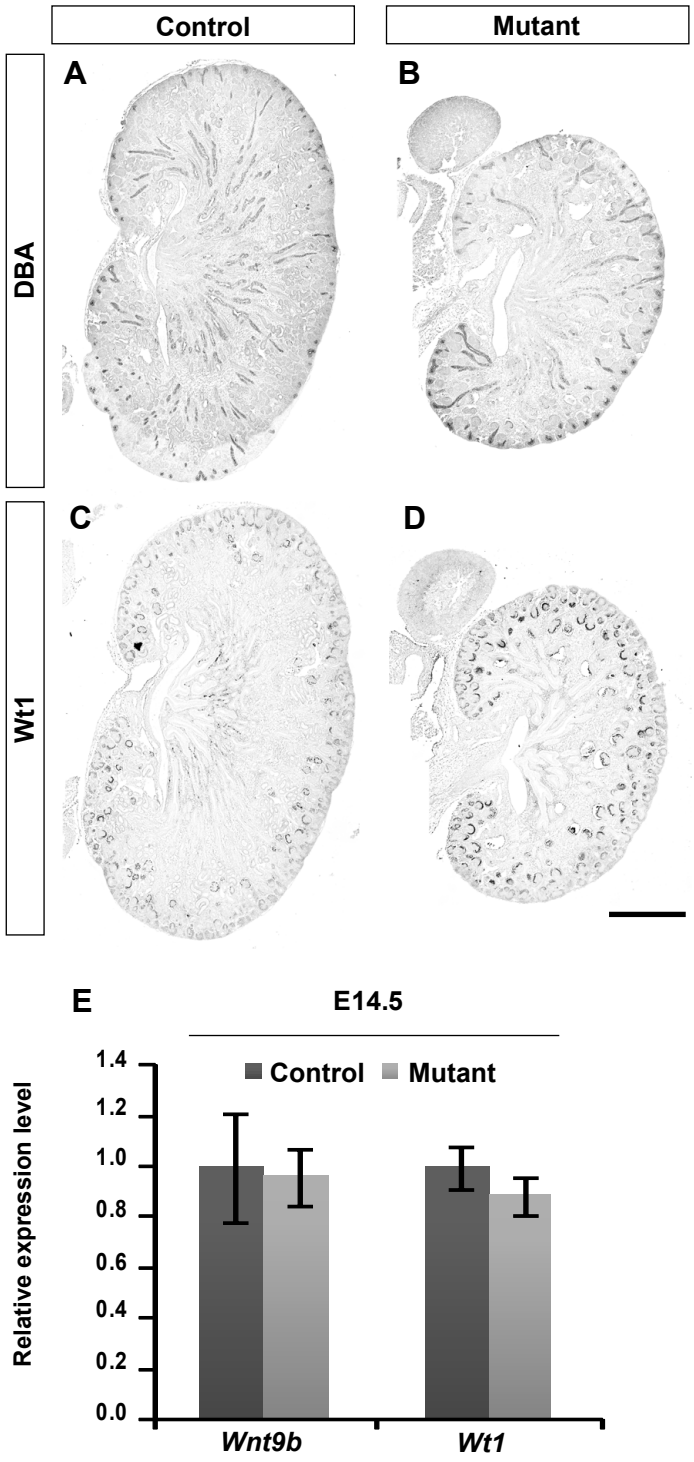

Fig. S1. The absence of HNF1β in metanephric mesenchyme does not affect UB branching and podocyte differentiation. (**A-C**) Kidney sections of newborns from control and mutant showed a similar staining for collecting ducts with Dolicho biflorus agglutinin (DBA) (A,B) and for Wt1 (C,D). (**E**) qRT-PCR analysis of specific markers of collecting ducts (*Wnt9b*) and podocytes (*Wt1*) did not show any difference between control and mutant kidneys at E14.5. Scale bar: 500 μm.

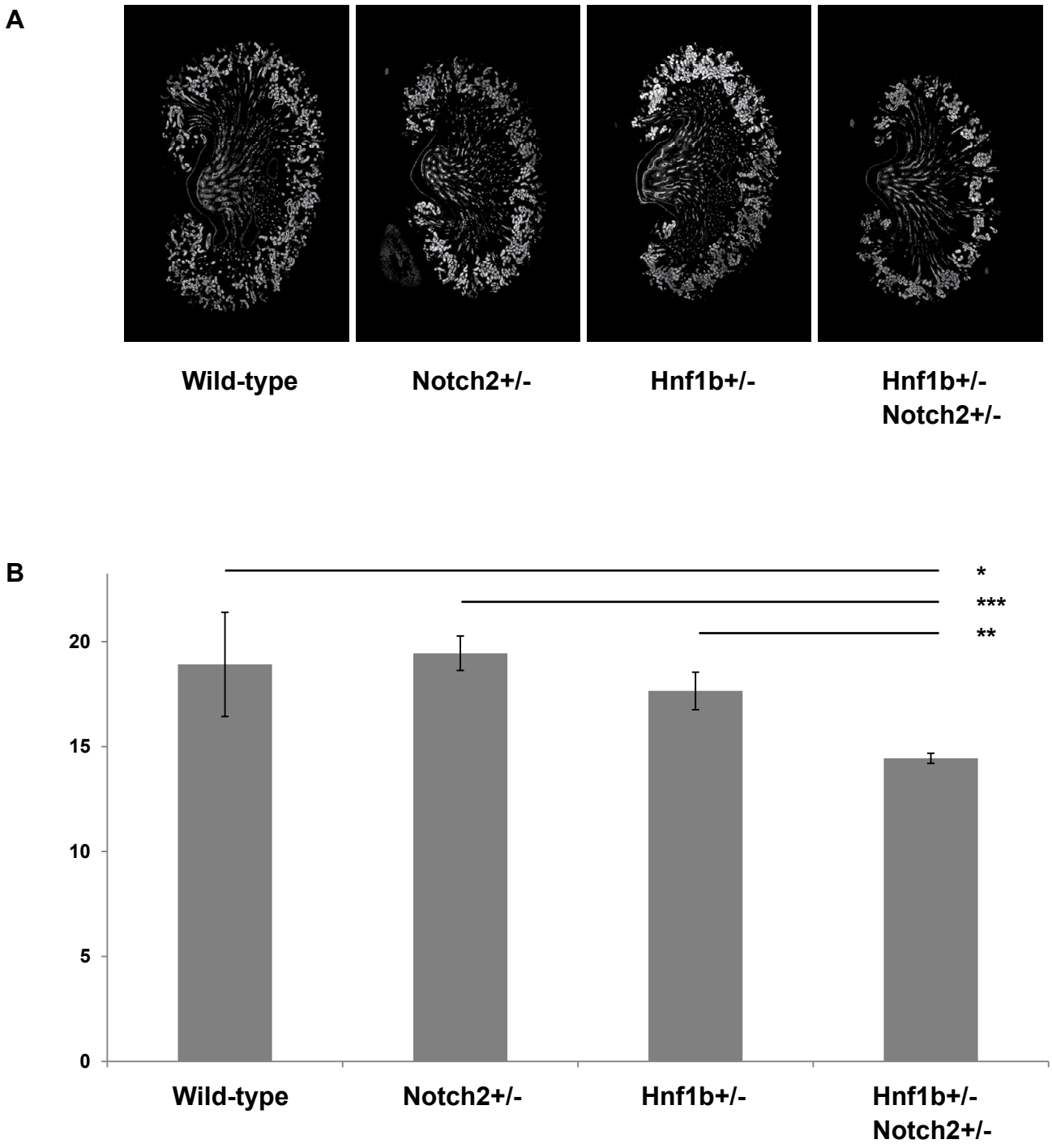

Fig. S2. Genetic interaction between *Hnf1b* and *Notch2* in proximal tubule expansion. (**A**) Immunofluorescence detection of *Lotus tetragonolobus* lectin (LTL; proximal tubules) showing the slight decrease in expansion of proximal tubules in double-heterozygous pups (*Notch2*$^{+/-}$*; Hnf1b*$^{+/-}$). (**B**) Quantification of the relative (percentage) surface of proximal tubules per kidney section. *n*=3, 5, 4 and 6 for wild type, *Notch2*$^{+/-}$, *Hnf1b*$^{+/-}$ and *Hnf1b*$^{+/-}$*; Notch2*$^{+/-}$, respectively. Student's *t*-test: **P*=0.015, ***P*=0.0015, ****P*<0.001.

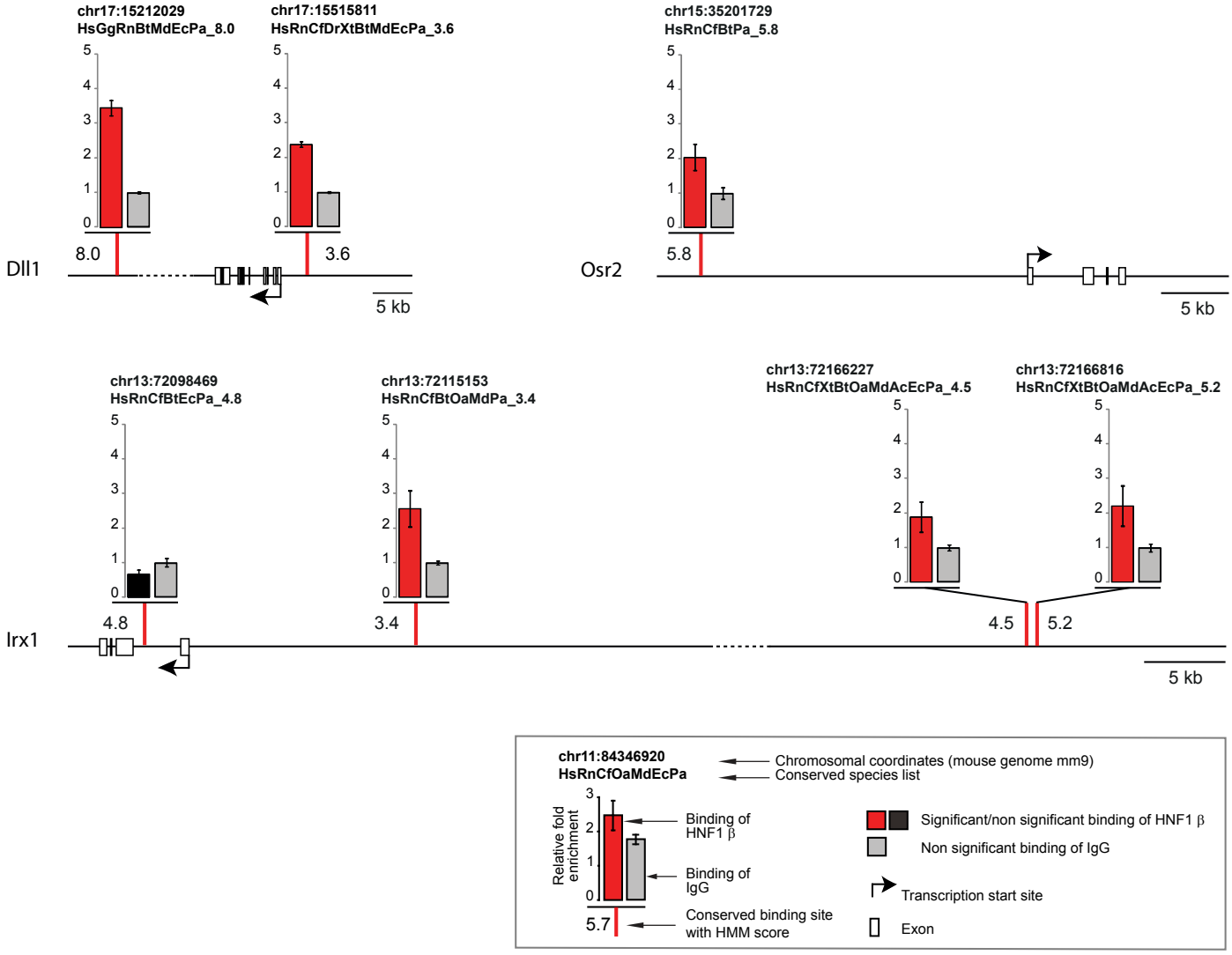

Fig. S3. In vivo binding of HNF1β to its chromatin target sites in genes involved in tubular differentiation. Predicted *in silico* HNF1 binding sites (vertical bars) in *Dll1*, *Osr2* and *Irx1* genes were tested in ChIP experiments for *in vivo* HNF1β binding. The relative enrichment for each DNA fragment upon immunoprecipitation of HNF1β is illustrated in histograms. Colored bars represent HNF1 binding sites with enrichments significantly higher than background (gray bars). PCR experiments were performed in triplicate and the standard errors of these quantifications are shown as error bars. Species list of conserved sites: Ac, *Anolis carolinensis*; Bt, *Bos taurus*; Cf, *Canis familiaris*; Dr, *Danio rerio*; Ec, *Equus caballus*; Gg, *Gallus gallus*; Hs, *Homo sapiens*; Md, *Monodelphis domestica*; Oa, *Ornithorhynchus anatinus*; Pa, *Pongo pygmaeus abelii*; Rn, *Rattus norvegicus*; Xt, *Xenopus tropicalis*.

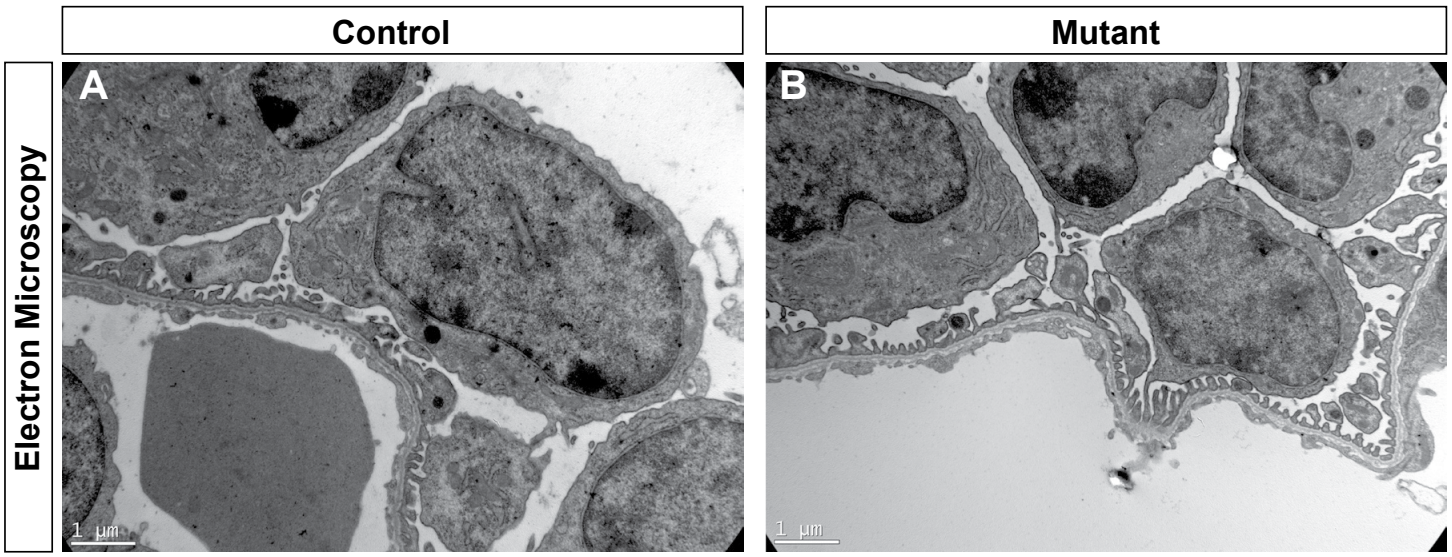

Fig. S4. Podocytes develop normally in the absence of HNF1β. Transmission electron microscopy of glomerular sections showing similar extent of foot process differentiation in podocytes of control (**A**) and mutant (**B**) newborn pups.

Table S1. Antibodies

Host species	Target protein	Source	Dilution
Mouse	WT1	Dako (M356101)	1:100
Rabbit	Laminin	Sigma (L9393)	1:200
Rabbit	HNF4α	FRH4 (homemade)	1:100
Rabbit	JAG1	Santa Cruz (SC-8303)	1:200
–	*Lotus tetragonolobus* lectin (LTL)	Vector (B-1325)	1:200
–	*Dolichos biflorus* agglutinin (DBA)	Vector (B-1035)	1:200
Mouse	HNF1β	HNF1b-3-12 (homemade)	1:100

Table S2. qRT-PCR primers

Gene	Primer	Sequence
Vil1	Reverse	GCGAGACTTTCCGGAGCTACT
	Forward	CCCCTTTCCGGATCACAAG
Hnf4a	Reverve	ATCACCTGGCAGATGATCGAA
	Forward	AGGTTGTCAATCTTGGCCATG
Slc12a1	Reverse	CTGGCCTCATATGCGCTTATT
	Forward	AGATTTGGCATACGAGGCATG
Slc12a3	Reverse	GGCCTACGAACACTATGCTAAC
	Forward	AGTCAGCTCACGACCTTGC
Pvalb	Reverse	CAGACTCCTTCGACCACAAAAA
	Forward	AACCCCAATCTTGCCGTCC
Dll1	Reverse	GAACAACCTAGCCAATTGCCA
	Forward	GCCCCAATGATGCTAACAGAA
Jag1	Reverse	ACTCGGAAGTGGAGGAGGATG
	Forward	AGCGGACTTTCTGCTGGTGT
Jag2	Reverse	CAATGCTGAGCCTGACCAATAC
	Forward	GACGGACAGTGGCATTCAAA
Notch2	Reverse	CCCTGATCATCGTGGTGCT
	Forward	AATGCGCAAGTTGGTGTGG
Hes5	Reverse	TCAACAGCAGCATAGAGCAGC
	Forward	TCCAGGATGTCGGCCTTCT
Hey1	Reverse	CCGACGAGACCGAATCAATAAC
	Forward	TCAGGTGATCCACAGTCATCTG
Cdh6	Reverse	CTAGTGGCTTCCCAGCAAAG
	Forward	CTGATAATCGGATCCCGTGT
Pou3f3	Reverse	CAGCCTACAGCTGGAAAAGG

	Forward	GGTACCCACCTGCGAGTAGA
Hnf1a	Reverse	AACCACCCTCTCTCCCAGTAA
	Forward	GCCGCAGACACTGTGACTAA
Osr2	Reverse	CCACGGACTGTACACCTGTC
	Forward	GAAAGATCGCATGTTCAGCA
Irx1	Reverse	ATTCACGAGAGGACCCACAC
	Forward	TCCTTTCCCACACTCCTGAC
Pax2	Reverse	CAAAGTTCAGCAGCCTTTCC
	Forward	GTTAGAGGCGCTGGAAACAG
Lhx1	Reverse	TGCGTCCAGTGCTGTGAAT
	Forward	AACCAGATCGCTTGGAGAGAT
Wt1	Reverse	GGTTTTCTCGCTCAGACCAG
	Forward	GGTGTGGGTCTTCAGATGGT
Wnt9b	Reverse	GTGAGGTCCTGACACCCTTC
	Forward	GCCTGGACAGCTTCAGTAGG

Table S3. ISH probe primers

Gene	Primer	Sequence
Osr2	Reverse	GCTGCAGCTCACCAATTACTCC
	Forward	ACTTTGCCGCACTGCTCGCAGC
Irx1	Reverse	ACCCTCACACAGGTCTCCAC
	Forward	GGAAAGATCGCATGTTCAGCA
Dll1	Reverse	CTAGAACACTCTGGGAGCGG
	Forward	GTCTTCAAAGACCCAGGGATG
Lhx1	Reverse	ACAAATGGTTCCCGTAGCTG
	Forward	CAACATGCGTGTTATCCAGG
Pvalb	Reverse	CTGGAGAACCTGTTCGCTTC
	Forward	CAGAGGCATCTCTCACCACA
Slc12a1	Reverse	CTGGTATGGTGAAGGCAGGT
	Forward	CAAACCAAAAGCAAGCCATT

Table S4. ChIP primers

Gene	Sites	Primer	Sequence
Dll1	17_15515811_HsRnCfDrXtBtMdEcPa_3.6 chr17:15515812-15515826	Reverse	AGGGTCTGAGCTATGCTTGC
		Forward	GCTGTGTCCAACAGGGACTT
	17_15212029_HsGgRnBtMdEcPa_8.0 chr17:15212030-15212044	Reverse	AAGAGCGGCCTCAGTCATTA
		Forward	CAGACCATAGCCACAGGACA
Irx1	13_72166227_HsRnCfXtBtOaMdAcEcPa_4.5	Reverse	ACTCATGCCTGCGATAATCC

	chr13:72166228-72166242	Forward	TTCCCACCAACCTCATTTTC
	13_72166816_HsRnCfXtBtOaMdAcEcPa_5.2	Reverse	CGGCTGCTAATCCAGTGTCT
	chr13:72166817-72166831	Forward	GGGAGGACTTTCTCCTGTCC
	13_72115153_HsRnCfBtOaMdPa_3.4	Reverse	ATGATGGTTCCAGGCTGTTC
	chr13:72115154-72115168	Forward	TGTGTGGATTGCTCATGGAT
	13_72098469_HsRnCfBtEcPa_4.8	Reverse	TCCAGGGCACTCTTCAGTCT
	chr13:72098470-72098484	Forward	ACCTGTCACCGCTACAGACC
Osr2	15_35201729_HsRnCfBtPa_5.8	Reverse	ATGCTGGCCTTTTATGTTGC
	chr15:35201730-35201744	Forward	TGTGGGAAAATCAGACAGCA