**Figure S1**: A phylogeny depicting the phylogenetic relationships of mouse (C57BL/6) and human IGHV (blue), IGLV (red), and IGKV (black) gene segment sequences (coding bases only), distinguished by open (mouse) and filled (human) symbols. The topology of the tree reveals species-specific expansions and contractions of gene subfamilies; for example, the contraction of IGLV genes and large expansion of family IGHV1 genes in mouse. To construct the tree, sequences for \*01 of human IGHV, IGKV, and IGLV, as well as mouse IGHV and IGKV were first downloaded from the IMmunoGeneTics Information System (IMGT; www.imgt.org/vquest/refseqh.html); for mouse, only sequences from the C57BL/6 strain were used. In addition, mouse (C57BL/6) IGLV sequences were extracted from the mm10 genome reference assembly. A multi-sequence alignment, involving 287 nucleotide sequences in total, was performed using MUSCLE (1) within the MEGA7 software package (2). Using MEGA7, the phylogeny was constructed using the Neighbor-Joining method (3), and evolutionary distances were computed using the Maximum Composite Likelihood (4); gaps and missing data were not considered.

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