SIGNIFICANCE STATEMENT

The glomerular filtration unit consists of three tightly intertwined cell types: the endothelium, the mesangium, and podocytes. Despite established physiologic cues acting on these cells within a single glomerulus, cellular heterogeneity in the healthy glomerulus remains poorly characterized. To address this problem, the authors performed large-scale transcriptional profiling of 13,000 mouse glomerular cells. They provide a comprehensive atlas of gene expression for the known glomerular cell types and describe potential subpopulations for endothelium and podocytes. An interactive, freely accessible web tool allows for querying and visualizing the data. The study highlights the power of single-cell RNA sequencing to study gene expression in the kidney and sets the stage for future investigations of glomerular dysfunction in disease.