

Table S4: Summary of selected Gene Ontology (GO) biological process categories or Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways for which expression programs discovered in the infection time-series data are significantly enriched. As expected, many significant GO categories and KEGG pathways were specifically involved with response to infection. Interestingly, a substantial number of significant categories or pathways corresponded to signaling cascades. Further, there were also a number of significantly enriched biological processes or pathways not directly labeled as being infection-related, but that are involved with alterations in cellular physiology consistent with infection. Finally, there were some unexpected significant categories or pathways.

Infection response	Signaling pathways	Other
<ul style="list-style-type: none"> - Inflammatory response (GO:0006954) - Response to virus (GO:0009615) - Chemotaxis (GO:0006935) - Positive regulation of T-cell proliferation (GO:0042102) - Endogenous antigen processing via MHC class II (GO:0019886) - Cytokine-cytokine receptor interaction (KEGG:hsa04060) - Natural killer cell mediated cytotoxicity (KEGG:hsa04650) - Leukocyte transendothelial migration (KEGG:hsa04670) - Complement and coagulation cascades (KEGG:hsa04610) 	<ul style="list-style-type: none"> - MAPKKK (GO:0000165 and KEGG:hsa04010) - JAK-STAT (GO:0007259 and KEGG:hsa04630) - Toll-like receptor (KEGG:hsa04620) - B-cell receptor (KEGG:hsa04662) - T-cell receptor (KEGG:hsa04660) - Insulin (KEGG:hsa04910) - VEGF (KEGG:hsa04370) - Calcium (KEGG:hsa04020) - Wnt (KEGG:hsa04310) - Phosphatidylinositol (KEGG:hsa04070) - I-κB kinase/NF-κB (GO:0043123) - Transmembrane receptor protein tyrosine kinase (GO:0007169) 	<ul style="list-style-type: none"> - Apoptosis (GO:0006915) - Nucleotide-excision repair (GO:0006289) - Nuclear mRNA splicing (GO:0000398) - Glycolysis (GO:0006096) - Glycogen metabolism (GO:0005977) - Anti-apoptosis (GO:0006916) - Cell cycle (GO:00070490) - Positive regulation of cell proliferation (GO:0008284) - Tricarboxylic acid cycle (GO:000609) - Regulation of adenylate cyclase activity (GO:0045761) - Chloride transport (GO:0006821) - Focal adhesion (KEGG:hsa04510) - Oxidative phosphorylation (KEGG:hsa00190) - Proteasome (KEGG:hsa03050) - Androgen and estrogen metabolism (KEGG:hsa00150) - Regulation of actin cytoskeleton (KEGG:hsa04810) - Gap junction (KEGG:hsa04540) - Fatty acid metabolism (KEGG:hsa00071) - Ribosome (KEGG:hsa03010) - Neuroactive ligand-receptor interaction (KEGG:hsa04080)