

GUDMAP: GenitoUrinary Development Molecular Anatomy Project

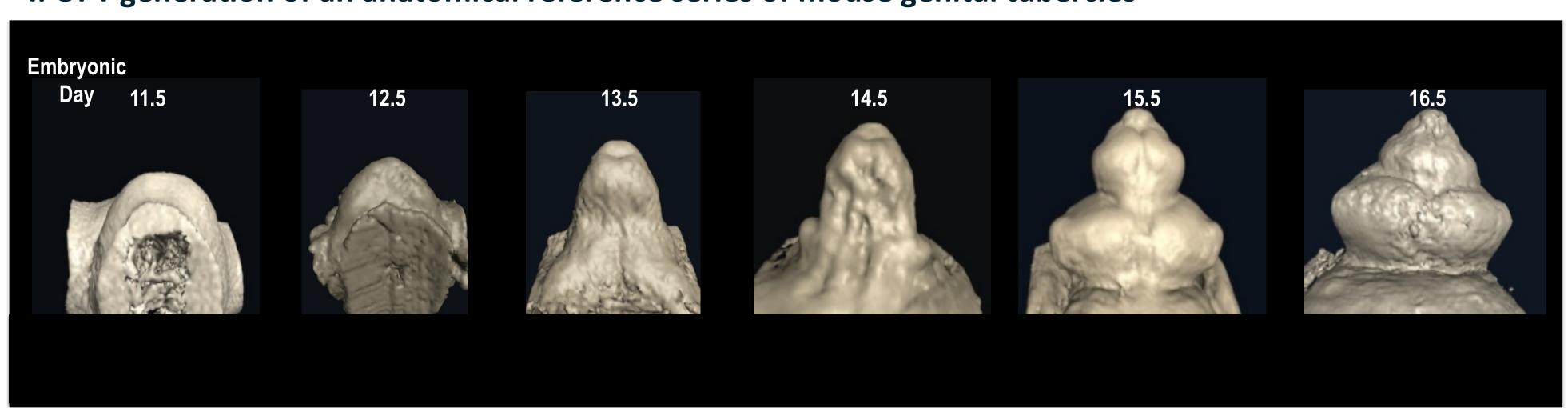
is a consortium of laboratories working to provide the scientific and medical community with tools to facilitate research. (http://www.gudmap.org/)

GUDMAP Database and Website developed and maintained by Duncan Davidson, Richard Baldock, Simon Harding, Xingjun Pi, Bernard Haggarty, Yogmatee Roochun AND Jamie Davis, Jane Brennan, Jane Armstrong, Sue Lloyd-MacGilp, Mathieu Unbekandt **University of Edinburgh**

A 3-D Atlas of Gene Expression During Lower Genitourinary Development Using Optical Projection Tomography (OPT)

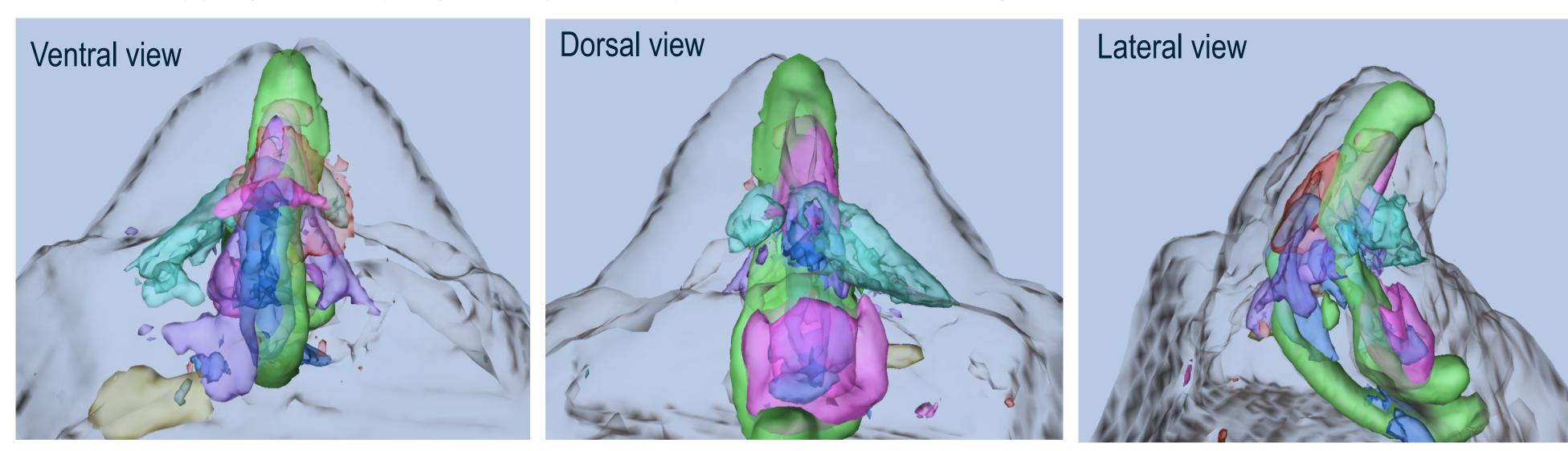
Monique Welten, Brooke Armfield, W. Bradley Barbazuk and Martin J. Cohn HHMI, Departments of Molecular Genetics & Microbiology and Biology, University of Florida, PO Box 103610, Gainesville, Florida, 32610

I. OPT generation of an anatomical reference series of mouse genital tubercles



This digital anatomical reference series allows users to map multiple gene expression patterns, produced using standard in situ hybridization, to embryonic anatomy. The 3D space can be interrogated online to identify, for example, regions of syn-expression, molecular anatomy, and interactomes in the context of morphological space.

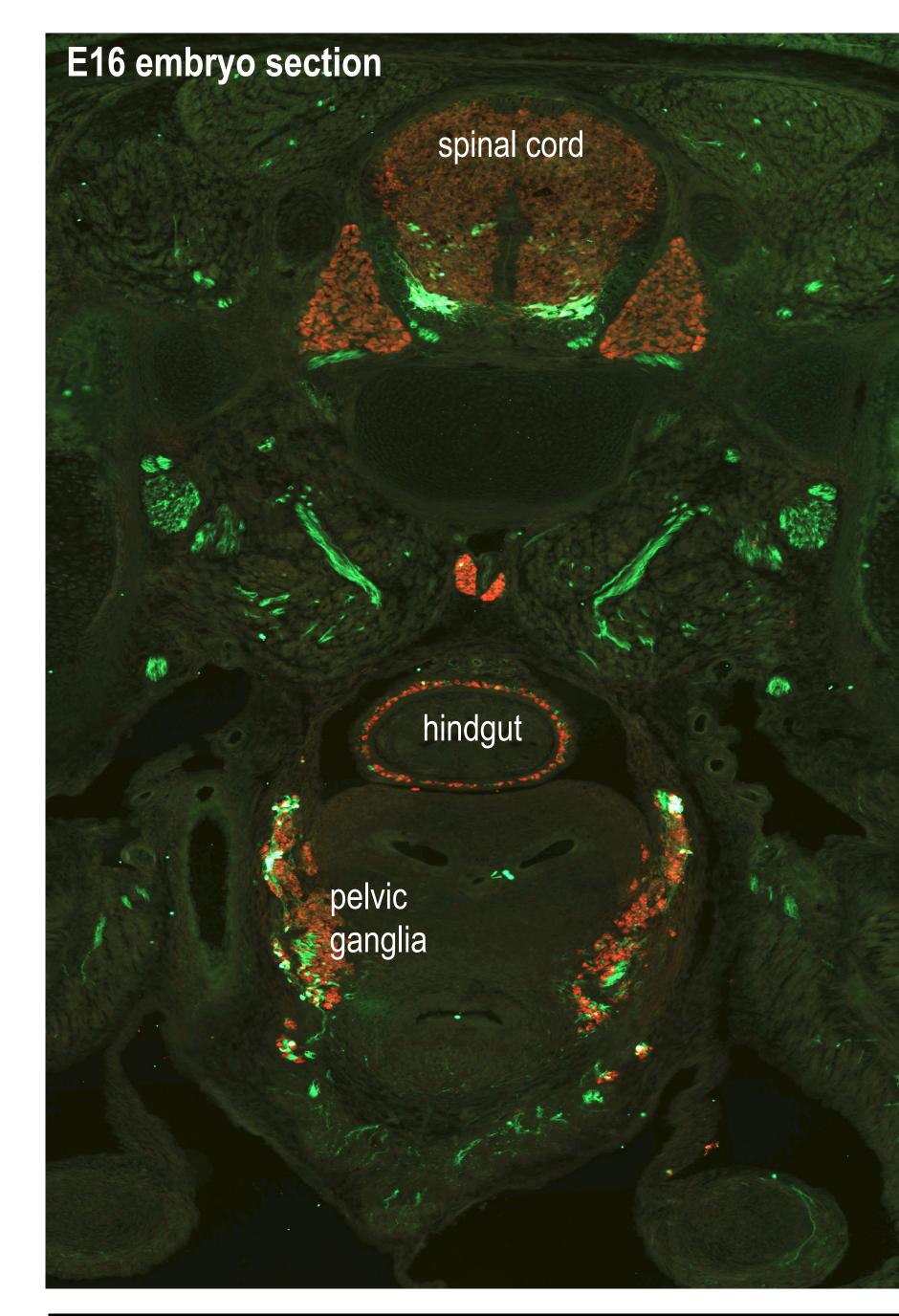
II. 3-D mapping of multiple gene expression patterns to the mouse genital tubercle at E12.5

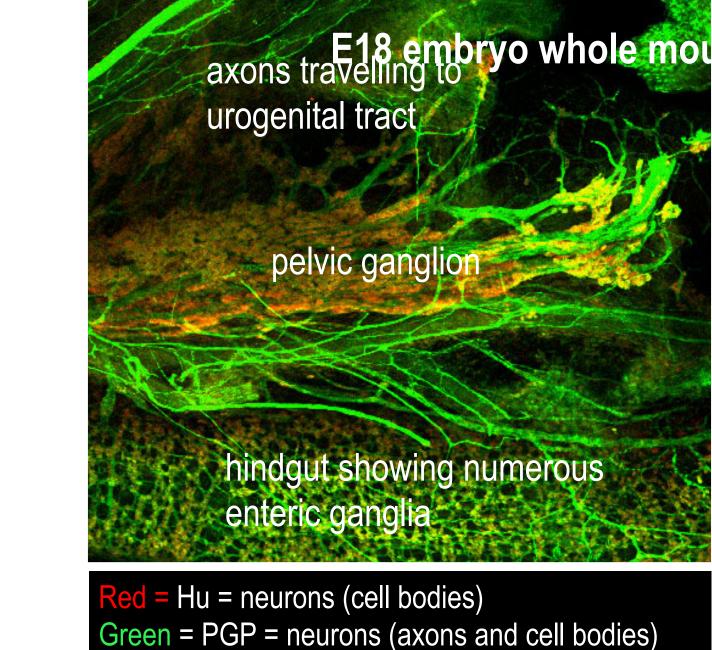


OPT-generated reconstructions of genital tubercles from an E12.5 mouse embryo showing expression of six different genes using unique colors. Urethral epithelium is genetically labeled and segmented in green. OPT mapping reveals novel molecular subcompartments.

Mapping the Development of Pelvic Autonomic Ganglia Adam S. Wallace and Janet R Keast

Department of Anatomy & Neuroscience, University of Melbourne.





Green = Tuj1 = neurons (axons)

E18 embryo whole mount

axons travelling to

urogenital tract

= Hu = neurons (cell bodies) = ChAT = choline acetyltransferase* = marker of cholinergic neurons *from ChAT-Cre mouse

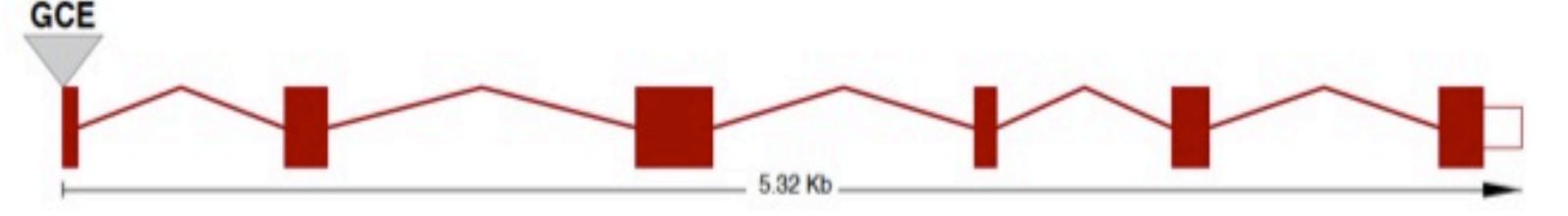
Tamoxifen Dependent Regulation of Gene Activity in the Urothelium

Jill McMahon1, Jin-jin Guo¹, JrGang Chen², Manfred Baetscher¹,

Todd Valerius³, Andrew McMahon¹

¹Department of Stem Cell and Regenerative Biology, Harvard University, ²UNC Chapel Hill, ³Beth-Israel Deaconess Hospital, Boston.

GENERATING A UPK3A – GFP::CRE::ERT2 BAC TRANSGENIC LINE:



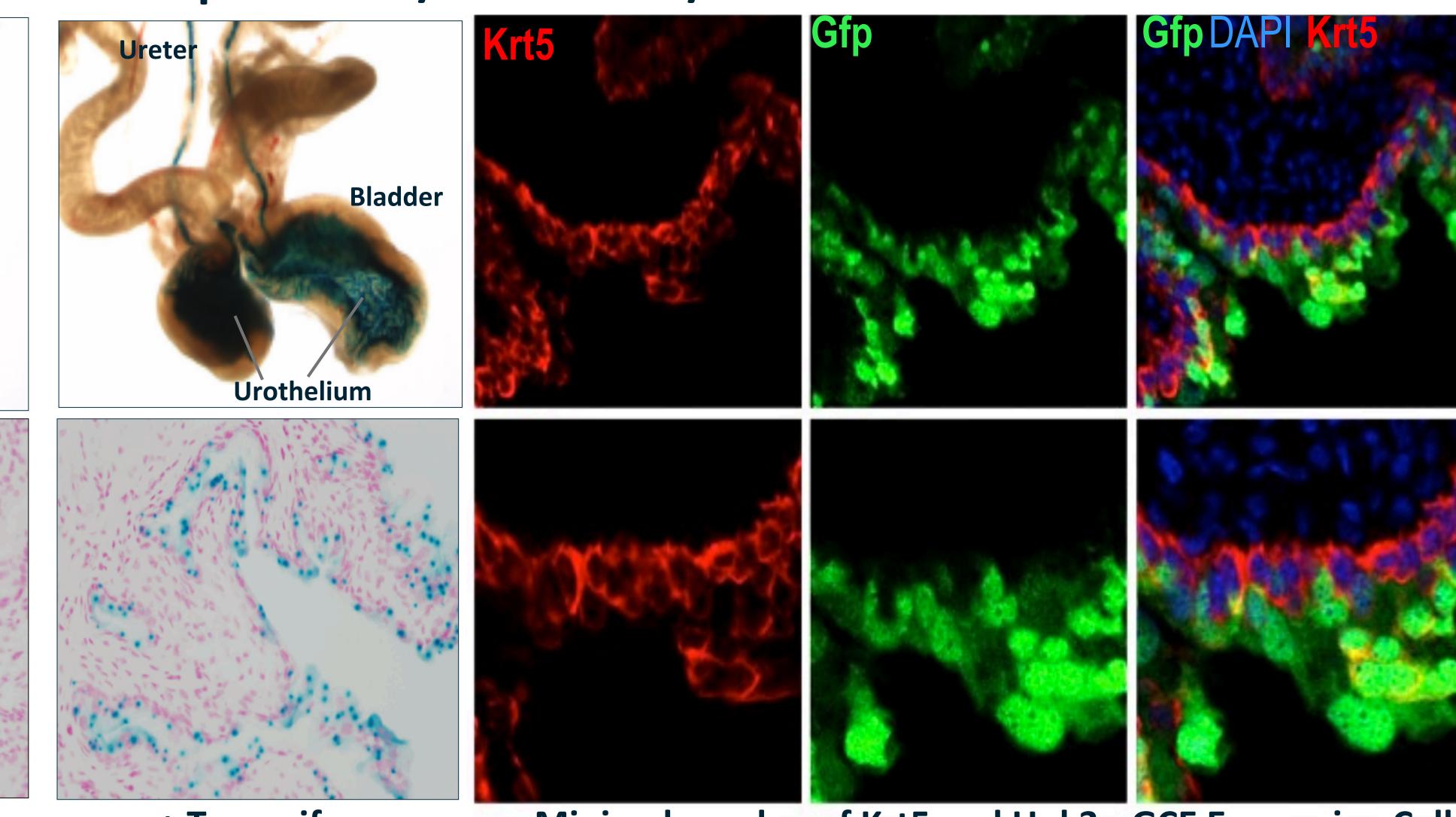
Upk3a 201 – ENSMUST00000053070

A GFP::CRE::ERT2 cassette is place into the Upk3a gene in a BAC construct

UPK3A-GCE CONTSTRUCT OVERVIEW CREATED 30 AUGUST 2010 UPDATED 6 SEPTEMBER 2010

See strain report at: WWW.GUDMAP.ORG

Upk3a-GDE/+:R26RlacZ/+



- Tamoxifen

Urothelium

+ Tamoxifen

Minimal overlap of Krt5 and Upk3a-GCE Expressing Cells

Identifying Novel Urothelial Cell Types And Genes That Label Them:

Andrei Molotkov, Kerry Schneider & Cathy L. Mendelsohn

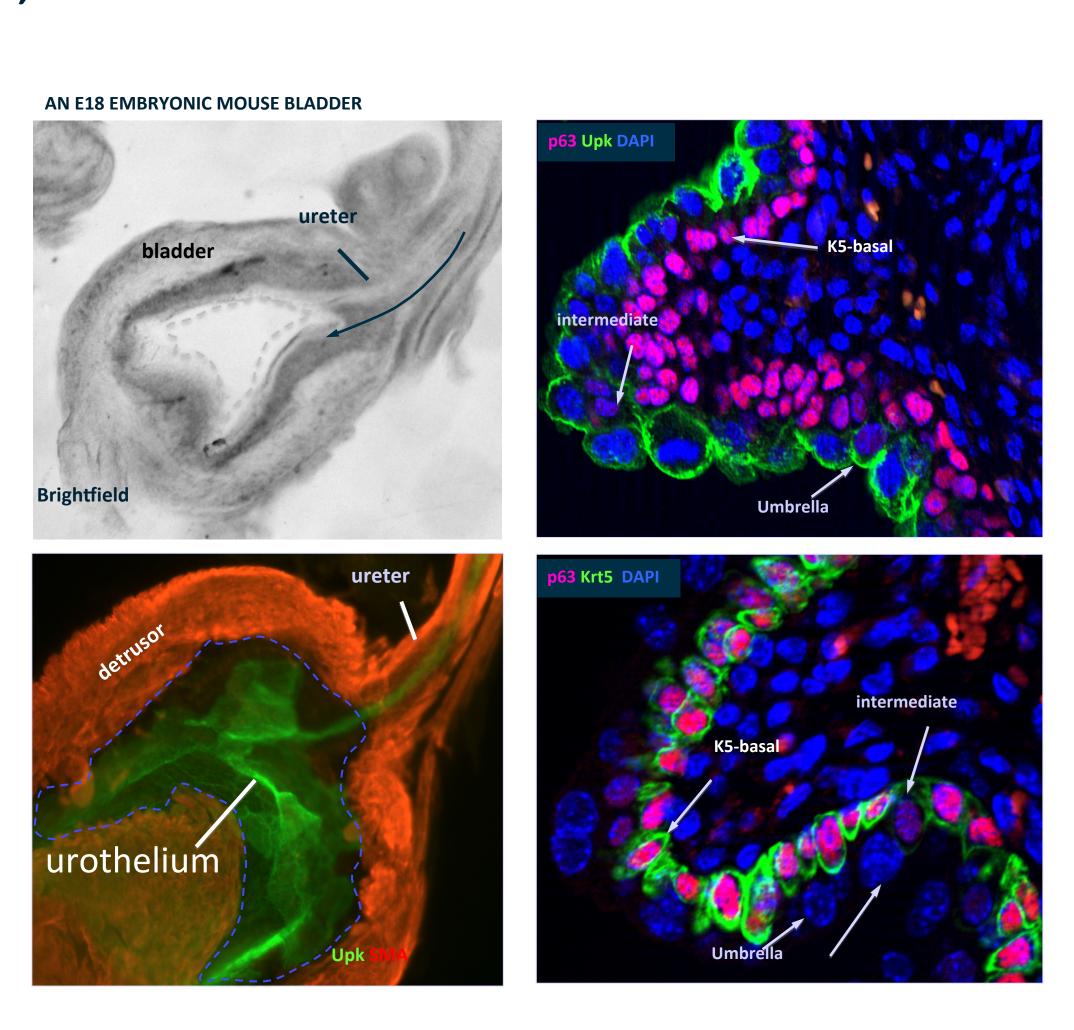
Departments of Urology, Genetics & Development, and Pathology, Columbia University, ICRC, 1130 St. Nicholas Avenue, New York, New York, 10032

At present we can only identify 3 cell types in the urothelium based on marker expression. A number of important questions need to be addressed, including the identity of progenitors that give rise to these urothelial cell types during development, and the identity of progenitors that give rise to the different types of bladder cancers

Identifying markers that label distinct urothelial sub-populations will be important for reaching these goals.

Three populations known at present:

K5-BASAL (KRT5+ P63+ UPK-) INTERMEDIATE: (KRT5- P63+ UPK+) (KRT5- P63- UPK+) **SUPERFICIAL**



In situ hybridization as a primary screen for novel urothelial cell markers identified from microarray and RNA-seq

