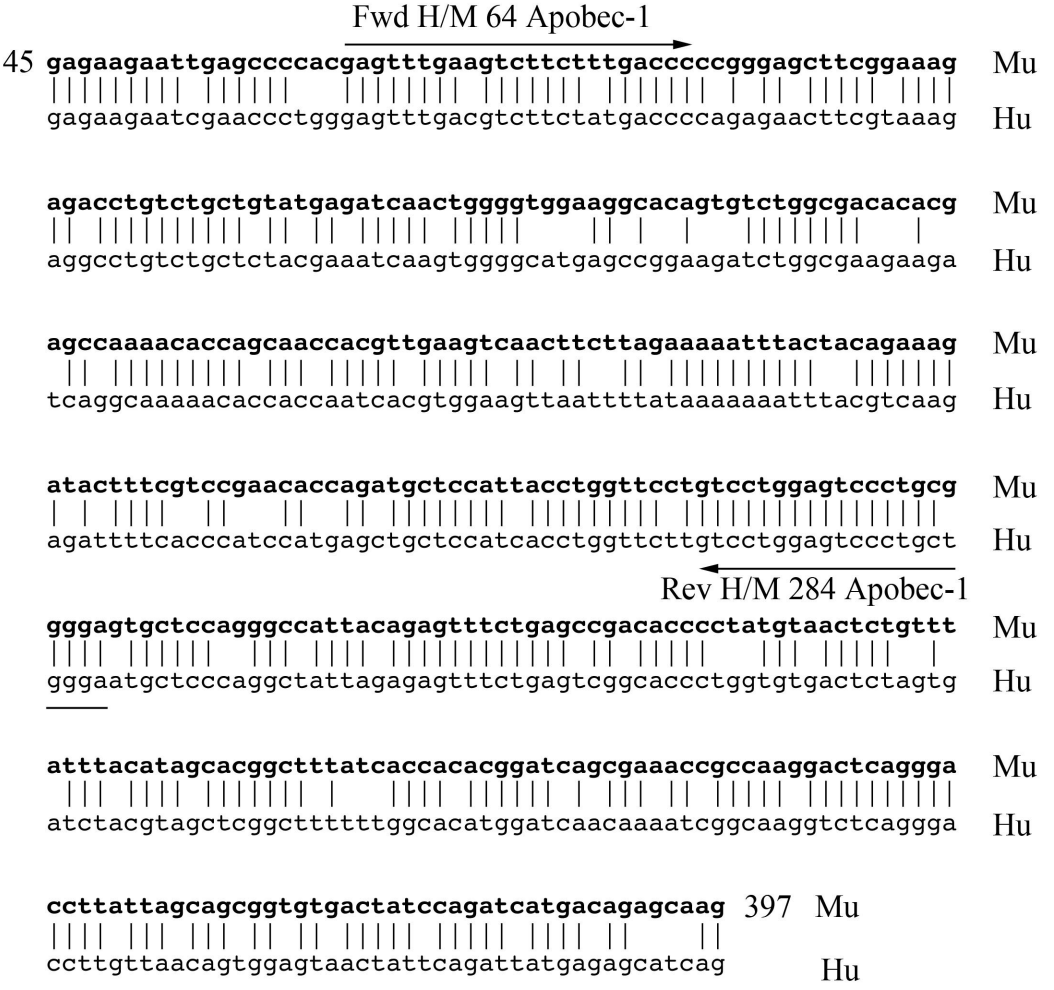
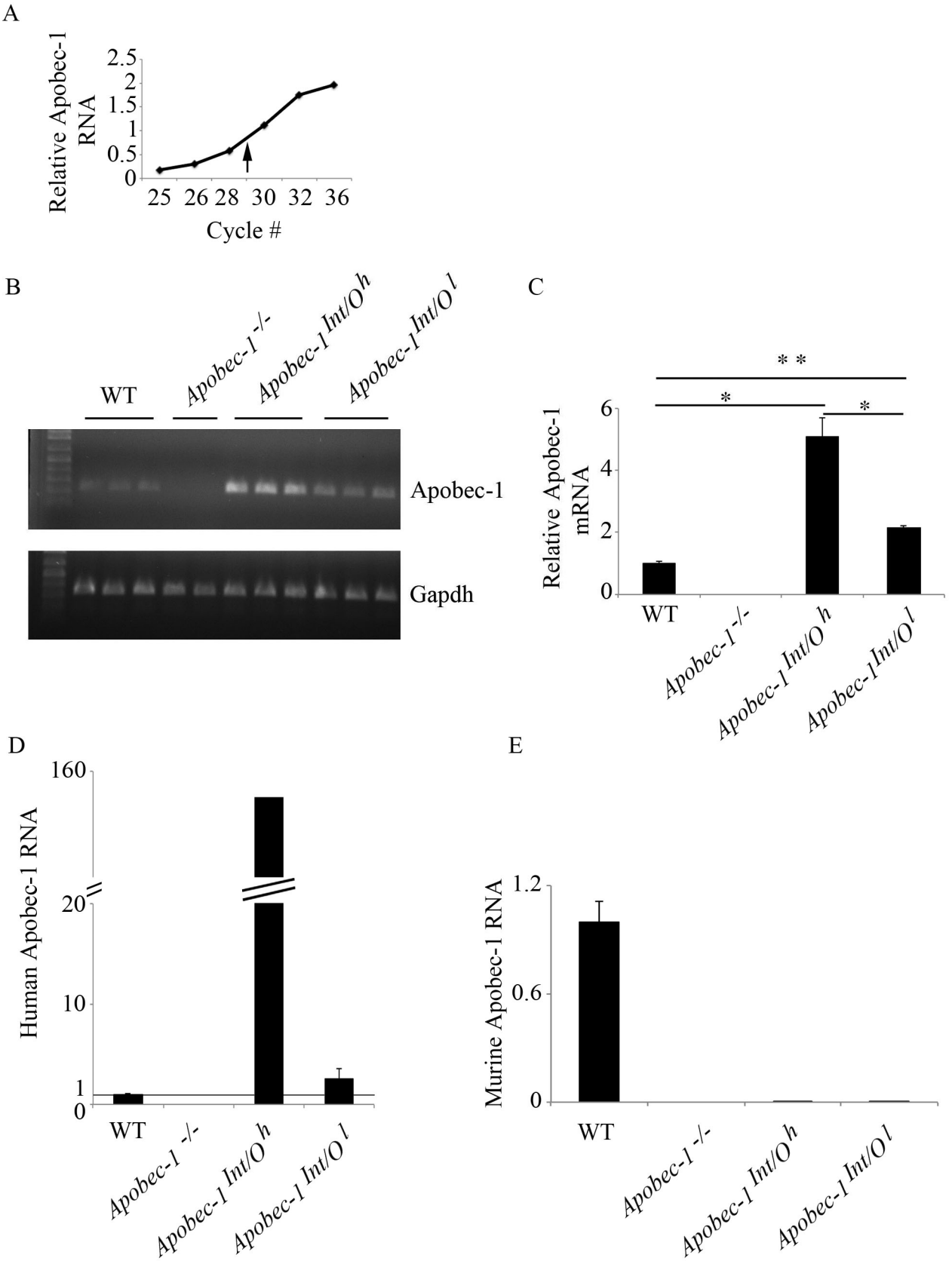
Supplemental Figure 1





Supplemental Figure 2

Supplemental Figure 1. Sequence alignment of murine (Mu) apobec-1 exon6 (bold) with human apobec-1 (Hu). Nucleotides are numbered starting from the ATG. Arrows indicate the position of primers used for the semi-quantitative evaluation of human Apobec-1 RNA expression. Sequences of the primers are given in Methods section.

Supplemental Figure 2. Determination of transgenic human Apobec-1 RNA expression. A. RNA was isolated from separate WT animals and used in an RT-PCR reaction with forward and reverse H/M primers (recognizing both murine and human apobec-1 within exon 6) as detailed in Methods. PCR reactions were performed in duplicate at the indicated cycle number (25-36). The number of cycles chosen to analyze Apobec-1 RNA expression was determined from the exponential phase of amplification (arrow) to be at cycle 29. B-C. Total RNA isolated from intestinal mucosa of individual WT, *Apobec-1* $^{-/-}$, *Apobec-1* $^{Int/Oh}$ and *Apobec-1* $^{Int/Ol}$ mice was RT-PCR for 29 cycles. Relative RNA expression of human apobec-1 was normalized to Gapdh and calculated as fold expression relative to murine apobec-1 in wild-type animals. Data represent mean ± SE (n=3 animals per genotype). * $P < 0.01$; ** $P < 0.001$. D-E. Expression of human and murine Apobec-1 RNA evaluated by quantitative PCR, using species-specific primers (Methods). D. Relative expression of human apobec-1 RNA was determined using human-specific primers. Data represent mean ± SE (n= 3-4 animals per genotype). R. Relative expression of murine apobec-1 RNA using murine-specific primers. Data represent mean ± SE (n=3-4 animals per genotype).