Figure S1 (Fujihara et al)

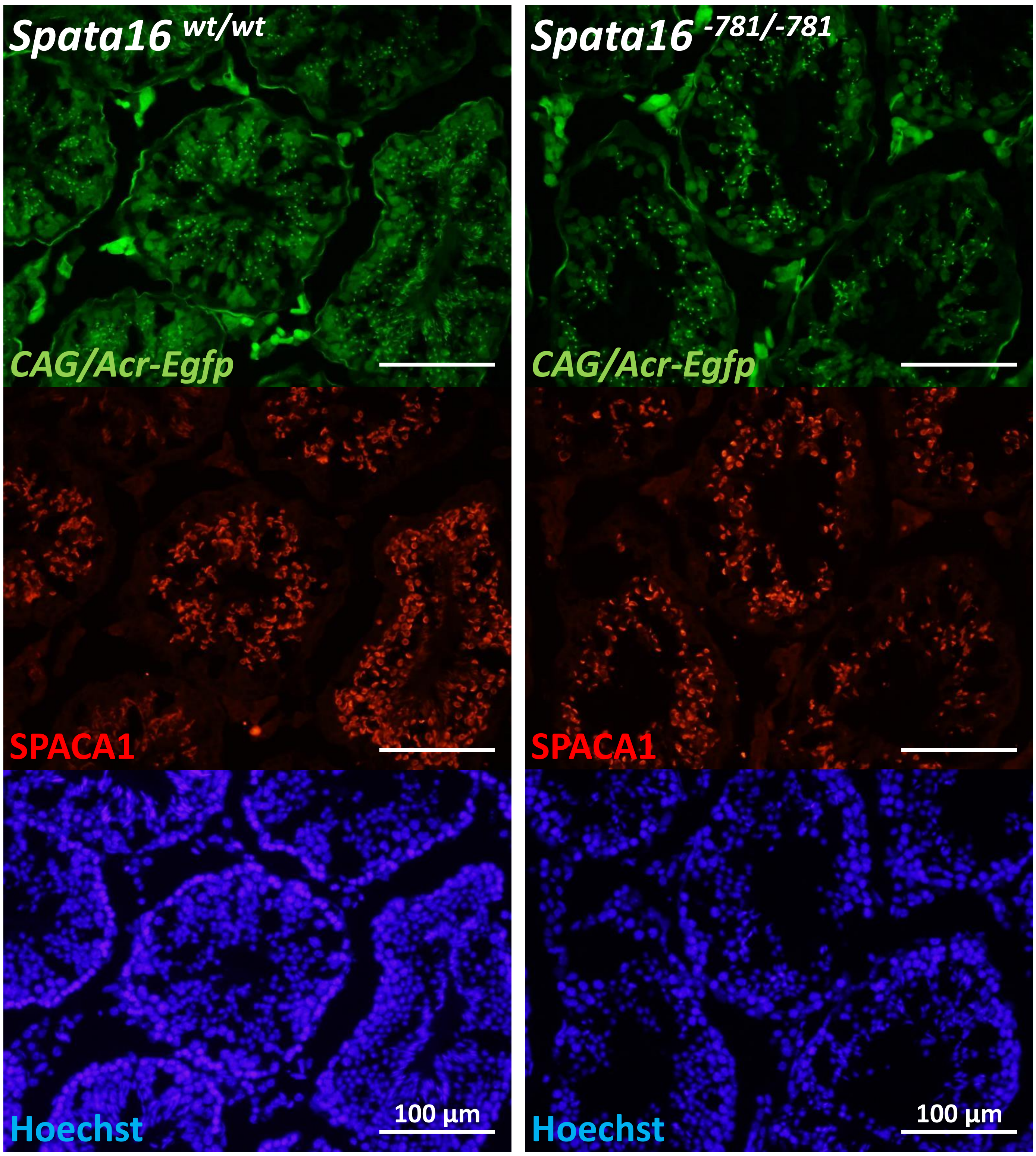

Figure S1. Histological sections of wild-type and *Spata16*$^{-781/-781}$ testes.
Acrosomal formation was observed using *CAG/Acr-EGFP* transgenic mouse testis. Red signals indicate the acrosomal membrane protein SPACA1 by immunostaining. Nuclei were stained with Hoechst 33342 (blue). Scale bars: 100 µm.

Figure S2 (Fujihara et al)

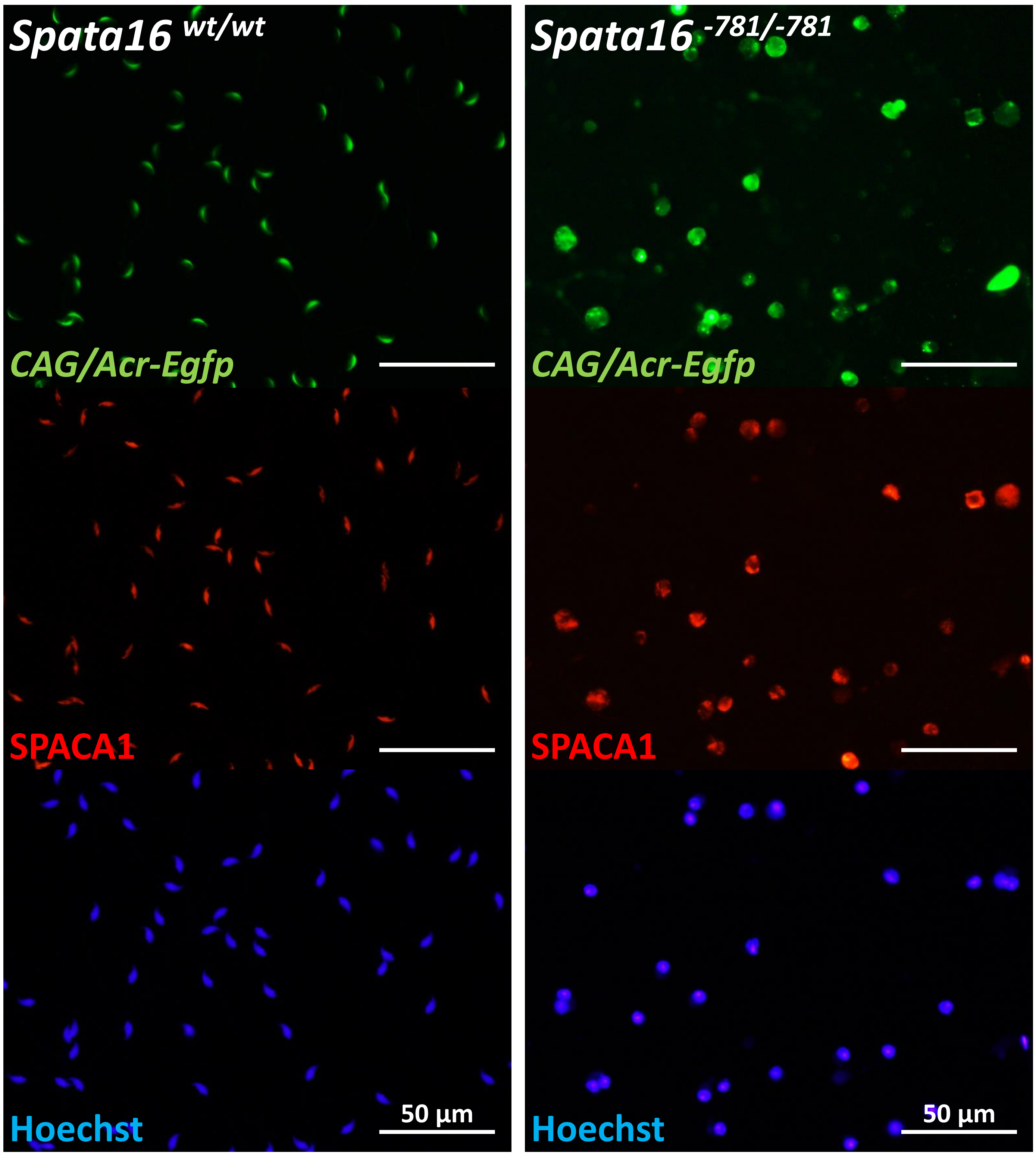

Figure S2. Observation of extracted cells from cauda epididymis in wild-type and *Spata16*$^{-781/-781}$ mice.
Acrosomal formation was observed using *CAG/Acr-EGFP* transgenic mouse testis. Red signals indicate the acrosomal membrane protein SPACA1 by immunostaining. Double-positive cells were haploid germ cells with acrosome, round spermatid and spermatozoa. The testicular remnants included round spermatids migrated from testis to the cauda epididymis in *Spata16*$^{-781/-781}$ mice. Nuclei were stained with Hoechst 33342 (blue). Scale bars: 50µm.

Figure S3 (Fujihara et al)

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Human SPATA16 intron4 (1-200)   1 GTATGTTTGTTTTAACTTTTGTGAGGATTTATATCAAGTCAAATTAATTTTATTCTCAAA 60
Mouse Spata16 intron4 (1-200)   1 GTATGTTTGTTACAACTTTC-TGAAGATTTATTTAAAGTTAAATTAATTTTACCCTCAGA 59

Human SPATA16 intron4 (1-200)  61 TTCTGGTAATAGCATAACAGAACTCTCCATTTCTCTCATGGAATATGATTTTATCCAAAT 120
Mouse Spata16 intron4 (1-200)  60 TTCTGGTAATAGCATAAGAGGACATTCCATTTCTCTCATGGAATATGATTTTATCCGAAT 119

Human SPATA16 intron4 (1-200) 121 TATTGTCT-ATCAACGTCAAACCAGCAATTATTGACTATCTTTCTCTTTAATTAAAGCTA 179
Mouse Spata16 intron4 (1-200) 120 TATTGTCTTATAAATGTCAAGCCAACAATTATTGAGTATCTTTTTCTTTAATTAAAGCTA 179

Human SPATA16 intron4 (1-200) 180 TTCCATGTTCATAGCTCTTAA                                        200
Mouse Spata16 intron4 (1-200) 180 TTTCATGTTCATAGCTCTTAG                                        200
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Figure S3. Sequence similarity of the fourth intron of SPATA16.
Sequence alignment was used for the 1st to 200th nucleotides of fourth intron of *SPATA16*. Black indicates a match in humans and mice. 88% of the nucleotide sequence is identical between humans and mice.

Table S1 (Fujihara et al)

Table S1. List of primer sequences

Figure	Sequence (5' to 3')	Name
1A, 1B, 2D, 3D, 3E	GGAGCAGCTCTGGGGAAACCC	*Spata16*, Pr.c/d
	CCAGTCGGCTGTCTGCGGC	
1A, 1B	AAGTGTGACGTTGACATCCG	*Actb*
	GATCCACATCTGCTGGAAGG	
1B	GGGAGTCAGTTAGGAGGTCTGATTACAGTAG	*Dpy19l2*
	CTGAAATTTGCTTGGCTCAATGTATCCCAC	
	GGCTCGAGCCCGCTTCTC	*Pick1*
	GCCTTGGTTAGGGCCATAGGC	
	GTTATACTGACAAATGACTCAGCAGTCTTGG	*Spaca1*
	CATAGAGCTCAGCTCGGACTGTATCTC	
2A	AGGTGAGCGCATGTGCAAGG	5'-arm
	GATATCTCTCCAGACATCTAAACACGG	
	GATACTCAGAAGCTGCCCAGTATGTTTGTTACAACTTTCTG	3'-arm
	TCTGGGGCTGAGAACATTAGC	
2B, 3B, 3C	GCCCACTCTGGTTAACTGGGACCC	Pr.a/b
	GGGTGCCAAGGACCCAAACTCAG	
2C	CTACGTCAGTGCTGCCAAGTAGC	Point mutation
	CCATCATCACTAATGACCTCATGGCTGG	