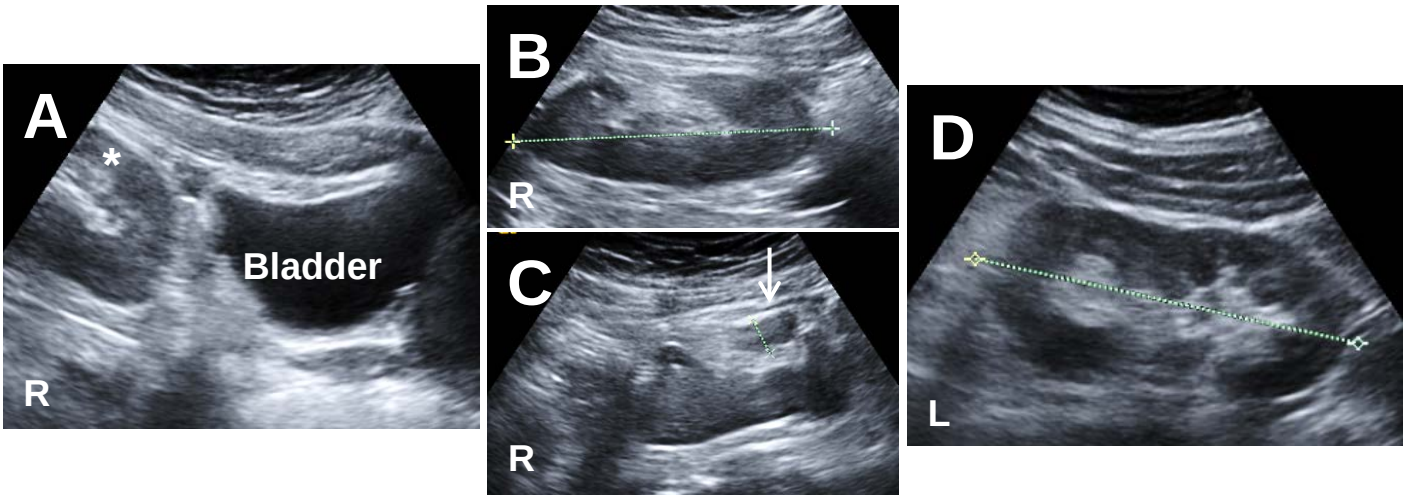
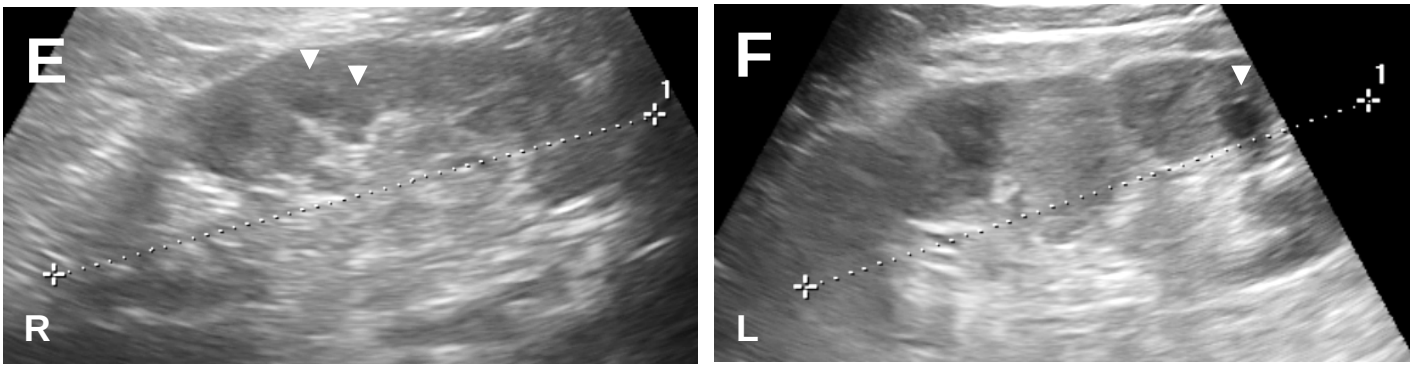
SUPPLEMENTAL DATA

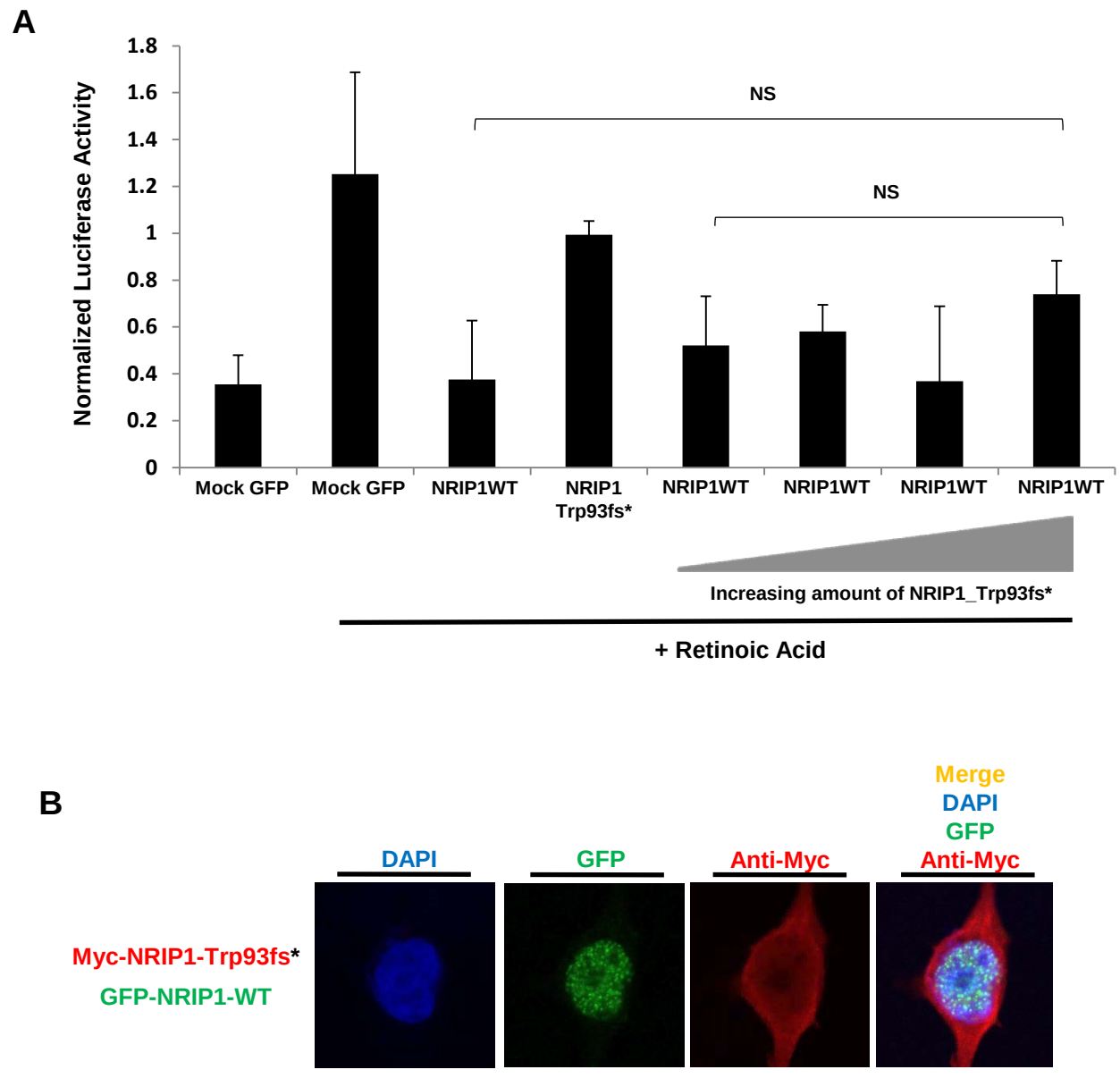
Family H: Patient II:8



Family H: Patient II:1



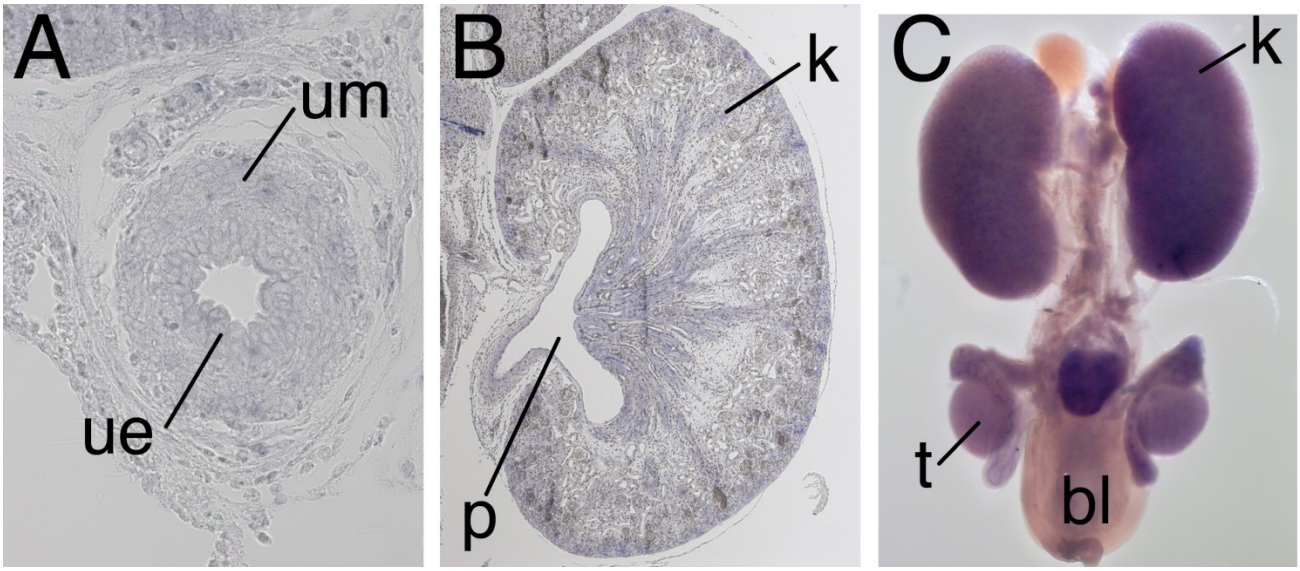
Supplemental Figure 1. Renal imaging in selected patients with *NRIP1* mutations.
A, B and C. Renal US of patient II8 shows right (R) ectopic small pelvic kidney (**A**, white asterisk). The kidney is 9.9 cm in length (**B**) and has 1.2 cm dilatation of its collecting system (**C**, white arrow).
D. Renal US of the same patient (II8) shows normal left (L) kidney. Left renal length is 12.7 cm.
E and F. Right and left renal US imaging of patient II1 show normal appearing kidneys (right renal length is 14 cm; left renal length is 14.9 cm) with small bilateral cysts (white arrow heads).



Supplementary Figure 2. The NRIP1 p.Trp93fs* mutation does not act in a dominant negative fashion.

A. Luciferase assay of HEK293 cells transfected with GFP-tagged WT NRIP1 (200 ng) and increasing amounts of GFP-tagged NRIP1 p.Trp93fs* (50 ng, 100 ng, 200 ng and 300 ng). WT NRIP1 transcriptional suppression of retinoic acid induced transcriptional activity is not suppressed by increasing doses of the p.Trp93fs* altered protein.

B. Immunofluorescence staining of HEK293 cells co-transfected with GFP-tagged WT NRIP1 and Myc-tagged NRIP1 p.Trp93fs*. When co-transfected, WT NRIP1 localizes to the nucleus while the mutant form remains in the cytoplasm, suggesting that the two do not dimerize.



Supplementary Figure 3. Nrip1 is not expressed in the urogenital system at E18.5.

Panel A-C: In situ hybridization analysis of expression of Nrip1 on transverse ureter sections (A), on coronal kidney sections (B) and in whole urogenital systems (C). No specific staining for Nrip1 can be detected in the ureter and kidneys at this stage. bl, bladder; k, kidney; p, pelvis; t, testis; u, ureter; ue, ureteric epithelium; um, ureteric mesenchyme.

Supplemental Table 1

Filtering process for genetic variants resulting from whole exome sequencing of individuals III:3, III:4, III:5, IV:7, IV:8 and IV:9 of family H with congenital anomalies of the kidneys and urinary tract (CAKUT).[a]

Remaining variants shared between 6 affected individuals from family H after applying listed filtering criteria	Number of variants
Variants with MAF<1%	10,751
Above criteria AND heterozygous	6,563
Above criteria AND non-synonymous or splice variants	148
Above criteria AND MAF<0.1%[b]	62
Above criteria AND critical inspection within the exome alignment	4
Above criteria AND Sanger confirmation and segregating	1
Remaining singular truncating gene (mutation)	*NRIP1* (p.Trp93fs*)

[a]See **Figure 1** and **Table 1**.
[b]Minor allele frequencies were assessed using data from dbSNP138, Exome variant server (EVS), 1,000 Genomes Project, and the Exome Aggregation Consortium data base (ExAC) of the Broad Institute.
MAF=minor allele frequency. NRIP1= nuclear receptor interacting protein 1.