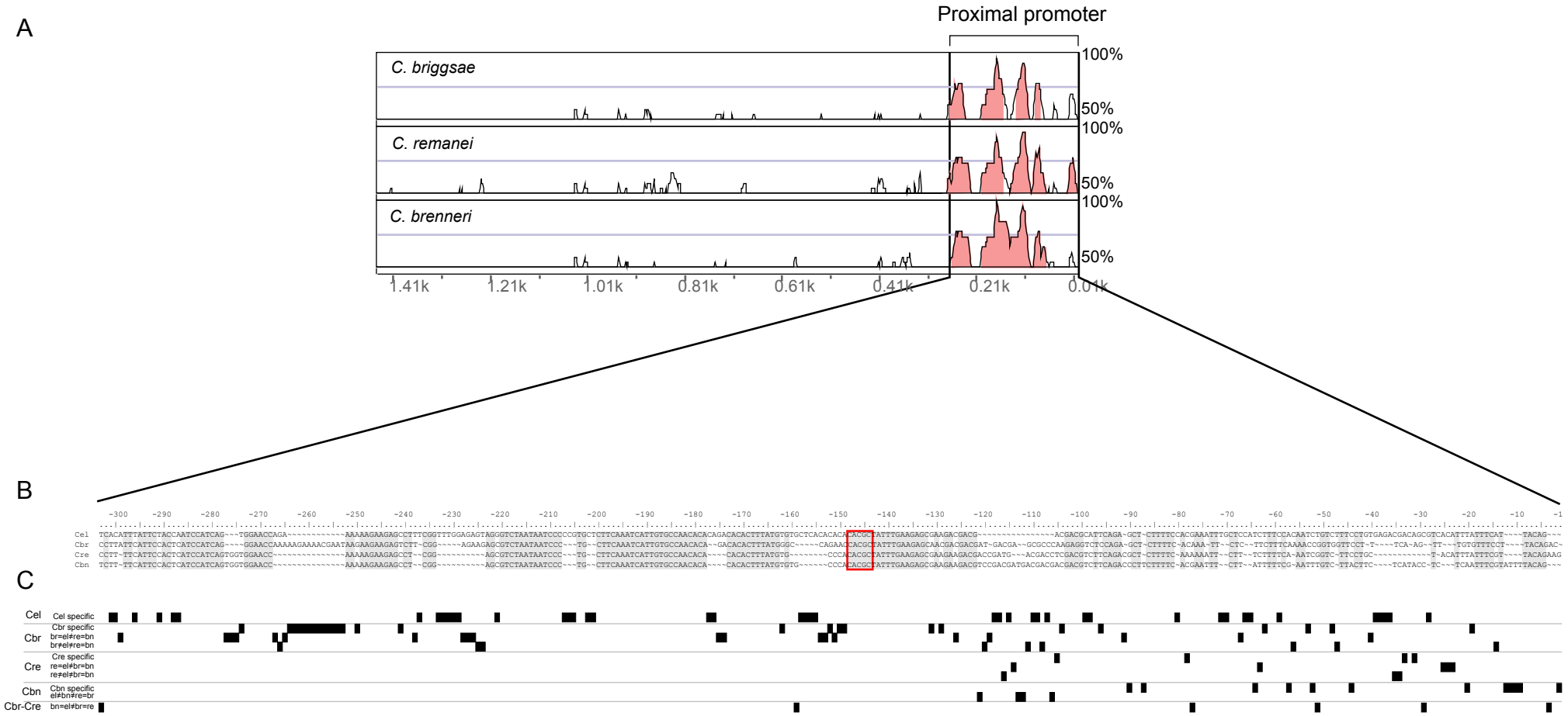

Figure S6. Pattern of sequence conservation in the proximal promoter of *unc-47*.
(A) VISTA plot of primary sequence conservation in the *unc-47 cis*-regulatory regions from *C. briggsae*, *C. remanei,* and *C. brenneri* aligned to *C. elegans*. Window size = 20 bp, threshold = 70%. (B) In the alignment of the proximal promoters from *C. briggsae, C. remanei, C. brenneri,* and *C. elegans*, conserved nucleotides are shaded in gray. Position -1 is the first nucleotide upstream of the translation start site. The conserved AHR-1 core consensus motif is boxed in red. (C) Insertions, deletions, and substitutions on each lineage are depicted as black boxes. The number of lineage-specific changes was counted by two methods. In the less stringent method, for *C. briggsae*, *C. remanei,* and *C. brenneri*, sites conserved between two species but divergent in the third were counted as branch-specific. The number of affected sites and events calculated in this way are reported in Figure 5E. In a more stringent analysis, only sites that were different from a nucleotide conserved with *C. elegans* and two other species were counted as species-specific. Using this method, *C. briggsae* has 14 substitutions, one insertion of 12 nucleotides, and a single deletion. *C. remanei* has 2 substitutions and one deletion of 2 nucleotides. *C. brenneri* has 6 substitutions and 3 insertions affecting a total of 6 sites. Eight sites for which the polarity of mutations could not be determined are not represented. In the region extending upstream of position -122, *C. briggsae* has 10 substitutions, 6 insertions affecting 26 nucleotides, and one deletion of 4 nucleotides. In contrast, in this region, there were no *C. remanei* or *C. brenneri* specific events.