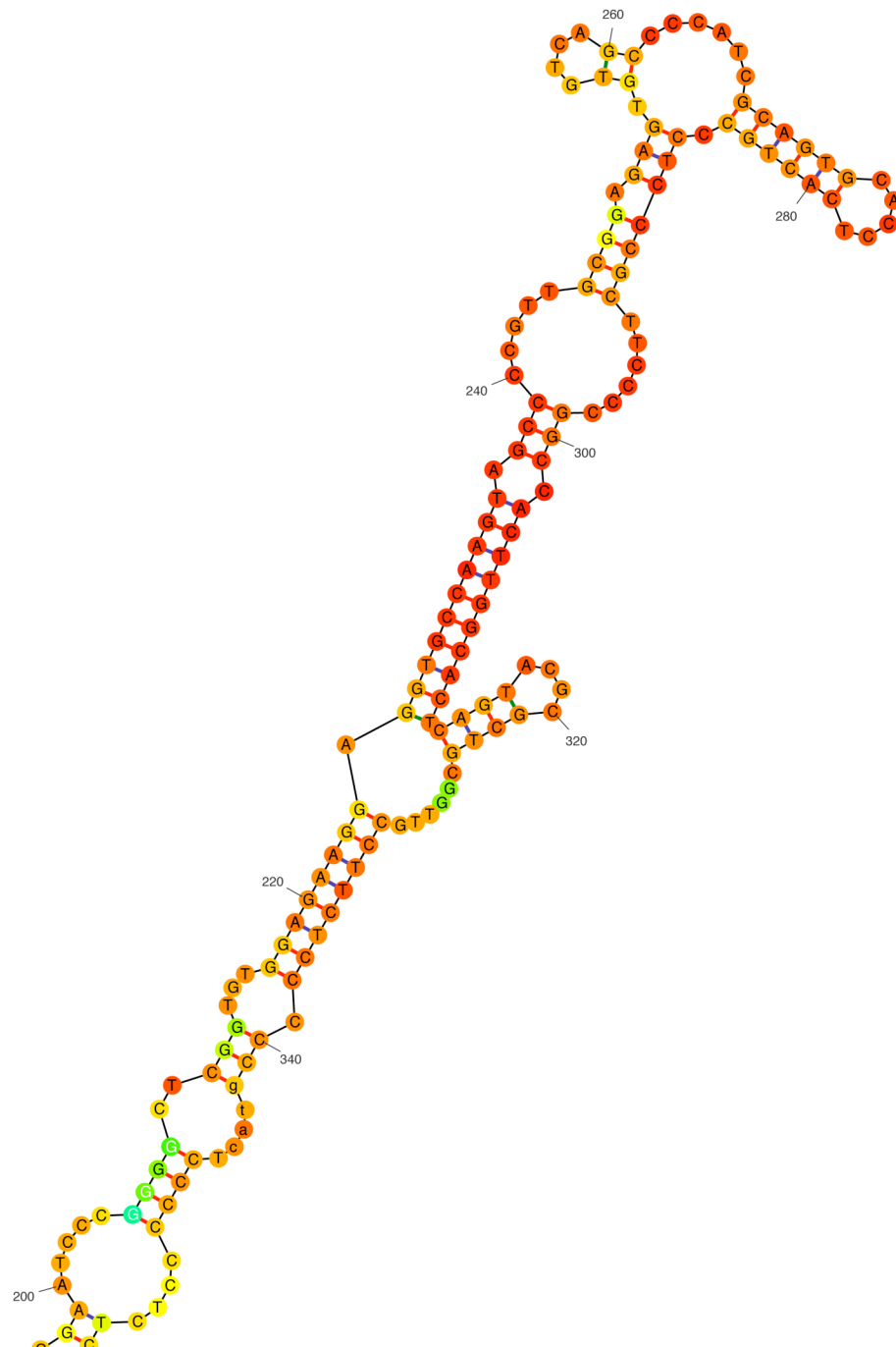


A.



dG = -197.8

1-472 C->G exchange 315-327

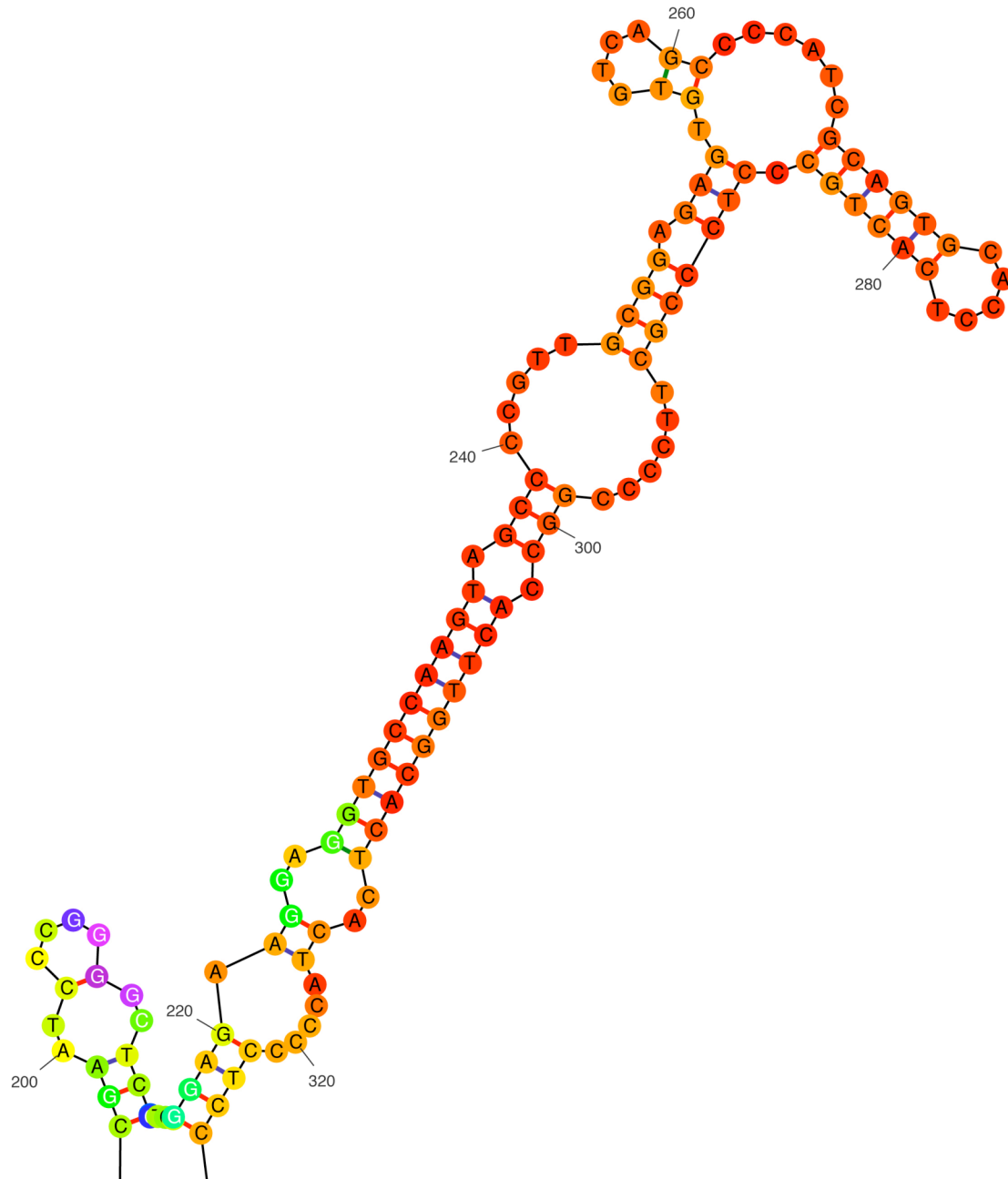
B.



dG = 190.2

1-472 Δ 332-341

C.



dG = -187.2 1-472 Δ 350-364

Supplementary Figure 1. Structure prediction of mutated 1-472 3' UTRs.

Structure prediction by UNAFold V3.4-1 was performed for the complete 1-472 fragment carrying the mutation. However, for better visualization, only the enlarged regulatory arm is shown for each mutant. **A.** 1-472 C->G exchange 315-327; **B.** 1-472 Δ 332-341; **C.** 1-472 Δ 350-364