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Single-cell transcriptome atlas in C57BL/6 mice encodes morphological phenotypes in the aging kidneys

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Objectives : C57BL/6 mice are frequently utilized as murine models with the desired genetic background for alteration in multiple research contexts. So far, there is still a lack of comprehensive kidney morphology and single-cell transcriptome atlas at all stages of growth of C57BL/6 mice. To provide an interactive set of reference standards for the scientific community, we performed the current study to investigate the kidney's development throughout the capillary-loop stage until senescence.

Methods : Eight groups, with five to six mice each, represented embryonic stage (embryos 18.5 days), suckling period (1 day after birth), juvenile stage (1 month old), adulthood (containing 3 months old, 6 months old and 10 months old), reproductive senescence stage (20 months old), and post-senescence stage (30 months old), respectively.

Results : With age, the thickness of the glomerular basement membrane (GBM) were increased. Notably, GBM knobs appeared at three months and became frequent with age. Using single-cell transcriptome data, we evaluated how various biological process appear in particular cell types and investigated the potential mechanism of formation of GBM knobs.

Conclusions : In conclusion, having access to detailed kidney morphology and single-cell transcriptome maps from C57BL/6 mice at various developmental stages of C57BL/6 mice would be a novel and major resource for biological research and testing of prospective therapeutic approaches.