Table S3. Gene ontology (GO) 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 GO categories at P value cut-off of 10^{-5} are shown.

Enriched GO Categories	Observed Number of Genes	Expected Number of Genes	Fold Enrichment	Enrichment P Value
response to stimulus	122	50.83	2.4	1.20×10^{-25}
response to other organism	40	4.94	8.1	4.00×10^{-25}
response to biotic stimulus	43	6.62	6.5	5.50×10^{-23}
immune system process	67	17.63	3.8	9.30×10^{-23}
immune response	54	11.74	4.6	1.10×10^{-21}
response to virus	27	2.23	12.1	1.10×10^{-21}
defense response	49	10.00	4.9	6.70×10^{-21}
response to external stimulus	54	14.21	3.8	9.50×10^{-18}
multi-organism process	49	12.25	4	5.80×10^{-17}
response to stress	75	28.85	2.6	2.80×10^{-15}
response to wounding	36	8.51	4.2	3.70×10^{-13}
inflammatory response	27	5.40	5	1.60×10^{-11}
response to chemical stimulus	57	21.92	2.6	1.60×10^{-11}
taxis	18	2.73	6.6	9.80×10^{-10}
chemotaxis	18	2.73	6.6	9.80×10^{-10}
response to molecule of bacterial origin	13	1.78	7.3	1.30×10^{-07}
response to lipopolysaccharide	12	1.58	7.6	2.90×10^{-07}
locomotory behavior	18	4.09	4.4	5.10×10^{-07}
locomotion	22	6.29	3.5	8.40×10^{-07}
regulation of defense response	14	2.59	5.4	1.30×10^{-06}
response to bacterium	15	3.00	5	1.30×10^{-06}
response to organic substance	32	12.80	2.5	2.40×10^{-06}
innate immune response	13	2.32	5.6	2.70×10^{-06}
cell-cell signaling	22	6.67	3.3	2.90×10^{-06}
regulation of response to stimulus	25	8.62	2.9	3.30×10^{-06}
regulation of cytokine production	16	3.72	4.3	3.70×10^{-06}
cell communication	28	10.37	2.7	4.20×10^{-06}
cellular di-, tri-valent inorganic cation homeostasis	15	3.41	4.4	6.50×10^{-06}