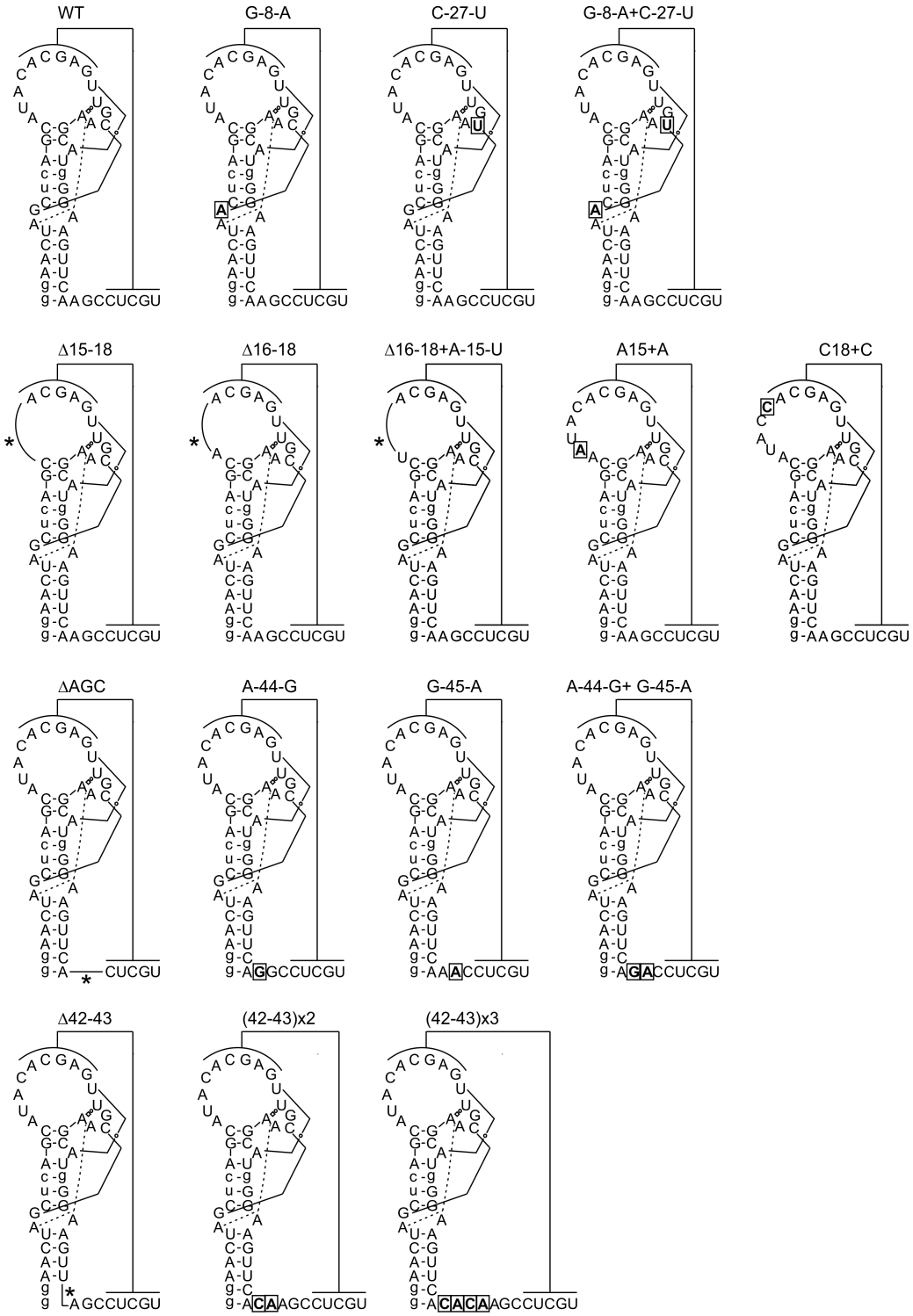

Supplemental Figure S7: Predicted secondary structures of the mutants used in functional assays. Secondary structures of wild-type and mutant PLRV xrRNA constructs used in *in vitro* assays. Substitution and insertion mutations are shown boxed and in bold, deletion mutations are shown as lines and indicated by an asterisk (*). For RNAs used in *in vitro* RNA degradation assays, the sequence shown was usually preceded by a 34 nucleotide leader based on the endogenous viral genomic context (5'-GCCACCACAAAAGAACACUGAAGGAGCUCACUAA-3'), to allow efficient loading of Xrn1. Only exception: RNAs in Fig. S2B had a 15 nucleotide leader (5'-GAAGGAGCUCACUAA-3') where indicated.