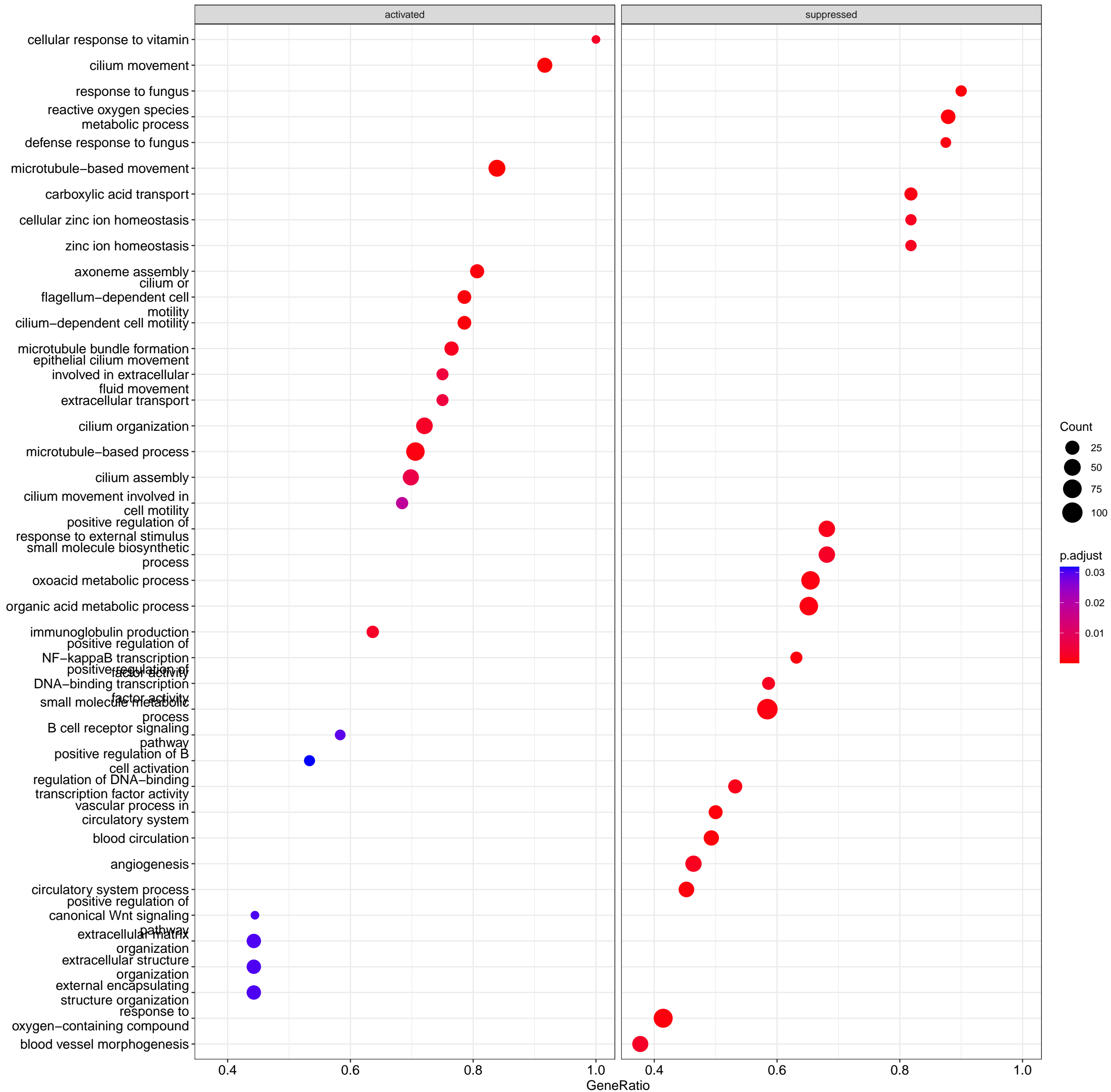
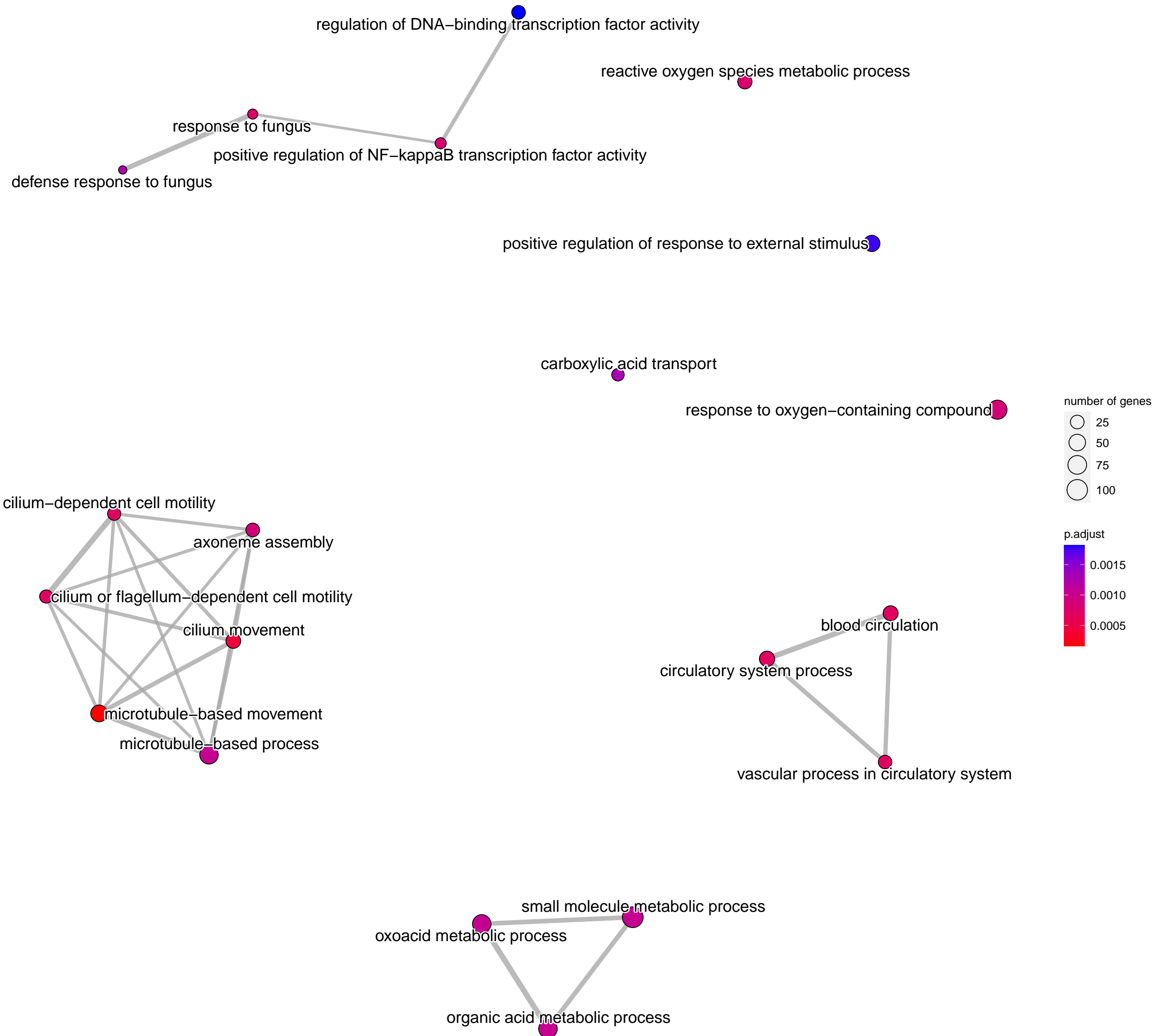
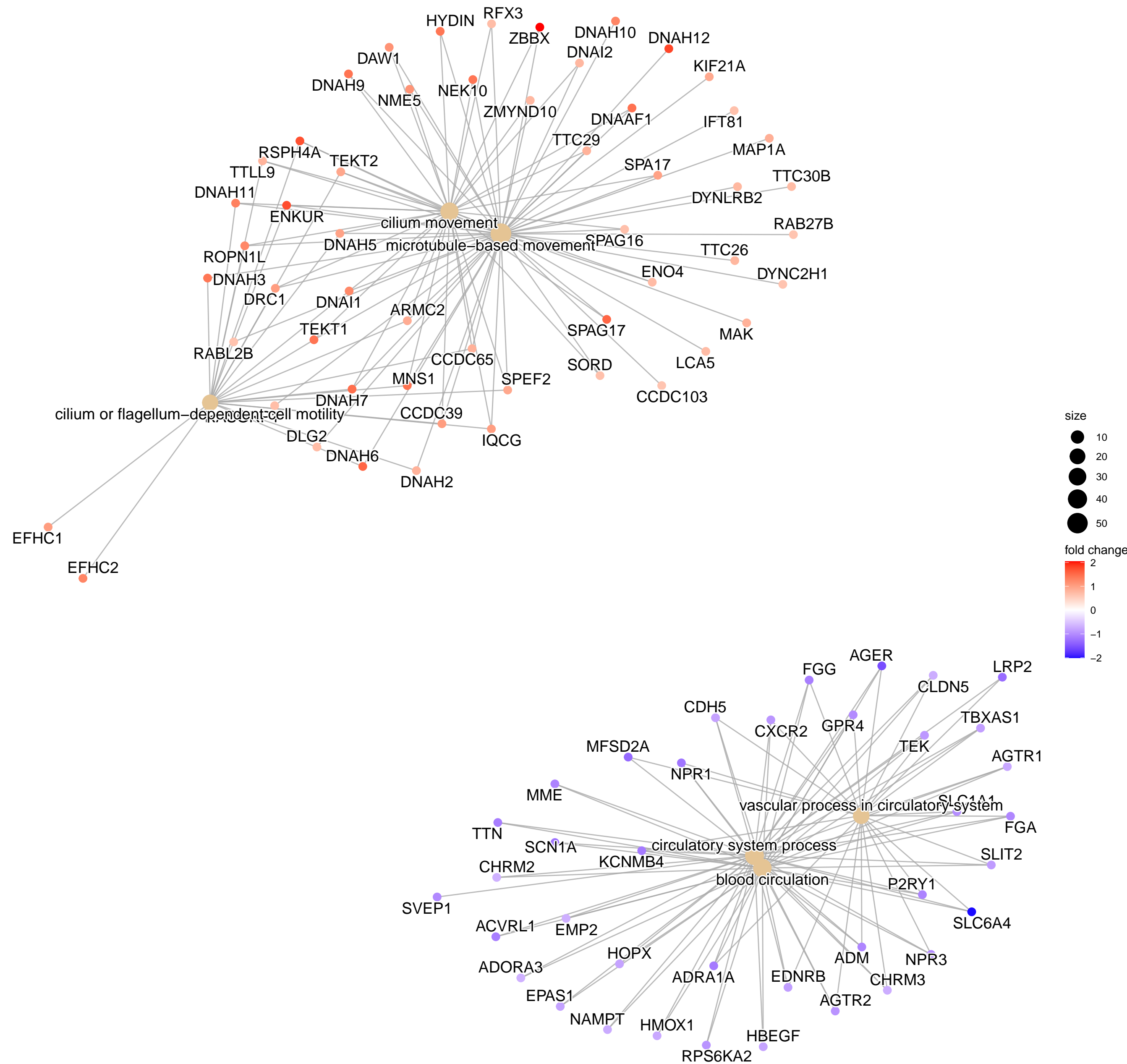
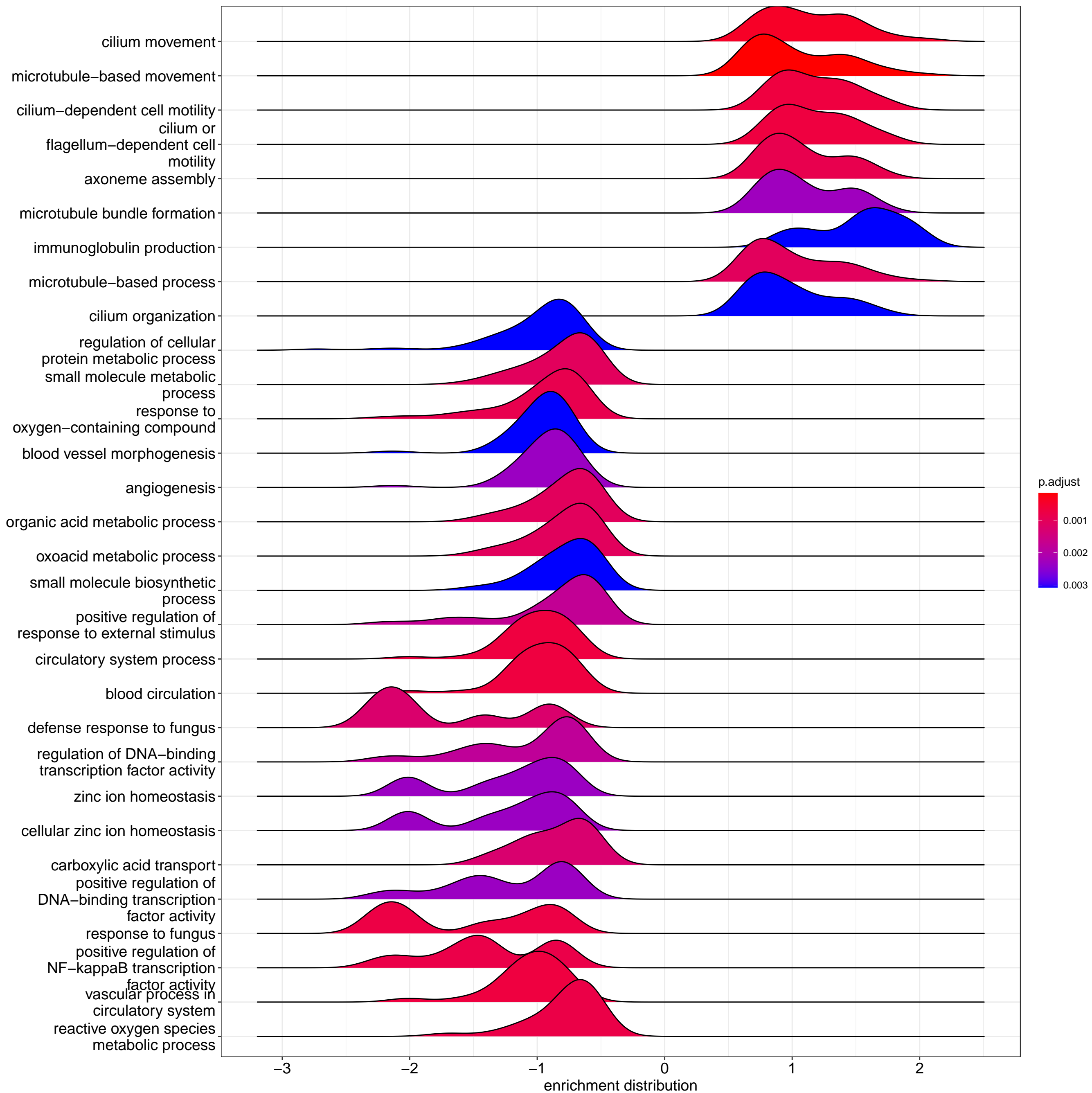


all BP

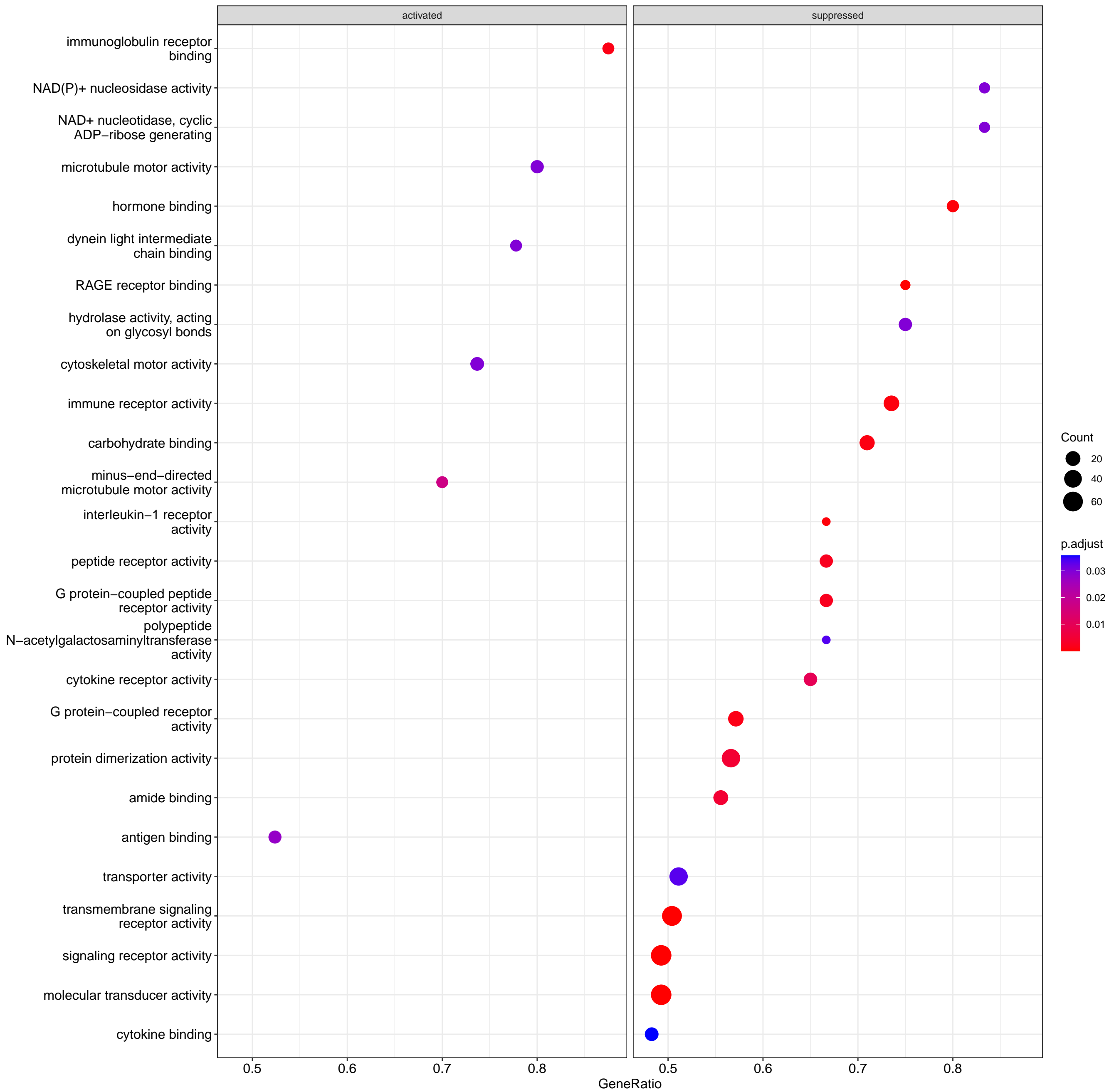


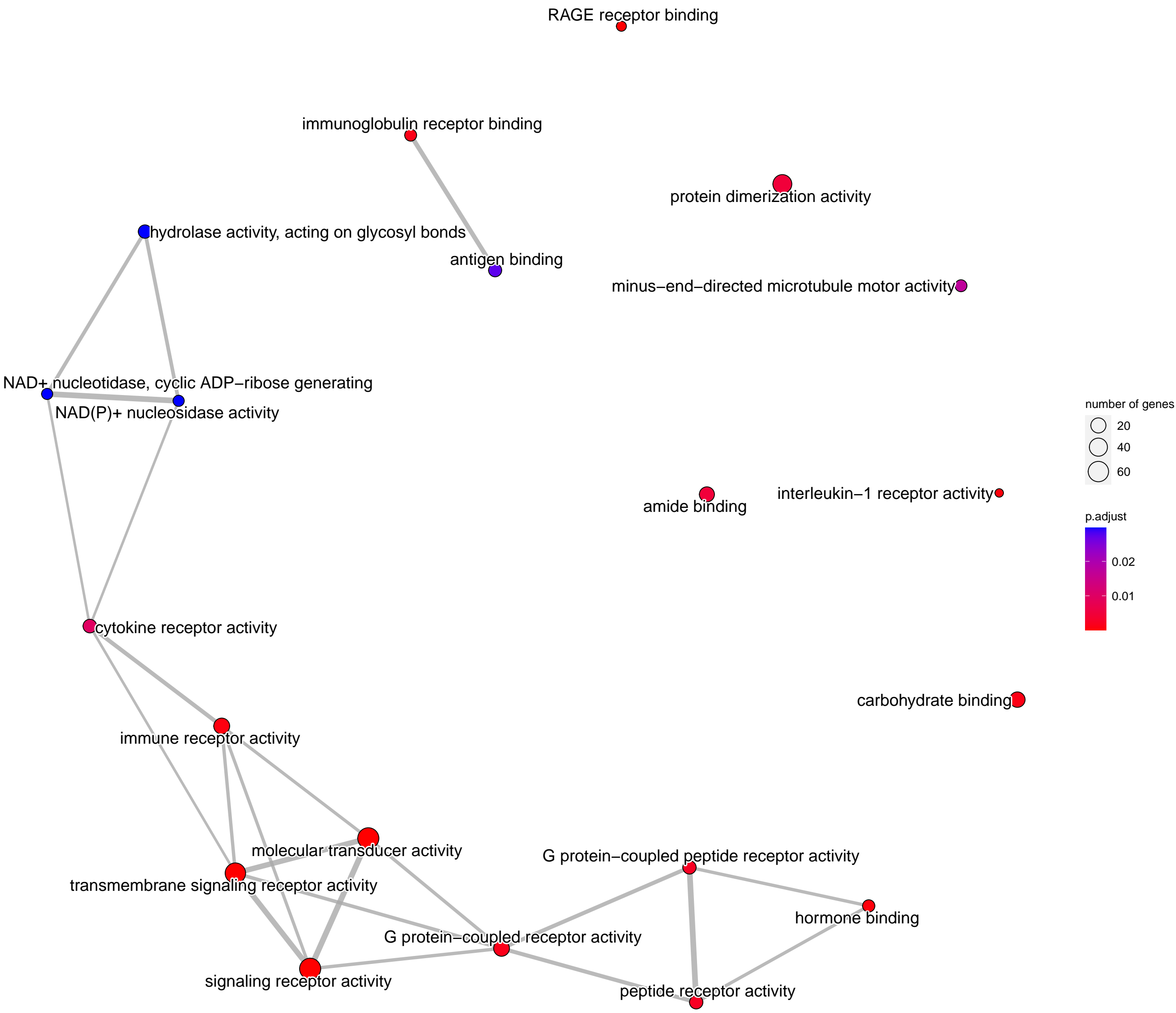


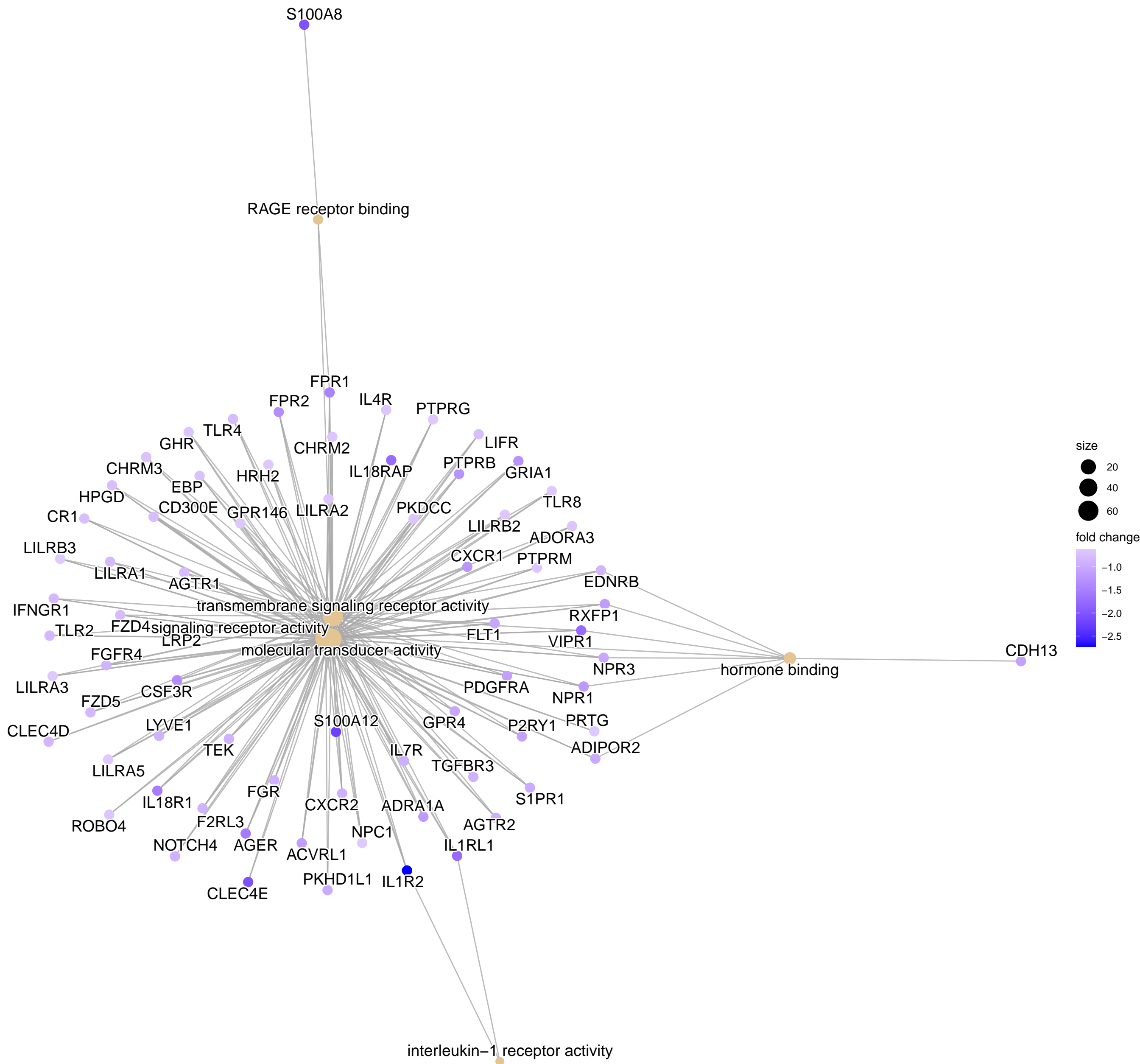


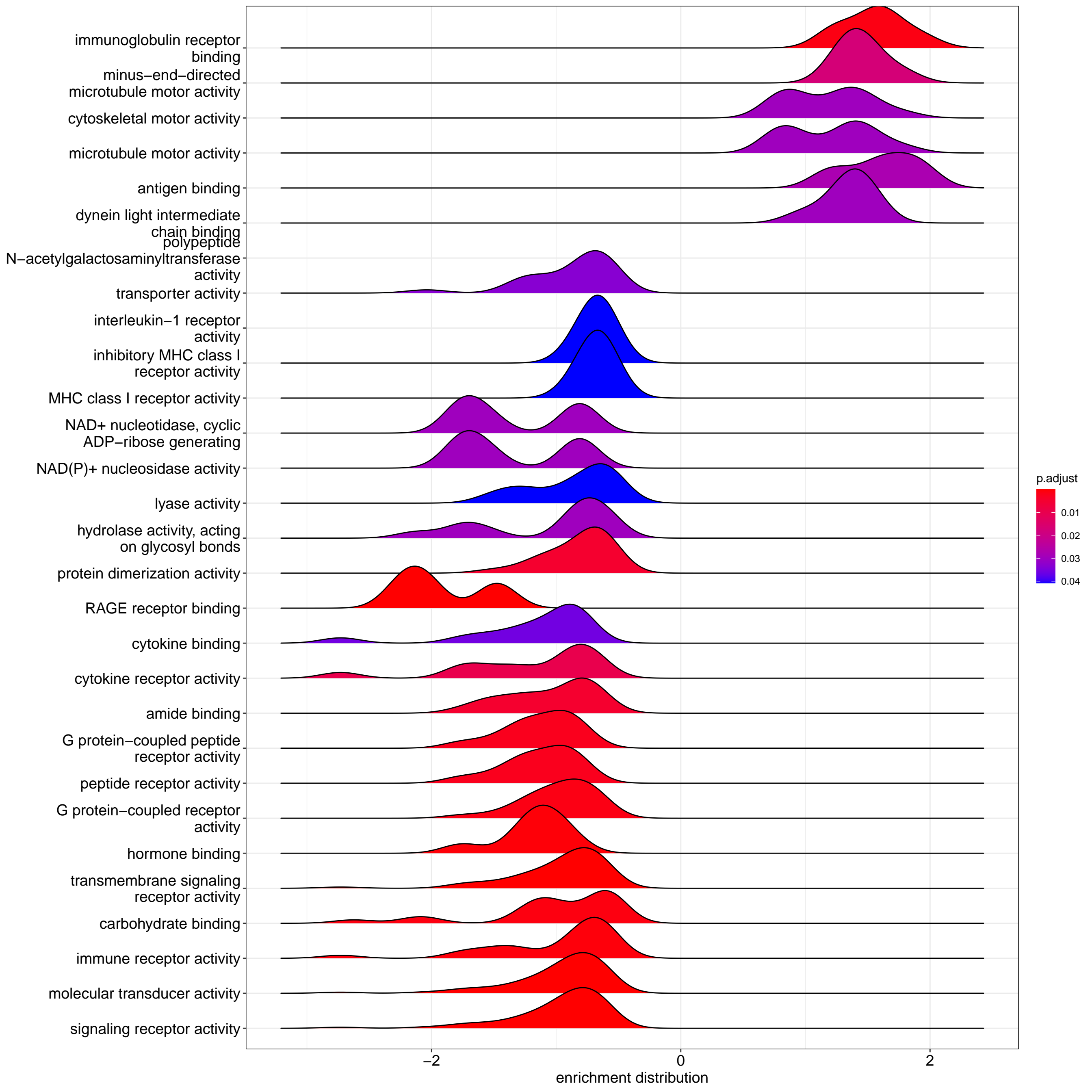


all MF

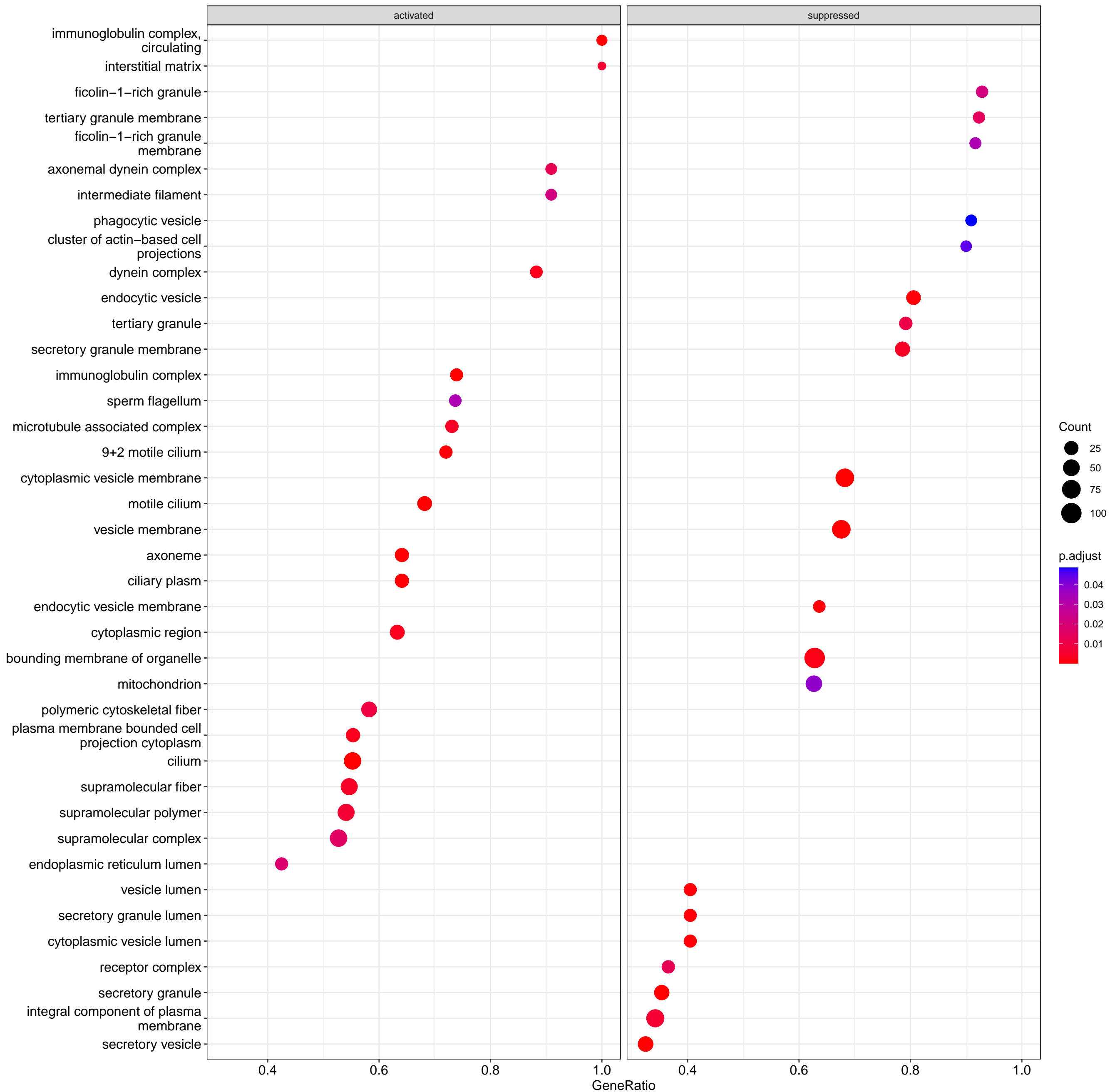


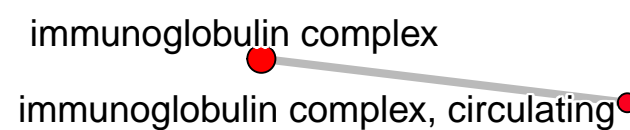
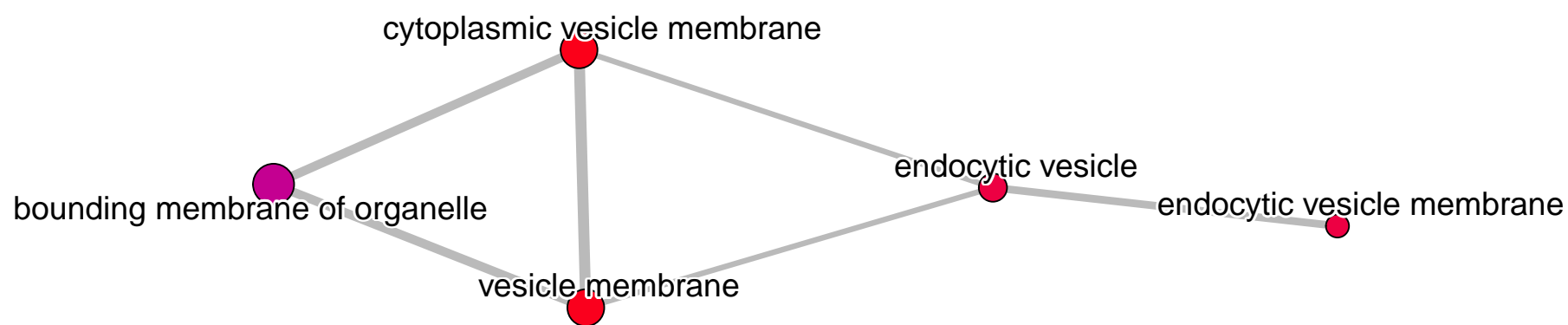




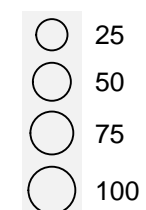


all CC

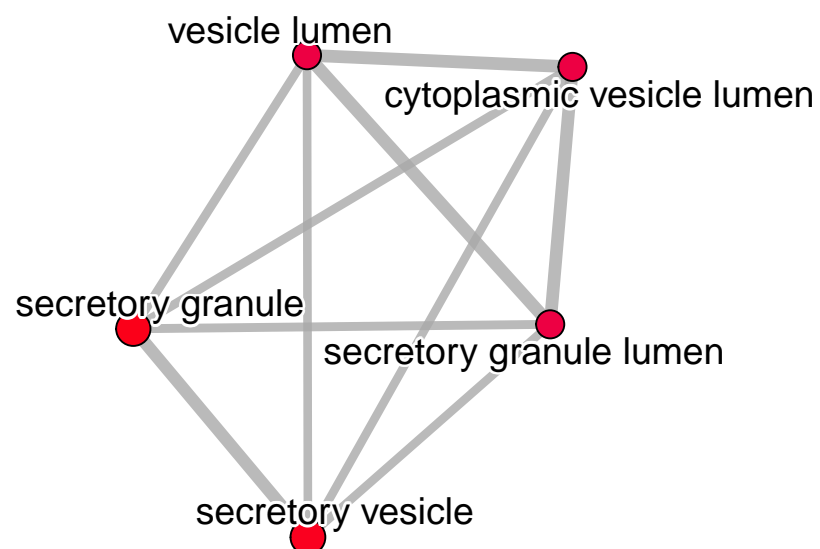
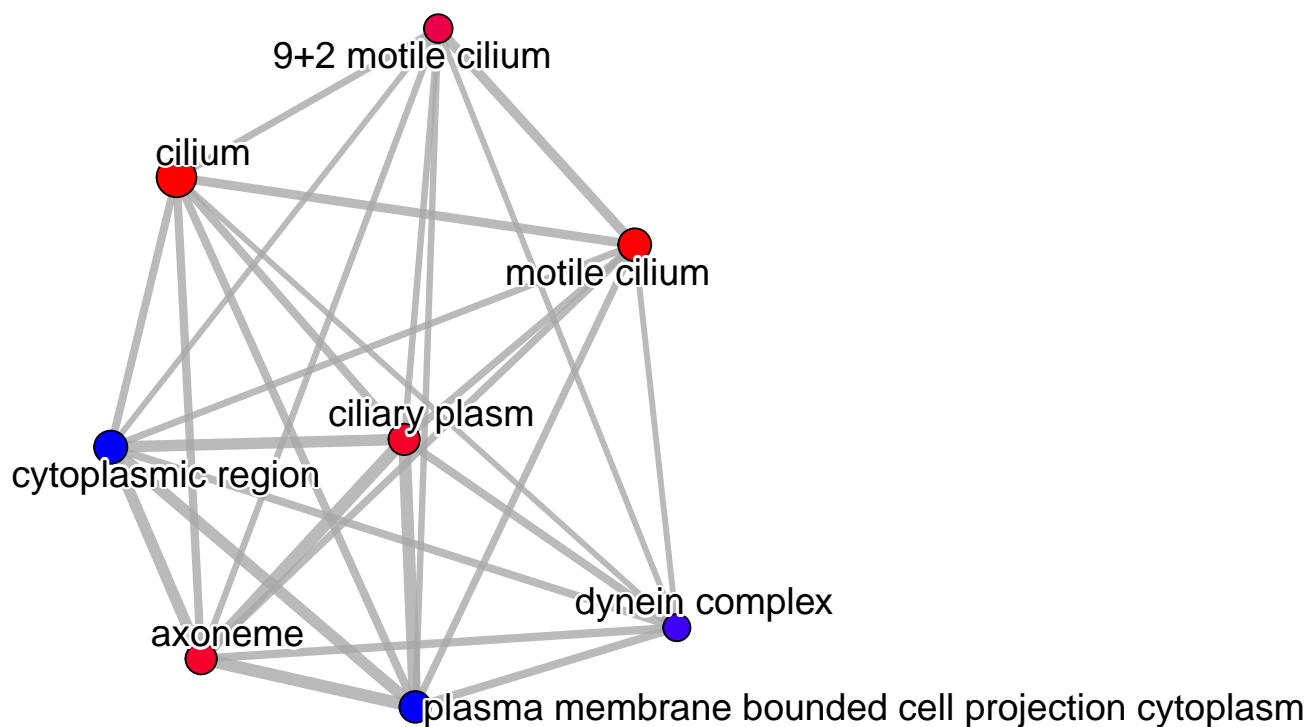
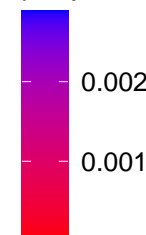


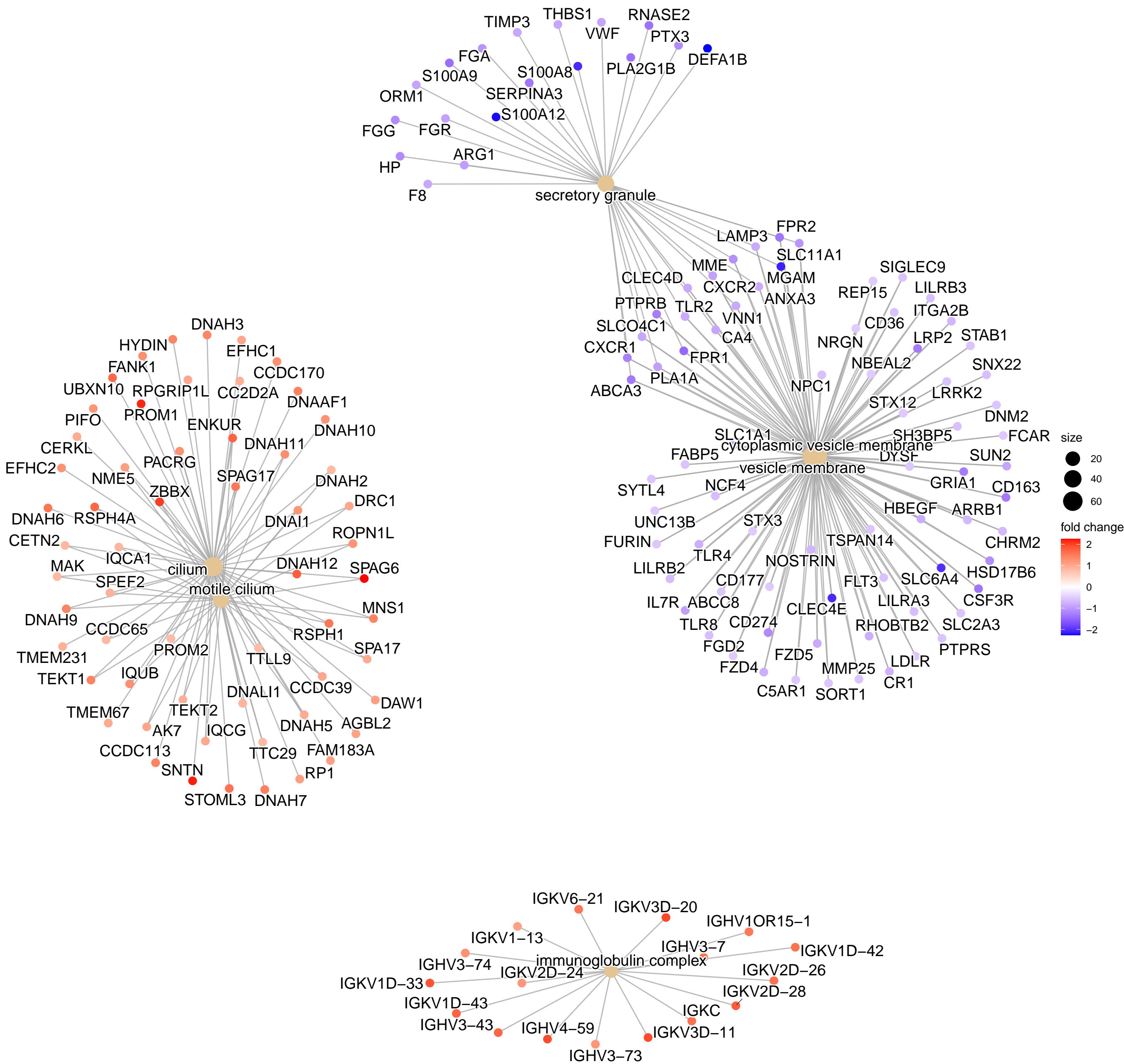


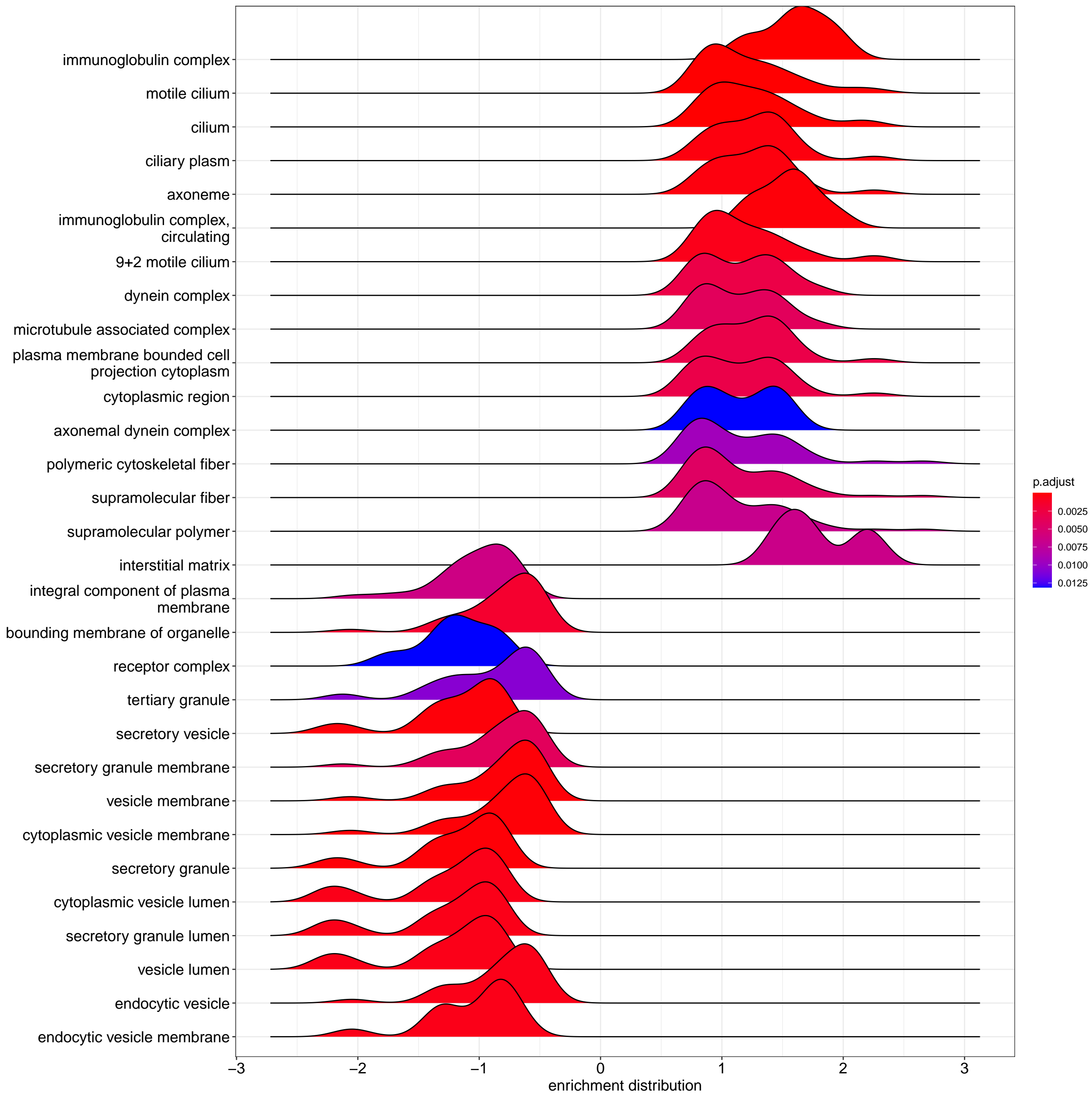
number of genes



p.adjust







Enriched Pathways

suppressed

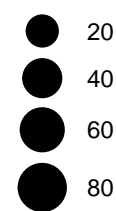
Neutrophil extracellular
trap formation

Fatty acid metabolism

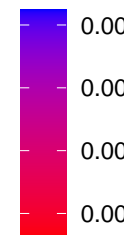
Metabolic pathways

Neuroactive ligand–receptor
interaction

Count



p.adjust



0.6

0.7

0.8

0.9

GeneRatio



