



Figure S1 Complementary R1 elements from the cholinergic loci of eight *Caenorhabditis* species. (A) R1 stem-loop structures. The fractional pairing of the stem is given below each species name; the length of the putative loop is shown above each stem. The consensus sequence (see below) is boxed. The solid black circles represent standard (A-U and G-C) pairing; circles with white centers represent G-U pairing. (B) Identification of an 11-nucleotide R1 consensus sequence (AAACCACCAAC) in the upstream stem sequences shown in panel A. The consensus (containing nucleotides present in the stems of at least six of the eight species) is boxed. Nucleotides in **Red** are paired (in the stem); nucleotides in **Black** are unpaired; the nucleotides in **Blue** 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).