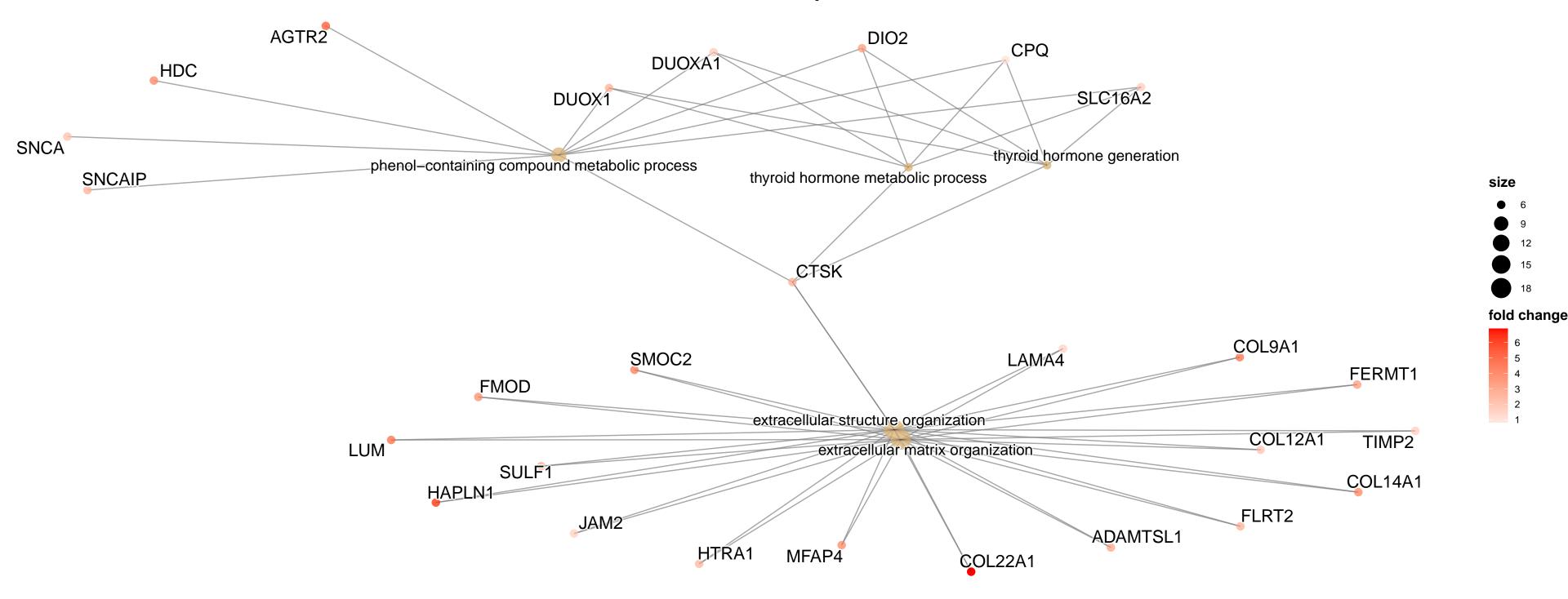
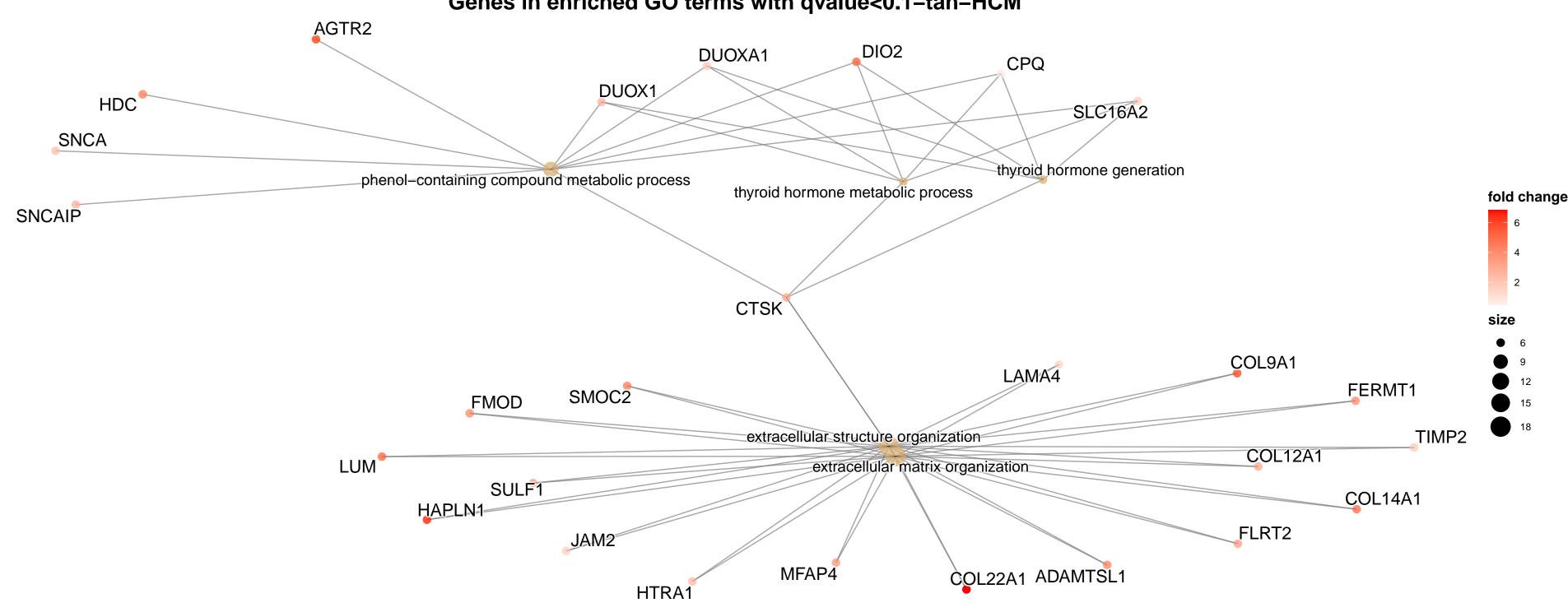
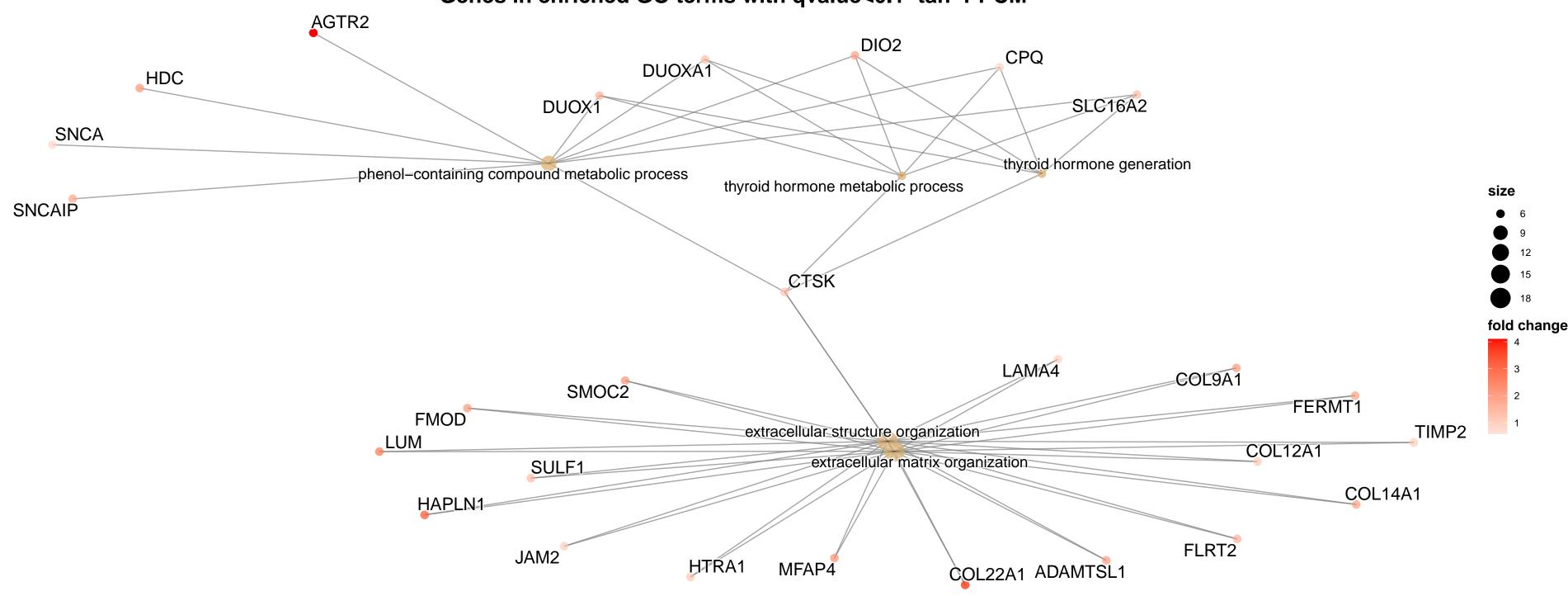
Genes in enriched GO terms with qvalue<0.1-tan-DCM



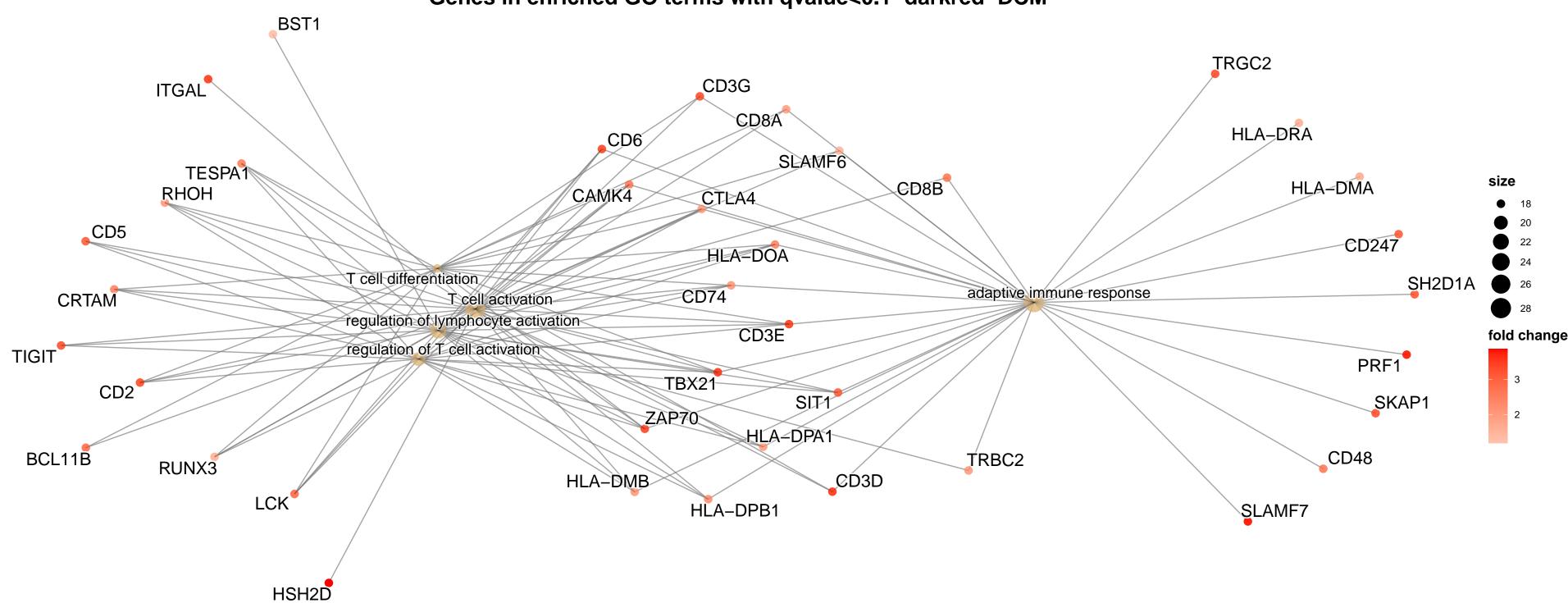
Genes in enriched GO terms with qvalue<0.1-tan-HCM



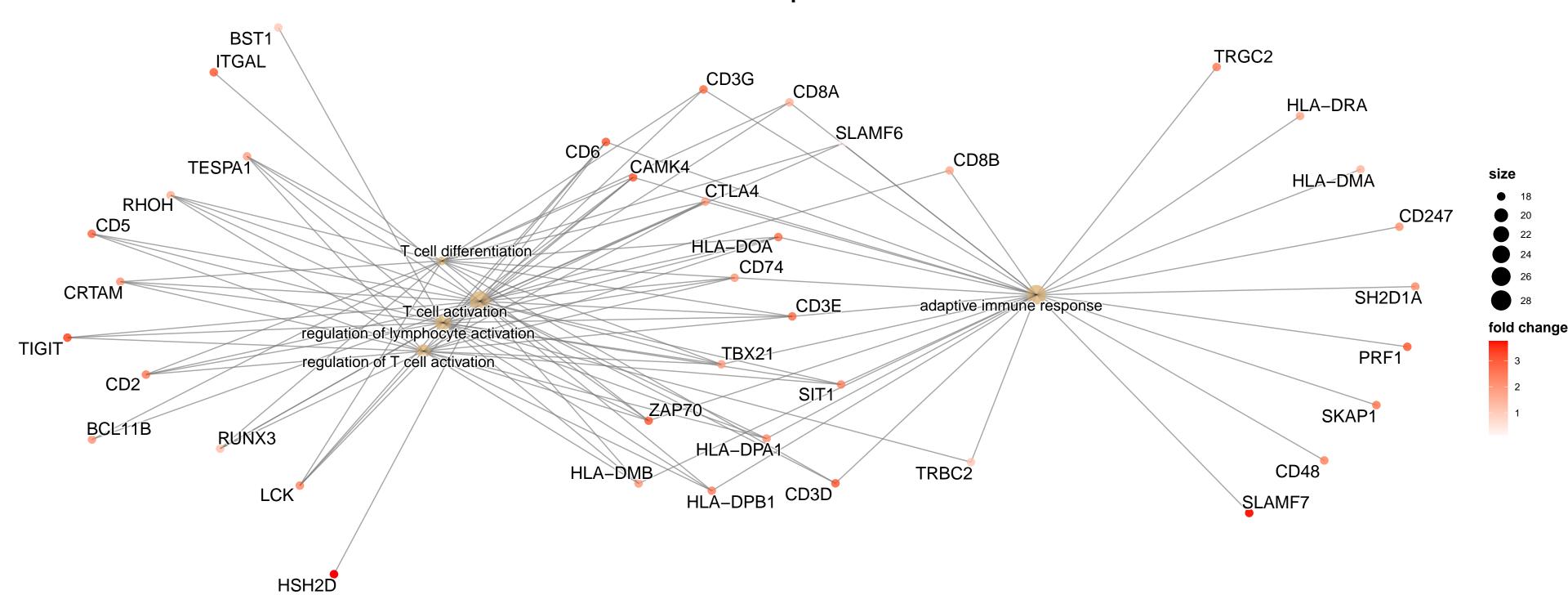
Genes in enriched GO terms with qvalue<0.1-tan-PPCM



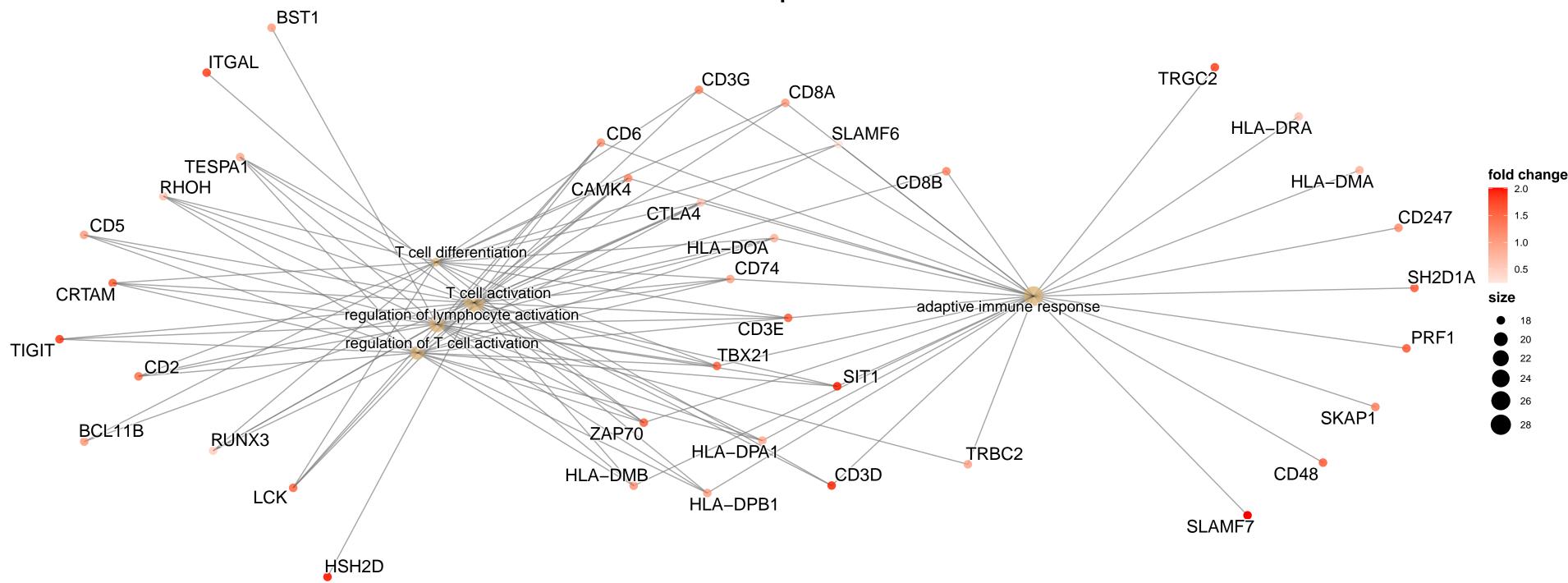
Genes in enriched GO terms with qvalue<0.1-darkred-DCM



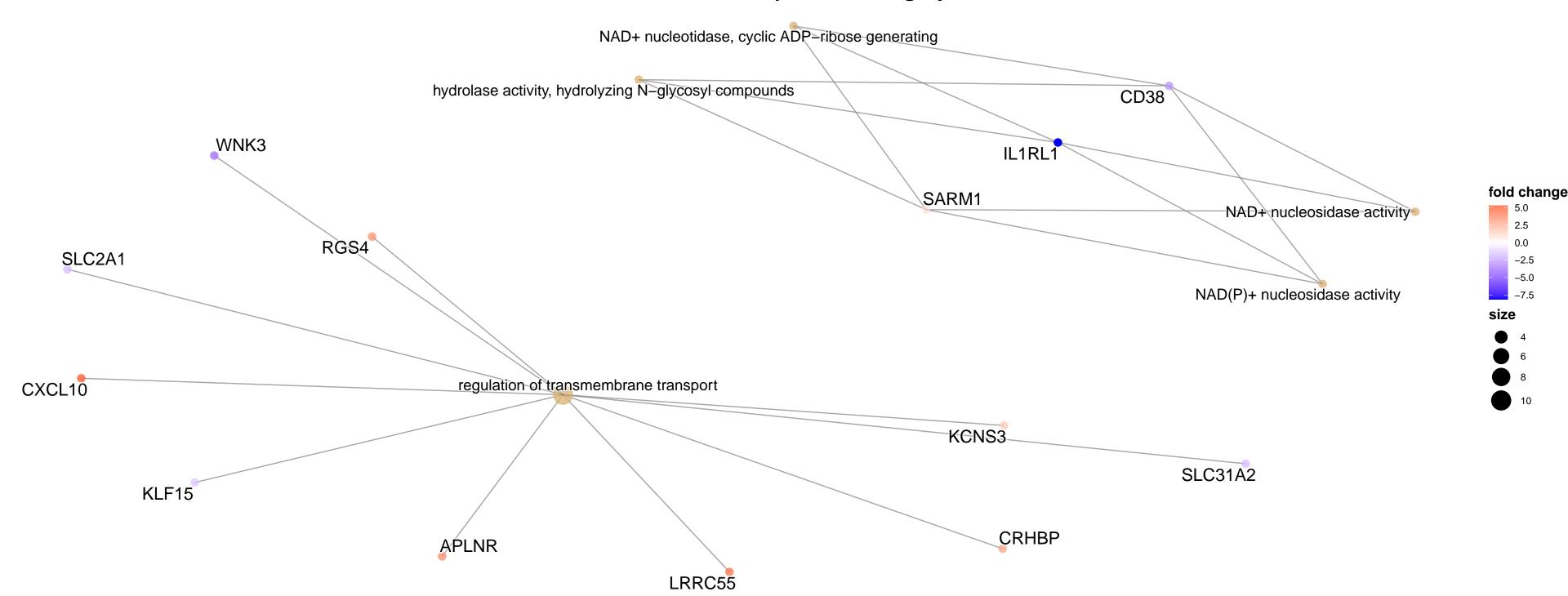
Genes in enriched GO terms with qvalue<0.1-darkred-HCM



Genes in enriched GO terms with qvalue<0.1-darkred-PPCM

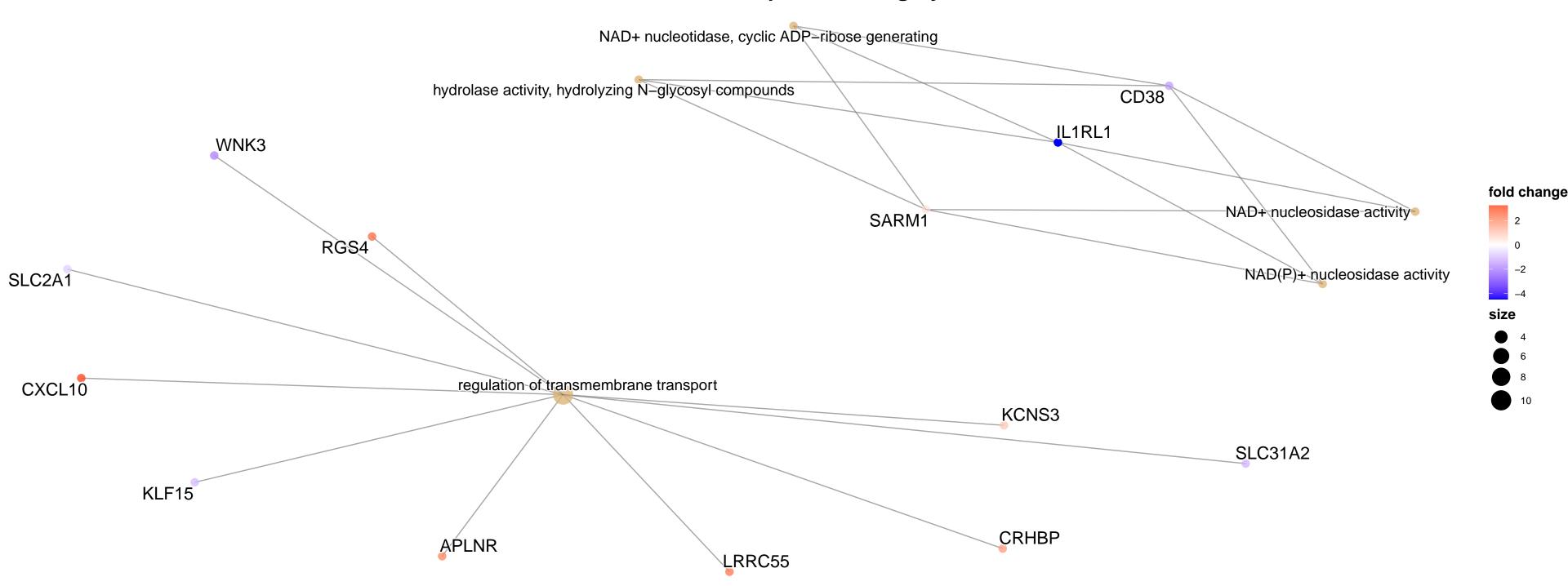


Genes in enriched GO terms with qvalue<0.1-lightyellow-DCM

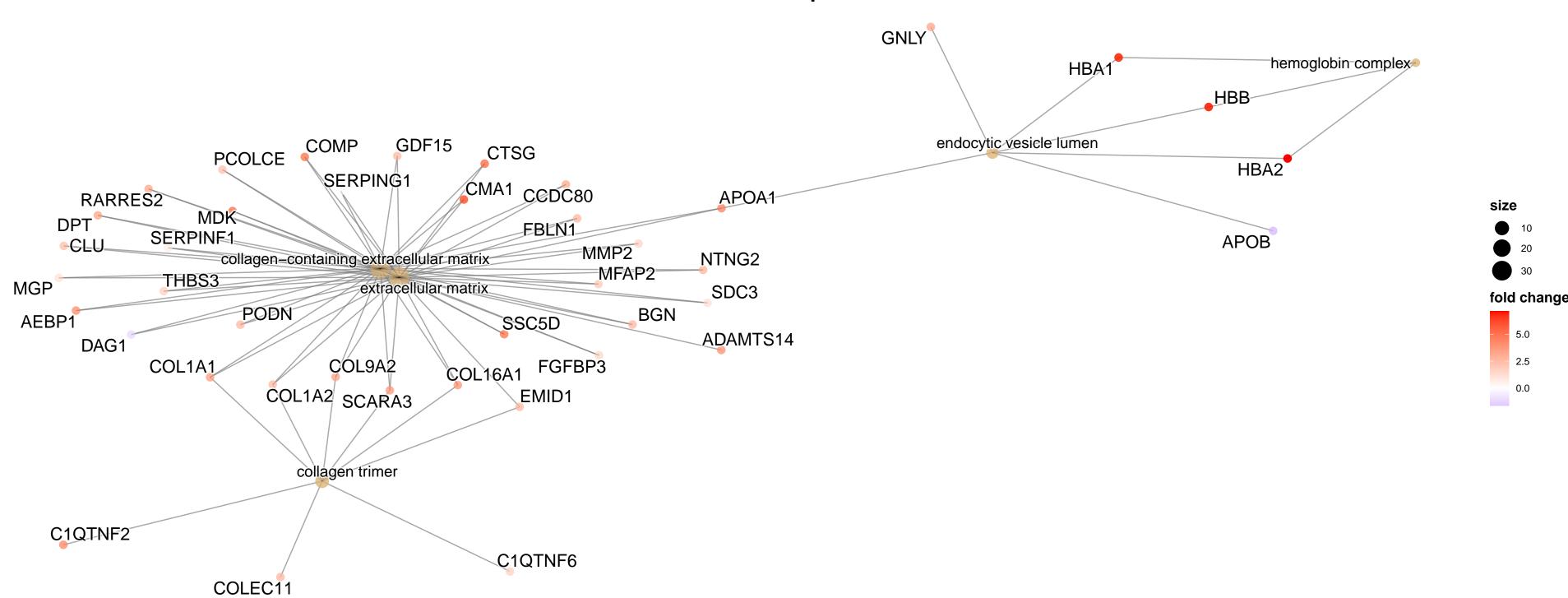


Genes in enriched GO terms with qvalue<0.1-lightyellow-HCM NAD+ nucleotidase, cyclic ADP-ribose generating CD38 hydrolase activity, hydrolyzing N-glycosyl compounds WNK3 IL1RL1 size NAD+ nucleosidase activity SARM1 RGS4 SLC2A1 NAD(P)+ nucleosidase activity fold change CXCL10 regulation of transmembrane transport KCNS3 SLC31A2 KLF15 CRHBP LRRC55 APLNR

Genes in enriched GO terms with qvalue<0.1-lightyellow-PPCM



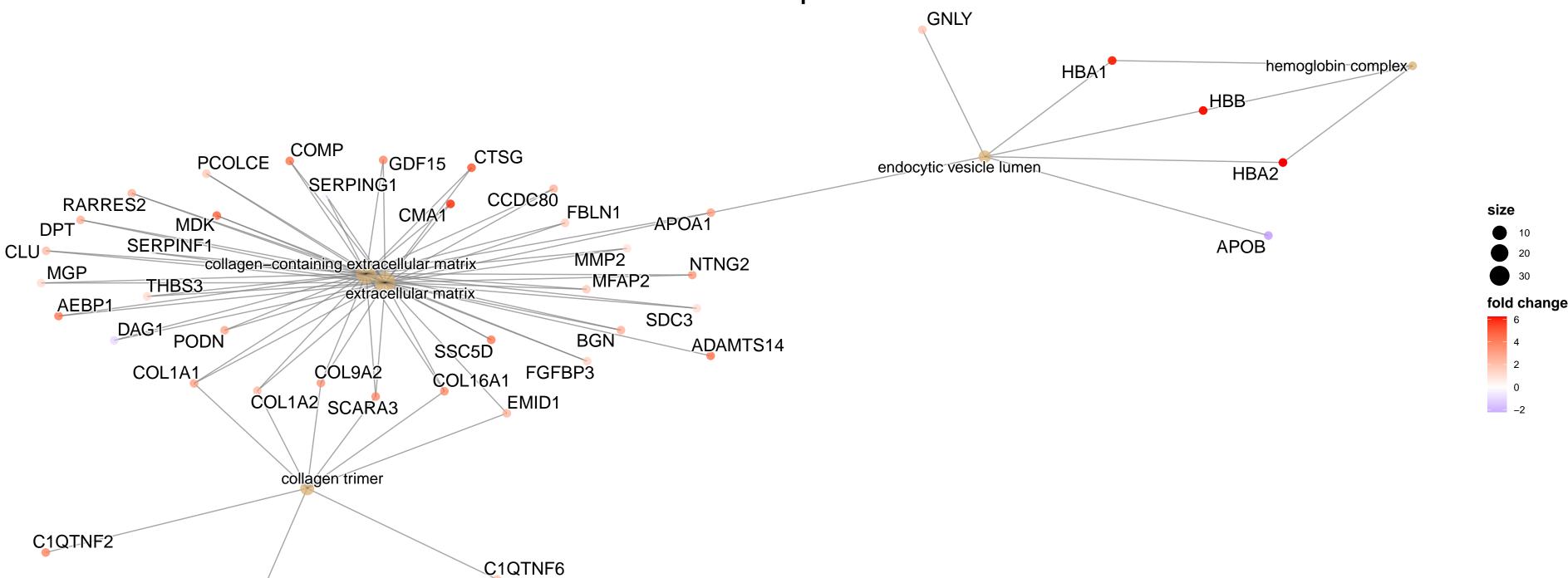
Genes in enriched GO terms with qvalue<0.1-red-DCM



5.0

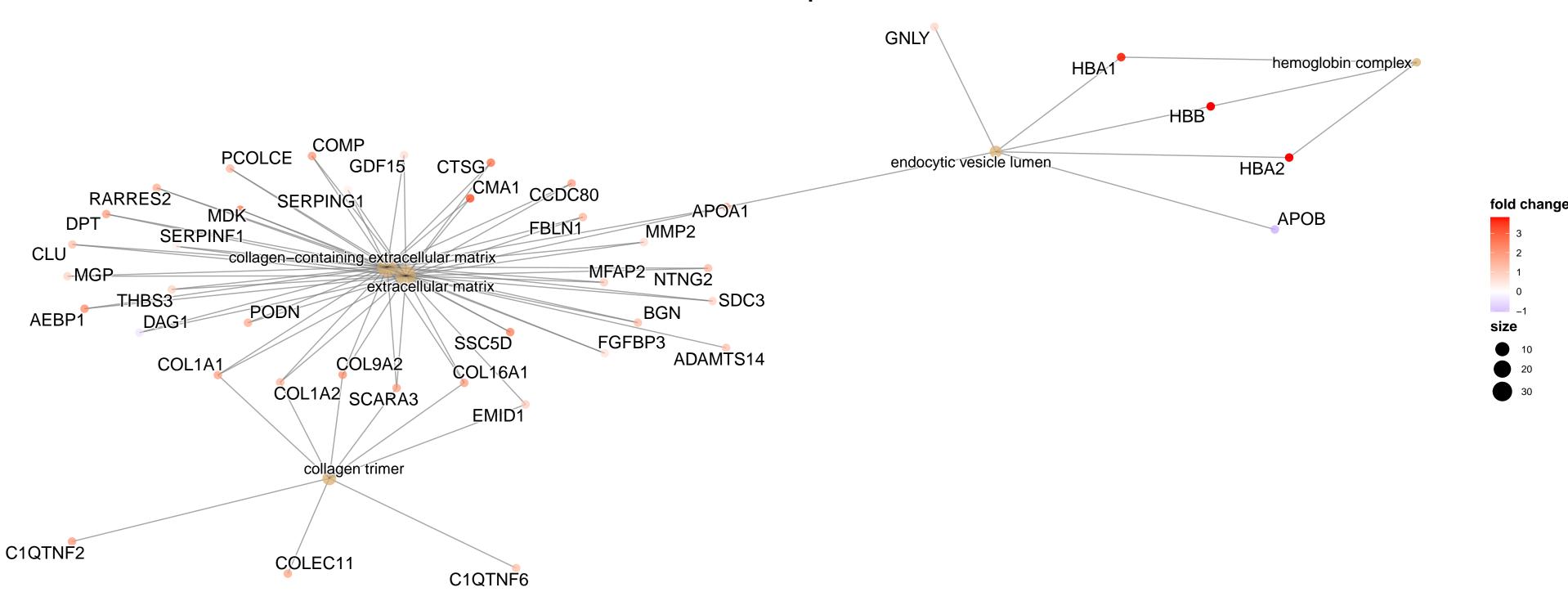
2.5

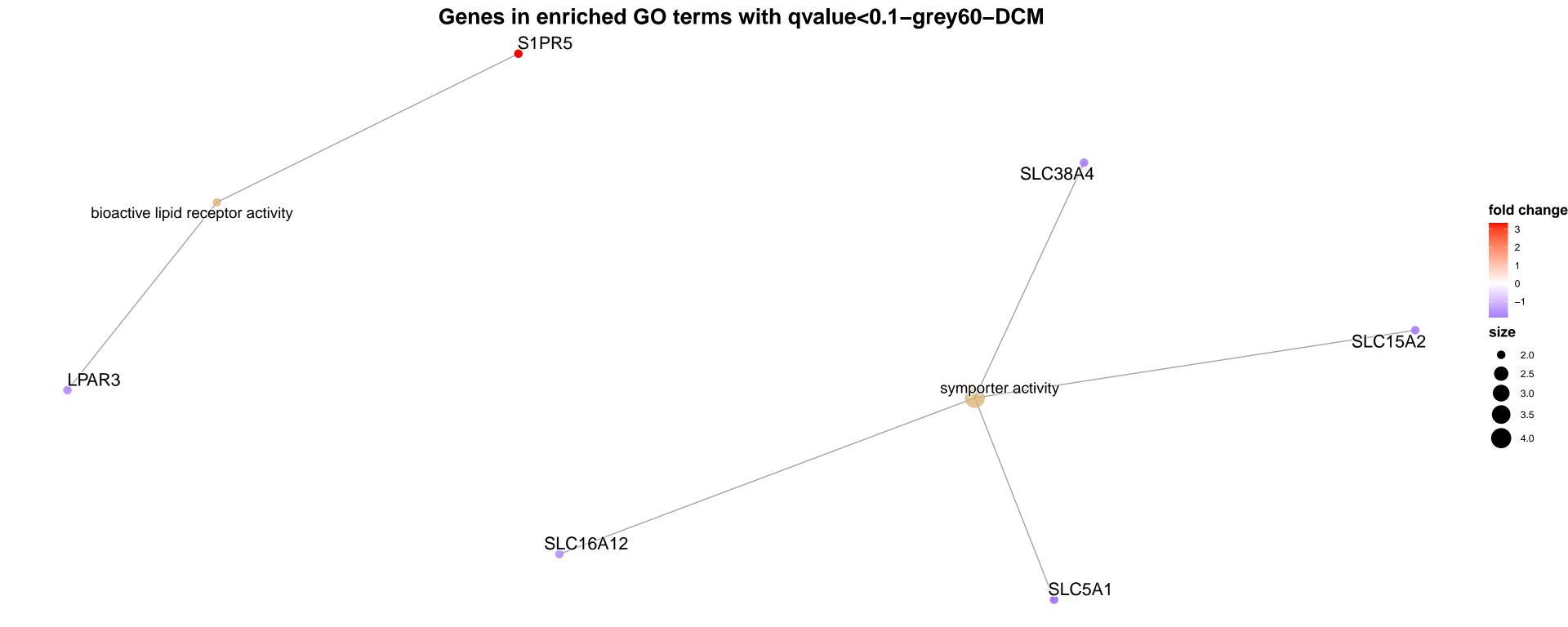
Genes in enriched GO terms with qvalue<0.1-red-HCM

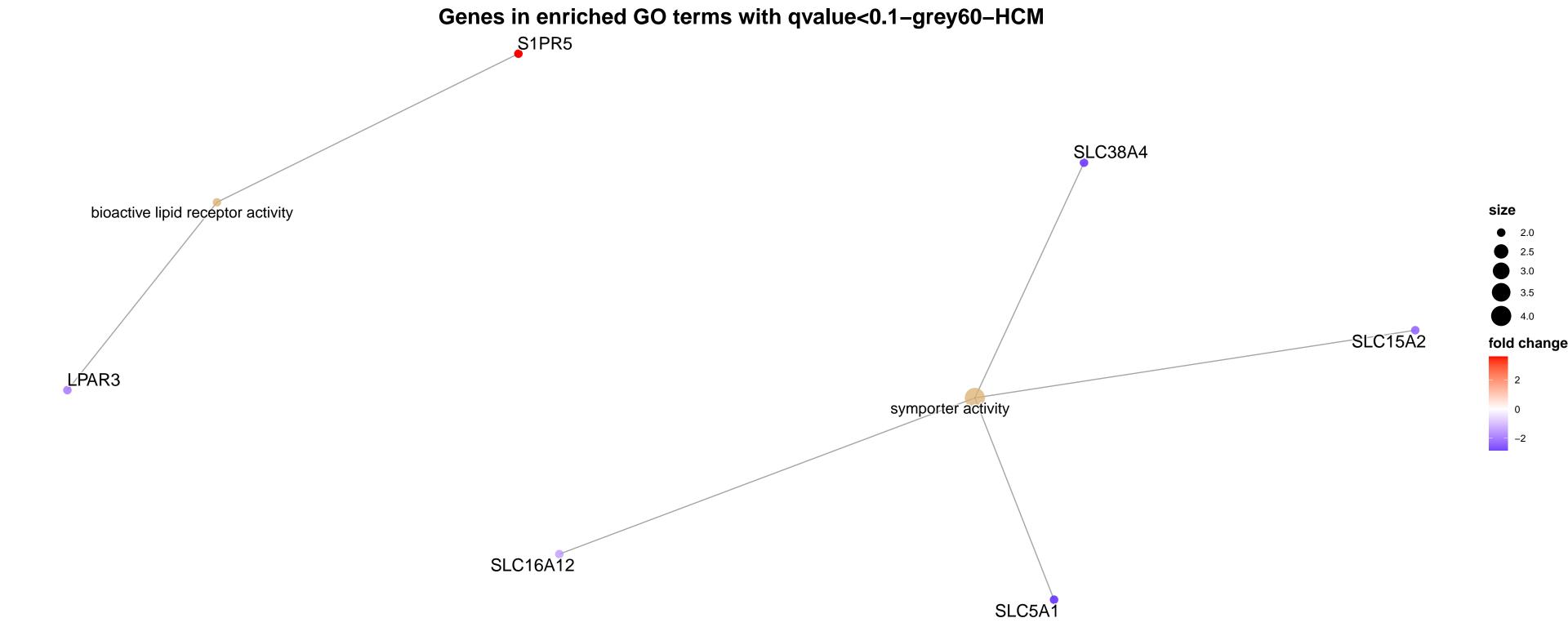


COLEC11

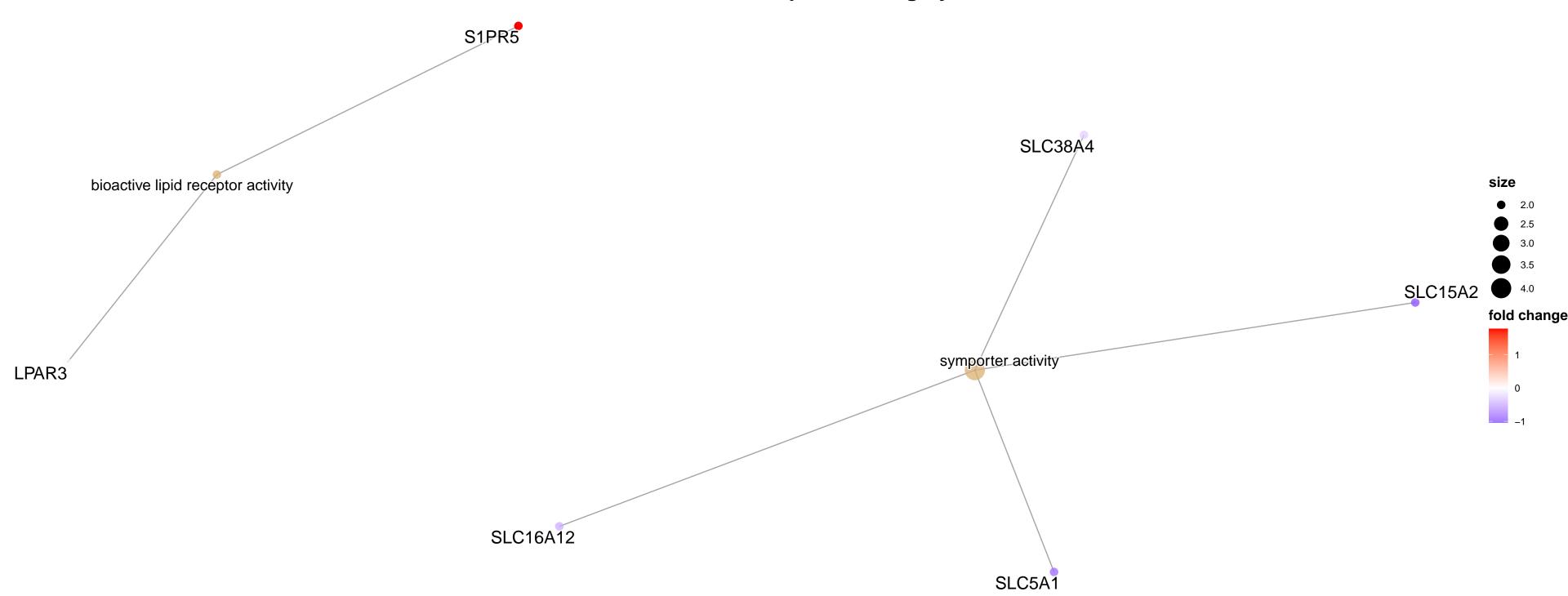
Genes in enriched GO terms with qvalue<0.1-red-PPCM





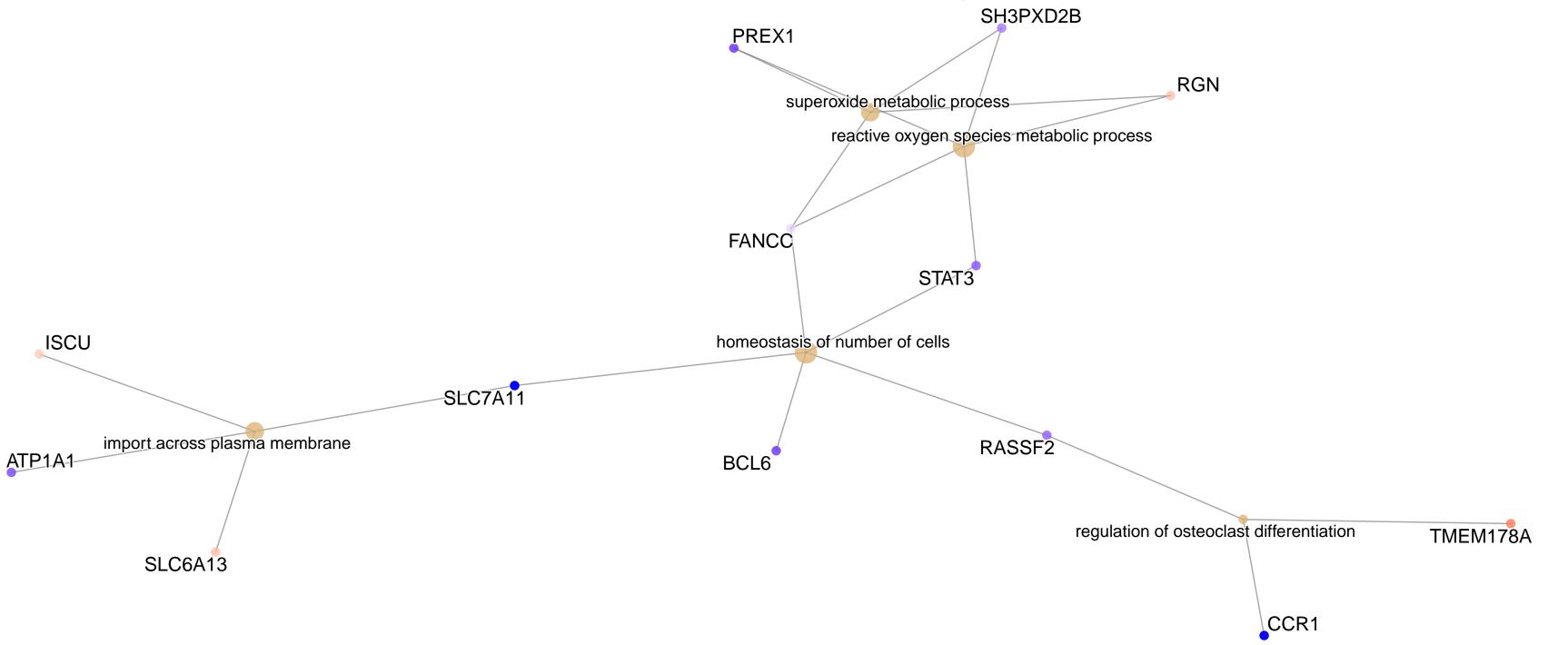


Genes in enriched GO terms with qvalue<0.1-grey60-PPCM



Genes in enriched GO terms with qvalue<0.1-royalblue-DCM SH3PXD2B PREX1 RGN superoxide metabolic process reactive oxygen species metabolic process fold change FANCC STAT3 ISCU homeostasis of number of cells SLC7A11 import across plasma membrane RASSF2 ATP1A1 BCL6 regulation of osteoclast differentiation TMEM178A SLC6A13 CCR1

Genes in enriched GO terms with qvalue<0.1-royalblue-HCM



size

fold change

Genes in enriched GO terms with qvalue<0.1-royalblue-PPCM SH3PXD2B PREX1 RGN superoxide metabolic process reactive oxygen species metabolic process FANCC STAT3 homeostasis of number of cells ISCU SLC7A11

