Justin St. Cloud

Genuine Parts Award

Biology Major

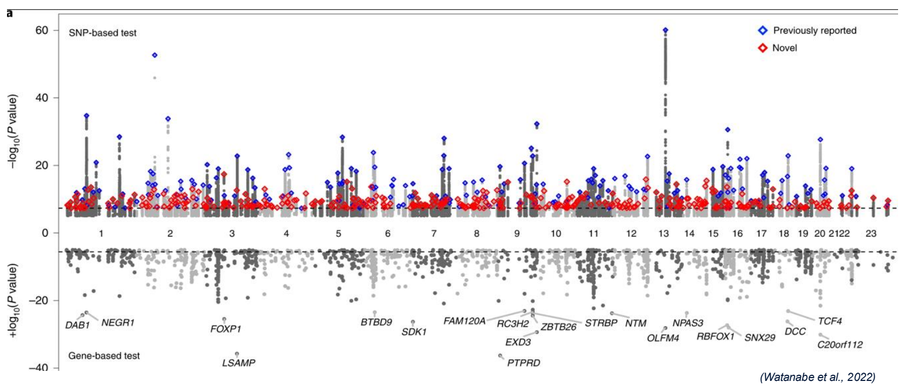
First Year ARCS Scholar

MOREHOUSE COLLEGE

Shared Molecular pathways Between Shank3 Disruption and Centrosomal Genes in Autism Spectrum Disorder

Utilized bioinformatic tools in R to perform principal component analysis on differentially expressed genes, revealing overlapping patterns in cytoskeletal regulation and mitotic timing that suggest converging developmental pathways in autism.

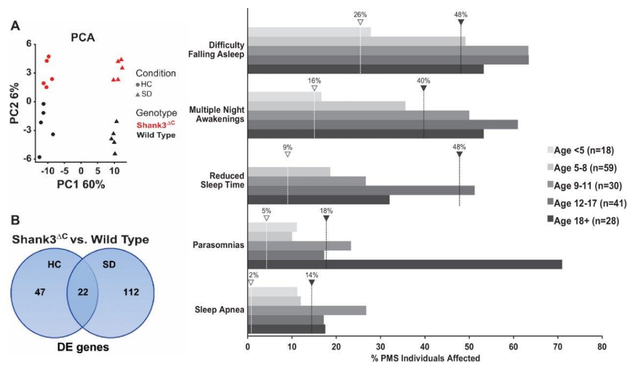
Autism and Sleep



(Watanabe et al., 2022)

Shank3 in Previous Studies

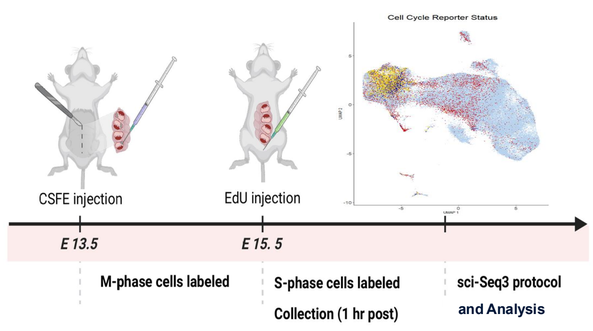
- Has essential functions in synaptic scaffolding and sleep pressure regulation.
- High-confidence ASD risk gene.
- Implicated in Phelan-McDermid Syndrome (PMS).



(Ingiosi et al., eLife 2019)

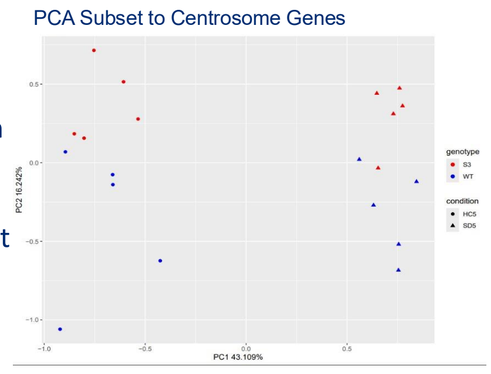
Methodology

- Integrated transcriptomic data from sleep-deprived 12-week-old *Shank3* knockout mice with a list of 164 differentially expressed genes identified in E15.5 mouse embryos exhibiting centrosome dysfunction.



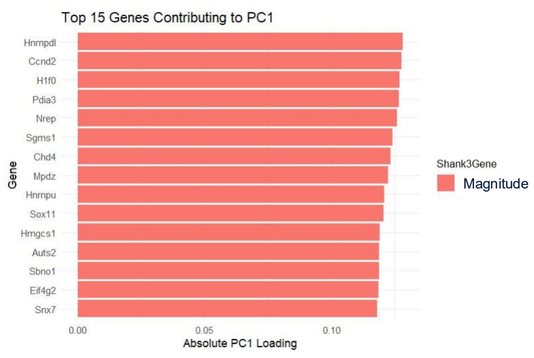
Similar PCA Loadings

- Principal component analysis using genes affected by centrosomal perturbations showed clear separation between *Shank3* knockout and wild-type mice along PC1 and PC2. Despite a narrower gene set, the knockout group's variance mirrored the full dataset, suggesting overlapping molecular functions.



Top Variance Contributors

- These genes share roles in actin cytoskeleton regulation, ciliary signaling, and neurogenesis.
- Many of these genes are critical for neurodevelopment such as CCND 2 (cell-cycle), SOX11 (neuron differentiation), and Auts2 (autism risk).



Scholar Awards Celebration

November 12, 2025

SCHOLAR AWARDS CELEBRATION ARCS FOUNDATION ATLANTA

Igniting Innovation in Georgia