

# Supplemental Figures

## Single-cell chromatin and gene-regulatory dynamics of mouse nephron progenitors

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**Supplemental Figure 1. Quality control for the Singleome scATAC-seq data (E16.5/P2).**

- (A) Insert size distribution of the scATAC-seq samples showing characteristic nucleosomal periodic patterns.
- (B) Transcription start sites (TSS) signal enrichment of the scATAC-seq samples.

**Supplemental Figure 2. TSS and unique nuclear fragments enrichment in Singleome scATAC-seq data (E16.5/P2).**

- (A) Violin plots showing TSS enrichment scores per sample at E16.5 and P2.
- (B) Violin plot showing the log(base10) of unique nuclear fragments per sample.
- (C) scRNA seq: median number of genes (left) and reads (right) per cell.

**Supplemental Figure 3. Quality control of Multiome scATAC/GEX (E16.5/P2).**

- (A) scATAC-seq: unique fragments/TSS, TSS enrichment scores, unique nuclear fragments, fragment size and TSS enrichment profiles
- (B) scRNA-seq: median genes/reads per cell.

**Supplemental Figure 4. Differential gene-specific chromatin accessibility across cell clusters.** Representative genes of progenitors (*Six2*), early (*Wnt4*, *Lef1*) and late (*Lhx1*, *Hnf1b*) differentiating, proximal (*Hnf4a*), LOH/distal (*Pou3f3* and *Tfap2b*) segments are shown.

**Supplemental Figure 5. Chromatin accessibility identifies new markers of tubular differentiation.**

(A, B) scATAC-seq UMAPs: *Mcmduc2* chromatin accessibility is higher in proximal than distal precursors. *Nabp1* chromatin accessibility is seen in both proximal and distal precursors.

(C-J) Confocal images of RNAscope. *Mcmduc2* is expressed in LTL-positive proximal tubules (C, D) and in Slc12a3+ distal tubules (H,I). *Nabp1* is expressed in LTL-positive as well as LTL-negative/Slc12a3-positive segments (E, F, H, J). *Mcmduc2* and *Nabp1* are not expressed in nascent nephron of the nephrogenic zone (NZ) (G).

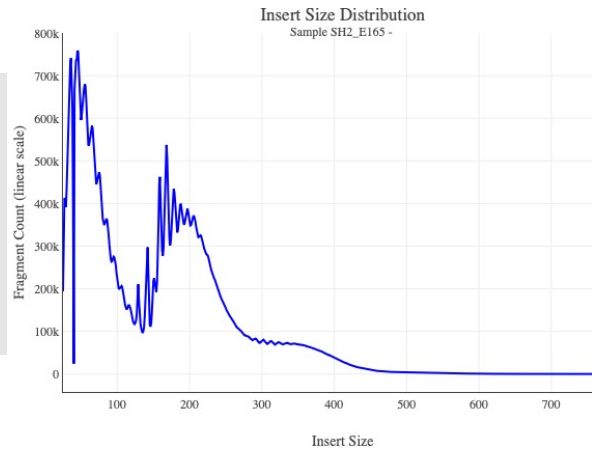
**Supplemental Figure 6. *Meis2* is expressed in stroma and NPCs.**

(A) Section IF for Six2 and Meis (1/2/3) factors in E14.5 kidney. In addition to expression in stroma, there is a low-level expression in Six2<sup>+</sup> cells.

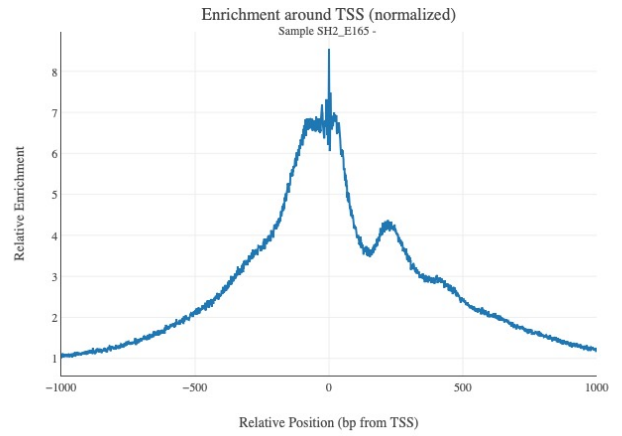
(B,C) UMAPs of E16.5/P2 multiome showing expression of *Meis2* in NPC clusters.

(D) scRNA derived UMAPs from published (GSE108291, GSE149134) and our unpublished (E14.5, P0) databases showing co-expression of *Meis2*/*Six2* especially prominent prior to P0.

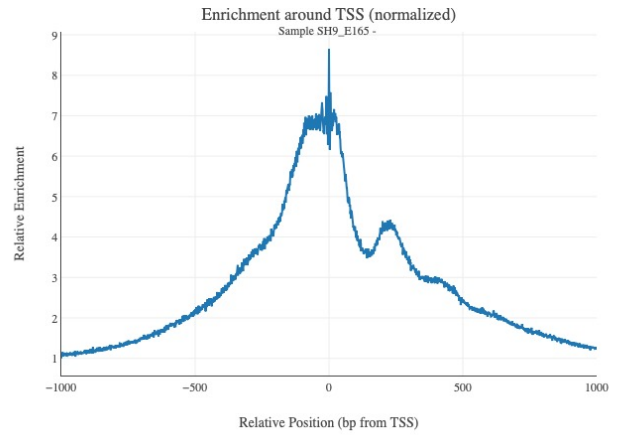
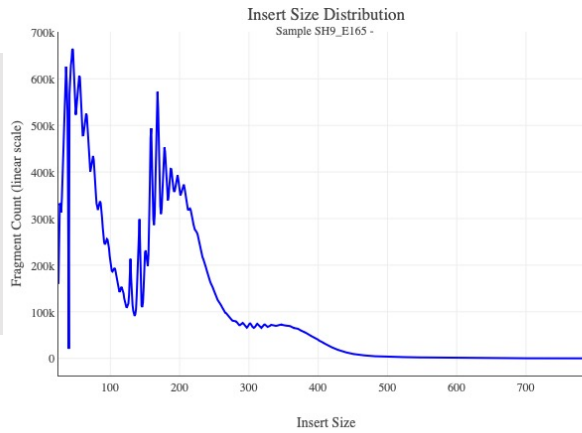
A



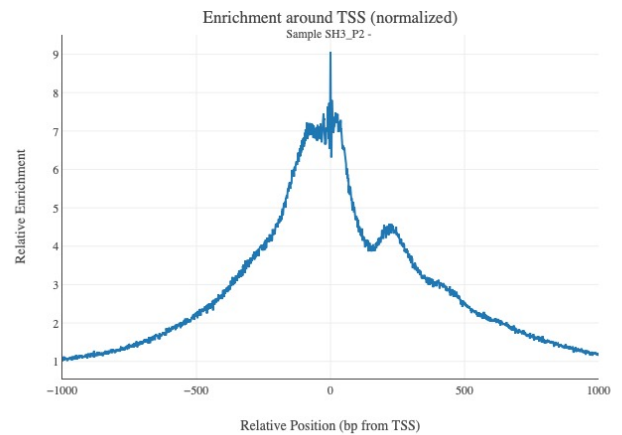
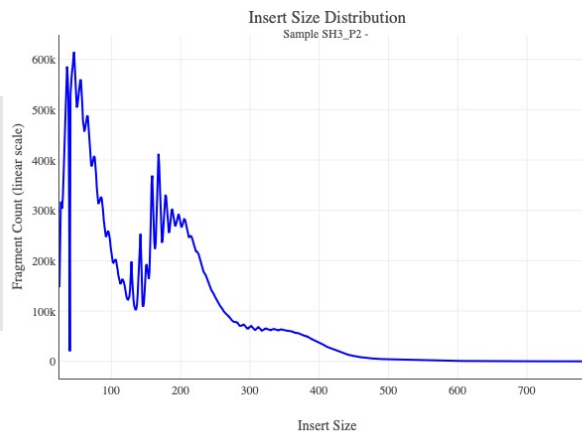
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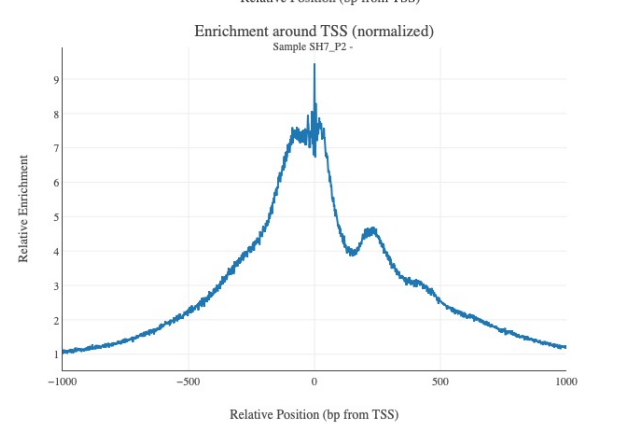
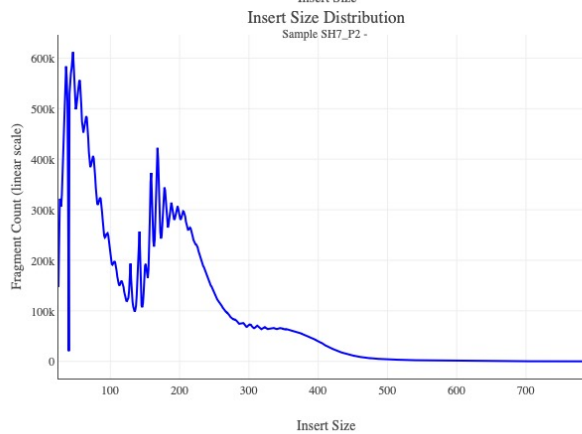
E16.5\_sample 1



E16.5\_sample 2

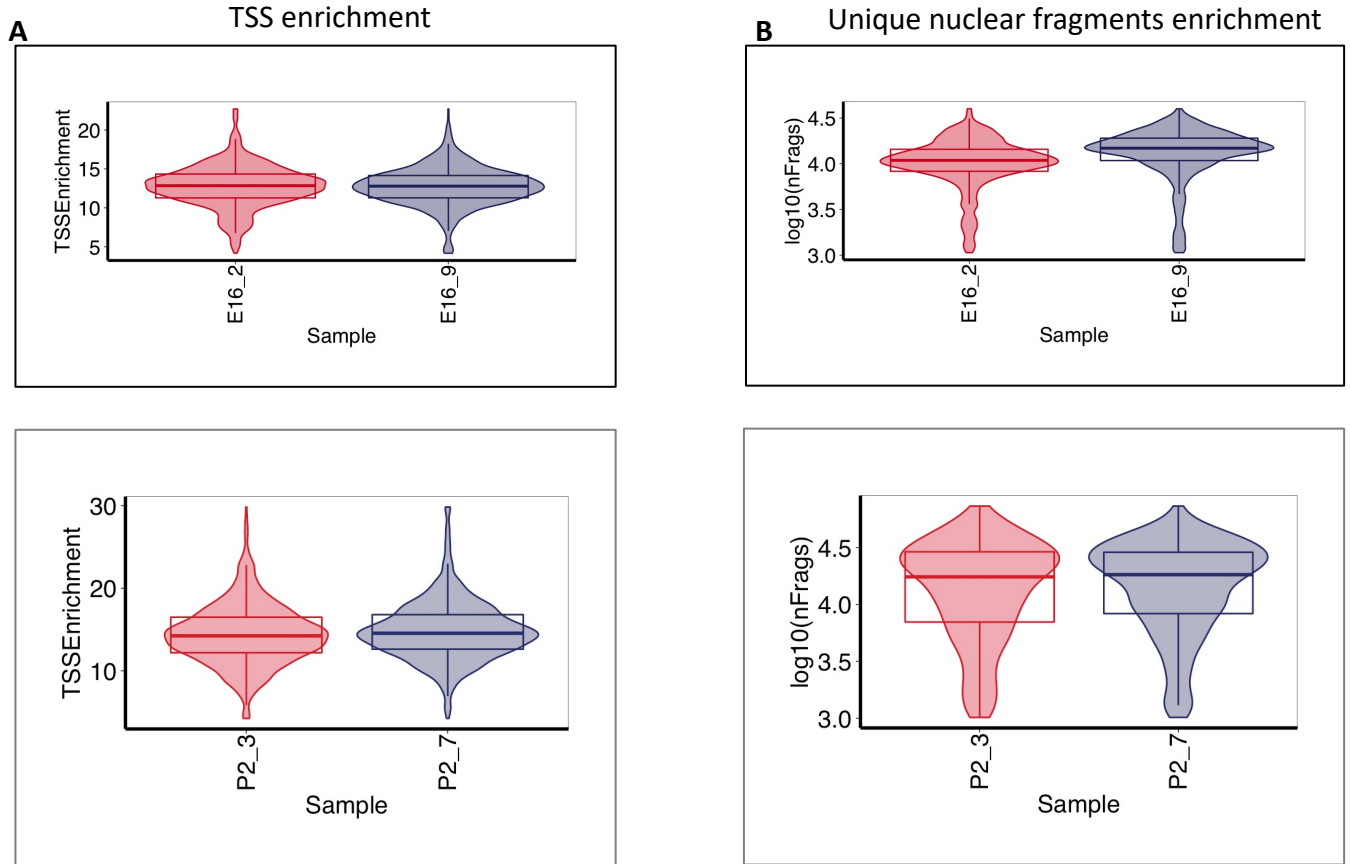
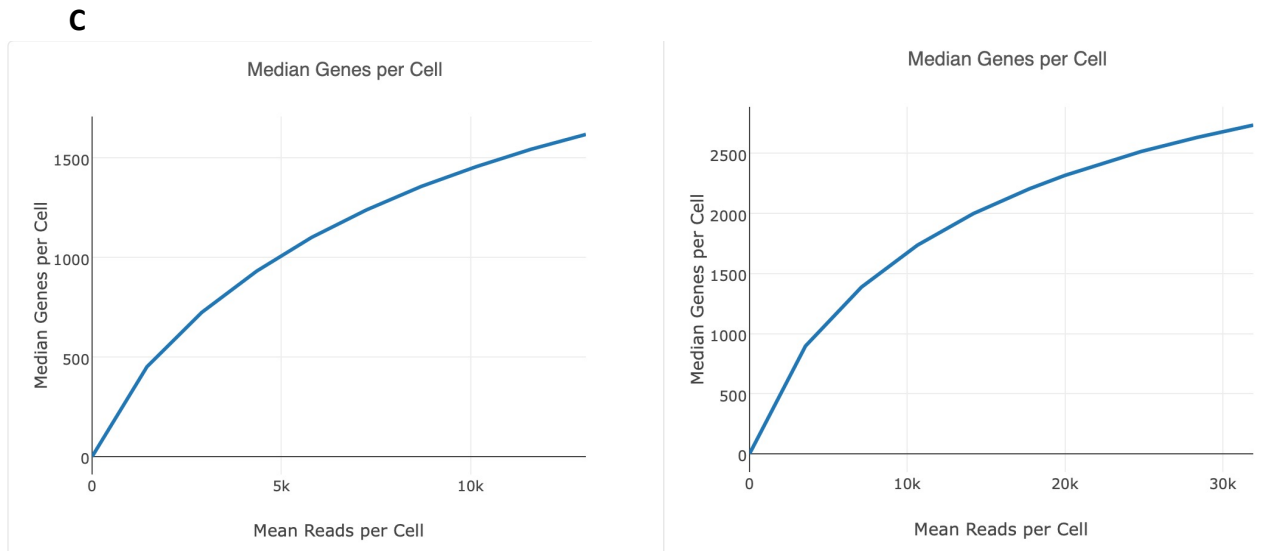


P2\_sample 1

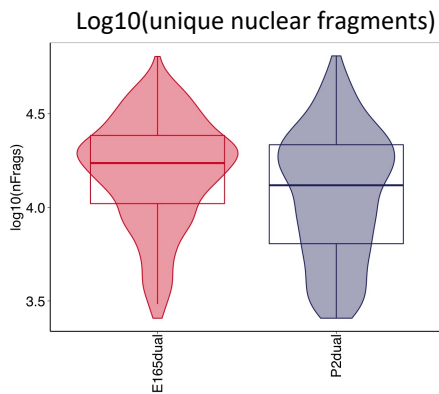
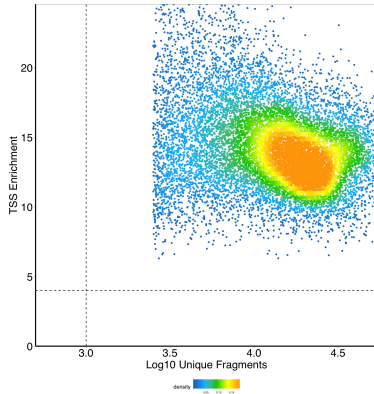


P2\_sample 2

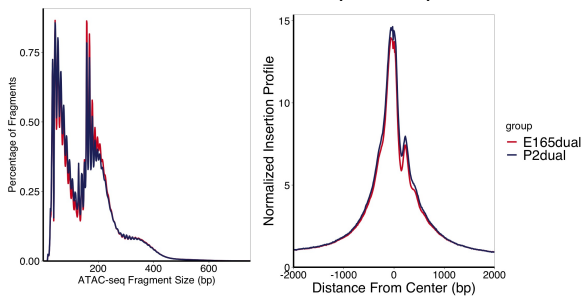


Singleomes: Six2<sup>GFP</sup> scATAC - TSS and unique nuclear fragments enrichmentSingleomes: Six2<sup>GFP</sup> scRNA-seq

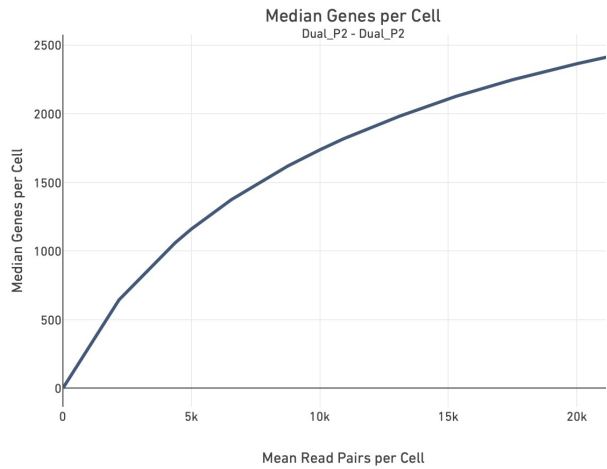
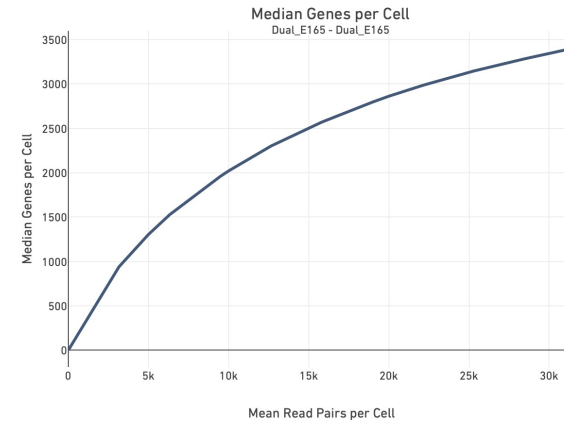
**A** **scATAC-seq**  
log10(Unique Fragments) vs TSS  
enrichment score



**Fragment size distribution profiles** **TSS enrichment profiles per sample**



**B** **scRNA-seq**



# Differential gene-specific chromatin accessibility

Fig. S4

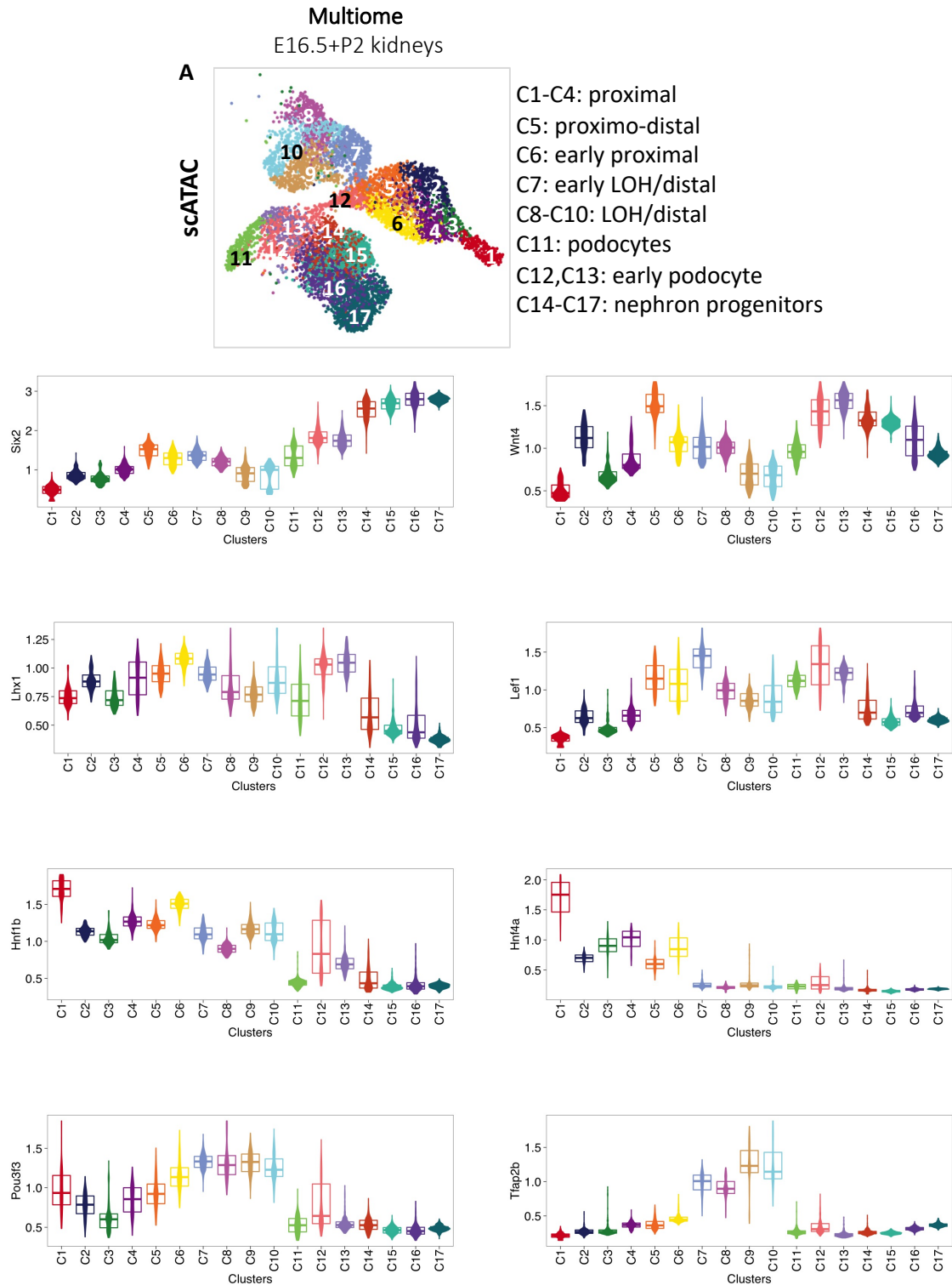
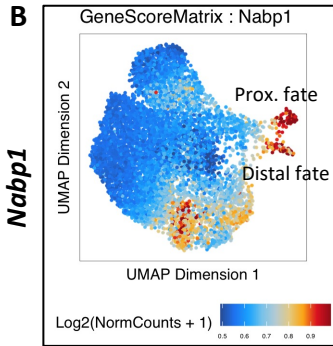
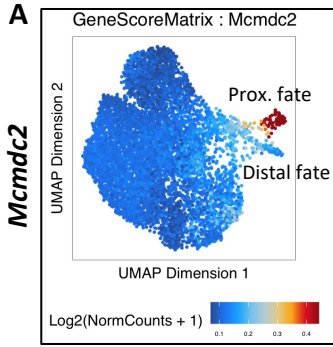


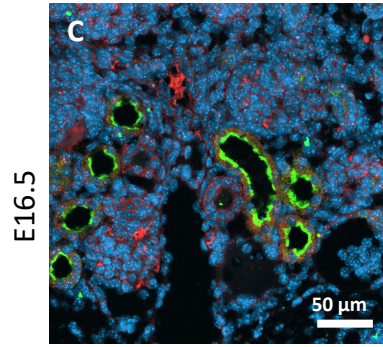


Fig. S5

scATAC-seq



*Mcmdc2* LTL Dapi



*Nabp1* LTL Dapi

