



Figure S4 Genomic structures of the cholinergic loci in *Globodera pallida* and *Meloidogyne hapla*, two nematode species with an abundance of UNC-17 exons. The structure of the *C. elegans* locus (at the same scale) is shown for comparison. Because the common exon is non-coding, it could not be identified easily by homology. Instead, the criteria used for provisional identification of the common exon in *G. pallida* and *M. hapla* were: 1) good matches to canonical splice acceptor and donor sequences; 2) size was 50 - 90 bp; and 3) the sequence contained no ATG triplets. The predicted extent of the 3'-UTRs for *G. pallida* and *M. hapla* were based on location of AATAAA sequences. Red and blue arrows indicate the locations of the sequences corresponding to the R1 and R2 complementary elements, respectively.