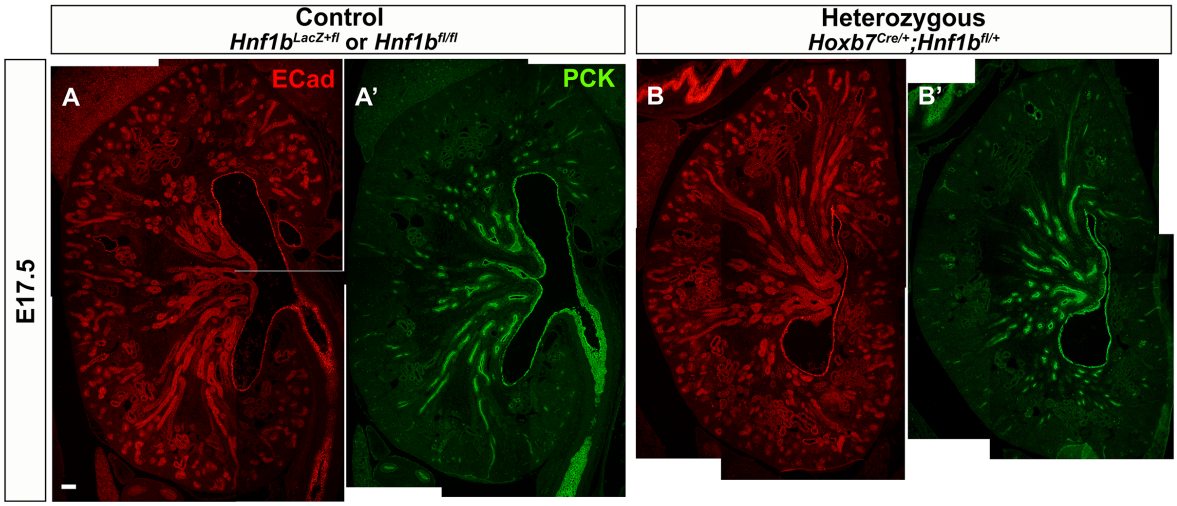
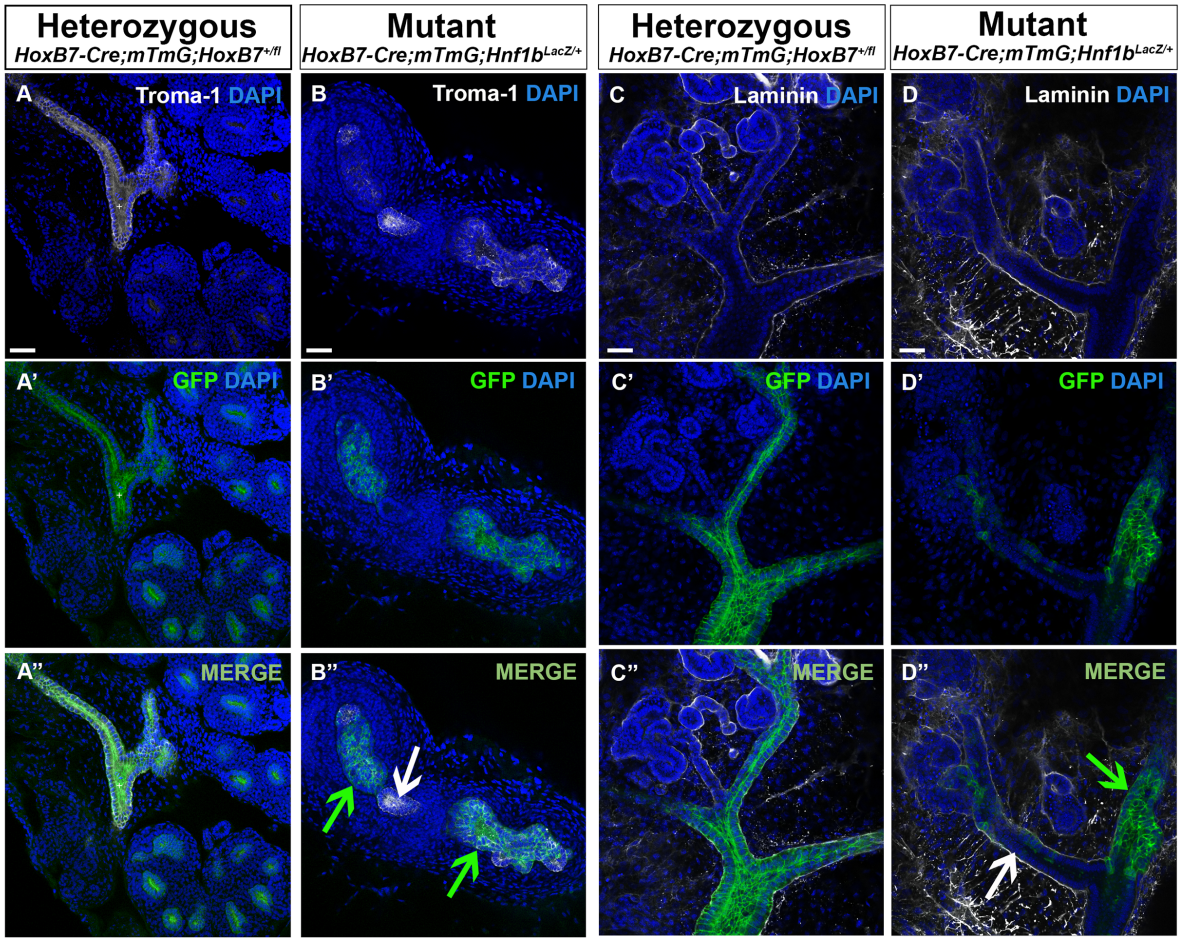
SUPPLEMENTARY DATA



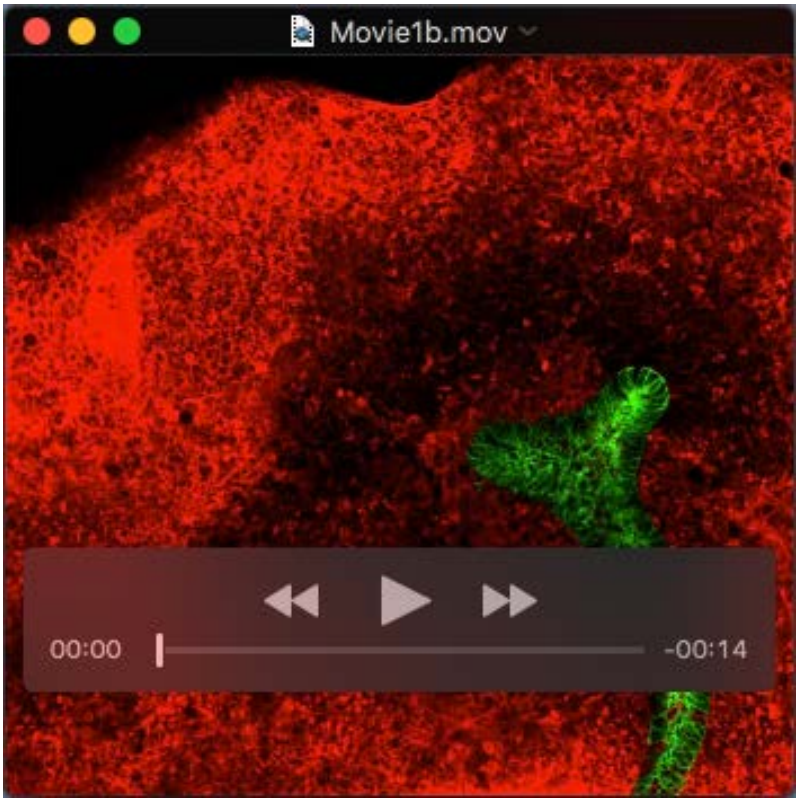
Supplementary figure S1: Comparative staining of collecting ducts and nephrons in control and heterozygous kidneys

Ecad and PCK staining of kidney tubules and collecting duct system, respectively show no difference between control (A, A') and heterozygous kidneys (B, B'). Scale bar, 100 μm.



Supplementary figure S2: *Hnf1b* invalidation leads to loss of apico-basal polarity *in vitro*

Confocal images of Troma-1 (A–B'') and Laminin (C–D'') immunostainings after 5 days of culture show specific loss of the apical and basal markers in mutant ureteric bud regions (that are GFP-positive). White arrows, WT cells; green arrows, GFP+ cells. Scale bar, 50 µm



Supplementary Movie 1

Time-lapse imaging of *Hoxb7*$^{Cre/+}$*;mTmG;Hnf1b*$^{fl/+}$ kidney shows first branching events. Tip domain with active cell movements and trunk with lumen formation can both be seen. By the end of the movie, nascent nephrons (Red cells) are observed. One image is taken every 10 minutes. Green is mG expression in Cre expressing cells. Red is mT expression in Cre non-expressing cells. Mitotic cells can be easily detected as they become round before division.

Supplementary Movie 2

Time-lapse imaging of *Hoxb7*$^{Cre/+}$*;mTmG;Hnf1b*$^{fl/LacZ}$ kidney shows defective branching pattern. Tip domain show active cell movements but lumen in the trunk is barely visible. By the end of the movie, WT cells appear to be recruited at the UB tip domain and correctly formed nascent nephrons are observed. One image is taken every 10 minutes. Green is mG expression in Cre expressing cells. Red is mT expression in Cre-non expressing cells. Mitotic cells can be easily detected as they become round before division.

Supplementary Table 1:

A- Selected down-regulated genes in E15.5 mutant kidneys: Using the gene expression data available in Gudmap (www.gudmap.org), genes expressed in the UB, medullar and cortical collecting ducts but also in the urothelium were selected from the whole data set of 499 down-regulated genes with a FDR or adjusted p-value threshold of 0.05 and a fold-change cutoff value of 1 in a $\log_2$ scale. This reduced the whole list to 256 down-regulated genes.

Note that several genes express additionally in early nephron segment tubules.

B- HNF1B target genes down-regulated under the fold-change cutoff value of 1 in a $\log_2$ scale

C- Selected dowregulated genes containing HNF1B binding sites identified by ChIP-seq on E14.5 kidneys. Only are shown the genes containing strong HNF1B binding peaks identified by ChIP sequencing on embryonic kidneys (C.H. and S.C. unpublished data). The chromosomal location of binding peak score is indicated.

D- Complete list of up-regulated genes in E15.5 mutant kidneys

Click here to Download Table S1

Supplementary Table 2: Selected Gene ontology terms enriched in down-regulated and up-regulated genes in E15.5 mutant kidneys.

Click here to Download Table S2