



**Figure S1 Bacterial choice behavior of introgression strain with chromosome II QTL predicted by RIAIL analysis.** Bacterial choice index of N2, HW and *ew/R20* (II ~0 - ~3.4 Mb, CB4856 >N2), which contains the chromosome II sequence near 2,808,858 predicted to contain a HW QTL by RIAILS (Figure 2). \*\*\* $p < 0.001$  compared to N2 by ANOVA with Dunnett test,  $n \geq 5$  assays. Error bars represent S.E.M. The strain *ew/R20* may have an N2-like phenotype because this region does not contain a QTL or because this region must interact epistatically with other QTLs to generate a HW-like phenotype. Note that control values for N2 and HW in this set of experiments are slightly different from those in Figure 1.