Figure S7. Group RSCA scores (R_α^S) of 0, 1, 2, and 3 G/C nucleotides in codons after introducing +1nt frameshift to the coding region (i.e., examining the first 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.