Supplementary Figure S2

A

ENO1p CAS9 CYC1t

SNR52p sgRNA ENO1t

ACT1p SAT1 URA3t

RT

ACT1p SAT1 URA3t

GOI

GOI

ACT1p SAT1 URA3t

B

SAT1 integration check

1 3

ACT1p SAT1 URA3t

2 6

5' integration check

3' integration check

ORF check

1 5

GOI

4 6

5' ORF check

3' ORF check

C

***SAT1* integration check**

ORF check

5' **3'** **5'** **3'**

SS +/+ +/- -/- -/- C

ctn1

cyb2

ecm3

hcm1

nce103

osm2

* *pho84*

try4

* *try6*

600bp

400bp

200bp

Supplementary Figure S2. Genotyping of *C. albicans* mutants. Homozygous null mutants were made in the *C. albicans* clinical isolate SC5314 using CRISPR-Cas technology. The primers used for mutant construction and PCR diagnosis are described in Supplementary Table 4. **(A)** The open reading frame of the target gene of interest (GOI) was deleted and replaced with a disruption cassette carrying the *SAT1* marker expressed from the *ACT1* promoter and *URA3* terminator. This was driven by *CAS9* expression from the *ENO1* promoter and *CYC1* terminator. **(B)** The genotypes of mutants were confirmed by diagnostic PCR using primers that checked integration of the *SAT* marker and loss of the target gene of interest (GOI) at both the 5' and 3' ends of the deletion/insertion. The approximate positions of the PCR primers, and their numbers are shown. **(C)** PCR confirmation of the mutants for the nine genes of interest (labelled to the left): SS, size standards, with their lengths shown by the left hand panels; +/+, SC5314 parental strain; +/-, heterozygous deletion mutant; -/-, homozygous deletion mutants A and B; C, control lacking template DNA. * No heterozygotes were identified for *PHO84* and *TRY6.*