

Supplementary Figure 1: Template outline of one HYAAC channel as designed in AutoCAD.



**Supplementary Figure 2:** Original buckets of HYAA chip filled with *C. neoformans*. Numerous issues were found with the original buckets where cells could outgrow through the top or clump and cluster together.



**Supplementary Figure 3:** Retention rate for cells that landed in a trap and replicated at least once. 28% of cells were lost within the first 7 generations and there was an overall retention rate of 62% for the 50 wildtype cells assessed.



**Supplementary Figure 4**: RLS of WT cells as measured by microdissection (n = 30) of in the HYAAC device (n = 100). P = 0.450 by Wilcoxon rank sum test. Center line is median, box limits are upper and lower quartiles, whiskers are minimum and maximum.

**Supplementary Table 1:** All strains used in this paper.

Strain	Reference	
WT	H99 - Provided as a gift from Dr. John Perfect of Duke University.	
RC2-ALL2:mCherry	Jain et. al, Infection and Immunity (2016)	
H99 ∆ <i>CNAG_05431</i>	Provided as a gift from Dr. Andrew Alspaugh of Duke University.	
H99 ∆ <i>CNAG_03465</i>	Provided as a gift from Dr. Peter Williamson of the National Institute for Health.	
KN99α ΔCNAG_00003 KN99α ΔCNAG_04956 KN99α ΔCNAG_00028	Purchased from the Madhani knockout collection managed by the Fungal Genetics Stock Center.	
KN99α ΔCNAG_04546 KN99α ΔCNAG_04313 KN99α ΔCNAG_06909	Provided as a gift from Dr. Maurizio Del Poeta at Stony Brook University who purchased from the Madhani knockout collection managed by the Fungal Genetics Stock Center.	

Supplementary Table 2: Media used in this paper. Each recipe is adjusted for 1L of media in

dH<sub>2</sub>O.

Media	Recipe (in 1L dH <sub>2</sub> O)	
YPD broth	10 g yeast extract, 20 g peptone, 20 g dextrose (Difco)	
YPD agar	10 g yeast extract, 20 g peptone, 20 g dextrose, 15 g agar (Difco)	
Sabourad Dextrose (SAB) broth	5 g peptic digest of animal tissue, 5 g pancreatic digest of casein, 20 g dextrose (Difco)	
RPMI 1640	10.4 g RPMI 1640 (with L-glutamine, without sodium bicarbonate), 165 ml 1M MOPS, adjusted to pH 7	
SCA media	1.7 g yeast nitrogen base without amino acids, 1 g drop out mix, 0.4% ethanol, 5 g $(NH_4)_2SO_4$ , 3.3 g NaCl, 20 g glucose	
SCA - 0.05%	1.7 g yeast nitrogen base without amino acids, 2 g drop out mix, 0.4% ethanol, 5 g (NH <sub>4</sub> ) <sub>2</sub> SO <sub>4</sub> , 3.3 g NaCl, 0.5g glucose	

Supplementary Table 3: Primers used in this paper.

Gene Name	Forward	Reverse
CNAG_04956	ACGGTATCGTCTCCACCAAC	CCAAAGCCTCGGTAGGTACA
CNAG_00028	AACAATGCGGGAAGTGAATC	TTCCGCCTTATCCCTTTTCT
CNAG_03465	TTTGGGGGCCCCTTAATTATC	GGATAGGTGCATGAGGAGGA
CNAG_04313	GGAGCGATTCATTGGTCATT	GTCGGTACGATCGTTGGAGT
CNAG_06909	GCCCATAGCACTAGGAGTCG	ATGTCATCCTGCGAATAGCC
CNAG_00003	GTGAAACTCGGAGCTTGGTC	TACAATGGGCTCCATGAACA
CNAG_04546	TTATCGCATGTCTCCCCTTC	GTGGAATAGGAATGGCATGG
ACT1	CCCACACTGTCCCCATTTAC	AACCACGCTCCATGAGAATC