

Figure 1.

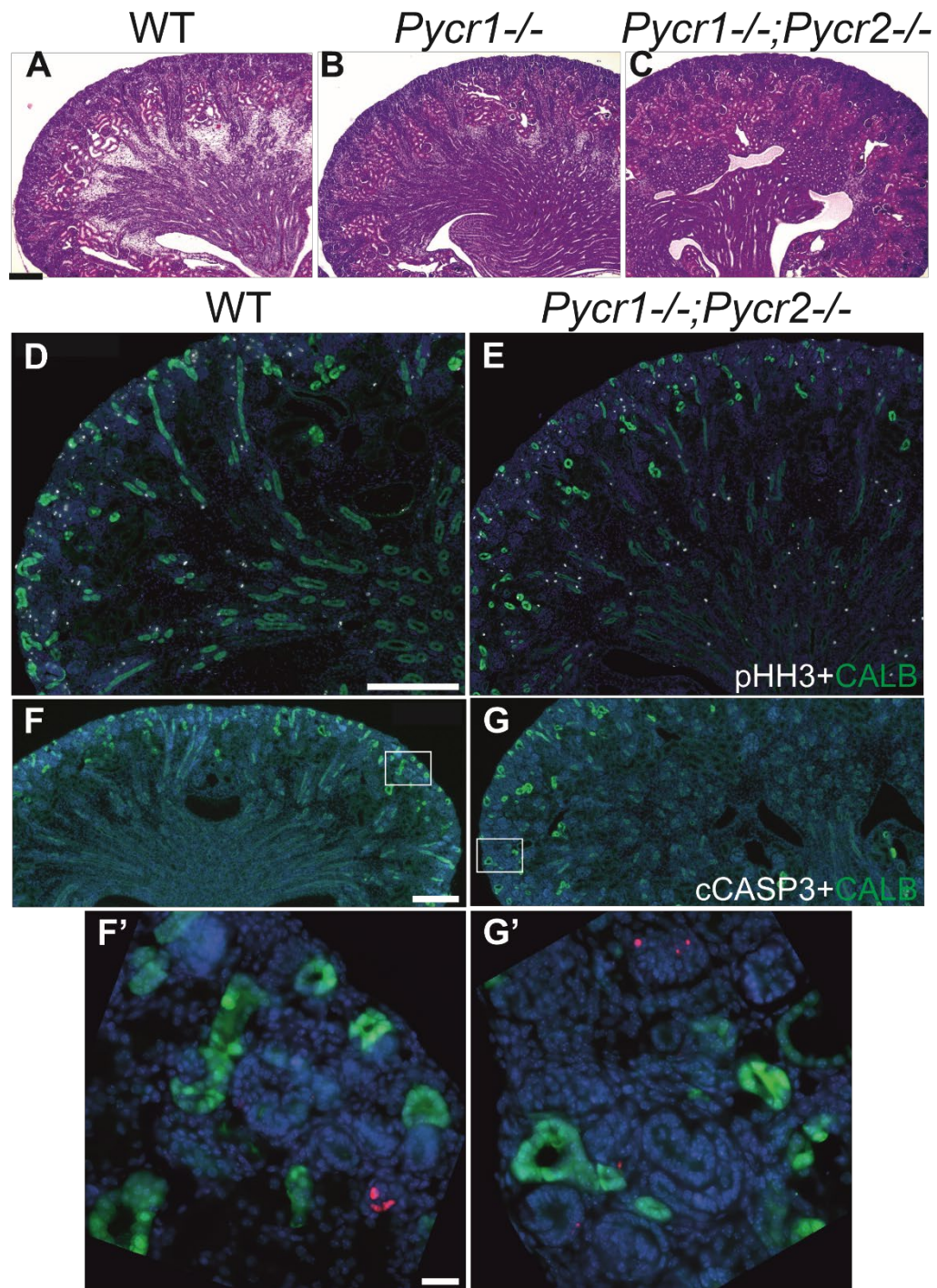


Fig. S1. *Pycr1* and -2 knockout kidney characterization. HE-staining of (A) wild type, (B) *Pycr1* and (C) *Pycr1*^{-/-};*Pycr2*^{-/-} kidneys at postnatal day 1 (P1). Representative examples of proliferation analyses in (D) wild type (WT) and (E) *Pycr1*^{-/-};*Pycr2*^{-/-} kidneys at P1 by phospho-histone H3 (white) staining. Representative examples of apoptosis detection in (F) wild type (WT) and (G) *Pycr1*^{-/-};*Pycr2*^{-/-} kidneys at P1 by cleaved-Caspase 3 (white) staining. CALBINDIN (green) visualizes ureteric bud epithelium in D-G'. Squared areas indicated in F and G are shown with higher magnification in (F') and (G'). Scale bar: A-G; 200µm, F'-G'; 20µm.

Figure 2.

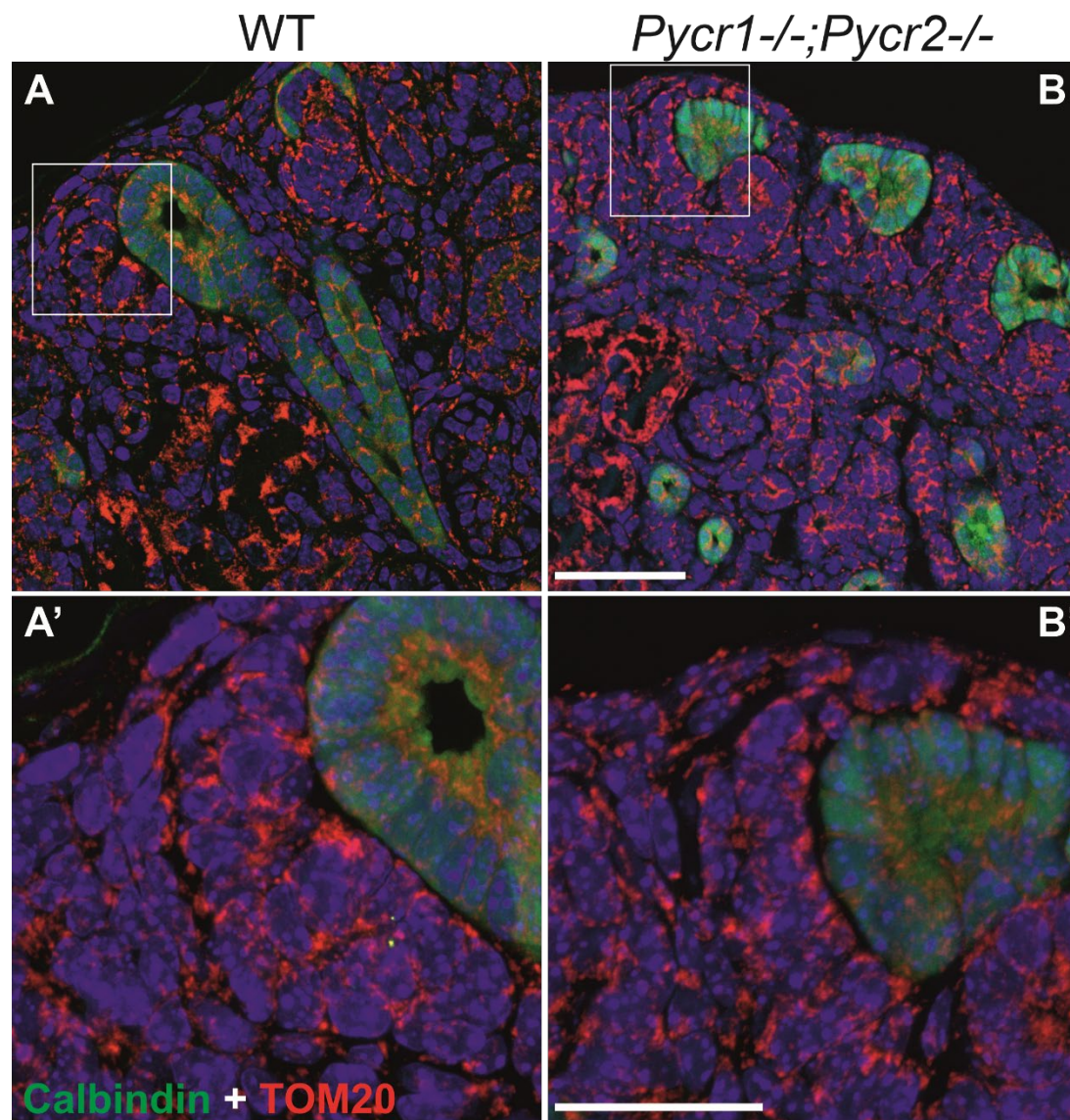


Fig. S2. Mitochondrial morphology in nephron progenitors of *Pycr1* and -2 knockout kidney. Representative examples of mitochondrial morphology and localization in (A) wild type (WT) and (B) *Pycr1^{-/-};Pycr2^{-/-}* kidneys at P1 as visualized by TOM20 (red) staining. CALBINDIN (green) visualizes ureteric bud epithelium. Scale bar: A-B; 50µm, A'-B'; 25µm

Table S1. List of differentially expressed genes

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Table S2. Metabolite marker identification

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Table S3. Metabolic set enrichment analysis (MSEA) of identified metabolites

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Table S4. The correlations between identified metabolites and differentially expressed genes

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Table S5. Comparison of our transcriptional changes to scRNA-seq by Brunskill et al 2014

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Table S6. Analysis of MAPK/ERK target and oxidative stress related gene expressions in MAPK/ERK-deficient nephron progenitors

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Table S7. The metabolite inclusion list of parallel reaction methods

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