Supplemental Information

for

Priyadarshini, Y. and Natarajan K. (2016).

Reconfiguration of Transcriptional Control of Lysine Biosynthesis in *Candida albicans* Involves a Central Role for the Gcn4 Transcriptional Activator.

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Supplementary Table S1. List of plasmids and strains

Plasmid	**Relevant Description**	**Source**
pGAL-HA	HA$_3$ tagging plasmid in pESC-LEU	Sawhney and Natarajan
pGH14-2	P$_{GAL1-}$Ca*LYS141-HA*$_3$, *LEU2*	This work
pGH142-1	P$_{GAL1-}$Ca*LYS142-HA*$_3$, *LEU2*	This work
pGH143-9	P$_{GAL1-}$Ca*LYS143-HA*$_3$, *LEU2*	This work
pGH144-1	P$_{GAL1-}$Ca*LYS144-HA*$_3$, *LEU2*	This work
pYPC24	CIp10-*LEU2*+Ca*GCN4*	This work
pHAH	HAH1 disruption cassette	(1)
***S. cerevisiae* strain**	**Relevant Genotype**	**Source**
BY4741	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0*	(2)
3973	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 lys14Δ::kanMX4*	Open Biosystems
PY1-a	[pGH14-2] in strain 3973	This work
PY9	[pGH142-1] in strain 3973	This work
PY13	[pGH143-9] in strain 3973	This work
PY17	[pGH144-1] in strain 3973	This work
249	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 gcn4Δ::kanMX4*	Open Biosystems
KNY164	*MATα leu2-3, 112 ura3-52 ino1 trp1::hisG*	(3)
KNY124	*MATα leu2-3, 112 ura3-52 ino1 trp1::hisG gcn4Δ-103*	(3)
***C. albicans* Strain**	**Relevant Genotype**	**Source**
SN152	*arg4Δ/arg4Δ leu2Δ/leu2Δ his1Δ/his1Δ URA3/ura3Δ::imm*^{434} *IRO1/iro1Δ::imm*^{434}	(4)
RPC206	*his1Δ/his1Δ::<pFA-HIS1> RPS1/rps1::<CIp10-C.d.ARG4>*derived from SN152	(5)
PC2	*LYS141/lys141Δ::C.d. ARG4* derived from SN152	This work
PC6	*LYS142/lys142Δ::C.d. ARG4* derived from SN152	This work
PC9	*LYS143/lys143Δ::C.d. ARG4* derived from SN152	This work
PC12	*LYS144/lys144Δ::C.d. ARG4* derived from SN152	This work
PC20	*lys141Δ::C.d.HIS1/lys141Δ::C.d.ARG4* derived from PC2	This work
PC27	*lys142Δ::C.d.HIS1/lys142Δ::C.d.ARG4* derived from PC6	This work
PC31	*lys143Δ::C.d. HIS1/lys143Δ::C.d. ARG4* derived from PC9	This work
PC37	*lys144Δ::C.d. HIS1/lys144Δ::C.d.ARG4* derived from PC12	This work
PC43	*lys2Δ::C.d. HIS1/lys2Δ::C.d.ARG4* derived from SN152	This work

PC205	*LYS141::TAP-C.m.LEU2/lys141Δ::C.d.ARG4* derived from PC2	This work
PC206	*LYS142::TAP-C.m.LEU2/lys142Δ::C.d.ARG4* derived from PC6	This work
PC209	*LYS143::TAP-C.m.LEU2/lys143Δ::C.d.ARG4* derived from PC9	This work
PC212	*LYS144::TAP-C.m.LEU2/lys144Δ::C.d.ARG4* derived from PC12	This work
PC222	*GCN4::TAP-CmLEU2/ GCN4* derived from SN152	This work
PC227	*GCN4::TAP-C.m.LEU2/ GCN4::TAP-C.d.HIS1* derived from PC222	This work
PC234	*gcn4Δ::C.d.ARG4/gcn4Δ::C.d.HIS1* derived from SN152 * the strain requires Arg for growth, likely due to the *gcn4* mutation	This work
PC291	*CaGCN4* (pYPC24) integrated in PC234	This work

Supplementary Table S2. List of oligonucleotides

Oligo Name	**Sequence (5'-3')**	**Notes**
ON364	5'- CGAATCAAATTAACAACCATAGGA -3'	*ScGAL1* promoter
ONC47	5'- ccggaattCTATTGCTACCACAGTCA -3'	5' cloning primer for *CaGCN4*
ONC110	5'- cggtggcacatttcacac-3'	3' Primer for sequencing *HIS1*-TAP
ONC164	5’ CCGctcgagGCACTGAGCAGCGTAATC-3’	Rev Primer for HA tagging
ONC305	5'-TAC CAA GGA ACA CCA ATA TCT AGT CAC T-3'	Forward Primer for Chr1
ONC306	5'-GAT CAC TTT TGT CCT TGG CAG TC-3'	Reverse Primer for Chr1
ONC350	5'-cgggaATGTCACAATCACCATCT-3’	5' cloning primer for *CaLYS141*
ONC351	5'-tttgtcgacGTATATCAATGTATCATCATTT-3'	3' cloning primer for *CaLYS141*
ONC352	5'-cgggaATGTCTACTTCCAAGAGA-3	5' cloning primer for *CaLYS142*
ONC353	5'-TTTgtcgacGTAGGCAACATTATCGAT	3' cloning primer for *CaLYS142*
ONC354	5'-cgggaATGGCGTCAAATATTTCA-3'	5' cloning primer for *CaLYS143*
ONC355	5'-TTTgtcgacGTATGATAACAAATCCTCG-3'	3' cloning primer for *CaLYS143*
ONC356	5'-cgggaATGGGTTCATCTAGCCCAAACC-3'	5' cloning primer for *CaLYS144*
ONC357	5'-TTTgtcgacTGAAAATGGTATAATTTCCGAATCAAA-3'	3' cloning primer for *CaLYS144*
ONC362	5'-GGTGCTGATTTGAATGTTTTAAC-3'	Forward Internal primer for *LYS14*
ONC363	5'-GACCAACAACTTTAATACTGAAAC-3'	Forward Internal primer for *LYS142*

ONC364	5'-TTGTTGTGGGCACGGAAT-3'	Reverse Internal primer for *LYS142*
ONC365	5'-CCATCAATATCATCTAACTCATCG-3'	Forward Internal primer for *LYS143*
ONC366	5'-TCGATCCCTAATTTGTTGAATG-3'	Forward Internal primer for *LYS143*
ONC367	5'-AGGATATTACTTGAGACTTGTTG-3'	Reverse Internal primer for *LYS143*
ONC368	5'-AATGATCAAGCTTTGCCTAAT-3'	Forward Internal primer for *LYS144*
ONC369	5'-ACCATCTACAACATTATCACCG-3'	Forward Internal primer for *LYS144*
ONC370	5'-TTGTTCACTCCAATCGTACC-3'	Reverse Internal primer for *LYS144*
ONC378	5'-ATCAACCAACTATCATCCCAACCACTACAACTATTCATAAA C CAA GTACTGACTTCGTCCTTCGTACGCTGCAGGTC-3'	5' Primer with 60bp homology to *LYS14*
ONC379	5'-ACTAAAACAGTACGTACAGACTTTTAAATGTTTTCCTAATTG TAGACA ACCAAATATTTTCTGATATCATCGATGAATTCGAG-3'	3' Primer with 60bp homology to *LYS14*
ONC380	5'- GCTTTGTTTTGTTTGTTGTTCCT -3'	5' upcheck Primer for *LYS141*
ONC381	5'- TCCCTGTCGCCAGAGAAC -3'	3' downcheck Primer for *LYS141*
ONC382	5'-AAGCGGAGTTGATTTCCCTGTAGTTGTCAAATTCATATTCAC CAGCACCAAGATATCATCCTTCGTACGCTGCAGGTC-3'	5' Primer with 60bp homology *LYS142*
ONC383	5'-GATGGTAGTGTTATTTCAAATGATCCATCTTTGTCAACTTAC AAAGAATAAATACCCCTACTGATATCATCGATGAATTCGAG-3'	3' Primer with 60 bp homology to *LYS142*
ONC384	5'- GTTGGTCTTTCGAATATTTGGG -3'	5' upcheck Primer for *LYS142*
ONC385	5'- ATGAGGTAAGAAATGAAGAGCC -3'	3' downcheck Primer for *LYS142*

ONC386	5'-CCTGAATCCAGAAAGAGGCCCATACTATTATCATATCCCCATATCTTTATTAGTTTATCTCTTCGTACGCTGCAGGTC-3'	5'Primer with 60 bp homology to *LYS143*
ONC387	5'-TATTTAATAATACAAAATTCTAATTTTATTTTAAAAGCTATAAACATATACATCT GTAGTCTGATATCATCGATGAATTCGAG-3'	3' Primer with 60 bp homology to *LYS143*
ONC388	5'- AACTAAACAAGCGAAAAAAAAAGAG -3'	5' upcheck Primer for *LYS143*
ONC389	5'- TCATTTGGTAGAGCAAGTTATG -3'	3' downcheck Primer for *LYS143*
ONC390	5'-AGGCATCATTATTCCTTTCCATAACTCAAAACCAATTACAGTAATTGAAGATAA GATCAACTTCGTACGCTGCAGGTC-3'	5'Primer with 60 bp homology to *LYS144*
ONC391	5'-ACAAAATCTATAAAACCGTGACACACAAAACTAAACTTACACTTACAAGCAATATCTATTCTGATATCATCGATGAATTCGAG-3'	3' Primer with 60bp homology to *LYS144*
ONC392	5'- AAAATCCCCAATGACCGC-3'	5' upcheck Primer for *LYS144*
ONC393	5'- CATATGTGTGTTTGACAGTTTTC -3'	3' downcheck Primer for *LYS144*
ONC394	5'-ATTTTATTTCATTTTCTTTATTTGAAATAACTTTAACGACCTTCAATTAATTCCACAACACTTCGTACGCTGCAGGTC-3'	5'Primer with 60bp homology to *LYS2*
ONC395	5'-TATATACTACAACTAAGACATAAGTTCTCCTTTCCTGGTATTTTAACTTTGAAGTATTACCTGATATCATCGATGAATTCGAG-3'	3'Primer with 60bp homology to *LYS2*
ONC396	5'- CTTGTACTGTTTTGCACGAC-3'	5' upcheck Primer for *LYS2*
ONC397	5'- ACACATTGTAACATGGTAATAGC -3'	3' downcheck Primer for *LYS2*
ONC460	5'-TTTACAAACCGATGCCGAAAT-3'	5' qRT-PCR Primer for *LYS141*
ONC461	5'-TCTCTCAACACTTCAATCTCAAATTCA-3'	3' Real time Primer for *LYS141*
ONC462	5'-TGTCTATTACCAGGACCAATTTCCA-3'	5' qRT-PCR Primer for *LYS142*
ONC463	5'-TGTGGGCACGGAATCGA-3'	3' qRT-PCR Primer for *LYS142*

ONC464	5'-GCAAGCAACGGTACTGCTGAT-3'	5' qRT-PCR Primer for *LYS143*
ONC465	5'-AACGACATCCTTCTTGTGTTGAATT-3'	3' qRT-PCR Primer for *LYS143*
ONC466	5'-AACGTGGTTTTTTGCAATTGAA-3'	5' qRT-PCR Primer for *LYS144*
ONC467	5'-AATGGTTCCGCCCAAAGG-3'	3' qRT-PCR Primer for *LYS144*
ONC468	5'-TCCGAAGCTGACGATTTACAAG-3'	5' qRT-PCR Primer for *LYS2*
ONC469	5'-TGGATTGTCCATATCCGTTTCC-3'	3' qRT-PCR Primer for *LYS2*
ONC540	5'-TGGGTTATTGAAAGATGGAGAAGTT-3'	5' qRT-PCR Primer of *LYS4*
ONC541	5'-CAATGCATCTTTTGAACCCATTC-3'	3' qRT-PCR Primer of *LYS4*
ONC548	5'-CTGGCGGTAAAATCGTATCATTC-3'	5' qRT-PCR Primer of *LYS9*
ONC549	5'-AATAAAACCCCTCTTGAACTCCAA-3'	3' qRT-PCR Primer *LYS9*
0NC561	5’-AGTATTATGATCTTCATATTAAGCATGAAAATGGTGAAATT GACGGAATTCATATCGATAATGTTGCCTACGGATCCATGGAAAAGAGA-3'	5' Primer for c-term TAP tagging Primers for *CaLYS142*
0NC562	5'-ATATATCCAGATGGTAGTGTTATTTCAAATGATCCATCTTTG TCAACTTACAAAGAATAAATACCCCTAGTGTGATGGATATCTGCA3'	3' Primer for C-term TAP tagging Primers for *CaLYS142*
0NC563	5'-TGGAATAAAAGAGATAATATCGAAGAAAGCGATAACGAT GACAACGAGAACGAGGATTTGTTATCATACGGATCCATGGAAAAGAGA-3'	5' Primer for c-term TAP tagging Primers for *CaLYS143*
0NC564	5'-TTTTAAGAATATTTAATAATACAAAATTCTAATTTTATTTTA AAAGCTATAAACATATACATCTGTAGTGTGTGATGGATATCTGCA	3' Primer for c-term TAP tagging Primers for *CaLYS143*
0NC565	5'-TCTATACAAATCTTACTAAAACATTGGAAAGGGACAATTGA TATTGAAAATGATGATACATTGATATACGGATCCATGGAAAAGAGA-3"	5' Primer for c-term TAP tagging Primers for *CaLYS14*
0NC566	5'-AAATAAAGAACTAAAACAGTACGTACAGACTTTTAAATGTT TTCCTAATTGTAGACAACCAAATATTTTGTGTGATGGATATCTGCA-3'	3' Primer for c-term TAP tagging Primers for *CaLYS14*
0NC567	5'-TTCATTGACGGTAAAGATGTAGATGATGACGTTGATTTAGC ATTTGATTCGGAAATTATACCATTTTCAGGATCCATGGAAAAGAGA-3'	5' Primer for c-term TAP tagging Primers for *CaLYS144*

0NC568	5'-AATAACAAAACAAAATCTATAAAACCGTGACACACAAAAC TAAACTTACACTTACAAGCAATATCTATTGTGTGATGGATATCTGCA-3'	3' Primer for c-term TAP tagging Primers for *CaLYS144*
ONC620	5'-GCGTTTCGTGGAGTCATTGAA	5' ChIP Primer for *LYS2*
ONC621	5'-GCACGACTTCCAATTATCAAGGA	3' ChIP Primer for *LYS2*
ONC622	5'-CTACCAAGTGACTCATTAGAGGCG	5' ChIP Primer for *LYS2*
ONC623	5'-TGTGACTAATCAAAGAAAGCGGC	3' ChIP Primer for *LYS2*
ONC624	5'-TCACTTGTTCTACTCTTTCTTCTCTTTTTC	5' ChIP Primer for *LYS9*
ONC625	5'-ACCCCTTCCACCAACTCTCTC	3' ChIP Primer for *LYS9*
ONC626	5'-GGGAAGTGATAAGATTGCCGC	5' ChIP Primer for *LYS9*
ONC627	5'-CGTGTATTTATGGTAGATAATGAGTTGACTC	3' ChIP Primer for *LYS9*
ONC628	5'-GCCGCATATGCTATTCACATTG	5' ChIP Primer for *LYS9*
ONC629	5'-CAATAAGCTCTAATTCAATGATGACATG	3' ChIP Primer for *LYS9*
ONC634	5’-GAAAAGCAAGCTTTACAAGATCAAGTTGAAAGATTACAAG AATTGTTAAGAGTTAATGGTATTCAATTTGGATCCATGGAAAAGAGA-3'	5' Primer for TAP-tagging of *GCN4*
ONC635	5'-AACAATAATAATTTTCTAAATTTTTCTTTTTTTAAAAAAATA ACGAGAGGTATATATAGTAGTAACTTTGTGTGATGGATATCTGCA	3' Primer for TAP-tagging of *GCN4*
ONC657	5'- TTATTATATTTACTGTTGCTATTTAAATTAAATTACATTA CATTAATTAGCTTTGTTACCCTTCGTACGCTGCAGGTC -3'	5' Primer with 60bp homology to *GCN4*
ONC658	5’-TAACGAGAGGTATATATAGTAGTAACTTTTTAAAATTGAAT ACCATTAACTCTTAACAATCTGATATCATCGATGAATTCGAG-3'	3' Primer with 60bp homology to *GCN4*

ONC659	5'-ACTACTTAGAAAGTCCTG -3'	5' Upcheck Primer of Ca*GCN4*
ONC660	5'- ATACTATCTGGACGAAGA -3'	3' Downcheck Primer of Ca*GCN4*
ONC1011	5'- TTT GTC GAC GAC TAT CCT ACA CTC A -3'	Forward primer for cloning *GCN4*
ONC1012	5'- ATC GAT GTC TAC CAT CAA TTA AAC T -3'	Reverse primer for cloning *GCN4*

Supplementary Table S3. Location of single nucleotide differences in the *LYS14* coding sequences and their alleles in the *C. albicans* genome sequence assembly and the corresponding sequence in the cloned *LYS14* genes.

Hap A Chromosome	Hap A Upstream Coord	Hap A Down-stream Coord	Hap B Chromosome	Hap B Upstream Coord	Hap B Downstream Coord	Change Type	Hap A Seq	Hap B Seq	Affected Features	Amino acid Change: Y/N; residue	Nucleotide change	Amino acid change
Ca22chr6A_C_albicans_SC5314	567324	567326	Ca22chr6B_C_albicans_SC5314	567295	567297	1 nt subs	CAG	CGG	C6_02750C/LYS14		CGG	
Ca22chr1A_C_albicans_SC5314	2020319	2020321	Ca22chr1B_C_albicans_SC5314	2020354	2020356	1 nt subs	GCT	GTT	C1_09200W/LYS142		GCT	
Ca22chr1A_C_albicans_SC5314	2020373	2020375	Ca22chr1B_C_albicans_SC5314	2020408	2020410	1 nt subs	CTA	CCA	C1_09200W/LYS142		CTA	
Ca22chr1A_C_albicans_SC5314	2020896	2020898	Ca22chr1B_C_albicans_SC5314	2020931	2020933	1 nt subs	GCC	GTC	C1_09200W/LYS142	P233S	GTC	P233S
Ca22chr1A_C_albicans_SC5314	2021018	2021020	Ca22chr1B_C_albicans_SC5314	2021053	2021055	1 nt subs	GCG	GGG	C1_09200W/LYS142		GCG	
Ca22chr1A_C_albicans_SC5314	2021123	2021125	Ca22chr1B_C_albicans_SC5314	2021158	2021160	1 nt subs	GGG	GTG	C1_09200W/LYS142		GGG	
Ca22chr1A_C_albicans_SC5314	2021132	2021134	Ca22chr1B_C_albicans_SC5314	2021167	2021169	1 nt subs	TTT	TAT	C1_09200W/LYS142		TTT	
Ca22chr1A_C_albicans_SC5314	2022097	2022099	Ca22chr1B_C_albicans_SC5314	2022132	2022134	1 nt subs	GGG	GAG	C1_09200W/LYS142	G633E	GGG	
Ca22chr1A_C_albicans_SC5314	2015059	2015061	Ca22chr1B_C_albicans_SC5314	2015094	2015096	1 nt subs	AAG	AGG	C1_09180W/LYS143		AAG	
Ca22chr1A_C_albicans_SC5314	2015148	2015150	Ca22chr1B_C_albicans_SC5314	2015183	2015185	1 nt subs	ATA	ACA	C1_09180W/LYS143	I109T	ATA	
Ca22chr1A_C_albicans_SC5314	2015215	2015217	Ca22chr1B_C_albicans_SC5314	2015250	2015252	1 nt subs	CCC	CTC	C1_09180W/LYS143		CCC	
Ca22chr1A_C_albicans_SC5314	2015257	2015259	Ca22chr1B_C_albicans_SC5314	2015292	2015294	1 nt subs	AAC	AGC	C1_09180W/LYS143		AAC	
Ca22chr1A_C_albicans_SC5314	2015272	2015274	Ca22chr1B_C_albicans_SC5314	2015307	2015309	1 nt subs	CGC	CTC	C1_09180W/LYS143		CGC	
Ca22chr1A_C_albicans_SC5314	2015321	2015323	Ca22chr1B_C_albicans_SC5314	2015356	2015358	1 nt subs	AGT	ACT	C1_09180W/LYS143		AGT	
Ca22chr1A_C_albicans_SC5314	2015473	2015480	Ca22chr1B_C_albicans_SC5314	2015508	2015515	6 nt subs	GGCCACAC	GCCCACCC	C1_09180W/LYS143	H219P	GGCCACAC	
Ca22chr1A_C_albicans_SC5314	2015621	2015623	Ca22chr1B_C_albicans_SC5314	2015656	2015658	1 nt subs	ATT	ACT	C1_09180W/LYS143		ATT	
Ca22chr1A_C_albicans_SC5314	2015641	2015643	Ca22chr1B_C_albicans_SC5314	2015676	2015678	1 nt subs	CGG	CAG	C1_09180W/LYS143		CGG	
Ca22chr1A_C_albicans_SC5314	2015671	2015673	Ca22chr1B_C_albicans_SC5314	2015706	2015708	1 nt subs	CCG	CTG	C1_09180W/LYS143		CCG	
Ca22chr1A_C_albicans_SC5314	2015694	2015696	Ca22chr1B_C_albicans_SC5314	2015729	2015731	1 nt subs	GCT	GTT	C1_09180W/LYS143		GCT	

Ca22chr1A_C_albicans_SC5314	2015704	2015706	Ca22chr1B_C_albicans_SC5314	2015739	2015741	1 nt subs	GCA	GTA	C1_09180W/LYS143		GCA	
Ca22chr1A_C_albicans_SC5314	2015716	2015718	Ca22chr1B_C_albicans_SC5314	2015751	2015753	1 nt subs	GCA	GTA	C1_09180W/LYS143		GCA	
Ca22chr1A_C_albicans_SC5314	2015743	2015745	Ca22chr1B_C_albicans_SC5314	2015778	2015780	1 nt subs	ATG	ACG	C1_09180W/LYS143		ATG	
Ca22chr1A_C_albicans_SC5314	2016601	2016603	Ca22chr1B_C_albicans_SC5314	2016636	2016638	1 nt subs	CCC	CGC	C1_09180W/LYS143		CGC	
Ca22chr1A_C_albicans_SC5314	2016764	2016766	Ca22chr1B_C_albicans_SC5314	2016799	2016801	1 nt subs	ATT	ACT	C1_09180W/LYS143		ACT	
Ca22chr1A_C_albicans_SC5314	2016838	2016840	Ca22chr1B_C_albicans_SC5314	2016873	2016875	1 nt subs	TCG	TTG	C1_09180W/LYS143		TTG	
Ca22chr1A_C_albicans_SC5314	2016865	2016867	Ca22chr1B_C_albicans_SC5314	2016900	2016902	1 nt subs	TCC	TTC	C1_09180W/LYS143		TTC	
Ca22chr1A_C_albicans_SC5314	2016930	2016935	Ca22chr1B_C_albicans_SC5314	2016965	2016970	4 nt subs	GCTATA	GTTACA	C1_09180W/LYS143	I704T	GTTACA	I704T
Ca22chr1A_C_albicans_SC5314	2017073	2017075	Ca22chr1B_C_albicans_SC5314	2017108	2017110	1 nt subs	TCG	TGG	C1_09180W/LYS143	R751G	TGG	R751G
Ca22chr1A_C_albicans_SC5314	2017168	2017170	Ca22chr1B_C_albicans_SC5314	2017203	2017205	1 nt subs	TGC	TAC	C1_09180W/LYS143		TAC	
Ca22chr3A_C_albicans_SC5314	140495	140510	Ca22chr3B_C_albicans_SC5314	140494	140506	3 nt indel	TACCACCACCACCACA	TACCACCACCACA	C3_00750W/LYS144	T22_	TACCACCACCACCA	
Ca22chr3A_C_albicans_SC5314	141210	141212	Ca22chr3B_C_albicans_SC5314	141206	141208	1 nt subs	GGA	GAA	C3_00750W/LYS144	G260E	GGA	
Ca22chr3A_C_albicans_SC5314	141649	141651	Ca22chr3B_C_albicans_SC5314	141645	141647	1 nt subs	TTC	TCC	C3_00750W/LYS144		TTC	
Ca22chr3A_C_albicans_SC5314	141764	141766	Ca22chr3B_C_albicans_SC5314	141760	141762	1 nt subs	TCT	TTT	C3_00750W/LYS144		TCT	
Ca22chr3A_C_albicans_SC5314	141805	141807	Ca22chr3B_C_albicans_SC5314	141801	141803	1 nt subs	ATA	ACA	C3_00750W/LYS144		ATA	
Ca22chr3A_C_albicans_SC5314	142285	142287	Ca22chr3B_C_albicans_SC5314	142281	142283	1 nt subs	GCG	GTG	C3_00750W/LYS144		GCG	
Ca22chr3A_C_albicans_SC5314	142711	142715	Ca22chr3B_C_albicans_SC5314	142707	142711	3 nt subs	ACACG	ATAAG	C3_00750W/LYS144	T761K	ACACG	
Ca22chr3A_C_albicans_SC5314	142838	142840	Ca22chr3B_C_albicans_SC5314	142834	142836	1 nt subs	TAG	TGG	C3_00750W/LYS144	S803G	TAG	
Ca22chr3A_C_albicans_SC5314	142969	142971	Ca22chr3B_C_albicans_SC5314	142965	142967	1 nt subs	ATG	AGG	C3_00750W/LYS144		ATG	
Ca22chr3A_C_albicans_SC5314	143018	143020	Ca22chr3B_C_albicans_SC5314	143014	143016	1 nt subs	GAA	GCA	C3_00750W/LYS144		nt subs after stop codon	

Supplementary Table S4. Location of CTG codons in *C. albicans LYS14*-like Genes

CaLys14-like sequence	No. of CTG codons/ Leu-to-Ser in *S.cerevisiae*	Amino acid Position of CTG → Ser in the translated protein	Zinc Finger domain
Lys141	1	22	32-~82
Lys142	5	86, 168, 347, 399, 610	5-~55
Lys143	6	68, 86, 130, 184, 781, 835	20-~70
Lys144	8	95, 123, 286, 304, 360, 554, 613, 793	36-~86

Supplementary Figure Legends

FIG S1. *S. cerevisiae* lysine biosynthetic pathway genes are induced under amino acid starvation conditions**.** Summary of genome-wide microarray data of *S. cerevisiae LYS* genes under His starvation (+/-3AT) (6)or under Ile-Val starvation (+/- SM) conditions (7).

FIG S2. *CaLYS14*-like genes do not complement the lysine auxotrophy of *S. cerevisiae lys14*Δ strain. *S. cerevisiae lys14*Δ strain was transformed with plasmids containing P_{GAL1}-driven *CaLYS141*, *CaLYS142, CaLYS143* or *CaLYS144* and the transformants as well as the control strains wild-type BY4741 and the parental *lys14*Δ (strain 3973) were grown overnight in SC medium at 30°C. Saturated cultures were diluted and spotted on synthetic complete media containing glucose or galactose plus raffinose as carbon sources and with or without lysine supplementation.

FIG S3. Deletion of *CaLYS14*-like genes does not lead to lysine auxotrophy in *C. albicans*. *C. albicans* strain RPY206 (WT) and the different mutant strains *lys141*Δ/Δ, *lys142*Δ/Δ, *lys143*Δ/Δ, *lys144*Δ/Δ, and *lys2*Δ/Δ as control, were grown overnight in YPD, and 10-fold serial dilutions were spotted on SC-Lys, SC-Lys+0.1mM Hyl, or on control plate SC+Lys+0.1mM Hyl, and grown for 2 days and image acquired.

FIG S4. Lysine starvation does not lead to upregulation of *C. albicans LYS14* gene expression. The wild-type strain RPC206 was grown in SC+Lys (lysine-replete), SC-Lys (lysine-deficient) or SC-Lys+Hyl (lysine-starved) media, extracted total RNA and the mRNA levels of *LYS141*, *LYS142, LYS143* and *LYS144* were quantified using qRT-PCR. The *scR1* transcript was used as normalization control, and relative expression calculated with respect to SC+lys, and data from 2-3 independent experiments were plotted. The error bars indicate SEM.

FIG S5. CaLys14-like protein levels are not altered by lysine starvation conditions. *CaLYS14* genes were TAP-tagged at their carboxyl-termini and the tagged strains PC205, 206, 209 and 212 expressing Lys141-TAP, Lys142-TAP, Lys143-TAP and Lys144-TAP respectively, were grown in SC+Lys, SC-Lys and SC-Lys +Hyl to OD_{600} ~2.0, and harvested. Whole cell extracts were prepared and 2-fold serial dilutions, starting from 50μg, were analyzed by Western blot. The TAP-tagged Lys14 expression was probed with PAP antibody (1:6000; Open Biosystems) and anti-Glucose 6-phosphate dehydrogenase antibody (1:1000; Sigma) as loading control.

FIG S6. Comparison of the *S. cerevisiae* and *C. albicans LYS* biosynthetic gene promoters. Schematic diagram comparing the presence or absence of the binding sites for Lys14 and Gcn4 on the promoters of the lysine biosynthetic pathway genes in *S. cerevisiae* and *C. albicans* based on their analyses at the yTFaSCo database.

FIG S7. Comparison of the *LYS* biosynthetic gene promoters in *Candida* clade genomes. Schematic diagram comparing the presence or absence of the binding sites for Lys14 and Gcn4 on the promoters of the lysine biosynthetic pathway genes in *S. cerevisiae, C. albicans* and other *Candida* clade genomes *L. elongisporus, C. tropicalis, C. lusitaniae*, and *C. guilliermondii* based on their analyses at the yTFaSCo database.

Supplementary References

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3. **Natarajan K, Jackson BM, Zhou H, Winston F, Hinnebusch AG.** 1999. Transcriptional activation by Gcn4p involves independent interactions with SWI/SNF complex and SRB/mediator. Molecular cell **4:**657-664.
4. **Noble SM, Johnson AD.** 2005. Strains and strategies for large-scale gene deletion studies of the diploid human fungal pathogen *Candida albicans*. Eukaryotic cell **4:**298-309.
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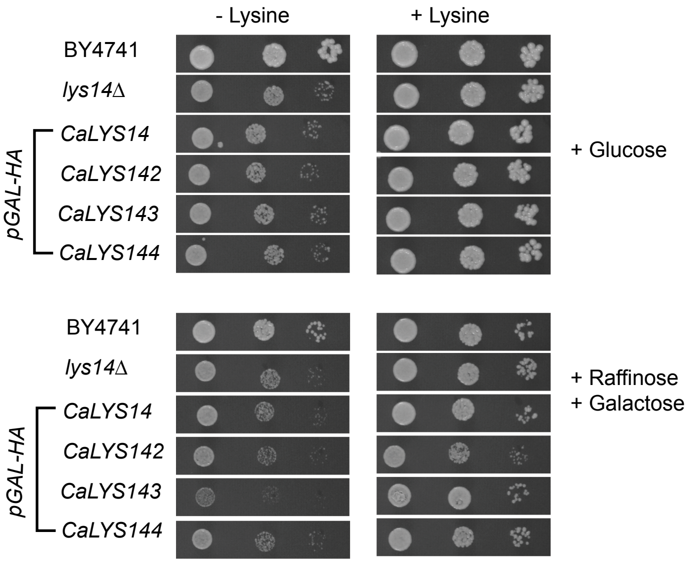
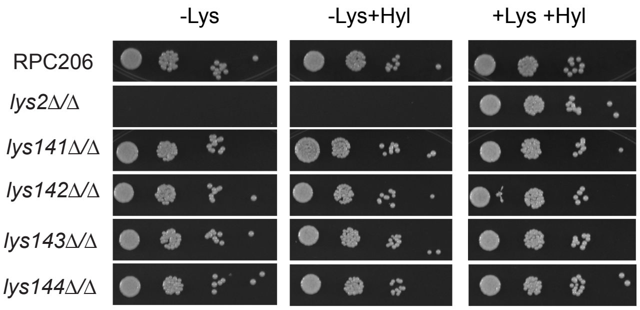
6. **Natarajan K, Meyer MR, Jackson BM, Slade D, Roberts C, Hinnebusch AG, Marton MJ.** 2001. Transcriptional profiling shows that Gcn4p is a master regulator of gene expression during amino acid starvation in yeast. Molecular and cellular biology **21:**4347-4368.
7. **Saint M, Sawhney S, Sinha I, Singh RP, Dahiya R, Thakur A, Siddharthan R, Natarajan K.** 2014. The TAF9 C-terminal conserved region domain is required for SAGA and TFIID promoter occupancy to promote transcriptional activation. Molecular and cellular biology **34:**1547-1563.

	WT +/- SM	WT +/- 3AT
	log2fc	log2fc
LYS20	2.8	3.0
LYS21	1.5	2.4
LYS4	1.8	1.6
LYS12	2.1	n.d.
LYS14	1.9	2.7
YER152C	no change	n.d.
ARO8	1.1	2.5
ARO9	4.1	5.4
LYS2	2.8	3.4
LYS5	2.2	2.7
LYS9	2.9	2.5
LYS1	3.8	4.5

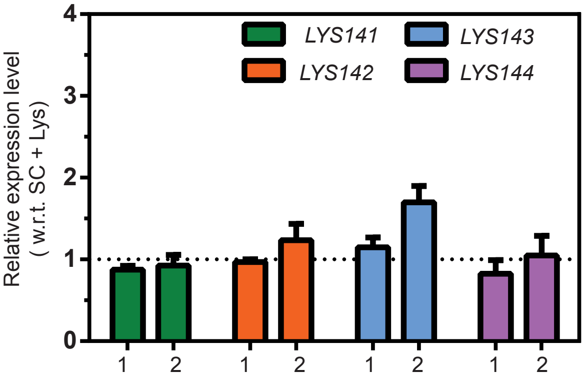
Priyadarshini_Fig. S1



Priyadarshini_Fig. S2



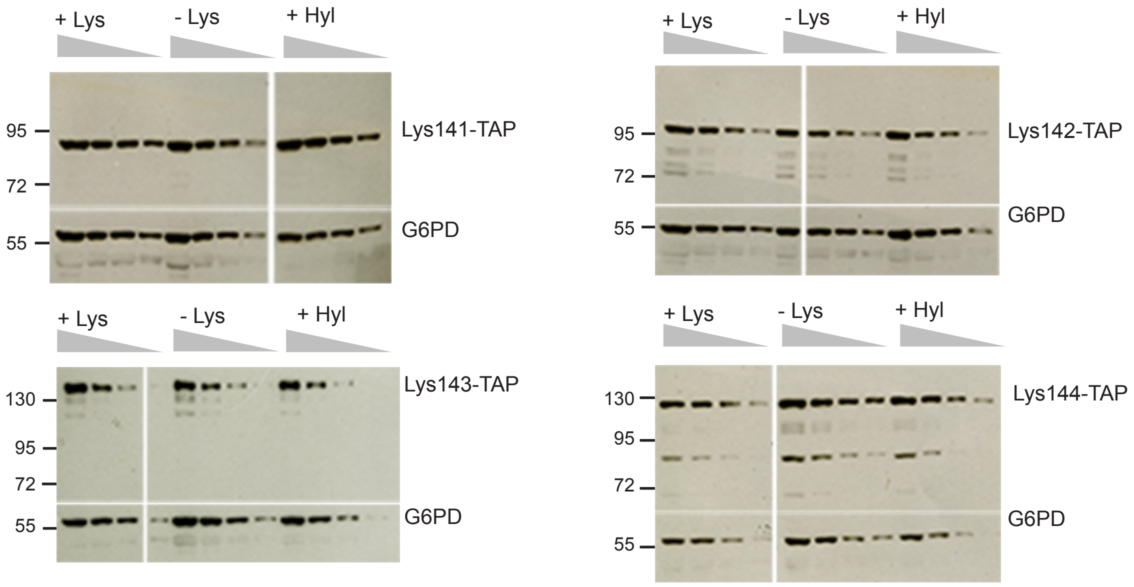
Priyadarshini_Fig. S3



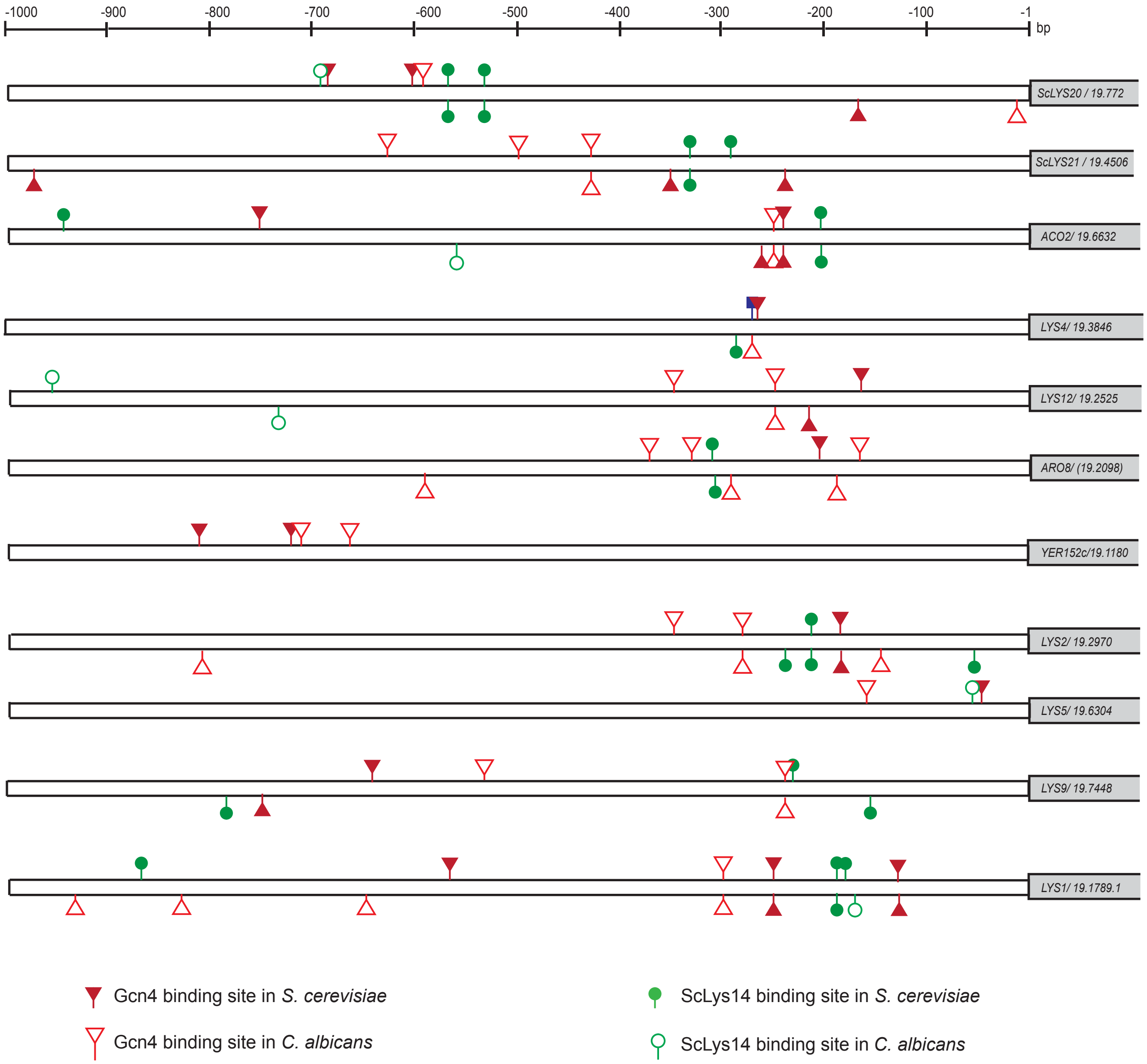
1 - SC-Lys

2 - SC-Lys+Hyl

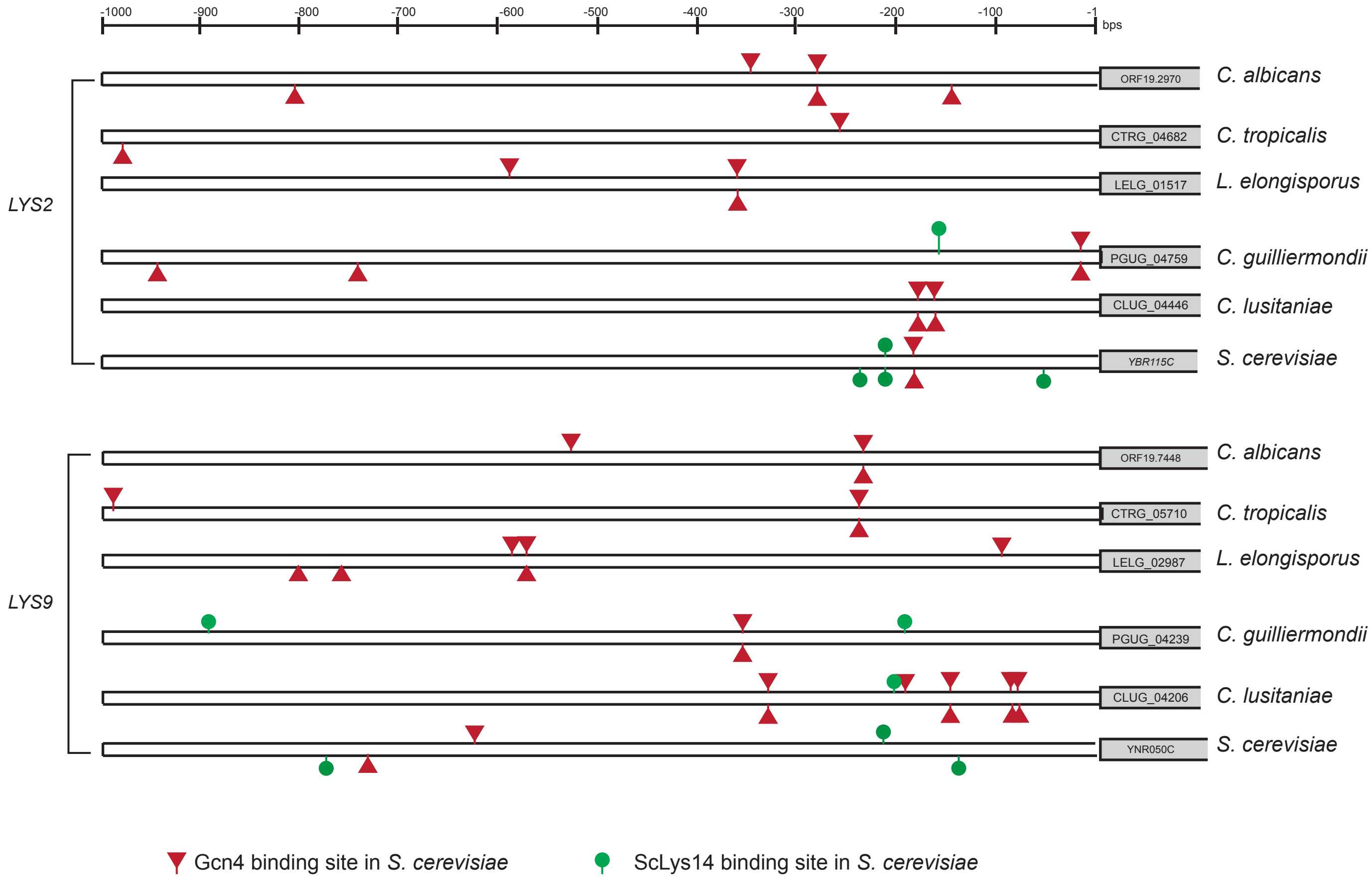
Priyadarshini_Fig. S4



Priyadarshini_Fig. S5



Priyadarshini_Fig. S6



Priyadarshini_Fig. S7