Establishment of an RNA polymerase II-driven reverse genetics system for Nipah virus strains from Malaysia and Bangladesh

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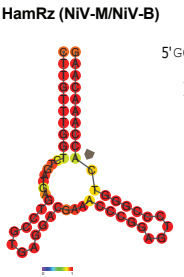
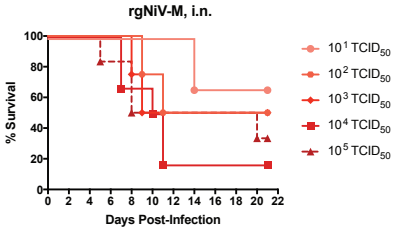
A



B

	Rescue efficiency (pos/total)	Time to rescue (days)
rgNiV-M/EGFP	3/4	5-7
rgNiV-B/EGFP	3/4	5-7

C



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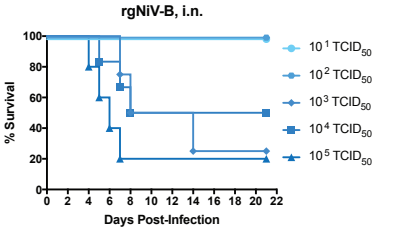
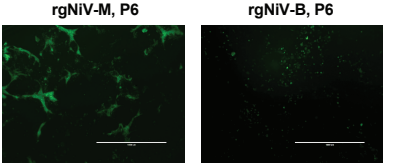


E



Supplementary Figure S1. **A**, Complete sequence of the hammerhead ribozyme (HamRz) (left panel) and the hepatitis delta virus ribozyme (HdRz) (right panel) sequences used to generate the rgNiV constructs. The HamRz structure was predicted using RNAFold 2.4.11. The cleavage site is indicated by a grey arrowhead. **B**, Efficiency of rescue. Rescue efficiency is depicted as the number of positive wells (pos) divided by the number of total wells. The time to rescue in BHK cells is indicated. **C/D**, Kaplan-Meier curves representing survival data are shown. Groups of five-to-six-week week-old female hamsters were inoculated with the indicated doses of rgNiV-M (C, n= 5-6) or rgNiV-B (D, n= 5-6) by the intranasal route (i.n.). Hamsters were observed daily to assess the clinical signs and survival. **E**, Stability of EGFP-expressing viruses. The rgNiV-M/EGFP or rgNiV-B/EGFP were serially passaged in Vero E6 and the EGFP fluoresence of the passage 6 (P6) viruses was visualized by fluorescence microscopy.