Molecular Signatures of Diabetic Kidney Disease Hiding in a Patient with Hypertension-Related Kidney Disease: A Clinical Pathologic Molecular Correlation

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**Supplemental Methods**

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A common overlapping set of 25,294 genes expressed was identified in our patient and nine nephrectomy samples for the glomerulus, proximal tubule, thick ascending loop of Henle, collecting duct, and interstitium (without tubules). Expression data can be found on [www.kpmp.org](http://www.kpmp.org). All samples and subsegments were quantile normalized together. The dispersion means biologic coefficient of variation (BCV) value for each gene was estimated from the nine KPMP nephrectomy samples in EdgeR. The BCV value constant was increased from 0.05 to 0.1 to be more conservative, assuming increased heterogeneity in disease. Differential expression was then tested between the case subject for each subsegment with the corresponding nephrectomy sub-segments using a negative binomial exact test. Individual genes were considered significant if they passed a Bonferroni multiple testing correction. For pathway enrichment, a Fisher’s exact test of KEGG pathways was employed using all significant genes.