The comprehensive single-cell atlas of mouse kidney with regional information

Background

The kidney is a highly heterogeneous organ, it is estimated that it has about 40 functionally different cell types. Single-cell RNA sequencing is a powerful technology for detecting cell types in highly complex tissues. However, no single study has comprehensively identified all cell populations residing in the kidney. For example, glomeruli are the functional units of the kidney, but they account for only about 1% -1.5% of the volume. Most whole kidney single-cell or single-nucleus RNA sequencing datasets do not include components of the glomeruli. Another exception is the neuron components, whose cell bodies are located paravertebrally and whose axons extend into the kidney through renal hilus. However, their expression is largely unknown, especially their interactions with other renal components, through which they participate in the regulation of renal function. In this study, we used cutting-edge integration algorithms to integrate information from five sequencing datasets and generate a comprehensive single-cell atlas of mouse kidneys. Two of the datasets used micro-dissection to dissect different regions of the kidney for sequencing, and regional information is also retained in this dataset.

Introduction

Methods

Results

Discussion