

Supplementary Table 3: List of enriched pathways for 113 differentially expressed genes in BAL for genotype effects

Function	FDR	Genes in network	Genes in genome
inflammatory response	6.13E-14	20	684
cell chemotaxis	2.28E-11	12	293
leukocyte chemotaxis	6.36E-10	11	215
positive regulation of response to external stimulus	6.12E-09	10	296
negative regulation of viral process	2.09E-08	8	90
positive regulation of inflammatory response	3.26E-08	7	135
regulation of viral genome replication	5.18E-08	7	89
negative regulation of multi-organism process	1.09E-07	8	169
negative regulation of viral genome replication	1.09E-07	6	53
regulation of inflammatory response	1.09E-07	10	321
leukocyte migration	2.37E-07	12	476
viral genome replication	2.63E-07	7	116
regulation of viral process	7.90E-07	9	174
chemokine receptor binding	9.31E-07	6	66
regulation of symbiosis, encompassing mutualism thrc	1.32E-06	9	202
myeloid leukocyte migration	1.82E-06	9	200
chemokine activity	3.88E-06	6	49
cytokine receptor binding	1.94E-05	8	282
granulocyte migration	2.07E-05	9	136
MHC protein binding	7.31E-05	4	35
lymphocyte chemotaxis	0.00013979	5	62
granulocyte chemotaxis	0.000252009	8	120
MHC class I protein binding	0.000529168	3	16
chemokine-mediated signaling pathway	0.000658133	8	87
neutrophil chemotaxis	0.000921607	8	103
neutrophil migration	0.000921607	9	115
cellular response to tumor necrosis factor	0.00175818	10	239
response to tumor necrosis factor	0.003894631	11	259
eosinophil migration	0.006964945	4	26
CCR chemokine receptor binding	0.010603936	4	43