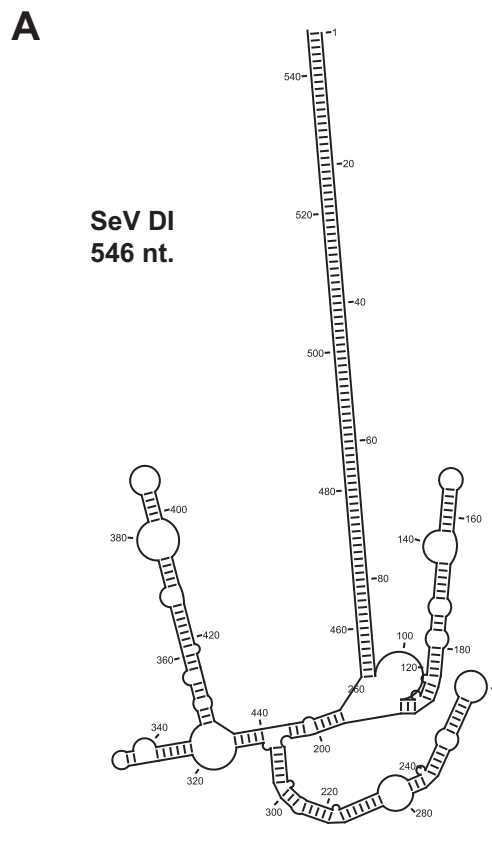

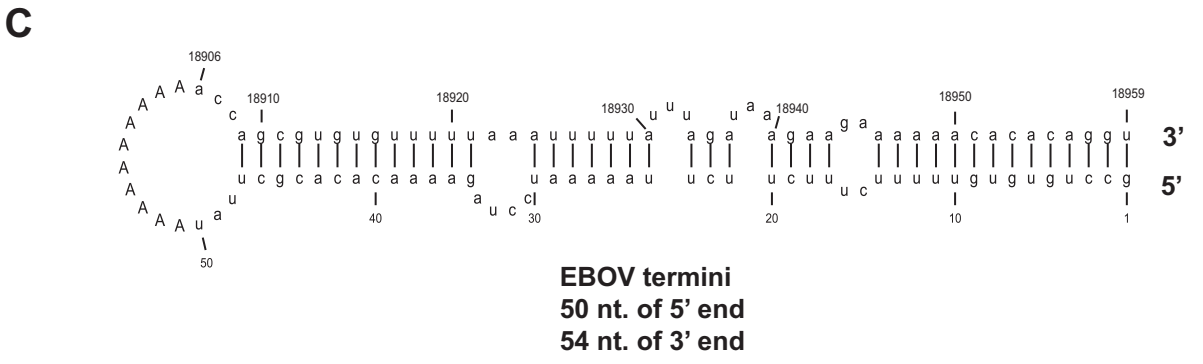

S1 Fig. Secondary structure of the Sendai Virus (SeV) and PAICS, the most significantly enriched host RNA bound by VP35, contain stable stem structures. RNA secondary structures of RNA molecules bound by EBOV VP35 protein were predicted using CLC Genomics Workbench 8.5 (QIAGEN Bioinformatics). (A) RNA secondary structure of the 546 nucleotide defective interfering (DI) genome of SeV. (B) RNA secondary structure of the 3,350 nucleotide host cell transcript PAICS (transcript variant 1, NM_001079525). (C) RNA secondary structure of the termini of the EBOV genome. The 5’ most 50 nucleotides and the 3‘ most 54 nucleotides were joined by adding ten “A”s (capital “A”s in left bulge). VP35 is required for EBOV genome packaging and is assumed to bind the genome (29). Panhandle structure of the EBOV termini has been previously predicted (J. Virol. 2005 Aug; 79(16): 10660-10671: PMID: 16051858). While we do not directly show VP35 binding this EBOV genomic region in our study, it represents a viral stem loop predicted to be present during EBOV infection which could serve as a binding target of VP35.