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LOH data contains the frequency of LOH at the *GAL1* locus calculated by enumerating the number of colonies on 2-DOG selective media divided by the number of colonies on non-selective media (YPD). These data correspond to Figures 1 and S2.

Diploid *in vitro* data contains the G1 mean, determined by FITC-A signal or ploidy (calculated by and R-script) for all three diploid strain backgrounds (laboratory, bloodstream, and oral). Data are separated by the time passaged *in vitro* (Day XX). The replicate line on day 0 corresponds to the same replicate line on days 4, 7, 14, and 28. If more than one ploidy/ G1 mean is present for an individual replicate line, this indicates that there were multiple G1 peaks (aka a mixed population) observed. These data correspond to Figure 2.

Tetraploid *in vitro* data contains the G1 mean, determined by FITC-A signal for all three tetraploid strain backgrounds (laboratory, bloodstream, and vaginal). Data are separated by the time passaged *in vitro* (Day XX). The replicate line on day 0 corresponds to the same replicate line on days 4, 7, 14, and 28. If more than one G1 mean is present for an individual replicate line, this indicates that there were multiple G1 peaks (aka a mixed population) observed. These data correspond to Figure 3.

Diploid *in vivo* data contains the location in the 96-well block, the tube number for tracking flow cytometry data, the corresponding G1 mean calculated by the FITC-A signal intensity, and the G1 mean relative to the mean of G1 means for the no host treatment of the corresponding yeast strain. Each G1 mean under the host treatment represents an individual colony that was picked after extraction from the nematode host following four days of infection. These data correspond to Figures 2, and S2, as well as Table S3.

Tetraploid *in vivo* data contains the location in the 96-well block, the tube number for tracking flow cytometry data, the corresponding G1 mean calculated by the FITC-A signal intensity, and the G1 mean relative to the mean of G1 means for the no host treatment of the corresponding yeast strain. Each G1 mean under the host treatment represents an individual colony that was picked after extraction from the nematode host following four days of infection. These data correspond to Figures 3, and S2, as well as Table S3.

Growth rate data contains the growth rate calculated by a custom R-script that measures the OD600 over a 24-hour period for the three diploid strains (laboratory, bloodstream, and oral) and the three tetraploid strains (laboratory, bloodstream, and vaginal). (P) represents the growth rate of the parental strain for that genetic background. 1-12 are individual isolates from the same genetic background as the parent that were extracted from the host environment. These data correspond to Figures 4 and S2 and Table 2.

The fecundity data file is broken up by strain background. Each genetic background has its own tab for fecundity data. Each separate experiment is divided by a solid blue line. OP50 is the strain of *E. coli* used to set a baseline for the number of offspring produced by *C. elegans*. 10 nematodes were infected individually with either *E. coli* (OP50) or a mixture of *E. coli* and *C. albicans.* Again, P represents the parental strain of *C. albicans* and MHXX-1-12 represents an individual isolate of the same genetic background that was extracted from the nematode host. Total progeny produced by a single nematode was counted daily (0-7) and the total number of offspring produced per nematode was also calculated. The total number of progenies produced per nematode was divided by the mean progeny produced for nematodes infected with OP50 only (Total progeny rel. to OP50). This was used in order to measure any changes in host fitness when infected with *C. albicans*. Finally, any black squares indicate when an individual nematode died. The progeny produced from nematodes that died were not taken into account in the overall mean for the population. These data correspond to Figures 4, S2 and Tables 3 and S3.

Specific methods can be found in the mSphere paper: **DOI:** 10.1128/mSphere.00433-20