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MS TITLE: A 1.1 Mb Segmental Deletion on the X Chromosome Causes Meiotic Failure in Male Mice

Supplemental information

Table S1. Genes in the *Nxf2-Nxf3* genomic interval on the X chromosome

Table S2. RT-PCR primer sequences

FIG. S1. Dynamic expression and subcellular localization of PRAMEL3 in male germ cells. **A-C)** Expression of PRAMEL3 in representative seminiferous tubules. Testis sections from 8-week-old mice were immunostained with anti-PRAMEL3 antibody (green). Nuclei were stained with DAPI. The morphology of nuclei and the association of various types of germ cells are used to determine the stages of tubules. An early stage tubule (I-IV) is shown in panel A. Stage IX tubules (**B**) are characterized by the presence of elongating spermatids and leptotene spermatocytes. Stage XII tubules (**C**) contain metaphase spermatocytes. Bottom panels show nuclear staining to visualize the distinct nuclear morphology of germ cells at different stages. **D)** Graphic of PRAMEL3 protein (green) localization during spermatogenesis. Stages (I-XII) of spermatogenesis are indicated below. Abbreviations: SG, spermatogonium; PL, preleptotene spermatocytes; L, leptotene spermatocytes; Z, zygotene spermatocytes; Pa, pachytene spermatocytes; M, metaphase spermatocytes; RS, round spermatids; ES, elongating/elongated spermatids. Scale bar, 50 μ m.

FIG. S2. Diagram of the conditional (floxed) and recombined alleles. Rectangles represent *Nxf2* and *Nxf3* exons. Triangles indicate the location and direction of the loxP sites contained within the previously generated *Nxf2^{fl}* and *Nxf3^{fl}* alleles [21, 22]. The loxP sites in *Nxf2^{fl}* and *Nxf3^{fl}* alleles are in the same orientation, permitting Cre recombinase-mediated deletion of the 1.1 Mb floxed segment.

FIG. S3. Analyses of 4-month-old mice. **A)** Body weight was not significantly different between wild type and mutant mice. **B)** Significantly reduced testis weight in *Nxf^{fl/y} Ddx4-Cre* males. **C-F)** Histological analysis of testes from 4-month-old mice. Sections were stained with hematoxylin and eosin. **C, E)** wild type. **D, F)** *Nxf^{fl/y} Ddx4-Cre*. Pa, pachytene spermatocytes; RS, round spermatids; ES, elongating/elongated spermatids. Scale bar, 50 μ m.

FIG. S4. Expression analysis of genes in the 1.1 Mb *Nxf* region and genes on either side of this region in testes from wild type and *Nxf^{fl/y} Ddx4-Cre* males of various ages. Semi-quantitative RT-PCR was performed on total RNAs from wild type and mutant testes. Three genes on either side of the *Nxf* region were analyzed: *Armcx6*, *Armcx3*, and *Armcx2* map close to *Nxf2*, whereas *5730412P04Rik*, *Bex4*, and *Tceal8* map close to *Nxf3*. *Gapdh* served as a positive control. Primer sequences are listed in supplemental Table S2. Reactions without reverse transcriptase were negative (data not shown). Notably, *Nxf2* was completely deleted in testes from *Nxf^{fl/y} Ddx4-Cre* males of all ages. Because the *Nxf2* gene harbors two closely located loxP sites (See supplemental Fig. S2), the deletion of *Nxf2* alone is more efficient and thus its deletion is not a good indicator of complete deletion of the 1.1 Mb *Nxf* segment. In contrast, deletion of genes such as *Pramel3* reflects the deletion of the entire *Nxf* segment.

Table S1. Genes in the *Nxf2-Nxf3* genomic interval on the mouse X chromosome

Gene symbol	Gene name	Comments
<i>Nxf2</i>	nuclear RNA export factor 2	reduced fertility in <i>Nxf2</i> -null males; germ cell-specific
<i>Zmat1</i>	zinc finger, matrin type 1	a C2H2-type zinc finger protein
3632454L22Rik	transcribed sequence	small putative coding region with homology to ZMAT1; a putative lincRNA
<i>Gm6207</i>	predicted gene 6207	pseudogene
<i>Gm15023</i>	predicted gene 15023	nearly identical to <i>Pramel3</i>
<i>Tceal6</i>	transcription elongation factor A (SII)-like 6	contains the BEX (Brain-expressed X-linked) domain
<i>Pramel</i>	preferentially expressed antigen in melanoma-like	LRR (leucine-rich repeat)-containing protein
<i>Pramel3</i>	preferentially expressed antigen in melanoma-like 3	germ cell-specific in testis
<i>Gm6215</i>	predicted gene 6215	lincRNA
<i>Gm5128</i>	predicted gene 5128	nearly identical to <i>Pramel3</i>
<i>Gm6221</i>	predicted gene 6221	nearly identical to <i>Gm6215</i>
<i>Gm7903</i>	predicted gene 7903	nearly identical to <i>Pramel3</i>
<i>Gm7905</i>	predicted gene 7905	nearly identical to <i>Gm6215</i>
AV320801	expressed sequence AV320801	nearly identical to <i>Pramel3</i>
<i>Gm6228</i>	predicted gene 6228	pseudogene
<i>Nxf7</i>	nuclear RNA export factor 7	NXF7 localizes to cytoplasmic granules such as stress granules and P bodies
<i>Prame</i>	preferentially expressed antigen in melanoma	member of <i>Prame</i> gene family
<i>Tcp1113</i>	t-complex 11 (mouse) like 3	RIKEN cDNA 1700008I05 gene with extensive homology to <i>Tcp11</i>
<i>Tmsb15a</i>	thymosin beta 15a	member of thymosin beta-4 family
<i>Armcx5</i>	Armcx5 armadillo repeat containing, X-linked 5	the armadillo-like repeats (Arm2) domain mediates protein interactions; 5' exons are shared with <i>Gprasp1</i>
<i>Gprasp1</i>	G protein-coupled receptor associated sorting protein 1	decreased behavioral responses to cocaine in <i>Gprasp1</i> -null mice; contains an Arm2 domain
<i>mmu-mir-1970</i>	microRNA	mapped within the <i>Gprasp1</i> gene
<i>Gprasp2</i>	G protein-coupled receptor associated sorting protein 2	contains an Arm2 domain
<i>Bhlhb9</i>	basic helix-loop-helix domain containing, class B9	contains an Arm2 domain
<i>Gm15016</i>	predicted gene 15016	pseudogene
<i>Arxes2</i>	adipocyte-related X-chromosome expressed sequence 2	signal peptidase subunit
<i>Arxes1</i>	adipocyte-related X-chromosome expressed sequence 1	signal peptidase subunit
<i>Bex2</i>	brain expressed X-linked 2	a putative tumor suppressor in human glioma; contains the BEX domain
<i>Nxf3</i>	nuclear RNA export factor 3	normal fertility in <i>Nxf3</i> -null males; Sertoli cell-specific

Notes: 1) The "20 genes" in this region do not include three predicted pseudo genes: *Gm6207*, *Gm6228*, *Gm15016* (in red).

2) *Pramel3* and its four close homologues (*Gm15023*, *Gm5128*, *Gm7903*, and *AV320801* in green) are counted once.

3) *Gm6215*, *Gm6221*, and *Gm7905* (in blue) are nearly identical and are counted once.

Table S2. RT-PCR primer sequences

Gene symbol	Primer sequence	PCR product size (bp)
<i>Armcx6</i>	GACTTGAGAAGAAGCAACCCG TGCCATCCAACCCATTTC	334
<i>Armcx3</i>	GGAAGGAAATTAACCAGATCGG CCCAGAACAGTCCCCAGCA	480
<i>Armcx2</i>	GTATTCCTGCCCTTCAACCC GCACTCGCCCCAATCACTA	397
<i>Nxf2</i>	CTGAACTGTTGTCCTTGAAGT AAGGAACTGACAAGGAGAAGC	657
<i>Zmat1</i>	ATGGAGAACAAGCGAAGTGC TTCAGGAAGGGTGGAGGTGC	274
<i>3632454L22Rik</i>	TGCCAAACCTTCCCTCCCA TGTGAAGGCACCCATAGAGCTG	340
<i>Tceal6</i>	TGGGTCTCCTCAGGTCTCTGC CTCATCTTGCCCCTGCTCAT	292
<i>Pramel</i>	GTCTACACAGATTGCTCAGAGTCCT TTTCAGCTCCATTAGTGGTAGTAAGT	377
<i>Pramel3</i>	TATGATGGACACCAAGGACCC CAGCATCCTGCCTTAAATCTAGG	335
<i>Gm6215</i>	GATCTTTTCCTTGATGGCTCCT GAAAGACCACAGAATGGCAGATAC	434
<i>Nxf7</i>	ATTTTGTCAATCCCTCGGTT TTCAGCCCTTTCATCTTCTCC	383
<i>Prame</i>	GAGGTCTGCGTCAACTGGG CAAAGCGAGGATGGGTCTC	498
<i>Tcp1113</i>	AACTGTCACAAACCCTCCTG TCTGTGGCAGCTCTAGTCATCC	466
<i>Tmsb15a</i>	ACTGCAAGGGCAGCATCAGT CCAGTGTTGGCATTATTTGTTG	263
<i>Armcx5</i>	GCTATGTAGTCGCTTCGTGAGG TGTGGAGGGTGGTGGTCTTC	440
<i>Gprasp1</i>	AGATCTTGGAGGACTCCCTGC TGACAATTCAGCACTCAGTGAGG	273
<i>Gprasp2</i>	AGATCTTGGAGGACTCCCTGC TAAATGACCAACTAATCCAGTACCA	281
<i>Bhlhb9</i>	GGTTTTGGGAAGGCGATGA GCAAGCGAAGGGCTTGATG	386
<i>Arxes</i>	GGCTTCATCACCTTCCACATC ATCCCAGCAATCGGTATCACT	278
<i>Bex2</i>	GCGAGCGGGACAGATTGACT TGTCTCACATCATCCCCAAACC	375
<i>Nxf3</i>	CAGCATCCCTTTCCTCCG AGAGTTCACCTGGGTCATATCC	334
<i>5730412P04Rik</i>	CACGGTTAGACCTTATGCTGG GGAGGATTGCCTTATCTTGGA	384
<i>Bex4</i>	AGAAAGAGGAGAAGGCAAGGAT GAAACCGTTAAGTGAAACACC	498
<i>Tceal8</i>	GCTACTTCCAGCACTCTTGATCT CTCTCCTCTATGGCTCCCTTC	267

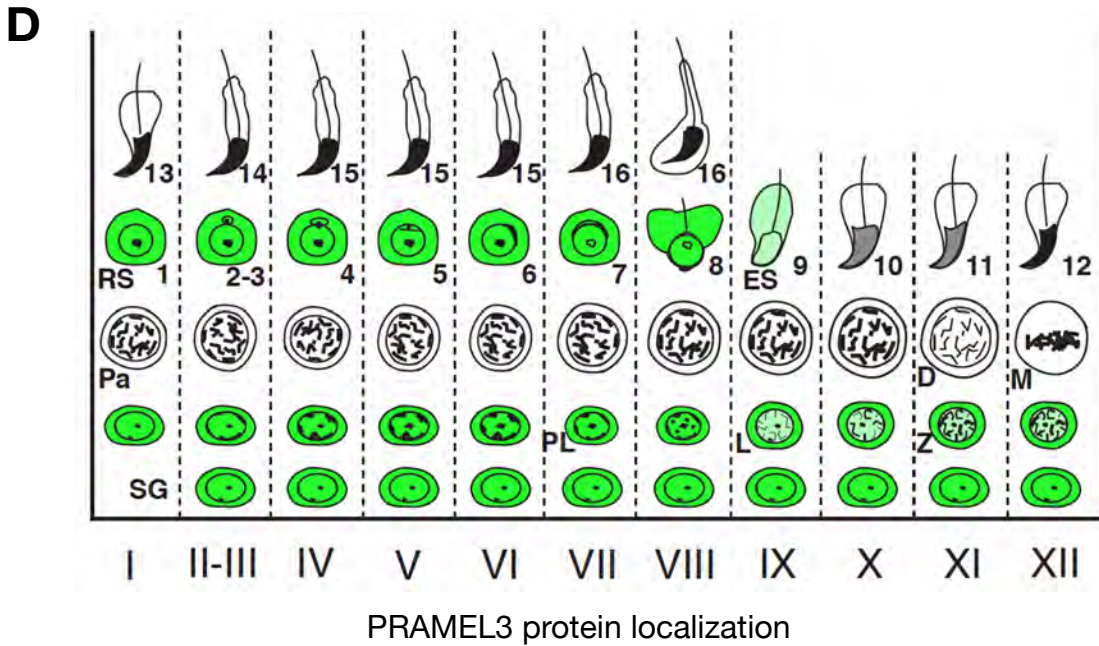
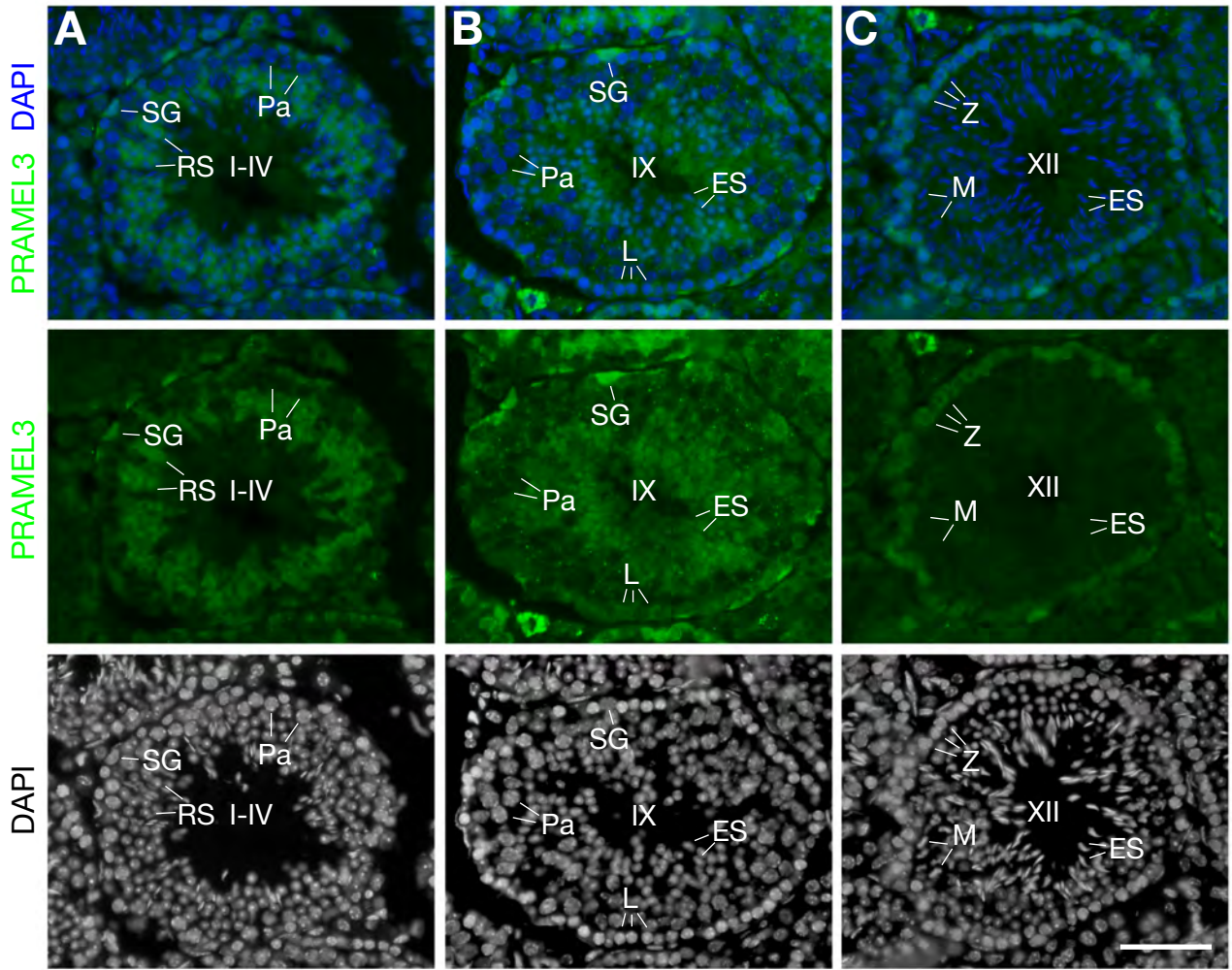


Fig. S1

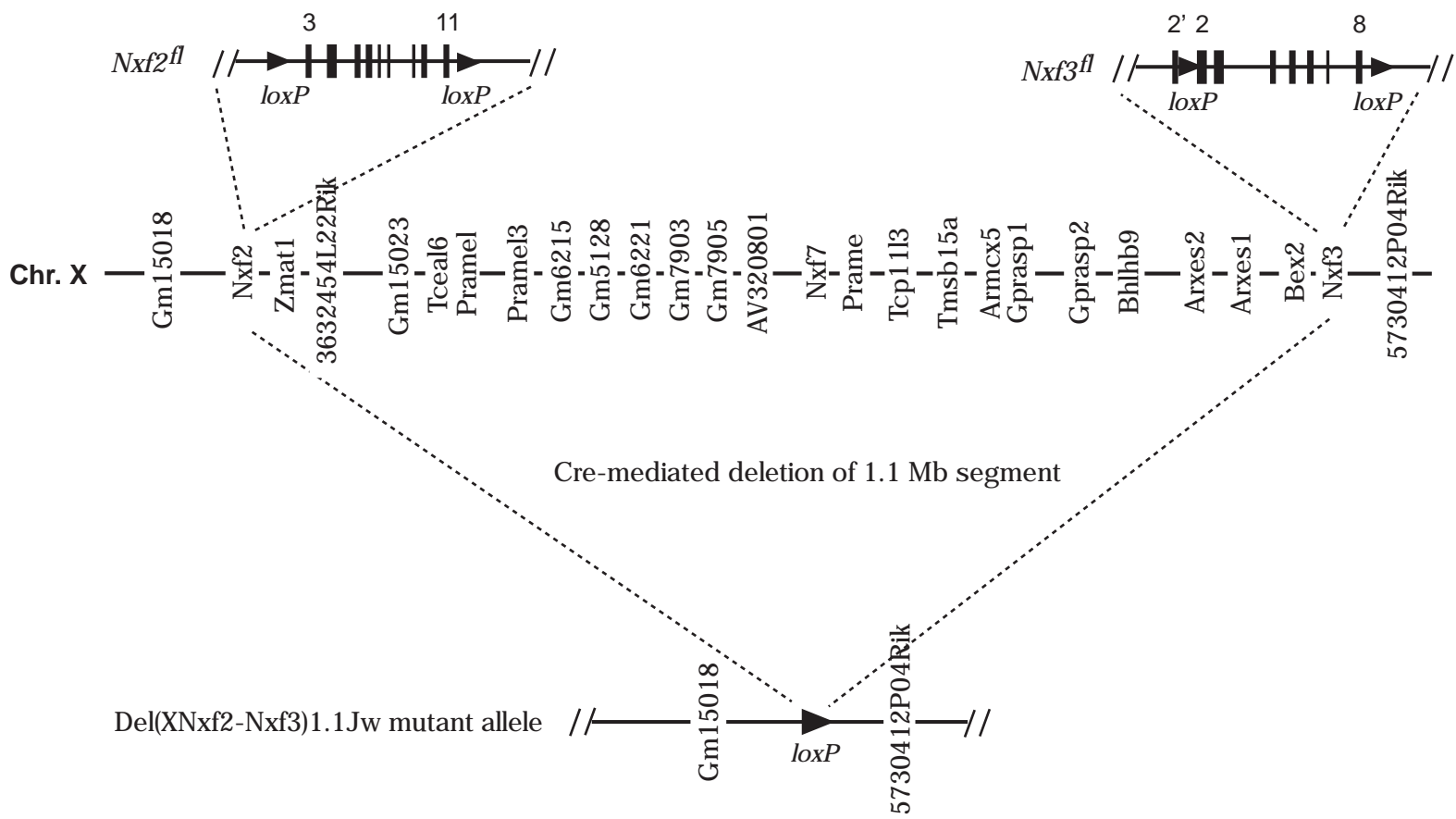
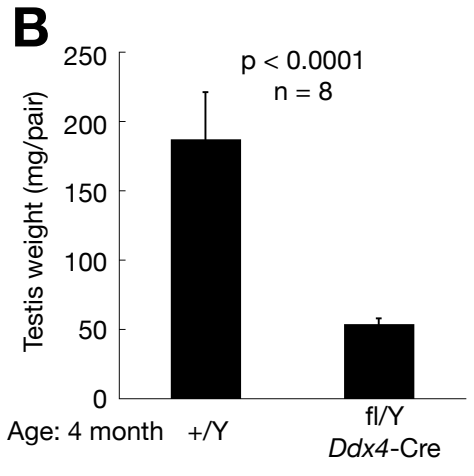
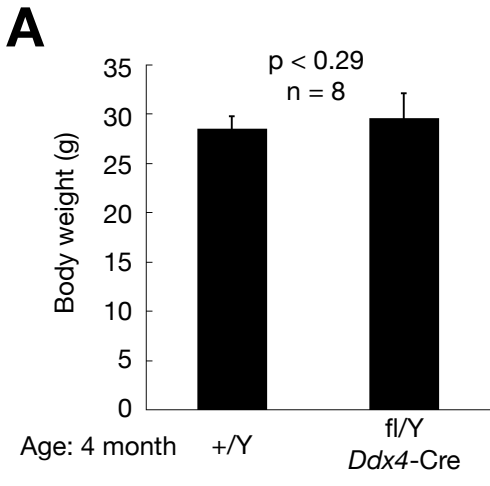


Fig. S2



+/Y (4-month)

fl/Y *Ddx4-Cre* (4-month)

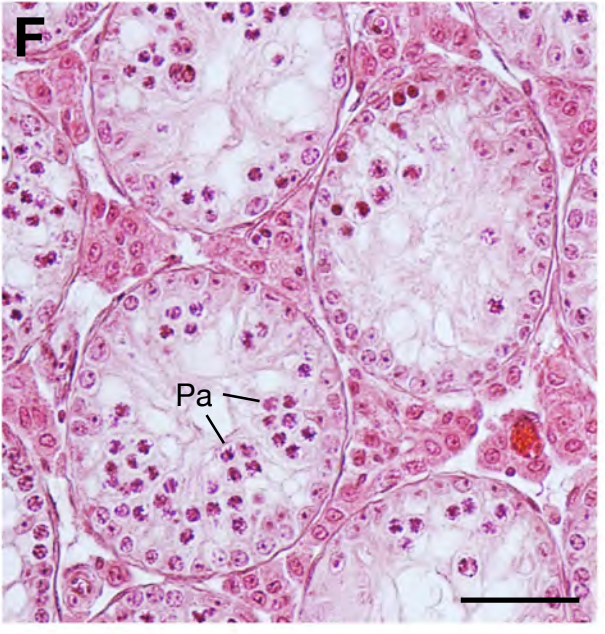
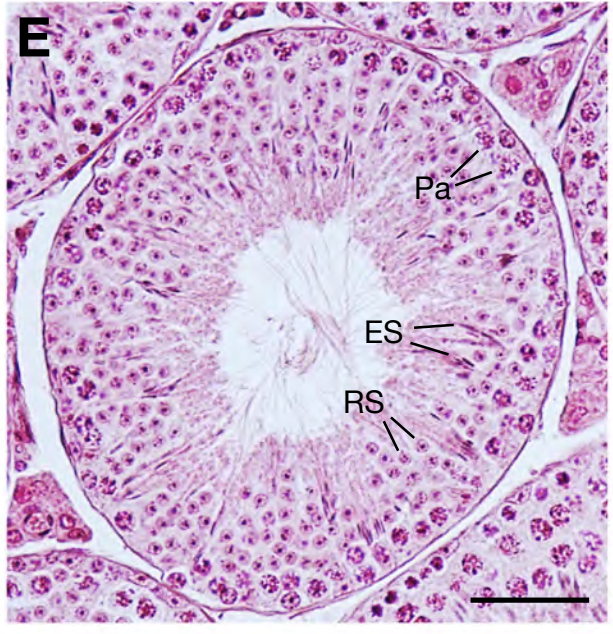
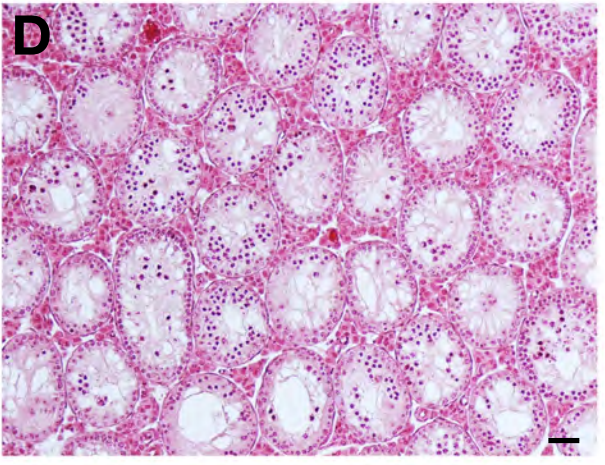
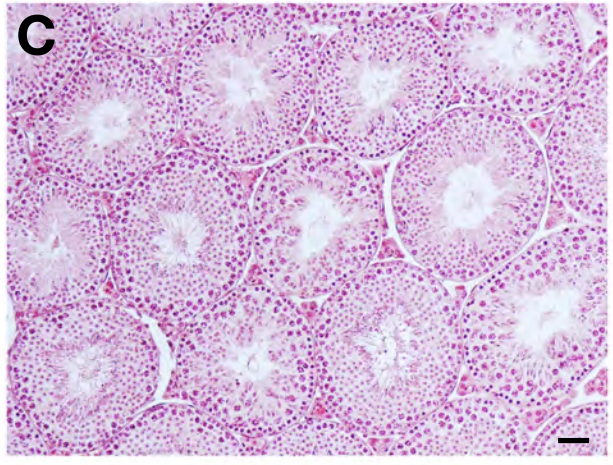


Fig. S3

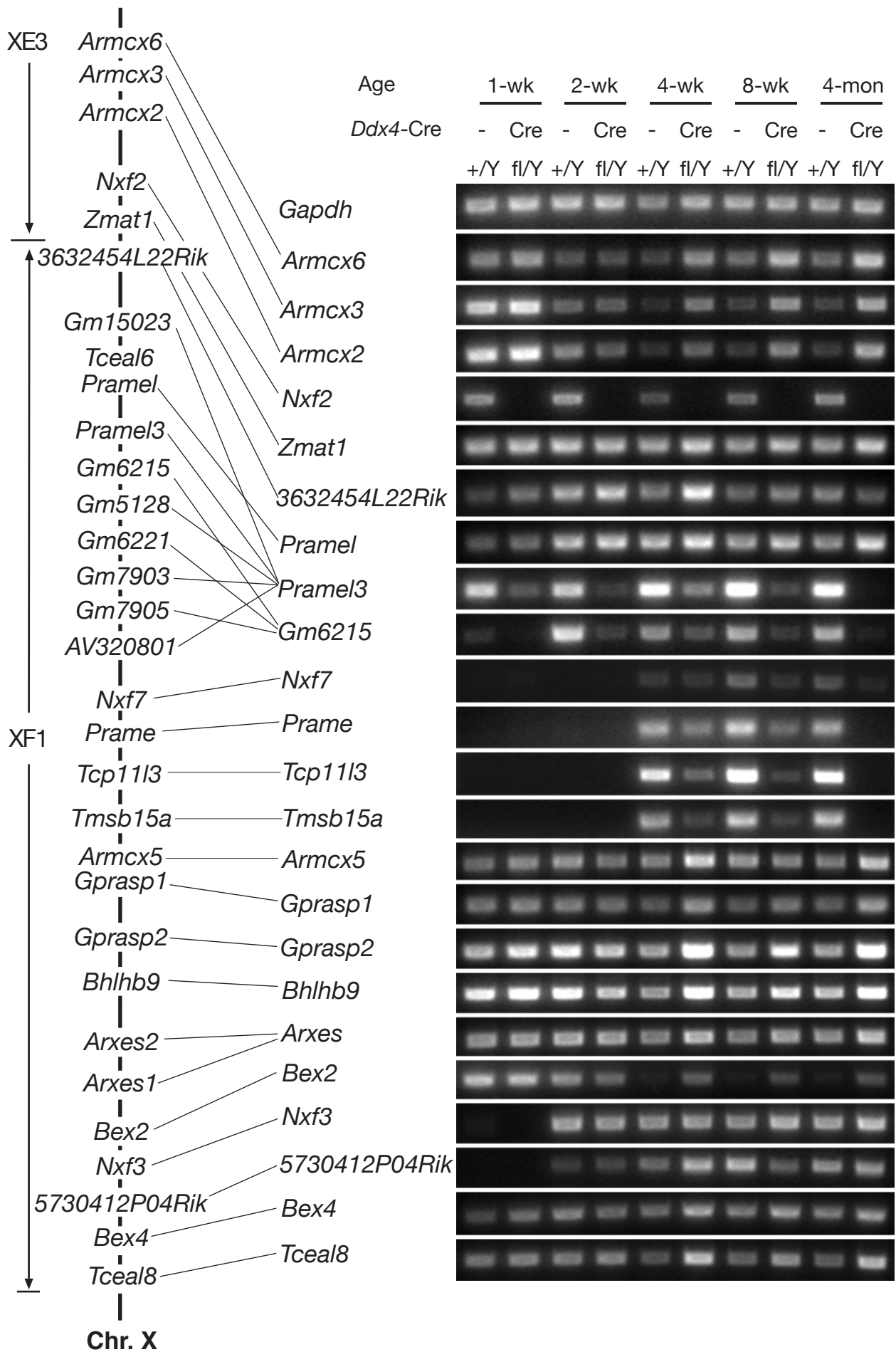


Fig. S4