DUSP1 regulates apoptosis and cell migration, but not the JIP1-protected cytokine response, during Respiratory Syncytial Virus and Sendai Virus infection.

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Figure S1: Cytokine production elicited during SeV and RSV infection is protected from DUSP1-mediated inhibition of JNK and p38.

A549 cells were either (A) pre-treated with DMSO (vehicle) or SB203580 (10 μ M) + SP600125 (10 μ M) for 30 min prior to infection, (B) transfected with empty or DUSP1-expressing plasmids or (C and D) transfected with Control (Ctrl) or DUSP1-specific siRNA before infection with SeV at 40 HAU/10⁶ cells (A to C) or RSV at MOI of 3 (D). Release of cytokines measured in each biological replicates was quantified using Luminex-based multiplex assays. Data are represented as mean +/- SEM of n≥3 independent replicates and statistical analyzes were done using unpaired t-test. P<0.05 (*), P<0.01 (**) or P<0.001 (***).





Figure S2: DUSP1 expression does not alter cytokines mRNA levels induced by SeV infection.

A549 cells were transfected with an empty- or DUSP1-expressing plasmid before infection with SeV at 5 HAU/10⁶ cells for the indicated times. IFN β , CXCL8 and CCL2 mRNA levels were quantified by qRT-PCR. Data are represented as mean +/- SEM of n=3 independent experiments and analyzed using two-way ANOVA with Bonferroni's post-test.



Figure S3: Full-length blots of Figure 1.

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Figure S4: Full-length blots of Figure 2.

Fig. 2A

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Figure S5: Full-length blots of Figure 3.

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Figure S6 Full-length blots of Figure 4.

Fig. 4A

Fig. 4B





Figure S7: Full-length blots of Figure 5.

Fig. 5A



Fig. 6C



Figure S8: Full-length blots of Figure 6.

Fig. 6B





Figure S9: Full-length blots of Figure 7.

SUPPLEMENTARY INFORMATION

MATERIALS AND METHODS

qRT-PCR

Specific mRNA levels were quantified by qRT-PCR as described in the Material and Methods using either Fast start SYBR Green Kit (Roche) for *IFNB* (S: gaactttgacatccctgaggagattaagcagc, AS: gttccttaggatttccactctgactatggtcc) and *IL8* (S: tctcttggcagccttcctgatttc, AS: gtgtggtccactctcaatcactct) or using TaqMan Gene Expression Assays (Applied biosystems) for *CCL2* (#Hs00234140_m1). Results were analyzed by the $\Delta\Delta$ CT method after normalization to S9 mRNA levels (S: cgtctcgaccaagagctga, AS: ggtccttctcatcaagcgtc) or S9 (Hs02339424_g1) for *CCL2*.