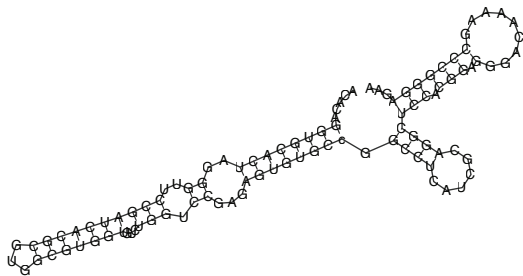
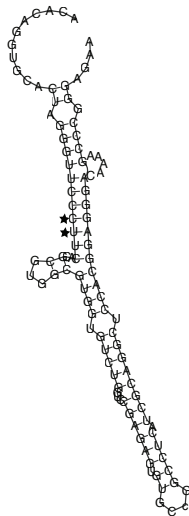


wt



mu1



mu2

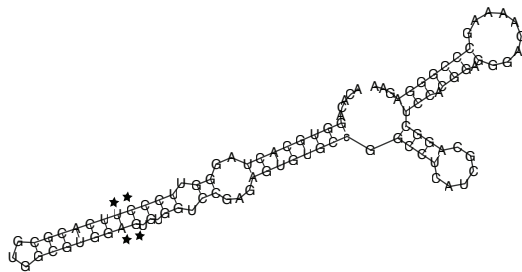


Figure S9. Guanidine I riboswitch. Secondary structure prediction with RNAfold for three different construction RNAs. The predicted structure fits the conserved structure from alignment (Fig. S4B, top). The disruptive mutation (mu1) disrupts the structure and compatible mutation (mu2) restores the structure.