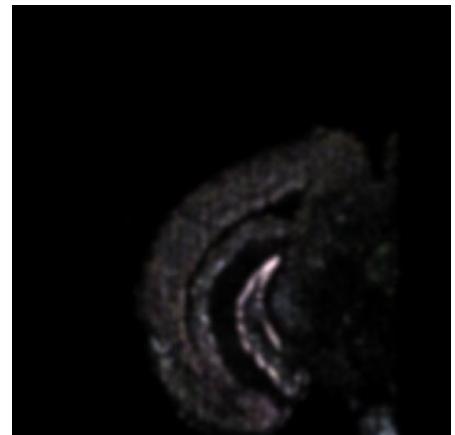
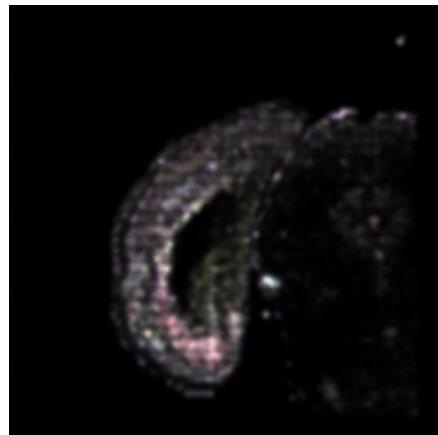
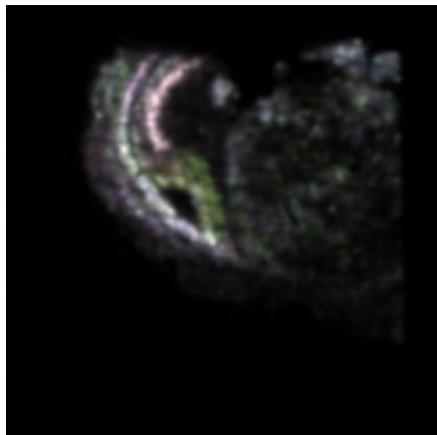
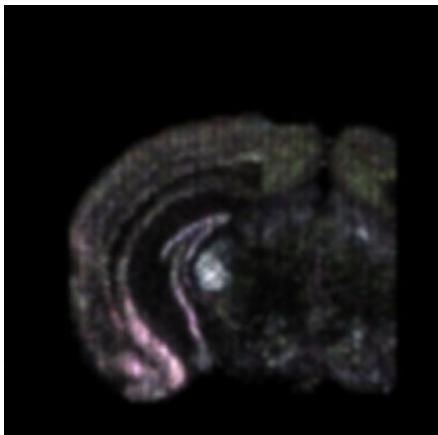


# Spatially map single cell RNA-seq to spatial coordinates

without prior knowledge of cell locations for scRNASeq (BAR-seq2)



# Motivation

Growing better organoids to form organ tissues for organ repair and regeneration

Mapping single cells to spatial structures improves interpretation of spatial developmental biology

For example, key kidney paper on SIX2 gene in progenitor kidneys involved spatial knowledge:

*Six2 activity is required for maintaining the mesenchymal progenitor population in an undifferentiated state by opposing the inductive signals emanating from the ureteric bud.*

*Six2-expressing cells give rise to all cell types of the main body of the nephron during all stages of nephrogenesis.*



[EMBO J.](#) 2006 Nov 1; 25(21): 5214–5228.

Published online 2006 Oct 12. doi: [10.1038/sj.emboj.7601381](https://doi.org/10.1038/sj.emboj.7601381)

Six2 is required for suppression of nephrogenesis and progenitor renewal in the developing kidney

[Michelle Self](#),<sup>1</sup> [Oleg V Lagutin](#),<sup>1</sup> [Beth Bowling](#),<sup>1</sup> [Jaime Hendrix](#),<sup>1</sup> [Yi Cai](#),<sup>2</sup> [Gregory R Dressler](#),<sup>2</sup> and [Guillermo Oliver](#),<sup>1,a</sup>

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PMCID: PMC1630416

PMID: [17036046](#)

## Cell Stem Cell

Volume 3, Issue 2, 7 August 2008, Pages 169-181



Article

Six2 Defines and Regulates a Multipotent Self-Renewing Nephron Progenitor Population throughout Mammalian Kidney Development

Akiyo Kobayashi<sup>1</sup>, M. Todd Valerius<sup>1</sup>, Joshua W. Mugford<sup>1</sup>, Thomas J. Carroll<sup>1,3</sup>, Michelle Self<sup>2</sup>, Guillermo Oliver<sup>2</sup>, Andrew P. McMahon<sup>1,2,3</sup>

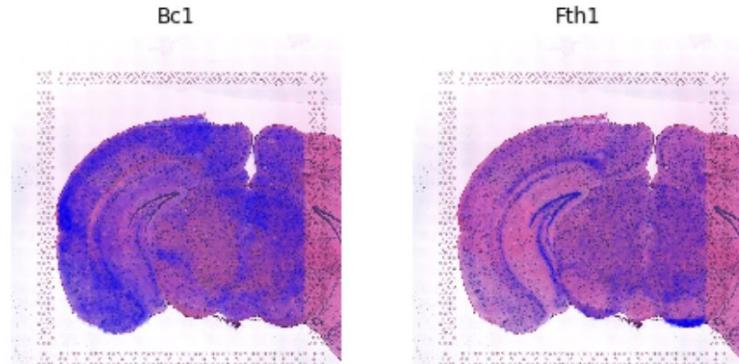
# Datasets

**Spatial Transcriptomic** data from the Allen Brain Institute is used from:

<https://github.com/almaan/spacetx/>

This is purposed for the **BAR-seq2** data of the **Competition from the Allen Brain Institute**:

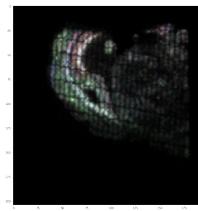
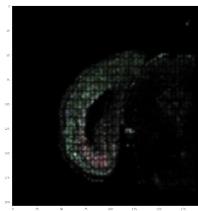
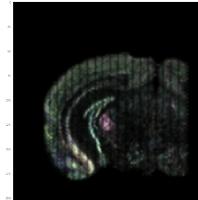
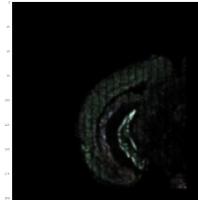
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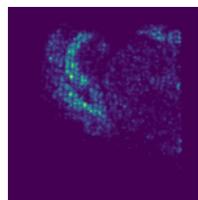
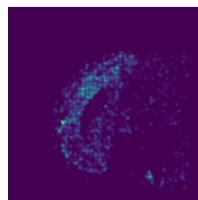
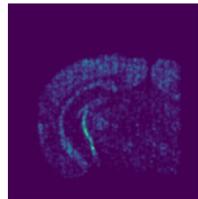
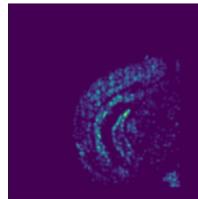
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<a href="#">barseq2.rds</a>	2022-04-16 11:27	27M	
<a href="#">readme.txt</a>	2022-04-16 11:27	1.2K	

# Training set

Predicted image tissue histology pixels matched to observed image tissue histology pixels

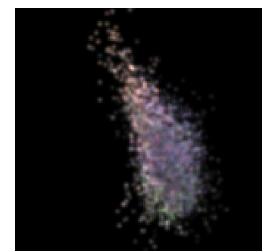
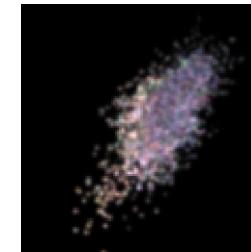
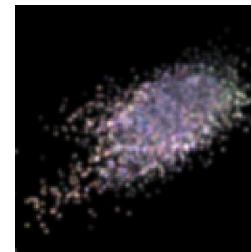


Predicted gene expression of SLC24A2 on spatial histology matched to observed spatial gene expression

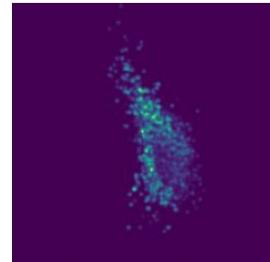
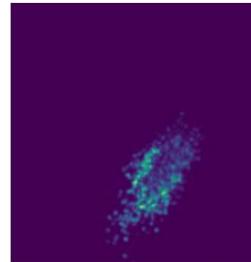
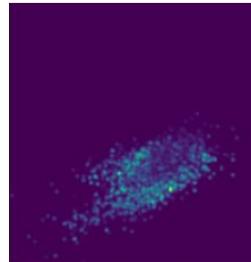


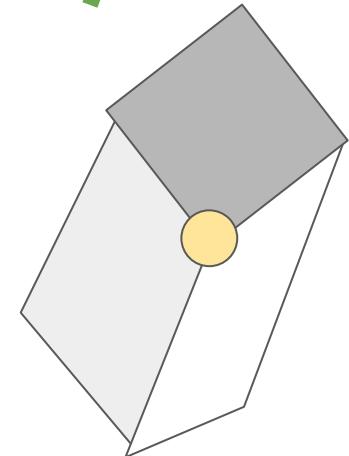
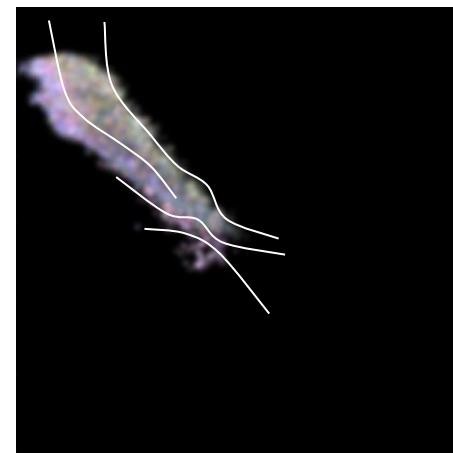
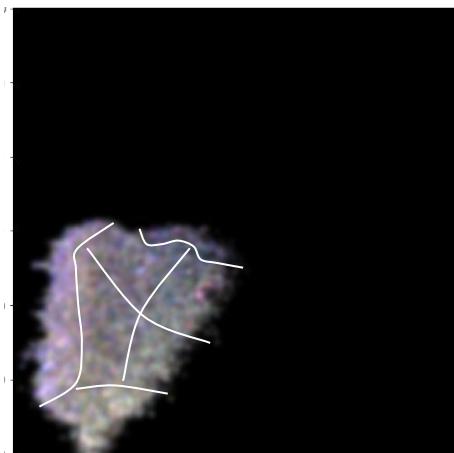
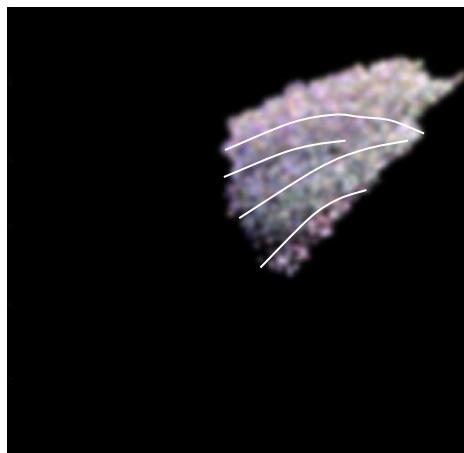
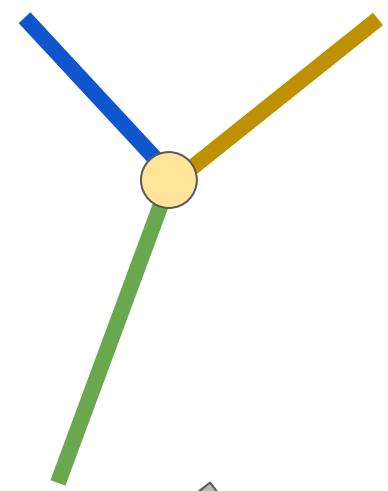
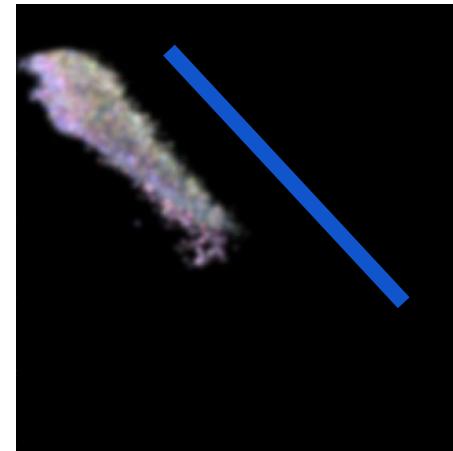
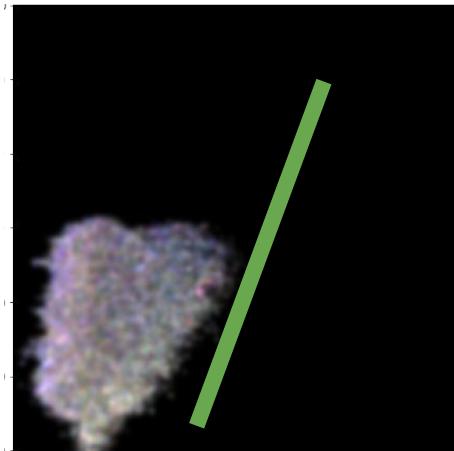
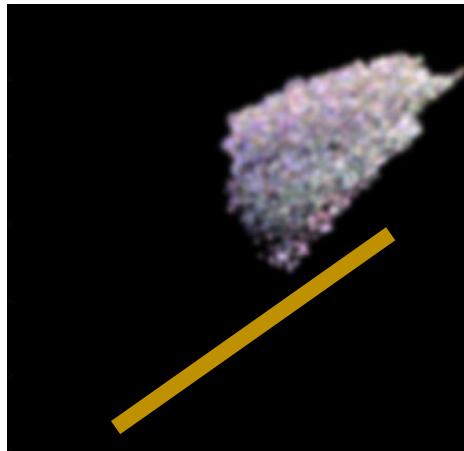
# Test set

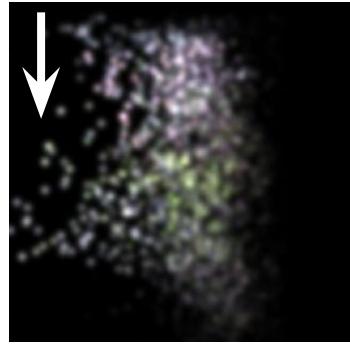
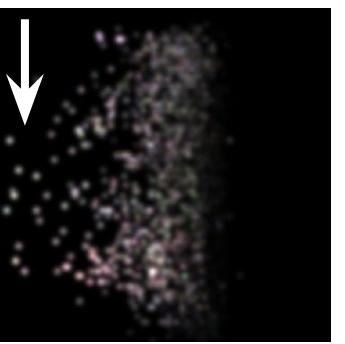
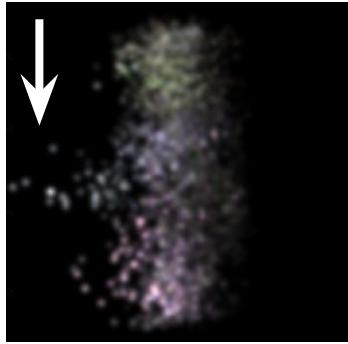
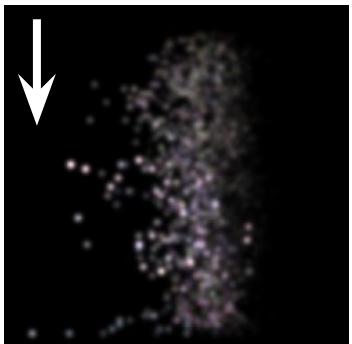
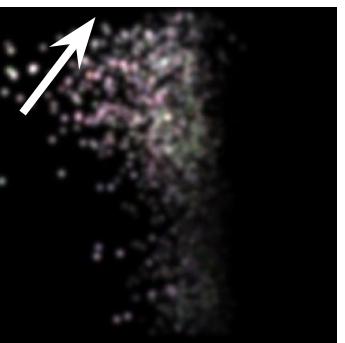
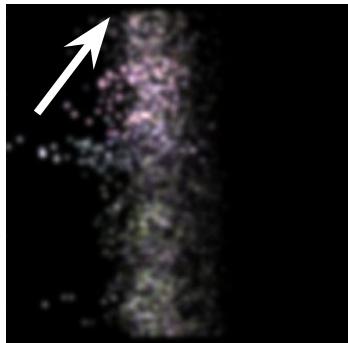
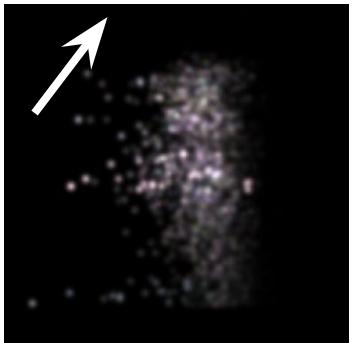
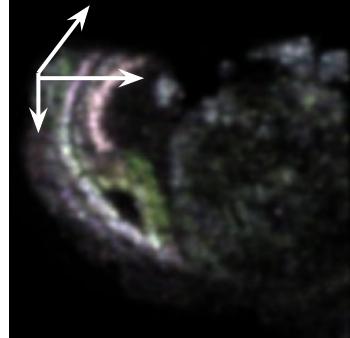
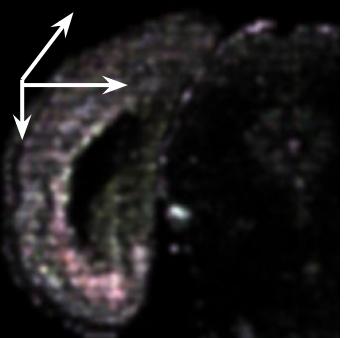
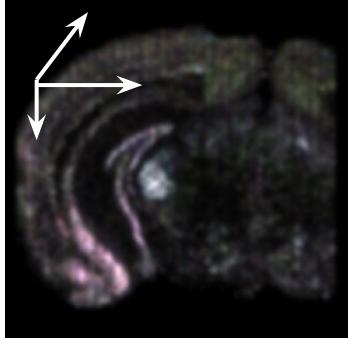
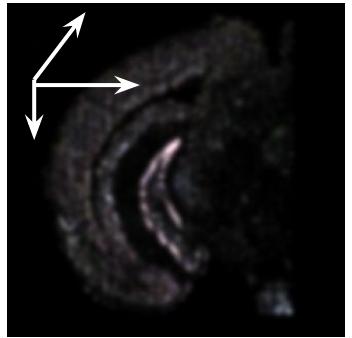
Predicted image tissue histology based on scRNAseq + model



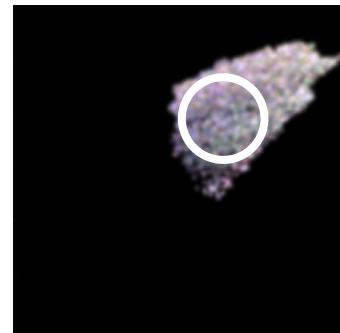
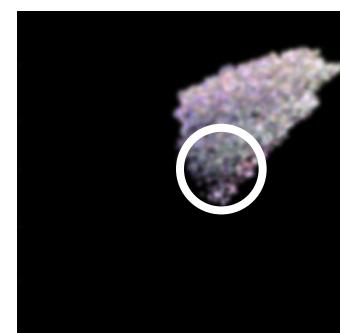
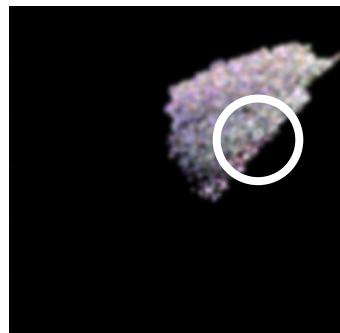
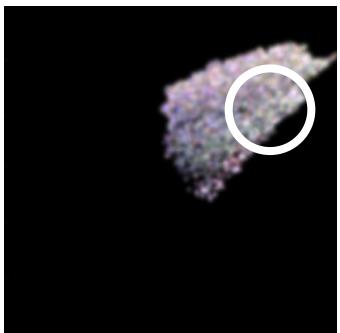
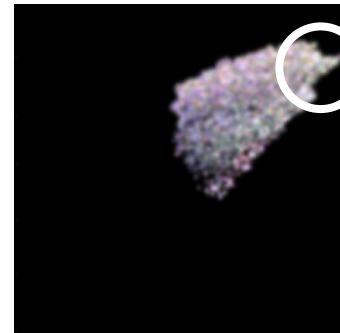
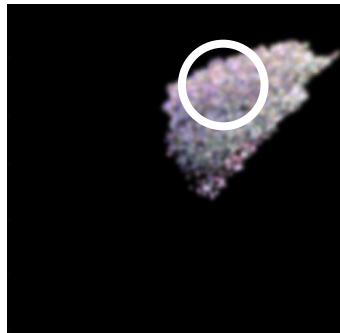
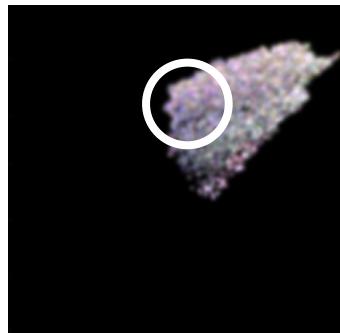
Predicted gene expression for SLC24A2 based on scRNAseq + model



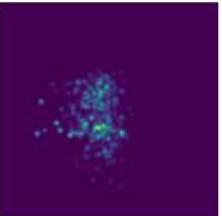
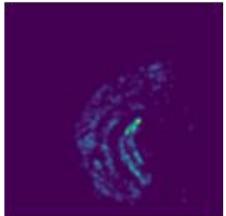




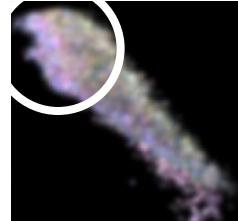
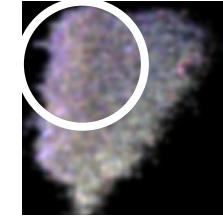
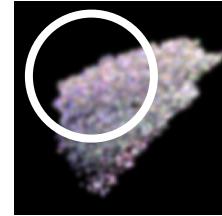
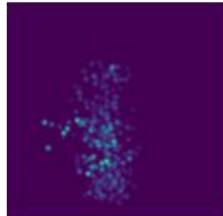
Next set of slides show the trajectory of gene expression based on location for different genes



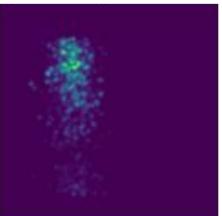
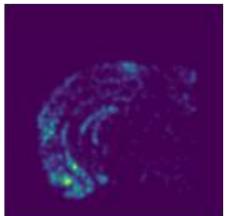
Real GEX (Tissue 1) - X-Y-Z-axis



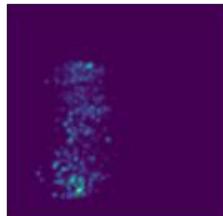
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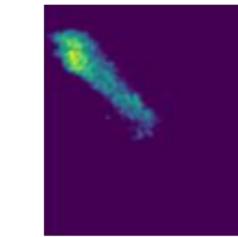
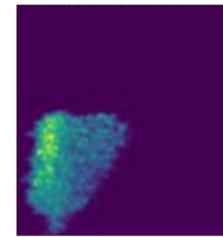
Real GEX (Tissue 2) - X-Y-Z-axis



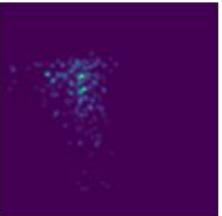
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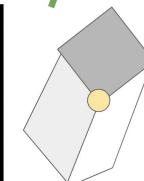
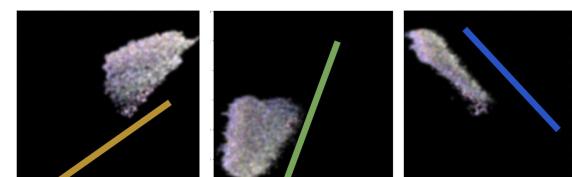
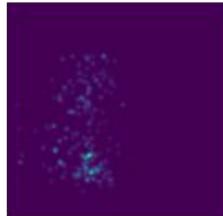
In-Silico GEX - X-Y-Z-axis



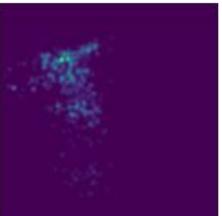
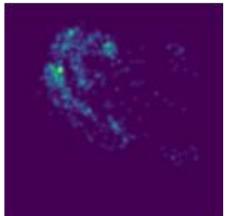
Real GEX (Tissue 3) - X-Y-Z-axis



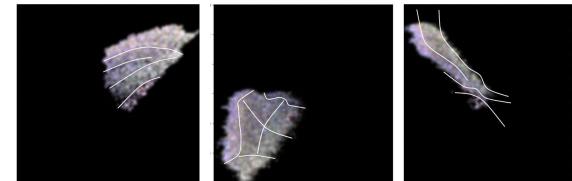
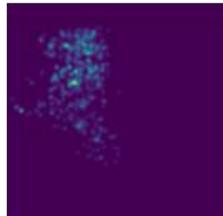
C1q|3



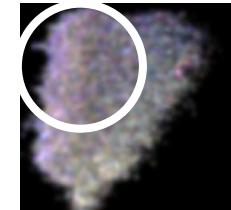
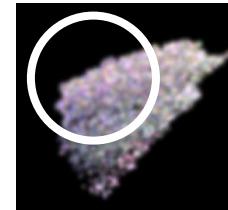
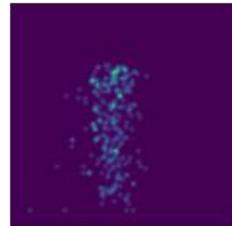
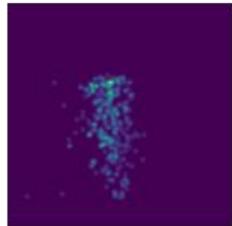
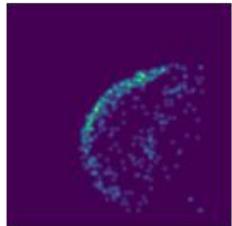
Real GEX (Tissue 4) - X-Y-Z-axis



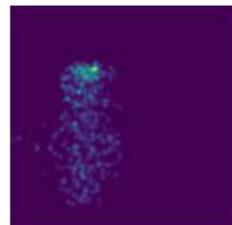
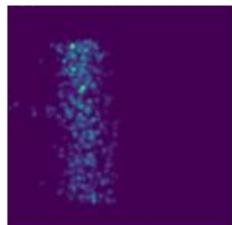
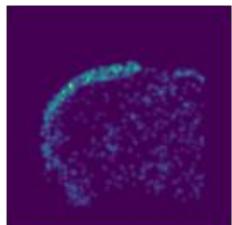
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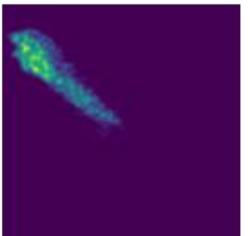
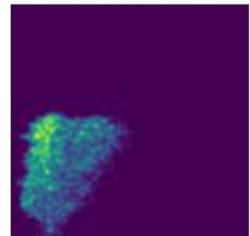
Real GEX (Tissue 1) - X-Y-Z-axis Cux2



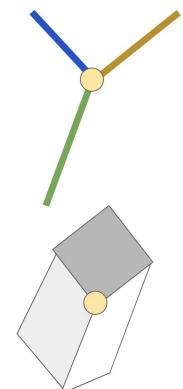
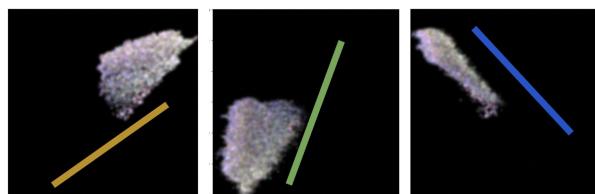
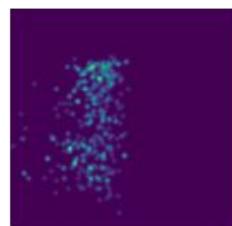
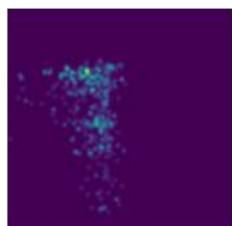
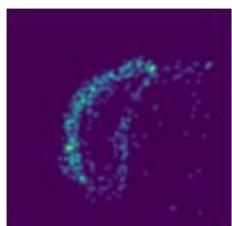
Real GEX (Tissue 2) - X-Y-Z-axis Cux2



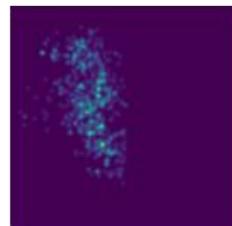
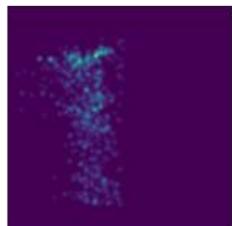
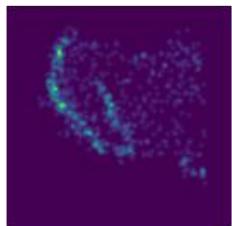
In-Silico GEX - X-Y-Z-axis Cux2



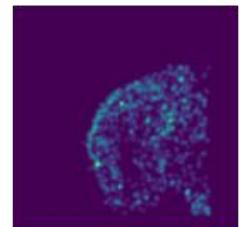
Real GEX (Tissue 3) - X-Y-Z-axis Cux2



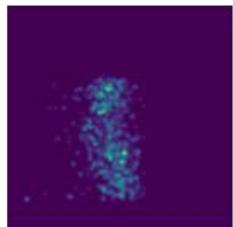
Real GEX (Tissue 4) - X-Y-Z-axis Cux2



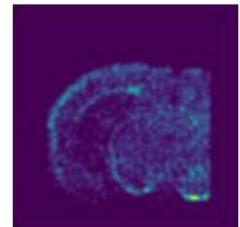
Real GEX (Tissue 1) - X-Y-Z-axis



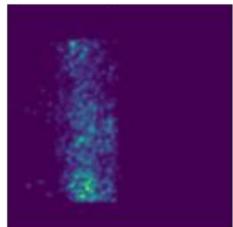
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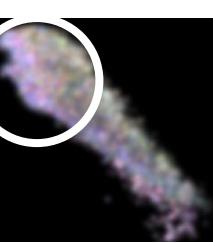
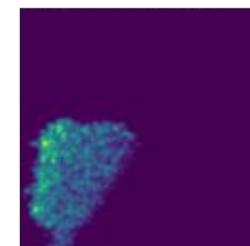
Real GEX (Tissue 2) - X-Y-Z-axis



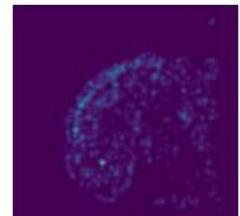
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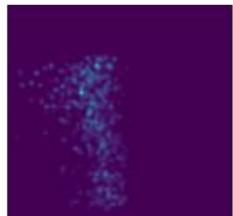
In-Silico GEX - X-Y-Z-axis    Enpp2



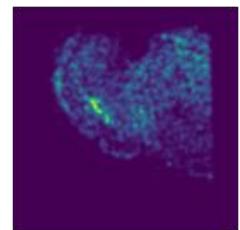
Real GEX (Tissue 3) - X-Y-Z-axis



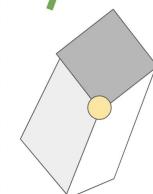
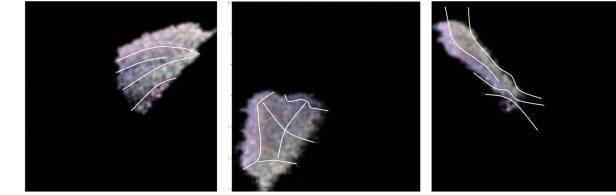
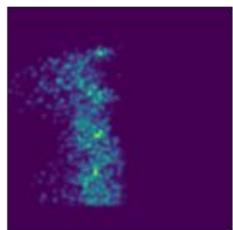
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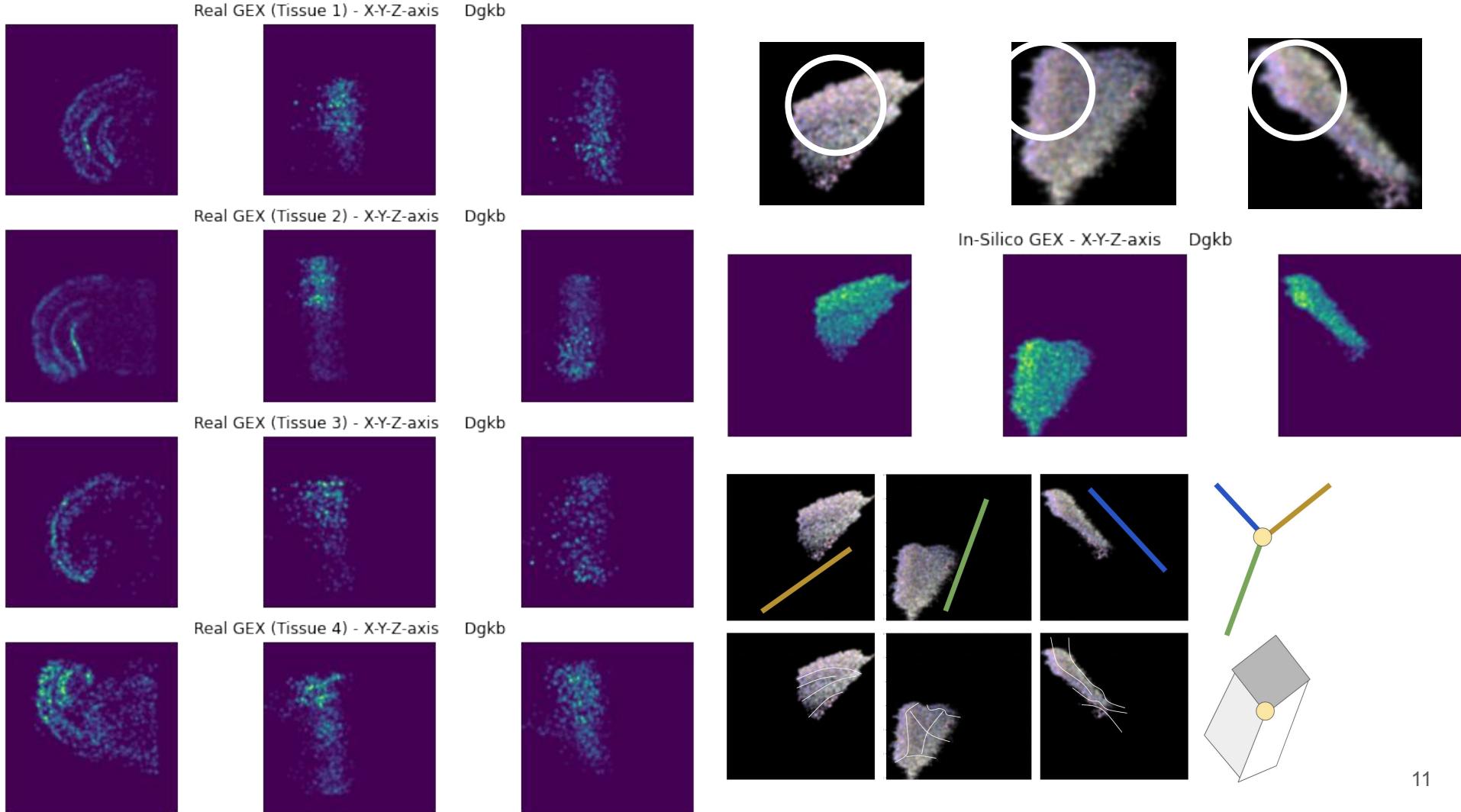


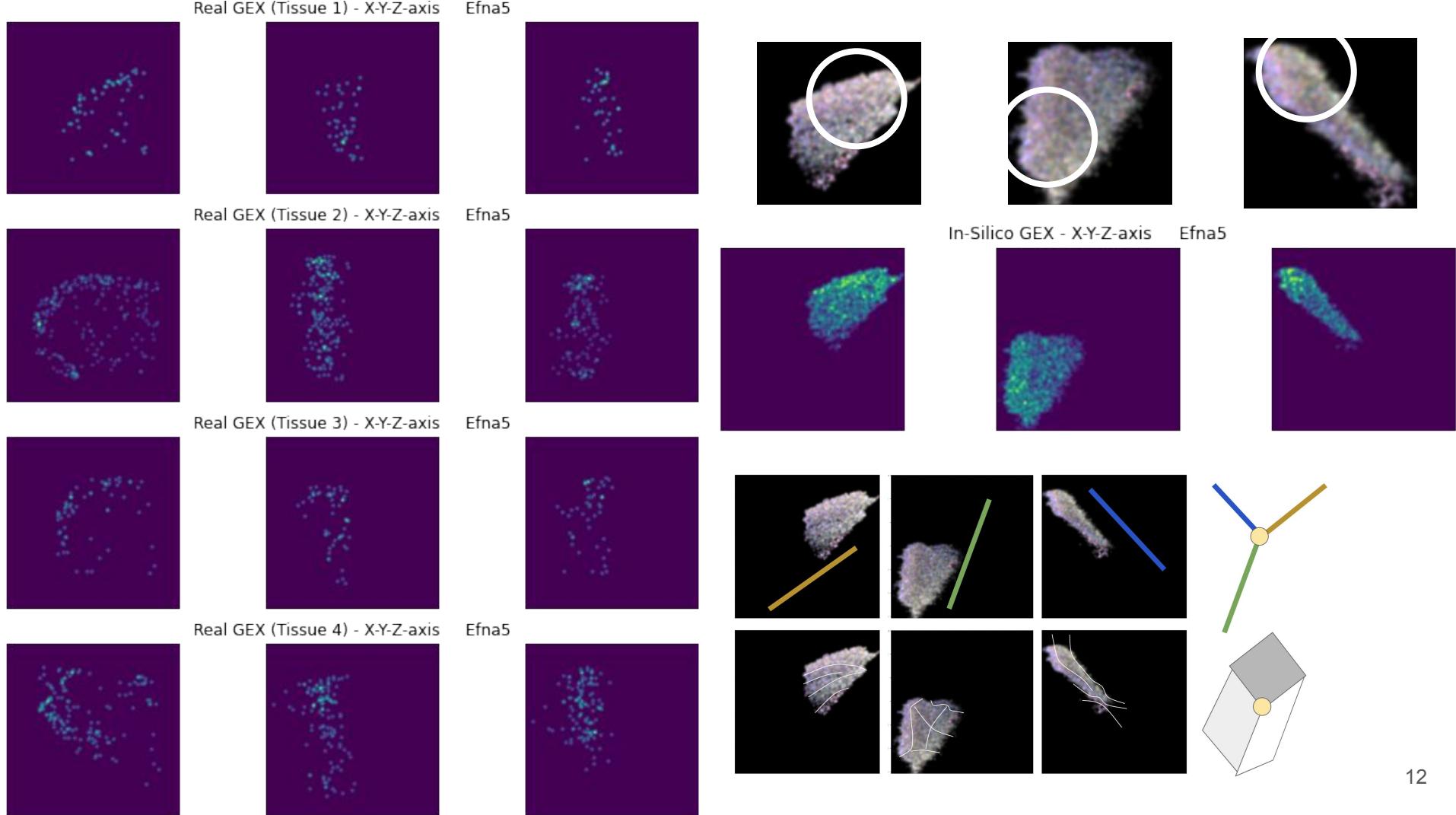
Real GEX (Tissue 4) - X-Y-Z-axis



Enpp2



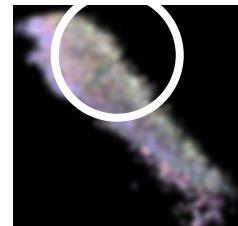
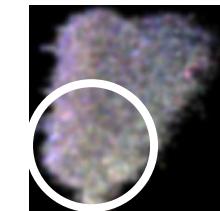
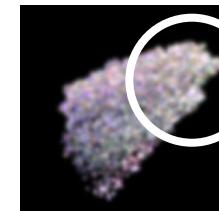
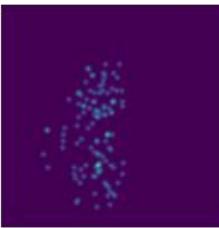




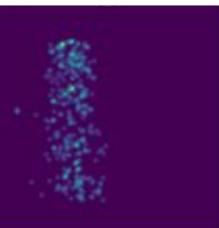
Real GEX (Tissue 1) - X-Y-Z-axis



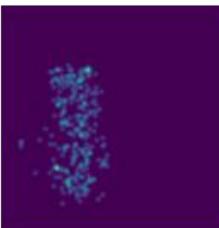
Fat3



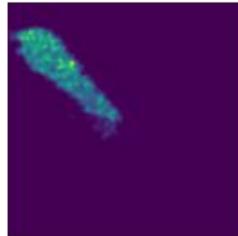
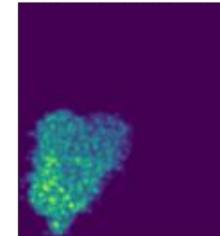
Real GEX (Tissue 2) - X-Y-Z-axis



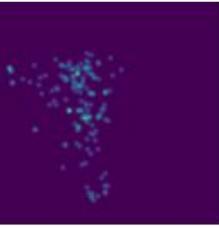
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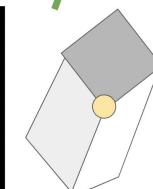
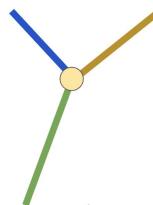
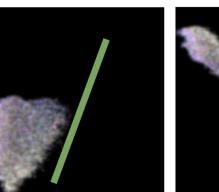
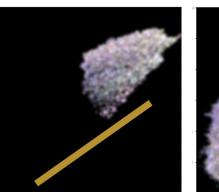
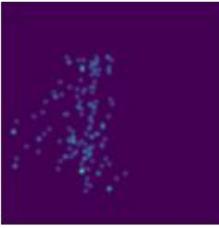
In-Silico GEX - X-Y-Z-axis



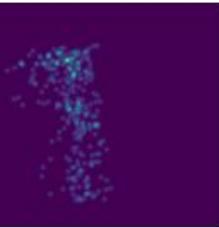
Real GEX (Tissue 3) - X-Y-Z-axis



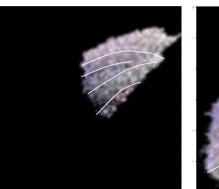
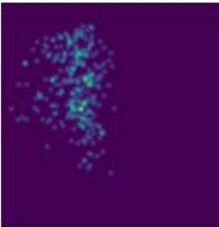
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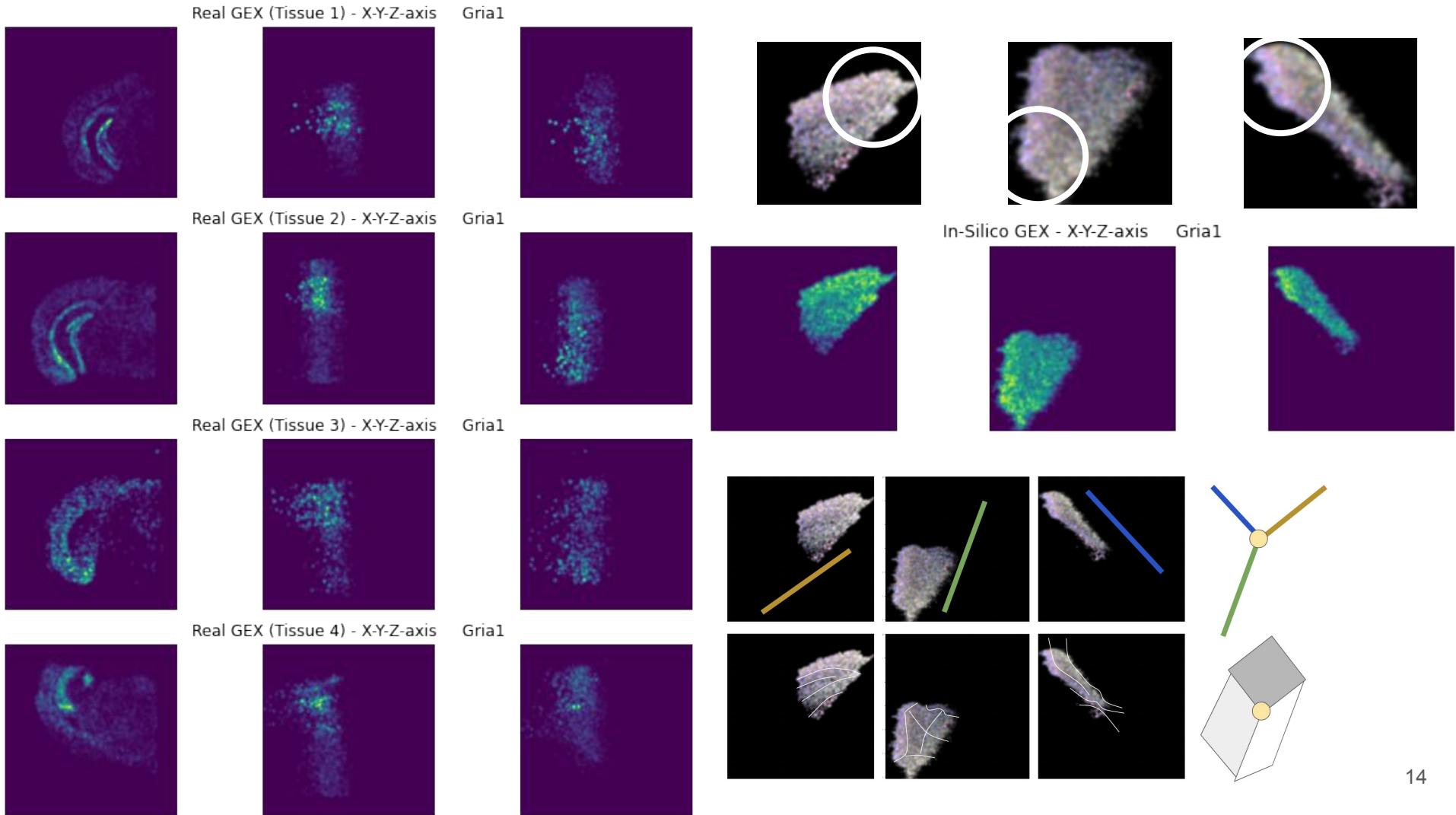


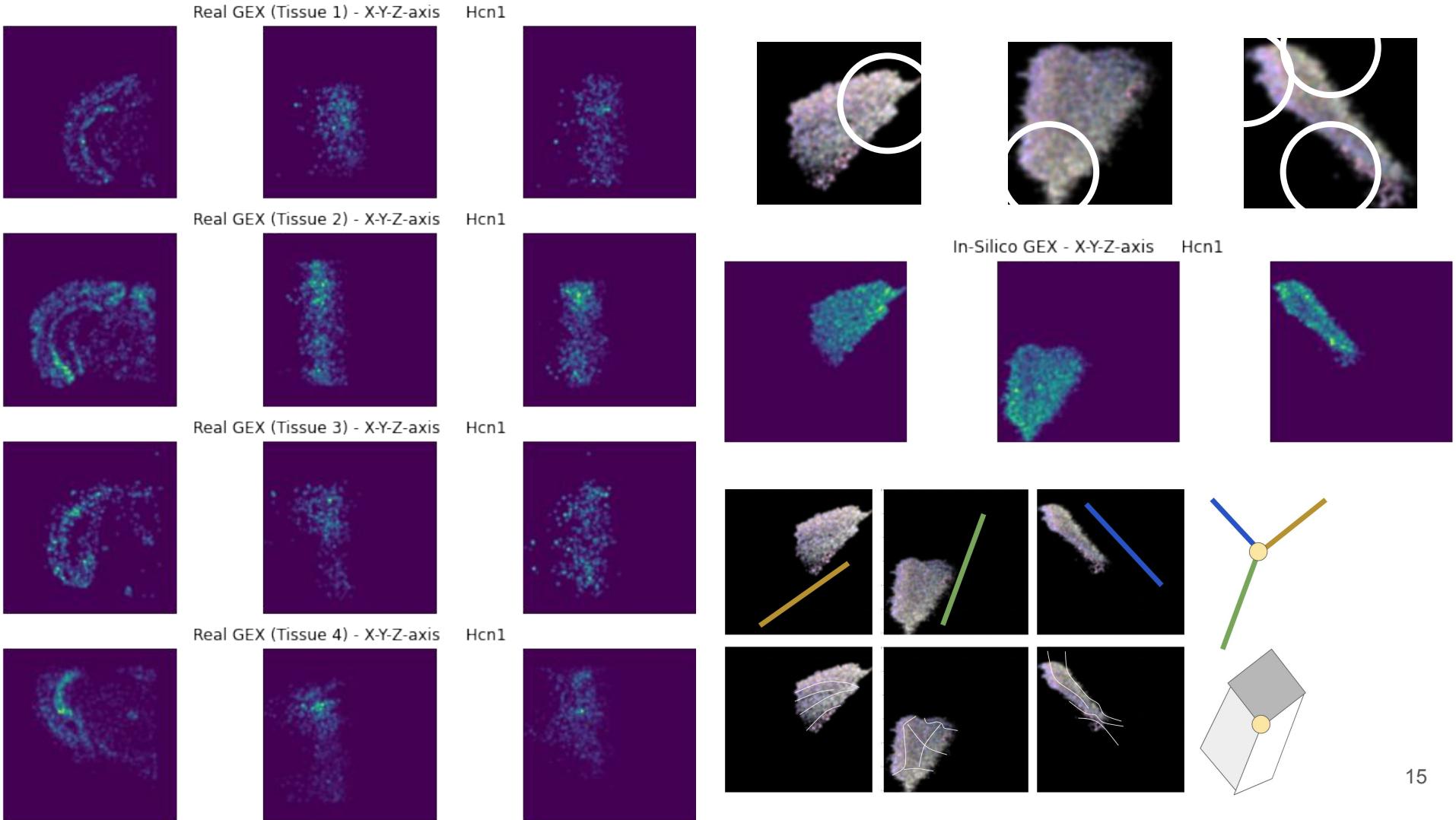
Real GEX (Tissue 4) - X-Y-Z-axis

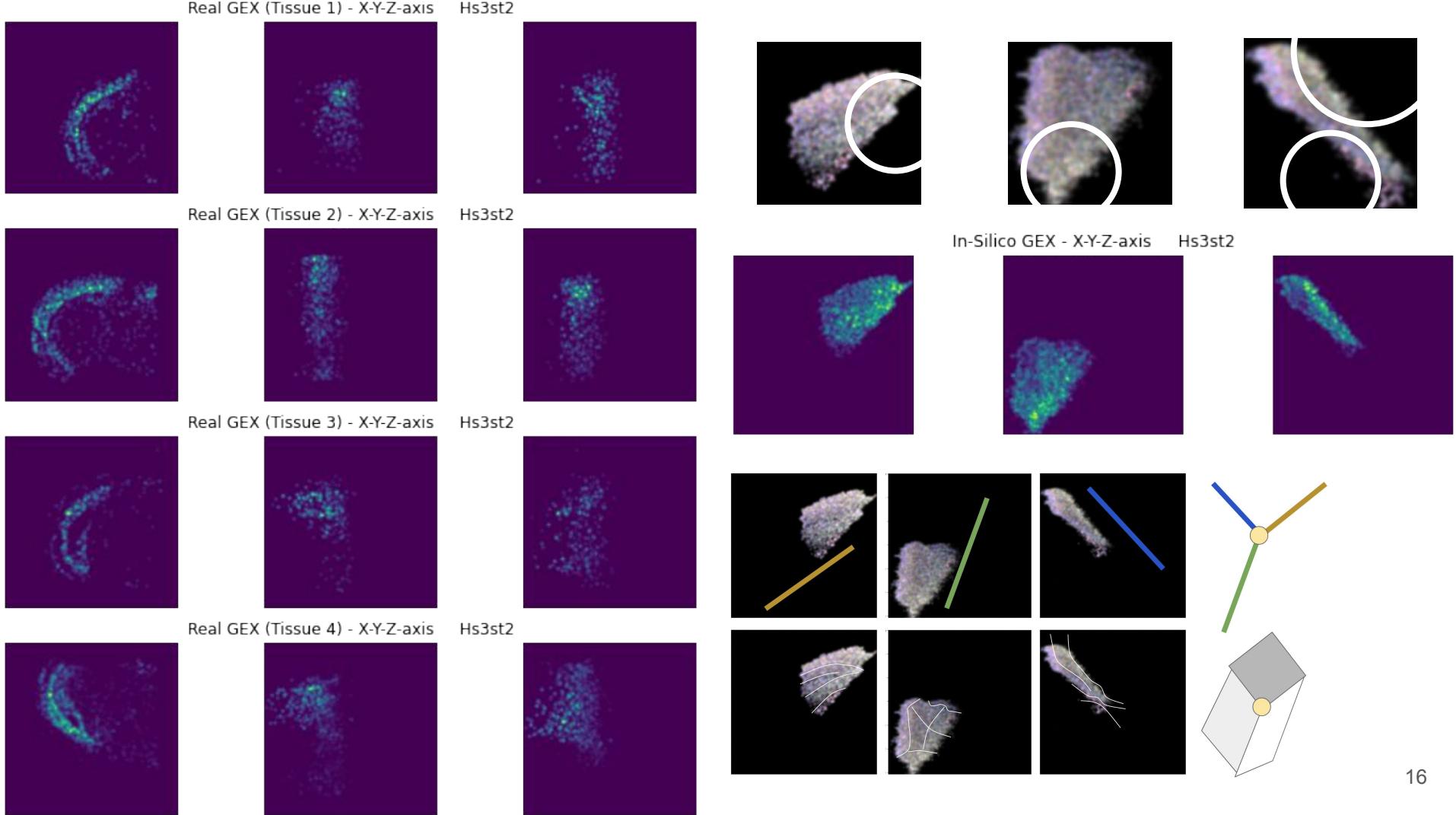


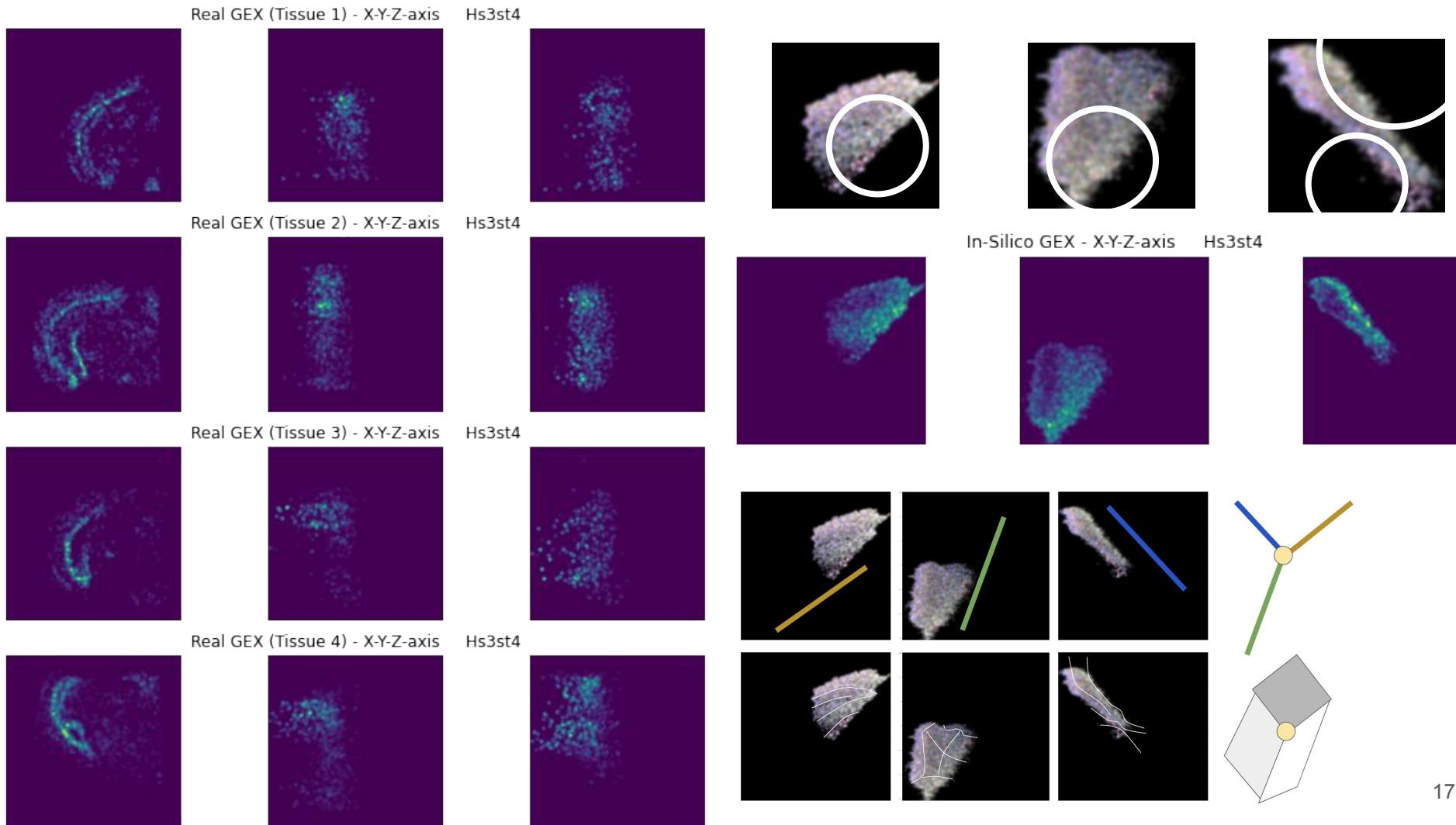
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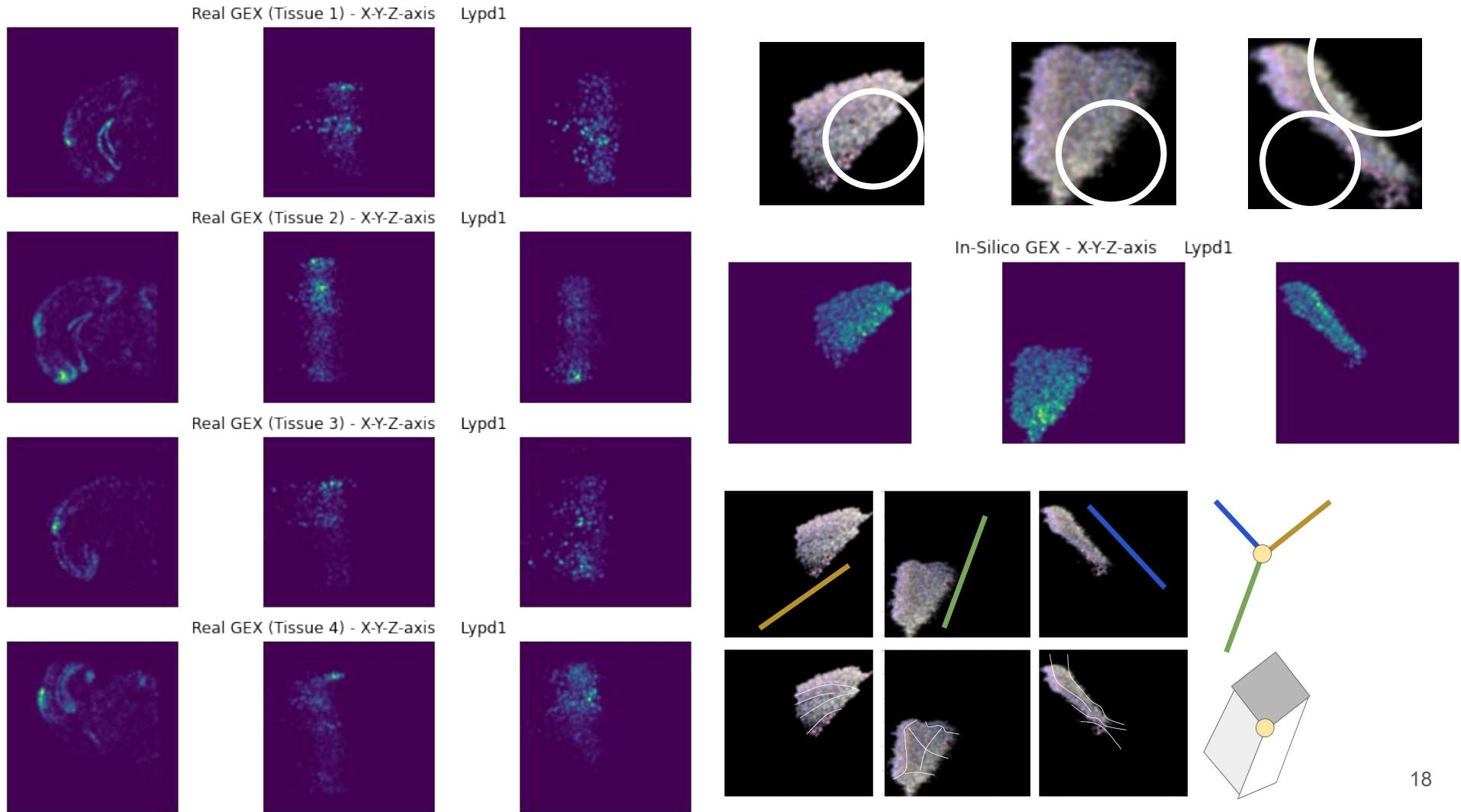


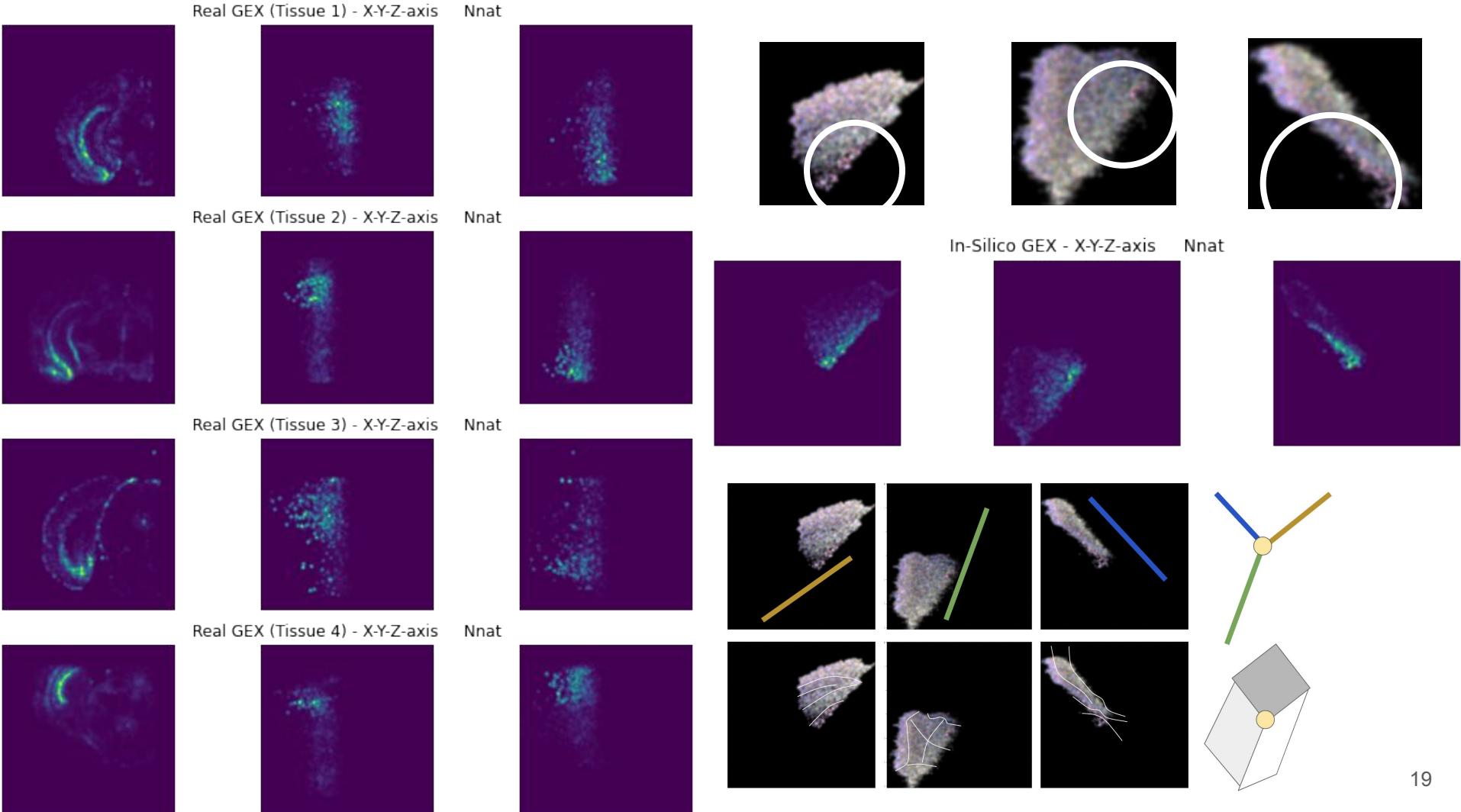


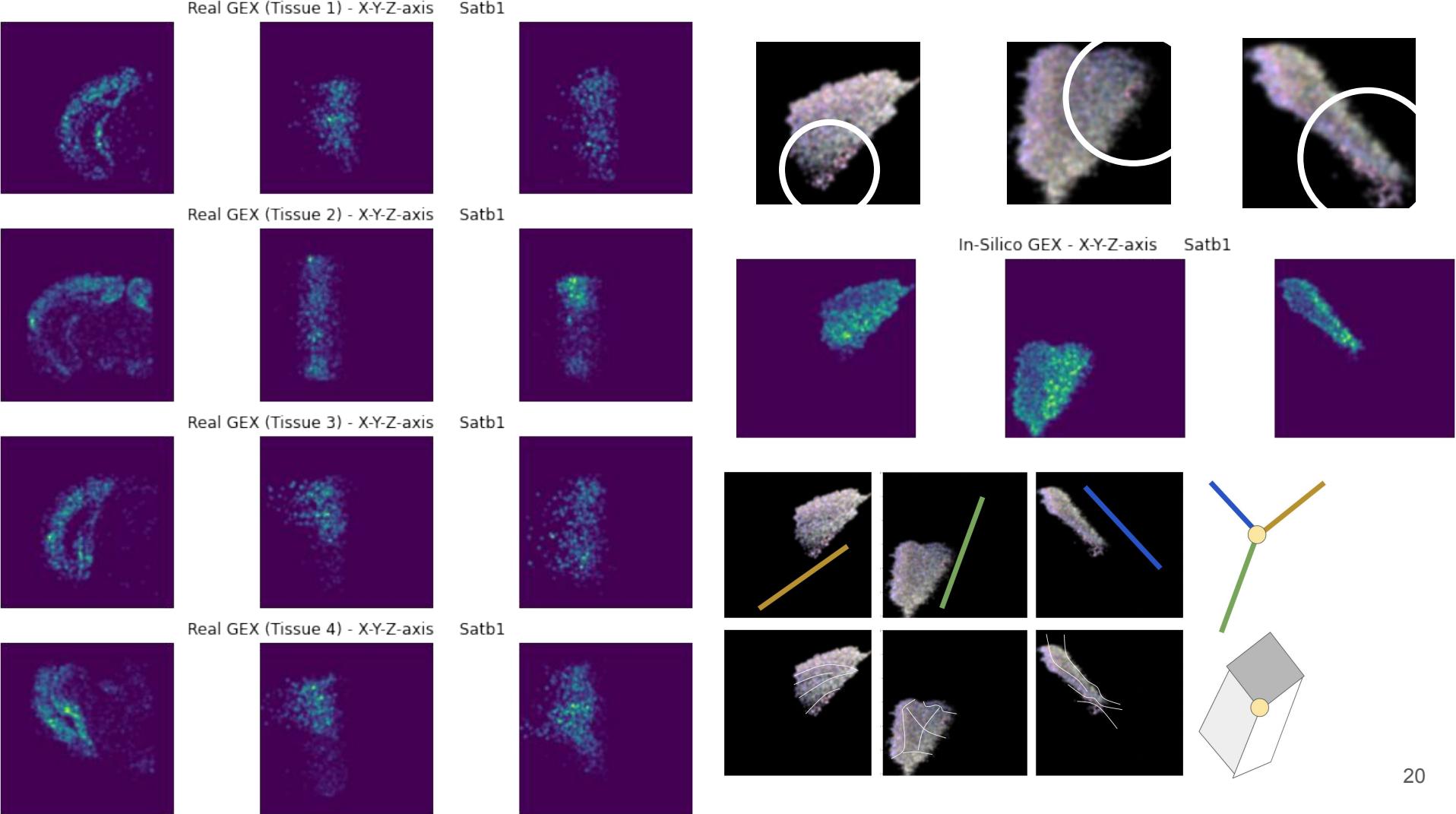












# Model primer

*arg min (*

*{ {*

A: How accurate are cell distributions compared to training?

*A +*

B: Whether the parameters for the new cell locations are actual signals?

*B +*

C: Whether gene to pixel transformations are learned correctly?

*C +*

D: Whether pixel image prediction is aligned with reality on a local predicted imaging spot level?

*D +*

E: Whether pixel image prediction is aligned with reality on a global predicted imaging tissue level?

*E +*

F: Whether the movement of cells around fits well with the idea of Waddington's marble analogy?

*F*

*}<sup>2</sup> }<sup>1/2</sup>*

F: Whether the movement of cells around fits well with the idea of Waddington's marble analogy?

)

# Actual model layers ...

```
# beta is to learn gene expression
# spatial signals from scRNAseq only
self.summary_beta = nn.Linear(10,window_size*2*window_size*2*106,bias=False)

# gex and pix are to learn transformation parameters that
# assign based on image similarity to real histology
self.summary_gex = nn.Linear(len(genes),100,bias=False)
self.summary_pix = nn.Linear(32*32*3,100,bias=False)
```

... and that's it!

A fully interpretable linear neural network

- beta : maps KNN gene convolutions to **predict coordinates**
- gex : maps gene to **shared space** with images
- pix : maps images to **shared space** with genes

# How are coordinates predicted?

1

Cells are randomly distributed onto a grid (e.g.  $1000 \times 1000 \times G$ ) with  $G$  gene channels and a spatial kernel applied to diffuse genes

2

Convolutions around each cell are taken, giving a small window of about  $5 \times 5 \times G$ , where  $G$  are the gene channels

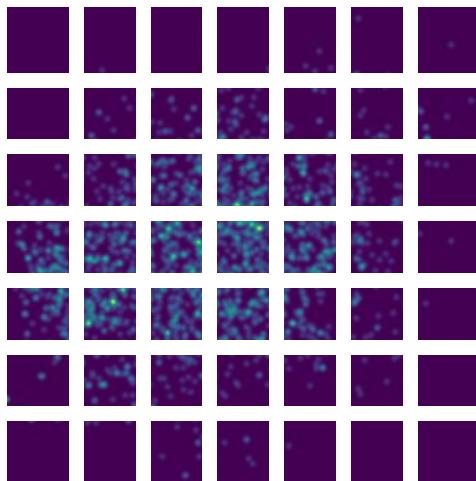
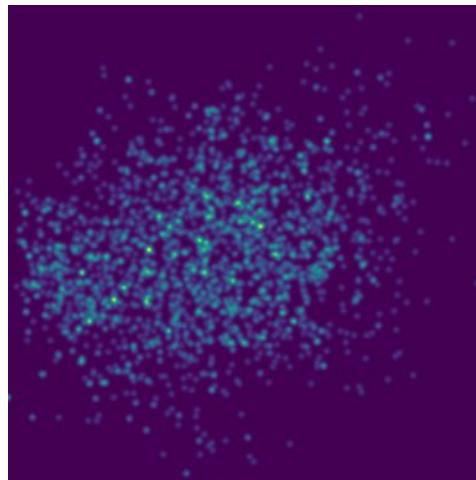
3

Convolutions of cells are put through a Neural Network to predict where the cell is next likely to occur

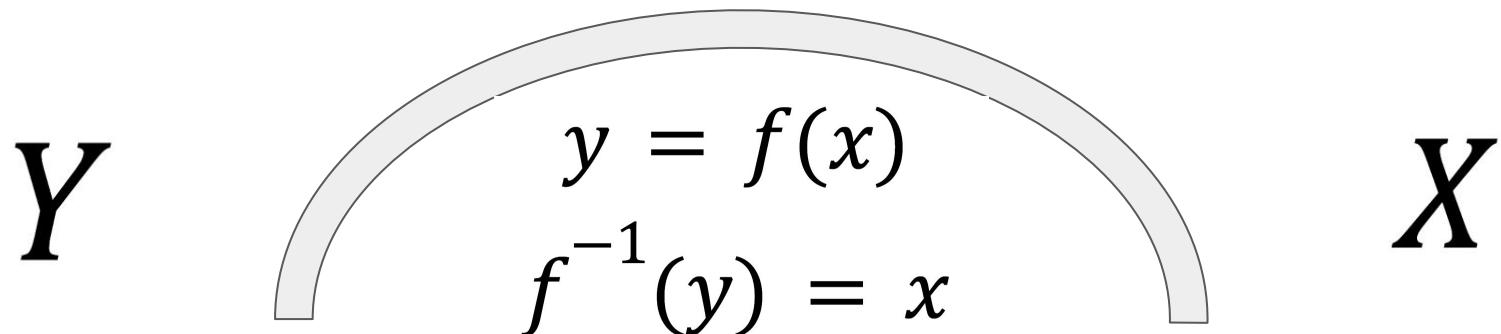
4

This is a repeated process to continuously update a walking process of the cell to the next likely location based on gene expression around the grid ...

**... like Waddington's marble analogy!**



# What is a shared space?

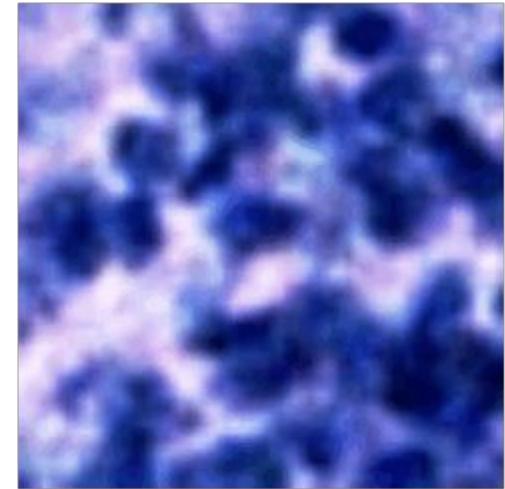
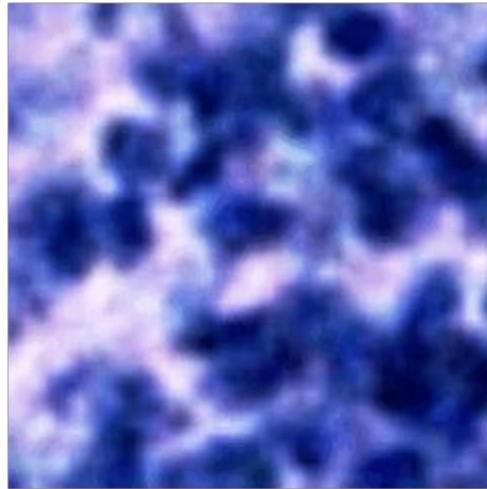
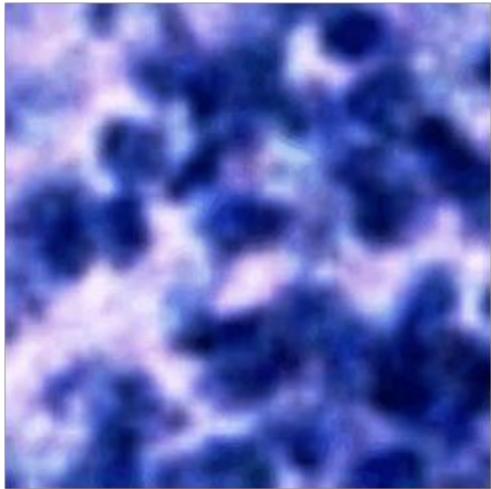


Spatial Histology to Spatial Transcripts

Methylation to Chromatin Accessibility to Chromatin Conformation to Chromatin Profiles

Genomics to Epigenomics to Transcriptomics to Proteomics

# What can a shared space do?





**[https://github.com/AskExplain/scRNA\\_maps/](https://github.com/AskExplain/scRNA_maps/)**

# Acknowledgements for inspiration

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University of Queensland

Dr Jessica Mar

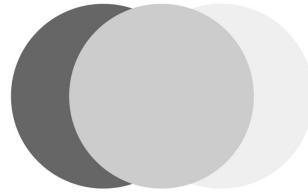
University of Queensland

Dr Ruth Pidsley

Garvan Institute of Medical Research

## **Our vision is to create great collaborations from science to industry**

Through an interest and passion for science to progress, our commitment is to  
work on, communicate around, and support collaborations



AskExplain  
[david.b@askexplain.com](mailto:david.b@askexplain.com)

# How about some interesting genes?

pg#	Gene	pg#	Gene	pg#	Gene	pg#	Gene	pg#	Gene
23	Brinp3	28	Cbln2	33	Efna5	34	Kcnip1	39	Scnn1a
24	C1ql3	29	Cdh3	34	Gnb4	35	Lypd1	40	Nrg1
25	Col19a	30	Cpne4	35	Hgf	36	Otof	41	Zfpm2
26	Calb1	31	Cux2	36	Hs6st3	37	Oprk1	42	Zfp804b
27	Car3	32	Dcc	37	Htr2a	38	Sgcd	43	Zfp804a

