

Analysis of Single-Cell RNAseq in PKD Kidneys

Re-analysis by

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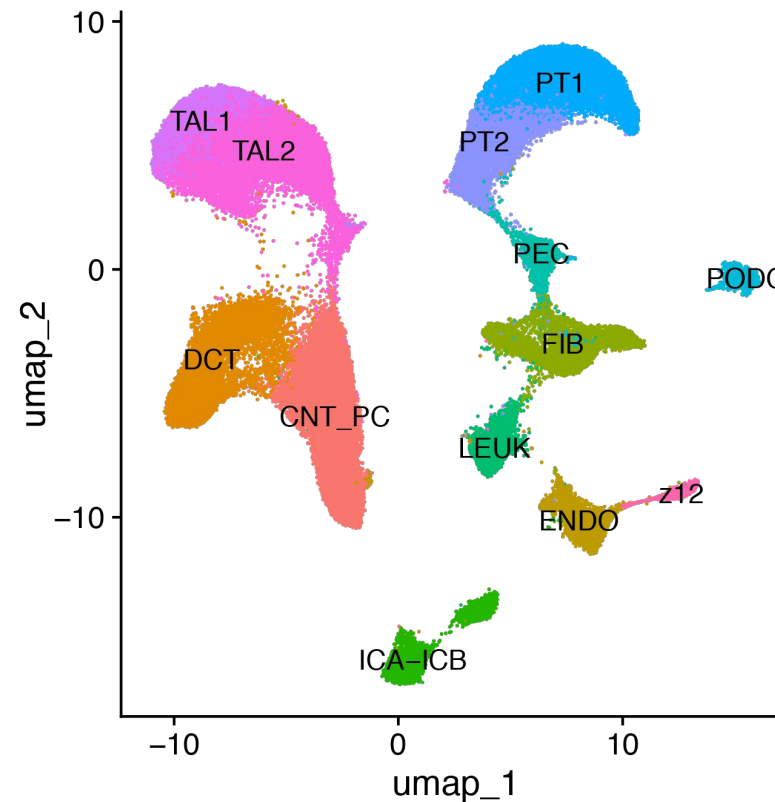
Data Source: Muto, et al.(2022). “Defining cellular complexity in human autosomal dominant polycystic kidney disease by multimodal single cell analysis”. [Nat Commun.](#)

Cell types

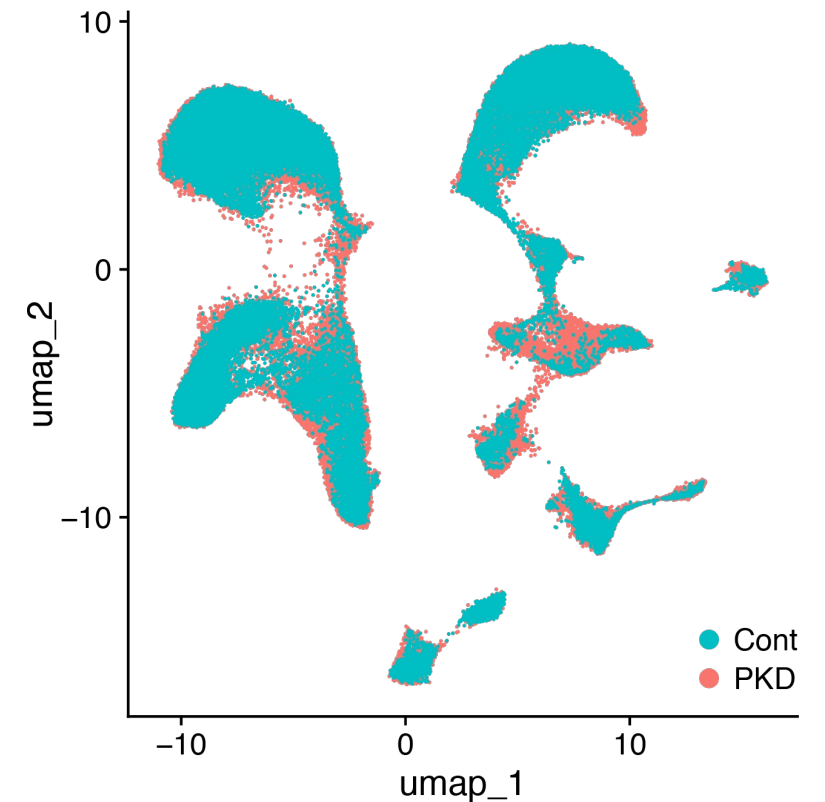
Bioinformatics workflow:

1. Integrate across samples
2. Normalize between PKD and Ctrl
3. Obtain cell clusters (n=12)
4. Map cell types based on marker genes
5. Perform DE analysis

- Number of samples:
Ctrl (n=5); PKD (n=7)
- Number of cells:
Ctrl (n=40,637); PKD (n=51161)
- Number of genes:
n=2,000 variable genes



- CNT_PC: connecting tubule and principal cells
- DCT: distal convoluted tubule
- ENDO: endothelial cells
- FIB: fibroblasts
- ICA: Type A intercalated cells
- ICB: Type B intercalated cells



- LEUK: leukocytes
- PEC: parietal epithelial cells
- PODO: podocytes
- PT: proximal tubule
- TAL: thick ascending limb of Henle's loop
- Z12: unknown

Differential Gene Expression Analysis between Ctrl and PKD

cell_type	gene	up/down	sub group
CNT_PC	AC017002.5	-	0
	HSD11B2	-	0
	LINC01098	-	0
	LINC01099	-	0
	SLC8A1	-	0
	SLC8A1-AS1	-	0
	TEX41	-	0
	UPP1	-	0

DCT	AC078980.1	-	0
	AL355612.1	-	1
	BACE2	-	0
	BTBD11	-	0
	CACNB4	-	1
	CNNM2	-	0 & 1
	DEPDC1B	-	0
	KLHL3	-	0
	LINC01762	-	1
	SLC12A3	-	1
	TMEM52B	-	1
	TRPM6	-	0

ENDO	ADGRF5	-	
	NOSTRIN	-	
	SEC14L1	-	
	SLCO2A1	-	
	TEK	-	

FIB	PIP5K1B	-	0
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ICA-ICB	ADAMTSL1	-	1
	CELF2	-	0
	CNTNAP5	-	1
	IQGAP2	-	0
	LINC01187	-	0
	PDZD2	-	0
	PLCL2	-	0
	SHOC1	-	1
	THRB-AS1	-	1
	UAP1	-	1
	VAT1L	-	1
	VWA5B1	-	1

cell_type	gene	up/down	sub group
LEUK	CD74	+	

PODO	AC040168.1	+	0
	ATP10A	-	1
	DACH2	-	2
	GRK5	-	1
	LINC00839	-	0
	NECAB1	-	1
	NLRP1	-	0
	TRPC6	-	0
	TSPAN2	-	0
	ZBTB7C	-	1

PT1	AC003044.1	-	0
	AC007364.1	-	0
	ACSM2B	-	0
	AGXT2	-	0
	CUBN	-	0
	RHEX	+	0
	SLC13A1	-	0
	SLC16A9	-	0
	SLC17A1	-	0
	SLC28A1	-	0

PT2	ACSM2A	-	1
	ACSM2B	-	1
	CUBN	-	1
	SLC17A1	-	1

TAL1	AC092078.2	-	
	GP2	-	
	UMOD	-	

TAL2	GP2	-	0
	UMOD	-	0

Z12	AC008050.1	-	0
	CHRM3	-	1
	NKAIN2	-	1
	TACR1	-	1

