Infectious DNAs derived from insect-specific flavivirus genomes enable identification of pre- and post-entry host restrictions in vertebrate cells

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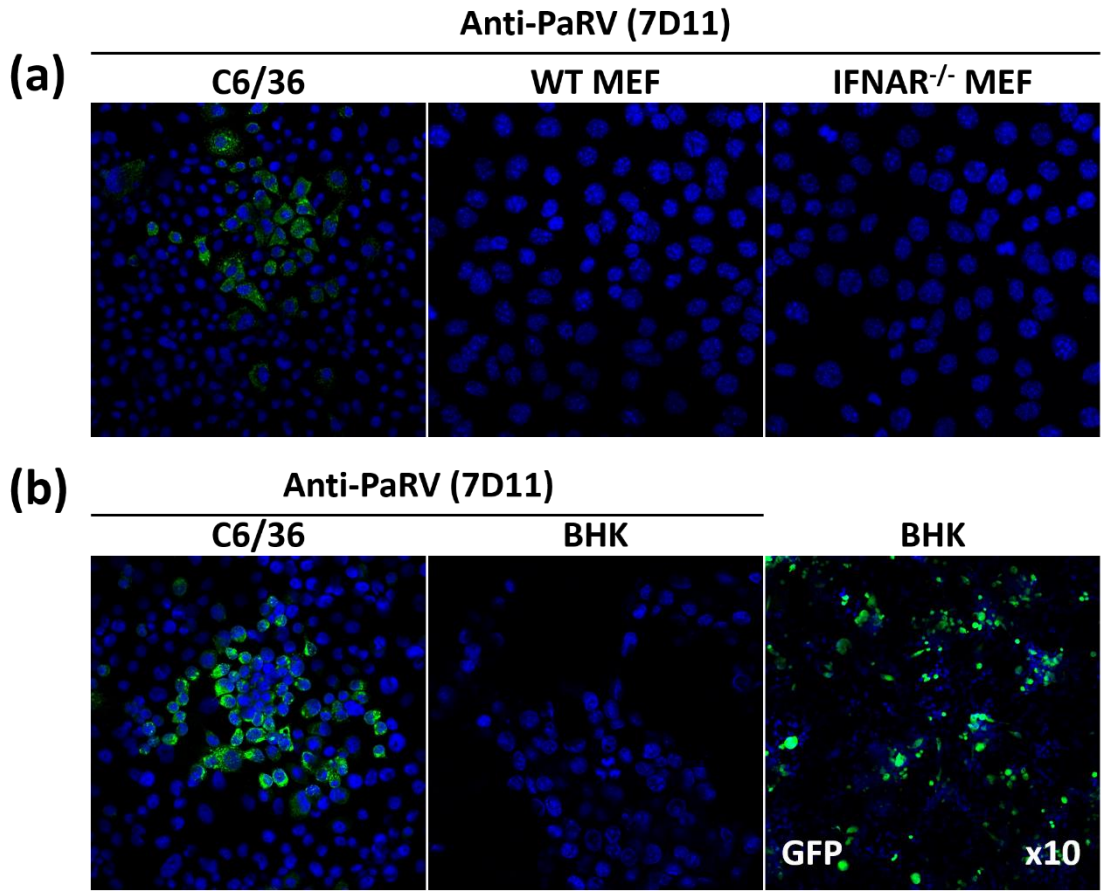
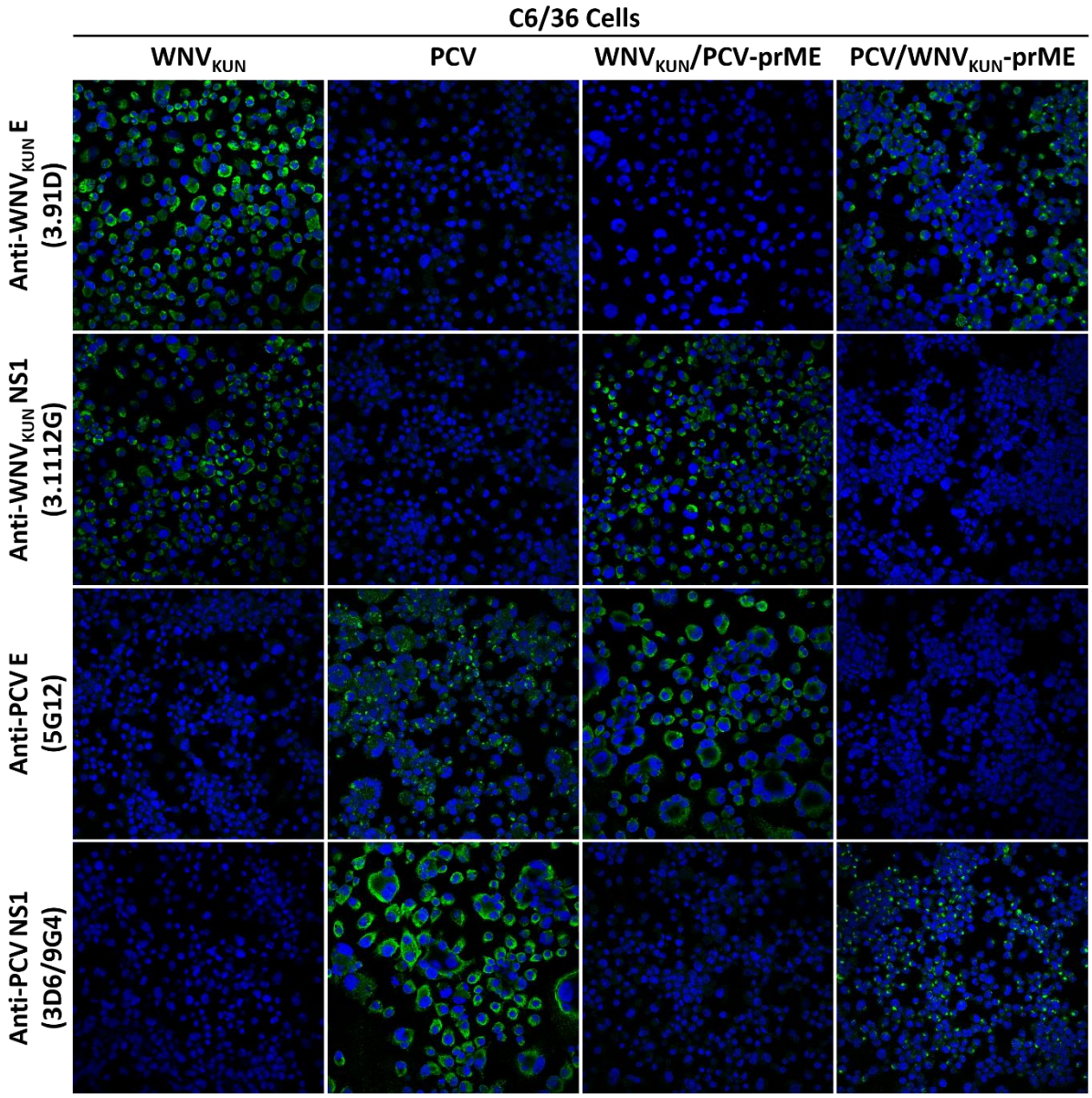
Supplementary Data

Supplementary Table S1. Sequence comparison between $PaRV_{CPEC}$ and $PaRV_{CPECM1}$ showing a 15 nucleotide change in $PaRV_{CPECM1}$.

Sequence Name	Sequence
$PaRV_{WT}$	ACCTTGGAA - - - AGAGCCTCACGTGCGGAAGAGAAGGGAA
$PaRV_{CPEC}$	ACCTTGGAA - - - AGAGCCTCACGTGCGGAAGAGAAGGGAA
$PaRV_{CPECM1}$	ACCTTGGAAAGACGCAGCAGAAGGGCGGAAGAGAAGGGAA



Supplementary Fig. S1. IFA visualisation of independent transfections of PaRV RNA into C6/36 cells and either (a) WT and IFNAR$^{-/-}$ MEF cells or (b) BHK cells. RNA from a GFP-nanoLuc fusion protein expressing WNV replicon was also included as a transfection control in BHK cells. IFA analysis was performed by probing with anti-PaRV E (7D11). Monolayers were fixed 72 hrs post-infection. IFA analysis was performed by probing with PaRV mouse anti-sera. The nucleus of each cell was stained with Hoechst 33342. Images were taken at ×40 magnification or as indicated.



Supplementary Fig. S2. Visualisation of C6/36 cells infected with either WNV_{KUN}, PCV, PCV/WNV_{KUN}-prME or WNV_{KUN}/PCV-prME at an MOI of 1. Monolayers were fixed 72 hrs post-infection. IFA analysis was performed by probing with anti-PCV E (5G12), anti-PCV NS1 (3D6/9G4), anti-WNV E (3.91D) and anti-WNV NS1 (3.1112G) mouse monoclonal antibodies. The nucleus of each cell was stained with Hoechst 33342. Images were taken at ×40 magnification.