

Table S4. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis for the 271 genes that were both statistically differentially expressed and had a fold change of ≥ 2 in response to RV infection. Enriched KEGG pathways at P value cut-off of 0.05 are shown.

Enriched KEGG Pathways	Observed Number of Genes	Expected Number of Genes	Fold Enrichment	Enrichment P Value
Cytosolic DNA-sensing pathway	14	1.87	7.5	1.20×10^{-08}
Toll-like receptor signaling pathway	16	3.33	4.8	5.20×10^{-07}
Cytokine-cytokine receptor interaction	21	6.00	3.5	9.50×10^{-07}
RIG-I-like receptor signaling pathway	13	2.32	5.6	1.70×10^{-06}
Autoimmune thyroid disease	8	0.98	8.2	2.80×10^{-05}
Antigen processing and presentation	10	1.96	5.1	9.10×10^{-05}
Chemokine signaling pathway	14	5.19	2.7	1.70×10^{-03}
Regulation of autophagy	6	0.94	6.4	1.80×10^{-03}
Jak-STAT signaling pathway	12	4.14	2.9	2.00×10^{-03}
PPAR signaling pathway	6	1.40	4.3	1.10×10^{-02}
Natural killer cell mediated cytotoxicity	9	3.75	2.4	3.00×10^{-02}
Arachidonic acid metabolism	4	0.85	4.7	4.90×10^{-02}