



**Supplementary Fig. 2.** Nucleotide substitution patterns (given as percentages) of the mutations in the 3'-flanking region of VDJH rearrangements in Peyers patch germinal centre B cells of [hSMUG1]-transgenic and control mice in different genetic backgrounds. Mutations identified in groups of mice of the same genotype (see Table II) were pooled (n = total mutation number in each pool).