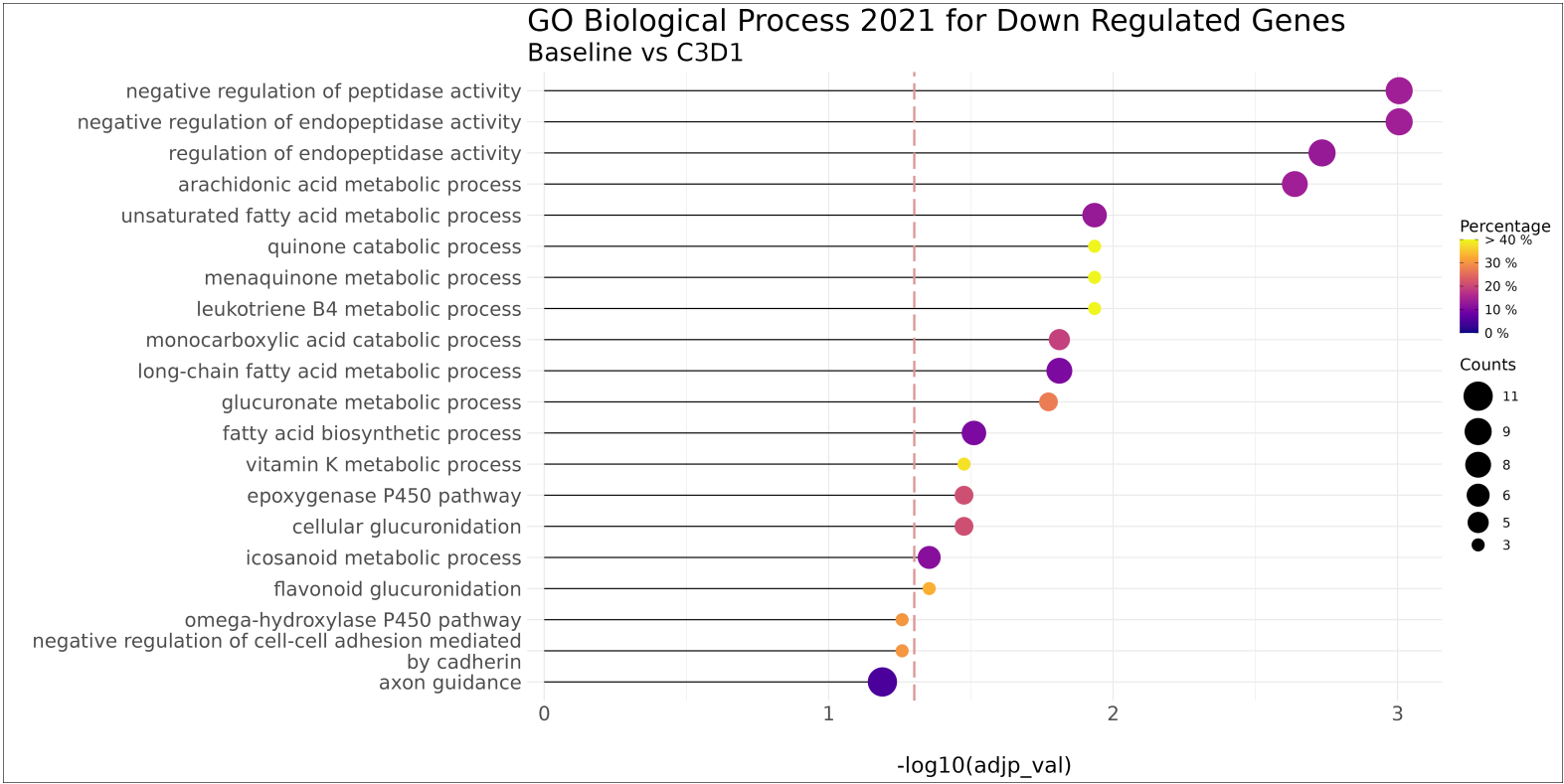


Pathway Enrichment Analysis Bar Plot of the top 20 enriched **Biological Processes** detected during Gene Ontology (GO) analysis of **downregulated** differentially expressed genes. The length of each bar refers to the statistical significance ( $-\log_{10}$  p-value), indicating the strength of association between the gene set and each process.



Pathway Enrichment Analysis Lollipop Chart of the top 20 enriched **Biological Processes** detected during Gene Ontology (GO) analysis of **downregulated** differentially expressed genes. Circle size refers to the number of DEGs associated with each GO term, while the color gradient reflects the percentage of downregulated genes within the total gene set for each term