Rhinovirus-induced modulation of gene expression in bronchial epithelial cells from subjects with asthma

YA Bochkov, KM Hanson, S Keles, RA Brockman-Schneider, NN Jarjour, and JE Gern

Online supplementary materials

Supplementary Figure 1 Clustering analysis of gene expression patterns. Hierarchical clustering of gene expression profiles based on 42 genes differentially expressed in asthmatic cells using fold change ratios (infection / mock) fails to differentiate samples according to the asthma phenotype.

Supplementary Figure 2 Optimization of the HRV1A infection procedure in PBE cells. (**a**) Representative microphotographs (magnification X100) of cells either mock-infected or infected with increasing doses of HRV1A. With increasing doses of HRV1A, the yield of viral RNA increased (**b**), while total cellular (floating and adherent cells) RNA decreased (**c**). Each bar represent the mean data from two independent experiments using cells from different donors.

Log2 fold change
(infected / mock)
  -3   0   3

a

mock-infected

HRV, MOI of 2

HRV, MOI of 10

HRV, MOI of 50

b

Viral RNA yield

PCR units (x10^6)

■ adherent cells
□ sups with detached cells

MOI of 2   MOI of 10   MOI of 50

c

Total RNA yield

RNA (μg/well)

■ adherent cells
□ sups with detached cells

MOI of 2   MOI of 10   MOI of 50