**Description of Supplementary Files**

File Name: Supplementary Information
Description: Supplementary Figures, Supplementary Tables and Supplementary References

File Name: Supplementary Data 1
Description: RNA PolII ChIP-seq data comparing wild type and *cas5Δ/cas5Δ* mutant strains under basal condition.

File Name: Supplementary Data 2
Description: RNA PolII ChIP-seq data for the wild type strain comparing basal and caspofungin treatment conditions.

File Name: Supplementary Data 3
Description: RNA PolII ChIP-seq data for the *cas5Δ/cas5Δ* mutant strain under basal and caspofungin treatment condition.

File Name: Supplementary Data 4
Description: RNA PolII ChIP-seq data comparing wild type and *cas5Δ/cas5Δ* mutant strains under caspofungin treatment condition.

File Name: Supplementary Data 5
Description: Common and unique differentially bound genes between the comparisons of the *cas5Δ/cas5Δ* mutant to the wild type strain and of wild type strain in the presence and absence of caspofungin treatment.
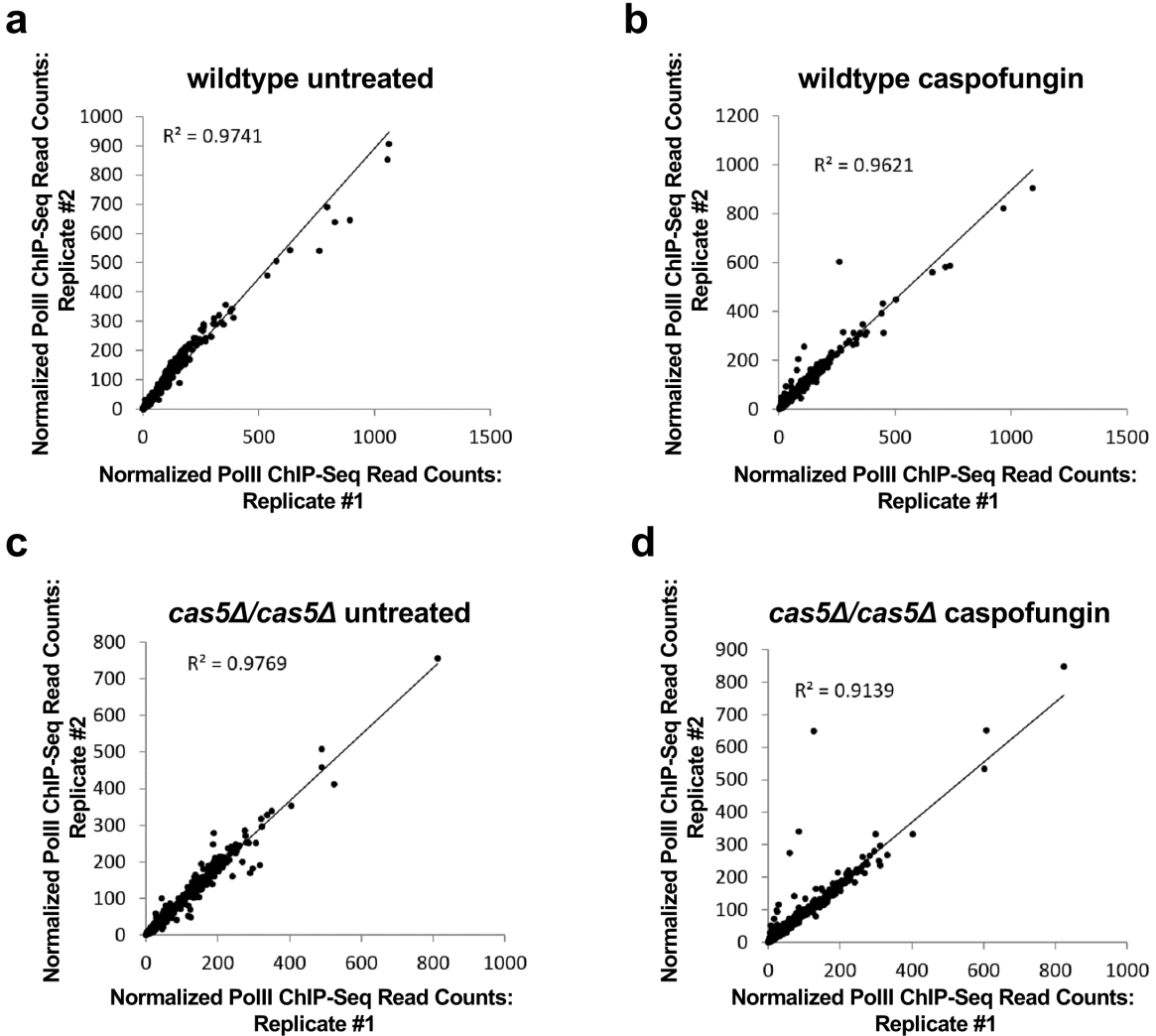
File Name: Supplementary Data 6
Description: Cell cycle expression pattern of genes differentially bound in *cas5Δ/cas5Δ* mutant in comparison to the wild type strain under basal caspofungin treatment conditions.
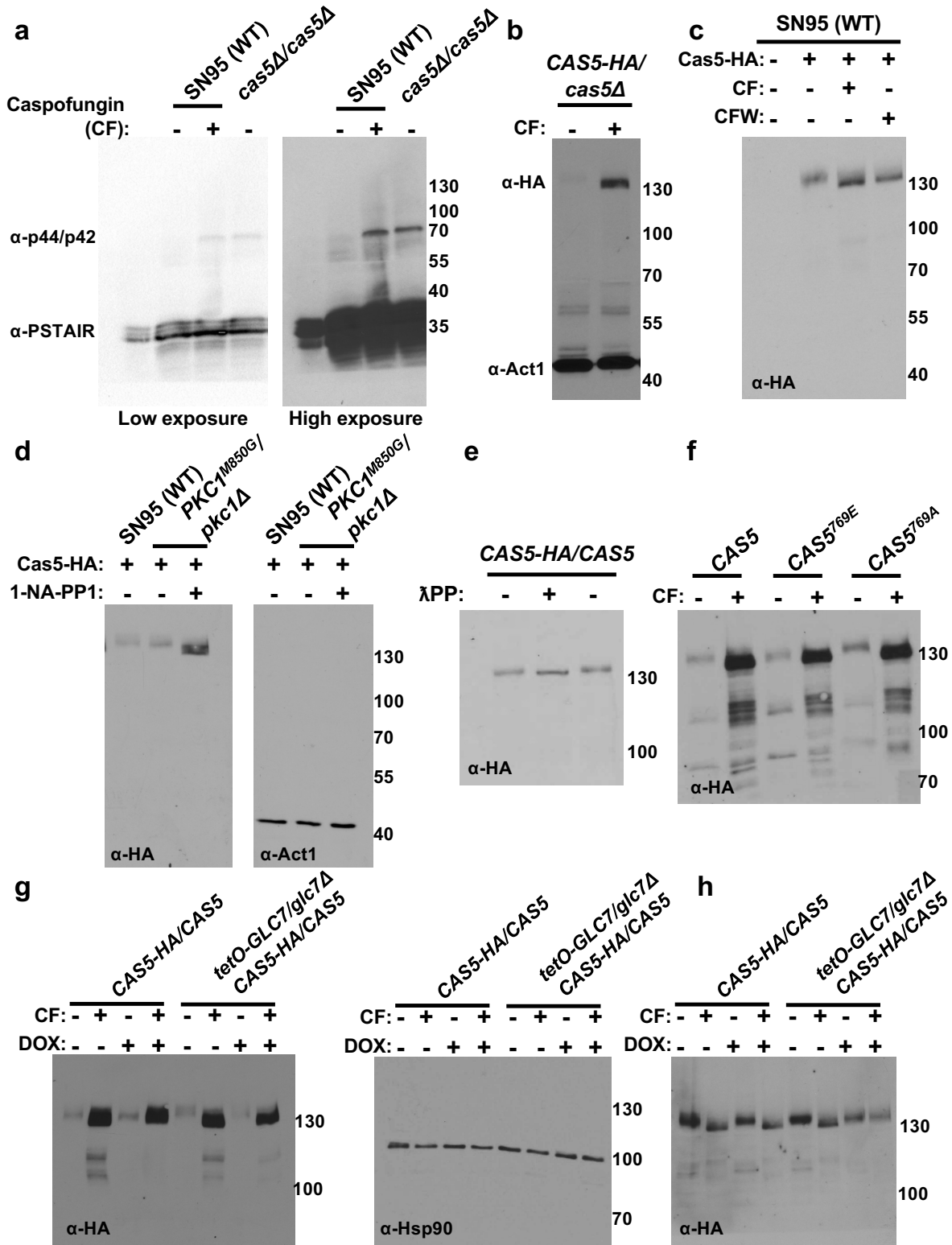
File Name: Supplementary Data 7
Description: Physical interactors of Cas5 identified by co-immunoprecipitation coupled with mass spectrometry.

File Name: Peer Review File

**a**

### wildtype untreated

$R^2 = 0.9741$

Normalized PolII ChIP-Seq Read Counts: Replicate #2

Normalized PolII ChIP-Seq Read Counts: Replicate #1

**b**

### wildtype caspofungin

$R^2 = 0.9621$

Normalized PolII ChIP-Seq Read Counts: Replicate #2

Normalized PolII ChIP-Seq Read Counts: Replicate #1

**c**

### *cas5Δ/cas5Δ* untreated

$R^2 = 0.9769$

Normalized PolII ChIP-Seq Read Counts: Replicate #2

Normalized PolII ChIP-Seq Read Counts: Replicate #1

**d**

### *cas5Δ/cas5Δ* caspofungin

$R^2 = 0.9139$

Normalized PolII ChIP-Seq Read Counts: Replicate #2

Normalized PolII ChIP-Seq Read Counts: Replicate #1

**Supplementary Fig. 1: Correlation plots for RNA PolII ChIP-Seq analysis.** Scatterplots highlighting the correlation of normalised PolII ChIP-Seq read counts between biological replicates of PolII ChIP-Seq experiments for **(a)** wild type untreated, **(b)** wild type with caspofungin, **(c)** *cas5Δ/cas5Δ* mutant untreated, and **(d)** *cas5Δ/cas5Δ* mutant with caspofungin.

**a**

SN95 (WT) cas5Δ/cas5Δ    SN95 (WT) cas5Δ/cas5Δ

Caspofungin (CF):   -   +   -     -   +   -

α-p44/p42

α-PSTAIR

130
100
70
55
40
35

Low exposure    High exposure

**b**

*CAS5-HA/ cas5Δ*

CF:   -   +

α-HA

α-Act1

130
100
70
55
40

**c**

SN95 (WT)

Cas5-HA:   -   +   +   +
CF:   -   -   +   -
CFW:   -   -   -   +

α-HA

130
100
70
55
40

**d**

SN95 (WT) PKC1^{M850G}/ pkc1Δ    SN95 (WT) PKC1^{M850G}/ pkc1Δ

Cas5-HA:   +   +   +     +   +   +
1-NA-PP1:   -   -   +     -   -   +

α-HA    α-Act1

130
100
70
55
40

**e**

*CAS5-HA/CAS5*

λPP:   -   +   -

α-HA

130
100

**f**

CAS5    CAS5^{769E}    CAS5^{769A}

CF:   -   +   -   +   -   +

α-HA

130
100
70

**g**

CAS5-HA/CAS5    tetO-GLC7/glc7Δ CAS5-HA/CAS5    CAS5-HA/CAS5    tetO-GLC7/glc7Δ CAS5-HA/CAS5

CF:   -   +   -   +   -   +   -   +
DOX:   -   -   +   +   -   -   +   +

α-HA    α-Hsp90

130
100

130
100
70

**h**

CAS5-HA/CAS5    tetO-GLC7/glc7Δ CAS5-HA/CAS5

CF:   -   +   -   +   -   +   -   +
DOX:   -   -   +   +   -   -   +   +

α-HA

130
100

**Supplementary Fig. 2: Images of complete Western blots shown in main figures. (a)** Deletion of *CAS5* leads to the activation of the cell wall integrity pathway in the absence of cell wall stress. A SN95 wild-type strain and a *cas5Δ/cas5Δ* mutant were left untreated (-) or treated for 1 hour with 125 ng/ml of caspofungin (+), as indicated. Phosphorylated Mkc1 was monitored by Western blot and detected with α-p44/42 antibody. **(b)** Cas5 increases in response to caspofungin. Levels of Cas5 were monitored by Western blot and detected with an α-HA antibody. Actin was detected with an α-β-actin antibody as a loading control. **(c)** Cas5 is post-translationally modified upon cell wall stress treatment. Cells were grown to log phase and subsequently treated with 125 ng/ml of caspofungin or 50 μg/ml of calcofluor white for 1 hour. Total protein was resolved by SDS-PAGE and the blot was hybridized with an α-HA to monitor Cas5 migration. **(d)** Cas5 is post-translationally modified upon Pkc1 inhibition. Cas5 migration and actin detection were monitored as part **b**. **(e)** Cas5 is phosphorylated in the absence of stress. Cas5 migration was monitored by Western blot and detected with an α-HA antibody. Treatment of protein lysate with lambda phosphatase resulted in a faster migrating band, indicative of a loss of phosphate groups. **(f)** Phosphomutations in *CAS5* do not affect band shifts associated with activation of the cell wall stress response, as observed upon caspofungin treatment. Cas5 was monitored by Western blot and detected using an α-HA antibody. **(g)** Upregulation of Cas5 expression does not depend on Glc7. *CAS5-HA/CAS5* and *CAS5-HA/CAS5 tetO-GLC7/glc7Δ* strains were cultured in the absence or presence of doxycycline and caspofungin, as indicated. Cas5 was monitored by Western blot and detected with an α-HA antibody. Hsp90 protein levels served as a loading control. **(h)** Post-translational modification of Cas5 is absent upon *GLC7* depletion. The Western blot was performed as described in **b,** except caspofungin treated samples were diluted 5-fold to achieve equal loading of Cas5

**Supplementary Fig. 3: Genetic validation of mutant strains. (a)** HA-tagged allele of *CAS5* is functional. Caspofungin susceptibility assays were conducted in YPD medium. Growth was measured by absorbance at 600 nm after 48 hours at 30°C. Optical densities were averaged for duplicate measurements. Data was quantitatively displayed with colour using Treeview (see colour bar). **(b)** ATP analogue 1-NA-PP1 specifically inhibits Pkc1 kinase activity. Caspofungin susceptibility assays were conducted in YPD medium in the presence of 0.05% DMSO or 5 μM

1-NA-PP1. Growth was measured by absorbance at 600 nm after 48 hours at 30°C. Data was analyzed and plotted as in part **a.**
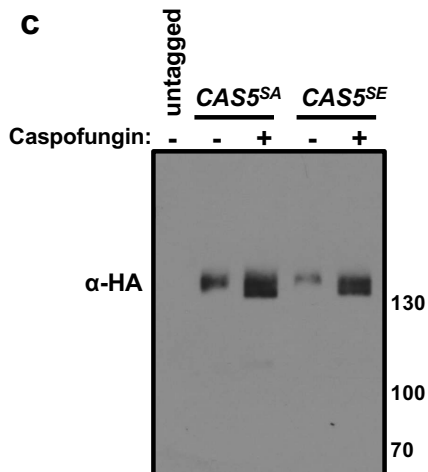
**a**
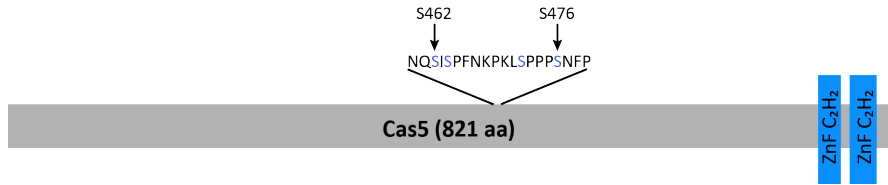


**b**
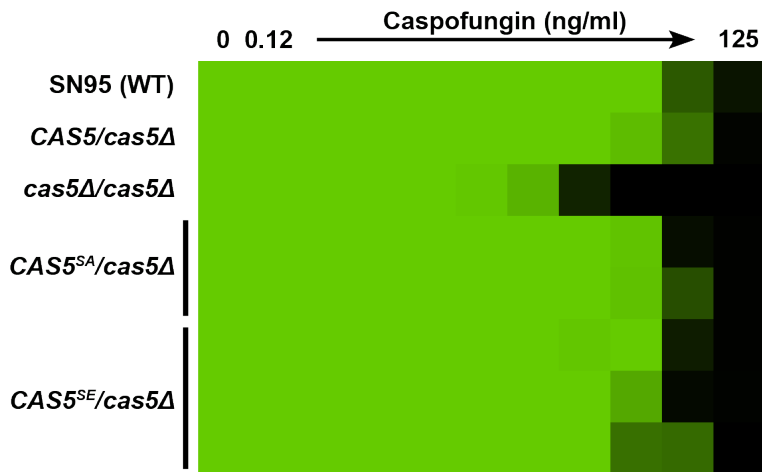


**c**

**Supplementary Fig. 4: The phosphorylation sites identified by mass spectrometry are not sufficient for regulation of Cas5 function in response to cell wall stress. (a)** A schematic showing the phosphorylated serine residues identified in Cas5 by the mass spectrometry analysis. **(b)** Both phosphomimetic and phosphodeficient substitutions of the Cas5 serine residues did not affect caspofungin tolerance. The phosphomimetic (SE) and phosphodeficient (SA) alleles of *CAS5*, consisting of four substitutions at serine residues 462, 464, 472, and 476, were introduced into a *cas5Δ/cas5Δ* mutant individually as the only *CAS5* allele in the strain. Caspofungin susceptibility assays were conducted in YPD medium. Growth was measured by absorbance at 600 nm after 48 hours at 30°C. Optical densities were averaged for duplicate measurements. Data was quantitatively displayed with colour using Treeview (see colour bar in Fig. S2). **(c)** The phosphomimetic (SE) and phosphodeficient (SA) substitutions of the serine residues on Cas5 do not affect the band shift associated with activation of the cell wall stress response. Cells were subcultured in YPD for 3 hours to reach log phase, and subsequently treated with 125 ng/ml of caspofungin for 2 hours. Levels of Cas5 were monitored by Western blot and detected with an α-HA antibody. Full blot is shown in the Figure.
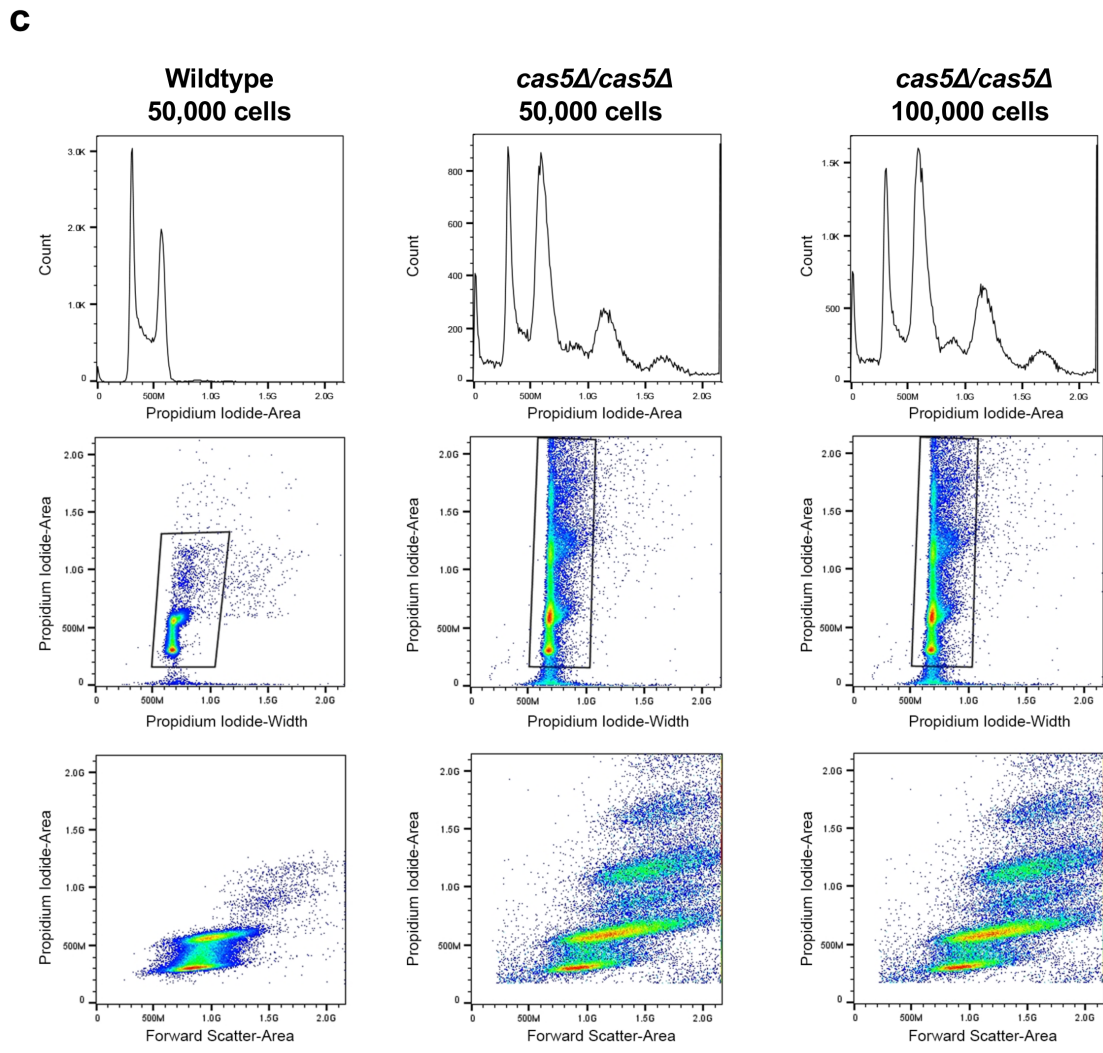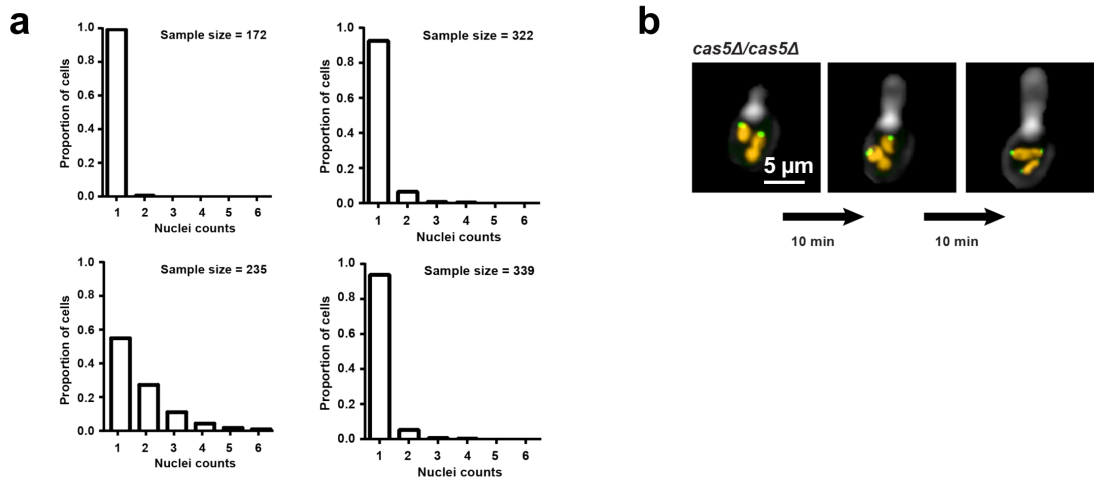
**a**



**b**
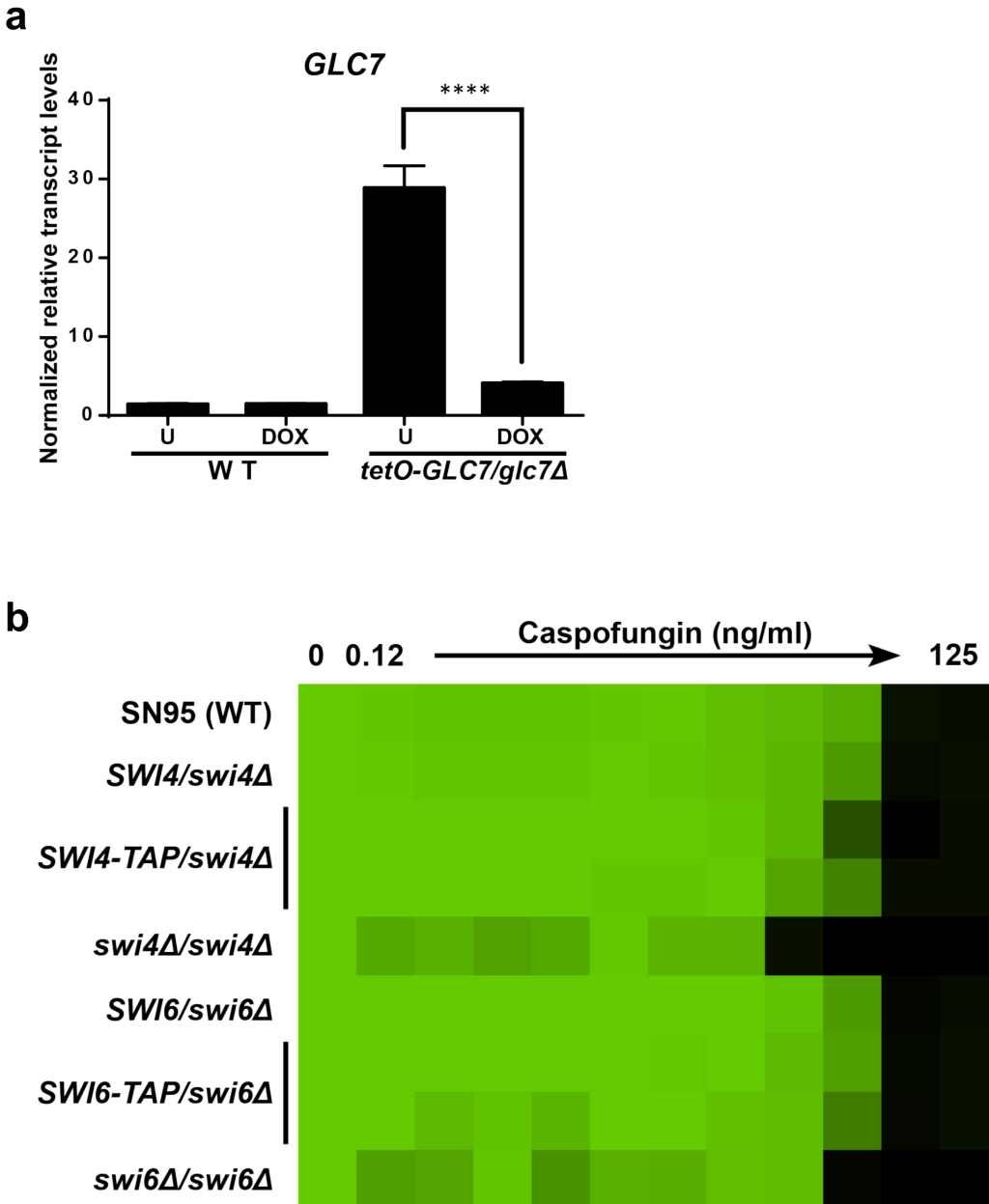


**Supplementary Fig. 5:** *GLC7* **is depleted upon doxycycline treatment in the** *tetO-GLC7/glc7Δ* **strain, and the TAP tagged versions of Swi4 and Swi6 are functional. (a)** Wild-type and *tetO-GLC7/glc7Δ* strains were grown for 24 hours in the presence or absence of 0.02 μg/ml of doxycycline. The strains were subcultured again in the same conditions for 3 hours and subsequently treated with or without caspofungin for 1 hour. The transcript level of *GLC7* was

monitored by qRT-PCR and normalized to *GPD1*. Error bars represent standard deviation (s.d.) from the mean of triplicate samples.  Levels of *GLC7* upon transcriptional repression with doxycycline were compared using Tukey's multiple comparisons test in GraphPad Prism (**** *P*<0.0001). **(b)** Caspofungin susceptibility assays were conducted in YPD medium. Growth was measured by absorbance at 600 nm after 48 hours at 30°C. Optical densities were averaged for duplicate measurements. Data was quantitatively displayed with colour using Treeview (see colour bar in Fig. S2).
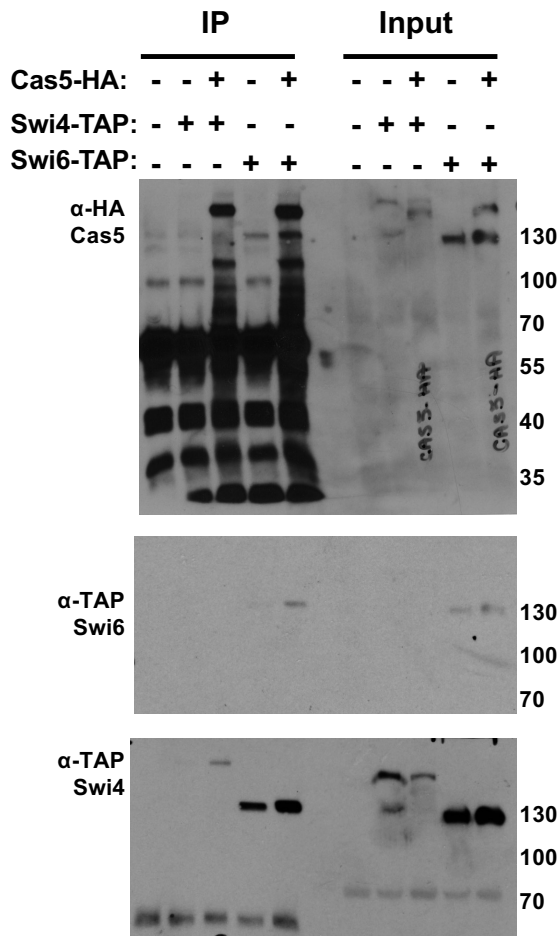
**Supplementary Fig. 6: Images of complete immunoprecipitation Western blots shown in Figure 8.** Swi4 and Swi6 co-purify with Cas5. C-terminally HA-tagged Cas5 was immunoprecipitated with α-HA beads. Swi4 and Swi6 co-purification was monitored by Western blot and detected with an α-TAP antibody. Cas5 pull down was confirmed with detection using an α-HA antibody. Input samples confirm the expression of tagged proteins. Top panel, middle panel, and bottom panel represent full blots used for corresponding panels in Figure 8.

**a**

Sample size = 172

Sample size = 322

Sample size = 235

Sample size = 339

(y-axis: Proportion of cells; x-axis: Nuclei counts)

**b**

*cas5Δ/cas5Δ*

5 µm

10 min → 10 min →

**c**

Wildtype
50,000 cells

*cas5Δ/cas5Δ*
50,000 cells

*cas5Δ/cas5Δ*
100,000 cells

(Top row: Count vs Propidium Iodide-Area)

(Middle row: Propidium Iodide-Area vs Propidium Iodide-Width)

(Bottom row: Propidium Iodide-Area vs Forward Scatter-Area)

**Supplementary Fig. 7: Cas5 regulates proper nuclear division. (a)** Histograms highlighting the number of nuclei present per cell in wild-type, *cas5Δ/cas5Δ, swi4Δ/swi4Δ,* and *swi6Δ/swi6Δ* strains. Plotted are results from a representative biological replicate. A minimum of 172 cells were counted for each strain. **(b)** Mitotic spindles are misaligned during cell division in a mutant lacking Cas5, monitored as in Fig. 9. Scale bar represents 5 μm. **(c)** Cellular DNA content measured by propidium iodide and flow cytometry of the (left panel) wild-type diploid (SN95), and the (middle and right panels) *cas5Δ/cas5Δ* mutant strain. Either 50,000 cells (left and middle panels) or 100,000 cells (right panel) were analyzed per strain. No difference was detected between the 50,000 or 100,000 cell populations. The top row of each column is the number of cells (Count) plotted by propidium iodide flurorescence (Propidium Iodide-Area). This is to rule out the possibility that the increased ploidy levels in the *cas5Δ/cas5Δ* mutant were due to cell aggregates. In the middle row, aggregates were detected by Propidium Iodide-Area versus Propidium Iodide-Width. Because single cells (G0/1 or G2/M) will have similar pulse width values (or transit time across the laser beam), we observed a near vertical line on the Propidium Iodide-Width axis that represents the width of a singlet population. Aggregates, however, will have larger width values and are detected only minimally to the right of the singlet population (> 1.0G). Furthermore, in the *cas5Δ/cas5Δ* mutant strain, the fluorescence intensity of the Propidium Iodide-Area increased with the ploidy intervals detected in the top row (indicated by red/orange/yellow). Using this singlet population gate, we then plotted the Propidium Iodide-Area by Forward Scatter-Area (bottom row). This plot shows that ploidy increases with cell size (Forward Scatter-Area), and this cell size increase is not due to cell aggregates because this population is derived from the singlet population.

**Supplementary Table 1.** *Candida albicans* **strains used in this study.**

| Strain Name | Genotype | Source |
|---|---|---|
| CaLC191 (DAY185) | *pARG4::URA3::arg4::hisG/arg4::hisG pHIS1::his1::his1/his1::hisG* | [1] |
| CaLC1349 | DAY185 *cas5::ARG4/cas5::URA3* | [2] |
| CaLC1350 | DAY185 *cas5::ARG4/cas5 ::URA3 pCAS5::HIS1::his1::hisG/his1::hisG* | [2] |
| CaLC239 (SN95) | *arg4Δ/arg4Δ his1Δ/his1Δ URA3/ura3Δ::imm434 IRO1/iro1::imm434* | [3] |
| CaLC2034 | SN95 *cas5::FRT/CAS5* | This study |
| CaLC2056 | SN95 *cas5::FRT/cas5::FRT* | This study |
| CaLC2087 | SN95 *FKS1$^{F641S}$/FKS1* | [4] |
| CaLC3908 | SN95 *FKS1$^{F641S}$/FKS1 cas5::FRT/cas5::FRT* | This study |
| CaLC3909 | SN95 *FKS1$^{F641S}$/FKS1 cas5::FRT/cas5::FRT* | This study |
| CaLC1255 | *SN95 CaTAR-FRT pkc1::FRT/pkc1::FRT* | [5] |
| CaLC1256 | *SN95 CaTAR-FRT pPKC1-FRT/pkc1::FRT* | [5] |
| CaLC3067 | *SN95 CaTAR-FRT PKC1$^{M850G}$-FRT/pkc1::FRT* | [6] |
| CaLC3378 | *SN95 CaTAR-FRT PKC1$^{M850G}$-FRT/pkc1::FRT CAS5-HA-HIS1/CAS5* | This study |
| CaLC3859 | SN95 *CaTAR-FRT-tetO-CAS5/cas5::FRT* | This study |
| CaLC3113 | SN95 *CAS5-HA-HIS1/cas5::FRT* | This study |
| CaLC3151 | SN95 *CAS5-HA-HIS1/cas5::FRT* | This study |
| CaLC2213 | SN95 *CAS5-HA-HIS1/CAS5* | This study |
| CaLC3044 | SN95 *CAS5-HA-HIS1/CAS5-HA-ARG* | This study |
| CaLC4285 | DAY286 *CAS5-HA-HIS/CAS5* | This study |

| | | |
|---|---|---|
| CaLC3209 | SN95 *CAS5$^{S769E}$-HA-HIS1/cas5::FRT* | This study |
| CaLC3189 | SN95 *CAS5$^{S769A}$-HA-HIS1/cas5::FRT* | This study |
| CaLC4036 | SN95 *swi4::FRT/swi4::FRT* | This study |
| CaLC4330 | SN95 *swi6::FRT/swi6::FRT* | This study |
| CaLC3391 | SN95 *SWI4-TAP-ARG4/SWI4* | This study |
| CaLC3393 | SN95 *SWI6-TAP-ARG4/SWI4* | This study |
| CaLC3395 | CaLC3151 *SWI4-TAP-ARG4/SWI4* | This study |
| CaLC3398 | CaLC3151 *SWI6-TAP-ARG4/SWI6* | This study |
| CaLC3932 | SN95 *CaTAR-FRT-tetO-GLC7/glc7::FRT* | This study |
| CaLC3952 | CaLC3932 *CAS5-HA-HIS1/CAS5* | This study |
| CaLC3672 | CaLC2056 *CAS5S462A/S464A/S472A/S476A-HA-HIS1/cas5::FRT* | This study |
| CaLC3673 | CaLC2056 *CAS5S462A/S464A/S472A/S476A-HA-HIS1/cas5::FRT* | This study |
| CaLC3693 | CaLC2056 *CAS5S462E/S464E/S472E/S476E-HA-HIS1/cas5::FRT* | This study |
| CaLC3694 | CaLC2056 *CAS5S462E/S464E/S472E/S476E-HA-HIS1/cas5::FRT* | This study |
| CaLC3695 | CaLC2056 *CAS5S462E/S464E/S472E/S476E-HA-HIS1/cas5::FRT* | This study |
| CaLC4471 | SN95 *SWI4-TAP-ARG4/swi4::FRT* | This study |
| CaLC4499 | SN95 *SWI6-TAP-ARG4/swi6::FRT* | This study |
| CaLC4705 | SN95 *HHF1-RFP-NAT/HHFR DAD2-GFP-HIS/DAD2* | This study |
| CaLC4707 | SN95 *cas5::FRT /cas5::FRT HHF1-RFP-NAT/HHFR DAD2-GFP-HIS/DAD2* | This study |

**Supplementary Table 2. Bacterial plasmids used in this study.**

| Strain Name | Description | Source |
|---|---|---|
| pLC49 | *FLP-CaNAT, NATr, ampR* | [7] |
| pLC383 | *GFP-HIS, ampR* | [8] |
| pLC435 | *Clp1-ADH1-CHERRY, ampR* | [9] |
| pLC447 | *CaCherry-NAT, NATr, ampR* | This study |
| pLC575 | *pFA-HA-HIS1, ampR* | [10] |
| pLC576 | *pFA-HA-ARG4, ampR* | [10] |
| pLC790 | pLC49 $CAS5^{DBD\ domain}$-HA-HIS1, NATr, ampR | This study |
| pLC791 | pLC49 $CAS5^{S769E}$-HA-HIS1, NATr, ampR | This study |
| pLC800 | pLC49 $CAS5^{S769A}$-HA-HIS1, NATr, ampR | This study |
| pLC573 | *pFA-TAP-ARG4, ampR* | [10] |
| pLC605 | *CaTAr-FLP-CaNAT, ampR* | [11] |
| pLC818 | pLC49 *CAS5-HA-HIS1, NATr, ampR* | This study |
| pLC857 | pLC49 $CAS5^{S462E/S464E/S472E/S476E}$-HA-HIS1, NATr, ampR | This study |
| pLC858 | pLC49 $CAS5S^{462A/S464A/S472A/S476A}$-HA-HIS1, NATr, ampR | This study |

**Supplementary Table 3. Oligonucleotides used in this study.**

| Name | Description | Sequence |
|------|-------------|----------|
| oLC274 | pJK863down-F | CTGTCAAGGAGGGTATTCTGG |
| oLC275 | pJK863up-R | AAAGTCAAAGTTCCAAGGGG |
| oLC300 | Tetp-F-NotI | ATAAGAATGCGGCCGCGTTTGGTTCAGCACCTTGTCG |
| oLC534 | CaTAR-797-R | GATGGAGATAGTTTACGG |
| oLC600 | JB-GFP+344-R | CCTTCAAACTTGACTTCAGC |
| oLC752 | GPD1+570-F | AGTATGTGGAGCTTTACTGGGA |
| oLC753 | GPD1+766-R | CAGAAACACCAGCAACATCTTC |
| oLC1593 | TAP-R | TAAACTTTGGATGAAGGCG |
| oLC1594 | ARG4-F | ATGTTGGCTACTGATTTAGCTG |
| oLC1645 | HIS-F | ACAAACCTACTAATATCAGAT |
| oLC1752 | CaEcm331 664-F | AACTTGACTAGTGTCAACGG |
| oLC1753 | CaEcm331 961-R | CTTGGAAATCACCAGATACC |
| oLC2017 | CaCas5-70F M13R | CTATTCTAATTTATTTACTTTGCTTTT CATCCCACCCCTTTGTTGGTAAATATAGAC TTTAACATATACTGGAAACAGCTATGACCATG |
| oLC2018 | CaCas5+2536R M13F | AAAATACGAATTATCTATATGGATT ATACTTTAAATAATACCGTCTTTTAATG CATAGTCTATATAATGTGTAAAACGACGGCCAG |
| oLC2029 | CaHA-R | GGCGAGGTATTGGATAGTTC |
| oLC2034 | CaCas5-465F | GCTTGGATTTTCCCCCATTAG |
| oLC2035 | CaCas5+3422R | GTTGTCATAATCCTACAGG |
| oLC2047 | CaCas5+1349F | CCAATGACTTCATATCCACC |
| oLC2048 | CaCas5+1559R | CCACCTGAAGTTGAATTGG |
| oLC2088 | CaCAS5_pLC605F | CTATTCTAATTTATTTACTTTGCTT TTCATCCCACCCCTTTGTTGGTAAATATA GACTTTAACATATACTGGAAACAGCTATGACCATG |
| oLC2089 | CaCAS5_pLC605R | GTAAACTATTTGTACCATCATCATA TGGCTGTGATAGCTGTGTCGGCGAAC TTAATAAATAATTCTCCATCGACTATTTATATTTGTATG |
| oLC2161 | CaCAS5 HA-ARG4 F | AAAGATTCATGGACTTGTGAAAGG ACAAGAAGAGTTTACAAGAGTGTTGAAT GAAAACAAAGAAGTTTCCCCCGGGTACCCATACGATGT |
| oLC2162 | CaCAS5 HA-ARG4 R | AAAATACGAATTATCTATATGGATTA TACTTTAAATAATACCGTCTTTTAATGCATAG TCTATATAATGTTCGATGAATTCGAGCTCGTT |
| oLC2163 | CaCAS5+2276F | GACCAGAACATGTTAAACGTC |
| oLC2164 | CaCAS5+2737R | GTCATCATGCGAGTTATGG |
| oLC2256 | CaPGA13+468-F | CCAACCACTACATCTACTTC |
| oLC2257 | CaPGA13+665-R | GGAACAACAACTGTAGTTGG |
| oLC2470 | CaRLM1+868F | CCGGGAATGTTCCAAATACC |
| oLC2471 | CaRLM1+1114R | GGAACTGTTGATACTGCTG |

| oLC3052 | CaCAS5+1812-F | GGCTGTTGTTAAACAGGAAAAG |
|---------|---------------|------------------------|
| oLC3371 | CaCAS5+1812-R | CTTTTCCTGTTTAACAACAGCC |
| oLC3424 | CaSWI4+3144F TAP | TGGTGTTAAAGTTGAAGAAATTGAC AGTTTAATTGATGGAATTGCCGAATCATT AACTGAAGGTATGACGGGTCGACGGATCCCCGGGTT |
| oLC3425 | CaSWI4+3286R HIS/ARG | CATCGAGTCAATTTAATAAAACTGTC CTCTTTCAATTTTGTTCCGATTTAATTTC CCCCATCTATCGTAATCGATGAATTCGAGCTCGTT |
| oLC3426 | CaSWI4+2914F | GTTGAACAACATGAGTCAAG |
| oLC3427 | CaSWI4+3581R | GTGTTTCCCTCTGTTATTG |
| oLC3428 | CaSWI6+2118F TAP | TACAAATGTTGGTGTAAACGAAGTT GATGAATTTTTAGACGGGTTGTTGGAAGC AGTGGAAGGACAACAGGGTCGACGGATCCCCGGGTT |
| oLC3429 | CaSWI6+2260R HIS/ARG | GAATAAACATACAAAGAATAGGA ATCGTTTTTTTTTTTGATTTTTTTTTTGTTTGA GTTGGTGATATTGATCGATGAATTCGAGCTCGTT |
| oLC3430 | CaSWI6+1739F | CCAATAATCGTTTCAACACC |
| oLC3431 | CaSWI6+2844R | GTTGCAACAATGGTACAAAG |
| oLC3472 | CaSWI4-70F M13R | GTTTGTATCACCCATATTTAATTTC ATTATATCCTTTTGATACTTCATTGATACTT AAAACTACTACATAGGAAACAGCTATGACCATG |
| oLC3473 | CaSWI4+3286R M13F | CATCGAGTCAATTTAATAAAACT GTCCTCTTTCAATTTTGTTCCGATTTAA TTTCCCCCATCTATCGTAAGTAAAACGACGGCCAG |
| oLC3474 | CaSWI4-988F | CGTTGATCACACTTCATTTC |
| oLC3490 | CaGLC7-70F | TATATTTTTTTTTTTTTTTATTTGGTG TGTCCAATTGCTTACTAACAACATTTAG TAATATAGCCTATAGGAAACAGCTATGACCATG |
| oLC3491 | CaGLC7+1063R pLC49 | AAACAGGAATAATAAAATAACAATAGT GACAATAATTTTATCAATTTCAAGACTC ATCGTGTAAACTCGAGTAAAACGACGGCCAG |
| oLC3492 | CaGLC7+62R **pLC605** | TCCAAAAGACGGTCGACAATATTGTCAAC GGAAATGGAATCGTCTTCGATATTGTTTGACATCGACTA TTTATATTTGTATG |
| oLC3494 | CaGLC7-1520R | GAAGAAAGTAGGTGTTGTTG |
| oLC3495 | CaGLC7+237R | GAATAAACGGAGTAGATCG |
| oLC3558 | CaGLC7-432F-KpnI | GGGGTACCGAAGAAGAATTGAGCGAGAG |
| oLC3561 | CaGLC7+1431R-SacI | CCCGAGCTCGACTCTATATATGGTACAAC |
| oLC3641 | CaSWI6A-70F M13R | CATACTTATTTCATTGAAAGGAAGCTGAACG TTATCATTATAAACGCTGGCTCAAGTTTATTAAC AAACTGGAAACAGCTATGACCATG |
| oLC3642 | CaSWI6A+2191R M13F | GAATAAACATACAAAGAATAGGAATCGTTTTTTTTTT TGTTTTTTTTTTGTTTGAGTTGGTGATATTGAGTAAAACG ACGGCCAG |
| oLC3645 | CaSWI6-449F | CAGAAATGTGTACATGCTAG |
| oLC3654 | CaSWI6+2660R | GCATTGAGTATAACCAGTAG |
| oLC3793 | CaGLC7AB-320-F pLC605 | AGTGAGTGAGAAAATTTTCTAATTAAACAAGAACAA AAAGGAAGGAAAAAAAAAAACACATCATTTTTTTGG |

| | | AAACAGCTATGACCATG |
|---|---|---|
| oLC3794 | CaGLC7AB-448-F | GGATGGAAAAAAAGAGGAAG |
| oLC4260 | CaGLC7AB+392F | CAGTATCAACCGTATCTATG |
| oLC4261 | CaGLC7AB+700R | CATCAGGTCCAAAAGTAAAC |
| oLC4417 | yEmRFP+571R | AGCACCTGGTAATTGAACTGG |
| oLC4748 | CaDAD2+314-F-linker-GFP | AAGAAGAAGCAGATGAAGAAGAAGGTGTTAGAGATAGTG AAGAAGTTGAAGAATCCACGGAAGGTGGTGGTTCTAAA GGTGAAGAATTAT |
| oLC4749 | HIS-CaDAD2-R | GCCAGAATTTAGAGTTATTATATGTACACATTTTTTTTAA TATA AACATGTAGCAATATACTTTAGAATTCCGGAATATTTAT GAGAAAC |
| oLC4751 | CaDAD2+49-F | GCAAACTTGGAACGATTTAG |
| oLC4750 | CaDAD2+525-R | CAACGAGTCATTGTTAAGTC |
| oLC4752 | CaHHF1-pLC447-F | TTCATTGGATGTTGTTTACGCTTTGAAGAGACAAGGTAG AACCTTGTATGGTTTCGGTGGTGGTGGTGGTGTTTCAA AAGGTGAAGAAGA |
| oLC4753 | CaHHF1-GFP/NAT-R | ACTTCTTAAATTAATACTATACAATAAAGAAAACGAACT AAAAAGACAATTAGAAATACAACCCAGTGTAAAACGAC GGCCAGTGAATTC |
| oLC4754 | CaHHF1+28-F | GGTAAAGGTTTAGGAAAAGG |
| oLC4755 | CaHHF1+486-R | CATTTTACTAGGCAACTGAC |
| oLC5247 | CaWSC1+443-F | CAATAACTGGATCTCCTAAC |
| oLC5248 | CaWSC1+672-R | CTTTTCTGATTTCCCATCAG |
| oLC5259 | CaWSC2+589-F | CCATCTACATCTACATCTTC |
| oLC5260 | CaWSC2+839-R | GGATGTTGTTCCATTTCTTG |
| oLC5277 | CaMCM2+964-F | CATCAAGAAGTTCACGTTAG |
| oLC5278 | CaMCM2+1168-R | CAGTATTCGAATCTTGAACG |
| oLC5279 | CaMCM3+1124-F | CCAAATCTCAAGTATTACGG |
| oLC5280 | CaMCM3+1357-R | GTTCCATAACTTCGTGAATG |

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