Supplementary Material for:

"Variation in filamentous growth and response to quorum-sensing compounds in environmental isolates of *Saccharomyces cerevisiae*"

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Generation of an F5 Mapping Population

An overnight 5ml YPD culture of HMY7 was sporulated on solid medium for 2 days, gently scraped off using sterile water and a cell scraper, and digested using a zymolyase- β-glucuronidase procedure (Goddard et al. 2005, Granek et al. 2013). The random spore preparation was pipetted in a concentrated drop onto a YPD + G418 plate and incubated overnight to allow for germination and mating. The patch of cells was gently scraped and collected in 1ml of water, which was used to inoculate 5ml of YEPD + G418. After ~24hrs, 100ul was used to inoculate 5 ml of YPD + G418 for a further day of growth. This culture was then washed and sporulated, beginning the cycle again. After 4 cycles, spores were plated to a density of ~100 colonies per plate and 360 segregants were isolated and phenotyped. Each colony was presumed diploid due to self-mating.

HMY7 Genome

HMY7 reads were aligned to the *S. cerevisiae* reference genome (version 64) using BWA (Li and Durbin 2009), and SNPs were called using Freebayes (Garrison and Marth 2012) with the default settings for a diploid organism. SNPs were filtered for quality and read depth; an HMY7 genome was generated from the reference genome by replacing SNPs with a frequency over 0.9 (~23,000 sites), which were presumed to represent fixed differences. There were ~46,000 SNPs with a frequency between 0.25-0.75, presumed to represent heterozygous sites, and available for mapping studies. Aneuploidy was detected at chromosomes 1 and 6 (Figure S1).

References Cited

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