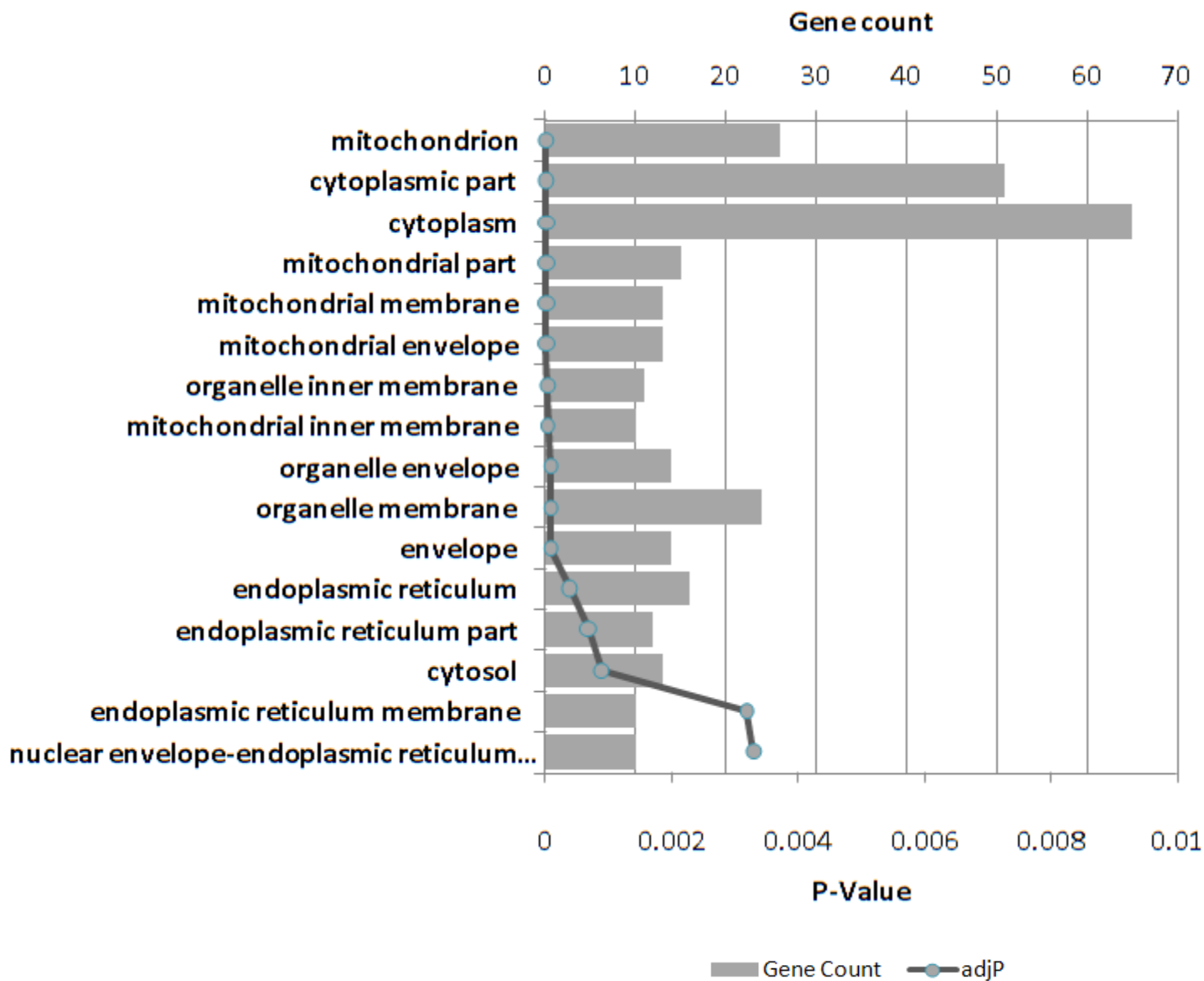


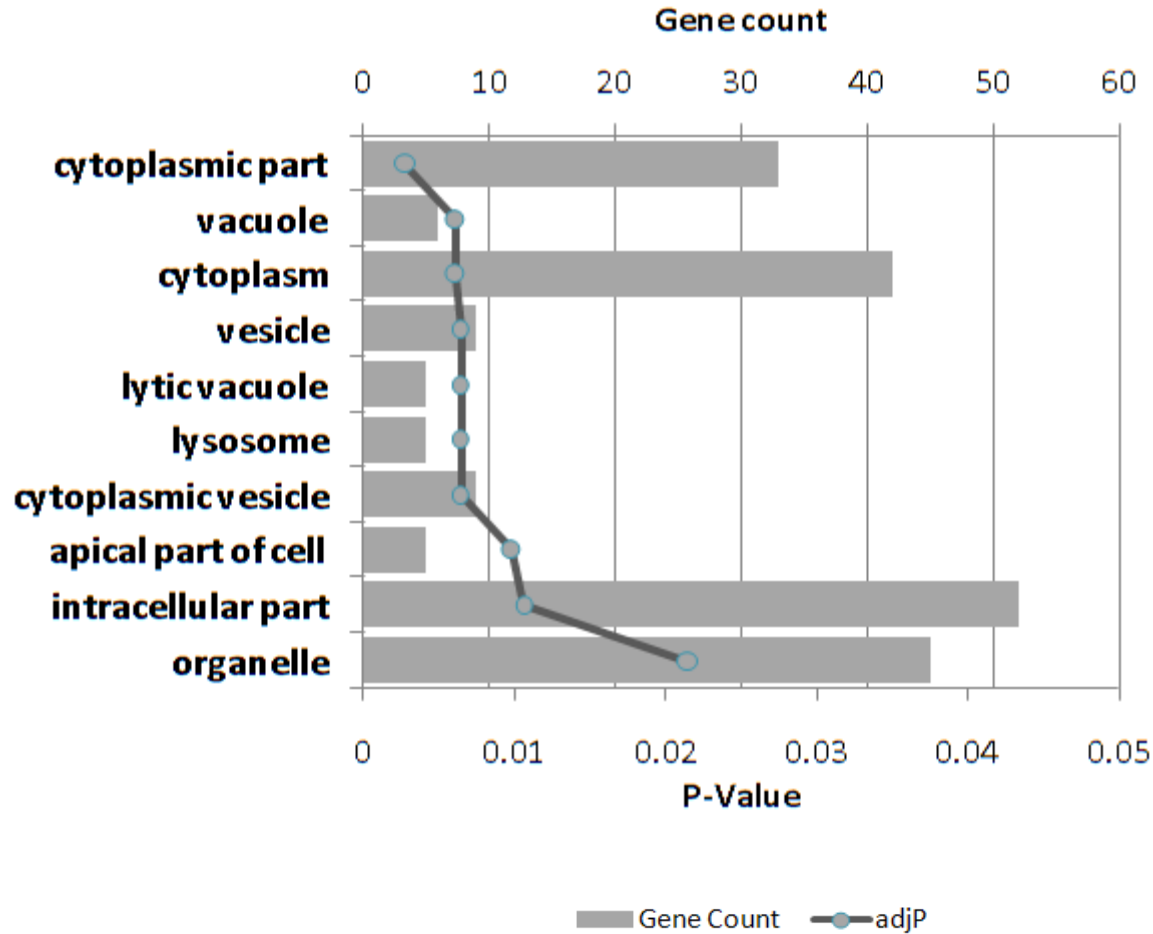
Gene Ontology Analyses - Supplemental Data

Using the GOTree Machine web application, the 214 differentially expressed genes were categorized as being associated with specific biological processes, molecular functions and cellular compartments. Statistically significant over represented biological processes were determined using the hypergeometric test.

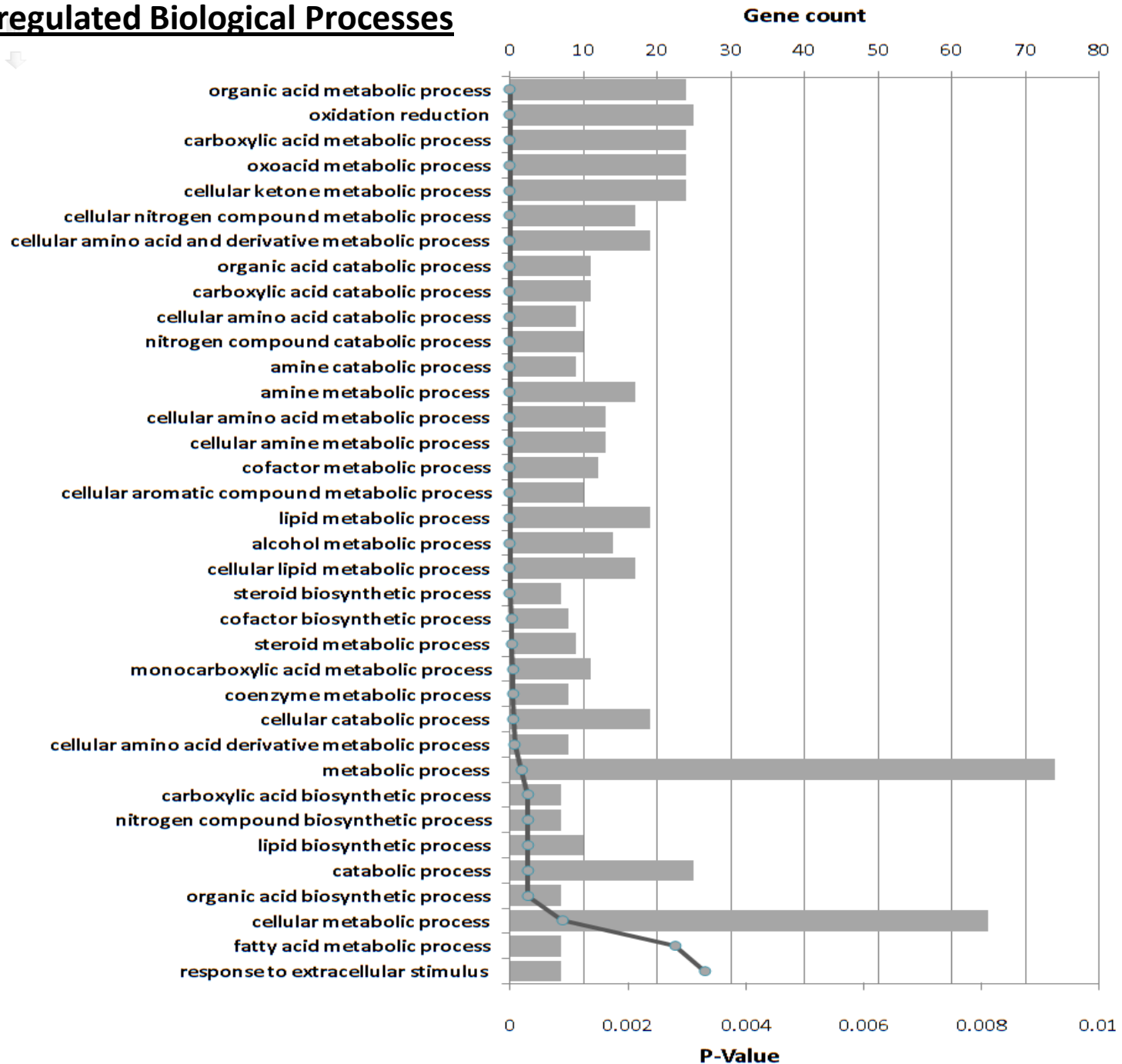
Downregulated Cellular Compartments



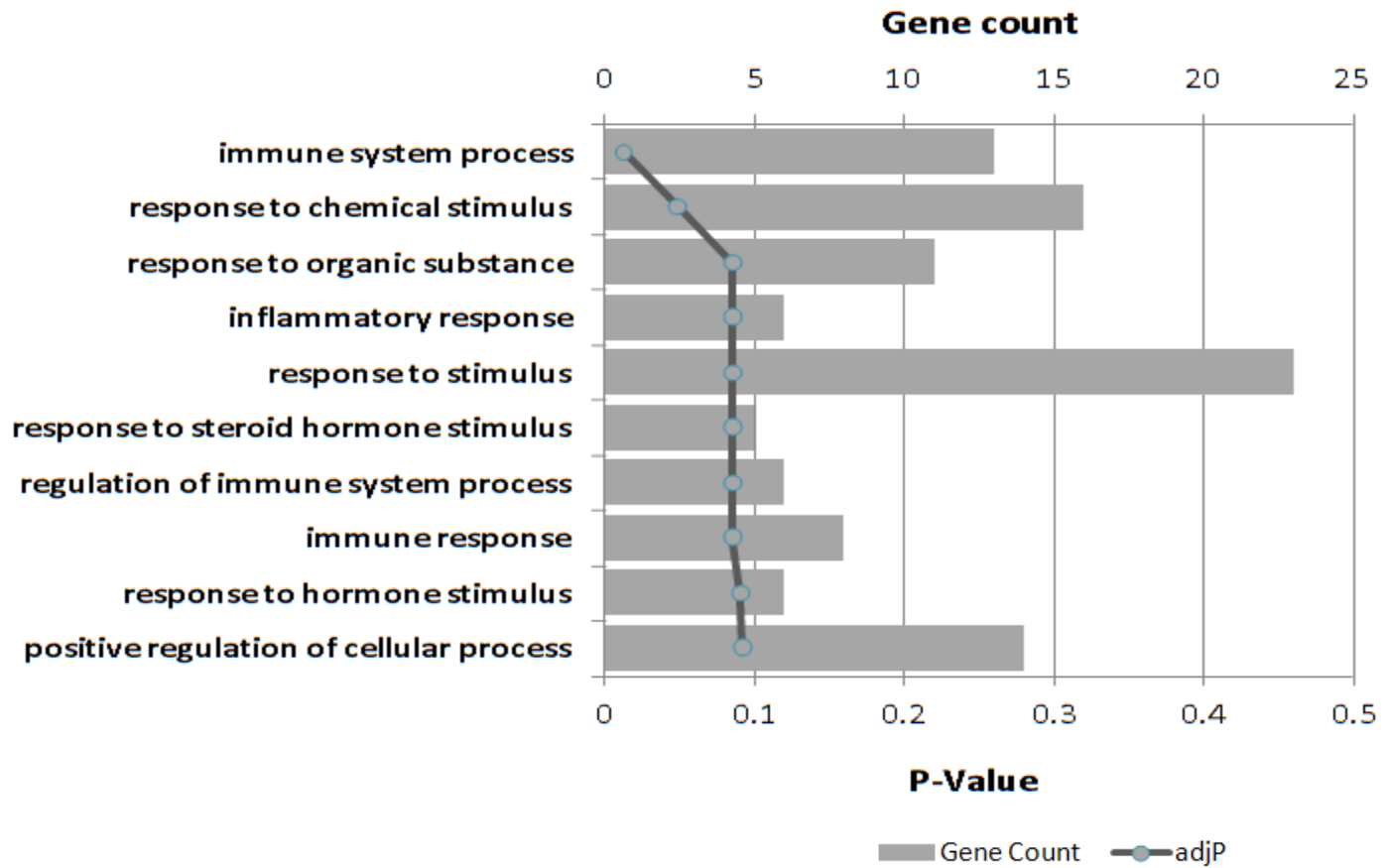
Upregulated Cellular Compartments



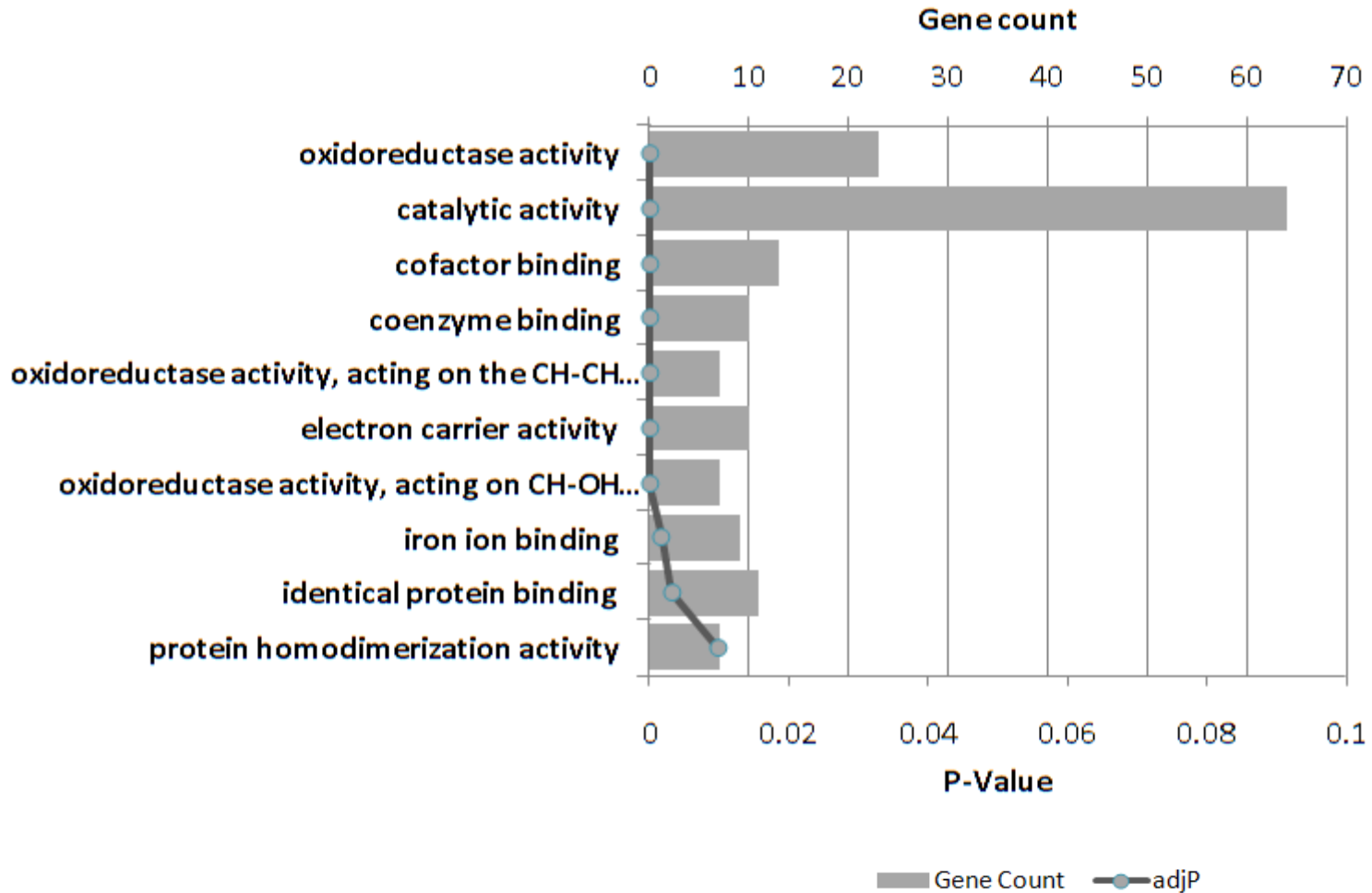
Downregulated Biological Processes



Upregulated Biological Processes



Downregulated Molecular Functions



Upregulated Molecular Functions

