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Cross-platform single cell analysis of kidney development shows stromal cells express Gdnf

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Abstract

The developing kidney provides a useful model for study of the principles of organogenesis. In this report we use three independent platforms, Drop-Seq, Chromium 10x Genomics and Fluidigm C1, to carry out single cell RNA-Seq (scRNA-Seq) analysis of the E14.5 mouse kidney. Using the software AltAnalyze, in conjunction with the unsupervised approach ICGS, we were unable to identify and confirm the presence of 16 distinct cell populations during this stage of active nephrogenesis. Using a novel integrative supervised computational strategy, we were able to successfully harmonize and compare the cell profiles across all three technological platforms. Analysis of possible cross compartment receptor/ligand interactions identified the nephrogenic zone stroma as a source of GDNF. This was unexpected because the cap mesenchyme nephron progenitors had been thought to be the sole source of GDNF, which is a key driver of branching morphogenesis of the collecting duct system. The expression of *Gdnf* by stromal cells was validated