



S11 Figure. Matches to motifs responsible for the *C. elegans unc-25* gene expression pattern can be found in orthologous sequences. Cartoons depicting all orthologous upstream *unc-25* sequences fused to *mCherry* (*C. elegans*) or *GFP* (all others) near the translation start site (bent arrow), or further downstream. Exons are thick black boxes, introns are gray lines. UNC-30 (box arrow) consensus motifs are shown above, in uppercase letters; conserved flanking nucleotides shown in lowercase. Locations of motifs relative to the endogenous translation start site are indicated. Daggers denote binding sites found to be bound by UNC-30. See S1 Text.