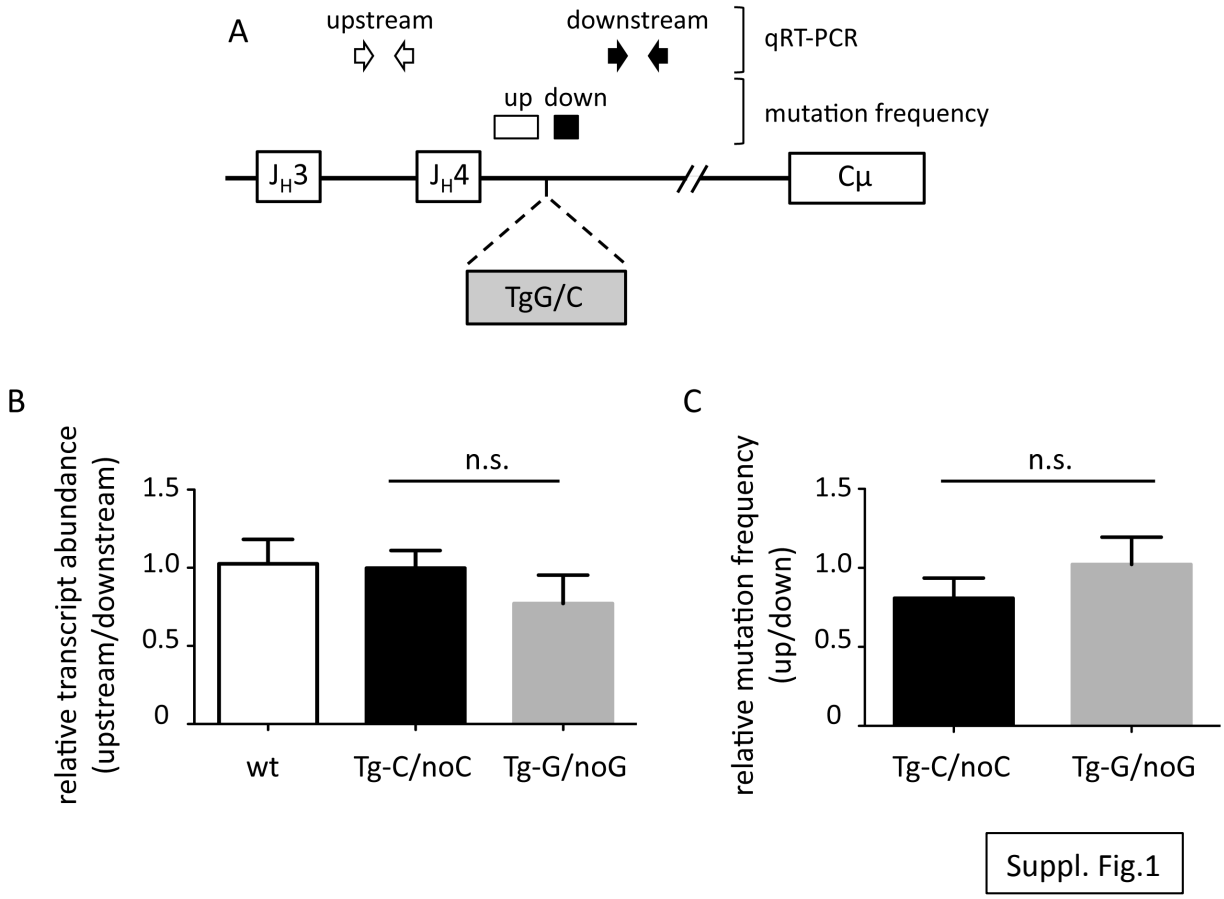

Legend to Supplementary Figure 1. Insertion of the oligonucleotide transgenes does not affect transcription elongation at the heavy chain locus.

A) Localization of primers used to quantify the relative abundance of heavy chain pre-mRNA transcripts located upstream and downstream of the transgene insertion site and of the DNA regions sequenced to determine the relative mutation frequency of both sides of the transgene (up/down). B) Absence of interference of the specific transgene insertion with transcription elongation. The relative abundance of Ig pre-mRNA segments located upstream and downstream of the different oligonucleotide transgenes was measured by qRT-PCR. The values represent the average [upstream pre-mRNA]/[downstream pre-mRNA] ratio for 2 wild-type mice (wt), three homozygous Tg-C mice (Tg-C/-NoC) and two homozygous Tg-noG and one homozygous Tg-GxUngKO (Tg-G/noG). The contamination with genomic DNA was negligible, as assessed by qPCR without reverse-transcription step (not shown). C) Absence of interference of the specific transgene insertion on the mutation frequency of the 5' and 3' flanking DNA segments. The values represent the average [up frequency]/[down frequency] ratio calculated for the different categories of transgenic mice (Tg-C, Tg-NoC and TgCxUngKO ; Tg-G, Tg-NoG and Tg-GxUngKO). The mutation numbers in 5' (up) and 3' (down) J_H4 DNA segments are shown in Table 1 for each mouse genotype. The error bars correspond to standard deviations; n.s., non-significant (unpaired, two-tailed Student's *t*-test).