

Supplementary Figure 1: ISG annotations. Differentially expressed interferon-induced genes were annotated using two approaches: the Interferome database helped to identify and classify genes depending on their induction by either type I IFN (α , β), type II IFN (γ), or both IFN types. In addition, Geneious software was used to annotate ISGs depending on the presence of either GAS, ISRE, or both sequence motifs within the 2,000 bp upstream of the 5'UTR of each gene. (**A**) Schematic diagram of annotations. (**B**) ISRE and GAS sequences.