Figure S1 A) Heritabilities of the sixty-six behavioral components in the wild isolate and the RIAIL population in response to ΔT~0.4ºC. **B)** Correlation of six representative components of the avoidance behavior among wild isolates. We analyzed 66 traits for pattern of correlation in the RIAIL population. For the traits that are speed at different time points there were two uncorrelated groups. The speeds between 0.72 and 1.96 seconds were uncorrelated to the speeds at the other time points which were strongly correlated. For simplicity, representative speeds are included in the plot: one at early time point (sp0.18s), one at late time point (sp8.1s) and one in the 0.72-1.96 range (sp1.61s). The behavioral components are: sp0.18s: speed at 0.18 seconds, sp1.61s: speed at 1.61 seconds, sp8.1s: speed at 8.1 seconds after start of the assay, pFR: probability of responding by reversals, W=number of body bends during reversals, pRO: probability of inducing omega turns. The magnitude of significant Pearson correlation coefficients ($p < 0.01$) among these behavioral metrics are shown for wild isolates in circles. Absence of circles represents an absence of significant correlations. The phenotypes are hierarchically clustered and cut into two clusters bordered by red lines. **C,D)** Common naturally occurring variation on chromosomes IV and X contribute to natural variation in speed at early time points (C) and acceleration (D) during escape behavior. Plots of the results of genome wide association mapping for acceleration and speed at 0.2 seconds. Significantly associated markers are indicated by red lines.