

Spatial Architecture Changes in Kidney Cancer

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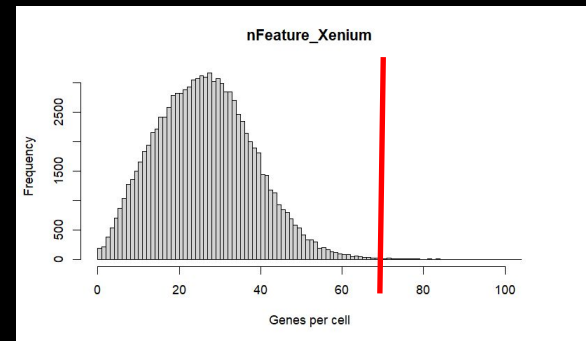
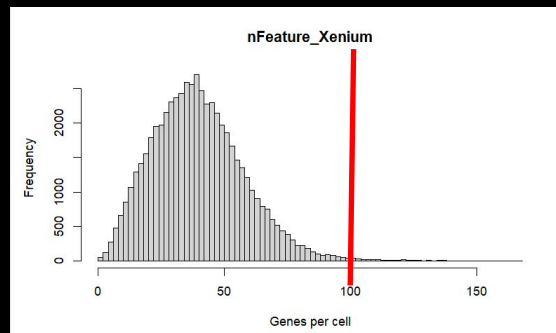
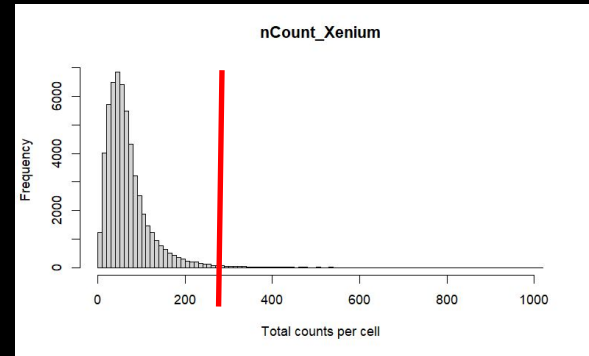
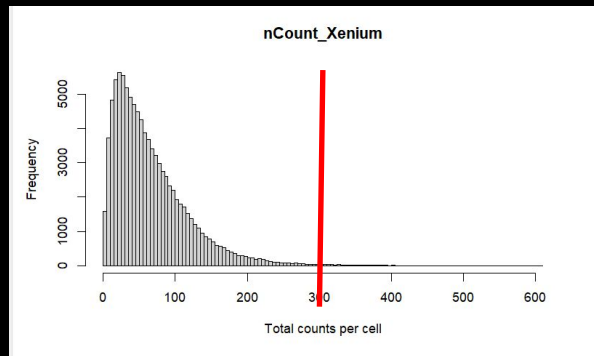
Rajam Arunprakash

In a healthy versus a diseased kidney...

how do cell type **spatial relationships**
and cell type **proportions** differ?

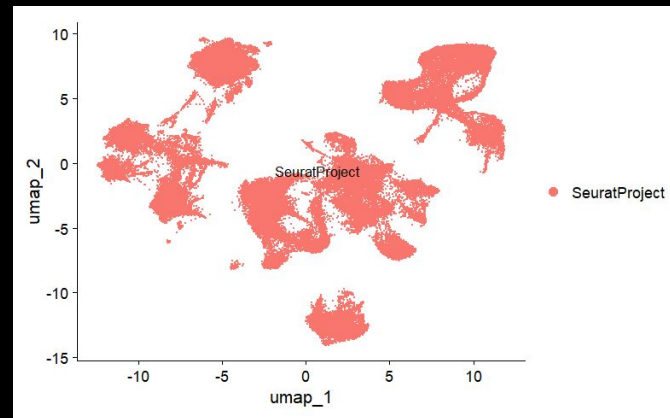
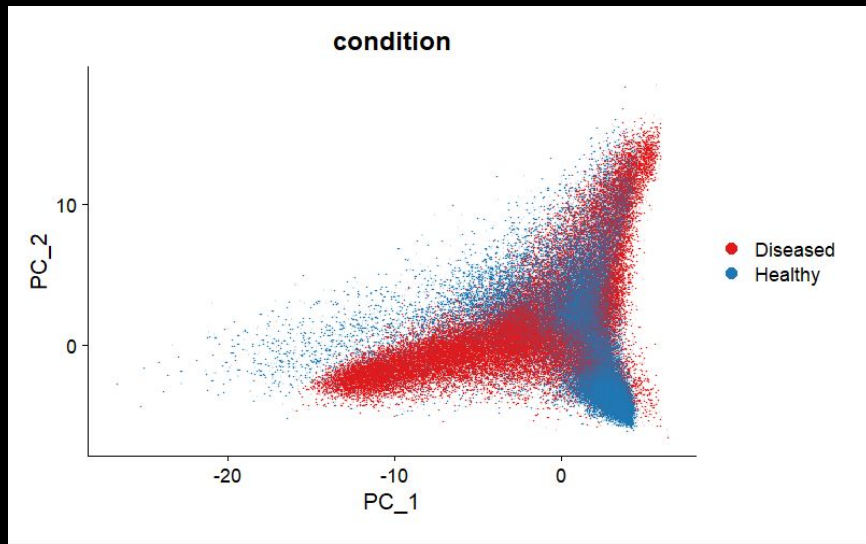
Obtaining the Data

Healthy: ~90k
Diseased: ~50k



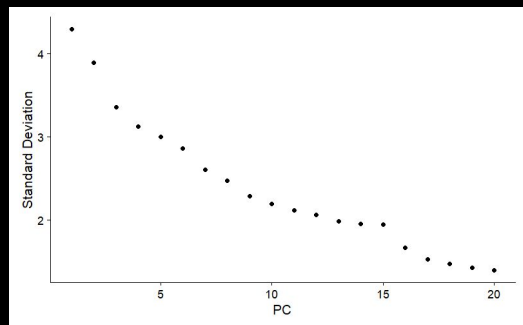
source:

<https://www.10xgenomics.com/datasets/human-kidney-preview-data-xenium-human-multi-tissue-and-cancer-panel-1-standard>

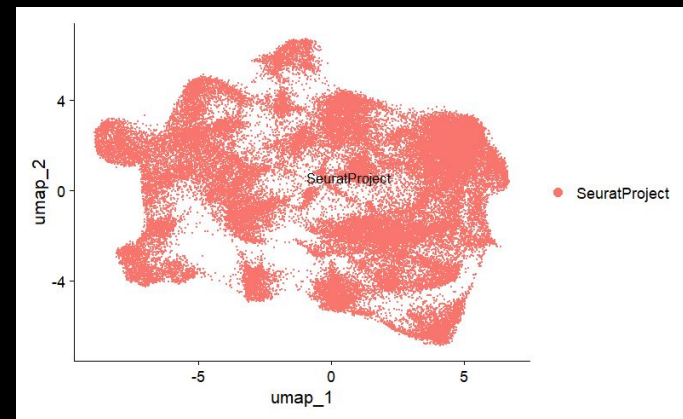


above: Healthy UMAP below: Diseased UMAP

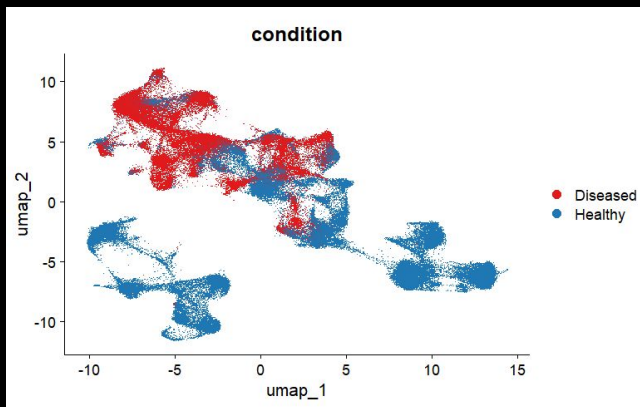
PC Graph for Diseased & Healthy



← Elbow Plot

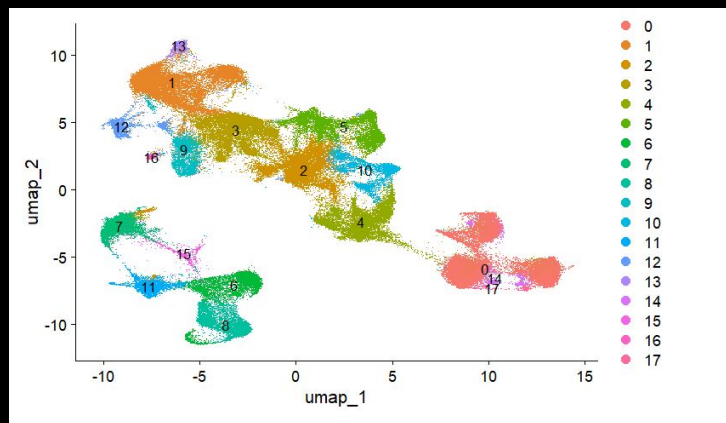


Sorting the Data



← UMAP
after
integration

UMAP
with
colored
clusters →

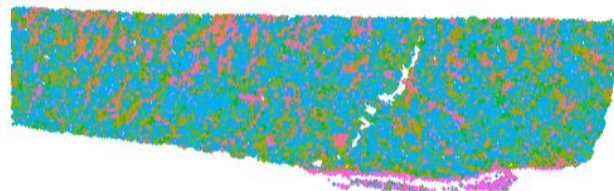


- B cells
- C. duct principal cells - inflammatory
- Collecting duct/distal epithelial
- Distal convoluted tubule (DCT)
- Endothelial cells
- Fibroblasts
- Intercalated cells (A/B)
- Mast cells
- Monocytes/macrophages
- NK cells
- Parietal epithelial cells (PECs)
- Perivascular
- Proximal tubule (S1/S2)
- Proximal tubule S3 (metabolic)
- PT-S3 metabolic
- Smooth muscle / pericytes
- T cells
- Thick ascending limb (TAL)

Annotated Cell Types



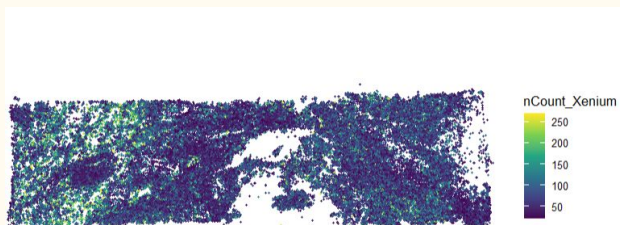
Diseased



Healthy

celltype

- B cells
- C. duct principal cells - inflammatory
- Collecting duct/distal epithelial
- Distal convoluted tubule (DCT)
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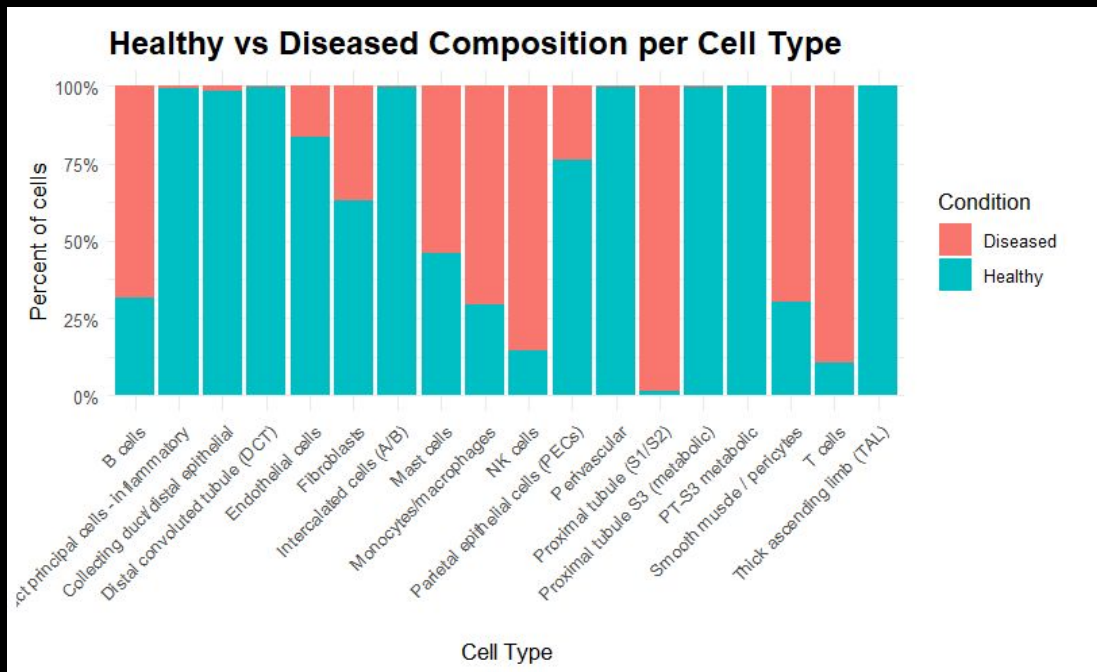
Diseased

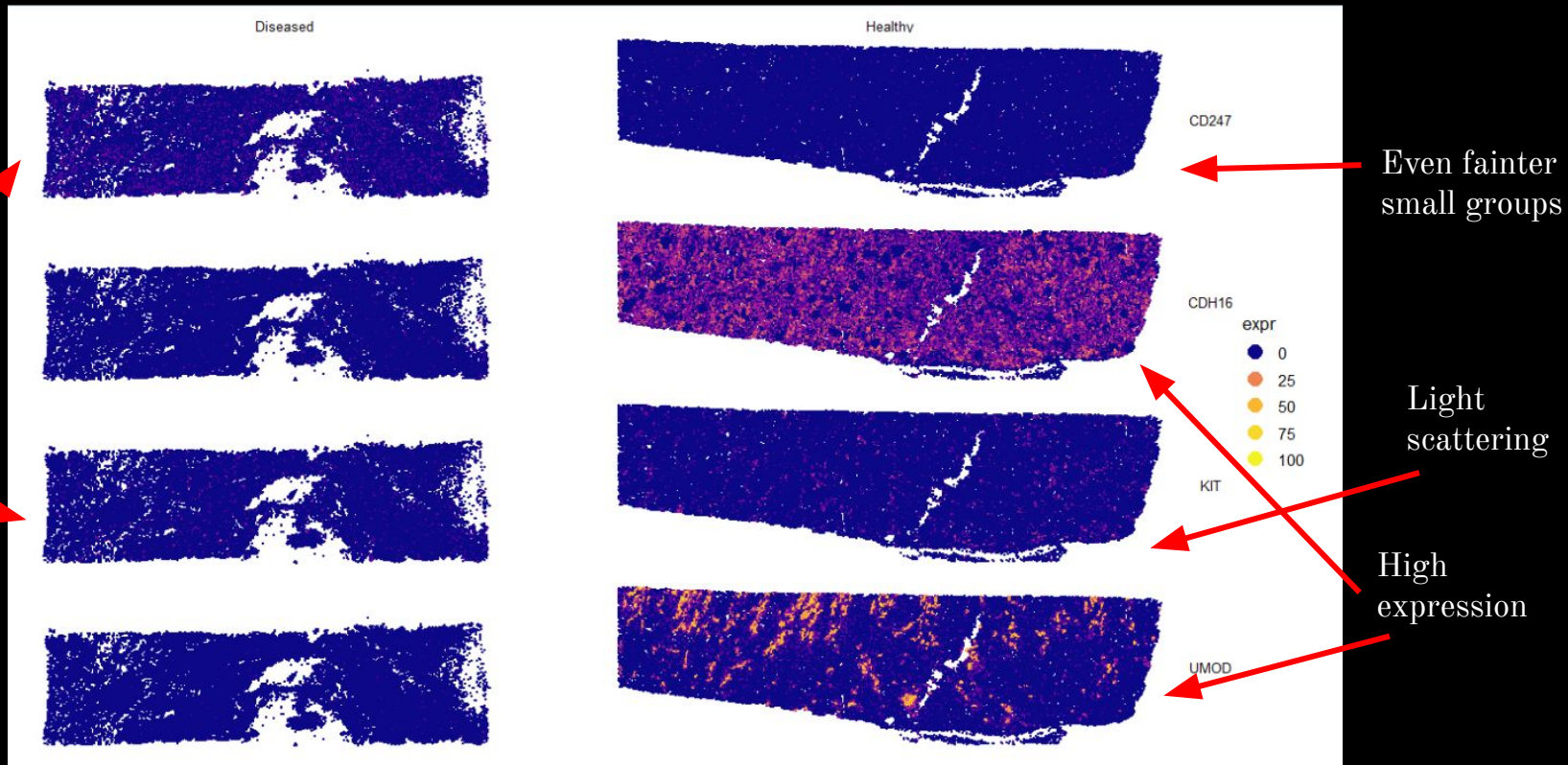
Cell Visualization



Healthy

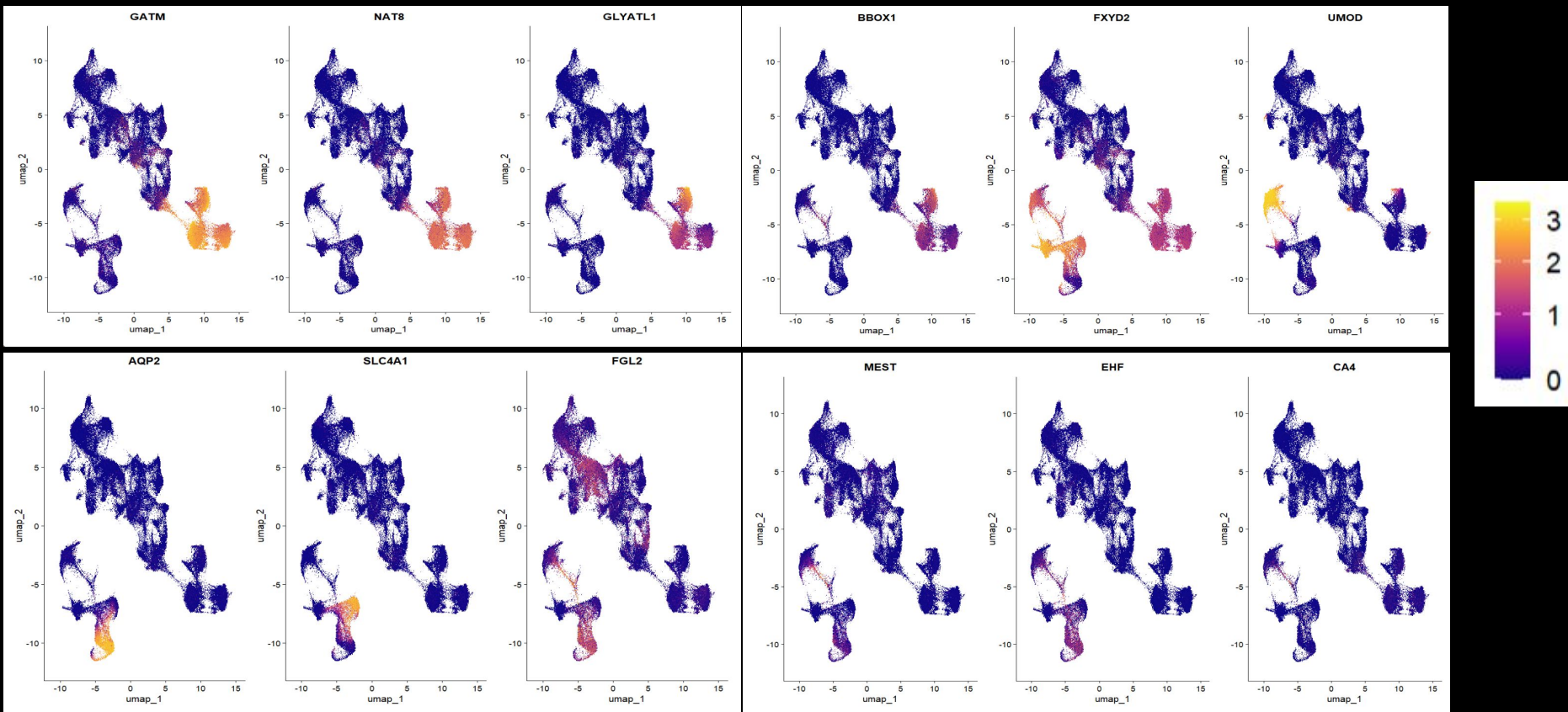
Other Conclusions





Selected genes: CD247, CDH16, KIT, UMOD

Gene Expression Distributions



Statistical Analysis

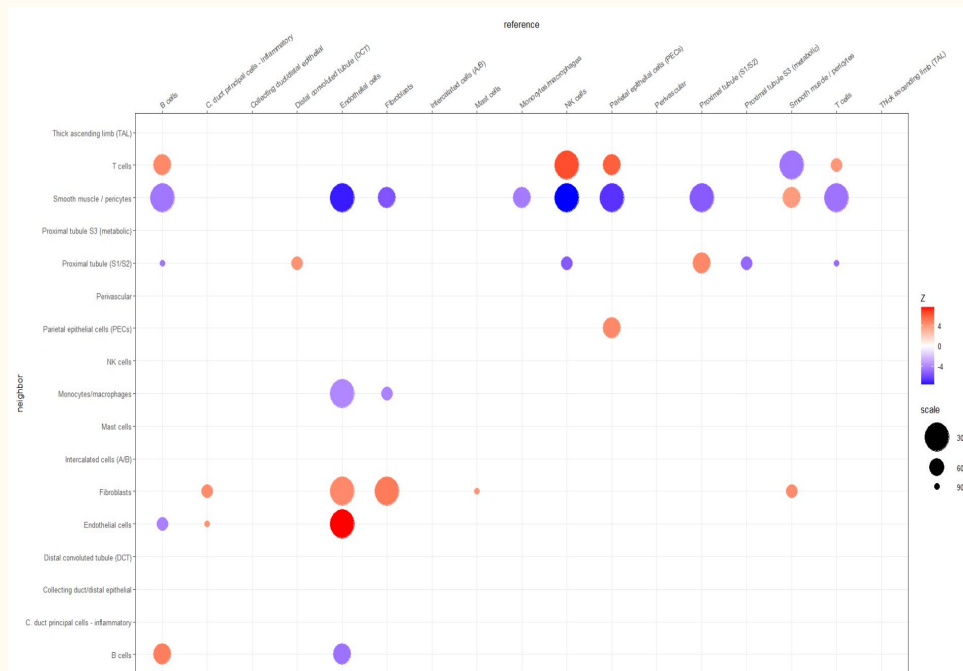
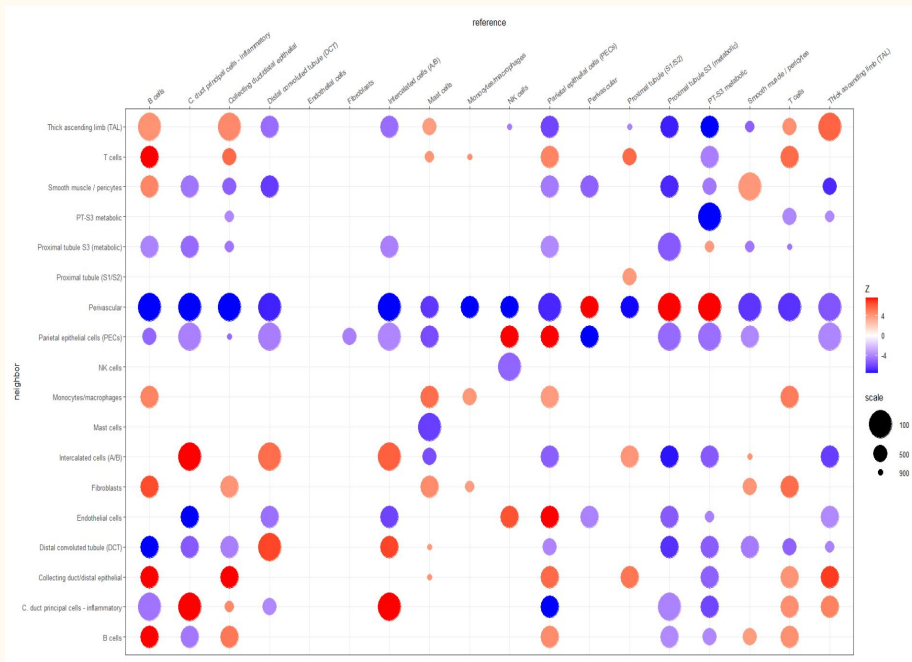
- Chi-Square Test
- Fisher's Exact Test
- Explanations

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# A tibble: 18 x 3
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	celltype <chr>	odds_ratio <dbl>	p_value <dbl>
1	Perivascular	582.	0
2	Monocytes/macrophages	0.222	0
3	Parietal epithelial cells (PECs)	2.01	4.07e- 98
4	T cells	0.0486	0
5	Fibroblasts	1.06	7.26e- 4
6	B cells	0.277	2.13e-243
7	Endothelial cells	3.44	0
8	C. duct principal cells - inflammatory	128.	0
9	Intercalated cells (A/B)	662.	0

CRAWDAD pt. 2

Healthy



Diseased

CRAWDAD pt. 2



Conclusion

Compositionally, disease typically increases immune and injury-associated populations and decreases certain tubular populations.

Spatially, this disease in particular caused major rewiring of cellular neighborhoods

Future

- More detailed cell-type annotation (subclusters, tweaking parameters, etc)
- Add more biological replicates, perhaps something that can be aligned
- Code optimization