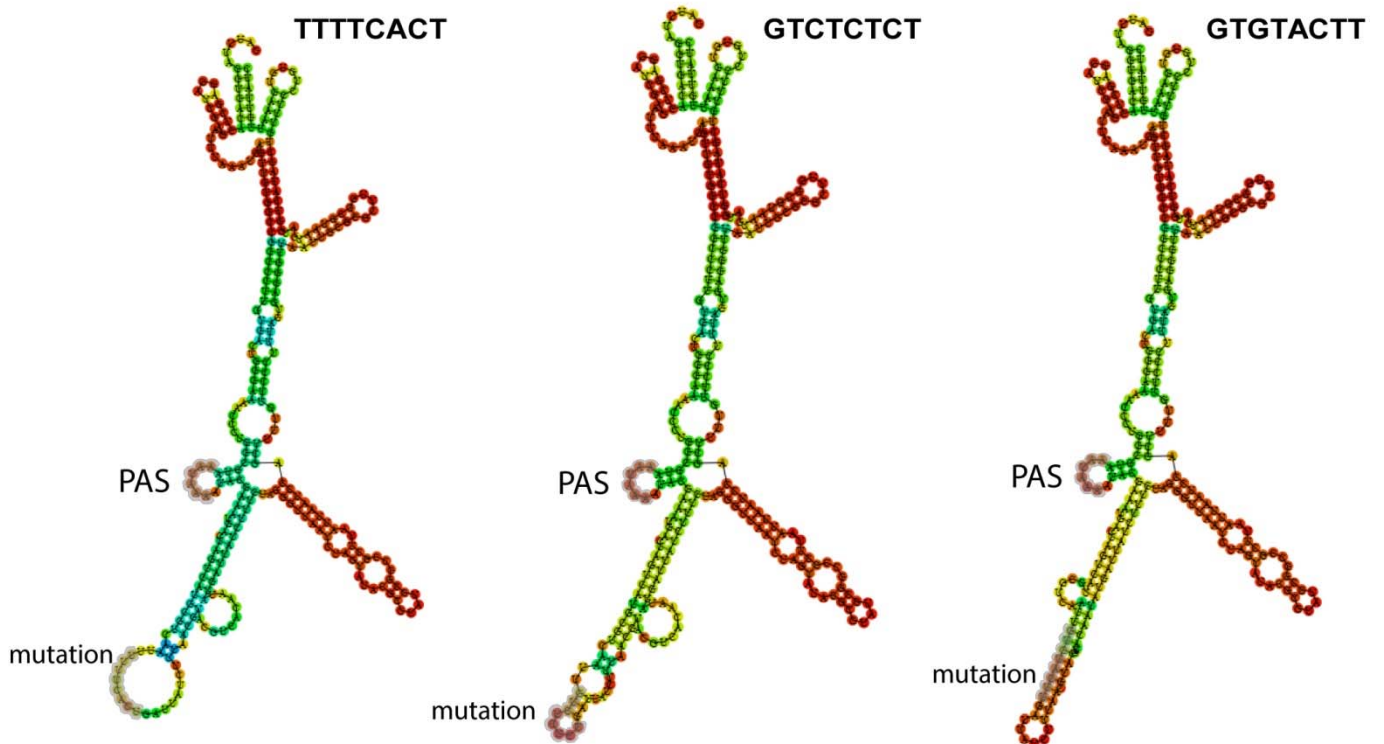


RNAfold Minimum Free Energy prediction

High expression mutations



Low expression mutations

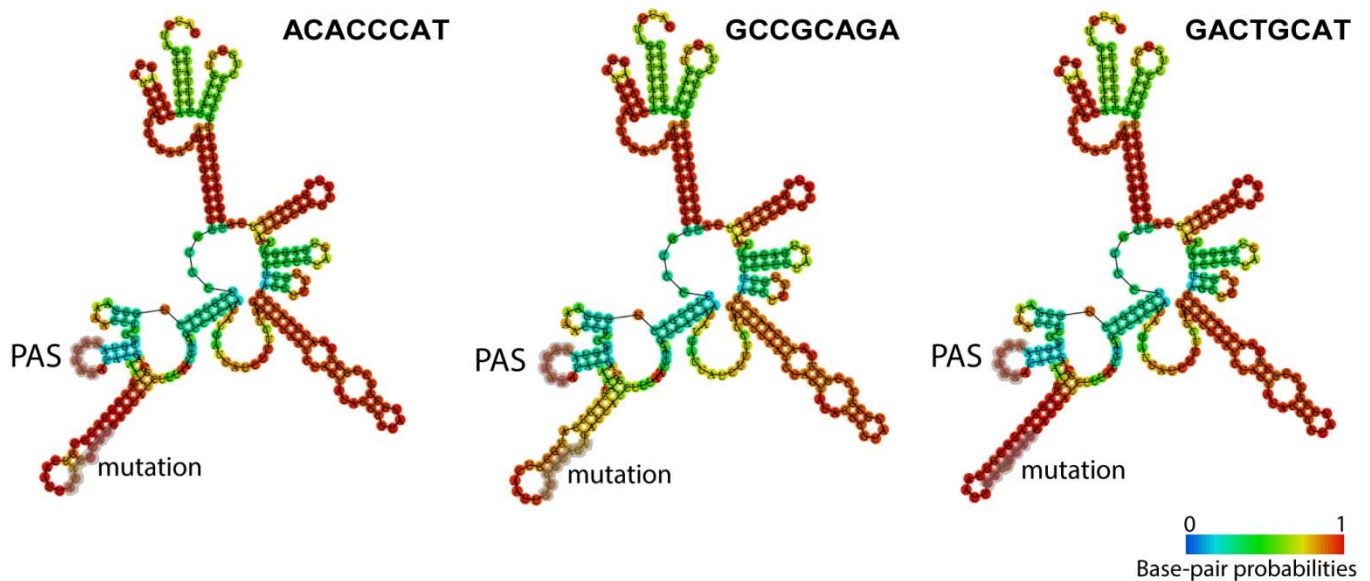


Figure S1. Prediction of the optimal secondary structure of the 3' region of *eGFP* mRNA for three “high” and three “low” expression mutations based on a minimum free energy of -75.70 kcal/mol using the RNAfold web server (<http://rna.tbi.univie.ac.at/>) [113,114]. The mRNA region used for the calculations spans from -75 nt to +200 nt relative to the PAS. The colour scale shows base-pair probabilities from 0 to 1. PAS – polyadenylation signal position; mutation – region of mutation. The regions of PAS and mutations are shown in grey.