

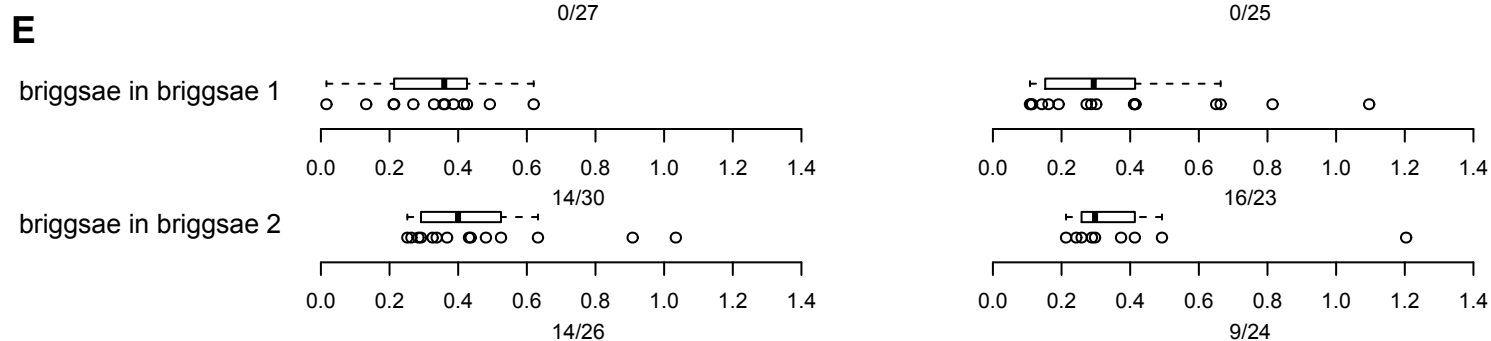
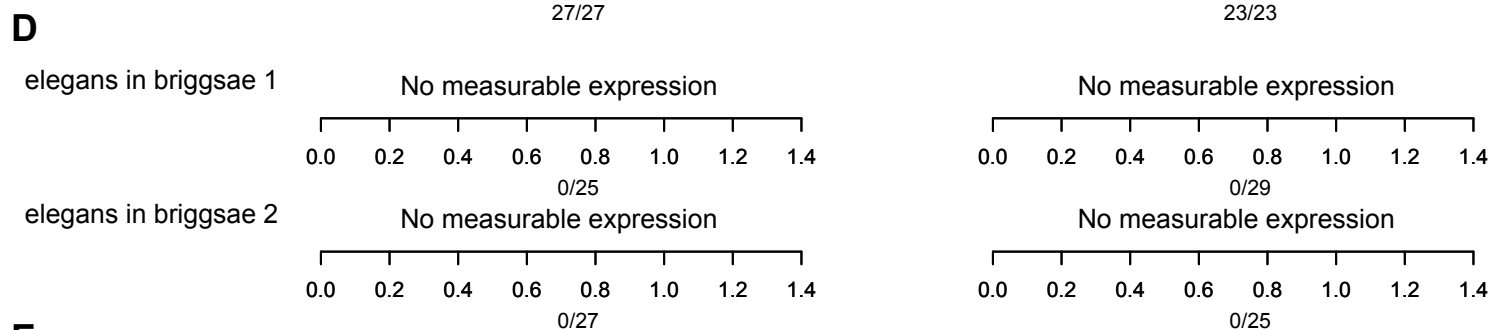
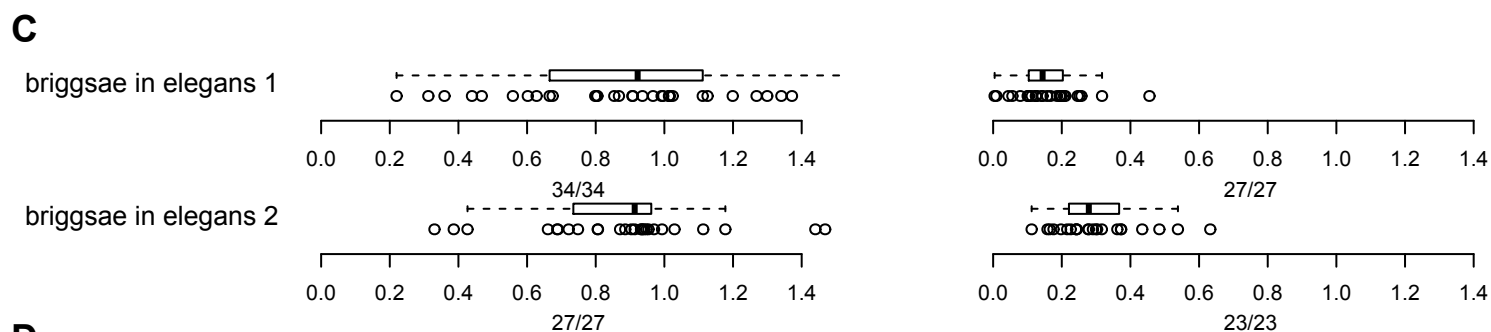
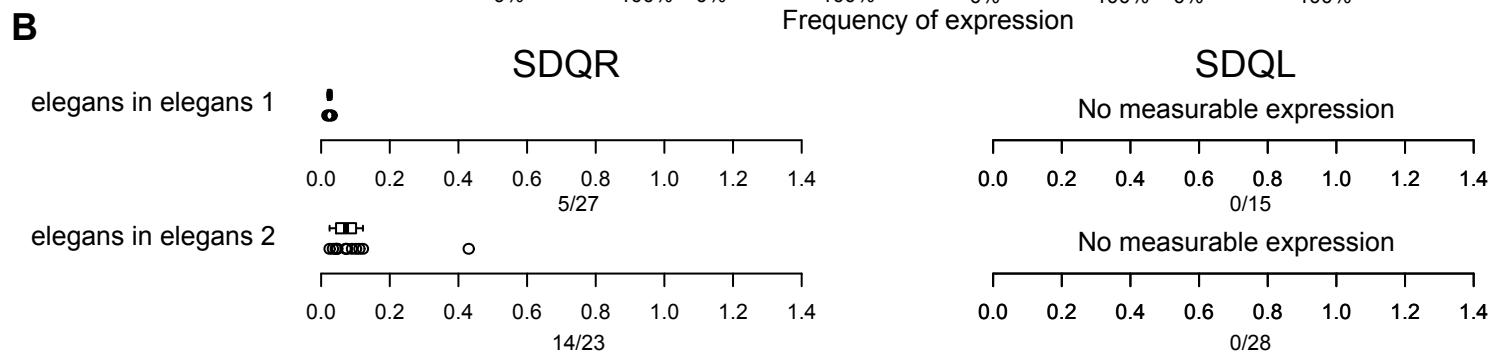
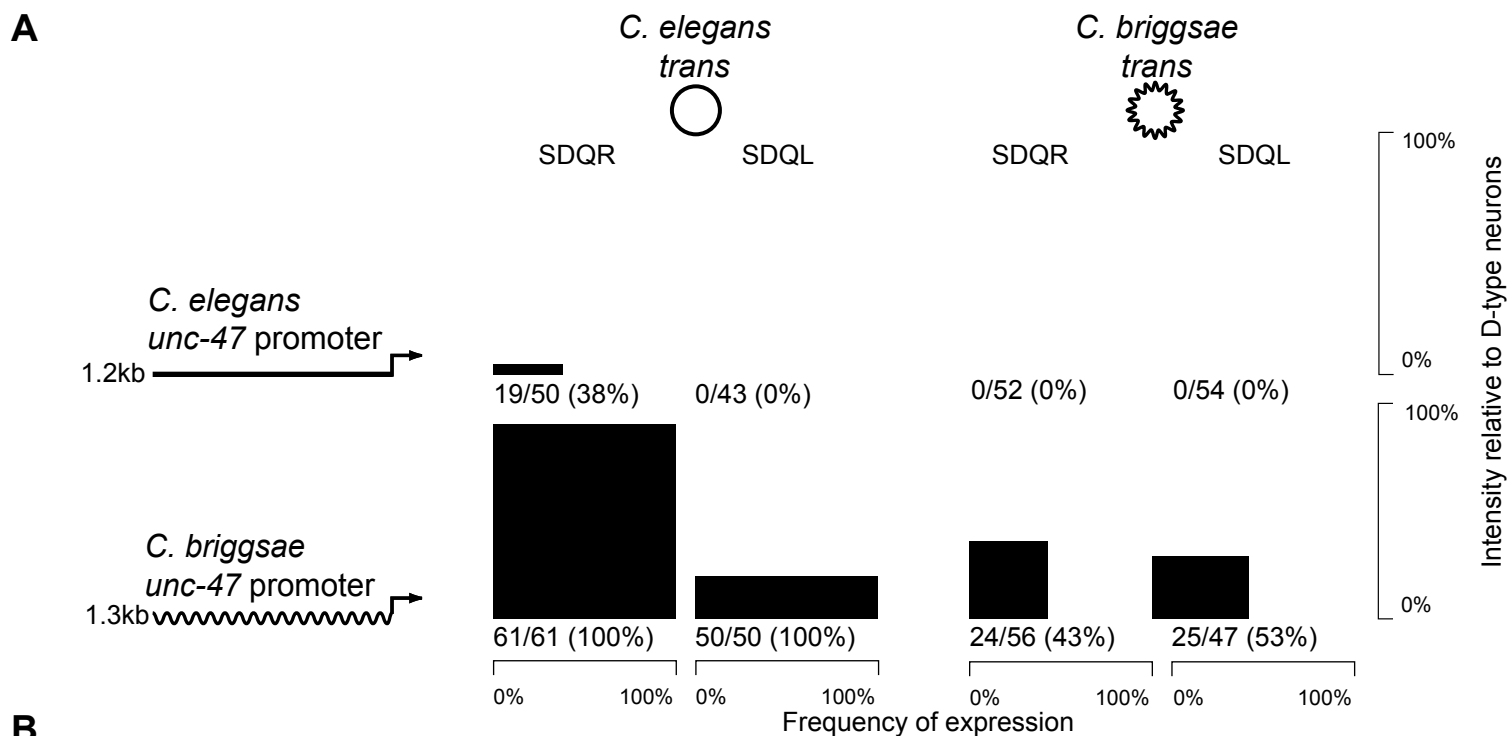


Figure S2. Expression driven by integrated transgenes is consistent with expression driven by extrachromosomal arrays and between independent strains.

(A) For each combination of promoter and *trans*-regulatory environment, expression in SDQR and SDQL is presented. *C. elegans* is represented by straight lines, *C. briggsae* by wavy lines. Frequency of expression is represented by the width, and intensity of expression relative to D-type neurons by the height of black boxes. Compare with Figure 1C. Number of individuals expressing and total number of individuals scored is indicated underneath. Individuals were only scored if their cell was clearly visible, unobstructed by the intestine. The distribution of expression intensity in SDQR and SDQL relative to D-type neurons is plotted. The fraction of individuals showing expression over individuals scored is indicated underneath. Two independent strains carrying integrated transgenes were measured for (B) *C. elegans* promoter in *C. elegans*, (C) *C. briggsae* promoter in *C. elegans*, (D) *C. elegans* promoter in *C. briggsae*, (E) *C. briggsae* promoter in *C. briggsae*.