



Figure S2. VP7 sequences of Wa strain and clinical isolates RV7 and RV39. Three aligned VP7 sequences of the clinical isolates RV7, RV39 and the cell culture-adapted Wa strain are presented. Sequence alignments were obtained with Bioedit software version 7.0.5.3.

Table S1. Viral loads of each one of the clinical filtrates utilized to infect the different cell lines and the HIEs. The viral load indicates the number of genome equivalents calculated by qPCR as previously described (Jothikumar, et al., 2009, doi: 10.1016/j.jviromet.2008.09.025).

Strain	Viral load/well
V1	$2.71 \cdot 10^9$
V3	$7.62 \cdot 10^9$
V5	$3.54 \cdot 10^{10}$
V6	$5.58 \cdot 10^{10}$
V7	$1.69 \cdot 10^{10}$
V9	$4.3 \cdot 10^{10}$
V10	$6.83 \cdot 10^{10}$
V11	$1.2 \cdot 10^{11}$
V12	$2.25 \cdot 10^{10}$
V13	$2.26 \cdot 10^{10}$
V14	$1.88 \cdot 10^{11}$
V15	$2.6 \cdot 10^{10}$
V16	$1.4 \cdot 10^{10}$
V17	$3.43 \cdot 10^9$
V18	$7.84 \cdot 10^8$
V22	$6.62 \cdot 10^8$
V28	$4.4 \cdot 10^7$
V30	$2.04 \cdot 10^9$
V31	$3.08 \cdot 10^9$
V39	$2.1 \cdot 10^9$
V41	$2.33 \cdot 10^9$