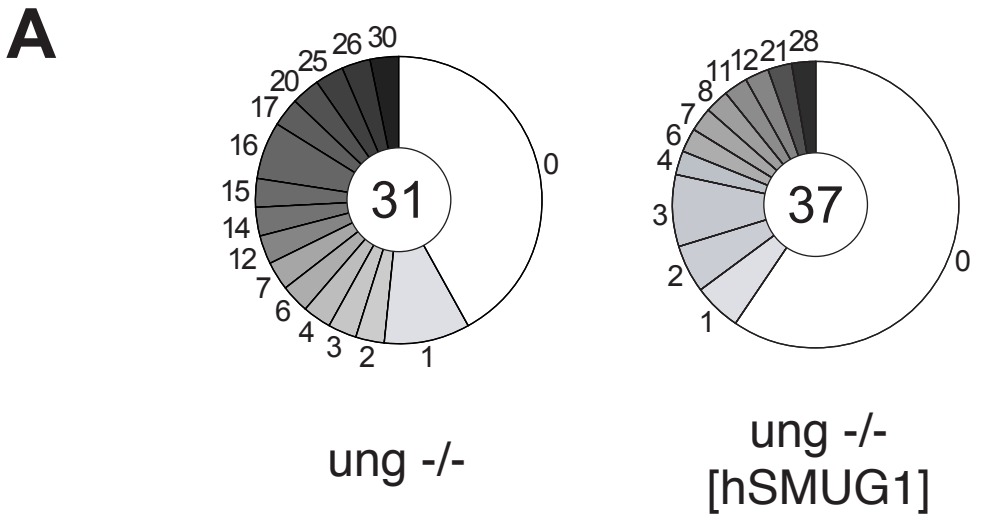

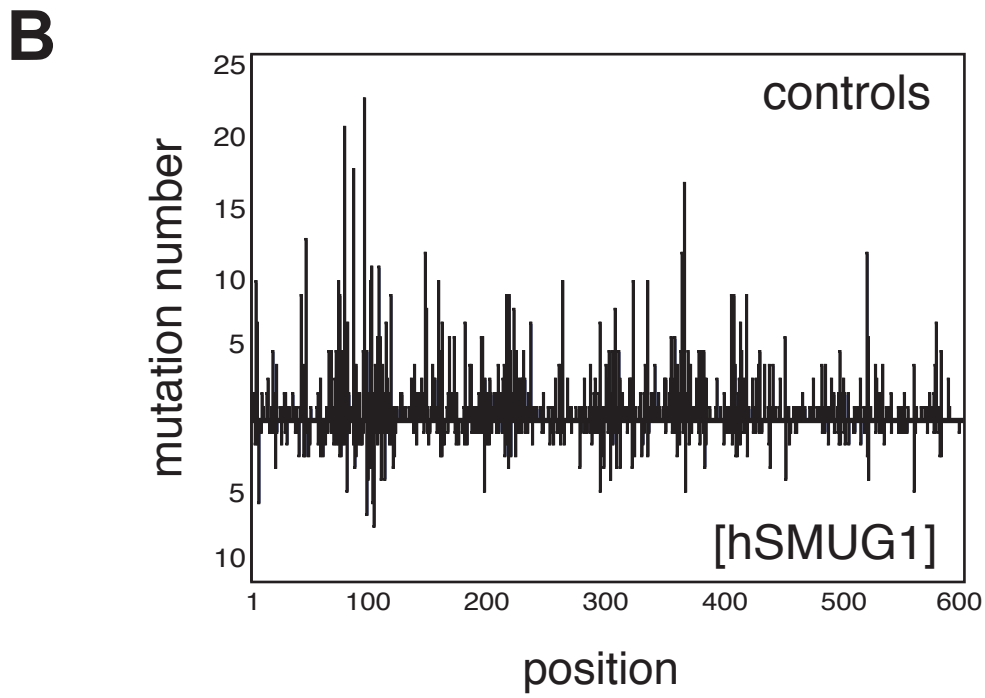

Supplementary Fig. 1. (A) Comparison of mutation accumulation in the 3'-flanking region of VDJH rearrangements in Peyers patch germinal centre B cells in a hSMUG1-transgenic ung-/- mouse versus a non-transgenic ung-/- littermate control (both 9 month old). The pie charts indicate the proportion of sequences carrying the indicated number of mutations with the total number of sequences analyzed for each mouse indicated in the centre of the corresponding pie. Repeat counting of the same mutation was avoided by randomly eliminating from the analysis all but one of the sequences in each data set that shared the same VDJH rearrangement. **(B)** Distribution along the VDJH4 3'-flank of independently-occurring mutations in the database of control (above the line) or hSMUG1-transgenic (below the line) mice. The profiles were obtained by pooling the mutation data described in Figure 4(C) with the stringent criteria described in Rada et al. (2004) used to avoid mutation overcounting in dynastically-related sequences.