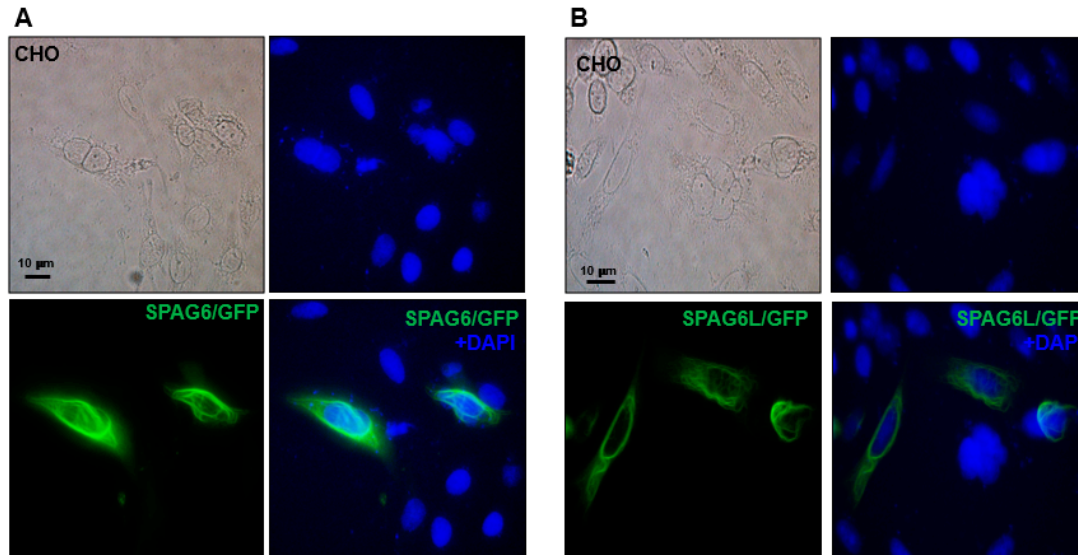


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Spag6 (Chr2)	61	GTGCAGATGTTGGCGGAGCAGGCGACCAACCCAGAACATCGAGACACTGCGAAGTGG	120
Spag6l (Chr16)	61	GTGCAGATGTTGGCGAGAGCTGGCGACAAGACCCAAACATCGAAACGCTGCGAAGTGA	120
Spag6 (Chr2)	121	GGTATAATGTCCTTTGCTGAGGCGCTCTCTCTGCGACGTGGTCCCAACATTGACGAGACT	180
Spag6l (Chr16)	121	GGTGTAAATGTCCTTTGCTAAGGCGCGCTCTCTCTGGATGGTCCCAACATTCACAGACT	180
Spag6 (Chr2)	181	GCTGCCTTGGCTCTGGGGAGGCTGGCCAACTACACGATGACTTAGCAGAGCAGTCTGTG	240
Spag6l (Chr16)	181	GCAGCTTTGGCTCTGGGGAGACTGGCCAAATACATGATGACTTAGCAGAGCAGTCTGTG	240
Spag6 (Chr2)	241	AAGGGTGACATTCTTCCACAGCTTGTGTATTATTGGCAGAGCAGAAATGCTGTCTACAAG	300
Spag6l (Chr16)	241	AAAGGTGACATTCTTCCACAGCTTGTATTATTATTGGCAGAACAAATGTTTTTACAAG	300
Spag6 (Chr2)	301	AAGGCAGCTGCGTTTGTGCTGCGAGCGGTTGGTAAACACTCTCCTCAGCTGGCGCAGGCC	360
Spag6l (Chr16)	301	AAGGCAGCTGCGTTTGTGTTGAGAGCAGTTGGGAACACTCTCCTCAGCTGGGCCAGGCC	360
Spag6 (Chr2)	361	ACAGTTGACTGTGGTGCCCTGGACTCACTGGTGATCTGCTTGGAAAGTTTGGACCTGGA	420
Spag6l (Chr16)	361	ATAGTTGACTGCGGGAGCTCTGGATACACTGGTGATCTGCTTGGAGGATTTGACCCCTGGG	420
Spag6 (Chr2)	421	GTCAGGAGGCTGCGAGCTGGGCACTTGCATATATTGCAAGGCATAATGCGAGAACTGCG	480
Spag6l (Chr16)	421	GTCAGGAGGCTGCGAGCTGGGCACTCGGATACATTGCAAGCACACACAGAAATTATCT	480
Spag6 (Chr2)	481	CAAGCTGTGGTGATGCGGGAGCTGTTCCCTTTTAGTCTCTGTATCCAGGAGCCGAG	540
Spag6l (Chr16)	481	CAAGCCGTGGTGATGCGAGGCAATTCCCTTTTAGTCTTTGTATCCAGGAGCCAGAA	540
Spag6 (Chr2)	541	ACTGCTTTGAAAGGATCGCTGCTCGGCCCTCAGTGATATTTCAAAGCACTCCCCAGAG	600
Spag6l (Chr16)	541	ATTGCTTTGAAAGGATCGCTGCTCGGCCCTCAGTGATATCTCAAAGCACTCCCCAGAG	600
Spag6 (Chr2)	601	TTAGCACAAACGGTGGTGATGTAGGAGCTATTGCTCACTTAGCCAGATGATCCTCAAC	660
Spag6l (Chr16)	601	TTAGCACAGAGCGTGGTGAGCGAGGAGCTATTGCTCACTTAGCCAGATGATCCTCAAC	660
Spag6 (Chr2)	661	CCCGATGAGAACTGAAGCAGAGGCTCTCTCAGCTCTGAGTCACATGCGAGCACTCG	720
Spag6l (Chr16)	661	CCTGATGCAAACTGAAGCGCAGGCTCTCTCAGCTCTCAGTCAGATTGCAAGGATCTCT	720
Spag6 (Chr2)	721	GTGGACCTGGCAGAGATGGTTGTGGAGGAGAGATTTTCCAGTTGTTCTCACCTGTCTG	780
Spag6l (Chr16)	721	GTGGACTTGGCAGAGATGGTTGTGAAGCAGAGATTTTCCCTGTTGACTTAACCTGCTG	780
Spag6 (Chr2)	781	AAGGACAAAGTGAATCTCGTGAAGAAGATGCTGTACTCTGATTAGAGAGATCGCAAAA	840
Spag6l (Chr16)	781	AAGGACAAAGTGAATATGTGAAGAAAATGCTTGACCTTAATCAGAGAGATTGCAAAA	840
Spag6 (Chr2)	841	CATACACGAGGCTCTCGCAGCTGATTGTTAATGCGGAGGTGTGGCTGCCGTGATCGAC	900
Spag6l (Chr16)	841	CACACGCTGAGCTCTCGCAGCTGATTGTTAATGAGGAGGCGTGGCTGCCGTGATCGAT	900
Spag6 (Chr2)	901	TGCATCGGGTCTGCAAAAGGGAACATACGGCTGCGTGGCATCATGATGCTGGGTTACATG	960
Spag6l (Chr16)	901	TGCATTTGGGTCTGCAAAAGGGAACATACGGCTGCGTGGCATCATGATGCTGGGTTAAGTG	960
Spag6 (Chr2)	961	GCTGCTCATTTCTGAGAACCTGGCCATGGCGGTGATCATCTCCAGGGGTGACCCCACTTG	1020
Spag6l (Chr16)	961	GCTGCTCATTTCTGAGAACCTGGCCATGGCGGTGATCATCTCCAGGGGTGATCCCACTTG	1020
Spag6 (Chr2)	1021	TCAGACTGCTGTGAGAACCTGGGAGAGATCATATTAAGGCTGGGCTGCTGGGCTCTA	1080
Spag6l (Chr16)	1021	TCAATCTGCTGTGAGAACCTGGGAGAGATCATATTAAGGCTGCTGCTGGGCTCTTG	1080
Spag6 (Chr2)	1081	GGGCAGGTTGGGAGGCACACTCCAGAACATGCTCGGGCTGTGCGCATCAAAACACGTTG	1140
Spag6l (Chr16)	1081	GGGCAGCTGGGAGGACACACTCCAGAGCATGCCAGGCTGTGGCTGTCAAAACACGCTG	1140
Spag6 (Chr2)	1141	CCCGTGTGCTGGCTTTGTACATGTCCCGAGAGGCTCTGAGGACCTGCAAGTGAAGT	1200
Spag6l (Chr16)	1141	CCAGTCTGCTGCTTTGTACATGTACCGAGAGGCTCTGAGGACCTACAGCTCAAAAGT	1200
Spag6 (Chr2)	1201	AAAAAGCCATAAAGAAATATCATCCAAAATGCACCTAOCCTCCCGGCGCTTGAGCCGTTT	1260
Spag6l (Chr16)	1201	AAAAAGCCATAAAGAAATATCCTTCAGAAATGCACCTAOCCTCCCGGCGCTTGAGCCGTTT	1260
Spag6 (Chr2)	1261	CTCTATGATGCGCCTCCCAATATCCTGAAGTATGTGCTGGACAGTTCACTAAGGTGCTG	1320
Spag6l (Chr16)	1261	CTGTACGACGACCTCCCAATATCCTGAACATGTTGTGGGAGTTCACTAAGGTGCTG	1320
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Spag6l (Chr16)	1321	CCACATGACAGCAAGCCCGCGGCTTTTGTGACTAGTGGTGGACTTAAAAAGGTTTCA	1380
Spag6 (Chr2)	1381	GAGATCAAGCAGAACCTGGTCCATCCTCCAAGAGTATATCAACAACTCAACAGCTGC	1440
Spag6l (Chr16)	1381	GAGATAAAGCAGAACAGGCTCTCTCTGAGGAATACATCAACAGCATCAACAAATTGT	1440
Spag6 (Chr2)	1441	TACCCAGAGGAATAGTAAGGTACTATTCTCCTGGTACTCAGACATACTTCTGCAAGG	1500
Spag6l (Chr16)	1441	TACCCAGAGGAATAGTAAGGTATTATTCACTGGTACTCCGATACACTTCTGCAAGG	1500
Spag6 (Chr2)	1501	ATCGACAGCTATCAGCCTCTTATTAACTGAACGAAGTATA---TTATAACTCAGATTC	1557
Spag6l (Chr16)	1501	GTGGACAGCTACCAACACT-----GTGAACAAAGCATATTTTATTCTCTCGGTTTT	1554
Spag6 (Chr2)	1558	ACAGGAGAGTAAAGGATAACAATTGTTAA 1585	
Spag6l (Chr16)	1555	CCAGGAGAGTGTGAATATGATTGTTAA 1582	

**Supplemental Figure S1. The ancient *Spag6* gene shares high homology with the evolved gene, *Spag6l*.**

*Spag6* and *Spag6l* share high homology in nucleotide sequences. The coding sequences of the two genes were compared. Nucleotide sequence comparison using Basic Local Alignment Search Tool (BLAST) demonstrates high similarity between the two genes.



**Supplemental Figure S2. Localization of SPAG6L/GFP in transfected CHO cells.**

The SPAG6/pEGFP-N<sub>2</sub> (A) and SPAG6L/pEGFP-N<sub>2</sub> (B) plasmids were transfected into CHO cells. 48 hrs after transfection, the cells were fixed with 4% paraformaldehyde and mounted with a medium containing DAPI. Images were taken with a fluorescence microscope.

A				B			
WILD-TYPE	1	---CCGGTTTGTGCAGATGGTGGCGGAGCAGGCGACCAAAACCCAGAAACA	47	<i>Spag6</i> KO	1	----CGGTTTGTGCAGATGGTGGCGGAGCAGGCGACCAAAACCCAGAAACA	46
<i>Spag6</i> CDNA	51	GACCCGGTTTGTGCAGATGGTGGCGGAGCAGGCGACCAAAACCCAGAAACA	100	<i>Spag6</i> CDNA	51	GACCCGGTTTGTGCAGATGGTGGCGGAGCAGGCGACCAAAACCCAGAAACA	100
WILD-TYPE	48	TCGAGACACTGCAGAATGCGGGTATAATGTCTTTGCTGAGGCCCTCTTCTT	97	<i>Spag6</i> KO	47	TCGAGACACTGCAGAATGCGGGTATAATGTCTTTGCTGAGGCCCTCTTCTT	96
<i>Spag6</i> CDNA	101	TCGAGACACTGCAGAATGCGGGTATAATGTCTTTGCTGAGGCCCTCTTCTT	150	<i>Spag6</i> CDNA	101	TCGAGACACTGCAGAATGCGGGTATAATGTCTTTGCTGAGGCCCTCTTCTT	150
WILD-TYPE	98	CTGGAGCTGGTCCCAACCATTCAGCAGACTGCTGCTTGGCTCTGGGGAG	147	<i>Spag6</i> KO	97	CTGGAGCTGGTCCCAACCATTCAGCAGACTGCTGCTTGGCTCTGGGGAG	146
<i>Spag6</i> CDNA	151	CTGGAGCTGGTCCCAACCATTCAGCAGACTGCTGCTTGGCTCTGGGGAG	200	<i>Spag6</i> CDNA	151	CTGGAGCTGGTCCCAACCATTCAGCAGACTGCTGCTTGGCTCTGGGGAG	200
WILD-TYPE	148	GCTGGCCAATCACACGATGACTTAGCAGAGCAGCTGCTGAAGGGTGACA	197	<i>Spag6</i> KO	147	GCTGGCCAATCACACGATGACTTAGCAGAGCAGCTGCTGAAGGGTGACA	196
<i>Spag6</i> CDNA	201	GCTGGCCAATCACACGATGACTTAGCAGAGCAGCTGCTGAAGGGTGACA	250	<i>Spag6</i> CDNA	201	GCTGGCCAATCACACGATGACTTAGCAGAGCAGCTGCTGAAGGGTGACA	250
WILD-TYPE	198	TTCTTCCACAGCTTGTGTAATTCATTGGCAGAGCAGAAATGTGTCTACAAG	247	<i>Spag6</i> KO	197	TTCTTCCACAGCTTGTGTAATTCATTGGCAGAGCAGAAAT-----	234
<i>Spag6</i> CDNA	251	TTCTTCCACAGCTTGTGTAATTCATTGGCAGAGCAGAAATGTGTCTACAAG	30	<i>Spag6</i> CDNA	251	TTCTTCCACAGCTTGTGTAATTCATTGGCAGAGCAGAAATGTGTCTACAAG	300
WILD-TYPE	248	AAGGCAGCTGCGTTTGTGCTGCGAGCGGTTGGTAAACACTCTCTCAGCT	297	<i>Spag6</i> KO	235	-----	234
<i>Spag6</i> CDNA	301	AAGGCAGCTGCGTTTGTGCTGCGAGCGGTTGGTAAACACTCTCTCAGCT	350	<i>Spag6</i> CDNA	301	AAGGCAGCTGCGTTTGTGCTGCGAGCGGTTGGTAAACACTCTCTCAGCT	350
WILD-TYPE	298	GGCGCAGGCCACAGTTGACTGTGGTGGCTTGGACTCACTGGTGAATCTGCT	347	<i>Spag6</i> KO	235	-----	234
<i>Spag6</i> CDNA	351	GGCGCAGGCCACAGTTGACTGTGGTGGCTTGGACTCACTGGTGAATCTGCT	400	<i>Spag6</i> CDNA	351	GGCGCAGGCCACAGTTGACTGTGGTGGCTTGGACTCACTGGTGAATCTGCT	400
WILD-TYPE	348	TGGAAGATTTTGACCTGGATTCAAGGAGGNTGCAGCTGGGTACTTGCA	397	<i>Spag6</i> KO	235	-----	234
<i>Spag6</i> CDNA	401	TGGAAGATTTTGACCTGGATTCAAGGAGGNTGCAGCTGGGTACTTGCA	450	<i>Spag6</i> KO	235	-----	234
WILD-TYPE	398	TATATTGCAAGGATAATGAGAACTGWCAGCAAGCTGTGGTGGATGCGGG	447	<i>Spag6</i> CDNA	401	TGGAAGATTTTGACCTGGATTCAAGGAGGNTGCAGCTGGGTACTTGCA	450
<i>Spag6</i> CDNA	451	TATATTGCAAGGATAATGAGAACTGTGCAAGCAAGCTGTGGTGGATGCGGG	500	<i>Spag6</i> KO	235	-----AACTGTGCAAGCTGTGGTGGATGCGGG	262
WILD-TYPE	448	AGCTGTCCCTCTTNTAGTCTTTGTATCCAGGAGCCCGAATTTGCTNTGN	497	<i>Spag6</i> CDNA	451	TATATTGCAAGGATAATGAGAACTGTGCAAGCAAGCTGTGGTGGATGCGGG	500
<i>Spag6</i> CDNA	501	AGCTGTCCCTCTTNTAGTCTTTGTATCCAGGAGCCCGAATTTGCTTTGA	550	<i>Spag6</i> KO	263	AGCTGTCCCTCTTTAGTCTCTGTATCCAGGAGCCCGAATTTGCTTTGA	312
				<i>Spag6</i> CDNA	501	AGCTGTCCCTCTTTAGTCTCTGTATCCAGGAGCCCGAATTTGCTTTGA	550

C

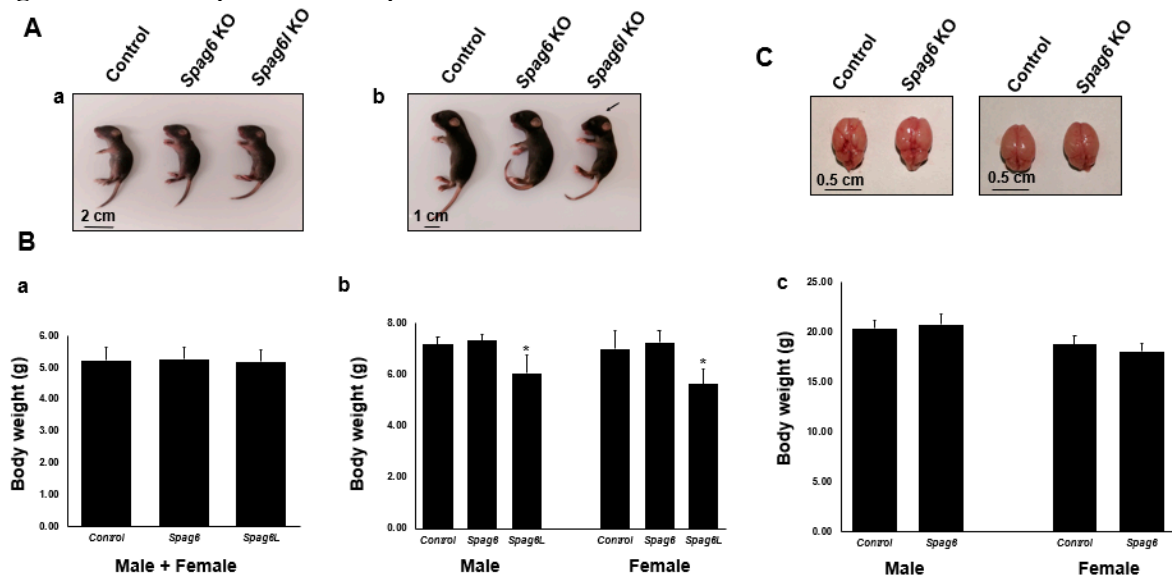
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Y N D D L A E A V V K G D I L P Q L V F S L A E Q N
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E Q N N C R K L W W M R E L F L F - S S V S R S P X
AACTGTGCGAGCTGTGGTGGATGGGAGCTGTCTCTTTAGTCTCTGTATCCAGGAGCCCAHACTGCTTGA

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### Supplemental Figure S3. Examination of exon 4 deletion in *Spag6* KO mice by Sanger sequencing.

The full-length mouse *Spag6* coding regions were amplified by RT-PCR using testicular cDNA from a control mouse and a *Spag6* KO mouse. The two PCR products were sequenced using the forward primer, and the sequencing results were compared to the coding sequence of the mouse *Spag6* cDNA (GenBank: NM\_001001334.2). A. BLAST results using the PCR product from the control mouse; B. BLAST results using the PCR product from the *Spag6* KO mouse. Notice that the control mouse contained an intact exon 4 sequence, but exon 4 was deleted in the KO mouse. C. Analysis of the amino acid sequence of the *Spag6* KO mice. The EMBOSS TranSeq program was used to analyze the amino acid sequence of the *Spag6* KO cDNA. Deletion of exon 4 of mouse *Spag6* resulted in a premature stop codon.



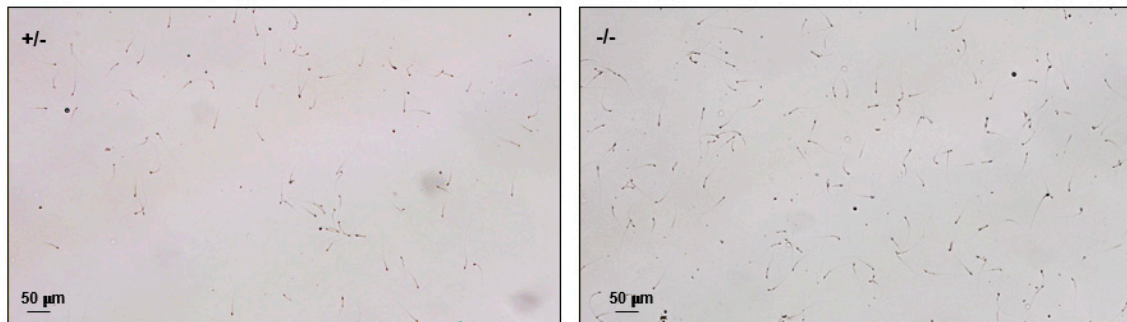
### Supplemental Figure S4. Normal development of *Spag6* KO mice.

A. Representative images of the mice at the indicated ages. Notice that no difference was observed between the control and the *Spag6* KO mice at any of age analyzed. However, the *Spag6L* KO mice

were smaller at two weeks of age. a. One-week-old mice; b. Two-week-old mice. The arrow points to the head of a two-week-old *Spag6l* KO mouse with hydrocephalus.

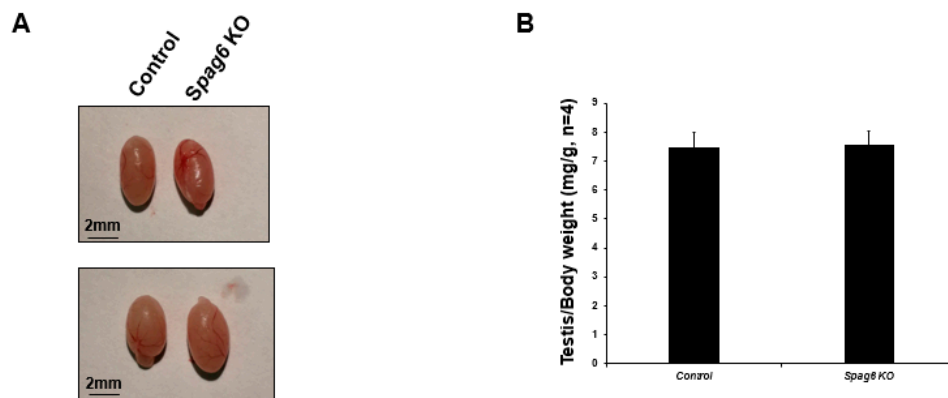
B. Body weight of the control and *Spag6* KO mice at the indicated ages. Notice that there was no significant difference between the two groups. However, the body weight of the *Spag6l* KO mice was significantly lower at two weeks after birth.  $n=6$ . \*  $P<0.05$  compared to the control mice.

C. Representative images of brains of two-month-old control and *Spag6* KO mice. Hydrocephalus was not identified in any of the mice analyzed in this study.



**Supplemental Figure S5. Morphological examination of epididymal sperm of *Spag6* KO mice by light microscopy at low magnification.**

Representative images of sperm at low magnification. Sperm density is similar between the control and the *Spag6* KO mice at the same dilutions.

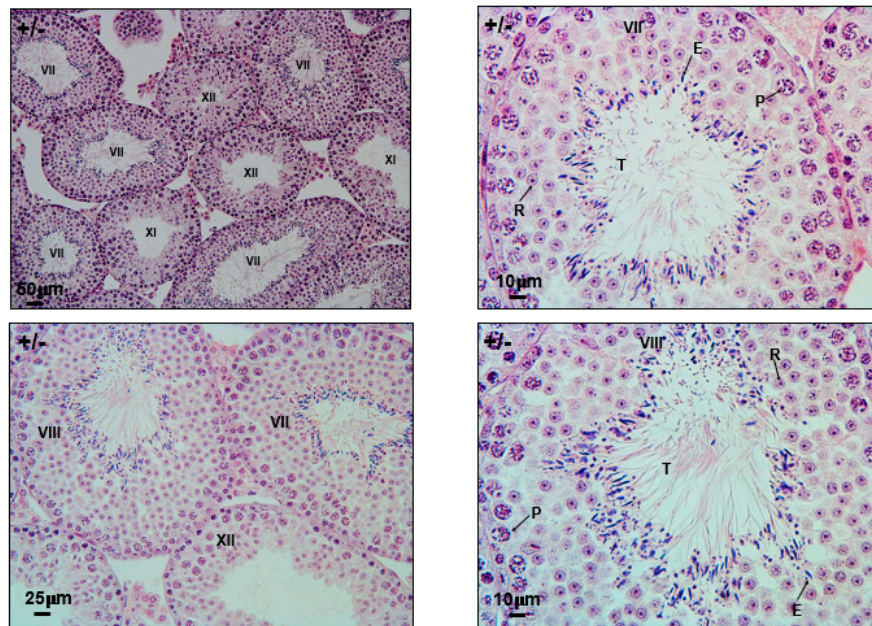


**Supplemental Figure S6. *Spag6* KO mice have normal testis weight.**

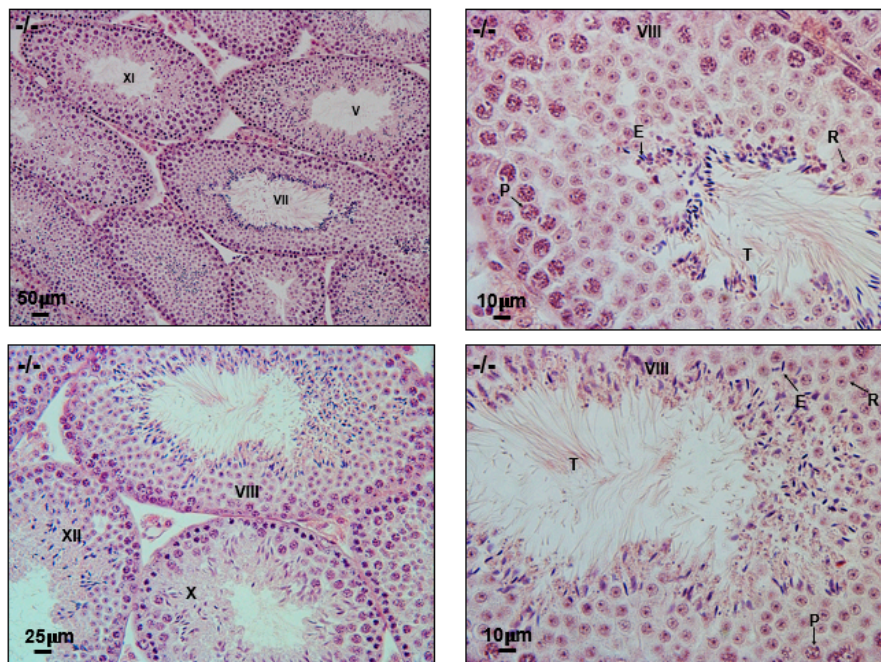
A. Representative image showing two pairs of testes from 4-month-old *Spag6* KO mice and their littermates;

B. A statistical analysis to compare the testis weight/body weight between the control and the *Spag6* KO mice.  $n=4$ . No significant difference was found ( $P>0.05$ ).





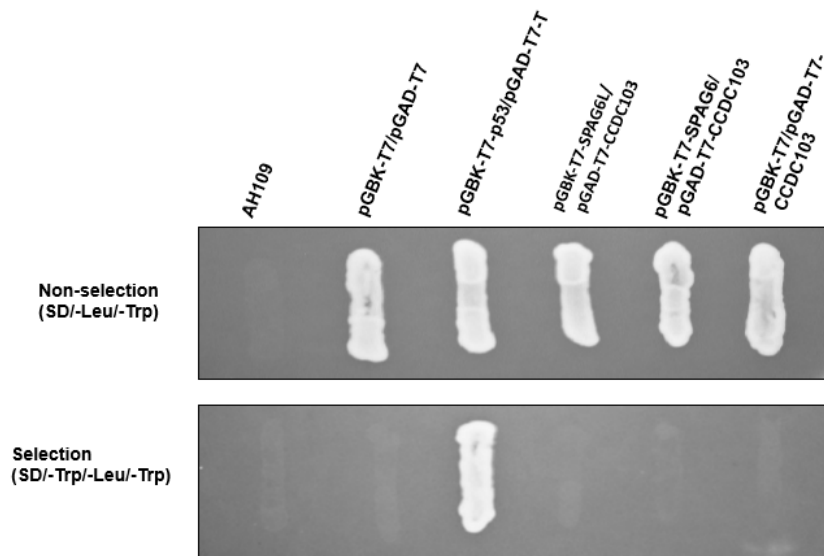
A



B

**Supplemental Figure S7. Low and high magnification of testis histology.**

Notice that both the control (A) and the *Spag6* KO (B) mice show normal seminiferous tubule structure at low (left) and high (right) magnification. P, pachytene spermatocytes, R, round spermatids, E, elongating spermatids, T, tail of sperm being released.



**Supplemental Figure S8. The two mouse SPAG6 proteins do not bind to CCDC103.**

Direct yeast two-hybrid assay to analyze interactions between the two mouse SPAG6 proteins and CCDC103. Neither of the two SPAG6 proteins bind to CCDC103.