Table S1. Sequences for PCR primers to generate templates for RNA probe synthesis

Gene name		Primer sequence	Product size
Slc34a1, probe 1	F	5′-CTTCTTCAACATCTCGGGCATC-3′	
	R	5′-TCTGTCTTTCTACTGTGGGCATTG-3′	556 bp
Slc34a1, probe 2	F	5′-CGCTGGTGTTTGGCATTTCC-3′	
	R	5′-GCACTAATGGTCACACAGGCTCAG-3′	580 bp
Slc12a3, probe 1	F	5′-CCTTTGATACCCAGAGCCATAATG-3′	
	R	5′-AATGAATGCAGGTCAGCCAGG-3′	290 bp
Slc12a3, probe 2	F	5′-GTGGCACCTATTTCCTTATTTCCC-3′	
	R	5′-CCCTTACGGTTTCTGCAAAGC-3′	129 bp
Wnt4, probe 1	F	5′-GGAGACGTGCGAGAAACTCAAAG-3′	
	R	5′-TGTGTCACCACCTTCCCAAAGAC-3′	192 bp
Wnt4, probe 2	F	5′-CGCTAAAGGAGAAGTTTGACGGTG-3′	
	R	5′-GGTCCTCATCTGTATGTGGCTTG-3′	111 bp
Podxl, probe 1	F	5′-GCCAAGCAACCCTACACCATTC-3′	
	R	5′-TCGCTGTGCTCGGTGAAGAATC-3′	359 bp
Podxl, probe 2	F	5′-AATGGTCTGTGATGGTCACGGG-3′	
	R	5′-GCCTCATTCTGCTGGACATTCC-3′	394 bp
T7 sequence		5′-ATTGTAATACGACTCACTATAGGG-3′	

To generate probes for the genes listed, we amplified two different PCR products specific for exon sequences of each gene using mouse genomic DNA as a template. The reverse primers had a 5′ extension that included the T7 promoter for in vitro transcription. The two resulting probes for each gene were combined in the hybridization solution.

F, forward primer; R, reverse primer.

The sequence of the T7 promoter is highlighted.

Table S2. Total number of collecting duct tips in kidneys of normal and mutant littermates

	Number of collecting duct tips		
	E13.5	E15.5	E17.5
Normal littermates	89.6±25.5	337.4±39.2	874±61.9
Fgf8-MM-KO	40.3±10.1 (45%)	90.5±25.1 (27%)	148±25.3 (20%)
Normal littermates	79.5±22.7	397.2±33.9	1098±147
Severe *Fgf8* hypomorph	60.1±15.3 (76%)	284.3±55 (72%)	518±61 (47%)

Total number of collecting duct tips in kidneys of normal and mutant littermates was quantified as previously described (Cebrián et al., 2004). Briefly, 100 μm vibratome-sectioned kidneys were permeabilized and assayed for immunofluorescent staining using primary antibodies against Calbindin D_{28K}(CD). CD-positive duct tips were visualized under fluorescent microscopy and quantified in all sections of a given kidney. A minimum of seven kidneys at each developmental stage was analyzed with values expressed as mean±s.d.

Reference

Cebrián, C., Borodo, K., Charles, N. and Herzlinger, D. A. (2004). Morphometric index of the developing murine kidney. *Dev. Dyn.* **231**, 601-608.

Table 3. Total number of renal corpuscles in kidneys of normal and mutant littermates

	Number of renal corpuscles	
	E15.5	E18.5
Normal littermates	379±28	2519±374
Mild *Fgf8* hypomorph	265±32 (70%)	912.5±83.3 (36%)
Normal littermates	427±34	2812±409
Severe *Fgf8* hypomorph	201±37 (47%)	531±76.5 (19%)

Samples were analyzed as described in Table S2, using primary antibodies against Wilms' tumor 1 protein (WT1). Overprojection bias was corrected as previously described by Cebrián et al. (Cebrián et al., 2004). A minimum of five kidneys at each developmental stage was analyzed with values expressed as mean±s.d.

Reference

Cebrián, C., Borodo, K., Charles, N. and Herzlinger, D. A. (2004). Morphometric index of the developing murine kidney. *Dev. Dyn.* **231**, 601-608.