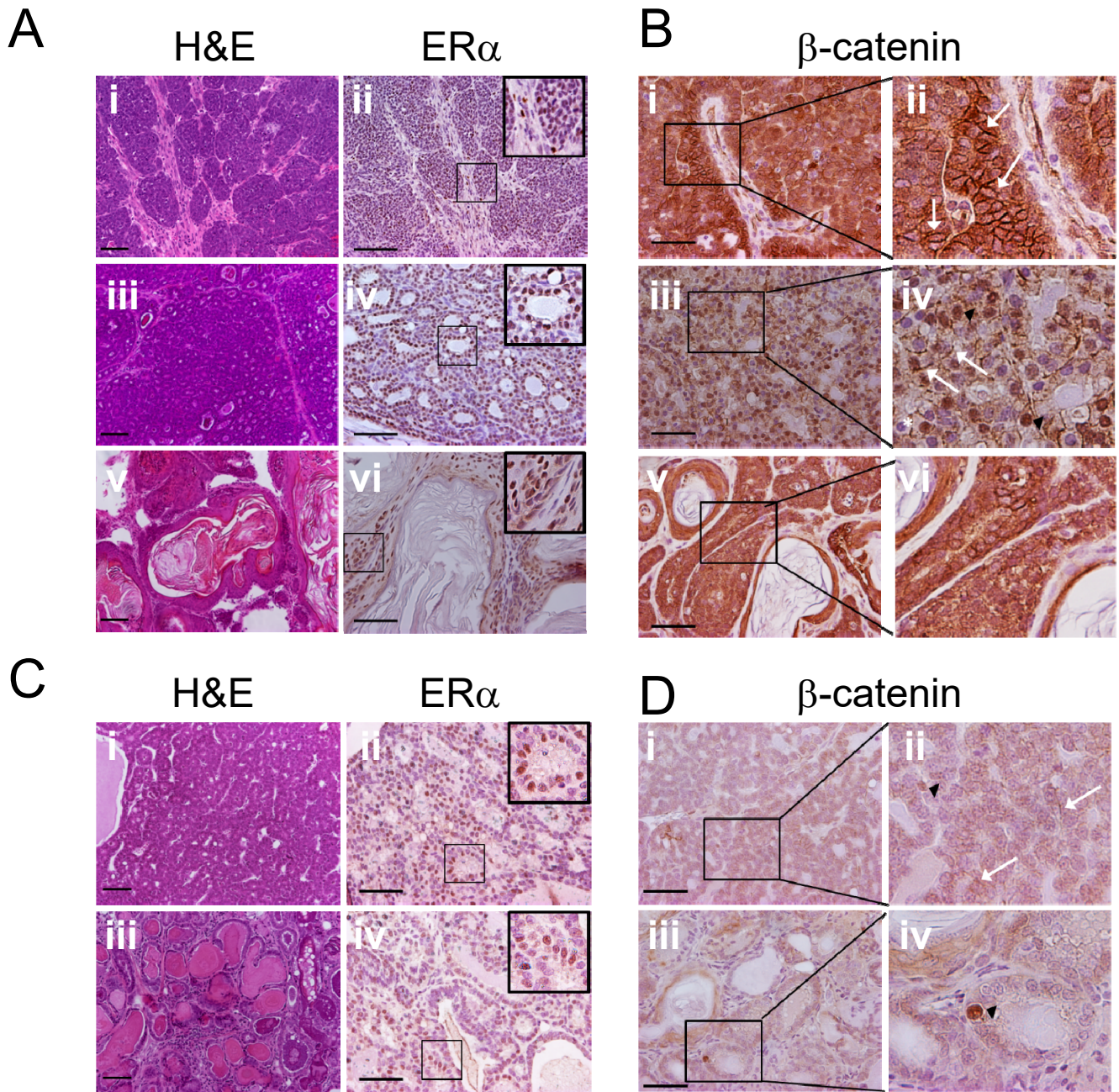


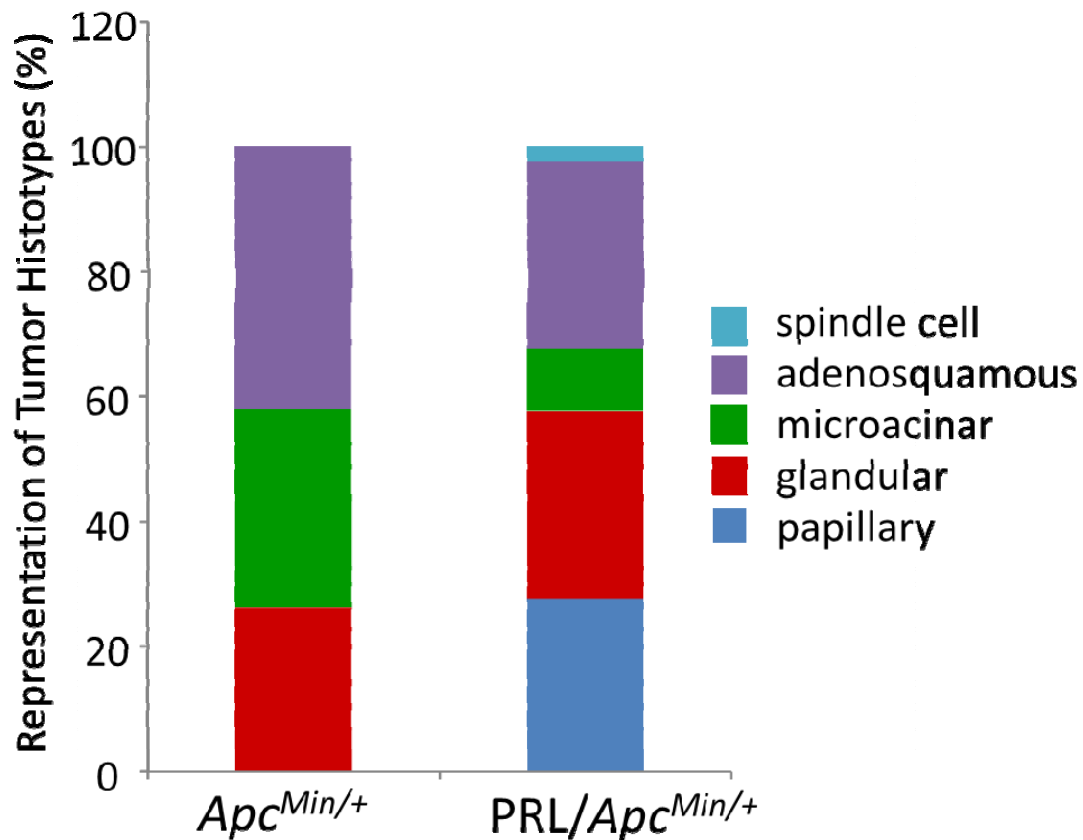
**Supplemental Table S1. PCR Primers**

<p><b>Genetic manipulations</b></p> <p>rPRL transgene</p> <p><i>Apc</i><sup>Min</sup> germline mutation</p> <p><i>Apc</i> hotspot region (aa 1512-1579), sequencing tags in bold</p>	<p>5' CCTCCTCATTCTCTGCTCTTC 3' 5' CCAATCACCTTGCTCTAAACCC 3'</p> <p>5' TGAGAAAGACAGAAGTTA 3' 5' TTCCACTTTGGCATAAGGC 3' Internal control, 5'GCCATCCCTTCACGTTAG</p> <p>5' <b>GTT TTC CCA GTC ACG ACC</b> CAA GCA GAA GCA AAA CCC C 3' 5' <b>CAG GAA ACA GCT ATG ACC</b> CTC GCT GAG CAT CAT CTG T 3'</p>
<p><b>qRT-PCR</b></p> <p><i>18S</i></p> <p><i>Axin2</i></p> <p><i>Ccnd1</i></p> <p><i>Ccne1</i></p> <p><i>Cdkn2c</i></p> <p><i>Hes1</i></p> <p><i>Hey1</i></p> <p><i>Nrarp</i></p> <p><i>Notch1</i></p> <p><i>Notch2</i></p>	<p>F, 5' CGC CGC TAG AGG TGA ATT TCT 3' R, 5' CGA ACC TCC GAC TTT CGT TCT 3'</p> <p>F, 5' CCA GGC TGG AGA AAC TGA AAC T 3' R, 5' CCT GCT CAG ACC CCT CCT TT 3'</p> <p>F, 5' CAT CAA GTG TGA CCC GGA CTG 3' R, 5' CCT CCT CCT CAG TGG CCT TG 3'</p> <p>F, 5' GCC AAG ATT GAC AAG ACT GTG AAA 3' R, 5' GGT CCA CGC ATG CTG AAT TA 3'</p> <p>F, 5' CAA CGC CCC GAA CTC TTT C 3' R, 5' AGC AGA AGA GCT GCT ACG TGA A 3'</p> <p>F, 5' TAC CCC AGC CAG TGT CAA CA 3' R, 5' CCT TCG CCT CTT CTC CAT GA 3'</p> <p>F, 5' GGT ACC CAG TGC CTT TGA GA 3' R, 5' GGC GTG CGC GTC AAA ATA A 3'</p> <p>F, 5' CCA GCG TTG TGA AGG CTG TT 3' R, 5' GCA GCC CTT CCA CTC ATT CA 3'</p> <p>F, 5' ACA ACA ACG AGT GTG AGT CC 3' R, 5' ACA CGT GGC TCC TGT ATA TG 3'</p> <p>F, 5' TAC CTA CCA CAA CGG CAC AG 3' R, 5' TCT CAC AGG GGT CTC GAT GT 3'</p>

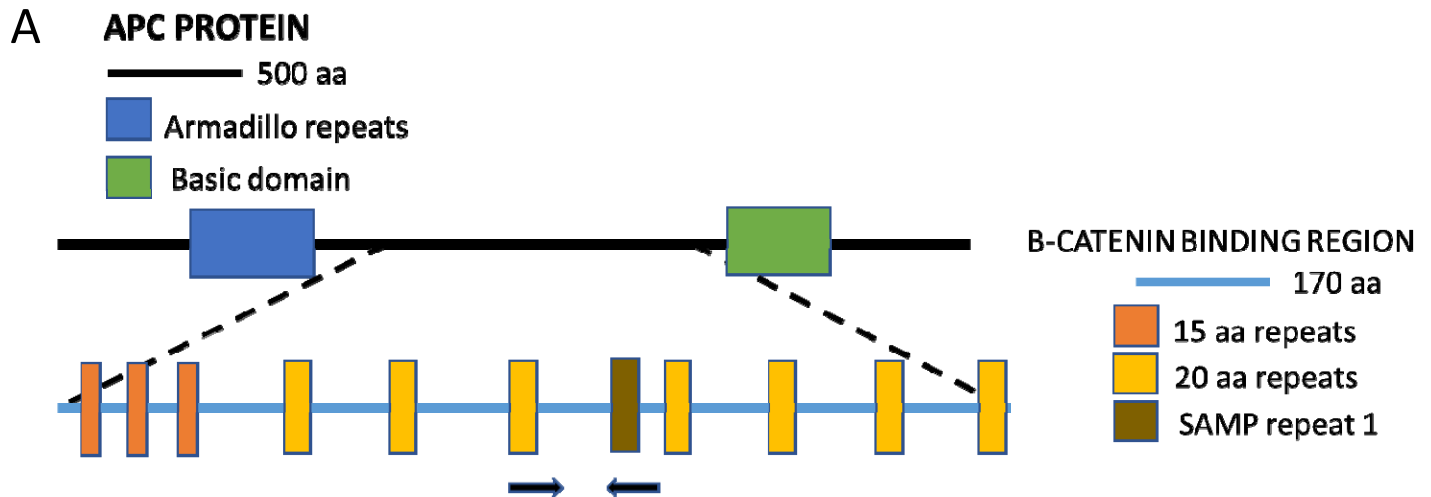
<i>Notch3</i>	F, 5' AGA TCA ATG AGT GTG CAT CC 3' R, 5' GCA GAC TCC ATG ACT ACA GG 3'
<i>Notch4</i>	F, 5' AAT GGG GGT ACC TGT GTG AA 3' R, 5' GTA TAG CCA GGG CTG CAG AG 3'
<i>Sox2</i>	F, 5' CCA CCA ATC CCA TCC AAA TT 3' R, 5' CAA AAA GAA GTC CCA AGA TCT CTC A 3'
<i>Sox9</i>	F, 5' CGA GCA CTC TGG GCA ATC TC 3' R, 5' CCT CTC GCT TCA GAT CAA CTT TG 3'
<i>Tcf4</i>	F, 5' CCT CGT CAT CTC CCA ATT ATG AA 3' R, 5' GTC TTT CCA AAC GGT CTT CGA T 3'



**Suppl. Fig. S1. Tumors from *Apc<sup>Min/+</sup>* (A,B) and NRL-PRL (C,D) females.** (A) *Apc<sup>Min/+</sup>* tumors. Left, hematoxylin and eosin (H&E) stained representative histotypes (i, ii, glandular; iii, iv, microacinar; v, vi, adenosquamous). Right, ER $\alpha$  expression by immunohistochemistry; insets as shown. (B) Tumors from *Apc<sup>Min/+</sup>* females exhibited heterogeneous cellular localization of  $\beta$ -catenin; insets as shown. (i, ii, glandular; iii, iv, microacinar; v, vi, adenosquamous). (C) Tumors from NRL-PRL females. Left, H&E stained histotypes (i, ii, glandular; iii, iv, papillary). Right, ER $\alpha$  expression by immunohistochemistry; insets as shown. (D) Tumors that developed NRL-PRL females exhibited lower  $\beta$ -catenin expression compared to tumors from *Apc<sup>Min/+</sup>* and NRL-PRL/*Apc<sup>Min/+</sup>* females; insets as shown. (i, ii, glandular; iii, iv, papillary). White arrows indicate membrane  $\beta$ -catenin, black arrowheads indicate nuclear  $\beta$ -catenin, and white asterisk shows cell with negligible detectable  $\beta$ -catenin. Scale bars, 100  $\mu$ m. Original magnifications, H&E, x100;  $\beta$ -catenin, ER $\alpha$ , x200.



**Suppl. Fig. S2. Tumors that develop in *Apc*<sup>Min/+</sup> and NRL-PRL/*Apc*<sup>Min/+</sup> females exhibit similar spectra of histotypes, except that papillary carcinomas develop only in the presence of PRL. N= 19 tumors in *Apc*<sup>Min/+</sup> females; N=40 tumors in NRL-PRL/*Apc*<sup>Min/+</sup> females. Tumors in NRL-PRL females are not shown because of the low number of tumors (2 x papillary, 1 glandular. N=3).**



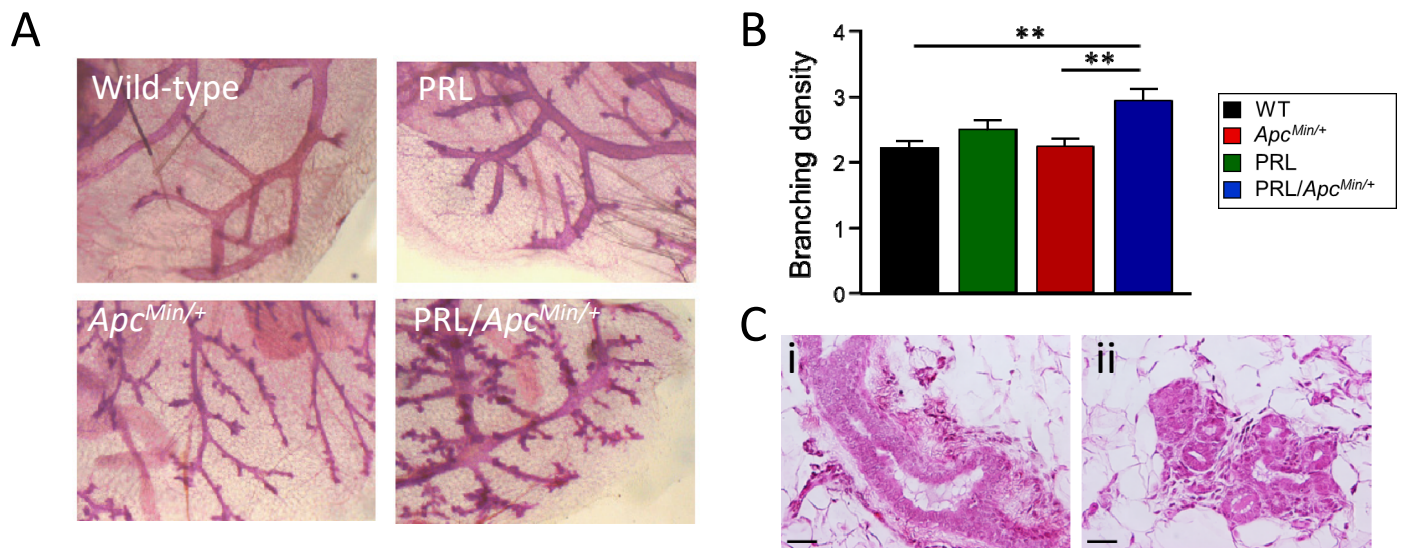
**B**

Mutation	<i>Apc</i> <sup>Min/+</sup>	PRL/ <i>Apc</i> <sup>Min/+</sup>	Histotype
None		4	adenosquamous, papillary, 2 x glandular
AA1512 (G/T)AG		1	adenosquamous
AA1516 (C/T)AG		2	2 x adenosquamous
AA1521 T(T/A)A		1	papillary
AA1521 T(T/G)A		3	adenosquamous, 2 x glandular
AA1528 (C/T)AG	1		adenosquamous
AA1529 (G/T)AA	1		adenosquamous
AA1531 <b>GGAC</b>		1	glandular
AA1539 (G/T)AA	1	1	2 x glandular
AA1540 (C/T)AG	1	2	adenosquamous, 2 x papillary
AA1548 (C/T)AG		1	glandular
AA1561 T(T/A)A	1		adenosquamous
AA1562 T(T/G)A	1		microacinar
AA1568 <del>GAT</del>	1	1	glandular, adenoquamous
AA1569 <del>GAT</del>	1		adenosquamous
AA1576 TG(T/A)	1		glandular
<b>TOTAL</b>	9/9 (100.0%)	13/17 (76.5%)	
#/ total #(percentage)			

⚭-strikethrough: deletion

**NN** bold: insertion

**Suppl. Fig. S3. Tumors in PRL/ *Apc*<sup>Min/+</sup> and *Apc*<sup>Min/+</sup> females acquire a somatic mutation in the second *Apc* allele.** (A) Diagram of the APC protein. Expanded area,  $\beta$ -catenin binding region. Arrows indicate the region where somatic mutations cluster in mammary tumors in mutant *Apc* models (Kuraguchi et al., 2009; Keller et al., 2016). This region was sequenced in a subset of tumors in this study. aa, amino acids. (B) Somatic mutations detected in tumors in this region of the *Apc* gene in *Apc*<sup>Min/+</sup> and NRL-PRL-*Apc*<sup>Min/+</sup> ENU-treated females.



**D** Incidence of microscopic mammary abnormalities in 120 d.o. ENU-treated females<sup>a</sup>

	WT	<i>Apc<sup>Min/+</sup></i>	NRL-PRL	NRL-PRL/ <i>Apc<sup>Min/+</sup></i>
Focal Irregular ductal epithelium <sup>b</sup>	(0/7)	(5/7)	(2/6)	(5/6)
Focal epithelial hyperplasias				
Small <sup>c</sup>	(2/7)	(7/7)	(6/6)	(6/6)
Large <sup>d</sup>	(0/7)	(7/7)	(0/6)	(6/6)
Squamous changes <sup>e</sup>	(0/7)	(6/7)	(0/6)	(5/6)

<sup>a</sup>Number of mice exhibiting lesions/ total number of mice examined in H&E stained sections.

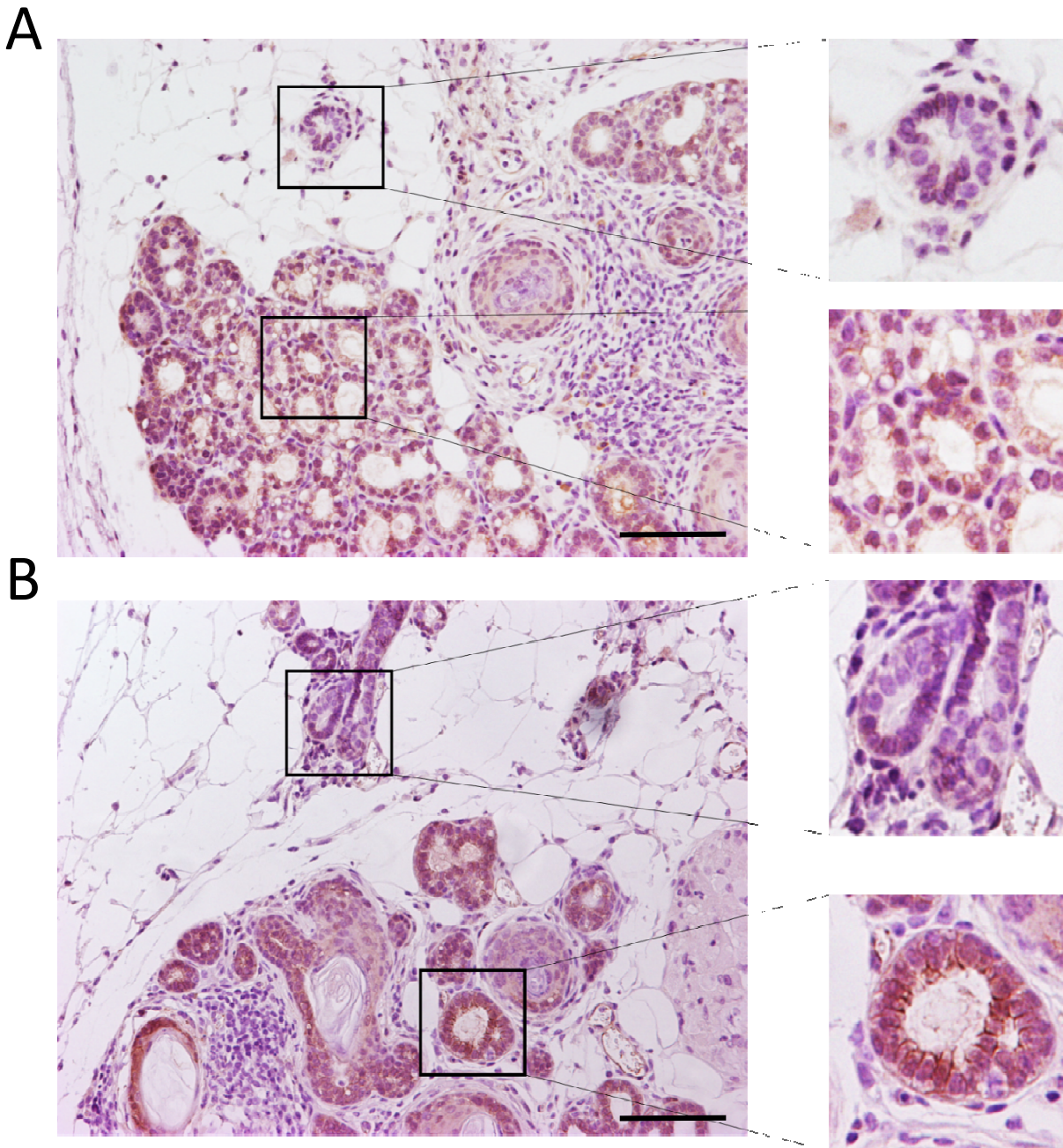
<sup>b</sup>Illustrated in Fig. S4CI

<sup>c</sup>Small epithelial hyperplasias were defined as structures with 5-20 lumens, each surrounded by cuboidal epithelial cells (illustrated in Fig. S4CII).

<sup>d</sup>Large epithelial hyperplasias were defined as structures with more than 20 lumens, each surrounded by cuboidal epithelial cells (illustrated in Fig. 4A)

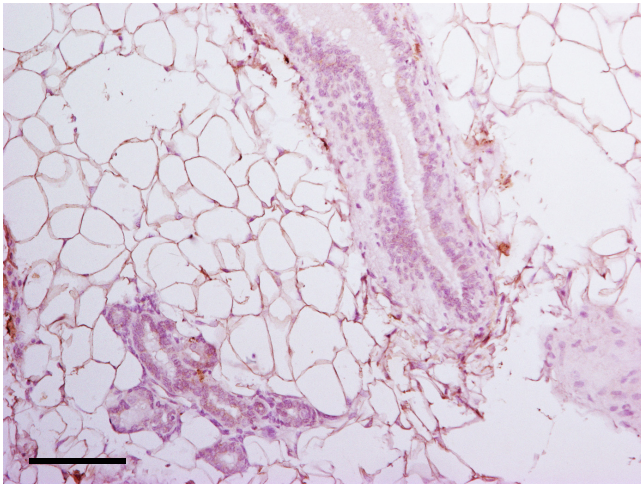
<sup>e</sup>Illustrated in Fig. 4A.

**Suppl. Fig. S4. PRL influences epithelial structures in 120 d.o. ENU-treated females, but in the absence of *Apc<sup>Min/+</sup>*, few mammary abnormalities are observed.** (A) PRL cooperates with *Apc<sup>Min/+</sup>* to increase ductal branching. Representative mammary whole mounts, stained with carmine alum. (B) Quantitation of ductal branching (mean ± S.E.M. \*\*,  $p < 0.01$ ;  $N = 4-7$ ). (C) Image of (i) irregular ductal epithelium; and (ii) small epithelial hyperplasia (Hematoxylin/eosin stain). Scale bars, 100  $\mu\text{m}$ . Original magnifications,  $\times 200$ . (D) Incidence of microscopic mammary abnormalities.

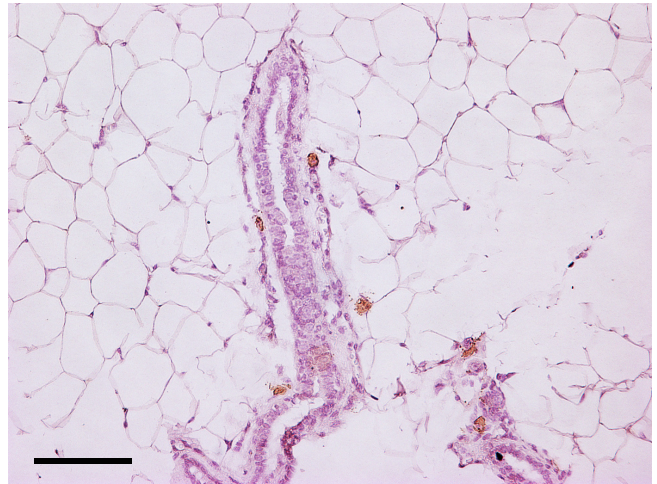


**Suppl. Fig. S5. Ductal luminal epithelium does not accumulate  $\beta$ -catenin in either *Apc<sup>Min/+</sup>* or NRL-PRL/*Apc<sup>Min/+</sup>* 120 d.o. ENU-treated females.** (A) Large epithelial hyperplasias in mammary glands of ENU-treated *Apc<sup>Min/+</sup>* females exhibited abundant nuclear  $\beta$ -catenin, which was not evident in ductal structures. (B) Epithelial hyperplasias in mammary glands of ENU-treated NRL-PRL *Apc<sup>Min/+</sup>* females exhibited abundant  $\beta$ -catenin at the plasma membrane, which was not evident in ductal structures. (A,B) Upper right insets, ductal structures; lower insets, epithelial hyperplasias. Scale bar, 500  $\mu$ m. Original magnifications, x100.

**A** *Apc*<sup>Min/+</sup>



**B** NRL-PRL/*Apc*<sup>Min/+</sup>



**Suppl. Fig. S6. Ductal luminal epithelium expresses little NOTCH1 in either *Apc*<sup>Min/+</sup> or NRL-PRL/*Apc*<sup>Min/+</sup> 120 d.o. ENU-treated females. (A) Mammary gland from *Apc*<sup>Min/+</sup> female. (B) Mammary gland from NRL-PRL/*Apc*<sup>Min/+</sup> female. Scale bar, 500  $\mu$ m. Original magnifications, x100.**