

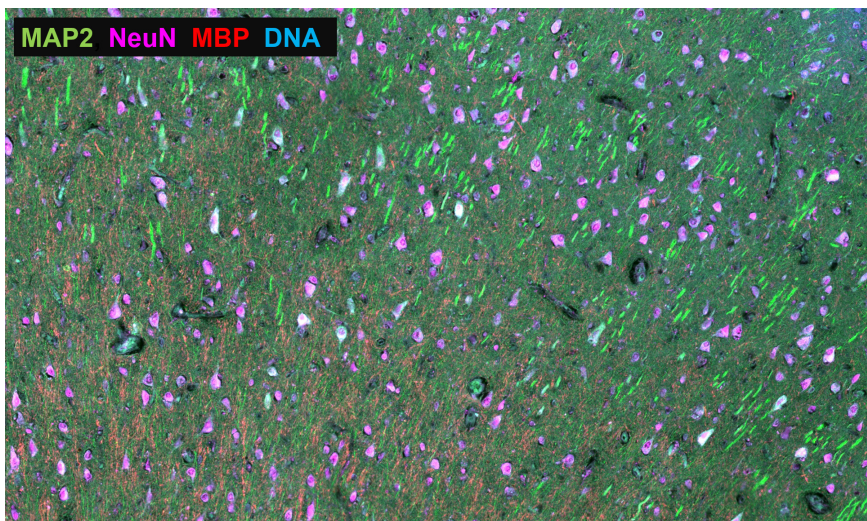
Brain Schizophrenia

Study Purpose

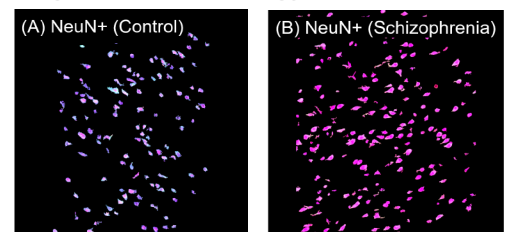
Previous studies have shown that brain tissue from patients with Schizophrenia have altered density of neurons in the white matter compared to control normal tissue. To better understand transcriptomic changes that occur in neurons in Schizophrenia, the GeoMx Human Whole Transcriptome Atlas was used to profile neurons in different cortical regions of brain tissue sections taken from patients with and without Schizophrenia.

Study Summary

Sample Type	FFPE
Species	Human
AOI* Strategy	Cell-type specific
Assay	Human Whole Transcriptome Atlas
Morphology Markers	MAP2, MBP, NeuN, DNA
Targets Detected	2,420 targets in Neurons
Application	Biomarker discovery

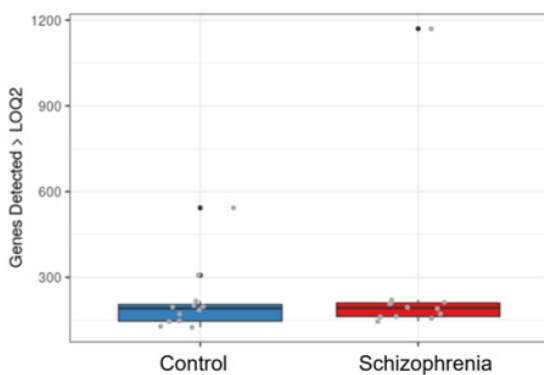


Segmentation Strategy



Legend

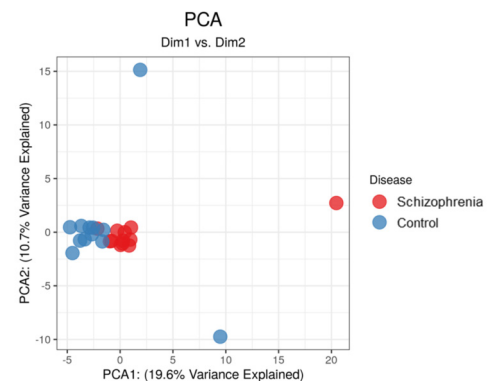
Neurons in control (A) and Schizophrenia (B) were enriched by segmenting NeuN positive cells.



Legend

Left:
The number of targets detected above the background (LOQ2*) by AOI groups.

Right:
Principal component analysis (PCA) plot.



*AOI = Area of Illumination

Acknowledgement: We sincerely thank Dr. Ken-ichiro Kubo from The Jikei University School of Medicine for sharing these images.

For more information, please visit

<https://nanosttring.com/geomx-morphology-markers/>

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