Additional File 4

Table S3 - Selective pressure in ruprintrivir contacts.

Data S3 – Consensus structures HRVA and HRVB 5'NCR elements R1-R7.

Consensus secondary structure and sequence of HRVA and HRVB 5'NCR elements identified in Witwer, C et al., 2001). Circled residues, positions where compensatory substitutions are detected in the alignment. Gray residues indicate positions where substitutions that disrupt basepairing potential are detected in the alignment. (PDF)

Data S4 – Consensus structures HRVA and HRVB 3'NCR element.

Consensus secondary structure and sequence of HRVA and HRVB 3'NCR element identified in Witwer, C et al., 2001). Circled residues, positions where compensatory substitutions are detected in the alignment. Gray residues indicate positions where substitutions that disrupt basepairing potential are detected in the alignment. (PDF)

Figure S8 – Analysis of HRVA and HRVB cis-replicating elements (CREs).

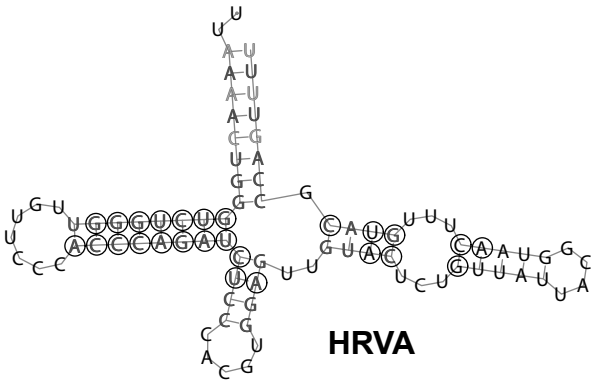
ClustalW alignment of HRVA (A) and HRVB (B) region of the P2A gene (HRV002 nucleotides 3268 – 3302) in which the minimal functional CRE has been identified for a member of the HRVA subgroup (Gerber, K. et al., 2001). ClustalX alignment of HRVA (A) and HRVB (B) region of the VP1 gene (HRV014 nucleotides 2353 to 2386) in which the minimal functional CRE has been identified for a member of the HRVB subgroup (McKnight, KL and Lemon, SM, 1998; Yang, Y et al., 2002). Shorthand for consensus secondary structures deduced from each of these alignments (Hofacker, I et al., 2004) are depicted above with parentheses above the clustalx alignment indicate base-paired nucleotides, while dots or commas indicate unpaired nucleotides.. (PDF)

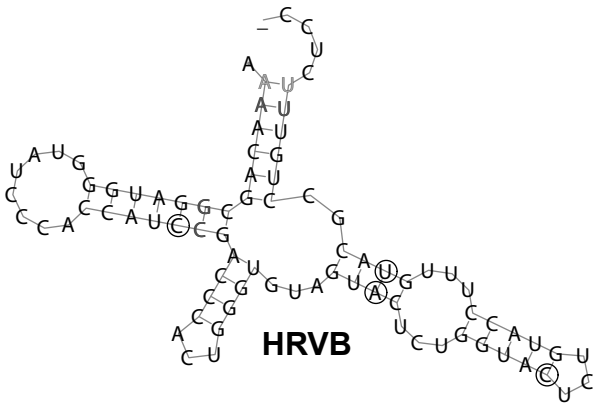
Table S3: Selective pressure in ruprintrivir contacts[a]

Residue number[b]	dN/dS value
25	0.05
40	0.05
71	0.05
125	0.05
127	0.05
128	0.05
130	0.05
142	0.05
147	0.05
161	0.05
163	0.05
164	0.05
165	0.05

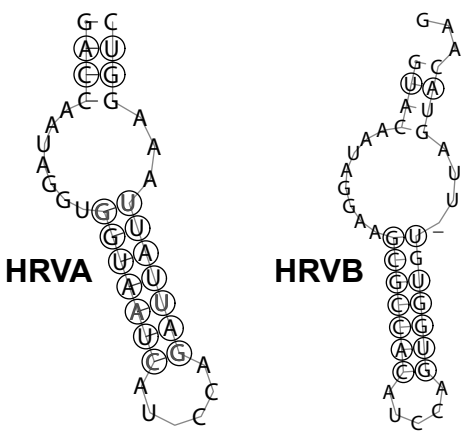
[a]HRV2 contacts with ruprintrivir, a protease inhibitor targeted to the 3C protease active site (Binford, SL et al., 2005. Antimicrobial Agents Chemother. 49, 619-26). [b]Residue number indicates residue within the 3C protease relative to N-terminal proteolytic cleavage site.

A. R1 cloverleaf element

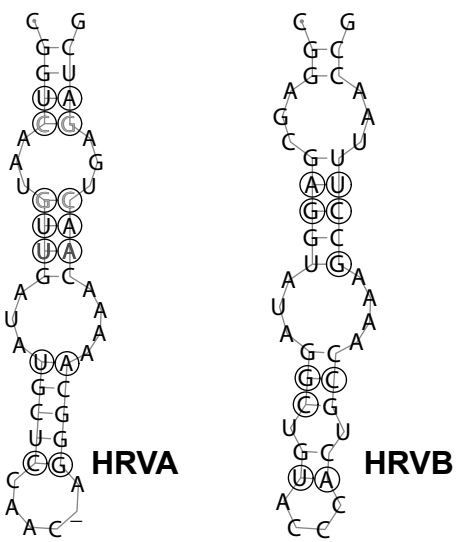




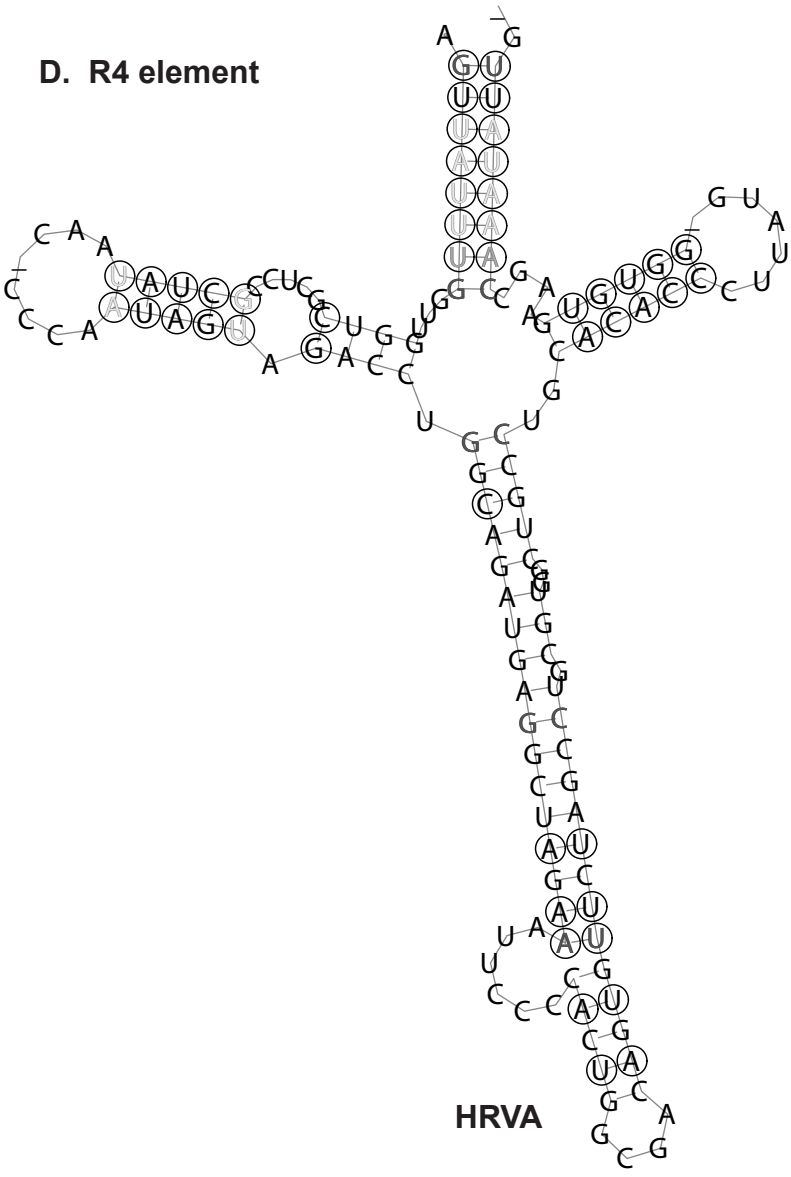
B. R2 element

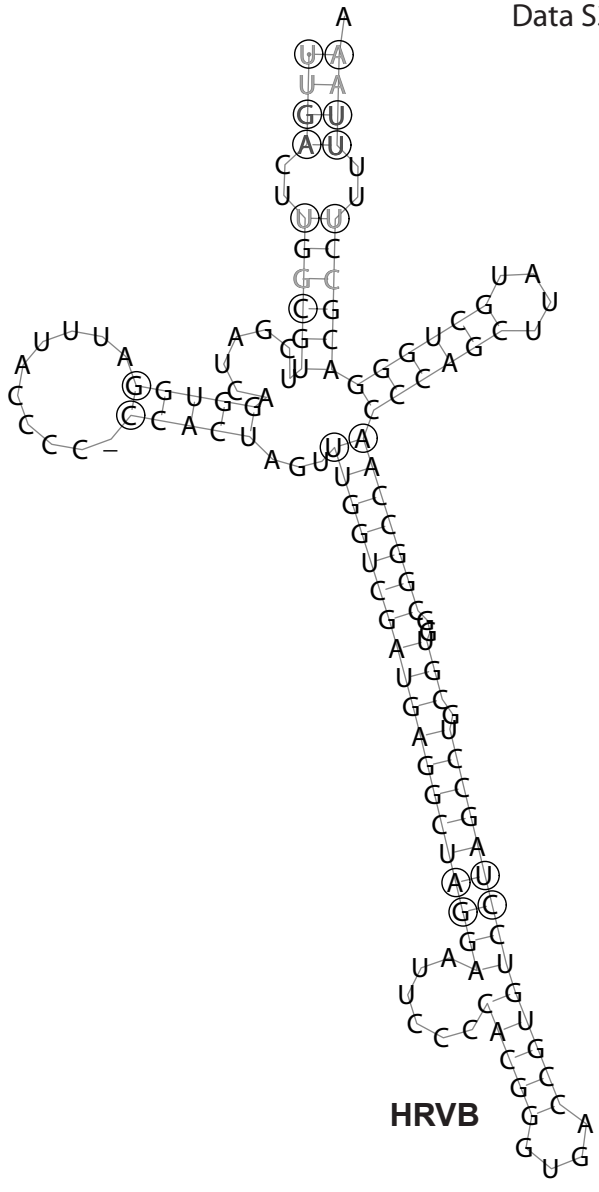


C. R3 element

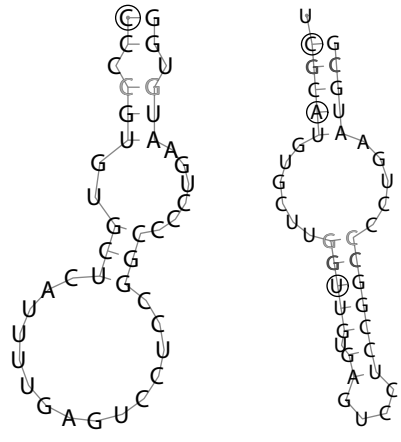


D. R4 element

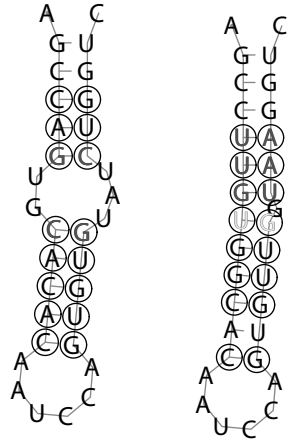




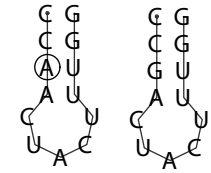
E. R5 element



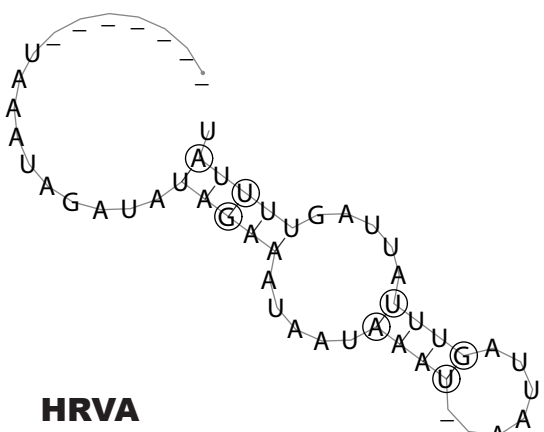
F. R6 element



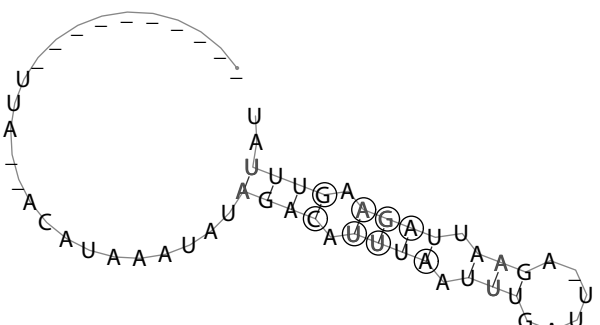
G. R7 element



3'NCR stem loop element

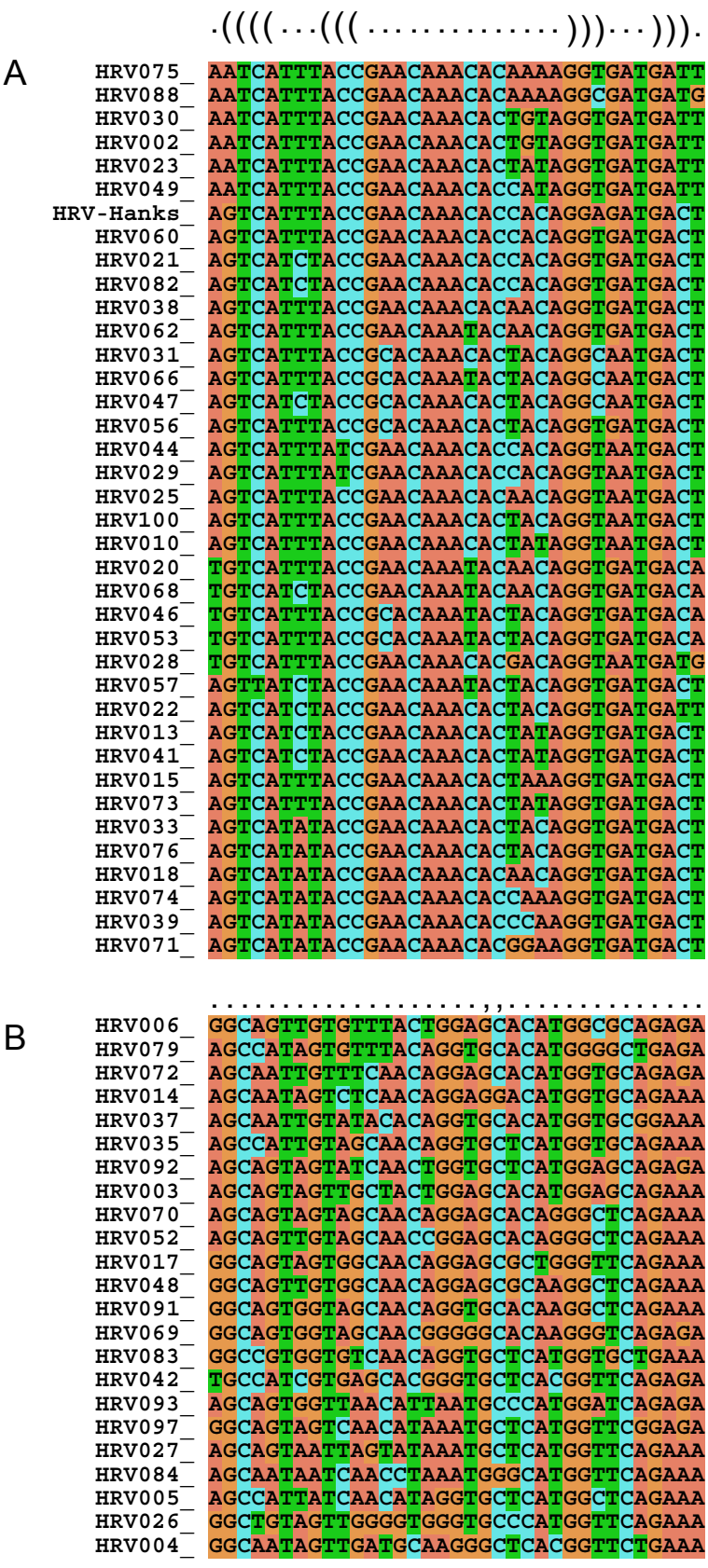


HRVA



HRVB

Fig. S8AB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HRV-Hanks_ AGTCATTTACCGAACAAACACCACAGGAGATGACT
HRV060_ AGTCATTTACCGAACAAACACCACAGGTGATGACT
HRV021_ AGTCATCTACCGAACAAACACCACAGGTGATGACT
HRV082_ AGTCATCTACCGAACAAACACCACAGGTGATGACT
HRV038_ AGTCATTTACCGAACAAACACAACAGGTGATGACT
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.....,,.....
B
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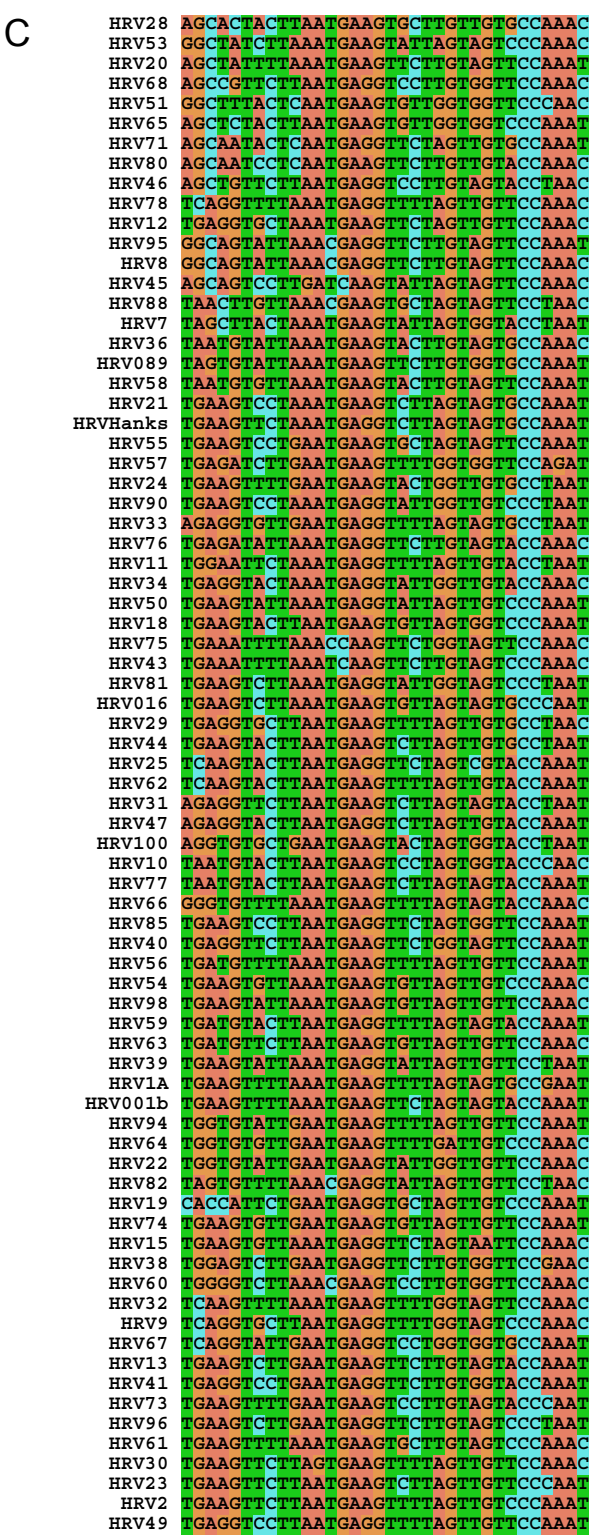
Fig. S8CD

C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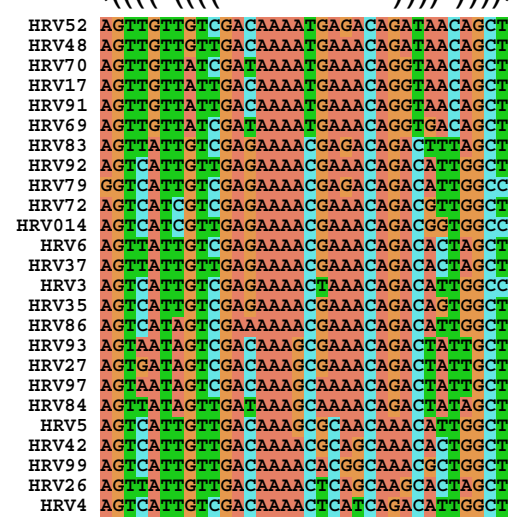
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