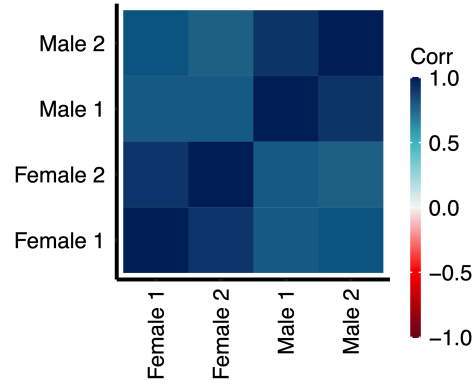
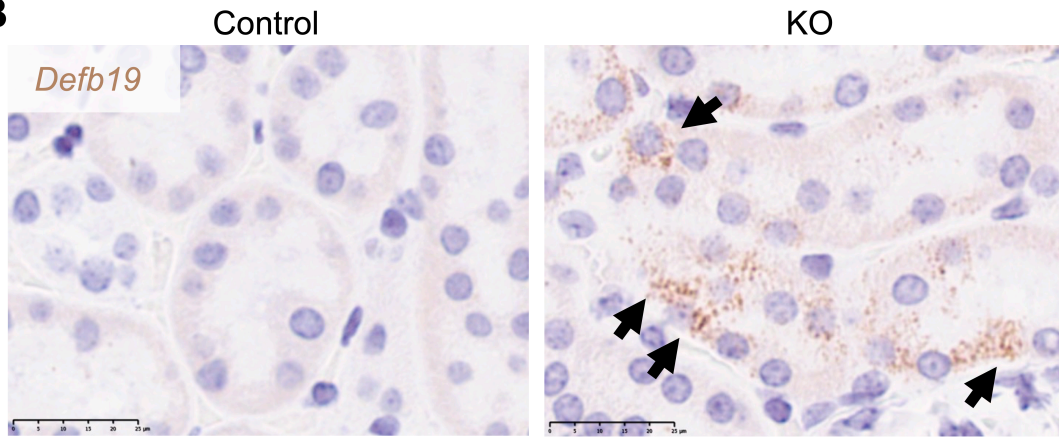


# Supplementary Figure S2

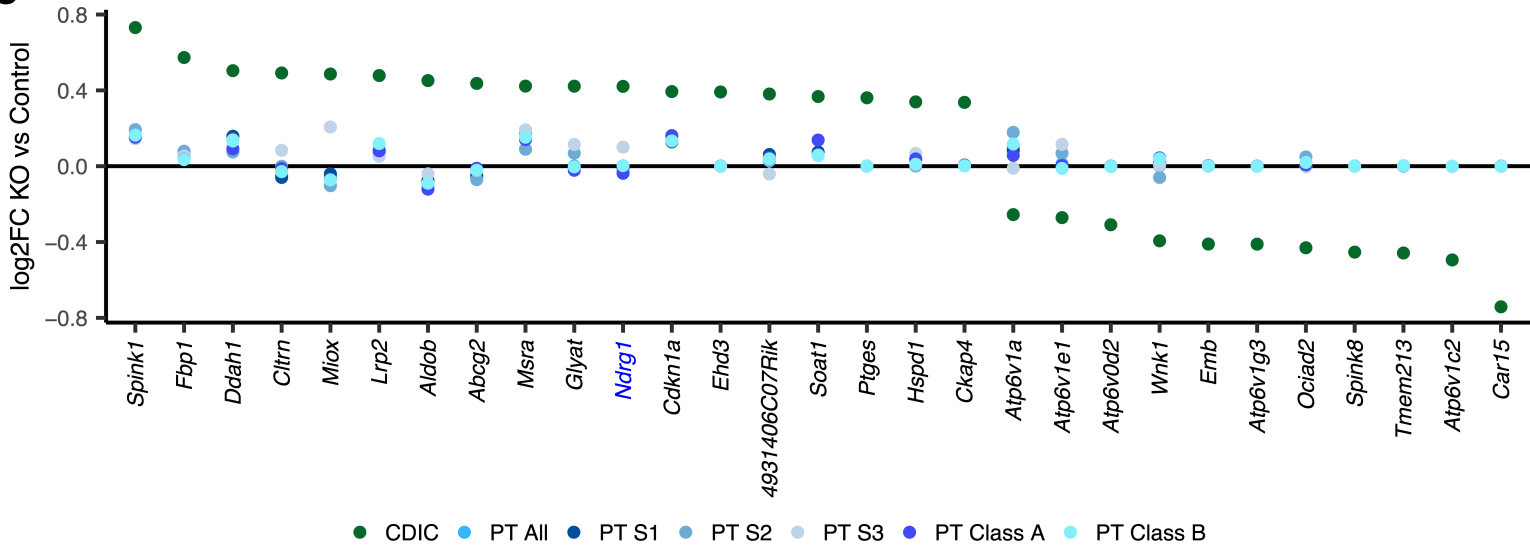
**A**



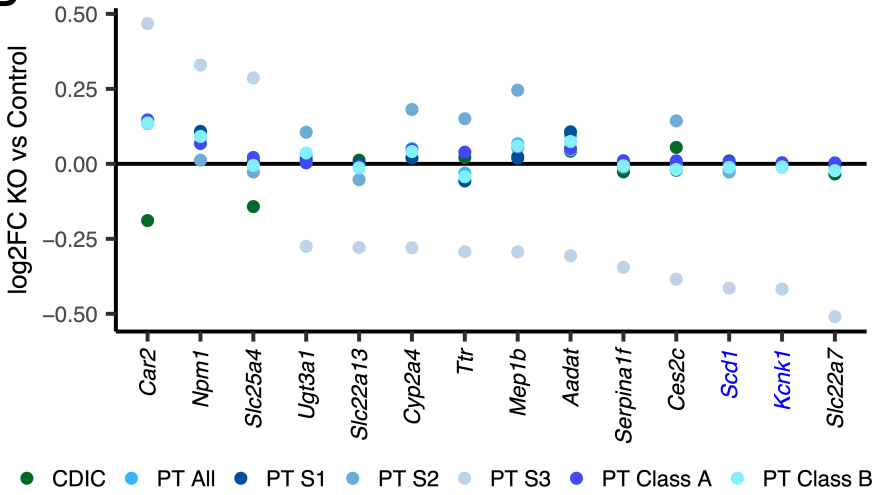
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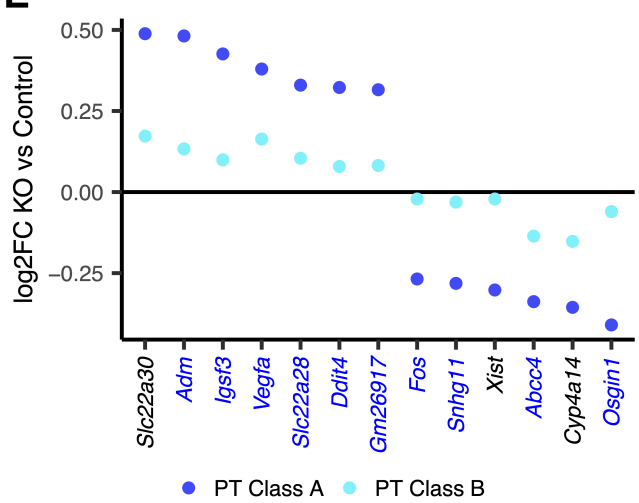
**C**



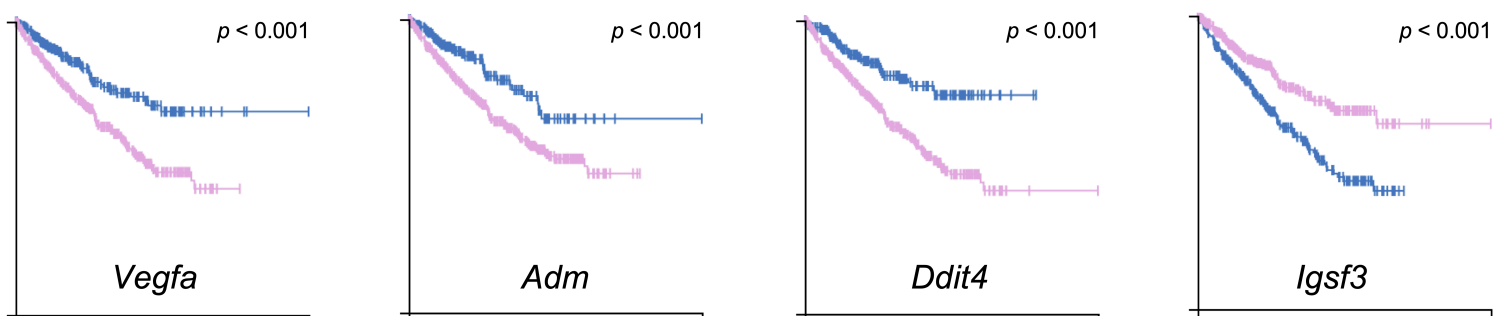
**D**



**E**



**F**



**Supplementary Figure S2: Biallelic *Vhl* loss entrains early cell-specific transcriptomic changes in renal tubular cells.** (A) Heatmap depicting Spearman correlation coefficients for changes in *Vhl*-regulated genes in tdTomato-positive cells derived from individual KO mice. (B) Representative *in situ* RNA hybridization for *Defb19* mRNA in kidneys from Control or KO mice (n = 2F, 2M per genotype) harvested at the early timepoint. *Defb19* signal depicted by black arrows. Scale bar denotes 25  $\mu$ m; 40x magnification. (C-E) Scatter plot depicting log<sub>2</sub>-fold change (log<sub>2</sub>FC) between tdTomato-positive cells from KO *versus* Control for genes specifically regulated in (C) CDIC, (D) PT S3 cells, and (E) PT Class A cells. Names of HIF target genes (blue). (F) Survival analysis of renal cancer patients stratified by expression of genes specifically regulated in PT Class A cells after *Vhl* inactivation. Cases with high (blue) and low (pink) expression. Data from The Human Protein Atlas, accessed on 23 July 2023. (A-E) scRNA-seq data shown for n = 3F, 1M mice for Control positive samples; n = 2F, 2M mice for KO positive samples.