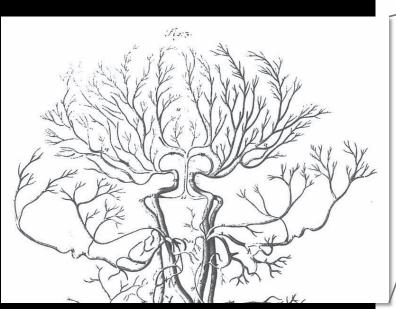
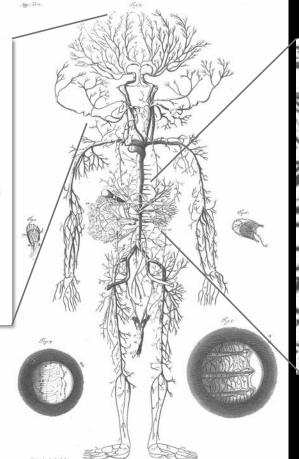
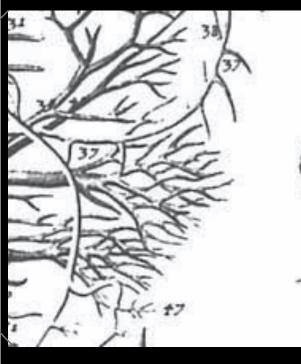
The Vasculome – Mapping Knowledge about Human Vasculature Across Body Scales



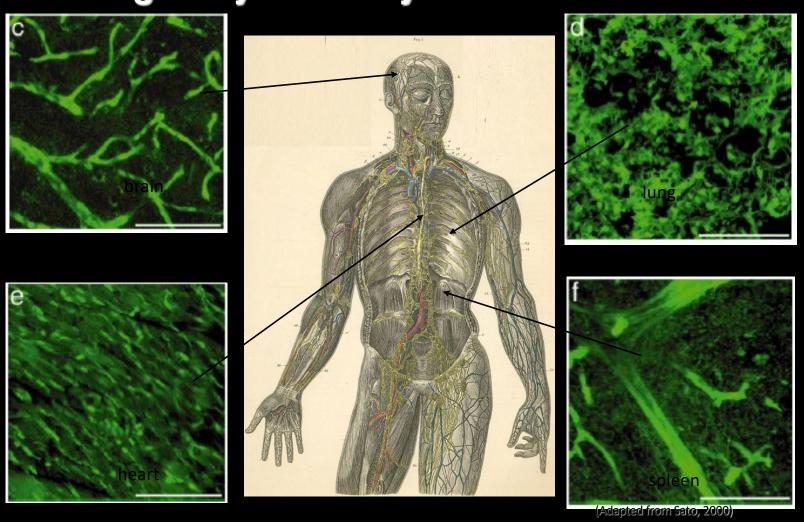
Ondine Cleaver, Dept Molecular Biology
Center for Regenerative Science and Medicine (CRSM),
UT Southwestern Medical Center

Mapping the Vasculome, NAVBO August 31st, 2021

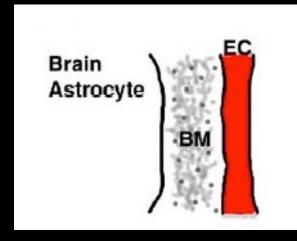


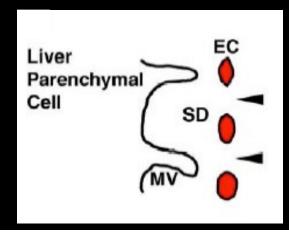


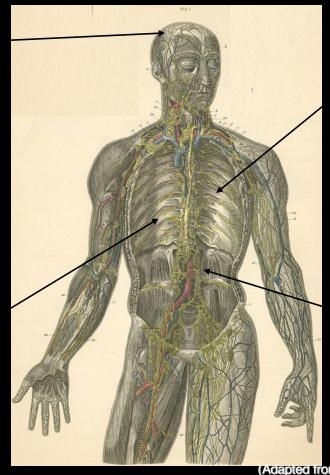
EC heterogeneity: Anatomy - vessel size and density

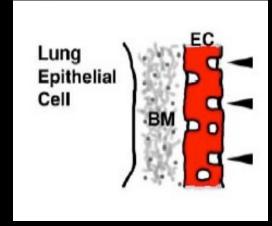


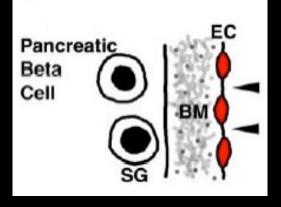
EC heterogeneity: cellular ultrastructure





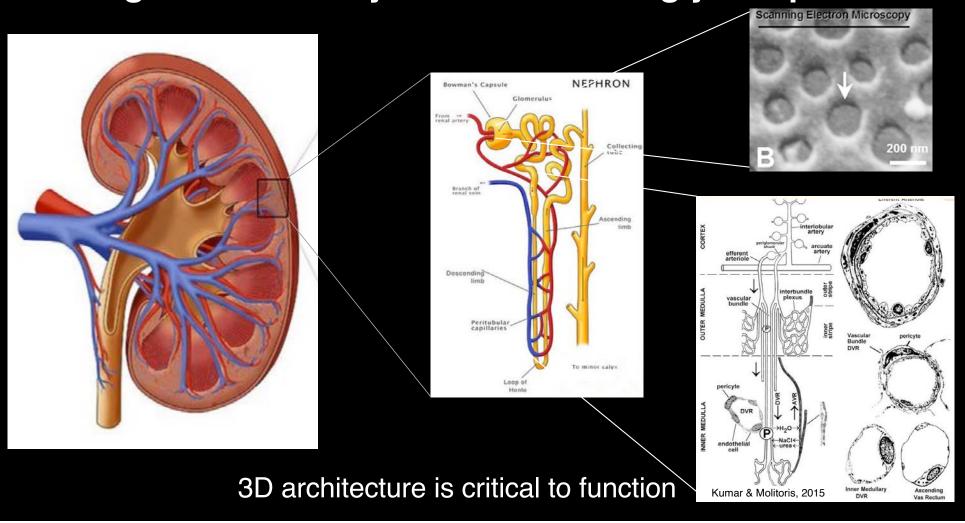




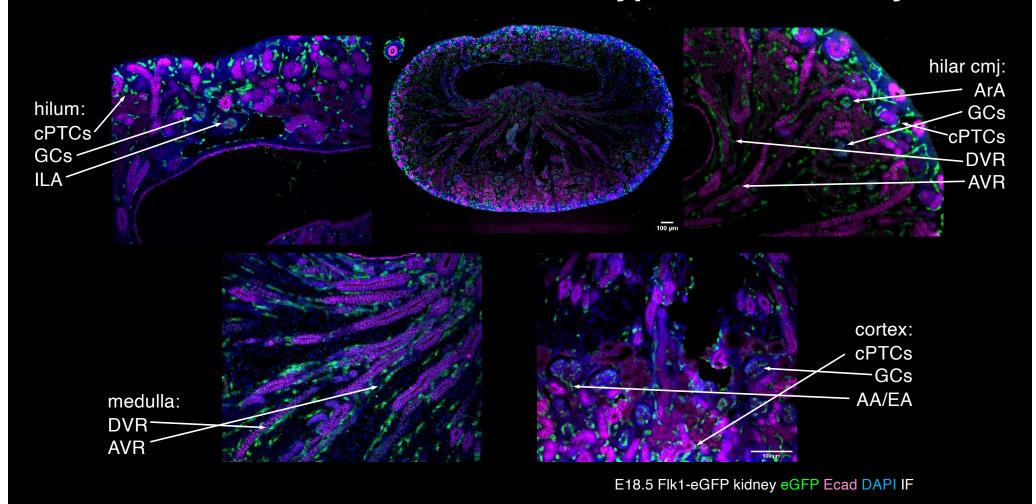


(Adapted from Nikolova and Lammert, 2003)

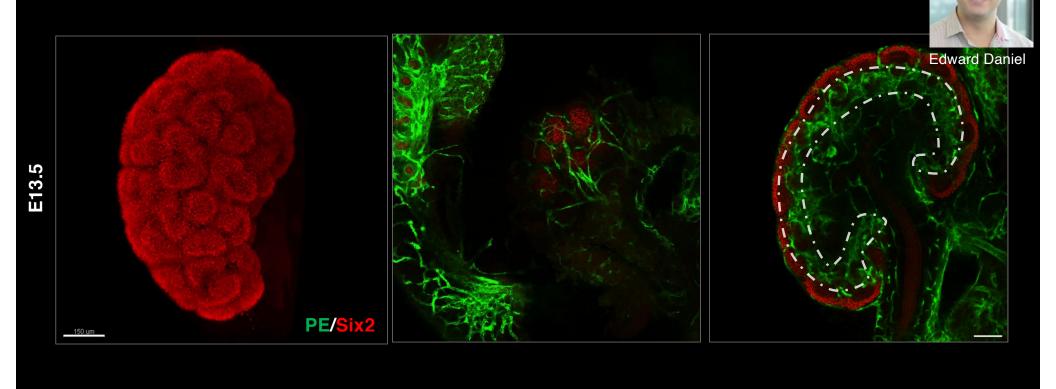
Organ 3D anatomy can be exceedingly complex

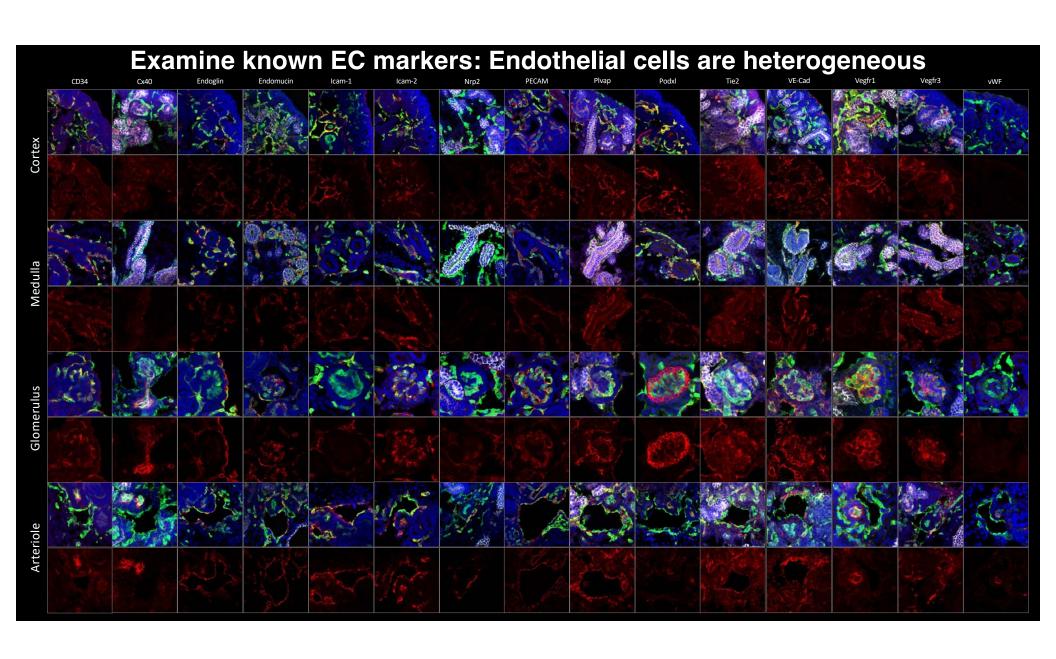


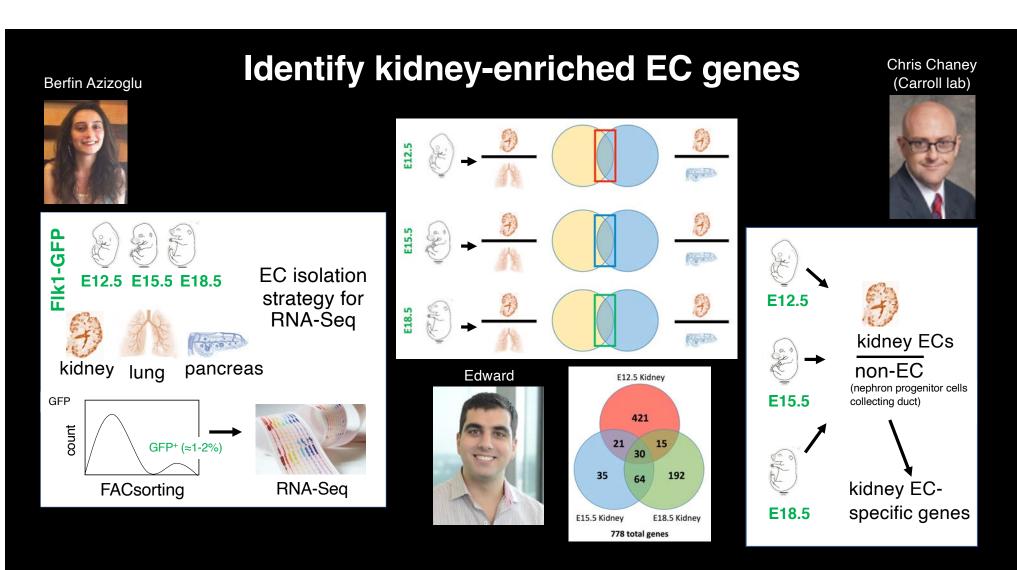
Identification of vessel subtypes in the kidney



Endothelial cells form dense plexus next to progenitor cells (red) during kidney development

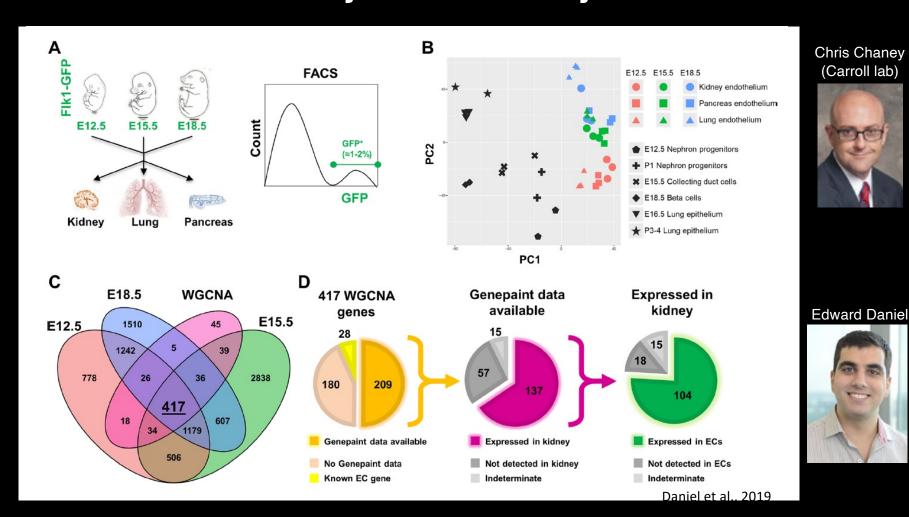






Transcriptional profiling of ECs by EC isolation, RNAseq & comparison

We isolated and analyzed the kidney endothelium

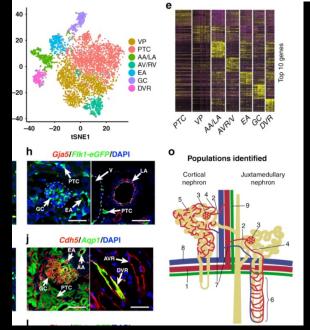


Recent papers on kidney vasculature

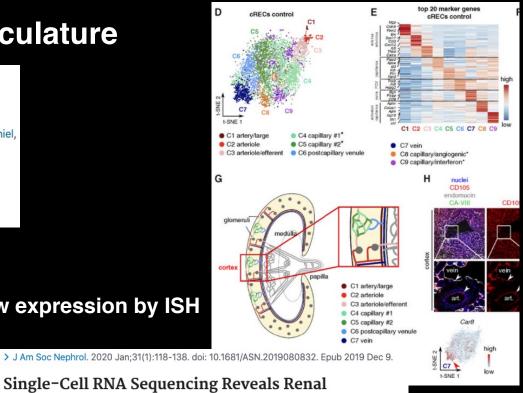
Molecular determinants of nephron vascular specialization in the kidney

David M. Barry ☑, Elizabeth A. McMillan, Balvir Kunar, Raphael Lis, Tuo Zhang, Tyler Lu, Edward Daniel, Masataka Yokoyama, Jesus M. Gomez-Salinero, Angara Sureshbabu, Ondine Cleaver, Annarita Di Lorenzo, Mary E. Choi, Jenny Xiang, David Redmond, Sina Y. Rabbany, Thangamani Muthukumar & Shahin Rafii

Nature Communications 10, Article number: 5705 (2019) | Cite this article



Less than 5% show expression by ISH



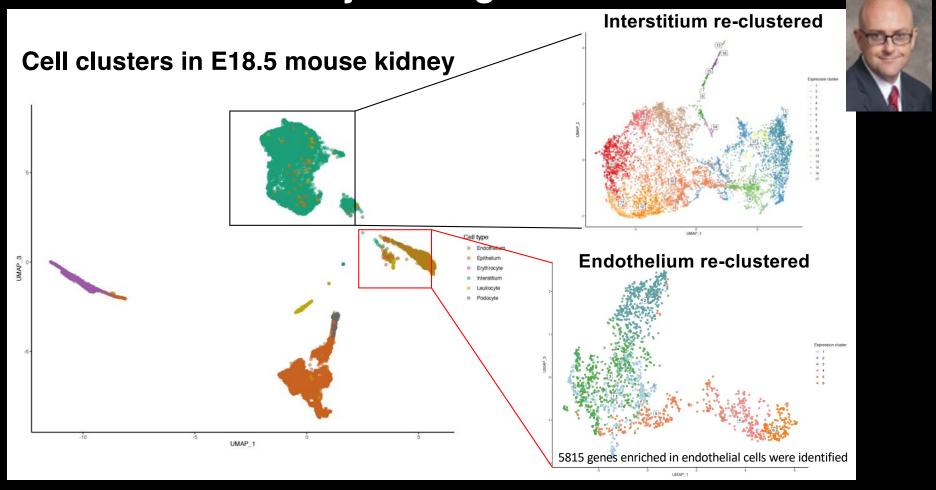
Single-Cell RNA Sequencing Reveals Renal **Endothelium Heterogeneity and Metabolic**

Adaptation to Water Deprivation

```
Sébastien J Dumas 1 2, Elda Meta 1 2, Mila Borri 1 2, Jermaine Goveia 1 2,
Katerina Rohlenova 12, Nadine V Conchinha 12, Kim Falkenberg 12, Laure-Anne Teuwen 12,
Laura de Rooij <sup>1 2</sup>, Joanna Kalucka <sup>1 2</sup>, Rongyuan Chen <sup>3</sup>, Shawez Khan <sup>1 2</sup>.
Federico Tayerna 12, Weisi Lu3, Magdalena Parys 12, Carla De Legher 12,
Stefan Vinckier 1 2, Tobias K Karakach 1 2, Luc Schoonjans 1 2 3, Lin Lin 4 5, Lars Bolund 4 5,
Mieke Dewerchin 1 2, Guy Eelen 1 2, Ton J Rabelink 6, Xuri Li 7, Yonglun Luo 8 5 9 10
Peter Carmeliet 11 2 3
```

The kidney stroma (which includes ECs) is very heterogeneous

Chris Chaney (Carroll lab)





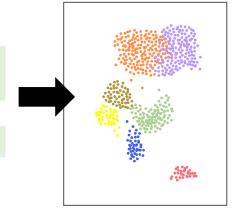
Data sourcing and analysis pipeline



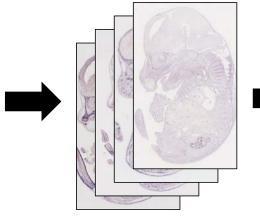
Annie Ryan

RNA seq data compilation

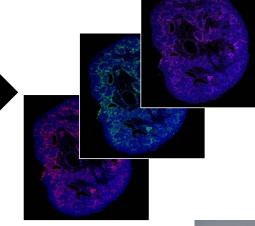
Kidney ECs



in silico analysis



Genepaint, online database review and our in situs



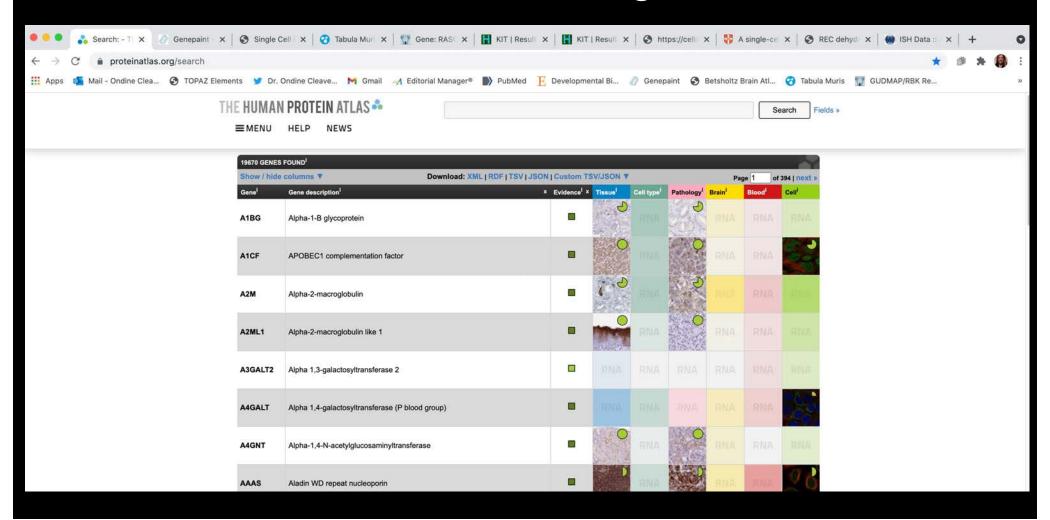
FISH Validation



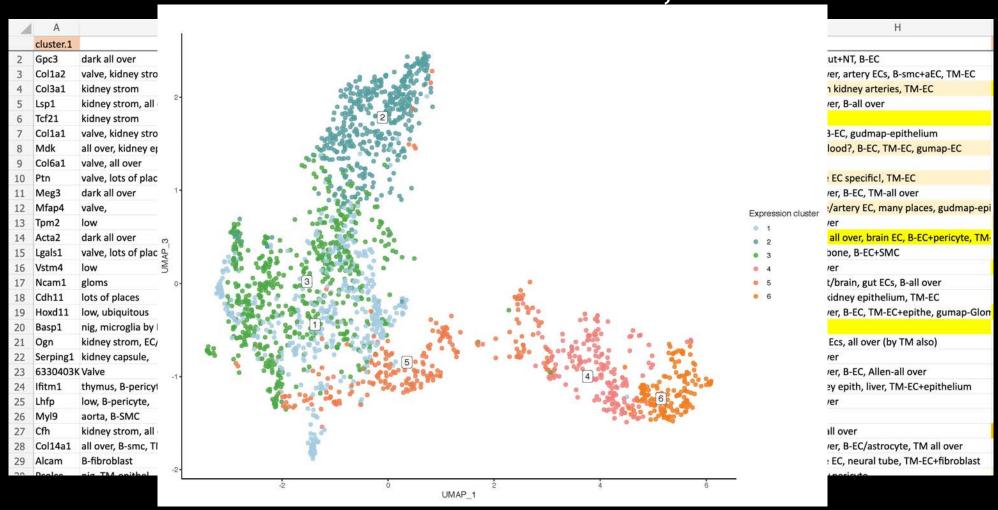
Peter Luo

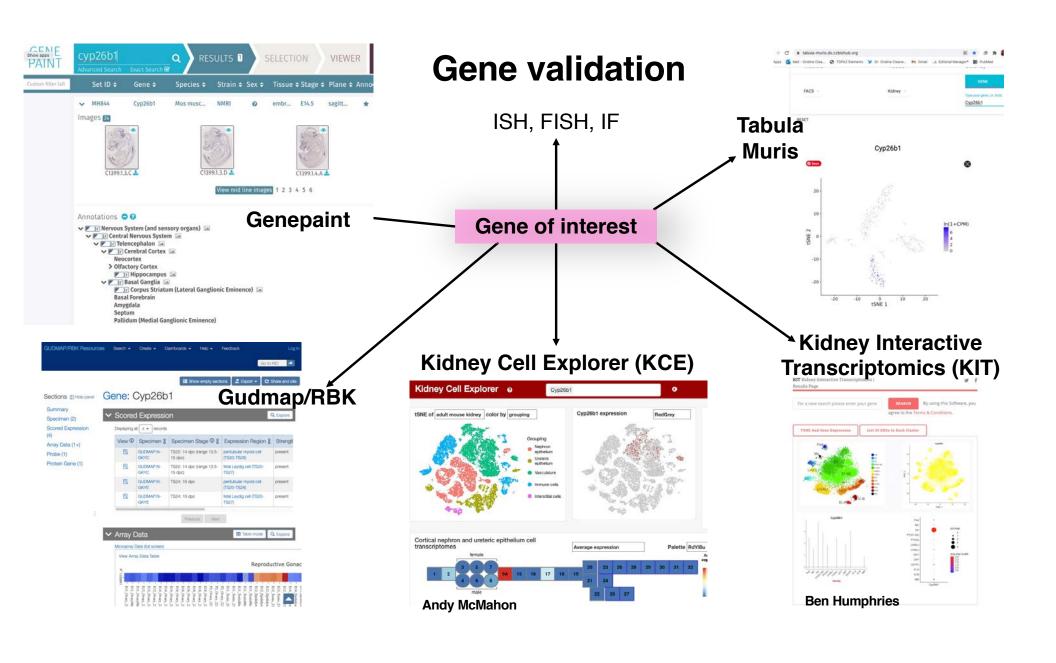


We must VALIDATE our gene lists



How much of what we find is useful, or even real?

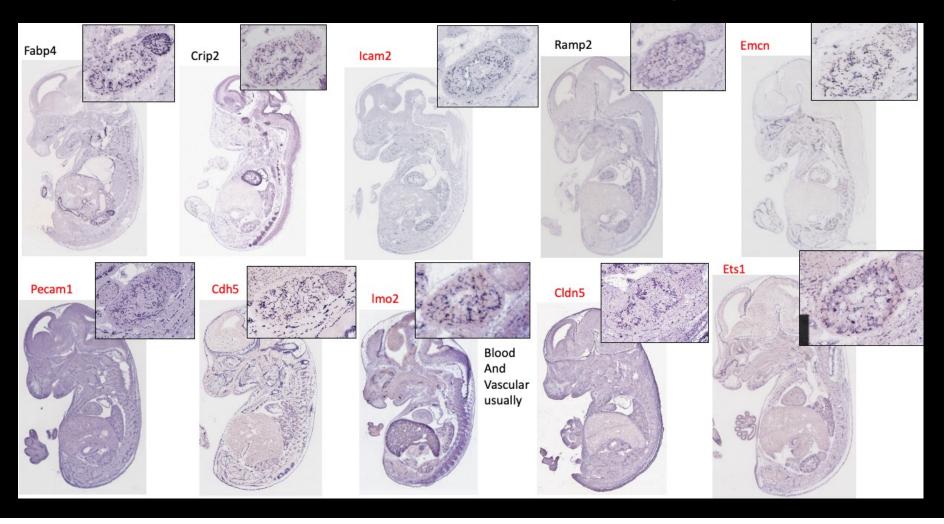




Transcriptomic Index based on multiple website analysis

	Α	В	С	D	E	F	G	Н	1	J K	L
1	Gene	genepaint	KEC	KIT	Gudmap	Betsholtz	Tabula Muris	Allen Brain A	Human Protein Atla	Single Cell Mouse	Index
2	Ramp2	2	1	2.7	2.1	1	2	1	1	2	1.64
3	Plvap	2.8	1	1	1.1	2.9	1	na	2.4	1.4	1.71
4	lgf2r	2.5	2	1.8	2.5	2.9	2.5		2.7	2.7	2.45
5	Ppfibp1	2.9	1.5	2	2.5	1.8	1		2.5	2.7	2.11
6	Rnf130	na	2.5	2.9	2.5	2.5	2.6		2.8	2.6	2.63
7	Tm6sf1	na	2.5	2.3	3	2.1	2.7		2.8	2	2.49
8	Lpp	2.5	2.7	2.8	2.3	2.7	1.8		2.8	2.3	2.49
9	Ifit1	3	1	1.3	2.6	1.8	1.3		2.5	3	2.06
10	Ctso	2.9	2.1	2.7	2.6	2.2	2		2.7	2.8	2.5
11	Lfng	na	2.1	1.3	2.2	2.6	2.5		2.8	2.7	2.31
12	ltpr1	3	2.8	2.9	2.8	2.8	2.7		2.8	2.6	2.8
13	Stx3	3.5	2.7	2.8	2.9	1	2.9		2.9	2.8	2.69
14	Stox2	2.9	1.8	2.9	2.5	2.7	2		2.5	2	2.19
15	Filip1	2.9	2.5	1.5	2.5	2.1	1		2.8	2.2	2.19
16	Oasl2	4	1.5	1.3	na	1	2		na	2	1.97
17	Plau	2.8	2.8	2.8	2.1	3	2.6		2.9	1.5	2.56
18	Kank3	3.5	1.3	1.3	1.1	1	1		1.3	1.1	1.45
19	Tmem252	3.5	2.1	2.8	4	1	na		4	1.4	2.69
20	Herpud1	2.8	2.3	2.8	2.7	2.3	2.5		2.8	2.8	2.63
21	Gbp7	4	1	1.3	na	1	1		2.6	2	1.84
22	Tgm2	3.7	1.3	2.3	2.1	1.8	1.7		2.5	2.2	2.2
23	Tmem37	3.7	2.9	2.9	2.4	2.8	2.9		2.9	1.3	2.73
24	Exoc3l4	2.2	1	2.9	3	2.9	1		3	1	2.13
25	Mapk3	2.7	1.7	2.2	2.2	2.2	1.8		2.8	1.3	2.11
26	Kras	na	2.5	2.9	2.4	1.2	2.6		2.6	2.4	2.37
27	Picalm	2.7	2.6	2.9	2	2.5	2.3		2.3	2.7	2.5
28	Lama5	3.5	2.6	2.9	2.3	2.5	1.4		2.5	2.6	2.53
29	Fabp4	2	1	1.1	2.7	2.8	1		2.6	2.6	1.98
	Grasp	na	1.7	1.1	2.1	1	1.2		2.4	1.4	1.56
31	Agrn	3	2.5	2.9	2	2	1.5		2.8	2.6	2.41
	Ankrd37	na	2	2.6	2.7	1			2.8	2.6	2.33

Lots of known and novel EC genes

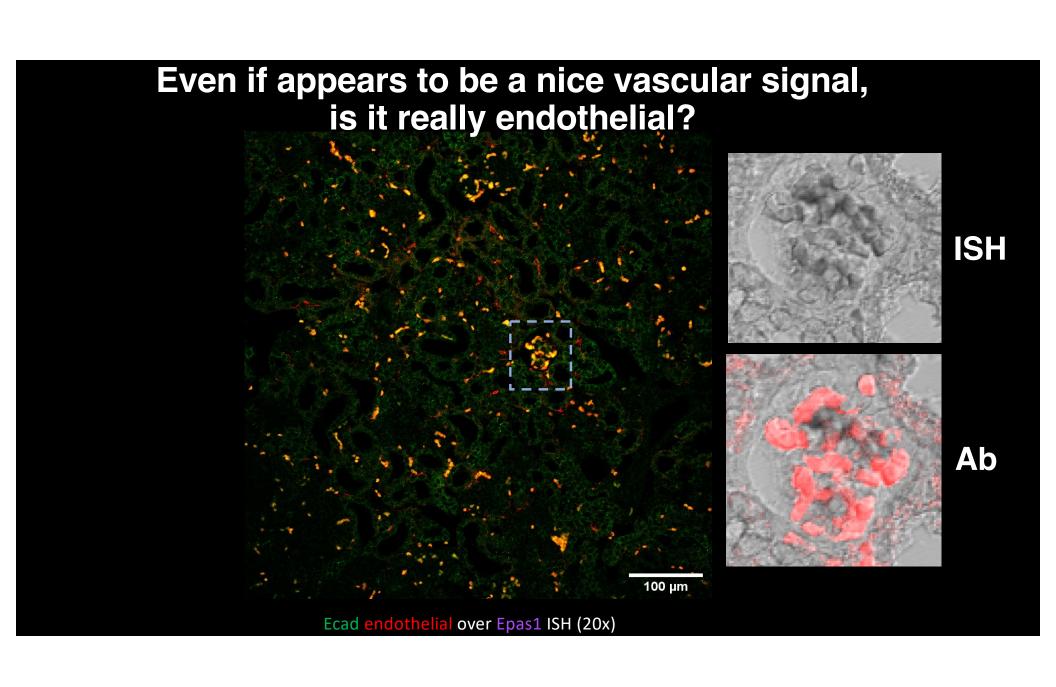


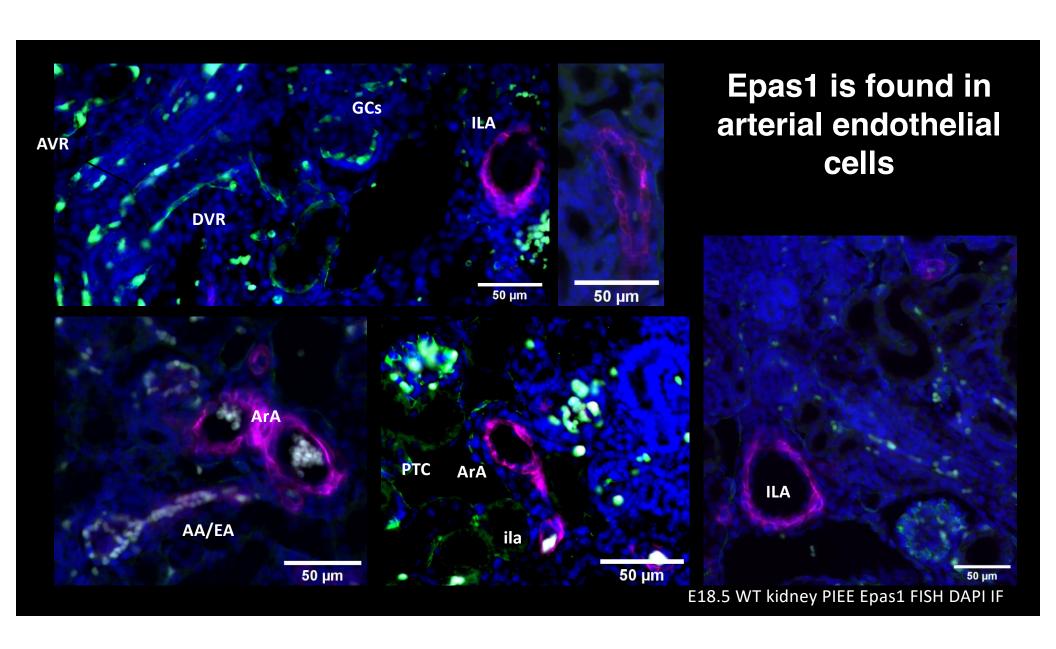
Genes identified by scRNAseq require validation

21 probes synthesized
10 working ISHs
5 potentially
endothelial genes
1 gene with
convincingly
heterogeneous
expression

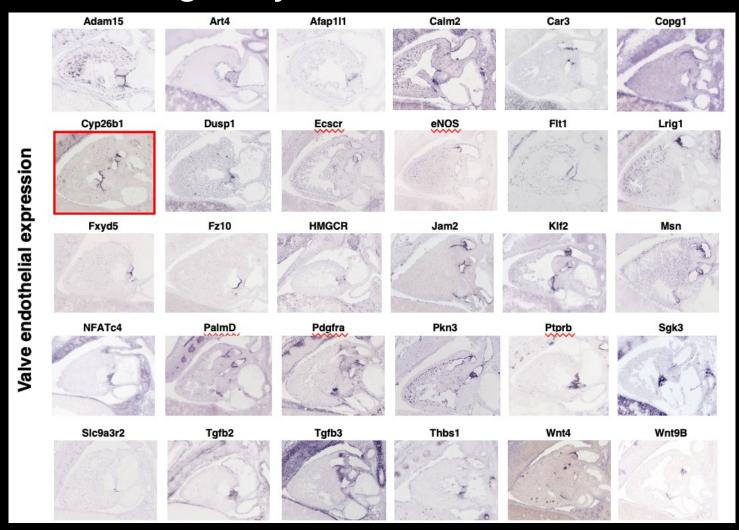
	present
	Likely present
	Likely absent
	Absent
**	Reported as present
??	Unclear – could not visualize

Gene	ILA	AA	ila	AA/EA	GC	PTC	DVR	AVR	Veins	Epithelia
Aqp1			??	??						
Ptprb										
Epas1										
Tm4sf1										
Irx3										
Cd93										
Ifi44			??	??						
Neat1										
Sgk1										
Rassf9										





Heterogeneity of the valve vasculature



Papers on single cell RNAseq in ECs

PMCID: PMC2919381

Original Paper | Open Access | Published: 01 June 2021

Endothelial cell plasticity at the single-cell level

Alessandra Pasut, Lisa M. Becker, Anne Cuypers & Peter Carmeliet ™

Angiogenesis 24, 311-326 (2021) | Cite this article

2931 Accesses | 18 Altmetric | Metrics

PLoS One. 2010; 5(8): e12034.

Published online 2010 Aug 10. doi: <u>10.1371/journal.pone.0012034</u> PMID: <u>20706631</u>

Gene Expression Programs of Mouse Endothelial Cells in Kidney Development and Disease

Eric W. Brunskill and S. Steven Potter*

Comparative Study > Cancer Cell. 2007 Jun;11(6):539-54. doi: 10.1016/j.ccr.2007.04.017.

Genes that distinguish physiological and pathological angiogenesis

Steven Seaman 1, Janine Stevens, Mi Young Yang, Daniel Logsdon, Cari Graff-Cherry, Brad St Croix

Affiliations + expand

PMID: 17560335 PMCID: PMC2039723 DOI: 10.1016/j.ccr.2007.04.017

Free PMC article

Cell Reports

Volume 26, Issue 7, 12 February 2019, Pages 1934-1950.e5



Resource

Single-Cell Transcriptome Analysis Maps the Developmental Track of the Human Heart

Yueli Cui ^{1, 3, 6}, Yuxuan Zheng ^{1, 3, 5, 6}, Xixi Liu ^{1, 2, 3, 4, 6}, Liying Yan ^{1, 2, 4}, Xiaoying Fan ^{1, 3}, Jun Yong ^{1, 2, 4}, Yuqiong Hu ^{1, 3, 5}, Ji Dong ^{1, 3}, Qingqing Li ^{1, 3}, Xinglong Wu ^{1, 3, 5}, Shuai Gao ^{1, 3}, Jingyun Li ^{1, 3, 5}, Lu Wen ^{1, 3}, Jie Qiao ^{1, 2, 4, 5} ⊗ ≅, Fuchou Tang ^{1, 3, 5, 7} ⊗ ≅

RESEARCH ARTICLE | 14 JUNE 2019

Single cell expression analysis reveals anatomical and cell cycle-dependent transcriptional shifts during heart development [RES]

In collection: Cardiovascular development and regeneration

Guang Li ≥ 0, Lei Tian, William Goodyer, Eric J. Kort 0, Jan W. Buikema, Adele Xu, Joseph C. Wu, Stefan Jovinge ≥ 0, Sean M. Wu ≥ 0

+ Author and article information

Development (2019) 146 (12): dev173476.

J Am Soc Nephrol. 2018 Aug; 29(8): 2060-2068.

Published online 2018 May 24. doi: 10.1681/ASN.2018030238

PMCID: PMC6065081

PMID: 29794128

A Single-Cell Transcriptome Atlas of the Mouse Glomerulus

Nikos Karaiskos,¹ Mahdieh Rahmatollahi,² Anastasiya Boltengagen,¹ Haiyue Liu,¹ Martin Hoehne,² Markus Rinschen,^{2,3} Bernhard Schermer,^{2,4,5} Thomas Benzing,^{2,4,5} Nikolaus Rajewsky,¹ Christine Kocks,[⊠]¹ Martin Kann,² and Roman-Ulrich Müller,[©]2,4,5

▶ Author information ▶ Article notes ▶ Copyright and License information <u>Disclaimer</u>

The Vasculome

"Mapping knowledge about human vasculature across body scales"

NAVBO Zoom panel on Tuesday August 31st, 1-2:30pm

WHY?



Ondine Cleaver, PhD
UT Southwestern Medical Center

WHAT?



Zorina Galis, PhD Chief of Vascular Biology & Hypertension, NIH NHLBI HuBMAP

HOW?



Griffin Weber, MD PhD Biomedical Informatics Harvard Medical School VCCF & HuBMAP

Point being

Each of us is generating lots of EC data ☺

Let's assemble it to generate a full map of the kidney vasculature!

