

## **Diabetic Complications Consortium**

**Application Title: Single Cell Sequencing of Human Diabetic Kidney Disease**

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### **1. Project Accomplishments:**

We have collected human kidney tissue samples

We performed histological analysis and collected clinical information.

We successfully performed single cell RNAsequencing on 10 human kidney samples. Sequencing data has been obtained data matrix generate.

We have performed preliminary bioinformatic analysis of control and diabetic human kidney samples including cell type identification.

### **Specific Aims:**

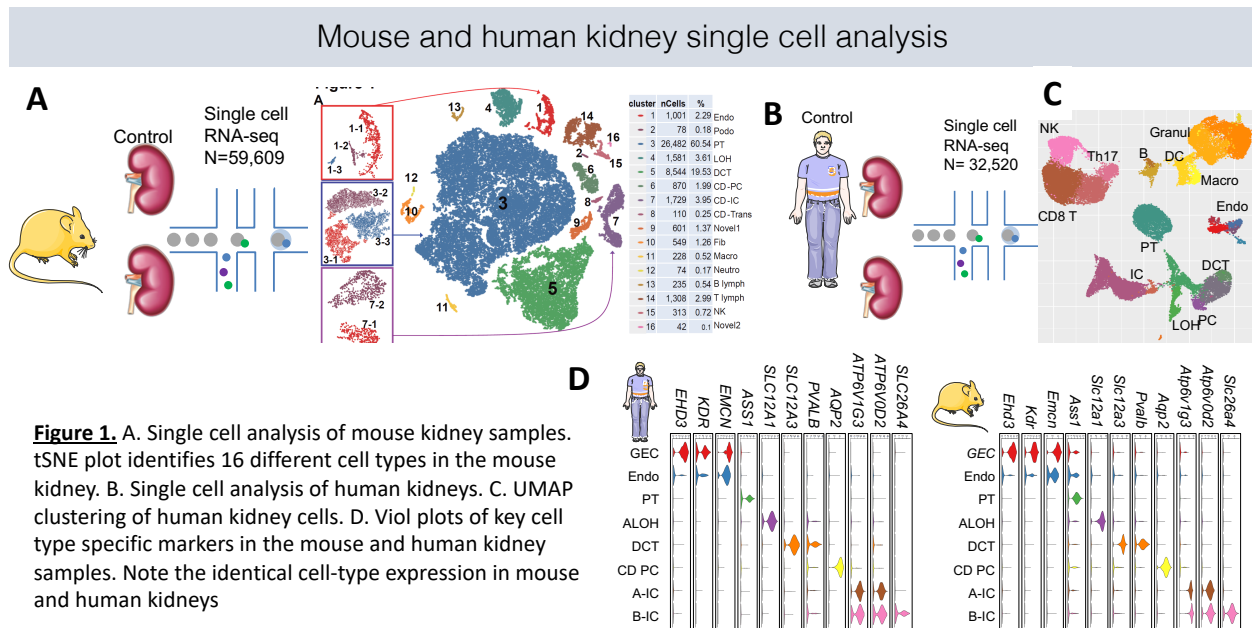
**Aim1. Generate a comprehensive single cell kidney transcriptome atlas for healthy and diabetic human kidney samples. Define cell types and the cell type specific transcriptome.**

**Aim2. Define cell-type specific and cell-type composition transcriptomic changes in human diabetic kidney disease and trace origin of cell types in DKD.**

**Results:** 1. We completed the single cell analysis for the following 10 human kidney tissue samples. The clinical information is shown under table 1.

<b>FIG 1.</b>	<b>HK NUM</b>	<b>NON TUM DX</b>	<b>CKD STAGE</b>	<b>GFR (CKD- EPI)</b>	<b>DM- TYPE</b>	<b>HTN</b>	<b>AGE</b>	<b>GENDER</b>	<b>RAC</b>
Human2	HK1584	DKD/HTN	3	57.60987	2	1	59	1	1
Human3	HK1585	CONTROL	1	95.44299	0	0	69	1	1
Human4	HK1588	CONTROL	2	80.87882	0	0	57	1	1
Human5	HK1593	CKD	3	53.88228	0	0	56	1	1
Human6	HK1594	CONTROL	2	62.7923	0	0	60	0	1
Human7	HK1595	DKD/HTN	3	39.07191	2	1	55	0	1
Human10	HK1632	DKD	3	53	2	0	56	1	1
Human12	HK1634	DKD	2	63	2	1	63	0	1
Human13G	HK1635	DKD	2	62	2	1	70	0	1
Human13T	HK1635	DKD	2	62	2	1	70	0	1
Human 24	HK1997	CONTROL	1	69	0	1	71	0	1

2. After quality control we have retained a total of 32,520 cells. The initial clustering



of these cells are shown on Figure1. We noticed that the cell type discriminatory gene signature was identical in the human and the mouse data.

- While single nuclear data has been generated for human kidneys this is the first whole human kidney single cell data. In the single cell data compared to the single nuclear data we can identify much larger number of immune cells. Unfortunately the precise identification of immune cell in the single cell data is still fairly difficult. We are working on correct identification of immune cells in the human kidney data using transfer learning methods.
- Finally, we are also working on the identification of differentially expressed genes between control diabetic samples.

## 5. Publications:

We are in the process of finalizing the results and writing up the manuscript. We expect to complete the manuscript by the end of January. We plan to deposit the manuscript to BioRx and the accompanying gene expression data into GEO.