Figure S6. Group RSCA scores (R_α^S) of A-ending, T-ending, C-ending, and G-ending codons after introducing +2nt frameshift to the coding region (i.e., examining the second codon position in the original coding sequence) along the last 50 codons of the gene. Rows denote species, columns denote positions. Species within domains are sorted from high (top) to low (bottom) GC-content.