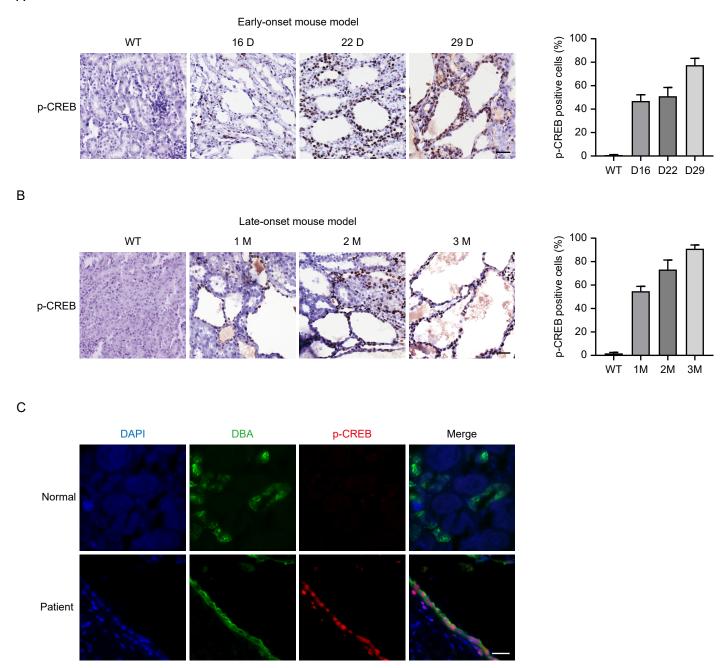
1 SUPPLEMENTAL MATERIAL

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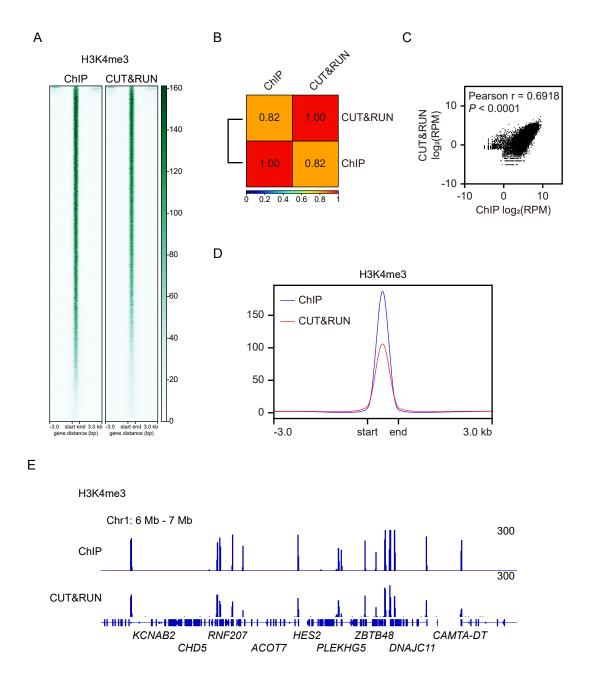
- 3 Supplemental Table 1. ADPKD patient information.
- 4 Supplemental Table 2. Annotation of p-CREB binding peaks in DBA+ cells from
- 5 ADPKD kidney.
- 6 Supplemental Table 3. Comparison of differentially expressed genes in DBA+ cells
- 7 from WT and ADPKD mice treated with or without 666-15.
- 8 Supplemental Figure 1. Phosphorylation of CREB increases steadily in ADPKD
- 9 kidneys.
- Supplemental Figure 2. Comparison of p-CREB CUT&RUN and ChIP-seq.
- Supplemental Figure 3. Comparison of H3K4me3 CUT&RUN and ChIP-seq.
- Supplemental Figure 4. Function enrichment analysis of p-CREB binding genes.
- Supplemental Figure 5. Inhibition of CREB transactivity by 666-15 treatment.
- Supplemental Figure 6. p-CREB target genes previously reported as cystogenesis-
- 15 associated genes.
- Supplemental Figure 7. 666-15 suppresses cystic cell proliferation in the early-onset
- model.
- Supplemental Figure 8. Inhibition of CREB by overexpressing A-CREB.
- 19 Supplemental Figure 9. 666-15 suppresses cystic cell proliferation in the kidney-
- 20 specific mouse model.

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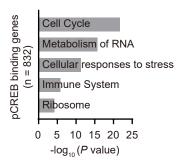


Supplemental Figure 1. Phosphorylation of CREB increases steadily in ADPKD kidneys. (A and B) Immunostaining of p-CREB in kidney sections from early-onset (A) or late-onset (B) ADPKD mouse model at the indicated times. The proportion of p-CREB-positive cells in normal tubular or cystic epithelial cells were was counted. (C) Immunofluorescence analysis of p-CREB level in normal kidneys and kidneys from ADPKD patient. Scale bars represent 50 μ m in A and B (200 \times magnification), 25 μ m in C (650 \times magnification).

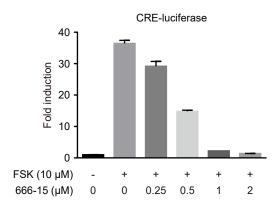
Supplemental Figure 2. Comparison of p-CREB CUT&RUN and ChIP-seq. (A) Heatmap of normalized p-CREB signals from ChIP-seq or CUT&RUN in WT 9-12 cells (n=1). (B) Genomic distribution of p-CREB peaks from ChIP-seq or CUT&RUN. (C) Pearson correlation matrix between p-CREB ChIP-seq and CUT&RUN. (D) Dot plots of p-CREB signals from ChIP-seq and CUT&RUN. (E) Composite plots of normalized p-CREB signals from ChIP-seq or CUT&RUN in WT 9-12 cells. (F) Representative ChIP-seq and CUT&RUN tracks of p-CREB.



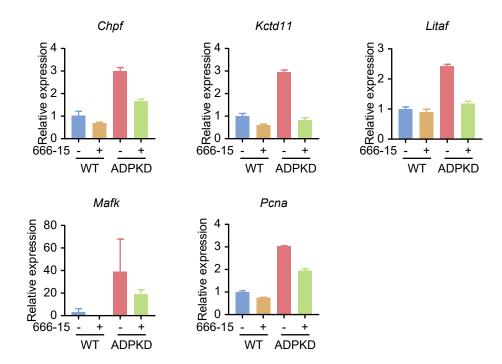
Supplemental Figure 3. Comparison of H3K4me3 CUT&RUN and ChIP-seq. (A) Heatmap of normalized H3K4me3 signals from ChIP-seq or CUT&RUN in WT 9-12 cells (n = 1). (B) Pearson correlation matrix between H3K4me3 ChIP-seq and CUT&RUN. (C) Dot plots of H3K4me3 signals from ChIP-seq and CUT&RUN. (D) Composite plots of normalized H3K4me3 signals from ChIP-seq or CUT&RUN in WT 9-12 cells. (E) Representative ChIP-seq and CUT&RUN tracks of H3K4me3.



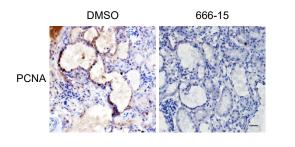
Supplemental Figure 4. Function enrichment analysis of p-CREB binding genes.

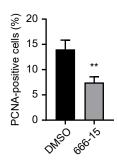


Supplemental Figure 5. Inhibition of CREB transactivity by 666-15 treatment. CRE-luciferase activity in 293T cells with 666-15 and forskolin (FSK) treatment.



Supplemental Figure 6. p-CREB target genes previously reported as cystogenesis-associated genes. qPCR validation of previously reported cystogenesis-associated genes in DBA-positive cells from the indicated groups.



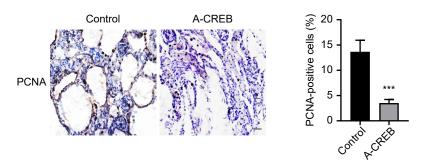


Supplemental Figure 7. 666-15 suppresses cystic cell proliferation in the early-onset model. Immunohistochemistry analysis of PCNA level in kidney sections from early-onset ADPKD mice treated with DMSO or 666-15. Proportion of PCNA-positive cells in cystic epithelial cells was determined. ** P < 0.01. Scale bar represents 50 µm (200× magnification).

DMSO

Supplemental Figure 8. Inhibition of CREB by overexpressing A-CREB. (A) WB analysis of overexpressed FLAG-A-CREB in 293T cells. (B) CRE-luciferase activity in 293T cells from the indicated groups. (C) WB analysis of FLAG-A-CREB in mice from the indicated groups.

FSK



Supplemental Figure 9. 666-15 suppresses cystic cell proliferation in the kidney-specific mouse model. Immunohistochemistry analysis of PCNA level in kidney sections from ADPKD mice with or without A-CREB expression. Proportion of PCNA-positive cells in cystic epithelial cells was determined. *** P < 0.001. Scale bar represents 50 µm (200× magnification).