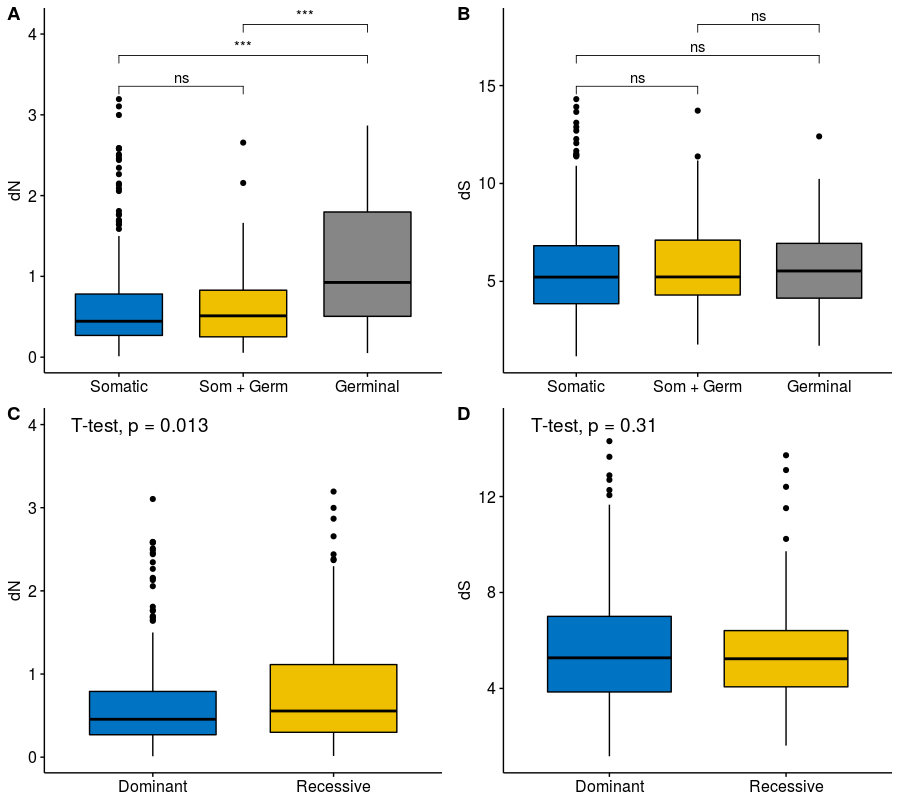
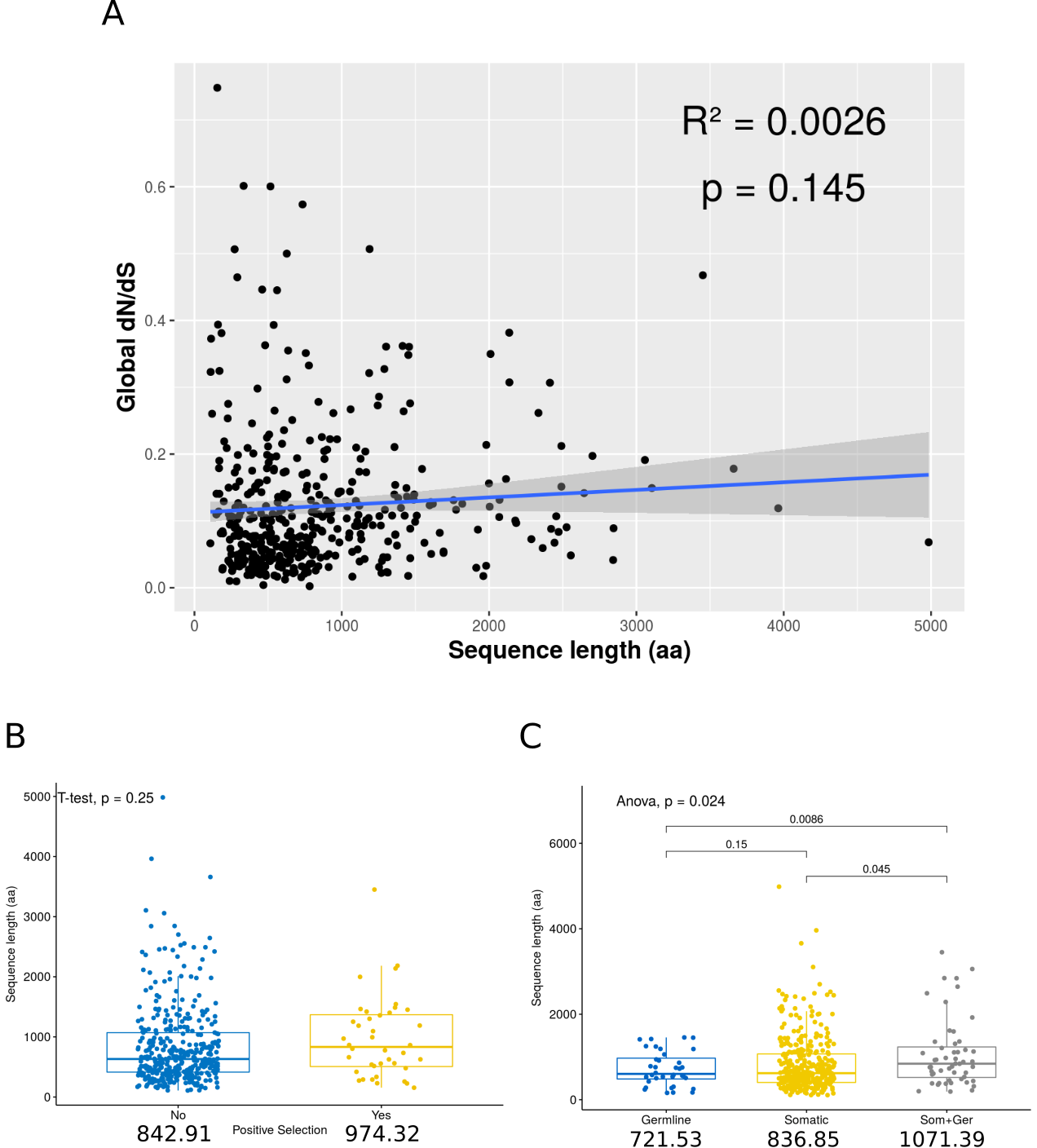


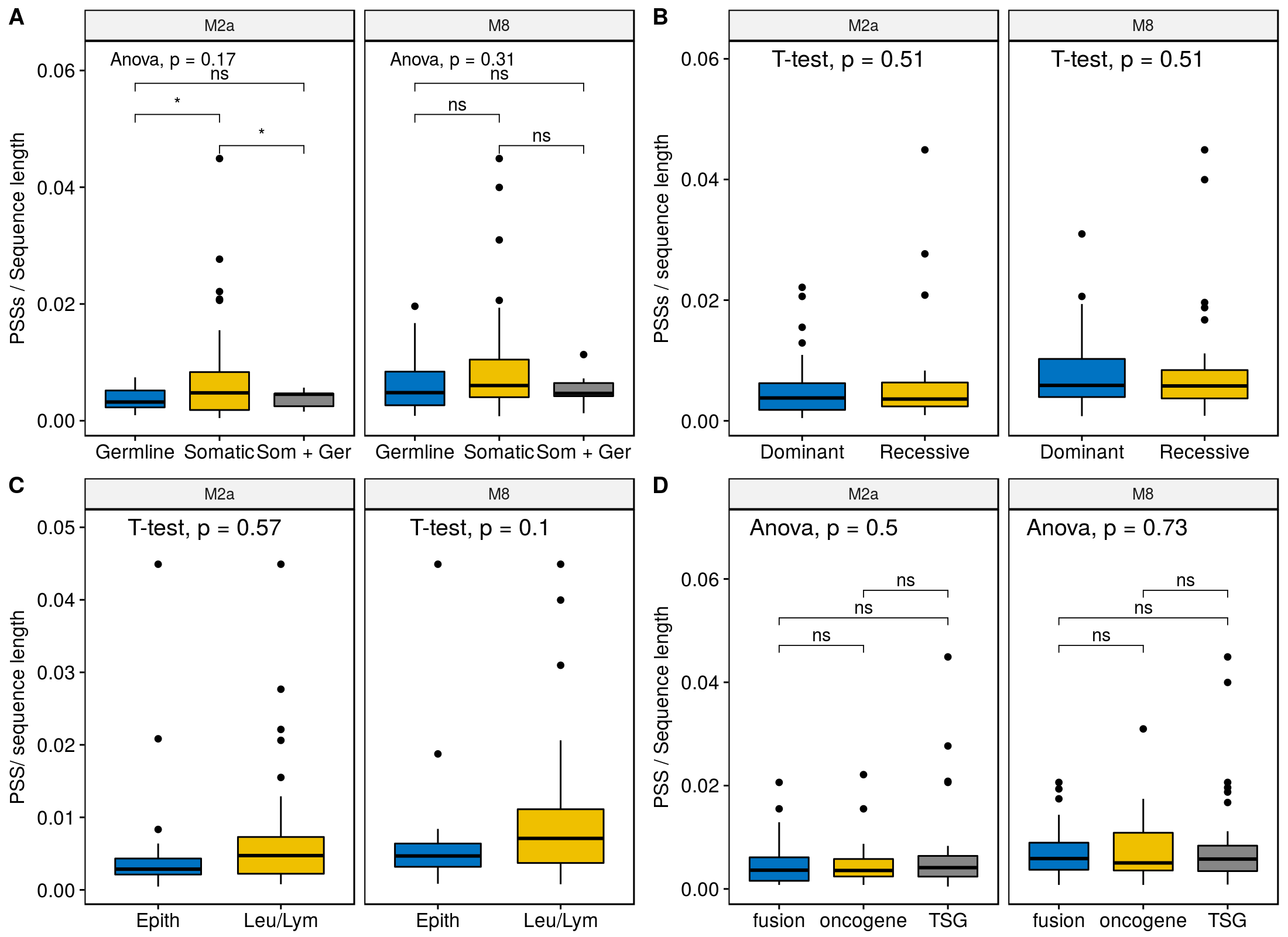
**Figure S1.** Mammal phylogenetic tree of mammalian species assembled for this study.



**Figure S2.** Global dN and dS values according to mutation type (A,B) and inheritance (C,D).



**Figure S3.** (A) Correlation between protein sequence length and global dN/dS estimates; (B) Comparison of protein length between positively selected and not selected genes; (C) Comparison of protein length among mutation-type categories. Statistical *p*-values are shown for multiple and pairwise comparisons. Mean of sequence length is indicated below each category in (B,C).



**Figure S4.** Proportion of positively selected sites across COSMIC categories: (A) mutation type; (B) genetic dominance; (C) tissue type; and (D) cancer role. The number of genes in each category is indicated within each square. Significance levels for chi-square tests are indicated below each plot: non-significant (ns) and significant *p*-value < 0.05 (\*). Abbreviated categories: Som + Ger: Genes bearing both somatic and germline mutations; TSG: tumor suppressor genes.