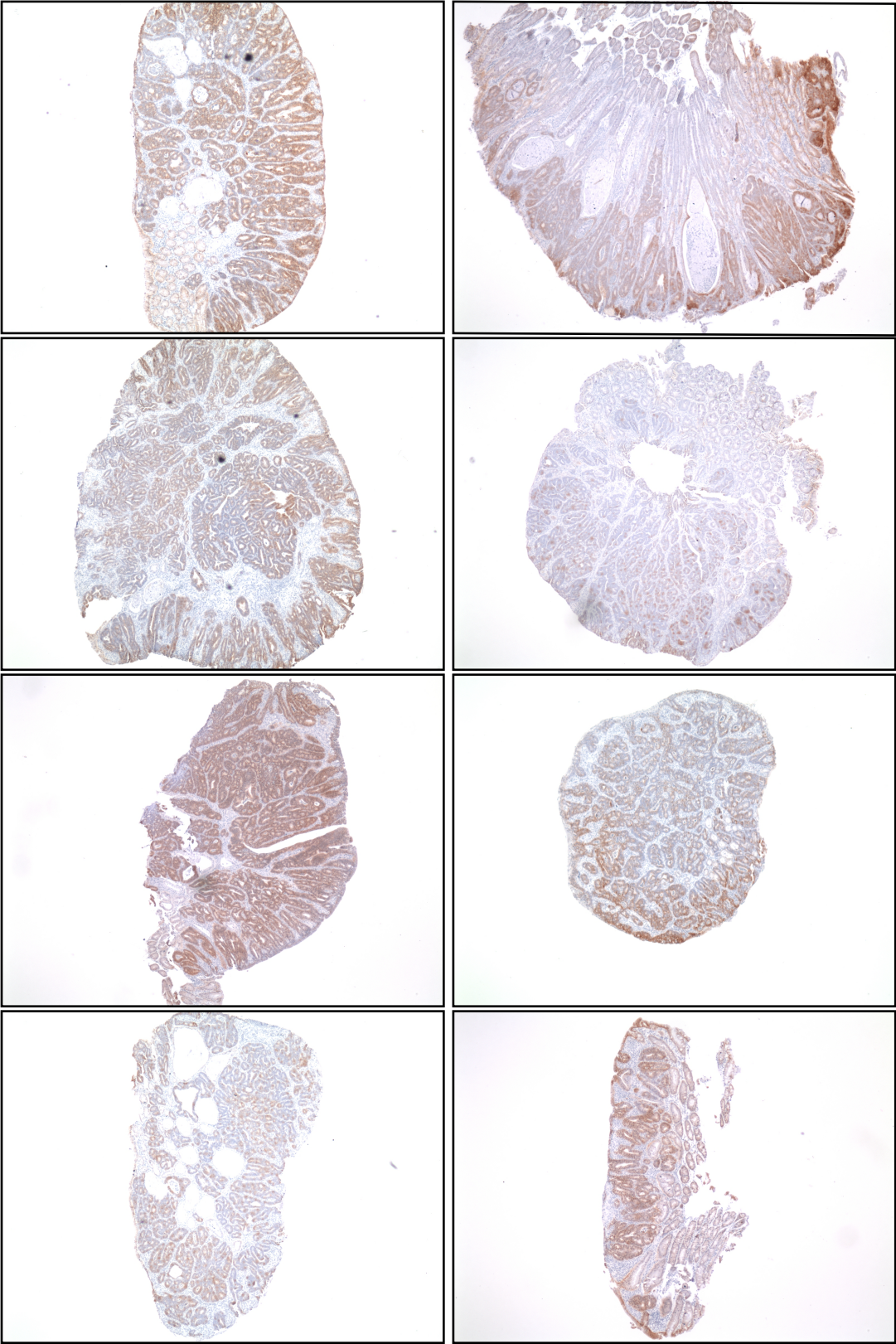


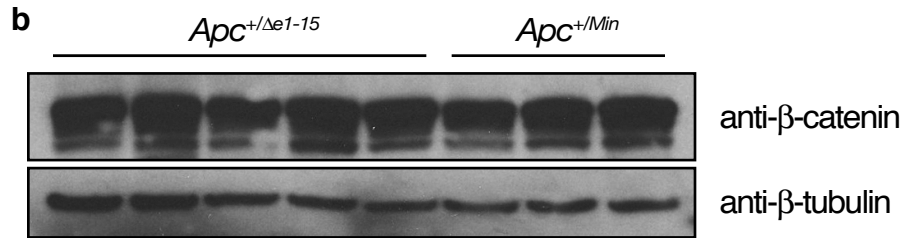
Supplemental Figure 1.

a

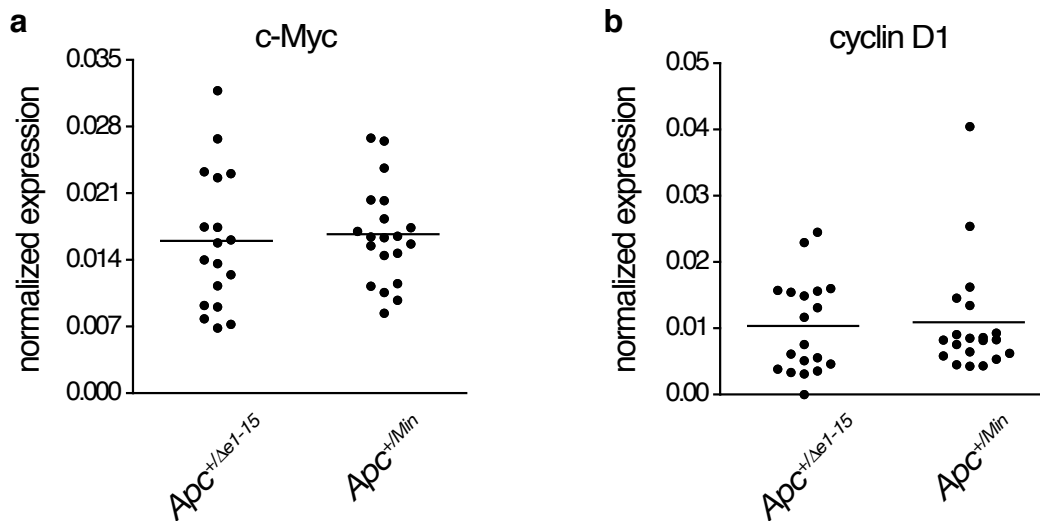
Apc^{+/ Δ e1-15}

Apc^{+/*Min*}





Supplemental Figure 1. No difference in β-catenin protein abundance is apparent between colon tumors from *Apc*^{+/Δe1-15} and *Apc*^{+/Min} mice. a. Immunohistochemistry and b. Western blot detection of β-catenin (anti-β-catenin mouse mAb, BD Transduction Laboratories cat# 610154) in colon tumors from aged *Apc*^{+/Δe1-15} and *Apc*^{+/Min} mice. Representative samples are shown. Immunohistochemistry was performed on formalin-fixed paraffin sections as previously described (Haigis et al., 2008). Samples for Western blot were prepared by flushing freshly dissected colons with cold PBS, plucking colonic tumors from intestinal surface, and snap freezing in liquid nitrogen. Tissues were thawed and homogenized on ice in RIPA lysis buffer and cell debris was pelleted. Samples were subject to SDS-PAGE under reducing condition and transferred onto PVDF membranes. Membranes were blocked and hybridized with primary and secondary antibodies in TBS-T supplemented with 5% BSA and developed using Amersham ECL Plus detection kit.



Supplemental Figure 2. Transcript levels of c-Myc and cyclin D1 remain comparable between colon tumors from $Apc^{+/\Delta e1-15}$ and $Apc^{+/Min}$ mice. Quantitative Real-time PCR for a. c-Myc and b. cyclin D1 in colon tumors from aged $Apc^{+/\Delta e1-15}$ and $Apc^{+/Min}$ mice. Bars, mean. Samples were prepared by flushing fresh colons with cold PBS and plucking colonic tumors from intestinal surface. Tissues were then minced with a razor blade before Trizol extraction for RNA. RNA was quantified by spectrophotometer, and RNA quality was assessed by agarose gel electrophoresis and visualization of 28S and 18S ribosomal RNA bands. Non-degraded samples were subjected to cDNA synthesis using random primers and Superscript III reverse transcriptase. Samples were treated with RNase H to degrade template RNA after cDNA synthesis was complete. Taqman probes and reagents were purchased from Applied Biosystems. Relative expression of transcripts was determined by normalization to GAPDH.