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# Epigenetic variation in neurons from multiple brain regions

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Opioid addiction is a brain disorder known to be impacted by genetic, environmental, and lifestyle factors. We focus our research on the impact of non-coding genetic variants in defining disease risk. In order to evaluate the impact of noncoding DNA variants involved in addiction a thorough map of the regulatory regions active in different regions and cell types in the brain is required. Previous mental disorder studies investigating the epigenetic signatures of different cell types typically derive populations from either the pre-frontal cortex or hippocampus. This becomes a pitfall for studying addiction where multiple brain regions are likely to play a role in its development, progression, and relapse. We utilize H3K27ac chromatin immunoprecipitation to identify active regulatory elements in post-mortem human brain tissue from control patients and opioid addiction patients to create a epigenomic map of brain regions involved in decision making, reward, and emotional memory. We aim to identify whether neuronal and non-neuronal epigenetic landscapes differ across different brain regions. We will present our findings comparing H3K27ac enrichment in the amygdala to the prefrontal cortex and hippocampus. Our data supports previous findings that regulatory element activity varies most significantly between neuronal and non-neuronal cell populations. We also observe modest differences in the amygdala neurons relatives to neurons isolated from the frontal cortex. We will present preliminary findings on the critical differences that distinguish the neurons in these two brain regions.