Supplemental data

Supplemental Figure 1. Principal components analyses for urine excretion of metabolites per day (A) and blood concentrations of metabolites (B) show segregation of CKD vs. healthy controls. The figures show the plot of principal components 1 vs. 2 (x vs. y axis). Black circles and red triangles denote CKD and healthy controls, respectively.

Supplemental Figure 2. The urinary excretion of citric acid (TCA) cycle metabolites and the renal expression of genes that regulate these metabolites were significantly reduced among participants with versus without non-diabetic CKD. Urine excretion of citric acid cycle metabolites in the proximal part of the pathway were reduced in samples from patients with non-diabetic CKD, as was the mRNA expression of the enzymes catalyzing the proximal steps of the citric acid cycle in the glomerular compartment in biopsies of patients with non-diabetic CKD (tubulointerstitial compartment shown in main text).

Supplemental Table 1. Influence of glomerular and tubular kidney function on metabolite levels.

Note: Urine data show the correlations between the renal excretion of the metabolite and eGFR. Blood data show the correlation between 1/plasma metabolite concentration and eGFR. Analysis includes both controls and CKD participants on placebo. Fractional excretion describes the effect of tubular reabsorption and secretion (e.g. FE 5% means that 95% of the filtered amount is reabsorbed). The median of the differences are displayed with 95% confidence intervals and pvalues based on Wilcoxon rank sum test.

Supplemental Table 2: Fractional excretion (FE %) of metabolites in CKD patients on paricalcitol versus placebo treatment.

Supplemental Table 3. Precision of citric acid cycle metabolites

Supplemental table 4. Metabolites measured in primary study population (Paricalcitol trial).

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Supplemental methods

Replication study population, the SUGAR study

For replication of TCA cycle findings, 45 participants with non-diabetic CKD and 15 matched controls from the SUGAR (StUdy of Glucose And insulin in Renal disease) study were used. Urine metabolites were quantified in 24-hour urine samples using GC-MS analysis at Northwest Metabolomics Research Center, University of Washington, Seattle. A 100 µL aliquot of each urine sample was transferred to a clean 2 mL Eppendorf microcentrifuge tube followed by addition of 100 U urease to remove urea from the sample. After incubation at 37 °C for 1 hour, the urease was precipitated with 850 µL methanol and mixed for 5 min at room temperature. Subsequently, samples were centrifuged for 10 min at 14000 rpm, 750 μ L of the supernatant was transferred to a clean 2.0 mL Eppendorf tube and centrifuged under vacuum until dry. For derivatization, 25 µL of methoxyamine in pyridine (20 mg/mL) was added to each sample and incubated for 90 min at 30 °C. Metabolites were silvlated with 75 μ L MSTFA (1% TMCS v/v) for 30 min at 37 °C and 2 μ L of FAMEs (fatty acid methyl-esters) containing myristic acid – d27 were added to provide a retention time index. GC-MS experiments were conducted using an Agilent 7890A gas chromatograph equipped with an Agilent DB-5ms column 30 m in length and 0.25 mm i.d. column with an additional integrated 10 m guard column coupled to an Agilent 5975C MSD. A total of 1 μL of each sample was injected into a single tapered, split less injector liner with glass wool heated at 230 °C. Metabolites were separated using a temperature gradient consisting of a 60 °C hold for 1 min, ramp at 10 °C/min until a final temperature of 325 °C and a holding for 5 min, for a total run time of 32.5 min. The method was retention time locked using the myristic acid – d27 with a targeted elution time of 16.75 min. Spectral deconvolution and metabolite identification were conducted using AMDIS software (Agilent) and the NIST library, respectively. Typically, relative quantitation of approximately 150 metabolites, along with approximately 200 unidentified metabolite signals are observed for each urine sample. The retention times on the LC-MS platform for TCA cycle metabolites citrate, isocitrate, succinate, and cis-aconitate were 16.62, 16.88, 10.58 and 13.56 minutes, respectively. The retention times using the GC-MS platform for these metabolites were as follows: citrate 13.84, isocitrate 13.10, succinate 7.93, 2-oxoglutarate 15.36, and cis-aconitate 13.10 minutes.

Gene expression in human kidney tissue

Total RNA was isolated from micro-dissected glomerular and tubulointerstitial compartments from kidney biopsies of 155 patients from the ERCB cohort with biopsy-proven, non-diabetic CKD. RNA was reverse-transcribed and amplified, fragmented and hybridized to Affymetrix GeneChip Human Genome U133A 2.0 and U133 Plus 2.0 Array. The Cel files were uploaded on Gene Omnibus website (http://www.ncbi.nlm.nih.gov/geo/) under reference numbers GSE32591, $GSE37455$, $GSE35488$, and $GSE47185$.³ Gene expression data for 20 TCA cycle enzymes, and 11 genes regulating mitochondrial biogenesis was extracted from above datasets for further analysis

References

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