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Project Title: *Validation and Characterization of Long Non-coding RNAs in Sjögren's Syndrome*

Abstract: The human genome contains ~22,000 genes that are expressed as the result of very complex mechanisms that involve both proteins (such as transcription factors) and thousands of non-coding regulatory RNAs. Recent work by the ENCODE project has found that ~80% of the human genome is biochemically active while only 3-5% contains protein-coding sequences. In several diseases, such as prostate and breast cancer, lncRNAs have recently been shown to be important diagnostic markers, prognostic indicators, and targets for successful therapeutic interventions. Our preliminary RNAsequencing studies using whole blood from Sjögren's syndrome (SS) patients have found a substantial number of dysregulated long non-coding RNAs (lncRNAs). We propose to validate these candidates in disease relevant cell types and test potential functional mechanisms. Understanding the role of lncRNAs in SS has significant potential to open completely novel lines of investigation and significantly impact diagnosis and treatment.