

Figure S5. Expression patterns driven by chimeric *unc-47* promoters.

(A) An alignment of the sequences flanking the conserved AHR-1 consensus motif (boxed in red). Regions conserved between all four species are shaded in gray. In (B-J) bold face letters represent *C. briggsae* sequence, regular font represents *C. elegans*. All transgenes were tested in *C. elegans*. Full-length *C. elegans* promoter (B) drives inconsistent expression in SDQR, no expression in SDQL, and consistent expression in DVB. Full-length *C. briggsae* promoter (C) drives consistent expression in SDQR, SDQL and DVB. *C. elegans* promoter with *C. briggsae* Region A (D) or Region B (E) drives *C. briggsae*-like expression in SDQR, *C. elegans*-like expression in SDQL, while expression in DVB is unaffected. Additionally, expression in AVL and RIS is either severely reduced or abolished. Partial replacement of *C. elegans* Region B by 10 nucleotides of *C. briggsae* Region B (F) completely abolishes expression in SDQR/L and reduces the intensity of expression in DVB. This phenotype is similar to that observed with the *C. briggsae* promoter mutated in the conserved AHR-1 consensus motif (Figure 3B in the text), indicating that these nucleotides are critical for SDQR/L and DVB expression. *C. briggsae* promoter with *C. elegans* Region A (G) or Region B (H) drives *C. briggsae*-like expression in SDQR, *C. elegans*-like expression in SDQL, while expression in DVB is unaffected. These chimeric promoters also drive strong ectopic expression in several head neurons and the pharyngeal-intestinal valve. A partial replacement of *C. briggsae* Region B by 10 nucleotides of *C. elegans* Region B (I) does not affect expression in SDQR/L in the context of the full-length promoter. However, in the context of the proximal promoter (J), the percentage of individuals expressing in SDQR is reduced and expression in SDQL is completely eliminated. Compare to Figure 3D in the text.