Toward a Human Reference Atlas: Anatomical Structures, Cell Types, and Biomarkers

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HuBMAP

https://commonfund.nih.gov/HuBMAP

Vision

Catalyze the development of an open, global framework for comprehensively mapping the human body at cellular resolution.

Goals

1. Accelerate the development of the next generation of tools and techniques for constructing high resolution spatial tissue maps
2. Generate foundational 3D tissue maps
3. Establish an open data platform
4. Coordinate and collaborate with other funding agencies, programs, and the biomedical research community
5. Support projects that demonstrate the value of the resources developed by the program

The Human Body at Cellular Resolution:
The NIH Human Biomolecular Atlas Program.
Snyder et al. *Nature*. 574, p. 187-192.

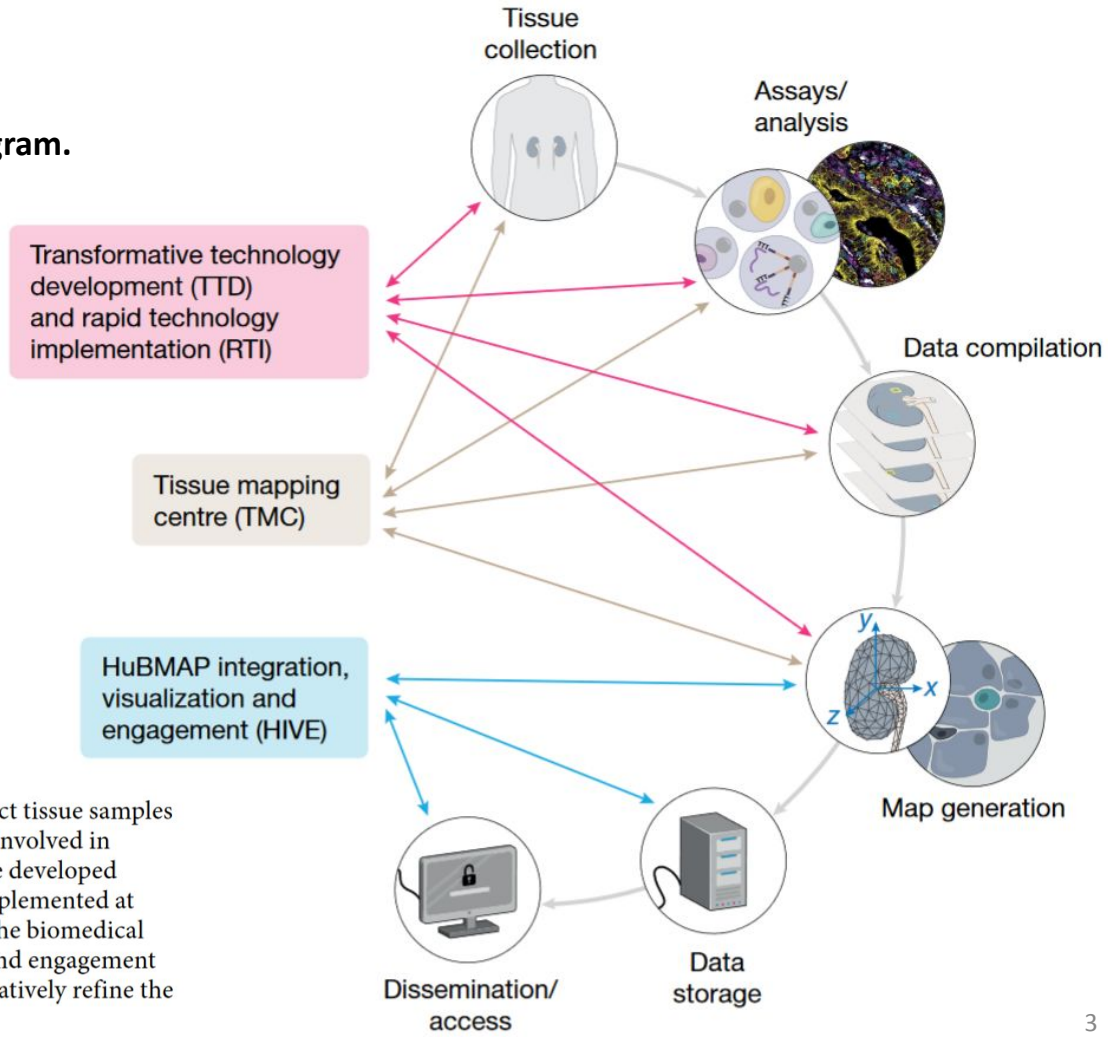


Fig. 1 | The HubMAP consortium. The TMCs will collect tissue samples and generate spatially resolved, single-cell data. Groups involved in TTD and RTI initiatives will develop emerging and more developed technologies, respectively; in later years, these will be implemented at scale. Data from all groups will be rendered useable for the biomedical community by the HuBMAP integration, visualization and engagement (HIVE) teams. The groups will collaborate closely to iteratively refine the atlas as it is gradually realized.

The Human Body at Cellular Resolution:
The NIH Human Biomolecular Atlas Program.
Snyder et al. *Nature*. 574, p. 187-192.

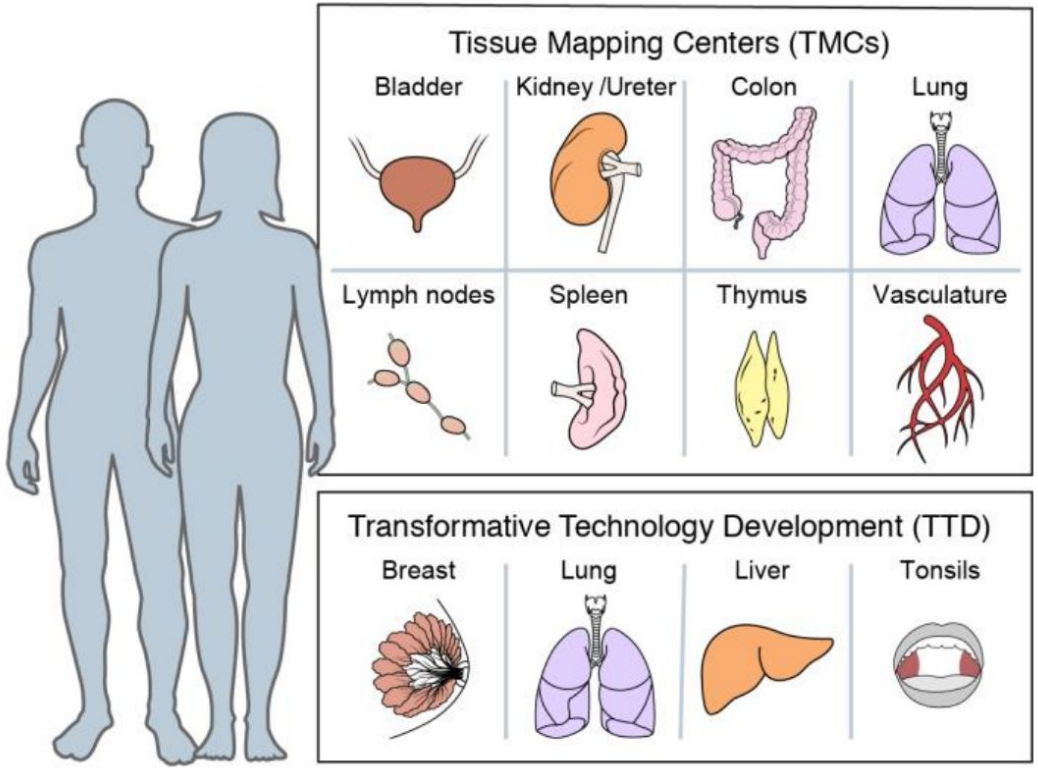


Fig. 2 | Key tissues and organs initially analysed by the consortium. Using innovative, production-grade ('shovel ready') technologies, HuBMAP TMCs will generate data for single-cell, three-dimensional maps of various human tissues. In parallel, TTD projects (and later RTI projects) will refine assays and analysis tools on a largely distinct set of human tissues. Samples from individuals of both sexes and different ages will be studied. The range of tissues will be expanded throughout the program.

The Human Body at Cellular Resolution: The NIH Human Biomolecular Atlas Program. Snyder et al. *Nature*. 574, p. 187-192.

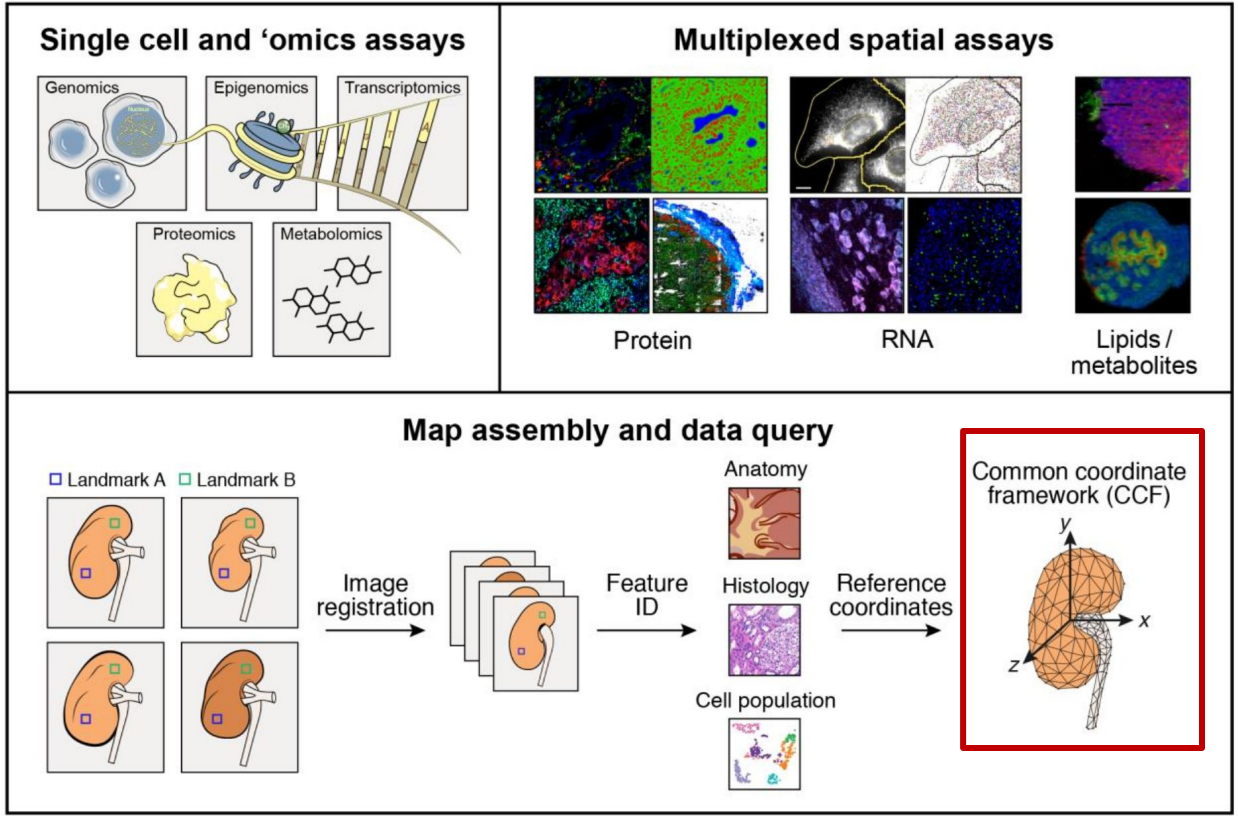


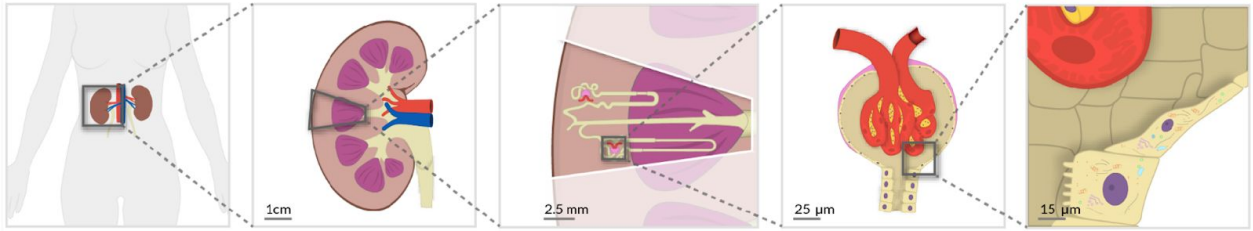
Fig. 3 | Map generation and assembly across cellular and spatial scales. HuBMAP aims to produce an atlas in which users can refer to a histological slide from a specific part of an organ and, in any given cell, understand its contents on multiple 'omic levels—genomic, epigenomic, transcriptomic, proteomic, and/or metabolomic. To achieve these ends, centres will apply a combination of imaging, 'omics and mass spectrometry techniques to specimens collected in a reproducible manner from specific sites in the body. These data will be then be integrated to arrive at a high-resolution, high-content three-dimensional map for any given tissue. To ensure inter-individual differences will not be confounded with collection heterogeneity, a robust CCF will be developed.

CCF ASCT+B Tables

CCF Requirements

The CCF must capture major **anatomical structures, cell types, and biomarkers** and their interrelations across **multiple levels of resolution**.

It should be **semantically explicit** (using existing ontologies, e.g., Uberon, CL) and **spatially explicit** (e.g., using 3D reference organs for registration and exploration).



Body	Organ	Functional Tissue Unit	FTU Sub-structure(s)	Cellular
• Body	• Renal capsule	• Nephron	• Bowman's capsule	• Parietal epithelial cell
• Kidney (Left, Right)	• Renal pyramid	• Renal corpuscle	• Glomerulus	• Capillary endothelial cell
• Aorta	• Renal cortex	• Proximal convoluted tubule	• Efferent arteriole	• Mesangial cell
• Renal artery	• Renal medulla	• Loop of Henle	• Afferent arteriole	• Podocyte
• Renal vein	• Renal calyx	• Distal convoluted tubule		
• Ureter	• Renal pelvis	• Connecting tubule		
		• Collecting duct		

ASCT+B Tables

Anatomical Structures, Cell Types, and Biomarkers (ASCT+B) tables aim to capture the partonomy of anatomical structures, cell types, and major biomarkers (e.g., gene, protein, lipid or metabolic markers).

Structure/Region	Substructure/Subregion	Cell Type	Subset of Marker Genes
Renal Corpuscle	Bowman's Capsule	Parietal epithelial cell	*CRB2*, CLDN1**
	Glomerulus	Podocyte	*NPHS2*, PODXL*, NPHS1**
		Capillary Endothelial Cell	*EHD3*, EMCN*, HECW2*, FLT1*, AQP1**
		Mesangial Cell	*POSTN*, PIEZO2*, ROBO1*, ITGA8**

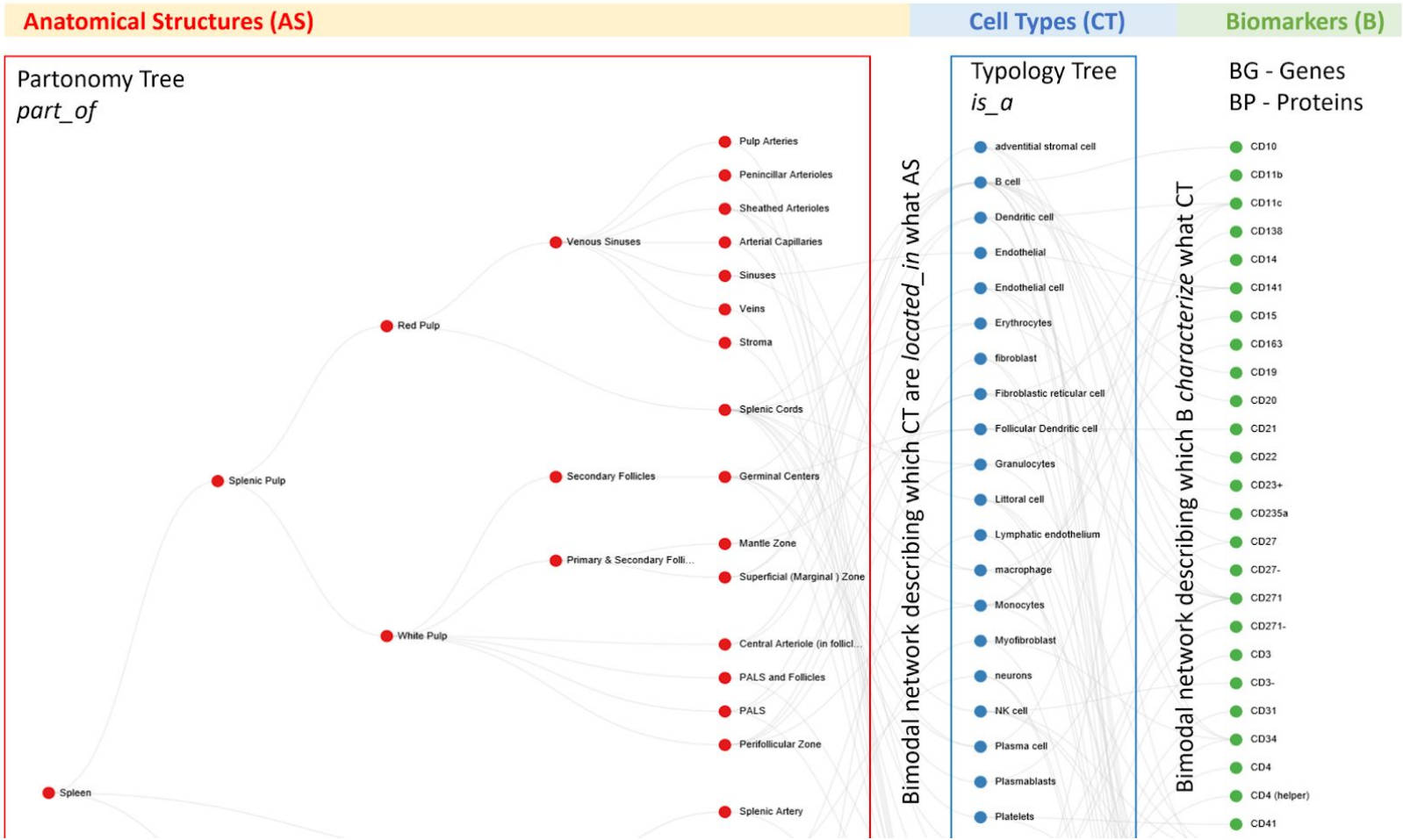
Partial ASCT+B Table from

- El-Achkar et al. A Multimodal and Integrated Approach to Interrogate Human Kidney Biopsies with Rigor and Reproducibility: The Kidney Precision Medicine Project. bioRxiv. 2019, Updated Aug 2020. doi:10.1101/828665

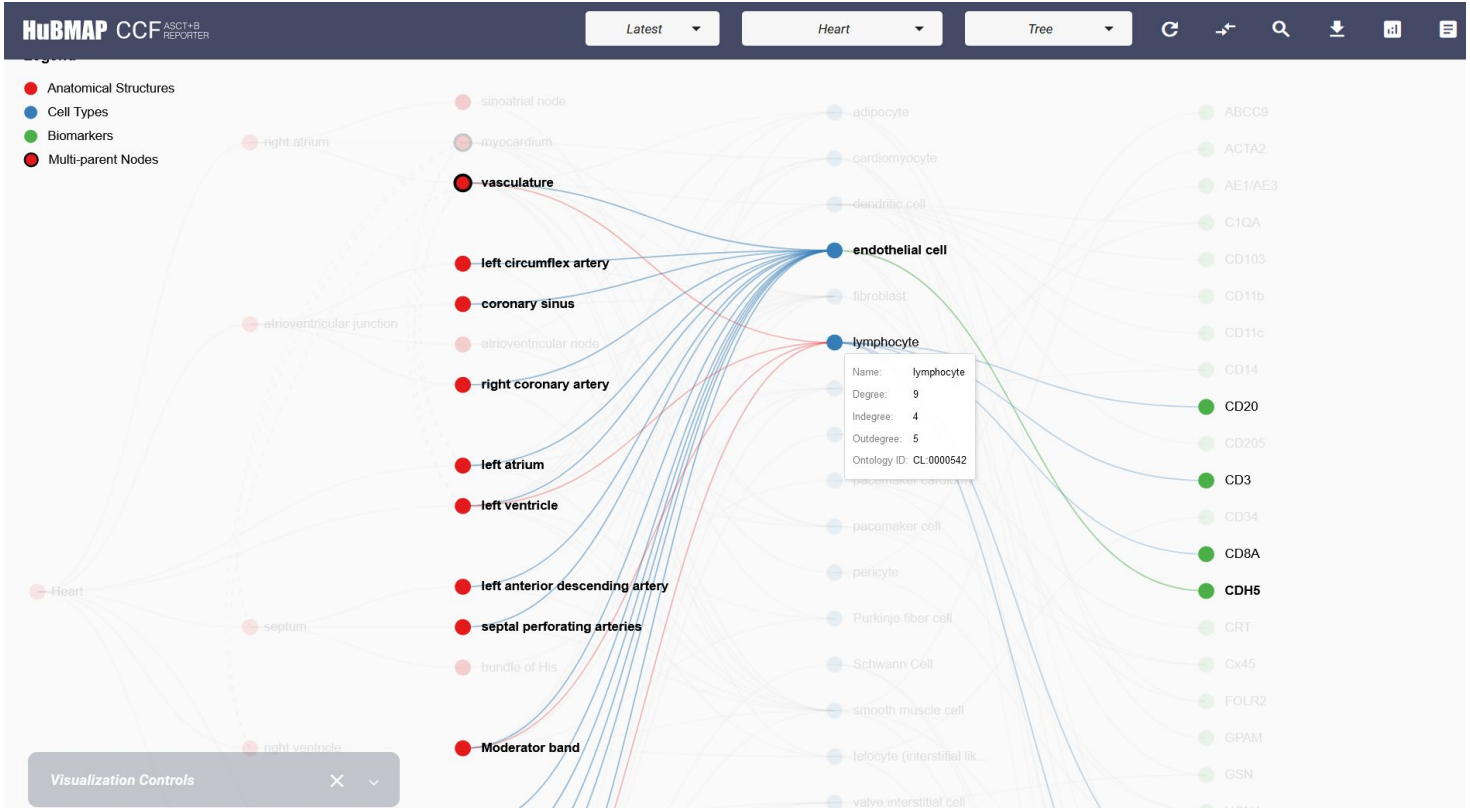
Table 3: Cell types and associated markers from KPMP Pilot 1 transcriptomic studies. Asterisk denotes genes detected by more than one technology. *Italics*, genes detected by a single technology.

Structure/Region	Sub structure/Sub region	Cell Type	Abbreviation	Subset of Marker Genes	Pertinent negatives/comments
Renal Corpuscle	Bowman's Capsule	Parietal epithelial cell	PEC	*CRB2*, CLDN1**	
	Glomerulus	Podocyte	POD	*NPHS2*, PODXL*, NPHS1**	
		Capillary Endothelial Cell	GC-EC	*EHD3*, EMCN*, HECW2*, FLT1*, AQP1**	
		Mesangial Cell	MC	*POSTN*, PIEZO2*, ROBO1*, ITGA8**	
Tubules	Proximal Tubule	Proximal Tubule Epithelial Cell (general)	PT	*CUBN*, LRP2*, SLC13A1*, ALDOB*, GATM**	
		Proximal Convoluted Tubule Epithelial Cell Segment 1	PT-S1	*SLC5A2*, SLC5A12**	There is overlap among the segments
		Proximal Tubule Epithelial Cell Segment 2	PT-S2	*SLC22A6**	
		Proximal Tubule Cell Epithelial Segment 3	PT-S3	*PDZK1IP1*, MT1G**	
	Loop of Henle, Thin Limb	Descending Thin Limb Cell (general)	DTL	*CRYAB*, VCAM1*, AQP1*, SPP1**	*CLDN10* low
		Ascending Thin Limb Cell (general)	ATL	*CRYAB*, TACSTD2*, CLDN3**	*AQP1* low to none
	Loop of Henle, Thick Limb	Thick Ascending Limb Cell (general)	TAL	*SLC12A1*, UMOD**	*SLC12A3* low to none
		Cortex-TAL cell	C-TAL	*SLC12A1*, UMOD**	
		Medulla-TAL cell	M-TAL	*SLC12A1*, UMOD**	
		TAL-Macula Densa cell	TAL-MD	*NOS1*, SLC12A1**	
	Distal Convolution	Distal Convoluted Tubule Cell (general)	DCT	*SLC12A3*, TRPM6**	
		DCT type 1 cell	DCT-1	*SLC12A3*, TRPM6*	*SLC8A1, HSD11B2* (low to none)
		DCT type 2 cell	DCT-2	*SLC12A3*, SLC8A1*, HSD11B2*	Has CNT and DCT signature
	Connecting Tubule	Connecting Tubule Cell (general)	CNT	*SLC8A1*, CALB1, TRPV5*	*SLC12A3* low to none. IC or PC without *SLC8A1* could be in the CNT structure
		CNT-Principal Cell	CNT-PC	*SLC8A1*, AQP2*, SCNN1G**	
		CNT-Intercalated Cell	CNT-IC	*SLC8A1*, CA2, ATP6VOD2**	
		CNT-IC-A cell	CNT-IC-A	*SLC8A1*, SLC4A1*, SLC26A7**	
		CNT-IC-B cell	CNT-IC-B	*SLC8A1*, SLC26A4*, SLC4A9**	
	Collecting Duct	Collecting duct (general) cell	CD	*GATA3**	*GATA3* may be in subpopulation of DCT, CNT and vSMC/P. SLC8A1, CALB1, TRPV5
		CD-PC (general)	CD-PC	*AQP2*, AQP3*, FXYD4*, SCNN1G*, GATA3**	
		C-CD-PC	C-CD-PC		
		M-CD-PC	M-CD-PC		
		Outer medulla-CD-PC	OM-CD-PC		
		Inner Medulla-CD cell	IM-CD	*AQP2*, SLC14A2*	
		Transitional PC-IC cell	tPC-IC	*FXYD4*, SLC4A9*/SLC26A7**	(low to none); Low to No *CALCA* and *KIT* in C-CD-IC-A. It may not be possible to assign IC or PC to CNT or CD structures without regional information of their source.
		CD-IC (general) cell	CD-IC	*CA2, ATP6VOD2**	
		CD-IC-A (general) cell	CD-IC-A	*SLC4A1, SLC26A7*, TMEM213**	
		C-CD-IC-A cell	C-CD-IC-A	*SLC26A7*, SLC4A1**	
		M-CD-IC-A cell	M-CD-IC-A	*SLC26A7*, SLC4A1, KIT*, CALCA*	
		CD-IC-B (general) cell	CD-IC-B	*SLC4A9*, SLC26A4**	
		C-CD-IC-B cell	C-CD-IC-B		
		M-CD-IC-B cell	M-CD-IC-B		
Vessels	Endothelial Cells (non-glomerular)	Endothelial Cell (general)	EC	*EMCN*, PECAM1*, FLT1**	
		EC-Afferent/Efferent Arteriole	EC-AEA	*SERPINE2*, TM4SF1**	likely *PALMD*
		EC-Peritubular capillaries	EC-PTC	*PLVAP**	
		EC-Descending Vasa Recta	EC-DVR	*TM4SF1*, PALMD*	
		EC-Ascending Vasa Recta	EC-AVR	*DNASEIL3**	low to none
		EC-Lymphatics	EC-LYM	*MMRN1*, PROX1*	
Structure/Region	**Sub structure/Sub region**	**Cell Type**	**Abbreviation**	**Subset of Marker Genes**	**Pertinent negatives/comments**
Interstitium	Stroma (non-glomerular)	Vascular Smooth Muscle/Pericyte (general)	vSMC/P	*TAGLN*, ACTA2*, MYH11*, NTRK3, MCAM*	
		vSMC/P-Renin	vSMC/P-REN	*REN*	
		Fibroblast	FIB	*DCN*, ZEB2, C7, LUM*	
	Immune	Macrophages-Resident	MAC-R	*CD163*, IL7R**	
		Macrophage	MAC	*S100A9*	
		Natural Killer Cell	NKC	*NKG7*	
		Dendritic Cell	DC	*APOE*	
		Monocyte	MON	*C1QA, HLA-DRA*	
		T lymphocyte (general)	T	*CD3*	
		T Cytotoxic	T-CYT	*GZMA*	
		B lymphocyte	B	*IGJ*	

El-Achkar et al. A Multimodal and Integrated Approach to Interrogate Human Kidney Biopsies with Rigor and Reproducibility: The Kidney Precision Medicine Project. bioRxiv. 2019, Updated Aug 2020. doi:10.1101/828665


Anatomical Structures (AS)
Cell Types (CT)
Biomarkers (B)
Partonomy Tree
part_of
Spleen
Splenic Pulp
Red Pulp
Venous Sinuses
Pulp Arteries
Penicillar Arterioles
Sheathed Arterioles
Arterial Capillaries
Sinuses
Veins
Stroma
Splenic Cords
Secondary Follicles
Germinal Centers
Primary & Secondary Folli...
Mantle Zone
Superficial (Marginal) Zone
White Pulp
Central Arteriole (in follicl...
PALS and Follicles
PALS
Perifollicular Zone
Splenic Artery
Bimodal network describing which CT are located_in what AS
Typology Tree
is_a
adventitial stromal cell
B cell
Dendritic cell
Endothelial
Endothelial cell
Erythrocytes
fibroblast
Fibroblastic reticular cell
Follicular Dendritic cell
Granulocytes
Littoral cell
Lymphatic endothelium
macrophage
Monocytes
Myofibroblast
neurons
NK cell
Plasma cell
Plasmablasts
Platelets
BG - Genes
BP - Proteins
Bimodal network describing which B characterize what CT
CD10
CD11b
CD11c
CD138
CD14
CD141
CD15
CD163
CD19
CD20
CD21
CD22
CD23+
CD235a
CD27
CD27-
CD271
CD271-
CD3
CD3-
CD31
CD34
CD4
CD4 (helper)
CD41

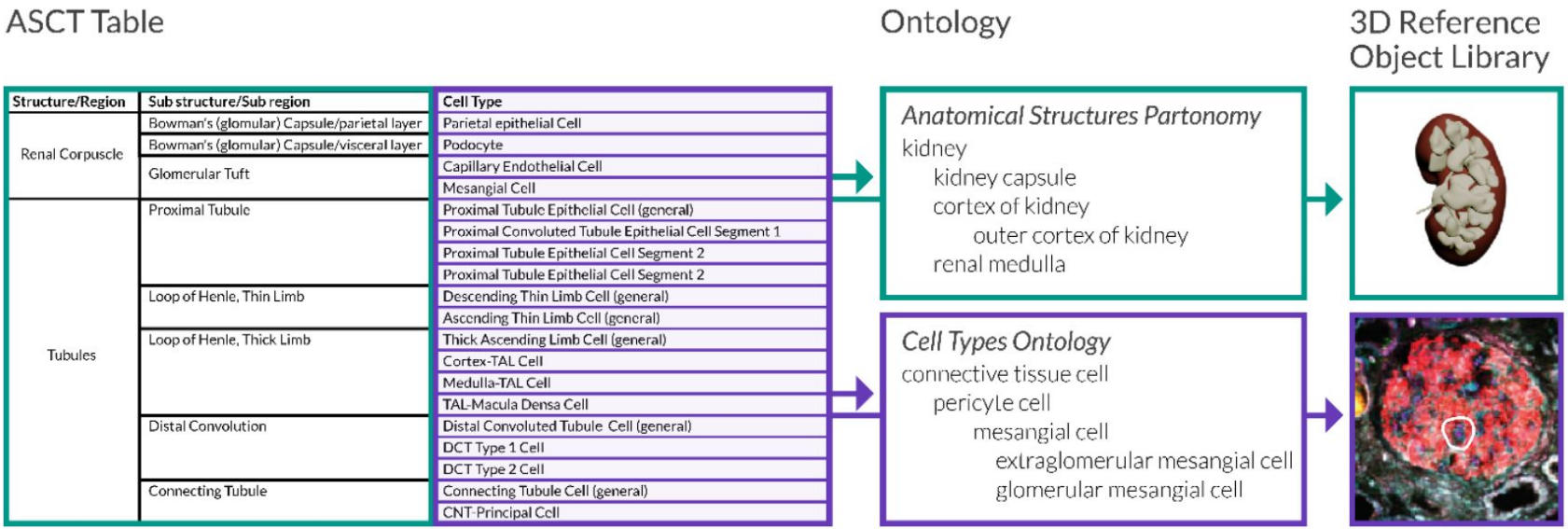
CCF ASCT+B Reporter UI

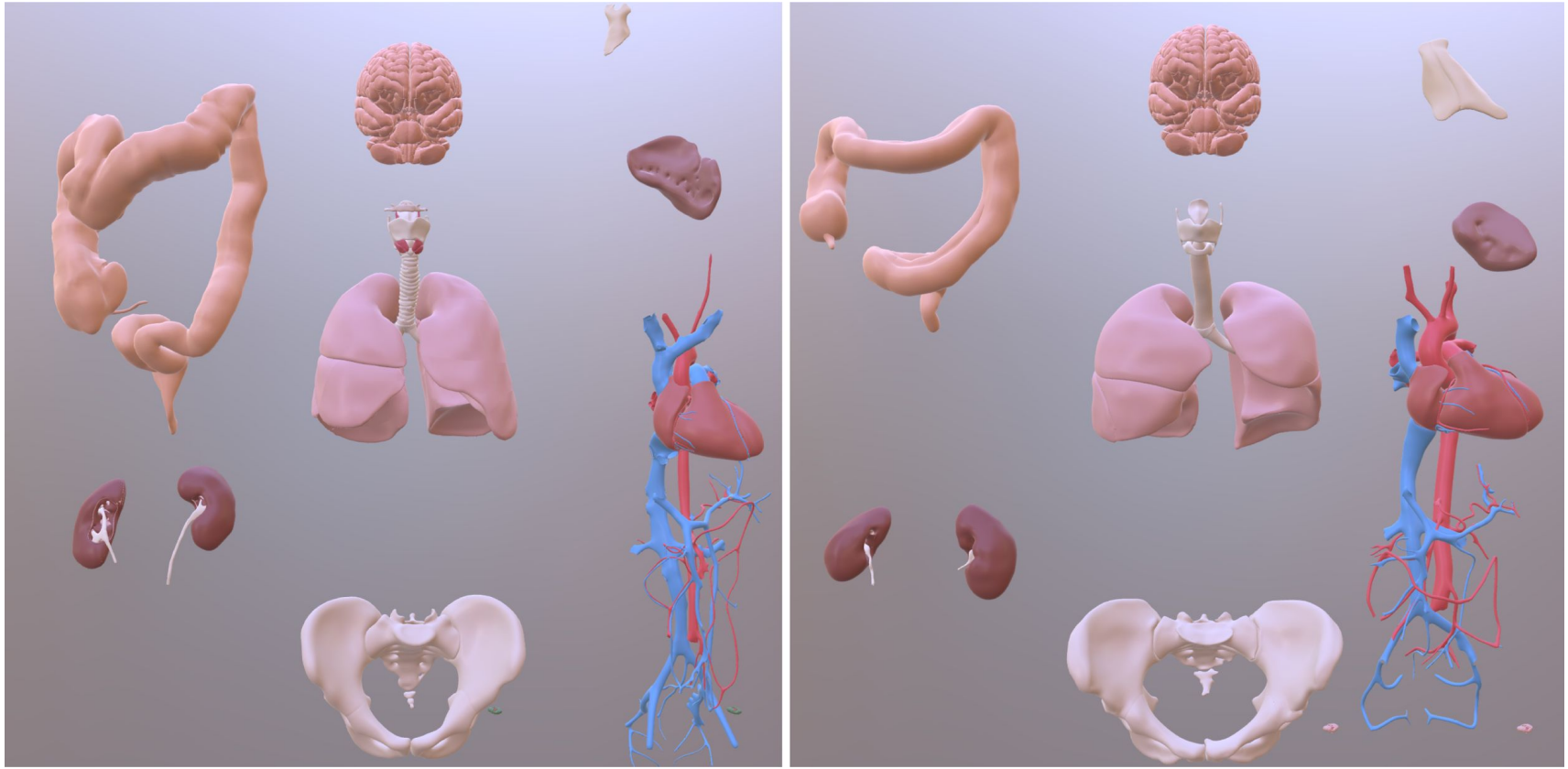


https://hubmapconsortium.github.io/ccf-asct-reporter/

ASCT+B Tables

Anatomical Structures (AS), Cell Types (CT), and Biomarkers (B) or ASCT+B tables aim to capture the partonomy of anatomical structures, cell types, and major biomarkers (e.g., gene, protein, lipid or metabolic markers).





Overview of CCF 3D Reference Models

ASCT+B Table Working Group

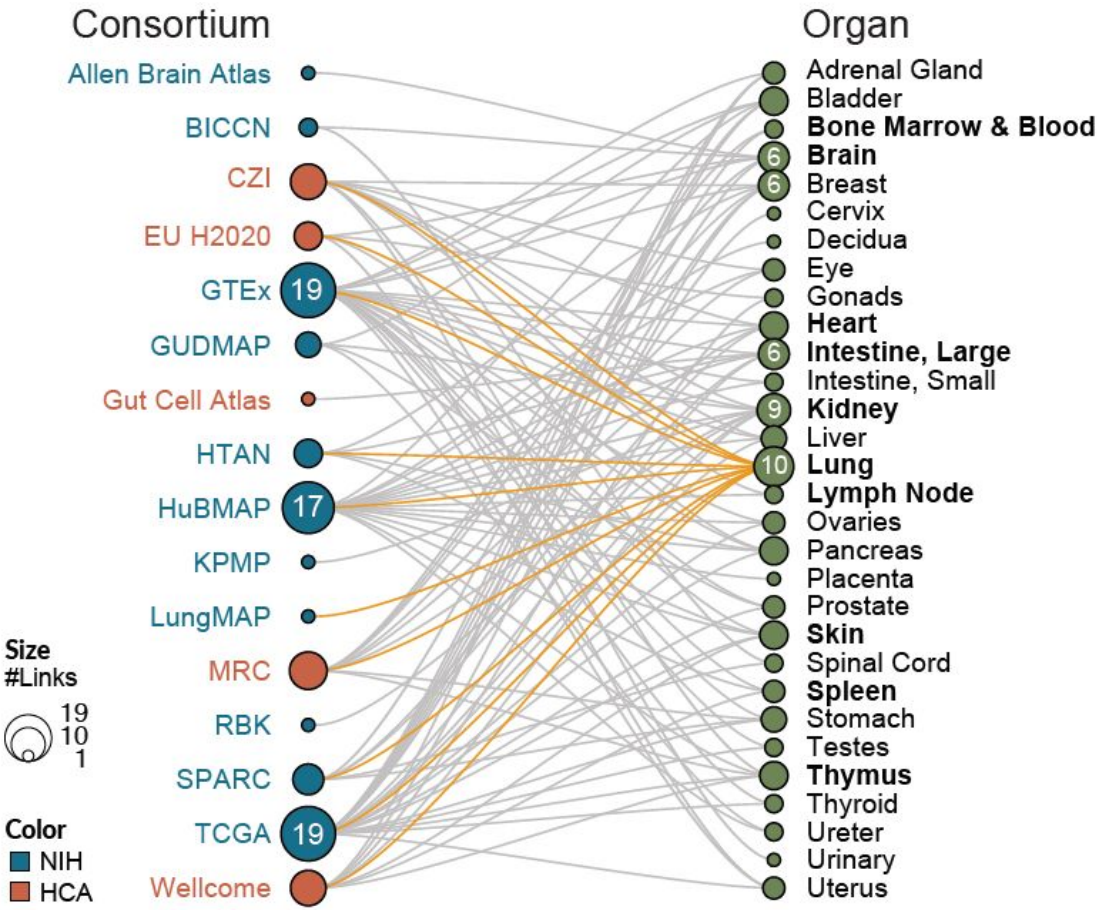
Lead by Katy Börner and Jim Gee; Ellen M Quardokus serves as Knowledge Manager

Meetings take place monthly to review and approve tables, formalize and unify table design language, discuss and expand table usage, see WG Charter.

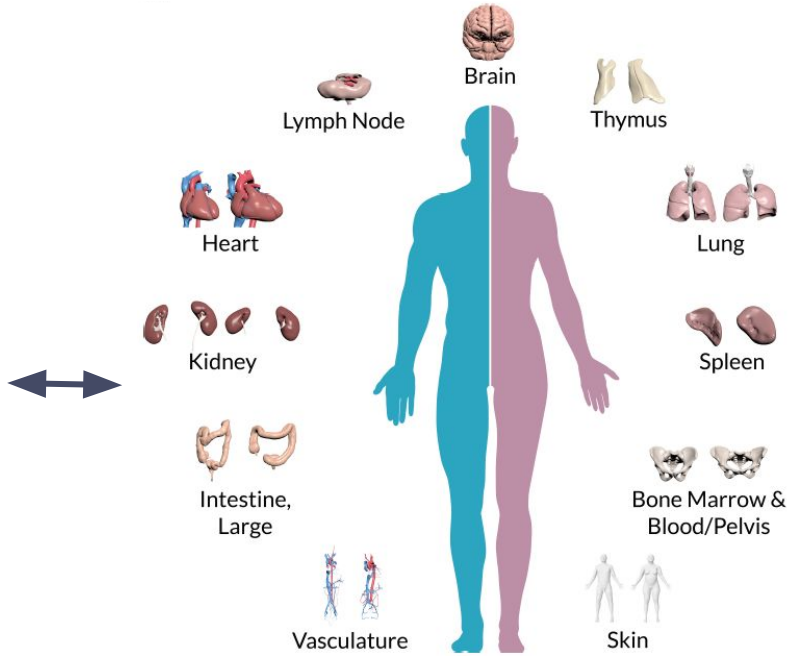
Upcoming meetings in **2021:** May 5, June 2, 11a-noon ET.
Please register to receive invites and updates.

	HuBMAP	RBK	KPMP	SPARC	LungMAP	HTAN	HCA	GUDMAP	Gut Cell Atlas	BICCN	Allen Brain	TCGA	Wellcome	MRC	H2020	GTEx	Total
Kidney	1	1	1	0	0	0	1	1	0	0	0	1	1	1	0	1	9
Liver	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	1	3
Spleen	1	0	0	0	0	0	1	0	0	0	0	0	1	0	0	1	4
Heart	1	0	0	1	0	0	1	0	0	0	0	0	0	0	0	1	4
Lung	1	0	0	1	1	1	1	0	0	0	0	1	1	1	1	1	10
L intestine/Colon	1	0	0	1	0	1	1	0	1	0	0	1	0	0	0	1	7
S intestine	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2
Bladder	1	0	0	1	0	0	0	1	0	0	0	1	0	0	0	1	5
Ureters	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	2
Thymus	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	2
Lymph nodes	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	2
mediastinal lymph node	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Eye	1	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	3
Brain	0	0	0	0	0	0	1	0	0	1	1	1	0	0	1	1	6
Brain stem	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
Cerebellum	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	1	3
Spinal cord	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	2
Pancreas	0	0	0	0	0	1	1	0	0	0	0	1	0	0	1	1	5
Breast	0	0	0	0	0	1	1	0	0	0	0	1	1	0	0	1	5
Skin	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	1	3
Pediatric systems	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	2
Ovaries	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	2
Testes	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	2
Cervix	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
Uterus	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	5
Blood	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	2
Bone	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Placenta	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Decidua	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Embryo	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
esophagus	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	1	3
hematopoietic system	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	2
immune system bulk	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
Stomach	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	1	3
Thyroid	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	2
Prostate	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	1	3
Adrenal gland	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	1	3
Totals	11	1	1	7	1	6	21	4	1	2	2	20	7	5	4	21	114

Table compiled for, during, and after the NIH-HCA Joint Meeting in March 2020, https://hubmapconsortium.org/nihhca2020


Consortium
Allen Brain Atlas
BICCN
CZI
EU H2020
GTEx
19
GUDMAP
Gut Cell Atlas
HTAN
HuBMAP
17
KPMP
LungMAP
MRC
RBK
SPARC
TCGA
19
Wellcome
Size
#Links
19
10
1
Color
NIH
HCA
Organ
Adrenal Gland
Bladder
Bone Marrow & Blood
Brain
6
Breast
6
Cervix
Decidua
Eye
Gonads
Heart
Intestine, Large
6
Intestine, Small
Kidney
9
Liver
Lung
10
Lymph Node
Ovaries
Pancreas
Placenta
Prostate
Skin
Spinal Cord
Spleen
Stomach
Testes
Thymus
Thyroid
Ureter
Urinary
Uterus

Organ	#AS	#CT	#B Total	#BG	#BP	#AS-AS	#AS-CT	#CT-B
Bone Marrow & Blood/Pelvis	3	46	327	201	126	2	70	710
Brain	187	127	254	254	0	187	127	330
Heart	52	25	48	48	0	61	164	78
Intestine, Large	65	69	94	88	6	389	1,361	197
Kidney	68	63	152	152	0	67	59	257
Lung	161	92	176	172	4	1,633	12,094	286
Lymph Node	41	49	266	108	158	62	135	544
Skin	16	42	70	0	70	17	19	105
Spleen	46	66	255	80	145	68	172	414
Thymus	25	41	511	388	123	38	180	657
Vasculature	870	2	1	1	0	869	606	2
Totals:	**1,534**	**622**	**2,154**	**1,492**	**632**	**3,393**	**14,987**	**3,580**



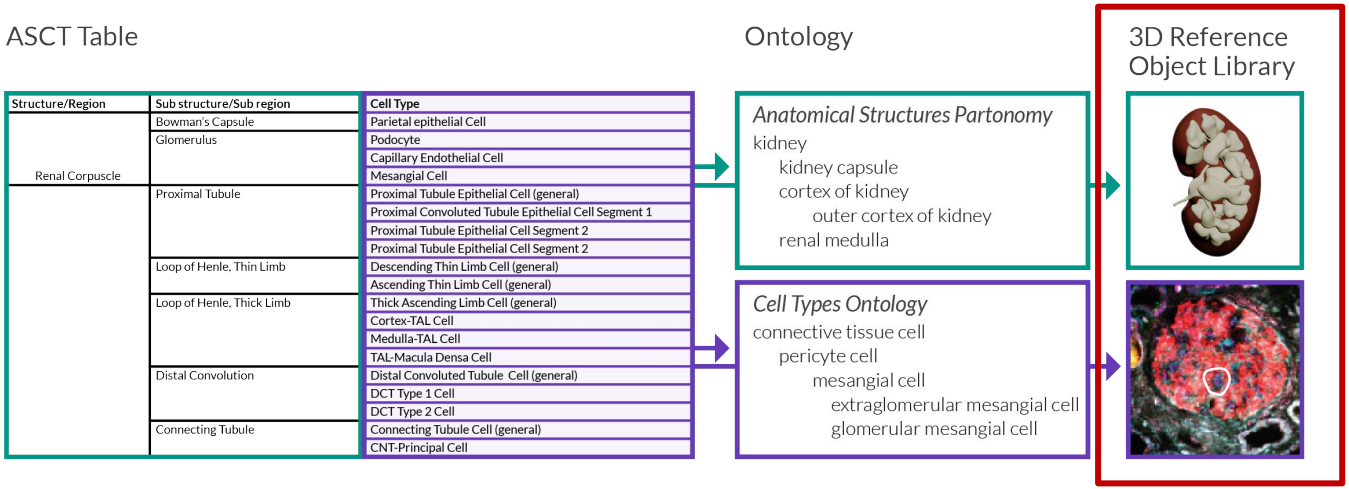
https://hubmapconsortium.github.io/ccf/pages/ccf-anatomical-structures.html

https://hubmapconsortium.github.io/ccf/pages/ccf-3d-reference-library.html (NLM VH organs)
https://community.brain-map.org/t/allen-human-reference-atlas-3d-2020-new/ (brain)
https://www3.cs.stonybrook.edu/~ari/ (male colon)

CCF Registration User Interface (RUI)

ASCT+B Table Usage

ASCT+B tables guide **CCF Ontology** and **3D Reference Object Library** design that semantically name and spatially place tissue data from different donors into one CCF (i.e., mapping).



Tissue blocks are registered into the CCF using the Registration User Interface (RUI), and they can be explored via the Exploration User Interface (EUI).

Document the tissue extraction site by registering tissue blocks within a 3D reference organ.

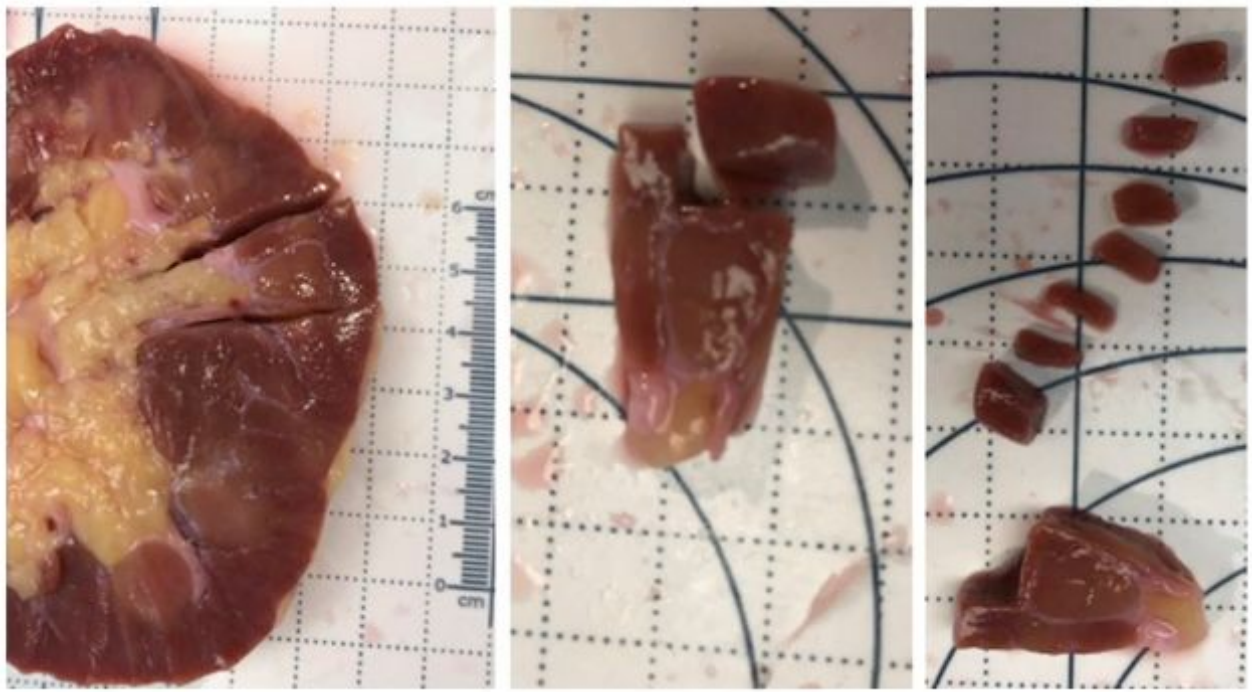
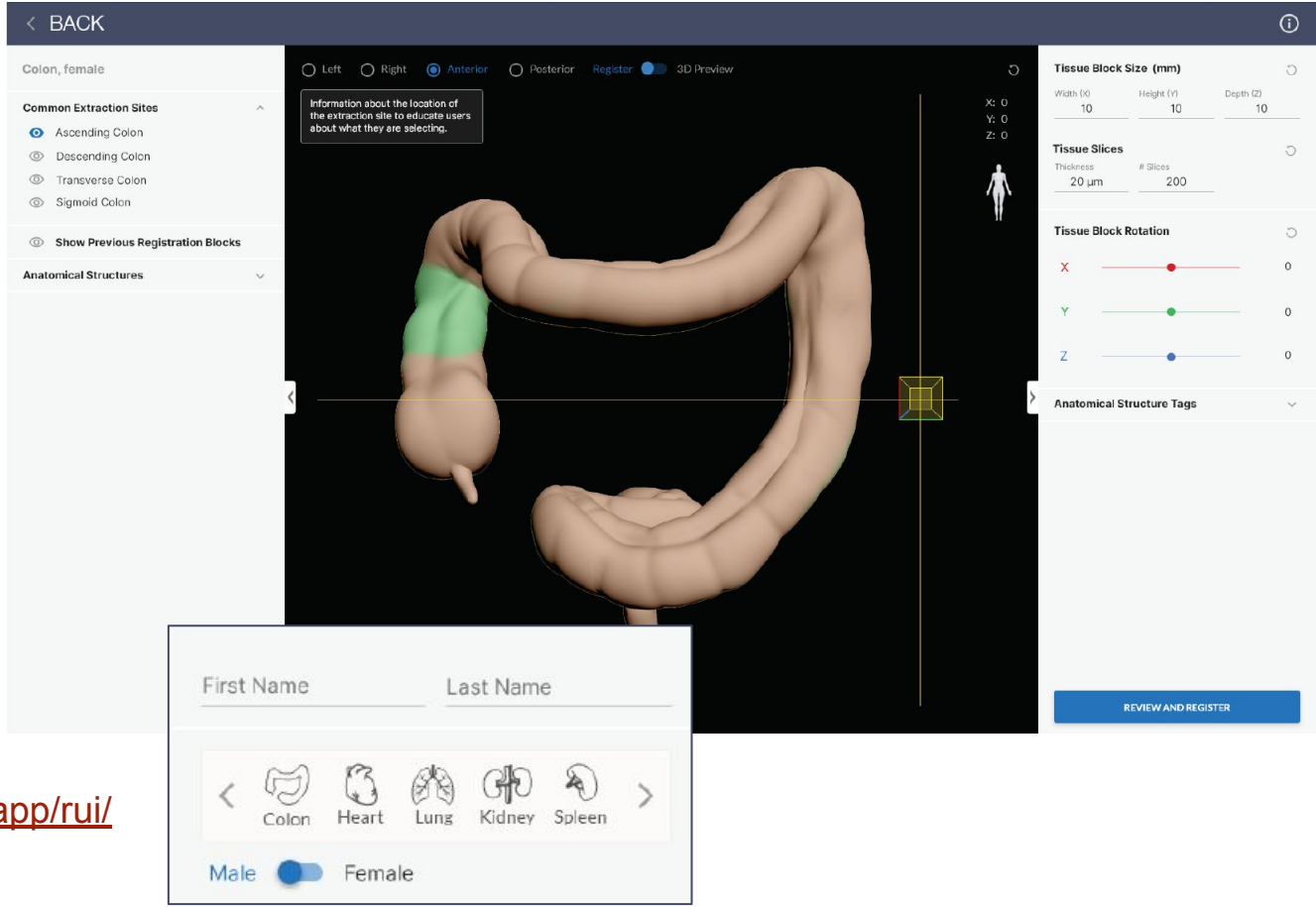


Image provided by Sanjay Jain, TMC-UCSD

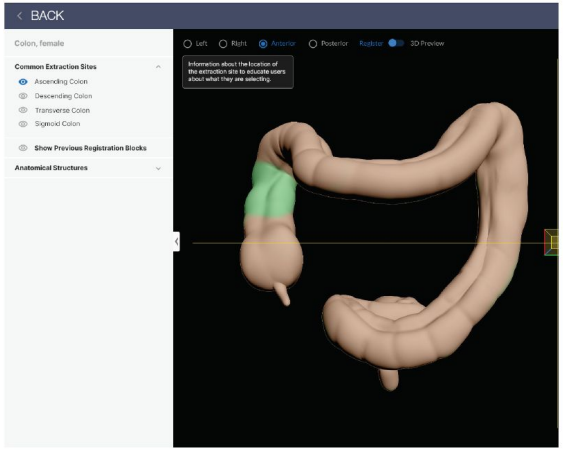
CCF Registration User Interface (RUI) v1.0.0

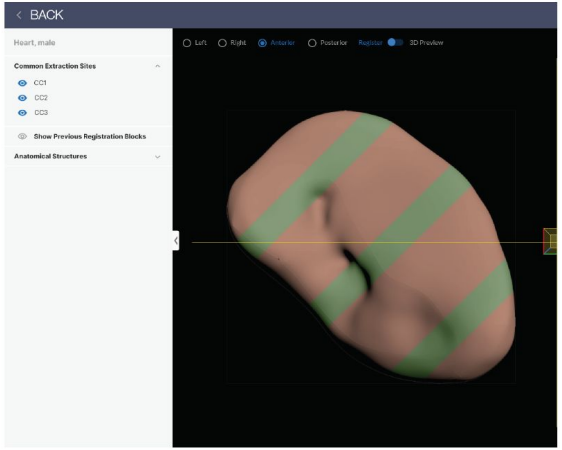
New Features:

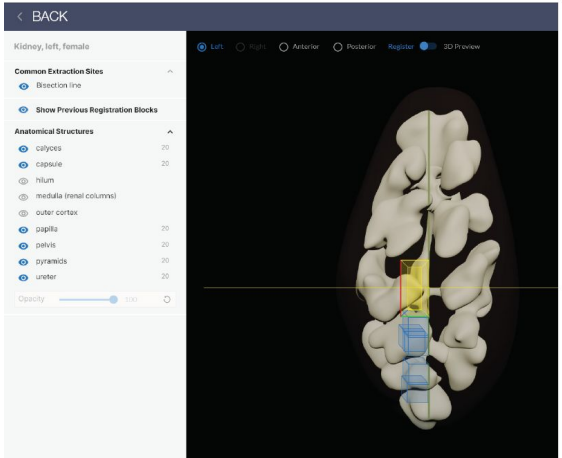
- Organ carousel with 4 reference organs
- Support for tissue extraction sites
- Expanded ontology
- Semantic annotation via collision detection & manual annotation
- Support for non-HuBMAP usage

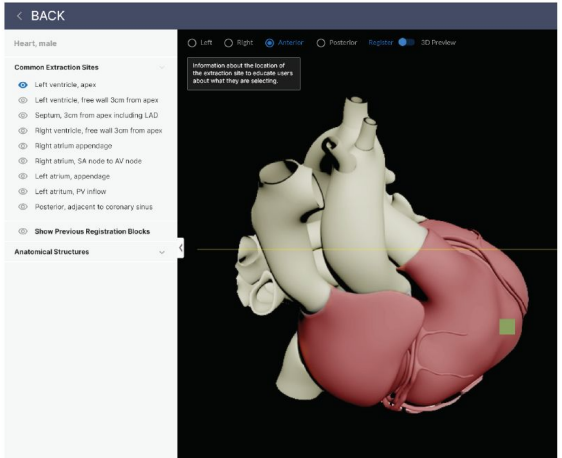


https://hubmap-ccf-ui.netlify.app/rui/









Kidney

- Bisection Line

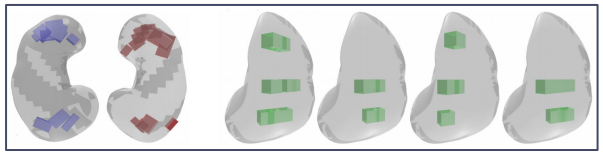
Spleen

- CC1
- CC2
- CC3

Colon

- Ascending Colon
- Descending Colon
- Transverse Colon
- Sigmoid Colon

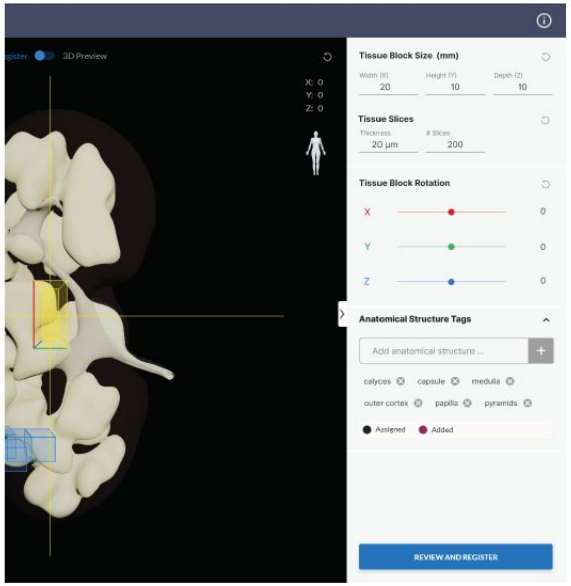
Heart	Extraction Site Mapping
Left atrium, appendage	7
Left atrium, PV inflow	8
Left ventricle, apex	1
Left ventricle, free wall 3cm from apex	2
Septum, 3cm from apex including LAD	3
Posterior, adjacent to coronary sinus	9
Right atrium appendage	5
Right atrium, AV (atrioventricular) node	6a
Right atrium, SA (sinoatrial) node	6b
Right ventricle, free wall 3cm from apex	4



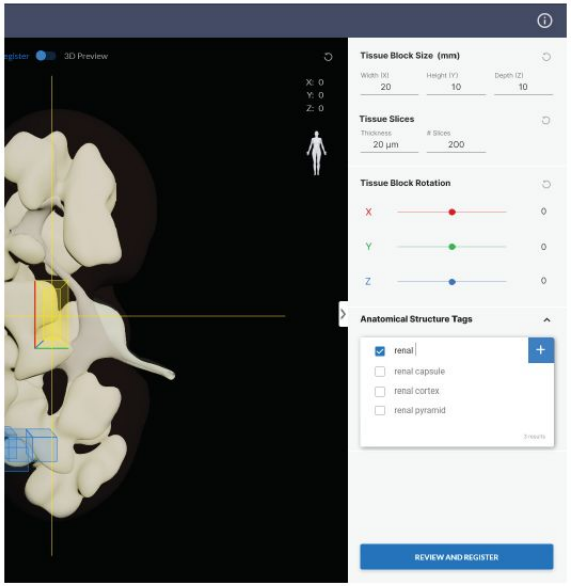
For the first HuBMAP portal release, 48 tissue blocks were registered.

CCF Registration User Interface (RUI) v1.0.0 cont.

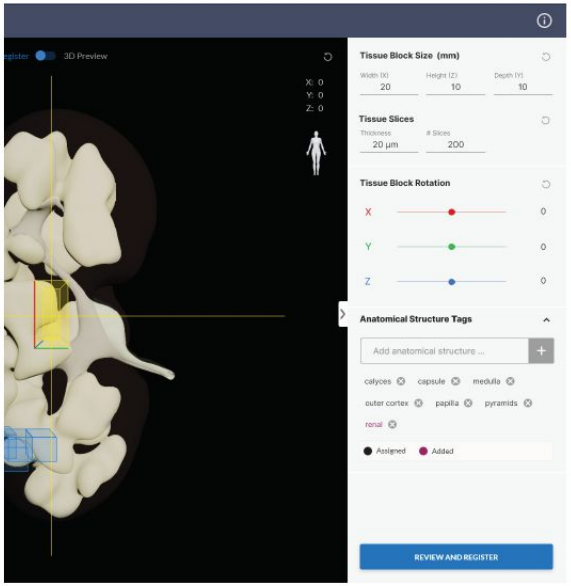
Collision when Tissue Block hits Reference Organ



Tag Search behavior



Custom tag added to list

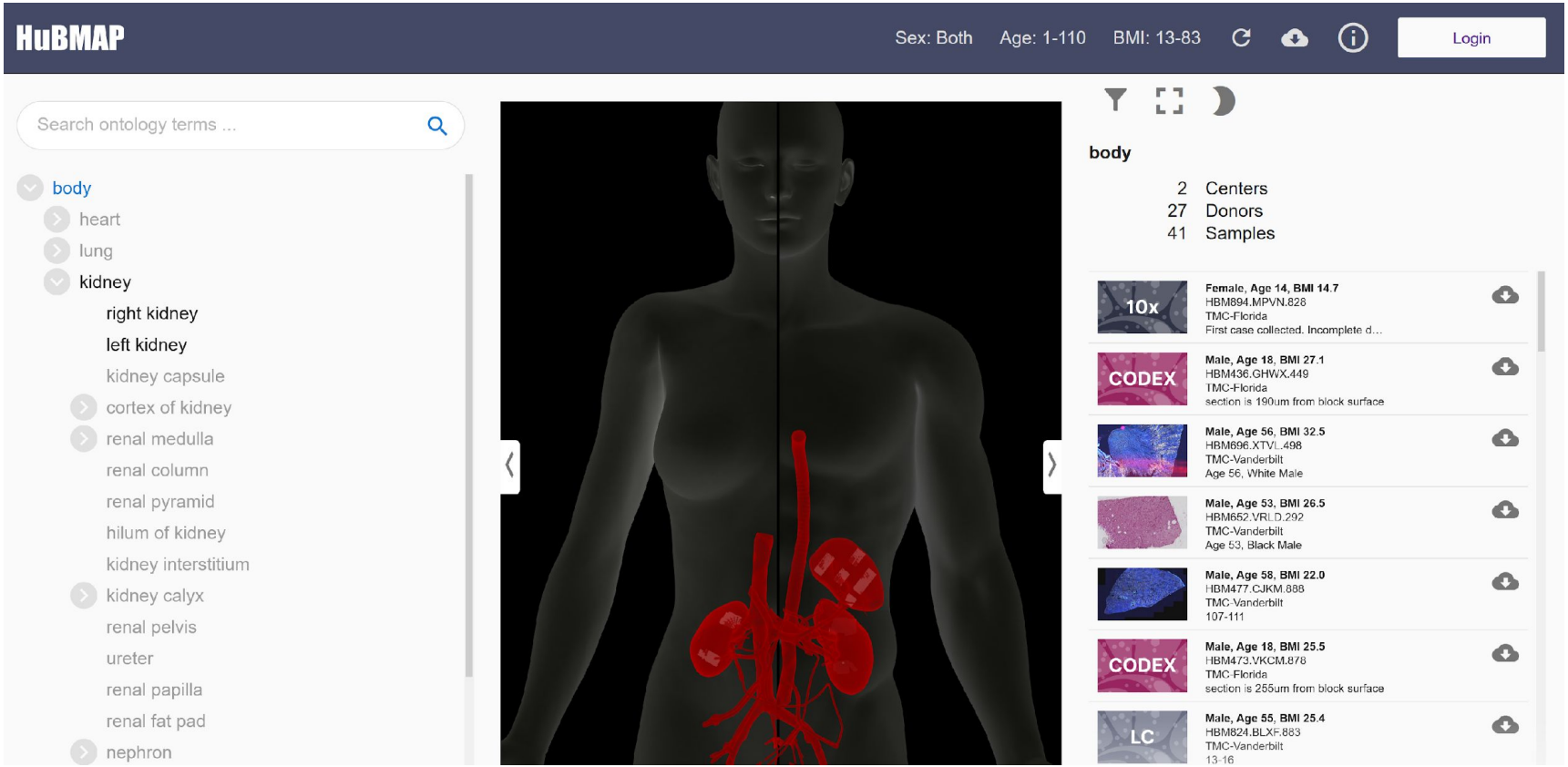


CCF Registration User Interface (RUI)

https://hubmapconsortium.github.io/ccf-ui/rui/

CCF Exploration User Interface (EUI)

CCF Exploration User Interface (EUI)



https://portal.hubmapconsortium.org/ccf-eui

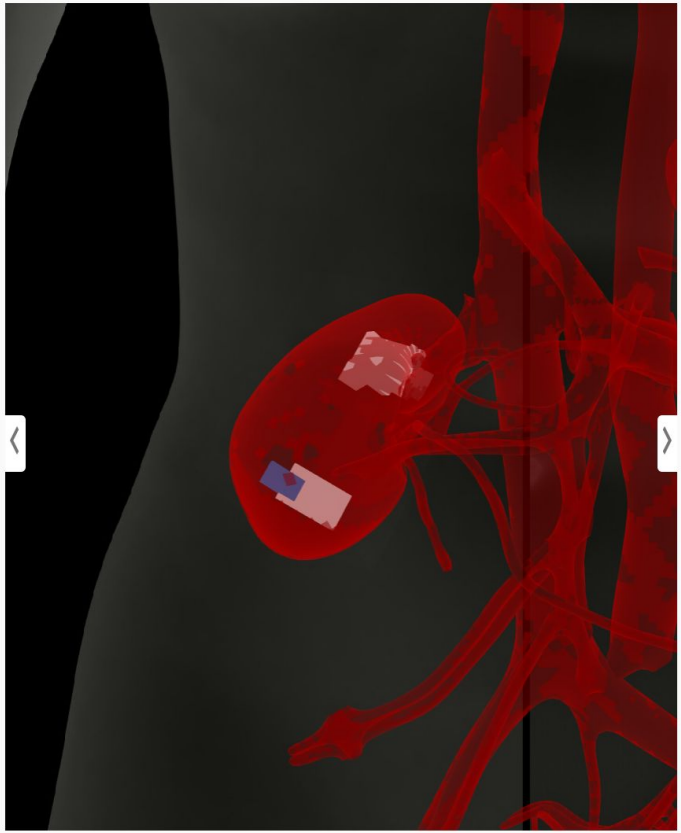
HuBMAP

Sex: Both Age: 1-110 BMI: 13-83

Logout

Search ontology terms ...

- body
  - heart
  - lung
  - kidney
    - right kidney
    - left kidney
    - kidney capsule
    - cortex of kidney
    - renal medulla
    - renal column
    - renal pyramid
    - hilum of kidney
    - kidney interstitium
    - kidney calyx
      - major calyx
      - minor calyx
    - renal pelvis
    - ureter
    - renal papilla
    - renal fat pad
  - nephron
  - spleen
  - colon

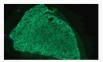


body

1 Centers
9 Donors
40 Samples

Male, Age 55, BMI 25.4
HBM695.RTLJ.484
TMC-Vanderbilt
13-16

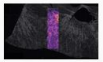
Male, Age 21, BMI 21.8
HBM634.MMGK.572
TMC-Vanderbilt
Age 21 , White Male, Trauma Patient



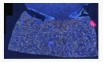
Female, Age 44, BMI 28.0
HBM457.NNQN.252
TMC-Vanderbilt
Age 44, white female.

Female, Age 44, BMI 28.0
HBM465.VKHL.532
TMC-Vanderbilt
Age 44, white female.

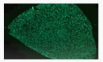
Male, Age 21, BMI 21.8
HBM693.HFFJ.752
TMC-Vanderbilt
Age 21 , White Male, Trauma Patient



Female, Age 58, BMI 23.0
HBM536.LDTZ.757
TMC-Vanderbilt
Age 58, White Female

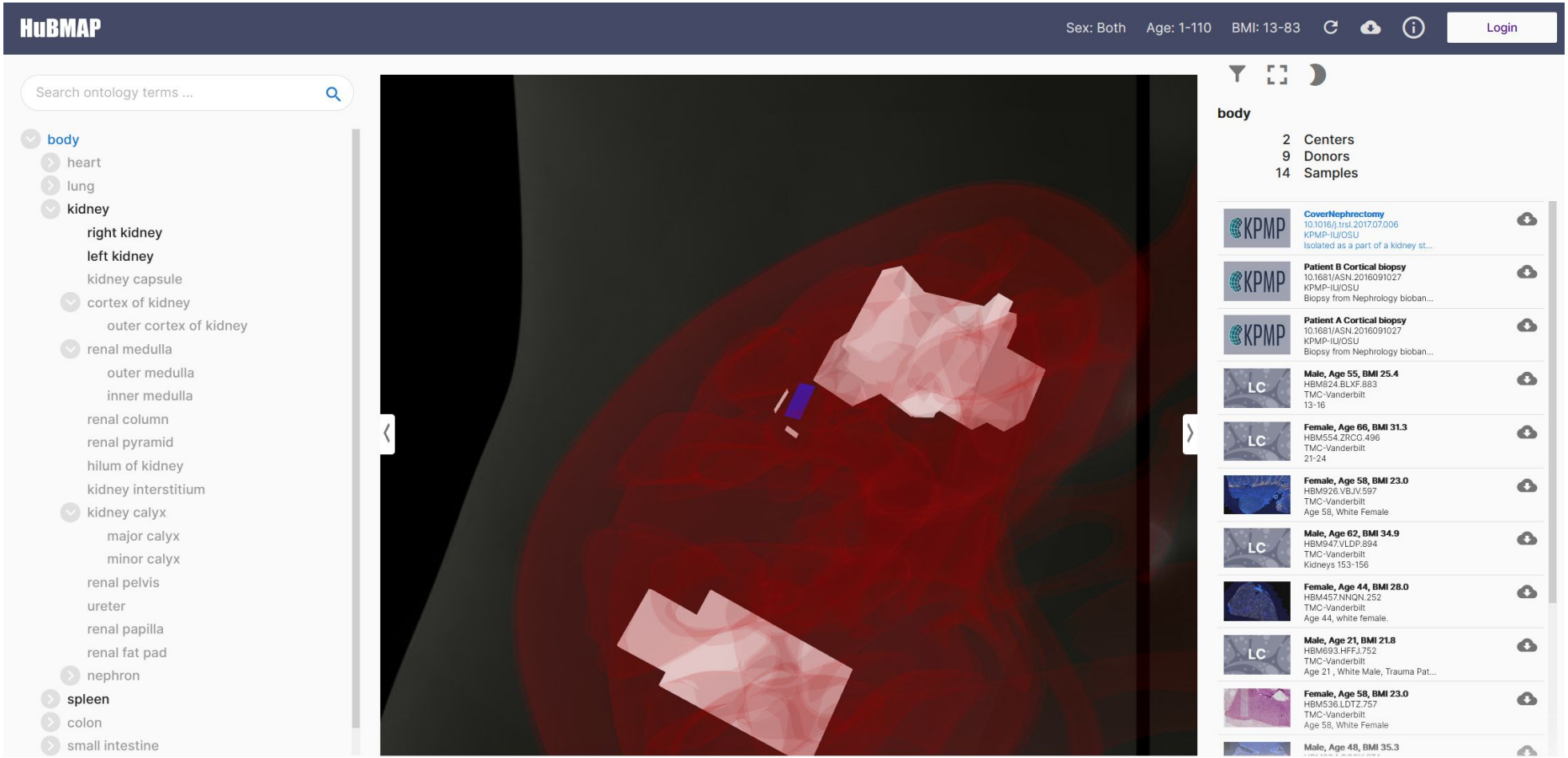


Male, Age 48, BMI 35.3
HBM334.GCCX.874
TMC-Vanderbilt
Age 48, White Male

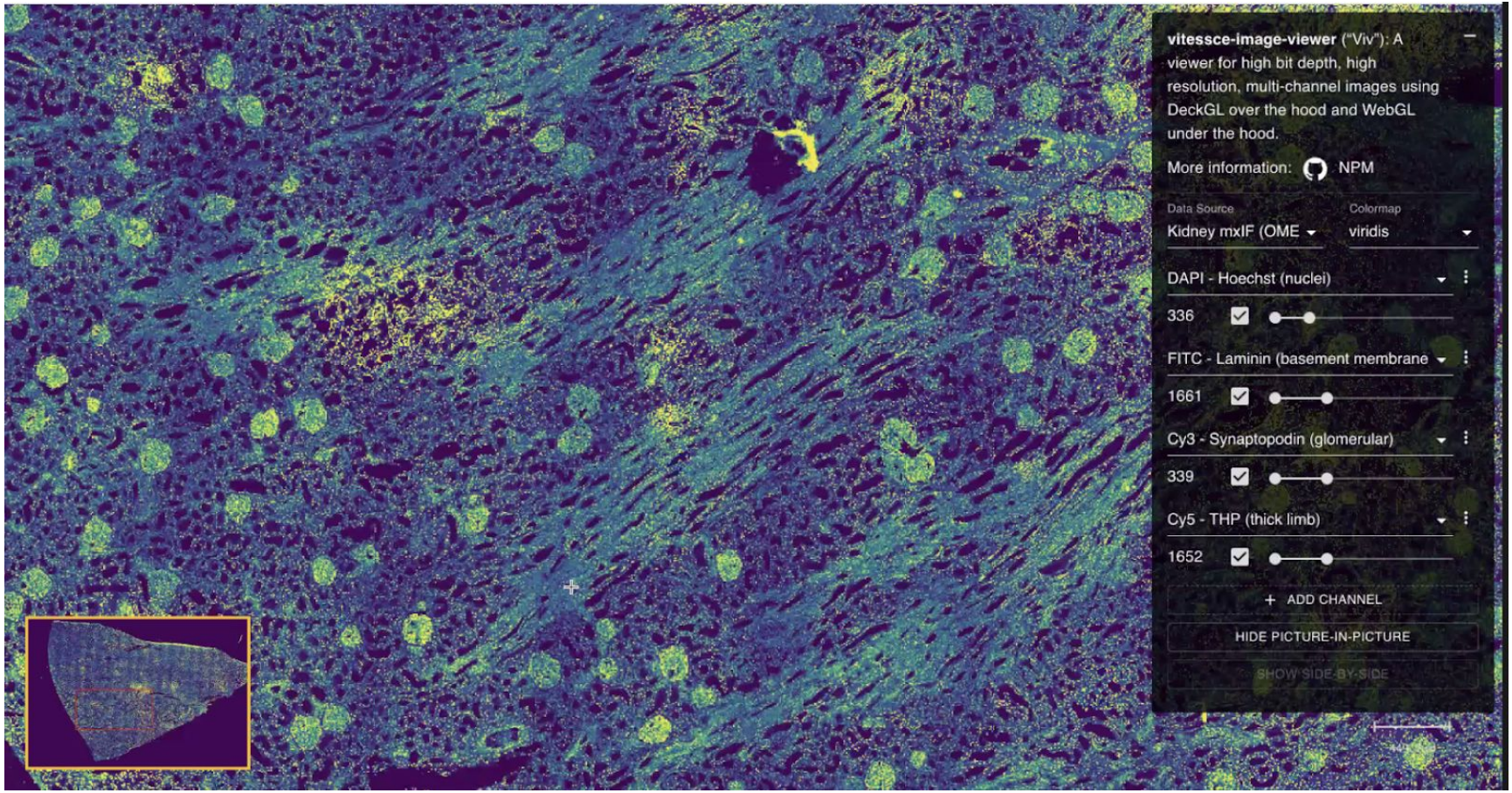


Male, Age 31, BMI 32.6
HBM776.PKJF.786
TMC-Vanderbilt
Age 21, White Male

Female, Age 66, BMI 31.3
HBM284.TRCV.726



Register your data via https://hubmap-ccf-ui.netlify.app/rui/ so it can be spatially/semantically explored in EUI.



http://gehlenborglab.org/research/projects/vitessce/

DAY TWO: 15 APRIL 2021

16:00 - 16:30

Interactive Session: Demo of HuBMAP Tools

Presentation 1: Cellar: Interactive Single Cell Data Annotation Tool

JUN DING, Assistant Professor, Department of Medicine, **McGill University**

Presentation 2: Vitessce: A Framework For Integrative Visualization Of Multi-Modal Single-Cell Data

MARK S. KELLER, PhD Program in Bioinformatics and Integrative Genomics, Division of Medical Sciences, **Harvard Medical School**

Presentation 3: CCF Tissue Registration User Interface (RUI)

ANDREAS BUECKLE, PhD Program in Information Science, Luddy School of Informatics, Computing, and Engineering, **Indiana University**

Visible Human MOOC (VHMOOC)

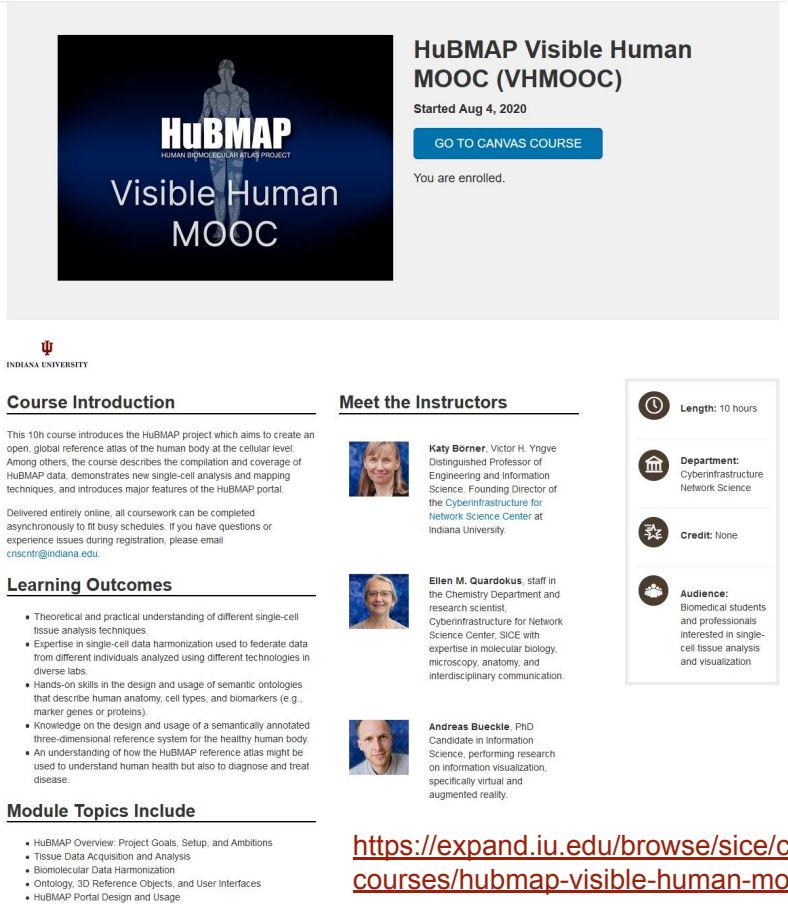
VH Massive Open Online Course (VHMOOC)

Goals

- Communicate tissue data acquisition and analysis,
- Demonstrate single-cell analysis and CCF mapping techniques, and
- Introduce major features of the HuBMAP portal.

Learning modules come with

- Videos (incl. interviews, tool demos)
- Hands-on exercises
- Self-quizzes



https://expand.iu.edu/browse/sice/cns/courses/hubmap-visible-human-mooc

Acknowledgements

HuBMAP Consortium (https://hubmapconsortium.org)

Thanks go to all the **patients** that agreed to volunteer healthy tissue and open use of their data.

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KIDNEY PRECISION MEDICINE PROJECT
kpmp.org

NSF

TMCs

Jeffrey Spraggins
TMC-Vanderbilt
Vanderbilt University

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Washington University, St. Louis

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Marda Jorgensen
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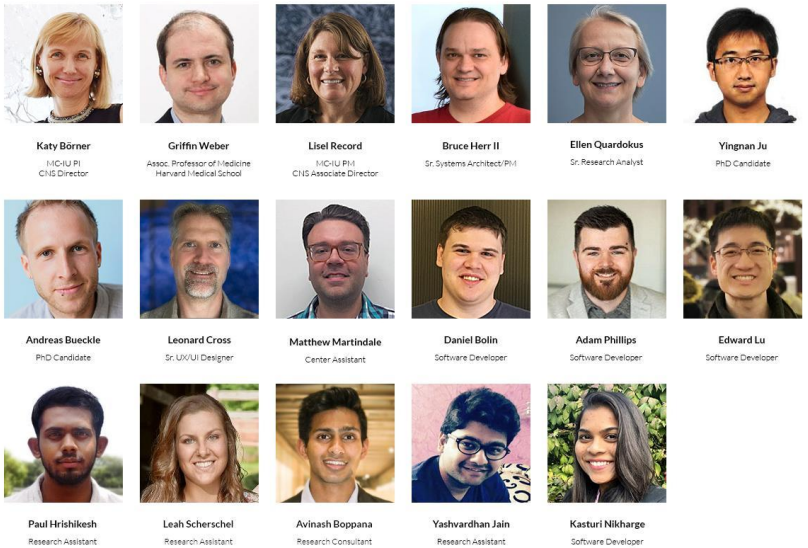
University of Florida

3D Models

Kristen Browne
Medical Imaging and 3D Modeling Specialist
NIAID

MC-IU HIVE Team



Spatial Biology Europe: *ONLINE*

LIVE & INTERACTIVE CONTENT SCHEDULE

Please see the full programme for the conference below. Where possible, sessions will be made available OnDemand after the scheduled time slot.

Please note: Access to OnDemand sessions will only be available to delegates who purchase a full access pass

DAY TWO: 15 APRIL 2021

PROFILING & IMAGING

Panel Discussion: Human Reference Atlas

Moderator: KATY BÖRNER, Victor H. Yngve Distinguished Professor of Engineering and Information Science, **Indiana University**

15:30 - 16:00

Panellists:

JAMES GEE, Associate Professor of Radiologic Science in Radiology. Director, Penn Image Computing and Science Laboratory, Department of Radiology, Perelman School of Medicine, **University of Pennsylvania**

XUEGONG ZHANG, Professor of Pattern Recognition and Bioinformatics, Director, Bioinformatics Division, TNLIST (Tsinghua National Laboratory for Information Science &Technology), Department of Automation, **Tsinghua University**

AMY BERNARD, Director, Science & Technology Strategy, **Allen Institute**

BERNARD DE BONO, Principal Investigator, Associate Professor, **University of Auckland**

Q&A