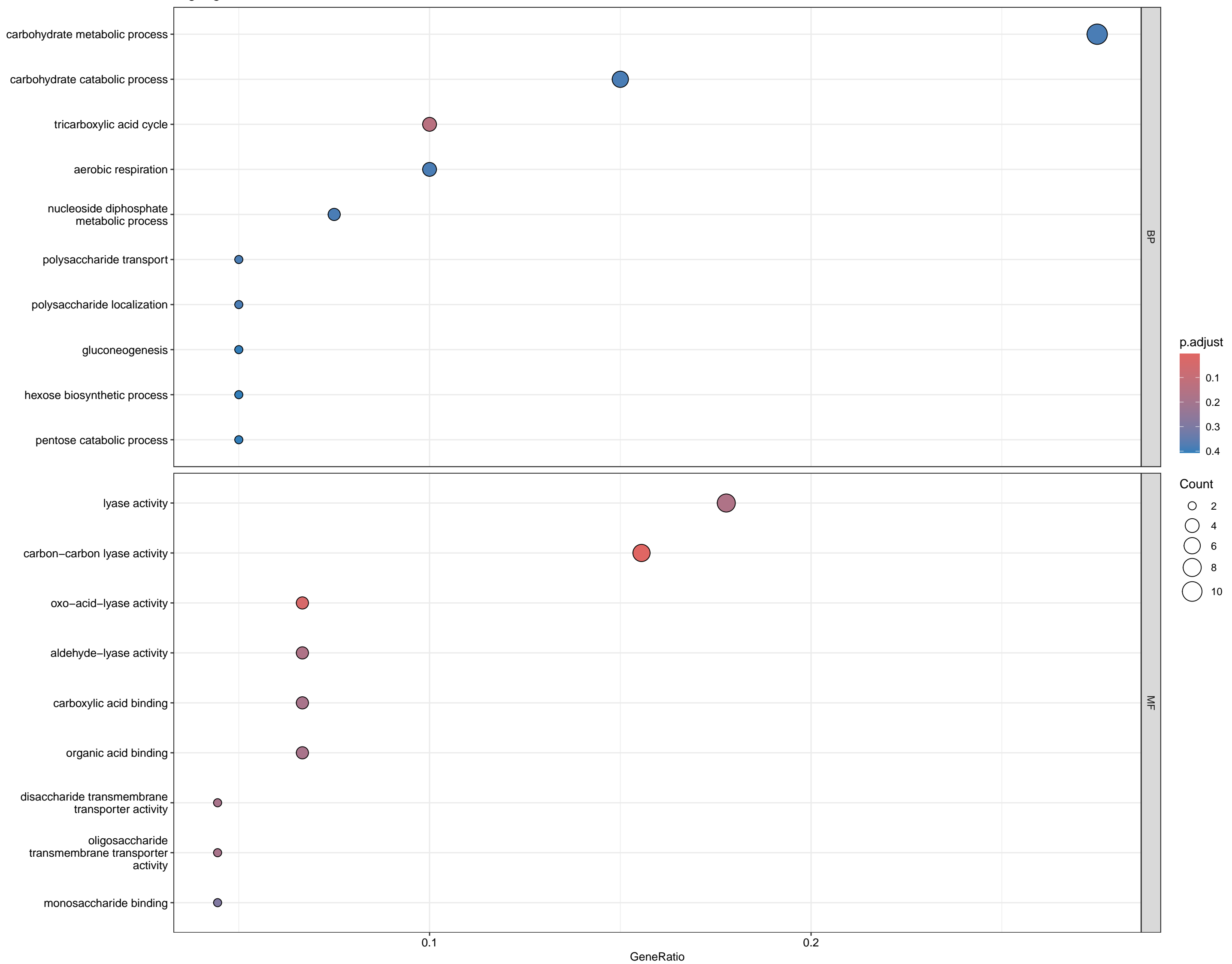
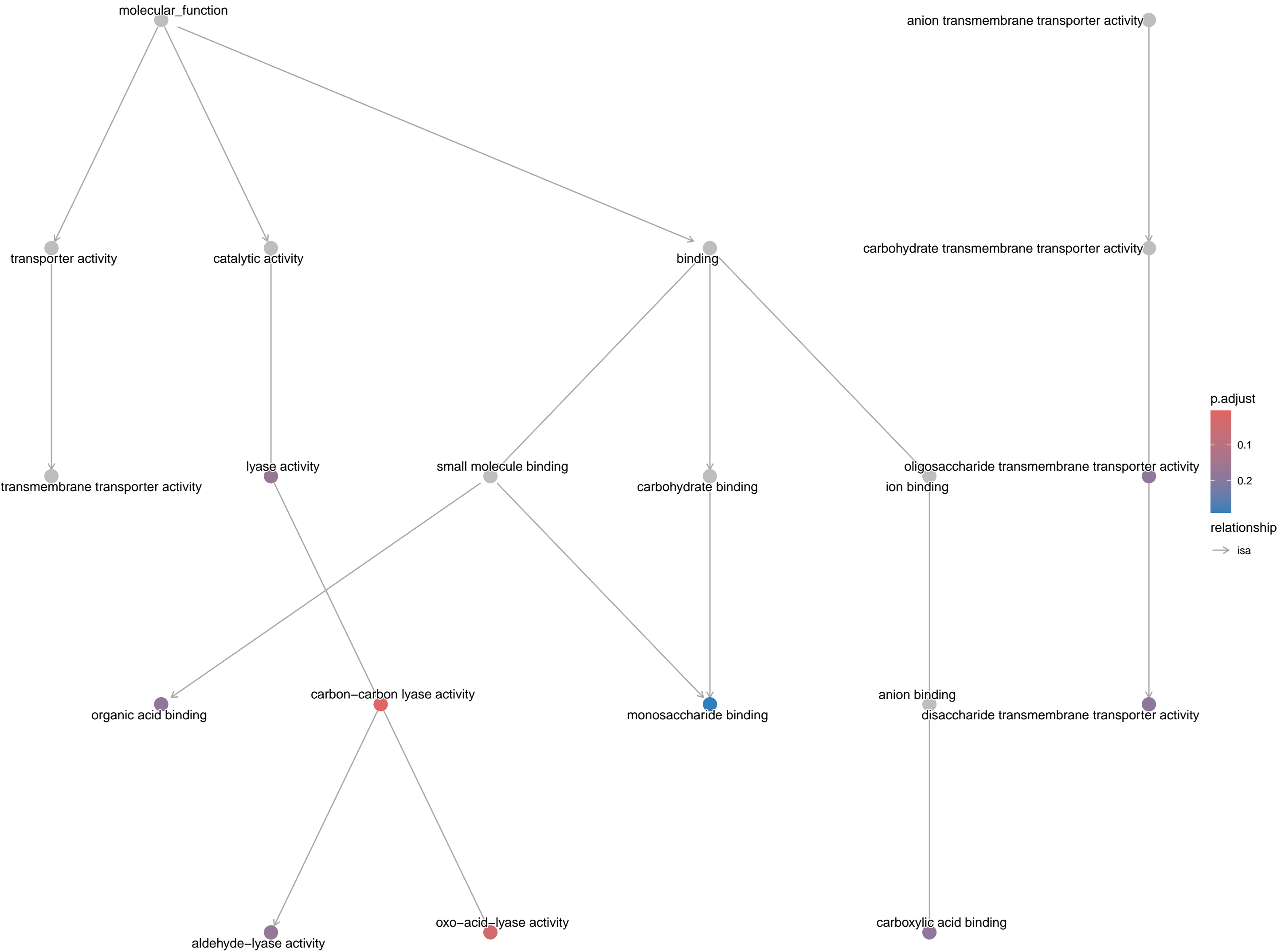
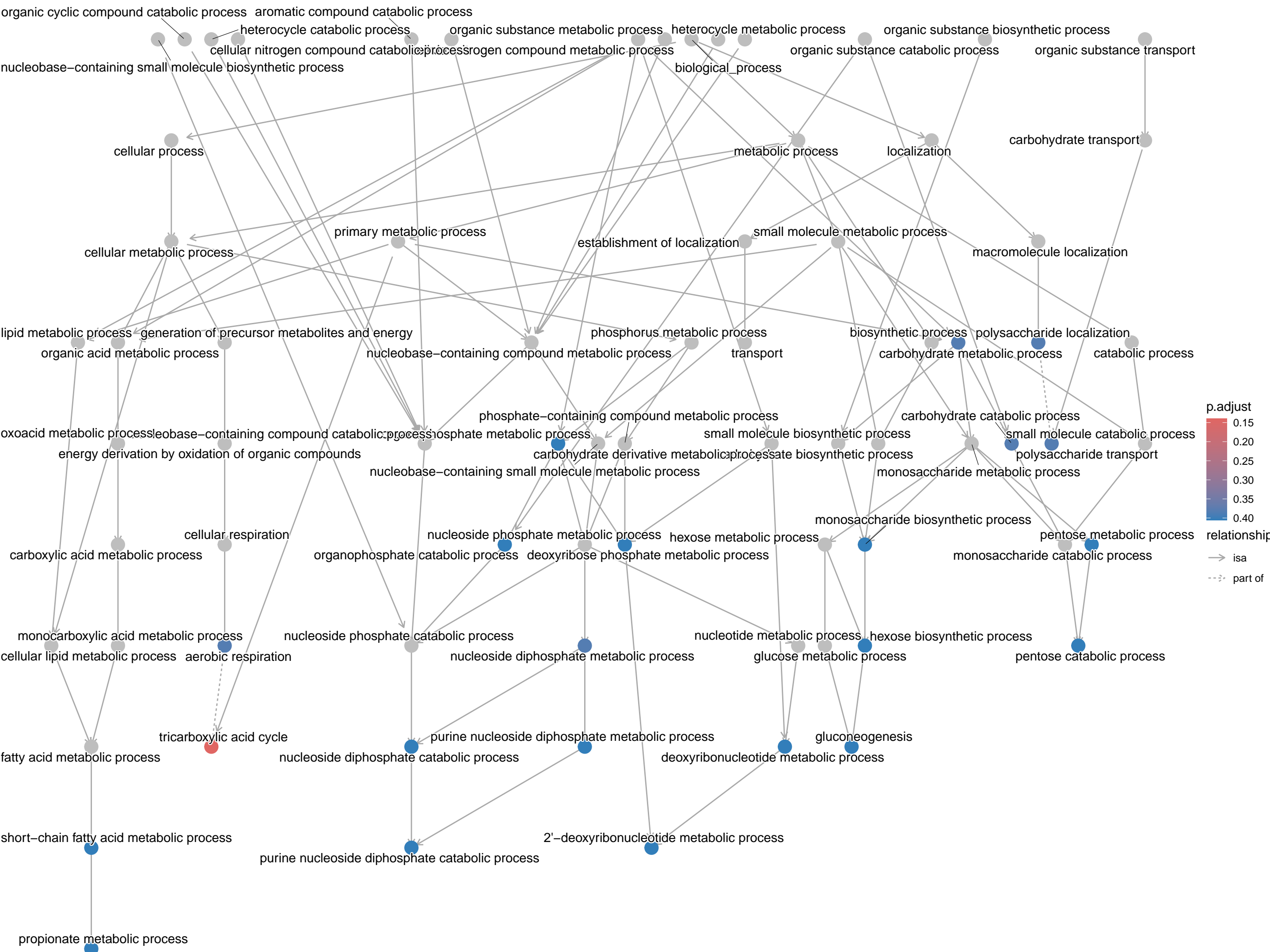


Right genes, nd=1

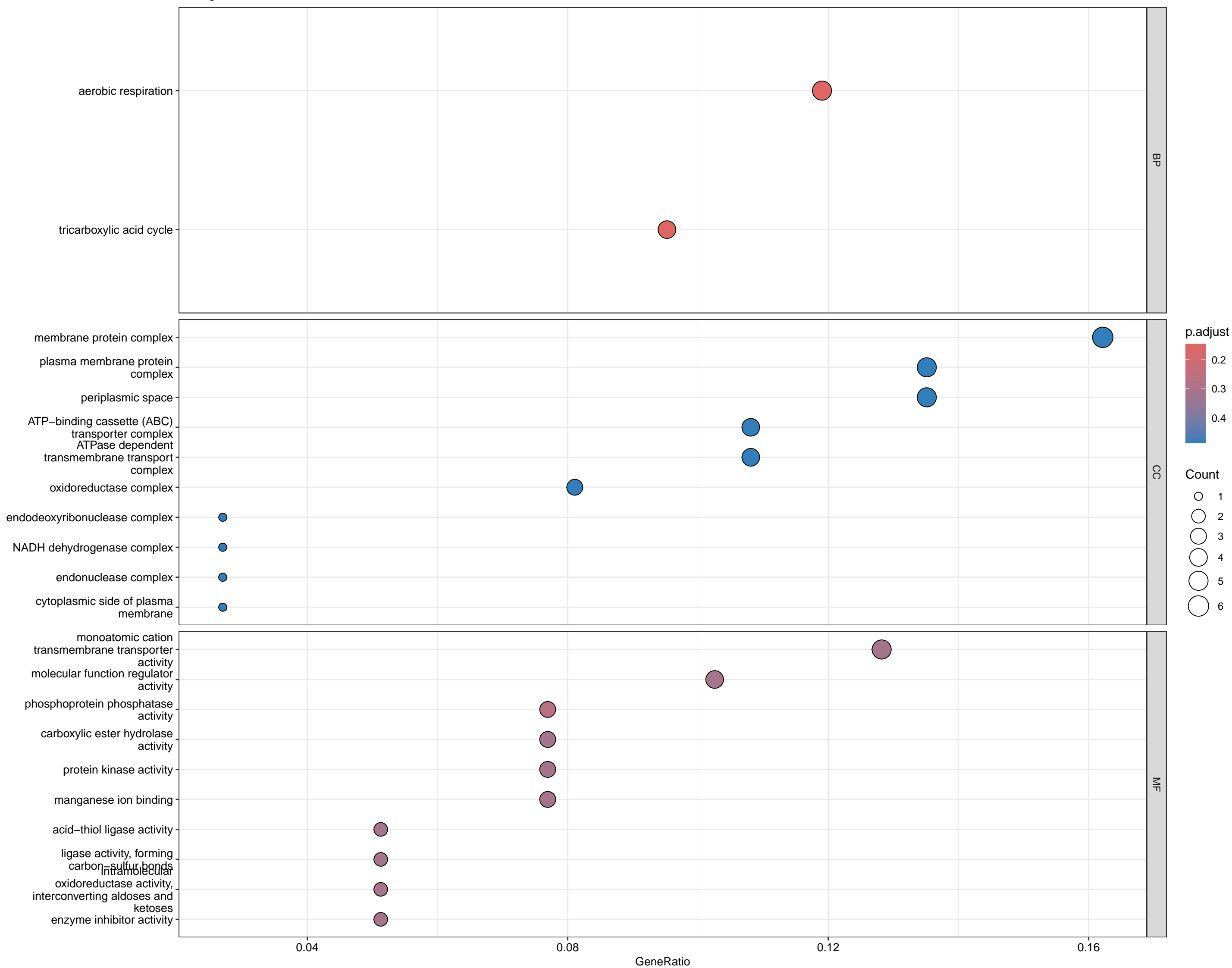




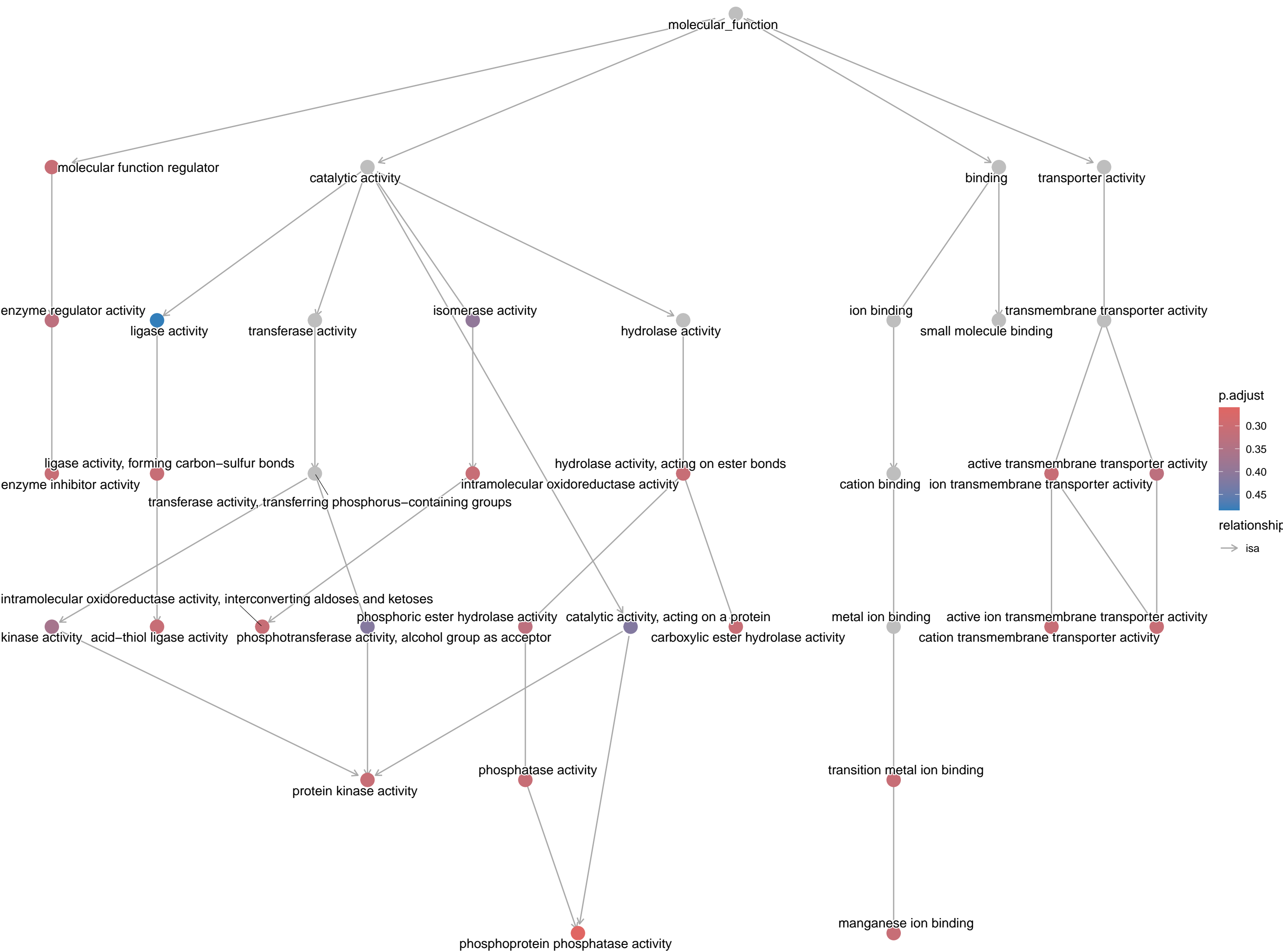
Right genes, Biological Process ontology, nd=1

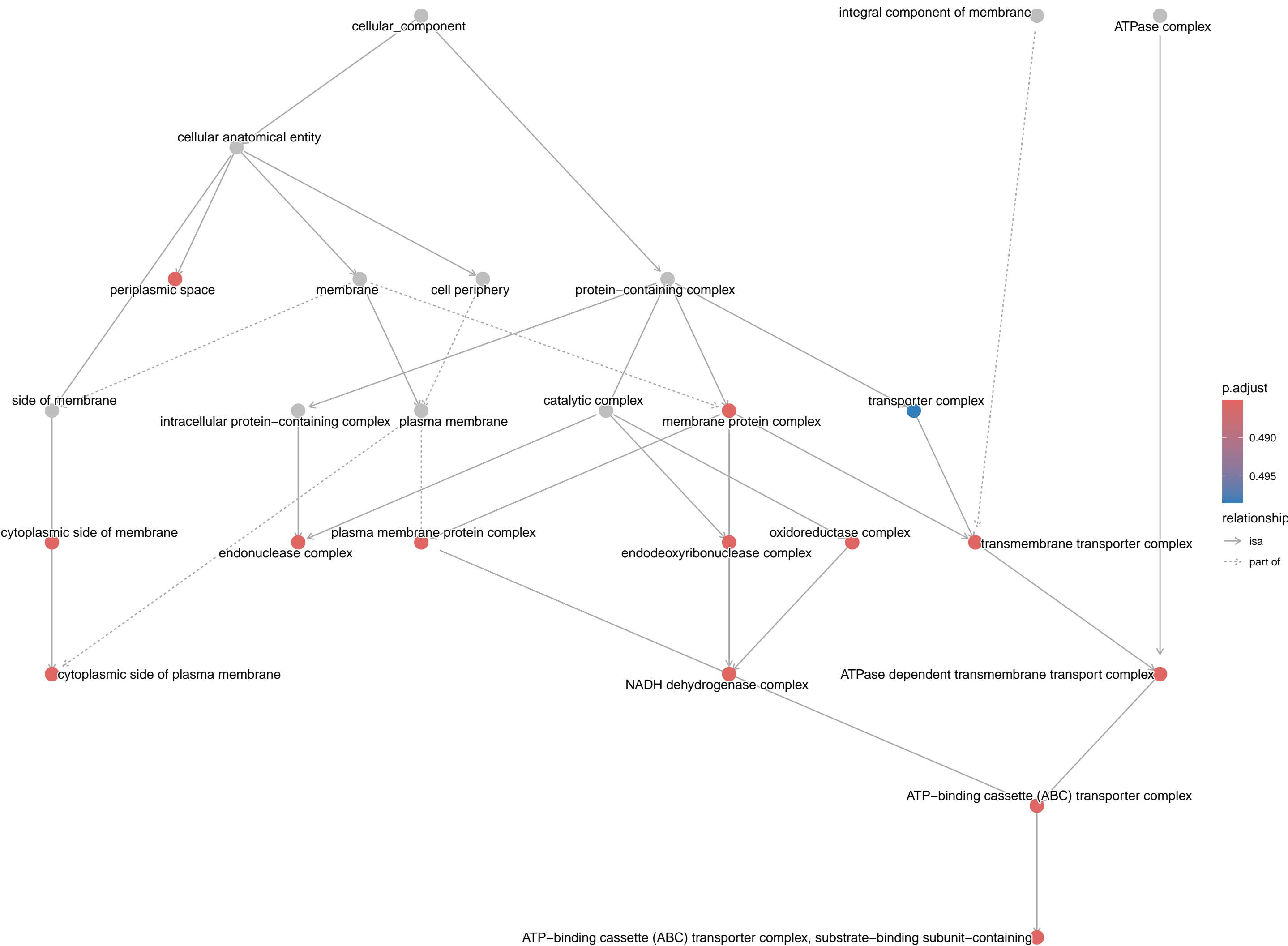


Left genes, nd=1



Left genes, Molecular Function ontology, nd=1





metabolic process

cellular respiration

primary metabolic process

aerobic respiration

tricarboxylic acid cycle

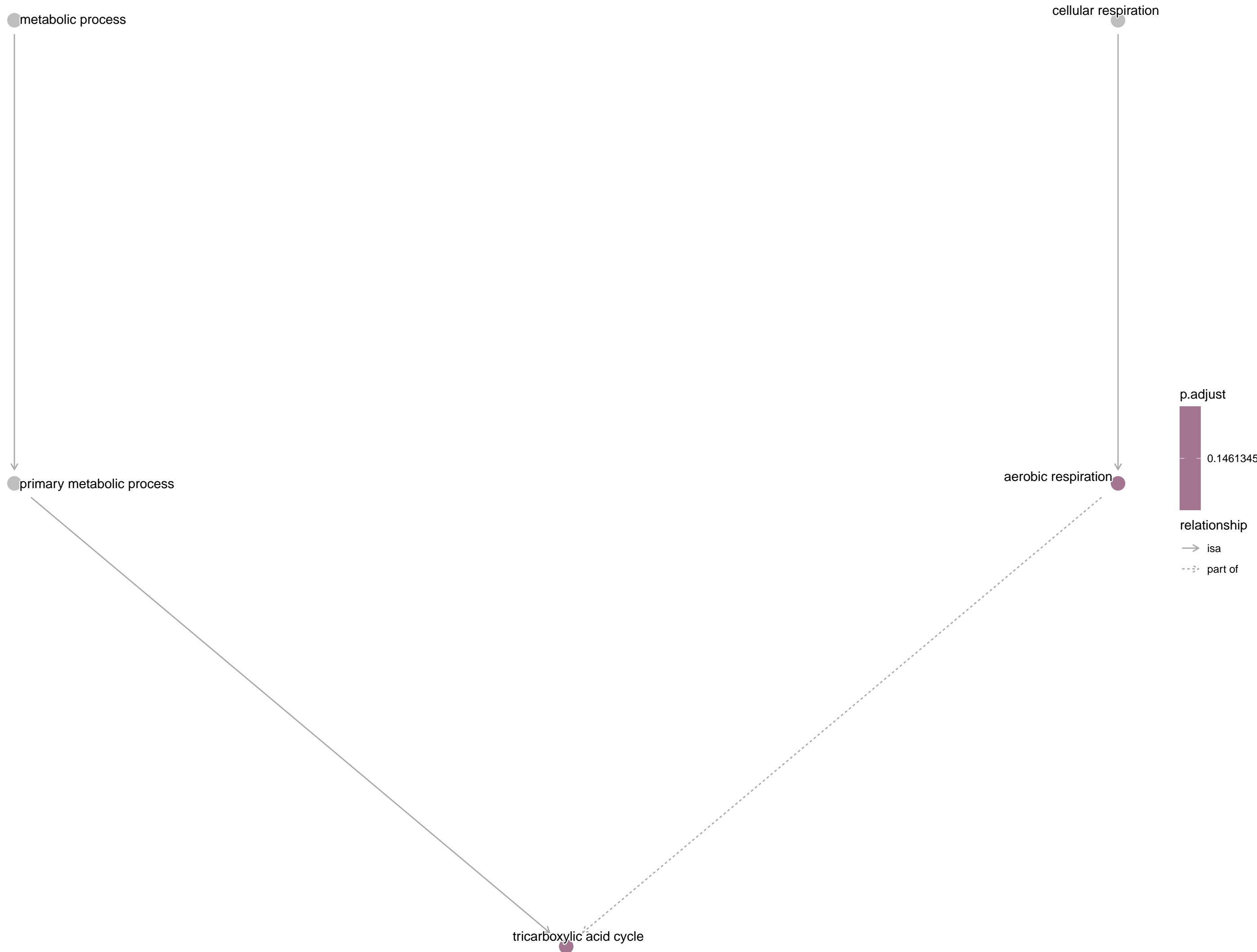
p.adjust

0.1461345

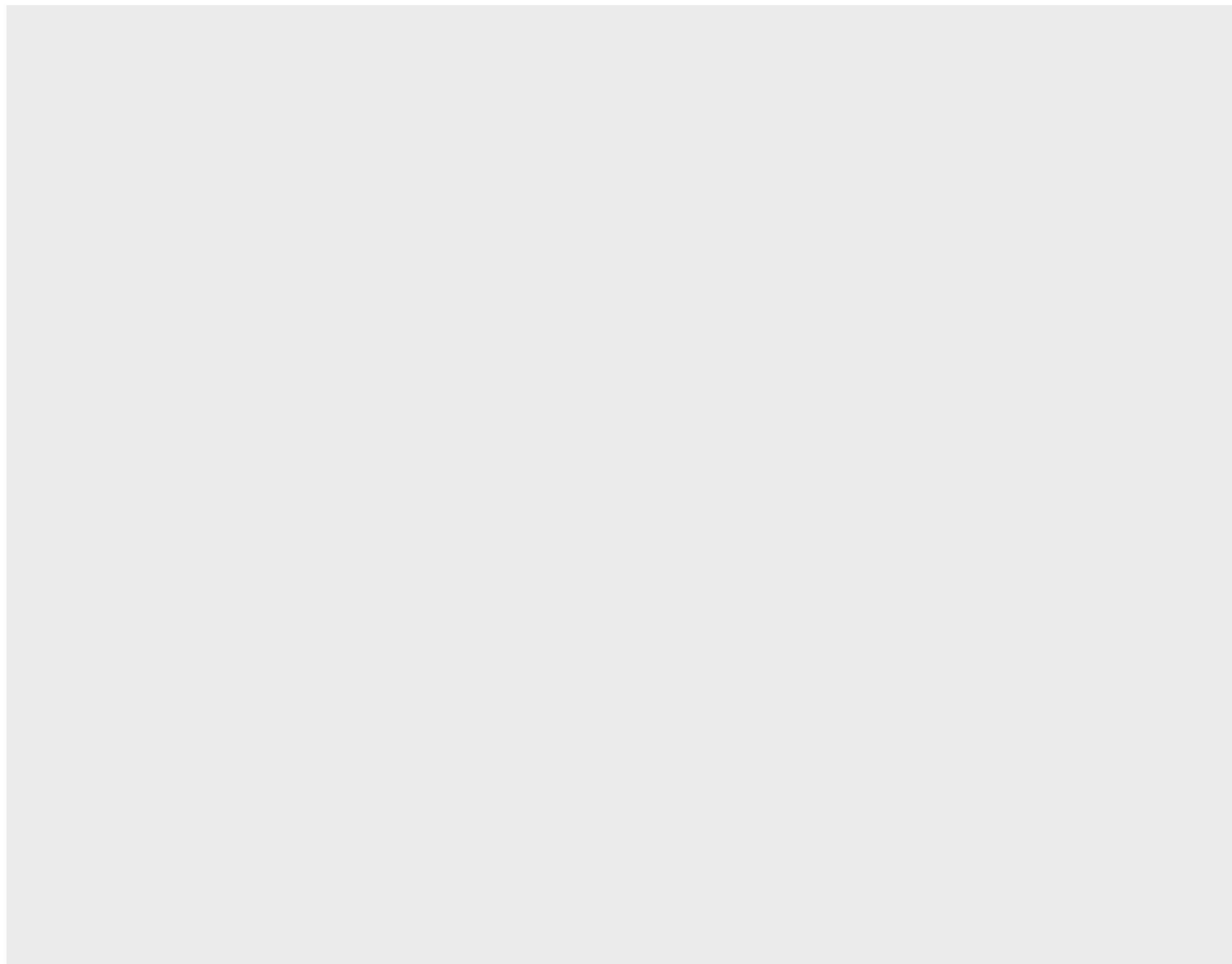
relationship

→ isa

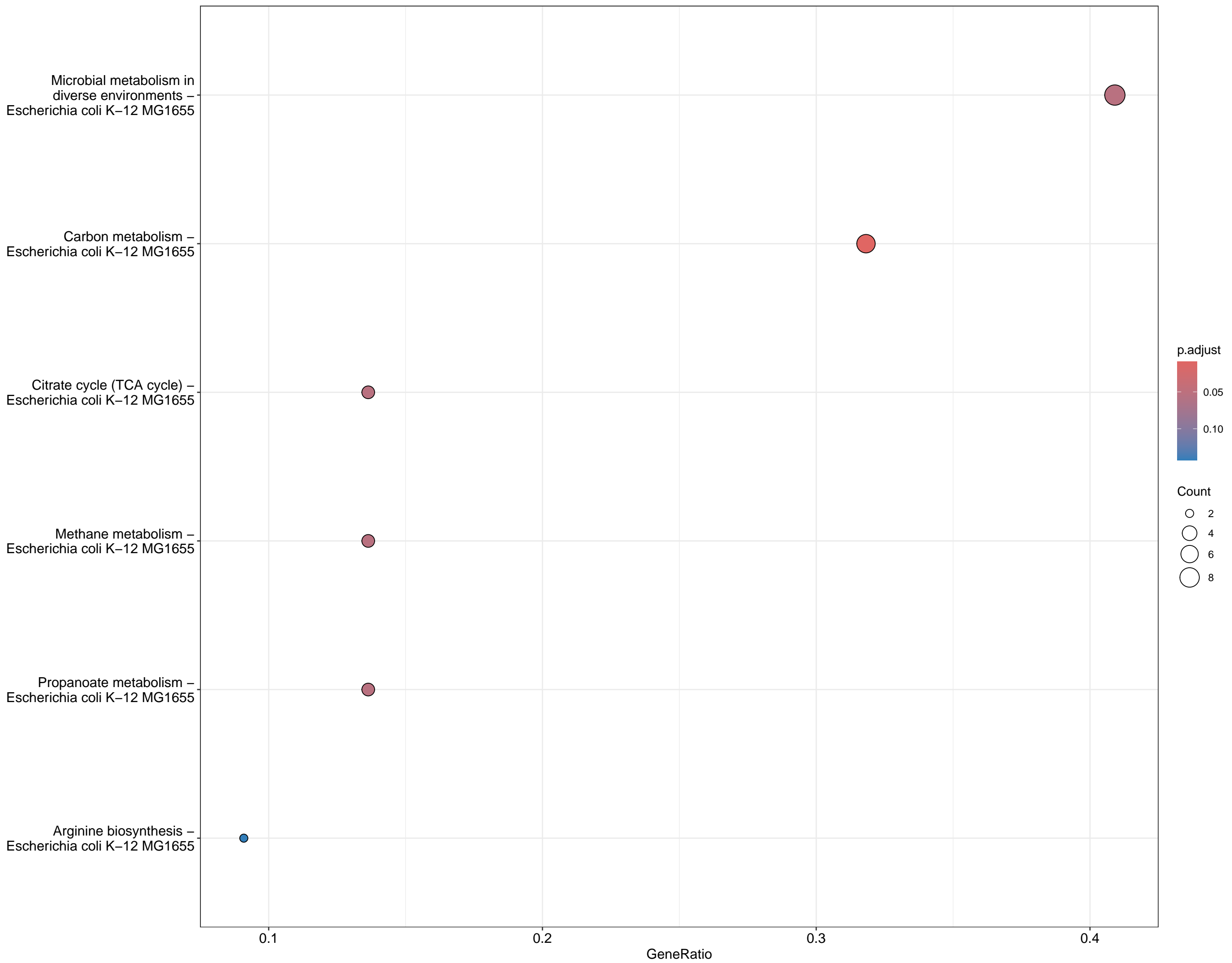
-.-> part of



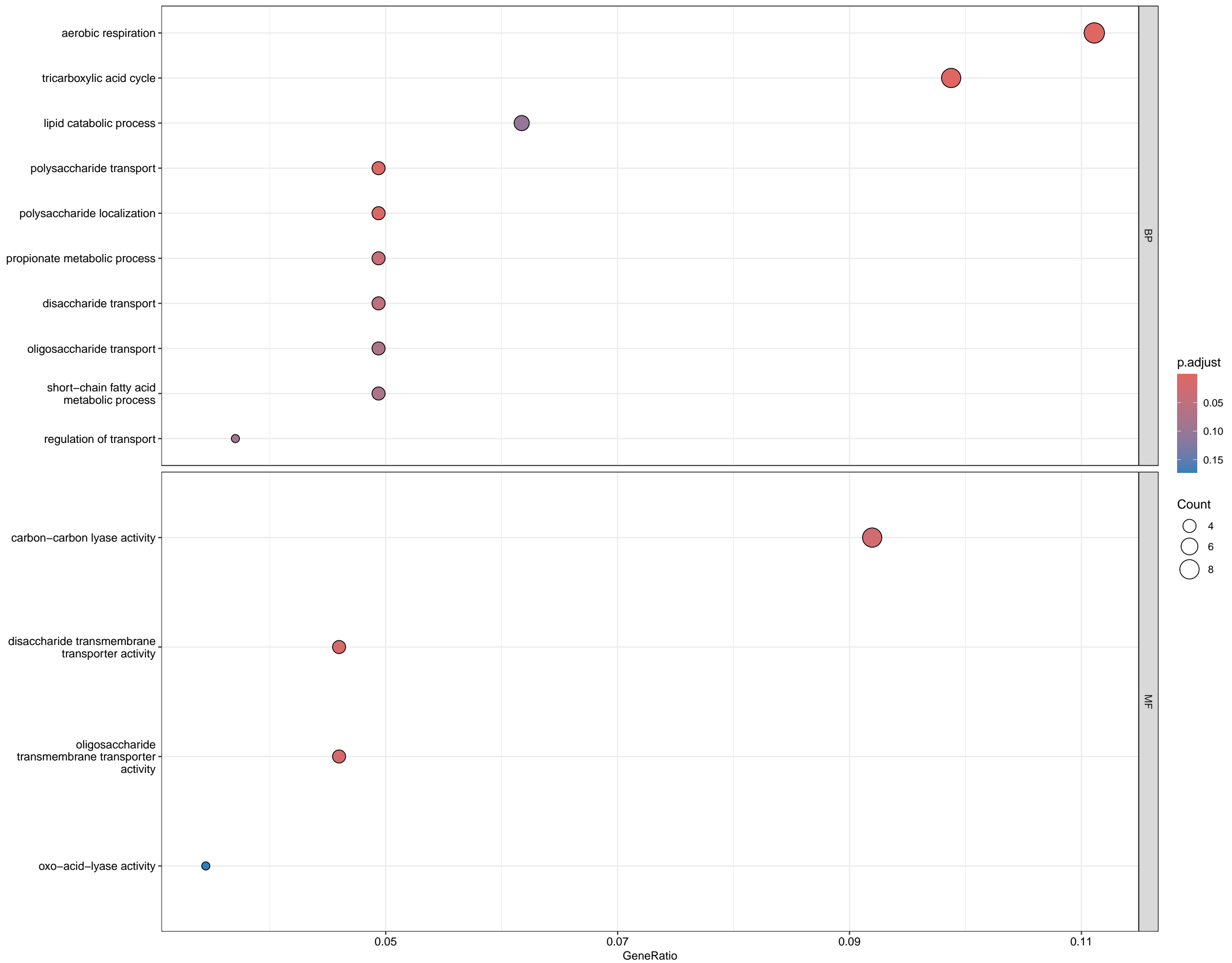
No KEGG enrichment found for right genes, nd=1

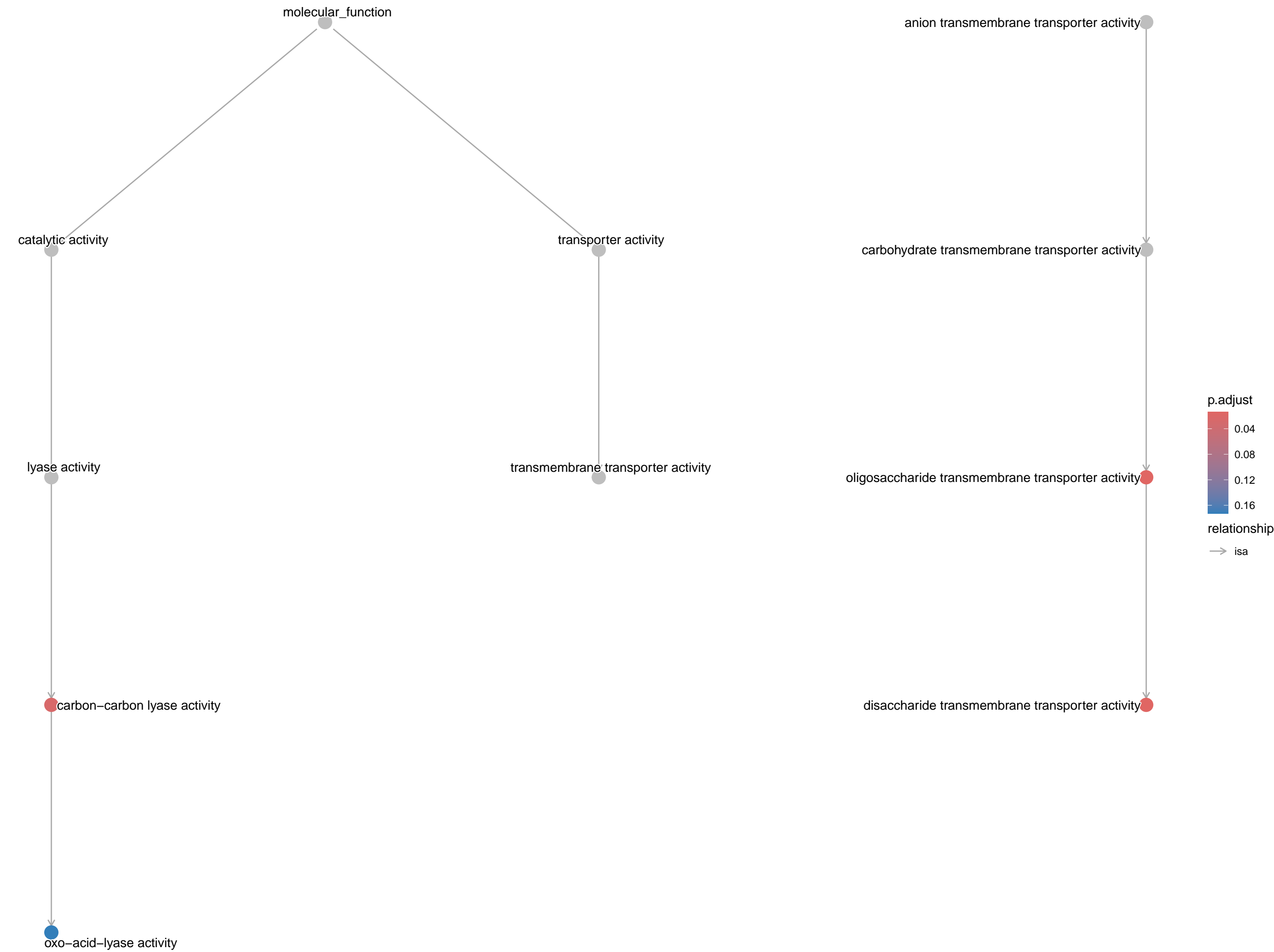


Left genes, KEGG, nd=1

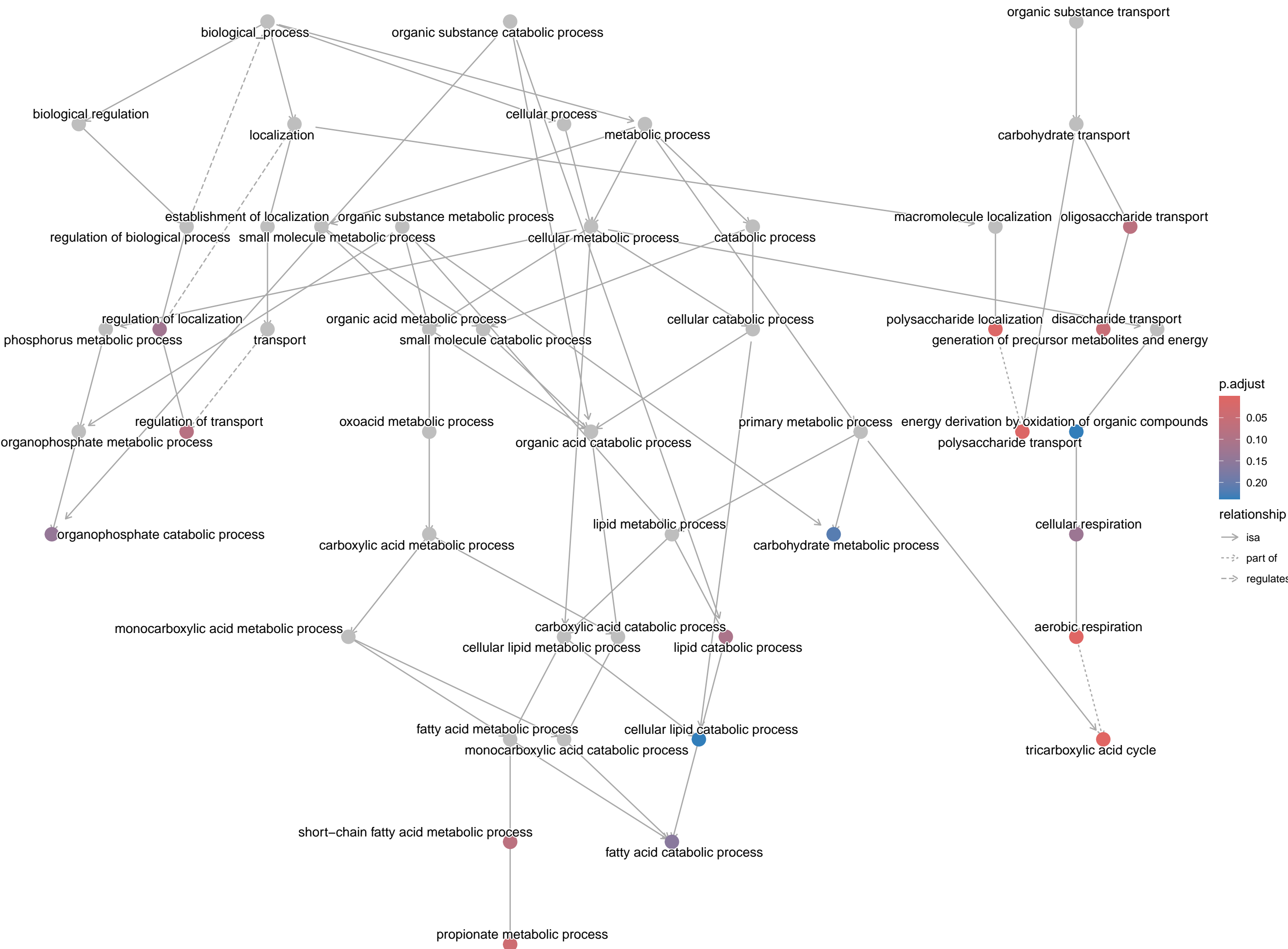


Right genes, nd=2

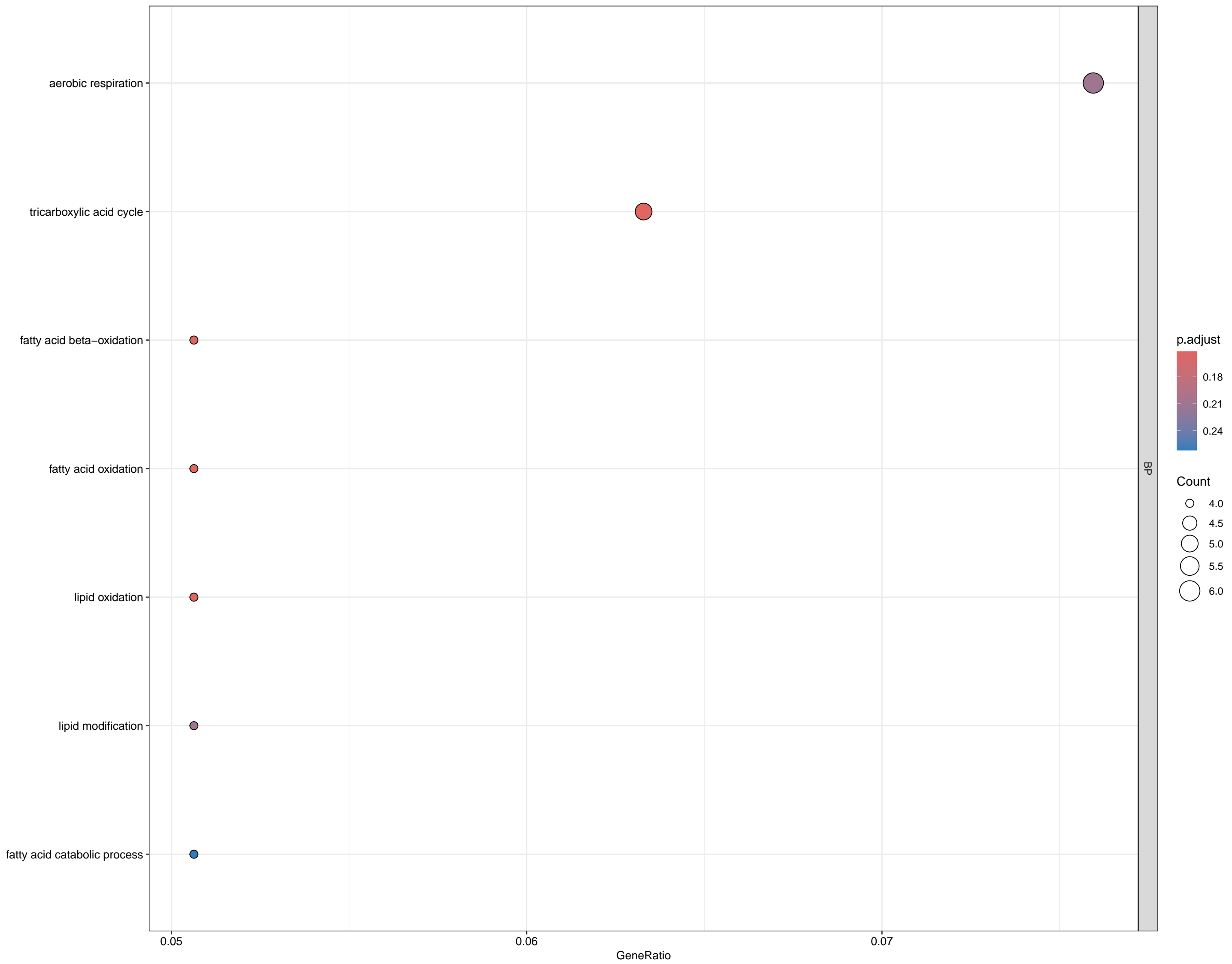




Right genes, Biological Process onthology, nd=2

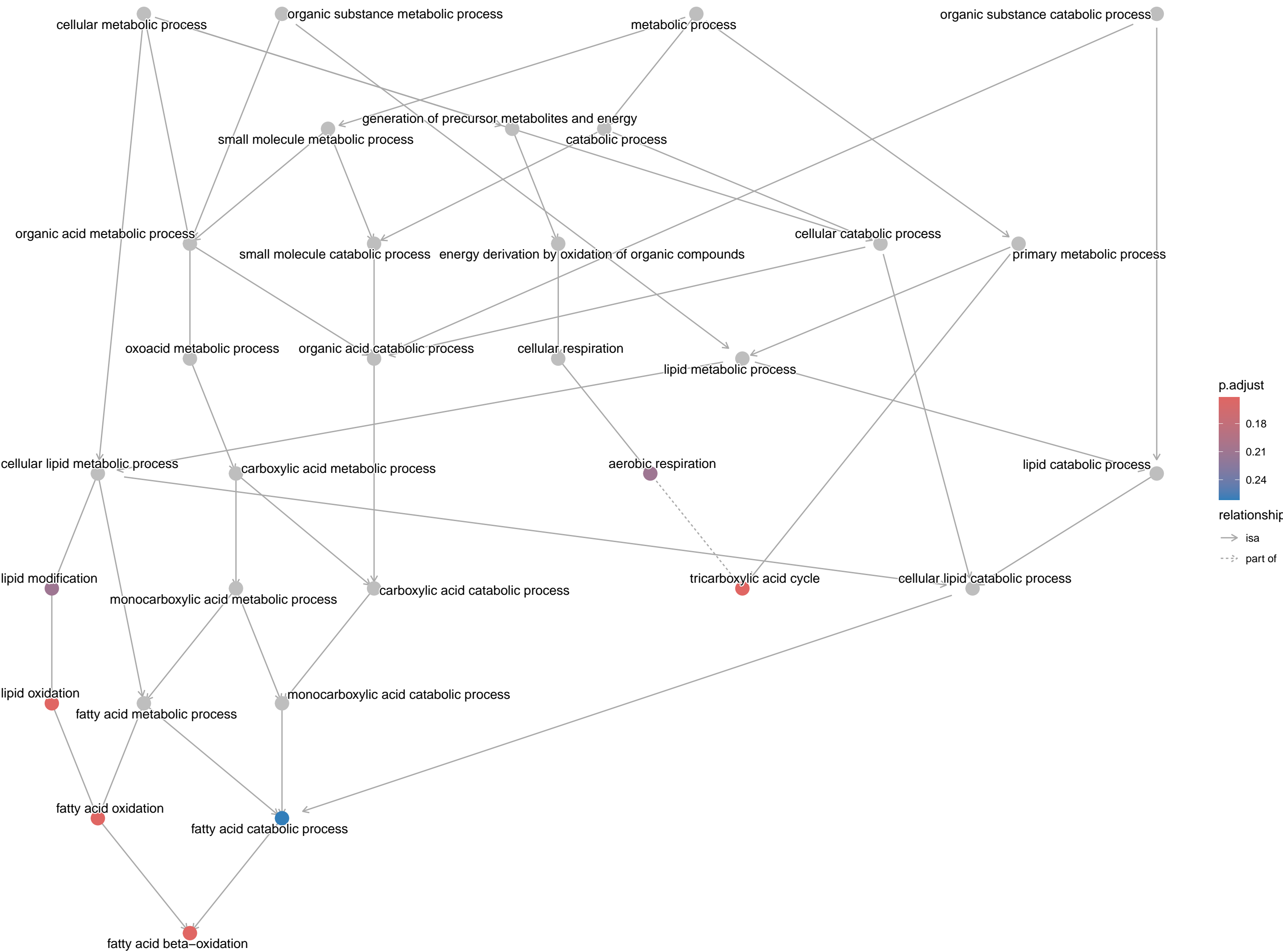


Left genes, nd=2

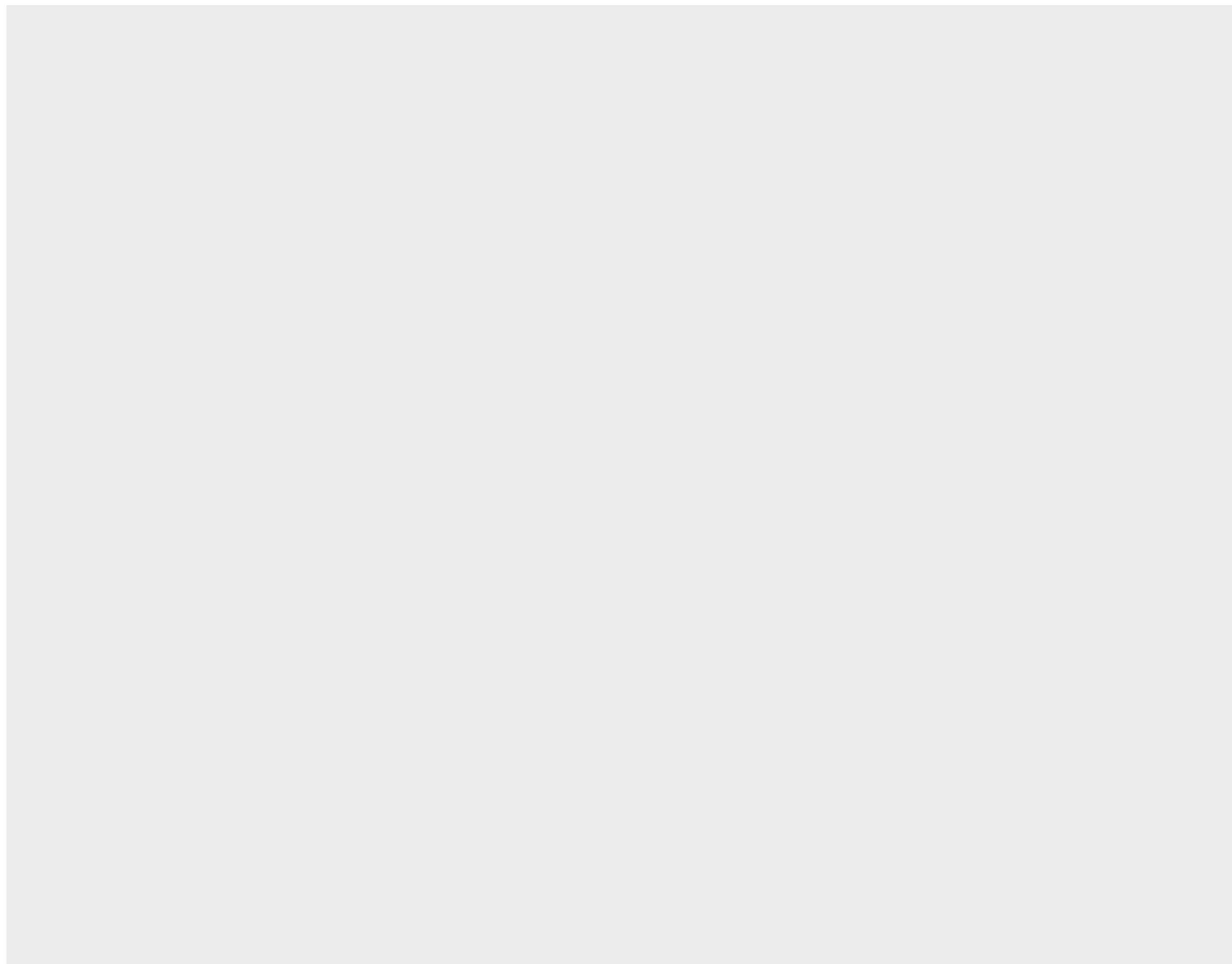


Left genes, Molecular Function onthology, nd=2

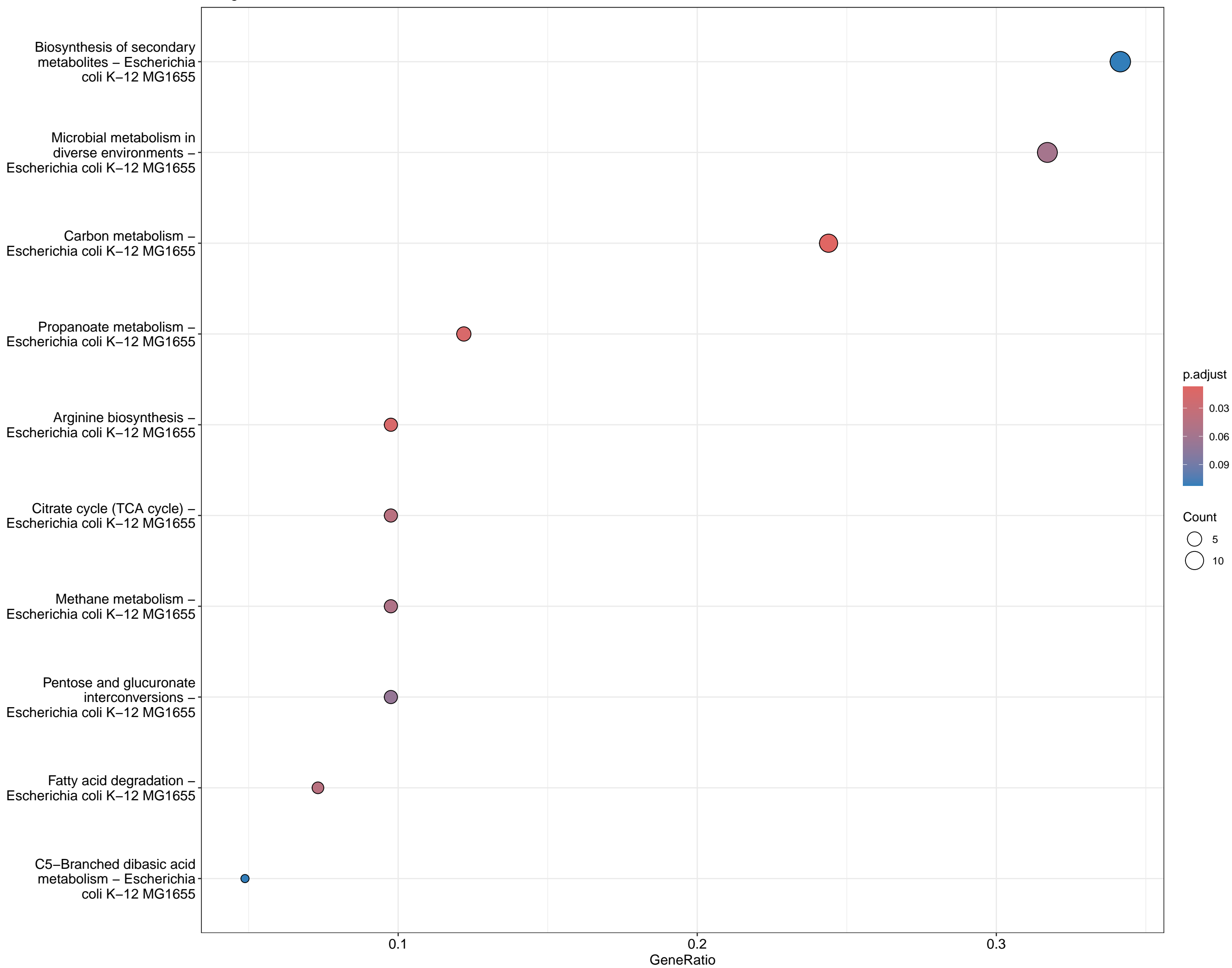
Left genes, Cellular Component onthology, nd=2



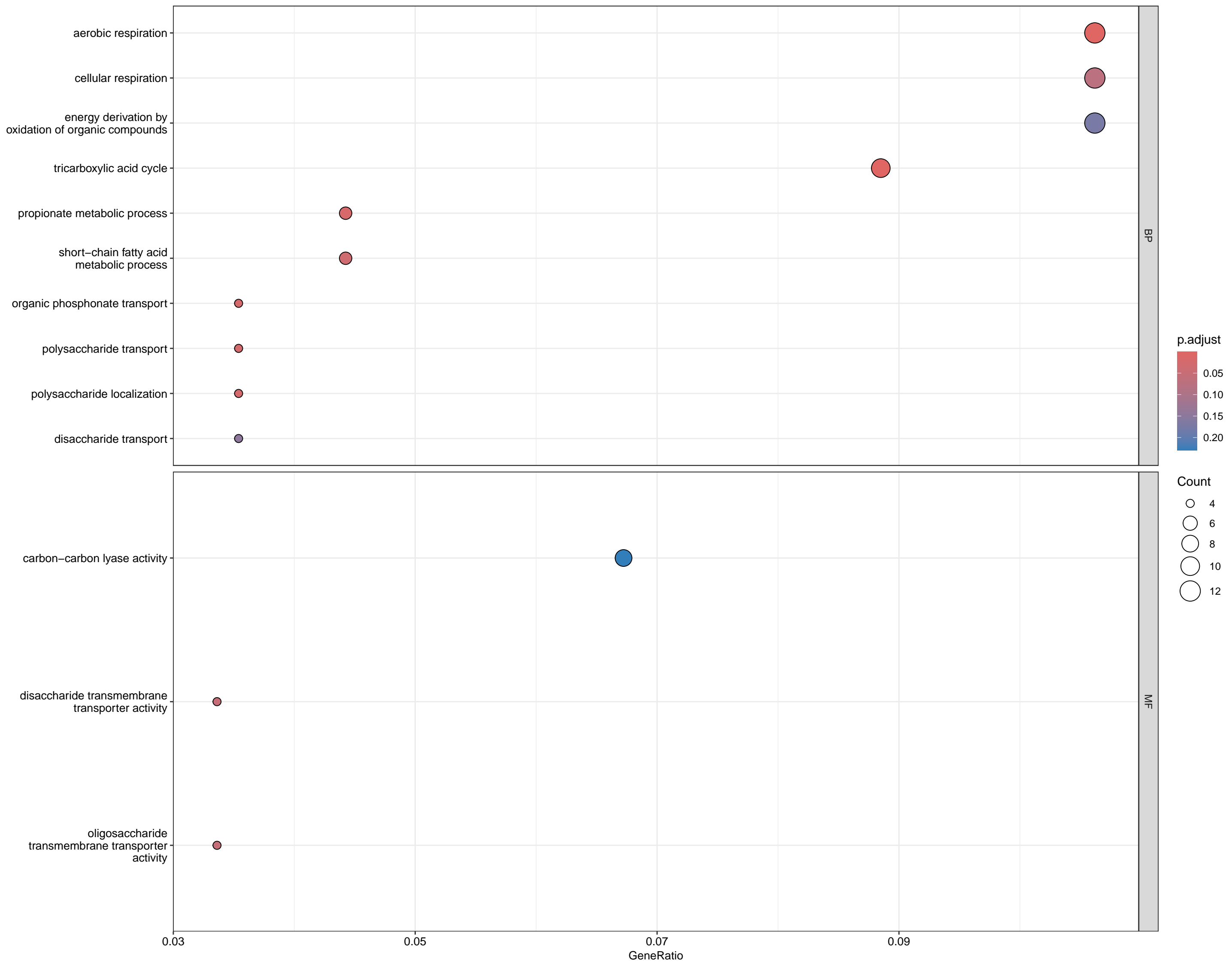
No KEGG enrichment found for right genes, nd=2

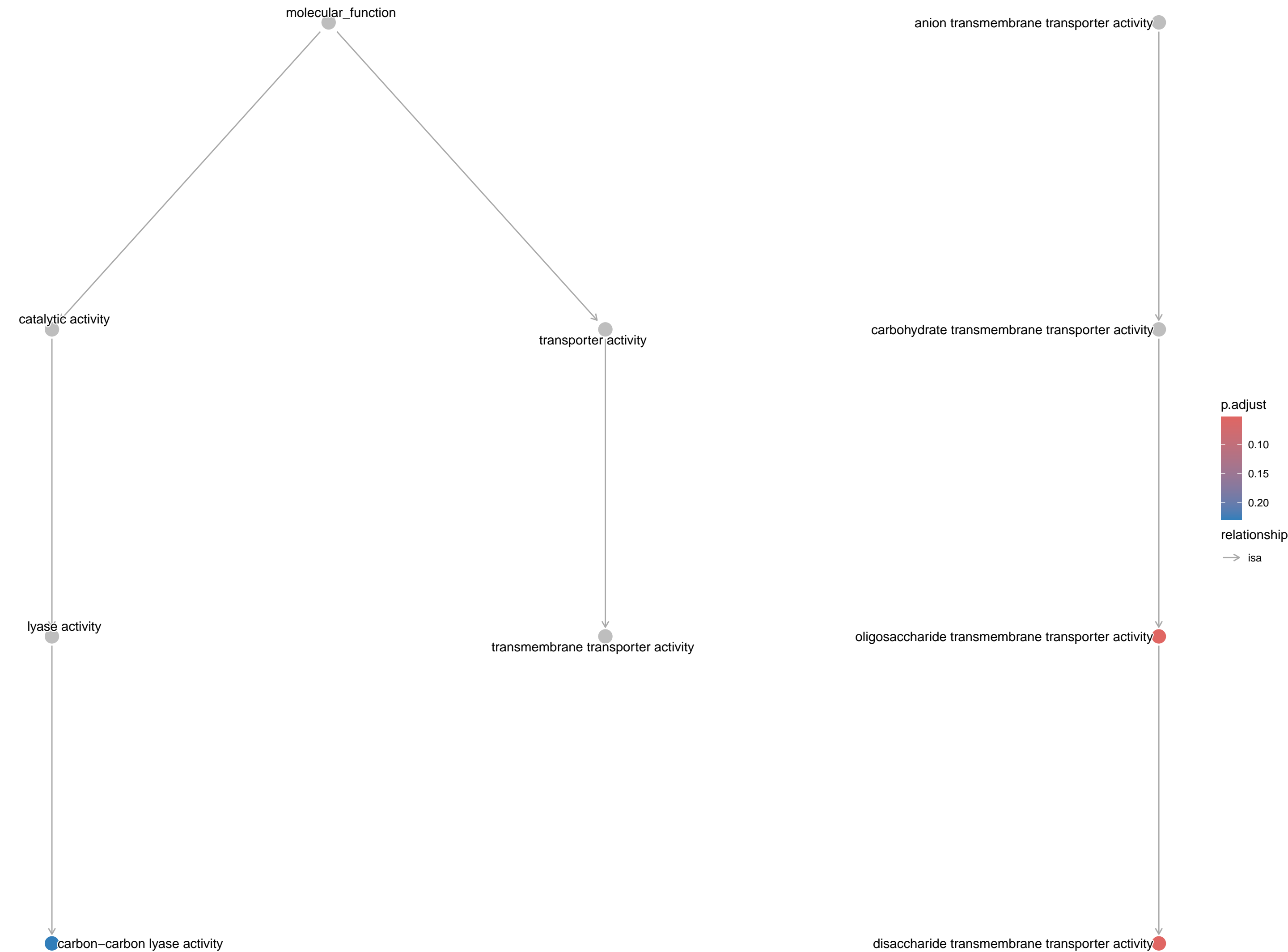


Left genes, KEGG, nd=2

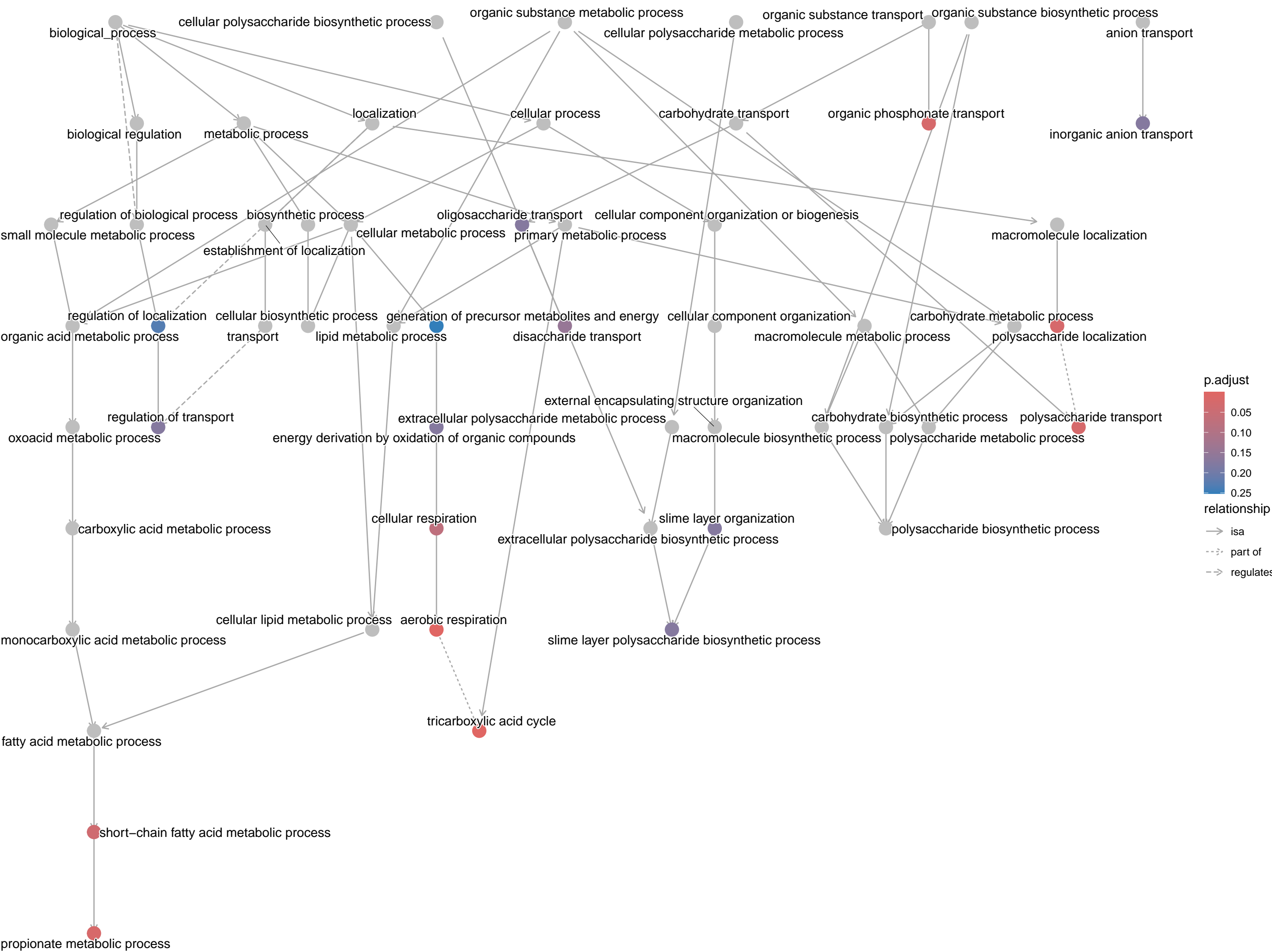


Right genes, nd=3





Right genes, Biological Process ontology, nd=3

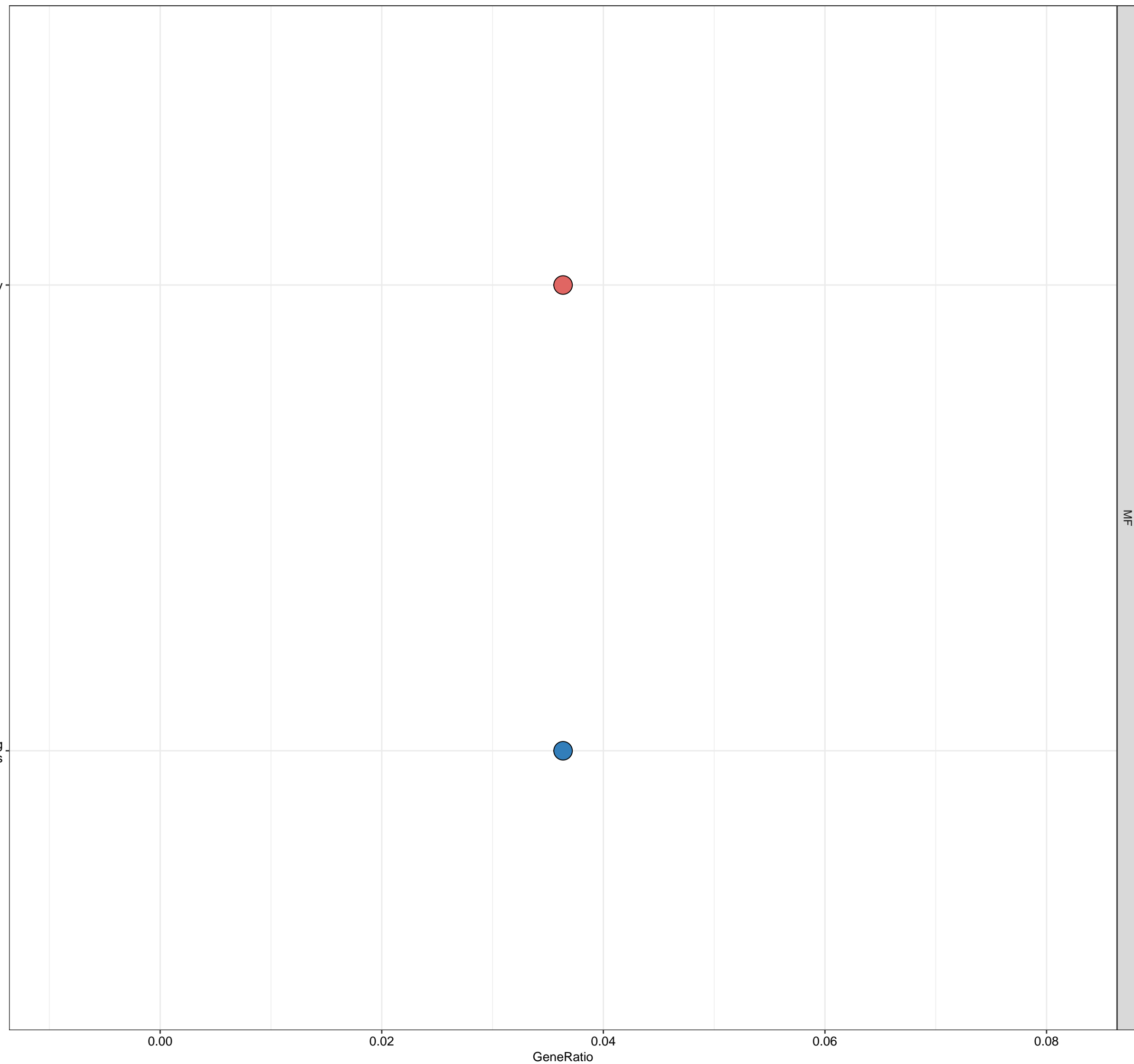
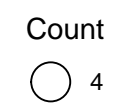
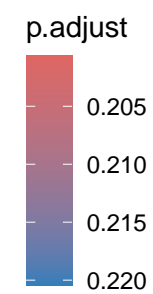


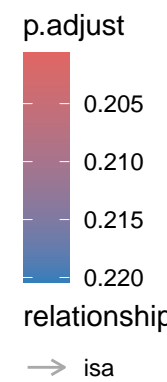
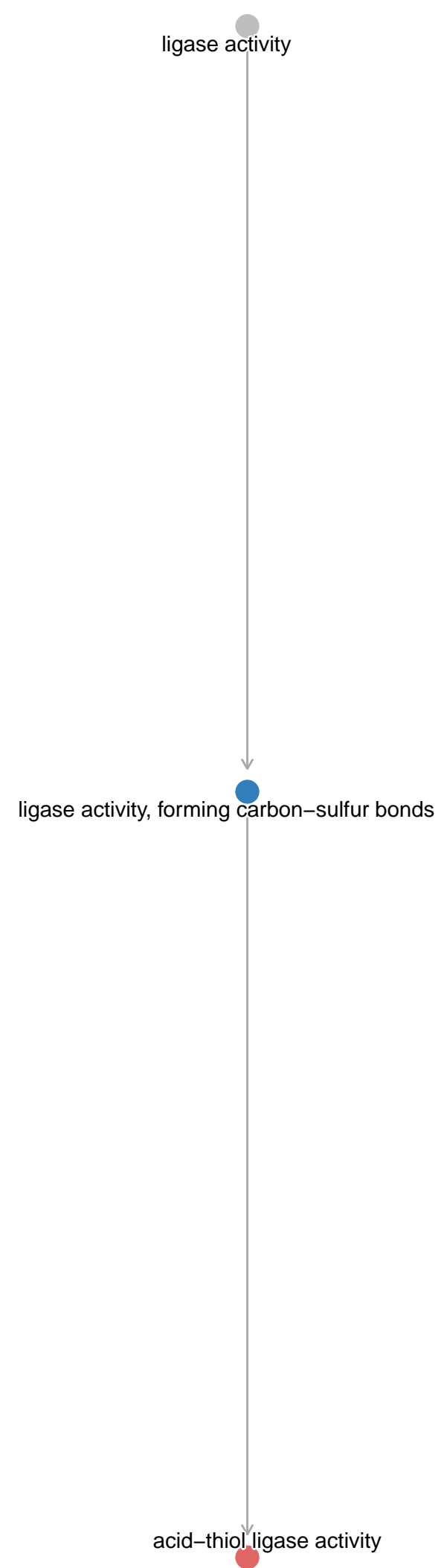
Left genes, nd=3

acid–thiol ligase activity

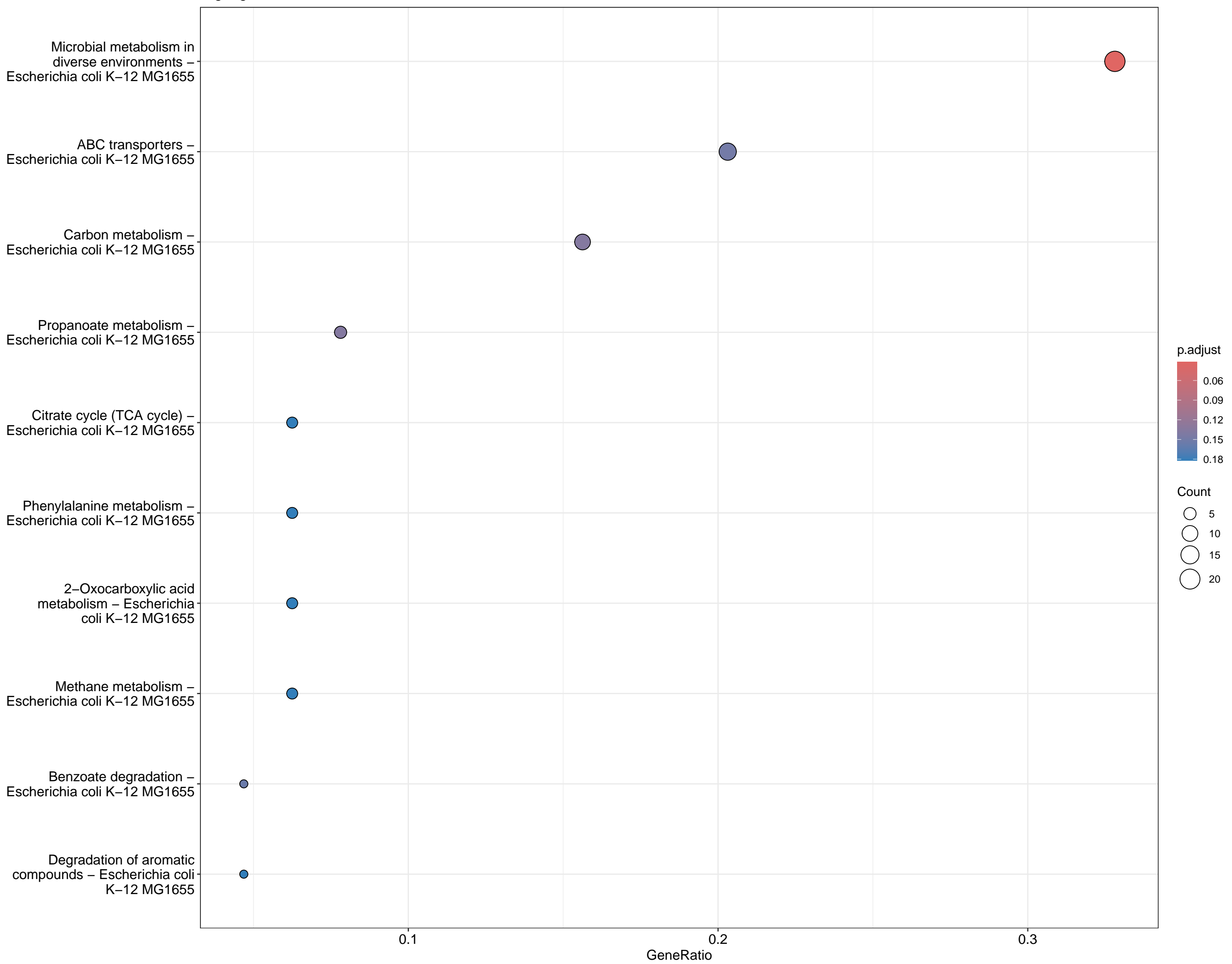
ligase activity, forming
carbon–sulfur bonds

MF





Left genes, Cellular Component onthology, nd=3



Left genes, KEGG, nd=3

