© 2015. Published by The Company of Biologists Ltd | Development (2015) 142, 1893-1908 doi:10.1242/dev.117903

RESEARCH ARTICLE

TECHNIQUES AND RESOURCES

An illustrated anatomical ontology of the developing mouse lower urogenital tract

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ABSTRACT

Malformation of the urogenital tract represents a considerable paediatric burden, with many defects affecting the lower urinary tract (LUT), genital tubercle and associated structures. Understanding the molecular basis of such defects frequently draws on murine models. However, human anatomical terms do not always superimpose on the mouse, and the lack of accurate and standardised nomenclature is hampering the utility of such animal models. We previously developed an anatomical ontology for the murine urogenital system. Here, we present a comprehensive update of this ontology pertaining to mouse LUT, genital tubercle and associated reproductive structures (E10.5 to adult). Ontology changes were based on recently published insights into the cellular and gross anatomy of these structures, and on new analyses of epithelial cell types present in the pelvic urethra and regions of the bladder. Ontology changes include new structures, tissue layers and cell types within the LUT, external genitalia and lower reproductive structures. Representative illustrations, detailed text descriptions and molecular markers that selectively label muscle, nerves/ganglia and epithelia of the lower urogenital system are also presented. The revised ontology will be an important tool for researchers studying urogenital development/malformation in mouse models and will improve our capacity to appropriately interpret these with respect to the human situation.

KEY WORDS: Mouse embryogenesis, Murine urogenital system development, Lower urinary tract, Lower reproductive tract, Urogenital sinus, Urethral plate, External genitalia, Genital tubercle, Bladder, Trigone, Ureter, Urethra, Pelvic urethra, Phallic urethra, Prostate gland, Pelvic ganglion

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Received 2 November 2014; Accepted 1 April 2015

INTRODUCTION

The urogenital tract is composed of urinary (kidneys, ureters, bladder, urethra) and reproductive (gonads, reproductive ducts, external genitalia) systems. The anatomy of this large, interconnected system is complex and changes rapidly during embryogenesis. In addition, hormonal signalling leads to dimorphism between male and female systems. With such complexity, even small perturbations in differentiation processes or timing in one tissue can translate into functional defects affecting the entire system. Congenital anomalies of the LUT have been described in both mouse models and humans (Rasouly and Lu, 2013). The embryonic origins and morphogenesis of the urogenital tract (bladder, urethra, vagina, external genitalia) and terminal hindgut (rectum and anus) are closely linked, which might explain the co-occurrence of genital anomalies (ambiguous genitalia, hypospadias, chordee and micropenis in males, cleft clitoris in females) with anorectal defects (Rasouly and Lu, 2013). Lower urinary and reproductive system development in mouse and human are not equivalent, and there have been historical instances in which terms have been drawn from human anatomy to incorrectly describe similar but distinct structures in the mouse. Clarity around the morphogenesis of these closely linked and intersecting organ systems in mouse will allow us to better appreciate differences between mouse and human, to re-evaluate the lessons that can or cannot be drawn from mouse models of human anomalies and, in some instances, to revise our thinking about the origin of some structures in the human.

Previously, we created a high-resolution anatomical ontology for the Genitourinary Development Molecular Anatomy Project (GUDMAP), a publicly available expression database for the mouse genitourinary system (Little et al., 2007). With the recent application of three-dimensional (3D) imaging techniques, the identification of cell-type specific markers and the application of genetic lineage tracing, our understanding of the developmental anatomy of the LUT and genitalia in the mouse have significantly improved. We have incorporated this new knowledge, together with additional studies presented here, into an updated anatomical ontology of the LUT and reproductive systems, including the sites and signalling centres important for establishing connections with the upper urogenital tract.

RESULTS

Early development: E10.5-14.5 (TS18-23)

Urogenital development involves epithelia derived from two embryological lineages, the nephric duct (ND, also called mesonephric or Wolffian duct) and cloaca, giving rise to the upper and lower urinary tract, respectively (reviewed in

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supplementary material). At E11, the urogenital sinus (UGS) is a simple epithelial tube extending from the cloaca, to which paired NDs are attached via the common nephric duct (CND), defined as the region of ND caudal to the ureter (Fig. 1). Caudal NDs connect at the UGS ridge, a thickened, raised proportion of the UGS epithelium (Fig. 1A-C,I-M). The UGS ridge is a signalling centre, important for regulating CND remodelling and apoptosis during ureter maturation and repositioning (Shapiro et al., 2000). From E11-13, the anterior UGS above the UGS ridge is the primitive bladder, and below this site, including the UGS ridge itself, is the caudal UGS. We define the UGS region, in which the epithelia of the primitive bladder and caudal UGS meet, as the transition zone. The cranial UGS will elongate and expand, becoming the bladder, while the caudal UGS becomes the pelvic urethra (PLUR, Fig. 1). The hindgut and anorectal sinus will form the colon, rectum and anus.

From E13, the term urethra is introduced, composed of pelvic and phallic regions. The PLUR develops within the embryo body and the phallic urethra (PHUR) within the GT (Fig. 1C,G,H). Alongside the NDs, paired paramesonephric ducts (derived from the mesonephric coelomic epithelium) elongate caudally and have reached the UGS ridge by E13.5 (Fig. 1C,M) (Guioli et al., 2007; Orvis and Behringer, 2007). From E14, the primitive bladder becomes the bladder. UGS is retained in the developmental ontology as a parental term, encompassing bladder, bladder-PLUR transition zone and PLUR.

The genital tubercle (GT) is the precursor of the penis and clitoris (supplementary material). Located within the GT of both sexes, the PHUR develops from a bilaminar epithelial extension of the cloacal

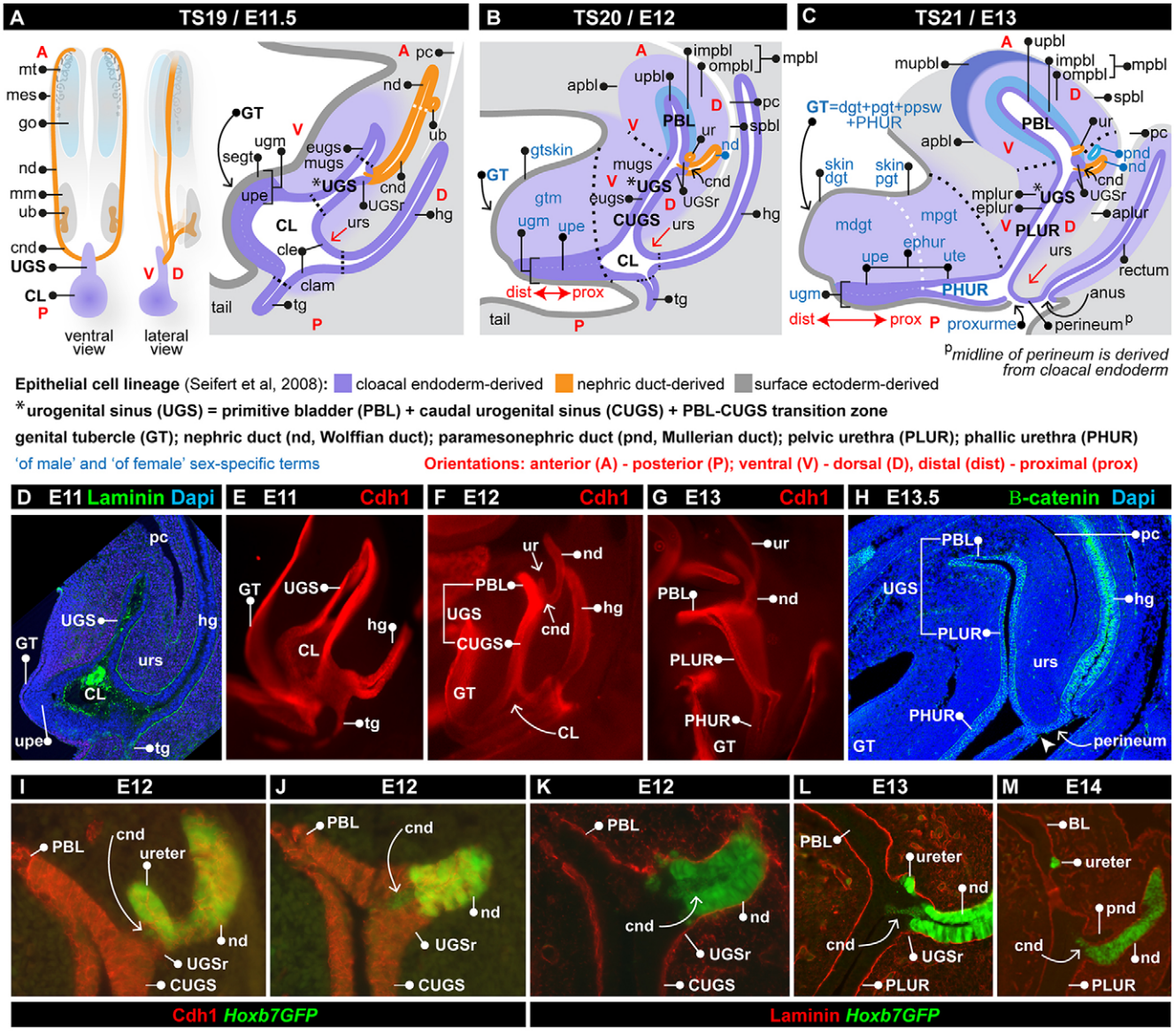

Fig. 1. Urogenital sinus development. (A-C) Schematics illustrating early development. (D-M) Immunohistochemistry of sagittal sections. Mesenchymal growth (red arrows, A-C) separates the hindgut and UGS. When it reaches the surface, the proximal urethral meatus is formed (C; arrowhead in H). Here, the perineum midline is derived from cloacal endoderm (C) and is β-catenin^{+} (H). NDs connect the UGS ridge (A-C) and are Cdh1^{+} (F,G). CND remodelling and ureter repositioning occur between E12 and E14 (B,C,I-M). NDs and CNDs are Hoxb7GFP^{+} (I-M). UGS ridge is Cdh1^{+} (I,J), Laminin^{+} (K-M) and surrounds the CNDs at E11-12 (A,B,I,J). The ureter directly connects the bladder at E13 (C; Hoxb7GFP^{+} in L). Very few Hoxb7^{+} CND cells remain at E14 (M). For abbreviations in all Figures, see supplementary material.

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epithelium, called the urethral plate epithelium (UPE). At the ventral midline, the endodermal cloacal epithelium is in direct contact with the surface ectoderm and together they are known as the cloacal membrane. By E11.5, genital swellings have merged to form a single GT, and the UPE grows out from between these swellings (Fig. 1A,D and Fig. 2A). As the urorectal septum expands, the UPE is forced into its ventral GT position and is in direct contact with the surface ectoderm/skin. Together, these structures are termed the urogenital membrane (Fig. 1A-C). At E13, the urorectal septum reaches the embryo surface, resulting in complete separation of the UGS and hindgut. Here, proportions of the cloacal membrane disintegrate in mice and humans, contributing to formation of the anal opening and an opening in the PHUR called the proximal urethral meatus (Fig. 1C,H and Fig. 2C; Nievelstein et al., 1998; Perriton et al., 2002; Sasaki et al., 2004; Seifert et al., 2008, 2009a,b; Lin et al., 2009; Ng et al., 2014; Ching et al., 2014; Miyagawa et al., 2014).

Except for very early in development (prior to E12), the GT and reproductive ducts are parts of the reproductive ontology. Whereas the PHUR in females plays no reproductive role, the term is included in both urinary and reproductive systems because of its anatomical location in the female external genitalia.

From E13, the GT is morphologically subdivided into proximal and distal regions (Fig. 1C and Fig. 2C). Laterally, in the proximal GT, two mesenchymal preputial swellings appear that enclose the preputial glands, epithelial glands seen from E13.5 (Cunha, 1975; Seifert et al., 2008). The PHUR epithelium remains in contact with the surface ectoderm of the ventral GT. The ventral ectoderm forms a small invagination, the urethral groove (or urethral seam), on the GT surface, where it meets the urethral endoderm (Baskin et al., 2001; Perriton et al., 2002). As seen in histological sections, the mouse urethra is actually closed within the GT, and therefore this groove has been referred to as a ‘closed urethral groove’ (Baskin

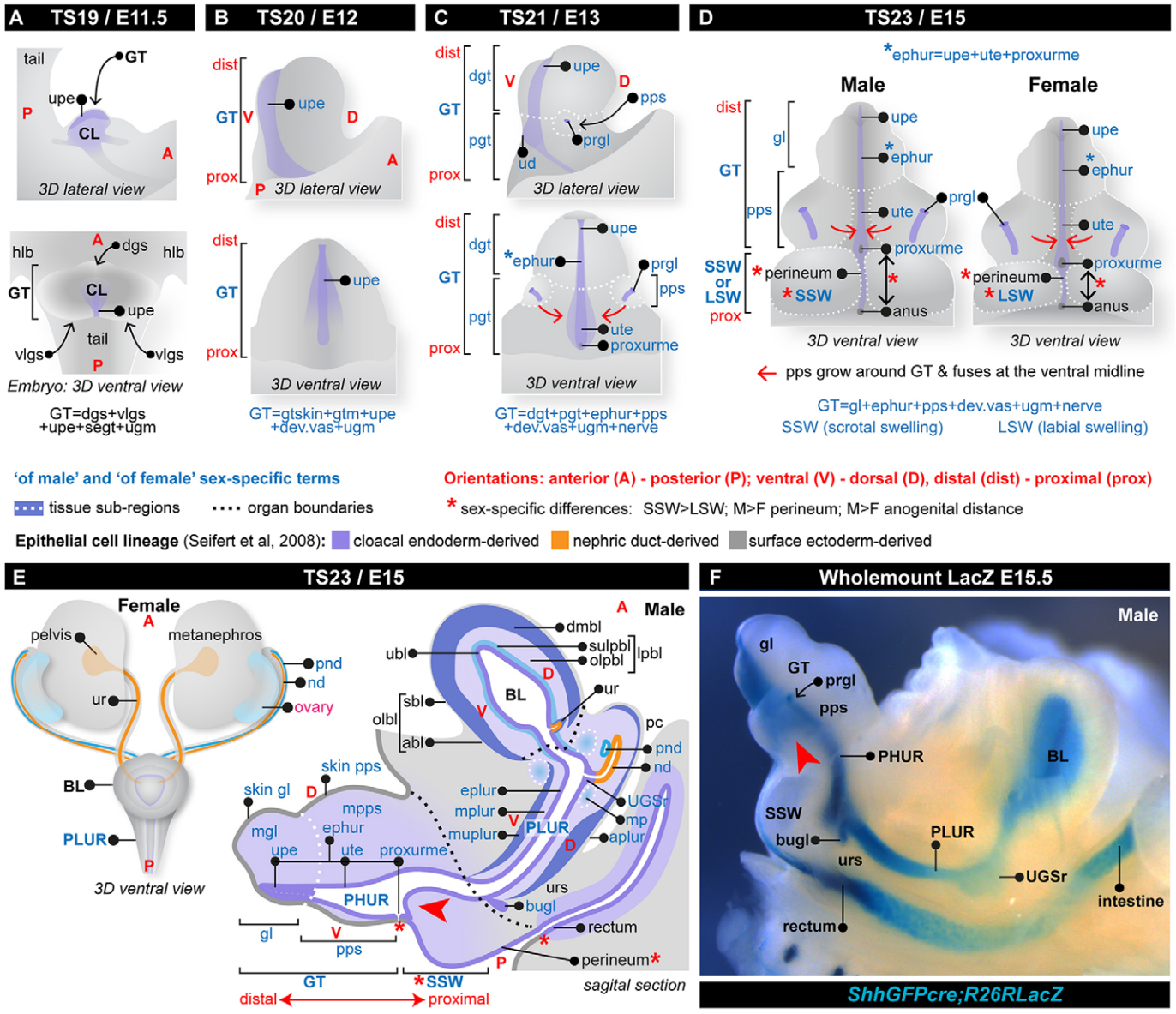

Fig. 2. Genital tubercle development. (A-E) Schematics illustrating GT development. Preputial swellings grow ventrally around the GT (red arrows). Anogenital distance, perineum and scrotal swellings are larger in males (red asterisks). (F) Whole-mount β-galactosidase staining of *ShhGFPCre;Rosa26RlacZ* embryo shows lineage of *Shh*-expressing cells (blue) in epithelia lining the PHUR, PLUR, bladder, rectum, intestine, perineum, bulbourethral glands, preputial glands and UGS ridge. In males, the mesenchyme begins to septate the PHUR epithelium (red arrowheads in E,F).

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et al., 2001). This is in contrast to humans that develop an open urethral groove, with the PHUR lumen exposed on the ventral GT surface until fusion of the urethral folds results in closure (Glenister, 1954). The UPE commences as a cord that canalises in a proximal-to-distal wave, with the lumen forming between the two epithelial layers. From E13, the PHUR is composed of the distal UPE, proximal urethral tube epithelium and external orifice defined as the proximal urethral meatus (Fig. 1C and Fig. 2C). By E14 in both sexes, the preputial swellings become more apparent, and mesenchyme at the GT base expands and will become the labioscrotal swellings (Fig. 2D-F).

In histological section, mesenchymal swellings are found just lateral to the ventral-most urethral tube epithelium. This mesenchyme has been referred to as the 'urethral folds' (Yamada et al., 2003). We note that the 'urethral folds' described in the mouse are distinct from those structures of the same name in humans. Tubulogenesis of the human urethra is analogous to neurulation, in that the lateral edges of the urethral plate are brought together medially, eventually fusing to close the urethral tube. Fusion of the urethral folds in humans results in formation of the urethra proper internally and penile raphe externally, a structure that is not seen in the mouse. By contrast, the mouse UPE is a bilaminar epithelium that extends from the centre of the GT to the ventral margin, and lumen formation occurs as the two layers separate medially. In the mouse, the mesenchyme referred to as 'urethral folds' on either side of the plate might function to separate the definitive urethra from the ventral urethral seam, which will be remodelled away (Baskin et al., 2001).

Sex-specific anatomical differentiation of LUT and external genitalia: E15.5 to adult (TS23-S28)

From E15, the GT is divisible proximo-distally into a proximal region surrounded by preputial swellings (and later, prepuce) and a distal region of exposed glans (Fig. 2D-F). During GT outgrowth (E11.5-14.5), males and females are anatomically indistinguishable. However, from E15.5, morphological differences between male and female phalluses are observed. In males, mesenchyme begins to invade the ventral-proximal GT, thereby partially closing the proximal urethral meatus and separating the definitive PHUR from the surface ectoderm in a proximal-distal wave that continues until postnatal stages (Seifert et al., 2008). This event is thought to occur by fusion of the mesenchymal urethral folds, although invasion by mesenchyme from the perineum has also been proposed (Baskin et al., 2001; Yamada et al., 2003; Seifert et al., 2008). In addition, beginning at E15.5, the distance between the urethral meatus and anus (anogenital distance) is longer in males than in females (Figs 2,3).

Sexual dimorphism becomes more apparent at E16.5 with differentiation of the penis and scrotum in males, as highlighted using *ShhGFPCre;Rosa26RlacZ* reporter mice (Fig. 3). In males, concurrent with internalisation of the urethra by fusion of the urethral folds, the mesenchyme of the preputial swellings (termed 'prepuce' from E16 onwards) fuses at the ventral midline, also in a proximal-distal wave. As the prepuce continues to expand, it envelops the glans (Fig. 3G-L). Mesenchyme fusion at the ventral midline of the GT and remodelling of the urethra result in an indentation on the external surface, called the preputial seam (Fig. 3M-O; Baskin et al., 2001; Yamada et al., 2003; Seifert et al., 2008).

The proximal urethral meatus is nearly closed in males by E16.5, whereas it remains open at the GT/clitoris base in females (Fig. 3; Baskin et al., 2004; Seifert et al., 2008; Wang et al., 2011; Guo et al., 2014). At E17, the GT has differentiated sufficiently to be recognised as the penis/clitoris, and the PHUR becomes the penile urethra in males. Mesenchymal growth also results in a bend in the male urethra at the glans-body junction, which is prominent from E17 and results in the glans penis being positioned at a right angle bend to the body of the penis (Fig. 3; Cunha and Baskin, 2004; Rodriguez et al., 2011). By contrast, the female urethra is more linear and positioned ventral to the clitoris (Fig. 3A-T).

In females, the UPE can still be seen at E17.5, whereas, in males, it is no longer present and the definitive urethral meatus has formed (Fig. 3Q-V). Although the urethra has opened in the distal glans of the male at this stage (Fig. 3U), urethral maturation and internalisation by invading mesenchyme is not complete until postnatal stages (Baskin et al., 2001; Rodriguez et al., 2012). In female mice, the UPE also continues to canalise; however, because the mesenchyme does not internalise the female urethra, it remains ventral to the clitoris. The proximal urethral meatus remains open at the base of the clitoris. By P8, this opening in the proximal urethral meatus has closed (Kurita, 2010), and its prior location will become the site of the vaginal opening.

In recent years, several publications have provided new insights into the postnatal anatomy of murine external genitalia (Rodriguez et al., 2012, 2011; Schlomer et al., 2013; Weiss et al., 2012; Yang et al., 2010). We have modified the ontology to incorporate these findings (supplementary material). In both sexes, mesenchymal condensations develop into bone (os penis/clitoridis). Males develop cartilage and bands of erectile tissue, called corpora cavernosum. The adult male urethra is subdivided into penile, pelvic and prostatic urethra. The structure of the adult penis is illustrated in Fig. 3W-Y. At the distal tip of the adult glans penis is a tapered extension of the os penis called the male urogenital mating protuberance (MUMP; Rodriguez et al., 2011; Weiss et al., 2012). The glans penis is covered with keratinised epidermal spines. It is positioned internally, within the preputial space, and is completely surrounded by the prepuce externally. The prepuce contains the preputial glands, the ducts of which drain into the preputial space. The glans can be exposed when the prepuce is retracted.

The morphology of the adult mouse clitoris has only recently been described in detail (Yang et al., 2010). Like the penis, the clitoris is surrounded by a prepuce containing preputial glands; however, the clitoris is much smaller and is ventrally tethered to the prepuce, as the clitoral epithelial lamina does not completely enclose the clitoris. Because of this anatomy, the urethra resides partially within the preputial mesenchyme and partially within the clitoris. This is in contrast to humans, in which the urethra is not housed within the clitoris but opens proximal and ventral to the clitoris and is circumscribed by the labia minora.

The PLUR becomes sex specific in the ontology from E15 (Fig. 2E and Fig. 4; supplementary material). Circulating androgens in the male initiate seminal vesicle bud formation from the NDs and, from E16, the ducts become the ductus deferens (Fig. 4A-C). Both seminal vesicles and ductus deferens are connected to the UGS ridge via the ND-derived ejaculatory ducts, and disrupting ND development in males results in loss of these structures (Fig. 4C,D; Guo et al., 2011). The male UGS ridge becomes the verumontanum (Fig. 4C,D; Levin et al., 2007; Yucel and Baskin, 2004).

In females, the UGS ridge blocks the patent opening of the NDs to the PLUR, and from E16 on becomes the sinovaginal bulb (SVB, Fig. 4E,F). By E16.5, the caudal paramesonephric ducts have fused and enlarged to become the upper vagina (Fig. 4F-H). By E18, the upper vagina has fused to the SVB and the vagina comprises both the upper vagina and lower vagina or SVB. These are unique structures with different origins and gene expression profiles (Fig. 4H; Drews et al., 2002; Kurita, 2010). The SVB, a solid epithelial cord, is a transient structure only seen during development

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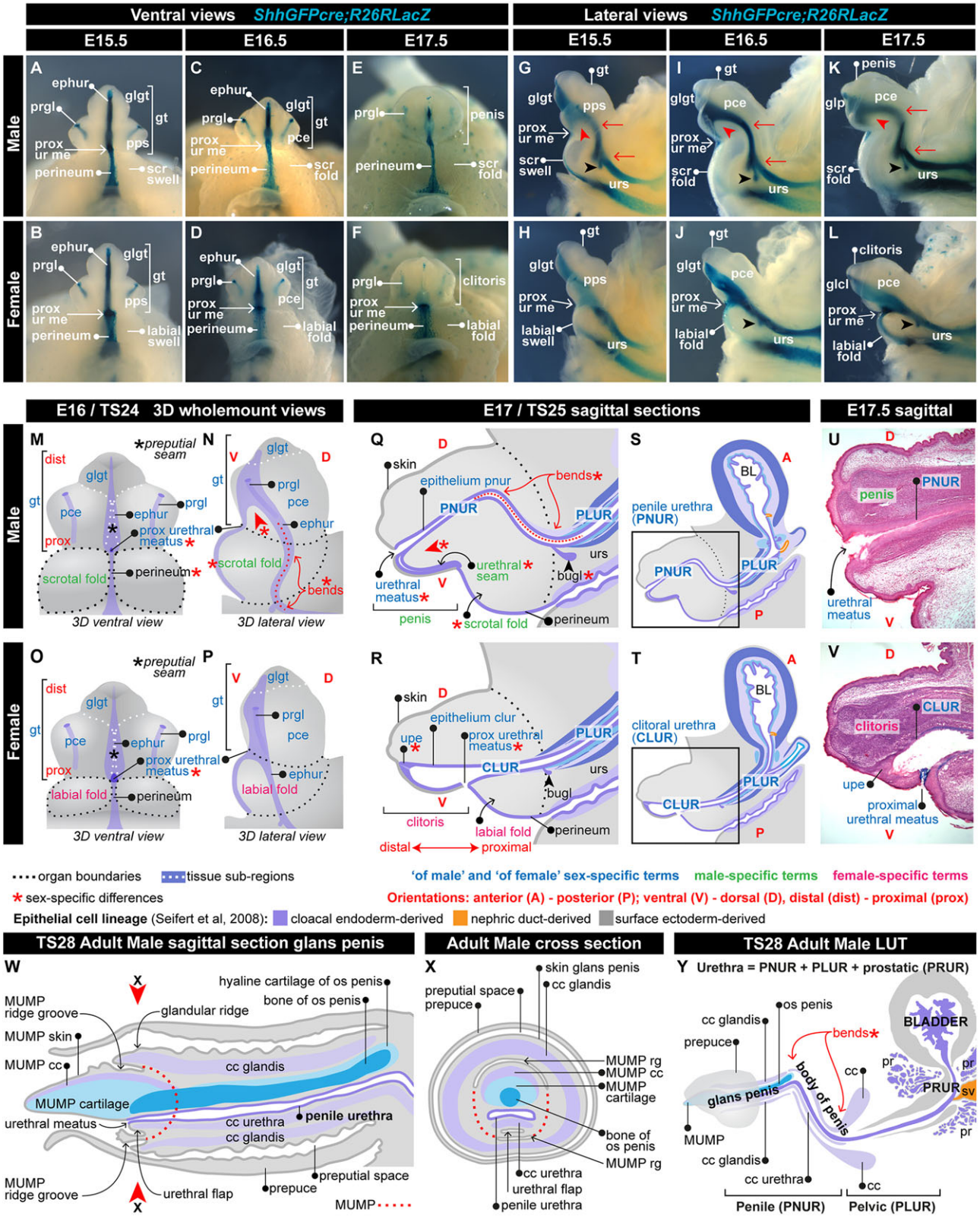

Fig. 3. See next page for legend.

(Kurita, 2010). The upper vagina becomes the adult vagina and the SVB contributes to the vulval epithelium (Kurita, 2010).

Morphological sex differences in the PLUR itself are first seen around E16.5 (Fig. 5; supplementary material). The urethral epithelium gives rise to accessory glands, including the prostate, bulbourethral glands and numerous urethral glands. Only the prostate glands are male specific. Female bulbourethral glands (new to the ontology), although smaller than the male, are also known as

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Fig. 3. Sexual differentiation of the external genitalia. (A-L) Whole-mount β-galactosidase staining of *ShhGFPCre;Rosa26RlacZ* embryos. Descendants of the *Shh*-expressing lineage (blue) contribute to preputial glands, epithelium of PHUR, perineum, rectum/intestine and hair follicles. (M-T) Schematics illustrate external genitalia. From E15.5-17.5 in males, mesenchyme grows distally, the urethra septates (red arrowheads), the proximal urethral meatus closes, the urethral seam forms and two right-angle bends develop in the urethra (red arrows). Male bulbourethral glands (black arrowheads), scrotal swelling/fold and perineum are larger. In both sexes, the preputial seam is seen as an indentation along the prepuce ventral midline (black asterisks in M,O). (U,V) H&E-stained external genitalia sections. (Q-V) At E17.5, the male urethra is patent along its length and open at the urethral meatus; in females, the urethral plate (upe) is present and the urethra opens at the proximal urethra meatus. (W-Y) Schematics illustrating adult male anatomy, showing the male urogenital mating protuberance (MUMP), corpora cavernosa (light purple), cartilage/bone (blue). Red arrowheads (in W) indicate position of cross-section (X). (Y) Two right-angle bends are present in the adult male urethra. The prostatic urethra (PRUR) is surrounded by prostate glands. Paired corpus cavernosum extend anteriorly to join the pubic bone (cc in Y).

Bartholin's glands (Bloomfield, 1927). Like their male counterparts, they are derived from cloacal endoderm and marked by *Shh* (Fig. 2F and Fig. 3G-L).

Prostate gland anatomy is extremely complex (Fig. 5; supplementary material). Several studies describing early murine prostate development (Allgeier et al., 2010, 2009; Cook et al., 2007) have instructed modifications to the ontology. Numerous prostate buds develop from the PLUR epithelium in distinct locations (Fig. 5A-D). Number, size, morphology, location and patterning of the different prostate regions have been described (Allgeier et al., 2010, 2009; Lin et al., 2003; Timms et al., 1994). Bud formation is complete by E18.5 (Lin et al., 2003); however, extensive branching morphogenesis does not begin until after birth. The glands later develop a patent lumen and the adult prostate secretes a variety of products dependent on region. In adult males, the urethra region surrounded by prostate glands is called the prostatic urethra (Fig. 5I,J).

Urethral glands also form as buds that develop from the PLUR epithelium in both sexes (Fig. 5; supplementary material). Ventral urethral gland buds develop at the male bladder-urethra junction in the same location as ventral prostate buds, but at early stages these are indistinguishable, as both express the early prostatic marker *Nkx3-1* (Allgeier et al., 2010). Consequently, it is difficult to definitively identify any ventral budding structure in the developing male, although there is evidence that *Edar* and *Wnt10b* mRNA staining intensity can separate prostatic gland buds (high expression) from urethral gland buds (low to non-detectable expression; Keil et al., 2012). However, the ontology now includes the indefinite term, ventral epithelial bud, first introduced by Allgeier et al. (2010) (Fig. 5A-H). Female mice can develop functional prostate glands from ventral epithelial buds if exposed to exogenous androgens (Price and Williams-Ashman, 1961; Raynaud, 1938, 1942). In the past, these have been referred to as female prostate buds. The ontology uses ventral epithelial bud in favour of prostate bud for the female mouse. Whereas these buds might go on to form Skene's glands in females, no lineage tracing is available to confirm this and, even in males, not all ventral buds go on to form prostate glands (Allgeier et al., 2010).

Regional and cellular updates to the bladder and urethra ontology

In the literature, the bladder has been divided into three different regions: fundus, neck and trigone (supplementary material). We

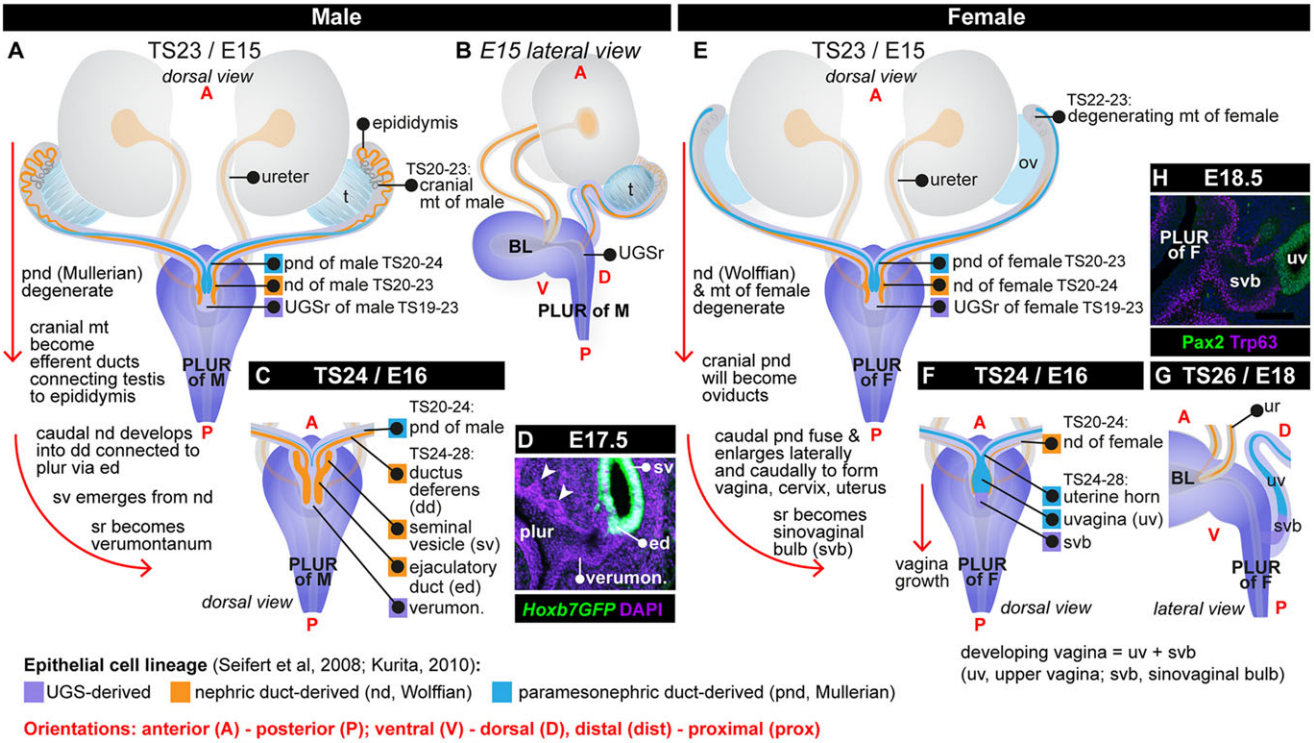

Fig. 4. Sexual differentiation of the reproductive ducts. Schematics illustrate 3D anatomy of reproductive ducts and their connection to the PLUR. At E15, the sexes are identical. Red arrows and associated text indicate sex-specific changes. Nephric and paramesonephric duct degeneration is complete by E17.5. (D) Section immunofluorescence of *Hoxb7GFP* embryo shows *Hoxb7GFP*$^{+}$ ejaculatory ducts and seminal vesicles. Anterior prostate buds are seen (arrowheads). (F,G) The vagina grows in a posterior direction along the PLUR (red arrow), eventually separating from the PLUR and opening at the base of the clitoris (postnatally). (H) Section immunofluorescence shows differential expression in upper vagina (Pax2^{+}) and SVB (Trp63^{+}).

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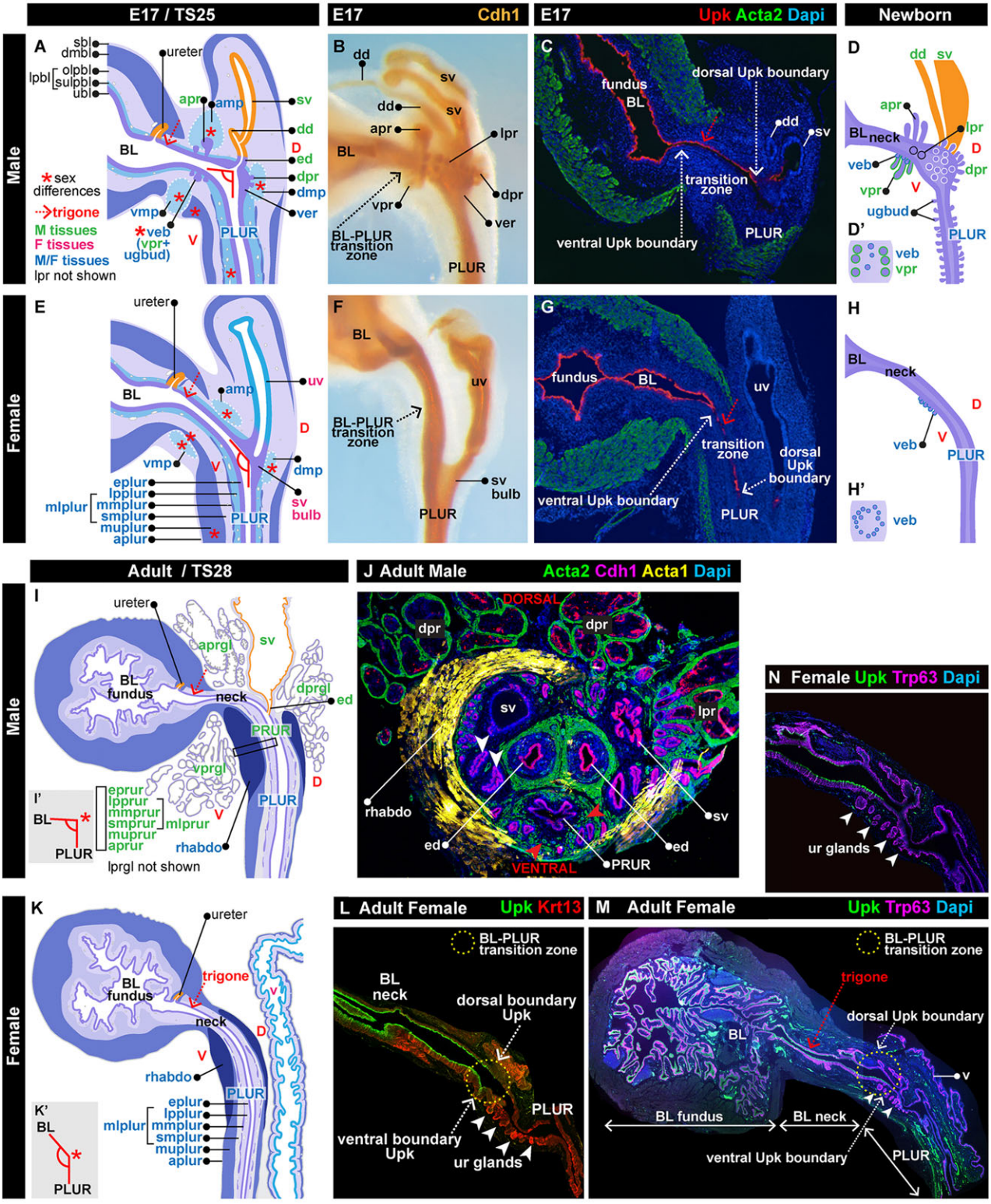

Fig. 5. Sexual differentiation of the pelvic urethra. Schematics illustrate sagittal sections of bladder-PLUR junction at E17 (A,E) and adult (I,K). Sex differences (red asterisks) include: mesenchymal pad size/shape; thicker male lamina propria (lpplur) and thicker female muscle (muplur); muscle layer (muplur) continuous with detrusor in females (gap in males); and the bladder-PLUR (BL-PLUR) connection angle, close to 90° in males (I′), more linear in females (K′). (B,F) Whole-mount immunolabelling shows epithelial structures (Cdh1^{+}). (C,G) Immunofluorescence of sagittal sections shows smooth muscle (green) and Upk (red) expression. Upk marks the bladder urothelium boundary (dotted arrows). (D,H) 3D illustrations of PLUR epithelium at birth (purple) shows prostate, ventral epithelial and urethral gland bud location; lateral (black), dorsal (white) and ventral (green) prostate glands and ventral epithelial buds (veb, blue) are outlined. (D′,H′) Underside views of ventral PLUR. (J) Cross-section through adult male PRUR shows labelling of epithelia (red), smooth muscle (green) and striated muscle (yellow), which marks the rhabdosphincter. Blood vessels (Acta2^{+}, red arrowheads) and prostate glands (Cdh1^{+}, white arrowheads) are seen. (K-N) In female adults, the vagina has elongated and a rhabdosphincter develops. (L-N) Sagittal BL-PLUR sections labelled with Upk (bladder urothelium) shows the adult BL-PLUR transition zone (dotted arrows). Urethral glands (arrowheads, L-N) are located close to the BL-PLUR boundary.

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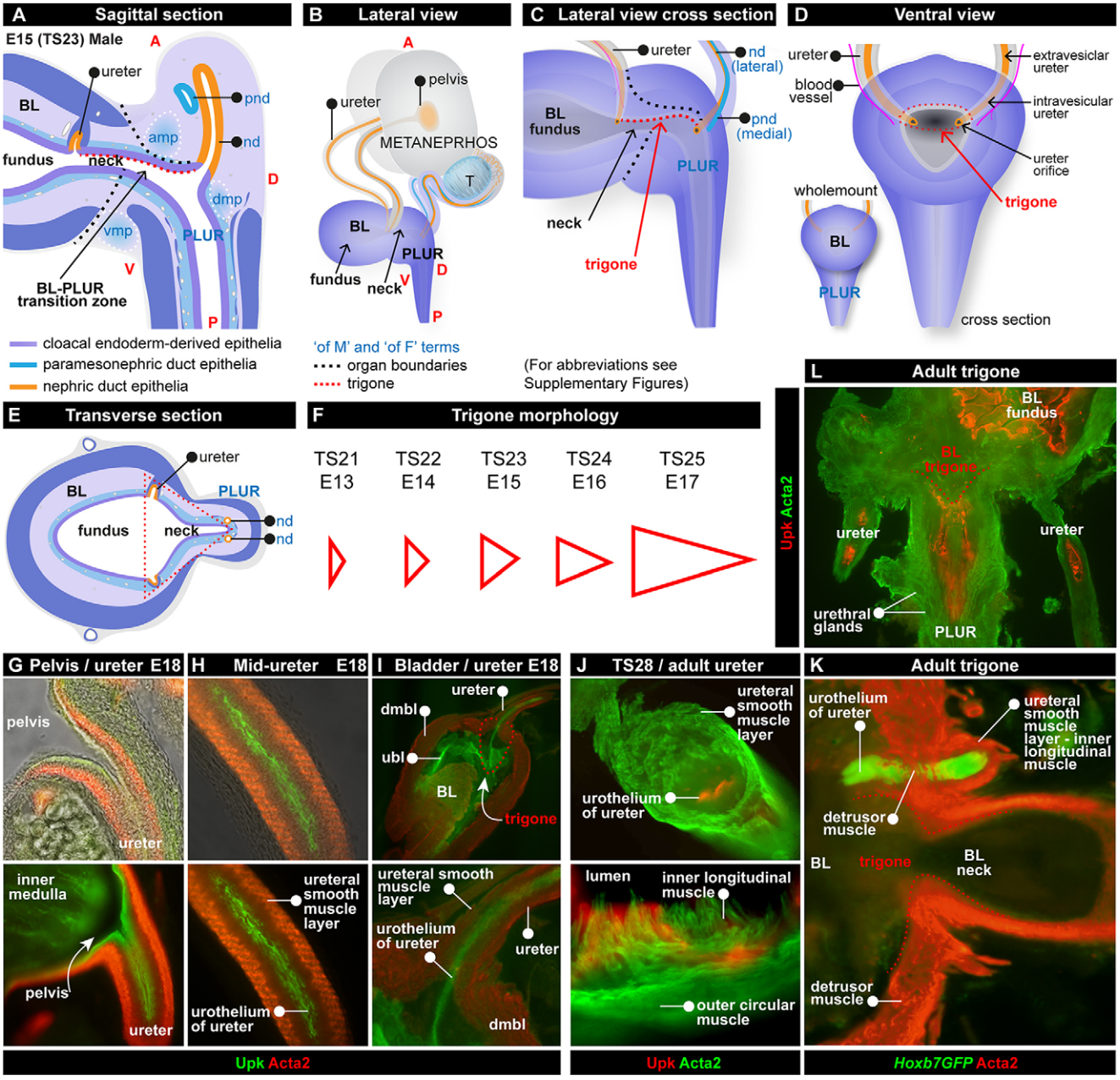

Fig. 6. Morphology of the bladder fundus, neck, trigone and ureters. (A-E) Schematics illustrating location and morphology of the bladder regions, ureter and urethra connections at E15. Trigone and BL-PLUR boundaries are shown (red/black dotted lines). The bladder neck is more elongated in the adult (see Fig. 5M). (F) As the bladder grows, trigone morphology changes from an equilateral to an isosceles triangle. (G-L) Immunofluorescence of vibratome sections and whole-mounts of E18 ureter (G-I), adult ureter (J) and trigone (K,L), with labelling of urothelium (Upk), ureter muscle layer and detrusor muscle (Acta2) and *Hoxb7-GFP* in ureter urothelium (K). Approximate trigone boundary is shown (red dotted lines in I,K,L).

have reviewed the definition of these regions and modified the ontology as a result. Anatomically, the bladder is divided into the fundus (or dome), the rounded blind-end of the bladder and the neck, which is the narrow open end of the bladder located between the ureter orifices and the PLUR opening (Figs 5 and 6). The dorsal bladder neck forms a triangular-shaped region called the trigone. The ureter orifices form the trigone base and the urethra opening forms the apex (Fig. 6E). Trigone morphology changes as the bladder and urethra expand, increasing the distance between the ureters and urethral opening (Fig. 6F) (Carpenter et al., 2012). The ureters are muscular tubes that transport urine from the renal pelvis to the bladder (Fig. 6G-J; supplementary material). The ureters are inserted in a stereotypical position in the trigone, where ureteral muscle and bladder muscle intersect to form the anti-reflux valve (Carpenter et al., 2012; Viana et al., 2007) (Fig. 6K,L).

The bladder urothelium is lined by an apical barrier of urothelial plaque, composed of uroplakin family proteins (Upk1a, Upk1b, Upk2, Upk3a and Upk3b). Expression of multiple Upk proteins is required to create the plaque. The urethra epithelium does not produce uroplakin plaque and therefore has not been described as an urothelium. However, both epithelia are derived from cloacal endoderm, and the exact location of the bladder-urethra boundary is not precise. In the adult, the distribution of urothelial plaque and

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Upk protein expression may be used to determine the boundary (Fig. 5L,M). However, during development, Upk expression not only differs between stages, but also differs between dorso-ventral surfaces (Fig. 5C,G). During early development (E11.5-13.5), we have defined the bladder-urethra boundary as the site where the reproductive ducts insert into the urethra (Fig. 1). Later in development, as the ducts differentiate, this boundary becomes difficult to define, especially in the female, when the SVB and vagina move caudally. In order to facilitate the annotation of gene expression within this region at later stages, and at early stages when the reproductive ducts are not visible, we have introduced the term bladder-urethra transition zone, from E11.5 to adult. This zone (Figs 5 and 6) marks the region where these two different epithelia meet and is similar to transitional zones in other organs, such as the female cervix and the oesophagus *Z*-line.

The bladder is able to stretch to store urine and to contract under autonomic control to expel urine via the urethra. These dynamic movements are facilitated by the detrusor muscle, which is composed of irregularly oriented smooth-muscle fibre bundles that, together with the urothelium, expand and contract in response to stretching. Correct patterning and differentiation of bladder smooth muscle is therefore crucial for bladder function. The muscle forms via interactions between the urothelium and surrounding mesenchyme (Cunha, 1999). Recent studies of environmental factors, epithelial-to-mesenchymal interactions and signalling pathways required for bladder smooth muscle formation have advanced our understanding of this developmental process (Cao et al., 2008, 2010; Cheng et al., 2008; DeSouza et al., 2013; Haraguchi et al., 2007; Liu et al., 2010; Shiroyanagi et al., 2007; Tasian et al., 2010). We have updated the bladder ontology to incorporate these findings (Fig. 7).

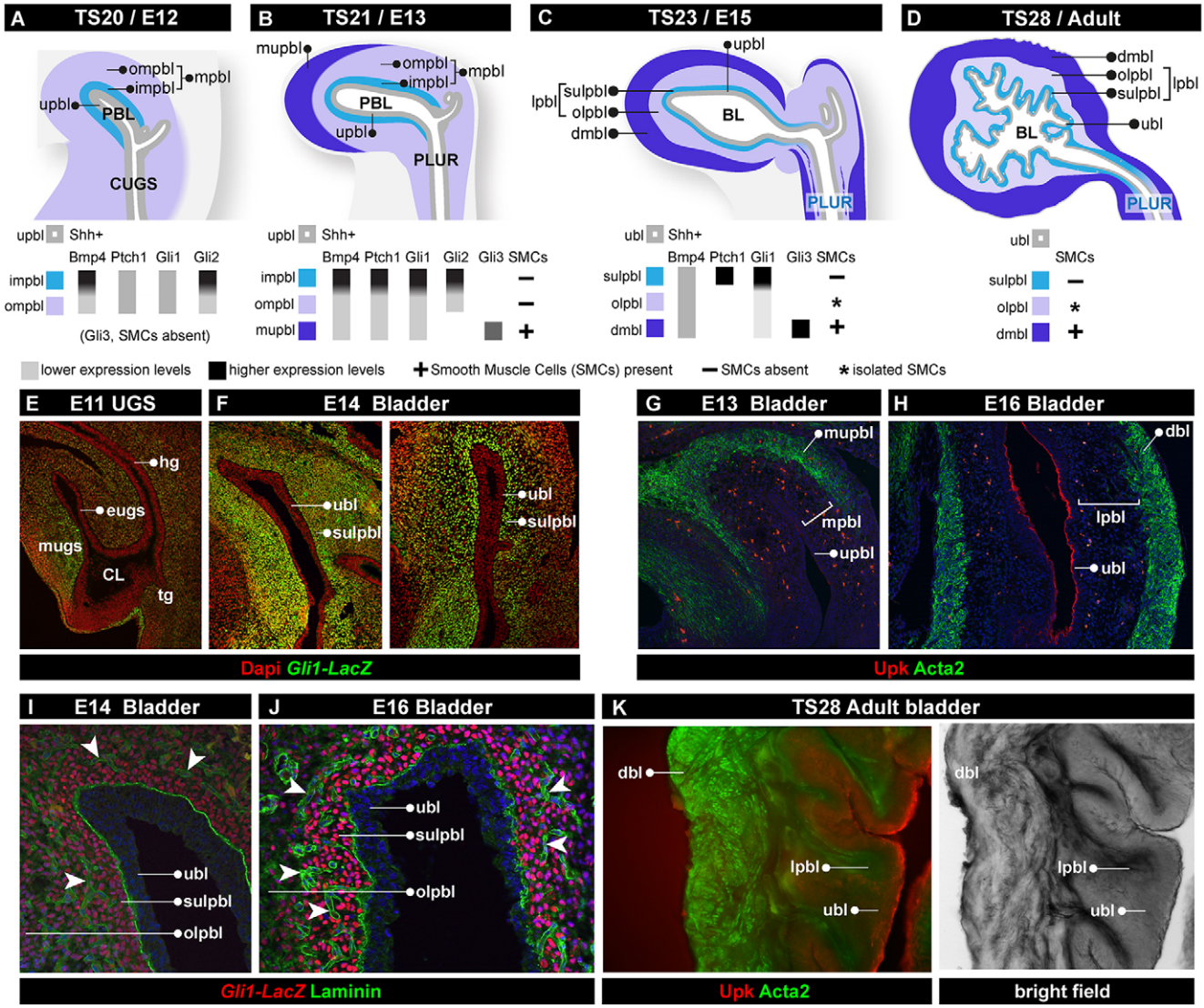

Fig. 7. Radial patterning of the bladder mesenchyme activates and maintains smooth muscle differentiation. (A-D) Schematics illustrate mesenchymal and smooth muscle layers. The urothelium expresses *Shh*, signalling the mesenchyme to express *Bmp4*, *Ptch1* and *Gli1-3*. Relative gene expression (lower-higher) and presence/absence of smooth muscle cells are shown. Muscle differentiation begins at the fundus and progresses towards the PLUR (B,C). (E,F) β-galactosidase-labelled *Gli1-lacZ* tissue sections show differential *Gli1* expression in the UGS and bladder mesenchyme. (G,H) Immunolabelled bladder sections show urothelium (Upk) and smooth muscle (Acta2). (I,J) β-galactosidase-labelled *Gli1-lacZ* tissue sections show location of *Gli1* and Laminin. Expression of *Gli1* is strongest in the suburothelial lamina propria (sulpbl) at E14 (I) and E16 (J) and weak or absent in the outer lamina propria (olpbl). The sulpbl also contains numerous blood vessels (Laminin^{+}, white arrowheads, I,J). (K) Immunolabelled vibratome sections show urothelium (Upk) and detrusor muscle (Acta2). Bright field (on the right) shows the convoluted adult bladder urothelium.

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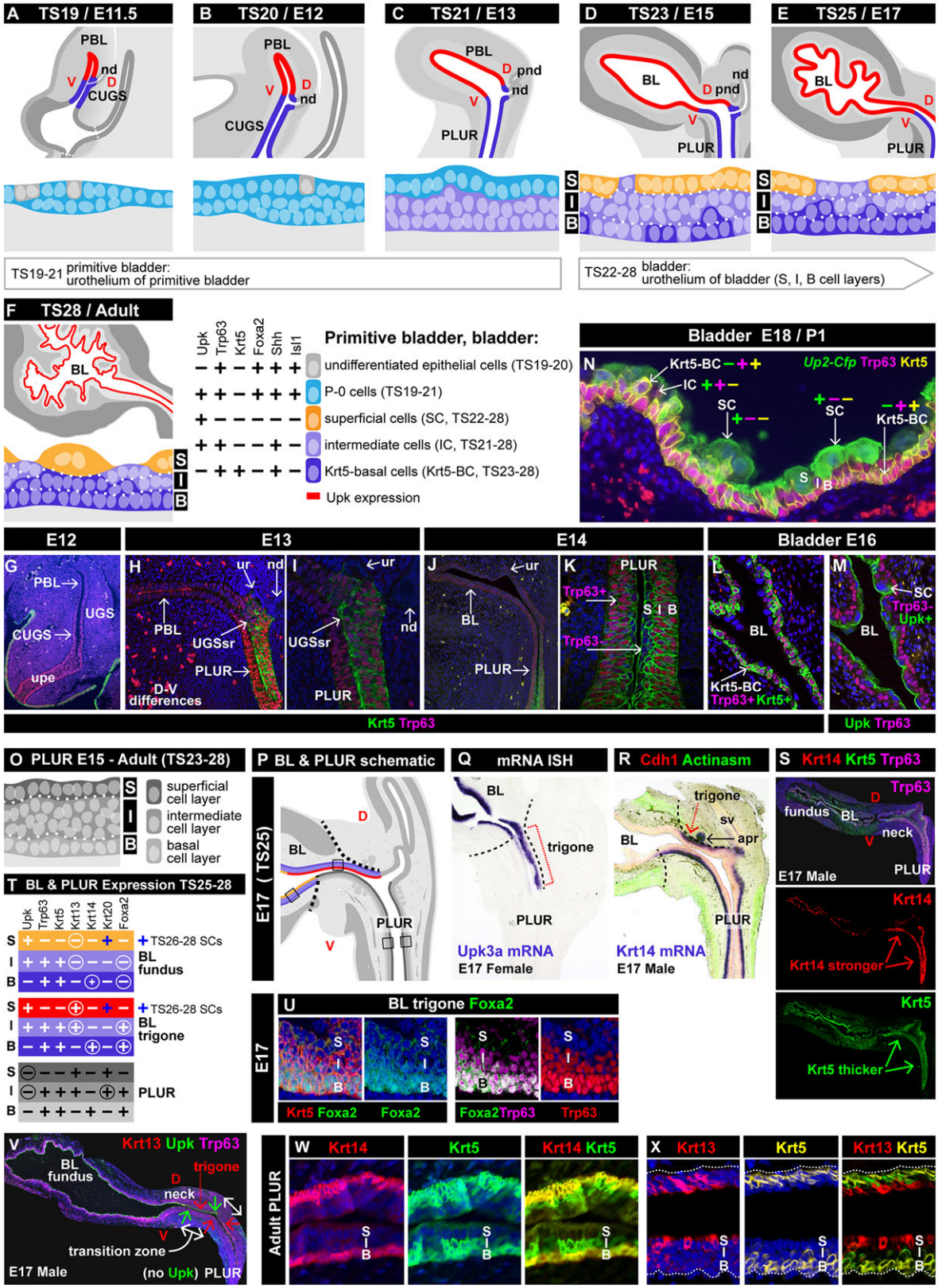

Fig. 8. See next page for legend.

Differentiation of smooth muscle cells from the bladder mesenchyme begins at E13.5 in the outer peripheral zone of the primitive bladder and progresses inwards towards the urothelium. Differentiation is dependent on *Shh* signalling from the cloacal endoderm-derived epithelium to the surrounding mesenchyme, which upregulates target genes, including *Bmp4*, *Ptch1* and *Gli1*, although their expression is seen much earlier, in the peri-cloacal mesenchyme at E10.5 (Cao et al., 2010; Cheng et al., 2008;

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Fig. 8. Protein expression defines the bladder urothelium and PLUR epithelium cell types. (A-F) Schematics illustrate epithelial layers; urothelium (red) and caudal UGS (CUGS)/PLUR epithelium (blue). Cross-sections below each panel illustrate location and gene expression of urothelial cell types. (D-F) From E14, bladder urothelium is divided into superficial (S), intermediate (I) and basal (B) cell layers. (G-N) Immunolabelling of LUT tissues. Expression of Trp63 is stronger in CUGS at E12 (G). Krt5 is not expressed in the bladder until after E14; however, expression is seen in the dorsal PLUR epithelium at E13 (H,I), which also shows stronger Trp63 expression. The PLUR superficial cell layer does not express Trp63 at E14 (J,K). (L-N) In the E16 (L,M) and E18 (N) urothelium, Upk is expressed by superficial (SC) and intermediate (IC) cells, Trp63 by ICs and Krt5-basal cells (BCs), and Krt5 exclusively by Krt5-BCs; however, these cells are found in both the basal and intermediate layers. By birth, SCs (or umbrella cells) are large and multi-nucleated (N). *Up2-Cfp* reporter mice show *Upk*-expressing cells (green, N). (O-X) Expression patterns in PLUR versus bladder regions (trigone, red dotted lines/arrows). (O) From E15, the PLUR epithelium is subdivided into superficial (S), intermediate (I) and basal (B) cell layers (S), which are thicker than the bladder urothelium. (P) Schematic shows bladder fundus/ventral neck (yellow), bladder dorsal neck/trigone (red) and PLUR epithelium (grey). (Q) All bladder regions express *Upk*. (R) *Krt14* expressed in bladder neck/trigone and PLUR at E17. (S,U-X) Immunolabelling in the BL-PLUR. (S) Krt14, Krt5 and Trp63 expression. (T) Summary of BL-PLUR expression profiles in the cell layers from E17 to adult (TS25-28). White circles indicate differences between bladder regions; black circles indicate differences between PLUR and bladder. Krt20 is expressed by mature SCs of the bladder from E18 to adult (blue '+' in T). (U) Foxa2 is expressed in bladder neck/trigone (U) and PLUR, but absent in the bladder fundus (data not shown). (V) E17 BL-PLUR showing tissue regions, Upk (green arrows) and Krt13 (red arrows) expression borders, with BL-PLUR transition zone in between (white arrows). (W,X) Adult PLUR showing Krt14, Krt5 and Krt13 expression in the epithelial layers.

DeSouza et al., 2013; Haraguchi et al., 2007; Liu et al., 2010; Shiroyanagi et al., 2007; Tasian et al., 2010; Suzuki et al., 2012). Fig. 7A-D summarises the relative expression levels of genes in the mesenchyme from E12-15. In the primitive bladder, the strongest expression is seen in a thin layer of the mesenchyme immediately underneath the urothelium, resulting in radial patterning of the mesenchyme. This sub-urothelial layer remains devoid of smooth muscle cells throughout development (Cao et al., 2008, 2010; Shiroyanagi et al., 2007; Fig. 7). We have used *Gli1-lacZ* reporter mice to illustrate this radial patterning (Fig. 7E,F,I,J). The mesenchyme also shows differential cell proliferation between inner and outer layers, also regulated by *Shh* (Tasian et al., 2010), and the inner layer contains numerous blood vessels (Fig. 7I,J). As a result of these findings, the primitive bladder mesenchyme (E12-13) has been subdivided into inner and outer layers (Fig. 7A,B). As smooth muscle cells are detectable at E13.5, before a distinct detrusor muscle is recognised, we have added muscle layer of primitive bladder (Fig. 7B,G). Smooth muscle cells express *Tgfb1* and *Myocd*, together with smooth muscle actins and myosins. Actin alpha-smooth muscle (*Acta2*) is utilised as a marker of early differentiation (Fig. 7G,H,K) and smooth muscle heavy chain myosin (*Myh11*) marks more advanced differentiation (Cheng et al., 2008; DeSouza et al., 2013; Liu et al., 2010; Shiroyanagi et al., 2007).

From E14 to adult, the bladder is composed of urothelium, lamina propria and detrusor muscle, surrounded by either serosa or adventitia, depending on location (Fig. 7 and Fig. 9B). The lamina propria is also subdivided into suburothelial and outer lamina propria layers (Fig. 7C,D,H-K). *Shh* signalling from the urothelium continues throughout development, and genetic markers of the primitive bladder inner mesenchyme maintain their expression in the suburothelial lamina propria of the bladder (Fig. 7A-D). An absence of smooth muscle cells continues to be characteristic of the suburothelial layer through to adult.

The 3D pattern of detrusor muscle differentiation in the mouse bladder has also recently been analysed (Carpenter et al., 2012). Differentiation begins in the distal fundus and advances towards the bladder neck (Fig. 7B). As development progresses and the bladder grows in size, the percentage of urothelium remains constant, whereas the percentage of lamina propria decreases as the outer mesenchyme differentiates into smooth muscle cells of the detrusor.

A smooth muscle layer also differentiates from the PLUR mesenchyme. Unlike the bladder, PLUR mesenchyme does not form a thick muscular layer and was therefore not subdivided into inner and outer layers. There is some evidence that testosterone and oestradiol control smooth muscle differentiation in PLUR of rats and mice (Chrisman and Thomson, 2006; Thomson et al., 2002), and *TGFb* signalling might also play a role (Tomlinson et al., 2004). At E13.5, the PLUR is composed of an epithelium, mesenchyme and outer adventitia and, at E14.5, develops a muscle layer. From E15.5 to adult, the mesenchymal layer further differentiates into a thin lamina propria, discontinuous muscularis mucosa (containing smooth muscle cells) and underlying submucosa (Fig. 5 and Fig. 9C). Recent gene expression analysis in the E17 PLUR has provided many markers to distinguish these tissue layers (Abler et al., 2011a). Originally, the terms 'muscularis mucosa' and 'muscularis submucosa' were present in bladder ontology. However, unlike the PLUR, the mouse bladder does not contain a distinct muscularis layer and therefore these layers have been removed.

Late during development, the rhabdosphincter, another muscular structure, which is new to the ontology, develops in the PLUR of both sexes (Fig. 5I-K). The development of this structure is important for normal function of the urinary tract in mice and humans, because decreased sphincter tone and/or thickness, especially in aging multiparous women, has been associated with stress urinary incontinence (Athanasiou et al., 1999; Rortveit et al., 2003). Urethral sling and pelvic mesh surgeries to repair stress urinary incontinence are often ineffective and can lead to complications. Regenerative therapies involving stem cells are a hot research topic as an alternative to these therapies, and understanding sphincter muscle lineage is therefore central to these studies. This suggests a need for lineage studies to define the rhabdosphincter origin. Striated muscle cells develop in the anterior PLUR forming the rhabdosphincter (Borirakchanyavat et al., 1997), which is marked by actin α-skeletal muscle expression (Acta1, Fig. 5J). Although seen in the mouse at E17 (E.M.S.-S., unpublished data) and in rats at birth (Borirakchanyavat et al., 1997), the stage at which the rhabdosphincter forms in the mouse is not known.

Marker expression and lineage analyses define cell types in the bladder urothelium and urethra epithelium

The adult bladder urothelium is stratified, containing a basal layer of Krt5-expressing basal cells (Krt5-BCs), one or more layers of intermediate cells (ICs), and a superficial (or luminal) layer of superficial cells (SCs) (Gandhi et al., 2013). Lineage analysis in mouse suggests that ICs are progenitors that self-renew and generate SCs in the adult, whereas, during development, P-0 cells, a newly identified population undetectable in the adult, serve as transient progenitors that generate ICs and SCs in the embryo (Gandhi et al., 2013). The bladder urothelial ontology has been revised to include cell types, while retaining urothelial layers. This enables the annotation of data without knowing the cell type, and allows for the incorporation of data from previous publications referring to layer.

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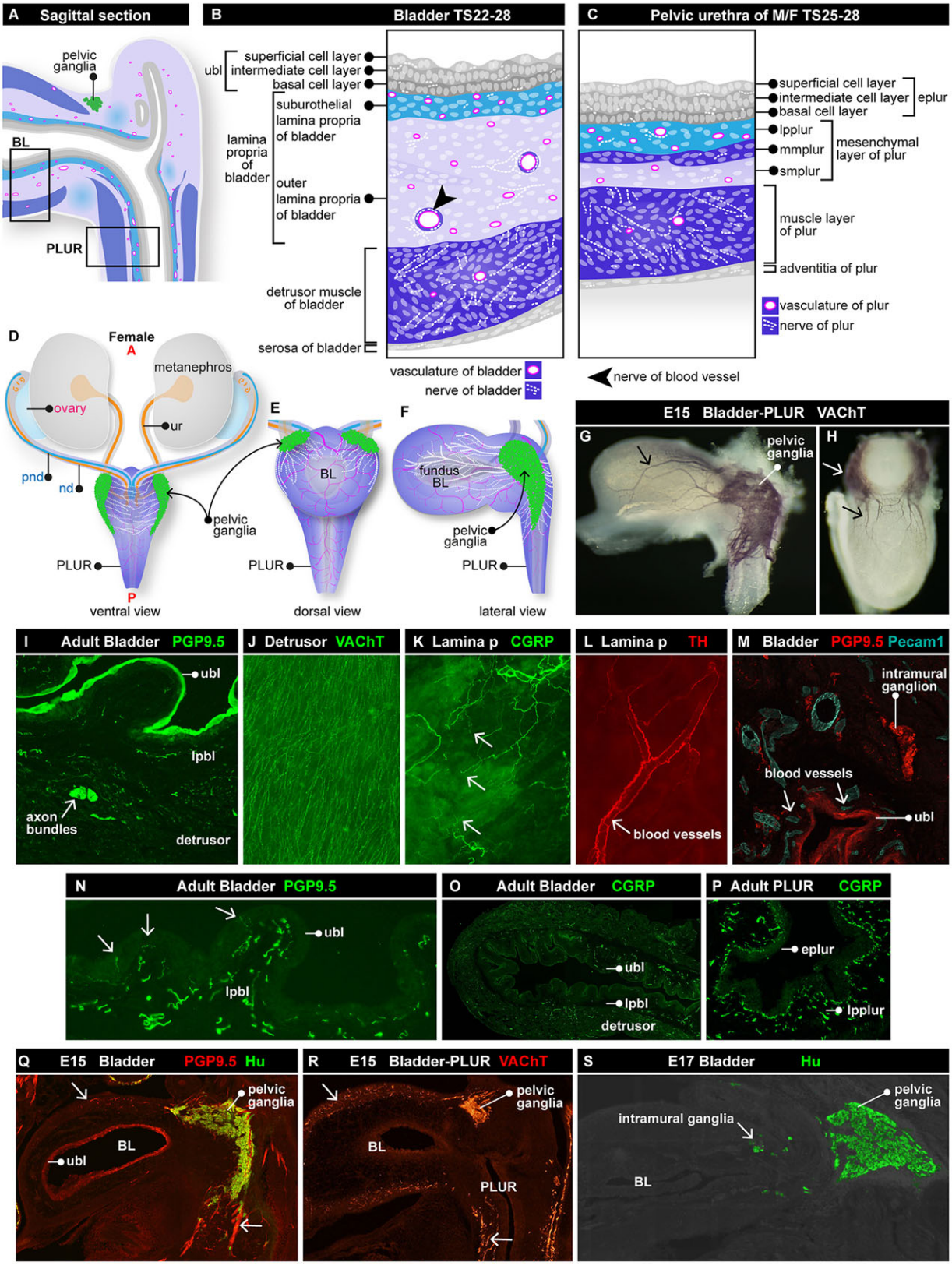

Fig. 9. See next page for legend.

Urothelial cell types have been defined by marker expression and relative position (Gandhi et al., 2013). During development, the cellular composition of the urothelial layers changes considerably (Fig. 8A-M; supplementary material). The urothelium expresses a series of endodermal markers (Shh, Trp63, Isl1, Foxa2). From E11-12, a small number of endodermal epithelial cells (Upk^{-}) are seen; however, most of the primitive bladder is lined by P-0 cells, transient progenitors expressing Upk and endodermal markers but

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Fig. 9. Nerves, pelvic ganglia and vasculature of the LUT. (A-F) E15 schematics illustrate nerves, pelvic ganglia (green) and vasculature. Pelvic ganglia extend their processes towards the PLUR midline (D) and bladder fundus (E,F). Only small areas of pelvic ganglia are visible in midline sagittal sections (A). (B,C) Bladder (E14 to adult) and PLUR (E17 to adult) ontology terms. Nerves are present in each tissue layer, in addition to nerves of blood vessels (arrowhead, B). (G,H) Whole-mount bladder-PLUR immunolabelled for VAChT show pelvic ganglion (white arrow), with axonal processes extending towards the bladder fundus (black arrows). (I) The pan-neuronal marker PGP9.5 labels axons, axon bundles (white arrow) and urothelial superficial cells in transverse section. (J) VAChT, marking cholinergic autonomic axons, labels varicose axons in whole-thickness adult detrusor. (K) CGRP marks a major population of sensory axons in whole-thickness lamina propria of adult bladder (focusing on suburothelial lamina propria). Arrows indicate terminating axons. (L) Tyrosine hydroxylase marking noradrenergic autonomic axons in whole-thickness lamina propria of adult bladder showing blood vessel innervation. (M) Pecam1-labelled vasculature (vascular endothelial cells) beneath the adult urothelium (PGP9.5^{+}). Clustered PGP9.5^{+} neuronal cell bodies form an intramural ganglion. (N,O) CGRP-labelled sensory axons form a network in the lamina propria, especially the suburothelial region (transverse section). Usually terminating in basal and intermediate urothelial layers, some axons penetrate the superficial cell layer (arrows, N). CGRP^{+} axons show even density in the bladder fundus, but there is an increase in suburothelial axons closer to the bladder neck (right hand of image, O). (P) Anterior PLUR transverse section shows the dense plexus of CGRP^{+} sensory axons in the lamina propria. (Q-S) BL-PLUR sagittal sections showing pelvic ganglia. At E15, neuronal bodies (Hu^{+}) within pelvic ganglia begin segregating into distinct clusters. Axonal processes (PGP9.5^{+}) extend towards the bladder fundus and distal urethra (arrows, Q). VAChT immunolabelling highlights nerve fibre density and penetration, showing axons in the distal bladder fundus and PLUR (arrows, R). At E15, nerve fibres have not penetrated the detrusor. By contrast, urethral innervation is denser and close to the epithelium (R). At E17, clusters of Hu^{+} neuronal bodies are evident within intramural ganglia of the bladder neck (S).

not Krt5 (C.M., unpublished data). By E13, ICs make up most of the urothelium.

From E14, the ontology subdivides urothelium into superficial, intermediate and basal cell layers (Fig. 8A-M). By E14, the basal layer is lined with ICs and the superficial layer mostly with SCs. The intermediate layer consists solely of ICs until E13. Krt5-BCs, first identified between E14 and E15, are seen in intermediate and basal layers. By E17, they line the entire basal layer, displacing ICs to the intermediate layer. In the adult, Krt5-BCs make up 90% of the urothelium, whereas ICs and SCs each make up 5% (Gandhi et al., 2013). Interestingly, our analysis suggests that a second Krt5-BC population (Krt5^{+}, Krt14^{+}, Trp63^{+}) emerges after E17 (C.M., unpublished data). Krt5-BC populations self-renew (Colopy et al., 2014) and are known to arise from cloacal endoderm; however, whether they have a distinct progenitor in the bladder is unclear.

Early in development, the UPE, primitive bladder and caudal UGS all express Shh, Trp63, Isl1 and Foxa2. Trp63 expression is shown in the bladder-PLUR (Fig. 8G-K). Krt5, a marker of Krt5-BCs in the bladder urothelium, is also expressed by the PLUR (Fig. 8H-K). Although not expressed by the bladder until after E14, it is seen as early as E12 in the caudal UGS (Fig. 8G) and UGS ridge at early stages (Fig. 8H,I).

Like the urothelium, the PLUR epithelium is stratified and, from E15, has been subdivided into superficial, intermediate and basal cell layers (Fig. 8O,P). We have used protein expression analysis to examine the distinct cell types that populate the PLUR epithelium compared with the bladder neck/trigone and fundus (Fig. 8). The PLUR basal cell layer is populated by cells expressing Trp63, Krt5, Krt14 and Foxa2. A second cell type (Trp63^{+}, Krt5^{+}, Foxa2^{+}, Krt14^{-}, Krt13^{+}) resides in the intermediate layer, and the superficial layer is populated by a third cell type (Trp63^{-}, Krt5^{-}, Krt14^{-}, Foxa2^{-}, Krt13^{+}). *Kremen1* expression marks the PLUR intermediate and basal cell layers at E17 (Abler et al., 2011a). As is the case with bladder Krt5-BCs, the lineage of these PLUR cell types is not clear; however, these cells persist into adulthood (Fig. 8W,X).

The epithelium transitions from bladder urothelium to PLUR epithelium. Even late in development, there is a distinct zone where the epithelium transitions (Fig. 8V). Between these regions the epithelial expression profile changes. The bladder-PLUR regions are shown at E17 (Fig. 8P-S,V), although the bladder neck is more elongated in the adult (Fig. 5M). PLUR epithelium is thicker than bladder urothelium (see Krt5, Fig. 8S). E17 bladder shows *Upk3a* mRNA and Upk protein in the intermediate and superficial cell layers of the bladder fundus, neck and trigone, but not in the PLUR (Fig. 8Q,V) (Abler et al., 2011a). The PLUR, bladder neck and trigone basal cell layers all strongly express Krt14 (Fig. 8R-T,W), which is weakly expressed by the bladder fundus (Fig. 8S,T). Foxa2 and Krt13 are exclusively expressed by the PLUR, bladder neck and trigone (Fig. 8V,X,U). Therefore, the combined expression patterns of Foxa2, Krt13, Krt14 and Upks can be used to identify distinct epithelial regions (Fig. 8T).

Nerves, vasculature and pelvic ganglia

The adult lower urogenital tract receives an extensive supply of nerves and vasculature, forming well before birth (supplementary material). In this update, nerves and vasculature have been added as components of the major organs and tissues. In addition, from E15 to adult (TS23-28), nerves of the bladder and PLUR have been described in much more detail and have been added as components of each tissue layer within these organs (Fig. 9). This updated ontology also defines blood vessels within each of the tissue layers so that nerves supplying those vessels can be annotated. However, prior to E15, the ontology has not been updated to the same level of detail. This will require further refinement once innervation and vascularisation of earlier stages and other LUT tissues have been examined more closely.

Numerous developing neural subpopulations have been identified and show distinct patterns of distribution among LUT tissues (Fig. 9I-P). LUT nerves can be sensory or motor (autonomic). Although each should produce distinctive transmitters or related signalling molecules, they are structurally indistinguishable, and no data currently exists on the spatiotemporal distinction between these populations. For this reason, the different types are not distinguished in the ontology. The pelvic ganglia are paired ganglia that develop in the LUT close to the anterior PLUR (Fig. 9D-H,Q-S). They comprise a mixture of both sympathetic and parasympathetic neurons (Keast, 1995; Wanigasekara et al., 2003). The intermixing of sympathetic and parasympathetic neurons within the one ganglion is unique in the autonomic nervous system. In rodents, pelvic ganglia also show considerable sexual dimorphism (Greenwood et al., 1985) (supplementary material).

DISCUSSION

Presented here is a definitive spatiotemporal description of the developing lower urinary and reproductive tracts, at the level of organ, tissue and, where possible, component cell type. This information has been incorporated into a text-based anatomical ontology spanning developmental time, space and gender. The improved ontology will provide a common language for those in the field, and enable higher resolution annotations of gene and protein expression in the developing and adult lower urogenital tract of both

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wild type and genetically altered mouse models. This will in turn facilitate the identification of markers of novel subcompartments at a finer microanatomical resolution. As such, the revised ontology will provide a basis for understanding congenital lower urogenital tract abnormalities commonly seen, but not well understood, in humans.

MATERIALS AND METHODS

Literature review

A comprehensive literature review was performed to improve accuracy of the mouse lower urogenital tract ontology from E10.5 to adult (supplementary material). Ontology changes were made based upon this review and group consensus of the authors.

Modifications to the GUDMAP ontology

The structure and principles of the GUDMAP ontology have been described (supplementary material; Little et al., 2007). The updated ontology and definitions (including features, synonyms, molecular markers and lineage relationships where established) are available on the GUDMAP website (http://www.gudmap.org/Resources/Ontology/index.php). The ontology has been entered into the EMAP mouse embryo ontology (Hayamizu et al., 2013) and published on the Open Biological and Biomedical Ontologies web resource (http://www.obofoundry.org/).

Mouse strains, tissue collection and processing

All procedures involving animals were approved by the relevant animal ethics committees (details in supplementary material, including transgenic staining). Wild-type mice were C57BL/6, C57BL/6J or Swiss Webster. Timed matings were established and foetal tissues collected at stages indicated in the Figures. Adult mice were euthanized by isoflurane overdose or cervical dislocation. Tissues were dissected in phosphate-buffered saline (PBS) and fixed before proceeding to whole-mount methods or sectioning.

Immunohistochemistry (IHC) and immunofluorescence (IF)

Detailed methods are included as supplementary material. For whole-mount IHC (Fig. 5B,F) (Keil et al., 2012), section IHC (Fig. 8R) (Abler et al., 2011a), E15 whole-mount IHC (Fig. 9G,H) (Wiese et al., 2012) and whole adult bladders (Fig. 9J-L) (Yan and Keast, 2008), tissues were immunostained as described previously.

For IF of tissues from Swiss Webster (Fig. 1D-G, Fig. 2F, Fig. 4H, Fig. 5C,F, J-L, Fig. 6G,H,K, Fig. 7G-J and Fig. 8G-N,S,U-X), *Hoxb7GFP* (Fig. 1I-M and Fig. 4D) and *Gli-lacZ* (Fig. 6E,F,I,J) mice, sectioned tissues (paraffin, frozen, vibratome) were pre-treated with 10% HIHS, 0.1% Triton-PBS for 1-2 h (25°C). Antigen retrieval was performed by boiling samples for 30 min. Primary antibodies (in 1% HIHS, 0.1% Triton-PBS) were incubated overnight (4°C). Slides were washed in 0.1% Triton-PBS, incubated with secondary antibodies 1-2 h (25°C), followed by DAPI (5-10 min) and cover-slipped with mounting medium (Dako). Antibodies detecting *Hoxb7-GFP* and *Gli-lacZ* were chicken anti-GFP (AVES, #GFP-1020; 1:300) and goat anti-β-galactosidase (Biogenesis, #4600-1409; 1:1000).

For IF of C57BL/6J tissues (Fig. 1H, Fig. 8R and Fig. 5J), 5-µm paraffin sections were labelled as described previously (Abler et al., 2011a). In Fig. 5J, two consecutive sections are shown, one stained with anti-Acta1 antibody and DAPI, the other with anti-Cdh1 and anti-Acta2 antibodies. Acta1 staining was pseudo-coloured yellow and the images were merged. For IF (Fig. 9I,N-P,Q-S), cryosections (14-20 µm thickness) were processed according to described methods (Yan and Keast, 2008; Wiese et al., 2012).

Section mRNA *in situ* hybridisation (SISH)

SISH using C57BL/6J E17 tissues (Fig. 8P,R) was conducted as described previously (see supplementary material; Abler et al., 2011a,b). IF (Fig. 8R) was performed post-SISH, using the C57BL/6J protocol described above.

β-galactosidase staining

For β-galactosidase activity detection (Figs 2,3) fixed *ShhGFPCre; Rosa26RlacZ* embryos were washed in *lacZ* buffer (1 M sodium phosphate pH 7.4, 0.1% sodium deoxycholate, 1 M $MgCl_2$, 0.2% NP40). For staining, X-gal (1 mg/ml), $K_3[Fe(CN)_6]$ and $K_4[Fe(CN)_6]$ (0.05 M) were added to the *lacZ* buffer, and embryos were incubated overnight (25°C). Embryos were washed in PBS and stored in 4% PFA.

Acknowledgements

The authors would like to thank Michael Wicks (MRC IGMM) for providing assistance with OBO file processing and for implementing the version control system, and Elsbeth Richardson for providing expert cryostat sectioning and immunostaining of nerves in adult mouse bladder. The anti-Hu antibody was a generous gift from Vanda A. Lennon (Department of Laboratory Medicine and Pathology, Mayo Clinic, Rochester, MN, USA). The GUDMAP Database and Website www.gudmap.org are funded by the National Institutes of Health (NIH).

Competing interests

The authors declare no competing or financial interests.

Author contributions

K.M.G., J.A., J.R.K., K.M.M., E.M.S.-S., M.J.C., M.H.L., C.M.V. and C.M. contributed to the conception and design of the manuscript. J.R.K., C.E.L., E.M.S.-S., M.J.C., E.B., H.D., K.S., D.P.B., C.B.W., C.M.V. and C.M. contributed to acquisition of experimental data. K.M.G., J.R.K., C.E.L., K.M.M., E.M.S.-S., M.J.C., E.B., H.D., K.S., D.P.B., C.B.W., C.M.V. and C.M. contributed to analysis and interpretation of data. K.M.G., J.R.K., C.E.L., K.M.M., E.M.S.-S., M.J.C., M.H.L., C.M.V. and C.M. contributed to the preparation and critical revision of the manuscript. K.M.G., J.R.K., C.E.L., E.M.S.-S., C.M.V. and C.M. contributed to figure design. J.A., J.B., J.A.D., S.D.H. and R.A.B. contributed to the implementation of the ontology and associated GUDMAP website data.

Funding

The research of the authors was supported by the National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK) [grant R01DK085242 to K.M.M.] and National Institutes of Health (NIH) grants [DK070136 to M.H.L.], [DK083425 to C.M.V.], [DK092983 to J.A.D. and R.A.B.], [DK094523 and ES017099 to M.J.C.], [UO1 DK094479 to J.R.K.], [R56 DK078158 R01 DK078158 and subcontract on U01 DK070219 to E.M.S.-S.]. M.H.L. is a National Health and Medical Research Council of Australia Senior Principal Research Fellow. Deposited in PMC for release after 12 months.

Supplementary material

Supplementary material available online at
http://dev.biologists.org/lookup/suppl/doi:10.1242/dev.117903/-/DC1

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Development (2015) 142, 1893-1908 doi:10.1242/dev.117903

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An illustrated anatomical ontology of the developing mouse lower urogenital tract

Supplementary material

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DETAILED METHODS AND MATERIALS

Modifications to the GUDMAP ontology

The ontology was written as a partonomic, hierarchical ontology to describe the subcompartments of the developing murine UGT (Little et al., 2007). The ontology uses Theiler staging (TS) to define developmental time, with modifications to the lower UGT ontology being made between TS18 (10.5dpc) and TS28 (representing the adult but defined as postnatal day 4 onwards). The original published UGT ontology listed anatomical terms for each TS separately, with every term appended with a unique stage-specific numerical identifier (EMAP:ID). An "abstract" (non-stage-specific) version of the ontology has subsequently been developed (Hayamizu et al., 2013). Here anatomical terms are given an EMAPA:ID with a TS range, indicating the developmental time frame that the term is present. The abstract ontology includes the introduction of the "is-a" relationship; for example nerve of bladder "is-a" nerve of urinary system and "part-of" bladder, together with the removal of the "group" relationship.

The modified version of the ontology is stored as an OBO formatted file, allowing it to be handled by text-editing software. The open source, Java-based ontology editor OBO-Edit2 was used to view the OBO file and make modifications to the ontology (Day-Richter et al., 2007). Editorial control of the revision process has been implemented, with version monitoring being provided by a Git revision control system (https://github.com/). The ontology is available from the GUDMAP website (http://www.gudmap.org/Resources/Ontology/index.php) and will be published on the Open Biological and Biomedical Ontologies (OBO) web resource (http://www.obofoundry.org/). Definitions of anatomical terms in the lower urogenital tract ontology, including defining features, synonyms, molecular markers and lineage relationships where established, can be found on the GUDMAP website (http://www.gudmap.org/Resources/Ontology/index.php) and also downloaded by following the Link to associated supplementary ontology documents.

Mouse strains

All procedures involving animals were approved by the appropriate institutional animal ethics committees, including; Animal Ethics Committee of the University of Melbourne and compliance with the Australian Code of Practice for the Care and Use of Animals for Scientific Purposes (NHMRC); Institutional Animal Care and Use Committee at Vanderbilt University; the University of Florida Institutional Animal Care and Use Committee; University of Wisconsin-Madison Animal Care and Use Committee; and the Institutional animal care and use committee of Columbia University. Mice were housed and bred in controlled animal facilities at each of the institutions, where the humidity, temperature and light/dark periods were kept constant. Animals were allowed access to food and water ad libitum. Transgenic mouse strains used (Supplementary Table 1) have been described previously (Ahn et al., 2004; Gandhi et al., 2013; Harfe et al., 2004; Rosselot et al., 2010; Seifert et al., 2008; Soriano, 1999; Srinivas et al., 1999; Sun et al., 2000).

Collection and processing of tissues

Embryos collected for whole-mount *lacZ* staining (Figures 2 and 3) were fixed for 1hour in 4% paraformaldehyde (PFA) at room temperature or overnight at 4°C in 0.2% PFA. In Figure 9M, Q-S, tissues for cryo-embedding were fixed by immersion in buffered formalin. In Figure 9I-L, N-P, tissues for cryo-embedding were collected after mice were anaesthetised with ketamine and xylazine (100 and 10mg/kg respectively, i.p.) then fixed by intracardiac perfusion with freshly prepared buffered 4% PFA (Kalous et al., 2012). In Figure 9M, adult tissues were collected after transcardiac perfusion and a subsequent 8 hours of fixation at 4°C in neutral buffered formalin. In Figure 9J-L, for adult bladders to be processed as whole mounts, after cervical dislocation, the bladder was removed, briefly rinsed in PBS, then the bladder was cut open along the dorsal midline, pinned flat and slightly

stretched in a dish lined with silicon polymer, then fixed by immersion in 4% PFA as above. E17 tissues, were dehydrated into 100% methanol post-fixation. For sectioning, tissues were embedded in paraffin or frozen in OCT and sectioned at various thicknesses (5-20µm) or embedded in 3% agarose and vibratome-sectioned (100-150µm). Paraffin sections were deparaffinised with Histoclear and rehydrated via an ethanol-series. Cryosections were prepared for immunolabelling by removing OCT by washing in PBS.

For Haematoxylin and eosin stained E17.5 sections in Figure 3U-V, sectioned CD1 females were crossed to males carrying the *ShhGFPcre;R26RlacZ* allele. Embryos were fixed overnight in 4% PFA and dehydrated through a graded ethanol series (25-50-75-100%) followed by Xylene washes. The embryos were incubated in 2 changes of paraffin wax at 55°C under vacuum. The embryos were then embedded in paraffin wax and sectioned at 10µm. Sections were dewaxed in Xylene, rehydrated through ethanol, stained with Harris haematoxylin and Eosin-Y, and finally dehydrated before mounting in Cytoseal.

Wholemount and section immunohistochemisty

For wholemount immunohistochemistry (IHC) of C57BL/6J E17 tissues (Figure 5B, F), labelling was conducted as previously described (Keil et al., 2012). For section IHC of C57BL/6J E17 tissues (Figure 8R), 5µm sagittal sections of paraffin embedded tissues were labelled as described previously (Abler et al., 2011a). For wholemount IHC of E15 bladder-urethra (Figure 9GH), labelling was performed according to methods described previously (Wiese et al., 2012). For whole adult bladders (Figure 9J-L), tissues were immunostained as described previously for studies of whole mount ganglion preparations (Yan and Keast, 2008). All primary antibodies are listed in Table 2.

Section immunofluorescence

For section IF of C57BL/6J fetal tissues at E13 (Figure 1H), E17 (Figure 8R), 5µm sections of paraffin-embedded tissues were labelled as described previously (Abler et al., 2011a). Primary antibodies (Table 2) were followed by species-specific secondary antibodies; Dylight 488 conjugated goat-anti mouse IgG (Jackson ImmunoResearch, #115-487-003, 1:250-500 dilution), Dylight 549 conjugated goat-anti-rabbit IgG (Jackson ImmunoResearch, #115-487-003, 1:500 dilution). For IF of adult tissue shown in Figure 5J: two consecutive 5µm sections are shown, one section was stained with anti-Acta1 mouse monoclonal and DAPI, the other section was stained with anti-Cdh1 rabbit monoclonal and anti-Acta2 mouse monoclonal (see Table 2) and secondary antibodies were Dylight 488 conjugated goat-anti mouse IgG (Jackson ImmunoResearch, #115-487-003, 1:500 dilution), and Dylight 549 conjugated goat-anti-rabbit IgG (Jackson ImmunoResearch, #115-487-003, 1:500 dilution).

For IF of C57BL/6 cryosectioned tissues (Figure 9I, N-P), 14µm cryosections were processed for direct label IF, as described previously (Yan and Keast, 2008). Primary antibodies (Table 2) were detected using species-specific secondary antibodies labelled with fluorophores; Cy3, FITC, AF488 or AF594 (Jackson ImmunoResearch, 1:1000-1:2000 dilution). IF of fetal tissues cryosectioned at 15-20µm (Figure 9Q-S) was performed according to methods described previously, using primary antibodies listed in Table 2 (Wiese et al., 2012).

Section mRNA *in situ* hybridisation

Section mRNA *in situ* hybridisation (SISH) using C57BL/6J E17 tissues (Figure 8P, R), sectioned at 50µm, was conducted as described previously (Abler et al., 2011a, Abler et al., 2011b). Primer sequences used to generate the riboprobe templates were as follows: *Krt14* (nucleotides 1275-1625

of NM_016958.1, 5'-TGCTGGATGTGAAGACAAGG-3' and 5'-CGATGT**TAATACGACTCACTATAGGG**CAGGAAGGACAAGGGTCAAG-3') and *Upk3a* (nucleotides 327 to 933 of NM_023478.2, 5'-TCCCACTGAGCACCACTTTC-3' and 5'-CGATGT**TAATACGACTCACTATAGGG**AGCTTGCTGGAGAACACCTC-3'). Bold, underlined sequences represent a synthetic T7 RNA polymerase binding site incorporated into the PCR primer. Annotated SISH expression patterns for *Krt14* and *Upk3a* are available on the GUDMAP website (www.gudmap.org) with the Accession IDs, GUDMAP:14299 and GUDMAP:14338, respectively. In Figure 8R, IF was performed post-SISH using primary antibodies (Table 2) and secondary antibodies; Fluo-549-labeled polyclonal goat anti-rabbit IgG (Jackson ImmunoResearch Laboratories Inc., 1:500 dilution) and Fluo-488-labeled polyclonal goat anti-mouse IgG (Jackson ImmunoResearch Laboratories Inc., 1:500 dilution), using the IF protocol described above for E17 tissue.

DETAILED LITERATURE REVIEW

Connecting the upper and lower urogenital tract

In the mouse, UGT development begins with formation of the nephric ducts (NDs, also called mesonephric or Wolffian ducts), paired epithelial tubes derived from intermediate mesoderm. From E9-11, the NDs elongate down the embryo and insert into the cloaca, establishing a primary connection between the upper and lower urogenital tract. The cloaca, an epithelial lined cavity derived from endoderm, undergoes septation from E11-13, forming the UGS ventrally and the hindgut dorsally, separated by a strip of mesenchyme called the urorectal septum (URS, Figure 1A-C) (Sasaki et al., 2004; Seifert et al., 2008). Correct cloacal insertion of the NDs is dependent on a number of signalling pathways including *Ret*, *Gata3*, *Retinoids* and *Fgf*, and is crucial to proper positioning of the ureters later in development (Chia et al., 2011; Walker et al., 2013).

Kidney development begins at E10.5, when epithelial ureteric buds (UBs) emerge from the caudal nephric ducts and grow into the adjacent metanephric mesenchyme (MM), in a position anterior to the cloaca. The buds then branch to form a T-shape. Seen at E11.5, the T-shaped UBs are comprised of a ureteric stalk and tips (Figure 1A). Mesenchyme condenses around the tips, forming the cap mesenchyme, the nephron progenitor source during kidney development. Throughout embryogenesis, the ureteric tree will undergo successive rounds of branching morphogenesis to form the renal collecting duct system and renal pelvis of the paired kidneys. The UB stalks will form the ureters, muscular tubes that conduct urine from the renal pelvis to the bladder, where it is stored and excreted. At E11, the UB stalks have not yet established independent insertion sites in the UGS and connect indirectly via the common nephric duct (CND, Figure 1A). The CNDs are defined as the caudal ND segments, below the level of the UB stalk attachment site. From E12-13, the CNDs undergo apoptosis and the ureters make contact with, then merge with the primitive bladder (PBL, Figure 1BC, I-L). As the UGS grows, the ureter orifice moves cranially, while the NDs remain joined to the urogenital sinus ridge (UGS ridge, Figure 1C, L) (Batourina et al., 2005). By E14.5, the ureters and NDs are separated and the CND has regressed (Figure 1M) (Batourina et al., 2005; Mendelsohn, 2009; Viana et al., 2007).

Failure of the ureters to enter the bladder at the correct position can result in urinary obstruction, megaureter and hydronephrosis, or vesicoureteral reflux (Murawski et al., 2008; Wu et al., 2009b). Hydronephrosis commonly results from defective peristalsis (Feeney et al., 2014) or mis-positioned distal ureters, which can be caused by a number of defects including delayed ND insertion (Chia et al., 2011; Walker et al., 2013), abnormal sprouting of the UB (Mackie et al., 1975) or failure in CND remodelling (Batourina et al., 2005; Hoshi et al., 2012; Uetani et al., 2009). Insertion of ureters lateral to the regular insertion site can cause vesicoureteral reflux (Murawski et al., 2007), while insertion at a posterior position, for example in the urethra, can result in urinary obstruction,

impeding the flow of urine from the kidney to the bladder (Hutch, 1972; Tanagho, 1981; Weiss, 1988). Due to the intimate connection with the kidneys, the resulting backflow of urine can lead to hydronephrosis and ultimately renal failure.

Emergence of the genital tubercle and urethral plate epithelium

As occurs in the urinary tract, epithelial-to-mesenchymal interactions play a critical role during genital tubercle (GT) development. *Shh* is expressed by the entire cloacal epithelium and urethral plate epithelium (UPE) and plays a critical role during GT development (Seifert et al., 2010). *Shh* in the UPE regulates gene expression in the adjacent mesenchyme, including *Ptch1, Gli1, Bmp4, Hoxd13*, and *Fgf10* (Haraguchi et al., 2001; Haraguchi et al., 2007; Haraguchi et al., 2000; Lin et al., 2009; Miyagawa et al., 2009; Perriton et al., 2002; Seifert et al., 2009b). *Shh* also promotes GT outgrowth by regulating cell cycle kinetics in GT mesenchyme (Seifert et al., 2010). At E10.5, prior to any obvious GT outgrowth, *Fgf8* is seen at the cloacal membrane, where the surface ectoderm meets the cloacal epithelium (Haraguchi et al., 2001; Haraguchi et al., 2007; Haraguchi et al., 2000; Perriton et al., 2002; Seifert et al., 2009b). Although *Fgf8* has no endogenous role in GT development, its transcription serves as a marker of the endodermal component of the cloacal membrane (Seifert et al., 2009b). Mesenchymal growth from paired ventrolateral genital swellings, which develop in a slightly anterior position adjacent to the cloaca, pushes the epithelial walls of the cloaca together at the cloacal membrane (Perriton et al., 2002). At E11.5, the GT is subdivided into ventrolateral genital swellings and a dorsal genital swelling (Figure 2A) (Perriton et al., 2002; Yamada et al., 2006). At E13, the GT has extended distally out from the embryo and is subdivided into distal (dgt) and proximal (pgt) regions, each comprised of mesenchyme (mpgt/mdgt) and skin (Figure 1C, 2C), and two laterally-positioned preputial swellings (pps, Figure 2C).

Growth from the urorectal septum completely separates the hindgut and UGS. In mice, the urorectal septum is marked by strong *Bmp7* expression, and persistent cloaca and rectourethral fistula are seen in *Bmp7* null embryos (Wu et al., 2009a). In humans, we refer to the skin between the urethral opening and the anus as the perineum. In the mouse, rupturing of the cloacal membrane exposes the terminus of the urorectal septum, which is covered by cloacal endoderm-derived epithelium, between the urethral and hindgut openings (proximal urethral meatus and anus) (Seifert et al., 2008). Consequently, the cloacal endoderm overlying the urorectal septum forms the midline of the perineum, and in mice, is marked by the *Shh+* endodermal cell lineage (Figure 1C) and β-catenin expression (Figure 1H). The skin on either side of the perineum midline is however, surface ectoderm derived (Figure 1C) (Seifert et al., 2008). Endodermally-derived cells remain on the perineum surface until P0, although whether they persist or are replaced after birth remains to be determined.

At E13, the UPE has begun to canalise into a tube (urethral tube epithelium, UTE), forming the phallic urethra (PHUR, Figure 1C). Canalisation is aided by mesenchymal growth from the base of the GT, which surrounds the tube. This mesenchyme is sometimes referred to as the urethral folds. The PHUR epithelium is proximo-distally patterned throughout development. The UPE and UTE show varying degrees of differentiation and different gene expression patterns (Suzuki et al., 2008). *Fgf8* becomes restricted to the growing distal tip, where *Shh* and *Bmp7* are also strongly expressed (Haraguchi et al., 2001; Haraguchi et al., 2000; Perriton et al., 2002; Seifert et al., 2009a; Suzuki et al., 2003).

Updated anatomy of the postnatal mouse penis and clitoris

The postnatal structure of the mouse penis and clitoris has recently been revisited (Rodriguez et al., 2012; Rodriguez et al., 2011; Schlomer et al., 2013; Weiss et al., 2012) and comparisons between human and mouse have been reviewed (Cohn, 2011; Yamada et al., 2003; Yamada et al., 2006). In humans, external genitalia sexual differentiation is completed early in the second trimester (Siiteri et al., 1974; Sinisi et al., 2003; Yiee et al., 2010). In mice however, even at birth, male and female external genitalia are more similar than in humans, both morphologically and morphometrically (Schlomer et al., 2013). Sexual differentiation in mice begins at E15.5 and continues postnatally, such that by 10 days after birth, males and females are quite different and begin to resemble the adult anatomy (Schlomer et al., 2013; Weiss et al., 2012). By 21 days, dramatic differences are seen between the sexes indicating that a significant amount of sexual differentiation occurs after birth in mice. Eight diagnostic anatomical features distinguishable in the adult mouse penis/clitoris have been described (Yang et al., 2010) and sex differences have been examined in the neonatal period (Schlomer et al., 2013) and adult (Weiss et al., 2012).

In males, the penis is subdivided into the glans penis and body of penis (Figure 3W-Y). The penile urethra (PNUR) lies ventrally along the length of the penis and below it lies the corpus cavernosum urethra, erectile tissue (Figure 3W-Y). The penile body also contains two lateral paired bands of erectile tissues, the corpora cavernosa (also called crura; or crus, singular) which attach to the pubic bone (Figure 3W-Y) (Rodriguez et al., 2011). From the body of the penis, the PNUR makes a right angle bend as it extends into the glans penis and it opens at the urethral meatus, located near the distal tip of the penis (Figure 3WY). Proximal to the male urogenital mating protuberance (MUMP), the glandular ridge encircles the glans and contains two linear corpora cavernosa glandis, which run ventrally and dorsally along the glans (Figure 3W-Y). The os penis is a ~3.8mm long bone (although its size is variable) surrounded by hyaline cartilage that lies in the centre of the glans above the

urethra, and overlaps the proximal end of the MUMP (Figure 3W-Y). Cartilage undergoes calcification to form the os penis bone at around 6 months of age. The MUMP is comprised of a cartilage core surrounded by corpus cavernosum and covered with skin and its boundary (red dotted line, Figure 3W-X) is defined by the MUMP ridge, a groove that encircles the distal glans penis. Externally, the preputial seam can be seen as a ventral cleft in the prepuce, extending from the urethral meatus to the tip of the glans penis, where it meets the MUMP. This cleft in the prepuce, which results from preputial fusion, is different to the seam along the ventral side of the glans penis, which is a remnant of the UPE.

The morphology of the adult penis and clitoris can be disrupted when the balance between androgen and estrogen action is altered during late prenatal or postnatal development. Changes to the shape and size of the external genitalia, MUMP size, amount of bone, cartilage and erectile tissue and other features, have all been shown to be influenced by changes in androgen and estrogen action in mice (Blaschko et al., 2013; Yang et al., 2010; Yucel et al., 2003). These changes can lead to abnormal morphology of the external genitalia, feminisation of males and masculinisation of females.

Sexual differentiation of the reproductive ducts and their connection to the pelvic urethra

At E15.5, in both sexes, the caudal ends of the paramesonephric ducts (PNDs, or Mullerian ducts) have laterally fused and the NDs remain connected to the PLUR at the urogenital sinus ridge (UGS ridge, Figure 2E, Figure 4A-B, E) (Iizuka-Kogo et al., 2007). However, the production of Anti-Mullerian Hormone by the testes has already initiated PND degeneration in males. PND degeneration, regulated by β-catenin signalling, progresses in a rostral-to-caudal wave (Figure 4A). Conversely in females, the NDs (also known as mesonephric or Wolffian ducts) degenerate in a

similar directional pattern (Figure 4E). Mesonephric tubules (mt) also degenerate in females (Figure 4E). By E16.5, sex-specific duct degeneration is almost complete, with only remnants of the ducts seen in both sexes (Figure 4C, F) (Iizuka-Kogo et al., 2007).

In developing female mice, the fused caudal portion of the PNDs becomes the upper vagina (UV), eventually becoming the adult vagina (Kurita, 2010). The oviducts, uterus and uterine horn are also derived from the PNDs. *Lhx1* is required in the PND epithelium for normal female development (Huang et al., 2014) and failure of the PNDs to either elongate or fuse can result in congenital absence or duplication of vagina, cervix and uterus, respectively, such as seen in *Dlgh1* KO mice (Iizuka-Kogo et al., 2007). At E16, the female UGS ridge becomes the sinovaginal bulb (SVB, Figure 4F). As development progresses, the SVB separates from the PLUR and the fused UV-SVB extends along the urethra in a caudal direction towards the clitoris (Figure 4F-G). At birth, the vagina is closed and the UV remains internally fused to the urethral epithelium via the SVB. When the SVB reaches the base of the clitoris by P8 (Kurita, 2010), it separates from the urethra, however, because the SVB is a solid epithelial cord, the vagina remains closed. It opens later during puberty, at approximately P28, via an apoptosis dependent process, which can be prevented by the overexpression of *Bcl2* (Kurita, 2010; Rodriguez et al., 1997). In the adult, the entire vaginal epithelium is derived from *Hoxb7-Cre* expressing PND epithelia and does not contain cells derived from the UGS, UGS ridge or NDs (Kurita, 2010). Vulvar epithelium does contain cells derived from UGS and it is thought that during vaginal opening, the remaining SVB epithelial cells become part of the vulvar epithelium (Kurita, 2010).

During development, the anterior reproductive ducts differentiate into other components of the reproductive system; in females, anterior PNDs will become the oviducts, connecting the uterus to the ovaries, and in males the anterior NDs will become the epididymis, while the cranial

mesonephric tubules will become the efferent ducts, completing the connection between the ductus deferens and the testes.

Morphological sex differences in the pelvic urethra

During PLUR development, three distinct clusters of condensed mesenchyme form at the bladder neck-urethra junction, centred on the midline at sites where the prostate buds develop in the male (Figure 4D, Figure 5A-B). These mesenchymal pads, seen from E17 to birth, are thought to play a role in bud differentiation (Timms et al., 1995). Females also develop mesenchymal pads though they are smaller and more elongated than the male (Figure 5E) (Abler et al., 2011). Mesenchymal pads of both sexes are subdivided into dorsal, ventral and lateral (Figure 5A, E). All pads are marked by F*gf10*, while *Scmh1* specifically marks the male and female ventral mesenchymal pads (Abler et al., 2011).

In the E17 male PLUR, the lamina propria and submucosa layers are thicker, whilst the female has a thicker muscle layer, which is also continuous with the detrusor muscle of the female bladder, where there is a large gap in males (Figure 5A-C, E-G) (Abler et al., 2011). The angle the PLUR connects to the bladder also differs between sexes. Seen at a right angle in males, and more linear in females, the angle is prominent at E17 and is maintained in the adult (Figure 5A, E, I', K'). As development progresses, continued sex-specific differentiation eventually results in an adult urethra that is highly sexually dimorphic (Figure 5I-N). This reflects the dual function of the male urethra in the transit of semen and urine from the body. The male urethra is much longer than the female as it extends into the penis (penile urethra, PNUR) (Yamada et al., 2003; Yang et al., 2010). As a result of development of the prostate gland and seminal vesicles, both contributing to seminal fluid, the adult male urethra is divided into the prostatic, pelvic and penile urethra (PRUR, PLUR, PNUR respectively; Figure 3Y).

The ejaculatory duct openings also located in the prostatic urethra and connect the seminal vesicles and testes, via the ductus deferens, to the urethra (Figure 5A-D, I-J).

Prostate gland anatomy and development

The anatomy of the adult prostate and its terminology has a confusing history (Timms, 2008). The adult mouse prostate is positioned at the bladder-urethra junction and surrounds the PRUR and ejaculatory ducts (Figure 5I-J). Unlike the human prostate, which is bounded distally by a thick fibromuscular capsule and divided into anatomical zones, the mouse prostate is subdivided into four bilaterally symmetrical regions (historically known as lobes); anterior, dorsal, lateral and ventral (Figure 5A-B, D, I). Each region has its own distinct morphology and function, specified during development via both common and region-specific genetic pathways (Cunha et al., 1987; Donjacour et al., 1987).

At E16.5, anterior and dorsal prostatic buds are the first to emerge, followed by lateral and ventral buds at E17 (Figure 5A-B). The buds emerge from the epithelium in response to androgen-induced paracrine-acting signals from the surrounding mesenchyme (Cunha et al., 1987). Buds are comprised of peri-prostatic mesenchyme and epithelium that is exclusively marked by *Wnt10b*, *Edar* and *Nkx3-1* in all four regions (Abler et al., 2011; Allgeier et al., 2008; Keil et al., 2012). *Bmp2* is selectively expressed by ventral prostatic buds (Abler et al., 2011) and loss of *Wnt5a* selectively inhibits ventral bud development (Allgeier et al., 2008).

Urethral gland development

Urethral gland buds are evident at E18 and are more numerous in males than females (Allgeier et al., 2008). In males, they are especially concentrated in the PLUR segment bounded cranially by the

ejaculatory ducts and caudally by the bulbourethral glands. In male mice at birth, urethral gland buds are usually distinguishable from the more developed, longer prostate gland buds. Newborn males have developed numerous urethral gland buds along the length of the PLUR (Figure 5D), however only ventral epithelial buds are seen in females (Figure 5H) (Allgeier et al., 2010). Female ventral epithelial buds are more numerous than those seen in the male, however they are short, only a few cells in diameter and uniformly distributed (Figure 5H'). In contrast, male ventral buds include two rows of longer ventral prostate buds and fewer, centrally positioned smaller ventral epithelial buds (Figure 5D') (Allgeier et al., 2010). Adult female urethral glands, also called Skene's glands, have been described in other rodents and in humans (Biancardi et al., 2010; Fochi et al., 2008; Wernert et al., 1992; Zaviacic et al., 2000). However in mice, little is known about the origin of these or the fate of the female ventral epithelial buds. Although a careful time course analysis to precisely determine their fate in adults has not been performed, it is likely that these buds become the urethral glands that are evident in the adult (Figure 5L-N, Figure 6L).

The bladder trigone

Trigone development is important for normal bladder function. As the bladder fills and pressure increases, the distal ureter segments (intravesicular, Figure 6D) that pass through the bladder wall are compressed, preventing backflow of urine to the kidneys (vesicoureteral reflux). This is commonly referred to as the anti-reflux valve. The trigone is first established at E13.5, when the ureter opens directly into the bladder lumen (Figure 1C, L). Although the trigone was initially thought to differentiate from the CND (Hutch, 1972; Mackie et al., 1975; Tanagho, 1981; Tanagho et al., 1968), lineage analysis has shown that the epithelial portion of the trigone derives from the UGS (Seifert et al., 2008). The muscular portion, which gives the trigone its distinct triangular structure (illustrated in Figure 6E-F) derives from intersecting detrusor and longitudinal ureteral muscle fibers (Figure 6K-L) (Viana et al., 2007). In the adult, the trigone urothelium has a smooth luminal surface,

in contrast to the folded surface seen in the rest of the bladder (see Figure 5M, Figure 7K), most likely due to the underlying muscular structure.

The ureters

The ureters are lined by a urothelium, comprised of superficial, intermediate and basal cell layers, and Uroplakin expression is seen along their length (Figure 6G-J). Superficial cells lining the lumen, intermediate cells and Krt5-expressing basal cells are seen in the ureter urothelium, however the layers are not subdivided into cell types in the ontology. Within the baldder trigone, the muscle layer of the ureters is distinct from that of the detrusor (Batourina et al., 2005; Viana et al., 2007). Interestingly, unlike the bladder, ureteral smooth muscle differentiation does not occur until E15 and progresses in a rostro-caudal wave beginning at the pelvic junction (Carpenter et al., 2012). Most of the ureters are encased by 2-3 layers of circular and longitudinal smuscle fibers, which are important for conducting peristaltic waves to propel urine from the renal pelvis to the bladder (Figure 6G-L). On the other hand, the muscle layer of the distal-most ureteral segment passing through the bladder wall contains only a thin layer of longitudinal fibers, a configuration that may be important for efficient compression and function of the anti-reflux valve (Figure 6K).

The bladder urothelium

The bladder urothelium differentiates into a highly specialized water-tight barrier that prevents exchange of water and toxic substances between the blood and urine (Hu et al., 2002; Khandelwal et al., 2009). The urothelium is one of the most quiescent epithelia in the body, but can rapidly regenerate in response to injury from urinary tract infection or toxins (Jost, 1986). Chronic irritation or injury can compromise barrier function leading to bladder pain disease and voiding dysfunction (Birder, 2011; Birder et al., 2007; Wyndaele et al., 2003).

Cell types in the urothelium of the bladder can be identified by their protein expression profiles (Gandhi et al., 2013) and relative positions in the urothelial cell layers (C.M., unpublished data illustrated in Figure 8A-F). From E11-E12, very few undifferentiated epithelial cells, expressing endodermal markers (Trp63, Krt5, Foxa2, Shh, Isl1) but not Upk, are seen in the primitive bladder urothelium, usually at the luminal surface. Although at these stages, most of the primitive bladder is lined by P-0 cells, a transient progenitor cell population expressing Trp63, Krt5, Foxa2, Shh, Isl1 and Upk, but not Krt5 (Figure 8A-B, G). However, by E13, intermediate cells (ICs; Upk^{+} $Trp63^{+}$ Shh^{+} $Foxa2^{-}$ Isl^{-} $Krt5^{-}$) make up most of the primitive bladder urothelium (Figure 8CH). At E14, the basal cell layer of the bladder urothelium is lined with ICs and the superficial layer is composed of superficial cells (SCs, or immature umbrella cells) which are Upk^{+} $Trp63^{-}$ Shh^{-} $Foxa2^{-}$ Isl^{-} $Krt5^{-}$ (Figure 8D, J). Superficial cells (SCs, also called umbrella cells) are specialized for the synthesis and transport of uroplakins, which assemble into the crystalline plaque that serves as the urothelial barrier (Khandelwal et al., 2009; Kong et al., 2004; Romih et al., 2005). Unlike their mature counterparts, an enormous, multinucleated population, immature SCs (or immature umbrella cells) are mononucleated and similar in size to other urothelial cell types. By E18, SCs are polyploid and resemble mature SCs (or mature umbrella cells, Figure 8N) (Romih et al., 2005). Fully-differentiated SCs uniquely express Krt20, from E18 to adult (see Figure 8T) (Erman et al., 2006). Krt5-expressing basal cells (K5-BCs; Krt5+, Shh+, Upk-, Isl1-, Foxa2-) are first observed in the basal layer at E14. By E15, K5-BCs populate most, if not all, of the basal layer and can also be found in the intermediate layers, interspersed with ICs (Figure 8D-F, L-N). By E17 and in the adult, Krt5-BCs line the entire basal cell layer and the intermediate cell layer remains a mixture of Krt5-BCs and ICs (Figure 8E, F, N).

Nerves and vasculature of the lower urogenital tract

Bladder nerves and vasculature have been described more thoroughly in adult rats (Gabella, 1995, 1999; Gabella et al., 1998; Inoue et al., 1991). The development of these structures during mouse embryogenesis has not been extensively characterized and the stage when urethral tissues are first innervated has not been determined, it is known that axonal processes have penetrated the bladder wall by E14 (Wiese et al., 2012). We do know that bladder innervation is well developed in the mouse by birth (Levin et al., 2007; Yan et al., 2008). This contrasts with the reproductive organs that show little or no innervation at birth, but in which nerves continue to mature until puberty (Keast, 2006; Yan et al., 2008).

Arterial and venous vessels, components of the vasculature, are found on the serosal and adventitial surface of the bladder and urethra, and continue to branch as they pass through the muscle and lamina propria layers (Figure 9A-FL). A complex vascular network lies close to the basal surface of the urethral epithelium and bladder urothelium (Figure 9LM). Although studies examining the architecture and morphology of vasculature in the adult mouse bladder have recently been performed (Hashitani et al., 2012; Hossler et al., 2013), vascular development in foetal mice is poorly understood.

Within the bladder wall, nerve fibres (axons) are present throughout each of the tissue layers (Figure 9I-O). Their primary functional targets are the detrusor muscle (Figure 9J), urothelium (Figure 9N,O) and vasculature (Figure 9L-M). Nerves are also found on the outer surface of the bladder (serosa and adventitia) and in the lamina propria as they pass through to their final target cells in the urothelium or blood vessels. The detrusor is evenly innervated throughout its depth but the urothelium is more densely innervated in the basal layer, with relatively few axons entering the intermediate and

superficial layers (Figure 9N). At a macroscopic level there is also a pronounced gradient of urothelial innervation, with many more urothelial nerves present within the bladder neck and pelvic urethra compared with the bladder fundus (or dome) (Figure 9O). The pelvic urethra shows a similar pattern of innervation as the bladder, although the urothelium has a higher density of axons (Figure 9P) and a more pronounced muscularis mucosa in which nerves can be found.

Sensory axons arise from lumbar and sacral dorsal root ganglia that lie close to the spinal cord, whereas most of the autonomic axons in the LUT arise from pelvic ganglia that lie very close to the urogenital organs (Figure 9G-HQ-S). A small number of autonomic neuronal cell bodies are also embedded in the outer wall of the bladder neck and form intramural ganglia (Figure 9S), although they are less common than reported in guinea pig, pig and human bladder (Dixon et al., 1983; Gabella, 1990; Gillespie et al., 2006; Pirker et al., 2005). Sensory and autonomic axons travel together in large bundles of hundreds of axons as they enter the organs of the LUT, and then branch into smaller bundles of axons, finally separating to single axons in their target tissue. Although larger bundles of axons can be seen in conventional histology preparations, the small diameter of a single axon (just a few microns or less) precludes visualization of individual axons, so they are typically assessed using immunohistochemistry or reporter mice. As in other organs, the part of the axon that is further from its termination (i.e. within larger bundles of multiple axons) is typically smooth (non-varicose), whereas in the final segment of the axon there are small, regularly spaced swellings (varicosities) (shown in Figure 9J). Varicosities are sites of neurotransmitter storage and release.

Pelvic ganglia

Pelvic ganglia are much larger in adult males, primarily due to the greater number of sympathetic neurons that innervate the male internal reproductive organs (Keast, 2006). In the embryo, when reproductive organs are still developing, the paired pelvic ganglia are closely opposed to the dorsolateral surface of the bladder neck and extend to the anterior PLUR (Figure 9D-HQ-S). However, as reproductive organs enlarge, their spatial relationship begins to change, having close proximity to the prostate gland in males and the uterine cervix in females. During this period of development, the compact pelvic ganglia also begin to become thinner and more dispersed across a broader area, such that discontinuities between regions of ganglia appear and some boundaries can be difficult to identify.

The pelvic ganglia provide all of the parasympathetic and most of the sympathetic innervation to lower urinary tract, distal colon and rectum, and reproductive tract. Most pelvic ganglion neurons innervate targets on the same side of the animal, but there is a small amount of contralateral innervation, and some crossing of axons between the dorsal aspects of the ganglia (Figure 9H). Numerous axon bundles emerge from consistent locations of the pelvic ganglia and comprise connections with the lumbar and sacral spinal dorsal root ganglia and spinal cord (hypogastric and pelvic nerves, respectively), and postganglionic axons projecting to specific targets (e.g. the cavernous nerve innervating erectile tissue of the penis; rectal nerves innervating the distal colon, rectum and internal anal sphincter). Most of these nerves contain both sensory and motor axons.

ABBREVIATIONS AND ACRONYMS

apbl, adventitia of primitive bladder

aplur, adventitia of pelvic urethra of M/F

apr, anterior prostate bud

aprgl, anterior prostate gland

aprur, adventitia of prostatic urethra

amp, anterior mesenchymal pad of M/F

BL, bladder

bugl, bulbourethral gland of M/F (syn: Bartholin's glands in F)

cc, corpus cavernosum

CL, cloaca

clam, cloaca associated mesenchyme

cle, cloacal epithelium (syn: cloacal endoderm)

CLUR, clitoral urethra

cnd, common nephric duct (syn: common mesonephric duct)

CUGS, caudal urogenital sinus (syn: primitive pelvic urethra)

dd, ductus deferens (syn: vas deferens)

dev.vas, developing vasculature of M/F GT

dgt, distal genital tubercle of M/F

dgs, dorsal genital swelling (syn: anterior genital swelling, dorsal genital tubercle)

dmbl, detrusor muscle of bladder (syn: smooth muscle layer of)

dmp, dorsal mesenchymal pad of M/F

dpr, dorsal prostate bud

dprgl, dorsal prostate gland

eclur, epithelium of clitoral urethra

ed, ejaculatory duct

ephur, epithelium of phallic urethra of M/F

epnur, epithelium of penile urethra

eprur, epithelium of prostatic urethra

eugs, epithelium of UGS

gl, glans of M/F GT

glcl, glans clitoris

glgt, glans of M/F gt

glp, glans penis (syn: penile glans)

go, gonad

GT, genital tubercle (of M/F) (syn: penis anlage / clitoris anlage)

gtm, genital tubercle mesenchyme of M/F

hg, hindgut

IC, intermediate cells of bladder urothelium

impbl, inner mesenchymal layer of primitive bladder (syn: suburothelial mesenchyme of)

Krt5-BC, Krt5-basal cells of bladder urothelium (syn: K5-basal cells of)

lpbl, lamina propria of bladder

lplur, lamina propria of PLUR of M/F

lpr, lateral prostate bud

lprgl, lateral prostate gland

lprur, lamina propria of prostatic urethra;

LSW, labial swelling

mdgt, mesenchyme of distal GT of M/F

mes, mesonephros

mgl, mesenchyme of glans of M/F GT

mlplur, mesenchymal layer of PLUR of M/F

mlprur, mesenchymal layer of prostatic urethra

mm, metanephric mesenchyme

mmplur, muscularis mucosa of PLUR of M/F

mmprur, muscularis mucosa of prostatic urethra

mpbl, mesenchyme of primitive bladder (syn: primitive bladder mesenchyme)

mpgt, mesenchyme of proximal genital tubercle of M/F

mpps, mesenchyme of M/F preputial swelling

mt, mesonephric tubule

mugs, mesenchyme of UGS

MUMP, male urogenital mating protuberance

MUMP rg, MUMP ridge groove;

mupbl, muscle layer of primitive bladder (syn: smooth muscle layer of)

muplur, muscle layer of PLUR of M/F

muprur, muscle layer of prostatic urethra

nd, nephric duct of M/F (syn: mesonephric duct, Wolffian duct)

olbl, outer layer of bladder

olpbl, outer lamina propria of bladder (syn: muscularis mesenchyme of)

ompbl, outer mesenchymal layer of primitive bladder (syn: peripheral mesenchyme of)

ov, ovary

PBL, primitive bladder (syn: cranial urogenital sinus)

pc, peritoneal cavity

pce, prepuce of M/F (from TS25 in F syn: clitoral hood)

pgt, proximal genital tubercle of M/F

PHUR, phallic urethra of M/F

PLUR, pelvic urethra of M/F

pnd, paramesonephric duct of M/F (syn: Mullerian duct)

pps, preputial swelling of M/F

PNUR, penile urethra

pr, prostate gland

prgl, preputial gland of M/F

PRUR, prostatic urethra

prox ur me, proximal urethral meatus of M/F (syn: urethral duct, proximal urethral opening)

sbl, serosa of bladder

SC, superficial cells of bladder urothelium (syn: umbrella cells of)

scr fold, scotal fold

scr swell, scrotal swelling

segt, surface ectoderm of gt

smplur, submucosa of PLUR of M/F

smprur, submucosa of prostatic urethra

spbl, serosa of primitive bladder

SSW, scrotal swelling

sulpbl, suburothelial lamina propria of bladder (syn: suburothelial stroma of)

sv, seminal vesicle (syn: vesicular gland, vesicular seminalis)

svb, sinovagnial bulb

t, testis

tg, tailgut

ub, ureteric bud

ubl, urothelium of bladder (syn: epithelium of primitive bladder)

ugbud, urethral gland bud of M/F

ugm, urogenital membrane of M/F

UGS, urogenital sinus

UGS ridge, urogenital sinus ridge (of M/F) (syn: sinus ridge)

upbl, urothelium of primitive bladder

upe, urethral plate epithelium (of M/F) (syn: urethral plate)

ur, ureter

ur gland, M/F urethral gland

uro ureter, urothelium of ureter

urs, urorectal septum

urseam, urethral seam

ute, urethral tube epithelium of M/F

uv, upper vagina

veb, ventral epithelial bud of M/F

ver, verumontanum (syn: seminal colliculus)

vlgs, ventrolateral genital swelling (syn: lateral plate mesoderm buds, ventrolateral genital tubercle)

vmp, ventral mesenchymal pad of M/F

vpr, ventral prostate bud

vprgl, ventral prostate gland

Table 1 Transgenic Mouse Strains

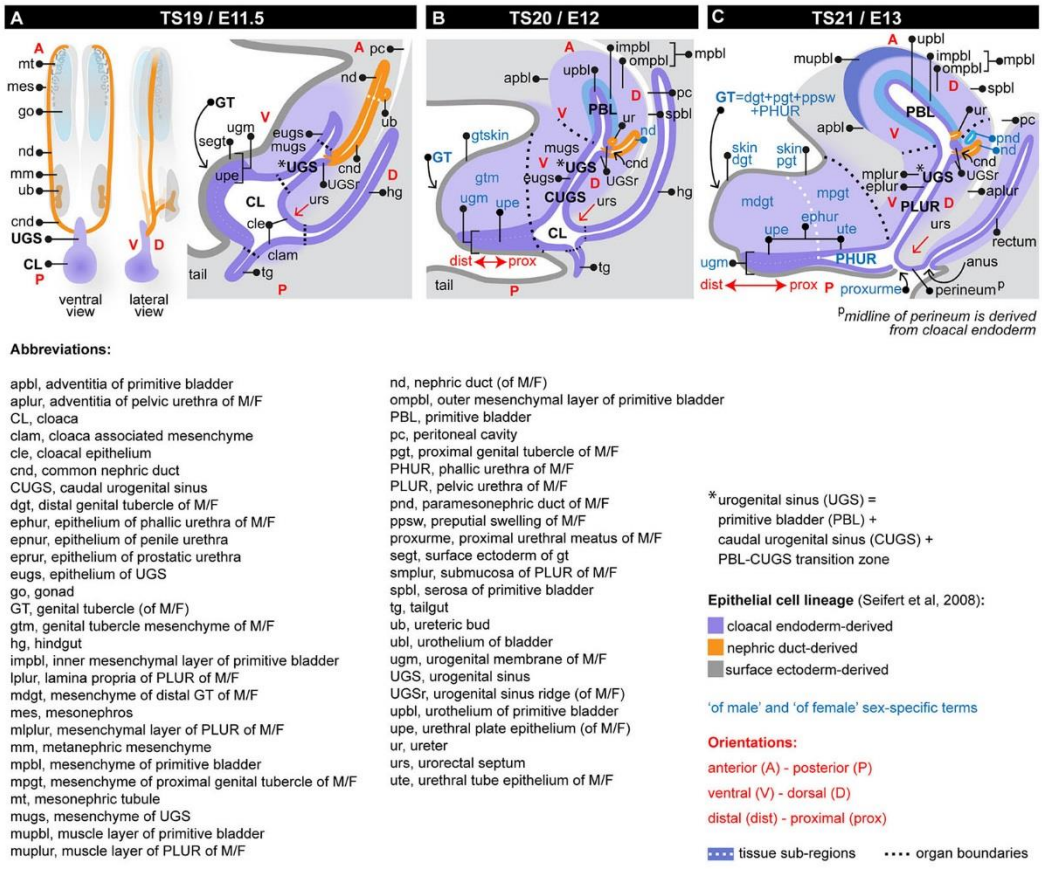
Allele	Strain name in text	Background strain	Figure	Source and Reference(s)
Tg(Hoxb7-EGFP)	*Hoxb7GFP*	mixed background; Swiss Webster were crossed to *Tg(Hoxb7-EGFP)*	1I-M, 4D, 6K	Sourced from and generated by Constantini lab, Columbia University, USA (Srinivas et al., 1999; Rosselot et al., 2010).
Gli1tm2Alj/J	*Gli1-lacZ*	mixed background; Swiss Webster were crossed to *Gli1tm2Alj/J*	7E, F, I, J	Sourced from the Jackson Labs (Ahn and Joyner, 2004).
Up2-Cfp	*Up2-Cfp*	mixed background; Swiss Webster were crossed to *Up2-Cfp*	8N	Generated by Mendelsohn lab, Columbia University, USA (Gandhi et al., 2013).
Shh$^{tm1(eGFP-Cre)}$ GtRosa26^{tm1Sor}	*ShhGFPCre; R26 lacZ*	mixed background; CD1 females were crossed to males carrying the *ShhGFPcre;R26RlacZ* allele (B6.Cg-Shhtm1(EGFP/cre)Cjt/J)	2F, 3A-L, 3U-V	*ShhGFPcre* and *Rosa26R^{lacZ}* (Soriano, 1999; Sun et al., 2000; Harfe et al., 2004). Cell lineage maps in the LUT using the *ShhGFPcre* and *Rosa26R^{lacZ}* strains have been described (Seifert, et al., 2008).

Table 2 Primary Antibodies

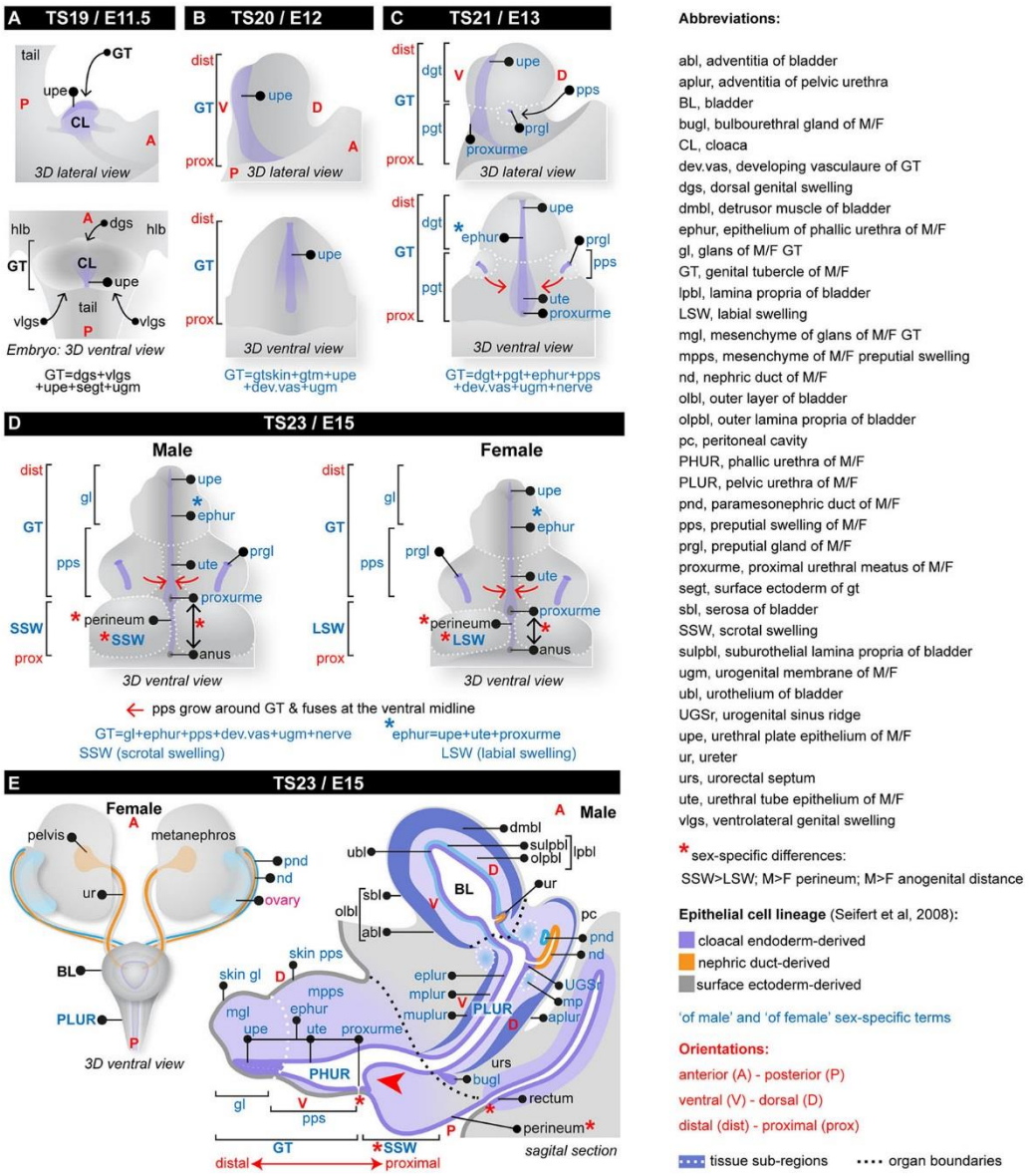
Antigen	Name(s)	MGI gene symbol	Species	Supplier	Catalogue Number	Dilution	Figure
Acta1	actin alpha-skeletal muscle	Acta1	Mouse (monoclonal)	Life Technologies	180177	1:250	5J
Acta2	actin alpha-smooth muscle	Acta2	Mouse (monoclonal)	Leica Microsystems	SMA-CE	1:250	5J, 8R
Acta2	actin alpha-smooth muscle	Acta2	Mouse (monoclonal)	Dako, Carpinteria, CA	M0851	1:100	5CG,6G-L,7GHK
β-catenin	catenin beta 1	Ctnnb1	Mouse (monoclonal)	BD Transduction labs	610153	1:100	1H
Cdh1	cadherin 1 (E-cadherin)	Cdh1	Rabbit (monoclonal)	Cell Signaling Technologies, Inc.	3195	1:1500	5BFJ, 8R
Cdh1	cadherin 1 (E-cadherin)	Cdh1	Goat (polyclonal)	R&D	AF748	1:400	1EFGIJ
CGRP	calcitonin/calcitonin-related polypeptide, alpha, (calcitonin gene-related peptide)	Calca	Goat (polyclonal)	AbD Serotec	1720-9007	1:2000	9KOP
FoxA2	forkhead box A2	FoxA2	Rabbit (polyclonal)	Seven Hills	WRAB-FOXA2	1:1000	8U
Hu	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4, (Hu antigen D, HuD)	Elavl4	Human	gift of V. Lennon	n/a	1:10000	9QS
Krt13	keratin 13	Krt13	Rabbit (polyclonal)	LSBio	c105651	1:400	5L
Krt13	keratin 13	Krt13	Rabbit (polyclonal)	LSBio	LS-B10431/49125	1:100	8VX
Krt14	keratin 14	Krt14	Rabbit (polyclonal)	Covance	Prb 155-P	1:500	8SW
Krt5	keratin 5	Krt5	Chicken (polyclonal)	Covance	SIG-3475-100	1:500	8G-LNSUWX
Laminin	laminin, (pan-laminin)	Laminin	Rabbit	Sigma	L-9393	1:200	1DKLM,7IJ

			(polyclonal)				
Pax2	paired box 2	Pax2	Rabbit (polyclonal)	Zymed	716000	1:70	4H
Pecam1	platelet/endothelial cell adhesion molecule 1 (Cd31)	Pecam1	Rat (monoclonal)	BDPharmingen	557355	1:1000	9M
PGP9.5	ubiquitin carboxy-terminal hydrolase L1	Uchl1	Rabbit (polyclonal)	AbD Serotec	7863-0504	1:4000	9LMQ
PGP9.5	ubiquitin carboxy-terminal hydrolase L1	Uchl1	Rabbit (polyclonal)	Chemicon/Millipore	CAB5925	1:2000	9IN
TH	tyrosine hydroxylase	Th	Rabbit (polyclonal)	Chemicon/Millipore	AB152	1:2000	9L
Trp63	transformation related protein 63, (p63)	Trp63	Rabbit (polyclonal)	GenTEX	GTX102425	1:300	4H,5MN,8G-NSUV
Upk	uroplakin, (pan-uroplakin)	Upk	Mouse (monoclonal)	Fitzgerald	10R-U103a	1:50	5CGL-N,6G-JL,7GHK,8MV
VAChT	solute carrier family 18 (vesicular monoamine), member 3, (VAT)	Slc18a3	Rabbit (polyclonal)	Synapic Systems	139 103	1:1000	9GHR
VAChT	solute carrier family 18 (vesicular monoamine), member 3, (VAT)	Slc18a3	Goat (polyclonal)	Chemicon/Millipore	ABN100	1:1000	9J

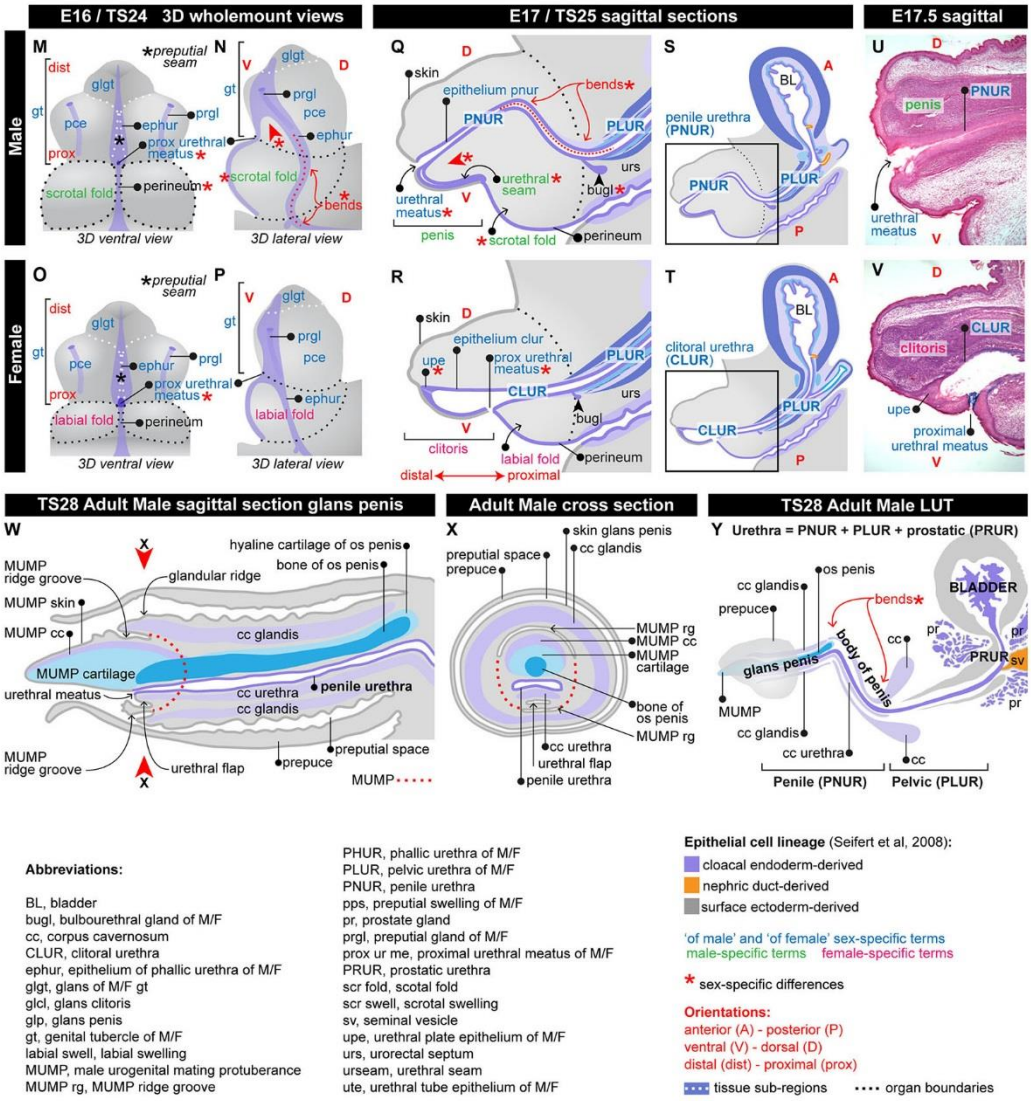
SUPPLEMENTARY FIGURES



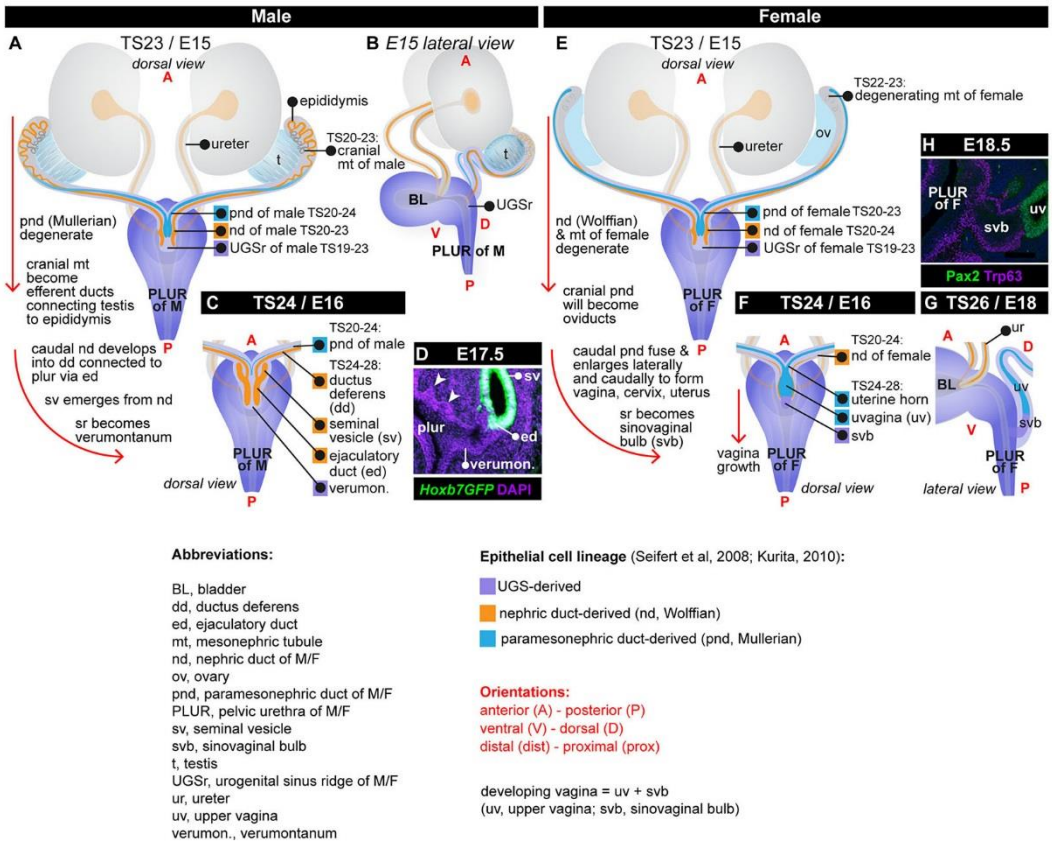
Supplementary Figure 1. Urogenital sinus development. Schematics illustrate early development. Three-dimensional views (**A**) and representative sagittal sections at the mid-line (**B-C**) are shown. Red arrows (**A-C**) indicate direction of mesenchymal growth, resulting in separation of the hindgut and UGS. Supplementary to Figure 1.



Supplementary Figure 2. Genital tubercle development. Schematics illustrate GT development. Red arrows (**C-D**) indicate direction of preputial swelling growth; towards the ventral midline of the genital tubercle. Red arrowhead (in **E**) indicates direction of mesenchymal growth seen in males, which begins to septate the epithelium of the PHUR (ephur). Supplementary to Figure 2.



Supplementary Figure 3. Sexual differentiation of the external genitalia. Schematics illustrate external genitalia. Red arrowheads in **N** and **Q** show direction of mesenchymal growth seen in males and epithelium of the penile urethra (PNUR) septation. Red arrows in **N**, **Q** and **Y** show the location of two right angle bends in the male urethra; at the glans-body junction of the penis and the penile urethra-pelvic urethra junction. Red arrowheads in **W** indicate position of cross section (**X**). Supplementary to Figure 3.



Abbreviations:

BL, bladder
dd, ductus deferens
ed, ejaculatory duct
mt, mesonephric tubule
nd, nephric duct of M/F
ov, ovary
pnd, paramesonephric duct of M/F
PLUR, pelvic urethra of M/F
sv, seminal vesicle
svb, sinovaginal bulb
t, testis
UGSr, urogenital sinus ridge of M/F
ur, ureter
uv, upper vagina
verumon., verumontanum

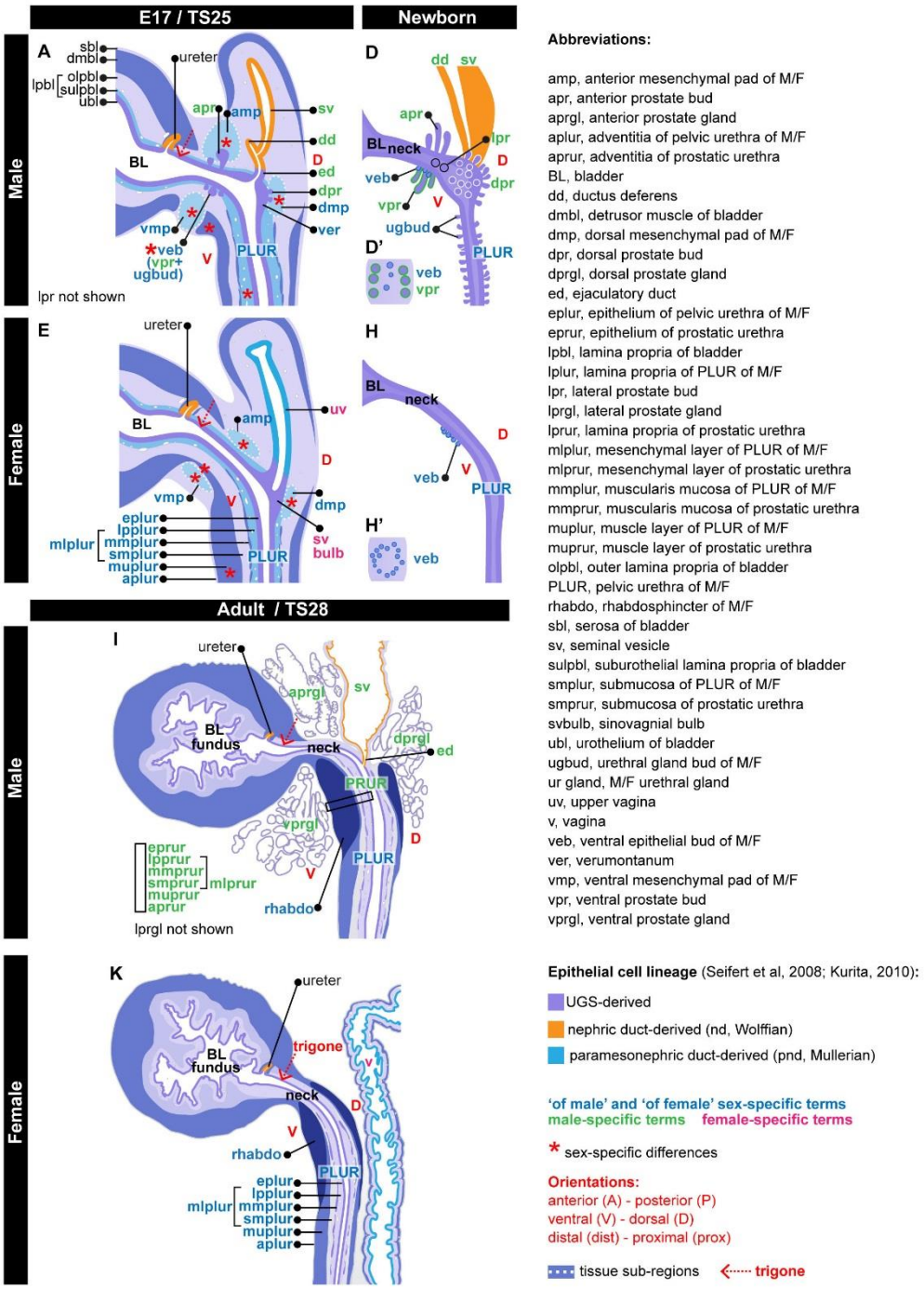
Epithelial cell lineage (Seifert et al, 2008; Kurita, 2010):

UGS-derived
nephric duct-derived (nd, Wolffian)
paramesonephric duct-derived (pnd, Mullerian)

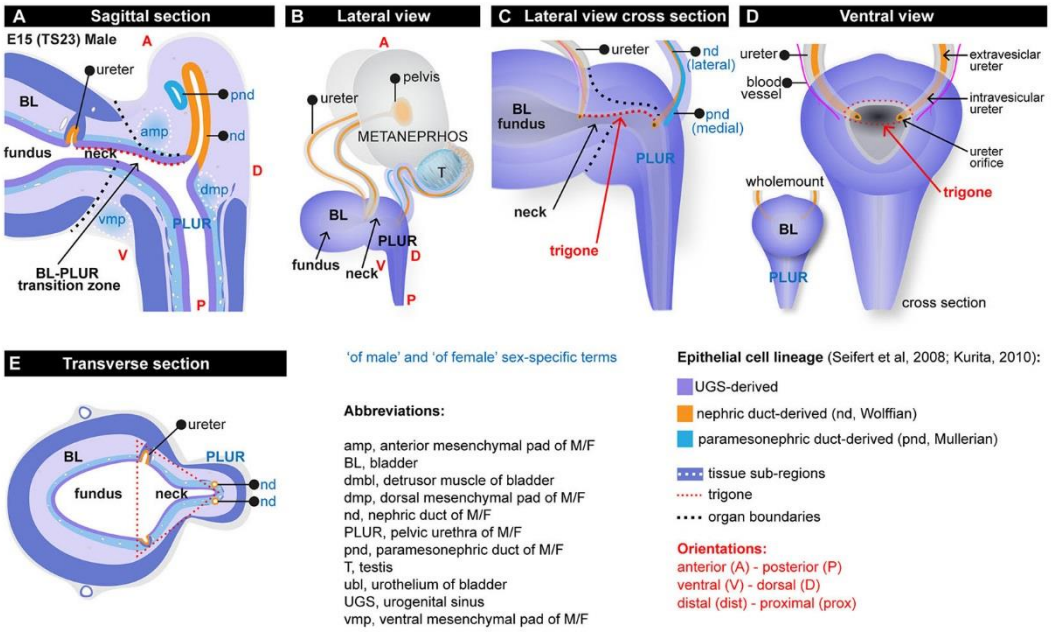
Orientations:
anterior (A) - posterior (P)
ventral (V) - dorsal (D)
distal (dist) - proximal (prox)

developing vagina = uv + svb
(uv, upper vagina; svb, sinovaginal bulb)

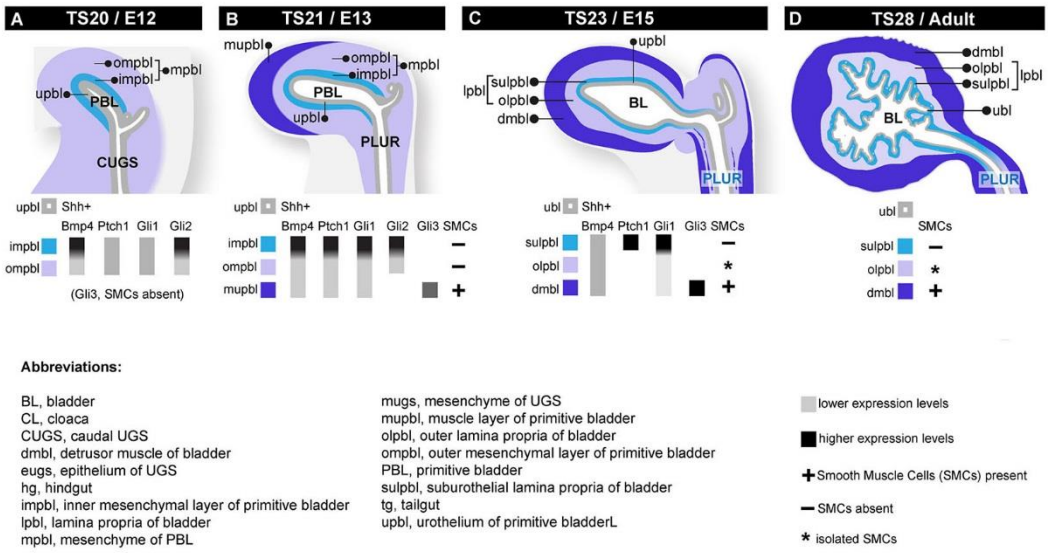
Supplementary Figure 4. Sexual differentiation of the reproductive ducts. Schematics illustrate 3-dimensional anatomy of the reproductive ducts and their connection to the pelvic urethra (PLUR). Red arrows in **A** and **E** indicate major anatomical changes that occur from TS23 to TS24. White arrows in **D** indicate anterior prostate buds. Red arrow in **F** indicates direction of vaginal growth. Supplementary to Figure 4.



Supplementary Figure 5. Sexual differentiation of the pelvic urethra. Schematics illustrate midline, sagittal sections of the bladder-pelvic urethra junction at E17 (**A, E**) and adult (**I, K**) and three-dimensional views of the PLUR epithelium (purple) at birth (**D, H**). Underside views of ventral PLUR epithelium are shown in **D'** and **H'**. Black rectangles in **I** show the tissue layers present in the prostatic urethra (PRUR). Supplementary to Figure 5.



Supplementary Figure 6. Morphology of the bladder fundus, neck, trigone and ureters. Schematics illustrate the location and morphology of the bladder regions and ureter and urethra connections at E15. Supplementary to Figure 6.

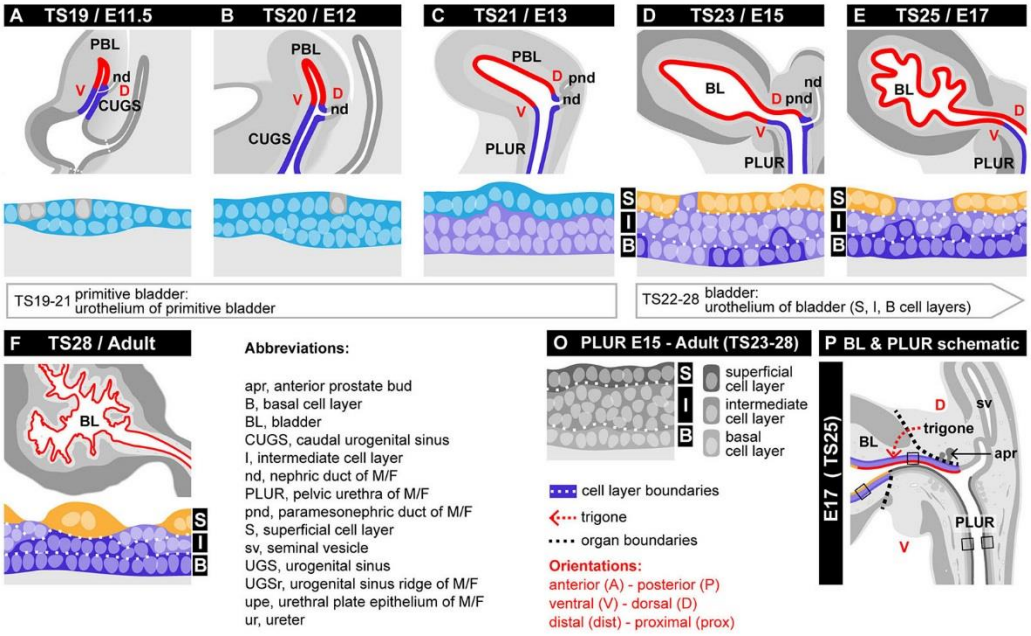


Abbreviations:

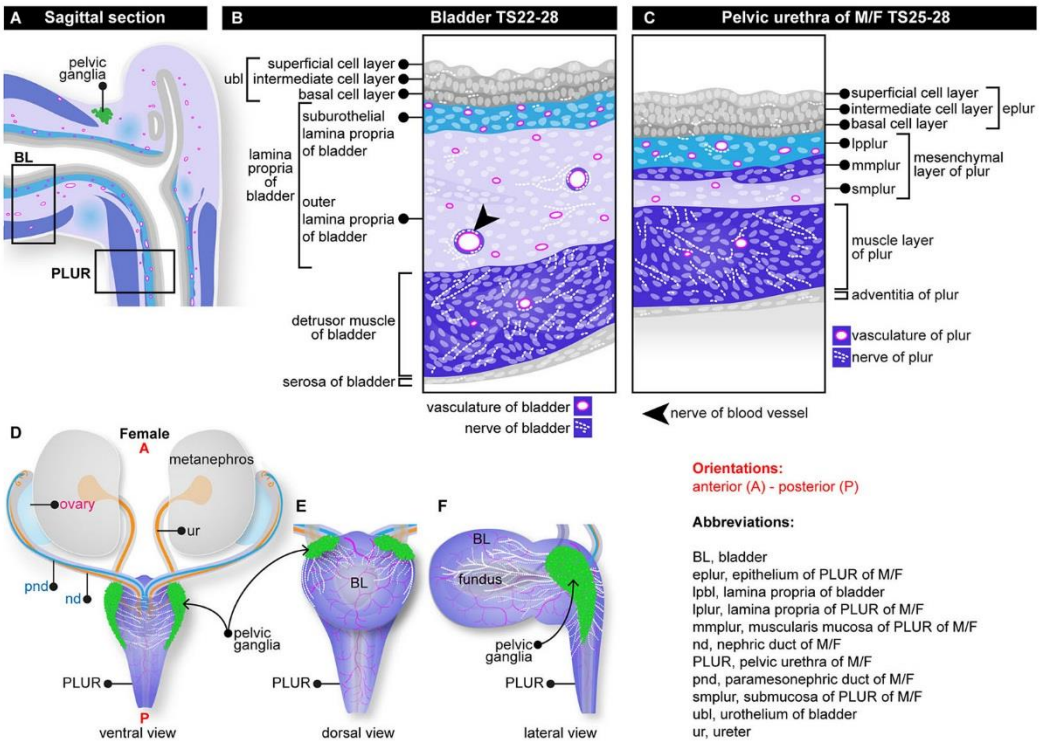
BL, bladder
CL, cloaca
CUGS, caudal UGS
dmbl, detrusor muscle of bladder
eugs, epithelium of UGS
hg, hindgut
impbl, inner mesenchymal layer of primitive bladder
lpbl, lamina propria of bladder
mpbl, mesenchyme of PBL
mugs, mesenchyme of UGS
mupbl, muscle layer of primitive bladder
olpbl, outer lamina propria of bladder
ompbl, outer mesenchymal layer of primitive bladder
PBL, primitive bladder
sulpbl, suburothelial lamina propria of bladder
tg, tailgut
upbl, urothelium of primitive bladderL

lower expression levels
higher expression levels
+ Smooth Muscle Cells (SMCs) present
– SMCs absent
* isolated SMCs

Supplementary Figure 7. Radial patterning of the bladder mesenchyme. Schematics representing midline sagittal sections, illustrate mesenchymal and smooth muscle layers of the primitive bladder (PBL) and bladder (BL). Supplementary to Figure 7.



Supplementary Figure 8. The bladder urothelium and PLUR epithelium cell types. A-F: Schematics illustrate midline sagittal sections. The epithelial layers are highlighted; urothelium of primitive bladder/bladder (PBL/BL) in red and epithelium of caudal urogenital sinus/pelvic urethra (CUGS/PLUR) in blue. Below, cross sections illustrate location and gene expression of urothelial cell types seen in the primitive bladder/bladder. **O-P:** PLUR schematics; a cross section illustrates the epithelial layers of the PLUR (**O**) and a sagittal section of the bladder-PLUR boundary at E17 (**P**). In **O-P**: epithelium of PLUR layers are shown in different shades of grey. In **P**: the urothelium of bladder layers are shown in red (superficial cell layer of urothelium of trigone), yellow (superficial cell layer of urothelium), light purple (intermediate cell layer of urothelium), and dark purple (basal cell layer of urothelium). Supplementary to Figure 8.



Supplementary Figure 9. Nerves, pelvic ganglia and vasculature of the LUT. Schematics illustrate nerves, pelvic ganglia and vasculature. Schematics are representative of sagittal sections (**A-C**) and three-dimensional views of the urogenital system (**D**) and bladder/pelvic urethra (**E-F**) at E15. Supplementary to Figure 9.

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