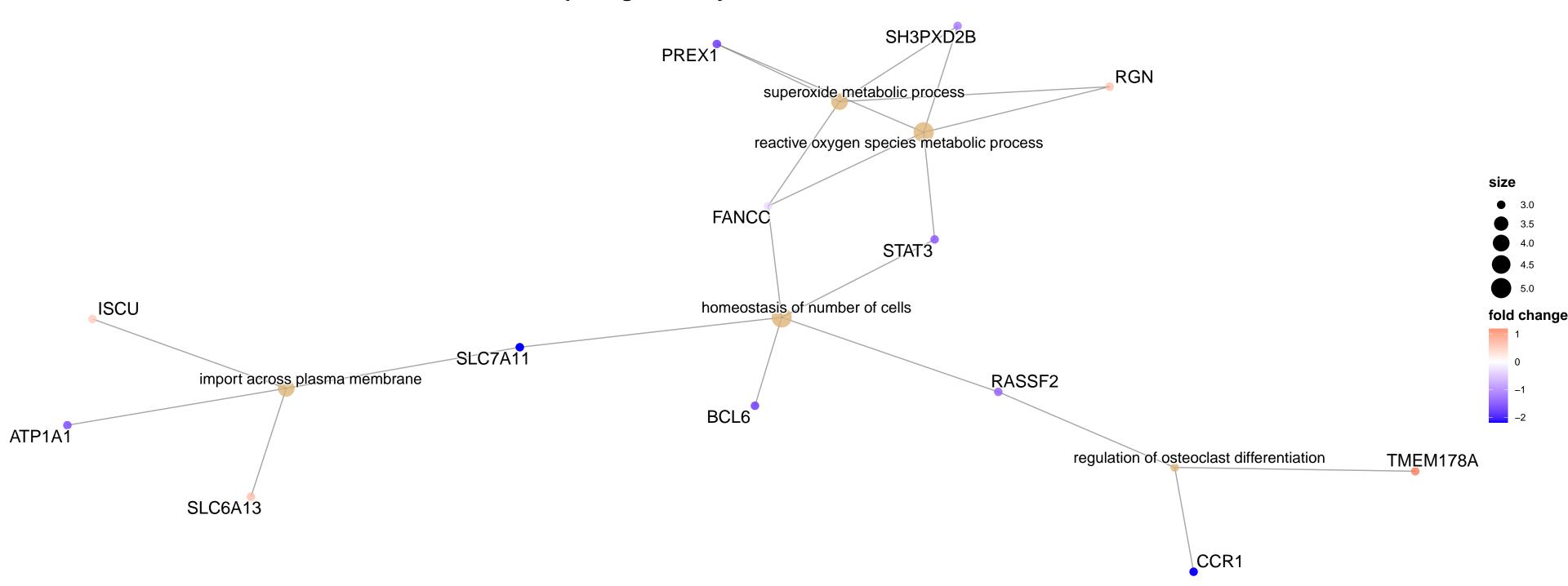
#### Genes in top 5 significantly enriched GO terms-PPCM-ALL

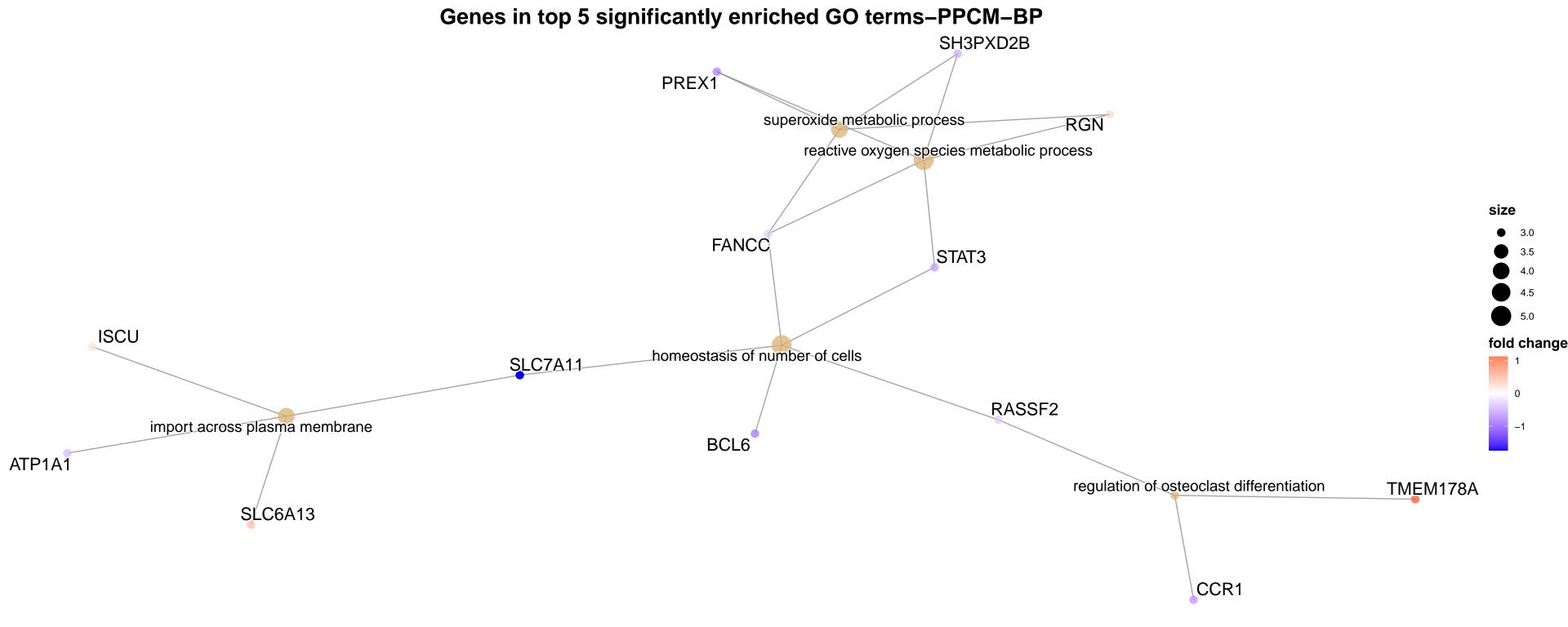


#### Genes in top 5 significantly enriched GO terms-DCM-BP

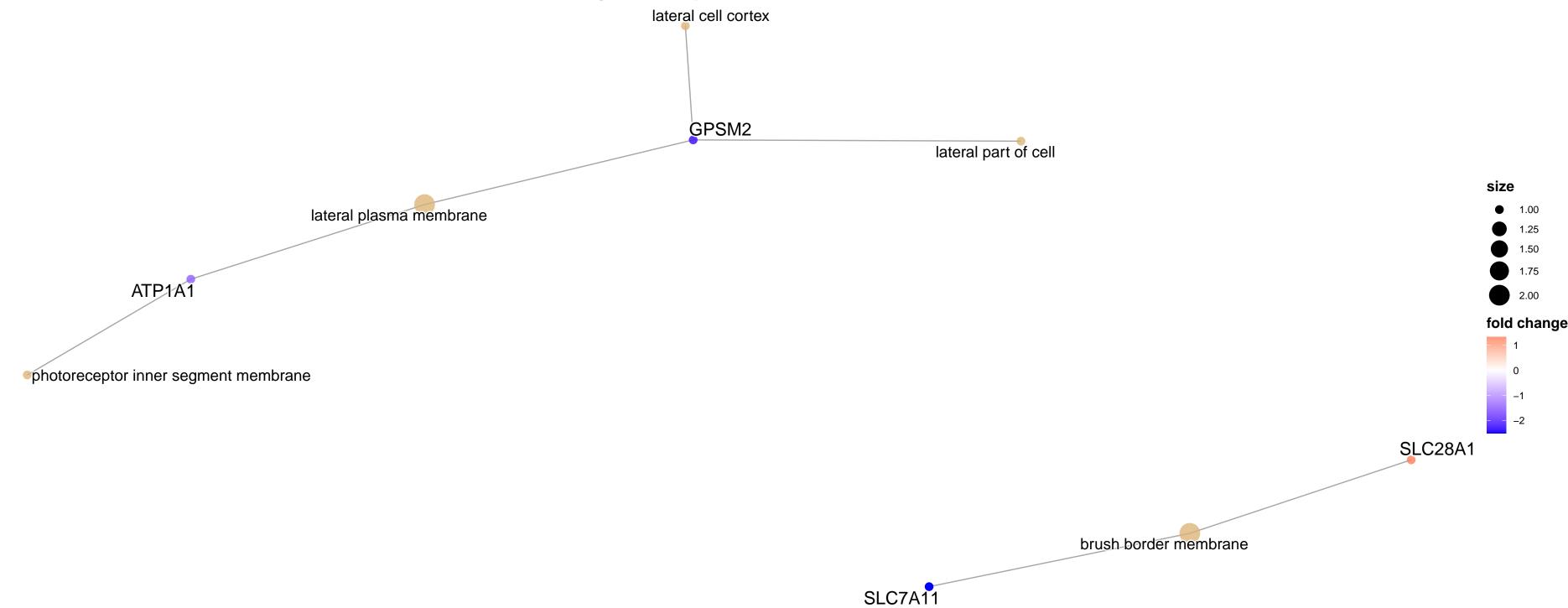


#### Genes in top 5 significantly enriched GO terms-HCM-BP

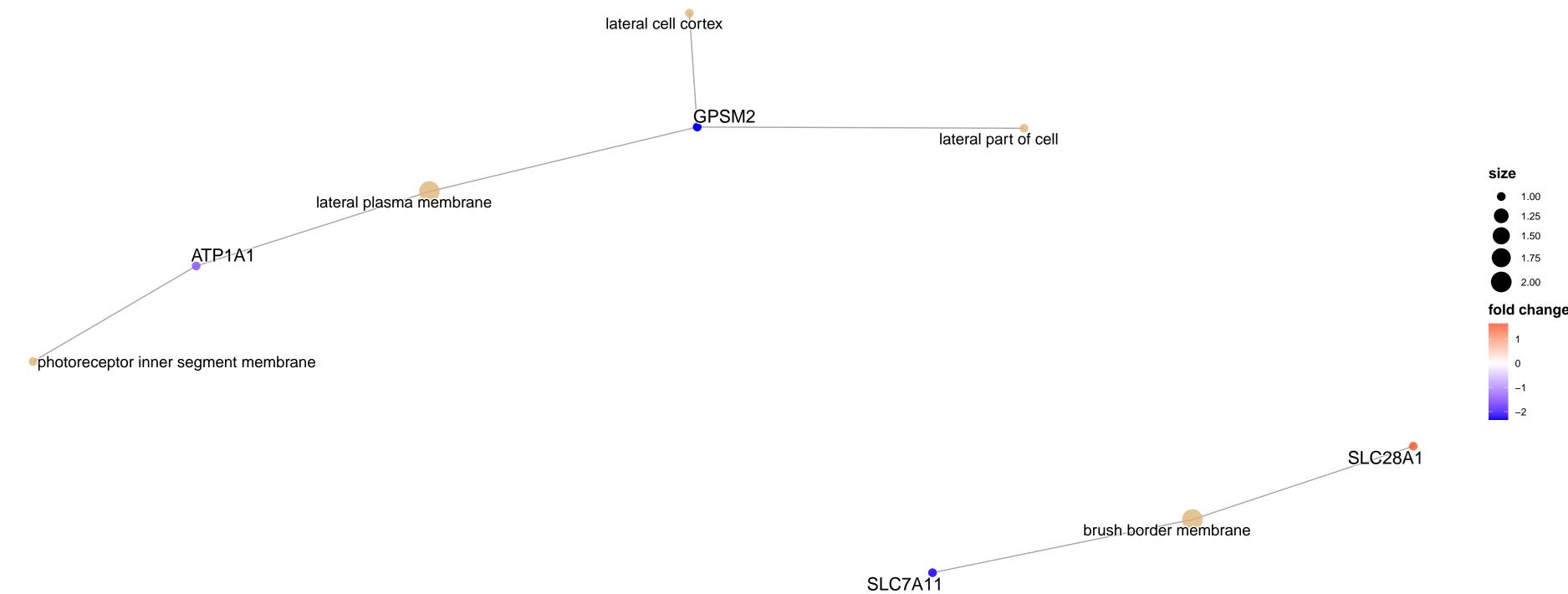




## Genes in top 5 significantly enriched GO terms-DCM-CC

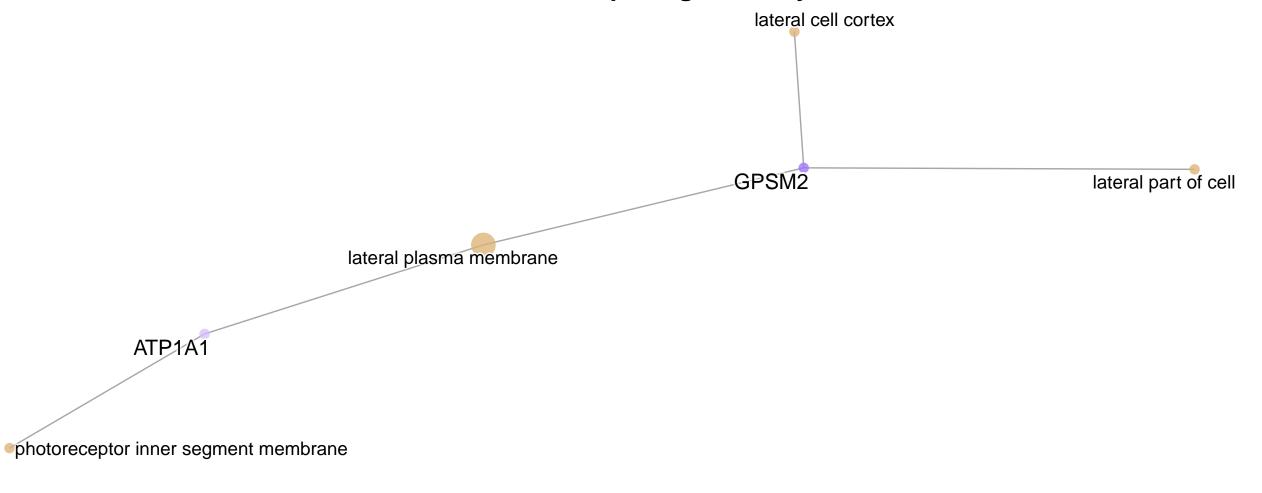


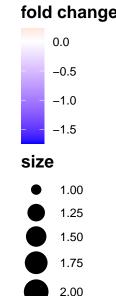
## Genes in top 5 significantly enriched GO terms-HCM-CC

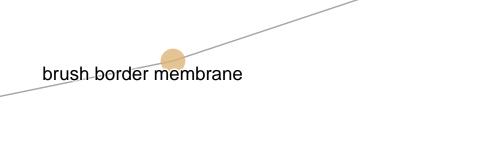


## Genes in top 5 significantly enriched GO terms-PPCM-CC

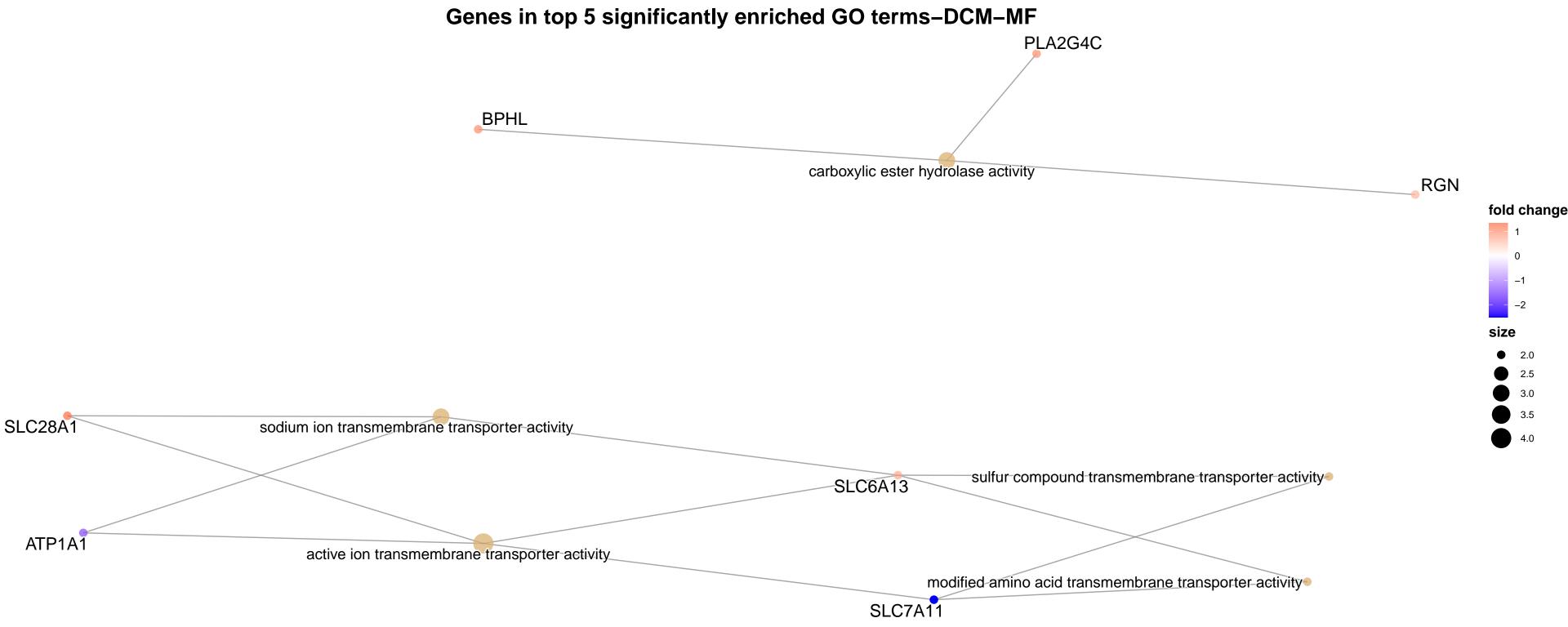
SLC7A11







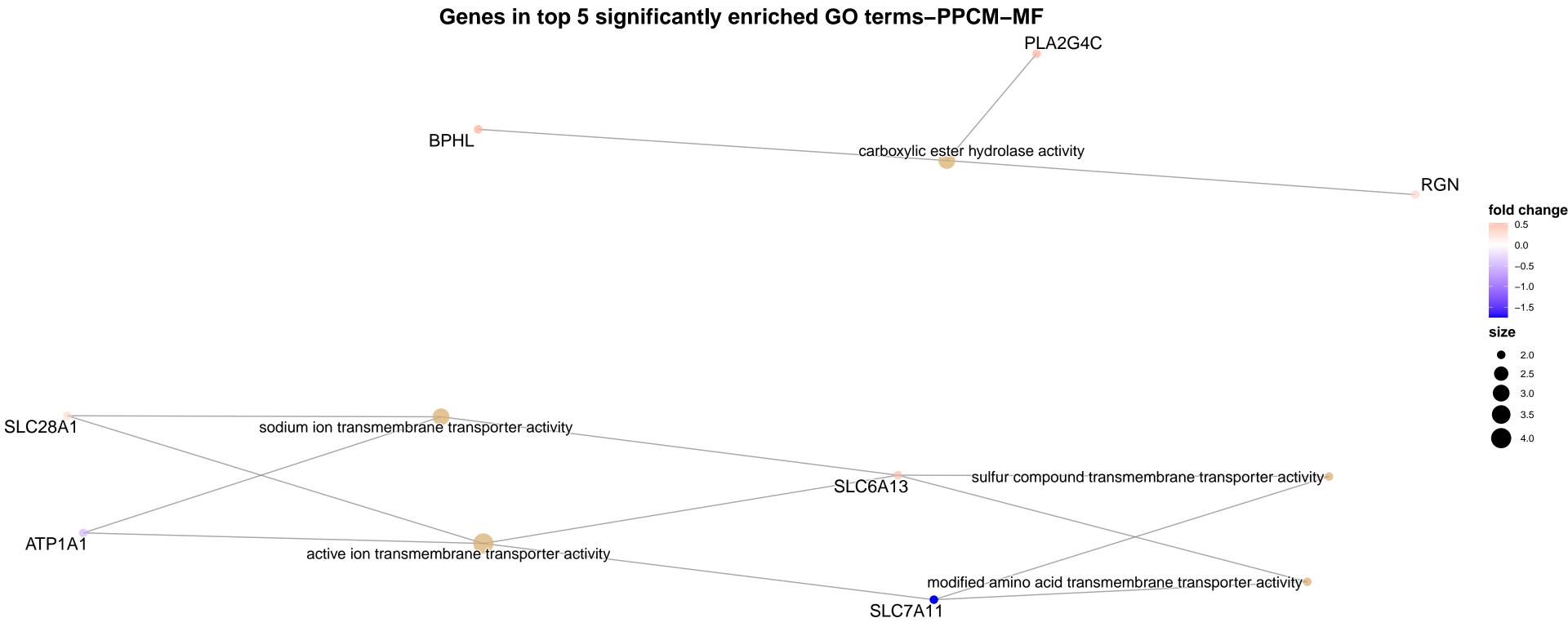
SLC28A1



#### Genes in top 5 significantly enriched GO terms-HCM-MF



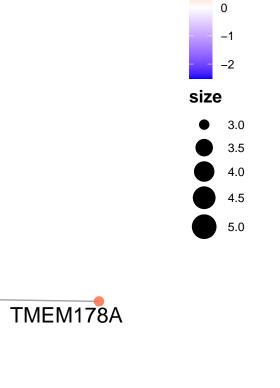
fold change



# Genes in top 5 significantly enriched GO terms-DCM-ALL SH3PXD2B PREX1 RGN superoxide metabolic process reactive oxygen species metabolic process fold change FANCC STAT3 homeostasis of number of cells ISCU SLC7A11 import across plasma membrane RASSF2 BCL6

ATP1A1

SLC6A13



regulation of osteoclast differentiation

CCR1

# Genes in top 5 significantly enriched GO terms-HCM-ALL SH3PXD2B PREX1 RGN superoxide metabolic process reactive oxygen species metabolic process size FANCC STAT3 fold change ISCU homeostasis of number of cells SLC7A11 import across plasma membrane RASSF2 BCL6 ATP1A1 TMEM178A regulation of osteoclast differentiation SLC6A13 CCR1

#### Genes in top 5 significantly enriched GO terms-PPCM-ALL

