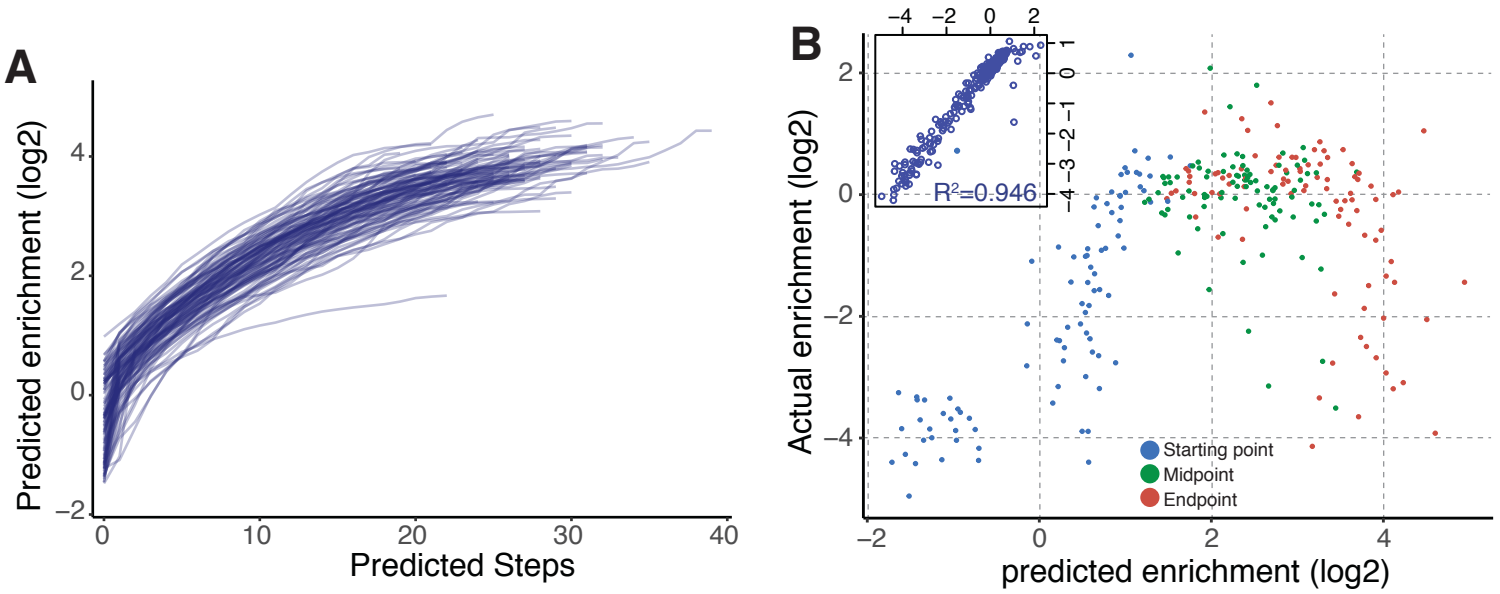

Supplemental Figure 7. (A) Using our convolutional neural network, we iteratively predicted the optimal single nucleotide change in 100 native 5' UTR sequences until no additional increase in enrichment was predicted. The resulting enrichment changes at each iteration step are shown. (B) The start, midpoint and endpoint sequences from evolutions shown in a were constructed and tested in a growth assay experimentally. The predicted and observed enrichments are plotted. Inset: enrichment values measured at two different 3-AT concentrations (1.5mM and 3mM) are well correlated.