



Figure S4 Match of sequence reads from 39 different wild isolates, N2 and CB4856 (HA) against the N2 genome and the CB4856 genome in a divergent region from chromosome I. The extent of the match is measured by ALE placement scores averaged across the region, with larger negative scores indicating a poorer fit. In (A) this region only the fourth strain (CB4854) resembles the CB4856 sequence. In (B) most strains are similar to the N2 pattern, but ED3049(9), JU258(19), MY6(38) and PX174(39) resemble HA. Others show an intermediate match, e.g. AB3(2) and CB4853(3). In (C), most strains again resemble N2, none resemble HA, a few are intermediate, e.g., AB3(2) and CB4853(3), and others are different from both N2 and HA, e.g., ED3052(10), JU1088(14) and JU1171(15). Figure S11 contains these same data for all of the divergent regions.