



Figure S2. Prediction of RNA secondary structures of mutated LCMV strain WE (LCMV-WE) S segment UTRs which have deletions or mutations between the 20th–40th nt in the 5' terminus or between the 20th–38th nt in the 3' terminus. (a to f) These RNAs were derived from (a) pRF-WE-SRG-UTR-comple, (b) pRF-WE-SRG-UTR 5-3 change, (c) pRF-WE-SRG- Δ 26–40, (d) pRF-WE-SRG- Δ 20–25, (e) pRF-WE-SRG- Δ 20–30, and (f) pRF-WE-SRG- Δ 31–40. RNA sequences of the mutated LCMV-WE S segment genome 5'-terminal and 3'-terminal UTRs and 50 nt of ORF regional RNA sequences that were directly downstream of the UTRs were linked, sent to the CENTROIDFOLD server, and analyzed using the CONTRAfold model (weight of base pairs: 2^2). Each predicted base pair is colored with heat-color gradation from blue to red, corresponding to the base-pairing probability from 0 to 1. "5'" and "3'" indicate 5' terminus and 3' terminus of RNA, respectively. Detailed information about the various mutated pRF-WE-SRGs is given in Table 1, 2 and Figure 1.