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      10      20      30      40      50      60      70      80      90     100
Wa      TTGGGGTCATGGAGAGATAAATGATTCTGACTACAGTAGAACCAATTTTAGATGGTCCTTATCAGCCAACTACATTACTCCACCTAATGATTATTGGATA
RV7     .....A.....A..G..G.....A..T.....A..C.....
RV39    .....A.....A..G..G.....A..T.....A..C.....

      110     120     130     140     150     160     170     180     190     200
Wa      CTTATTAAATTCAAATACAAATGGAGTAGTATATGAAAGTACAAATAATAGTGACTTTTGGACTGCAGTCGTTGCTATTGAACCGCACGTTAACCCAGTAG
RV7     .....CC.....C..G.....A.....G..A.....T.....
RV39    .....CC.....C..G.....A.....G..A.....T.....

      210     220     230     240     250     260     270     280     290     300
Wa      ATAGACAAATATACGATATTTGGTGAAAGTAAGCAATTTAATGTGAGTAACGATTCAAATAAATGGAAGTTTTTAGAAATGTTTAGAAGCAGTAGTCAAAA
RV7     .....ATG.....A..A.....A..A..T.....G.....G.....
RV39    .....ATG.....A..A.....A..A..T.....G.....G.....

      310     320     330     340     350     360     370     380     390     400
Wa      TGAATTTTATAATAGACGTACATTAACTTCTGATACTAGATTTGTAGGAATATTGAAATATGGTGGAAGAGTATGGACATTTTCATGGTGAACACCAAGA
RV7     ...T.....C.....C..C.....A.....G..G.....
RV39    ...T.....C.....C..C.....A.....G..G.....

      410     420     430     440     450     460     470     480     490     500
Wa      GCTACTACTGACAGTTCAGGTACTGCAAAATTTAAATAATATATCAATTACAATTCATTCAGAAATTTTACATTATTCGAAGTCCCAAGGAATCTAAATGTA
RV7     ...C.....T.....AC.....GG..CGG.....T.....G.....
RV39    ...C.....T.....AC.....GG..CGG.....T.....G.....

      510     520     530     540     550     560     570     580     590     600
Wa      ATGAATATATTAATAATGGTCTGCCCAATTCAAAATACTAGAAATGTAGTTCCATTGCCATTATCATCTAGATCGATACAGTATAAGAGAGACAAGT
RV7     .....C..C.....A..T.....A.....AT.....T.....
RV39    .....C..C.....A..T.....A.....AT.....T.....

      610     620     630
Wa      TAATGAAGACATTATAGTTTCAAAAACCTCATTATGGAA
RV7     .....C..A.....G.....
RV39    .....C..A.....G.....

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Figure S1. VP4 sequences of Wa strain and clinical isolates RV7 and RV39. Three aligned VP4 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.

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      10      20      30      40      50      60      70      80      90     100
Wa      ATATATTAAATCAGTGACTCGAATAATGGACTACATTATATATAGATTTTGTGATTACTGTAGCATATTGCTTTGACAAGAGCTCAGAATTATGG
RV7     .....T.A..A.TGCG.....TT.A..T.....C.T..AC..T..TATTGC..CAC...TGTT.A.A.A..A.....
RV39    .....T.A..A.TGCG.....TT.A..T.....C.T..AC..T..TATTGC..CAC...TGTT.A.A.A..A.....

      110     120     130     140     150     160     170     180     190     200
Wa      ACTTAACTTACCAATAACAGGATCAATGGACGCTGTATATACTAACTCTACTCAAGAAGAAGTGTTCCTAAGTCTACGTTATGTCTGTATTATCCAAC
RV7     .A...T...G..C..T..C..C...TA.A.C...G.A..T..AT.A..GC...ACA...T.G...A..AC...CT.A...T..A
RV39    .A...T...G..C..T..C..C...TA.A.C...G.A..T..AT.A..GC...ACA...T.G...A..AC...CT.A...T..A

      210     220     230     240     250     260     270     280     290     300
Wa      GAAGCAAGTACTCAAAATCAATGATGGTGACTGGAAGAGCTCATTGTGCGCAAAATGTTCTTACAAAGGGTTGGCCAAACAGGATCTGTTTACTTTAAAGAGT
RV7     .....TCA.....TGGA...ACG..A...GA.TA.TC...C..T.A..CT.G..T..A..G.....T...A..C..T.....A.
RV39    .....TCA.....TGGA...ACG..A...GA.TA.TC...C..T.A..CT.G..T..A..G.....T...A..C..T.....A.

      310     320     330     340     350     360     370     380     390     400
Wa      ACTCAAAATATTGTTGATTTTCTGTTGACCCACAGCTGTATTGTGACTATAATTTAGTACTTATGAAATATGACCAAGTCTTGAATTAGATATGTCAGA
RV7     .TAATG...C.C.TCA..C..AA...T...A..T.....T...G.T...G.....TTC..CGT.A..GC.....
RV39    .TAATG...C.C.TCA..C..AA...T...A..T.....T...G.T...G.....TTC..CGT.A..GC.....

      410     420     430     440     450     460     470     480     490     500
Wa      GTTAGCTGATTTAATAATTGAATGGTTATGTAAACCAATGGATGTAACATTATCTATTATCAACAATCGGGAGAAATCAAAATAAGTGGATATCGATG
RV7     A.....TC.A.....A.....A.....T.....G..A.A.AT..G.G...A.....
RV39    A.....TC.A.....A.....T.....G..A.A.AT..G.G...A.....

      510     520     530     540     550     560     570     580     590     600
Wa      GGATCATCATGTACCGTGAAAGTGTGTCGCTAAATACACAAACGTTAGGGATAGGTTGTCAAAACAACAAACGTAGACTCATTTGAAATGATTGCTGAGA
RV7     ...CAG..T.....A.A.....A...AT.G...G..G..T...A.....ATT..C.....TAC..CGA.G.....GA.G.G...ACA.
RV39    ...CAG..T.....A.A.....A...AT.G...G..G..T...A.....ATT..C.....TAC..CGA.G.....GA.G.G...ACA.

      610     620     630     640     650     660     670     680     690     700
Wa      ATGAGAAATTAGCTATAGTGGATGTCGTTGATGGGATAAATCATAAAAATAAATTTAACAACCTACGACATGTACTATTTCGAAATGTAAGAAATTAGGTCC
RV7     G.....TA...ACA..C..T.....TG..G..C.....C.TG..G.G..T..A..AT..C...A..A.G.....G...A..
RV39    G.....TA...ACA..C..T.....TG..G..C.....C.TG..G.G..T..A..AT..C...A..A.G.....G...A..

      710     720     730     740     750     760     770
Wa      AAGAGAAAATGTAGCTGTAAATACAGTTGGTGGTTCTAATGTGTTAGACATAACAGCAGATCCCAACAACATAATCC
RV7     .....GA.TG.....C...C..AG.....T..T.....T...GCA..
RV39    .....GA.TG.....C...C..AG.....T..T.....T...GCA..

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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	$2.33 \cdot 10^9$