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CORRECTION

Correction: Single cell analysis of the developing mouse kidney provides deeper insight into marker gene expression and ligand-receptor crosstalk (doi:10.1242/dev.178673)

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Edits have been made to *Development* (2019) **146**, dev178673 (doi:10.1242/dev.178673) to clarify that statements made comparing this and previous studies relate to the published analyses of data within those studies and not the detection of genes within the datasets themselves.

The changes made are shown below and both the online full-text and PDF versions have been updated.

In the Introduction, the following statement was changed:

Original

However, existing datasets have apparently not provided the transcriptional depth to identify the signalling pathways that operate within the human fetal kidney, and fail to detect several known ligand and receptor expression patterns in mouse.

Corrected

The analyses performed on existing datasets have not comprehensively identified the signalling pathway components known to be operating within the mouse fetal kidney.

In the Discussion, the following statements were changed:

Original

For example, although >20,000 cells were profiled at P1 (Adam et al., 2017), several known signalling molecules with functionally validated roles in the nephrogenic niche such as *Gdnf*, *Fgf20*, *Fgf9*, *Bmp7*, *Wnt4* and *Fgf8* were not detected in that analysis, precluding further insight into signalling interactions.

Corrected

Although >20,000 cells were profiled at P1 (Adam et al., 2017), several known signalling molecules with functionally validated roles in the nephrogenic niche were not highlighted in that analysis.

Original

The improved resolution of gene expression in our study may be due to sequencing depth (~3000 genes detected per cell), biological replication and differential expression analysis with the edgeR method, which has recently been shown to be a top performer in a comparison of 36 differential expression analysis methods for scRNA-seq data (Soneson and Robinson, 2018).

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In addition, a sentence (underlined) was moved as shown below:

Original

Lineage tracing was performed to investigate the possibility of these cells representing a transitional state. Using a constitutively active *Six2*-Cre (*Six2*TGC), *Six2*-derived cells were observed in the cortical and medullary stroma in all samples (Fig. 5F). However, as this *Six2*-Cre is active from E11.5 or earlier, labelled stromal cells may reflect the early plasticity between stromal and nephron lineages rather than continued transdifferentiation. Using an inducible *Six2*-Cre (*Six2*GCE, induced from E12.5) to assess nephron progenitor contributions to stroma after the establishment of the proposed lineage boundary did result in rare *Six2*-derived cells in the nephrogenic zone that did not express SIX2 protein, but labelled cells were observed at a frequency lower than expected based on NP7 cluster size, and most labelled cells were unusually small, suggesting they may be undergoing apoptosis (Fig. 5G). Evidence of lineage transition was also observed deeper in the kidney.

Corrected

Lineage tracing was performed to investigate the possibility of these cells representing a transitional state. Using a constitutively active *Six2*-Cre (*Six2*TGC), *Six2*-derived cells were observed in the cortical and medullary stroma in all samples (Fig. 5F). Evidence of lineage transition was also observed deeper in the kidney. However, as this *Six2*-Cre is active from E11.5 or earlier, labelled stromal cells may reflect the early plasticity between stromal and nephron lineages rather than continued transdifferentiation. Using an inducible *Six2*-Cre (*Six2*GCE, induced from E12.5) to assess nephron progenitor contributions to stroma after the establishment of the proposed lineage boundary did result in rare *Six2*-derived cells in the nephrogenic zone that did not express SIX2 protein, but labelled cells were observed at a frequency lower than expected based on NP7 cluster size, and most labelled cells were unusually small, suggesting they may be undergoing apoptosis (Fig. 5G).

The authors apologise for any lack of clarity in the original version of this paper. We believe the text now accurately reflects the contributions made by previous studies and the present work.