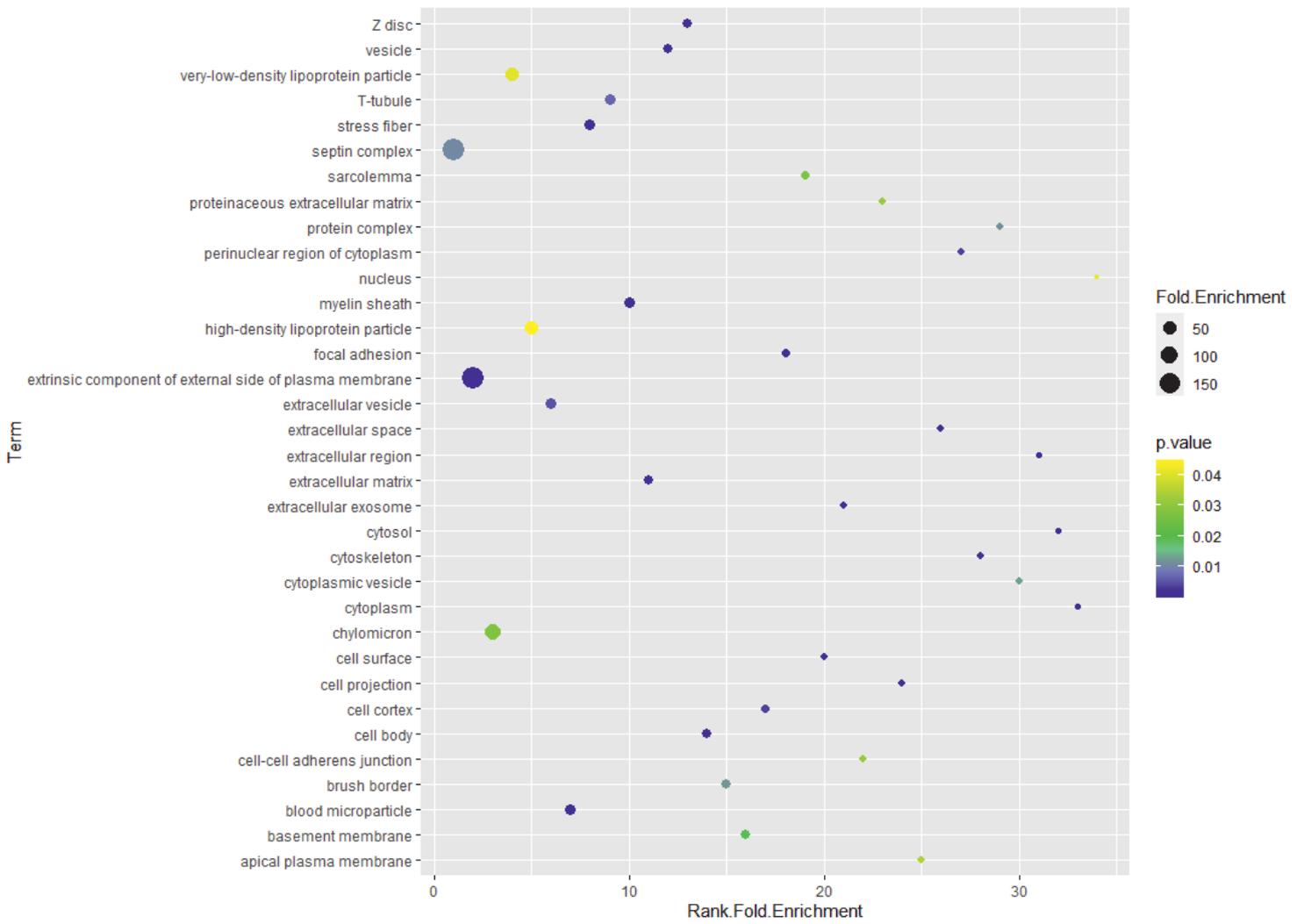


Supplementary Figure S1.

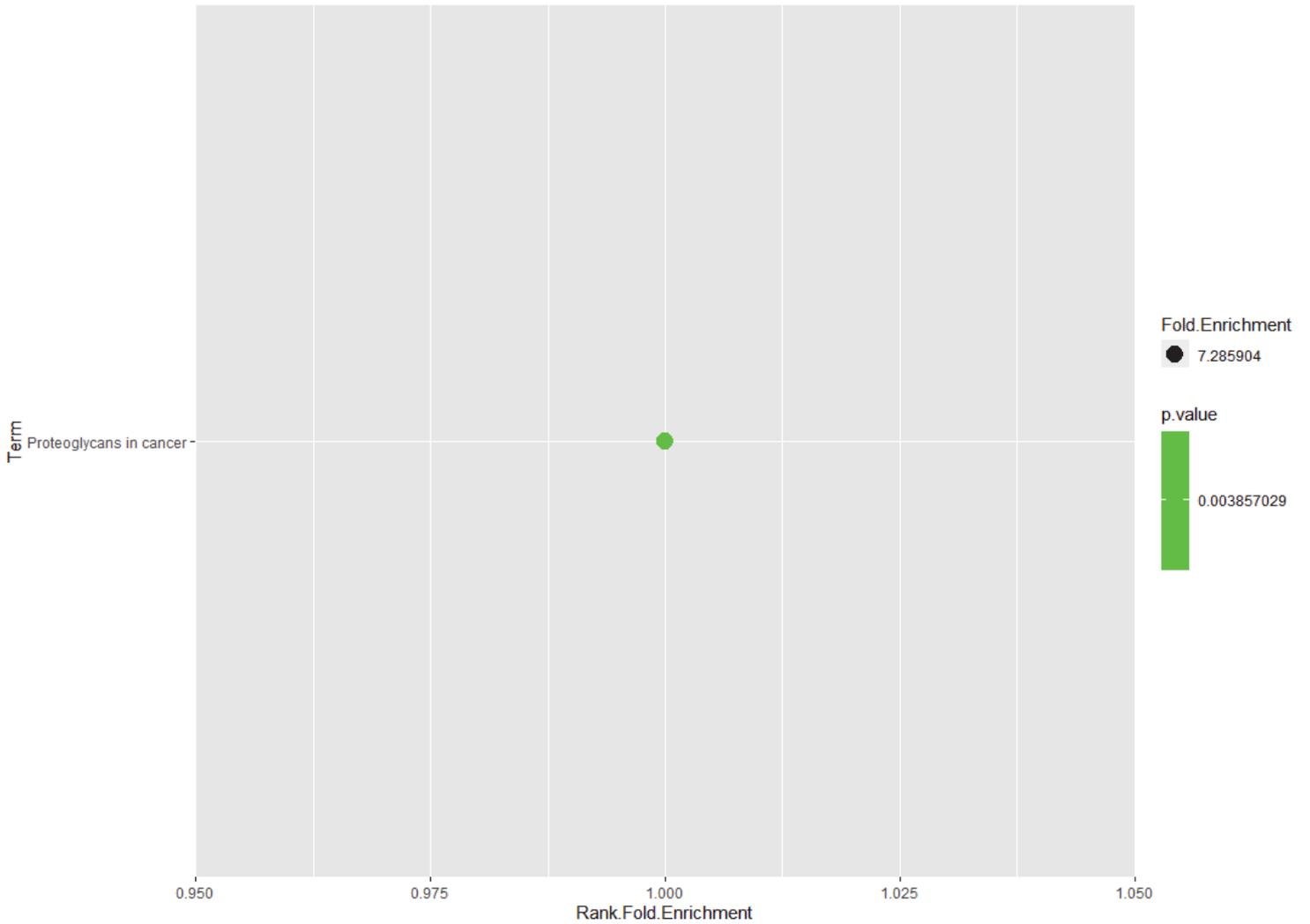
Bubble plot illustration of the “Gene Ontology (GO) term Cellular compartment (CC)” and “Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway” enrichments derived from hierarchical clustering of all quantitated proteins; see also Figure 6A and Table S1.

Terms and pathways were sorted alphabetically, dot sizes indicate fold enrichment values, color gradient corresponds to corrected p-values (Benjamini-Hochberg), and highest fold enrichment scores were sorted by rank (Rank Fold Enrichment).

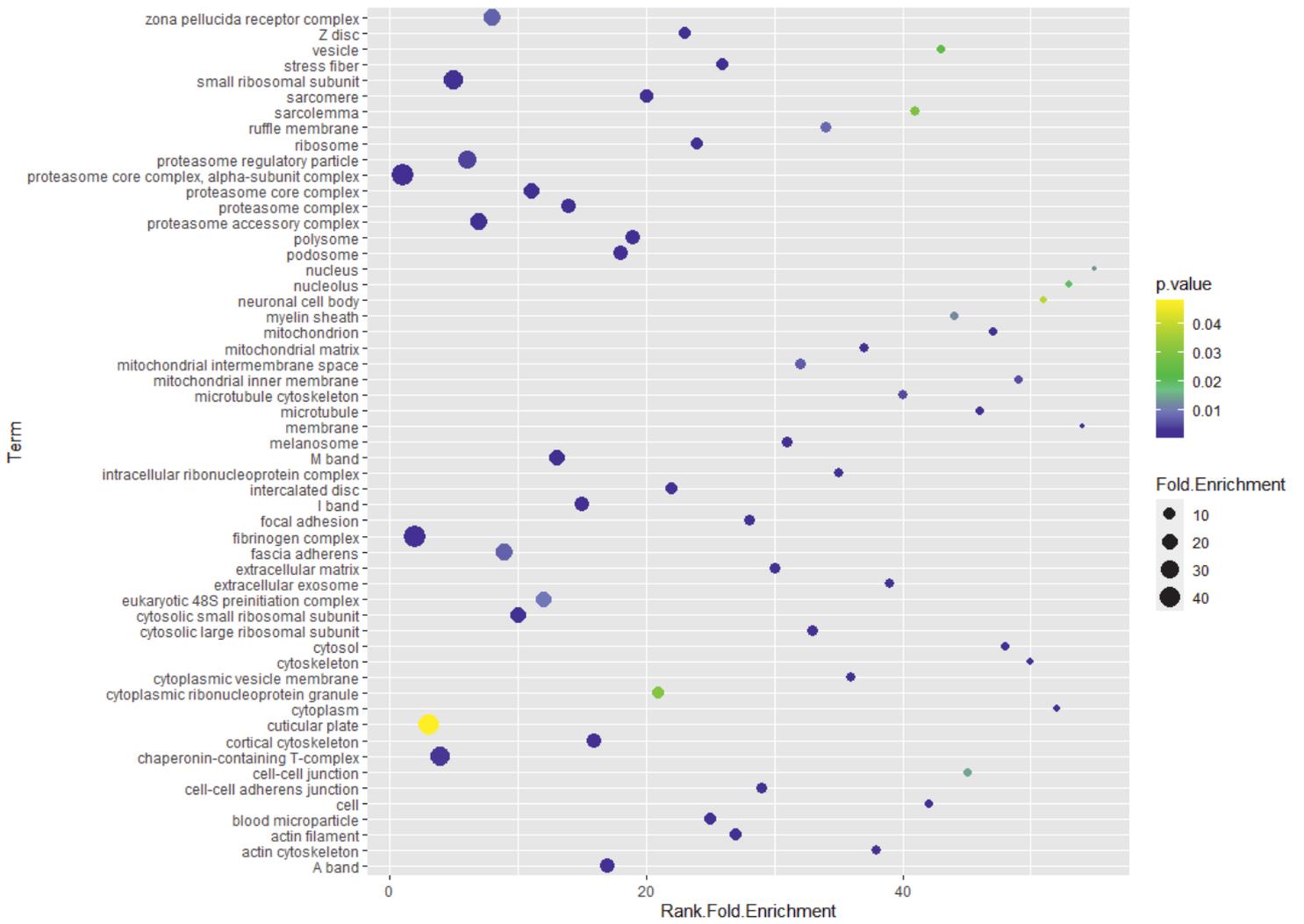
Cluster 1 GO Term CC



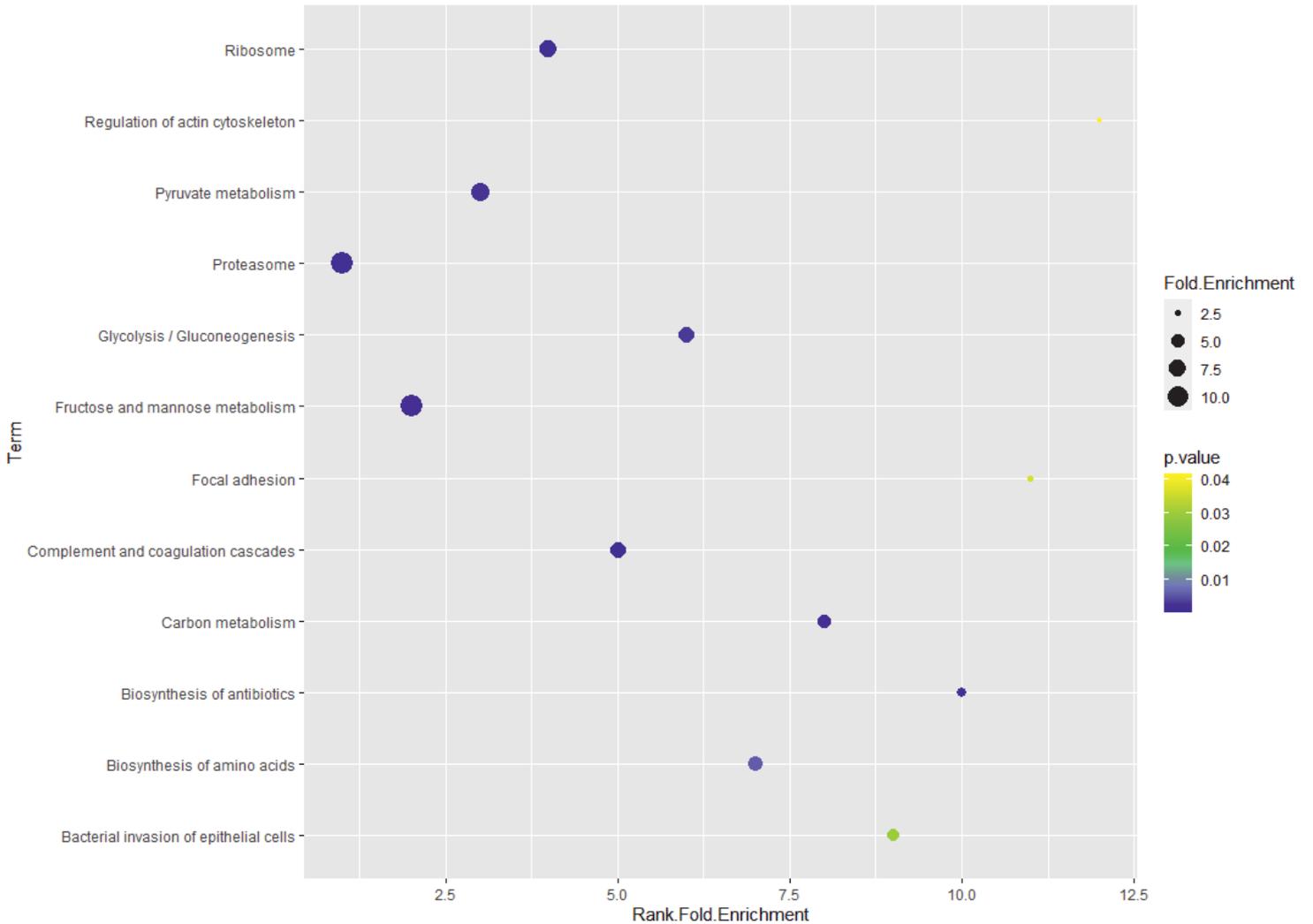
Cluster 1 KEGG Pathway



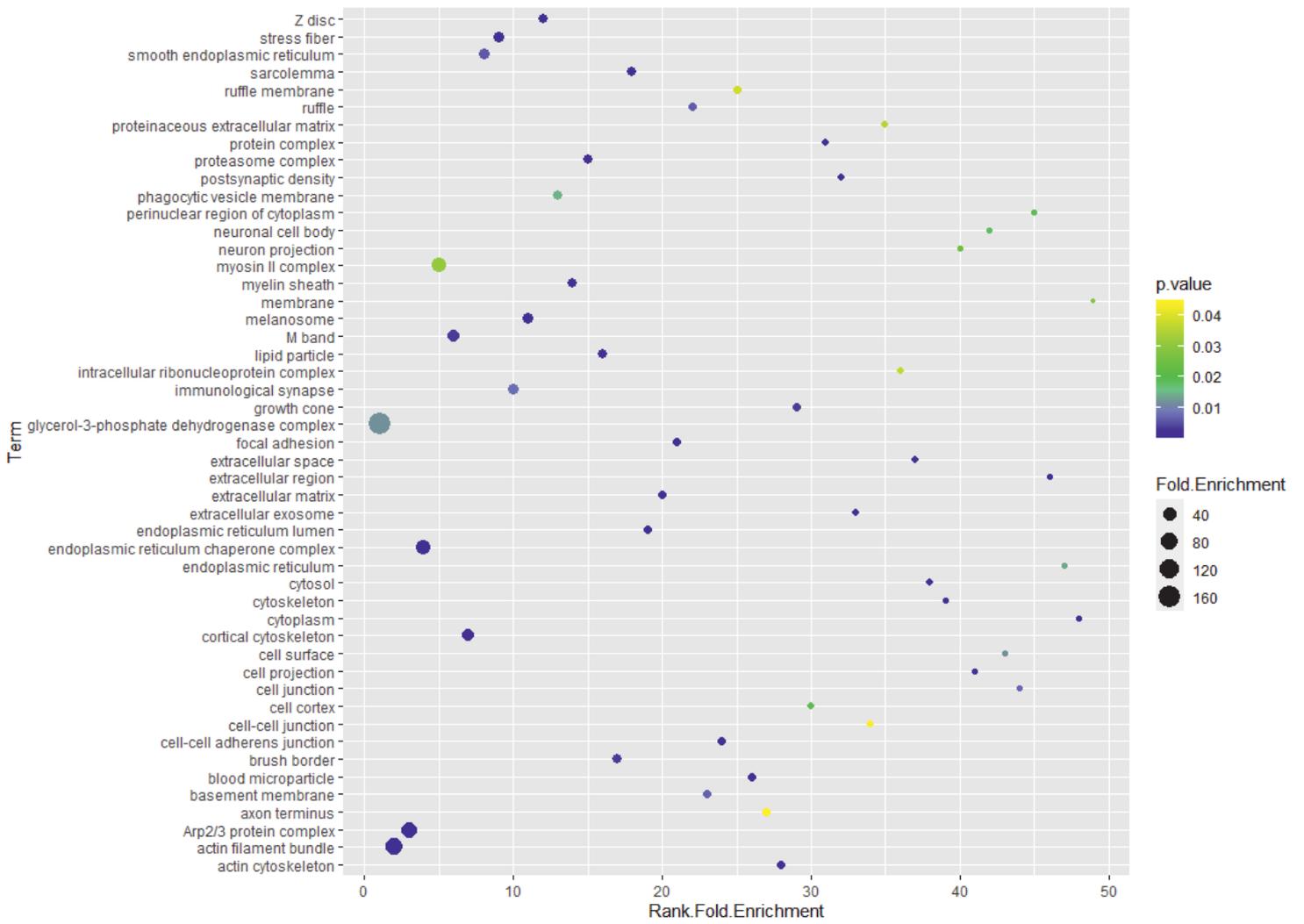
Cluster 2 GO Term CC



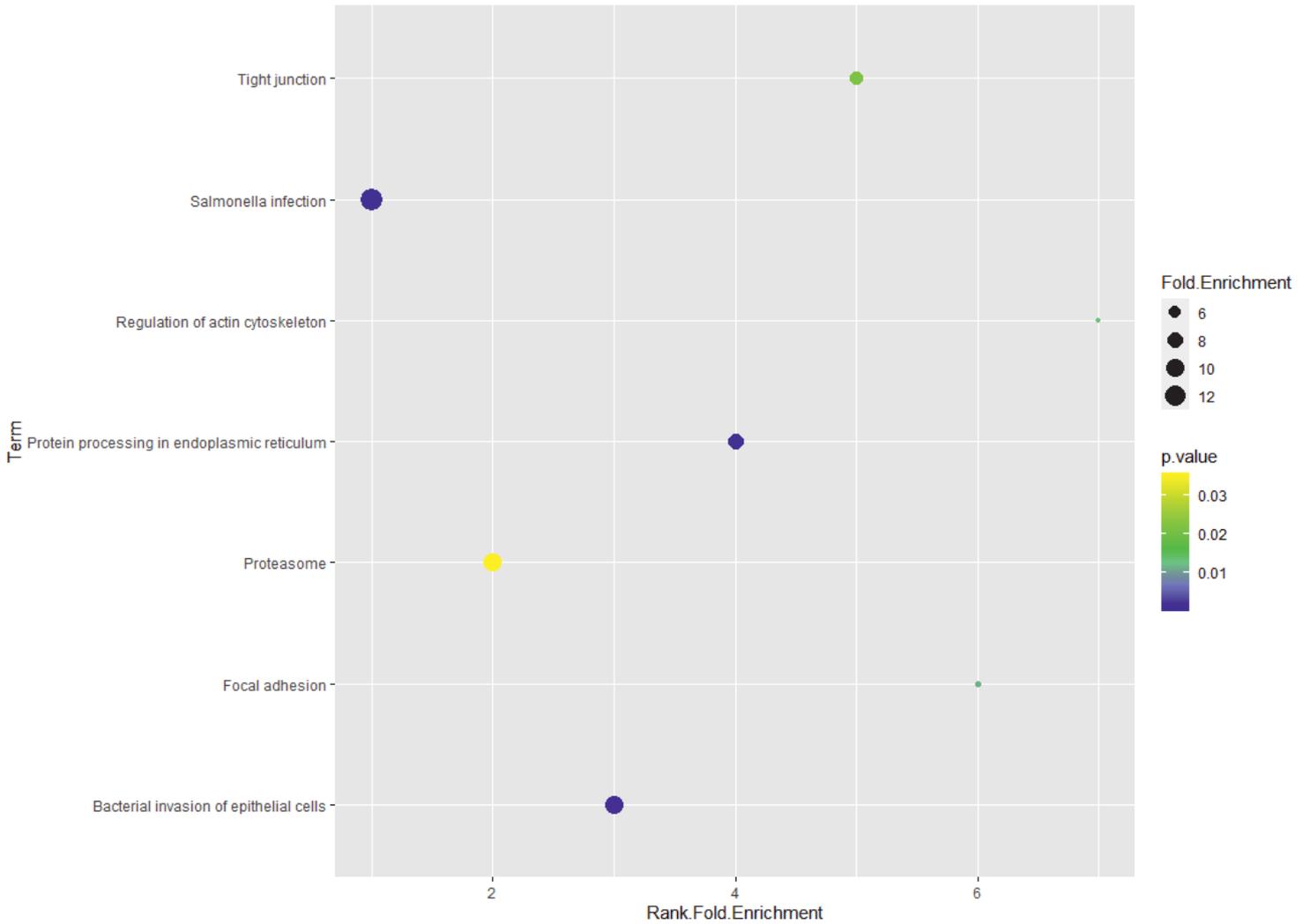
Cluster 2 KEGG Pathway



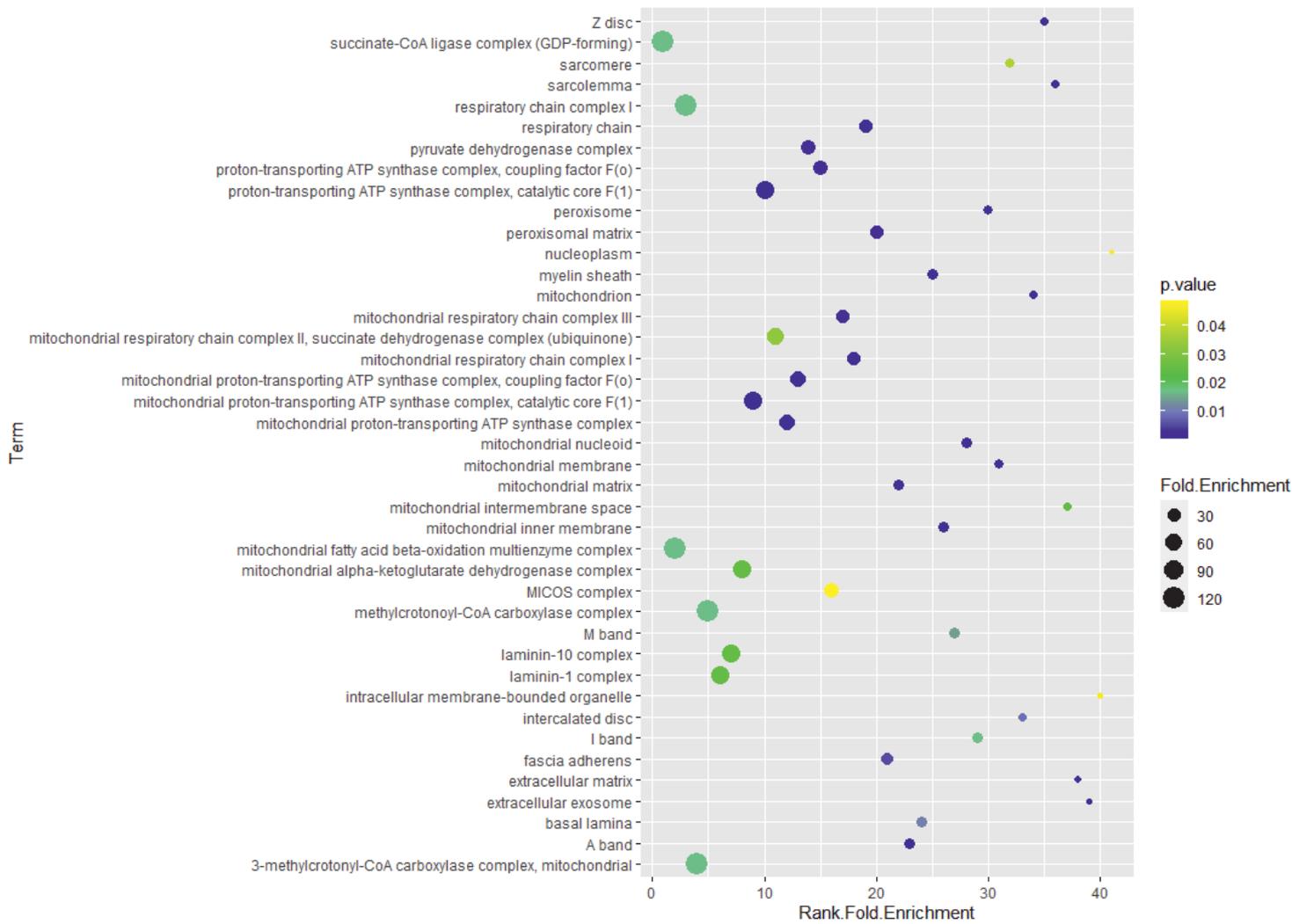
Cluster 3 GO Term CC



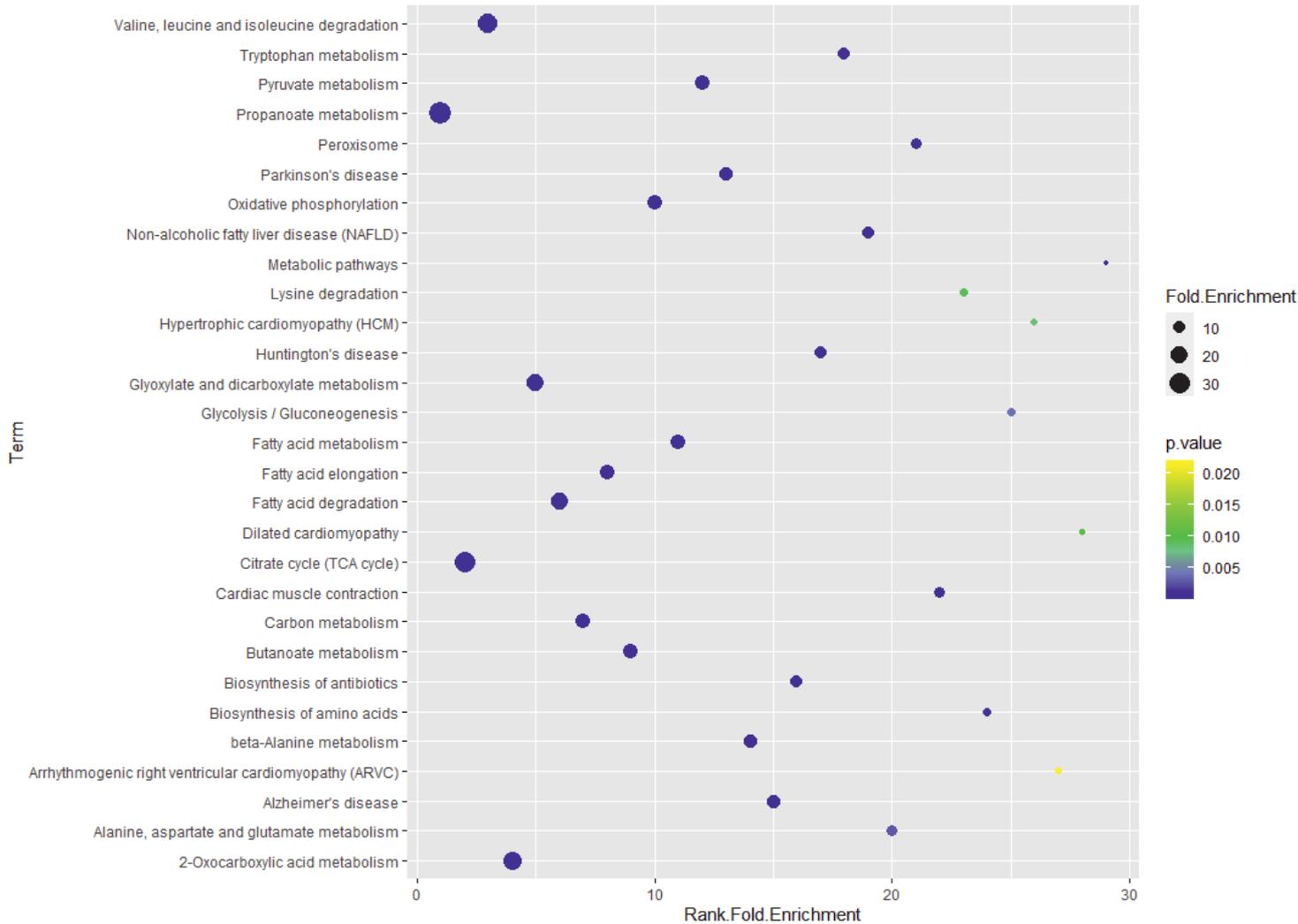
Cluster 3 KEGG Pathway



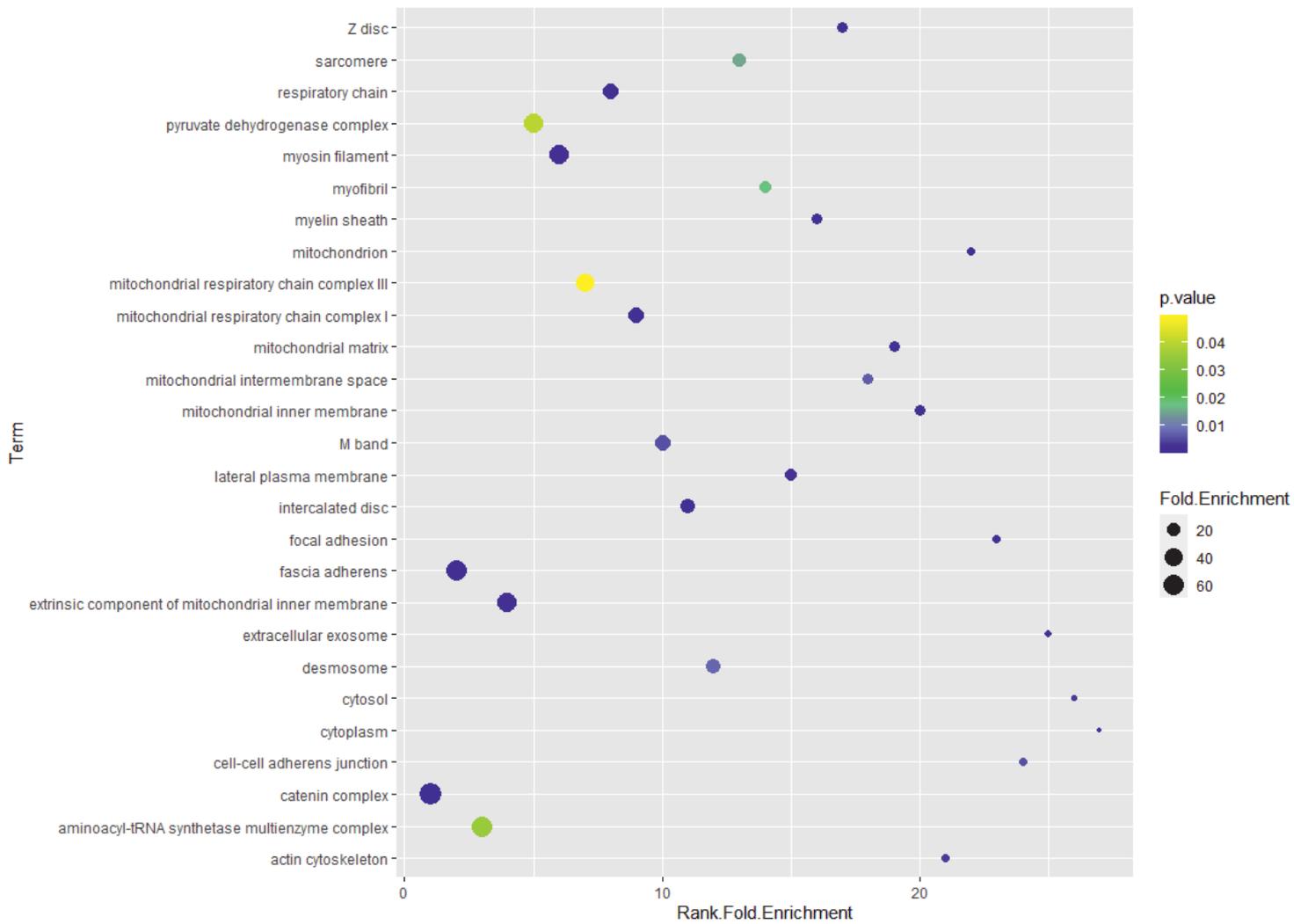
Cluster 4 GO Term CC



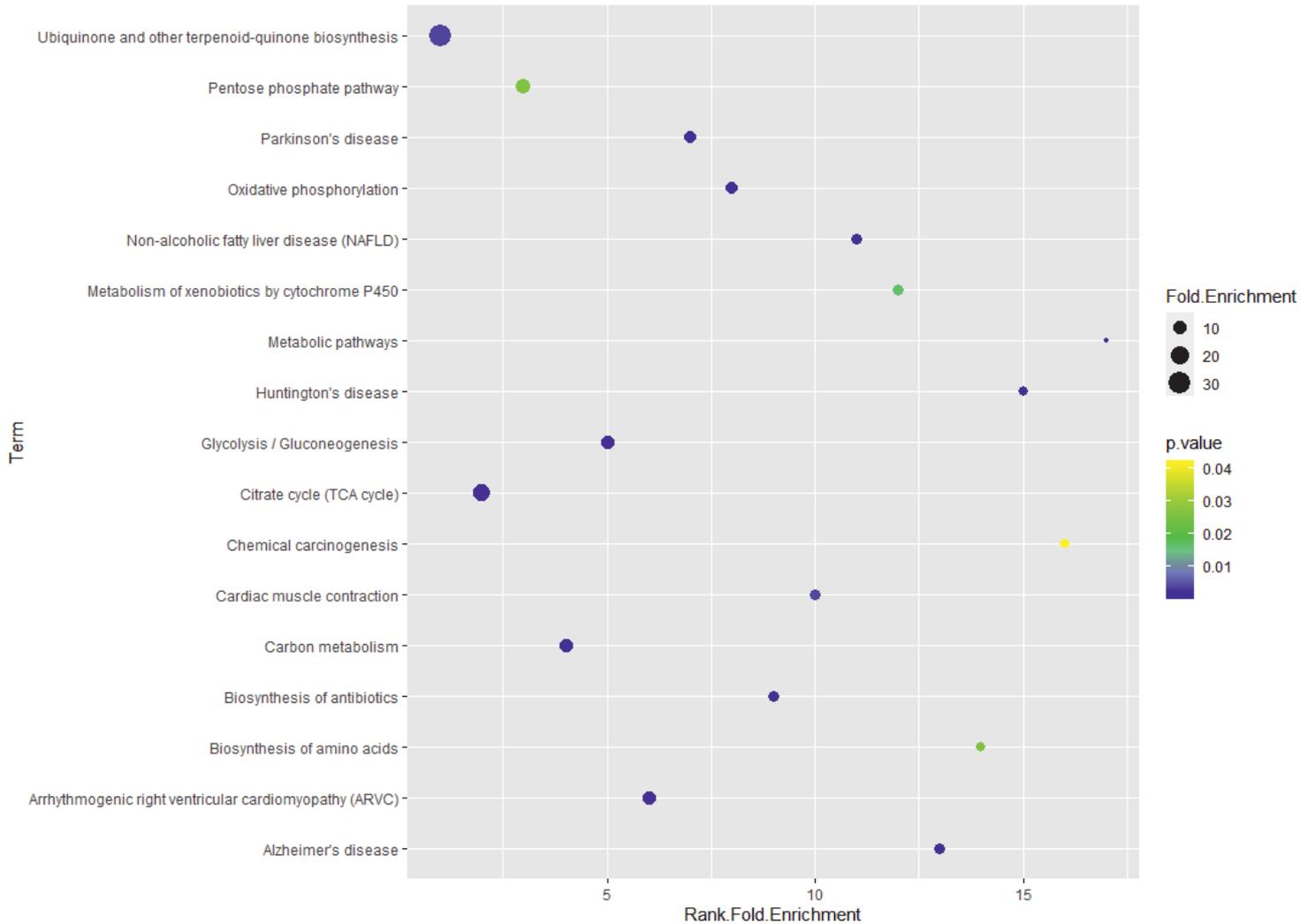
Cluster 4 KEGG Pathway



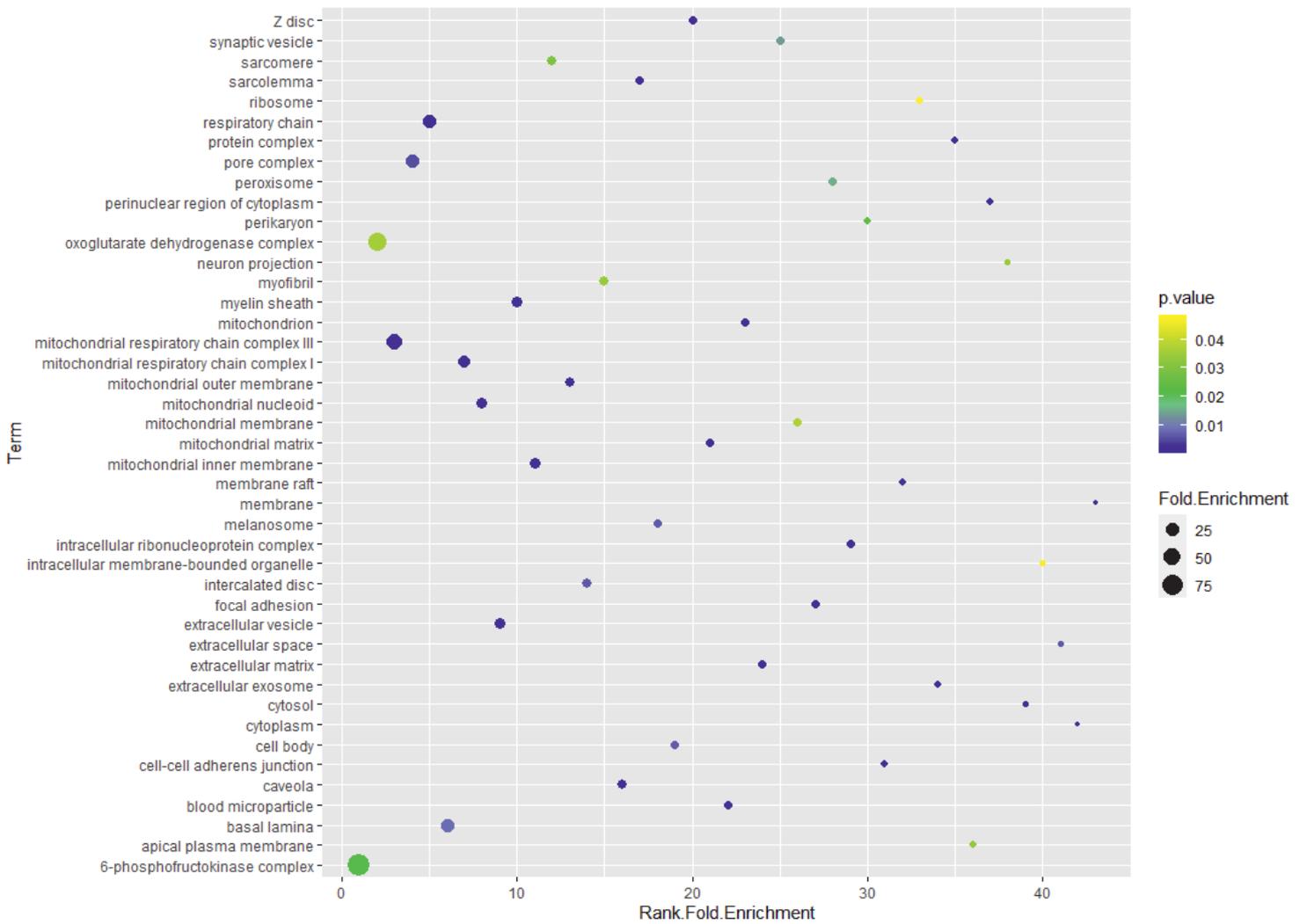
Cluster 5 GO Term CC



Cluster 5 KEGG Pathway



Cluster 6 GO Term CC



Cluster 6 KEGG Pathway

