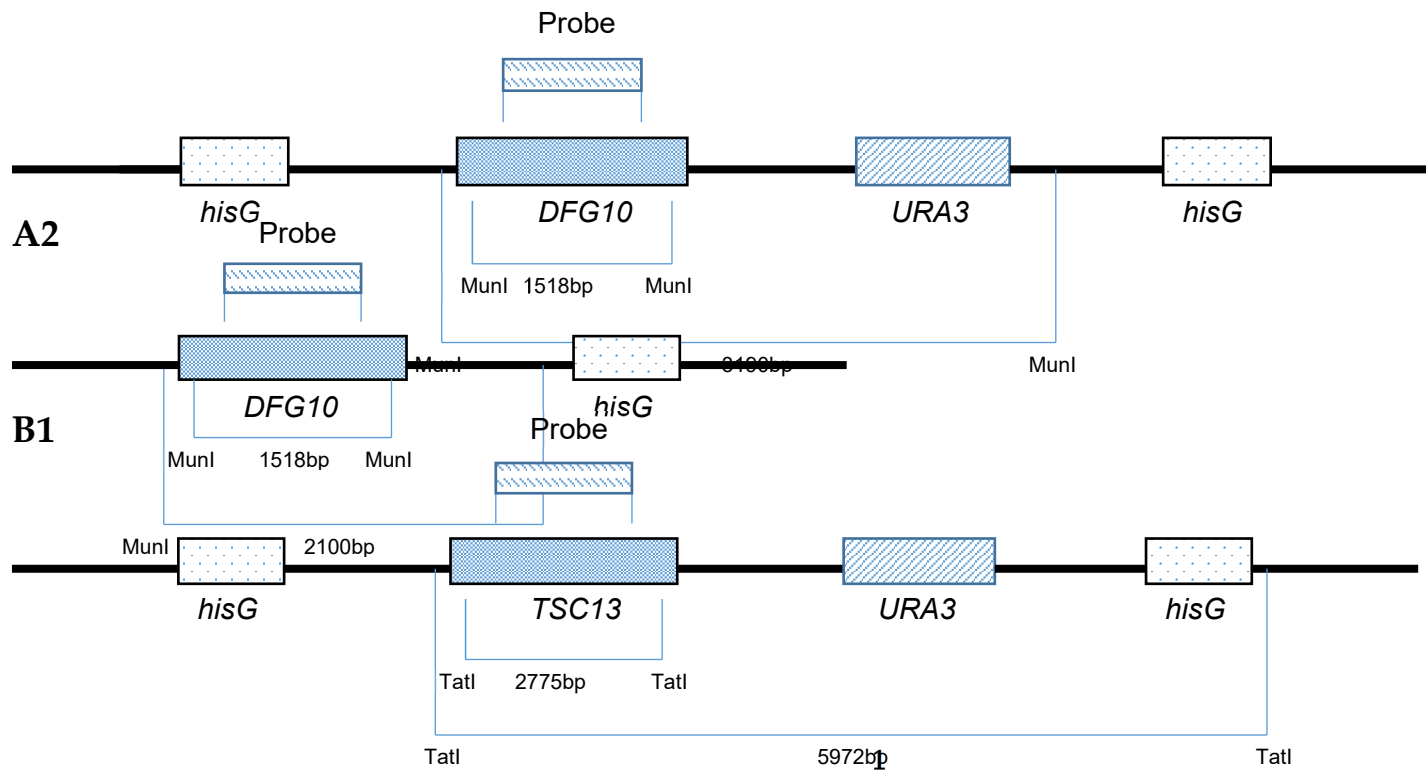
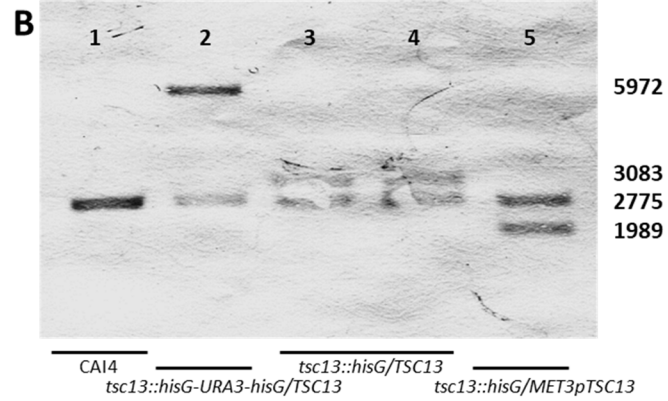
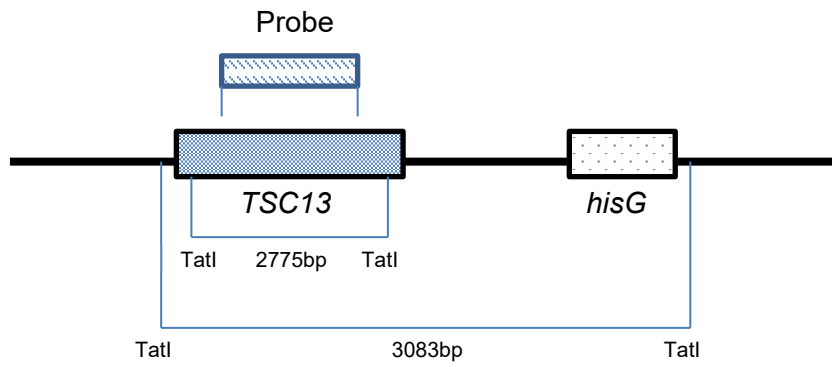


A1





B2



B3

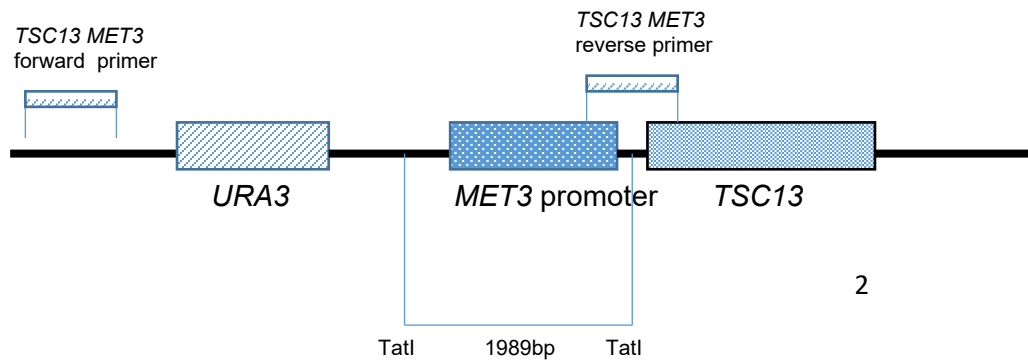


Figure S1. Southern analysis of *dfg1Δ0* (A) and *tsc1Δ13* (B) strains of *C. albicans* CAI4.

A- Analysis of *dfg10Δ* strain

MunI-digested DNA of control strain CAI4 (lane1), hemizygote *dfg10::hisG-URA3-hisG/DFG10* before *URA3* excision (lane 2, 3, 4)

hemizygote *dfg10::hisG/DFG10* after *URA3* excision (lane 5, 6), homozygote *dfg10::hisG/dfg10::hisG-URE3-hisG* strain (lane 7)

Blot was probed with digoxigenin-labeled *DFG10* fragment and visualized with NBT/BCIP

A1- restriction map of *DFG10* region before *URA3* excision

A2- restriction map of *DFG10* region after *URA3* excision

B- Analysis of *tsc13Δ*

TatI-digested DNA of control strain CAI4 (lane1), hemizygote *tsc13::hisG-URA3-hisG/TSC13* before *URA3* excision (lane 2), hemizygote

tsc13::hisG/TSC13 after *URA3* excision, *tsc13::hisG/MET3pTSC13* strain (lane 5).

Blot was probed with digoxigenin-labeled *TSC13* fragment and visualized with NBT/BCIP

B1- restriction map of *TSC13* region before *URA3* excision

B2- restriction map of *TSC13* after *URA3* excision

B3- restriction map of *TSC13* under the regulatable *MET3* promoter

Table S1

Profile of fatty acids in membranes from wild type and mutants of *C. albicans* strains

	CAI4	<i>tsc13Δ/MET3pTSC13</i> (Met/Cys -)	<i>tsc13Δ/MET3pTSC13</i> (Met/Cys +)	<i>dfg10Δ/dfg10Δ- tsc13Δ/MET3pTSC13</i> (Met/Cys -)	<i>dfg10Δ/dfg10Δ- tsc13Δ/MET3pTSC13</i> (Met/Cys +)	<i>dfg10Δ/dfg10Δ</i>
Fatty acid	Content of fatty acid (%)					
C14 Miristic	0,61±0,03	0,38 ±0,01	1,02 ±0,1	0,60 ±0,02	0,83 ±0,04	0,52 ±0,04
C16:0 Palmitic	19,83 ±0,08	18,03 ±0,28	17,08 ±0,52	17,35 ±0,12	18,09 ±0,17	16,93 ±0,58
C16:1 Palmitoleic	17,29 ±0,21	14,28 ±0,03	25,02± 1	15,05 ±0,21	18,21± 0,18	13,76± 0,66
C17:0 Margaric	0,46 ±0,34	0,36 ±0,04	0,55 ±0,02	0,75 ±0,01	1,29 ±0,03	0,46 ±0,04
C17:1 Margarinic	1,37 ±0,03	0,76 ±0,62	3,00 ±0,07	2,24 ±0,08	4,45 ±0,28	0,77 ±0,7
C18:0 Stearic	4,2± 0,08	4,04± 0,02	2,57± 0,13	3,73± 0,02	2,98 ± 0,24	4,05± 0,16
C18:1 Oleic	21,27± 0,13	17,44± 0,11	18,12 ± 0,33	19,86± 0,22	15,68± 0,23	16,66 ± 1,37
C18:2 Linoleic	26,52 ±0,4	34,43± 0,06	25,27 ±0,72	26,47± 0,05	26,30± 1,12	31,29± 1,03
C18:3 Linolenic	7,42 ± 0,09	7,88± 0,17	3,11± 0,22	7,26± 0,73	5,75± 0,42	7,62± 0,17

The values shown do not add to 100% because of a variable content of C17 fatty acids [between ca. 1 and 6% of all fatty acids analyzed, not shown].

Table S2 Primers used for mutant construction

Name	Sequence	Remarks
DFG10 F1F	<u>GAGCTC</u> TGGCAGCGGGTAGTTTAA	Restriction site for SacI underlined
DFG10 F1R	<u>AGATCT</u> CTACGTAAGTTTTGATGG	Restriction site for BglII underlined

DFG10 F2F	<u>GGATCC</u> GCTATGGCAAAAGAGCAA	Restriction site for BamHI underlined
DFG10 F2R	<u>CTGCAG</u> TCGCACTGTTATAGGGCA	Restriction site for PstI underlined
FverDFG10	CATAGTTTGTATGGACGTGTG	
RverDFG10	ATCTAGGCCATGTAGTAGCTG	
FverhisG	CGATACAGACCGGTTTCAGAC	
RverhisG	GCGCTTTCAGTTTCTCCATG	
TSC13 F1F	<u>GAGCTC</u> CAGTTGCAAGAGAGATTC	Restriction site for SacI underlined
TSC13 F1R	<u>AGATCT</u> TCTTGAAGTACGAGTCC	Restriction site for BglII underlined
TSC13 F2F	<u>GGATCC</u> CTTTGTTGATCTTGTGGGT	Restriction site for BamHI underlined
TSC13F2R	<u>CTGCAG</u> CCAATACCCCAGCTTCAG	Restriction site for PstI underlined
FverTSC13	TCCCAATCTGAAGACATGATCGAT	
RverTSC13	TGTGTAGACTGGTATATCCCT	
TSC13MET-F	TTTGAGGAAATAATCCACAGTTGGTTAGCACA CGAAAAGCAAGATTACAAGTAAAGATCTTTA GTGAGTGAATTGTCTATTCCAAGC	
TSC13TMET-R	TCAATTCATTGGAGGAAAAAGATTTAATGGAT CTGGAACGTGATTGACTTCAATGTCAGTCAT AAGTGACAACACTTGGAAGTTGAA	

Table S3 Primers used for RT qPCR analysis

Symbol	Name	Reference sequence	Primers		Efficiency (%)
DFG10	<i>Candida albicans</i> SC5314 putative polyprenol reductase	XM_707500.2	F	AACCTCAAAGATGAACGTGAGC	2.32
			R	CTTAGCCCCAAATAGGTAGCC	
TSC13	<i>Candida albicans</i> SC5314 trans-2-enoyl-CoA reductase (NADPH)	XM_713023.2	F	TGTCGTGGTTAGCCTATGCTTT	2.23
			R	GCCACATTGACCGGAACTAAC	
HMGR	<i>Candida albicans</i> SC5314 hydroxymethylglutaryl-CoA reductase (NADPH) (HMG1)	XM_708543.2	F	TGAACGTTTCTGTGTCAATGCC	2.21
			R	GTTGAGCATTTGCACCTGGATT	
ERG20	<i>Candida albicans</i> SC5314 bifunctional (2E,6E)-farnesyl diphosphate synthase/dimethylallyltransferase (ERG20)	XM_707824.2	F	TCCAGAACAAATTGGGAAAATC GG	2.35
			R	CGTTGTTTCAGGGGTAGCAATCA	
ACC1	<i>Candida albicans</i> SC5314 putative acetyl-coenzyme-A carboxylases (ACC1)	XM_713531.1	F	AGGTGAAGAGCGTCATGTCATT	
			R	ATGTGGCACCAGCAATTAAACC	
RER2	<i>Candida albicans</i> SC5314 ditrans, polycis-polyprenyl diphosphate synthase (RER2)	XM_716843.1	F	GTTGTGTGAGGAGTATGGAGTT	2.32
			R	ACACGGCACGAGTATTGTT	
SRT1	<i>Candida albicans</i> SC5314 ditrans, polycis-polyprenyl diphosphate synthase (SRT1)	XM_019475163.1	F	CCCTATACTGCTCGTGATGAAAT	2.11
			R	ACGATCATGAAGTTCTCCTGAAA	
NUS1	<i>Candida albicans</i> SC5314 ditrans, polycis-polyprenyl diphosphate synthase	XM_718081.1	F	CACAAGTGATTAGGGAGGACAT T	2.25
			R	GACCATGCTGTCAACTCACTAA	

ACT1	Candida albicans SC5314 actin (ACT1)	XM_019475182.1	F	TTGGATTCTGGTGATGGTGTTA	2.22
			R	TCAAGTCTCTACCAGCCAAATC	
CPA1	Candida albicans SC5314 carbamoyl-phosphate synthase (glutamine- hydrolyzing) (CPA1)	XM_717609.2	F	GGGAGAATTACGATTGGTGAAG A	2.25
			R	GGTGCCTTGGTGGTTACTTTA	
RPP2b	Candida albicans SC5314 ribosomal protein P2B (RPP2B)	XM_718047.1	F	TG GTAACACCTCTCCATCAGC	2.26
			R	GGATTCTTCGGCTTCAACACC	
RIP1	Candida albicans SC5314 ubiquinol-cytochrome-c reductase catalytic subunit (RIP1)	XM_019475318.1	F	GGTTCTGTCCATGTCACGGT	2.25
			R	GTTCAATGGAGCTGGACCCT	
LSC2	Candida albicans SC5314 succinate-CoA ligase (GDP-forming) subunit beta (LSC2)	XM_019475549.1	F	CACCACTCCAGAAGGTGCTT	2.23
			R	ACCACGACCACCAGTCAAAG	
PMA1	Candida albicans SC5314 H(+)-exporting P2-type ATPase (PMA1)	XM_712666.2	F	GCTGCCACAGTCAATGAAGC	2.20
			R	GCAATACCAACGGCATCACC	