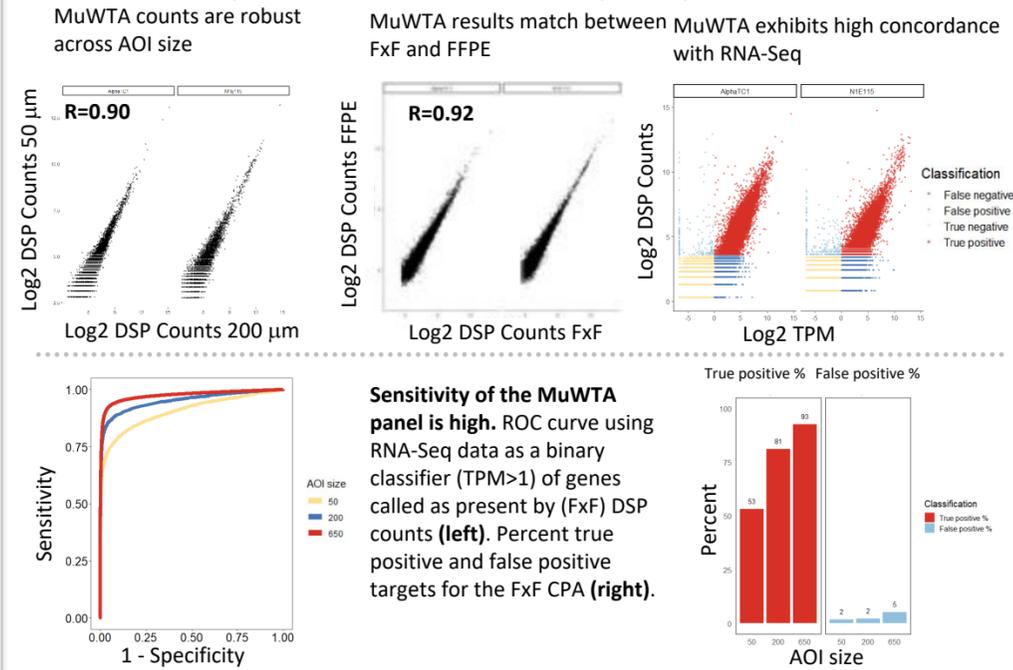


## Abstract

- The mouse Whole Transcriptome Atlas (MuWTA) targets >21,000 gene targets, 17 commonly used transgenes, and 210 negative controls.
- Using cell and tissue arrays and sagittal brain sections we investigated
  - Sensitivity and specificity
  - Fixed Frozen and FFPE correlations
  - The ability to characterize distinct gene expression profiles
  - The ability to utilize a variety of tissues
- Together these results show that MuWTA is a powerful tool to profile any mRNA in multiple mouse tissue types and preparations

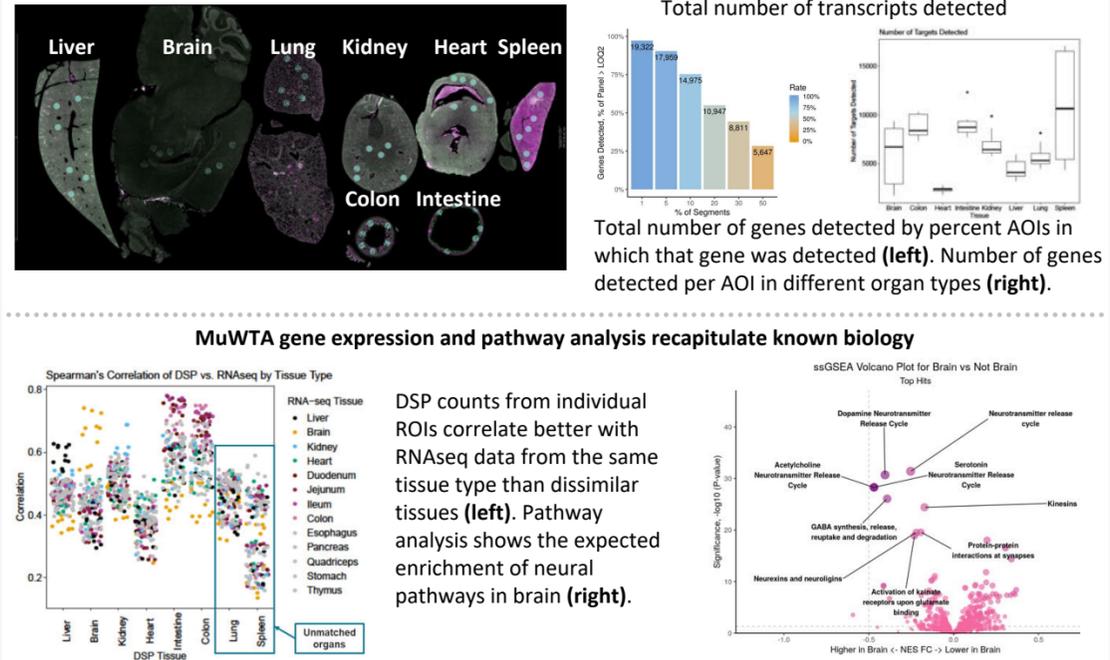
## MuWTA demonstrates high concordance with RNA-Seq

Twelve cell lines were profiled with GeoMx DSP and RNA-Seq. Two representative cell lines are shown



## MuWTA recapitulates known biology in FFPE tissue

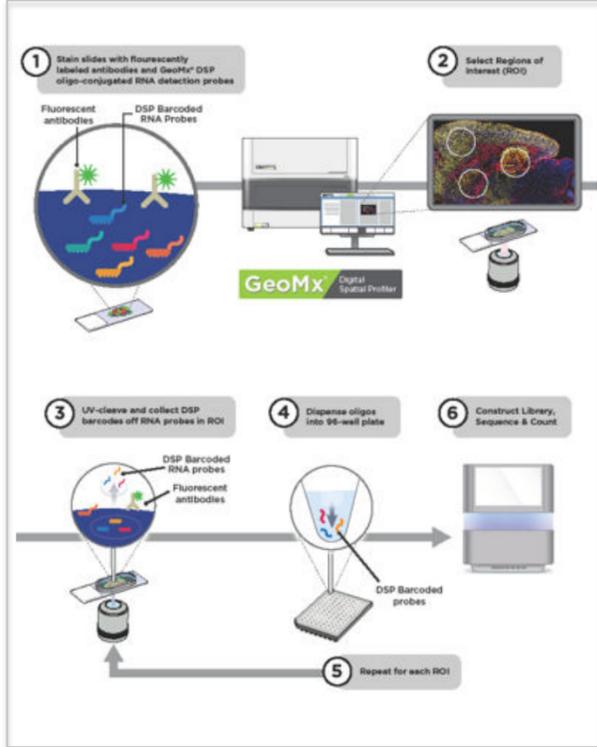
MuWTA captures biology across eight-organ array: 19,000+ genes detected across diverse tissues



## Conclusions

- MuWTA shows high sensitivity and specificity, detects ~5,000-10,000 genes per AOI across a range of tissues
- MuWTA exhibits high concordance across AOI sizes, between sample prep types, and to RNA-Seq
- MuWTA recapitulates known biology in an organ array
- MuWTA leverages targeted AOI design to capture biological differences in distinct brain structures
- Cell deconvolution allows spatial correlations of cell populations

## Digital Spatial Profiling



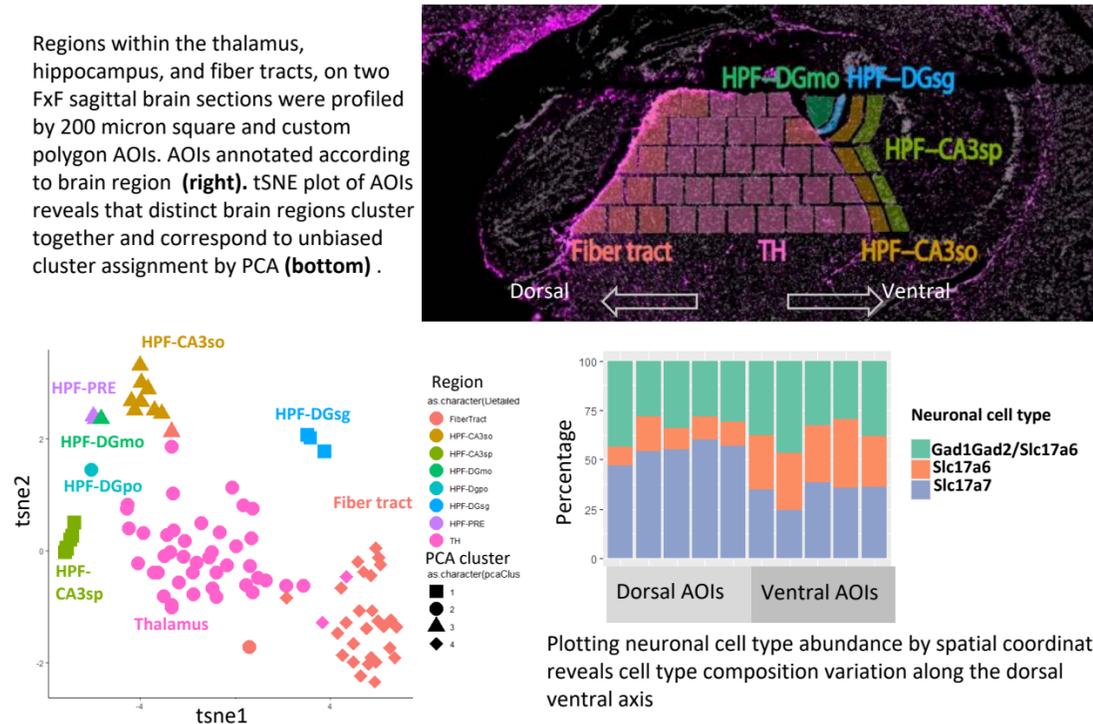
## Methods

The presence or absence of a gene was defined by the limit of quantitation (LOQ) which was determined by calculating the geometric mean of the negative probes, multiplied by the standard deviation raised to the power of 2. Cell type deconvolution was performed using the SpatialDecon R package, using cell types characterized by scRNA-Seq from thalamus regions in Saunders et al., 2018, Cell.

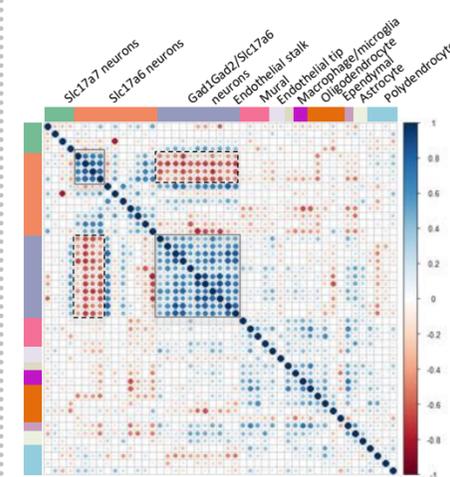
## Brain profiling with intelligent AOI selection enables distinct clustering of individual regions and identifies spatial variation in cell types

MuWTA uncovers structure-specific clustering and a spatial component to cell composition across a deeply profiled brain region

Regions within the thalamus, hippocampus, and fiber tracts, on two FxP sagittal brain sections were profiled by 200 micron square and custom polygon AOIs. AOIs annotated according to brain region (right). tSNE plot of AOIs reveals that distinct brain regions cluster together and correspond to unbiased cluster assignment by PCA (bottom).



MuWTA cell type deconvolution reveals anticorrelated populations across space



MuWTA detects biological differences between distinct anatomical regions of the same brain structure

