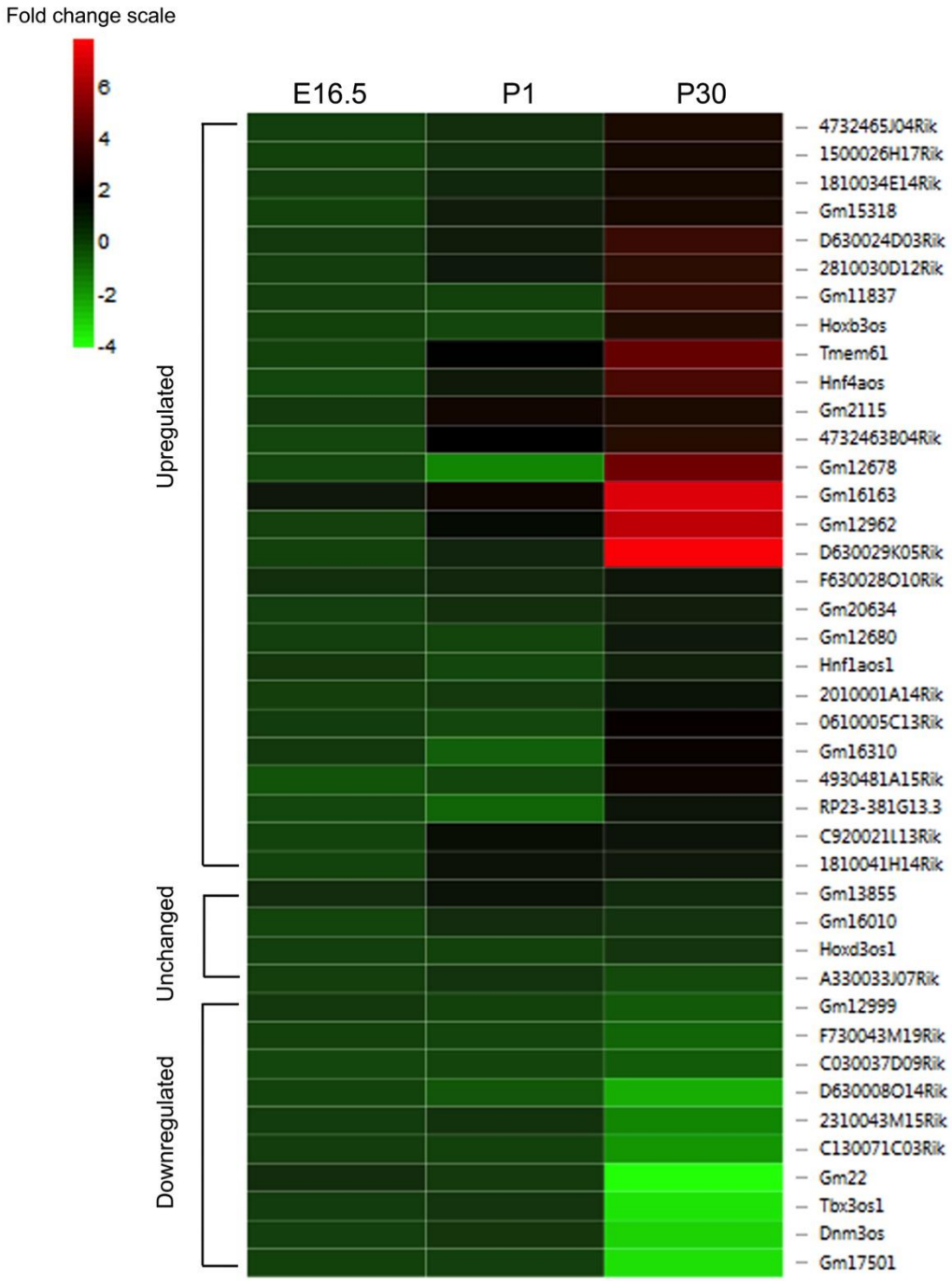
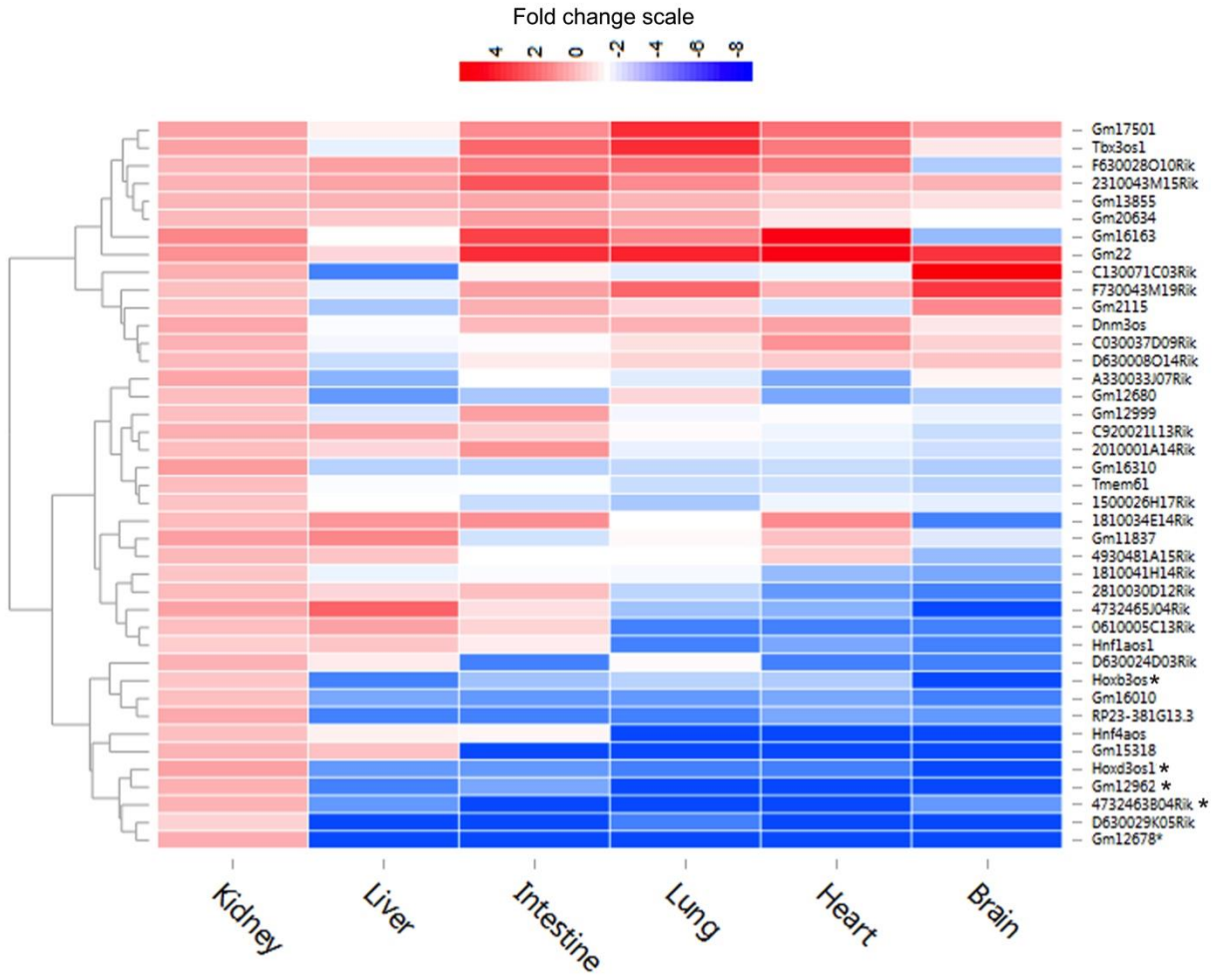
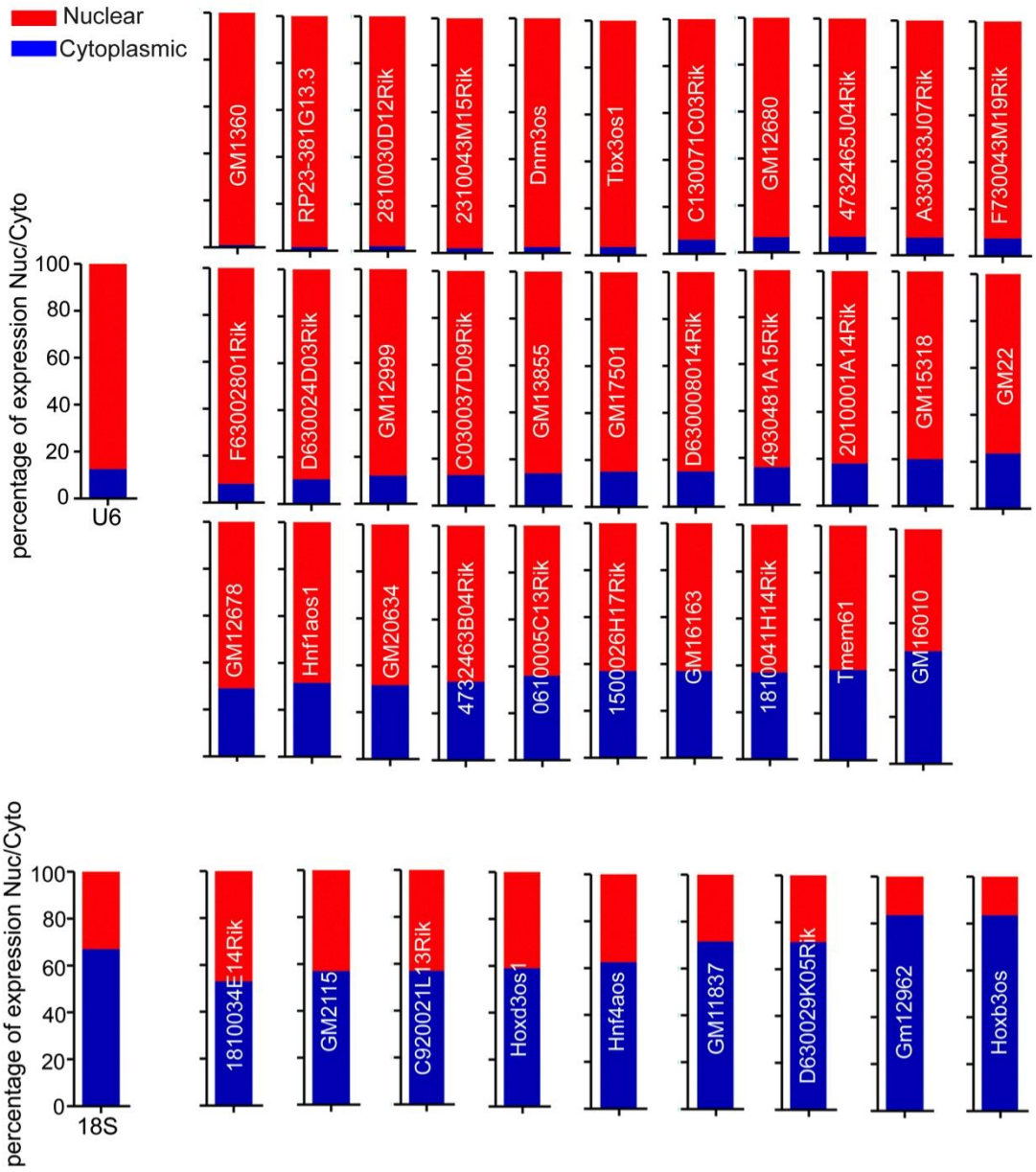


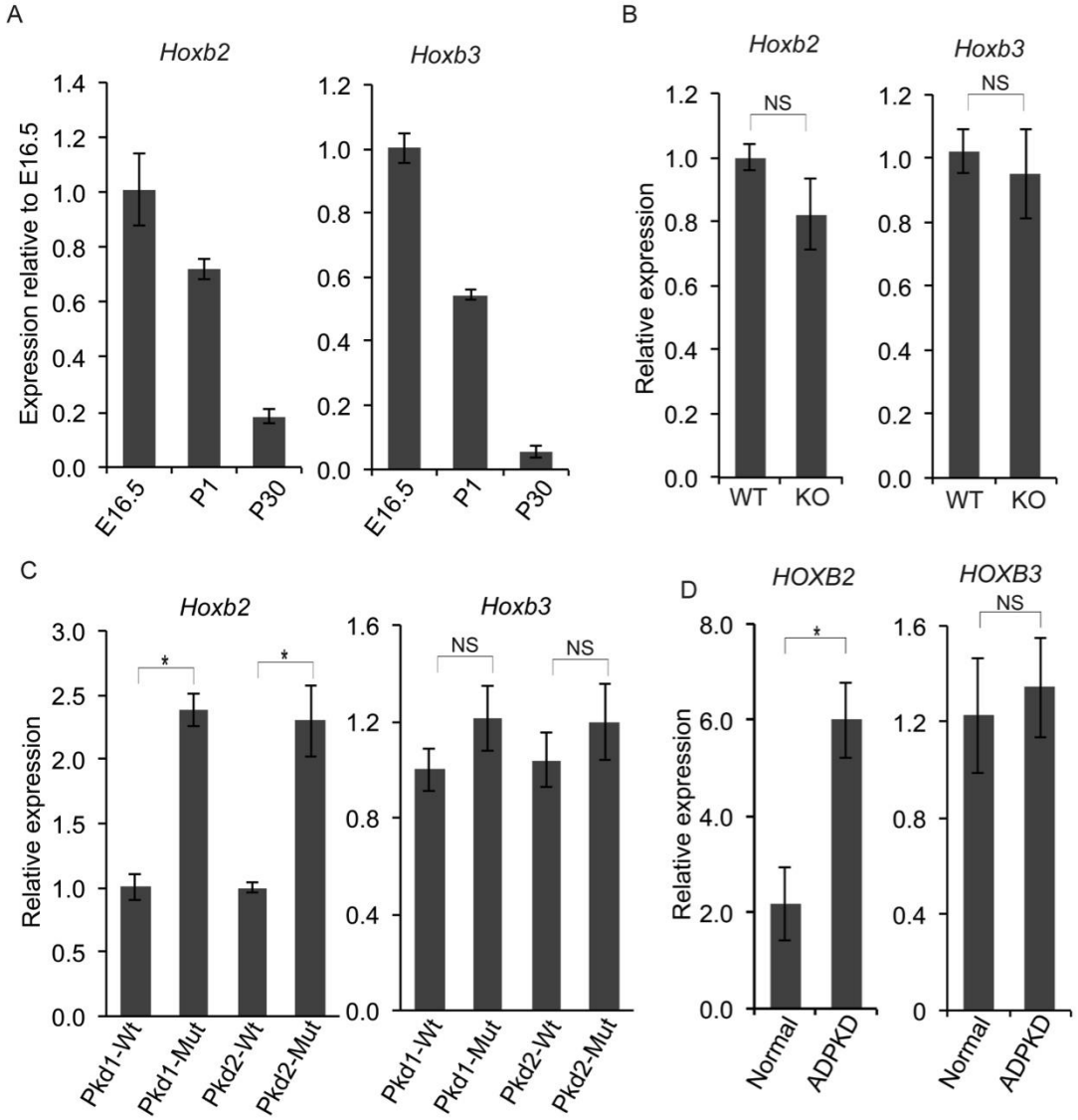
SUPPLEMENTARY FIGURE 1. Heat map showing developmental expression of the 41 most dysregulated lncRNAs in the embryonic (E16.5), newborn (P1) and adult (P30) mouse kidney measured by qRT-PCR. Expression at P1 and P30 was compared relative to E16.5.



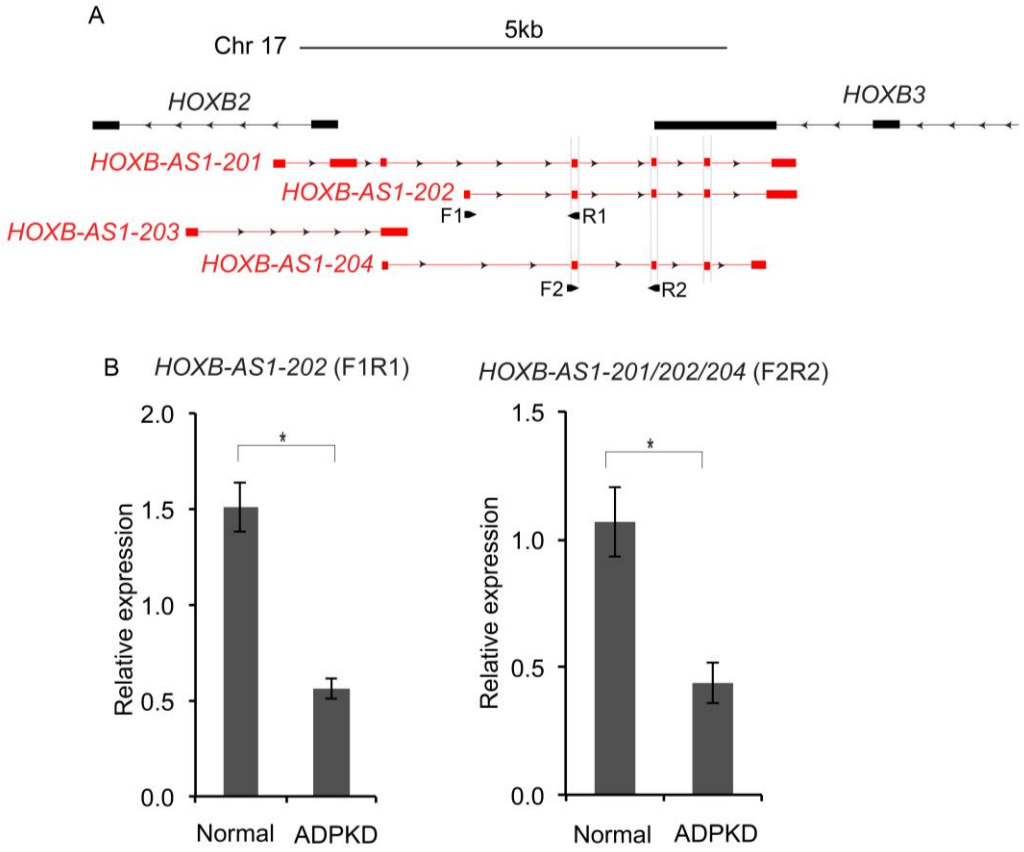
SUPPLEMENTARY FIGURE 2. Heat map of the 41 most dysregulated lncRNA in different organs measured by qRT-PCR. Expression was compared relative to the levels in kidney. Kidney-specific lncRNAs are indicated with an asterisk.



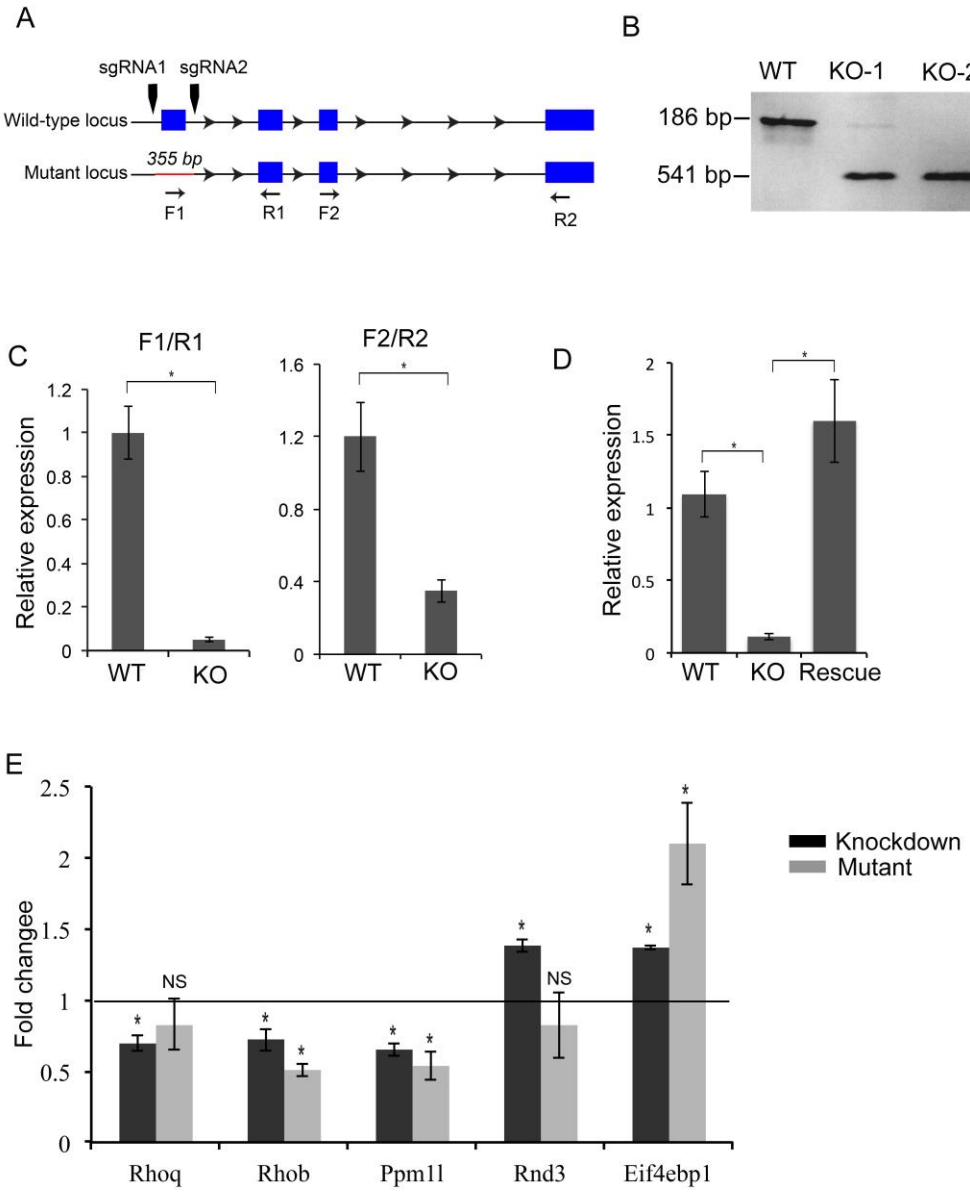
SUPPLEMENTARY FIGURE 3. RNA fractionation showing distribution of the 41 most dysregulated lncRNAs in cytoplasmic and nuclear fractions measured by qRT-PCR.



SUPPLEMENTARY FIGURE 4. Expression of *Hoxb2* and *Hoxb3* in the mamalian kidney. A) Developmental expression of *Hoxb2* and *Hoxb3* in the embryonic (E16.5), newborn (P1), and adult (P30) mouse kidney measured by qRT-PCR. B) Expression of *Hoxb2* and *Hoxb3* in wild type (WT) and *Hoxb3os*-knockout (KO) cells. C-D) Increased expression of *Hoxb2*, but not *Hoxb3*, in *Pkd1* (P10) and *Pkd2* (P20) mutant mice (C) and in human ADPKD kidney (D). Error bars indicate SEM. *, p <0.05. NS, not significant.



SUPPLEMENTARY FIGURE 5. A) Schematic of the human *HOXB3-AS1* locus (red) relative to *HOXB2* and *HOXB3* genes (black). Rectangles indicate exons and arrowheads indicate direction of transcription. Bold arrowheads indicate the location of the primer-set (F1/R1 and F2/R2) that amplifies *HOXB3-AS1* isoforms. B) Expression of the indicated *HOXB3-AS1* isoforms in normal and ADPKD human kidneys by qRT-PCR. Error bars indicate SEM. *, $p < 0.05$.



SUPPLEMENTARY FIGURE 6. A) Schematic of the *Hoxb3os* locus in the mouse indicating the location of the sgRNAs used to delete the promoter region and first exon (355 bp) by CRISPR/Cas9. Blue rectangles indicate exons and black arrowheads indicate direction of transcription. Black arrows indicate the location of the two primer-set (F1/R1 and F2/R2) used to measure the expression of *Hoxb3os* transcript. B) Confirmation of the deleted region by PCR of genomic DNA in three independent knockout cell lines. C) Decreased expression of *Hoxb3os* RNA in knockout cell lines measured by qRT-PCR using the indicated primer-set. D) Expression of *Hoxb3os* in mIMCD3 cells, *Hoxb3os* knockout cells, and *Hoxb3os* rescued cells by qRT-PCR (primer-set F1/R1). E) Quantitative RT-PCR analysis showing expression of five genes in mTOR pathways between *Hoxb3os*-Knockdown and *Hoxb3os*-mutant cells. Error bars indicate SEM. *, $p < 0.05$. NS, not significant.