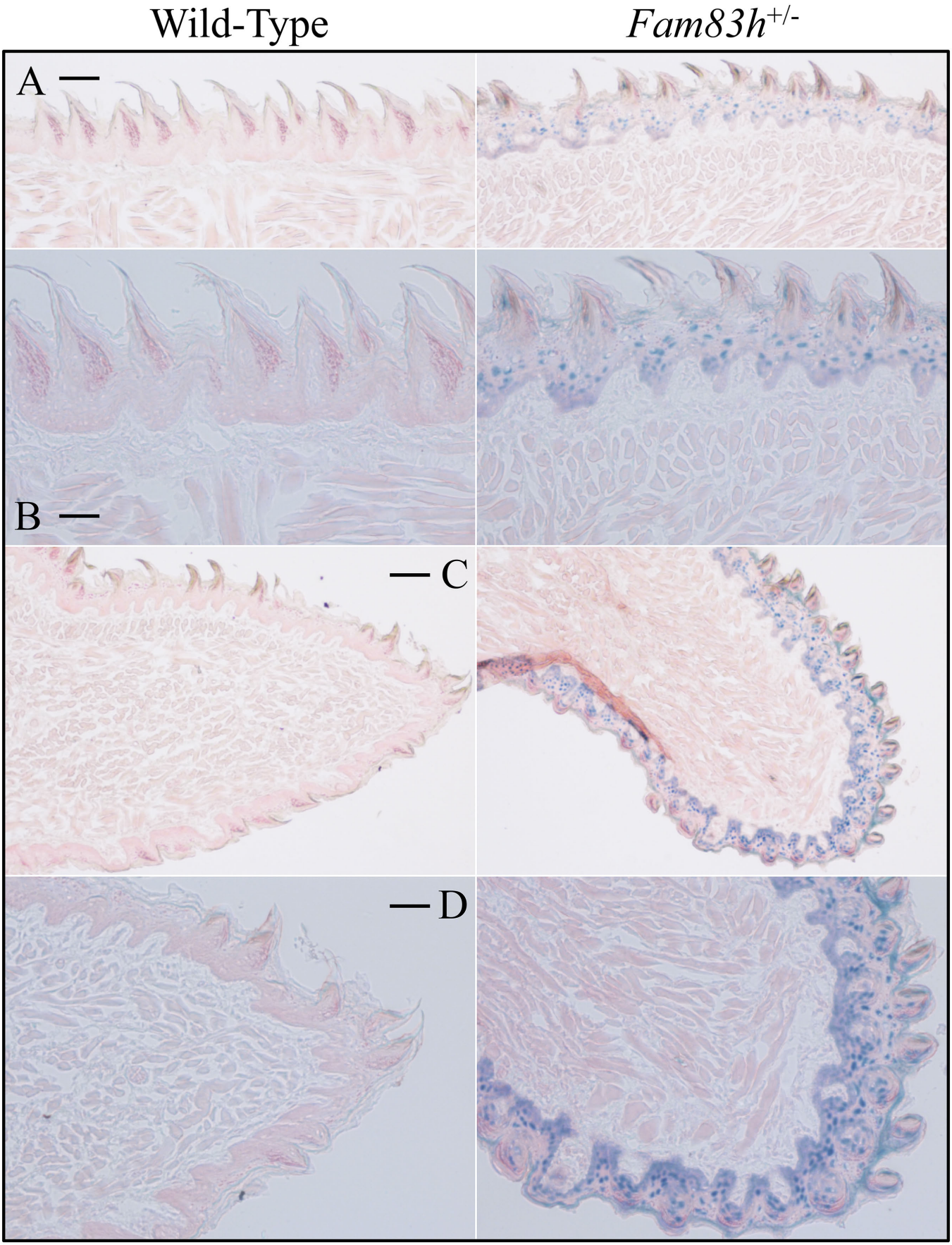

Fig. S20. *LacZ* Histochemistry of Tongue at 7-Weeks. The tongue dorsal epithelium stained positive. ***A:*** Scale bar 100 µm. ***B:*** Scale bar 50 µm. ***C:*** Scale bar 100 µm. ***D:*** Scale bar 50 µm.

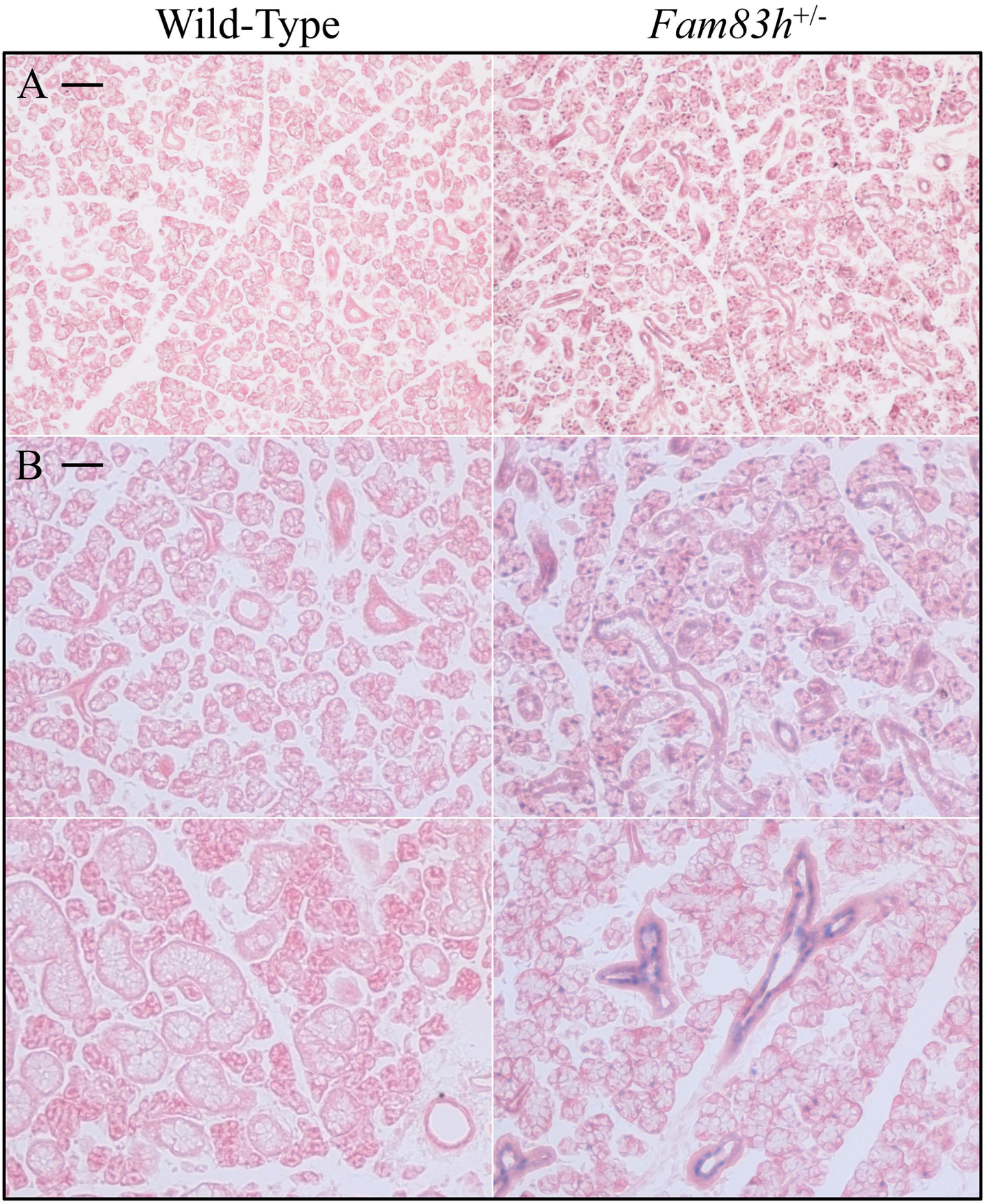

Fig. S21. *LacZ* Histochemistry of Submandibular Salivary Gland at 7-Weeks. The salivary gland duct epithelium reported positive. ***A:*** Scale bar 100 µm. ***B:*** Scale bar 50 µm.

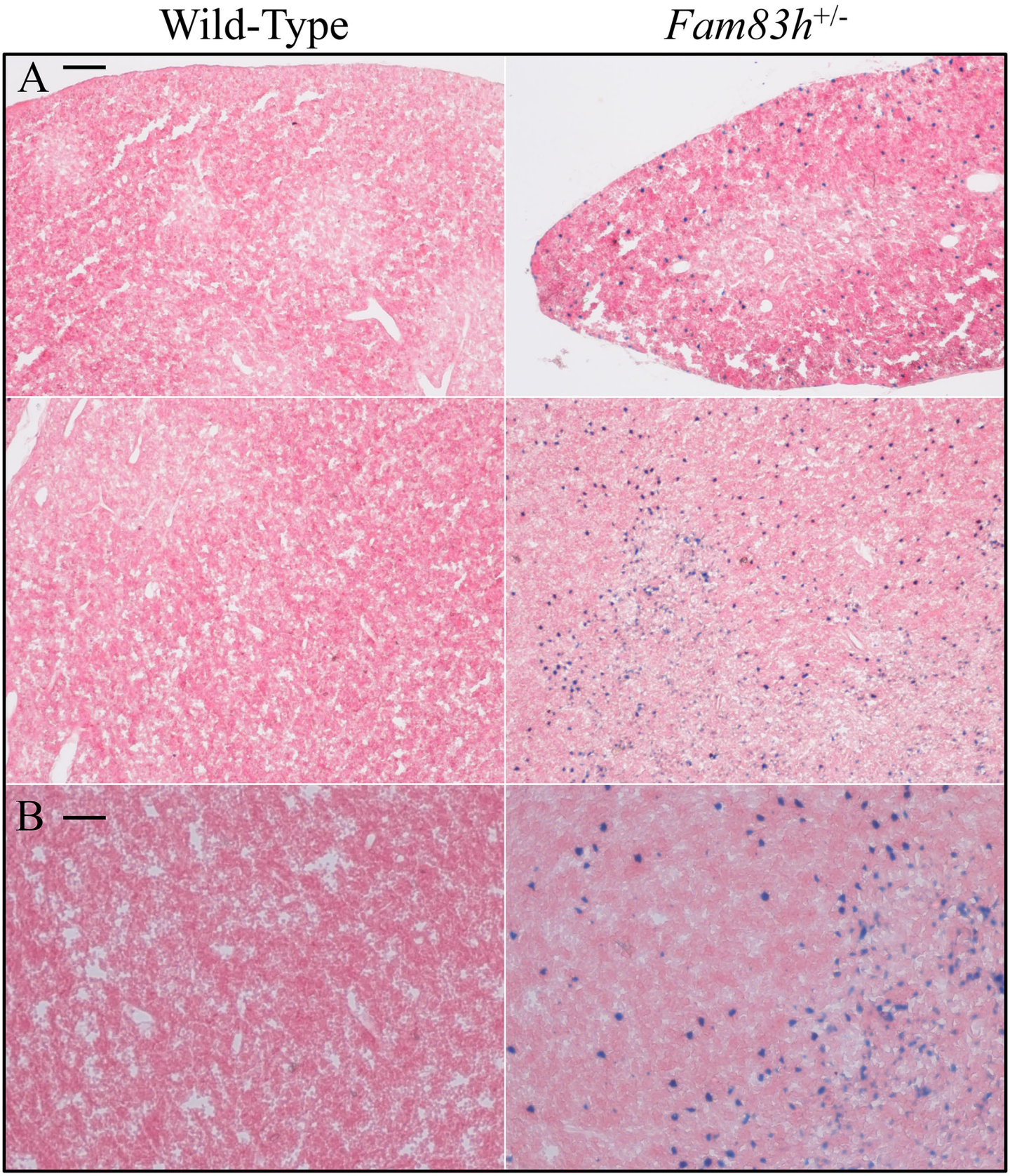

Fig. S22. *LacZ* Histochemistry of Thymus at 7-Weeks. Selected cells in the thymus reported positive. ***A:*** Scale bar 100 µm. ***B:*** Scale bar 50 µm.

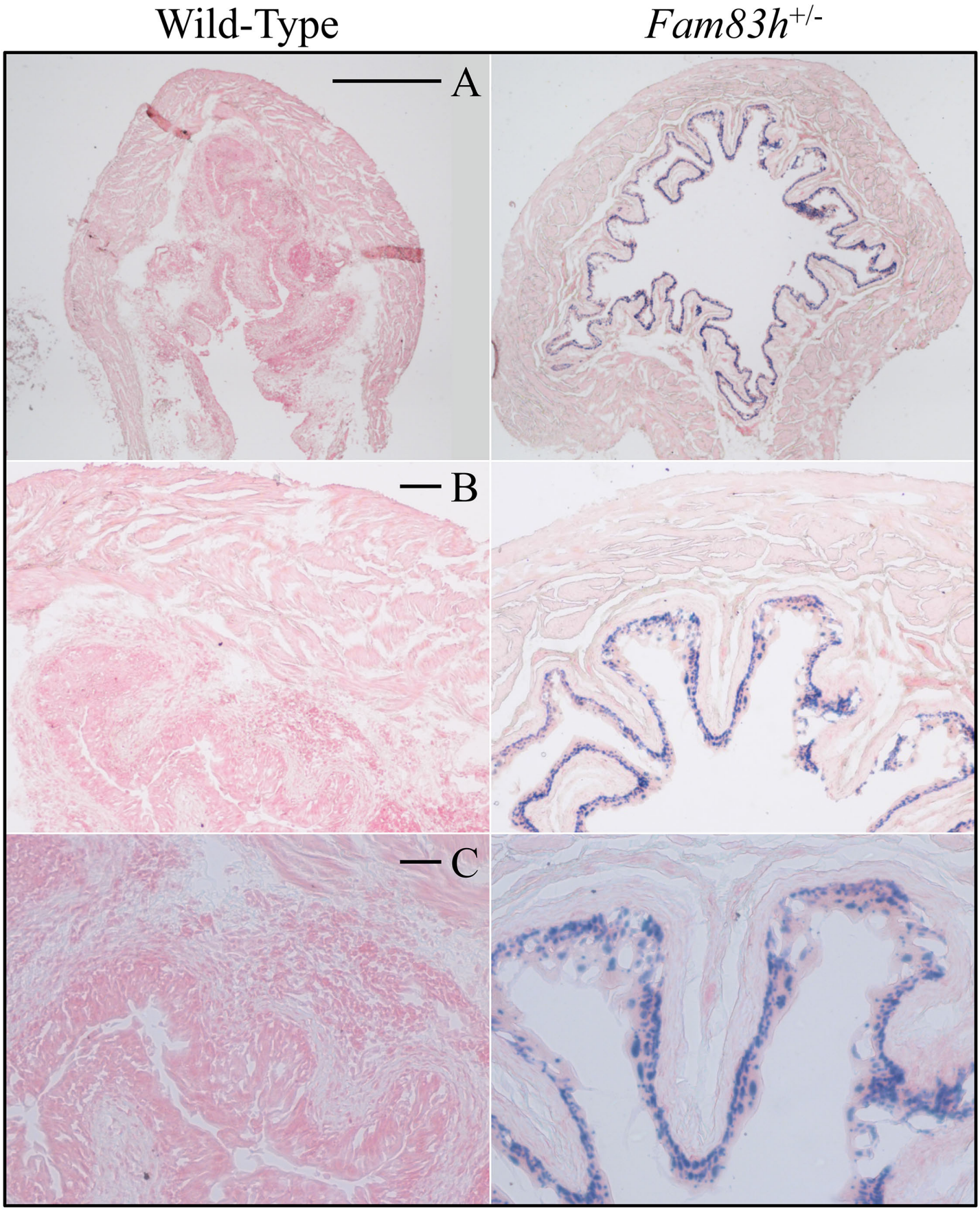

Fig. S23. *LacZ* Histochemistry of Urinary Bladder at 7-Weeks. The urinary epithelium reported postitive. ***A:*** Scale bar 500 µm. ***B:*** Scale bar 100 µm. ***C:*** Scale bar 50 µm.

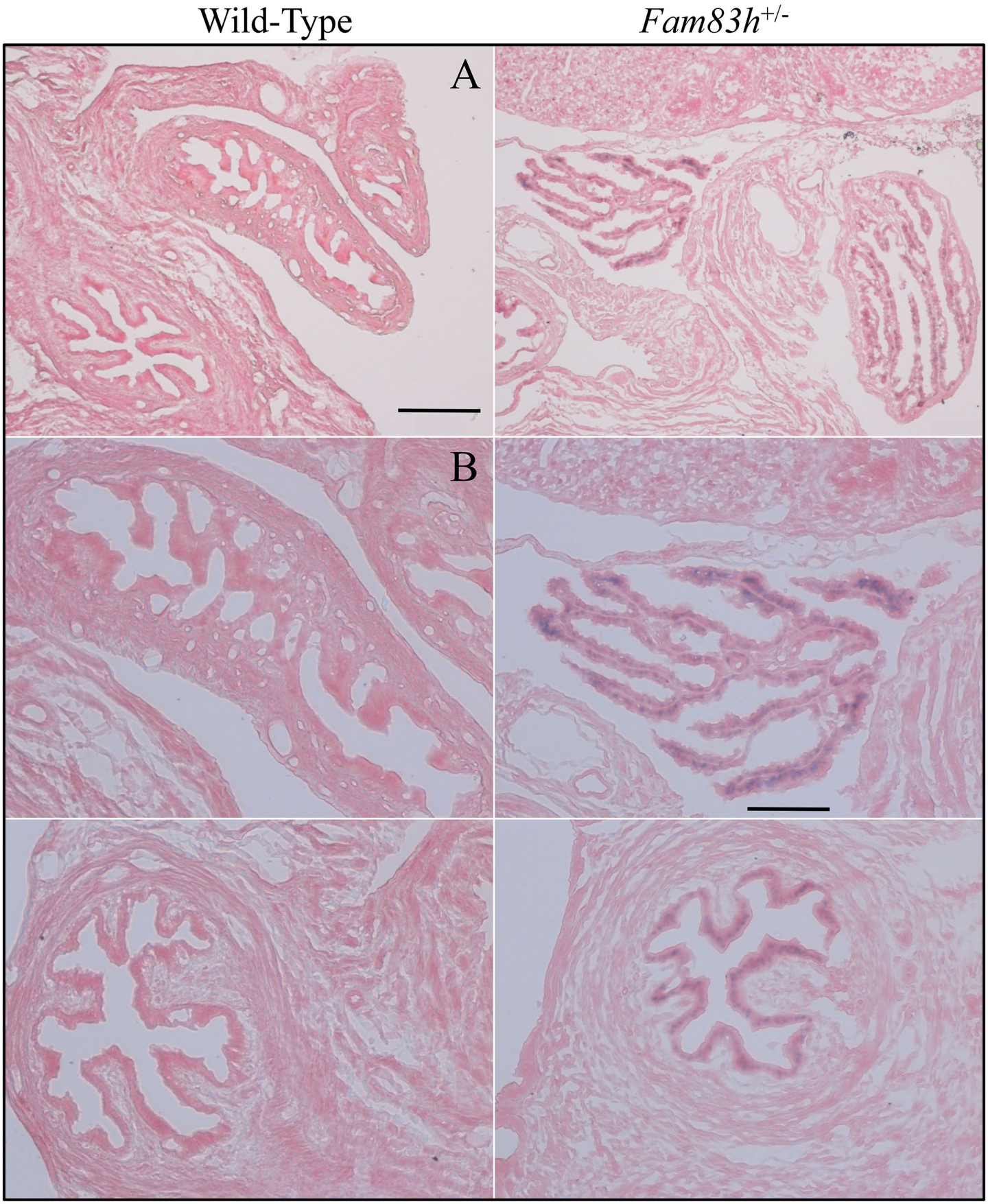

Fig. S24. *LacZ* Histochemistry of Oviduct at 7-Weeks. Columnary epithelium reported positive. ***A:*** Scale bar 200 µm. ***B:*** Scale bar 100 µm.

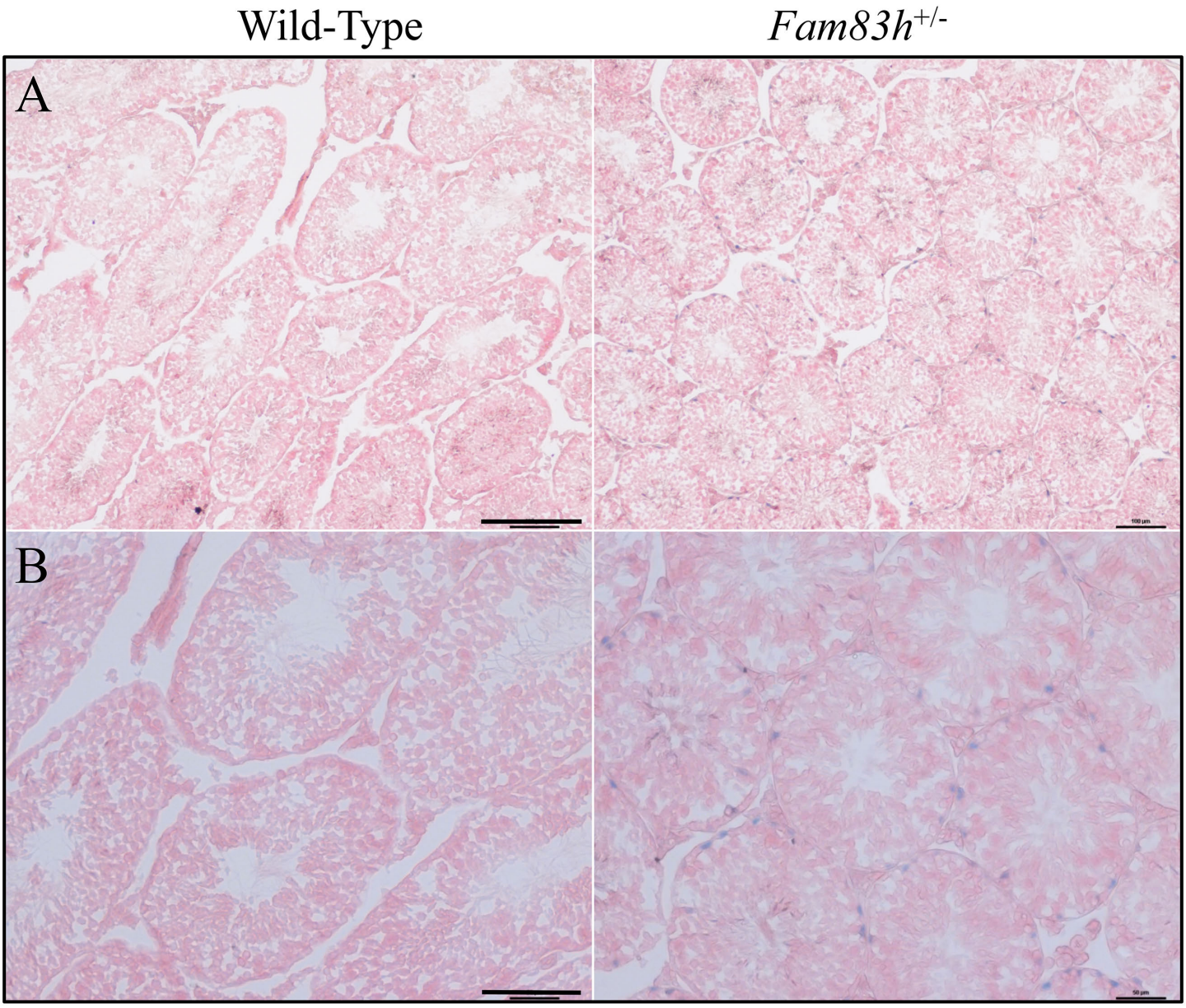

Fig. S25. *Lac*Z Histochemistry of Testis at 7-Weeks. Sertoli cells reported weakly postitive. ***A:*** Scale bar 200 µm. ***B:*** Scale bar 100 µm.

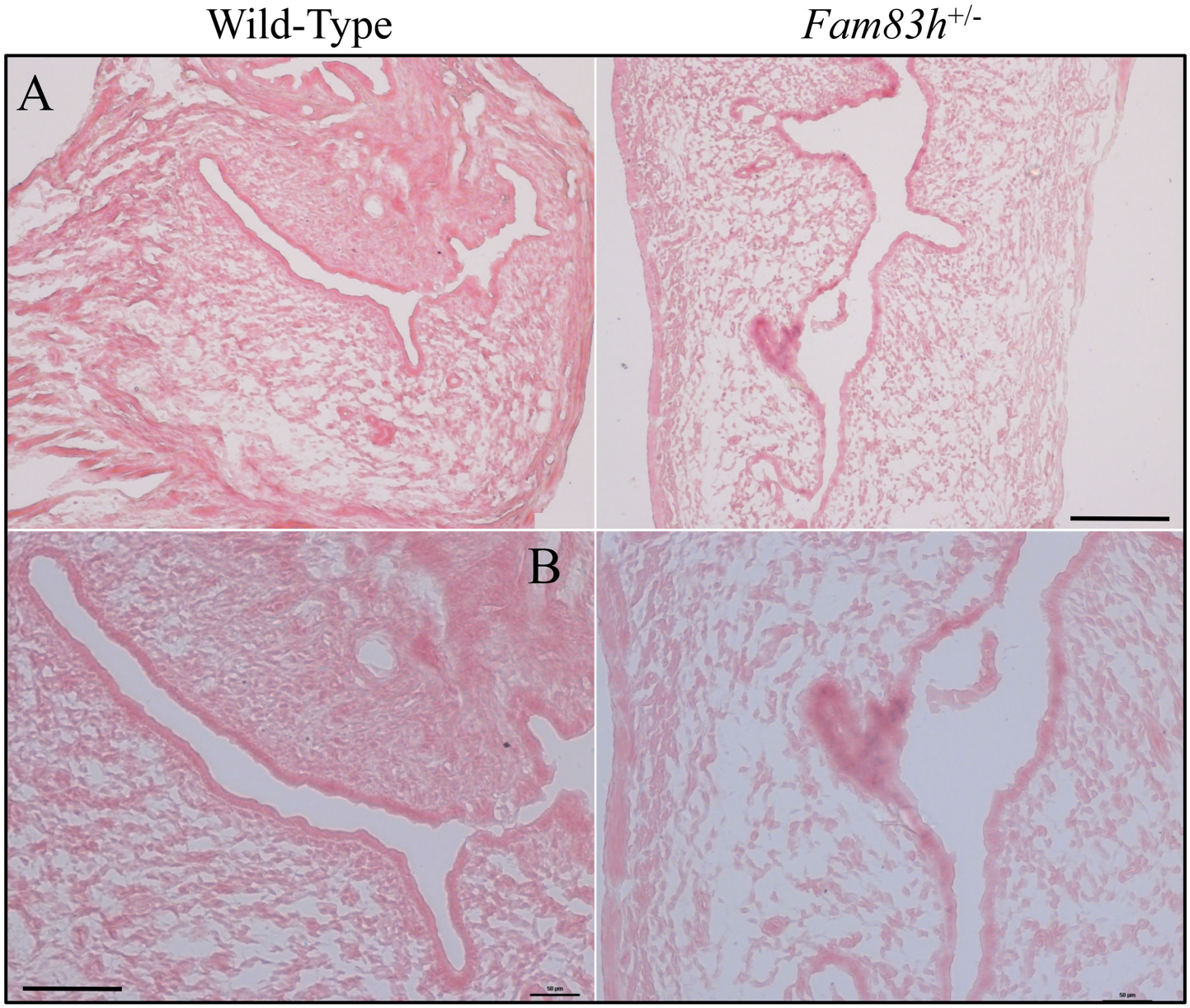

Fig. S26. *LacZ* Histochemistry of Uterus at 7-Weeks. Trace expression was reported in columnar epithelium. ***A:*** Scale bar 200 µm. ***B:*** Scale bar 100 µm.

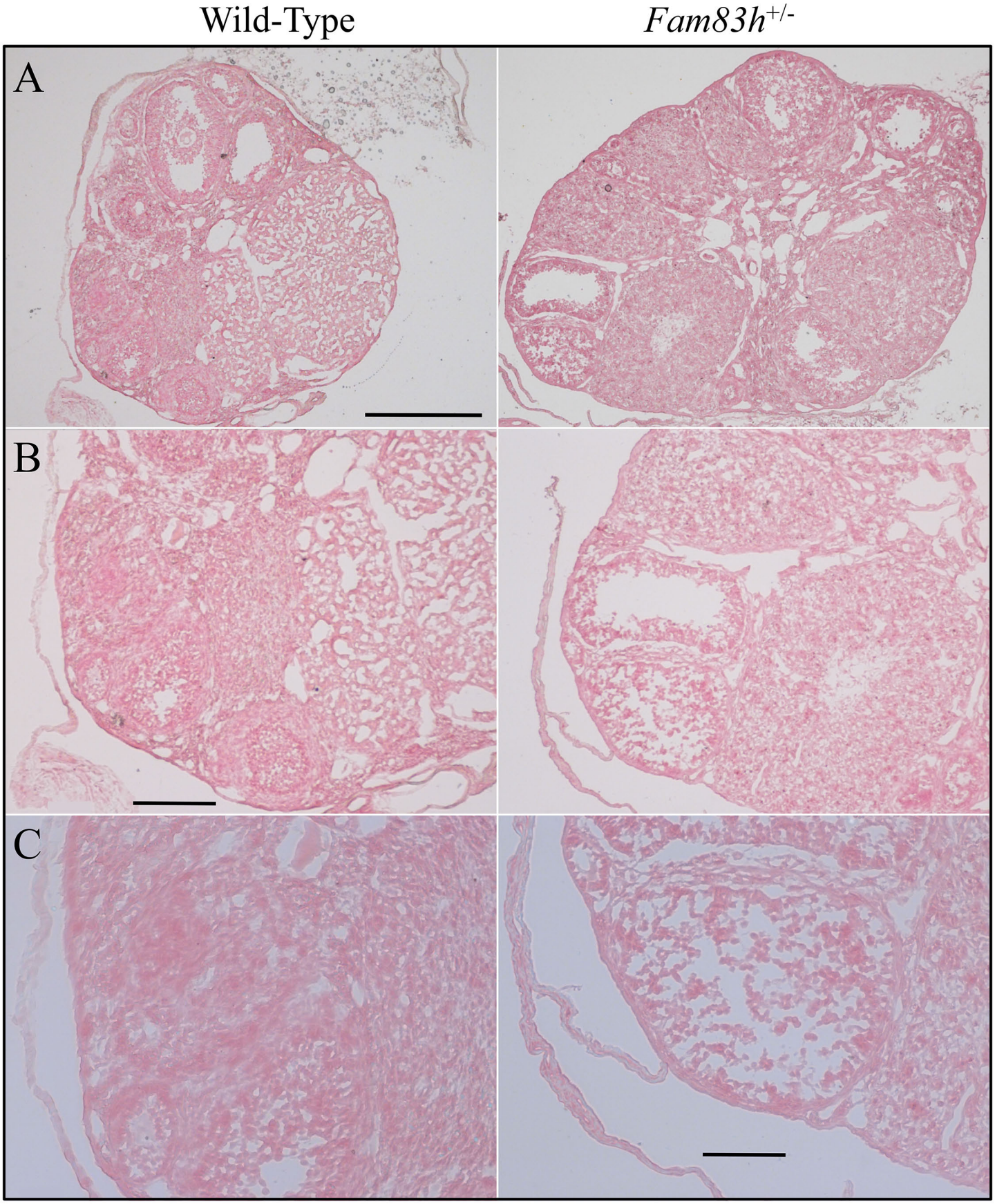

Fig. S27. *LacZ* Histochemistry of Ovary at 7-Weeks. No staining. ***A:*** Scale bar 500 µm. ***B:*** Scale bar 200 µm. ***C:*** Scale bar 100 µm.

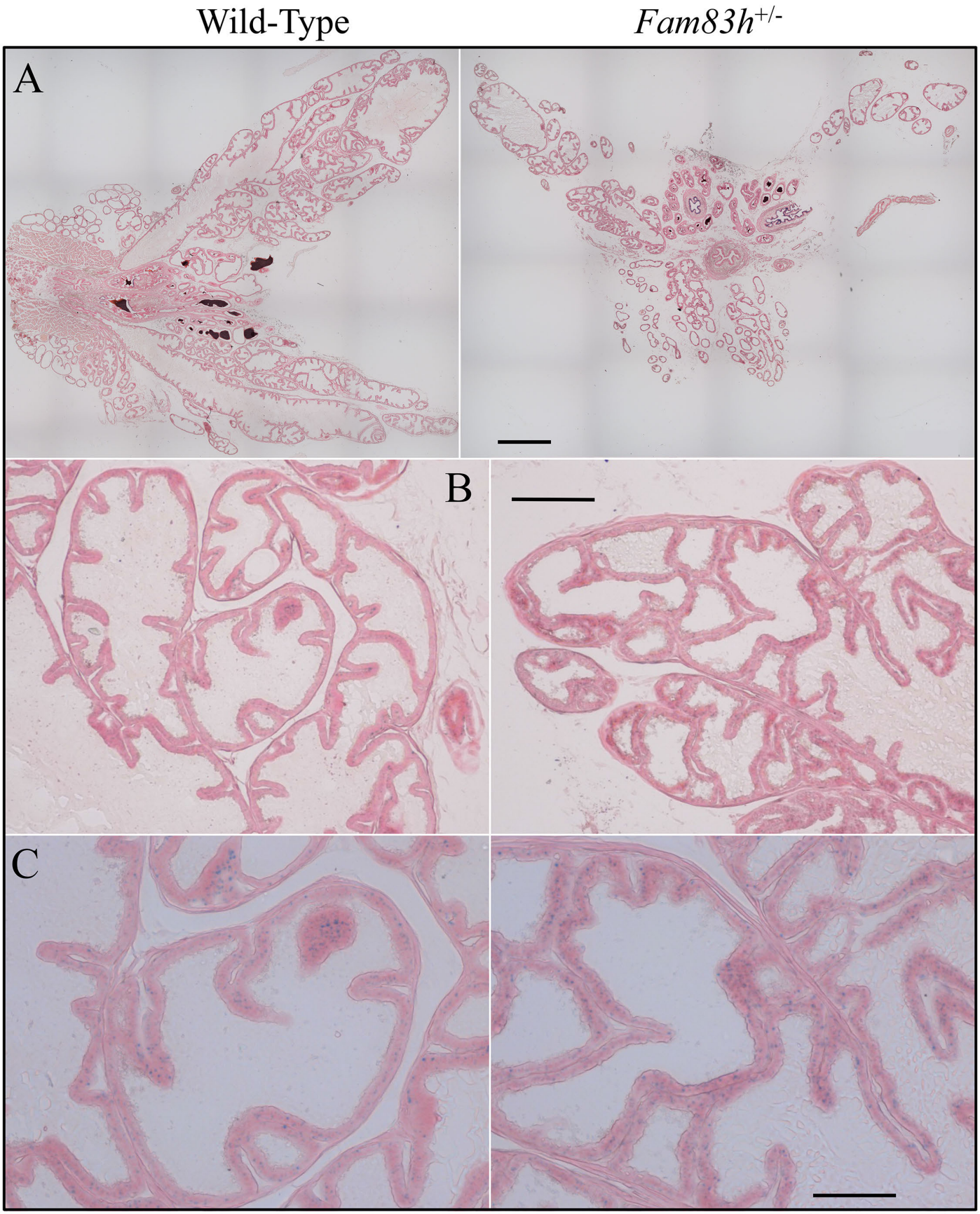

Fig. S28. *LacZ* Histochemistry of Prostate at 7-Weeks (Part 1). The dorsal prostate cuboidal epithelium cells reported weakly positive in both the wild-type and *Fam83h* mice. ***A:*** Scale bar 1 mm. ***B:*** Scale bar 200 µm. ***C:*** Scale bar 100 µm.

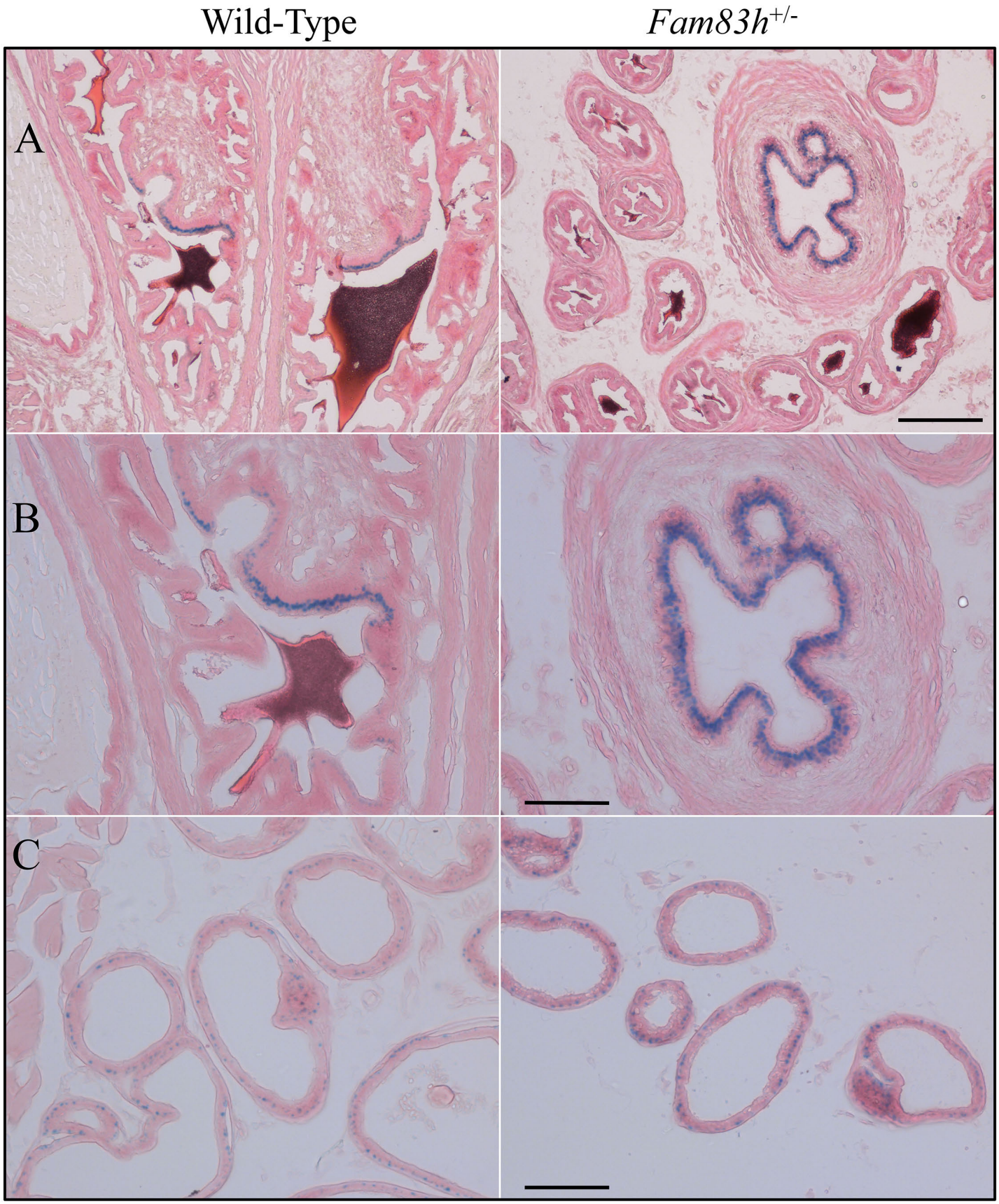

Fig. S29. *LacZ* Histochemistry of 7 Week Prostate (Part 2). The dorsal prostate cuboidal epithelium reported positive in both the wild-type and *Fam83h* mice. ***A:*** Scale bar 200 µm. ***B:*** Scale bar 100 µm. ***C:*** Scale bar 100 µm.

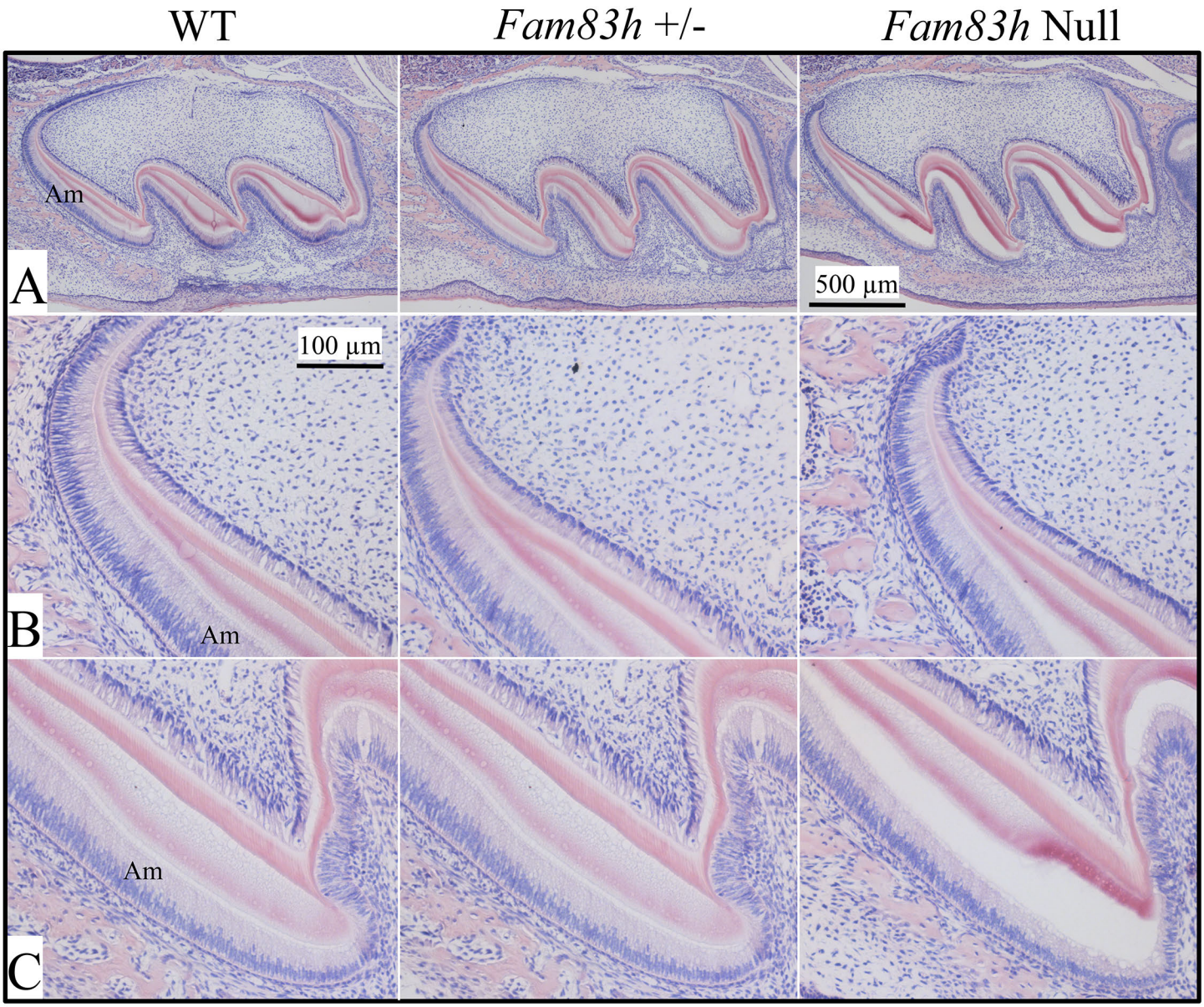

Fig. S30. Histology of Mouse Maxillary First Molars at PN5. Ameloblasts (Am) are in the secretory stage of amelogenesis. ***A:*** Low Magnification views. B: Higher magnification of youngest ameloblasts near the cervical loop. ***C:*** Higher magnification of the older ameloblasts on the cusp slopes and tip. No differences were observed among the ameloblasts from the 3 different genotypes.

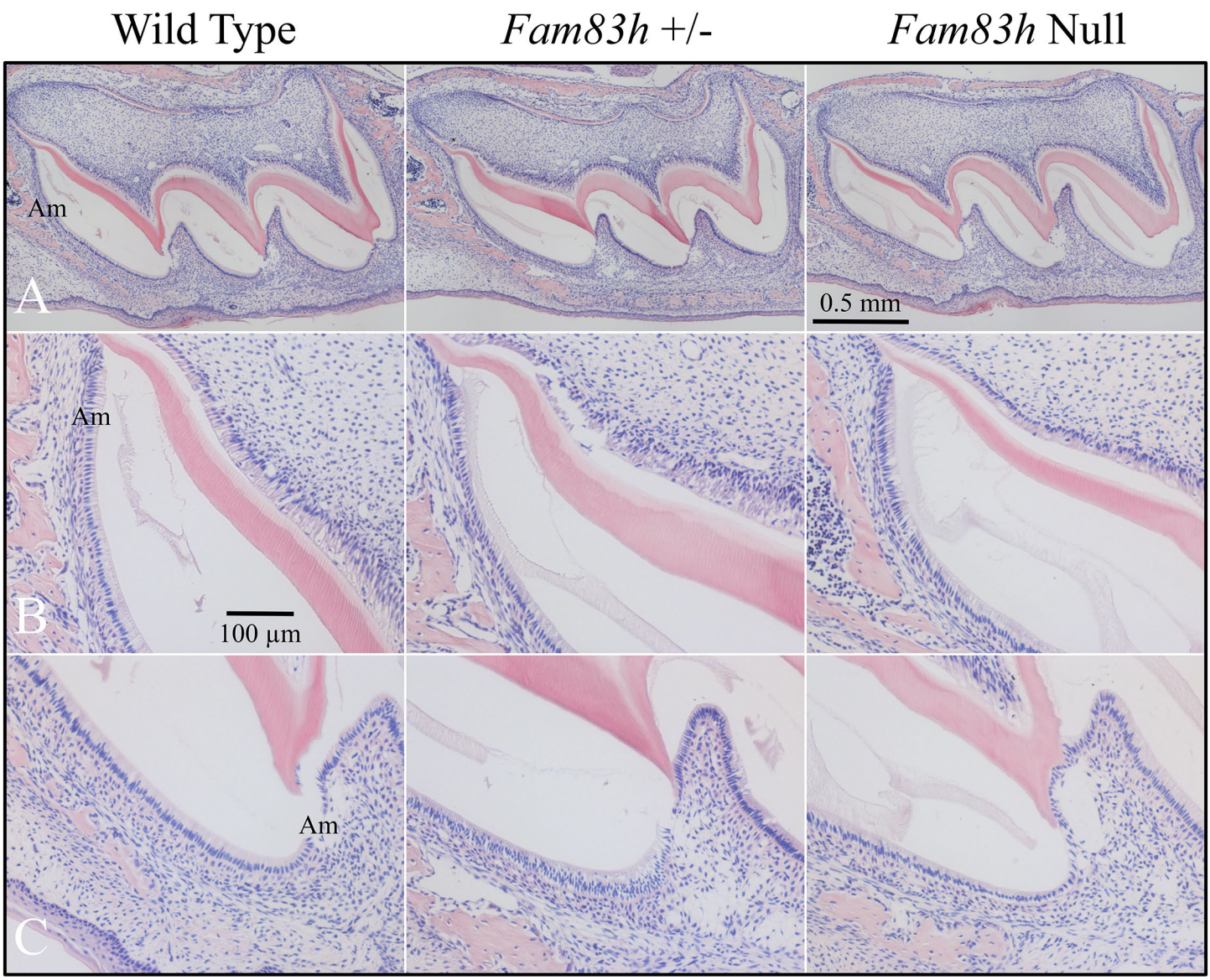

Fig. S31. Histology of Mouse Maxillary First Molars at PN11. Ameloblasts (Am) are in the maturation stage of amelogenesis. ***A:*** Low Magnification views. ***B:*** Higher magnification of youngest maturation stage ameloblasts near the cervical loop. ***C:*** Higher magnification of the older maturation stage ameloblasts on the cusp slopes and tip. No differences were observed among the maturation stage ameloblasts from the 3 different genotypes.

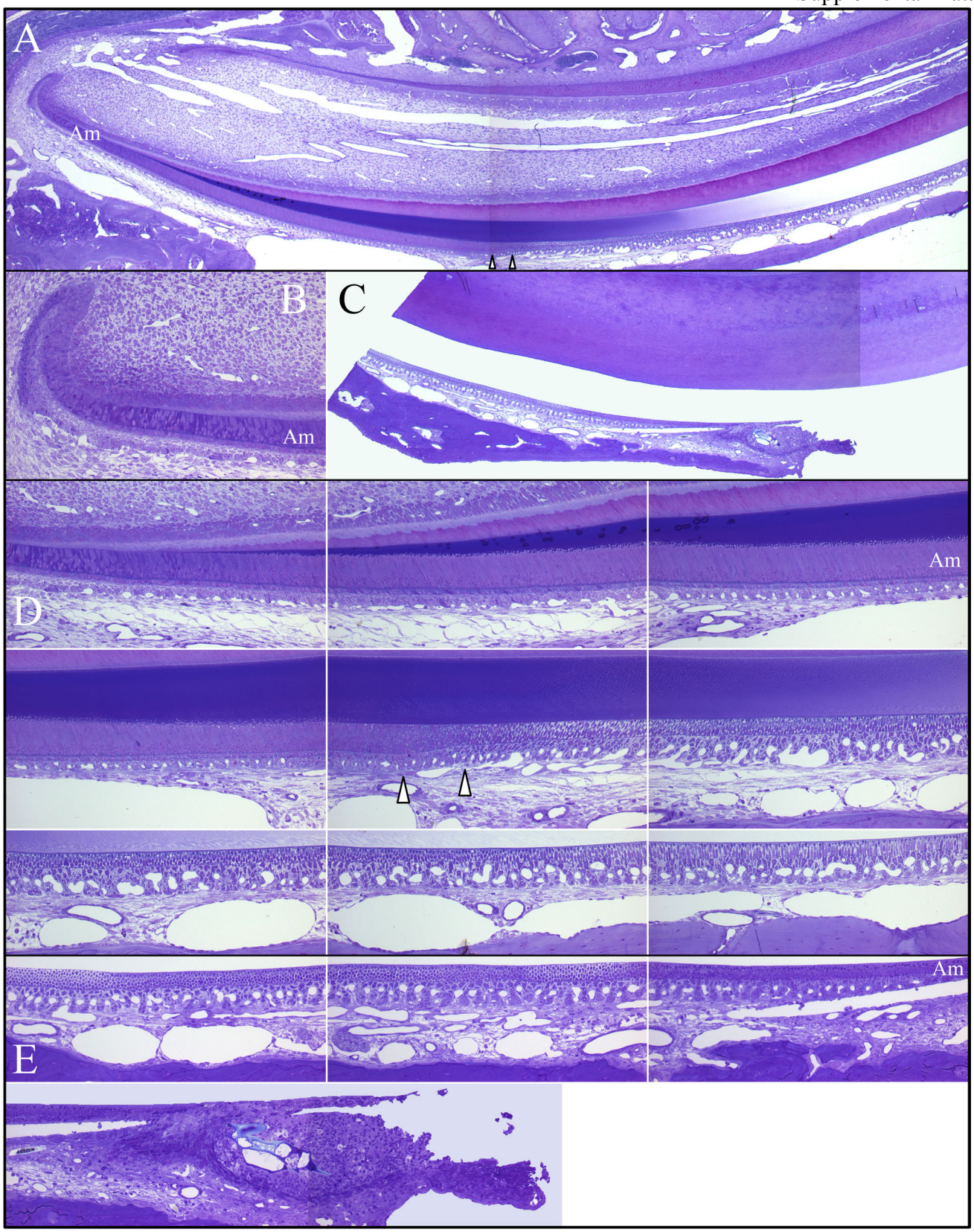

Fig. S32. Histology of *Fam83h* Null Mandibular Incisor at 7-weeks. ***A:*** Low magnification composite image of the mandibular incisor, block 1 and ***B:*** block 2. ***C:*** Basal end of incisor. ***D:*** Higher magnification views of ameloblasts (Am) from block 1 and ***E:*** block 2. Arrowheads mark the boundaries of the transition stage between the secretory and maturation stages of amelogenesis. Am, Ameloblasts.

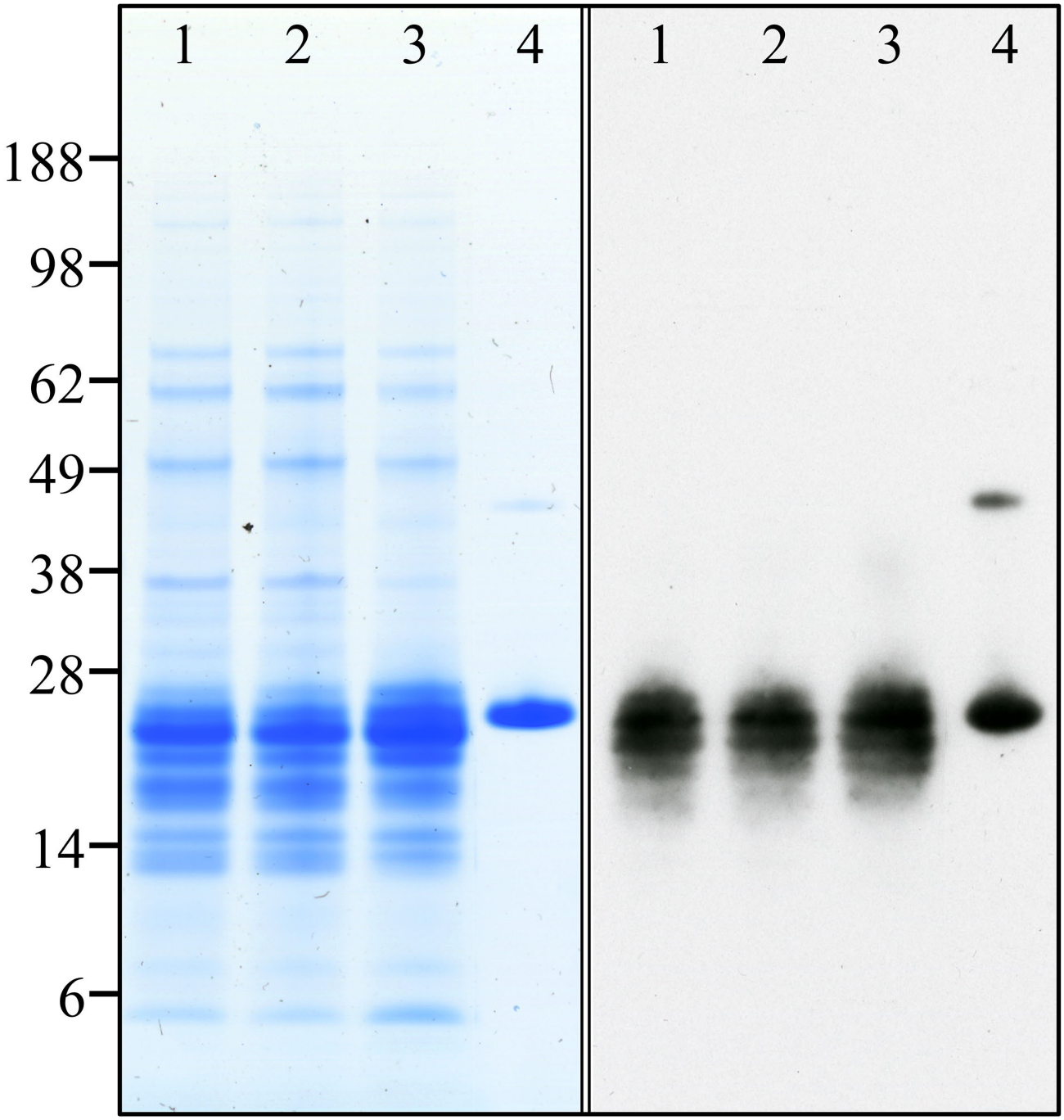

Fig. S33. SDS-PAGE and Western Blots of enamel proteins. ***Lane 1***: wild-type; ***Lane 2***: *Fam83h*$^{+/-}$; *Lane 3*: *Fam83h*$^{-/-}$; ***Lane 4***: rM179. Enamel proteins were extracted from D5 first molars. ~15% of the extracted proteins from a single molar was run down each lane and visualized by Coomassie Brilliant Blue staining. ~5% of a single molar extract was run down each lane and transblotted to a membrane and immunostained using an antibody raised against recombinant mouse amelogenin (rM179).

Protein Symbol	Protein Name	Protein Symbol	Protein Name	Protein Symbol	Protein Name
ACTB	actin, beta	**HNRNPA1**	heterogeneous nuclear ribonucleoprotein A1	**RCN1**	reticulocalbin 1, EF-hand calcium binding domain
ACTG1	actin, gamma 1	**HNRNPC**	heterogeneous nuclear ribonucleoprotein C (C1/C2)	**RCN2**	reticulocalbin 2, EF-hand calcium binding domain
ACTR2	ARP2 actin-related protein 2 homolog (yeast)	**HSPA1A**	heat shock 70kDa protein 1A	**RFC3**	replication factor C (activator 1) 3, 38kDa
ARF4	ADP-ribosylation factor 4	**HSPA9**	heat shock 70kDa protein 9 (mortalin)	**RPL22**	ribosomal protein L22
ATAD3A	ATPase family, AAA domain containing 3A	**IGF2BP1**	insulin-like growth factor 2 mRNA binding protein 1	**RPL27**	ribosomal protein L27
ATAD3B	ATPase family, AAA domain containing 3B	**KRT1**	keratin 1	**RPL28**	ribosomal protein L28
CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	**KRT10**	keratin 10	**RPLP0**	ribosomal protein, large, P0
CALU	calumenin	**KRT2**	keratin 2	**RPS13**	ribosomal protein S13
CAPZA1	capping protein (actin filament) muscle Z-line, alpha 1	**KRT9**	keratin 9	**RPS14**	ribosomal protein S14
CKAP5	cytoskeleton associated protein 5	**MYH10**	myosin, heavy chain 10, non-muscle	**RPS19**	ribosomal protein S19
CNOT1	CCR4-NOT transcription complex, subunit 1	**MYH14**	myosin, heavy chain 14	**RPS20**	ribosomal protein S20
CSNK1A1	casein kinase 1, alpha 1	**MYH9**	myosin, heavy chain 9, non-muscle	**RPS25**	ribosomal protein S25
CSNK1E	casein kinase 1, epsilon	**MYL6**	myosin, light chain 6, alkali, smooth muscle and non-muscle	**SEC16A**	SEC16 homolog A (S. cerevisiae)
DDX3X	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked	**NES**	nestin	**SLC25A13**	solute carrier family 25, member 13 (citrin)
DNAJB2	DnaJ (Hsp40) homolog, subfamily B, member 2	**NPM1**	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	**SNRNP200**	small nuclear ribonucleoprotein 200-kDa (U5)
DNAJB6	DnaJ (Hsp40) homolog, subfamily B, member 6	**PCBP1**	poly(rC) binding protein 1	**SNRPD2**	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa
FAM83H	family with sequence similarity 83, member H	**PPP1CA**	protein phosphatase 1, catalytic subunit, alpha isoform	**TIMM50**	translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae)
GAPDH	glyceraldehyde-3-phosphate dehydrogenase	**RBM14**	RNA binding motif protein 14	**TOMM22**	translocase of outer mitochondrial membrane 22 homolog (yeast)
HELZ	helicase with zinc finger	**RBM4**	RNA binding motif protein 4	**TRAFD1**	TRAF-type zinc finger domain containing 1

Fig. S34. Proteins that immunoprecipitated with FAM83H.

```
Hum ----------------------------------------------------------MARRS    5
Cow ----------------------------------------------------------MARRS    5
Dog ----------------------------------------------------------MARRS    5
Rat ----------------------------------------------------------MARRS    5
Mos ----------------------------------------------------------MARRS    5
Chk ----------------------------------------------------------MARRS    5
Xep MGPNLPRASQRHRPRMGPNLPRASQWHRPRMGPICPGLLSGTGPVPPLAPLWCSPMARRS   60
Zef ----------------------------------------------------------MARRS    5
                                                              *****

Hum QSSSQGDNPLAPGYLPPHYKEYYRLAVDALAEGGSEAYSRFLATEGAPDFLCPEELEHVS   65
Cow QSSSQGDNPLAPGYLPPHYKEYYRLAVDALAEGGPEAYSRFLASEGAPAFLCPEELEHVS   65
Dog QSSSQGDNPLAPGYLPPHYKEYYRLAVDALAEGGPEAYSRFLASEGAPAFLCPEELEHVS   65
Rat QSSSQGDNPLAPGYLPPHYKEYYRLAVDALTEGGQEAYNRFLASEGAPDFLCPEELEHVS   65
Mos QSSSQGDNPLAPGYLPPHYKEYYRLAVDALTEGGPEAYNRFLASEGAPDFLCPEELEHVS   65
Chk QSSSQGDNPLDPNYLPPHYKEYYRLALDILTEEGKESYERFLAEEGAPDFLCNSEVDHIL   65
Xep QSSSQGENPLDPNYLPPHYKEYYRIAIDALAENGPEAYEQFLMEEGAPDFLCPNEVEHIS  120
Zef QSSSLGDNPLDPNYLRPHYREEYRMAIDALVEDDIEGYYNFLQNANVVDFLSRSEIENIK   65
    **** * *** * ** *** * ** * * * *   * *  **       **   *

Hum RHLRPPQYVTREPP---EGSLLDVDMDGSSGTYWPVNSDQAVPELDLGWPLTFG--FQGT  120
Cow RHLRPPQHVAPEPP---DGSPPNLDFDGSSGTYWPVNSDQAVPELDLGWPLTFG--FQGT  120
Dog RHLRPPQHVAREPP---DGSPPNVDMDGSSGTYWPMNSDQAVPELDLGWPLTFG--FQGT  120
Rat RHLQPPQYVSREPP---EGAPPDVDMDGSSGTYWPVDSDQAVPELDLGWPLTFG--FQGT  120
Mos RHLQPPQYVAREPP---EGTPSDVDMDGSSGTYWPVNSDQAVPELDLGWPLTFG--FQGT  120
Chk QNLQKPQYANQEG---GTDTAGDNDVDGSSGTYWPMNSDLAVPELDLGWPMVFG--FRGT  120
Xep RSLQRPPESGQENPYPDSVYGSQEDADGSSGTYWPMDSDTAAPELDLGWPTIYG--FQGT  178
Zef STVQTPQSAGNVP----ELPYGEIDQDESSDTYWPLHSDLDAPGLDLGWPMQQHSFVGPT  121
         *                  * * ** ****  **   * ******         *

Hum EVTTLVQPPPPDSPSIKDEARRMIRSAQQVVAVVMDMFTDVDLLSEVLEAAARRVPVYIL  180
Cow EVTTLVQPPPPDSPSIKDEARRMIRSAQQVVAVVMDMFTDVDLLSEVLEAAARRVPVYIL  180
Dog EVTTLVQPPPPDSPSIKDEARRMIRSAQQVVAVVMDMFTDVDLLGEVLEAAARRVPVYIL  180
Rat EVTTLVQPPPPDSPSIKDEARRMIRSAQQVVAVVMDMFTDVDLLSEVLEAAARRVPVYIL  180
Mos EVTTLVQPPPPDSPSIKDEARRMIRSAQQVVAVVMDMFTDVDLLSEVLEAAARRVPVYIL  180
Chk EVTTLVQPPPPDNPSIKEEARRMIRAAQQVVAIVMDVFTDVDLLFEVLDAAARRVPVYIL  180
Xep EVTTLMHPPPPDNPTIKEEVRRMIRSAQQVIGIVMDIFTDADILSELLDAANRRIPVYII  238
Zef EVTMLVNPAEPERPSIKEQARRLIKNAHQVIAVVMDIFTDVDIFSDLLEAAARHVPVYIL  181
    *** *  *  *  * **   ** *  * **   *** *** *     * ** *  ****

Hum LDEMNAQHFLDMADKCRVNLQHVDFLRVRTVAGPTYYCRTGKSFKGHVKEKFLLVDCAVV  240
Cow LDEMNAQHFLDMADKCRVNLHHVDFLRVRTVAGPTYYCRTGKSFKGHVKEKFLLVDCAVV  240
Dog LDEMNAQHFLDMADKCRVNLHHVDFLRVRTVAGPTYYCRTGKSFKGHVKEKFLLVDCAVV  240
Rat LDEMNAQHFLDMADKCRVNLHHVDFLRVRTVAGPTYYCRTGKSFKGHLKEKFLLVDCAVV  240
Mos LDEMNAQHFLDMADKCRVNLHHVDFLRVRTVAGPTYYCRTGKSFKGHLKEKFLLVDCAVV  240
Chk LDEMNSQLFLDTAAKCRVNLNYVEFLRVRTVSGPTYYCRTGMSFKGHVKEKFLLVDCMVV  240
Xep LDQMNCQLFLDMAAKYRVNLNYVEFLRVRTVSGPTYFCRKGSTFKGNLQEKFLLVDCTMV  298
Zef LDEQNAHYFVNMVASCKVNLEMIHMMRVRTVSGVTYFCRTGKSFKGQVMDRFLLTDCRAV  241
    **  *   *        ***      ***** * ** ** *  ***     *** **  *
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Hum MSGSYSFMWSFEKIHRSLAHVFQGELVSSFDEEFRILFAQSEPLVPSAAALARMDAYALA  300
Cow MSGSYSFMWSFEKIHRSLAHVFQGELVSSFDEEFRILFAQSEPLVPSAGALARMDTYALA  300
Dog MSGSYSFMWSFEKIHRSLAHVFQGELVSSFDEEFRILFAQSEPLVPSAGALARMDAYTLA  300
Rat MSGSYSFMWSFEKIHRSLAHVFQGELVSSFDEEFRILFAQSEPLVPSAGALARMDAYALT  300
Mos MSGSYSFMWSFEKIHRSLAHVFQGELVSSFDEEFRILFAQSEPLVPSAGALARMDAYALA  300
Chk LSGNYSFMWSFEKIHRSIAHIFQGELVASFDEEFRILFAQSEPLVPPANVLAKAE----N  296
Xep LSGTYSFMWSFEKIHRSIAHIFQGELVSSFDEEFRILFAQSDPLIPSESALAKMD----K  354
Zef ISGNYSFMWSFEKIHRCIAHLFLGELVATFDEEFRILFAQSQPLVVENALVPMPQ-----  296
     ** ************  ** * ****  ************ **

Hum PYAGAGPLVGVPGVGAPTPFSFPKRAHLLFPPPREEGLGFPSF-LDPDRHFLSAFRREEP  359
Cow PYAGAGPLMGSQMPGAPTPFSFPKRAHLLFPPPREEGLGFPSF-LDPDRHFLSAFRREES  359
Dog PYTGAGPLMG-----APTPFSFPKRAHLLFPPPREEGLGFPSF-LDPDRHFLSAFRREEP  354
Rat PYSGAGPLVGVPGVGAPTPFSFPKRAHLLFPPPREEGLGFPSF-LDPDRHFLSAFRRDEL  359
Mos PYSGAGPLVGVPGVGAPTPFSFPKRAHLLFPPPREEGLGFPSF-LDPDRHFLSAFRREEL  359
Chk PFA-MTPFGN------NMPF-FPKKSPLMFQRDDNLFPSFMDR-VDPDRFFLSNFRRDDM  347
Xep SYMGMVPFAG------PRPM-FDRKLHFMFPREENPSQQFPSYGVDPDRHYFQPFRREDM  407
Zef -----DSYLG-------NQFGLKRTQSLRNPRGYLRQPELGGYQYGDRLDSILPFRRDDP  344
                                                         ***

Hum PRMPGGALEPHAGLRPLSRRLEAEAGPAGELAGARGFFQARHLE-MDAFKRHSFAT-EGA  417
Cow SRMPGGALEPHTGLRPLSRRLDAEAGPGGELSGPRGFFQARHLE-MDAFKRYSYAAADGA  418
Dog MRMPGGALEPHAGLRPLARRLDAEAGAGGELAGPRAFFQARHLE-MDAFKRHSFAAADGS  413
Rat QRMPGGALEPHTGLRPLAR--PGEAGPLGELPGPRGFFQSRHLE-MDAFKRHSYTAADGA  416
Mos QRMPGGALEPHTGLRPLAR--PTEAGPFGELAGPRGFFQSRHLE-MDAFKRHSYATPDGA  416
Chk LRHT---VEGSA-----MRMYKKVEMENAQMDPVRGFLRSKQLE-LDAFKRHSFAE----  394
Xep IRQT---MDPGG-----MRMYGKNLGDPMDKMQMS-FVQNKQLEAMEAFKRHSFAE----  454
Zef FRHT---IEPSAGPMQVTKYATQQFRMQQSFLDQGRSMLASRQLEMNAFKRHSYAE----  397
     *                                          **** *

Hum GAVENFAAARQVSRQTFLSHGDDFRFQTSHFHRDQLYQQQYQWDPQLTPARPQGLFEKLR  477
Cow GAVENLAAARQVSRQTFLSHGDDLRFQTSHFHRDQLYQQHYQWDPQLAPTRPQGLFEKLR  478
Dog GAVENFAAARQVSRQTFLSHGDDLRFQTSHFQRDQLYQQHYQWEPQLAPARPQGLFEKLR  473
Rat GAVENFAAARQVSRQTFLSHGDDFRFQTSHFQRDQLYQQHYQWDPQFAPARPQGLFEKLR  476
Mos GAVENFAAARQVSRQTFLSHGDDFRFQTSHFQRDQLYQQHYQWDPQFAPARPQGLFEKLR  476
Chk GTFENFASSKQYARQMFMNNMDEFKIQSSHFQKDQFYQY--QFEHPHLSGRPQGFFDRIR  452
Xep GTFENYTSSRQYSRQMFMNNNDEYRLQSSQVQKSQFMQ----FQSPLGTARPQGLFEKIR  510
Zef GTRETYASSRQYMKQRVMNN---LEETESHYQREQHYYQ-----SEGMGHDDRGHYDRFN  449
    *  *      *   *             *     *                  *

Hum GGRAGFADPDD---FTLGAG----PRFPELGPDG-HQRLDYVPSSASREVRHGSDPAFAP  529
Cow AGRPGFPDHDE---FMLGTG----PRFPELGLDG-HQRLDYVPSSASREVRHGSDPAFGP  530
Dog AGRPGFTEHDD---LALGLG----PRFPELGPDG-HQRLDYVPSSASREVRHGSDPAPGP  525
Rat AGRPGFADPDD---FALGAG----HRFPELGADV-HQRLEYVPSSASREVRHGSDPAFGP  528
Mos AGRPGFADPDD---FALGAG----HRFPELGADV-HQRLEYVPSSASREVRHGSDPAFGP  528
Chk GGRPGFNELEEGGPLPYGEGPRYHELESGFPQEGFPLRLDYVPSNSSREVRHGSD-QLNP  511
Xep GGRQGLQEMDEFDSRYPTKG---LPGEGHFALDGPPMRPGYNPSNSSREVRHGSD-QMVI  566
Zef YGLADQHSDSG--------------YPPELEAPG------NINVLSSDDLKSDSEKQYNI  489
     *                                              *      *
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Hum GPRGLEPSGAPRPNLTQRFPCQAAARPGPDPAP--------EAEPERRGGPEGRAGLRRW  581
Cow GPRGLEPGGAPRPNLGQRFSCQAMTRLGPEMAP--------EPEPEHRGGPEGRAGLRHW  582
Dog APRGLEPSGALRANLGQRFPCQAAARPGPEAAP--------DTEQERRGGPEGRAGLRHW  577
Rat SPRGLEPSGASRPNLGQRFPCQATLRQGLDTAT--------EAEPERRGGPEGRAGLRHW  580
Mos SPRGLEPSGASRPNLGQRFPCQATLRQGLDTAS--------EAEPERRGGPEGRAGLRHW  580
Chk AGNGPMGMMLRRQNIGQKFICQTSPTQKQSLEQRLFLQDKDEDQDQDKSTQENRTGLRNW  571
Xep GGEGRFGQRSLGR---QKFMCQISPTQKQGMEPKYFFHD----QDADKKPQENKQGLRSW  619
Zef GGR-YDPQGHKRPAAGHAYACQSSPTQPHPPDQKQLFSTG--DQVRQSQDPSVKQGLRSW  546
                       **                                 *** *

Hum RLASYLSGCHGEDGGDDGLPAPMEAEAYEDDVLA-------------------------  615
Cow RLTSYLSGCHSEDAGDEGLPTPMETEAYDDDVLV-------------------------  616
Dog RLASYLSGCHGDDAGDEGLPAPMDAEAYEDDVLG-------------------------  611
Rat RLASYLSGCHG-DGGEEGLP--MEAEACEDEVLA-------------------------  611
Mos RLASYLSGCHG-DGGEEGLP--MEAEACEDEVLA-------------------------  611
Chk RISSYLSAYQS-EP-EEGLPMPMESEAYNDVLG--------------------------  602
Xep RISSYLSGIQS-DQDEEGLPIPLDPELYDDALVPVERAVPASDTLFKYSMDPVPPYHPGT  678
Zef RINSYLSTYED--GGEEGLHQPMGSDAFEDSHQQPDSRLYGSEGPGIHSN----------  594
    *  ****          **          *

Hum ------------------------------------------PGGRAPAGDLLPSAFRV  632
Cow ------------------------------------------SGGRATAGDLLPSAFRV  633
Dog ------------------------------------------CAGRPSPGDLLPSATRV  628
Rat ------------------------------------------PGGR----DLLPSTFRT  624
Mos ------------------------------------------PGGR----DLLPSAFRT  624
Chk ------------------------------------------DPLTKHPTDLIPAFKSP  619
Xep APHDLPYDRANENPMKFSMDPVQLHRPNVPSQDVPMHLERAGNESLVKYSLDPIPPFKPN  738
Zef ---------------------------------------IRERPNIPTKPNLDLRPRFGKP  616
                                                        *  *

Hum PAA------------------------------FPTKVPVPGPGSGG-NGPEREGPEEPG  661
Cow PAP------------------------------FPGKGPAPGSGSGGGDGPEREGLEEVG  663
Dog PAA------------------------------FPAKGLEPCSGR--GDSPERETLEEAG  656
Rat PAP------------------------------FPAKGPKPGSGSGGGDSSEREGPEETG  654
Mos PAA------------------------------FPAKGPKPGSGSGGGDSSEREGPEETS  654
Chk IS-------------------------------FNSK-SLGVENAKEFADPERGG-EEAP  646
Xep VAGTDVPMPLERKPTANEILSRYSVDPIPPYKTFGSTGDLSVEKAKENPPAEKEK-EEGL  797
Zef IIQDRNQVKDNTSDLG-----------PTSTDTLKPAISASSLASSTDNEKELAEPREIS  665
                                                        *     *

Hum LAKQDSFRSRLNPLVQRSSRLRSSLIFSTSQAEGAAG-AAAATEKVQLLHKEQ--TVSET  718
Cow LAKQDSFRSRLNPLIQRSSRLRSSLIFSASQGEGTGGPTGASTEKVQLLHKEQ--TVSEM  721
Dog LAKQDSFRSRLNPLIQRSSRLRSSLIFSASPAEGAGGAPAAATERAQLLHKEQ--AVSET  714
Rat LIKQDSFRSRLNPLIQRSSRLRSSLIFAS-QAEGTAGTTAATTEKVQLMHKEQ--TISET  711
Mos LAKQDSFRSRLNPLIQRSSRLRSSLIFAS-QAEGAVGTAAATTEKVQLMHKEQ--TVSET  711
Chk MMKQDAFRTRINPLIQRSSRLRSSLIFNA----AKLDQPNTTVEKVQMIHKEQ--VSSEL  700
Xep LSRHDSFRTRTNPLIQRGSRLRSSLIFSS----SKLEQHTSTAESVQEMQKEQ--STSEL  851
Zef ITKHESFRTRINPMLQRSSRLRSSLIFSSSKLEQHNSSQAKSGGELQEEKEESEPIRYSS  725
          ** * **  ** *********                    *    *
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Hum LGPGGEAVRSAASTKVAELLEKYKGPARDPGGGAGAITVASHSKAVVSQAWREEVAAPGA  778
Cow LGPGNEAVRSAASTKVAELLEKYKGPSRDPGGVGTAVTAASHSKAVVSQAWREEVSAPGG  781
Dog LGPGGEATRSATSTKVAELLEKYKGPARDAGAVGAAVAVASHSKAVVSQAWREEVVAPGG  774
Rat LGPSGEAVRSSASAKVAELLEKYKGPARDPGGAGGAITASSHSKAVVSQAWREEVVAPGG  771
Mos LGPSGEAVRSSASAKVAELLEKYKGPARDPGGAGGAVTSSSHSKAVVSQAWREEVVAPGG  771
Chk TK-DNETIKTAASSKVAELLEKYKAVGKDAER-----ATVTHTKAVSSFLQEESQNAEKK  754
Xep VS-ENETGRTTS--KVAEILQKYRGINKDANS-----TTVTQAKAASRTIHEESEDGQSV  903
Zef IVAEILEKRRSLSREPFDWNKHKKADEKDVKHASTGDLTTIQDTKEEPIKEKEKPDNPKP  785
                                 *                       *

Hum VG--GERRSLESCLLDLRDSFAQQLHQEAERQPGAASLT--AAQLLDTLGRS--------  826
Cow GSG-SERRSLESCLLDLRESFAQQLHQEAERQPGAATLA--STQLLDTLGRGS-------  831
Dog G---SERRSLESCLLDLRDSFAQRLHQEAERQPGAATLT--ATQLLDTLGRG--------  821
Rat AG--AERRSLESCLLDLRDSFAQQLHQEAERHPGAASLT--AAQLLDTLG----------  817
Mos AG--TERRSLESCLLDLRDSFAQQLHQEAERHPGAASLT--AAQLLDTLG----------  817
Chk CTKSVQYKILESRVLESKDSCSTYK---------------MHGETDRTFGMS--------  791
Xep SAEEVAYKAVES-TVDTKGSMSHVQQESQYRSVASSHLESLLGKHQTTLSMSKVEQMTSS  962
Zef EENKVTQPTVPSASQQITSSLNMNDPASRLQYFKDQQEKRKTSKLELDLGTKSQEAAIKK  845
              *       *

Hum -------------GSDRLPSRFLSAQSHSTSPQGLDSPLPLEGSGAHQVLHNESKGSPTS  873
Cow ------------SGTDRLPSRFLSTQGHSTSPQGRDSPPP---EGPG-GQQSEPKGSPTL  875
Dog -------------GTDRLPSRFLSAQGRPGSPQGRDSPPP---EGPRQAPHPEPKGSPAS  865
Rat -------------GTDRLPSRFLSAQGRSLSPQGRDSPPP-EGLGTHQLPYSEPKGSPTP  863
Mos -------------GTDRLPSRFLSAQGRSLSPQGRDSPPP-EGLGTHQLPYSEPKGNPTP  863
Chk ---------------SSTPQLIDALSKDPLAHLG----------TKVDKLSSRFYPMENK  826
Xep IQTIGNISAAPSESGPTVPELSEVHKQSSISHMQQESHYKSVVTSKLEGLLNRDQQVMSM 1022
Zef --------PETLDTATKVPDVLLTSEQSTVKAQEPTVSQTDPVPHRPVIETKPKPSEVSV  897
                    *

Hum AYPERKGSPTP---------------------------------------------GFSTR  889
Cow AYPERKGSPTP---------------------------------------------GFPTR  891
Dog AYPERKGS------------------------------------------------------  873
Rat AYPERKGSPTPAYPERKGSPTPAYPERKGSPTPAYPERKGSPTPAYPERKGSPTSGFPNR  923
Mos AYPERKGSPTPAYPERKGSPTPAYPERKGSPTPAYPERKGSPTQAYPERKGSPTSGFPNR  923
Chk PALPEKESLIF---------------------------------------------VGDT  841
Xep SKVEQTSSTIQ---------------------------------------------TIGN 1037
Zef DRPYTTNKTLTESIADAP--------------------------------KKEPVKEPTKS  926

Hum RGSPTTGFIEQKGSPTSAYPERRGSPVPPVPERRSSPVPPVPERRGSLTLTISGESPKA-  948
Cow RGSPTAGFTEQKGSPTSAYPERRGSPVPPVPERRGSPVPPVPERRGSLTLPFSGESPKA-  950
Dog --------------PTSAFPERRASPVPPVPERRASPVPPVPERRASLTLTFAEESAKT-  918
Rat RGSPTTGLMEQKGSPTSTYPDRRSSPVPPVPERRGSPVPPVPERRG--SLTFAGESSKT-  980
Mos RGSPTTGLMEQKGSPTSTYPDRRGSPVPPVPERRGSPVPPVPERRG--SLTFAGESSKT-  980
Chk QKLALPEKKER-VTFKEDAEKLVSAELK--KPQVRTGATSAIENLSKGQGSDSSLNRSE-  897
Xep ISPAPPDSKESGPTITEVTEATQSSENLPTRPNSAFHFGSALESMSQNPTPSSSLNKSE- 1096
Zef LKPFPSPKFLKPFKSSQSSSRRISCGEEILTDATDAEKSELKKSRSFSTSGMSRTESRES  986
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Hum ----GPAEEGPSGPMEVLRKGSLRLRQLLSPKGERRMEDEGGFPVPQENGQPESPRRLSL 1004
Cow ----GPTEEAVGGPMEVLRKGSARLRQLMSPKGERRADDEGSFPTPQENGQPESPQWPSL 1006
Dog ----GTAEESAGGPMEVLRKGSLRLRQLLSPKGERRAEEDGGFPAPQENGQPESPRRPSL  974
Rat ----GPTEEVSGGPMEVLRKGSLRLRQLLSPKSERRGEDEVSFPAPQENGQPESPRRPSL 1036
Mos ----GPTEEVSSGPMEVLRKGSLRLRQLLSPKNERRGEDEGSFPTPQENGQPESPRRPSL 1036
Chk ----EECSKQEQNTMEFLRKGSLRLKQFLNPKGEKKLEEEPNSEIGKSDKQPMGLKRSSM  953
Xep ----EDLAKTDQN---FFRKGSMRLKQFLQSKAEKKAEEDLASDNAKAEKQHSTLRRLSK 1149
Zef LSSLGNSESKDTKALDFLKKQTQRLKGILGPKGDKKHSGVSNSQEDKSMKTVPEVQEEIS 1046
                        *   **      *

Hum GQGDSTEAATE------------------ERGPRARLSSATANALYSSNLRDDTKAILEQ 1046
Cow VRVDSTEAAAE------------------ERGPRARVASATANALYSSNLRDDTKAILEQ 1048
Dog GRADSTEAAAAA----------------DERGPRARTASATANALYSSNLRDDTKAILEQ 1018
Rat SRGDSTEAAAE------------------ERGSRVRLASATANALYSSNLRDDTKAILEQ 1078
Mos SRGDSTEAAAE------------------ERGSRVRLASATANALYSSNLRDDTKAILEQ 1078
Chk G--DCQEMLGE---EEKNHKFATLLPPKSSQPTQGRFPSSTANILYSSNLRDDTKVILEQ 1008
Xep S--DSQEVAASTDMEEKSAKSLSVSPPKTSSISQSRLSASTSNVIFSSNLRDDTKVILEQ 1207
Zef DKGKPSESISSS---------TAVENKPSAKPTTSRYQSSTSNIIFSSNLRDDTKVILEQ 1097
          *                            *    * *   ********* ****

Hum ISAHGQKHRAVPAPSPGPTHNSPELGRPPAAGVLAPDMSDKDKCSAIFRSDSLGTQGRLS 1106
Cow ISAHGQKHRGVPAPGPTPAHSSPELGHSPVAGGLAPDMSDKDKCSAIFRSDSLGTQGRLS 1108
Dog ISAHGQKHRAVPAPAPGLAHSSPELGRSPTAGGLAPDMSDKDKCSAIFRSDSLGTQGRLS 1078
Rat ISAHGQKHRAVPAP--GPAHNSSDVGRPTTAGDLAPDMSDKDKCSAIFRSDSLGTQGRLS 1136
Mos ISAHGQKHRGVPAP--GPAHSSPDVGRPTTAGDLAPDMSDKDKCSAIFRSDSLGTQGRLS 1136
Chk ISANSQKNRAELAKQLPSTSNP-DLSKSTMSLERKTE---KEKSCNIHRSESFGSQKRNL 1064
Xep ISANSQKNRAEMVKQAQQIQATGDPDPATSKPESKTEGTASTDAAAITRTGSFLSRSRFS 1267
Zef ISANSQKTRQQNEESGKGDGGKDDVANSP-----------------------FQSRNRFS 1134
    ***  ** *                                              *

Hum RTLPASAEERDRLLRRMESMRKEKRVYSRFEVFCKKEEASSPGAGEGPAEEGTRDSKVGK 1166
Cow RTLPAGAEERDRLLRRMESMRKEKRVYSRFEVFCKKEEPGALGAAEGPAEEDARDSKVGK 1168
Dog RTLPASAEDRDRLLRRMESMRKEKRVYSRFEVFCKKEEAGGPGAGEGPAEEDTRDSKVGK 1138
Rat RTLPASAEERDRLLRRMESMRKEKRVYSRFEVFCKKEDAGSSAAGDNLADEDTRDSKMGK 1196
Mos RTLPGSAEERDRLLRRMESMRKEKRVYSRFEVFCKKDEAGSSGAGDNLADEDTRDSKMGK 1196
Chk QRQPS--EDRDTLLKKMENMRKEKRVYSRFEVFCKKDE--HTSQSEEEYDTDAKDKKMGK 1120
Xep RPSPSSPEDRDILLKRMESIRKEKRVYSRFEVFCKKDE--QPSHAD-----DNDDKKAGK 1320
Zef -RAPVNPQERDNLLKRIESMRKEKKVYSRFEVLYRSREECCWERGS--------VEQANQ 1185
       *     ** **   *  **** *******

Hum FVPKILGTFKSKK 1179
Cow FMPKILGTFKSKK 1181
Dog FMPKILGTFKSKK 1151
Rat FVPKILGTFKSKK 1209
Mos FVPKILGTFKSKK 1209
Chk FMPKILGTFKTKK 1133
Xep IIPKLLGNLIKK- 1332
Zef FLIKSIE------ 1192
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Fig. S35. Protein sequence alignment of FAM83H orthologs from 8 vertebrates. The aligned protein sequences are from human (Hum) (*Homo sapiens*; gi|157311635, ref|NP_940890.3), cow (*Bos taurus*; gi|119906195, ref|XP_603315.3), dog (*Canis lupus familiaris*; gi|374091972, gb|AEY83660.1), rat (*Rattus norvegicus*; gi|194474062, ref|NP_001124037.1), mouse (Mos) (*Mus musculus*; gi|269914118, ref|NP_598848.2), chicken (Chk) (*Gallus gallus*; gi|118087467, ref|XP_423955.2), frog (Xep) (*Xenopus tropicalis*; gi|301629161, ref|XP_002943716.1), and zebrafish (Zef) (*Danio rerio*; gi|113682418, ref|NP_001038555.1). The number at the end of each line corresponds to the number of the amino acid with respect to the N-terminal Methionine. Asterisks (*) mark identical amino acids. The four F-X-X-X-F sequence motifs in human FAM83H that potentially mediate CK1-interactions (13) are highlighted in yellow: (F^{247}-X-X-X-F^{251}; F^{270}-X-X-X-F^{274}; F^{274}-X-X-X-F^{278}; F^{350}-X-X-X-F^{354}). Sites mutated in humans associated with disease-causing truncation mutations (nonsense or frameshift) are in bold and highlighted in cyan. Segments near the FAM83H C-terminus that show high sequence conservation during vertebrate evolution that may be important for FAM83H function are highlighted in green.

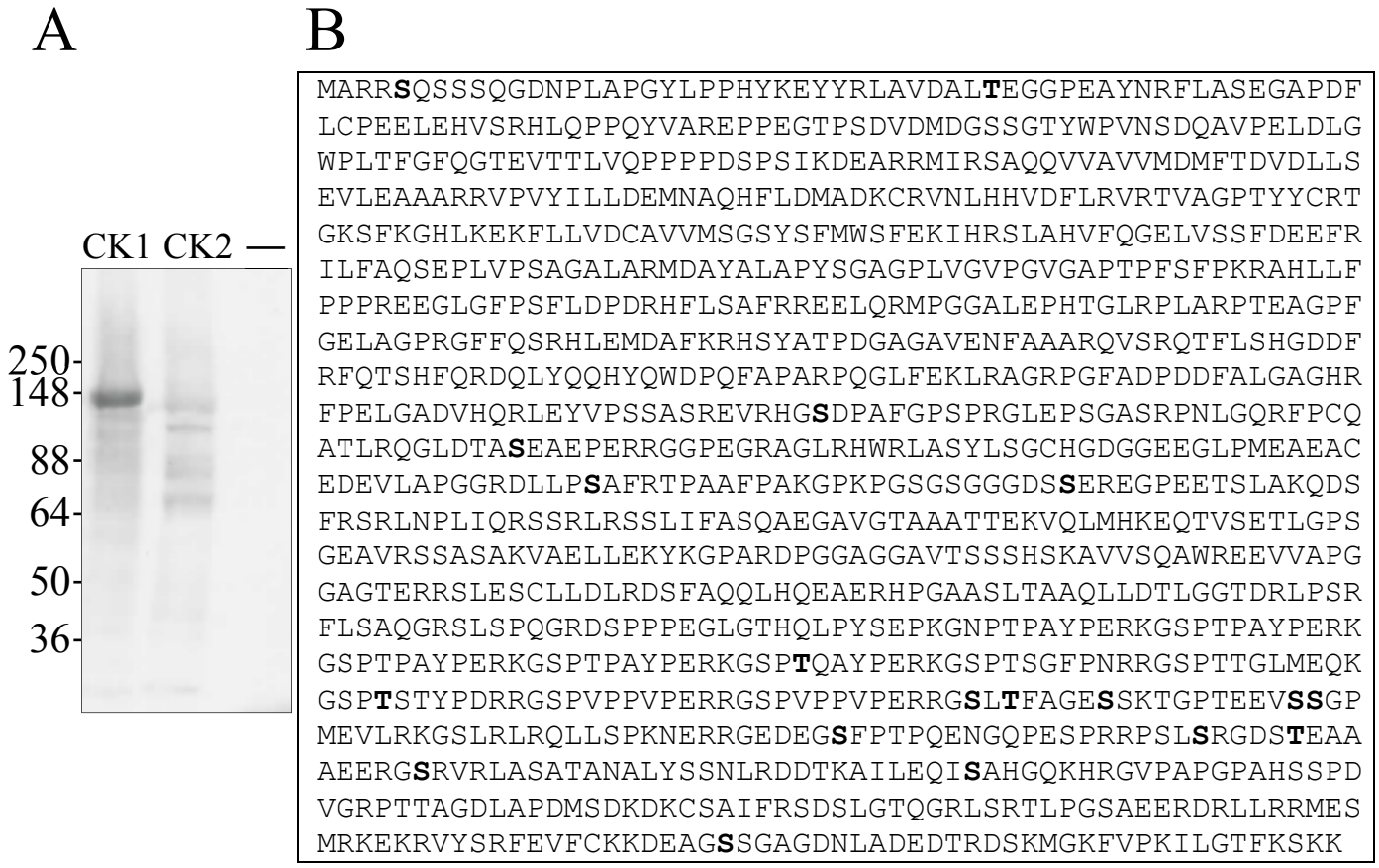

Fig. S36. FAM83H phosphorylation by CK1 *in vitro*. ***A:*** Autoradiograph of ^{33}P kinase assay. Purified mouse recombinant FAM83H was incubated with CK1, CK2, or no enzyme (–) as well as with radioactive ^{33}P-ATP. The reaction samples were separated by SDS-PAGE, and the dried gel was exposed to film. The CK1 reaction shows strong radioactivity at a specific band of ~130-kDa, demonstrating that CK1 can phosphorylate FAM83H *in vitro*. ***B:*** CK1 phosphorylation sites on FAM83H. The phosphorylation sites were determined by mass spectrometry of CK1-treated mouse FAM83H protein. The CK1-phosphorylated Serines and Threonines, which mainly locate at C-terminus of FAM83H, are marked bold.

Gene	Primer Name and Sequence	Amplicon Size
FAM83H 5.1	Fam5.1F: 5'AGGAGCCCTTGTCCTGTAGA Fam5.1R: 5'GAAGCTTCTCGAACAGGCCT	847 bp
FAM83H 5.2	Fam5.2F: 5'GGCACCTGGAGATGGACG Fam5.2R: 5'AGCCAGCACGTCGTCTTC	647 bp
FAM83H 5.3	Fam5.3F: 5'TTTGGCCTCCTACTTGAGCG Fam5.3R: 5'AAAGGAGTCGCGCAGGTC	646 bp
FAM83H 5.4	Fam5.4F: 5'CGGAGCTGCTGGAGAAGTAC Fam5.4R: 5'GATGGTAAGGGTGAGGCTGC	620 bp
FAM83H 5.5	Fam5.5F: 5'CTTCCCGCTTCCTCTCTGC Fam5.5R: 5'TCGGACATATCTGGGGCCA	763 bp
FAM83H 5.6	Fam5.6F: 5'ACGCCTTGTACAGCAGCA Fam5.6R: 5'CACTCAGCCAAGCCCCAA	593 bp

Fig. S37. *FAM83H* Exon 5 PCR primers and reaction conditions. 5 min at 94 ˚C followed by 35 cycles of denaturing at 94 ˚C for 30 s, annealing at 58 ˚C for 30 s and extension at 73 ˚C for 3 m, and a final extension at 72 ˚C for 5 m.