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## **Revealing the chromatin-bound long noncoding RNA landscape of the brain**

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Long noncoding RNAs (lncRNAs) are a diverse set of transcripts that bind the genome and regulate epigenetic states. They comprise approximately 58,000 genes in the human genome. Recently, there has been a growing interest in the role of lncRNAs in many psychiatric disorders, including drug addiction. While there have been many studies implicating histone-modifying enzymes and other epigenetic proteins, it has never been entirely clear what the mechanism is to bring an epigenetic modifier to a specific locus. Evidence has shown that lncRNAs can act as scaffolds to help recruit these complexes. To date, epigenetic regulation by lncRNAs has largely been studied on a single transcript basis. To better understand the global landscape of lncRNA in the brain, we are optimizing a recently published method which allows us to capture all chromatin-bound RNA and identify the RNAs as well as the loci to which they are bound. This will allow us to leverage available sequencing data from similar brain tissue-sets to determine how lncRNA are associated with histone marks, nuclear organization, expression levels, and more. While we troubleshoot this method, we will use computational techniques to uncover putative binding patterns using expression data and currently published RNA binding and ChIPseq datasets. This will lead to better understanding of how lncRNAs are regulating the epigenome in the brain both at baseline and in disease states.