Figure S1.—Total variant distribution of 16 sequenced mutant strains. (A) Accumulated representation of all variants from 16 genome sequenced strains (excluding OH9305 which was outcrossed against HA). Each hash mark represents a single variant position. Red lines indicate gene rich regions found on chromosomes I-V, but not on X. (B) Rate of retrieved variants is higher among non-gene rich regions than gene rich regions across all five autosomes. Variants on each chromosome for each strain were normalized to total variant number/strain to account for differences in coverage between strains. Variant rates inside and outside gene rich regions were then averaged between 16 sequenced genomes for each chromosome. Standard error of mean is shown. \( p \)-values (t-test) for each chromosome are as follows, I: \( 4 \times 10^{-5} \), II: \( 0.02 \), III: \( 0.06 \), IV: \( 0.5 \), V: \( 8 \times 10^{-3} \). (C) Same analysis as (B) with the following exception: variants linked to chromosomes harboring either the phenotype-causing mutant selected for, or the integrated transgene used to score phenotype, were excluded. Standard error of mean is shown. \( p \)-values (t-test) for each chromosome are as follows, I: \( 3 \times 10^{-9} \), II: \( 4 \times 10^{-4} \), III: \( 3 \times 10^{-3} \), IV: \( 0.3 \), V: \( 3 \times 10^{-4} \). (D) Rate of synonymous changes inside and outside gene rich regions. As synonymous variants are relatively infrequent when compared to non-synonymous variants, the presented numbers are the accumulation of all such variants among 16 strains (OH9305 was again excluded). Standard error bars are shown. Standard error of mean could not be calculated due to the method of obtaining synonymous change distribution. \( p \)-values (t-test) for each chromosome are as follows, I: .08, II: .4, III: .99, IV: .62, V: .06.