Supplementary figures

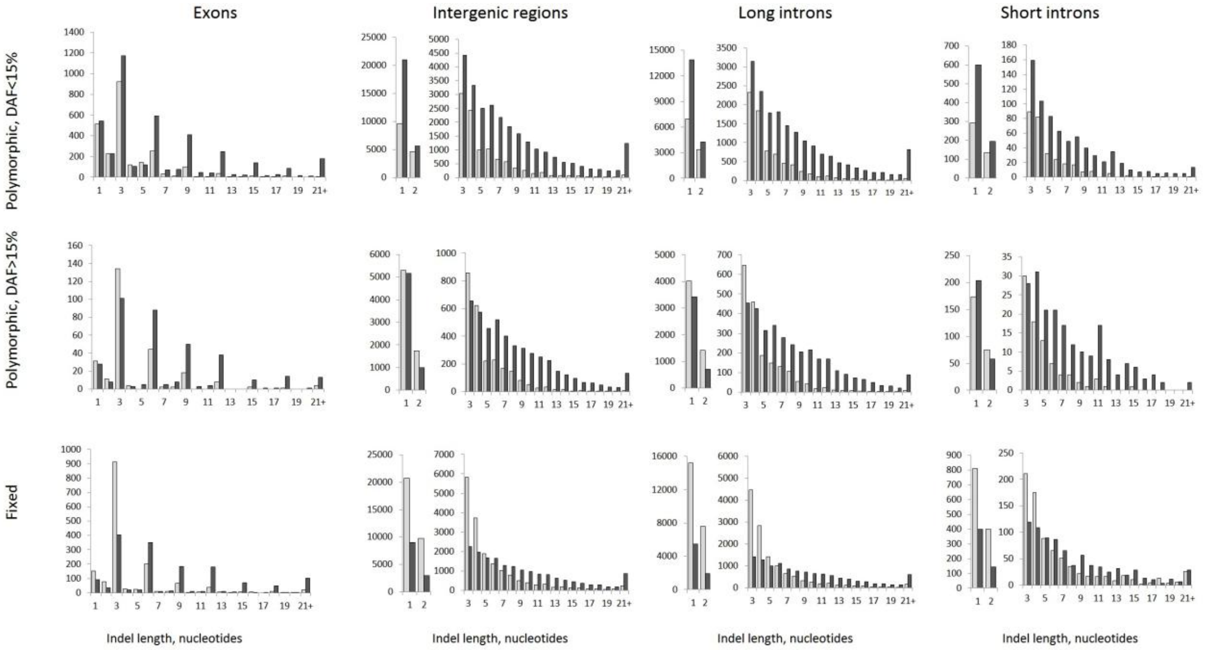

Figure S1. Length distribution of polymorphic and fixed indels and single-nucleotide substitutions in genome compartments of different kinds. Top row (A–D), polymorphisms with DAF < 15%; middle row (E–H), polymorphisms with DAF > 15%; bottom row (I–L), fixed mutations. A, E, I: exons (inframe indels and missense substitutions); B, F, J: intergenic regions; C, G, K: long (>300 nucleotides) introns; D, H, L: short (70-300 nucleotides) introns. Light gray, insertions; dark gray, deletions.

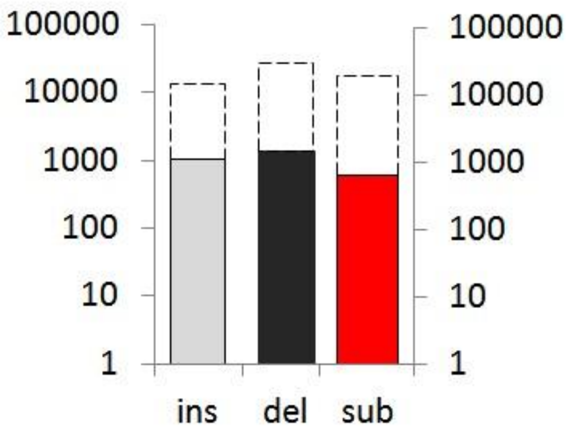

Figure S2. Number of frameshifting polymorphic indels and stop-codon inducing polymorphic single-nucleotide substitutions with DAF < 15%. Light gray, insertions; dark gray, deletions; red, nonsense substitutions. Broken lines show the expected values if polymorphism and the rate of divergence in the compartment were the same as in the short introns.

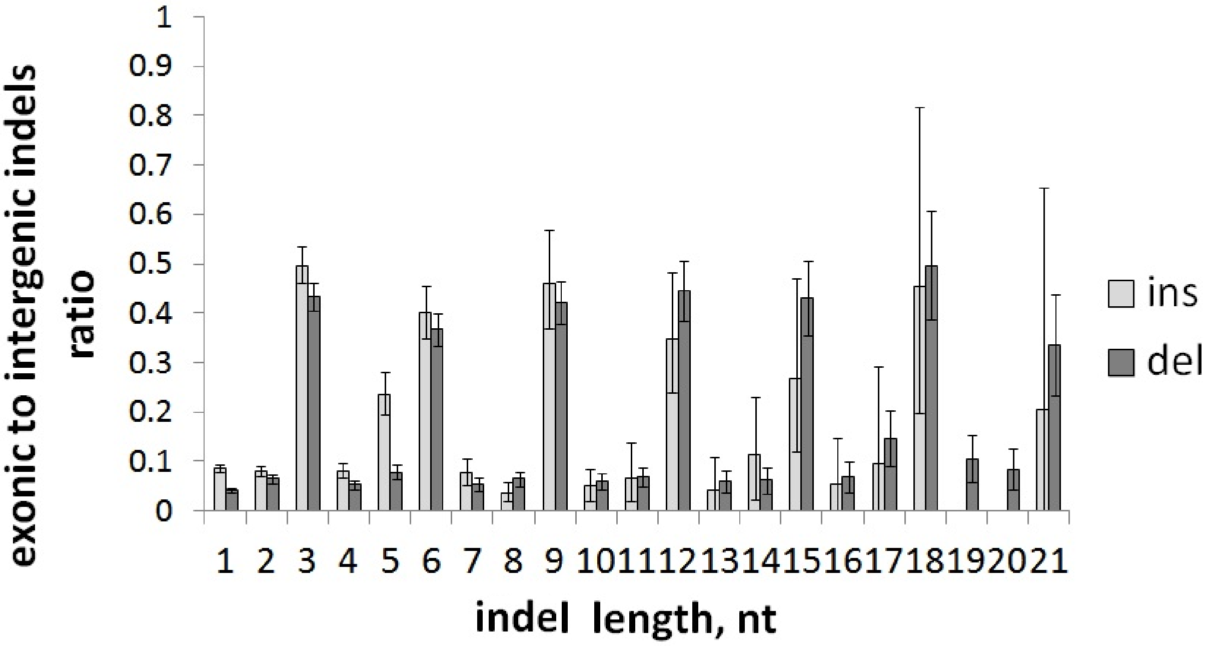

Figure S3 Ratio of low-frequency (DAF < 15%) indels in exons to low-frequency indels in intergenic regions. Error bars are 95% confidence intervals based on 1000 bootstrap trials.