



Identifying optimal untranslated regions (UTRs) for mRNA expression

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Background: Untranslated regions (UTRs) are key determinants of mRNA stability and translational efficiency. Identification of tissue-specific 5' and 3' UTR combinations that enhance expression of a gene of interest (GOI) could improve the design and performance of mRNA constructs for therapeutic applications. **Method:** We generated tissue-specific UTR libraries to assess the impact of different UTR combinations on expression of two GOIs, eGFP and IgG. Over 1000s of 5'UTR and 3'UTR combinations were screened from these libraries and compared for expression of the GOI. UTRs from highly abundant and/or tissue specific human genes were identified. UTRs were prioritized from genes with 5' UTRs