

Supplementary Materials

Zika Virus Infection of Sertoli Cells Alters Protein Expression Involved in Activated Immune and Antiviral Response Pathways, Carbohydrate Metabolism and Cardiovascular Disease

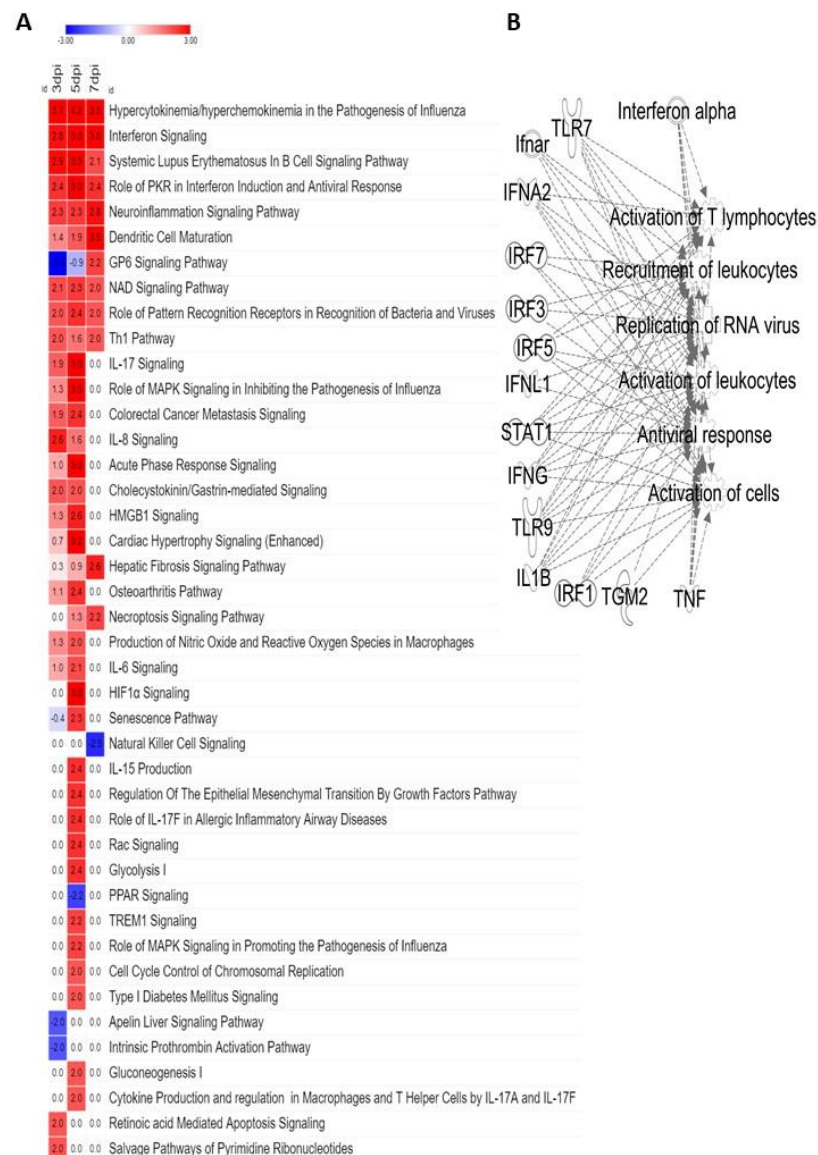


Figure S1. (A) Comparison of canonical pathways affected at 3, 5 and 7 dpi during ZIKV infection in HSerC. Red indicates up-regulation, blue indicates down-regulation. Numbers in the boxes show the significance of alteration measured by Z-score. (B) Top 15 upstream regulators associated with cellular function and disease.

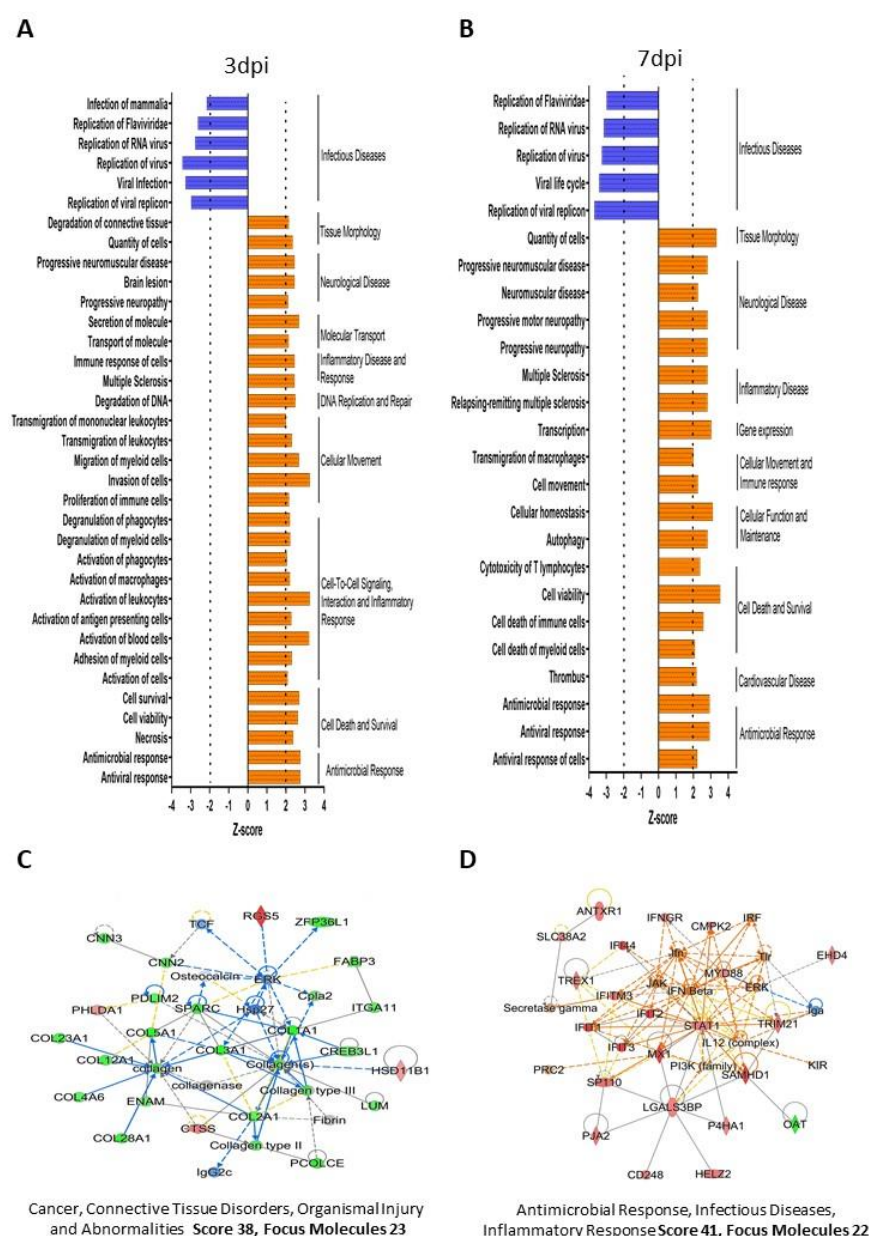


Figure S2. IPA-predicted activation and inhibition of bio-functions, and protein–protein network at 3 and 7 dpi in HSerC. Top bio-functions and their predicted activation or inhibition Z-scores indicated at (A) 3 and (B) 7 dpi. Activation is indicated by positive Z-Score and the inhibited bio-functions are indicated by negative Z-scores. The most effected protein–protein networks at (C) 3 dpi and (D) 7 dpi by ZIKV infection in HSerC. Red and green represent up-regulation and down-regulation, respectively; gray proteins denote that they were recognized in the present study, but not significantly regulated; colorless proteins interact with molecules in the network, but were not identified in our study. Abbreviations: dpi = Days post infection.

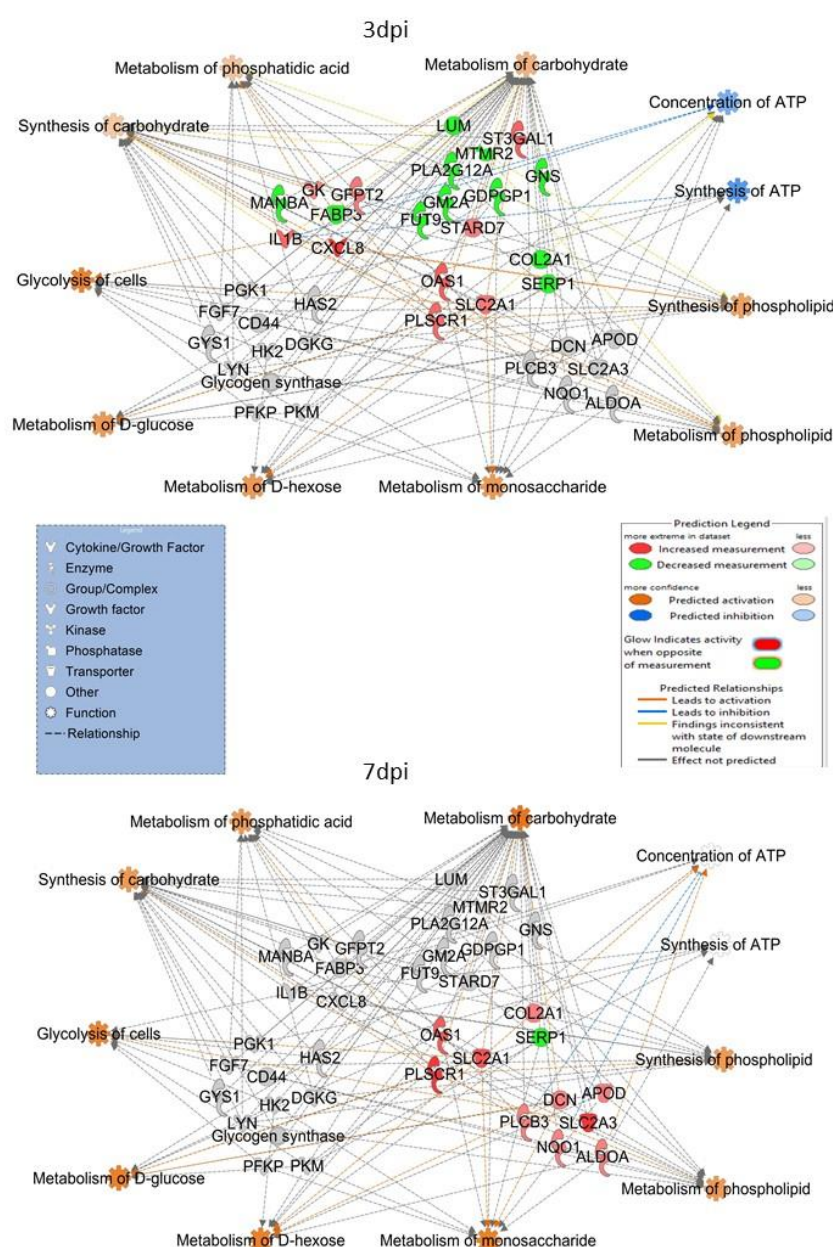


Figure S3. Proteins involved in the metabolism of carbohydrate and energy production in cells affected by ZIKV infection at 3 dpi and 7 dpi. Red and green represent up-regulation and down-regulation, respectively; gray proteins denote that they were recognized in the present study, but not significantly regulated; colorless proteins interact with molecules in the network, but were not identified in our study. Abbreviations: dpi = Days post infection.