

Supplementary Figure 2, Enrichment of KEGG pathways for differentially expressed genes in sepsis,

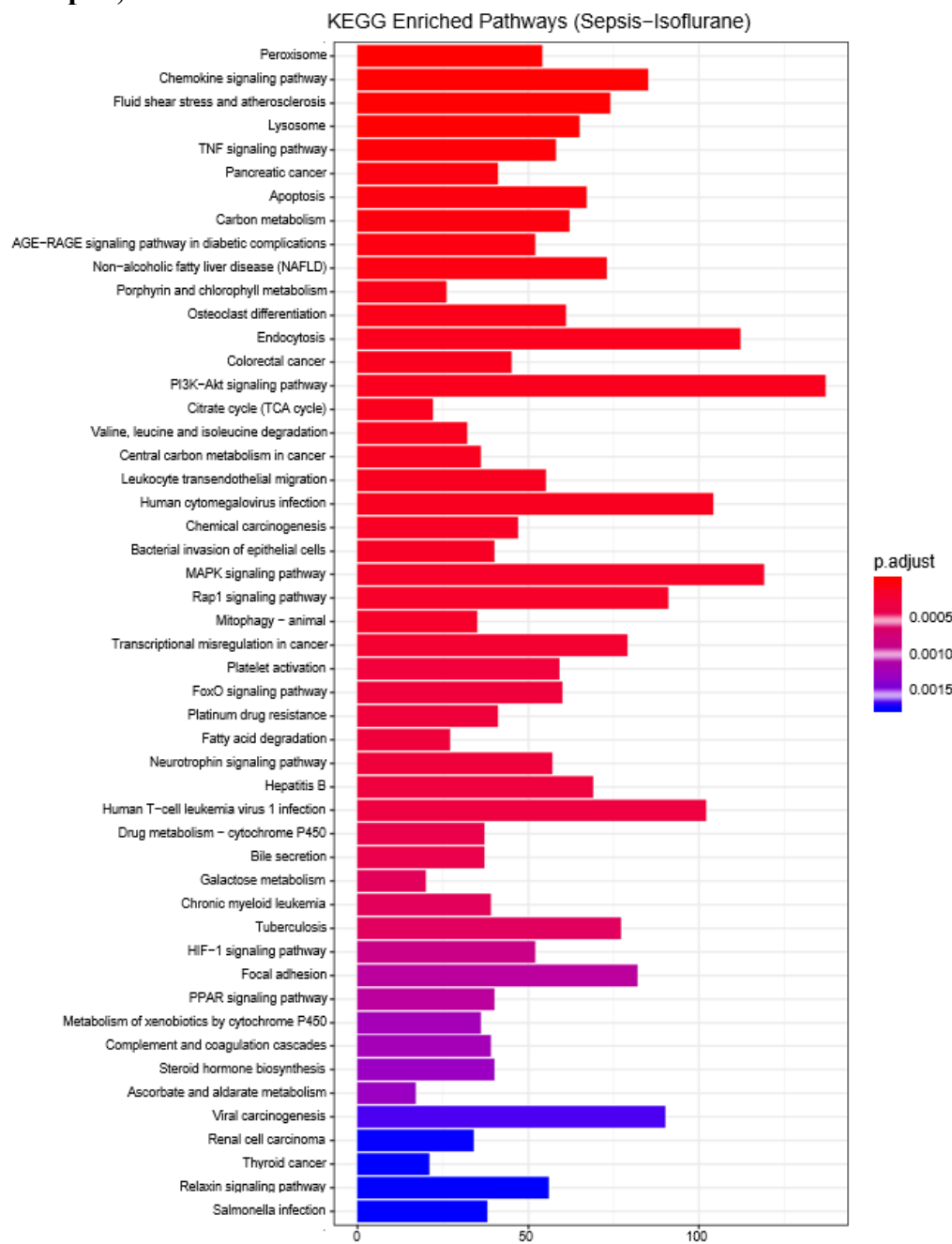


Figure 2. (A): Enrichment of KEGG pathways for differentially expressed genes in rat liver in response to Sepsis-inflammation with Isoflurane background: KEGG pathway enrichment p-value cutoff = 0.05; q-value cut off = 0.10; top 50; for differentially expressed genes the significance cut off level used was adjusted P-value > 0.05 for sepsis Vs. control. X-axis represents the gene counts. The most enriched pathways are those with the highest number of genes (e.g. PI3K-AKT signaling pathway in this figure).

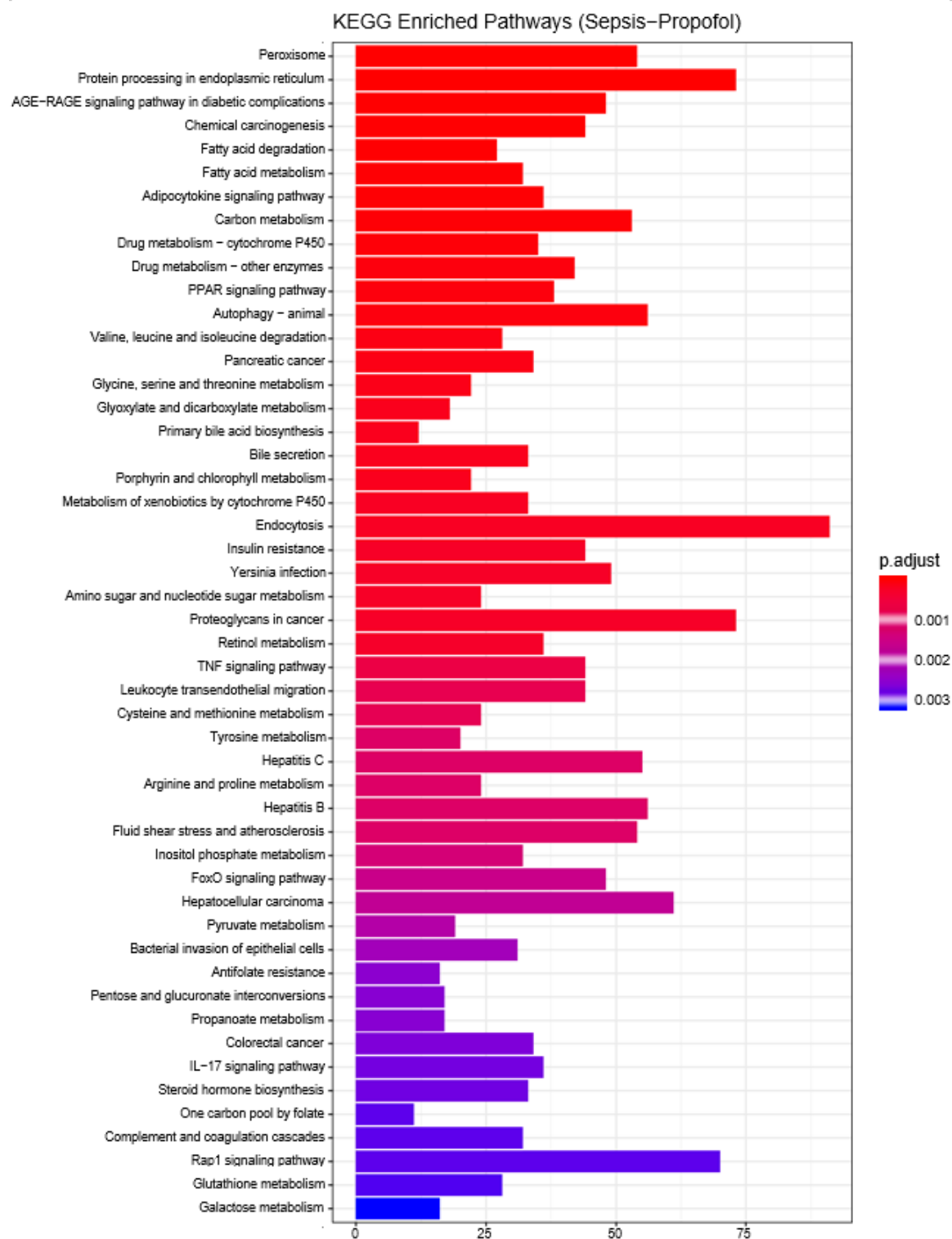


Figure 2. (B): Enrichment of KEGG pathways for differentially expressed genes in rat liver in response to Sepsis-inflammation with Propofol background: Significance cut off values are similar to S-Figure 5. A. The X-axis here represents the gene count.