



Figure S2 Complementary R2 elements from the cholinergic loci of eight *Caenorhabditis* species. (A) R2 stem-loop structures. The fractional pairing of the stem, the length of the putative loop, the consensus sequence, and the black circles are the same as in Figure S1. For each R2 structure, the splice acceptor site at the 5'-end of exon u2 (Figure 1) is indicated with a thin arrow, and the UNC-17 initiation (AUG) codon is indicated with a thick arrow. (B) Identification of a 16-nucleotide R2 consensus sequence (UCUGCGUCUCUCCCG when transcribed) in the upstream stem sequences shown in panel A. The consensus (containing nucleotides present in the stems of at least seven of the eight species) is boxed. Nucleotides in **Blue** are paired (in the stem); nucleotides in **Black** are unpaired; the three nucleotides in **Red** deviate from the consensus, but are paired with complementary downstream nucleotides; the nucleotide with the **Blue background** deviates from the consensus and is unpaired. The species previously known as *C. sp5* and *C. sp11* have recently been renamed *C. sinica* and *C. tropicalis*, respectively (Félix *et al.* 2014; Huang *et al.* 2014).