





Supplementary Figure 2: Identifiability of model parameters using the proposed estimation protocol. As described in methods, simulated data sets were generated using a range of values for (A) degradation rate (d), (B) rate of expression of gene by infected cells (k_i), (C) the level of IFNB1 for which the gene expression rate is 0.5 per cell (k), and (D) Hill coefficient (n). Parameters were then estimated from these data and compared to their actual values.