



**Supplemental Figure S8. MIP-MAP data for 6 strains categorized as class 0 or class 1 by mean FCR.** Strains were mapped by competitive selection using VC20019 with the y-axis representing the proportion of VC20019 present versus all reads for a MIP target at each locus across the genome. Strains were mapped in replicate (solid versus dotted lines) and sequenced at two timepoints each (ie. F2 vs F4). The strains mapped in this fashion were (A) VC30079, (B) VC30188, (C) VC40196, (D) VC40296, (E) VC40545, and (F) VC40611. X-axis units are in megabases across each chromosome. Green arrows indicate the suggested recombinant region associated with reduced fitness.