SIGNIFICANCE STATEMENT

Massively parallel single-cell RNA sequencing technologies provide powerful new possibilities to understand cell complexity, but which platform is best suited to study adult kidney in health and disease is undefined. The authors report that single-nucleus RNA sequencing offers comparable gene expression quantitation (despite reduced mRNA in the nucleus compared with the whole cell) as well as substantial advantages over single-cell RNA sequencing. These include representation of rare or fragile kidney cell types, the ability to use archival frozen samples, elimination of dissociation-induced transcriptional stress responses, and successful performance on inflamed fibrotic kidney. This work will guide future efforts to build a comprehensive single-cell atlas of healthy and diseased kidneys.