

## Description of Additional Supplementary Files

**Supplementary Data 1.** Raw data of kidney weight and body weight in mice without (Sham) or with unilateral nephrectomy (UNx) at different time points (Days 1, Day 3, and 30).

**Supplementary Data 2.** Histological analysis of kidney from mice without (Sham) or with unilateral nephrectomy (UNx) surgery at the 72 hour timepoint.

**Supplementary Data 3.** Morphological data of IF-stained microdissected S1 proximal tubules and cortical collecting duct (CCD) 30 days after surgery.

**Supplementary Data 4.** The hypothesis signaling pathways in kidney triggered by unilateral nephrectomy.

**Supplementary Data 5.** The enriched TF binding motifs identified by HOMER de novo motif analysis in chromatin regions that are more accessible in UNx (DAR-UP), those that are less accessible in UNx (DAR-down), and all chromatin regions that are identified in S1 segment of the proximal tubule.

**Supplementary Data 6.** A quantitative comparison of chromatin accessibility in microdissected S1 segment of proximal tubules at 24 h after UNx.

**Supplementary Data 7.** Target gene sets for individual transcription factors listed in

**Supplementary Table 1.**

**Supplementary Data 8.** Summary of transcription factor target gene sets analysis for ATAC-seq data (24h proximal tubule), RNA-seq data for proximal tubules at 24 h and 72 h after surgery.

**Supplementary Data 9.** Transcript abundance changes in microdissected S1 segment of PTs of mice at 24 h after UNx.

**Supplementary Data 10.** Upstream regulator analysis using QIAGEN's Ingenuity Pathway Analysis for S1 proximal tubule RNA-seq dataset at the 24h timepoint.

**Supplementary Data 11.** Transcript abundance changes in microdissected CCDs of mice at 24 h after UNx.

**Supplementary Data 12.** Transcript abundance changes in microdissected CCDs of mice at 72 h after UNx.

**Supplementary Data 13.** Transcript abundance changes in microdissected S1 segment of PTs of mice at 72 h after UNx.

**Supplementary Data 14.** Comparison of the core enrichments of genes annotated as either "G2M CHECKPOINT" or "E2F\_TARGET" between S1 proximal tubule RNA seq at the 72 hour time point and CCD RNA seq at the 24 hour timepoint.

**Supplementary Data 15.** Upstream regulator analysis using QIAGEN's Ingenuity Pathway

Analysis for S1 proximal tubule RNA-seq dataset at the 72 h timepoint.

**Supplementary Data 16.** Protein abundance changes in whole kidney of mice at 24 h after

UNx.

**Supplementary Data 17.** Upstream regulator analysis using QIAGEN's Ingenuity Pathway

Analysis for whole kidney proteomics dataset at the 24 h timepoint.

**Supplementary Data 18.** Protein abundance changes in kidney cortex of mice at 24 h after

UNx.

**Supplementary Data 19.** Upstream regulator analysis using QIAGEN's Ingenuity Pathway

Analysis for kidney cortex proteomics dataset at the 24 h timepoint.

**Supplementary Data 20.** Protein abundance changes in whole kidney of mice at 72 h after

UNx.

**Supplementary Data 21.** Upstream regulator analysis using QIAGEN's Ingenuity Pathway

Analysis for whole kidney proteomics dataset at the 72 h timepoint.

**Supplementary Data 22.** Phosphoprotein abundance changes in whole kidney of mice at 24 h

after UNx.

**Supplementary Data 23.** Phosphoprotein abundance changes in whole kidney of mice at 72 h after UNx.

**Supplementary Data 24.** Protein kinases that underwent changes in phosphorylation in contralateral kidney in response to unilateral nephrectomy (UNx) relative to Sham surgery at 72 h.

**Supplementary Data 25.** Data integration analysis using multi-omics datasets.

**Supplementary Data 26.** The changes in abundance of amino acid transporters in transcriptome and proteome.

**Supplementary Data 27.** Fatty acid (Gas chromatography) and lipid analysis (calorimetric assay) of kidney from Sham or UNx at 24 hour after surgery.

**Supplementary Data 28.** Body weight, kidney weight and histological parameters of the kidney from mice with or without fenofibrate treatments for 14 days.

**Supplementary Data 29.** Morphological data of IF-stained microdissected S1 proximal tubules from mice without (vehicle) and with fenofibrate treatments for 14 days.

**Supplementary Data 30.** Cell size assay for mouse livers with or without fenofibrates treatments for 14 days using NDP Nanozoomer.

**Supplementary Data 31.** Morphological data of IF-stained microdissected S1 proximal tubules from WT mice or PPAR $\alpha$ <sup>-/-</sup> mice 3 days after unilateral nephrectomy.