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>Consensus sequence RNA structure 1      Reverse reading direction      P= 0.671490
ACAAAACCCUGGCGCUGACUCUGGGGCUAUCUCUCUCCACGCCAGGGAGCUCUCAGGUCGUAUUGAGCGCUUUGCGUGUAGUGUCGGACAUUUGGUGACCCAGUCUCCUGGG
.....((.(((.(((.((((.((((.(.....)))....(((((((.((((.(.....)))....)))..)))..)))..)))..(((.(.....)))

>Consensus sequence RNA structure 2      Reverse reading direction      P= 0.994641
GGCCACGGGGCCUACGCUUUGUUUACCCAGUCUCCAGGGCAUGGGUUAACUCAGGACGACUCGCAUGGUCACAAAACCCUGGCGCUAUCUGGGUCCUUAUCCUCUCA
((((((((((.(.....)))(((.(.....(((.(.....)))..(((.(.....)))....)))..)))..))).....(((.(.....))).....

>Consensus sequence RNA structure 3      Foward reading direction        P= 0.976295
GCCACUAGCAUGCAGUGGUCUGGUAAGACAUCCGCCAGGUGGACUGGGUUAACAAAGCCGUAAGGCCCGUGGCCAAGCAAGGGGAUGGUGUGACCCUUGUGUAAGGACUAGAG
((((.....((.((((.(.(((.(.....)))..)))..)))..)).....(((.(.....)))....)))((.((((.(.....)))....))).....

>Consensus sequence RNA structure 4      Reverse reading direction      P= 0.846482
GGGUCUCCUCUAACCUUAGUCUUAACACAGGGUCACACCAUCCCUUGCUUGGGCCACGGGGCCUUAACGGCUUUGUUUACCCAGUCCACUGGGCAUGUCUUUAUCAGGCAGCA
((((.....))....(((.(.(((.(.....(((.(.....)))....)))..)))..)))(((.(.....))).....(((.(.....)))((.((((.(.....)))....)))

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LEGEND:
"." stands for an unpaired base, "(" corresponds to a paired base whose other base involved in the pair is further 3' and ")" corresponds to a paired base whose other base involved in the pair is further 5'.

Figure S1. Sequences of conserved structural RNA domains identified on the 3' UTR of Bagaza genomes used in this study. Analysis was performed using the RNAz method implemented in the Vienna RNA Websuite (Gruber, et al.; 2008 [22]). A classification probability above 0.5 was considered as significant. "." stands for an unpaired base, "(" corresponds to a paired base whose other base involved in the pair is further 3' and ")" corresponds to a paired base whose other base involved in the pair is further 5'.