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## **Single cell transcriptomic research in translational medicine**

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Single cell sequencing technologies have greatly advanced our understanding of kidney biology and disease. In this lecture I will present our most recent work using multiomic and spatially resolved transcriptomic approaches to better understand cellular diversity in kidney health and disease. Datasets generated from healthy human kidney, human polycystic kidney disease and mouse models of acute kidney injury and diabetic nephropathy will be reviewed. The integration of single cell transcriptome and chromatin accessibility datasets enables a deeper understanding of cell heterogeneity. As powerful as they are, these single cell approaches are also characterized by a loss of spatial information which hinders our interpretation of local intercellular communication networks and regional patterns of gene expression. New spatial transcriptomic sequencing platforms now make it possible to measure the spatial topography of gene expression at genome depth and these will be reviewed as well.