

Hôpital universitaire mère-enfant Robert-Debré







Institut national de la santé et de la recherche médicale

Contribution of transcriptomics in nephropathology

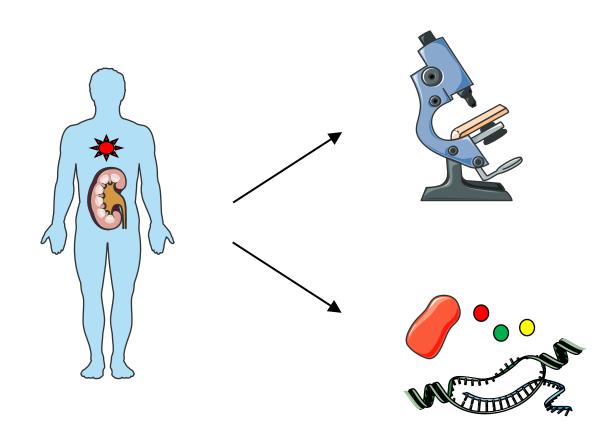
P. ISNARD

Hôpital Necker – Enfants Malades et Hôpital Robert Debré Université de Paris

Introduction (1)

The traditional tasks of the pathologist :

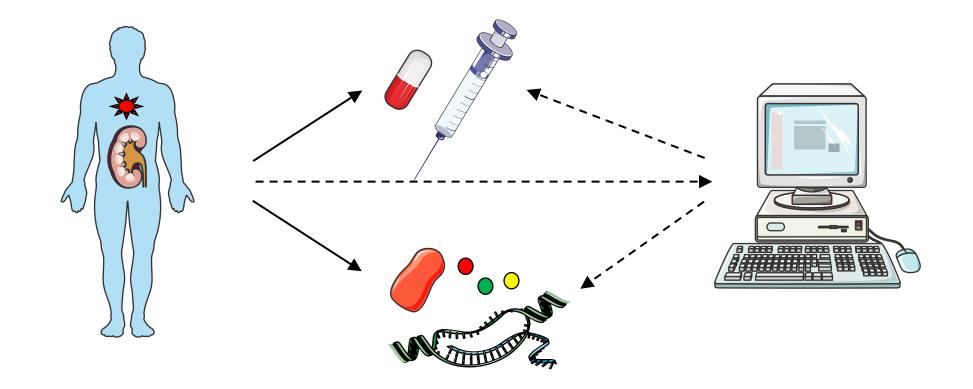
- Correct diagnosis of diseases
- Understand pathophysiology



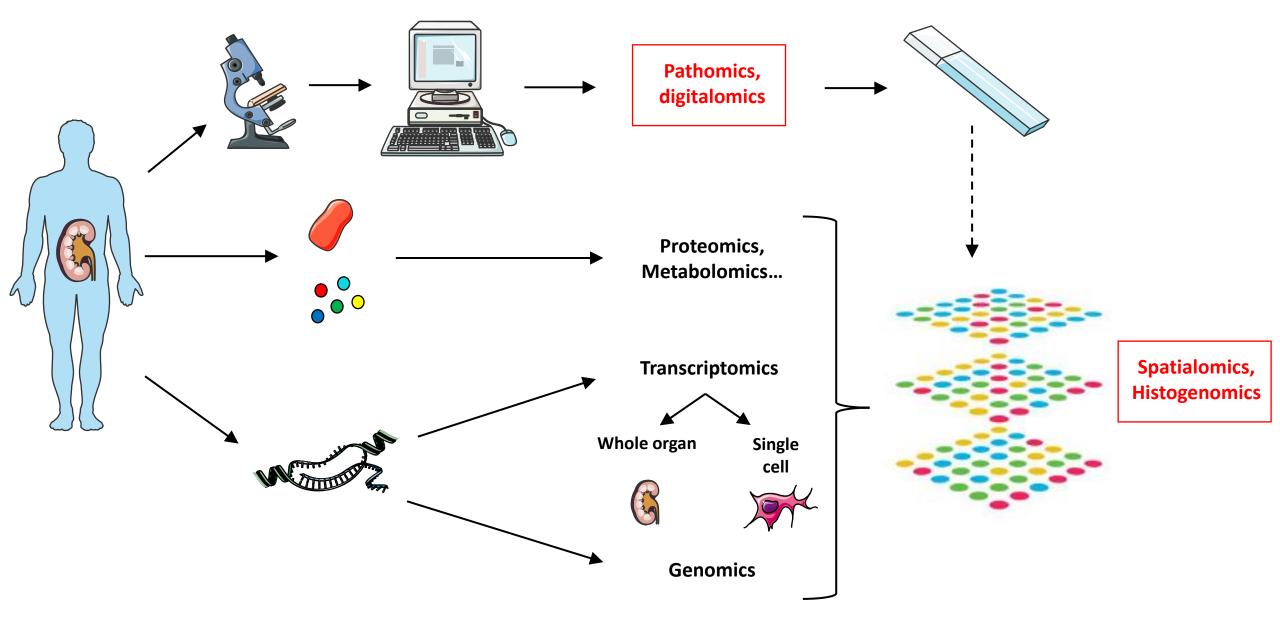
Introduction (2)

Personalized medicine

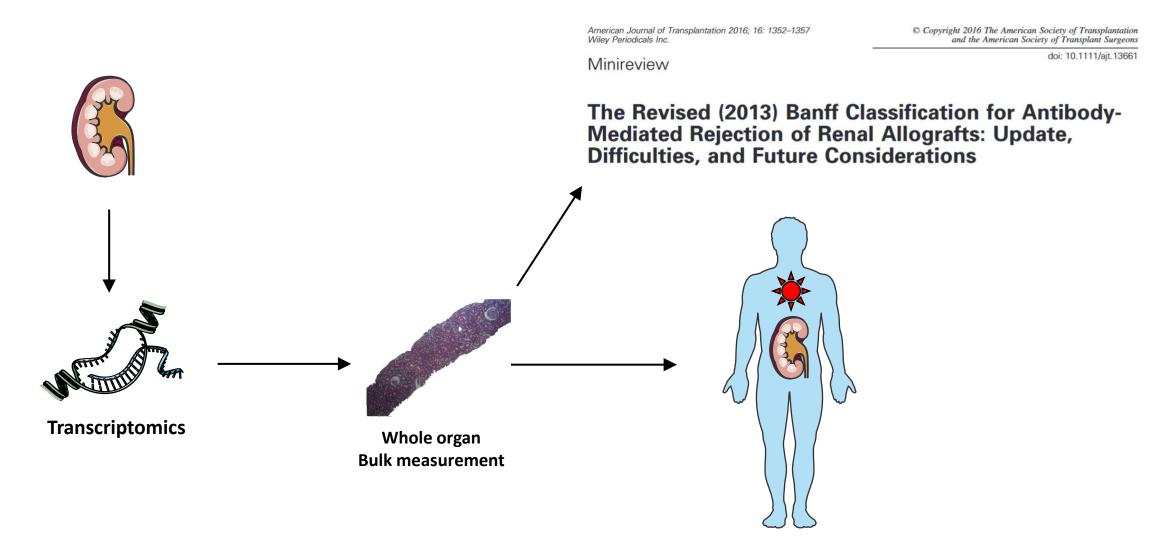
Collecting and analyzing the tremendous amounts of medical data



The concept of Pathomics



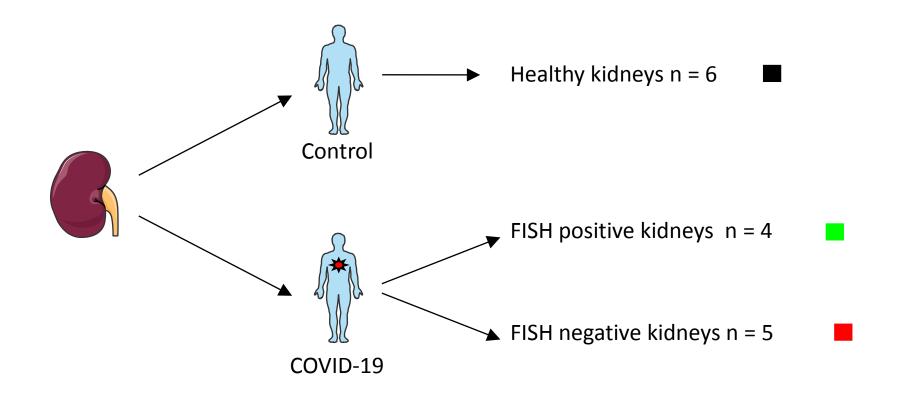
Whole Kidney Transcriptomics



Understanding the renal pathology of SARS-CoV-2



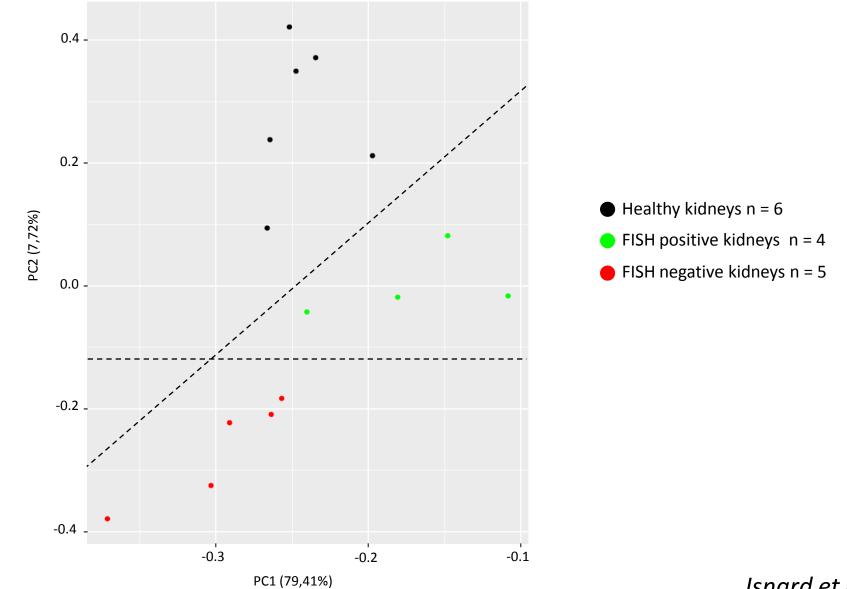
Understanding the renal pathology of SARS-CoV-2



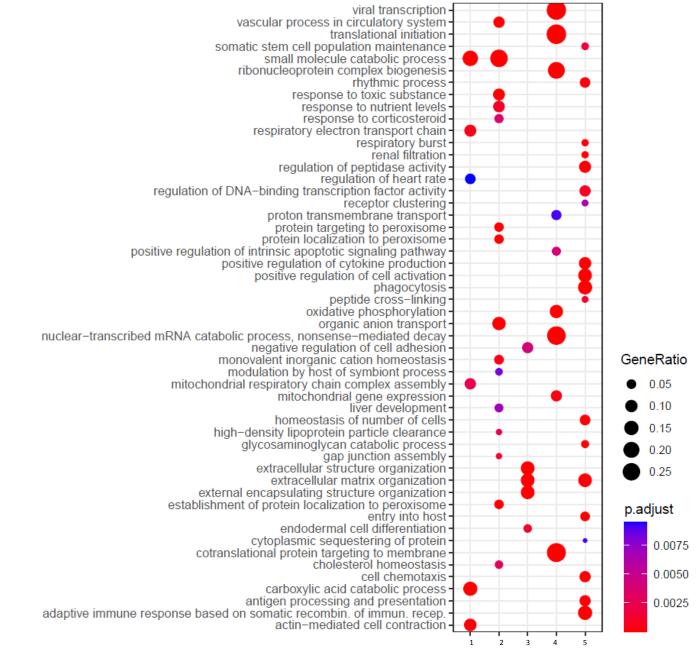
RNAseq analysis of COVID-19 Kidneys

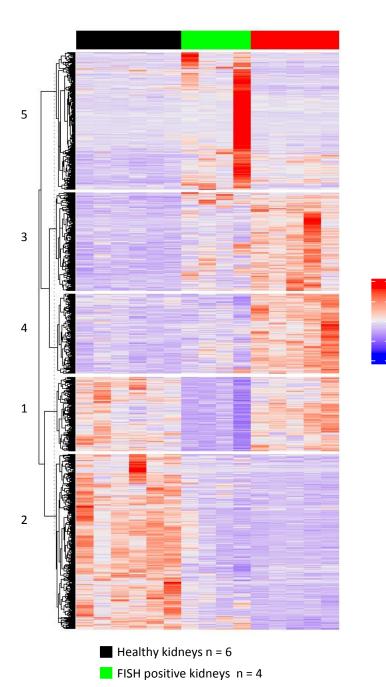
Isnard et al. Submitted

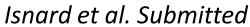
SARS-CoV-2 renal infection elicits a specific molecular signature



Isnard et al. Submitted

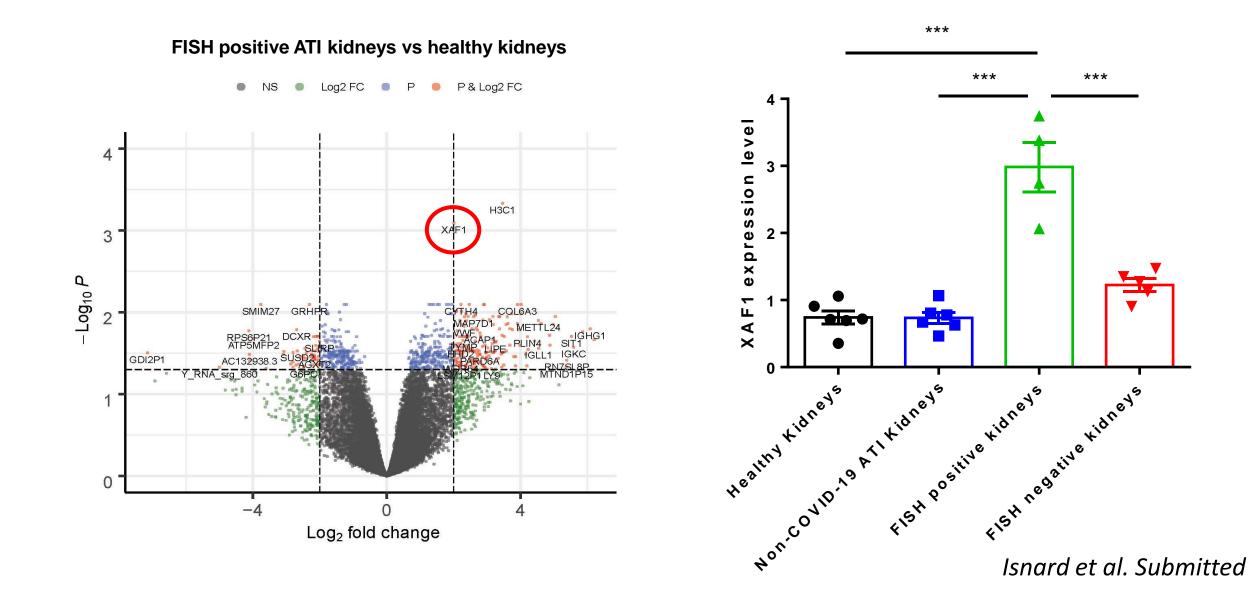




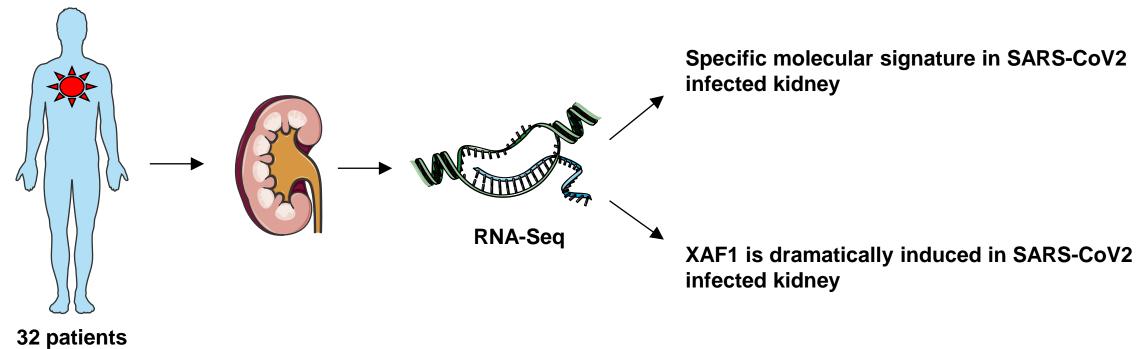


FISH negative kidneys n = 5

XAF1 is dramatically induced in SARS-CoV2 infected kidneys



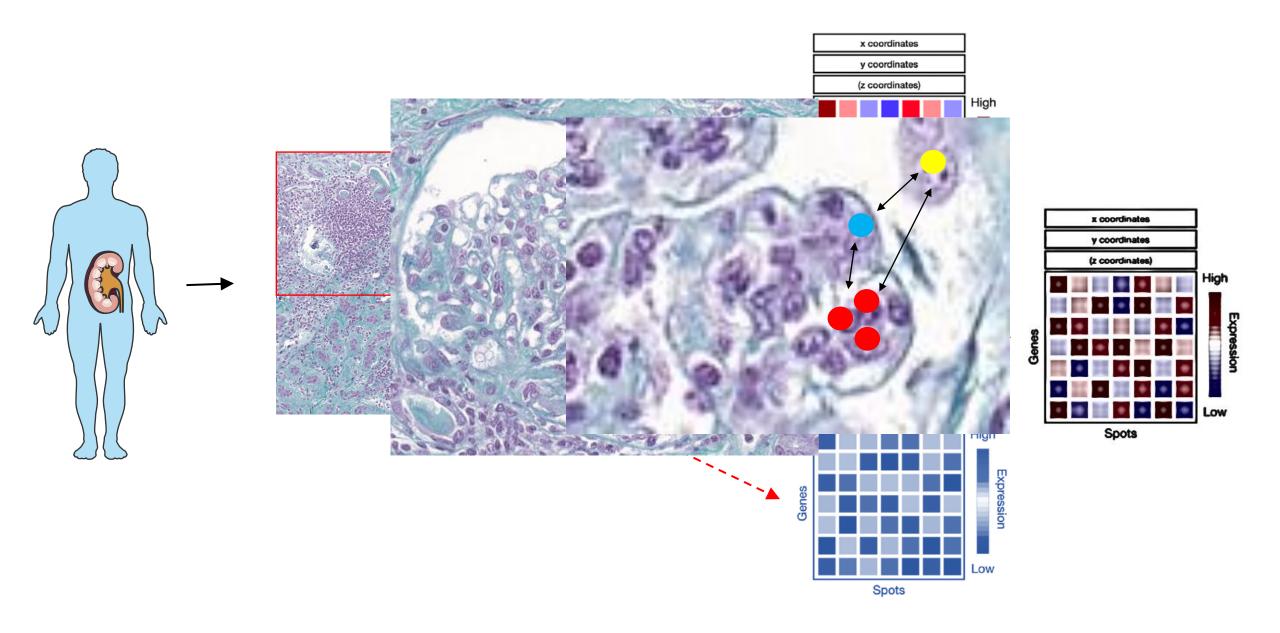
Conclusion

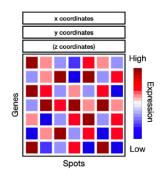


32 patients 7 French hospitals

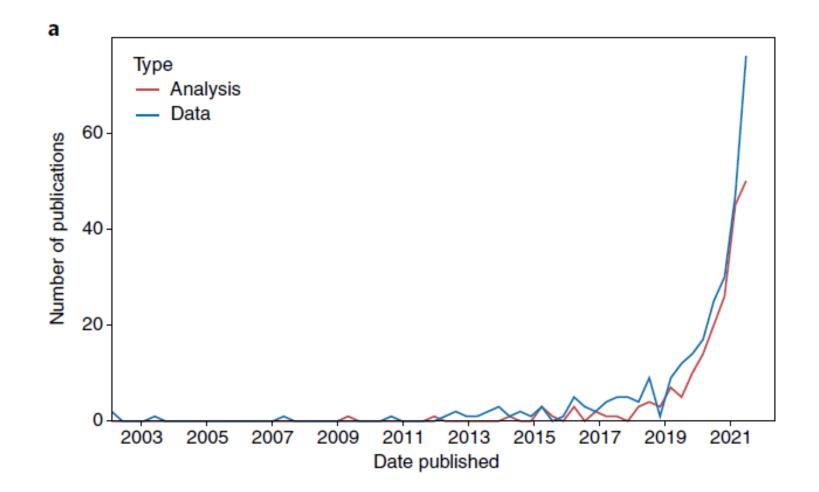
Isnard et al. Submitted

Exploring kidney pathology using spatial transcriptomics (1)

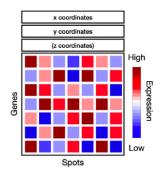




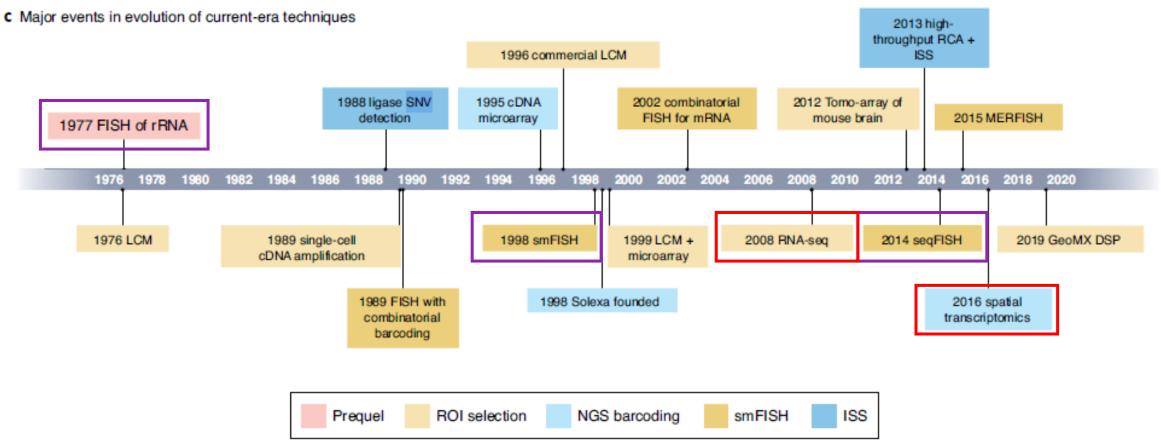
Exploring kidney pathology using spatial transcriptomics (2)



Moses et al. Nature Methods, March 2022

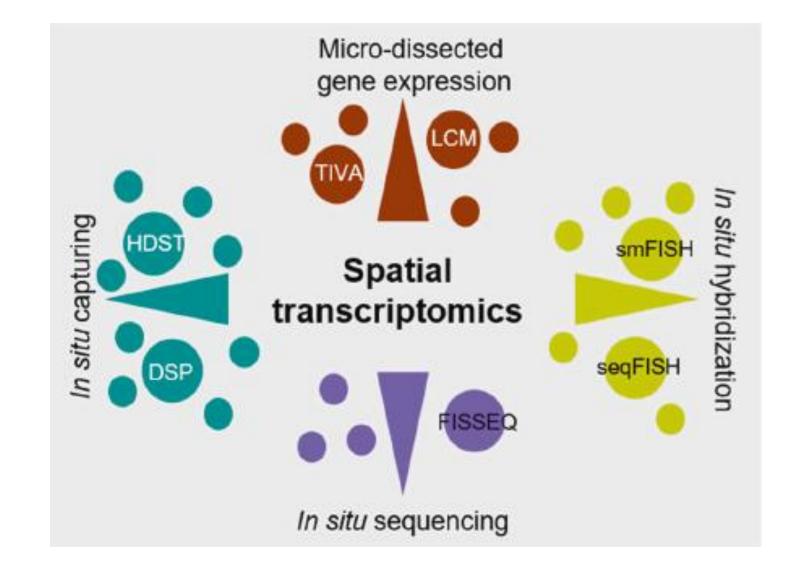


Exploring kidney pathology using spatial transcriptomics (4)

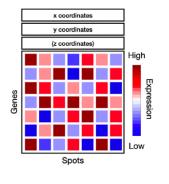


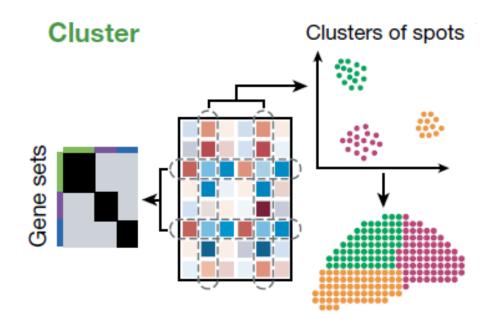
Moses et al. Nature Methods, March 2022

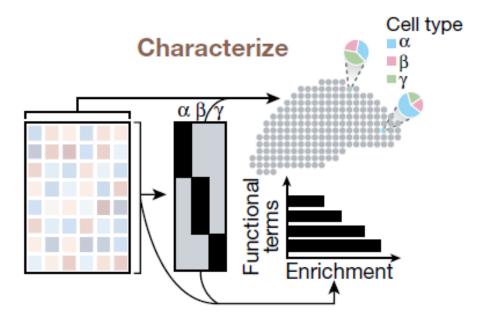


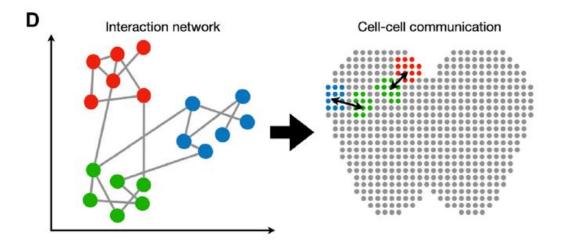


Zhang et al Signal Transduction and Targeted Therapy. March 2022

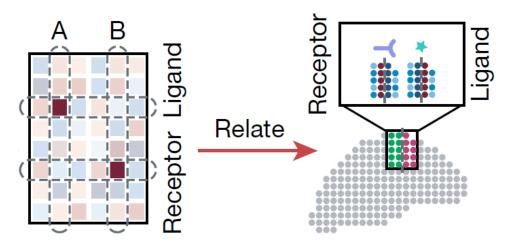






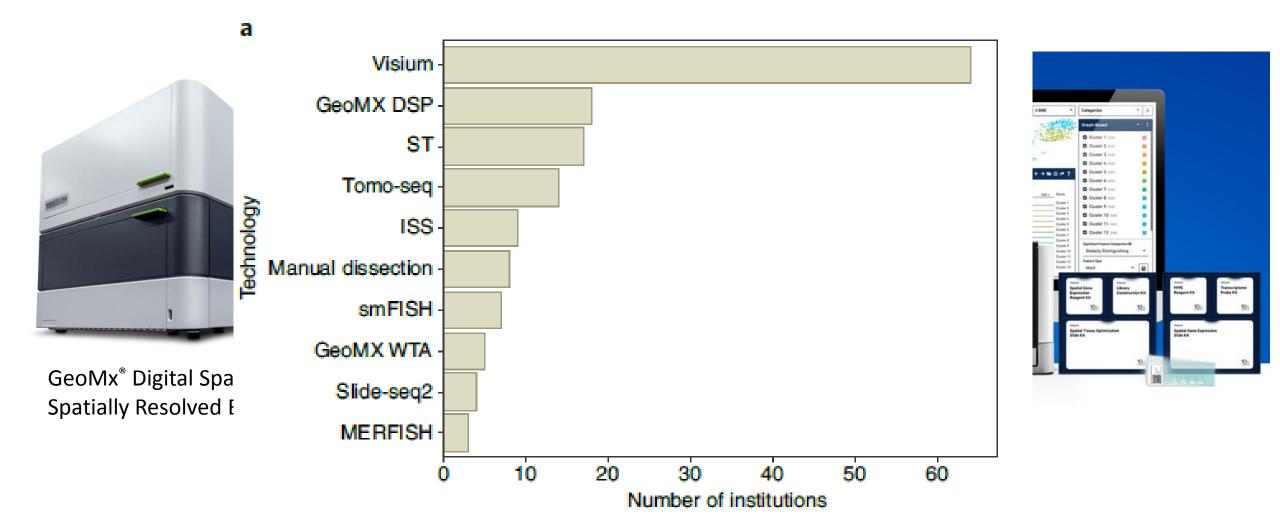


Correlation of gene expression

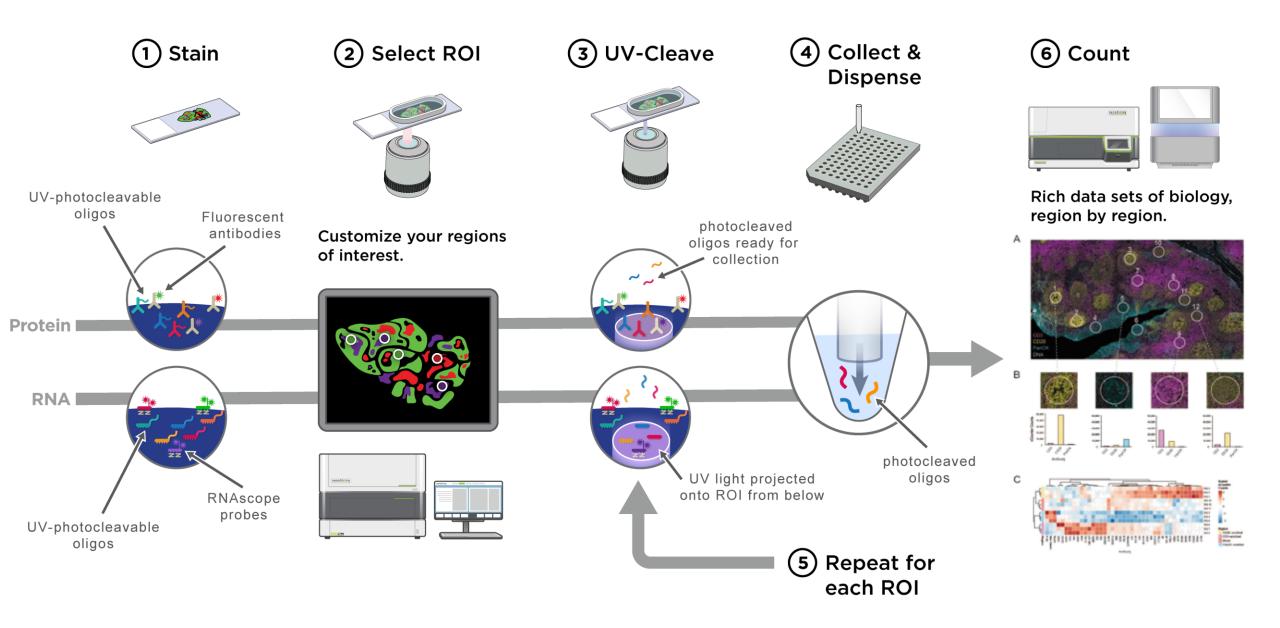


Liu et al Frontiers in Genetics Janurary 2022 Rao et Al. Nature, August 2021

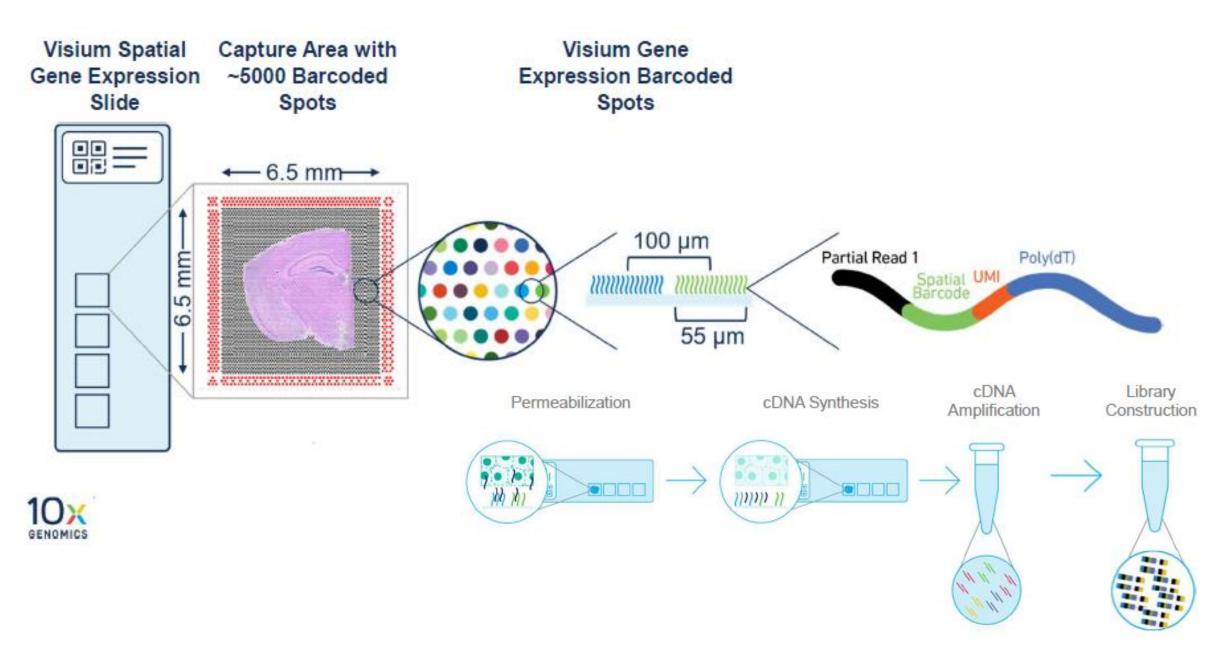
Exploring kidney pathology using spatial transcriptomics (7)



GeoMx DSP Workflow



10X Genomics Visium ST Workflow

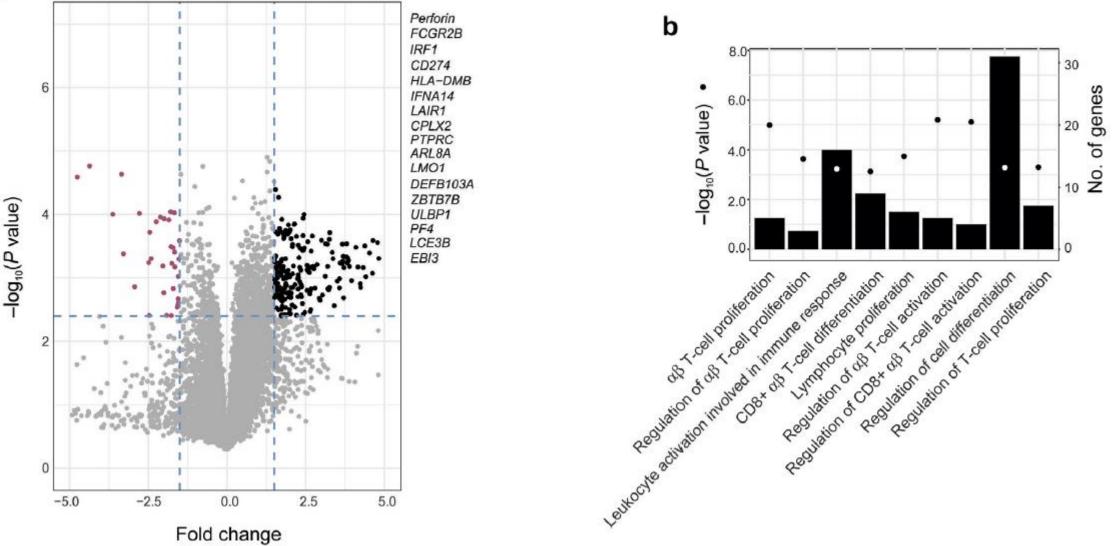


The spatially resolved transcriptional profile of acute T cell-mediated rejection in a kidney allograft

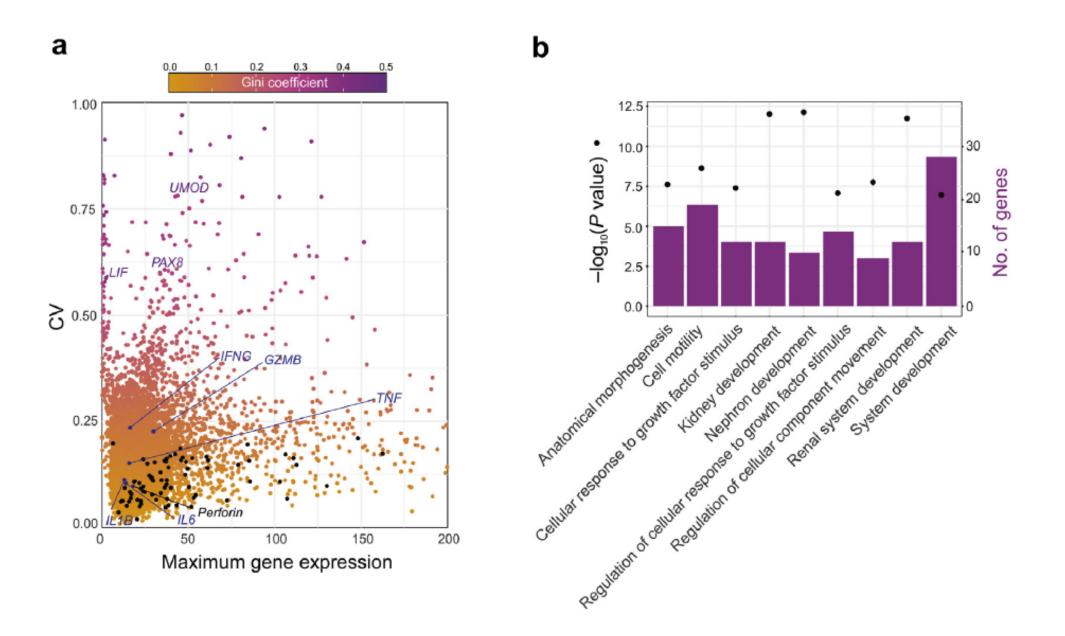


Fadi Salem^{1,8}, Laura Perin^{2,3,8}, Sargis Sedrakyan^{2,3}, Andrea Angeletti⁴, Gian Marco Ghiggeri⁴, Maria Cristina Coccia⁵, Marty Ross⁶, Miguel Fribourg^{7,9} and Paolo Cravedi^{7,9}

¹Department of Pathology and Molecular and Cell Based Medicine, Icahn School of Medicine at Mount Sinai, New York, New York, USA; ²GOFARR Laboratory for Organ Regenerative Research and Cell Therapeutics in Urology, Saban Research Institute, Division of Urology, Children's Hospital Los Angeles, Los Angeles, California, USA; ³Department of Urology, Keck School of Medicine, University of Southern California, Los Angeles, CA, USA; ⁴Nephrology, Dialysis and Transplantation Unit, Giannina Gaslini Scientific Institute for Research, Hospitalization and Healthcare, Genoa, Italy; ⁵Pathological Anatomy Unit, Giannina Gaslini Scientific Institute for Research, Hospitalization and Healthcare, Genoa, Italy; ⁶NanoString Technologies Inc., Seattle, Washington, USA; and ⁷Department of Medicine, Translational Transplant Research Center, Icahn School of Medicine at Mount Sinai, New York, New York, USA



Higher expression of inflammatory genes in tubular regions of interest (ROIs) in the acute cellular rejection (ACR) biopsy.



High variability in the kidney development transcriptional program across interstitial areas in a cellular rejection

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www.kidney-international.org

clinical investigation

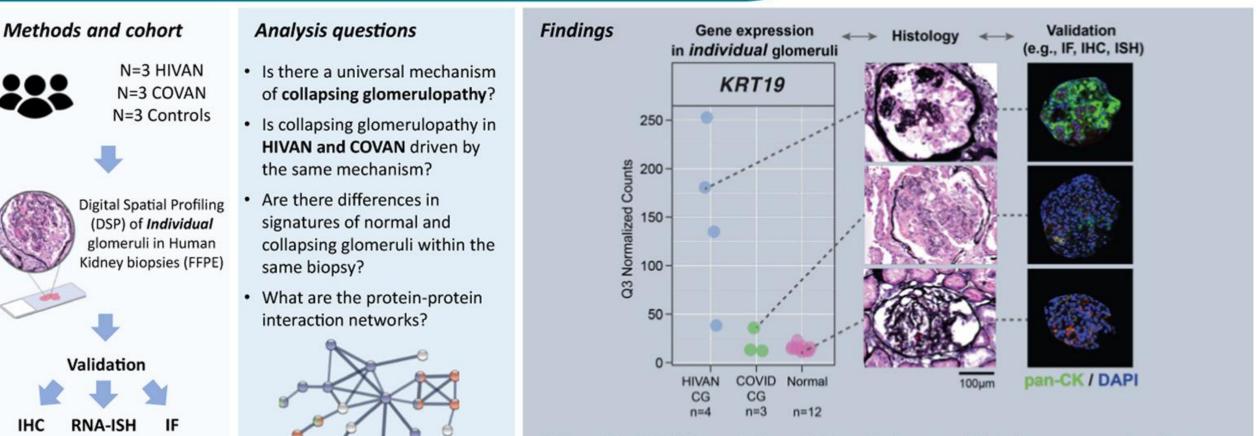
Digital spatial profiling of collapsing glomerulopathy

Kelly D. Smith^{1,2,4}, David K. Prince², Kammi J. Henriksen³, Roberto F. Nicosia¹, Charles E. Alpers^{1,2} and Shreeram Akilesh^{1,2,4}

¹Department of Laboratory Medicine and Pathology, University of Washington, Seattle, Washington, USA; ²Kidney Research Institute, Seattle, Washington, USA; and ³Department of Pathology, University of Chicago, Chicago, Illinois, USA

Digital Spatial Profiling of Collapsing Glomerulopathy

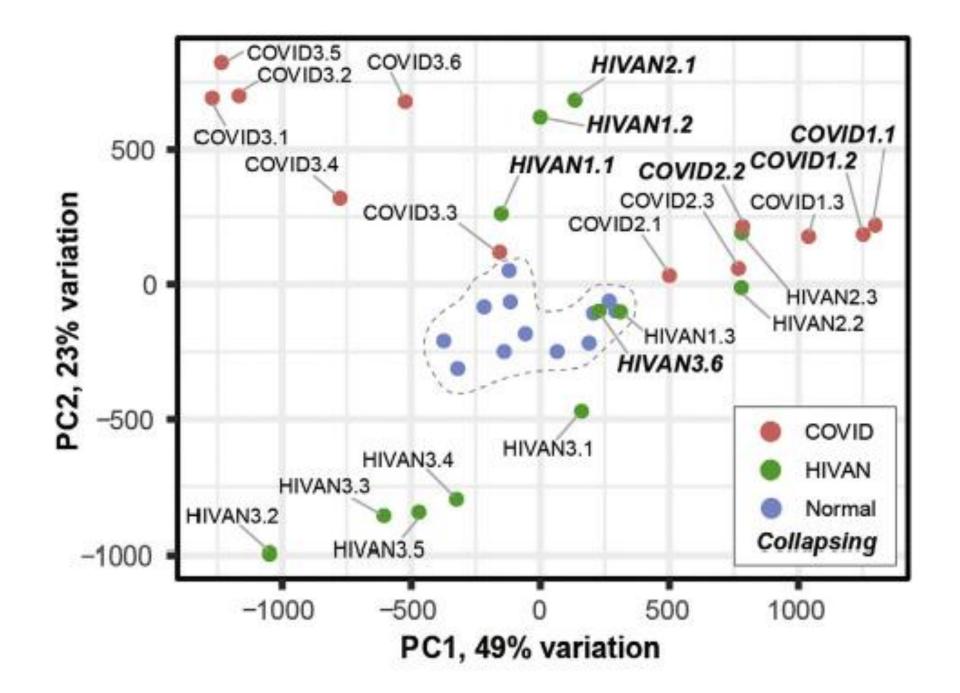


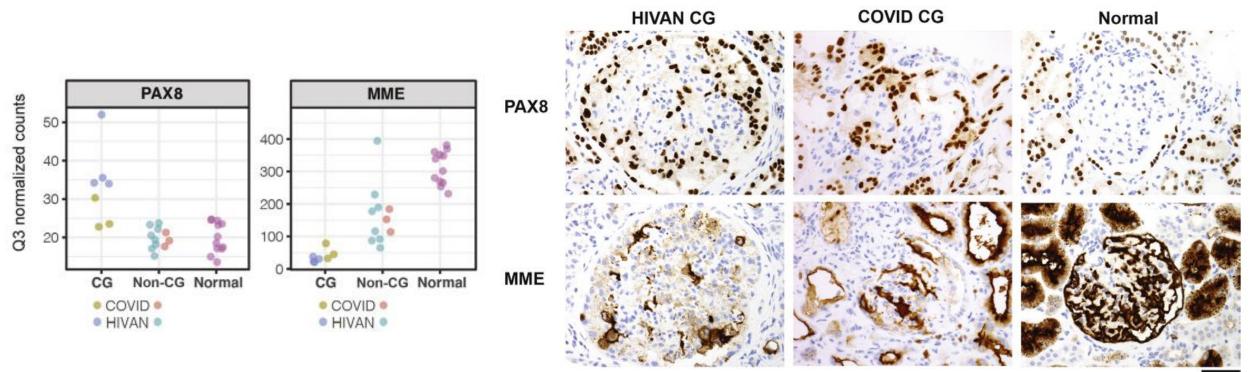


DSP enables DIRECT correlation of histopathology to validated gene expression signatures

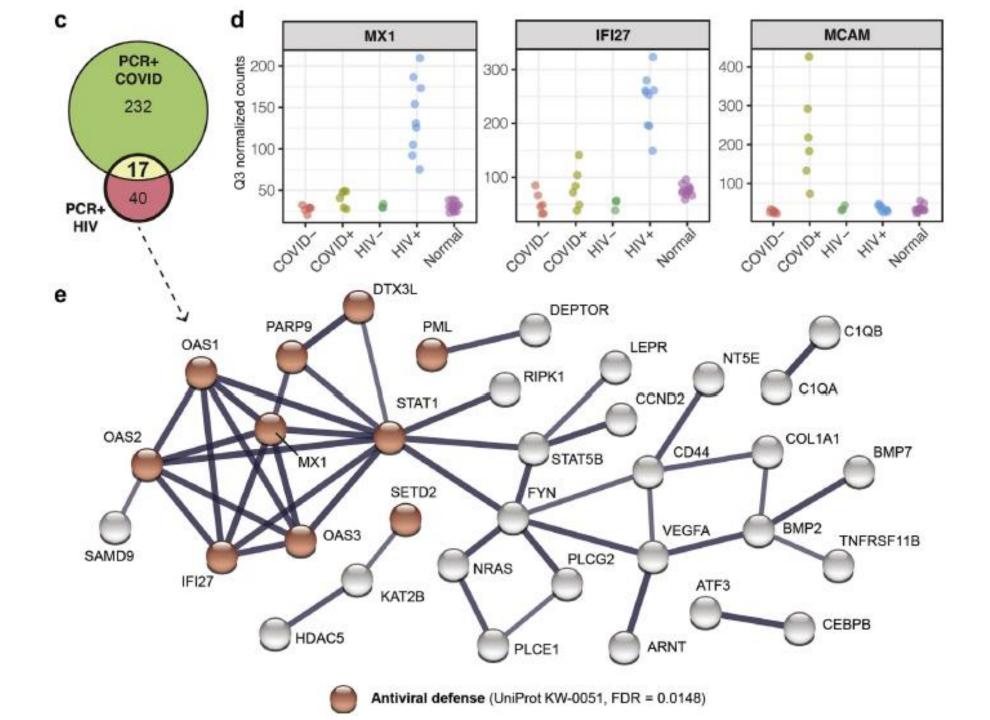
Smith, 2021

CONCLUSION: Digital spatial profiling can generate individual glomerular transcriptomes from single FFPE tissue sections of clinically procured human kidney biopsies without prior optimization. This enables direct correlation of histopathology with molecular signatures of disease.





50µm





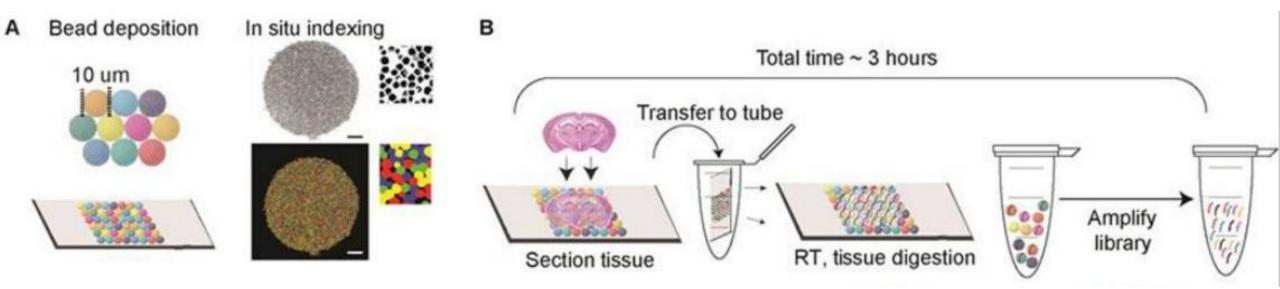


Article

High-resolution Slide-seqV2 spatial transcriptomics enables discovery of disease-specific cell neighborhoods and pathways

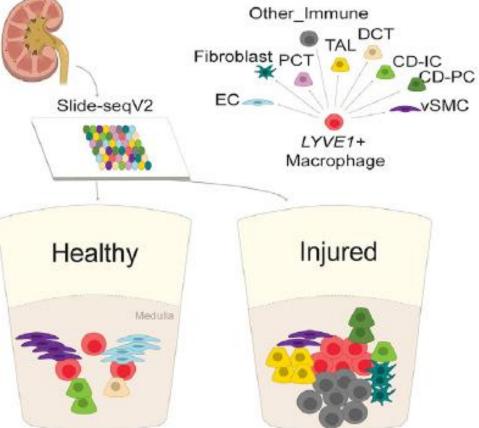
> Jamie L. Marshall, Teia Noel, Qingbo S. Wang, ..., Evan Z. Macosko, Fei Chen, Anna Greka

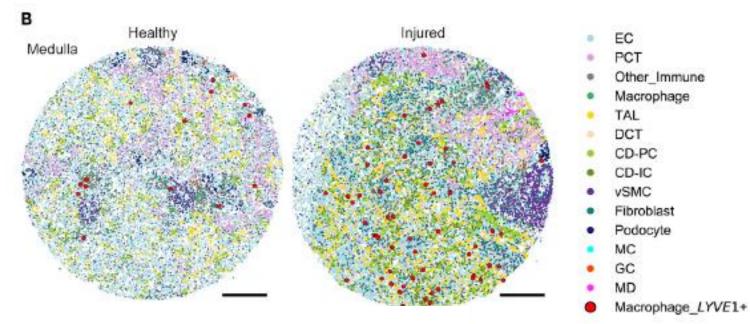
Slide-SeqV2 workflow

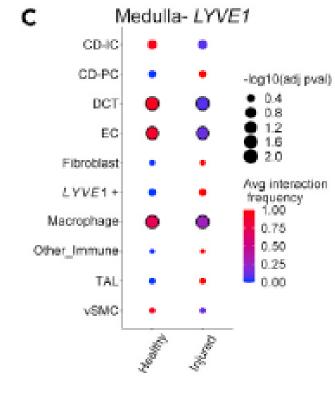


Rodriques et al. Science March 2020.

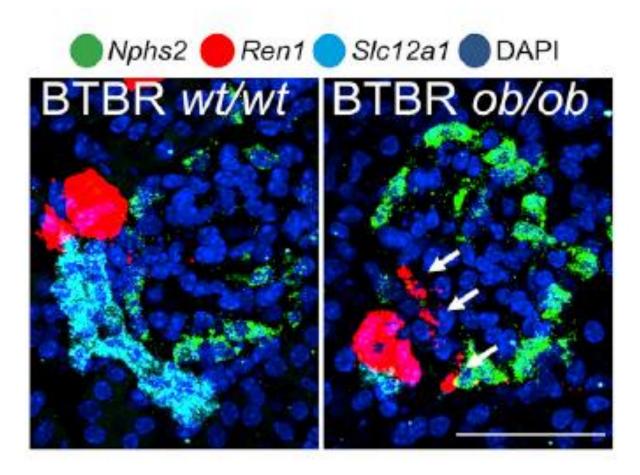
LYVE1+ Macrophage Neighborhoods in Injured Human Medulla

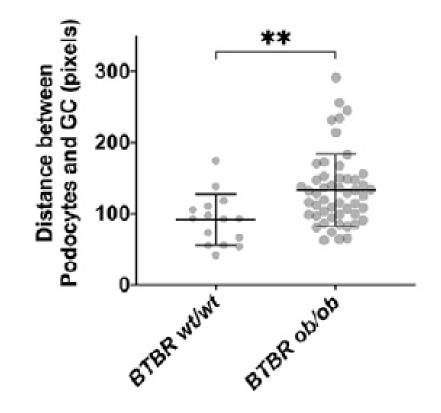




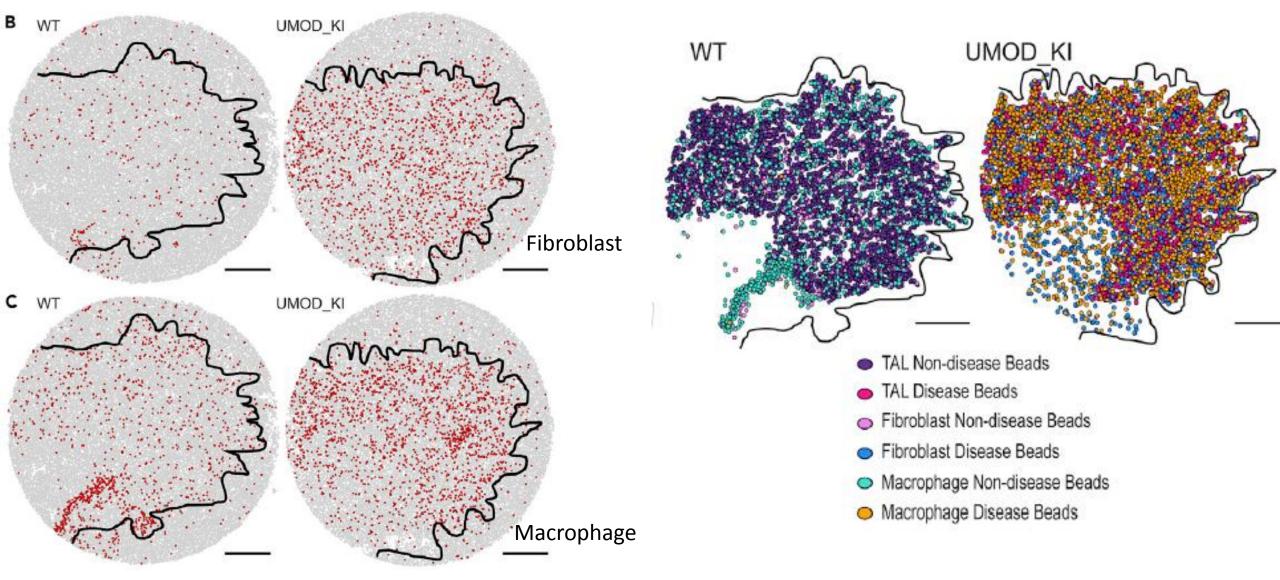


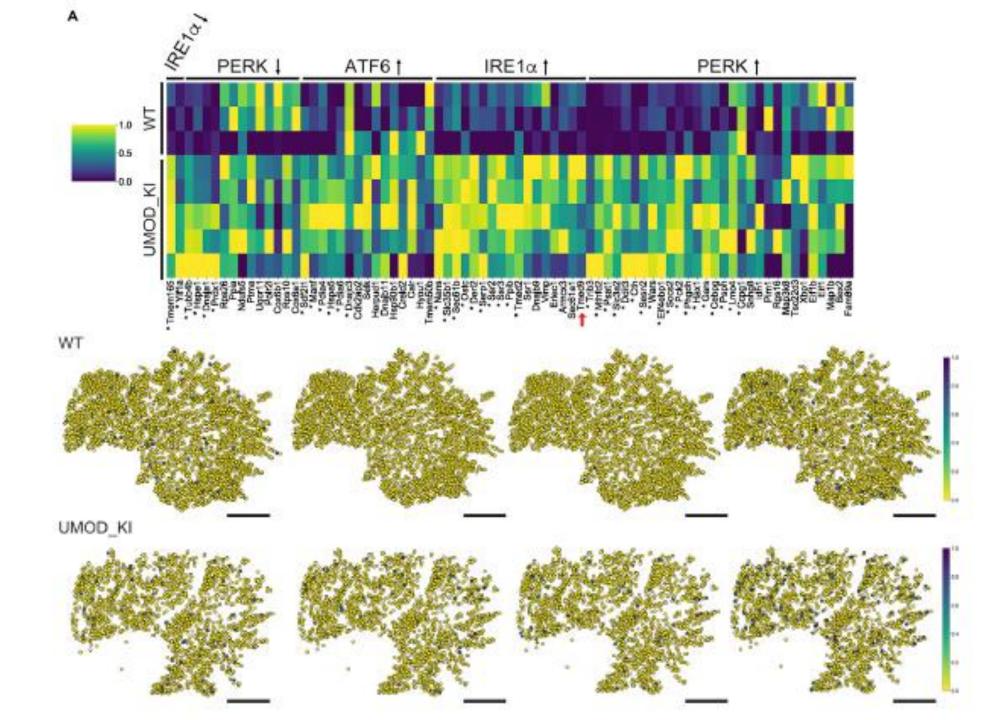
Re-organized Blood Flow Apparatus in Mouse Diabetic Kidney Disease



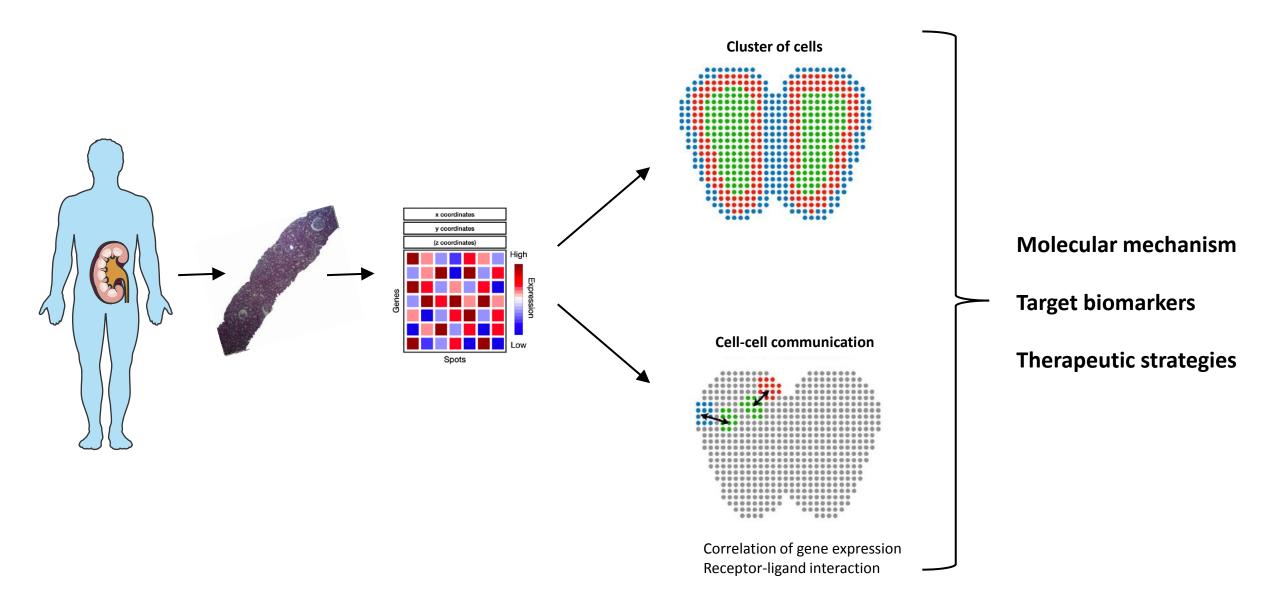


Trem2+ Cell Neighborhoods and Transcriptional Signatures of Disease in Mouse Medullary Toxic Proteinopathy





Conclusion



Remerciements



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Equipe Fabiola Terzi

Service de Néphrologie et Transplantation rénale Necker