Figure S9. Group RSCA scores (R_α^S) of efficient, moderately efficient, and inefficient codons ending by T along the last 50 codons of the gene. Rows denote species, columns denote positions. Species where none of the codons in a particular efficiency group end by T (missing data) are shown as white stripes. Species within domains are sorted from high (top) to low (bottom) GC-content.