

Transcriptome signatures associated with maternal immune activation in the developing brain and autism spectrum disorders

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Abstract: It is widely appreciated that there is correlation between inflammation and Autism spectrum disorders (ASD)¹. However, the molecular mechanisms underlying the impact of inflammation as an environmental risk factor for ASD etiology are largely understudied. Animal models of maternal immune activation (MIA) exhibit abnormal behaviors reminiscent of ASD². Therefore, they can serve as the basis to study the molecular mechanisms that underlie autism like behaviors. The purpose of this study is to gather and analyze data on broad transcriptome-wide studies on MIA offspring rodent models and compare it with autism gene data sets. With this approach we hope to identify a common gene signature that might underlie MIA associated neuronal phenotypes that might be relevant to autism pathophysiology.