

Supplemental Materials

Liu Z, Myers LC. ‘Mediator Tail Module is Required for Tac1 Activated *CDR1* Expression and Azole Resistance in *Candida albicans*.’

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Fig. S1

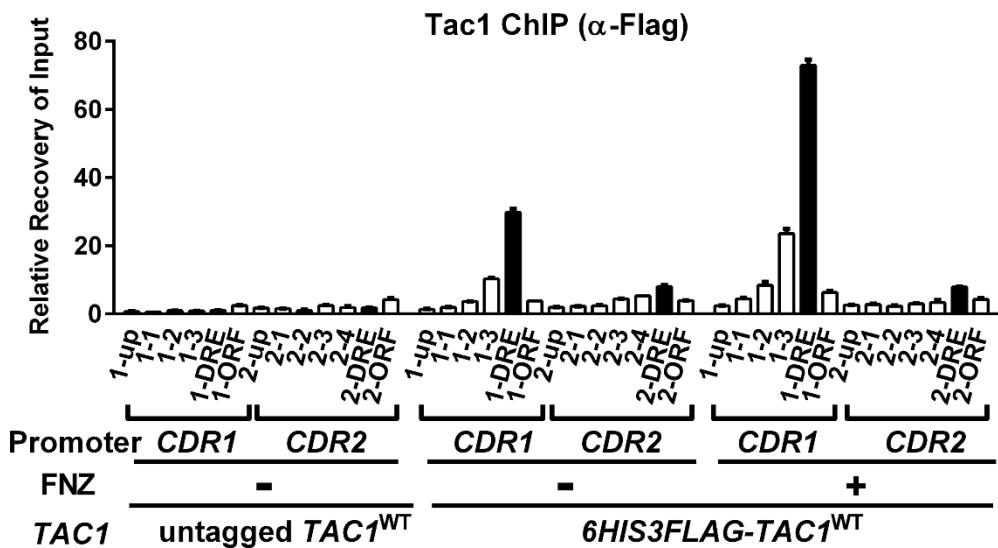


Fig. S1 Analysis of Tac1 occupancy at the *CDR1* and *CDR2* promoters using additional primer pairs

Anti-Flag ChIP products obtained from strains expressing 6His3Flag tagged Tac1 (yLM485) or untagged native Tac1 (DSY2937-35), in the absence or presence of fluphenazine (10 μ g/mL; 15 minutes), were analyzed for Tac1 occupancy profile across the *CDR1* and *CDR2* promoters. Recovery rate (% Input) of DNA fragments containing '1-DRE' amplicon in the ChIP product obtained from uninduced culture of the strain untagged Tac1 (DSY2937-35) was set to '1' to calculate relative recovery at additional regions. Columns representing the recovery at the two DREs were marked black.

Fig. S2

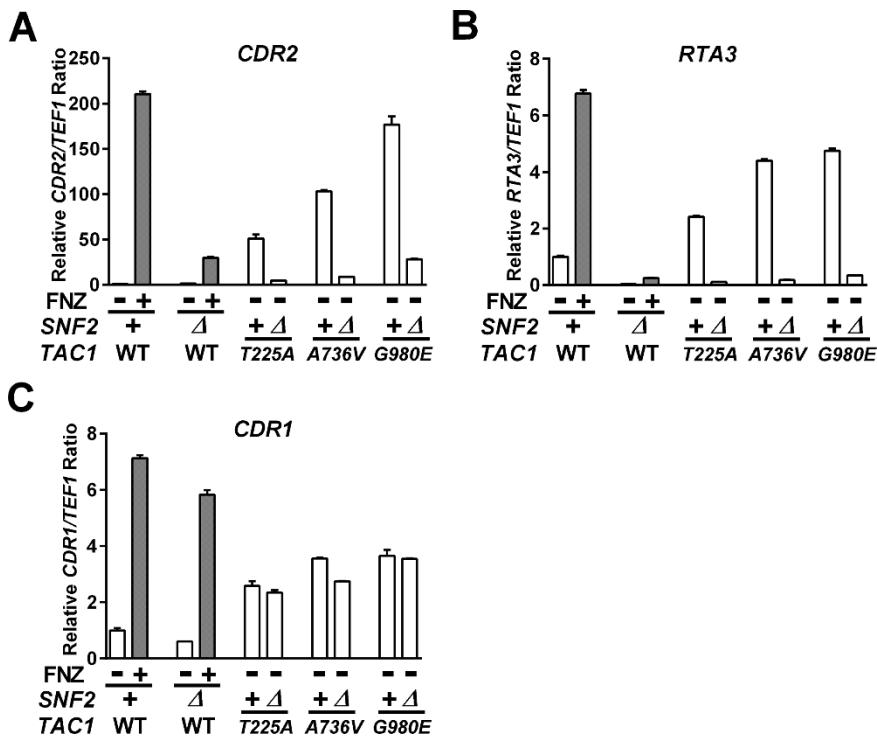


Fig. S2 Induction of Tac1 target genes in *snf2* deletion strains

RT-qPCR analysis of *CDR2* (A), *RTA3* (B) and *CDR1* (C) induction in *SNF2*^{+/+} ('+') strains bearing individual *TAC1* variants (WT (DSY2937-35), T225A (ACY67), A736V (ACY13) or G980E (ACY71)) and their *snf2* deletion derivatives ('Δ'; yLM472, yLM474, yLM476 and yLM478 respectively) were treated with 10 µg/mL fluphenazine or vehicle for 15 minutes as indicated. *TEF1* abundance was used as internal reference. Basal expression of each gene measured from the untreated *SNF2/TAC1* wild type strain (DSY2937-35) was set to '1' to calculate relative gene expression.

Fig. S3

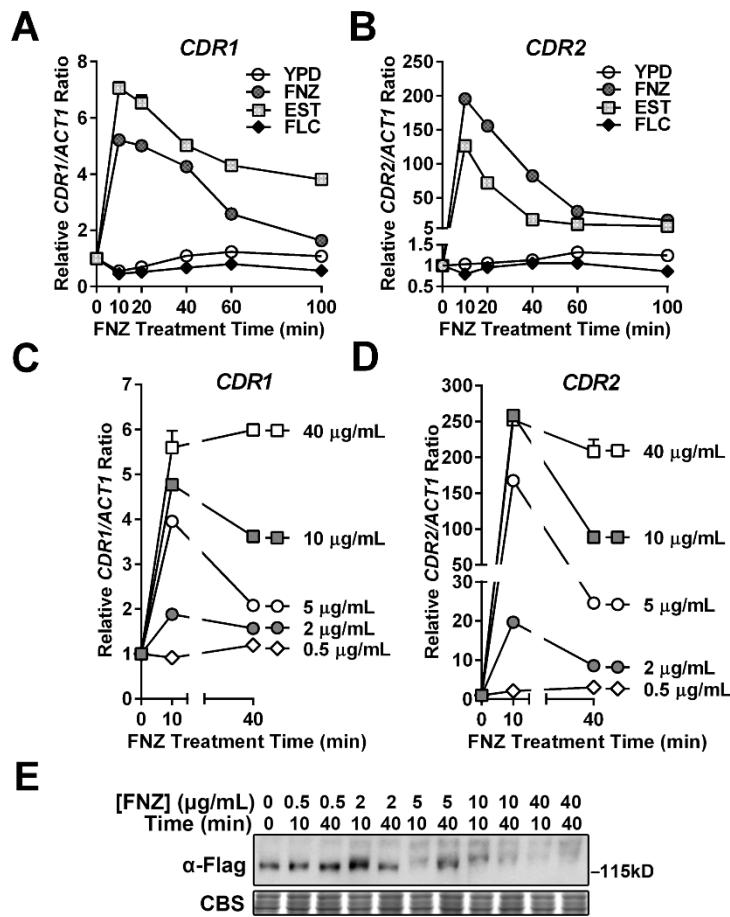


Fig. S3 Time Course analysis of SDS-PAGE mobility shift and corresponding *CDR1* and *CDR2* expression

(A-B) RT-qPCR analysis of *CDR1* and *CDR2* expression on RNA extracted from the samples collected in **Fig. 8A**. Basal expression of each gene, measured before any treatment, was set to ‘1’. (C) and (D) RT-qPCR analysis of *CDR1* and *CDR2* expression in a 6His3Flag tagged wild type Tac1 expressing strain (yLM485) grown in the presence of differing concentrations of fluphenazine for the indicated period of time. (E) Immunoblot of Tac1 mobility shift in lysates prepared from samples collected for the analysis in (C) and (D). Whole cell lysates were resolved on 6% SDS-PAGE gel and probed with an anti-Flag antibody. Coomassie blue staining (CBS) was used as the loading control.

Fig. S4

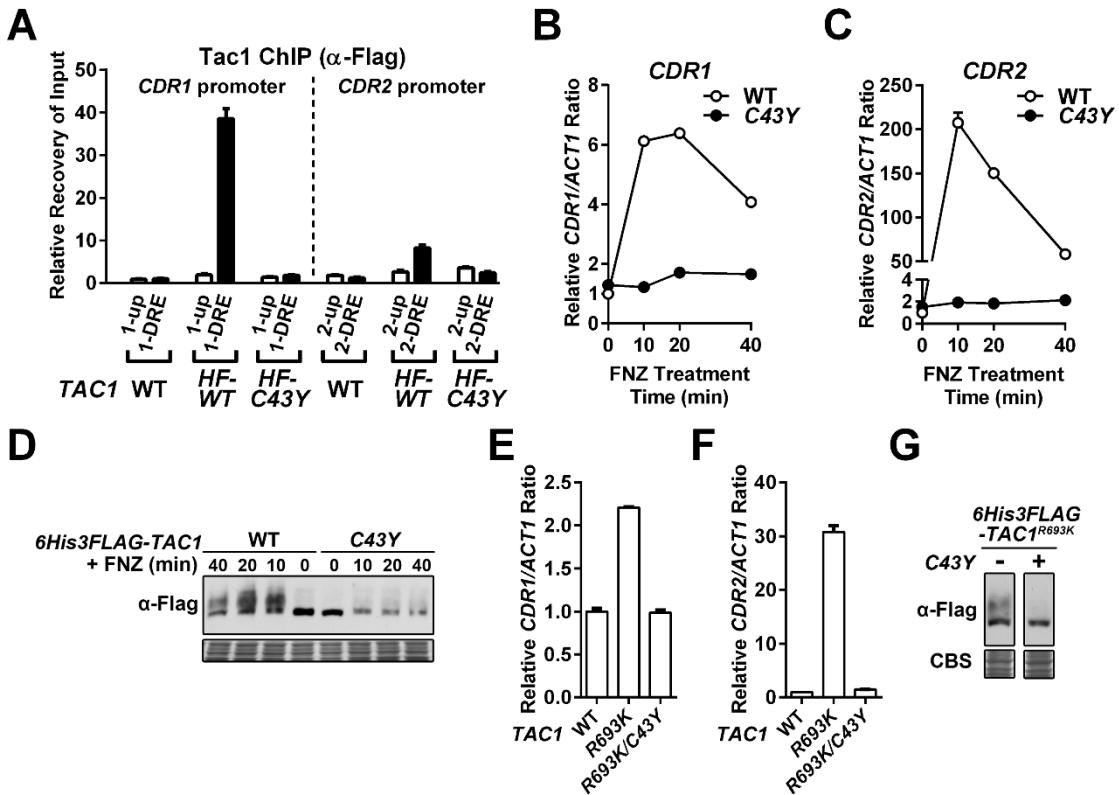


Fig. S4 A Tac1 C43Y mutant protein is unable to bind DNA, activate transcription of *CDR1* or *CDR2*, or undergo a phosphorylation mobility shift.

(A) Anti-Flag ChIP analysis of Tac1^{C43Y} occupancy at the *CDR1* and *CDR2* promoters in strains expressing 6His3Flag (HF) tagged wild type Tac1 ('HF-WT'; yLM485) or Tac1^{C43Y} ('HF-C43Y'; yLM537). Recovery rate (% Input) of DNA fragments containing the '1-DRE' amplicon in the ChIP product obtained from a strain expressing untagged native Tac1 ('WT'; DSY2937-35) was set to '1' to calculate relative recovery at additional regions. (B-C) RT-qPCR analyses of *CDR1* (B) and *CDR2* (C) expression in strains expressing 6His3Flag tagged wild type Tac1 ('WT'; yLM485) or Tac1^{C43Y} ('C43Y'; yLM537) treated with 10 µg/mL fluphenazine for the indicated period of time. *CDR1* and *CDR2* expression levels in the 6His3Flag-Tac1^{WT} strain (yLM485) were set to '1' individually. (D) Immunoblot analysis of the Tac1^{C43Y} phosphorylation shift in the lysates prepared from the samples collected for the analysis in (B) and (C) by using an anti-Flag antibody. The samples were resolved by 6% SDS-PAGE. Coomassie blue staining (CBS) was used as the loading control. (E-F) RT-qPCR analyses of *CDR1* (E) and *CDR2* (F) expression in strains expressing 6His3Flag tagged Tac1^{WT} (yLM485), Tac1^{R693K} (yLM532) or Tac1^{R693K/C43Y} (yLM538). (G) Immunoblot analysis of Tac1 in lysates from strains expressing 6His3Flag tagged Tac1^{R693K} (yLM532) or Tac1^{R693K/C43Y} (yLM538) using an anti-Flag antibody. Samples were resolved by 6% SDS-PAGE.

Coomassie blue staining (CBS) was used as the loading control. Panels originate from different lanes of the same exposure of the same blot and gel.

Fig. S5

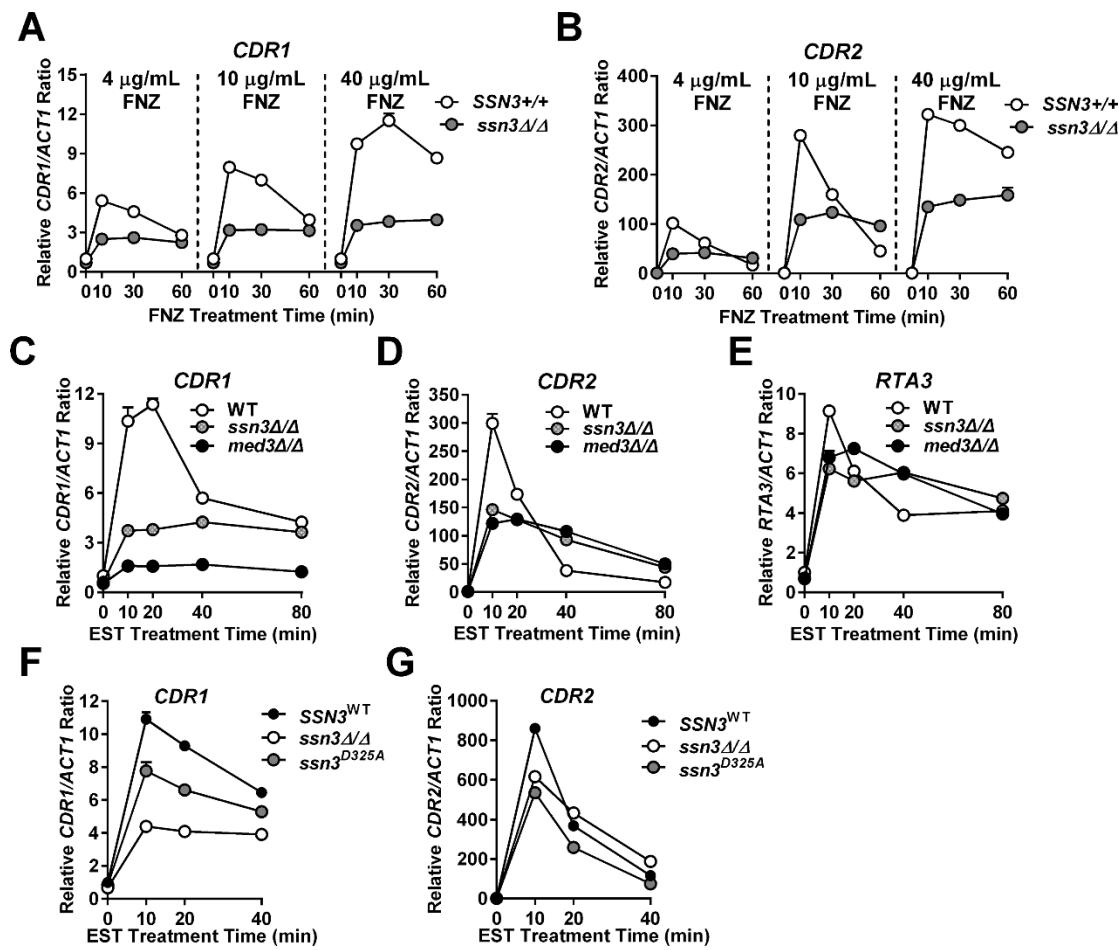


Fig. S5 Expression of Tac1 target genes, induced by estradiol treatment or different concentration of fluphenazine, in *ssn3* mutant strains

(A-B) RT-qPCR analyses of *CDR1* (**A**) and *CDR2* (**B**) induction in *SSN3*^{+/+} and *ssn3*^{Δ/Δ} strains expressing wild type Tac1 (DSY2937-35 and yLM236, respectively) by different concentrations of fluphenazine. The expression level of each gene in the untreated *SSN3*^{+/+} strain (DSY2937-35) was set to ‘1’. **(C-E)** RT-qPCR analysis of *CDR1* (**C**), *CDR2* (**D**) and *RTA3* (**E**) induction in an *ssn3*^{Δ/Δ} strain expressing wild type Tac1 (yLM236) by 10 µg/mL estradiol (EST). Parallel analysis of estradiol induction in a wild type (‘WT’; DSY2937-35) and a *med3*^{Δ/Δ} mutant (yLM232) strain are presented for comparison. The expression level of each gene measured in the untreated wild type strain (DSY2937-35) was set to ‘1’. **(F-G)** RT-qPCR analysis of estradiol induced *CDR1* (**F**) and *CDR2* (**G**) expression in an *ssn3*^{Δ/Δ} null strain (yLM265) complemented by either wild type *SSN3*^{WT} (yLM279) or a kinase dead allele *SSN3*^{D325A} (yLM276). The *CDR1* and *CDR2* expression levels in the *SSN3*^{WT} complementary strain culture (yLM279) collected before induction were individually set to ‘1’.

Table S1 RT-qPCR analysis of *CDR1* expression activated by *TAC1^{GOF}* mutants and xenobiotic exposure in wild type and *med3* deletion strains.

<i>TAC1</i> allele	Relative <i>CDR1</i> Expression Level ^a (mean ± SD)					
	<i>MED3</i> ^{+/+}		<i>med3</i> ^{Δ/Δ}			
	YPD	+FNZ	YPD	Fold Change ^b	+FNZ	Fold Change ^c
<i>tac1</i> ^{Δ/Δ}	1.32±0.01 ^d	1.55±0.05	ND ^e	ND	ND	ND
WT	1±0.07	7.18±0.12	0.59±0.02	0.59	1.34±0.08	0.19
<i>T225A</i>	2.91±0.06	7.28±0.06	1.32±0.03	0.45	1.29±0.01	0.18
<i>A736V</i>	4.23±0.12	10.52±0.35	1.60±0.12	0.38	1.67±0.01	0.16
<i>G980E</i>	5.46±0.11	10.87±0.07	2.05±0.12	0.38	2.02±0.16	0.19
<i>E461K</i>	2.32±0.19	5.90±0.3	1.23±0.04	0.53	1.07±0.07	0.18
<i>ΔM677</i>	3.26±0.22	6.81±0.05	1.21±0.03	0.37	1.11±0.01	0.16
<i>N972D</i>	4.54±0.06	7.01±0.03	1.30±0.11	0.29	1.05±0.01	0.15
<i>Δ962-969</i>	3.86±0.07	6.94±0.14	1.19±0.07	0.31	1.13±0.03	0.16
<i>N977D</i>	3.84±0.12	6.28±0.07	1.38±0.04	0.36	1.13±0.05	0.18

^a The *CDR1*^{+/+} *MED3*^{+/+} and *CDR1*^{+/+} *med3*^{Δ/Δ} strains tested in **Table 1** and a *CDR1*^{+/+} *MED3*^{+/+} *tac1*^{Δ/Δ} strain (DSY2906), were compared for *CDR1* expression under fluphenazine treated ('+FNZ'; 20 µg/mL for 30 minutes) and non-treated ('YPD') conditions. The *CDR1* level in the non-treated *CDR1*^{+/+} *MED3*^{+/+} *TAC1*^{WT} strain (DSY2937-35) was set to '1'.

^b *CDR1* mRNA level fold change caused by *med3* deletion under normal growth conditions

^c *CDR1* mRNA level fold change caused by *med3* deletion under FNZ inducing conditions

^d Data in *italics* is also shown in a bar graph in **Fig. 1A**.

^e ND: Not determined

Table S2. RT-qPCR analysis of *CDR2* expression activated by *TAC1^{GOF}* mutants in wild type and *med3* deletion strains

<i>TAC1</i> allele	Relative Expression Level of <i>CDR2</i> in YPD medium ^a		
	<i>MED3</i> ^{+/+}	<i>med3Δ/Δ</i>	Fold Change
WT	<i>1±0.08</i> ^b	<i>1.61±0.18</i>	1.61
<i>T225A</i>	<i>87.32±7.88</i>	<i>103.83±2.83</i>	1.50
<i>A736V</i>	<i>155.90±3.03</i>	<i>135.20±2.12</i>	0.87
<i>G980E</i>	<i>356.51±2.68</i>	<i>370.56±21.2</i>	1.04
WT ^c	<i>1±0.04</i>	<i>1.30±0.02</i>	1.30
<i>E461K</i>^c	<i>38.61±2.47</i>	<i>55.87±1.30</i>	1.45
<i>ΔM677</i>^c	<i>55.81±1.35</i>	<i>59.18±2.75</i>	1.06
<i>N972D</i>^c	<i>98.81±0.38</i>	<i>95.83±2.16</i>	0.97
<i>Δ962-969</i>^c	<i>65.79±0.84</i>	<i>68.09±2.48</i>	1.03
<i>N977D</i>^c	<i>97.84±1.83</i>	<i>97.62±2.66</i>	1.00

^a The *CDR1*^{+/+} *MED3*^{+/+} and *CDR1*^{+/+} *med3Δ/Δ* strains tested in **Table 1** were compared for *CDR2* expression under normal growth conditions (YPD).

^b Data in *italics* presents the first group of assays and is also shown in a bar graph form in **Fig. 1C**.

^c The second group of assays (denoted with a ‘^c’) were performed separately from the first (data in *italics*). Basal *CDR2* levels measured from the *TAC1*^{WT} *MED3*^{+/+} strain cultures were individually set to ‘1’ to calculate and compare *CDR2* relative expression between strains within each group.

Table S3 Fluconazole MIC in *med3Δ/Δ cdr2Δ/Δ* strains bearing *TAC1^{GOF}* mutations

<i>TAC1</i> allele	Fluconazole MIC ($\mu\text{g/mL}$) ^{a,b}		
	<i>med3Δ/Δ</i>	<i>med3Δ/Δ</i>	<i>CDR2+/+</i>
	<i>cdr2Δ/Δ</i>		
WT	0.5-0.75	0.5-0.75	
	(yLM232)	(yLM523)	
A736V	6-8	6-8	
	(yLM234)	(yLM525)	
ΔM677	4	4	
	(yLM504)	(yLM600)	
N972D	4	4	
	(yLM495)	(yLM527)	
N977D	4-6	4-6	
	(yLM498)	(yLM529)	

^a Fluconazole MIC was measured by E-test at 30°C on YPD plate. Plates were incubated for 36 hours before read-out. Intermediate values, between scale marks, are presented as intervals.

^b Exact strain used for each MIC measurement listed in parentheses.

Table S4 *C. albicans* strains used in this study

Strain Name	Parental strain	Constructs integrated	Genotype	Ref.
DSY2906 (yLM166)	-		<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i>	(1)
DSY2937-35 (yLM167)	-		<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1/URA3</i>	(2)
yLM208	DSY2937-35 (yLM167)	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1/URA3 med3Δ::FRT/MED3</i>	This study #
yLM232	yLM208	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1/URA3 med3Δ::FRT/med3Δ::FRT</i>	This study #
yLM216	DSY2937-35 (yLM167)	<i>pSFS2- SSN3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1/URA3 ssn3Δ::FRT/SSN3</i>	This study
yLM236	yLM216	<i>pSFS2- SSN3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1/URA3 ssn3Δ::FRT/ssn3Δ::FRT</i>	This study
yLM225	DSY2937-35 (yLM167)	<i>pSFS2-MEDI5KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1/URA3 med15Δ::FRT/MED15</i>	This study
yLM240	yLM225	<i>pSFS2-MEDI5KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1/URA3 med15Δ::FRT/med15Δ::FRT</i>	This study
ACY67 (yLM168)	-		<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1-T225A/URA3</i>	(3)
yLM210	ACY67 (yLM168)	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1-T225A/URA3 med3Δ::FRT/MED3</i>	This study
yLM233	yLM210	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1-T225A/URA3 med3Δ::FRT/ med3Δ::FRT</i>	This study
yLM218	ACY67 (yLM168)	<i>pSFS2- SSN3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1-T225A/URA3 ssn3Δ::FRT/SSN3</i>	This study
yLM237	yLM218	<i>pSFS2- SSN3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1-T225A/URA3 ssn3Δ::FRT/ssn3Δ::FRT</i>	This study
yLM226	ACY67 (yLM168)	<i>pSFS2-MEDI5KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1-T225A/URA3 med15Δ::FRT/MED15</i>	This study
yLM241	yLM226	<i>pSFS2-MEDI5KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1-T225A/URA3 med15Δ::FRT/med15Δ::FRT</i>	This study
ACY13 (yLM169)	-		<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1-A736V/URA3</i>	(3)
yLM212	ACY13 (yLM169)	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1-A736V/URA3 med3Δ::FRT/MED3</i>	This study
yLM234	yLM212	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i>	This study

			<i>LEU2::TAC1-1-A736V/URA3 med3A::FRT/ med3A::FRT</i>	
yLM220	ACY13 (yLM169)	<i>pSFS2-SSN3KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-A736V/URA3 ssn3A::FRT/SSN3</i>	This study
yLM238	yLM220	<i>pSFS2-SSN3KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-A736V/URA3 ssn3A::FRT/ssn3A::FRT</i>	This study
yLM229	ACY13 (yLM169)	<i>pSFS2-MED15KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-A736V/URA3 med15A::FRT/MED15</i>	This study
yLM242	yLM229	<i>pSFS2-MED15KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-A736V/URA3 med15A::FRT/med15A::FRT</i>	This study
ACY71 (yLM170)	-		<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-G980E/URA3</i>	(3)
yLM214	ACY71 (yLM170)	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-G980E/URA3 med3A::FRT/MED3</i>	This study
yLM235	yLM214	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-G980E/URA3 med3A::FRT/ med3A::FRT</i>	This study
yLM222	ACY71 (yLM170)	<i>pSFS2-SSN3KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-G980E/URA3 ssn3A::FRT/SSN3</i>	This study
yLM239	yLM222	<i>pSFS2-SSN3KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-G980E/URA3 ssn3A::FRT/ssn3A::FRT</i>	This study
yLM230	ACY71 (yLM170)	<i>pSFS2-MED15KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-G980E/URA3 med15A::FRT/MED15</i>	This study
yLM243	yLM230	<i>pSFS2-MED15KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-G980E/URA3 med15A::FRT/med15A::FRT</i>	This study
yLM490	DSY2906 (yLM166)	<i>TAC1Inte E461K</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-E461K/URA3</i>	This study
yLM491	yLM490	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-E461K/URA3 med3A::FRT/MED3</i>	This study
yLM492	yLM491	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-E461K/URA3 med3A::FRT/med3A::FRT</i>	This study
yLM493	DSY2906 (yLM166)	<i>TAC1Inte N972D</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-N972D/URA3</i>	This study
yLM494	yLM493	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-N972D/URA3 med3A::FRT/MED3</i>	This study
yLM495	yLM494	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-N972D/URA3</i>	This study

			<i>med3Δ::FRT/med3Δ::FRT</i>	
yLM496	DSY2906 (yLM166)	<i>TAC1Inte N977D</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG</i> <i>LEU2::TAC1-1-N977D/URA3</i>	This study
yLM497	yLM496	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG</i> <i>LEU2::TAC1-1-N977D/URA3 med3Δ::FRT/MED3</i>	This study
yLM498	yLM497	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG</i> <i>LEU2::TAC1-1-N977D/URA3</i> <i>med3Δ::FRT/med3Δ::FRT</i>	This study
yLM499	DSY2906 (yLM166)	<i>TAC1Inte</i> <i>A962-969</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG</i> <i>LEU2::TAC1-1-A962-969/URA3</i>	This study
yLM500	yLM499	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG</i> <i>LEU2::TAC1-1-A962-969/URA3</i> <i>med3Δ::FRT/MED3</i>	This study
yLM501	yLM500	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG</i> <i>LEU2::TAC1-1-A962-969/URA3</i> <i>med3Δ::FRT/med3Δ::FRT</i>	This study
yLM502	DSY2906 (yLM166)	<i>TAC1Inte ΔM677</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG</i> <i>LEU2::TAC1-1-ΔM677/URA3</i>	This study
yLM503	yLM502	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG</i> <i>LEU2::TAC1-1-ΔM677/URA3 med3Δ::FRT/MED3</i>	This study
yLM504	yLM503	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG</i> <i>LEU2::TAC1-1-ΔM677/URA3</i> <i>med3Δ::FRT/med3Δ::FRT</i>	This study
yLM505	DSY2937-35 (yLM167)		<i>tac1-1Δ::hisG/ tac1-2Δ::hisG</i> <i>LEU2::TAC1-1/URA3</i> <i>CDR1::CDR1-3HA/CDR1</i>	This study
yLM506	yLM232		<i>tac1-1Δ::hisG/ tac1-2Δ::hisG</i> <i>LEU2::TAC1-1/URA3</i> <i>med3Δ::FRT/ med3Δ::FRT</i> <i>CDR1::CDR1-3HA/CDR1</i>	This study
yLM507	ACY67 (yLM168)		<i>tac1-1Δ::hisG/ tac1-2Δ::hisG</i> <i>LEU2::TAC1-1-T225A/URA3</i> <i>CDR1::CDR1-3HA/CDR1</i>	This study
yLM508	yLM233		<i>tac1-1Δ::hisG/ tac1-2Δ::hisG</i> <i>LEU2::TAC1-1-T225A/URA3</i> <i>med3Δ::FRT/ med3Δ::FRT</i> <i>CDR1::CDR1-3HA/CDR1</i>	This study
yLM509	ACY13 (yLM169)		<i>tac1-1Δ::hisG/ tac1-2Δ::hisG</i> <i>LEU2::TAC1-1-A736V/URA3</i> <i>CDR1::CDR1-3HA/CDR1</i>	This study
yLM510	yLM234		<i>tac1-1Δ::hisG/ tac1-2Δ::hisG</i> <i>LEU2::TAC1-1-A736V/URA3</i> <i>med3Δ::FRT/ med3Δ::FRT</i> <i>CDR1::CDR1-3HA/CDR1</i>	This study
yLM511	ACY71 (yLM170)		<i>tac1-1Δ::hisG/ tac1-2Δ::hisG</i> <i>LEU2::TAC1-1-G980E/URA3</i> <i>CDR1::CDR1-3HA/CDR1</i>	This study
yLM512	yLM235		<i>tac1-1Δ::hisG/ tac1-2Δ::hisG</i>	This study

			<i>LEU2::TAC1-1-G980E/URA3 med3Δ::FRT/ med3Δ::FRT CDR1::CDR1-3HA/CDR1</i>	
yLM513	yLM502		<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-ΔM677/URA3 CDR1::CDR1-3HA/CDR1</i>	This study
yLM514	yLM490		<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-E461K/URA3 CDR1::CDR1-3HA/CDR1</i>	This study
yLM515	yLM492		<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-E461K/URA3 med3Δ::FRT/med3Δ::FRT CDR1::CDR1-3HA/CDR1</i>	This study
yLM516	yLM493		<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-N972D/URA3 CDR1::CDR1-3HA/CDR1</i>	This study
yLM517	yLM495		<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-N972D/URA3 med3Δ::FRT/med3Δ::FRT CDR1::CDR1-3HA/CDR1</i>	This study
yLM518	yLM496		<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-N977D/URA3 CDR1::CDR1-3HA/CDR1</i>	This study
yLM519	yLM498		<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-N977D/URA3 med3Δ::FRT/med3Δ::FRT CDR1::CDR1-3HA/CDR1</i>	This study
yLM520	yLM499		<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-Δ962-969/URA3 CDR1::CDR1-3HA/CDR1</i>	This study
yLM521	yLM501		<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-Δ962-969/URA3 med3Δ::FRT/med3Δ::FRT CDR1::CDR1-3HA/CDR1</i>	This study
yLM522	yLM208	<i>pSFS2-CDR2KO (two rounds)</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1/URA3 med3Δ::FRT/MED3 cdr2Δ::FRT/ cdr2Δ::FRT</i>	This study
yLM523	yLM522	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1/URA3 med3Δ::FRT/med3Δ::FRT cdr2Δ::FRT/cdr2Δ::FRT</i>	This study
yLM524	yLM212	<i>pSFS2-CDR2KO (two rounds)</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-A736V/URA3 med3Δ::FRT/MED3 cdr2Δ::FRT/ cdr2Δ::FRT</i>	This study
yLM525	yLM524	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/ tac1-2Δ::hisG LEU2::TAC1-1-A736V/URA3 med3Δ::FRT/med3Δ::FRT</i>	This study

			<i>cdr2Δ::FRT/cdr2Δ::FRT</i>	
yLM526	yLM494	<i>pSFS2-CDR2KO (two rounds)</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1-N972D/URA3 med3Δ::FRT/MED3 cdr2Δ::FRT/cdr2Δ::FRT</i>	This study
yLM527	yLM526	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1-N972D/URA3 med3Δ::FRT/med3Δ::FRT cdr2Δ::FRT/cdr2Δ::FRT</i>	This study
yLM528	yLM497	<i>pSFS2-CDR2KO (two rounds)</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1-N977D/URA3 med3Δ::FRT/MED3 cdr2Δ::FRT/cdr2Δ::FRT</i>	This study
yLM529	yLM528	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1-N977D/URA3 med3Δ::FRT/med3Δ::FRT cdr2Δ::FRT/cdr2Δ::FRT</i>	This study
SN152 (AZC22)			<i>arg4/arg4 leu2/leu2 his1 /his1 URA3/ura3 ::imm434 IRO1/iro1 ::imm434</i>	(4)
AZC32			<i>arg4/arg4 leu2/leu2 his1 /his1 URA3/ura3::imm434 IRO1/iro1::imm434 med5Δ::HIS1/med5Δ::LEU2</i>	(5)
AZC34			<i>arg4/arg4 leu2/leu2 his1 /his1 URA3/ura3::imm434 IRO1/iro1::imm434 med16Δ::HIS1/med16Δ::LEU2</i>	(5)
AZC42			<i>arg4/arg4 leu2/leu2 his1 /his1 URA3/ura3::imm434 IRO1/iro1::imm434 med9Δ::HIS1/med9Δ::LEU2</i>	(5)
AZC44			<i>arg4/arg4 leu2/leu2 his1 /his1 URA3/ura3::imm434 IRO1/iro1::imm434 med20Δ::HIS1/med20Δ::LEU2</i>	(5)
AZC46			<i>arg4/arg4 leu2/leu2 his1 /his1 URA3/ura3::imm434 IRO1/iro1::imm434 med1Δ::HIS1/med1Δ::LEU2</i>	(5)
AZC51 (yLM95)			<i>arg4/arg4 leu2/leu2 his1 /his1 URA3/ura3::imm434 IRO1/iro1::imm434 med3Δ::HIS1/med3Δ::LEU2</i>	(6)
cTTR01			<i>arg4/arg4 leu2/leu2 his1 /his1 URA3/ura3::imm434 IRO1/iro1::imm434 med15Δ::HIS1/med15Δ::LEU2</i>	(5)
AZC52			<i>arg4/arg4 leu2/leu2 his1 /his1 URA3/ura3::imm434 IRO1/iro1::imm434 med12Δ::HIS1/med12Δ::LEU2</i>	(5)
yLM485	DSY2906 (yLM166)	<i>TAC1InteHF-WT</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::P_{TAC1}-6HIS3FLAG-TAC1-1/URA3</i>	This study #
yLM530	DSY2906 (yLM166)	<i>TAC1InteHF- WT_{OE}</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::P_{TAC1}-6HIS3FLAG-TAC1-1/URA3</i>	This study
yLM531	DSY2906 (yLM166)	<i>TAC1InteHF-A73 6V</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::P_{TAC1}-6HIS3FLAG-TAC1-1-A736V/URA3</i>	This study
yLM532	DSY2906 (yLM166)	<i>TAC1InteHF-R69 3K</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::P_{TAC1}-6HIS3FLAG-TAC1-1-R693K/URA3</i>	This study
yLM533	DSY2906 (yLM166)	<i>TAC1InteHF-ΔM6 77</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::P_{TAC1}-6HIS3FLAG-TAC1-1-ΔM677/URA3</i>	This study

yLM534	DSY2906 (yLM166)	<i>TAC1InteHF-N97</i> 2D	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>LEU2::P_{TAC1}-6HIS3FLAG-TAC1-1-N972D/URA3</i>	This study
yLM535	DSY2906 (yLM166)	<i>TAC1InteHF-Δ96</i> 2-969	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>LEU2::P_{TAC1}-6HIS3FLAG-TAC1-1-Δ962-969/URA</i> 3	This study
yLM536*	DSY2906 (yLM166)	<i>TAC1InteHF-N97</i> 7D	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>LEU2::P_{TAC1}-6HIS3FLAG-TAC1-1-N977D/URA3</i>	This study
yLM537	DSY2906 (yLM166)	<i>TAC1InteHF-C43</i> Y	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>LEU2::P_{TAC1}-6HIS3FLAG-TAC1-1-C43Y/URA3</i>	This study
yLM538	DSY2906 (yLM166)	<i>TAC1InteHF-R69</i> 3K/C43Y	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>LEU2::P_{TAC1}-6HIS3FLAG-TAC1-1-R693K-C43Y/U</i> RA3	This study
yLM539	DSY2906 (yLM166)	<i>TAC1InteHF-TAC</i> IATAD	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>LEU2::P_{TAC1}-6HIS3FLAG-TAC1-1-ΔTAD(aa1-845)</i> /URA3	This study
yLM540	DSY2906 (yLM166)	<i>TAC1InteHF-R69</i> 3KO _E	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>LEU2::P_{ACT1}-6HIS3FLAG-TAC1-1-R693K/URA3</i>	This study
yLM541	DSY2906 (yLM166)	<i>TAC1InteHF-N97</i> 2D _{OE}	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>LEU2::P_{ACT1}-6HIS3FLAG-TAC1-1-N972D/URA3</i>	This study
yLM542	DSY2906 (yLM166)	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG med3Δ::FRT/MED3</i>	This study
yLM543	yLM542	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>med3Δ::FRT/med3Δ::FRT</i>	This study
yLM544	DSY2906 (yLM166)	<i>pSFS2- SSN3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG ssn3Δ::FRT/SSN3</i>	This study
yLM545	yLM544	<i>pSFS2- SSN3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>ssn3Δ::FRT/ssn3Δ::FRT</i>	This study
yLM546	yLM485	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>LEU2::P_{TAC1}-6HIS3FLAG-TAC1-1/URA3</i> <i>med3Δ::FRT/MED3</i>	This study
yLM547	yLM546	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>LEU2::P_{TAC1}-6HIS3FLAG-TAC1-1/URA3</i> <i>med3Δ::FRT/med3Δ::FRT</i>	This study
yLM548	yLM534	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>LEU2::P_{TAC1}-6HIS3FLAG-TAC1-1-N972D/URA3</i> <i>med3Δ::FRT/MED3</i>	This study
yLM549	yLM548	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>LEU2::P_{TAC1}-6HIS3FLAG-TAC1-1-N972D/URA3</i> <i>med3Δ::FRT/med3Δ::FRT</i>	This study
yLM550	yLM543	<i>TAC1InteHF-R69</i> 3K	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>med3Δ::FRT/med3Δ::FRT</i> <i>LEU2::P_{TAC1}-6HIS3FLAG-TAC1-1-R693K/URA3</i>	This study
yLM551	yLM543	<i>TAC1InteHF-</i> Δ962-969	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>med3Δ::FRT/med3Δ::FRT</i>	This study

			<i>LEU2::P_{TACI}-6HIS3FLAG-TACI-1-A962-969/URA3</i>	
yLM552	yLM545	<i>TAC1InteHF-WT</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG ssn3Δ::FRT/ssn3Δ::FRT LEU2::P_{TACI}-6HIS3FLAG-TACI-1/URA3</i>	This study
yLM553	yLM545	<i>TAC1InteHF-R69 3K</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG ssn3Δ::FRT/ssn3Δ::FRT LEU2::P_{TACI}-6HIS3FLAG-TACI-1-R693K/URA3</i>	This study
yLM554	yLM545	<i>TAC1InteHF- A962-969</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG ssn3Δ::FRT/ssn3Δ::FRT LEU2::P_{TACI}-6HIS3FLAG-TACI-1-A962-969/URA3</i>	This study
yLM555	yLM534	<i>pSFS2- SSN3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::P_{TACI}-6HIS3FLAG-TACI-1-N972D/URA3 ssn3Δ::FRT/SSN3</i>	This study
yLM556	yLM555	<i>pSFS2- SSN3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::P_{TACI}-6HIS3FLAG-TACI-1-N972D/URA3 ssn3Δ::FRT/ssn3Δ::FRT</i>	This study
yLM557	yLM504		<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TACI-1-ΔM677/URA3 med3Δ::FRT/med3Δ::FRT CDR1::CDR1-3HA/CDR1</i>	This study
SCMRR1M4A (yLM468)	-		<i>mrr1Δ::FRT/mrr1Δ::FRT</i>	(7)
yLM558	SCMRR1M4 A (yLM468)	<i>P_{MRR1}-HF-MD-TA C1^{WT}</i>	<i>mrr1Δ::FRT/mrr1Δ::P_{MRR1}-6HIS3FLAG-MRR1DB D(aa1-123)-TAC1^{ΔDBD}(aa130-981)</i>	This study
yLM559	DSY2906 (yLM166)		<i>tac1-1Δ::hisG/tac1-2Δ::hisG MED17-3HA-SAT1/MED17</i>	This study
yLM560	DSY2937-35 (yLM167)		<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TACI-1/URA3 MED8-3HA-SAT1/MED8</i>	This study
yLM482	DSY2937-35 (yLM167)		<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TACI-1/URA3 MED17-3HA-SAT1/MED17</i>	This study #
yLM483	yLM232		<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TACI-1/URA3 med3Δ::FRT/med3Δ::FRT MED17-3HA-SAT1/MED17</i>	This study #
yLM561	ACY13 (yLM169)		<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TACI-1-A736V/URA3 MED17-3HA-SAT1/MED17</i>	This study
yLM562	yLM234		<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TACI-1-A736V/URA3 med3Δ::FRT/ med3Δ::FRT MED17-3HA-SAT1/MED17</i>	This study
yLM563	yLM493		<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TACI-1-N972D/URA3 MED17-3HA-SAT1/MED17</i>	This study

yLM564	yLM495		<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1-N972D/URA3 med3Δ::FRT/med3Δ::FRT MED17-3HA-SAT1/MED17</i>	This study
yLM565	yLM496		<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1-N977D/URA3 MED17-3HA-SAT1/MED17</i>	This study
yLM566	yLM498		<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1-N977D/URA3 med3Δ::FRT/med3Δ::FRT MED17-3HA-SAT1/MED17</i>	This study
SSN3-3HA/ SSN3-3HA (yLM481)	BWP17		<i>ura3Δ::λimm434/ura3Δ::λimm434 his1Δ::hisG/his1Δ::hisG arg4Δ::hisG/arg4Δ::hisG SSN3::SSN3-3HA-HIS1/SSN3::SSN3-3HA-SAT1</i>	(8)
cRC106	-		<i>ura3Δ::λimm434/ura3Δ::λimm434 ade2::hisG/ade2::hisG::[pOPlacZ]</i>	(9)
yLM567	cRC106	Clp-LexA	<i>ura3Δ::λimm434/ura3Δ::λimm434 ade2::hisG/ade2::hisG::[pOPlacZ] RPS10/rps10Δ::[LexA]/URA3</i>	This study
yLM568	cRC106	Clp-LexA- Tac1 ¹³⁰⁻⁹⁸¹ WT	<i>ura3Δ::λimm434/ura3Δ::λimm434 ade2::hisG/ade2::hisG::[pOPlacZ] RPS10/rps10Δ:: [LexA-TAC1¹³⁰⁻⁹⁸¹ WT]/URA3</i>	This study
yLM569	cRC106	Clp-LexA- Tac1 ¹³⁰⁻⁹⁸¹ T225A	<i>ura3Δ::λimm434/ura3Δ::λimm434 ade2::hisG/ade2::hisG::[pOPlacZ] RPS10/rps10Δ:: [LexA-TAC1¹³⁰⁻⁹⁸¹ T225A]/URA3</i>	This study
yLM570	cRC106	Clp-LexA- Tac1 ¹³⁰⁻⁹⁸¹ E461K	<i>ura3Δ::λimm434/ura3Δ::λimm434 ade2::hisG/ade2::hisG::[pOPlacZ] RPS10/rps10Δ:: [LexA-TAC1¹³⁰⁻⁹⁸¹ E461K]/URA3</i>	This study
yLM571	cRC106	Clp-LexA- Tac1 ¹³⁰⁻⁹⁸¹ ΔM677	<i>ura3Δ::λimm434/ura3Δ::λimm434 ade2::hisG/ade2::hisG::[pOPlacZ] RPS10/rps10Δ:: [LexA-TAC1¹³⁰⁻⁹⁸¹ ΔM677]/URA3</i>	This study
yLM572	cRC106	Clp-LexA- Tac1 ¹³⁰⁻⁹⁸¹ A736V	<i>ura3Δ::λimm434/ura3Δ::λimm434 ade2::hisG/ade2::hisG::[pOPlacZ] RPS10/rps10Δ:: [LexA-TAC1¹³⁰⁻⁹⁸¹ A736V]/URA3</i>	This study
yLM573	cRC106	Clp-LexA- Tac1 ¹³⁰⁻⁹⁸¹ N972D	<i>ura3Δ::λimm434/ura3Δ::λimm434 ade2::hisG/ade2::hisG::[pOPlacZ] RPS10/rps10Δ:: [LexA-TAC1¹³⁰⁻⁹⁸¹ N972D]/URA3</i>	This study
yLM574	cRC106	Clp-LexA- Tac1 ¹³⁰⁻⁹⁸¹ Δ962-969	<i>ura3Δ::λimm434/ura3Δ::λimm434 ade2::hisG/ade2::hisG::[pOPlacZ] RPS10/rps10Δ:: [LexA-TAC1¹³⁰⁻⁹⁸¹ Δ962-969]/URA3</i>	This study
yLM575	cRC106	Clp-LexA- Tac1 ¹³⁰⁻⁹⁸¹ N977D	<i>ura3Δ::λimm434/ura3Δ::λimm434 ade2::hisG/ade2::hisG::[pOPlacZ] RPS10/rps10Δ:: [LexA-TAC1¹³⁰⁻⁹⁸¹ N977D]/URA3</i>	This study
yLM576	cRC106	Clp-LexA-	<i>ura3Δ::λimm434/ura3Δ::λimm434</i>	This study

		Tac1 ¹³⁰⁻⁹⁸¹ G980E	<i>ade2::hisG/ade2::hisG::[pOPlacZ] RPS10/rps10Δ::[LexA-TACI¹³⁰⁻⁹⁸¹ G980E]/URA3</i>	
yLM577	cRC106	Clp-LexA-Tac1 ¹³⁰⁻⁹⁸¹ G980W	<i>ura3Δ::λimm⁴³⁴/ura3Δ::λimm⁴³⁴ ade2::hisG/ade2::hisG::[pOPlacZ] RPS10/rps10Δ::[LexA-TACI¹³⁰⁻⁹⁸¹ G980W]/URA3</i>	This study
yLM578	cRC106	Clp-LexA-Tac1 ¹³⁰⁻⁹³¹ WT	<i>ura3Δ::λimm⁴³⁴/ura3Δ::λimm⁴³⁴ ade2::hisG/ade2::hisG::[pOPlacZ] RPS10/rps10Δ::[LexA-TACI¹³⁰⁻⁹³¹]/URA3</i>	This study
yLM579	cRC106	Clp-LexA-Tac1 ⁸⁵⁶⁻⁹⁸¹ WT	<i>ura3Δ::λimm⁴³⁴/ura3Δ::λimm⁴³⁴ ade2::hisG/ade2::hisG::[pOPlacZ] RPS10/rps10Δ::[LexA-TACI⁸⁵⁶⁻⁹⁸¹]/URA3</i>	This study
yLM580	cRC106	Clp-LexA-Tac1 ⁹³²⁻⁹⁸¹ WT	<i>ura3Δ::λimm⁴³⁴/ura3Δ::λimm⁴³⁴ ade2::hisG/ade2::hisG::[pOPlacZ] RPS10/rps10Δ::[LexA-TACI⁹³²⁻⁹⁸¹]/URA3</i>	This study
yLM581	cRC106	Clp-LexA-Tac1 ⁸⁵⁶⁻⁹⁸¹ N972D	<i>ura3Δ::λimm⁴³⁴/ura3Δ::λimm⁴³⁴ ade2::hisG/ade2::hisG::[pOPlacZ] RPS10/rps10Δ::[LexA-TACI⁸⁵⁶⁻⁹⁸¹ N972D]/URA3</i>	This study
yLM582	cRC106	Clp-LexA-Tac1 ⁸⁵⁶⁻⁹⁸¹ Δ962-969	<i>ura3Δ::λimm⁴³⁴/ura3Δ::λimm⁴³⁴ ade2::hisG/ade2::hisG::[pOPlacZ] RPS10/rps10Δ::[LexA-TACI⁸⁵⁶⁻⁹⁸¹ Δ962-969]/URA3</i>	This study
yLM583	cRC106	Clp-LexA-Tac1 ⁸⁵⁶⁻⁹⁸¹ N977D	<i>ura3Δ::λimm⁴³⁴/ura3Δ::λimm⁴³⁴ ade2::hisG/ade2::hisG::[pOPlacZ] RPS10/rps10Δ::[LexA-TACI⁸⁵⁶⁻⁹⁸¹ N977D]/URA3</i>	This study
yLM584	cRC106	Clp-LexA-Tac1 ⁸⁵⁶⁻⁹⁸¹ G980E	<i>ura3Δ::λimm⁴³⁴/ura3Δ::λimm⁴³⁴ ade2::hisG/ade2::hisG::[pOPlacZ] RPS10/rps10Δ::[LexA-TACI⁸⁵⁶⁻⁹⁸¹ G980E]/URA3</i>	This study
yLM585	cRC106	Clp-LexA-Tac1 ⁸⁵⁶⁻⁹⁸¹ G980W	<i>ura3Δ::λimm⁴³⁴/ura3Δ::λimm⁴³⁴ ade2::hisG/ade2::hisG::[pOPlacZ] RPS10/rps10Δ::[LexA-TACI⁸⁵⁶⁻⁹⁸¹ G980W]/URA3</i>	This study
yLM586	cRC106	pSFS2-MED3KO	<i>ura3Δ::λimm⁴³⁴/ura3Δ::λimm⁴³⁴ ade2::hisG/ade2::hisG::[pOPlacZ] med3Δ::FRT/MED3</i>	This study
yLM587	yLM586	pSFS2-MED3KO	<i>ura3Δ::λimm⁴³⁴/ura3Δ::λimm⁴³⁴ ade2::hisG/ade2::hisG::[pOPlacZ] med3Δ::FRT/med3Δ::FRT</i>	This study
yLM588	yLM587	Clp-LexA	<i>ura3Δ::λimm⁴³⁴/ura3Δ::λimm⁴³⁴ ade2::hisG/ade2::hisG::[pOPlacZ] med3Δ::FRT/med3Δ::FRT RPS10/rps10Δ::[LexA]/URA3</i>	This study
yLM589	yLM587	Clp-LexA-Tac1 ¹³⁰⁻⁹⁸¹ WT	<i>ura3Δ::λimm⁴³⁴/ura3Δ::λimm⁴³⁴ ade2::hisG/ade2::hisG::[pOPlacZ] med3Δ::FRT/med3Δ::FRT RPS10/rps10Δ::[LexA-TACI¹³⁰⁻⁹⁸¹ WT]/URA3</i>	This study
yLM590	yLM587	Clp-LexA-	<i>ura3Δ::λimm⁴³⁴/ura3Δ::λimm⁴³⁴</i>	This study

		Tac1 ¹³⁰⁻⁹⁸¹ A736V	<i>ade2::hisG/ade2::hisG::[pOPlacZ] med3Δ::FRT/med3Δ::FRT RPS10/rps10Δ:: [LexA-TAC1¹³⁰⁻⁹⁸¹A736V]/URA3</i>	
yLM591	yLM587	Clp-LexA-Tac1 ¹³⁰⁻⁹⁸¹ N977D	<i>ura3Δ::λimm⁴³⁴/ura3Δ::λimm⁴³⁴ ade2::hisG/ade2::hisG::[pOPlacZ] med3Δ::FRT/med3Δ::FRT RPS10/rps10Δ:: [LexA-TAC1¹³⁰⁻⁹⁸¹N977D]/URA3</i>	This study
yLM592	yLM587	Clp-LexA-Tac1 ¹³⁰⁻⁹⁸¹ G980E	<i>ura3Δ::λimm⁴³⁴/ura3Δ::λimm⁴³⁴ ade2::hisG/ade2::hisG::[pOPlacZ] med3Δ::FRT/med3Δ::FRT RPS10/rps10Δ:: [LexA-TAC1¹³⁰⁻⁹⁸¹G980E]/URA3</i>	This study
yLM593	yLM587	Clp-LexA-Tac1 ⁸⁵⁶⁻⁹⁸¹ WT	<i>ura3Δ::λimm⁴³⁴/ura3Δ::λimm⁴³⁴ ade2::hisG/ade2::hisG::[pOPlacZ] med3Δ::FRT/med3Δ::FRT RPS10/rps10Δ:: [LexA-TAC1⁸⁵⁶⁻⁹⁸¹]/URA3</i>	This study
yLM594	yLM587	Clp-LexA-Tac1 ⁹³²⁻⁹⁸¹ WT	<i>ura3Δ::λimm⁴³⁴/ura3Δ::λimm⁴³⁴ ade2::hisG/ade2::hisG::[pOPlacZ] med3Δ::FRT/med3Δ::FRT RPS10/rps10Δ:: [LexA-TAC1⁹³²⁻⁹⁸¹]/URA3</i>	This study
yLM595	yLM543	<i>TAC1InteHF-N97 2DoE</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG med3Δ::FRT/med3Δ::FRT LEU2::P_{ACT1}-6HIS3FLAG-TAC1-1-N972D/URA3</i>	This study
BWP17			<i>ura3Δ::λimm434/ura3Δ::λimm434 his1Δ::hisG/his1Δ::hisG arg4Δ::hisG/arg4Δ::hisG</i>	(10)
yLM265	BWP17		<i>ssn3Δ/ssn3Δ</i>	This study
yLM279	yLM265		<i>ssn3Δ/ssn3::SSN3^{WT}</i>	This study
yLM276	yLM265		<i>ssn3Δ/ssn3::SSN3^{D325A}</i>	This study
yLM596	yLM279	<i>TAC1InteHF-WT_O E</i>	<i>ssn3Δ/ssn3::SSN3^{WT} LEU2::P_{ACT1}-6HIS3FLAG-TAC1-1</i>	This study
yLM660	yLM276	<i>TAC1InteHF-WT_O E</i>	<i>ssn3Δ/ssn3::SSN3^{D325A} LEU2::P_{ACT1}-6HIS3FLAG-TAC1-1</i>	This study
yLM597	yLM485		<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::P_{TAC1}-6HIS3FLAG-TAC1-1/URA3 MED17-3HA-SAT1/MED17</i>	This study
yLM598	yLM539		<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::P_{TAC1}-6HIS3FLAG-TAC1-1-ΔTAD(aa1-845) /URA3 MED17-3HA-SAT1/MED17</i>	This study
yLM599	yLM503	<i>pSFS2-CDR2KO (two rounds)</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1-ΔM677/URA3 med3Δ::FRT/MED3 cdr2Δ::FRT/cdr2Δ::FRT</i>	This study
yLM600	yLM599	<i>pSFS2-MED3KO</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG LEU2::TAC1-1-ΔM677/URA3 med3Δ::FRT/med3Δ::FRT cdr2Δ::FRT/cdr2Δ::FRT</i>	This study

yLM471	DSY2937-35 (yLM167)	<i>pSFS2-SNF2KO</i>	<i>tacI-1Δ::hisG/tacI-2Δ::hisG LEU2::TACI-1/URA3 snf2Δ::FRT/SNF2</i>	This study #
yLM472	yLM471	<i>pSFS2-SNF2KO</i>	<i>tacI-1Δ::hisG/tacI-2Δ::hisG LEU2::TACI-1/URA3 snf2Δ::FRT/snf2Δ::FRT</i>	This study #
yLM473	ACY67 (yLM168)	<i>pSFS2-SNF2KO</i>	<i>tacI-1Δ::hisG/tacI-2Δ::hisG LEU2::TACI-1-T225A/URA3 snf2Δ::FRT/SNF2</i>	This study #
yLM474	yLM473	<i>pSFS2-SNF2KO</i>	<i>tacI-1Δ::hisG/tacI-2Δ::hisG LEU2::TACI-1-T225A/URA3 snf2Δ::FRT/snF2Δ::FRT</i>	This study #
yLM475	ACY13 (yLM169)	<i>pSFS2-SNF2KO</i>	<i>tacI-1Δ::hisG/tacI-2Δ::hisG LEU2::TACI-1-A736V/URA3 snf2Δ::FRT/SNF2</i>	This study #
yLM476	yLM475	<i>pSFS2-SNF2KO</i>	<i>tacI-1Δ::hisG/tacI-2Δ::hisG LEU2::TACI-1-G980E/URA3 snf2Δ::FRT/snF2Δ::FRT</i>	This study #
yLM477	ACY71 (yLM170)	<i>pSFS2-SNF2KO</i>	<i>tacI-1Δ::hisG/tacI-2Δ::hisG LEU2::TACI-1-G980E/URA3 snf2Δ::FRT/SNF2</i>	This study #
yLM478	yLM477	<i>pSFS2-SNF2KO</i>	<i>tacI-1Δ::hisG/tacI-2Δ::hisG LEU2::TACI-1-G980E/URA3 snf2Δ::FRT/snF2Δ::FRT</i>	This study #
yLM601	DSY2906 (yLM166)	<i>TACIInte</i> <i>HF-E461K</i>	<i>tacI-1Δ::hisG/tacI-2Δ::hisG LEU2::P_{TACI}-6HIS3FLAG-TACI-1-E461K/URA3</i>	This study
yLM602	DSY2906 (yLM166)	<i>TACIInte R693K</i>	<i>tacI-1Δ::hisG/tacI-2Δ::hisG LEU2::P_{TACI}-TACI-1-R693K/URA3</i>	This study
yLM603	DSY2906 (yLM166)	<i>TACIInteHF-E46</i> <i>IKATAD</i>	<i>tacI-1Δ::hisG/tacI-2Δ::hisG LEU2::P_{TACI}-6HIS3FLAG-TACI-1-E461K-ATAD(aa1-845)/URA3</i>	This study
yLM604	DSY2906 (yLM166)	<i>TACIInteHF-</i> <i>ΔMM677ATAD</i>	<i>tacI-1Δ::hisG/tacI-2Δ::hisG LEU2::P_{TACI}-6HIS3FLAG-TACI-1-ΔM677-ATAD(aa1-845)/URA3</i>	This study
yLM605	DSY2906 (yLM166)	<i>TACIInteHF-</i> <i>R693KATAD</i>	<i>tacI-1Δ::hisG/tacI-2Δ::hisG LEU2::P_{TACI}-6HIS3FLAG-TACI-1-R693K-ATAD(aa1-845)/URA3</i>	This study
yLM606	DSY2906 (yLM166)	<i>TACIInteHF-</i> <i>A736VATAD</i>	<i>tacI-1Δ::hisG/tacI-2Δ::hisG LEU2::P_{TACI}-6HIS3FLAG-TACI-1-A736V-ATAD(aa1-845)/URA3</i>	This study
yLM607	DSY2906 (yLM166)	<i>TACIInte</i> <i>E461KATAD</i>	<i>tacI-1Δ::hisG/tacI-2Δ::hisG LEU2::P_{TACI}-TACI-1-E461K-ATAD(aa1-845)/URA3</i>	This study
yLM608	DSY2906 (yLM166)	<i>TACIInte</i> <i>ΔM677ATAD</i>	<i>tacI-1Δ::hisG/tacI-2Δ::hisG LEU2::P_{TACI}-TACI-1-ΔM677-ATAD(aa1-845)/URA3</i>	This study
yLM609	DSY2906 (yLM166)	<i>TACIInte</i> <i>R693KATAD</i>	<i>tacI-1Δ::hisG/tacI-2Δ::hisG LEU2::P_{TACI}-TACI-1-R693K-ATAD(aa1-845)/URA3</i>	This study

yLM610	DSY2906 (yLM166)	<i>TAC1</i> <i>Inte</i> <i>A736V</i> <i>ATAD</i>	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>LEU2::P_{TAC1}-TAC1-1-A736V-ATAD</i> <i>(aa1-845)/URA3</i>	This study
yLM611	DSY2937-35 (yLM167)	<i>pSFS2-CDR1KO</i> ; Transient Cas9 system (11)	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>LEU2::P_{TAC1}-TAC1-1/URA3</i> <i>cdr1Δ::FRT/cdr1Δ::FRT</i>	This study
yLM612	ACY13 (yLM169)	<i>pSFS2-CDR1KO</i> ; Transient Cas9 system	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>LEU2::P_{TAC1}-TAC1-1-A736V/URA3</i> <i>cdr1Δ::FRT/cdr1Δ::FRT</i>	This study
yLM613	yLM493	<i>pSFS2-CDR1KO</i> ; Transient Cas9 system	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>LEU2::P_{TAC1}-TAC1-1-N972D/URA3</i> <i>cdr1Δ::FRT/cdr1Δ::FRT</i>	This study
yLM614	yLM496	<i>pSFS2-CDR1KO</i> ; Transient Cas9 system	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>LEU2::P_{TAC1}-TAC1-1-N977D/URA3</i> <i>cdr1Δ::FRT/</i> <i>cdr1Δ::FRT</i>	This study
yLM615	yLM234	<i>pSFS2-CDR1KO</i> ; Transient Cas9 system	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>LEU2::P_{TAC1}-TAC1-1-A736V/URA3</i> <i>med3Δ::FRT/med3Δ::FRT</i> <i>cdr1Δ::FRT/cdr1Δ::FRT</i>	This study
yLM616	yLM495	<i>pSFS2-CDR1KO</i> ; Transient Cas9 system	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>LEU2::P_{TAC1}-TAC1-1-N972D/URA3</i> <i>med3Δ::FRT/med3Δ::FRT</i> <i>cdr1Δ::FRT/cdr1Δ::FRT</i>	This study
yLM617	yLM498	<i>pSFS2-CDR1KO</i> ; Transient Cas9 system	<i>tac1-1Δ::hisG/tac1-2Δ::hisG</i> <i>LEU2::P_{TAC1}-TAC1-1-N977D/URA3</i> <i>med3Δ::FRT/med3Δ::FRT</i> <i>cdr1Δ::FRT/cdr1Δ::FRT</i>	This study

These strains were also used in a parallel study.

* yLM536 was found with ectopically high expression level of 6His3Flag-Tac1^{N977D}, and used for affinity purification of the 6His3Flag-Tac1^{N977D} sample analyzed in **Fig. 8C**.

Table S5 Plasmids used in this study

Plasmid ^a	Description	Checking Primers	Ref.
pDS1097	Vector for integrating <i>TAC1</i> promoter driven <i>TAC1</i>-I (wild type allele referred as <i>TAC1</i> ^{WT} in this study) with <i>URA3</i> marker to <i>LEU2</i> locus		(1)
pAC153	Vector for integrating <i>TAC1</i> promoter driven <i>TAC1</i>^{T225A} with <i>URA3</i> marker to <i>LEU2</i> locus		(3)
pAC97	Vector for integrating <i>TAC1</i> promoter driven <i>TAC1</i>^{A736V} with <i>URA3</i> marker to <i>LEU2</i> locus		(3)
pAC157	Vector for integrating <i>TAC1</i> promoter driven <i>TAC1</i>^{G980E} with <i>URA3</i> marker to <i>LEU2</i> locus		(3)
<i>TAC1</i> <i>InteE461K</i>	Vector for integrating <i>TAC1</i> promoter driven <i>TAC1</i>^{E461K} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteΔM677</i>	Vector for integrating <i>TAC1</i> promoter driven <i>TAC1</i>^{ΔM677} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteN972D</i>	Vector for integrating <i>TAC1</i> promoter driven <i>TAC1</i>^{N972D} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteN977D</i>	Vector for integrating <i>TAC1</i> promoter driven <i>TAC1</i>^{N977D} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteA962-969</i>	Vector for integrating <i>TAC1</i> promoter driven <i>TAC1</i>^{A962-969} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteR693K</i>	Vector for integrating <i>TAC1</i> promoter driven <i>TAC1</i>^{R693K} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteG980W</i>	Vector for integrating <i>TAC1</i> promoter driven <i>TAC1</i>^{G980W} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteHF-WT</i>	Vector for integrating <i>TAC1</i> promoter driven 6HIS3FLAG tagged <i>TAC1</i> ^{WT} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteHF-A736V</i>	Vector for integrating <i>TAC1</i> promoter driven 6HIS3FLAG tagged <i>TAC1</i> ^{A736V} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteHF-R693K</i>	Vector for integrating <i>TAC1</i> promoter driven 6HIS3FLAG tagged <i>TAC1</i> ^{R693K} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteHF-ΔM677</i>	Vector for integrating <i>TAC1</i> promoter driven 6HIS3FLAG tagged <i>TAC1</i> ^{ΔM677} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteHF-N972D</i>	Vector for integrating <i>TAC1</i> promoter driven 6HIS3FLAG tagged <i>TAC1</i> ^{N972D} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteHF-Δ962-969</i>	Vector for integrating <i>TAC1</i> promoter driven 6HIS3FLAG tagged <i>TAC1</i> ^{Δ962-969} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteHF-N977D</i>	Vector for integrating <i>TAC1</i> promoter driven 6HIS3FLAG tagged <i>TAC1</i> ^{N977D} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteHF-C43Y</i>	Vector for integrating <i>TAC1</i> promoter driven 6HIS3FLAG tagged <i>TAC1</i> ^{C43Y} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study

<i>TAC1</i> <i>InteHF-R693K/C43Y</i>	Vector for integrating <i>TAC1</i> promoter driven 6HIS3FLAG tagged <i>TAC1</i> ^{R693K/C43Y} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteHF-TAC1ΔTAD</i>	Vector for integrating <i>TAC1</i> promoter driven 6HIS3FLAG tagged <i>TAC1</i> ^{I-845} (<i>ΔTAD</i>) with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteHF-WT_{OE}</i>	Vector for integrating <i>ACT1</i> promoter driven 6HIS3FLAG tagged <i>TAC1</i> ^{WT} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteHF-R693KO_E</i>	Vector for integrating <i>ACT1</i> promoter driven 6HIS3FLAG tagged <i>TAC1</i> ^{R693K} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteHF-N972D_{OE}</i>	Vector for integrating <i>ACT1</i> promoter driven 6HIS3FLAG tagged <i>TAC1</i> ^{N972D} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteHF-E461K</i>	Vector for integrating <i>TAC1</i> promoter driven 6HIS3FLAG tagged <i>TAC1</i> ^{E461K} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteR693K</i>	Vector for integrating <i>TAC1</i> promoter driven <i>TAC1</i> ^{R693K} with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteHF-E461KΔTAD</i>	Vector for integrating <i>TAC1</i> promoter driven 6HIS3FLAG tagged <i>TAC1</i> ^{E461K} <i>ΔTAD</i> with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteHF-ΔM677ΔTAD</i>	Vector for integrating <i>TAC1</i> promoter driven 6HIS3FLAG tagged <i>TAC1</i> ^{ΔM677} <i>ΔTAD</i> with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteHF-R693KΔTAD</i>	Vector for integrating <i>TAC1</i> promoter driven 6HIS3FLAG tagged <i>TAC1</i> ^{R693K} <i>ΔTAD</i> with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteHF-A736VΔTAD</i>	Vector for integrating <i>TAC1</i> promoter driven 6HIS3FLAG tagged <i>TAC1</i> ^{A736V} <i>ΔTAD</i> with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteE461KΔTAD</i>	Vector for integrating <i>TAC1</i> promoter driven <i>TAC1</i> ^{E461K} <i>ΔTAD</i> with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteΔM677ΔTAD</i>	Vector for integrating <i>TAC1</i> promoter driven <i>TAC1</i> ^{ΔM677} <i>ΔTAD</i> with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteR693KΔTAD</i>	Vector for integrating <i>TAC1</i> promoter driven <i>TAC1</i> ^{R693K} <i>ΔTAD</i> with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>TAC1</i> <i>InteA736VΔTAD</i>	Vector for integrating <i>TAC1</i> promoter driven <i>TAC1</i> ^{A736V} <i>ΔTAD</i> with <i>URA3</i> marker to <i>LEU2</i> locus	ZL536/ZL537 ZL538/ZL539	This study
<i>pSFS2-MED3KO</i> ^{#b}	<i>SAT1</i> flipper construct for deleting <i>C. albicans</i> MED3 ORF	AZ146/Kpp063 Kpp062/AZ147' ZL257/AZ147'	This study
<i>pSFS2-SSN3KO</i> ^{#b}	<i>SAT1</i> flipper construct for deleting <i>C. albicans</i> SSN3 ORF	AZ357/Kpp063 Kpp062/AZ358 ZL177/ZL178	This study
<i>pSFS2-MED15KO</i> ^b	<i>SAT1</i> flipper construct for deleting <i>C. albicans</i> MED15 ORF	ZL082/Kpp063 Kpp062/ZL074 ZL085/ZL086	This study
<i>pSFS2-CDR2KO</i> ^b	<i>SAT1</i> flipper construct for deleting <i>C. albicans</i> CDR2 ORF	ZL528/Kpp063 Kpp062/ZL808 ZL542/ZL543	This study
<i>pSFS2-SNF2KO</i> ^{#b}	<i>SAT1</i> flipper construct for deleting <i>C. albicans</i> SNF2 ORF	ZL593/Kpp063	This study

		Kpp062/ZL594 ZL621/ZL622 ZL623/ZL594	
<i>pSFS2-CDR1KO</i> ^c	<i>SAT1</i> flipper construct for deleting <i>C. albicans CDR1</i> ORF		This study
CIp-LexA	Vector for expressing LexA protein in <i>C. albicans LacZ</i> reporter strains cRC106 and yLM587; targeting <i>RPS10</i> locus with <i>URA3</i> marker	ZL174/ZL093 ZL094/ZL173	(9)
CIp-LexA-Tac1 ¹³⁰⁻⁹⁸¹ WT	Vector for expressing LexA-Tac1 ¹³⁰⁻⁹⁸¹ WT protein in <i>C. albicans LacZ</i> reporter strains cRC106 and yLM587; targeting <i>RPS10</i> locus with <i>URA3</i> marker	ZL174/ZL093 ZL094/ZL485	This study
CIp-LexA-Tac1 ¹³⁰⁻⁹⁸¹ T225A	Vector for expressing LexA-Tac1 ¹³⁰⁻⁹⁸¹ T225A protein in <i>C. albicans LacZ</i> reporter strain cRC106; targeting <i>RPS10</i> locus with <i>URA3</i> marker	ZL174/ZL093 ZL094/ZL485	This study
CIp-LexA-Tac1 ¹³⁰⁻⁹⁸¹ E461K	Vector for expressing LexA-Tac1 ¹³⁰⁻⁹⁸¹ E461K protein in <i>C. albicans LacZ</i> reporter strain cRC106; targeting <i>RPS10</i> locus with <i>URA3</i> marker	ZL174/ZL093 ZL094/ZL485	This study
CIp-LexA-Tac1 ¹³⁰⁻⁹⁸¹ ΔM677	Vector for expressing LexA-Tac1 ¹³⁰⁻⁹⁸¹ ΔM677 protein in <i>C. albicans LacZ</i> reporter strain cRC106; targeting <i>RPS10</i> locus with <i>URA3</i> marker	ZL174/ZL093 ZL094/ZL485	This study
CIp-LexA-Tac1 ¹³⁰⁻⁹⁸¹ A736V	Vector for expressing LexA-Tac1 ¹³⁰⁻⁹⁸¹ A736V protein in <i>C. albicans LacZ</i> reporter strains cRC106 and yLM587; targeting <i>RPS10</i> locus with <i>URA3</i> marker	ZL174/ZL093 ZL094/ZL485	This study
CIp-LexA-Tac1 ¹³⁰⁻⁹⁸¹ N972D	Vector for expressing LexA-Tac1 ¹³⁰⁻⁹⁸¹ N972D protein in <i>C. albicans LacZ</i> reporter strain cRC106; targeting <i>RPS10</i> locus with <i>URA3</i> marker	ZL174/ZL093 ZL094/ZL485	This study
CIp-LexA-Tac1 ¹³⁰⁻⁹⁸¹ Δ962-969	Vector for expressing LexA-Tac1 ¹³⁰⁻⁹⁸¹ Δ962-969 protein in <i>C. albicans LacZ</i> reporter strain cRC106; targeting <i>RPS10</i> locus with <i>URA3</i> marker	ZL174/ZL093 ZL094/ZL485	This study
CIp-LexA-Tac1 ¹³⁰⁻⁹⁸¹ N977D	Vector for expressing LexA-Tac1 ¹³⁰⁻⁹⁸¹ N977D protein in <i>C. albicans LacZ</i> reporter strains cRC106 and yLM587; targeting <i>RPS10</i> locus with <i>URA3</i> marker	ZL174/ZL093 ZL094/ZL485	This study
CIp-LexA-Tac1 ¹³⁰⁻⁹⁸¹ G980E	Vector for expressing LexA-Tac1 ¹³⁰⁻⁹⁸¹ G980E protein in <i>C. albicans LacZ</i> reporter strains cRC106 and yLM587; targeting <i>RPS10</i> locus with <i>URA3</i> marker	ZL174/ZL093 ZL094/ZL485	This study
CIp-LexA-Tac1 ¹³⁰⁻⁹⁸¹ G980W	Vector for expressing LexA-Tac1 ¹³⁰⁻⁹⁸¹ G980W protein in <i>C. albicans LacZ</i> reporter strain cRC106; targeting <i>RPS10</i> locus with <i>URA3</i> marker	ZL174/ZL093 ZL094/ZL485	This study
CIp-LexA-Tac1 ¹³⁰⁻⁹³¹ WT	Vector for expressing LexA-Tac1 ¹³⁰⁻⁹³¹ WT protein in <i>C. albicans LacZ</i> reporter strain cRC106; targeting <i>RPS10</i> locus with <i>URA3</i> marker	ZL174/ZL093 ZL094/ZL485	This study
CIp-LexA-Tac1 ⁸⁵⁶⁻⁹⁸¹ WT	Vector for expressing LexA-Tac1 ⁸⁵⁶⁻⁹⁸¹ WT protein in <i>C. albicans LacZ</i> reporter strains cRC106 and yLM587; targeting <i>RPS10</i> locus with <i>URA3</i> marker	ZL174/ZL093 ZL094/ZL485	This study
CIp-LexA-Tac1 ⁹³²⁻⁹⁸¹ WT	Vector for expressing LexA-Tac1 ⁹³²⁻⁹⁸¹ WT protein in <i>C.</i>	ZL174/ZL093	This study

	<i>albicans LacZ</i> reporter strains cRC106 and yLM587; targeting <i>RPS10</i> locus with <i>URA3</i> marker	ZL094/ZL560	
CIp-LexA-Tac1 ⁸⁵⁶⁻⁹⁸¹ N972D	Vector for expressing LexA-Tac1⁸⁵⁶⁻⁹⁸¹N972D protein in <i>C. albicans</i> <i>LacZ</i> reporter strain cRC106; targeting <i>RPS10</i> locus with <i>URA3</i> marker	ZL174/ZL093 ZL094/ZL485	This study
CIp-LexA-Tac1 ⁸⁵⁶⁻⁹⁸¹ Δ962-969	Vector for expressing LexA-Tac1⁸⁵⁶⁻⁹⁸¹Δ962-969 protein in <i>C. albicans</i> <i>LacZ</i> reporter strain cRC106; targeting <i>RPS10</i> locus with <i>URA3</i> marker	ZL174/ZL093 ZL094/ZL485	This study
CIp-LexA-Tac1 ⁸⁵⁶⁻⁹⁸¹ N977D	Vector for expressing LexA-Tac1⁸⁵⁶⁻⁹⁸¹N977D protein in <i>C. albicans</i> <i>LacZ</i> reporter strain cRC106; targeting <i>RPS10</i> locus with <i>URA3</i> marker	ZL174/ZL093 ZL094/ZL485	This study
CIp-LexA-Tac1 ⁸⁵⁶⁻⁹⁸¹ G980E	Vector for expressing LexA-Tac1⁸⁵⁶⁻⁹⁸¹G980E protein in <i>C. albicans</i> <i>LacZ</i> reporter strain cRC106; targeting <i>RPS10</i> locus with <i>URA3</i> marker	ZL174/ZL093 ZL094/ZL485	This study
CIp-LexA-Tac1 ⁸⁵⁶⁻⁹⁸¹ G980W	Vector for expressing LexA-Tac1⁸⁵⁶⁻⁹⁸¹G980W protein in <i>C. albicans</i> <i>LacZ</i> reporter strain cRC106; targeting <i>RPS10</i> locus with <i>URA3</i> marker	ZL174/ZL093 ZL094/ZL485	This study
pV1093	A tool plasmid for <i>C. albicans</i> CRISPR-Cas9 system		(12)

^a Before transformation into *C. albicans*, vectors for introducing native or tagged *TAC1* variants (the ‘*TAC1Inte*’ plasmids) were linearized by **Sall**; vectors for expressing LexA fusion proteins (the ‘CIp-LexA’ plasmids) were linearized by **StuI**; *SAT1* flipper cassettes for gene disruption were released from the ‘*pSFS2*’ constructs by **SacI/ApaI** digestion.

^b When a *pSFS2* construct was used for a conventional two-round gene knock-out, positive PCR amplification by primer pairs in *italics* confirmed its correct integration at one of the two gene loci. Disruption of the remaining allele was identified by loss of specific amplification products by the primer pair(s) in **Bold** in genotyping PCR tests.

^c Use of *pSFS2-CDR1KO* plasmid as a repairing template in a transient CRISPR-Cas9 system (11) to delete *CDR1* was described in **Supplemental Methods** session in detail.

These DNA constructs are also used in a parallel study.

Table S6 Primers used in this study

Primer name	Primer sequence	Note ^a
AZ146	TGACGAACTTGTTCCAAAC	
AZ147'	TGGATAAGTGTGATCTATCG	
Kpp062	GTAATGGTACAGATGGTACTAGAC	
Kpp063	CACAGGATGACGCCAAC	
LM065	GAGAAGAGCTCACTGTCATTATTAGGGAGAG	SacI
LM066	GAGAACCGCGGTTGTGGTTTGATATCTTG	SacII
LM067	GAGAACTCGAGGGACATAGTCCTACTGTAC	XhoI
LM068	GAGAAGGGCCCCTTCTAATTGATGTCGTTGTC	Apal
LM069	GAGAAGAGCTCCTCAAAGTCAAACACAATCTT	SacI
LM070	GAGAACCGCGGCTAAATGAAGCTGAACACTATAACT	SacII
LM071	GAGAACTCGAGTGGTAGATAGATAGATAGATGTCA	XhoI
LM072	GAGAAGGGCCCTCATAACGATACAATTGGTGC	Apal
LM073	GAGAAGAGCTCCCACAATACAACCCCTACC	SacI
LM074	GAGAACCGCGGAATAGGCAATCCGGACAC	SacII
LM075	GAGAACTCGAGAGCTGACTTTAGTAATC	XhoI
LM076	GAGAAGGGCCCTAACGTTGATATGTGCC	Apal
AZ357	CAGGAGATAACAATAAGTTGAG	
AZ358	CAAGTCCTGAACTCATTGATTAAACC	
ZL082 (TRR05)	GACAATCAAAATTCTCATATCAAC	
ZL074 (TRR06)	GGAGGTTATGGTTGTTCC	
ZL085	TTACTGTTGTTGGGTACTAG	
ZL086	TCCATGGTATGCACITGC	
ZL177	GGCCATCAATTGCTGCAACAAAC	
ZL178	TATTCTCCTCTGAATGTACAGC	
ZL804	AATAAgagtcAAAGTTACTCACATCATAAGCTG	SacI
ZL805	TGCGAccggcgCGTGTGCAAGTACTCATATG	SacII
ZL806	CTGGTctcgagGAGTCCAAAAGGTAATAGAG	XhoI
ZL807	ATGAGggcccGGTGCTACCAATGTCCCACAC	Apal
ZL808	TCCTTGTCCTTAAGAGCAGCC	
ZL536	ATGGTCCAAAAGGTATTGGTGCC	
ZL537	Cttaaatgccccatcgagc	
ZL538	Gccctggactacatttgc	
ZL539	Cagctgttctatcacggttcg	
ZL540	ATTCTAAGATGTCGCGAAGATG	(13)
ZL541	AGTTCTGGCTAAATTCTGAATGTTTC	(13)
ZL542	TAGTCCATTCAACGGCAACATT	(13)
ZL543	CACCCAGTATTGGCATTGAAA	(13)

ZL712	TGGTGATGGTGTACTCACG	(14)
ZL713	GACAATTCTCTTCAGCAC	(14)
ZL544	AACTCAACAACTCTATCC	
ZL545	GAGGCACTAATGTAATCC	
LM077	gcaaggatccaagaagaagtggataattttgattaac	BamHI (1)
LM078	gcaactcgagagtatattctgtggaaaggggfag	XhoI (1)
LM085	attagattcgccaaaaattggcttcataga	
LM086	tctatgaagaccaattttggcgaatcta	
ZL558	ATTTACAGCCGAATTATCAATCAAATAGTC	
ZL559	GACTATTGATTGATAATTGGCTGTAAATTACCCAATTTC TTGACAATAATTG	
ZL560	CCAATTTCCTTGACgATAATTGGGGATTAA	
ZL561	TTAAATCCCCAATTATCgtCAAAGAAAAATTGG	
ZL564	GATTATAATCGATATCCATTAAATTGCTACCGAAGATTCC	
ZL565	GGAATCTCGGTAGCAATTAAATGGATATCGATTAATAATC	
ZL572	CAATTAAATAATTACCCgtTTTTCTTGACAATAATTG	
ZL573	CAAATTATTGTCAAAGAAAAatcGGTAAATTATTAAATTG	
ZL612	CGAGTAATAAAATTAAaAAATCTTCATTGGAT	
ZL613	ATCCAATGAAAGATTtTAAATTATTACTCG	
ZL552	AATATCATTCTACGGTGATCTTTATTGGTAGCTAGAGTTCAA AGGGTAACAGAGAGAAAAAAAATAAGAAAAGgtcgacggatcccc	
ZL553	CAATAGTCTAAAACGTCTATTATATTAGACGTTGAGATACC ACCATGTCAAAAAACAAACTGTTAATtcgtgaattcgagetcg	
ZL554	ATGTACAGATGTAATCCATTCA	
ZL555	CACATGACCACTAACCAACCACG	
ZL636	AGCTGGTACCCGTGGTGGTGGTGGTGCATTATTATGAGAGA AGGAGAAAGGC	KpnI
ZL637	tGTCCATacctccCTGcggtgaCTTGTCATCGTC	
ZL638	ccgCAGggaggATGGACACTTCACTGTCACTGGGA	
ZL639	TAATggatccAGTCTAATATTCTTTGGAC	BamHI
ZL640	GCTGGTACCCGTGGTGGTGGTGGTGCATTGAATGATTATA TTTTTTAATATTAATATCG	KpnI
ZL696	GAGTGGCATGTAGTTaTCGGAGAAAGAAAATTAAATGC	
ZL697	GCATTAAATTCTTCTCCGAtAACTATCACATGCCACTC	
ZL706	tggtgattcttgaattttacg	
ZL707	cgtaaaaattcaaagaatcaccaAATGACAACAAATCAAGTG	
ZL708	CATCggatccACCAATTACAACACTTTTAACCC	BamHI
ZL648	AACGTTCTACAGCTGGTTCAGTGATTCAATGAAATCGAAGAA TGCTGGATTGGTCGATCCAAAATTGTAAGgtcgacggatcccc	
ZL649	GAACAGTGATGTACAGTGGTTATATTACCTGAATGTTATAAT ACTTTCTTAAATACTTGTACATATAtcgtgaattcgagetcg	
ZL650	AACCTCTAATATGTTGGACG	
ZL651	GAGAGATGAAAAGTATTACCG	

LM023	TGAAAATAACTGCTGGTGGTCAAAAAAGTTGCATCCAAATCAA GTATTGAAATTATGTGTCAAGGACAGATAggtcgacggatccccg	
LM014	AACACACAGTAATATTACATAAACACCACATCTGTTCTTCTA CTTCATCCCCCTCTCCTAAAAATTtcgtatcgagctcg	
KPP017	AAGGATAAAGAATTGAACG	
KPP018	TATATAGATCAGAAACAACA	
LM21	CTAATTAACGTGTGTATGGATC	
ZL514	ATTGACGACGATGATGAC	1-up ^F
ZL515	ATAAGAAGTTGAGGCGAAG	1-up ^R
ZL849	ATCCTCGTTACTCAATAAG	1-1 ^F
ZL850	AGACACTAACTCCGTATT	1-1 ^R
ZL851	TGCGTGACCCAAACATAATCT	1-2 ^F
ZL852	TGTGACGAGGTGGCTGAT	1-2 ^R
ZL853	GTAAGAGGAGTAGCAAGTG	1-3 ^F
ZL854	TTAAGCGATTCTGGTAGTTAT	1-3 ^R
ZL518	tttcaacatattagaatcgaatcattacg	1-DRE ^F (15)
ZL519	gccccctgtgtgttgttg	1-DRE ^R (15)
ZL528	CATCTTGCCTTCTAATAG	2-up ^F
ZL529	CACTCTAACCTGATATGGTTC	2-up ^R
ZL855	TCAACTGTTAACGTCCGATAA	2-1 ^F
ZL856	TGTAGATTGTCTGAGTCTG	2-1 ^R
ZL857	GACTCAGACAATCTACAA	2-2 ^F
ZL858	AGTTTGACATCCTTGAAT	2-2 ^R
ZL859	CTGATAATATACCTCTGTCGAA	2-3 ^F
ZL860	GGTCACATCTGTCAACA	2-3 ^R
ZL861	TGTGACCAGGTAGTGATAGT	2-4 ^F
ZL862	GCATTGCTGAGAGTGGAA	2-4 ^R
ZL532	aattcaaacacaaacaataaggctgt	2-DRE ^F (15)
ZL533	gcaatcattgtggatacatcgga	2-DRE ^R (15)
ZL488	GGT CCA CGC GTT CCA GCA ACA TCA ACA TCG	MluI
ZL489	GGT CCA CGC GTT GGT GGT TGT GGT AGC AGG AAC	MluI
ZL490	GAA GCT GCA GAC CAA TTA CAA CTC TTT TTT AAC CC	PstI
ZL524	ccgcCTGCAGTTAAATCTCAAATTATTGTC	PstI
ZL525	ccgcCTGCAGTTAAATCCACAAATTATTGTC	PstI
ZL526	GCGCAAACTCGAgTTAAATCCACAAATTATTGTC	XhoI
ZL527	ccgcCTGCAGTTAAATCCCCAAATTATcGTCAAAGAAAAATTGG	PstI
ZL173	Gatgaagcaactgtcaaacgc	
ZL174	GGAATGCTTATTGAAAAAGACTGGC	
ZL093	CTCACGCACGCCATACTAC	

(SNR52/N)		
ZL919 (sgRNA/N)	GCAGCTCAGTGATTAAGAGTAAAGATGG	(11)
ZL926	ATACAAGTGAAAACATTCA GTC	
ZL927	CTGAATGTTTCACTTGTATGTTTAGAGCTAGAAATAGCAAGT TAAA	
ZL654	GTGCTGAACGTGAATATG	
ZL257	gttggggatccgtGTTGAAGGCCACCTCCAAG	

^a The ‘Note’ column denotes the restriction enzyme cutting site(s) added for cloning or the annealing region of a ChIP assay primer (referring to Fig. 3A).

Supplemental Methods

Construction of vectors for expression of Tac1 variants from *LEU2* locus

Gain-of-function point mutations were individually introduced into pDS1097 (1) to generate the corresponding '*TAC1Inte*' plasmids listed in **Table S5**. In details, PCR amplicons of ZL481/LM086, ZL481/ZL565, ZL481/ZL573, ZL481/ZL561 ZL481/ZL558 and ZL481/ZL613 from pDS1097, were respectively fused to amplicons of LM085/LM078, ZL564/LM078, ZL572/LM078, ZL560/LM078, ZL559/LM078 and ZL612/LM078 by fusion PCR. The resulting DNA fragments were digested by PstI and XhoI and ligated to pDS1097 vector cut by the same enzymes to generate *TAC1Inte-E461K*, *-ΔM677*, *-N972D*, *-N977D*, *-Δ962-969* and *-R693K*, respectively. *TAC1Inte-G980W* was constructed by ligating PstI/XhoI digested ZL481/ZL526 amplicon from pDS1097 to pDS1097 vector digested by the same enzymes.

Construction of vectors for expression of 6His3Flag tagged Tac1 variants from *LEU2* locus

6His3Flag tag coding sequence was first introduced to the 5' end of wild type *TAC1* ORF on pDS1097. Specifically, pDS1097 was used as the template and LM077/ZL636 as the primer pair, *TAC1* promoter (including the translation start codon) was amplified with 6His coding sequence added at 3' end. This fragment was digested by BamHI/KpnI and ligated to *pFA-6HIS3FLAG-SAT1* (6) vector digested by the same enzymes. LM077/ZL637 amplicon from the resulting plasmid, which contains *TAC1* promoter driven entire 6HIS3FLAG tag was fused to Tac1 (aa1-433) coding sequence amplified from pDS1097 by ZL638/ZL486 through fusion PCR. The product was digested by BamHI/PstI and ligated to pDS1097 cut at the same sites to generate *TAC1InteHF-WT*. After confirmed by DNA sequencing, the BamHI/PstI fragment was re-cleaved from *TAC1InteHF-WT* and sub-cloned into *TAC1Inte-E461K*, *-ΔM677*, *-N972D*, *-N977D*, *-Δ962-969* and *-R693K* between the

same sites, resulting in each corresponding ‘*TAC1InteHF*’ plasmid. To introduce C43Y mutation to Tac1 DNA binding domain, fusion PCR product sealing the amplicon of LM077/ZL697 and amplicon of ZL696/ZL486 both from *TAC1InteHF-WT*, was digested by BamHI/PstI and ligated to *TAC1InteHF-WT* and *TAC1InteHF-R693K* cut by the same enzymes. *TAC1InteHF-TAC1ΔTAD* was derived from *TAC1InteHF-TAC1* by replacing the sequence between the PstI and XhoI sites by a ZL481/ZL670 amplicon digested by the same enzymes. The same method was used to generate the plasmids for expression of 6His3Flag tagged Tac1^{GOF} TAD truncation mutants (*TAC1InteHF-E461KΔTAD*, *-ΔM677ΔTAD*, *-R693KΔTAD* and *-A736VΔTAD*) and their untagged forms (*TAC1InteE461KΔTAD*, *ΔM677ΔTAD*, *R693KΔTAD* and *A736VΔTAD*) from the corresponding ‘*TAC1InteHF*’ and ‘*TAC1Inte*’ constructs.

Construction of SAT1 flipper vectors for gene disruption

To generate SAT1 flipper (16) constructs for deleting *MED3*, *SSN3*, *MED15*, *CDR2*, *SNF2* and *CDR1* in *C. albicans*, 5' homologous regions (5' HRs) for each gene were respectively amplified by LM065/LM066, LM069/LM070, LM073/LM074, ZL804/ZL805, ZL589/ZL590 and ZL907/ZL908 from genomic DNA and 3' HRs respectively by LM067/LM068, LM071/LM072, LM075/LM076, ZL806/ZL807, ZL591/ZL592 and ZL909/ZL910. pSFS2 vectors with individual 5' HR inserted between the SacI/SacII sites and the corresponding 3' HR inserted between the XhoI/ApaI sites were named as *pSFS2-MED3KO*, *pSFS2-SSN3KO*, *pSFS2-MED15KO*, *pSFS2-CDR2KO*, *pSFS2-SNF2KO* and *pSFS2-CDR1KO* according to their gene targets.

Construction of vectors for over-expression of 6His3Flag tagged Tac1 variants

Using *C. albicans* genomic DNA as template and ZL639/ZL640 as primers, *ACT1* promoter (including the translation start codon) was amplified with 6His coding sequence added at its 3' end. This fragment was digested by BamHI/KpnI and

inserted into *pFA-6HIS3FLAG-SAT1* between the two sites. ZL639/ZL637 amplicon from the resulting plasmid, which contains *ACT1* promoter driven complete 6His3Flag tag sequence, after fused to Tac1 (aa1-433) coding sequence amplified from pDS1097 by ZL638/ZL486, was digested by BamHI/PstI and ligated to pDS1097 cut at the same sites to generate *TAC1InteHF-WTOE*. The BamHI/PstI insertion, after confirmed by DNA sequencing, was also sub-cloned into *TAC1InteHF-R693K* and *TAC1InteHF-N972D* to generate the corresponding over-expression vector *TAC1InteHF-R693KOE* and *TAC1InteHF-N972DOE*.

Construction of vectors for expression of LexA fused Tac1 fragments in *LacZ* reporter strains

DNA fragments encoding Tac1 TAD (aa856-981) variants (wild type, *N972D*, *Δ962-969*, *N977D*, *G980E* and *G980W*) were amplified respectively by ZL489/ZL490 from pDS1097, ZL489/ZL490 from *TAC1Inte-N972D*, ZL489/ZL490 from *TAC1Inte-Δ962-969*, ZL489/ZL527 from pDS1097, ZL489/ZL524 from pDS1097 and ZL489/ZL525 from pDS1097, digested by MluI/PstI and inserted into CIp-LexA (9) vector between the same sites. The shorter form of wild type Tac1 TAD (aa932-981) coding sequence amplified by ZL488 and ZL490 from pDS1097 was introduced into CIp-LexA in the same way.

Vectors expressing LexA-Tac1(aa130-981) variants (CIp-LexA-Tac¹³⁰⁻⁹⁸¹WT, -255A, -E461K, -ΔM677, -A736V, -N972D, -Δ962-969, -N977D, -G980E and -G980W) were constructed by inserting MluI/AscI digested ZL556/ZL557 amplicon respectively from pDS1097, ACY67, *TAC1Inte-E461K*, *TAC1Inte-ΔM677*, pAC97, *TAC1Inte-N972D*, *TAC1Inte-Δ962-969*, *TAC1Inte-N977D*, pAC157 and *TAC1Inte-G980W* into MluI linearized CIp-LexA vector. Correctly oriented insertion was selected by positive amplification of ZL185/ZL486 and negative amplification of ZL185/ZL485. In addition, ZL556/ZL630 amplicon from pDS1097 was inserted into CIp-LexA in the same way to generate CIp-LexA-Tac1¹³⁰⁻⁹³¹WT.

Deletion of *cdr1* by a transient CRISPR-Cas9 system

Deletion of *cdr1* was performed using the system and protocol described in (11) with modifications. A Cas9 cassette was amplified by ZL914/ZL915 from pV1093 (12). A sgRNA cassette was generated by a nest fusion PCR (11), where ZL918/ZL919 was used to seal the two fragments amplified from pV1093 by ZL916/ZL926 and ZL927/ZL917. Choose of the sgRNA sequence was guided by a genome-wide search described in (12). A DNA mixture containing 800 ng of Cas9 cassette, 800 ng of sgRNA cassette and 500 ng of SacI/ApaI digested *pSFS2-CDR1KO* plasmid, which serves as a repairing template, were used to transform *C. albicans* cells by electroporation. Transformants with deletions in both copies of *CDR1* were identified by loss of the ZL540/ZL541 and ZL654/ZL912 amplicons during PCR testing.

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