



Figure 1. LOGO diagram of base proportions in the observed spliced leader sequences.

The relative proportion of nucleotides retrieved within 50 bases of the 5-prime end of dinoflagellate transcripts is shown above the canonical spliced leader sequence from Zhang *et al* 2007. The “anchor” sequence used to retrieve potential spliced leader sequences bioinformatically is shown on the right side consisting of “GCTCAAG”.