The neuronal epigenome is composed of DNA and histone modifications and higher order chromatin structures. Its architecture changes during the course development and with respect to function in the normal and diseased mouse and human brain. We have begun to link the neuronal epigenome to functional behaviors and provide signatures of how changes in the neuronal epigenome affect behavior. Using publically available schizophrenia datasets we have predicted key transcriptional targets associated with the disorder. Overexpression of these targets in the prefrontal cortex of mice has revealed associations with working memory and social cognition behaviors. Furthermore, we have developed a tool to mark neuronal epigenomes over the course of development in the mouse brain to link previous exposures to present day behavior.

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