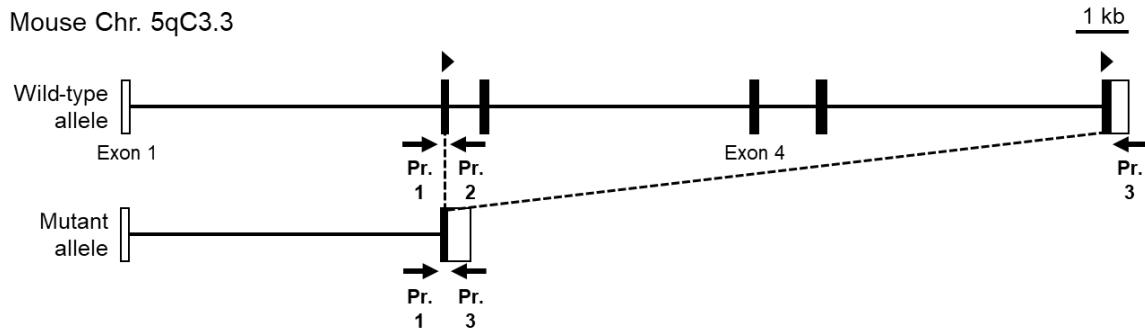


# Figure S1 (Fujihara et al.)

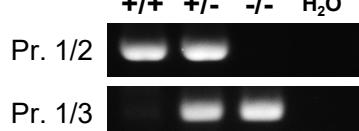
A

H. sapiens PDCL2	1	MQDPNEDTEWNDILRDFGILPPKEESKDEIEEMVLRLQKEAMVKPFEEKMT	50
M. musculus PDCL2	1	MQDPNEDTEWNEILRNFGILPPKEEPKDEIEEMVLRLQQEAMVKPYEKMT	50
H. sapiens PDCL2	51	LAQLKAEAEDEFDEEDDMQAVETYRKRLQEWKALKKKQKFGELEISGNQY	100
M. musculus PDCL2	51	LAQLKAEAEDEFDEEDIKAIEIYREKRLQEWKALKKKQKFGELEISGNQY	100
H. sapiens PDCL2	101	VNEVTNAEEDVWVIHLYRSSIPMCILLVNQHLSLLARKFPETKFVKAIVN	150
M. musculus PDCL2	101	VNEVTNAEKDLWVVIHLYRSSVPMCILVVNQHLSVLARKFPETKFVKAIVN	150
H. sapiens PDCL2	151	SCIHYHDNCLPTIFVYKNGQIEAKFIGIIIECGGINLKLLEELEWKLAEVG	200
M. musculus PDCL2	151	SCIHYHDNCLPTIFVYKNGQIEGKFIGIIIECGGINLKLLEELEWKLSSEVG	200
H. sapiens PDCL2	201	AIQSDLEENPKKGIADEMMVSSIRNISIYD-SDSSGSDTEAK	241
M. musculus PDCL2	201	AIQSDLEENPKKGIADEMMVSSIRNISIYD-SDSSGSDTEAK	240

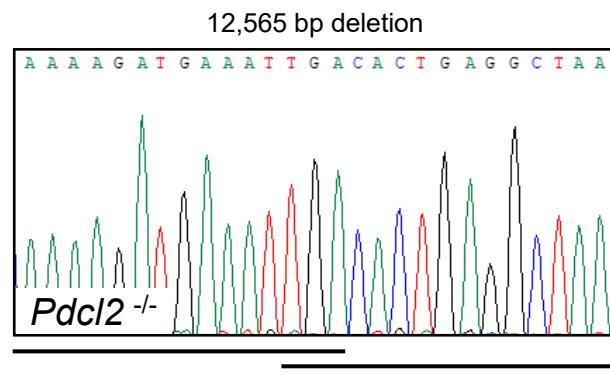
B



C



D



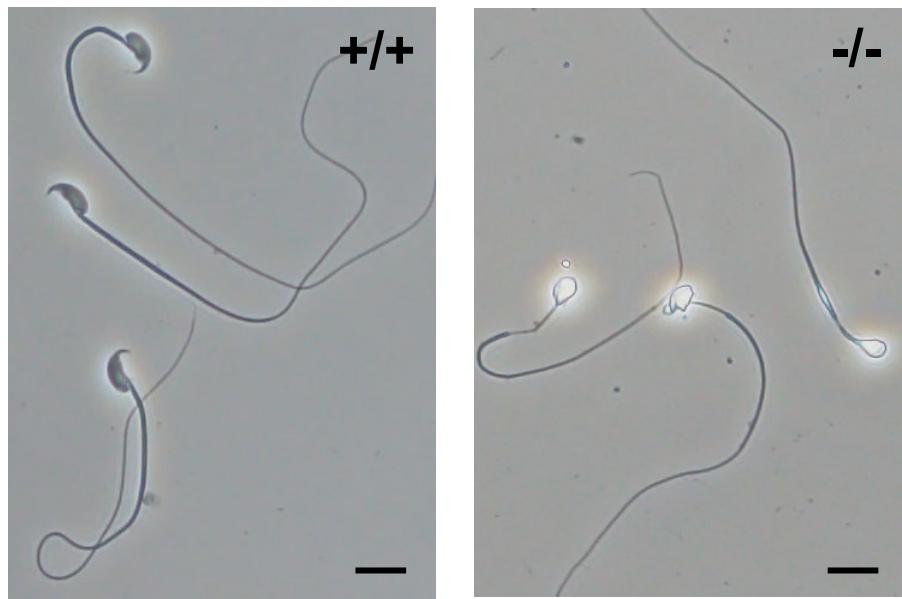
E

PDCL2 wild-type mice	1	MQDPNEDTEWNDILRDFGILPPKEEPKDEIEEMVLRLQQEAMVKPYEKMT	50
PDCL2 mutant mice	1	MQDPNEDTEWNEILRNFGILPPKEEPKDEIEEMVLRLQQEAMVKPYEKMT	35
PDCL2 wild-type mice	51	LAQLKAEAEDEFDEEDIKAIEIYREKRLQEWKALKKKQKFGELEISGNQY	100
PDCL2 mutant mice	35	-----	35
PDCL2 wild-type mice	101	VNEVTNAEEDVWVIHLYRSSIPMCILLVNQHLSLLARKFPETKFVKAIVN	150
PDCL2 mutant mice	35	-----	35
PDCL2 wild-type mice	151	SCIHYHDNCLPTIFVYKNGQIEGKFIGIIIECGGINLKLLEELEWKLSSEVG	200
PDCL2 mutant mice	35	-----	35
PDCL2 wild-type mice	201	AIQSDLEENPKKGIADEMMVSSIRNISIYD-SDSSGSDTEAK	240
PDCL2 mutant mice	35	-----	35

**Figure S1: Generation of *Pdcl2*<sup>-/-</sup> mice via the CRISPR-Cas9 system**

(A) Amino acid sequence similarity of PDCL2 in mice and humans. 87.5% of the sequence (210/240 amino acids) is identical. (B) Schematic of the *Pdcl2* locus and CRISPR-Cas9 targeting scheme. Arrows represent primers. (C) Genotyping *Pdcl2*<sup>-/-</sup> mice via PCR amplification. *Pdcl2*<sup>-/-</sup> mice had an amplified band using primers 1 and 3. (D) Wave pattern sequence of the *Pdcl2* mutant allele (12,565 bp deletion) in *Pdcl2*<sup>-/-</sup> mice. (E) Amino acid sequence of *Pdcl2*<sup>-/-</sup> mice. The 12,565 bp deletion caused a 205 (out of 240) amino acid deletion.

# Figure S2 (Fujihara et al.)



**Figure S2: Phase-contrast microscopy of spermatozoa from the cauda epididymis**  
Scale bars: 10  $\mu\text{m}$ .