Background & Aim
Various mouse models with differing disease etiologies are available in preclinical chronic kidney disease (CKD) research. Characterizing these models according to their renal transcriptomics enables better selection of the optimal model for preclinical drug discovery studies. We therefore characterized the kidney transcriptome signature of three well-established models of CKD, i.e. adenine-supplemented diet feeding (ADI), unilateral ureter obstruction (UUO) and unilateral ischemic reperfusion injury (uIRI).

Methods
Male C57BL/6J mice were used in all studies. Mice underwent UUO or uIRI surgery and were terminated two- and six-weeks post-surgery, respectively. Sham-operated mice served as controls. For ADI, mice received an adenine-supplemented diet or control diet for six weeks. Endpoints included plasma biochemistry and RNA sequencing.

Results

Expression signatures of Current clinical drug targets

Conclusion
The adenine-supplemented diet, unilateral ureter obstruction, and unilateral ischemic reperfusion injury mouse models displayed pronounced similarities in their transcriptomic signatures.

Distinct transcriptomic signatures were observed in both current clinical and preclinical drug targets across the three models.

These models exhibit different utility for preclinical research, emphasizing the importance of considering differences in transcriptomic signatures when designing experimental studies.