

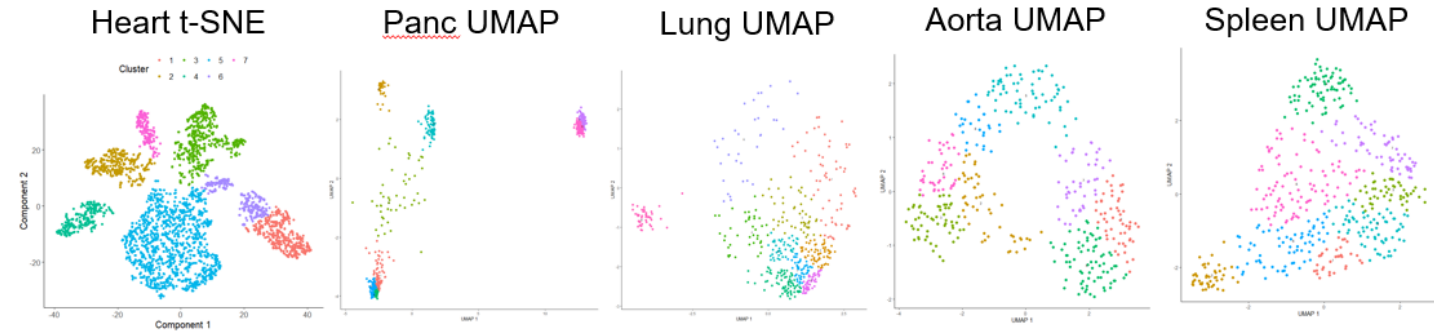
Caltech-UW TMC: A Spatially Resolved Molecular Atlas of Human Endothelium

Jay Shendure, Cole Trapnell, Shin Lin and Long Cai
09/23/2019

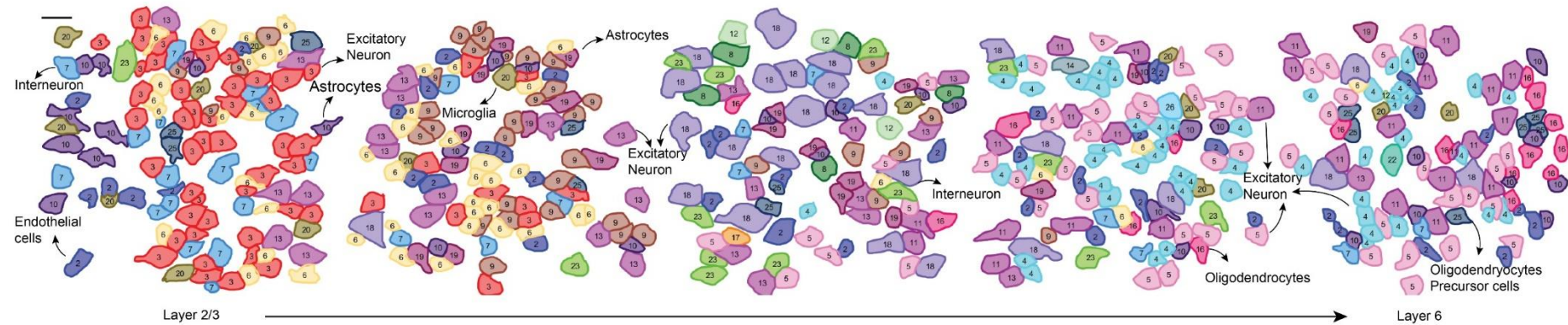


UW-Caltech TMC Progress to date

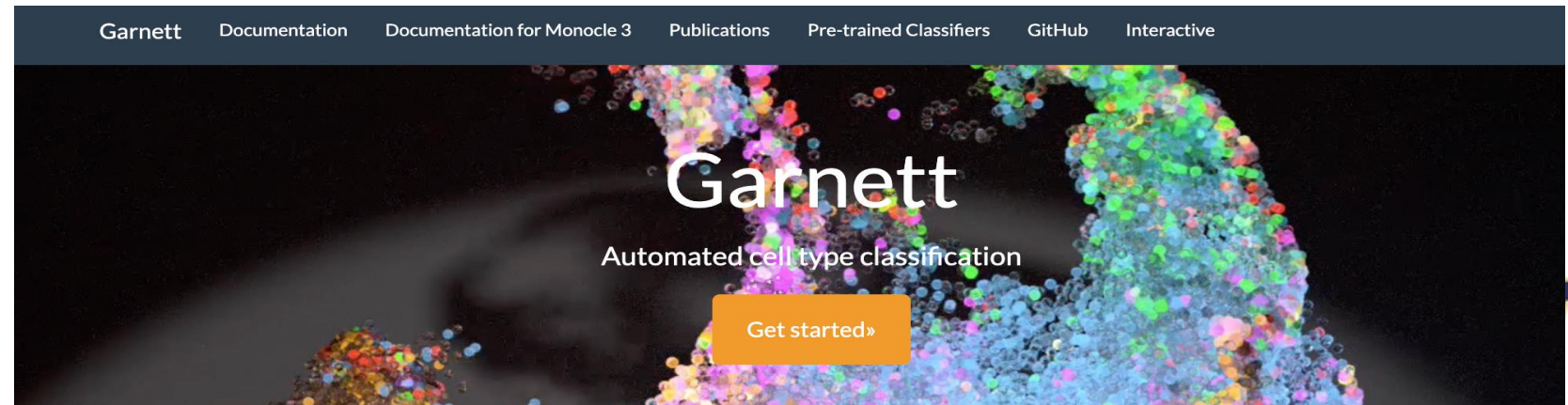
- *sci-RNA-seq*



- *seqFISH+*



- *Computational*



Next Year's Deliverable in 1 slide

- **Tissue Donors:** 1-2
- **Locations:** average of 5 sites from at least 2 organs (may not be heart).
- **Data Types:**
 - seqFISH: 10 fields will be imaged from each site using ~50 probes
 - paired sci-RNA-seq + sci-ATAC-seq: 10,000 cells for each site

Collaborations

A. with Stanford (colon)

1. Single nuclei data generation occurs independently

B. with University of Florida (spleen)

2. Collaborative analysis to establish probeset

C. TMC-wide collaborative project (TBD)

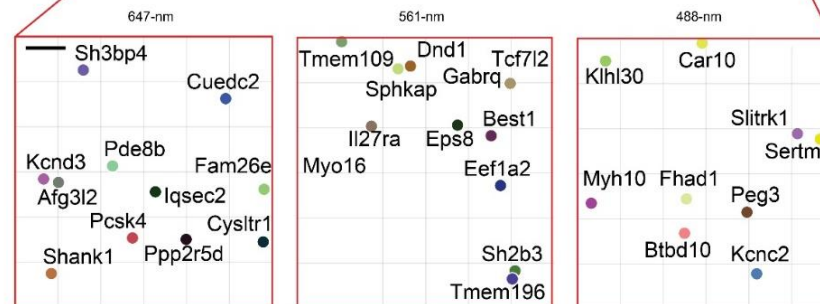
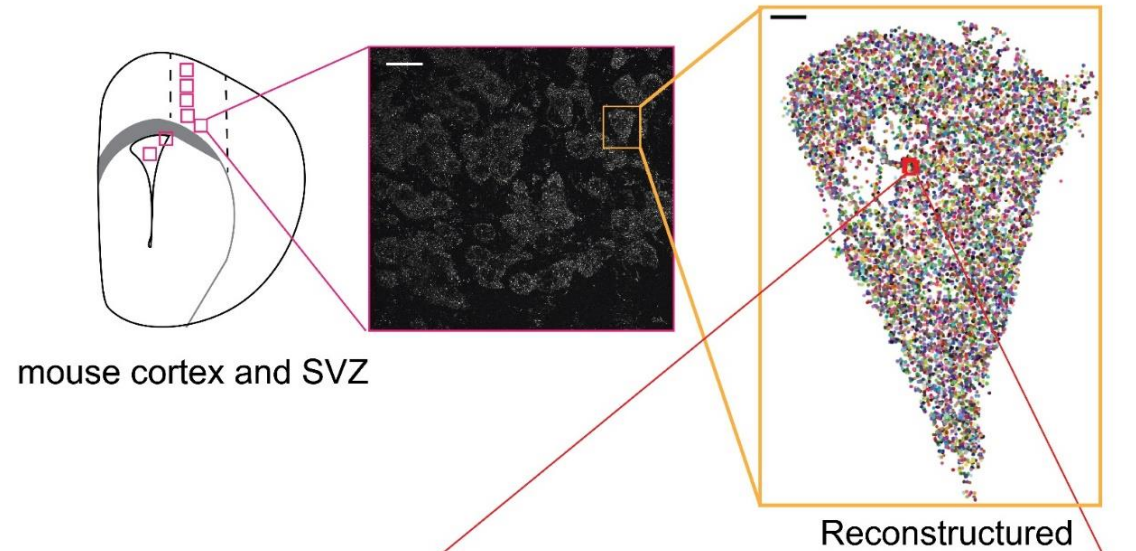
3. Spatial mapping

D. Integrating intron seqFISH with RNA seqFISH

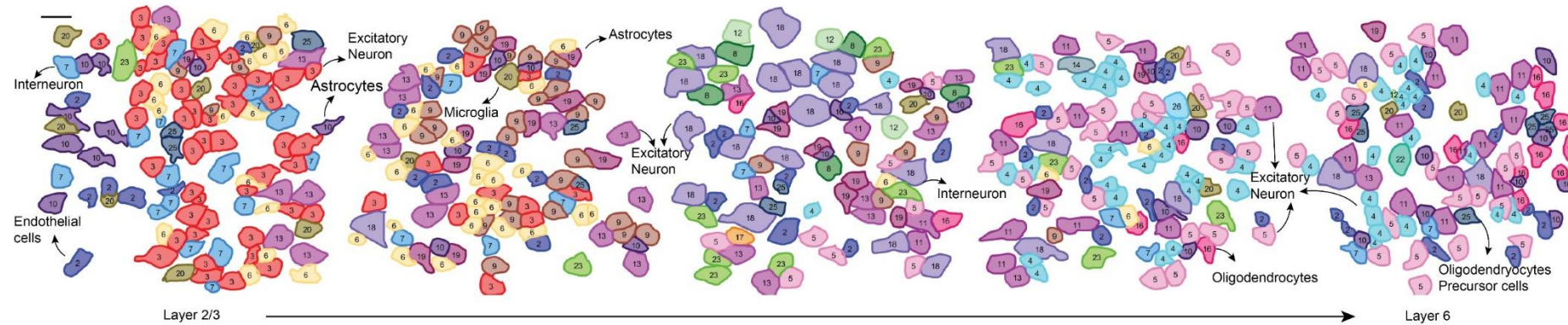
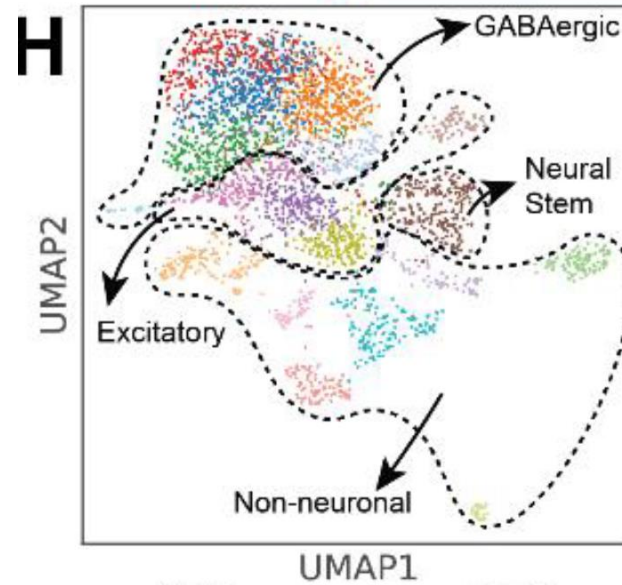
What should HuBMAP Do ?

- *support some studies into diseased tissues to showcase how the normal data may be used*

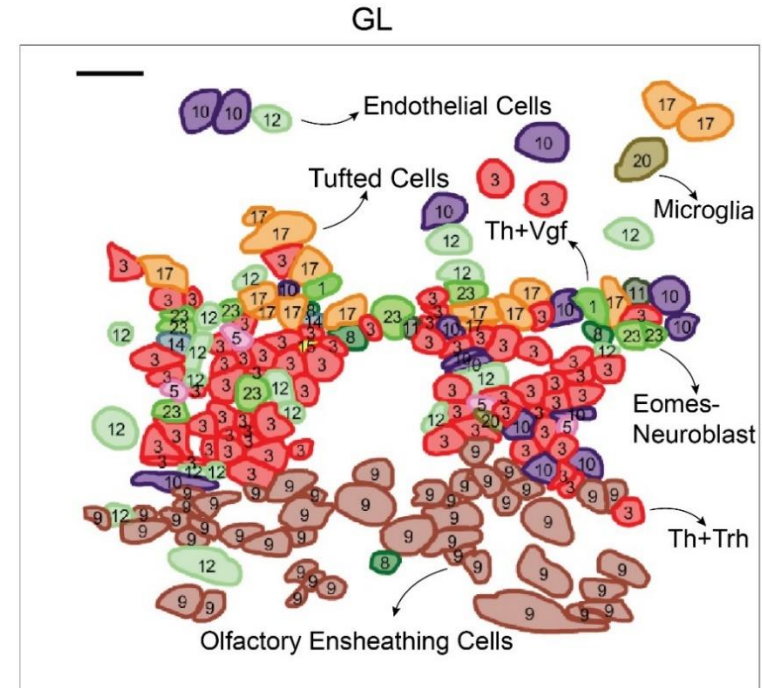
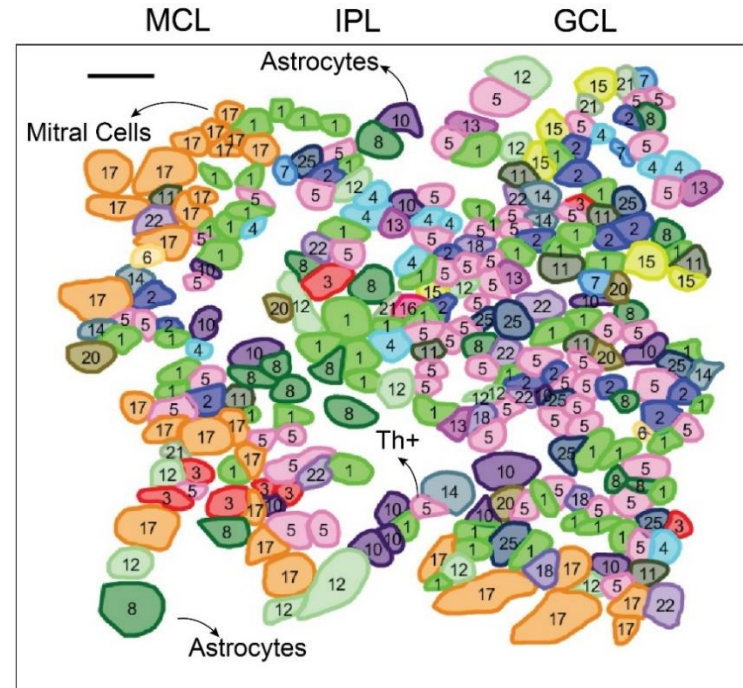
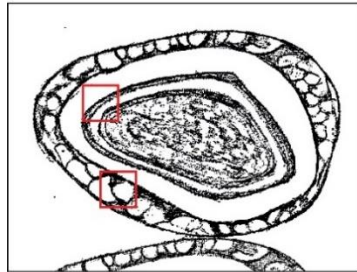
RNA seqFISH+ profiles 10,000 gene in mouse cortex, SVZ and Olfactory bulb



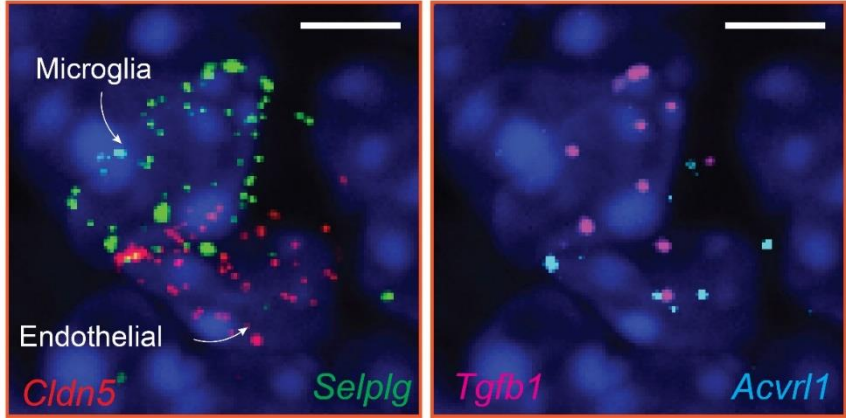
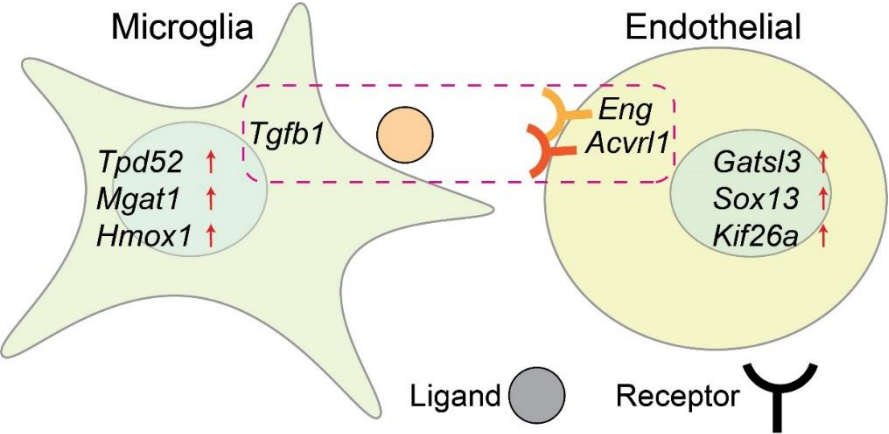
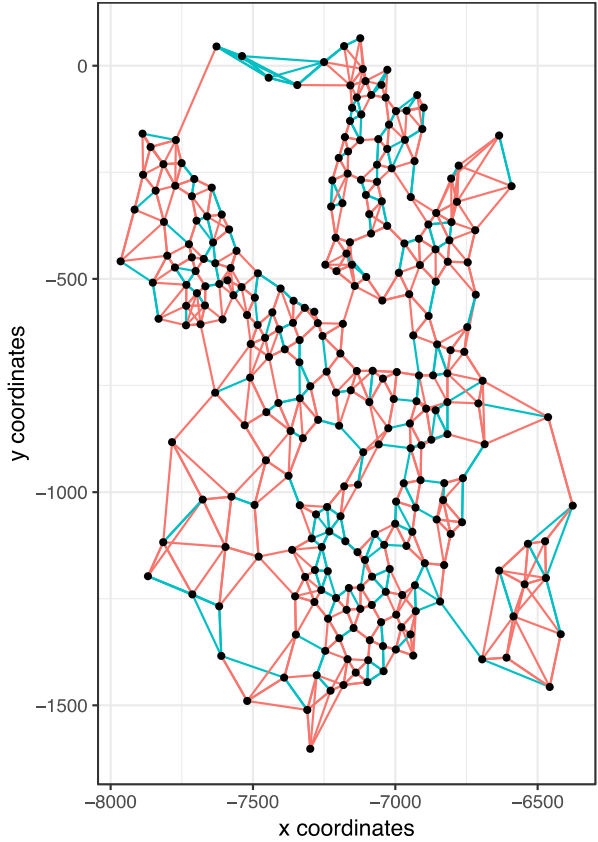
Spatial organizations of cells in cortex



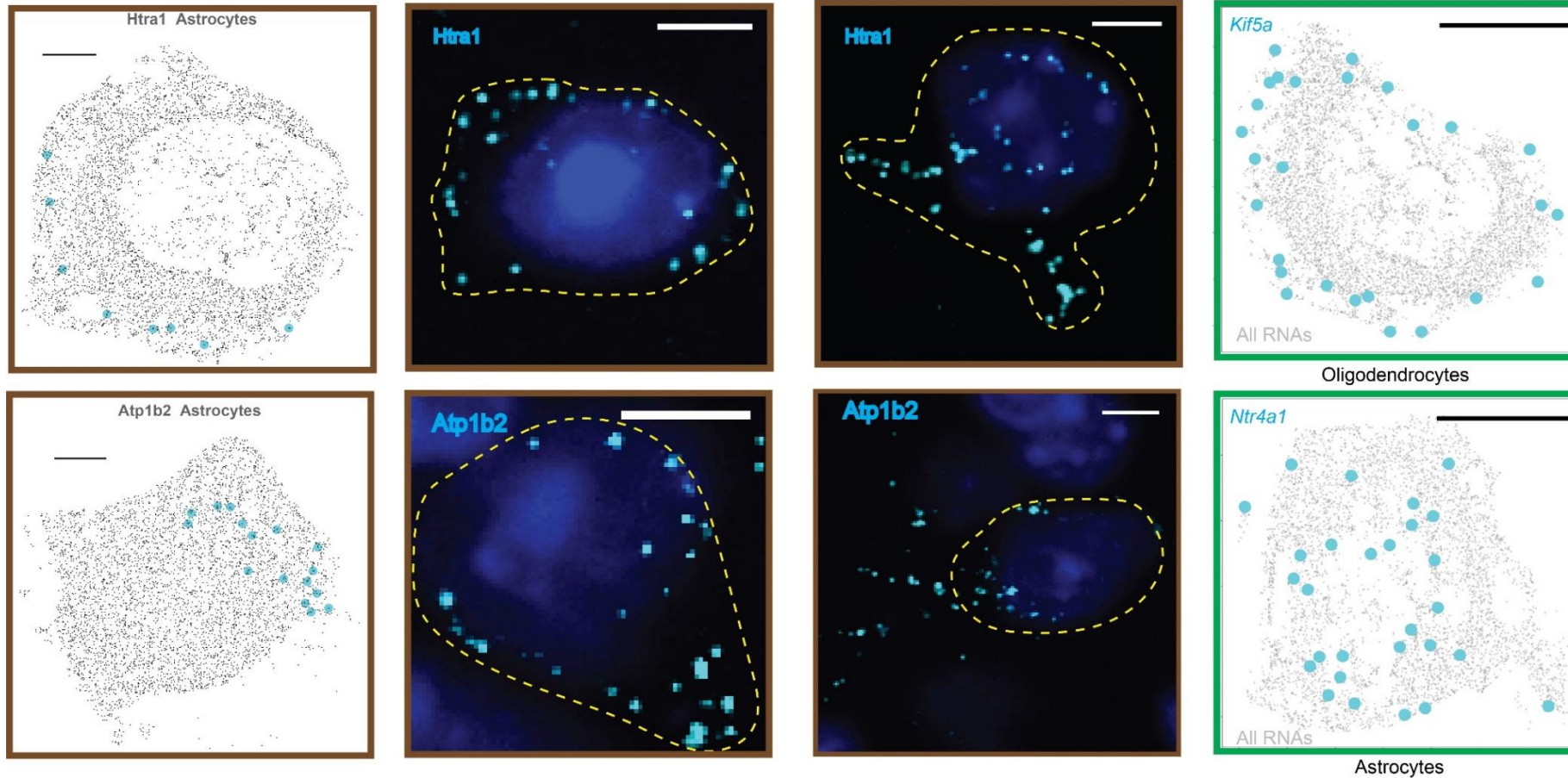
1. seqFISH+ can provide an independent measurement of the transcriptome



2. seqFISH+ enables *in situ* neighbor interaction analysis

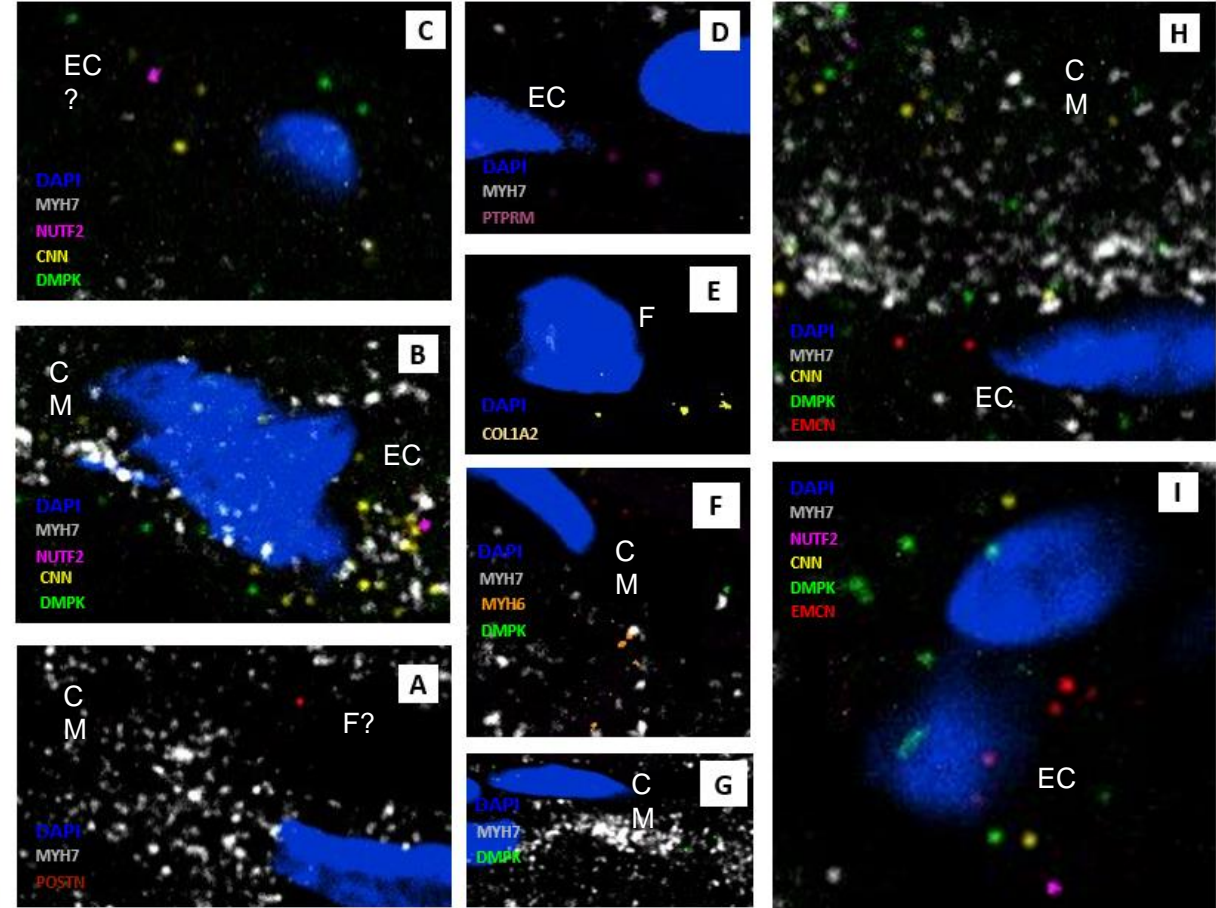
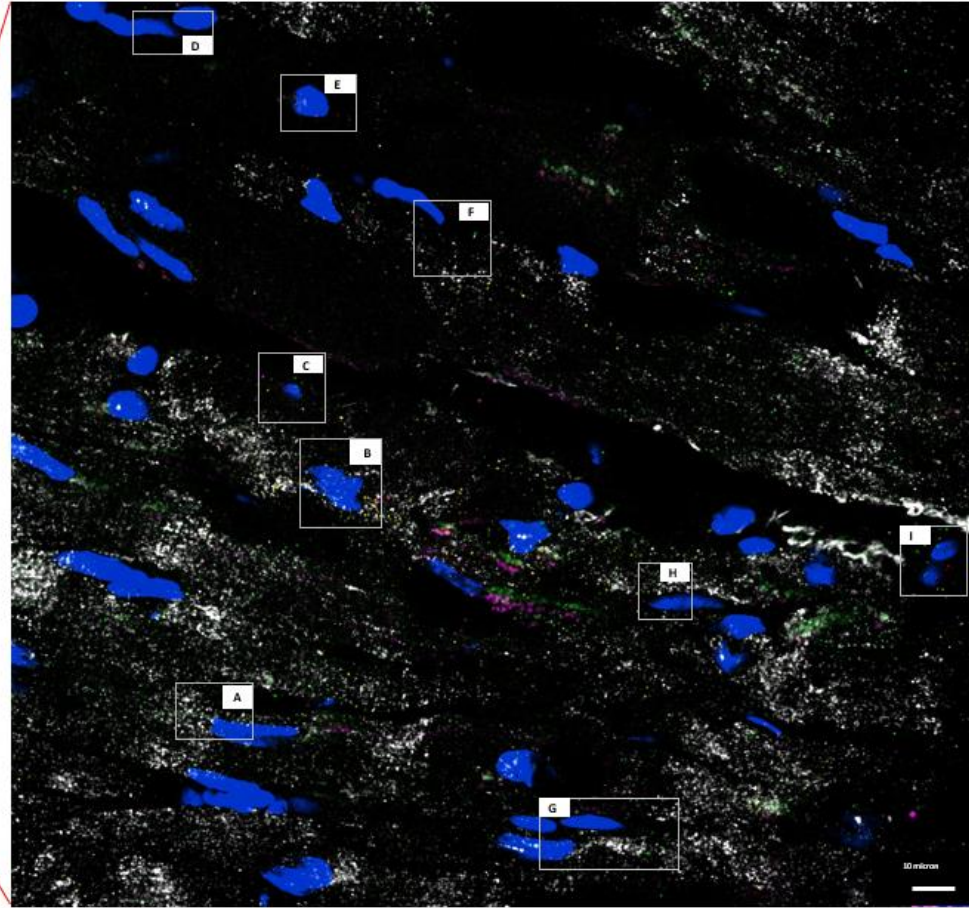
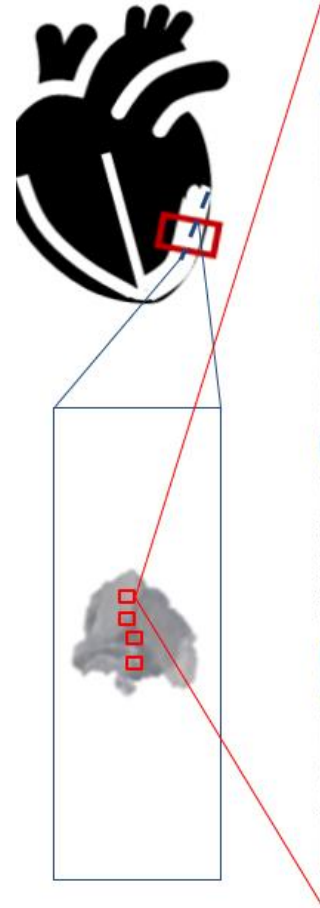


3. seqFISH+ enables imaging of subcellular localizations in distinct cell types



seqFISH+

smFISH



Cardiomyocytes	Endothelial cells	Fibroblasts	Other	Nuclei
MYH6	PTPRM	POSTN	NUTF2	DAPI
MYH7	CNN	COL1A2	PLS3	
DMPK	EMCN	DCN	FASN	
			LUM	