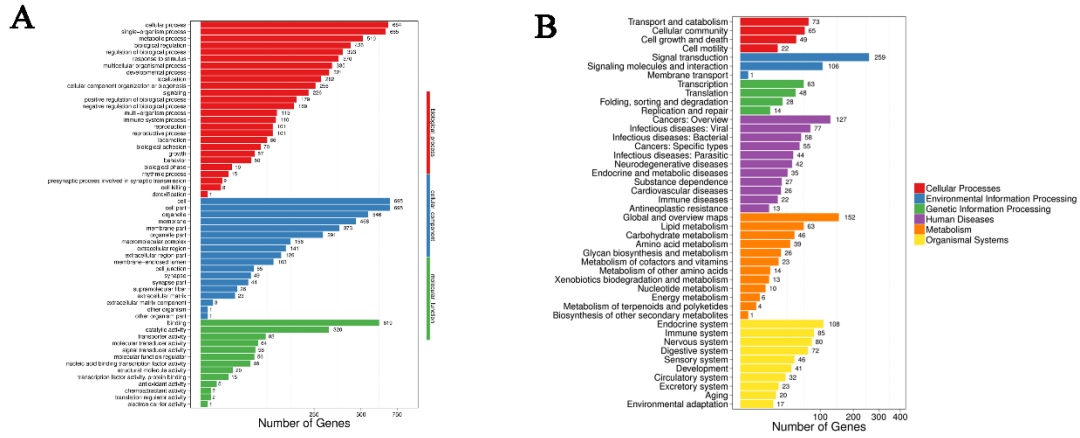


## Supplemental Data



**Fig. S1. Analysis of efferent ductule transcriptomics in WT and dKO mice. (A) GO analysis of DEGs. (B) KEGG pathway analysis of DEGs.**

**Table S1.** Functional description of DEGs based on GO analysis

| Description of GO terms | Genes  | P-Value | Classification of GO terms |
|-------------------------|--|---------|----------------------------|
| mitotic cell cycle      | <i>Ywhag</i> , <i>Kif20a</i> , <i>Pim2</i> , <i>Cep76</i> , <i>Id2</i> , <b><i>Ccnb1</i></b> , <i>Ptprv</i> , <i>Brsk2</i> , <i>Pak3</i> , <i>Spag5</i> , <i>Misp</i> , <i>Camk2a</i> , <i>Mcidas</i> , <i>Smc4</i> , <i>Dlgap5</i> , <i>Ckap2</i> , <i>Pcnt</i> , <i>Nek2</i> , <i>Nusap1</i> , <i>Cit</i> , <i>Rprm</i> , <i>Kif2c</i> , <i>Cdca2</i> , <i>Edn1</i> , <i>Pidd1</i> , <i>Birc3</i> , <i>Met</i> , <b><i>Ccna1</i></b> , <i>Trp63</i> , <i>E2f8</i> , <b><i>Cdk1</i></b> , <i>Cenpm</i> , <i>Rgs14</i> , <b><i>Cdc14a</i></b> , <b><i>Mbd4</i></b> , <i>Cenpj</i> , <i>Btg4</i> , <i>Aurka</i> , <i>Ska3</i> , <i>Cep126</i> , <i>Setdb2-phf11c</i> , <i>E2f7</i> , <i>Cntrl</i> , <i>Nedd1</i> , <i>Racgap1</i> , <i>Smc2</i> , <i>Camk2b</i>   | 0.00970 |                            |
| cell cycle process      | <i>E2f7</i> , <i>Nedd1</i> , <i>Ska3</i> , <i>Cep126</i> , <i>Sycp1</i> , <i>Smc2</i> , <b><i>Ccna1</i></b> , <i>Trp63</i> , <i>Cep120</i> , <i>Birc3</i> , <i>Spata22</i> , <i>Rgs14</i> , <i>Cenpm</i> , <b><i>Cdc20</i></b> , <i>Plk4</i> , <i>Pcnt</i> , <i>Tube1</i> , <i>Ckap2</i> , <i>Camk2a</i> , <i>Rprm</i> , <i>Cdca2</i> , <i>Edn1</i> , <i>Cit</i> , <b><i>Sass6</i></b> , <i>Fancd2</i> , <i>Nek2</i> , <i>Kif20a</i> , <i>Pim2</i> , <i>Brsk2</i> , <i>Spag5</i> , <i>Ptprv</i> , <i>Cep135</i> , <i>Aurka</i> , <i>Setdb2-phf11c</i> , <i>Cenpj</i> , <b><i>Mbd4</i></b> , <i>Camk2b</i> , <i>Cab39l</i> , <i>Ddias</i> , <i>Racgap1</i> , <i>Plk5</i> , <i>Met</i> , <i>Pidd1</i> , <b><i>Cdc14a</i></b> , <b><i>Cdk1</i></b> , <i>E2f8</i> , <i>Cep152</i> , <i>Smc4</i> , <i>Misp</i> , <i>Kif2c</i> , <i>Nusap1</i> , <i>Brdt</i> , <i>Hormad1</i> , <i>Cks2</i> , <i>Prkaca</i> , <i>Cenpe</i> , <i>Cep76</i> , <i>Id2</i> , <i>Ywhag</i> , <i>Tacc3</i> , <i>Ccdc67</i> , <b><i>Ccnb1</i></b> , <i>Fbxo43</i> | 0.01451 | biological process         |
| centriole assembly      | <i>Cenpj</i> , <i>Plk4</i> , <i>Ccdc67</i> , <i>Cep152</i> , <i>Cep135</i> , <i>Cep76</i> , <i>Ccdc78</i>  | 0.01678 |                            |
| cell cycle              | <i>E2f8</i> , <i>Ddit3</i> , <b><i>Cdk1</i></b> , <b><i>Cdc14a</i></b> , <i>Pidd1</i> , <i>Met</i> , <i>Rif1</i> , <i>Plk5</i> , <i>Racgap1</i> , <i>Ddias</i> , <i>Cab39l</i> , <i>Camk2b</i> , <b><i>Mbd4</i></b> , <i>Cenpj</i> , <i>Setdb2-phf11c</i> , <i>Aurka</i> , <i>Cep135</i> , <b><i>Ccnb1</i></b>   | 0.04202 |                            |

Fbxo43, Ccdc67, Tacc3, *Ywhag*, Id2, Cep76, Cenpe, Prkaca, Cks2, Hormad1, Brdt, Nusap1, Fignl1, Kif2c, Misp, Junb, Smc4, Cep152, **Cdc20**, Cenpm, Rgs14, Spata22, Birc3, Cep120, Trp63, **Ccna1**, Smc2, Sycp1, Sept3, Btg4, Cep126, Ska3, Cntrl, Nedd1, E2f7, Ptpv, Spag5, Pak3, Brsk2, Kif20a, Pim2, Nek2, Fancd2, **Sass6**, Cit, Cdca2, Edn1, Rprm, Camk2a, Mcidas, Ckap2, Tube1, Dlgap5, Pcnt, Plk4

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|             |   |         |                       |
|-------------|---|---------|-----------------------|
| centriole   | Ccdc78, Ccdc67, Cenpj, Cep76, Plk4, Nedd1, Cep152, Cep128, Pcnt, Cep120, Cep135 | 0.00352 | cellular<br>component |
| deuterosome | Cep152, Ccdc67, Plk4, Ccdc78  | 0.00339 |                       |

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Note: Red indicates significantly up-regulated DEGs; Blue indicates significantly down-regulated DEGs; Italic indicates target genes; Bold indicates DEGs validated subsequently.

**Table S2.** Functional description of DEGs based on KEGG pathway analysis

| Description of KEGG pathways | Genes   | P-Value    | Classification of KEGG pathways           |
|------------------------------|---|------------|---|
| p53 signaling pathway        | <b>Cdkn1a</b> , Igfbp1, Shisa4, Sfn, Rprm, Perp, Pidd1, Adgrb1, <b>Ccnb1</b> , Serpinb5, <b>Cdk1</b> , Cycs   | 0.05425801 |   |
| Cell cycle                   | Plk1, <b>Ccna1</b> , <b>Cdkn1a</b> , Smc1b, <b>Cdc20</b> , Dbf4, Gm5936, Sfn, <b>Ywhag</b> , <b>Ccnb1</b> , <b>Cdc14a</b> , <b>Cdk1</b> , Gm5640, <b>Cdc20b</b> | 0.1688805  | Cellular Processes: Cell growth and death |

Note: Red indicates significantly up-regulated DEGs; blue indicates significantly down-regulated DEGs; Bold indicates DEGs validated subsequently.

**Table S3.** Primer sequences for RT-qPCR

| Gene Symbol    | Forward primer (5'-3') | Reverse primer (5'-3')   |
|----------------|------------------------|--------------------------|
| Mbd4           | TTGGGATCGCTGCAAGGAAG   | CAGTGGGCTCTGGAGAAGG      |
| Sass6          | CTACTGGGCTTCTCACCTC    | CTCTGGGAAAGCTTCTGTGTA    |
| Cdkn1          | CAGAATAAAAGGTGCCACAGGC | CGTCTCCGTGACGAAGTCAA     |
| Cdk1           | ACACACGAGGTAGTGACGC    | TCTGAGTCGCCGTGGAAAAG     |
| Ccnb1          | CTCCAAGCCCAGTGGAAACA   | TGACTGCTCTTCTCCAGTTG     |
| Ccna1          | TTCCAAGCAGCAGCAGG      | CTAGCACGGTTCTCTGTGGG     |
| Cdc20          | CCCCAGAAGGCTACCAGAAC   | GATTCGGGGGCATCAAGGA      |
| Cdc20b         | GCACTTCCACACACAAGCTG   | GCACTTCCACACACAAGCTG     |
| Ywhag          | CGATCCTTTCAGCCCTGTG    | GTTTCAGCTCGGTCACGTTCT    |
| Cdc14a         | CAGGCTCGGTGATTGGGAC    | AATCGATCTTTCATGAACTCGCAA |
| $\beta$ -actin | ACTGTGCGATCGCGTCCA     | ATCCATGGCGAACTGGTGG      |