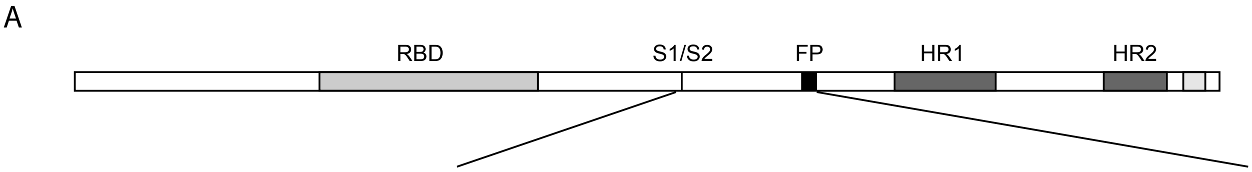
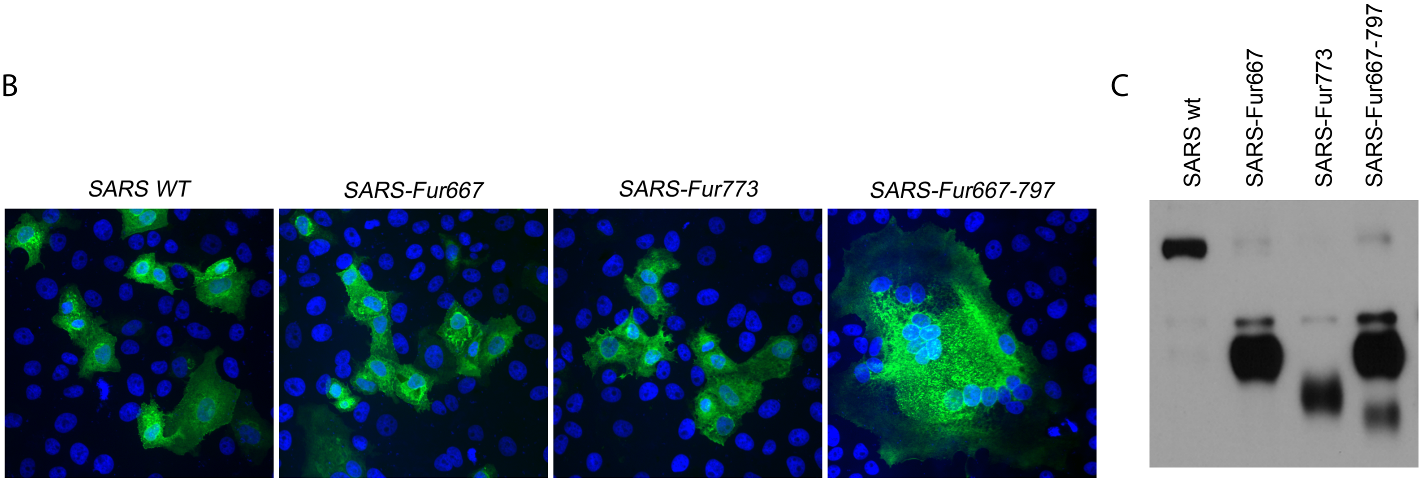
Supplemental Figure 1



SARS WT ....HTV SLLR STSQ..................VFAQV KQMYK TPTLKYFGGFNFSQILPDPLKPTKR*SFIEDLLFNKVTLADAGF*M.....
SARS Fur667 ....HTV **RRSRR** STSQ............... VFAQV KQMYK TPTLKYFGGFNFSQILPDPLKPTKR*SFIEDLLFNKVTLADAGF*M.....
SARS Fur773 ....HTV SLLR STSQ..................VFAQV **KRSRR**S TPTLKYFGGFNFSQILPDPLKPTKR*SFIEDLLFNKVTLADAGF*M.....
SARS Fur667-797 ....HTV **RRSRR** STSQ............... VFAQV KQMYK TPTLKYFGGFNFSQILPDPL**KRTKR***SFIEDLLFNKVTLADAGF*M.....



Effect of furin site insertion within SARS S S2. A) Cartoon representation of the SARS-CoV spike with the receptor-binding domain (RBD) in S1, the fusion peptide (FP), Heptad repeats 1 and 2 (HR1 and HR2) and the transmembrane domain (TM) in S2. As indicated in the mutant map, furin cleavage sites were introduced at positions 667, 773 and a double insertion at 667 and 797 of SARS S. B) VeroE6 cells expressing SARS-CoV S wild type (SARS wt) or the mutants SARS-Fur667, SARS-Fur773, or SARS-Fur667-797 were analyzed by immunofluorescence microscopy using an anti-S monoclonal antibody (green), with nuclei counterstained with Hoechst 33548 (blue). C) Western blot analysis of BHK cells expressing SARS-CoV S wild type (SARS WT) or furin mutants Fur667, Fur773, Fur667-797, with the C-terminal part of the spike protein detected with an anti-C9 antibody.