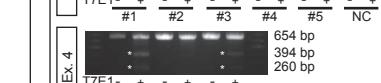
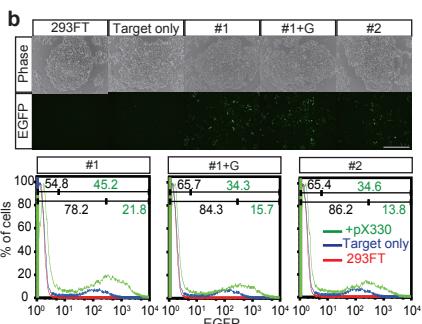
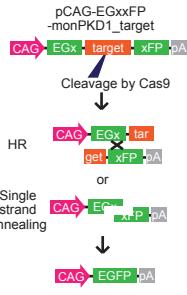
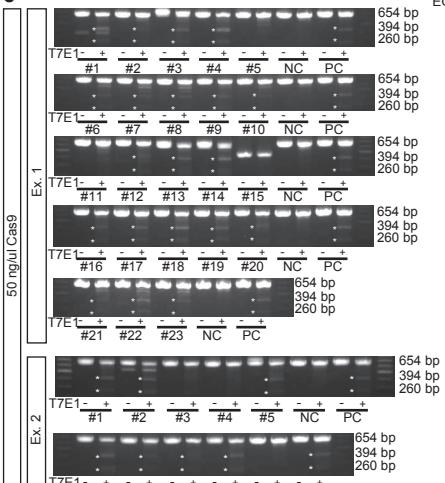
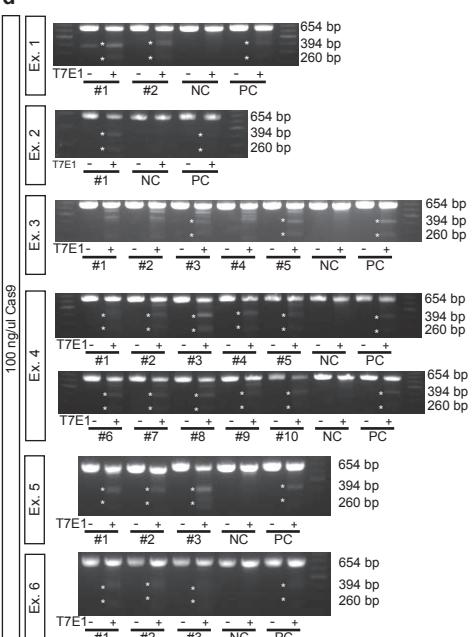


**Monkeys mutant for *PKD1* recapitulate human
autosomal dominant polycystic kidney disease.**

Tsukiyama, Kobayashi and Nakaya et al.

a**c****d**

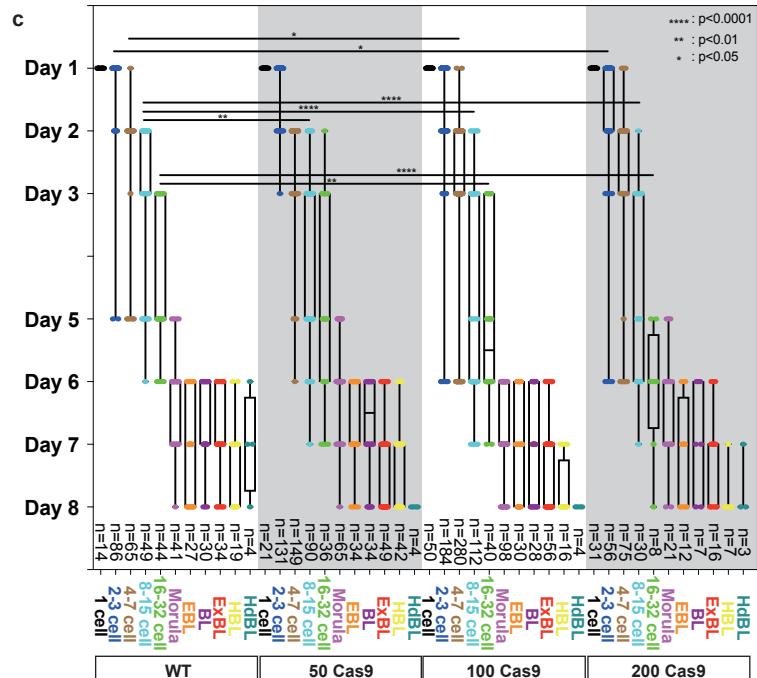
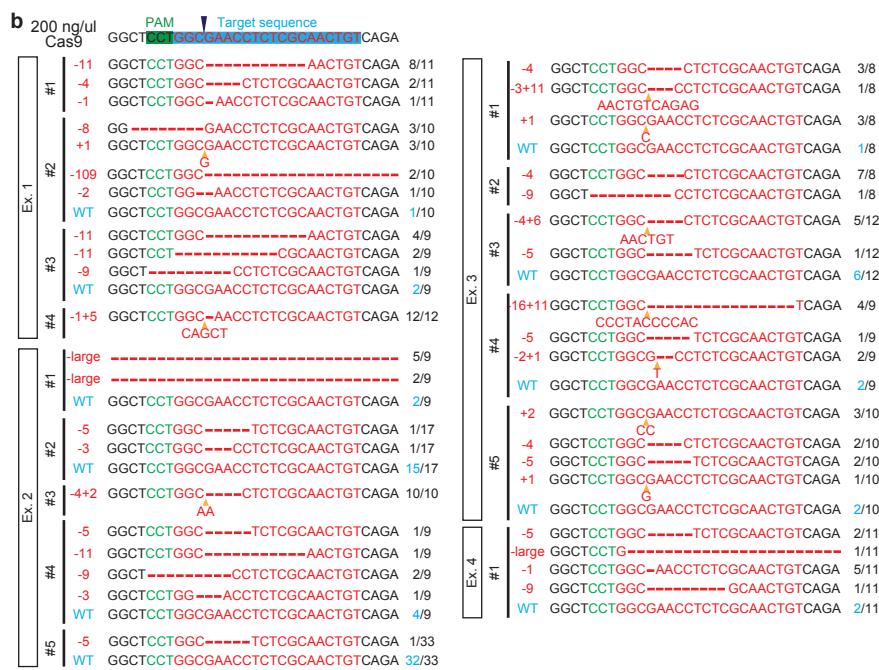
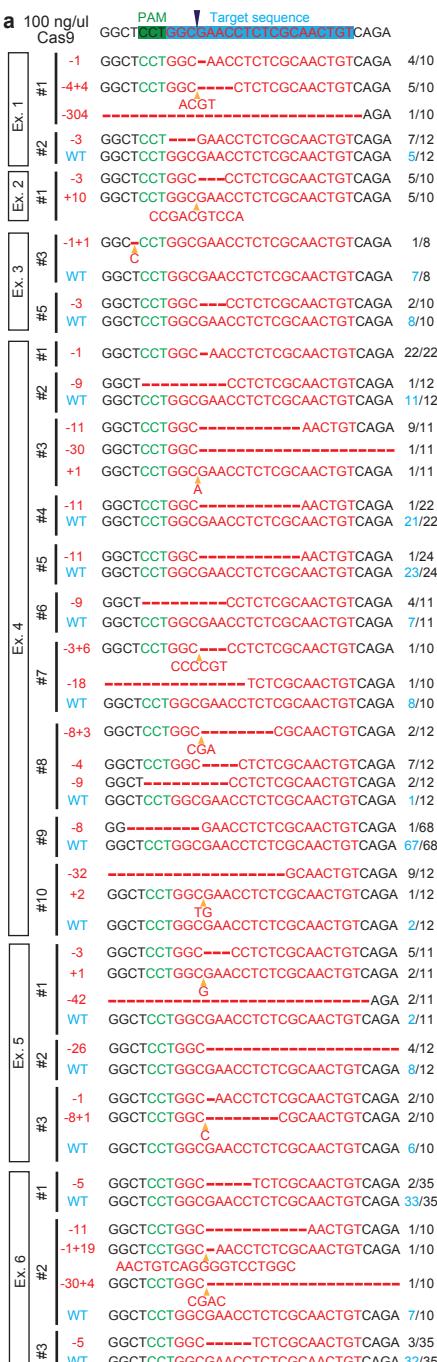
f

50 ng/ μ l Cas9 PAM Target sequence

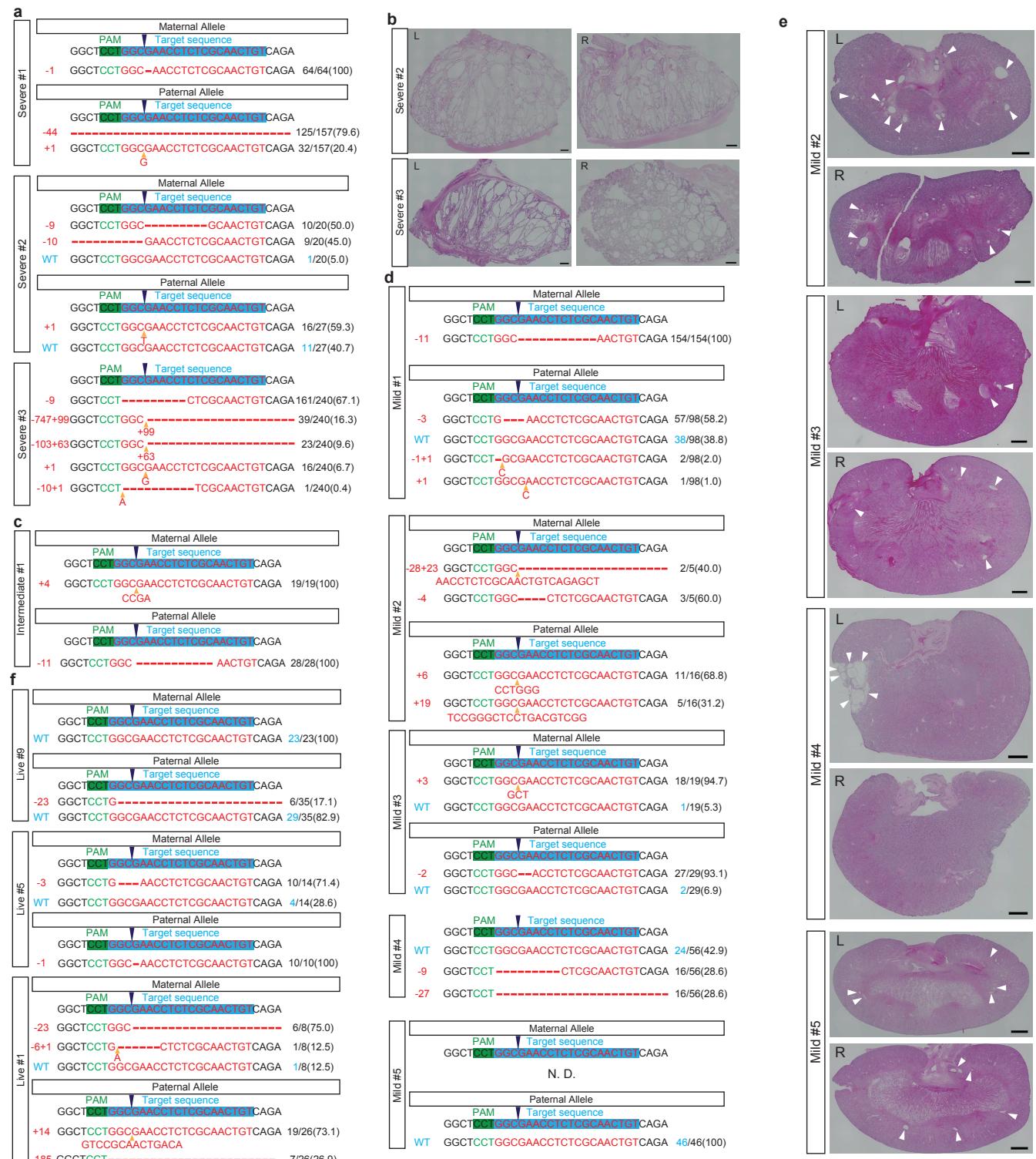
| | Ex. 1 | Ex. 2 | Ex. 3 | Ex. 4 |
|---------|--|-------|-------|-------|
| #1 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 3/11 | | | |
| -317+13 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 2/11 | | | |
| -2+6 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 5/11 | | | |
| +1 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 1/11 | | | |
| +1 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 11/11 | | | |
| -5 | GGCTCCTGGC-TCTCGCAACTGT CAGA 1/31 | | | |
| -23+33 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 1/31 | | | |
| -53 | GGCTCCTGGC-7/11 | | | |
| -21 | GGCTCCTGG-A 1/11 | | | |
| -3+1 | GGCTCCTGG-CCTCTCGCAACTGT CAGA 1/11 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 2/11 | | | |
| -5 | GGCTCCTGGC-TCTCGCAACTGT CAGA 1/31 | | | |
| -23+33 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 1/31 | | | |
| -53 | GGCTCCTGGC-7/11 | | | |
| -21 | GGCTCCTGG-A 1/11 | | | |
| -3+1 | GGCTCCTGG-CCTCTCGCAACTGT CAGA 1/11 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 2/11 | | | |
| -5 | GGCTCCTGGC-TCTCGCAACTGT CAGA 1/31 | | | |
| -11 | GGCTCCTGGC-AACTGT CAGA 2/21 | | | |
| +1 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 2/21 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 17/21 | | | |
| -23 | GGCTCCTGG-1/17 | | | |
| +1 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 7/17 | | | |
| -2+1 | GGCTCCTGGC-CCTCTCGCAACTGT CAGA 4/17 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 5/17 | | | |
| -351 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 1/43 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 42/43 | | | |
| -9 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 1/48 | | | |
| -5 | GGCTCCTGGC-TCTCGCAACTGT CAGA 1/48 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 46/48 | | | |
| -351 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 1/43 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 42/43 | | | |
| -351 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 1/18 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 17/18 | | | |
| -351 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 1/15 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 14/15 | | | |
| -42+3 | GGCTCCTGGC-9/14 | | | |
| +1 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 1/14 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 4/14 | | | |
| -28 | GGCTCCTGG-5/10 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 5/10 | | | |
| -9 | GGCTCCTGGC-GCAACTGT CAGA 1/21 | | | |
| -1+1 | GGCTCCTGGC-GCAACCTCTCGCAACTGT CAGA 1/21 | | | |
| WT | GGCTCCTGGC-GCAACCTCTCGCAACTGT CAGA 18/21 | | | |
| -28 | GGCTCCTGG-5/10 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 5/10 | | | |
| -9 | GGCTCCTGGC-GCAACTGT CAGA 1/21 | | | |
| -1+1 | GGCTCCTGGC-GCAACCTCTCGCAACTGT CAGA 1/21 | | | |
| WT | GGCTCCTGGC-GCAACCTCTCGCAACTGT CAGA 19/21 | | | |
| -4 | GGCTCCTGGC-CTCTCGCAACTGT CAGA 10/19 | | | |
| +1 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 4/19 | | | |
| -5 | GGCTCCTGGC-TCTCGCAACTGT CAGA 1/19 | | | |
| -9 | GGCTCCTGGC-GCAACTGT CAGA 1/19 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 3/19 | | | |
| -11 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 1/20 | | | |
| -5 | GGCTCCTGGC-TCTCGCAACTGT CAGA 1/20 | | | |
| -1 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 1/20 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 15/20 | | | |
| -146+25 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 1/20 | | | |
| -122+1 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 1/20 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 15/20 | | | |
| -1+1 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 1/17 | | | |
| -14 | GGCTC-GCAACTGT CAGA 4/17 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 12/17 | | | |
| -5 | GGCTCCTGGC-TCTCGCAACTGT CAGA 2/21 | | | |
| -4+2 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 1/21 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 18/21 | | | |
| -5 | GGCTCCTGGC-TCTCGCAACTGT CAGA 8/20 | | | |
| -4+4 | GGCTCCTGGC-TCTCGCAACTGT CAGA 1/20 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 11/20 | | | |
| -7 | GGCTCCTGGC-GAAATGT CAGA 1/20 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 11/20 | | | |
| -25+21 | GGCTCCTGGC-GTCAGA 1/11 | | | |
| WT | GGCTCCTGGC-GTCAGA 7/11 | | | |
| -1 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 3/10 | | | |
| -22+5 | GGCTCCTGGC-CGACA 1/10 | | | |
| WT | GGCTCCTGGC-CGACA 6/10 | | | |

| | Ex. 1 | Ex. 2 | Ex. 3 | Ex. 4 |
|--------|--|-------|-------|-------|
| #6 | | | | |
| #7 | | | | |
| #8 | | | | |
| #9 | | | | |
| -5 | GGCTCCTGGC-TCTCGCAACTGT CAGA 2/21 | | | |
| -4+2 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 1/21 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 18/21 | | | |
| -5 | GGCTCCTGGC-TCTCGCAACTGT CAGA 8/20 | | | |
| -4+4 | GGCTCCTGGC-TCTCGCAACTGT CAGA 1/20 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 11/20 | | | |
| -7 | GGCTCCTGGC-GAAATGT CAGA 1/20 | | | |
| WT | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 11/20 | | | |
| -25+21 | GGCTCCTGGC-GTCAGA 1/11 | | | |
| WT | GGCTCCTGGC-GTCAGA 7/11 | | | |
| -1 | GGCTCCTGGC-AACCTCTCGCAACTGT CAGA 3/10 | | | |
| -22+5 | GGCTCCTGGC-CGACA 1/10 | | | |
| WT | GGCTCCTGGC-CGACA 6/10 | | | |

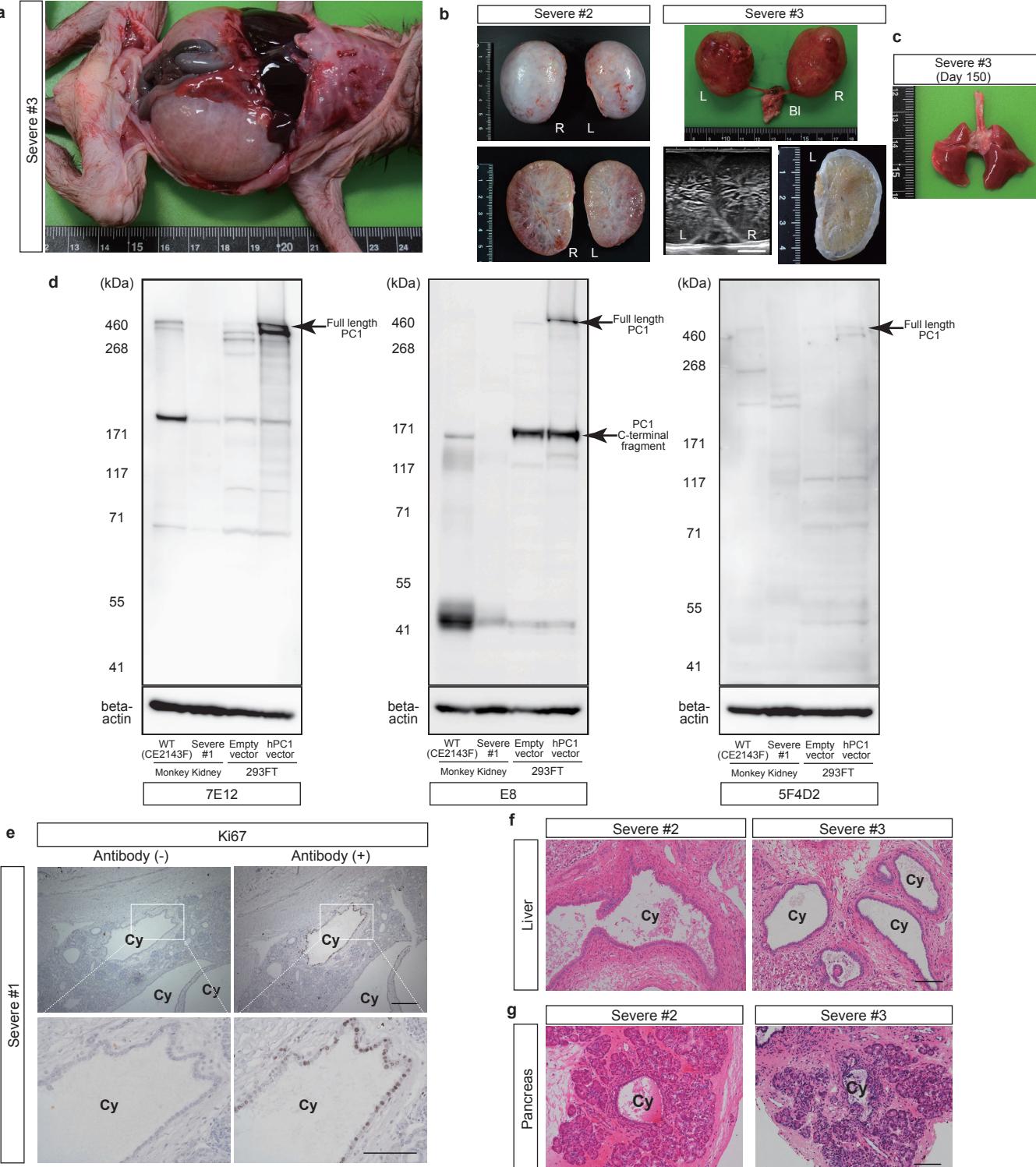
Supplementary Fig. 1. Single-strand annealing (SSA) assay and embryo genotypes. (a) Schematic diagram of the SSA assay using pCAG-EGxxFP. “HR” indicates homologous recombination. (b) EGFP signals 2 days after transfection of an EGxxFP vector and CRISPR/Cas9 vectors into 293FT cells. (c-e) T7E1 assay of embryos injected with 50, 100, or 200 ng/ μ l Cas9 mRNA and 50 ng/ μ l sgRNA. Asterisks indicate positive bands. “NC” indicates negative control, in which wild-type DNAs were used as the PCR template. “PC” indicates positive control, in which mutated DNAs were used as the PCR template. (f) Sequences of sgRNA targets in each mRNA-injected embryo. Source data are provided as a Source Data file.



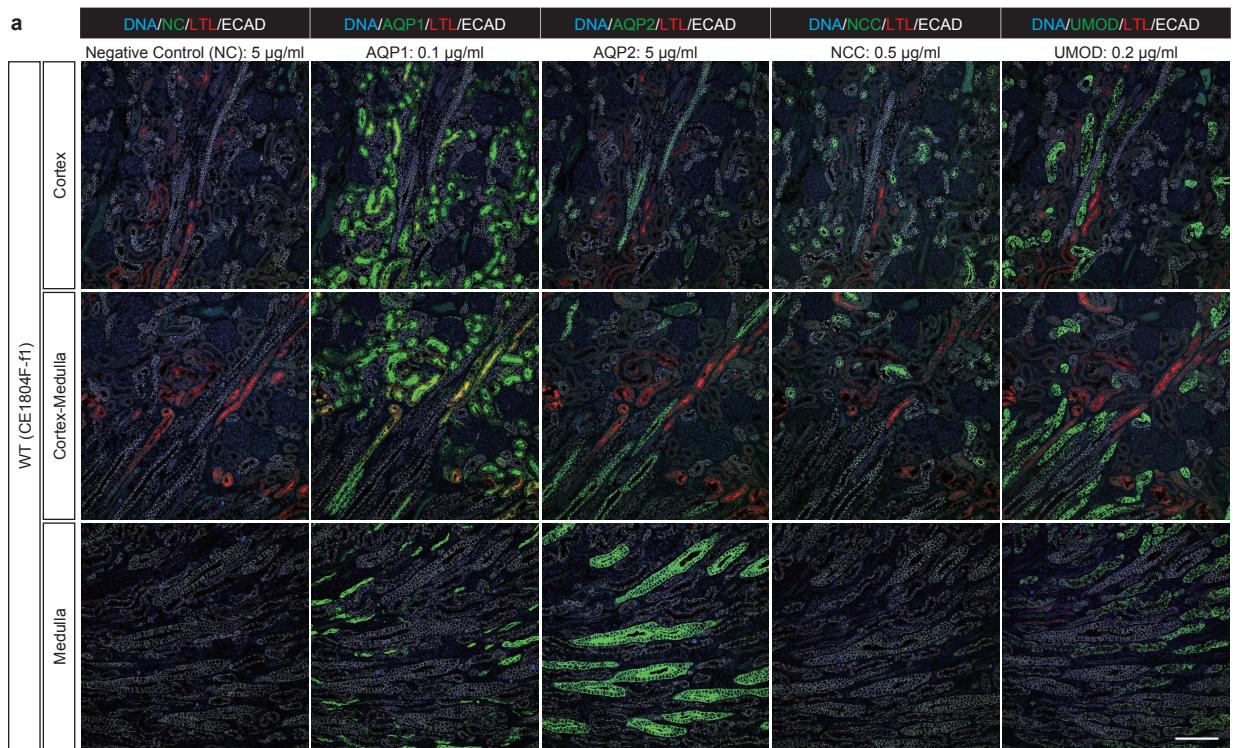
Supplementary Fig. 2. Genotypes and development of embryos. (a and b) Sequences of sgRNA targets in each mRNA-injected embryo. (c) Plot of days at each developmental stage for each type of mRNA-injected embryo. Source data are provided as a Source Data file.



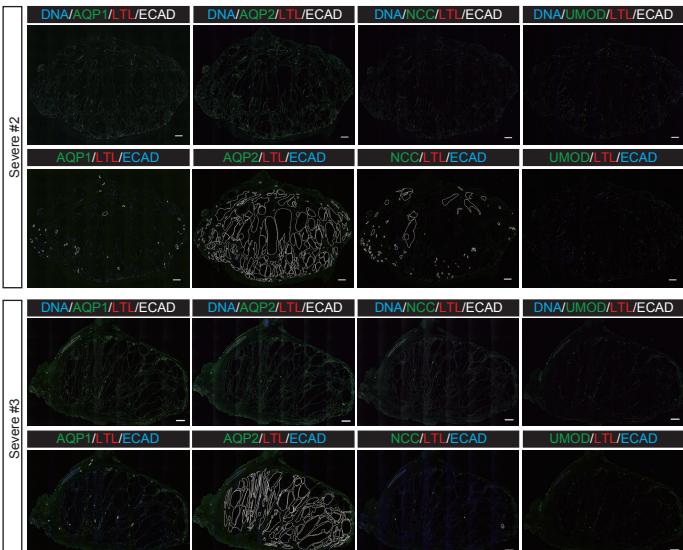
Supplementary Fig. 3. Genotypes and H&E-stained images of monkeys. (a) Sequences of sgRNA targets in the genomes of monkeys with severe-type kidneys. (b) Low-power, H&E-stained images of severe-type kidneys. “L” indicates left kidneys, and “R” indicates right kidneys. Scale bar, 1 mm. (c) Sequences of sgRNA targets in the genome of a monkey with intermediate-type kidneys. (d) Sequences of sgRNA targets in the genomes of monkeys with mild-type kidneys. N.D. indicates not detected. (e) Low-power, H&E-stained images of mild-type kidneys. Arrowheads indicate cyst formation. Scale bar, 1 mm. (f) Sequences of sgRNA targets in the genomes of PKD1-mutated live monkeys.



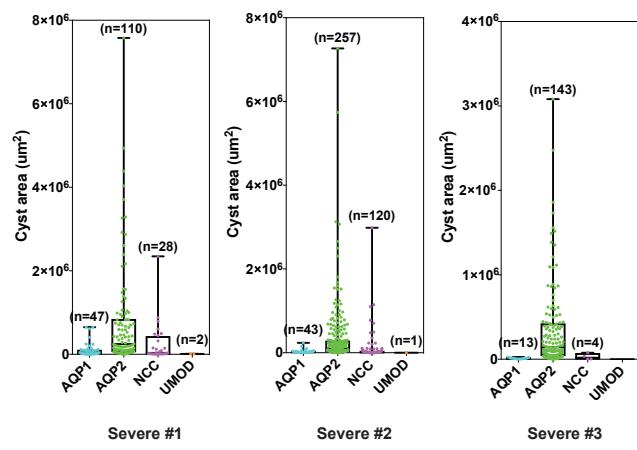
Supplementary Fig. 4. Severe phenotypes and expression of nephron segment markers in monkeys with severe-type kidneys. (a) A monkey with enlarged severe-type kidneys. (b) Ultrasonographic and cross-section appearance of severe-type kidneys. “L” indicates left kidneys, and “R” indicates right kidneys. “Bl” indicates a bladder. Scale bar in the ultrasonography image, 10 mm. (c) The immature lungs of a monkey with severe-type kidneys. “Day” indicates the day of abortion. (d) The expression levels of PC1 protein. “Empty vector” and “hPC1 vector” indicate the 293FT samples transfected with empty or human PC1-overexpression vectors, respectively. “7E12,” “E8,” and “5F4D2” indicate the clone names of anti-PC1 monoclonal antibodies. (e) Expression of Ki67 in cystic cells in a severe-type kidney. Small boxes indicate the regions that show at high magnification in the low column. “Cy” indicates cysts. Scale bar, 100 μ m. (f) Liver cysts. “Cy” indicates cysts. Scale bar, 100 μ m. (g) Pancreatic cysts. “Cy” indicates cysts. Scale bar, 100 μ m. Source data are provided as a Source Data file.



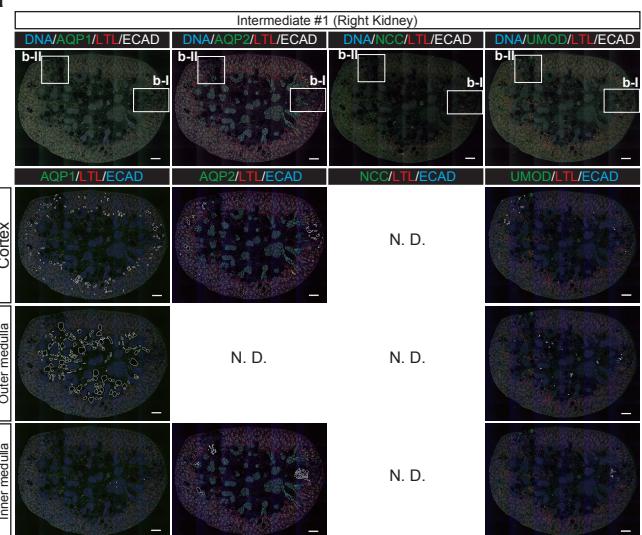
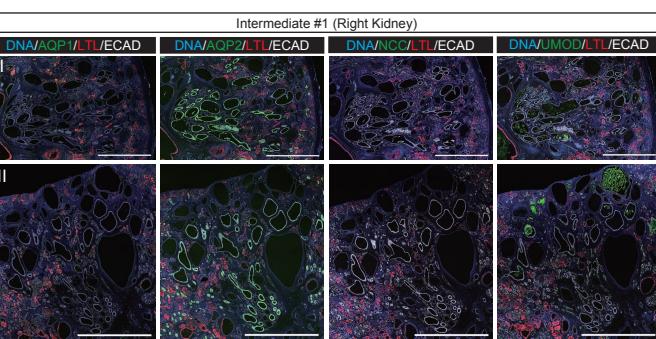
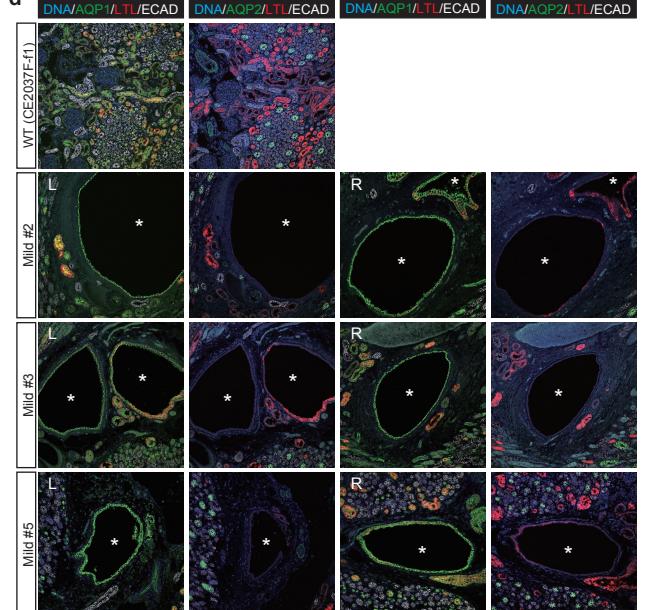
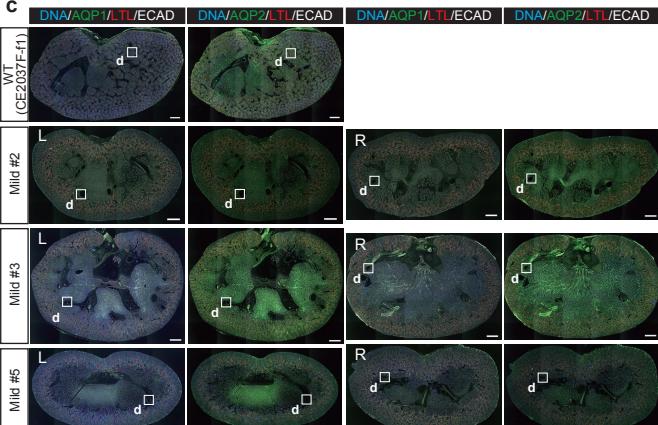
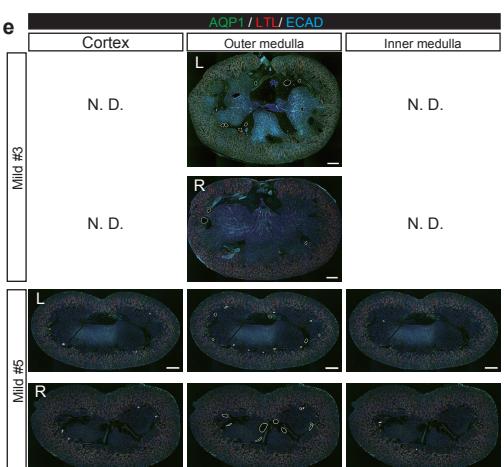
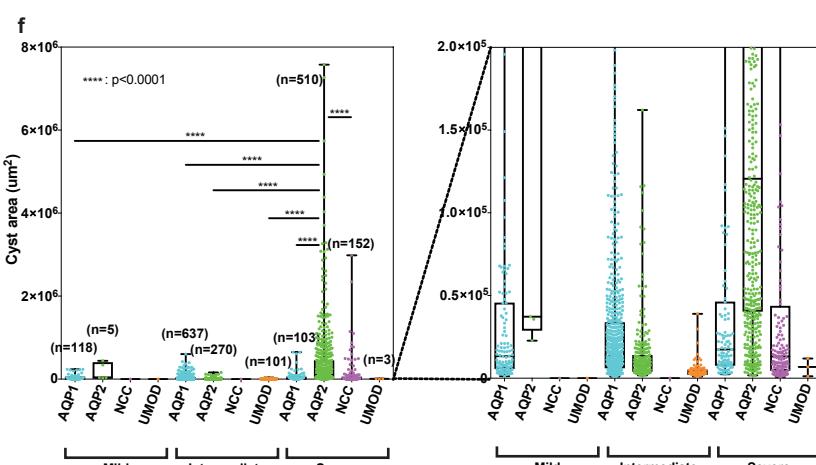
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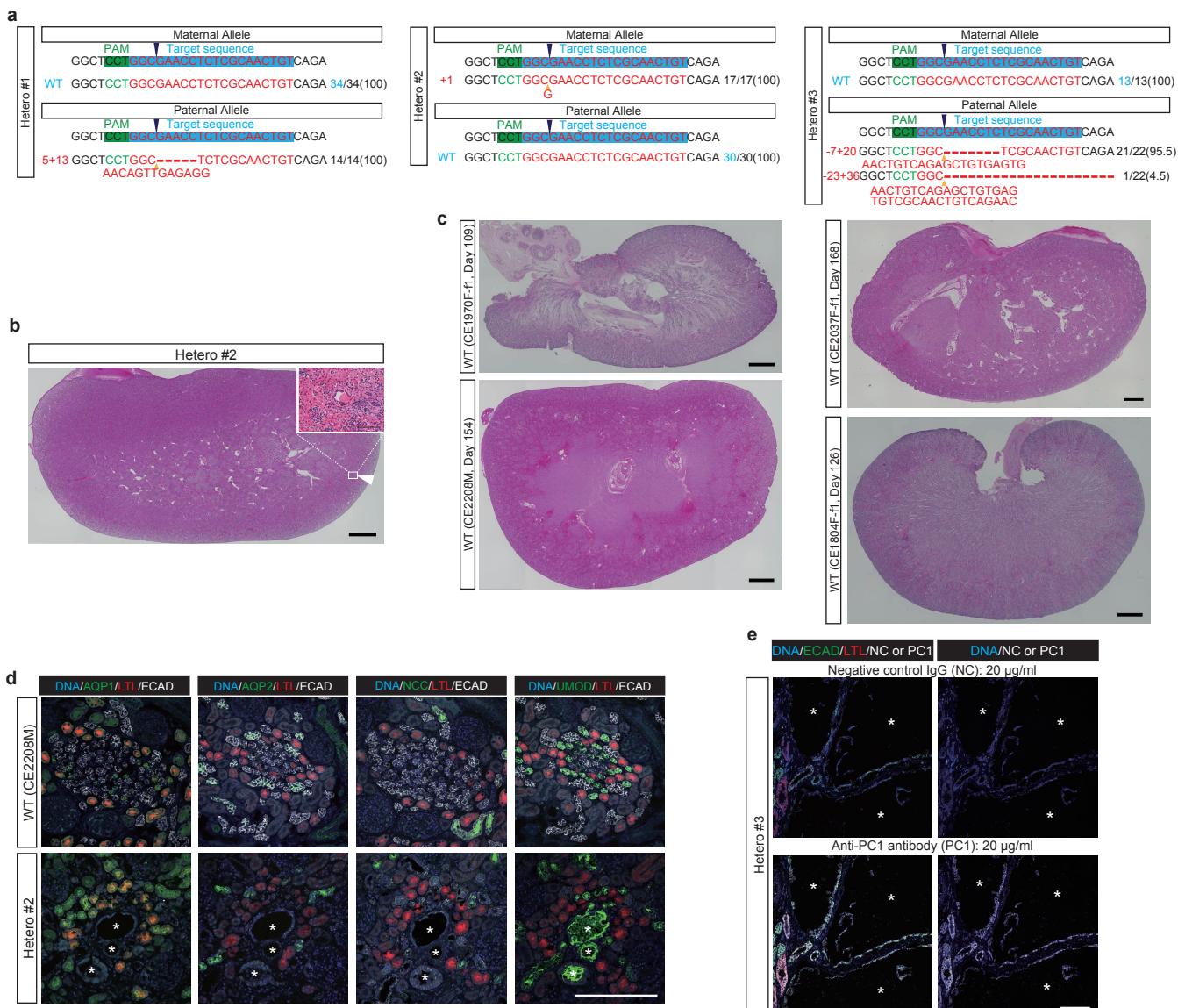
c



Supplementary Fig. 5. Expression of nephron segment markers in monkeys with severe-type kidneys. (a) Examination for autofluorescence or non-specific staining using negative control immunoglobulin. Scale bar, 100 μm . (b) Expression of nephron segment markers in severe-type kidneys. Cystic areas that are positive for AQP1, AQP2, NCC, or UMOD are surrounded by white lines. Scale bar, 1 mm. (c) Box plots of the areas of AQP1-, AQP2-, NCC-, or UMOD-positive cysts in severe-type kidneys. The top and bottom edges of boxes indicate the first and third quartiles, respectively; the center lines indicate the medians; and the ends of whiskers indicate the maximum and minimum values, respectively. Source data are provided as a Source Data file.

a**b****d****c****e****f**

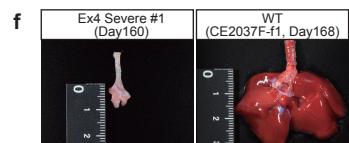
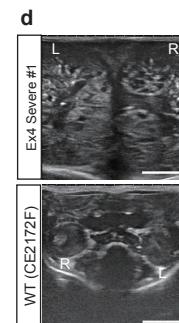
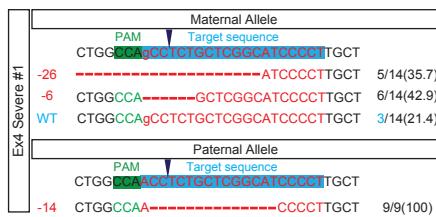
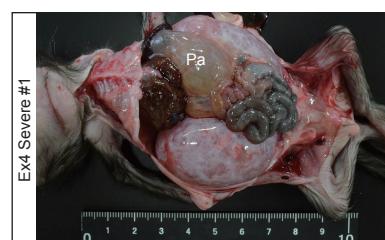
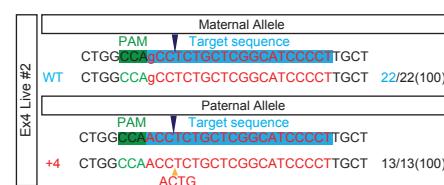
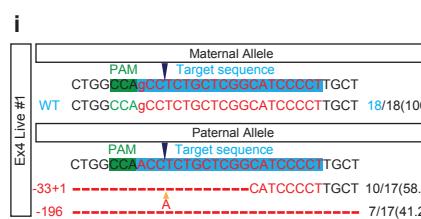
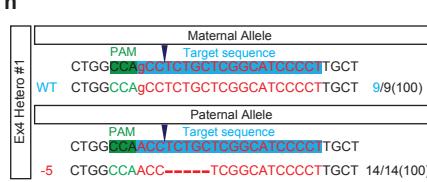
Supplementary Fig. 6. Expression of nephron segment markers in monkeys with intermediate- and mild-type kidneys. (a) Expression of nephron segment markers in an intermediate kidney. Small boxes indicate the regions shown in high magnification in (b). Cystic areas that are positive for AQP1, AQP2, or UMOD in the cortex, outer medulla, or inner medulla are surrounded by white lines. Scale bar, 1 mm. (b) Expressions of nephron segment markers in an intermediate-type kidney compartment containing multiple cysts similar to those in severe-type kidneys. Scale bar, 1 mm. (c) Expression of nephron segment markers in mild-type kidneys. Small boxes indicate the regions shown in high magnification in (d). “L” indicates left kidneys, and “R” indicates right kidneys. Scale bar, 1 mm. (d) Representative AQP1-positive and AQP2-negative cysts in mild-type kidneys. Asterisks indicate cysts. Scale bar, 100 μm . (e) Expression of nephron segment markers in mild-type kidneys. Cystic areas that are positive for AQP1 in the cortex, outer medulla, or inner medulla, are surrounded by white lines. Scale bar, 1 mm. (f) Comparison of cystic areas among mild-, intermediate-, and severe-type kidneys. The top and bottom edges of boxes indicate the first and third quartiles, respectively; the center lines indicate the medians; and the ends of whiskers indicate the maximum and minimum values, respectively. Source data are provided as a Source Data file.



Supplementary Fig. 7. Genotypes and phenotypes of exon 2 heterozygous monkeys. (a) Sequences of sgRNA targets in the genomes of exon 2 heterozygous monkeys. (b) Low-power, H&E-staining images of a heterozygous kidney. Arrowheads indicate cyst formation. Scale bar in a large image, 1 mm. Scale bar in a small box, 100 µm. (c) H&E-stained images of kidneys of wild-type monkeys. Low-power, H&E-stained images of the kidneys. Days indicate the aborted days. Scale bar, 1 mm. (d) Representative ECAD-positive cysts in a heterozygous kidney. Asterisks indicate cysts. Scale bar, 100 µm. (e) Expressions of PC1 in heterozygous kidneys. Representative PC1-positive cysts in Hetero #3 are shown. Asterisks indicate cysts. Scale bar, 100 µm.

a

| Recipients | Methods | gRNA types | Concentrations | Mutation detection rates (%) | | | ET |
|-------------------|-------------------------|-------------|----------------|------------------------------|---------------|---------------|----|
| | | | | Maternal | Paternal | Mosaic (%) | |
| Pronuclear Zygote | Cytoplasmic Injection | mRNA | 200 ng/ul | 0 / 90 (0) | 35 / 35 (100) | 3 / 8 (37.5) | |
| MII Oocyte | Co-injection with sperm | RNP complex | 200 ng/ul | 1 / 104 (0.96) | 72 / 72 (100) | 2 / 16 (12.5) | 35 |
| | | | 20 ng/ul | 0 / 26 (0) | 6 / 23 (26.1) | 4 / 5 (80.0) | |
| ICSI Embryo | Electroporation | RNP complex | 200 ng/ul | 0 / 24 (0) | 29 / 29 (100) | 0 / 5 (0) | 23 |

b**c****h**

Supplementary Fig. 8. Genotypes and phenotypes of exon 4 mutated monkeys. (a) The genotyping results of exon 4-mutated blastocyst embryos. The mutation detection rate per sequenced DNA and mosaic rate per embryo are shown. "ET" indicates the number of transferred embryos. (b) Sequences of gRNA targets in the genome of an exon 4 mutated monkey, Ex4 Severe #1. (c) Enlarged kidneys and pancreas in monkey Ex4 Severe #1. "Pa" indicates the enlarged pancreas. (d) Ultrasonographic appearance of the kidneys. "L" indicates left kidneys, and "R" indicates right kidneys. Scale bar, 10 mm. (e) The cross-sectional appearance of the kidneys. (f) Immature lung of monkey Ex4 Severe #1. "Day" indicates day of abortion. (g) Gross appearance of the liver and pancreas of monkey Ex4 Severe #1. "Day" indicates day of abortion. (h) Sequences of gRNA targets in the genome of an exon 4 mutated aborted monkey, Ex4 Hetero #1. (i) The sequences of gRNA target in the genomes of exon 4 mutated live monkeys, Ex4 Live #1 and #2.

| ID | Institute ID | Sex | Survival | Day of abortion | Day of birth | Day of death | Sequenced | Maternal genotype (%) | | | Paternal genotype (%) | | | Allele-indistinguishable genotype (%) | | | Cyst formation | | | |
|-----------------------------------|--------------|--------|----------|-----------------|--------------|--------------|-----------|-----------------------------------|------|------|-----------------------------------|------|------|---------------------------------------|------|------|----------------|-------|----------|---|
| | | | | | | | | In-frame (≥3AA) or missense | | WT | In-frame (≤2AA) or missense | | WT | In-frame (≥3AA) or missense | | WT | Kidney | Liver | Pancreas | |
| | | | | | | | | Frameshift | | | Frameshift | | | Frameshift | | | ++ | + | + | |
| Severe #1 | CE2104F-f1 | Female | Dead | 144 | | | 221 | Mosaic | 100 | | | 100 | | | | | +++ | + | + | |
| Severe #2 | CE2154F-f1 | Male | Dead | 163 | | | 47 | Mosaic | 45 | 50 | 5 | 59.3 | | | 40.7 | | +++ | + | + | |
| Severe #3 | CE1950F-f1 | Female | Dead | 150 | | | 240 | Mosaic | | | | | | | 32.5 | 67.5 | +++ | + | + | |
| Intermediate #1 | CE2170M | Male | Dead | | 161 | 2 | 47 | Non-mosaic | 100 | | | 100 | | | | | ++ | - | - | |
| Mild #1 | CE1788F-f1 | Female | Dead | 153 | | | 252 | Mosaic | 100 | | | 0 | | 60.2 | 38.8 | | + | - | - | |
| Mild #2 | CE2015F-f1 | Female | Dead | 114 | | | 21 | Mosaic | 100 | | | 31.2 | | 68.8 | | | + | - | - | |
| Mild #3 | CE1696F-f2 | Male | Dead | 148 | | | 48 | Mosaic | | | 94.7 | 5.3 | 93.1 | | 6.9 | | + | ND | ND | |
| Mild #4 | CE2158F | Female | Dead | | 160 | 8 | 32 | Mosaic | | | | | | | 28.6 | 28.6 | 42.8 | + | - | - |
| Mild #5 | CE1788F-f2 | Female | Dead | 125 | | | 46 | ND | | | | | | | | | + | ND | ND | |
| Hetero #1 | CE2002F-f1 | Female | Dead | 128 | | | 48 | Non-mosaic | | | 100 | 100 | | | | | + | - | - | |
| Hetero #2 | CE2196F | Female | Dead | | 160 | 4 | 47 | Non-mosaic | 100 | | | | | 100 | | | + | ND | ND | |
| Hetero #3 | CE2214F | Female | Dead | | 153 | 216 | 54 | Mosaic | | | 100 | 100 | | | | | + | ND | ND | |
| Live #1 | CE2215M | Male | Live | | 163 | | 34 | Mosaic | 87.5 | | | 12.5 | 100 | | | | ++ | ND | ND | |
| Live #2 | CE2209F | Female | Live | | 156 | | 33 | Mosaic | 100 | | | | 28.6 | 66.7 | 4.7 | | + | ND | ND | |
| Live #3 | CE2216F | Female | Live | | 164 | | 18 | Mosaic | 50 | 20 | | 30 | 75 | | 25 | | + | ND | ND | |
| Live #4 | CE2225M | Male | Live | | 164 | | 35 | Mosaic | 100 | | | | 39.1 | | 60.9 | | ++ | ND | ND | |
| Live #5 | CE1995F | Female | Live | | 160 | | 24 | Mosaic | | | 71.4 | 28.6 | 100 | | | | + | ND | ND | |
| Live #6 | CE2190F | Female | Live | | 149 | | 30 | Mosaic | 69.2 | | | 30.8 | 35.3 | | 64.7 | | + | ND | ND | |
| Live #7 | CE2191F | Female | Live | | 165 | | 34 | Mosaic | | | 18.2 | 81.8 | 69.6 | 30.4 | | | + | ND | ND | |
| Live #8 | CE2197F | Female | Live | | 167 | | 35 | Mosaic | 8.7 | 4.3 | | 87 | 75 | 25 | | | + | ND | ND | |
| Live #9 | CE1987M | Male | Live | | 156 | | 58 | Mosaic | | | 100 | 17.1 | | | 82.9 | | - | ND | ND | |
| Live #10 | CE2189F | Female | Live | | 162 | | 34 | Mosaic | 36.4 | | | 63.6 | | | 100 | | - | ND | ND | |
| No kidney sample (Mosaic) #1 | CE1980F-f1 | Female | Dead | 78 | | | 53 | Mosaic | | | | | | | 96.2 | | 3.8 | ND | ND | |
| No kidney sample (Mosaic) #2 | CE2102F-f1 | ND | Dead | 175 | | | 23 | Mosaic | | | 100 | 92.9 | | | 7.1 | | ++ | ND | ND | |
| No kidney sample (Mosaic) #3 | CE1942F-f1 | Female | Dead | 141 | | | 36 | Mosaic | 33.3 | | | 66.7 | | | 100 | | | ND | ND | |
| No kidney sample (Mosaic) #4 | CE2110F-f1 | ND | Dead | 165 | | | 24 | Mosaic | | | 100 | | 5 | 95 | | | ND | ND | ND | |
| No kidney sample (Hetero) #1 | CE1665F-f3 | ND | Dead | 51 | | | 22 | Non-mosaic | 100 | | | | | 100 | | | ND | ND | ND | |
| No kidney sample (Hetero) #2 | CE2075F-f1 | ND | Dead | 103 | | | 24 | Mosaic | | | 100 | 100 | | | | | ND | ND | ND | |
| No kidney sample (Genotype ND) #1 | CE2016F-f1 | ND | Dead | 83 | | | | ND | | | | | | | | | ND | ND | ND | |
| Ex4 Severe #1 | CE2344M | Male | Dead | 160 | | | 23 | Mosaic | 35.7 | 42.9 | 21.4 | 100 | | | | | +++ | + | + | |
| Ex4 Severe #2 | CE2348M | Male | Dead | | 158 | 5 | 24 | Mosaic | 30.8 | | 69.2 | 100 | | | | | +++ | ND | ND | |
| Ex4 Hetero #1 | CE0362F-f1 | Male | Dead | 159 | | | 23 | Non-mosaic | | | 100 | 100 | | | | | + | ND | ND | |
| Ex4 Live #1 | CE2345F | Female | Live | | 161 | | 35 | Mosaic | | | 100 | 100 | | | | | + | ND | ND | |
| Ex4 Live #2 | CE2346F | Female | Live | | 157 | | 35 | Non-mosaic | | | 100 | 100 | | | | | + | ND | ND | |
| Ex4 Live #3 | CE2347M | Male | Live | | 152 | | 34 | Non-mosaic | | | 100 | | | 100 | | | - | ND | ND | |
| Ex4 Live #4 | CE2373F | Female | Live | | 150 | | 36 | Non-mosaic | | | 100 | 100 | | | | | + | ND | ND | |
| Ex4 Live #5 | CE2374F | Female | Live | | 146 | | 36 | Non-mosaic | | | 100 | 100 | | | | | ND | ND | ND | |
| Ex4 No kidney sample (Hetero) #1 | CE2126F-f2 | ND | Dead | 63 | | | 36 | Non-mosaic | | | 100 | 100 | | | | | ND | ND | ND | |
| Ex4 No kidney sample (Hetero) #2 | CE2025F-f1 | Male | Dead | 140 | | | 23 | Non-mosaic | | | 100 | 100 | | | | | ND | ND | ND | |
| Ex4 No kidney sample (Hetero) #3 | CE2143F-f1 | Female | Dead | 148 | | | 23 | Non-mosaic | | | 100 | 100 | | | | | ND | ND | ND | |
| Ex4 No kidney sample (Hetero) #4 | CE2141F-f2 | Female | Dead | 154 | | | 24 | Non-mosaic | | | 100 | 100 | | | | | ND | ND | ND | |

Supplementary Table 1. Fetuses and offspring with their genotypes and pathologies. "Sequenced" indicates the number of sequences examined in this analysis. "++, "+, +" and "-" indicate the severity of cyst formation. "ND" indicates that the cyst formation was not determined. Source data are provided as a Source Data file.

Supplementary Table 2. Oligonucleotides used in this study.

| Names | Forward | Reverse | For |
|--|---|--|-------------------------------|
| monPKD1_Ex 2_1_#1_F,R | caccACAGTTGCGAGAGGTTCG CC | aaacGGCGAACCTCTCGCAA CTGT | sgRNA cloning |
| monPKD1_Ex 2_1_#1+G_F, R | caccGACAGTTGCGAGAGGTTC GCC | aaacGGCGAACCTCTCGCAA CTGTC | sgRNA cloning |
| monPKD1_Ex 2_1_#2_F,R | caccCAGCGCCGGAGCAAGTT AT | aaacATAACTTGCTCCGGGC GCTG | sgRNA cloning |
| | | | |
| monPKD1_tar get_EcoRI_F, NheI_R | ataGAATTGcgactgtggacaagaatt gcaggac | ataGCTAGCgccactgatacccaccc aaagaaccac | SSA assay |
| | | | |
| T7-Cas9_F,R | ttaatacgactcactatagGGAGAATGG ACTATAAGGACCACGAC | GCGAGCTCTAGGAATTCTT AC | In vitro transcriptio n |
| T7- sgRNA_monP KD1_Ex2_1_ 1_F,R | ttaatacgactcactataggACAGTTGCG AGAGGTTCGCC | AAAAGCACCGACTCGGTG CC | In vitro transcriptio n |
| | | | |
| monPKD1_tar get_EcoRI_F, NheI_R | ataGAATTGcgactgtggacaagaatt gcaggac | ataGCTAGCgccactgatacccaccc aaagaaccac | Genotyping (Ex2) |
| monPKD1_tar get_EcoRI_F, outer_R3 | ataGAATTGcgactgtggacaagaatt gcaggac | TGTCAATGGTCAGTGTGGG CCTAAGATG | Genotyping (Ex2 long) |
| monPKD1_Ex 4_gen_0_F,R | TCCCATTCCAGGCTTGAGACC AGATC | TGTCAGGGAGGCAGGCGA TATAC | Genotyping (Ex4) |
| monPKD1_Ex 4_gen_0_F,Int4 | TCCCATTCCAGGCTTGAGACC AGATC | ATAGCTAGCCAGGGAAGA CATGCTGGAGGAGGGTTG | Genotyping (floxed) |

| | | | |
|--|--|--|--------------------------------------|
| _target_NheI_R | | | Ex4, RFLP assay) |
| monPKD1_target_EcoRI_F, I nt4_target_Nh eI_R | ataGAATT Cgcactgtggacaagaatt gcaggac | ATAGCTAGCCAGGGAAAGA CATGCTGGAGGAGGGTTG | Genotyping (floxed Ex4, Sequencing) |
| | | | |
| monPKD1_flox_Ex4_5_arm_F, BbsI_R | CCTCTCTTCCAGGGATATAAG CAACAACAAG | GAAGACAATTATCCGGCA ACCAGGCCCTGGAG | Long ssODN production (1st PCR) |
| monPKD1_flox_Ex4_BbsI_1 oxP_F, R | GAAGACAAATAACTCGTAT AGCATA CATTATACGAAGTT ATTAAGGGGCTGGTAGAC CCTTCCCAC | GAAGACAAATAACTCGT ATAATGTATGCTATACGAA GTTATCTGCTCTTTGGCC CGGAGGC | Long ssODN production (1st PCR) |
| monPKD1_flox_Ex4_3_arm_BbsI_F, R | GAAGACAATTATCATGGGAG CCTGTGAGTGTGGC | GAACAGAAGGACAGGCAG GCGAAG | Long ssODN production (1st PCR) |
| monPKD1_flox_Ex4_5_Bam HI_BbsI_F, R | CCTCTCTTCCAGGGATATAAG CAACAACAAG | GAAGACAAATCCCGAGCA GAGGCTGGCCAGC | Long ssODN production (2nd PCR) |
| monPKD1_flox_Ex4_3_Bam HI_BbsI_F, R | GAAGACAAGGATCCCTTGCTGGACAGTGACTG | GAACAGAAGGACAGGCAG GCGAAG | Long ssODN production (2nd PCR) |