

Title of Project	Role of promoter features in RNA fate determination
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Summary of project

The aim of this project is to identify transcriptional features that distinguish the major RNA classes. In particular, we will test the hypothesis that the transcription complexes loaded onto mRNA and ncRNA genes are functionally distinct due to differences in the promoter regions, with consequences for the fate of the RNA transcripts. Bioinformatics and modelling will be used to define differences in the promoter regions of large groups of expression-matched ncRNAs and mRNAs. Most specific eukaryotic transcription initiates from promoter regions that are defined by nucleosome free regions (NFRs) flanked by precisely positioned nucleosomes. We will separate sequences from NFRs, +1 and -1 nucleosome locations, and the subsequent transcript regions of select mRNAs and unstable ncRNAs. These analyses will complement and inform a synthetic biology approach, that will generate large numbers of constructs based on mRNA or ncRNA promoters and flanking regions. These will be tested to determine the fate of the resulting transcripts. Data from these experiments will be used to refine the models, which will guide subsequent gene construct design for experimental testing.