

Supplementary Table S1. Single-guide RNAs targeting the genes' upstream (U) and downstream (D) regions used for generating knockout mice. Efficiency of embryo transplantation was presented using the number of total pups delivered by pseudopregnant mice divided by the number of total embryos used for oviduct transplantation (Total pups/embryos transplanted). Efficiency of genome editing was determined by the number of pups carrying enzymatic mutations divided by the number of pups subjected to genotyping (GM pups/pups genotyped).

Gene symbol	KO strategy	Total pups/embryos transplanted	GM pups/pups genotyped	PAM	sgRNA sequences	
<i>4921507P07Rik</i>	Zygote electroporation	14/90 (15.6%)	3/14 (21.5%)	CGG	U	GGCCGAATAGTTGTTTCGTA
				AGG	D	AACAGAATCCAGCAAATGC
<i>Allc</i>	Zygote electroporation	15/56 (27%)	1/15 (6%)	GGG	U	GATTGGCCTCTGAGTGCCT
				AGG	D	TAGGGAAACCCCTTGAGCCGA
<i>Cabs1</i>	Zygote injection	15/77 (19%)	5/11 (45%)	TGG	U	AGTCATTTACTGAAGTAACG
<i>Fam229b</i>	Zygote electroporation	16/75 (21%)	15/16 (94%)	AGG	U	CTTCTTGAGCCCGCTAGCTA
				GGG	D	ATCATTAAGTCTCTGTCGA
<i>Fscb</i>	Zygote electroporation	17/100 (23%)	10/17 (59%)	AGG	U	CCTGAAGAGCCTATATCATT
				AGG	D	TAAAGAACTGAGCTATCGTC
<i>Hdgf1</i>	Zygote electroporation	15/80 (18.8%)	9/15 (60%)	AGG	U	AGCAGCAGCGGGACCTCTCG
				GGG	D	GTTGAAGACTGGGCCCTAGT
<i>Iqca</i>	Zygote electroporation	20/80 (25%)	5/20 (25%)	AGG	U	GTTCCCCAACCTCGGCAGT
				AGG	D	TCTTCCTCCTCTCGGTACAC
<i>Lelp1</i>	Zygote electroporation	6/33 (18%)	3/6 (50%)	AGG	U	TGAAAGCTTCTCGAGAAAAC
				AGG	D	CCATGCCTACCCGAAAGTG
<i>Spata24</i>	Zygote electroporation	16/40 (40%)	13/16 (81%)	GGG	U	ACAGAGCACCCCTGGCAACCG
				AGG	D	GACAGTGCCTACTGCTCATGG
<i>Tmem97</i>	Zygote electroporation	4/46 (8.7%)	3/4 (75%)	TGG	U	CAGCTAGGCGCTGTGTCGAG
				TGG	D	GCAGTGCTGTGGTAGCGCTT
<i>Eddm3b</i>	Zygote electroporation	10/79 (13%)	1/10 (10%)	GGG	U	TCAGGCCTTGGTCACCGTCC
<i>Lrcol1</i>	Zygote electroporation	6/81 (7.4%)	3/6 (50%)	TGG	U	GTGAGATGTCTGTCTCGGTG
				TGG	D	CACATTCCAAAAACACGGTC
<i>Tmem114</i>	Zygote electroporation	20/65 (30.8%)	11/20 (55%)	TGG	U	TGCGGGTGGGATCGCGTAAG
				TGG	D	CCAGGAGGCGCAGGGCCTT

Supplementary Table S2. Primers and PCR conditions used for genotyping.

Gene symbol	Allele	Forward primer	Reverse primer	Band size	Annealing	Elongation
<i>4921507P07Rik</i>	WT	TAAGCCTCTGGTTTTGTGC	TACTCATGTTGCCCTCTCC	400 bp	65°C, 30 s	72°C, 30 s
	KO	TAAGCCTCTGGTTTTGTGC	GTCAGGACATTATTTGGTCC	346 bp	65°C, 30 s	72°C, 30 s
<i>Allc</i>	WT	GCCTTGCTGTGTTGAAGCC	ATGGACTTGGGTTCACCGAC	856 bp	65°C, 30 s	72°C, 1 min
	KO	CAGAGCTCTCACCGGTTCTC	AGCACCATAGGGTATGTA	649 bp	65°C, 30 s	72°C, 45 s
<i>Cabs1</i>	WT	CTGTGAGAGTGCTCAGTGCC	CCCTTAGGTTGGAGTTGG	350 bp	65°C, 30 s	72°C, 30 s
	KO	CTGTGAGAGTGCTCAGTGCC	CCCTTAGGTTGGAGTTGG	345 bp	65°C, 30 s	72°C, 30 s
<i>Fam229b</i>	WT	AGGCAGGAAGCTATGTGAAGG	TACACAAGGGATAGGAAAGGTGA	422 bp	65°C, 30 s	72°C, 30 s
	KO	AGGCAGGAAGCTATGTGAAGG	GCTTAGCATGCAGAGCGCTC	347 bp	65°C, 30 s	72°C, 30 s
<i>Fscb</i>	WT	GGAACTGTAGAACGACTGACTGC	GAGAAAATTTCAGCAGAGCCC	502 bp	65°C, 30 s	72°C, 30 s
	KO	GTCCTAACAGAAACAAACCAAG	TAAGCAATCATTGTCCATGG	545 bp	65°C, 30 s	72°C, 30 s
<i>Hdgfl1</i>	WT	ACCAACATTCTAACATGG	ACAAAGTTGATGTCAACTGG	1514 bp	60°C, 30 s	60°C, 30 s
	KO	ACCAACATTCTAACATGG	ACAAAGTTGATGTCAACTGG	419 bp	60°C, 30 s	60°C, 30 s
<i>Iqca</i>	WT	GGGGTTGCTGTGAAACAC	TCAACAGCCTCCTCGAGT	461 bp	63°C, 30 s	72°C, 60 s
	KO	CGGCTCACATAAACAGGGCA	TCCATCAAGAACGGAGGTGAG	978 bp	63°C, 30 s	72°C, 60 s
<i>Lelp1</i>	WT	CCATGCCTACCCGAAAGTG	CAGCCCCACAATGTTGAGG	968 bp	65°C, 30 s	65°C, 30 s
	KO	CCATGCCTACCCGAAAGTG	CAGCCCCACAATGTTGAGG	509 bp	65°C, 30 s	65°C, 30 s
<i>Spata24</i>	WT	TCTGTTGCAGATGGTCTCC	CAGGACTCTGCTTGTACAC	542 bp	65°C, 30 s	72°C, 30 s
	KO	TTGGGGGATGAAATCCAGTC	AGCTCAGTAGAGGCCGGGTGC	199 bp	55°C, 30 s	72°C, 30 s
<i>Tmem97</i>	WT	GTGACCCTAGGCCAATGG	GGCAATATACTAACCTAAGG	591 bp	60°C, 30 s	72°C, 30 s
	KO	CTATAGCCCCGCTATATGGG	GGTGAGGTGCCAGAGTAGGG	552 bp	65°C, 30 s	72°C, 30 s
<i>Eddm3b</i>	WT	CAAAAGAGAGGGCATATAGGAGG	AGCAGAAGCAGGGCCAGGC	296 bp	65°C, 30 s	72°C, 30 s
	KO	CAAAAGAGAGGGCATATAGGAGG	GAGCAGAAGCAGGGCCTTT	292 bp	65°C, 30 s	72°C, 30 s
<i>Lrcol1</i>	WT	CAGCCAGGGCTACACGGAAA	GATGGGGCTGCATGACGATTGGG	491 bp	65°C, 30 s	72°C, 30 s
	KO	CAGCCAGGGCTACACGGAAA	GGTCTTGATGAGCAGAACCC	489 bp	65°C, 30 s	72°C, 30 s
<i>Tmem114</i>	WT	ACTCAGTCTGATCGTGATGG	TCCGCTGCTTCTACTGTGG	567 bp	60°C, 30 s	60°C, 30 s
	KO	GGACGCTCGCCCCGATCCGG	AAAACCTACCGGGTGACTAGG	587 bp	60°C, 30 s	60°C, 30 s

Supplementary Table S3. Sanger sequencing of mutant alleles in all mouse lines. Bases in uppercase indicate exon sequences and the ones in lowercase indicate intron sequences.

Gene symbol	Upstream sequence (25 bp)	Mutation	Downstream sequence (25 bp)
<i>4921507P07Rik</i>	TACTCTAACGGACTGCACACCCGT	-22195	GGCTGGATTCTGTTCTGTATTAAG
<i>Allc</i>	GCAGCTGATTGATTGGCCTCTGAG	-19639	gggaagtattttagaattatcctc
<i>Cabs1</i>	AACTATTACCTCGGAAGGAGACCAC	-5	TTCAGTAAATGACTGCACACCGGAT
<i>Fam229b</i>	TTGGCCTATTTGGTAAGTCTATGT	-3266 +17*	TTCAGTAAATGACTGCACACCGGAT
<i>Fscb</i>	AATGTGAAGAACCTGAAGAGCCTAT	-3166	AGGTGTTAACTAAACTAATAATT
	AATGTGAAGAACCTGAAGAGCCTAT	-3164	TCAGGTGTTAACTAAACTAATAAT
<i>Hdgl1</i>	aggaagcggtgccaggcatcctcgag	-1095	GGGACAGGCCAGTTGACATCAACTT
<i>Iqca</i>	CTAGGGGGAGTTCCCCAACCTCGG	-107633	AGAGGAGGAAGAGAGTTAAGgtA
<i>Lelp1</i>	aggcccctaagaacacactgcttact	-577bp+118 [#]	AGTGAGGCACCATGGCAACACTCC
<i>Spata24</i>	CCTTGCACACAGAGGAAGTCCCCGC	-5638	ACTGTCTGTCTGCCTCCTATAGCAA
<i>Tmem97</i>	GGGCCTGGCAGCTAGGCCTGTGT	-8286	CGCTACCACAGCACTGCTAAAAAGG
<i>Tmem114</i>	TGGGCCGGAGCACGTGCGGGTGGGA	-15261	CCCATCTCAGTGGATGGCAACCTTT
<i>Eddm3b</i>	CCTGCTCTGATGTCCCTCTAAAAG	-5	GCCCTGCTTCTGCTCCTGCTGTGCC
<i>Lrcol1</i>	GGTCCAACGTGAGATGTCTGCTCG	-1196	AATGTGTGCCCTGGAGGAAGGTGAC

*+17: TTTCTTGAGCCCGCTAG

[#]+118:GAAGCTTCAATGTGTCAGTCTGACCACATCTCATTAAGAGCTGCCTGTGGACTTGGGTATGTCTAGATGCCTGCACTCTGATTTCT
CTTACTTTGTTCCATTCTAG

Supplementary Table S4. Testis weight relative to body weight in wild-type and mutant males.

Gene symbol	Testis/body weight ($\times 10^3$)	No. of males	No. of testis
Wild-type	3.0 \pm 0.4	6	12
<i>Fam229b</i>	3.3 \pm 0.1	3	6
<i>Lqca</i>	3.2 \pm 0.0	2	4
<i>Lelp1</i>	4.2 \pm 0.4	2	4
<i>Spata24</i>	3.8 \pm 0.6	2	4
<i>Tmem114</i>	3.2 \pm 0.5	3	6

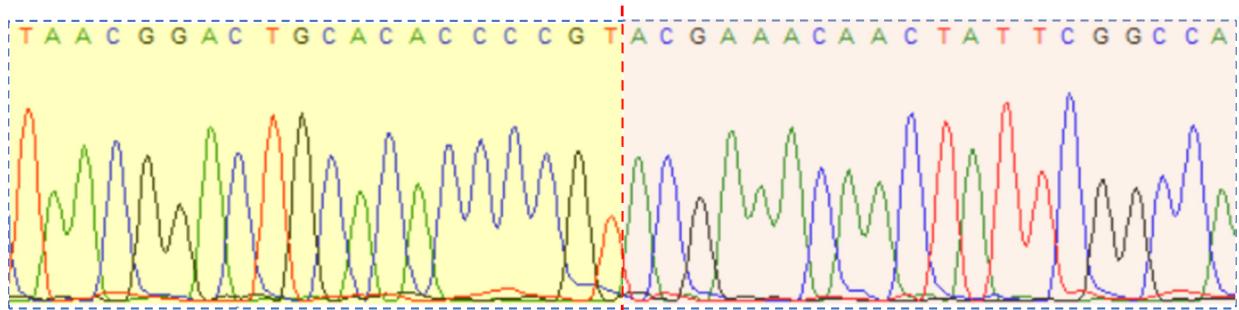
Supplementary Table S5. The 13 knockout mouse lines in this study. The RBRC No. and CARD ID are available for the mouse lines that have been deposited as frozen sperm to Riken BioResource Research Center and Center for Animal Resources and Development at Kumamoto University, respectively.

Gene symbol	Gene name	RBRC No.	CARD ID
<i>4921507P07Rik</i>	RIKEN cDNA 4921507P07 gene	11050	2957
<i>Allc</i>	Allantoicase	11054	2961
<i>Cabs1</i>	Calcium binding protein, spermatid associated 1	10333	2703
<i>Fam229b</i>	Family with sequence similarity 229, member B	11035	2942
<i>Fscb</i>	Fibrous sheath CABYR binding protein	11063	2970
<i>Hdgfl1</i>	HDGF like 1	11018	2925
<i>Iqca</i>	IQ motif containing with AAA domain	TBD	TBD
<i>Lelp1</i>	Late cornified envelope-like proline-rich 1	TBD	TBD
<i>Spata24</i>	Spermatogenesis associated 24	TBD	TBD
<i>Tmem97</i>	Transmembrane protein 97	11025	2932
<i>Eddm3b</i>	Epididymal protein 3B	10345	2715
<i>Lrcol1</i>	Leucine rich colipase like 1	TBD	TBD
<i>Tmem114</i>	Transmembrane protein 114	TBD	TBD

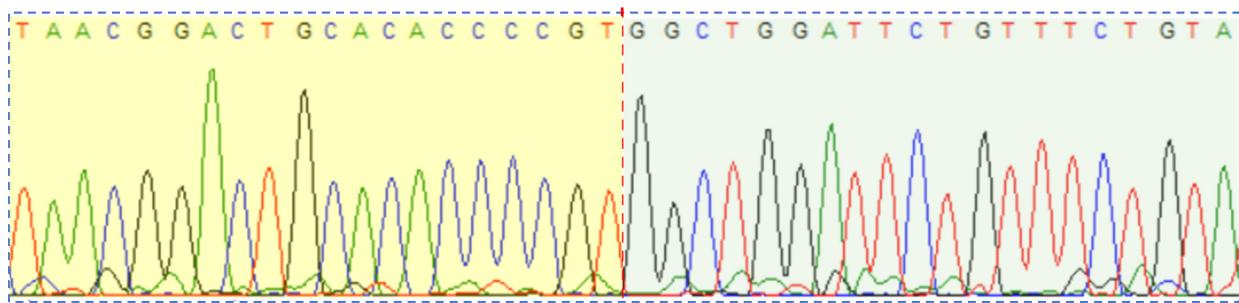
Supplementary Table S6. Additional information about the 13 mouse genes analyzed in this study. The presence of transmembrane (TM) domains and a signal peptide was predicted using TMHMM and SignalP, respectively.

Gene symbol	NCBI UID	MGI ID	Chromosome	No. of TM domain	Signal peptide	Human orthologs
<i>4921507P07Rik</i>	70821	1918071	6	0	N	<i>C7orf31</i>
<i>Allc</i>	94041	2136971	6	0	N	<i>ALLC</i>
<i>Cabs1</i>	70977	1918227	5	0	N	<i>CABS1</i>
<i>Fam229b</i>	66337	1913587	10	0	N	<i>FAM229B</i>
<i>Fscb</i>	623046	3646964	12	0	N	<i>FSCB</i>
<i>Hdgfl1</i>	15192	1194493	13	0	N	<i>HDGFL1</i>
<i>Iqca</i>	74918	1922168	1	0	N	<i>IQCA1</i>
<i>Lelp1</i>	149018	1916582	1	0	N	<i>LELP1</i>
<i>Spata24</i>	71242	1918492	18	0	N	<i>SPATA24</i>
<i>Tmem97</i>	69071	1916321	10	4	N	<i>TMEM97</i>
<i>Eddm3b</i>	219026	2684921	14	0	Y	<i>EDDM3B</i>
<i>Lrcol1</i>	381667	2686525	5	1	Y	<i>LROCL1</i>
<i>Tmem114</i>	74720	1921970	16	4	Y	<i>TMEM114</i>

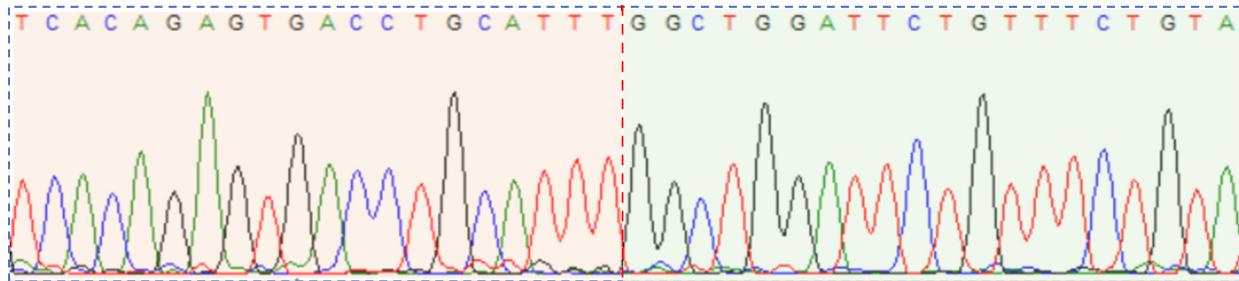
4921507P07Rik^{+/+} Upstream



4921507P07Rik^{-22195/-22195}

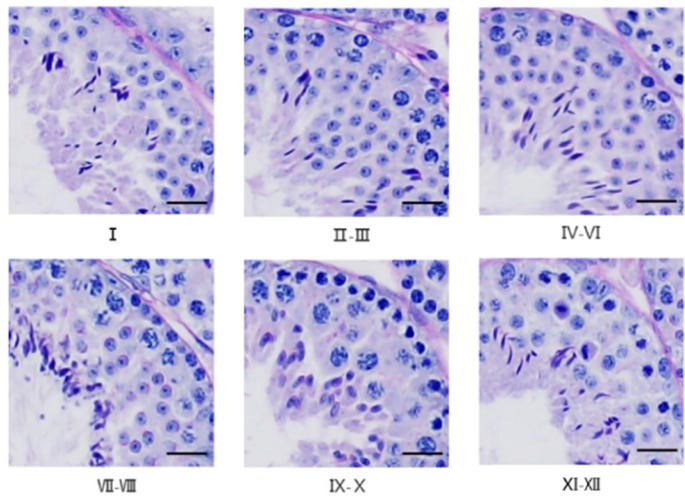


4921507P07Rik^{+/+} Downstream

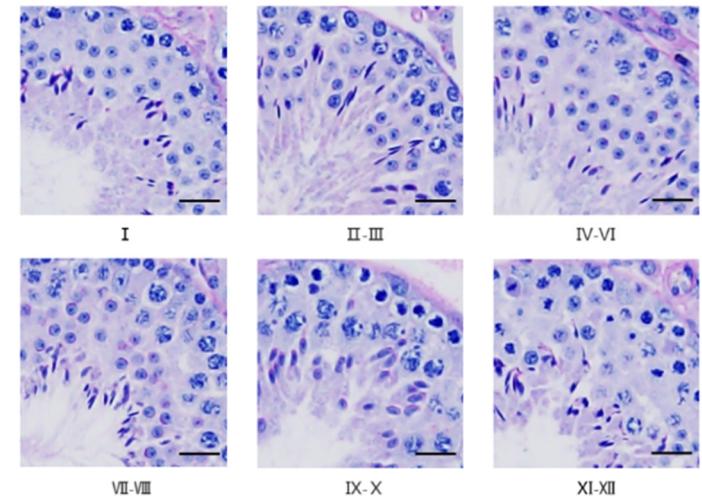


Supplementary Figure S1. Sanger sequencing of 4921507P07Rik wild-type and knockout alleles. The upper and lower graphs indicate the upstream and downstream sequences of the wild-type allele, whereas the middle graph shows the knockout allele. The sequences deleted in the knockout mice are highlighted in red. The regions immediately upstream and downstream of the deletion are highlighted in yellow and green, respectively.

(A) Het.

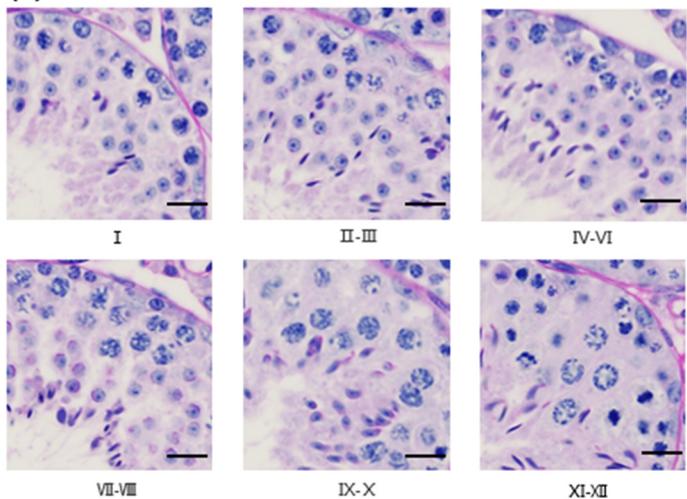


(B) Homo.

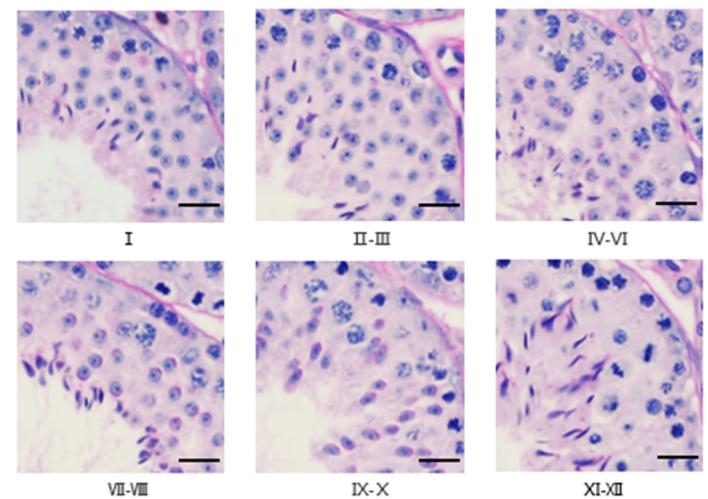


Supplementary Figure S2. Detailed analyses of spermatogenesis in **(A)** *A/Ic* heterozygous and **(B)** homozygous knockout mice. Scale bars = 20 μm .

(A) Het.

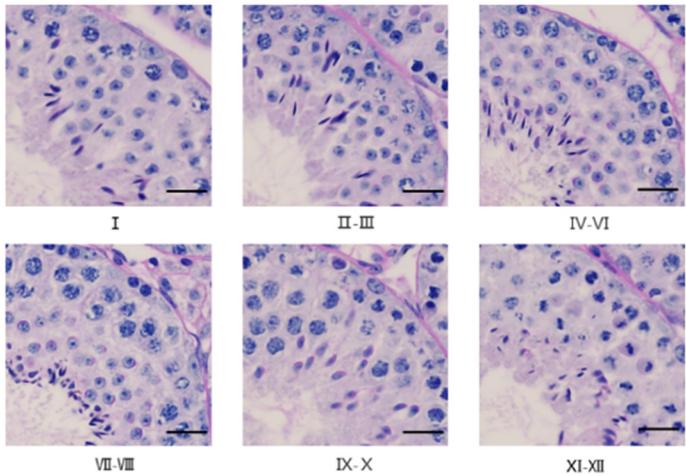


(B) Homo.

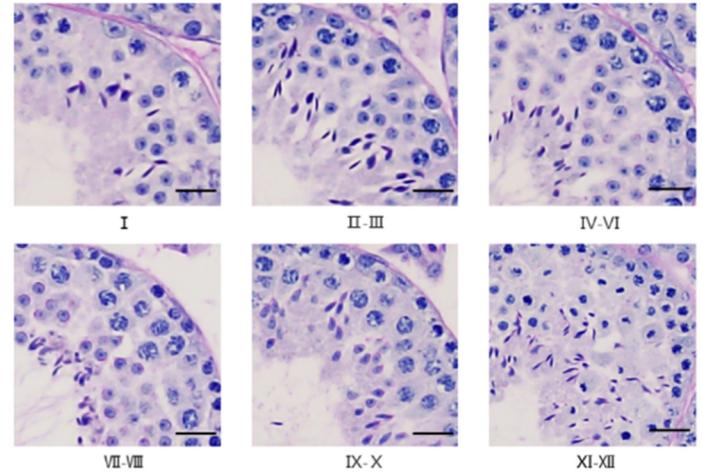


Supplementary Figure S3. Detailed analyses of spermatogenesis in **(A)** *Fscb* heterozygous and **(B)** homozygous knockout mice. Scale bars = 20 μ m.

(A) Het.

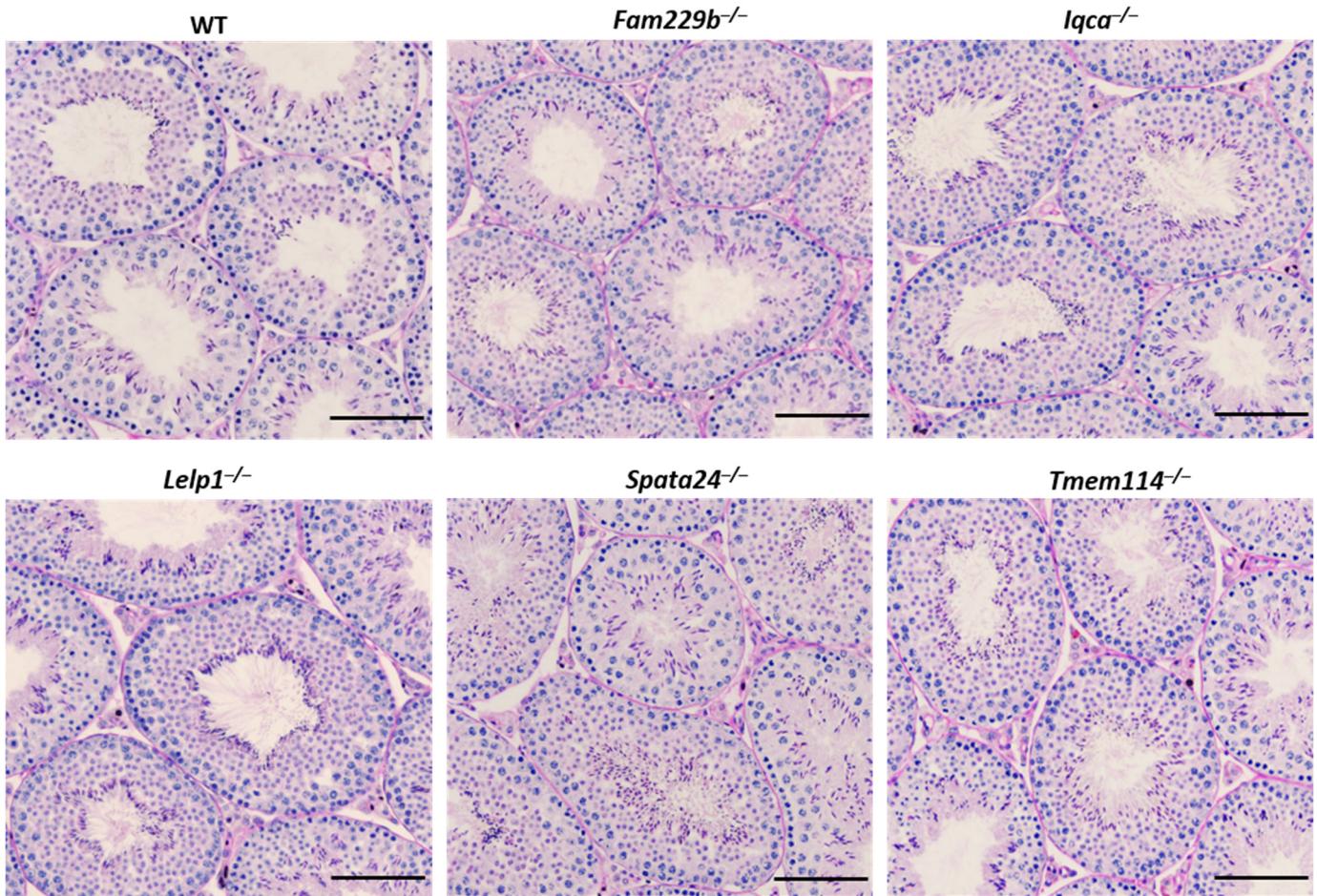


(B) Homo.

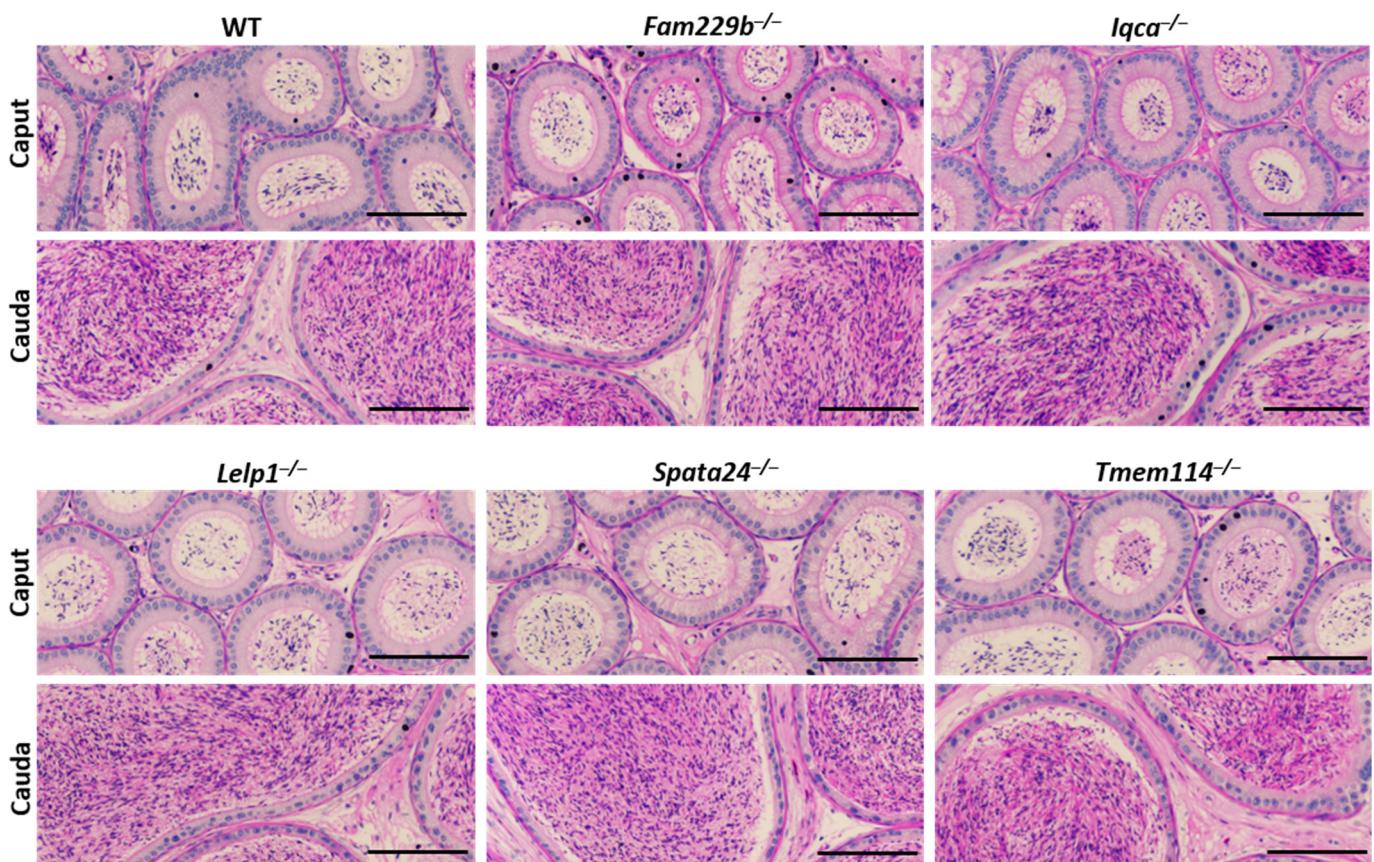


Supplementary Figure S4. Detailed analyses of spermatogenesis in **(A)** 4921507P07Rik heterozygous and **(B)** homozygous knockout mice. Scale bars = 20 μ m.

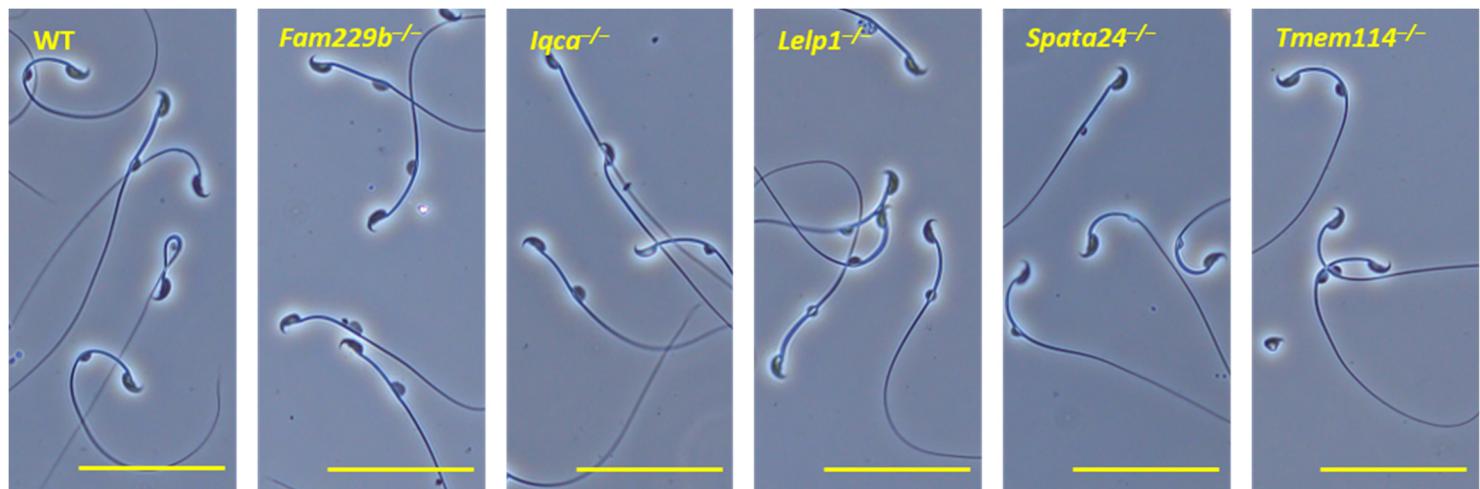
(A)



(B)



Supplementary Figure S5. Histological analyses of **(A)** testes and **(B)** epididymides in *Fam229b*, *Iqca*, *Lelp1*, *Spata24* and *Tmem114* knockout males. Scale bars = 100 µm.



Supplementary Figure S6. Morphology of spermatozoa in *Fam229b*, *Iqac*, *Lelp1*, *Spata24* and *Tmem114* knockout males. Scale bars = 50 μ m.

(A) 4921507P07Rik

Mouse	1	MEVIHGRPHCCRNLLEGADILSNTFYSNLHTPYTTIRPTASQARYQELREALPQCRLRWGADREYGGVLWVSLPEEHRPKCEPPRLMSKGHQHYGFGGEIWPKKLPIEQ	110
Human	1	MEVIHGRPYCERELEGADILSNTFYSNLHNPLQTIVTRPTASEDRYQELRESLQCRLPWGAEREYGGIIPISLPEDHRPKYEPFRVMGKGHQHYGFGGEIWPKLVEO	110
Mouse	111	YYMTQNKSDVYGNDSLIPKPPNSAVREICSPXPYIEHPYHTHSRGSVFPTFTSFKDLYTGIKARTQQFPPTVPTKACDTIILKTRGNPYRYELLDFPMDSKKKALTW	220
Human	111	YYLTQNKSDVYGNDSLIPKPPNSTVGEICLXPYIEHPYHTHICRGAMFTFTSFEDLYTGIKARTQQFPPTVPTKAYDSTVILKTRGNPYRYELIDIPMDSKKKALTW	220
Mouse	221	PGQGVYYDFPFKEVEKNKPVFPKPKPKTFAPNNTNPWDTMSSAKDANIQRNLERSHWLTSYHDFTGLGPMSPLEDDYHEKEIAELTGGIGDFQPQEKFHPAIFTPRP	330
Human	221	PGQGVYYDFPFKEVEKNKPVFPKPKPKTFAPNNTSWDPICSAKDANIQRNLERSHWLTSYHDFTGLGPMDPLEDDYHEKMAELTRMIGDFBEPQEKFHPVFPFPRP	330
Mouse	331	LDGRIARLTQNCRPLEATIVQIPP-PCPDCTPRVLCAFHTFIPSAPIMAMNNNLLSGITHKNQDVEEKIKEEGQGMSTCPLTCYESKDLTSYDVSFPKITDTKKTDD	439
Human	331	LDGRIARLIONRNRSEATIVQRRRSCPDCTPRVLCNFHTRVPSKEMVALSDNIPAGVTHKNODIEEKIIIEECSSLTYELPSCTKDLTSYDVKPFPKITDTKKTDD	440
Mouse	440	LYWRQOLEMKPLBISCSKSNHYDYEPLKSAYRDYAMCENPVRLSKSNILQNKTDIADFTFDNFLSKPEF-LGMNMEESNEETRELLDWIPRAVGPKHHHSNIRNLNFSK	548
Human	441	LYWRQOSLKTQETPYCPDPDHWTBYENLKSPLRDQYNMCEDEVSLSKESVLQNKQDTEAFTLEHFLSKPEEEFLNMENNEETREVLGWIPRAVGPKPQTNLLELKNFSK	550
Mouse	549	SMAQKRHLNSIOPQQEOKDLRDKLQGMRHOFFGYNGHHFYN	588
Human	551	TGAQKRHKSILEDHKDLRDNEHSGMKHQFYGHNSYYFYN	590

(B) ALLC

Human	1	-----MDMASESVGGKILIFATDDFFPAENLIKSDSFCFKEHEYTEFGKWMGWETRRKRIKGHDWCVLRLGIQGVIRGFDVDVSYFTGDYAPRVS	91
Mouse	1	MTDTPKEGKLTRFLDFTQLIDLASECVGGKVLIFATDDFFPAENLIKSDSPCFKEHEYTEFGKWMGWETRRKRIKGHDWCVLRLGIQGVIRGIDVDISYFSGNHAPRMS	110
Human	92	IQAANL-EEDKLPPIPERGTRTCAATPPEEFAIAELKSDDWSYLVPMTELKPGNPGASHNYFLVNSQQRWTHIRLNIFPDGGIARLRLVEGTGQKDWTADPKEPADLVA	200
Mouse	111	IQAANLSEEDTMSNIPPPRGVRMGAAATPPEEFAITELKSHSWDYLVPMSKELKQGDPSSSHNNYFVNSQQRWTHIRLNIFPDGGIARLRLVEGTGQDWAALDSTEPVVLVA	220
Human	201	IAFGGVCVGSNAFGHPNNIIGVGGAKSMADGWETARRLDRPFILENDENGILLVPGCEAWFRLAHPGVITRIEIDTKYFEGNAPDSCVKDGCLLTQEEEAIVRQK	310
Mouse	221	IAFGGVCVGSNAFGHPNNMIGVGEPKSIAADGWETARRLDRPFILEASENGILLVPGCEAWFRLAHPGVITIEIDTKYFEGNCPNSCKVDGCILTTLEEDDMIRHN	330
Human	311	ILPAHKWKFLLPVTKLSPNQSHLFDSDLTLELQDVITHARLTIVPDGGVSRLRLRGFPSSICLLRP-REKPMLKFSV--SFKANP	391
Mouse	331	NLPAHKWKSLLPVTKLIPNONHLDSDLTLELQDVITHAMITIAPDGGSVSRLRLKGFPSSICLLRPLREKPLLRESLKTGERANL	414

(C) CABS1

Human	1	MAEDGIPKIYSHPPTESSKTPTAATIFFGADNAIPKSETTITSEGHDVHTSVNEYMLSDFSTTIDNKLAKKEKLKSEDDIMGTDIFKSTTHLQEITSLTGTINSITRDS	110
Mouse	1	MAEDGSPKIYSPRPRDNSKTPTEADIFFGADNTIPKSETTITSEGHDVHTSVNDCTPDGDFSTTVN-KLPTKEKLKLEDDIE-GCLKLTTLPEKEITPTEPNSKPKGS	108
Human	111	ITEHFMPVKIGNISSPVTIVSLIDFSTDIAKEDILIAITDTGDAEISITSESGTLKDSSAGADAPAFFRKDEADMSNNSSIKSNVPADEAVQVTDSTIPEAEIPPA	220
Mouse	109	ITENFIPVKIGNISSPVTIVSLIDFSSNTAKEDIBLITIDTGEKEVVPPTERSGTLEDSAADEASGFPDESTEVDVP---SSATSDAPDGAQVQVTDSSFSPPEAGVPPS	215
Human	221	PEESFTTIPDITALEEEEKITEIDSVLEEDTSAVATLTDSE-KFIFTVFEITSAEIKDKREDTLLDEETEGASINMERDTANEAEHTSVLLTAVESRYDFVVPASI	329
Mouse	216	TEKEVTTIPDITINIAEENVTEIKIVSEDRKTVTKLSDSEEKFIFTVFEITNSAEIKDKNDVDEPL-NDEESTDGANDEMEKETASEAEHVAVLLTAVESRYDFVITASE	324
Human	330	ATNLVEESSTEE-DLSETDNTETPKITEPFSGTTSVLDTPDYKERTSTTETDIFELLKEEPPEFMI	395
Mouse	325	TDNVMEESHVNNTDLPENETTESVTNVTEELPSVTSIVDTLKDKEIISTNSGLFKLLKEEPPEFLMM	391

(D) FAM229B

Human	1	MPPQFGTQPRRFPVEGGDSSIELEPGLSSSAACNGKEMSPTRQLRRCPGSHCLTIDVPTVYATIRKPPAQSSKEMHPK	80
Mouse	1	MPPRFGTQPRRFPVEGGDSSIELESGLSSSACTGKETSPNROLRRCPGSHCLTIDVPTVYATIRKPPAQSSKEMHPK	80

(E) FSCB

Human	1	MVGKSQQTDVIEKKKHMAIPKSSSPKATHRIGHTSGSKGSYSAKAYESIRVSELQWTKRKHGQEMTSKSLQDTIVEEKKEVVLVEETVVPEEKSDADREAAIELPE	110
Mouse	1	-----MEECEEPEPISLGRQEYRRRRPSQPMVDKSQQTEIHEKRKAMASVQPPAKATHSIGNIPGSKDNYSRKEYESLRLSSQLQKLMKRK	90
Human	111	SVQDVEIPPNIIPSVQLKMDRSQQTSRTGYWTMMNIPPEKEVKDEEQQTYSFSESEIVVISREDSSSTSKEALKHKGSSGKF--ASEHPEFQPATNSNE-EIGQKNISRTS	217
Mouse	91	HVQDMTDKSLQTEPIVEEKVEVIFIDKTLKLENTAGVGEIAPLQPSIHEVEIPT-SRTHSLIDRSQQTSCTGDWSLIVICPKEVKDEQQTYSFSELEIIIRSIPGSS	199
Human	218	FQETKKGPFVLLDEPREFEVTPVVOQGSAVKKVASAEIEPPSTEKFPAKIQPLVVEATAKAPRPAEEHTHCVQPSSTEETPDRDAAATAVBNSTKVQPPAEEAPLV	327
Mouse	200	MTKSKEETIPIACEDPVE-INGSLEIIVLSPPELPDVMMSFTEGE-ISGEIQALSGNEATVKGLFLTEIPIQCAPSPAETSAARTATTAKDWDIOAPPADKLSSV	307
Human	328	EPPAECIOPPSAEEESPVELLAELPPSADESPSEPPAELPPPAEKSPSVELGEIRSPSAQKAPIEVQPLPAEGALEEAPAKVEFPTVEETLADQPLLPEEAPREA	437
Mouse	308	EPPADISPTLQVGALSDKPSDQQYQPGTEMAPSELPVED-LDFSE----EVIEKVQALTTDSM-LEDLGIAESTIAETSGKVQHPLSEITSKEVPAEVHFPIAADF	410
Human	438	RELQLSTAMETPAEEFAPTEFQSLPKETTAEEPSAEIILLAETTEPPADETPAFAKSPSSETSPEAHAEVQSPLAETTAEASAEIQLLA-IEAP-ADTPAFAQSP	545
Mouse	411	ESAILINEK-FATDEVFEEYKPIIEEVSAKDTAECVPPSAEADSEEEVAPSEVLPSTEQGTVBDLTAEVLISTPEEGPTVPPQPTEEGAEVPPPELSECPAEPVPA	519
Human	546	LSEETSAAE-EPAEVQSPSAKGSVIEEAPLELQPPSGEETTAAEA-SAIQLIAAT-EASAEPPAEEVPPPAEEAAPAEVQPPAEEAEVQPPAEEAEVQPPA	651
Mouse	520	PAEEAEPVLPPEEEAEPAEVPPPLTEEGPAAEVPEPLTEEGPAAEVPEVPLPTEEGPAAEVPEVPLTEEGPAAEVPEVPLPAAEEABTKVPSPA	629
Human	652	EEAPAEVQPPPAAEAAEPAEVQPPPAAEAEAEVQSLPAEETPIETTLAAVHSPPADDVP--AEEASWDKHSPPADLLTE-EHIGEAS-AEVSPPPSEQTPEDEALVENVS	757
Mouse	630	EKGSAEVSPPPQTEEGPAAEVPPPAEEBTEVPSSSAEGGSSEVLPPTAERPEEAPPATEEAPAEVPEVLPATEEAPAEVPEVQSAABEGLAEVBPPPTESPTHD----VP	734
Human	758	TEFQSPQVAGIEAVKLGSSVVLGEAKREEVSKINSVLKDSLNTNDGQAPTLEIESVPHIELKQREHEL-----	825
Mouse	735	TFVQVPOAKESPGQVL---PLSGESTAEEASAQVQPPSFKAPELSPLEEVETKHLNLPFEVQBLPTEDIAIGVPAESQALPADENPAREDVTETQPSSEFGAPIAEN	841
Human	825	-----	825
Mouse	842	PIEAPLPASEADTGREDSAVHPSSLAFTDEAPAEIQLQTDDIPTEMSPVENQPLPAEEGFPVVSEEEATAEVRFPLSEGAPAQEAETVAAQLTSVEESPKRASVDQ	951
Human	825	-----	825
Mouse	952	LSPETPVEESPVGVLPLKTNEMTMQEFRVEKMPAEDPLPPSEQTPADQVLLKEHRLSQVADISEKELESTTLSDKMSEGIDSVPEDVSGTKDDQISTFKIEGTIKIELK	1061
Human	825	-	825
Mouse	1062	N	1062

(F) HDGFL1

Human 1 MSAYGMMPMYKSGLVFAKLKGYAHWPARIEHMTQ[NRYQVFFFTHETA[SEKRLFPYKECEKEFGKPNKRGRFSAGLWEIENN[TVQASD--CPLASEKGSGDG[WPE 108
Mouse 1 MSCFSRSKYKTGLVFAKLKGYAHWPARIEHVAEANRYQVFFFTHETALLGRHLFPYEESEKEFGKPNKRGRGFSEGLWEI[EHDPMVEASSLCS-EEDQSYTEDPGLA 109

Human 109 PAAEGGDDKPTHAGGGDELGKPDDEKTEEEK[ELKRSAGD--PPEDA[P[KRPREAAPDQEEAEAE[RAAB[A[RAA[AATAVDEESPFLVAVENGSAPEPGLVCEP 216
Mouse 110 EEP[ELGQELVQELEPEFMPELEAPEMPEPETCEQEPQPAWDLDAVEE[PLTKAEPGDOQA[HVQEKHPEVAEAEAEAEAEAEAKAEV[EPGSLKRS[AEDEP 219

Human 217 PQEEEEE[REEEEV-[DEPASQW[HRAEPGGGRDDSL----- 251
Mouse 220 HQCLKRPRAAPG[LEMEPAEEREAACPFVEEPQDAQEQLPPL[EEATEKAVQGLIVGEIEGL 283

(G) IQCA

Human 1 MSNAMYNKWMWHQ[QEA[GLLDKEPKMIEPORNQVFIFQTLATTFVHYVQIFRNLENVYDQ[VHPQKRILIRKVLDGVGMGRILELKNE[VELE[TEFH[FDDILQDLKL 110
Mouse 1 MSNLMYNKMNHQ[QEA[NSLLDKEPKMIEPORNQVFIFQTLATTFVHYVQIFRNLENVYDQ[VHPQKRILIRKVLDGVGMGRILELKNE[VELE[TEFH[FDDILQDLKL 110

Human 111 APQQLDIPIPYFLKE[LEVIKGREKILA[QIA[SDGIDTSMDKYPVKSIPFDEAVKLIQIAERARQGRRLALFMKQIYLQEYRAQSKMLGKKV[DIWAALRIQKVWRR 220
Mouse 111 SPQQLDVPIPYFLKE[LEVIKGREKILA[QIA[SDGIDTSMDKYPVKSIPFDEAVKLIQIAERARQGRRLALFMKQIYLQEYRAQSKMLGKKV[DIWAALRIQKVWRR 219

Human 221 FHQRKETEK[REEEEM[FLGMNEPPLFNEVSATVIQAEKVDRLNNEVOLKHEEDYREALVTIKNDLKLIEGVDIKENLQDQIRHWFIECRNLTGTFPDYD[DV[EE[GGSAIIF 330
Mouse 220 FHOCKKTVK[REEEEM[FLGMNEPPLFNEVSDAIVOSKQVNTLDEVOLKHEEDYOEALVNIKE[DLKMLEGPDIKEHLDQDQIRHWFIECRNLTGTFPDYD[DV[EE[GGSAIIF 329

Human 331 SDKTIQOE-----EDEKKMSPSLFIPAMKECNAYKEIWMRKD[ESWNFSQDYDPEL[KEEKRKELQSEIRIO 398
Mouse 330 SNKTP[EVOMGDIIATQEEEELK[KKKKKEDKENKGKKKEKEKKDEDEWKMSPSLFQ[LMEEGNSLYD[IWLNKDESWNFPQDYDPEL[KEEKRKELEMEIRVQ 439

Human 399 VDELMRQELKNLKLA[VI[RER[RPVACK-KKD[KGKKKKKE[KA[KD[KDLTADRTIESLYKE[ELVEEGLLIQALKVNLSDYIGEYSYLGT[LRQV[SIEPMPSL[LDVRQLI 507
Mouse 440 VDELMRQELKNLKLA[VI[RER[RPVACK-KKD[KGKKKKKE[KA[KD[KDLTADRTIESLYKE[ELVEEGLLIQALKVNLSDYIGEYSYLGT[LRQV[SIEPMPSL[LDVRQLI 548

Human 508 TLYG[PLGSA[VPHE[APLVKSLLAGPSVGK[MLVHAIC[ETGANLFNLSSNIAGKYPGKNGLOMMIHA[VFKVARQLOPSVW[IE[DT[TEKTFYKKVPAEKMN[EPKRL 617
Mouse 549 TLYG[PLGSA[VPHE[APLVKSLLAGPSVGK[MLVHAIC[ETGANLFNLSSNIAGKYPGKNGLOMMIHA[VFKVARQLOPSVW[IE[DT[TEKTFYKKVPAEKMN[EPKRL 658

Human 618 KKHLQ[QILKLLKPD[DRILIVGTTRPFDAELOS[FCVYQKII[LVPRPDYASRYVLW[KIIERNGGV[LSALNVSCLA[KVTDGF[QGHIVEVVKGVLTDQ[IRRO[HKPLT 727
Mouse 659 KRYLPKLLKLLKPD[DRILIVGTTRPFDAELOS[FCVYQKII[LVPRPDYASRYVLW[KIIERNGGKLTNSLNISCLSKVTDGF[QGHIVEVVKGVLTDQ[IRRO[HKPLT 768

Human 728 AVEFITAIISMN[PVI[REEEESFKNWYAKTPLGKKR[AITG[ESTERAKDKGKKR----- 781
Mouse 769 AIEFITMMTNMN[PVI[REEEESFKNWYAKTPLGKKR[ISLTVG[KEKEAKDKGKKGKRGKKKK 829

(H) LELP1

Human 1 MSSDDKSKSNDP[TEPKNCDPKCEQKCESKCQPSCLKKLLQRCFEKOPWEK[APPKCLPCPSQSPSS--CP[COPCTK[CP[PKC[SSCPHAC[PPP--CP[PE----- 98
Mouse 1 ---MSSDDKSKSNDP[TEPKNCDPKCEQKCE[TCQPSCLNKLLQRCSEKQSLDKC[PSNP[CPCP[CPLVCQSC-CSTPTSP[CLC[PLCSP[RC[SGT[ACCP[PSCP[QKGCVK 106

Human 98 ----- 98
Mouse 107 PCPPKCPSP[CLPRK 120

(I) SPATA24

Human 1 MATPLGWSKAGSGSVCL[QDQLRDVIESQEELIHQLRNVMVLODENFVSKEE[QAVEKKLVEEKAHAKTVLLAKEEELKQFALGEVEVLSKQLEKEKLAF[EKA[LSSVK 110
Mouse 1 MATPLGWSQGGGSVCL[QDQLRDVIESQEELIHQLRNVMVLODENFVSKEE[HEI[EKKLVEEKAHAKTVLLAKEEELKQFALGEVEVLSKQLEKEKMAFEKA[LSSVK 110

Human 111 SKV[QESSKKDQLITKCNEIESHIKQEDILNGKENEIKELQ[QVISQ[Q[QI[FRNHMSDFRIQKQ[Q[SYMAQVLDQHKKAS[GTR[QARSHO[HEREK 205
Mouse 111 SRV[QESSKKDQLITKCNEIESHIKQEDILNGKENEIKELQ[QVISQ[Q[QI[FRNHISDFRIQKQ[Q[SYMAQVLDQHKKAS[GTR[QARSHO[HEREK 205

(J) TMEM97

Human 1 MGAPAT[RRC[VEWLLGLYFISHIPI[FLIDLQAVL[RELYFVEFRNLLKWYKEFKDPLLQEPFWFKSFLFCELVFQLPFFPIAYAFLGSC[WRIPAI[IYSVHIMTT 110
Mouse 1 MGALAARRC[VEWLLGLYFISHIPI[FLIDLQAVL[RELYFVEFRNLLKWYKEFKDPLLQEPFWFKSFLFCELVFQLPFFPIAYAFLGSC[WRIPAI[IYAAHTTT 110

Human 111 LIPILST[ELFEDFSKASCFKGQ[RE[ELH[ERLTLV[S[VYAPYLLIPI[ILLI[FLMLRS[PYYKYE[EKRKKK 176
Mouse 111 LIPILY[ELFEDFSKAVAFKGQ[RE[ELH[ERLTLV[S[VYAPYLLIPI[ILLI[FLMLRS[PYYKYE[EKRKKK 176

(K) EDDM3B

Human 1 -----MASSLKingTLL[LLCILCIL[LLVQSKEVSP[RE[FMKCHYLSPSRE[RE[YKCDVLMRENELKDKSSHMP[VI[ISWYKIEHIC[TSDNWMDRFRNAYVWV[CNPLKVK 104
Mouse 1 MSLVPALMSLKA[ALLL[LLCQHSLIAQST-[SRQFMEHHLSPNKM[SDVNCVLM[TDK-AV[KP[LSHMP[VI[MTWYKIEHIC[IGSNWDRYK[MYI[ACTEIKVIR 107

Human 105 CHQENSKNSYTESRSFNYIEFHCSMDGYVDSIEDL[RMV[EPIGN 147
Mouse 108 CQEWLSK[NR[YTERRSYSSVQFHONADGYVDSIEDIRALEPIL- 149

(L) LRCOL1

Human 1 MAGPGWTI[LL[LL[LL[LL[LL[LL[GSMAGYGPQKKLNL[SHKGIGEPCRRHEECQSN[OTINSIAPHTLCTPKT[FLQCLPWRKPNGYR[SHDSECOSCCV[RNNS-PQELO[TPQSV 109
Mouse 1 MSVSVWP[LL[LL[LL[LL[LL[LL[WAVPTFQDKNTRV[SAYKGIGE[CRNNSECQSD[COVINSI[NEQKF[ISQT[FL[EE[TECHSNC[IRTSSNPDRF[CSKTI 110

Human 110 FMOCPVWRKP[NG[DE[CSH[OCHSOCC[Q[REYSPF-RCI[PRTG[IL[QCLPL 159
Mouse 111 FMOCISWRK[PEGA[Q[HE[ECWD[CC[PL[SEN[SPSSH[CTK[RTG[LL[AD[CLPV 161

(M) TMEM114

Human	1	MRVHLGGLAGAAALTGALSFVLLAAAIGTDFWYIIDTERLER	TGPGAQDLIGSINRSQPEPLSSHSGLWRTRVQSPECTPLMNPFRLENVTVS	SSSRQLLTMHGTFVILL	110
Mouse	1	MRVHLGGLAGAAALTGALSFVLLAAAIGTDFWYIIDTERLER	SSQRMRDQ-GPANRSQQEPLSSHSGLWRTRVQSPECTPLMNPFWQENVTVS	SSSRQLLTMHGTFVILL	109
Human	111	PLSLIILMVFGGMTGFLSFLLQAYLLLLTGILFLFGAMVIIAGISVYIAYSAAAFREALCLLEEKALLDQVDISFGWSLALGWISFIAELLTC	AAFLAAARELSIRRRQD	220	
Mouse	110	PLSLIVMVFGGMTGFLSFLLRAHLLLLTGILFLFGAMVIIAGISVYIAYSAAAFREALCLLEERALLDQVDISFGWSLALGWISFVSELLTGVV	FLAAARALSLISQRQD	219	
Human	221	QAI			223
Mouse	220	QAI			222

Supplementary Figure S7. Alignment of mouse and human peptide sequences encoded by each gene. Dark regions indicate identities between mouse and human sequences. **(A)** 4921507P07Rik. **(B)** ALLC. **(C)** CABS1 **(D)** FAM229B. **(E)** FSCB. **(F)** HDGFL1. **(G)** IQCA. **(H)** LELP1. **(I)** SPATA24. **(J)** TMEM97. **(K)** EDDM3B. **(L)** LRCOL1. **(M)** TMEM114.

Cabs1

Wild-type	MAEDGSPKIYSRPPRDNSKTPTEADIFFGADNTIPKSETTITSEGDHVTS . . LKEEPDDLMM*
Mutant	MAEDGSPKIYSRPPRDNSKTPTEADIFFGADNTIPKSETTITSEGDHFSK*

Supplementary Figure S8. Amino acid sequences encoded by wild-type and mutant *Cabs1*.

Eddm3b

Wild-type MSLVPALMSSLKAWALLLLLCLQ...EDIKALEPIL*

Mutant MSLVPALMSSLKGPA~~SAPAVPAA~~*

Supplementary Figure S9. Amino acid sequences encoded by wild-type and mutant *Eddm3b*.