

Figure S1 Apoptosis phenotype of the *Nes*-Cre mutant e12.5 kidneys.

All experiments in this figure are undertaken in GFP-sorted cells from e12.5 embryonic kidneys.

A- RT-qPCR: The levels of *Wnt4* in FACS-sorted cells from kidneys from *Nes*-Cre *Wt1*^{co/GFP} and *Wt1*^{co/GFP} e12.5 embryos. The results are an average from cells isolated from at least 4 embryos in each case.

B- Percentage of FACS-sorted cells from embryonic kidneys from Nes-Cre Wt1^{co/GFP} and Wt1^{co/GFP} e12.5 embryos.

C-RT-qPCR: The levels of the indicated genes in embryonic kidneys from *Nes*-Cre *Wt1*^{∞/GFP} is divided by the levels of the same genes in *Wt1*^{∞/GFP} e12.5 embryos. **F & G**-FACS analysis of AnnexinV (staining of GFP positive cells isolated from e12.5 kidneys from control (F) and mutant (G)). The percentage of total cell death (i.e. apoptotic and necrotic cells) is indicated below each panel.

Figure S1 supports and corroborates the data presented in Figures 1A-F



Figure S2

The absolute Wnt4 expression levels in the e12.5 kidney mesenchyme primary cells and the M15 cell line.

A- The absolute levels of Wnt4 are compared between M15 control, miWt1, GFP+ and GFP- cells e12.5 kidney cells. GFP+ and GFP- cells either had Cre added (Cre+ and hence Wt1 is knocked out) or not (Cre- and hence Wt1 is still expressed). GFP is knocked in the *Wt1* gene. B- The fold of *Wnt4* repression in cells where Wt1 is silenced (M15) or knocked out (e12.5 embryonic kidneys). All data are from at least a biological triplicate. Figure S2 supports and corraborates the data presented in Figure 2.



Figure S3 RNA polymerase II (RNAPII) occupancy upstream and downstream of the *Wnt4* TSS

A- RNAPII occupancy upstream and downtream of Wnt4 TSS in the kidney mesnechymal cell line, M15.
B- RNAPII occupancy upstream and downtream of Wnt4 TSS in the epicardial cell line, MEEC.
Figure S3 supports and corraborates data in Figure 5.