

**Supplementary Data S4:** Venn diagram illustrating the overlap of significant (*p* < 0.05; -1 ≥ log2foldchange ≤ 1) differentially expressed genes (DEGs) between the *Babesia-*infected vs. control and the oil-contaminated vs. control groups. The right (green) circle represents the number of DEGs specific to Babesia infection (n = 412), the left (pink) circle represents the number of DEGs specific to oil contamination (n = 1,118), and the overlap area represents the number of DEGs shared between the two groups (n = 194). The results indicate that *Babesia* infection and oil contamination elicit mostly distinct patterns of gene expression, while a higher-than-expected number of genes were shared between both groups (Expected = 50.98). Of the 194 shared genes, 97% (n = 188) shared the same directional change in expression, indicating similar functionality.