

1 **FIGURE LEGENDS**

2 FIG S1 Analysis of caspofungin or anidulafungin susceptibility of the mutants lacking *CHT2*,
3 *CSU51* or *PGA4* by spot assay. (A and B) Shown are two independent repeats for growth of
4 all single- or double-deletion mutants vs their parental strain CAF4-2 on medium
5 supplemented with caspofungin (CAS) and for growth of representative double-deletion
6 mutants vs their parental strain CAF4-2 on medium supplemented with anidulafungin (ANI).
7 Strains are indicated on the left. From left to right, the number of cells that were spotted onto
8 each plate, were 10^4 , 10^3 , 10^2 , and 10^1 . Plates were incubated at 37°C.

9 FIG S2 Analysis of caspofungin (CAS) susceptibility of the representative double-deletion
10 mutants NAC4 a.k.a. *cht2*^{-/-}, NACS1 a.k.a. *csu51*^{-/-}, NAP88 a.k.a. *pga4*^{-/-} by standard broth
11 microdilution assay. (A and B) Shown are two independent repeats for growth of mutants vs
12 their parental strain CAF4-2 in different concentration of caspofungin as indicated. For more
13 explanations see the legend of Fig. 3B. Data are presented as the best fit curve (see Materials
14 and Methods).

15 FIG S3 Analysis of anidulafungin (ANI) susceptibility of the representative double-deletion
16 mutants NAC4 a.k.a. *cht2*^{-/-}, NACS1 a.k.a. *csu51*^{-/-}, NAP88 a.k.a. *pga4*^{-/-} by standard broth
17 microdilution assay. (A and B) Shown are two independent repeats for growth of mutants vs
18 their parental strain CAF4-2 in different concentration of caspofungin as indicated. For more
19 explanations see the legend of Fig. S3. Note that experiment was conducted on the same
20 microtiter plate.

21 FIG S4 Analysis of caspofungin susceptibility of *pga4*^{-/-} and FJS5 mutants with both copies
22 of either *PGA4* (1) or *CHT2* (2), respectively, disrupted with the *Tn7*-UAU1 cassette, as well
23 as of the mutant DSY1768 (3) having incomplete deletion of ORF of *CHT2*. Shown is the
24 spot assay for growth of the mutant FJS5 vs the control strain DAY286 (and also vs the

25 parental strain BWP17) or of the mutant DSY1768 or the mutant *pga4*^{-/-} vs the control strain
26 CAF2-1 on control YPD medium supplemented with arginine, histidine and uridine, as well
27 as on YPD medium supplemented with the aforementioned aminoacids and caspofungin
28 (CAS), as indicated. Strains are indicated on the left. From left to right, 10⁴, 10³, 10², and
29 10¹ cells were spotted on each plate and incubated for 3 days at 37°C.

30 FIG S5 Example of semiquantitative RT-PCR analysis of products amplified from total RNA
31 from deletion strain JMC200-3-3 and its parental strain JRCT1. The *CHT2*, *CSU51* or *PGA4*
32 gene was amplified and ran on a conventional electrophoresis gel, which was ethidium
33 bromide stained and photographed and the imaged was processed, as described in Materials
34 and Methods. Lanes show products sampled at increasing cycles. Values for the *CHT2*,
35 *CSU51* or *PGA4* gene were normalized against control *REX2*. *CHT2*, *CSU51* or *PGA4*
36 monosomic to disomic (JMC200-3-3/JRCT1) ratio was calculated, as averaged from three
37 consecutive cycles.

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39 TABLE S1 Calculated values^a of caspofungin MICs (ng/ml) for double-deletion
 40 mutants and CAF4-2 (2nd and 3rd set of experiments)

	NAC4		NACS1		NAP88	
	CAF4-2	a.k.a. <i>cht2</i> ^{-/-}	CAF4-2	a.k.a. <i>csu51</i> ^{-/-}	CAF4-2	a.k.a. <i>pga4</i> ^{-/-}
MIC ₅₀	91 ± 4	122 ± 1	31 ± 1	63 ± 14	45 ± 2	123 ± 1
MIC ₇₀	105 ± 5	125 ± 1	39 ± 1	107 ± 26	59 ± 3	123 ± 1
MIC ₈₀	115 ± 6	128 ± 1	46 ± 1	150 ± 36	70 ± 4	124 ± 1
MIC ₉₀	139 ± 1	171 ± 1	58 ± 1	248 ± 59	90 ± 5	124 ± 6

^a MIC₅₀, MIC₇₀, MIC₈₀, or MIC₉₀ refers to the concentration of caspofungin at which 50%, 70%, 80%, or 90% of growth is inhibited. See Materials and Methods for the calculation of MIC values. The differences between mutants and CAF4-2 were evaluated with Student's *t* test and all p-values were <0.05.

	NAC4		NACS1		NAP88	
	CAF4-2	a.k.a. <i>cht2</i> ^{-/-}	CAF4-2	a.k.a. <i>csu51</i> ^{-/-}	CAF4-2	a.k.a. <i>pga4</i> ^{-/-}
MIC ₅₀	117 ± 5	206 ± 11	96 ± 6	154 ± 25	60 ± 1	157 ± 4
MIC ₇₀	146 ± 6	233 ± 13	103 ± 6	260 ± 56	75 ± 1	193 ± 5
MIC ₈₀	167 ± 7	254 ± 14	107 ± 6	362 ± 101	87 ± 1	220 ± 6
MIC ₉₀	206 ± 9	284 ± 15	113 ± 6	331 ± 26	108 ± 1	267 ± 7

^a MIC₅₀, MIC₇₀, MIC₈₀, or MIC₉₀ refers to the concentration of caspofungin at which 50%, 70%, 80%, or 90% of growth is inhibited. See Materials and Methods for the calculation of MIC values. The differences between mutants and CAF4-2 were evaluated with Student's *t* test and all p-values were <0.05.

41 TABLE S2 Calculated values^a of anidulafungin MICs (ng/ml) for double-deletion
 42 mutants and CAF4-2 (2nd and 3rd set of experiments)

	CAF4-2	NAC4 a.k.a. <i>cht2</i> ^{-/-}	NACS1 a.k.a. <i>csu51</i> ^{-/-}	NAP88 a.k.a. <i>pga4</i> ^{-/-}
MIC ₅₀	8.5 ± 1	25 ± 2.1*	11.5 ± 1.2	64.5 ± 1.2*
MIC ₇₀	12 ± 1.4	22.7 ± 1.8*	14.6 ± 1.5	71.5 ± 3.1*
MIC ₈₀	15 ± 1.8	24.3 ± 1.9*	16.9 ± 1.8	68.8 ± 1.4*
MIC ₉₀	20.8 ± 2.5	27.0 ± 2.2	21.3 ± 2.2	73.4 ± 1.8*

^a MIC₅₀, MIC₇₀, MIC₈₀, or MIC₉₀ refers to the concentration of caspofungin at which 50%, 70%, 80%, or 90% of growth is inhibited. See Materials and Methods for the calculation of MIC values. The differences between mutants and CAF4-2 were evaluated with Student's *t* test and p-values indicated as an asterisk (*) were <0.001.

	CAF4-2	NAC4 a.k.a. <i>cht2</i> ^{-/-}	NACS1 a.k.a. <i>csu51</i> ^{-/-}	NAP88 a.k.a. <i>pga4</i> ^{-/-}
MIC ₅₀	9.1 ± 1.0	21.6 ± 0.9*	13.6 ± 0.8*	31.9 ± 1.6*
MIC ₇₀	11.1 ± 1.3	24.5 ± 1.0*	15.1 ± 0.9*	35.6 ± 1.8*
MIC ₈₀	12.6 ± 1.4	26.6 ± 1.1*	16.2 ± 1.0	38.1 ± 1.9*
MIC ₉₀	15.2 ± 1.7	30.1 ± 1.3*	17.9 ± 1.1	42.3 ± 2.1*

^a MIC₅₀, MIC₇₀, MIC₈₀, or MIC₉₀ refers to the concentration of caspofungin at which 50%, 70%, 80%, or 90% of growth is inhibited. See Materials and Methods for the calculation of MIC values. The differences between mutants and CAF4-2 were evaluated with Student's *t* test and all p-values indicated as an asterisk (*) were <0.05.

44 **REFERENCES**

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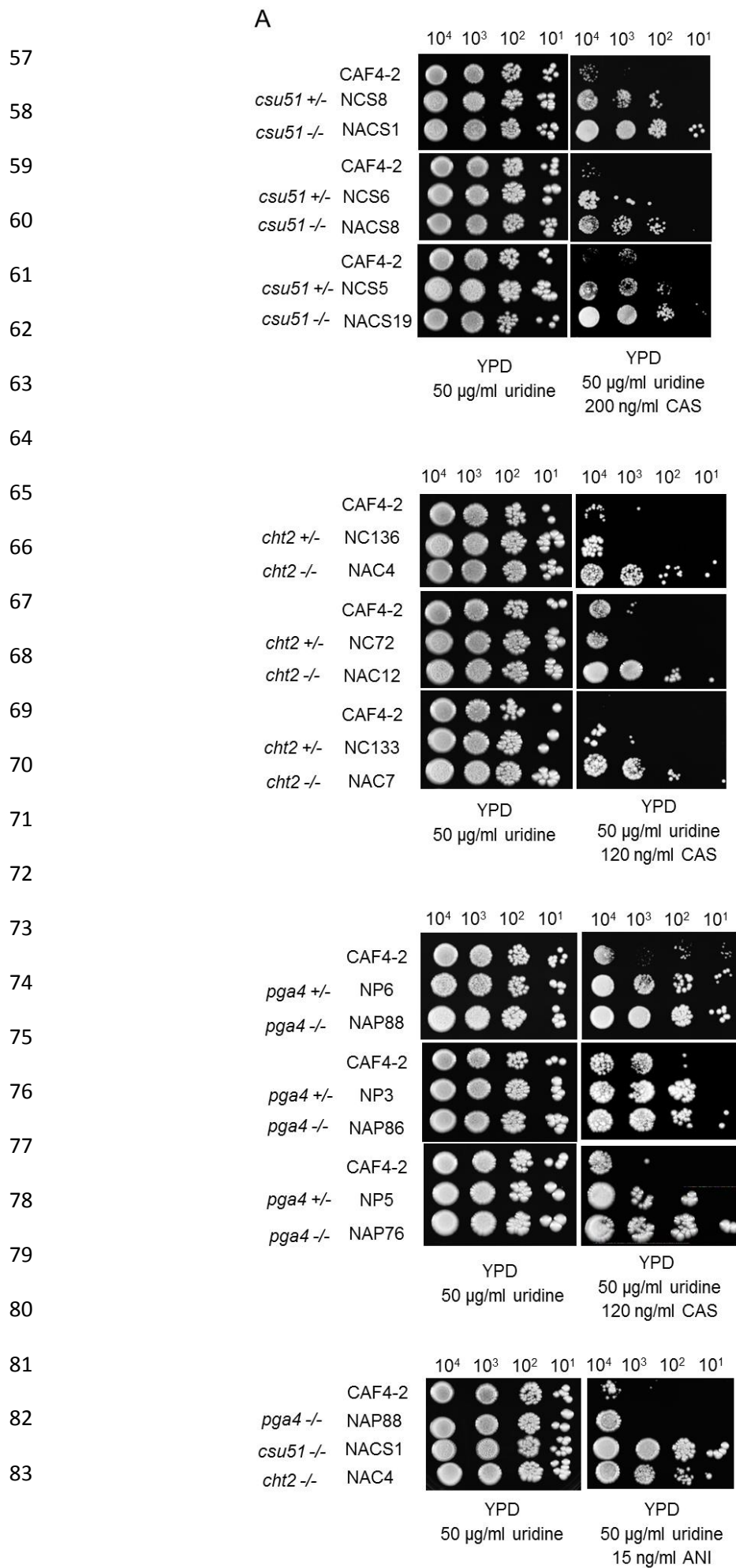
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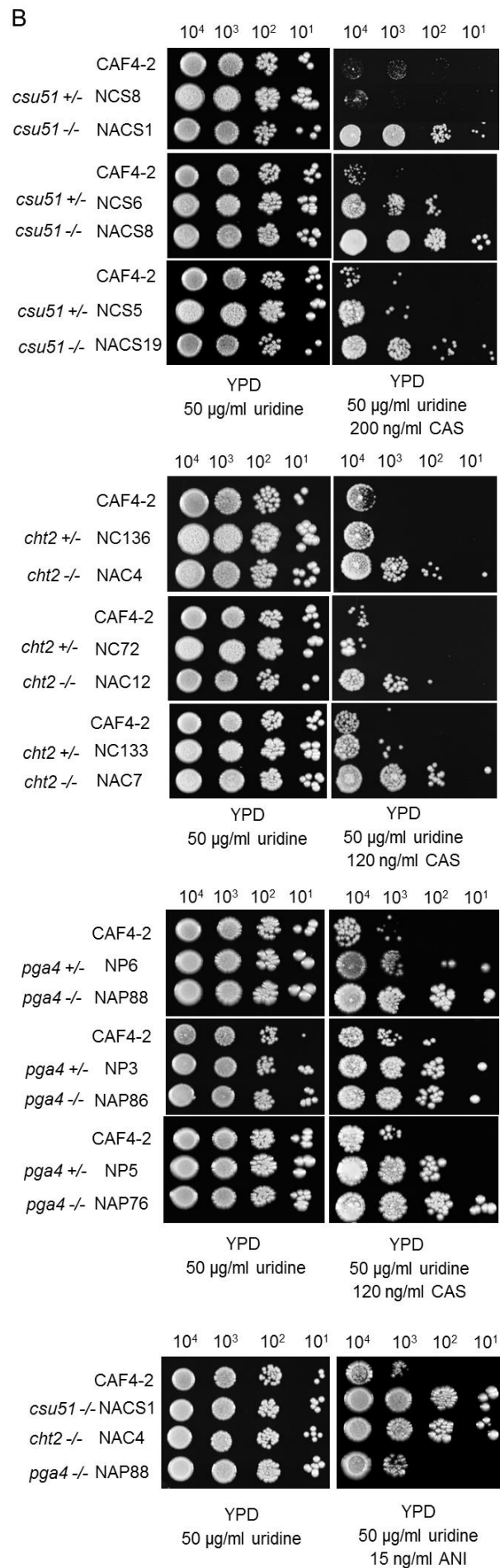
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Fig. S1



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Fig. S1



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115 mutants vs their parental strain CAF4-2 on medium supplemented with anidulafungin (ANI).
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117 each plate, were 10^4 , 10^3 , 10^2 , and 10^1 . Plates were incubated at 37°C.

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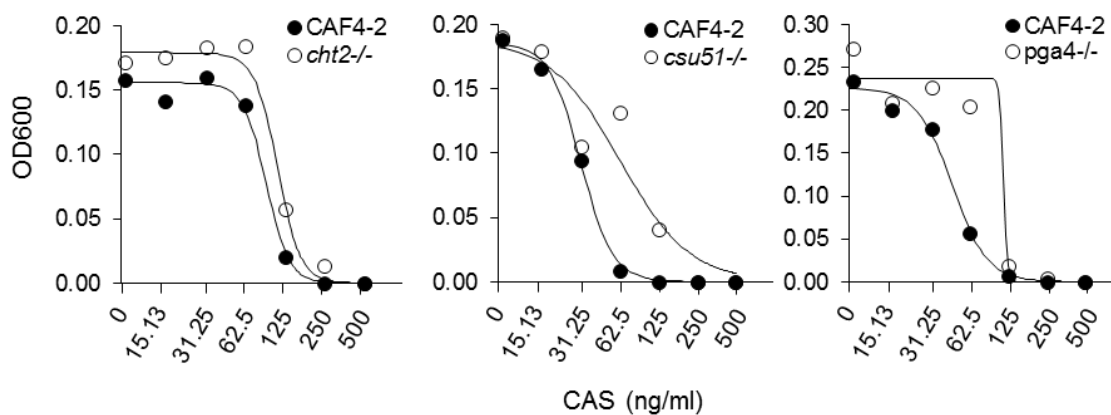
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Fig. S2

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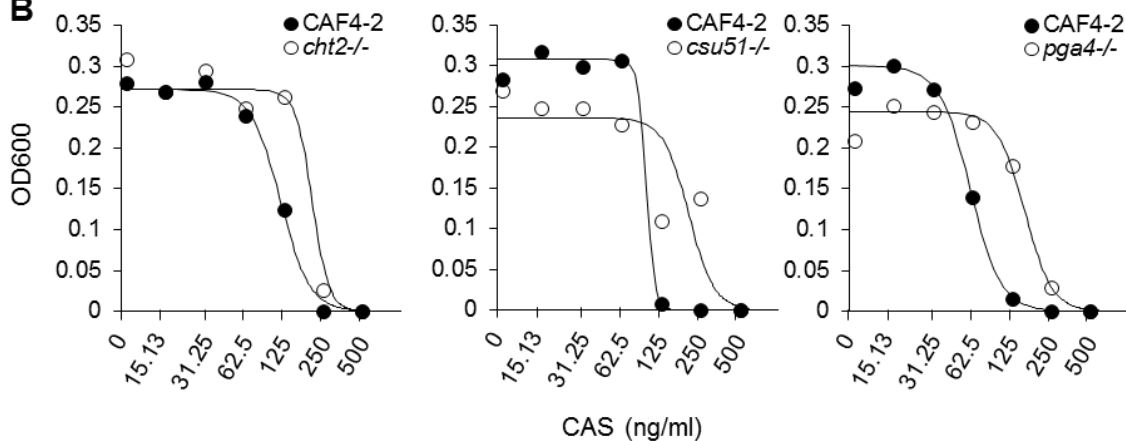


FIG S2 Analysis of caspofungin (CAS) susceptibility of the representative double-deletion mutants NAC4 a.k.a. *cht2*^{-/-}, NACS1 a.k.a. *csu51*^{-/-}, NAP88 a.k.a. *pga4*^{-/-} by standard broth microdilution assay. (A and B) Shown are two independent repeats for growth of mutants vs their parental strain CAF4-2 in different concentration of caspofungin as indicated. For more explanations see the legend of Fig. 3B. Data are presented as the best fit curve (see Materials and Methods).

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Fig. S3

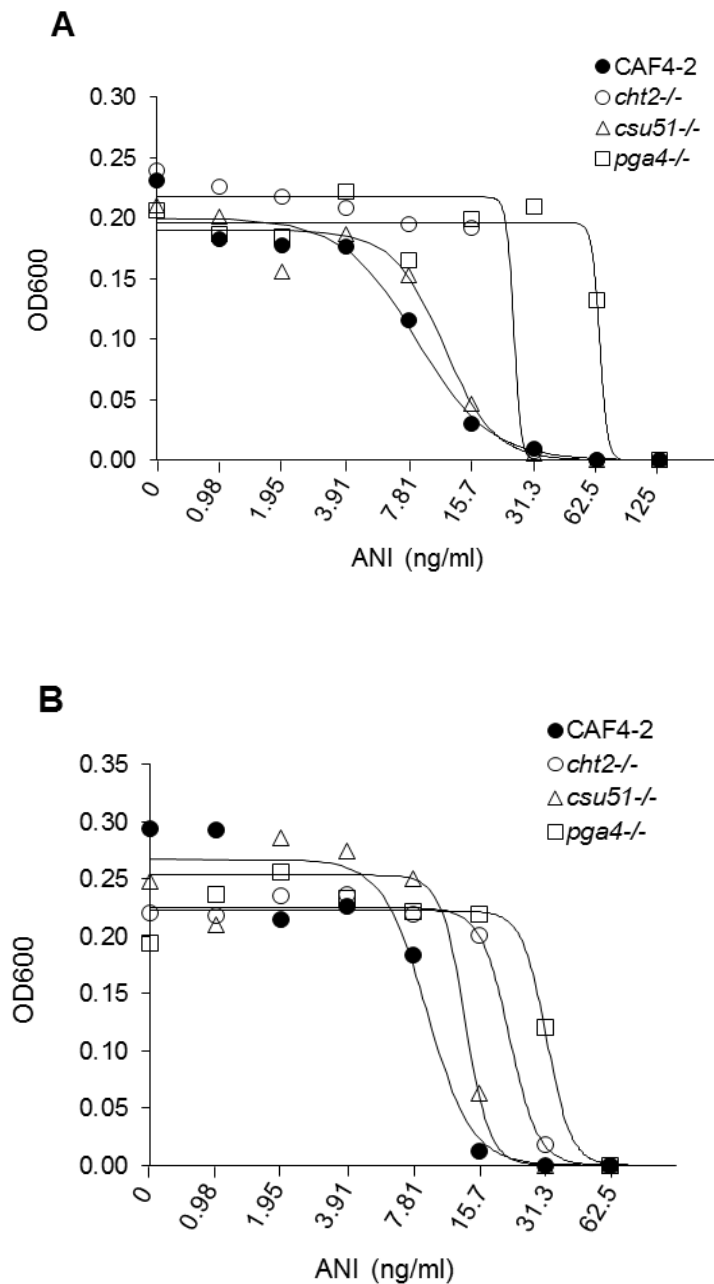


FIG S3 Analysis of anidulafungin (ANI) susceptibility of the representative double-deletion mutants NAC4 a.k.a. *cht2*^{-/-}, NACS1 a.k.a. *csu51*^{-/-}, NAP88 a.k.a. *pga4*^{-/-} by standard broth microdilution assay. (A and B) Shown are two independent repeats for growth of mutants vs their parental strain CAF4-2 in different concentration of caspofungin as indicated. For more explanations see the legend of Fig. S3. Note that experiment was conducted on the same microtiter plate.

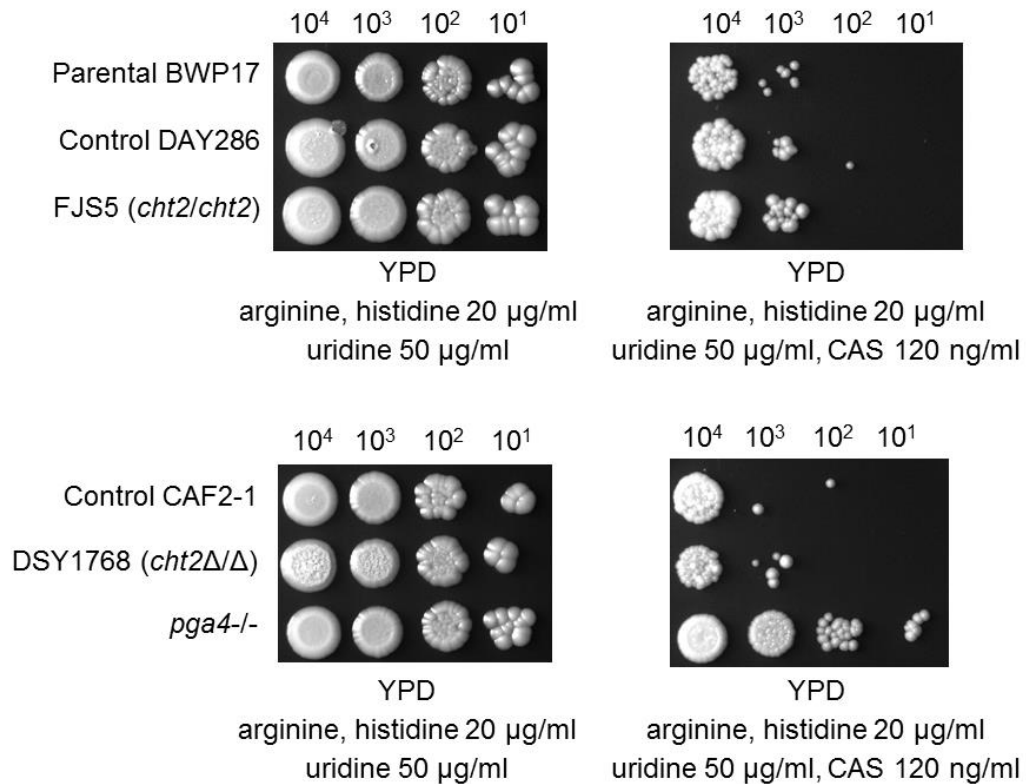
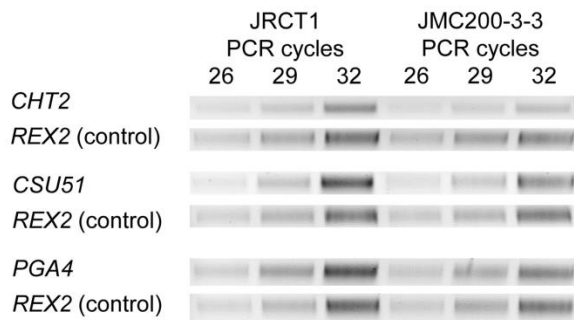
Fig. S4

FIG S4 Analysis of caspofungin susceptibility of *pga4*^{-/-} and FJS5 mutants with both copies of either *PGA4* (1) or *CHT2* (2), respectively, disrupted with the *Tn7*-UAU1 cassette, as well as of the mutant DSY1768 (3) having incomplete deletion of ORF of *CHT2*. Shown is the spot assay for growth of the mutant FJS5 vs the control strain DAY286 (and also vs the parental strain BWP17) or of the mutant DSY1768 or the mutant *pga4*^{-/-} vs the control strain CAF2-1 on control YPD medium supplemented with arginine, histidine and uridine, as well as on YPD medium supplemented with the aforementioned aminoacids and caspofungin (CAS), as indicated. Strains are indicated on the left. From left to right, 10^4 , 10^3 , 10^2 , and 10^1 cells were spotted on each plate and incubated for 3 days at 37°C.

Fig. S5

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213 FIG S5 Example of semi-quantitative RT-PCR analysis of products amplified from total RNA

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215 gene was amplified and ran on a conventional electrophoresis gel, which was ethidium

216 bromide stained and photographed and the imaged was processed, as described in Materials

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219 monosomic to disomic (JMC200-3-3/JRCT1) ratio was calculated, as averaged from three

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