

Figure S1 Schematic strategy for the construction of promoter replacement and GFP tagging strains. The promoter replacement strains were constructed in haploid H99 strain background and the 3xGFP tagging strain was constructed in the diploid AI187 strain background. (A, C, E, H, K, N and P) Schematic strategy for the construction of promoter replacement strains. (B, D, F, I, L, O and Q) The correct genotypes of the strains were confirmed by Southern blot analysis. (G, J and M) Northern blot analysis for measuring *TOR1*, *TLK1* and *HSF1* expression in $P_{H3}::TOR1$, $P_{H3}::TLK1$ and $P_{H3}::HSF1$ strains. Ethidium bromide staining result of rRNA is used for loading control.

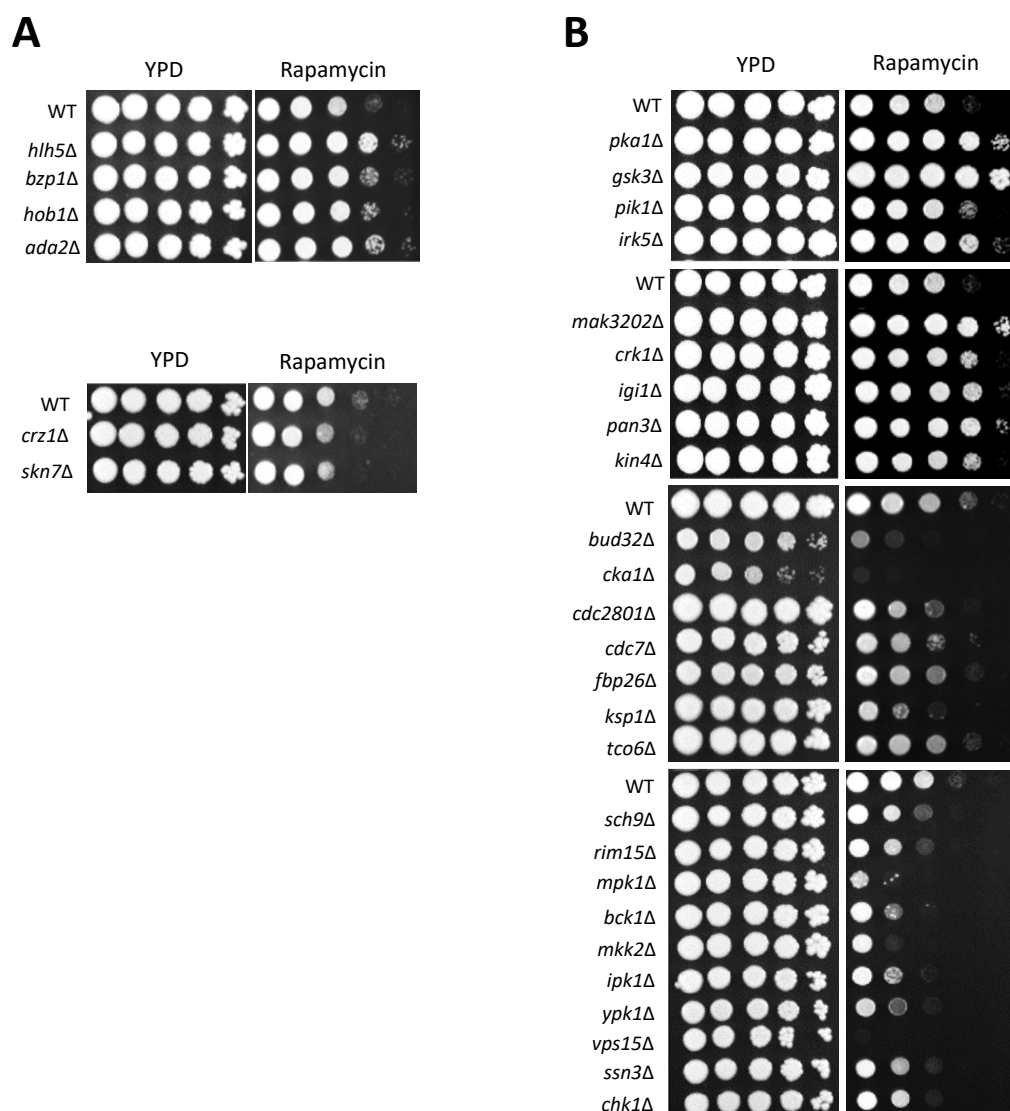


Figure S2 Screening of transcription factor and kinase mutants showing altered rapamycin-susceptibility. (A to B) *C. neoformans* strains were grown overnight at 30°C in liquid YPD medium. The 10-fold serially diluted cells (1 to 10⁴ dilutions) were spotted on YPD plates containing the rapamycin (10 ng/ml) and the plates were incubated at 30°C and photographed daily for 5 days. [Strains: WT H99, *hlh5Δ* (YSB2609), *bzp1Δ* (YSB723), *hob1Δ* (YSB2308), *ada2Δ* (YSB2381), *crz1Δ* (YSB1263), *skn7Δ* (YSB349), *pka1Δ* (YSB188), *gsk3Δ* (YSB2038), *pik1Δ* (YSB1493), *irk5Δ* (YSB2952), *mak3202Δ* (YSB3240), *crk1Δ* (YSB1709), *igi1Δ* (YSB1514), *pan3Δ* (YSB2809), *kin4Δ* (YSB2955), *bud32Δ* (YSB1968), *cka1Δ* (YSB3051), *cdc2801Δ* (YSB2370), *cdc7Δ* (YS2199), *fbp26Δ* (YSB4341), *ksp1Δ* (YSB1808), *tco6Δ* (YSB2469), *sch9Δ* (YSB619), *rim15Δ* (YSB1216), *mpk1Δ* (YSB3814), *bck1Δ* (YSB273), *mkk2Δ* (YSB330), *ipk1Δ* (YSB2157), *ypk1Δ* (YSB1885), *vps15Δ* (YSB1500), *ssn3Δ* (YSB3038), *chk1Δ* (YSB1825)]. This spot assay was repeated more than three times and one representative image was shown here.

Table S1. Strains used in this study

Strain	Genotype	Parent	Reference
<i>C. neoformans</i>			
H99	<i>MAT</i> α (Serotype A)		(PERFECT <i>et al.</i> 1993)
AI187	Diploid <i>ade2/ADE2 ura5/URA5 MAT</i> α / <i>MAT</i> α		(IDNURM 2010)
YSB3450	Diploid <i>ade2/ADE2 ura5/URA5 MAT</i> α / <i>MAT</i> α <i>TOR1/tor1</i> Δ	AI187	This study
YSB3176	<i>MAT</i> α <i>P</i> _{CTR4} : <i>TOR1::NAT</i>	H99	This study
YSB3178	<i>MAT</i> α <i>P</i> _{CTR4} : <i>TOR1::NAT</i>	H99	This study
YSB3180	<i>MAT</i> α <i>P</i> _{CTR4} : <i>TOR1::NAT</i>	H99	This study
YSB3043	<i>MAT</i> α <i>P</i> _{CTR4} : <i>TLK1::NAT</i>	H99	This study
YSB3044	<i>MAT</i> α <i>P</i> _{CTR4} : <i>TLK1::NAT</i>	H99	This study
YSB3045	<i>MAT</i> α <i>P</i> _{CTR4} : <i>TLK1::NAT</i>	H99	This study
YSB3144	<i>MAT</i> α <i>P</i> _{H3} : <i>TOR1::NEO</i>	H99	This study
YSB3147	<i>MAT</i> α <i>P</i> _{H3} : <i>TOR1::NEO</i>	H99	This study
YSB3115	<i>MAT</i> α <i>P</i> _{H3} : <i>TLK1::NEO</i>	H99	This study
YSB3118	<i>MAT</i> α <i>P</i> _{H3} : <i>TLK1::NEO</i>	H99	This study
YSB3153	<i>MAT</i> α <i>tlk1</i> Δ :: <i>NAT</i> STM#116	H99	This study
YSB3188	<i>MAT</i> α <i>tlk1</i> Δ :: <i>NAT</i> STM#116	H99	This study
YSB619	<i>MAT</i> α <i>sch9</i> Δ :: <i>NAT</i> -STM#169	H99	(LEE <i>et al.</i> 2016)
YSB620	<i>MAT</i> α <i>sch9</i> Δ :: <i>NAT</i> -STM#169	H99	(LEE <i>et al.</i> 2016)
YSB2200	<i>MAT</i> α <i>P</i> _{H3} : <i>HSF1::NEO</i>	H99	(YANG <i>et al.</i> 2017)
YSB3394	<i>MAT</i> α <i>P</i> _{H3} : <i>TOR1::NEO sch9</i> Δ	YSB3144	This study
YSB3342	<i>MAT</i> α <i>P</i> _{H3} : <i>TOR1::NEO P</i> _{H3} : <i>HSF1::NAT</i>	YSB3144	This study
YSB3785	<i>MAT</i> α CNAG_05216 Δ :: <i>NAT</i> -STM#184	H99	This study
YSB4869	<i>TOR1/TOR1-loxP-NEO'-loxP-3xGFP</i>	YSB4868	This study
YSB4870	<i>TOR1/TOR1-3xGFP</i>	YSB4868	This study
YSB64	<i>MAT</i> α <i>hog1</i> Δ :: <i>NAT</i> -STM#177	H99	(BAHN <i>et al.</i> 2005)
YSB676	<i>MAT</i> α <i>atf1</i> Δ :: <i>NAT</i> -STM #220 (CNAG_04090)	H99	(LEE <i>et al.</i> 2016)
YSB678	<i>MAT</i> α <i>atf1</i> Δ :: <i>NAT</i> -STM #220 (CNAG_04090)	H99	(LEE <i>et al.</i> 2016)
YSB2609	<i>MAT</i> α CNAG_02516 Δ :: <i>NAT</i> STM#210	H99	(LEE <i>et al.</i> 2016)
YSB3059	<i>MAT</i> α CNAG_02516 Δ :: <i>NAT</i> STM#210	H99	(LEE <i>et al.</i> 2016)
YSB1263	<i>MAT</i> α <i>crz1</i> Δ :: <i>NAT</i> -STM#231 (CNAG_00156)	H99	(LEE <i>et al.</i> 2016)
YSB1264	<i>MAT</i> α <i>crz1</i> Δ :: <i>NAT</i> -STM#231 (CNAG_00156)	H99	(LEE <i>et al.</i> 2016)
YSB349	<i>MAT</i> α <i>skn7</i> Δ :: <i>NAT</i> -STM#201	H99	(LEE <i>et al.</i> 2016)
YSB350	<i>MAT</i> α <i>skn7</i> Δ :: <i>NAT</i> -STM#201	H99	(LEE <i>et al.</i> 2016)
YSB723	<i>MAT</i> α <i>Cnhac1</i> (CNAG_06134):: <i>NAT</i> -STM #295	H99	(LEE <i>et al.</i> 2016)
YSB724	<i>MAT</i> α <i>Cnhac1</i> (CNAG_06134):: <i>NAT</i> -STM#295	H99	(LEE <i>et al.</i> 2016)
YSB2308	<i>MAT</i> α CNAG_01431 Δ :: <i>NAT</i> -STM#213	H99	(LEE <i>et al.</i> 2016)
YSB2309	<i>MAT</i> α CNAG_01431 Δ :: <i>NAT</i> -STM#213	H99	(LEE <i>et al.</i> 2016)
YSB2381	<i>MAT</i> α CNAG_01626 Δ :: <i>NAT</i> -STM#232	H99	(LEE <i>et al.</i> 2016)
YSB2382	<i>MAT</i> α CNAG_01626 Δ :: <i>NAT</i> -STM#232	H99	(LEE <i>et al.</i> 2016)
YSB1968	<i>MAT</i> α CNAG_02712 Δ :: <i>NAT</i> -STM#296	H99	(LEE <i>et al.</i> 2016)
YSB1969	<i>MAT</i> α CNAG_02712 Δ :: <i>NAT</i> -STM#296	H99	(LEE <i>et al.</i> 2016)
YSB1216	<i>MAT</i> α CNAG_03024 Δ :: <i>NAT</i> -STM #191	H99	(LEE <i>et al.</i> 2016)
YSB1217	<i>MAT</i> α CNAG_03024 Δ :: <i>NAT</i> -STM #191	H99	(LEE <i>et al.</i> 2016)
YSB1709	<i>MAT</i> α CNAG_06193 Δ :: <i>NAT</i> STM#43	H99	(LEE <i>et al.</i> 2016)
YSB1710	<i>MAT</i> α CNAG_06193 Δ :: <i>NAT</i> STM#43	H99	(LEE <i>et al.</i> 2016)
YSB2809	<i>MAT</i> α CNAG_04821:: <i>NAT</i> STM#204	H99	(LEE <i>et al.</i> 2016)
YSB2810	<i>MAT</i> α CNAG_04821:: <i>NAT</i> STM#204	H99	(LEE <i>et al.</i> 2016)
YSB2952	<i>MAT</i> α CNAG_03811:: <i>NAT</i> STM#213	H99	(LEE <i>et al.</i> 2016)

YSB2953	<i>MATα</i> CNAG_03811::NAT STM#213	H99	(LEE <i>et al.</i> 2016)
YSB3038	<i>MATα</i> CNAG_06086::NAT STM#219	H99	(LEE <i>et al.</i> 2016)
YSB3039	<i>MATα</i> CNAG_06086::NAT STM#219	H99	(LEE <i>et al.</i> 2016)
YSB3240	<i>MATα</i> CNAG_06033::NAT STM#169	H99	(LEE <i>et al.</i> 2016)
YSB3241	<i>MATα</i> CNAG_06033::NAT STM#169	H99	(LEE <i>et al.</i> 2016)
YSB2157	<i>MATα</i> CNAG_01294Δ::NAT STM#184	H99	(LEE <i>et al.</i> 2016)
YSB2158	<i>MATα</i> CNAG_01294Δ::NAT STM#184	H99	(LEE <i>et al.</i> 2016)
YSB278	<i>MATα tco1::NAT</i> STM#102	H99	(BAHN <i>et al.</i> 2006)
YSB279	<i>MATα tco1::NAT</i> STM#102	H99	(BAHN <i>et al.</i> 2006)
YSB3051	<i>MATα</i> CNAG_05694Δ::NAT STM#6	H99	(LEE <i>et al.</i> 2016)
YSB3053	<i>MATα</i> CNAG_05694Δ::NAT STM#6	H99	(LEE <i>et al.</i> 2016)
YSB1885	<i>MATα</i> CNAG_02389Δ::NAT STM#242	H99	(LEE <i>et al.</i> 2016)
YSB1886	<i>MATα</i> CNAG_02389Δ::NAT STM#242	H99	(LEE <i>et al.</i> 2016)
YSB1808	<i>MATα</i> CNAG_01905Δ::NAT STM#159	H99	(LEE <i>et al.</i> 2016)
YSB1809	<i>MATα</i> CNAG_01905Δ::NAT STM#159	H99	(LEE <i>et al.</i> 2016)
YSB1825	<i>MATα</i> CNAG_03167Δ::NAT STM#205	H99	(LEE <i>et al.</i> 2016)
YSB1828	<i>MATα</i> CNAG_03167Δ::NAT STM#205	H99	(LEE <i>et al.</i> 2016)
YSB1514	<i>MATα</i> CNAG_05600Δ::NAT STM#230	H99	(LEE <i>et al.</i> 2016)
YSB1515	<i>MATα</i> CNAG_05600Δ::NAT STM#230	H99	(LEE <i>et al.</i> 2016)
YSB1500	<i>MATα</i> CNAG_02680::NAT-STM #123	H99	(LEE <i>et al.</i> 2016)
YSB1501	<i>MATα</i> CNAG_02680::NAT-STM #123	H99	(LEE <i>et al.</i> 2016)
YSB3814	<i>MATα</i> CNAG_04514::NAT#240	H99	(LEE <i>et al.</i> 2016)
YSB3816	<i>MATα</i> CNAG_04514::NAT#240	H99	(LEE <i>et al.</i> 2016)
YSB264	<i>MATα ssk2::NATSTM#210</i>	H99	(BAHN <i>et al.</i> 2006)
YSB265	<i>MATα ssk2::NATSTM#210</i>	H99	(BAHN <i>et al.</i> 2006)
YSB330	<i>MATα mkk1::NATSTM#224</i>	H99	(LEE <i>et al.</i> 2016)
YSB331	<i>MATα mkk1::NATSTM#224</i>	H99	(LEE <i>et al.</i> 2016)
YSB273	<i>MATα mkh1(bck1)::NATSTM#43</i>	H99	(LEE <i>et al.</i> 2016)
YSB274	<i>MATα mkh1(bck1)::NATSTM#43</i>	H99	(LEE <i>et al.</i> 2016)
YSB188	<i>MATα pka1::NATSTM#191</i>	H99	(BAHN <i>et al.</i> 2004)
YSB189	<i>MATα pka1::NATSTM#191</i>	H99	(BAHN <i>et al.</i> 2004)
YSB2038	<i>MATα</i> CNAG_06730Δ::NAT STM#123	H99	(LEE <i>et al.</i> 2016)
YSB2039	<i>MATα</i> CNAG_06730Δ::NAT STM#123	H99	(LEE <i>et al.</i> 2016)
YSB2469	<i>MATα</i> CNAG_00363Δ::NAT STM#58 (TCO6)	H99	(LEE <i>et al.</i> 2016)
YSB2554	<i>MATα</i> CNAG_00363Δ::NAT STM#58 (TCO6)	H99	(LEE <i>et al.</i> 2016)
YSB2370	<i>MATα</i> CNAG_00415Δ::NAT STM#191	H99	(LEE <i>et al.</i> 2016)
YSB3699	<i>MATα</i> CNAG_00415Δ::NAT STM#191	H99	(LEE <i>et al.</i> 2016)
YSB123	<i>MATα pbs2Δ::NATSTM#213</i>	H99	(LEE <i>et al.</i> 2016)
YSB124	<i>MATα pbs2Δ::NATSTM#213</i>	H99	(LEE <i>et al.</i> 2016)
YSB1493	<i>MATα</i> CNAG_07744Δ::NAT STM#227	H99	(LEE <i>et al.</i> 2016)
YSB1494	<i>MATα</i> CNAG_07744Δ::NAT STM#227	H99	(LEE <i>et al.</i> 2016)
YSB261	<i>MATα ssk1Δ::NATSTM#205</i>	H99	(BAHN <i>et al.</i> 2006)

Table S2. Primers used in this study

Primer name	Sequence	Comments
B79	TGTGGATGCTGGCGGAGGATA	Screening primer on <i>ACT1</i> promoter
B1026	GTAAACGACGGCCAGTGAGC	M13 forward (extended)
B1027	CAGGAAACAGCTATGACCATG	M13 reverse (extended)
B1454	AAGGTGTTCCCGACGACGAATCG	NSL2
B1455	AACTCCGTCGCGAGCCCCATCAAC	NSR2
B1886	TGGAAGAGATGGATGTGC	NSL-NEO
B1887	ATTGTCTGTTGTGCCAG	NSL-NEO
B354	GCATGCAGGATTCGAGTG	<i>CTR4</i> promoter- left flanking primer 1
B355	GATTGGTGAAGTCGTTGTCCG	<i>CTR4</i> promoter- right flanking primer 2
B4017	GCATGCAGGATTCGAGTG	<i>H3</i> promoter- left flanking primer 1
B4018	GTGATAGATGTGTTGTGGTG	<i>H3</i> promoter- right flanking primer 2
B6081	TACACTGAAGTCGGAGCCTG	<i>TOR1</i> 5'-flanking region primer L1
B6084	CACTCGAATCCTGCATGCGGCGATGATTAGGGGGCCAT	<i>TOR1</i> 5'-flanking region primer L2 (<i>CTR4</i> promoter)
B6085	CGACAACGACTTCACCAATCATGTCTTCACAATCAGACGT	<i>TOR1</i> 3'-flanking region primer R1 (<i>CTR4</i> promoter)
B6092	GAAGGTAGTTTCGCAAAATGG	<i>TOR1</i> 3'-flanking region primer R2
B4090	ATCGCTTCTCGTTTGACC	<i>TLK1</i> 5'-flanking region primer L1 (<i>CTR4</i> promoter)
B6004	CACTCGAATCCTGCATGCTTCGGGGATATTGCTGGCCTC	<i>TLK1</i> 5'-flanking region primer L2 (<i>CTR4</i> promoter)
B6005	CGACAACGACTTCACCAATCATGACTGTCACTTCTAGAGTA	<i>TLK1</i> 3'-flanking region primer R1 (<i>CTR4</i> promoter)
B6006	GACGCATACTGTTTATTGTG	<i>TLK1</i> 3'-flanking region primer R2 (<i>CTR4</i> promoter)
B6003	TCGCAAGAGGATGTGAATC	<i>TLK1</i> promoter replacement screening primer
B6082	CACTCGAATCCTGCATGCGGCGATGATTAGGGGGCCA	<i>TOR1</i> 5'-flanking region primer L2 (<i>CTR4</i> promoter)
B6083	ACCACAACACATCTATCACATGTCTTCACAATCAGACGT	<i>TOR1</i> 3'-flanking region primer R1 (<i>CTR4</i> promoter)
B6120	AACGAGGGATTTGGCTTC	<i>TOR1</i> promoter replacement screening primer
B6079	CACTCGAATCCTGCATGCCTGGGACATATCATGAGTTGT	<i>TOR1</i> 5'-flanking region primer L2 (<i>H3</i> promoter)
B6080	ACCACAACACATCTATCACATGGTCGTTGATGAAACGAT	<i>TOR1</i> 3'-flanking region primer R1 (<i>H3</i> promoter)
B4088	CTTTGAAACCGACCATAGG	<i>TLK1</i> Diagnostic screening primer SO
B4089	GGACCGAGACACTACTACAAC	<i>TLK1</i> Southern blot probe primer PO
B4090	ATCGCTTCTCGTTTGACC	<i>TLK1</i> 5'-flanking region primer L1
B4091	TCACTGGCCGTCGTTTTACATCAACGACCATCTGGGAC	<i>TLK1</i> 5'-flanking region primer L2
B4092	CATGGTCATAGCTGTTTCTGTGGCTACTGCTGTGTATTGC	<i>TLK1</i> 3'-flanking region primer R1
B4093	GCGGTAAAGGTGGAAAGTC	<i>TLK1</i> 3'-flanking region primer R2
B6182	CACGAAAGATACAACGCC	<i>TLK1</i> Northern blot probe primer NP1
B6183	TGTTTTCCAGGTGGCAAG	<i>TLK1</i> Northern blot probe primer NP2
B6184	CCTTCCTCAGGTATGTGAATC	<i>TOR1</i> Northern blot probe primer NP1
B6185	AGCAAATGGGAACAGTCC	<i>TOR1</i> Northern blot probe primer NP2
B6937	ATCGATGGTGGCGGTGGCTCTGTG	1 ST <i>GFP</i> F
B6938	AGATCTCTGTACAGCTCGTCCAT	1 ST <i>GFP</i> R
B6939	AGATCTGTGAGCAAGGGCGAGGAG	2 ND <i>GFP</i> F
B6940	CTGCAGCTGTACAGCTCGTCCAT	2 ND <i>GFP</i> R
B6941	CTGCAGGTGAGCAAGGGCGAGGAG	3 RD <i>GFP</i> F
B6942	CTCGAGAGAGCCACCGCCACCTTGACAGCTCGTCCAT	3 RD <i>GFP</i> R
B6943	CTCGAGGAGTCTATCTGGGTTCTC	<i>TOR1</i> E5-2 F
B6944	TCTAGATCGTCTGCTGACAGATTG	<i>TOR1</i> E5-2 R
B6945	ACTAGTTCGACAACCTTAATAT	<i>loxP</i> NAT F
B6946	ATCGATACTACCTAATAACTTCGTA	<i>loxP</i> NAT R
B6947	GAGCTCACAGCCACAGCCACTTCC	<i>TOR1</i> E5-1 F
B6948	ACTAGTTGTCGAGCTGGCTTTGAG	<i>TOR1</i> E5-1 R
B6407	TCATAGAGGCGTAGAACCTTC	<i>TOR1</i> seq1

B6493	ATGGCGATGATTTAGGGG	<i>TOR1</i> seq2
B6506	AACAATACCATCCTTCCCAC	<i>TOR1</i> seq3
B6507	GAAAGACCTGTGCCATAC	<i>TOR1</i> seq4
B6759	GGGTATTCTTGGGTGTAAGC	<i>TOR1</i> seq5
B8577	GCTCTTATCTACCTGCCTTG	<i>TOR1-3xGFP</i> Probe primer1
B8578	CGCAAGGAGACGAAGAGC	<i>TOR1 3xGFP</i> Probe primer2
B7761	AGCTGCATATCCGCAACT	<i>TOR1</i> qRT1
B7762	CTCAACGAGGGAGATGATGG	<i>TOR1</i> qRT2
B7048	GCG GCC GCA CAG ATT TAC CTA CTT CC	<i>SCH9</i> 5'-flanking region primer L1
B7049	GCG GCC GCG TCC ATA TCG ACG TCG CA	<i>SCH9</i> 5'-flanking region primer L2
B1504	CATGGTCATAGCTGTTTCTCTGAATGAGAATGCGGTGGAC	<i>SCH9</i> 3'-flanking region primer R1
B1505	GGATGGATGGATGCTCAT	<i>SCH9</i> 3'-flanking region primer R2
B1502	TTCTTCGTGCTGAGAGGAG	<i>SCH9</i> Diagnostic screening primer SO1
B1704	AACCGAAACCCTCAGAACC	<i>SCH9</i> Southern blot probe primer PO
B7755	TCATTTTTTTGTGCCGAATGC	<i>HSF1</i> qRT1
B7756	ACATGTTGAGTTGACGGACA	<i>HSF1</i> qRT2
B7757	TAAGAAGCACTCCGAGTTCA	<i>HSP90</i> qRT1
B7758	ACCCTCCTTGACCTCCTCT	<i>HSP90</i> qRT2
B7759	ACCTGATTATGGCCGGGAAA	<i>HSP104</i> qRT1
B7760	GTGGCACCAATGACCTTGAG	<i>HSP104</i> qRT2
B8341	GCATACACTCACTTGACTACTC	<i>ERG11</i> qRT1
B8342	GACCGGACTTGATAAACTTC	<i>ERG11</i> qRT2
B9564	TGGTGGTGAGGGAAAATG	<i>RAD51</i> qRT1
B9565	GCACCTCTTCACCATCAAG	<i>RAD51</i> qRT2
B9566	GCAAAATCTTTCAGCGTGTG	<i>RAD54</i> qRT1
B9567	CACAAAGTTTCGGGGTTG	<i>RAD54</i> qRT2
B9568	AAAGCGATGAGGATGACC	<i>RDH54</i> qRT1
B9569	CTCGTCTTTTTTCAGCACG	<i>RDH54</i> qRT2
B9570	TAACACTCAGCGCCATCC	<i>RIG1</i> qRT1
B9571	CACATCGGCGTTCATCTCG	<i>RIG1</i> qRT2
B9572	ATTCGGGTGTAAAGCCTG	<i>RIG2</i> qRT1
B9573	AGAGGCTGGAATAGACGAGG	<i>RIG2</i> qRT2
B9574	ATATCAACCGCCGATCAGCAC	<i>BDR1</i> qRT1
B9575	TCCCTAATTCGTTGTTACGCAC	<i>BDR1</i> qRT2
ALID2261	gtaacgccagggttttcccagtcacgacgAATTCCACAGCCCGACATT	<i>TOR1</i> KO 5' Flanking region primer L1
ALID2262	GCTTATGTGAGTCTCCCGACTCTGTGAGCTGGCTTT	<i>TOR1</i> KO 5' Flanking region primer L1 (NAT)
ALID2263	CTCGTTTCTACATCTCTTCGCGAAGTTGTGAAGTGTC	<i>TOR1</i> KO 3' Flanking region primer R1 (NAT)
ALID2264	GcggataacaatttcacacaggaacagcAACAGGTCACAATGCAGCCT	<i>TOR1</i> KO 3' Flanking region primer R1
ALID2265	GCAATACCTCTATTACCTGC	<i>TOR1</i> KO diagnostic screening F
ALID2266	GGTTGCAAACGCAGATAGC	<i>TOR1</i> KO diagnostic screening R
ai006	GAAGAGATGTAGAAACGAG	pACT1 F
ai290	GGGAGGACTCACATAAGC	pTRP1 R
ai37	ATGGCGGCCGCCACTCTTGAC	NAT F
ai270	ACTTCTCGCAAAGTGAATCC	NAT R
ALID1229	gtaacgccagggttttcccagtcacgacg	F- Primer on pRS426 backbone for amplification of the constructs for targeted gene replacement R- Primer on pRS426 backbone for amplification of the constructs for targeted gene replacement
ALID1230	gcggataacaatttcacacaggaacagc	
ai144	GAAAAGGTTACGACAGAGG	PCR check MAT in serotype A strains
ai145	TGGGAAGAACTATCAGAGG	PCR check MAT in serotype A strains
ai151	CGCACCTTTTCTGTAGGG	PCR check MAT in serotype A strains
ai152	CAACAAATTCACGTACAGCC	PCR check MAT in serotype A strains
ALID0375	tgcaagagcggaagtgc	<i>URA5</i> F (Promoter)

ALID0376	gattgacagccaacaatc	<i>URA5</i> R (terminator)
ALID0380	ACTGGATCGACCTCATCG	<i>ADE2</i> F
ALID0381	CGATGACTGGCAAACCTGG	<i>ADE2</i> R
ALID2262	GCTTATGTGAGTCCTCCCGACTCTGTCGAGCTGGCTTT	<i>TOR1</i> KO 5' Flanking region primer L1 (<i>NAT</i>)
ALID2263	CTCGTTTCTACATCTCTTCGCGAAGTTGTGAAGTGTC	<i>TOR1</i> KO 3' Flanking region primer R1 (<i>NAT</i>)
ALID2264	GcggataacaatttcacacaggaacagcAACAGGTCACAATGCAGCCT	<i>TOR1</i> KO 3' Flanking region primer R1

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