Supplemental Data

Transcriptional Rewiring of Fungal Galactose-Metabolism Circuitry

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Supplemental References

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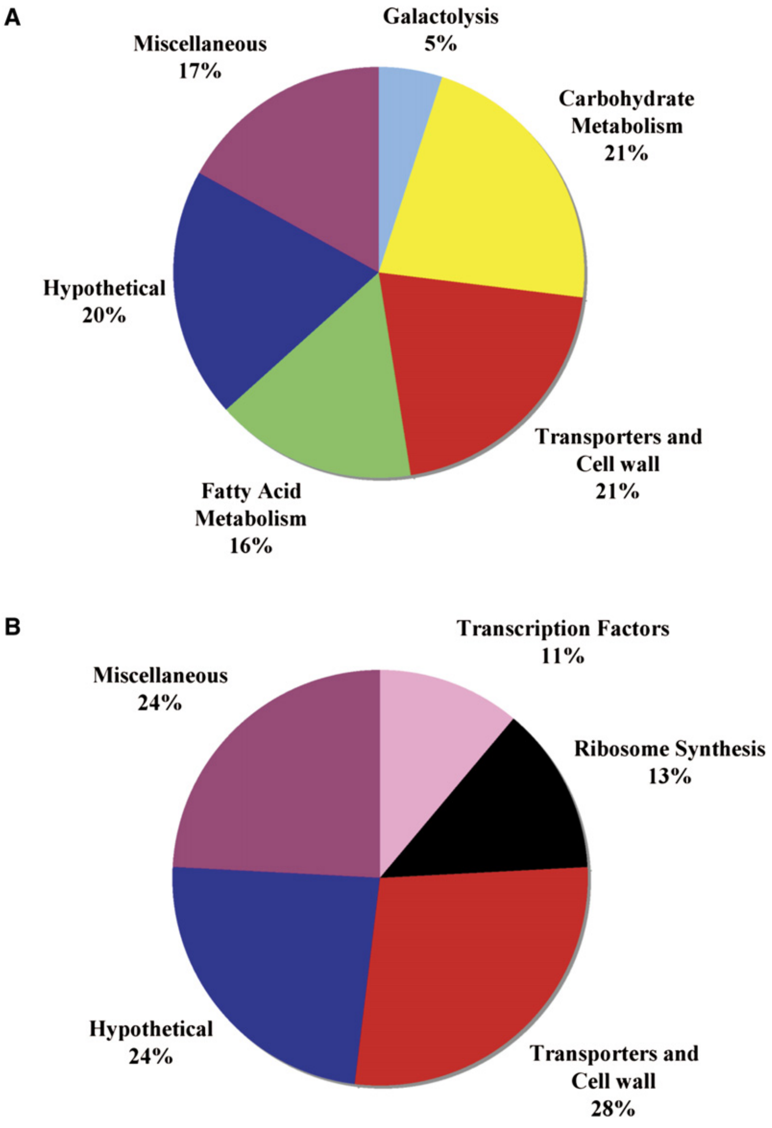

Figure S1. Galactose Leads to Elevated Expression of *CaGAL* Genes

Galactose leads to higher expression of 82 genes including *GAL1*, *GAL2*, *GAL7*, and *GAL10* (A), whereas dextrose leads to higher expression of 54 genes in *C. albicans* (B).

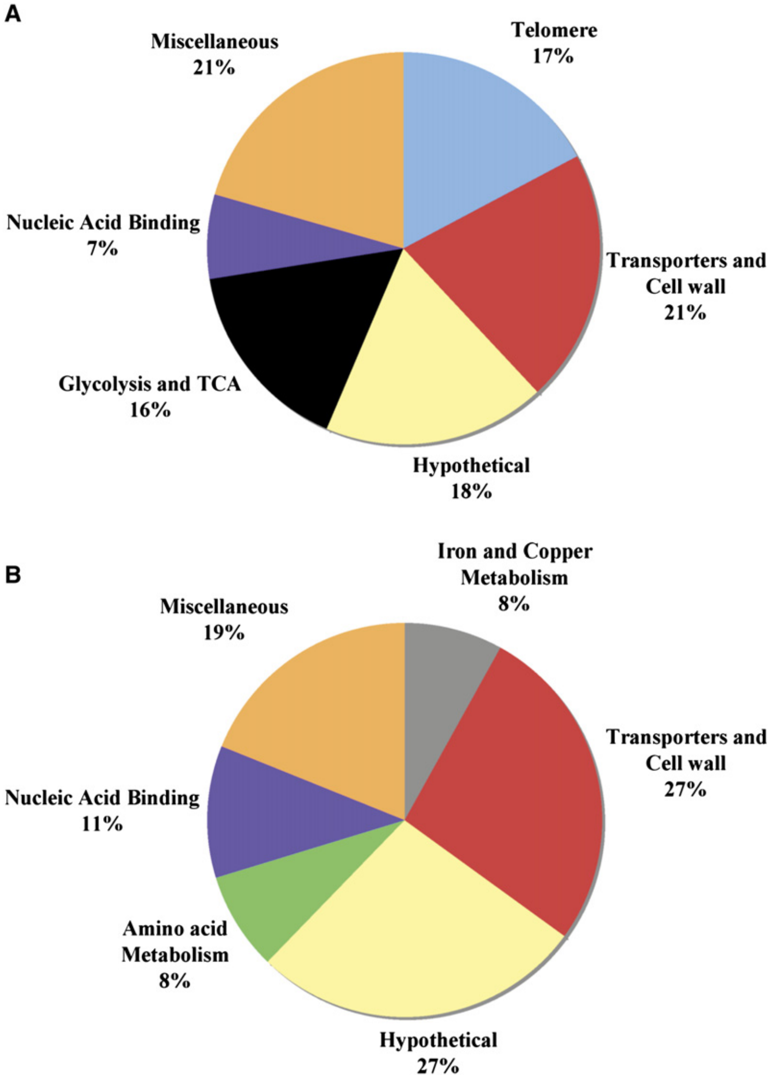

Figure S2. The Function of *C. albicans* Gal4p

The transcriptional-gene targets of *C. albicans* Gal4p were analyzed by microarrays. Loss of *C. albicans GAL4* led to reduced expression of 87 genes (A) and increased expression of 37 genes (B).

Table S1. Genes Whose Expression Was Upregulated in response to Galactose

Systematic	Fold Change	Common Name	Description
orf19.3668	7.75	*GAL2*	hexose transporter
orf19.6169	5.62		conserved hypothetical gene, DNA metabolism
orf19.3672	5.52	*GAL10*	UDP glucose-4-epimerase
orf19.7094	5.10	*HGT12*	glucose sensor or transporter protein
orf19.2849	4.78	*AQY1*	aquaporin
orf19.3670	4.18	*GAL1*	galactokinase
orf19.3675	4.13	*GAL7*	galactose-1-phosphate uridyl transferase
orf19.4384	3.76	*HXT5*	fructose symporter
orf19.7310	3.33	*MSC1*	meiotic sister-chromatid recombination
orf19.4527	3.32	*HGT1*	hexose transporter
orf19.4591	3.28	*CTN2*	carnitine acetyltransferase, amino acid metabolism
orf19.3359	3.13	*ARP8*	actin-related protein
orf19.5307	3.05	*JEN2*	carboxylic acid transporter
orf19.734	3.02	*GLK1*	aldohexose specific glucokinase
orf19.4555	2.87	*ALS4*	agglutinin-like protein 4
orf19.1408	2.70	*GLK2*	glucokinase
orf19.4980	2.66	*HSP70*	heat-shock protein 70
orf19.2882	2.63		putative purine permease
orf19.2496	2.58	*FUN34*	transporter involved in nitrogen utilization
orf19.6491	2.57		hypothetical protein
orf19.13	2.51	*GLK1*	glucokinase, aldohexose specific
orf19.111	2.45	*CAN2*	arginine permease
orf19.3160	2.41	*HSP12*	heat-shock protein; molecular chaperone
orf19.6116	2.40	*GLK4*	aldohexose-specific glucokinase
orf19.3637	2.40		hypothetical protein
orf19.7021	2.30	*GPH1*	glycogen phosphorylase
orf19.1097	2.20	*ALS2*	cell-wall protein
orf19.4539	2.19		putative rho GDP dissociation inhibitor
orf19.1794	2.19		hypothetical protein
orf19.4735	2.17		putative ornithine cyclodeaminase
orf19.7514	2.16	*PCK1*	phosphoenolpyruvate carboxykinase gluconeogenesis
orf19.2896	2.11	*SOU1*	peroxisomal dienoyl-CoA reductase, sorbitol utilization
orf19.2515	2.09		hypothetical protein
orf19.3131	2.09	*OYE32*	NADPH dehydrogenase
orf19.3684	2.08	*SPS20*	peroxisomal 2,4-dienoyl-CoA reductase
orf19.802	2.05	*UGA12*	4-aminobutyrate aminotransferase (nitrogen)
orf19.4274	2.05	*PUT1*	proline oxidase
orf19.1847	2.03	*ARO10*	Protein described as pyruvate decarboxylase, LEU catabolism
orf19.2121	2.02	*ALS4*	cell wall protein
orf19.4551	2.01	*CTN1*	mitochondrial carnitine acetyltransferase
orf19.744	2.01	*GDB1*	glycogen debranching enzyme
orf19.3070.1	2.00	*FOX3*	hydratase-dehydrogenase- epimerase
orf19.4317	1.93	*GRE3*	aldose reductase
orf19.1743	1.93	*ACS1*	acetyl-coenzyme A synthetase
orf19.3548.1	1.92	*WH11*	heat-shock protein
orf19.4682	1.91	*HGT17*	quinate permease
orf19.5037	1.91		conserved hypothetical protein
orf19.682	1.90		hypothetical protein
orf19.5525	1.90		conserved hypothetical protein
orf19.1862	1.83		conserved hypothetical protein
orf19.7566	1.82	*GNP1*	high-affinity glutamine permease
orf19.338	1.78		conserved hypothetical protein
orf19.272	1.74	*FAA2-2*	long-chain fatty acid CoA ligase
orf19.1974	1.73	*TFS1*	carboxypeptidase Y inhibitor
orf19.7520	1.71	*POT1*	peroxysomal 3-ketoacyl-CoA thiolase A
orf19.5604	1.70	*MDR1*	benomyl/methotrexate resistance protein
orf19.7531	1.69	*YMR90*	conserved hypothetical protein
orf19.6083	1.68		hypothetical protein
orf19.1152	1.67		hypothetical protein
orf19.3278	1.67	*GSY1*	glycogen (starch) synthase
orf19.1788	1.66	*XKS1*	xylulokinase
orf19.4477	1.66	*CSH1*	aryl-alcohol dehydrogenase
orf19.532	1.64	*RBR2*	cell-wall protein
orf19.5000	1.64	*CYB2*	cytochrome b2 precursor
orf19.7281	1.63	*PDK2*	pyruvate dehydrogenase kinase
orf19.1149	1.61	*ETR1*	mitochondrial 2-enoyl thioester reductase, respiration
orf19.4287	1.61		alcohol dehydrogenase (glucose catabolism to butanediol)
orf19.3325	1.60	*GLG1*	self-glucosylating initiator of glycogen synthesis
orf19.345	1.59	*UGA2*	succinate semialdehyde dehydrogenase

(*Continued on next page*)

Table S1. *Continued*

Systematic	Fold Change	Common Name	Description
orf19.1180	1.59		conserved hypothetical protein
orf19.1809	1.59	*FOX2*	peroxisomal hydratase-dehydrogenase-epimerase
orf19.2613	1.57	*ECM4*	involved in cell-wall biogenesis and architecture
orf19.7676	1.56	*SOR1*	sorbitol dehydrogenase
orf19.6443	1.56	*ECI12*	enoyl-CoA isomerase
orf19.6082	1.55	*GSF2*	ER localized promote secretion of GAL2
orf19.5640	1.55	*PEX5*	peroxisomal protein receptor
orf19.2737	1.55		kinase
orf19.3029	1.54	*EHD3*	enpyl-CoA hydratase
orf19.6637	1.53		predicted glycosilase
orf19.1325	1.52	*ECM38*	gamma-glutamyltransferase, cell wall organization
orf19.854	1.52	*UGA1*	4-aminobutyrate aminotransferase (GABA transaminase)
orf19.1652	1.51	*POX1-3*	fatty-acyl coenzyme A oxidase

Table S2. Genes Whose expression Was Upregulated in Response to Dextrose

Systematic	Fold Change	Common Name	Description
orf19.4737	4.88	*TPO3*	membrane transporter of the MFS-MDR family
orf19.1354	3.77	*YER67*	conserved hypothetical protein
orf19.6656	2.74	*DUR3*	urea transport protein
orf19.4941	2.57	*TYE7*	basic helix-loop-helix transcription factor
orf19.3707	2.55	*YHB1*	flavohemoglobin;dihydropteridine reductase
orf19.2659	2.52		conserved hypothetical protein
orf19.4716	2.40	*GDH3*	NADP-glutamate dehydrogenase
orf19.5288	2.26	*IFE2*	Zn-containing alcohol dehydrogenase
orf19.85	2.15	*GPX2*	glutathione peroxidase
orf19.5437	2.13	*RHR2*	DL-glycerol-3-phosphatase (glycewrol biosynthesis)
orf19.5626	2.07		conserved hypothetical protein
orf19.978	2.03	*BDF1*	transcription factor
orf19.889	1.96	*THI20*	thiamine biosynthesis;phosphomethylpyrimidine kinase
orf19.3448	1.96		hypothetical protein
orf19.1415	1.94	*FRE10*	ferric reductase
orf19.6249	1.93	*HAK1*	high affinity potassium transporter
orf19.5193	1.93	*FMA1*	benzil reductase
orf19.670.2	1.88		hypothetical protein
orf19.909	1.77	*STP4*	transcription factor
orf19.5305	1.75	*RHD3*	putative GPI-anchored protein
orf19.3712	1.73		hypothetical protein
orf19.3441	1.73	*FRP6*	putative transporter
orf19.2158	1.72	*NAG3*	related to MDR-family transporters
orf19.6586	1.71		conserved hypothetical protein
orf19.4779	1.71		multidrug-resistance transporter
orf19.740	1.71	*HAP41*	CCAAT-binding factor complex
orf19.23	1.70	*RTA3*	transporter upregulated during the acquisition of azole
orf19.2475	1.69	*PGA26*	putative GPI-anchored protein
orf19.5759	1.65	*SNQ2*	ABC transporter
orf19.5025	1.65	*MET3*	ATP sulfurlyas
orf19.5431	1.65		hypothetical protein
orf19.3676	1.61	*ABP140*	hypothetical protein
orf19.1855	1.60	*SEO2*	putative permease
orf19.339	1.56	*NDE1*	mitochondria directed NADH dehydrogenase
orf19.3088	1.56		TF
orf19.6770	1.56	*ENT4*	epsin N-terminal homology- containing protein
orf19.6766	1.56	*NOP13*	Nucleolar Protein 13
orf19.1264	1.55	*CFL2*	ferric reductase
orf19.183	1.55	*HIS3*	imidazoleglycerol-phosphate dehydratase
orf19.5992	1.55	*ZCF33*	zinc finger transcription factor
orf19.5305	1.55	*RHD3*	GPI-anchored protein
orf19.3393	1.55	*DBP9*	dead-box protein 9
orf19.449	1.55		possible phosphatidyl synthase
orf19.4033	1.54	*PRP22*	RNA-dependent ATPase
orf19.7657	1.53	*POP3*	RNase P and RNase MRP subunit
orf19.6902	1.53	*DBP7*	dead-box protein; RNA helicase
orf19.2308	1.53	*PFK26*	6-phosphofructose-2-kinase
orf19.6727	1.53	*RIT1*	ribosyltransferase of initiator tRNA methionine
orf19.3040	1.53	*EHT1*	alcohol acyl transferase, mitochondrial outer membrane
orf19.5010	1.52	*DIM1*	dimethyladenosine transferase, rRNA
orf19.409	1.52		conserved hypothetical protein, membrane
orf19.4459	1.51	*YNL234W*	weakly similar to mammalian globins
orf19.6014	1.50	*RRS1*	regulator of ribosome synthesis
orf19.3406	1.50		highly conserved hypothetical protein

Table S3. Genes Whose Expression Was Downregulated in *gal4* Strain

Systematic	Fold Change	Common Name	Description
orf19.5338	0.251	*GAL4*	domain similar to that of GAL4
orf19.6191	0.286	*TLO8*	hypothetical protein
orf19.3074	0.308	*TLO10*	hypothetical protein
orf19.3386	0.425	*TLO6*	transcription factor
orf19.5467	0.430	*TLO7*	transcription factor
orf19.710	0.453	*LSC2*	succinate-CoA ligase beta subunit (TCA)
orf19.4054	0.461	*TLO12*	transcriptional regulation
orf19.5383	0.471	*PMA1*	plasma membrane H+-ATPase (phosphate)
orf19.3182	0.475	*GIS2*	nucleic-acid-binding protein
orf19.6112	0.481	*TLO3*	putative transcriptional activator
orf19.3145.4	0.507	*PGI12*	glucose-6-phosphate isomerase (glycolysis)
orf19.2762	0.517	*AHP1*	alkyl hydroperoxide reductase
orf19.362	0.526	*TLO9*	transcriptional activation
orf19.7544	0.553	*TLO1*	hypothetical protein
orf19.4885	0.556	*MIR1*	mitochondrial phosphate transport protein
orf19.2777	0.566	*TOS3*	target of SBF (glucose repression)
orf19.7680	0.581	*TLO2*	transcriptional activation
orf19.6561	0.596	*LAT1*	dihydrolipoamide acetyltransferase component (TCA)
orf19.7127	0.596	*TLO16.5*	hypothetical protein
orf19.6435	0.600		conserved hypothetical protein
orf19.655	0.606	*PHO842*	high-affinity inorganic phosphate/H+ symporter
orf19.6337	0.609	*TLO13*	transcriptional activator
orf19.4155.12	0.614	*IDH1*	similar to protion of isocitrate dehydrogenase 1 alpha-4-beta-4 subunit (TCA)
orf19.7231	0.616	*FTR2*	plasma-membrane iron permease
orf19.1860	0.616	*LSC2*	hypothetical protein
orf19.631	0.617	*TLO34*	transcription factor
orf19.6165	0.619	*KGD1*	alpha-ketoglutarate dehydrogenase (TCA)
orf19.3642	0.625	*SUN4*	putative cell-wall protein
orf19.5451	0.625		hypothetical protein
orf19.2685	0.639	*PGA54*	GPI-anchored protein
orf19.7635	0.641	*DRS1*	ATP-dependent RNA helicase
orf19.7276.1	0.642	*TLO4*	transcriptional activator, 3-prime end
orf19.1124.2	0.644	*DPH52*	diphthamide methyltransferase
orf19.7127.1	0.662	*TLO16.3*	hypothetical protein
orf19.4211	0.663	*FET3*	multicopper ferro-oxidoreductase, high-affinity Fe uptake
orf19.7424	0.664	*NSA2*	Killer toxin Resistant; ribosomal biogenesis
orf19.5193	0.668		benzil reductase
orf19.1105.2	0.669	*PGA56*	Regulator of sorbose utilization; putative GPI-anchor
orf19.1536	0.669	*ZRC1*	zinc- and cadmium-resistance protein
orf19.968	0.673	*PGA14*	GPI-anchored protein
orf19.7443	0.681		hypothetical protein
orf19.5305	0.683	*PGA29*	GPI-anchored protein
orf19.6724	0.686	*FUM12*	mitochondrial fumarate hydratase, 5-prime end (TCA)
orf19.1591	0.686	*ERG10*	acetyl-CoA acetyltransferase;acetoacetyl CoA thiolase
orf19.903	0.689	*GPM1*	phosphoglycerate mutase (glycolysis)
orf19.5892	0.691	*HUL4*	ubiquitin-protein ligase
orf19.3223	0.697	*ATP3*	proton-transporting ATP synthase, central stalk
orf19.6676	0.701	*DPH5*	diphthamide biosynthesis methyltransferase
orf19.4309	0.701	*GRP2*	induced by osmotic stress
orf19.932	0.703	*DNF1*	phopholipid transporting ATPase
orf19.4263	0.706		hypothetical protein
orf19.3475	0.710		Gag-related protein; hyphal induced
orf19.7125	0.711		hypothetical protein
orf19.10	0.713	*ALK8*	cytochrome p450
orf19.3713	0.715		hypothetical protein
orf19.7673	0.715	*SMD1*	snRNA-associated protein, snRNP
orf19.6189	0.715		conserved hypothetical protein
orf19.339	0.722	*NDE1*	mitochondria directed NADH dehydrogenase (glycolysis)
orf19.3829	0.723	*PHR1*	pH-regulated GPI-anchored required for morphogenesis
orf19.5021	0.723	*PDX1*	pyruvate dehydrogenase complex protein X (TCA)
orf19.7534	0.723	*MIS1*	mitochondrial C1- tetrahydrofolate synthase precursor
orf19.7219	0.727	*FTR1*	plasma-membrane iron permease
orf19.717	0.727	*HSP60*	mitochondrial groEL-type heat shock protein
orf19.5684	0.730	*MRPL14*	mitochondrial ribosomal protein L14
orf19.3097	0.731	*PDA1*	alpha subunit of pyruvate dehydrogenase (TCA)
orf19.5052	0.733		conserved hypothetical protein
orf19.6948	0.734	*CCC1*	transmembrane Ca2+ transporter
orf19.4051	0.735	*HTS1*	histidine tRNA synthetase
orf19.301	0.735		hypothetical protein, likely to be cell wall localized and GPI-anchored

Table S3. *Continued*

Systematic	Fold Change	Common Name	Description
orf19.6090	0.735	*NSR1*	ribosomal-small-subunit assembly and maintenance
orf19.2346	0.737		highly conserved hypothetical protein
orf19.962	0.738		hypothetical protein
orf19.6105	0.739	*MVD*	mevalonate pyrophosphate decarboxylase
orf19.5112	0.740	*TKL1*	transketolase 1 (pentose)
orf19.327	0.742	*HTA3*	histone variant involved in chromatin and transcriptional control
orf19.252	0.742		conserved hypothetical protein
orf19.5943.1	0.743	*STM1*	maintain telomere structure
orf19.929	0.747		hypothetical protein
orf19.5989	0.748	*HRP1*	nuclear polyadenylated-RNA-binding protein
orf19.930	0.751	*PET9*	ATP/ADP translocator
orf19.1329	0.752		hypothetical protein
orf19.5444	0.753	*TIM44*	inner-membrane translocase component
orf19.6190	0.753	*SRB1*	GDP-mannose pyrophosphorylase cell wall
orf19.3038	0.756	*TPS2*	threalose-6-phosphate phosphatase
orf19.2200	0.756	*VIP36*	vesicular integral-membrane protein VIP36-like
orf19.2953	0.757	*TOM20*	mitochondrial outer membrane translocase complex
orf19.4826	0.759	*IDH1*	mitochondrial isocitrate dehydrogenase 1 (TCA)

Table S4. Genes Whose Expression Was Upregulated in *gal4* Strain

Systematic	Fold Change	Common Name	Description
orf19.6139	2.42	*FRE7*	ferric reductase
orf19.3646	1.93	*CTR1*	copper transport protein
orf19.2107.1	1.85	*STF2*	ATP synthase regulatory factor
orf19.7111.1	1.84	*SOD3*	superoxide dismutase
orf19.1862	1.83		conserved hypothetical protein
orf19.2344	1.68	*ASR1*	similar to heat-shock protein
orf19.2020	1.63	*HGT6*	hexose transporter
orf19.638	1.62	*FDH1*	formate dehydrogenase, glycine catabolism
orf19.4555	1.60	*ALS4*	agglutinin-like protein 4
orf19.3548.1	1.60	*WH11*	heat-shock protein
orf19.2048	1.58		hypothetical protein
orf19.670.2	1.58		hypothetical protein
orf19.1996	1.57	*CHA1*	catabolic serine/threonine dehydratase
orf19.7077	1.53	*FRE7*	transmembrane subunit of ferric reductase
orf19.5626	1.51		conserved hypothetical protein
orf19.2121	1.51	*ALS4*	cell-wall protein
orf19.7310	1.49	*MSC1*	meiotic sister-chromatid recombination
orf19.1354	1.47	*YER67*	conserved hypothetical protein
orf19.4941	1.46	*TYE7*	basic helix-loop-helix transcription factor
orf19.5288	1.45	*YAL60*	Zn-containing alcohol dehydrogenase
orf19.2849	1.42	*AQY1*	aquaporin
orf19.6816	1.42		aldehyde reductase
orf19.4682	1.42	*HGT17*	quinate permease
orf19.5514	1.42		conserved hypothetical protein
orf19.5876	1.39		hypothetical protein
orf19.3682	1.38	*CWH8*	generation of mannoprotein layer of the cell wall
orf19.3932	1.38		conserved hypothetical protein
orf19.1331	1.37	*HSM3*	MutS family (putative);mismatch repair
orf19.946	1.37	*MET14*	adenylylsulfate kinase
orf19.5000	1.37	*CYB2*	cytochrome b2 precursor
orf19.2292	1.36	*OPT4*	oligopeptide transporter protein
orf19.2584	1.35	*OPT9*	oligopeptide transporter
orf19.1974	1.35	*TFS1*	carboxypeptidase Y inhibitor
orf19.2693	1.35	*URE1*	nitrogen catabolite repression regulator
orf19.7284	1.34	*ASR2*	conserved hypothetical protein
orf19.3749	1.34	*IFC3*	oligopeptide transporter protein
orf19.2173	1.33	*MAF1*	nuclear-cytoplasmic transport

Table S5. Strains Used in This Study

Strain	Genotype	Source
SC5314	Wild-type isolate	[S1]
BWP17	*ura3Δ::λimm434/ura3Δ::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG*	[S2]
CMM1	*ura3Δ::λimm434/ura3Δ::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG GAL4/GAL4::*[p*His1-GAL4*]::[p*ARG4-GAL4*]	This study
CMM2	*ura3Δ::λimm434/ura3Δ::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG gal4Δ::HIS1/GAL4*	This study
CMM3	*ura3Δ::λimm434/ura3Δ::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG gal4Δ::ARG4/gal4Δ::HIS1*	This study
CMM4	*ura3Δ::λimm434/ura3Δ::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG GAL4/GAL4::*[p*His1-GAL4*]::[p*ARG4-GAL4*] *RPS1/RPS1::*[p*GAL10-lacZ*]	This study
CMM5	*ura3Δ::λimm434/ura3Δ::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG gal4Δ::ARG4/gal4Δ::HIS1 RPS1/RPS1::*[p*GAL10-lacZ*]	This study
CAI4	*ura3Δ::λimm434/ura3Δ::λimm434*	[S1]
CMM42	*ura3Δ::λimm434/ura3Δ::λimm434 RPS1/RPS1::*[p*GDH3-lacZ*]	This study
CMM41	*ura3Δ::λimm434/ura3Δ::λimm434 RPS1/RPS1::*[plac-poly]	This study
CMM43	*ura3Δ::λimm434/ura3Δ::λimm434 RPS1/RPS1::*[p*GAL10-lacZ*-840]	This study
CMM99	*ura3Δ::λimm434/ura3Δ::λimm434 RPS1/RPS1::*[p*GAL10-lacZ*-188]	This study
CMM100	*ura3Δ::λimm434/ura3Δ::λimm434 RPS1/RPS1::*[p*GAL10-lacZ*-176]	This study
CMM101	*ura3Δ::λimm434/ura3Δ::λimm434 RPS1/RPS1::*[p*GAL10-lacZ*-840Δ176-188]	This study
JKC19	*ura3Δ::λimm434/ura3Δ::λimm434 cph1::hisG/cph1::hisG-URA3-hisG*	[S3]
CMM102	*ura3Δ::λimm434/ura3Δ::λimm434 cph1::hisG/cph1::hisG*	This study
CMM105	*ura3Δ::λimm434/ura3Δ::λimm434 cph1::hisG/cph1::hisG RPS1/RPS1::*[p*GAL10-lacZ*-188]	This study
CMM106	*ura3Δ::λimm434/ura3Δ::λimm434 cph1::hisG/cph1::hisG RPS1/RPS1::*[p*GAL10-lacZ*-176]	This study
CMM54	*ura3Δ::λimm434/ura3Δ::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG GAL4/GAL4*::[pH]::[pA] *RPS1/RPS1::*[p*TLO-lacZ*-126]	This study
CMM55	*ura3Δ::λimm434/ura3Δ::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG gal4Δ::ARG4/gal4Δ::HIS1 RPS1/RPS1::*[p*TLO-lacZ*-126]	This study
CMM56	*ura3Δ::λimm434/ura3Δ::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG GAL4/GAL4*::[pH]::[pA] *RPS1/RPS1::*[p*TLO-lacZ*-114]	This study
CMM57	*ura3Δ::λimm434/ura3Δ::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG gal4Δ::ARG4/gal4Δ::HIS1 RPS1/RPS1::*[p*TLO-lacZ*-114]	This study
CMM65	*ura3Δ::λimm434/ura3Δ::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG GAL4/GAL4*::[pH]::[pA] *RPS1/RPS1::*[p*LAT1-lacZ*-270]	This study
CMM66	*ura3Δ::λimm434/ura3Δ::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG gal4Δ::ARG4/gal4Δ::HIS1 RPS1/RPS1::*[p*LAT1-lacZ*-270]	This study
CMM67	*ura3Δ::λimm434/ura3Δ::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG GAL4/GAL4*::[pH]::[pA] *RPS1/RPS1::*[p*LAT1-lacZ*-253]	This study
CMM68	*ura3Δ::λimm434/ura3Δ::λimm434 his1::hisG/his1::hisG arg4::hisG/arg4::hisG gal4Δ::ARG4/gal4Δ::HIS1 RPS1/RPS1::*[p*LAT1-lacZ*-253]	This study

Table S6. Plasmids Used in This Study

Plasmids	Genes	Source
pFA-*HIS1*	pFA6a backbone, *CaHIS1*	[S4]
pFA-*ARG4*	pFA6a backbone, *CaARG4*	[S4]
p*HIS1-GAL4*	pFA6a backbone, upstream flan 600 bp *CaHIS1* downstream flank 500 bp	This study
p*ARG4-GAL4*	pFA6a backbone, upstream flan 600 bp *CaARG4* downstream flank 500 bp	This study
plac-poly	*CaURA3, RPS1, lacZ*	[S5]
p*GDH3-lacZ*	*CaURA3, RPS1, lacZ*, promoter of *CaGDH3*	This study
p*TLO-lacZ-126*	*CaURA3, RPS1, lacZ*, 126 bp promoter of *CaTLO*	This study
p*TLO-lacZ-114*	*CaURA3, RPS1, lacZ*, 114 bp promoter of *CaTLO*	This study
p*LAT1-lacZ-270*	*CaURA3, RPS1, lacZ*, 270 bp promoter of *CaLAT1*	This study
p*LAT1-lacZ-253*	*CaURA3, RPS1, lacZ*, 253 bp promoter of *CaLAT1*	This study
p*GAL10-lacZ*	*CaURA3, RPS1, lacZ*, full-length promoter of *CaGAL10*	This study
p*GAL10-lacZ*-840	*CaURA3, RPS1, lacZ*, 840 bp promoter of *CaGAL10*	This study
p*GAL10-lacZ*-188	*CaURA3, RPS1, lacZ*, 180 bp promoter of *CaGAL10*	This study
p*GAL10-lacZ*-176	*CaURA3, RPS1, lacZ*, 176 bp promoter of *CaGAL10*	This study
p*GAL10-lacZ*-840Δ176-188	*CaURA3, RPS1, lacZ*, 840 bp Δ176-188 promoter of *CaGAL10*	This study

Table S7. Oligos Used in This Study

Oligonicleotides (Restriction Sites)	Sequence[a]	Used to Create
OMM87 (SunI)	ttcgtacgTGTTGGATTACCAAGCACTTAAGCAT	*gal4* knockout
OMM88 (BamHI)	acggatccGGCTGTTGGTAGTTTGGCGAA	*gal4* knockout
OMM89 (PmeI)	ctgtttaaacTGAGTTTGTTTTTTATCGTTTAGTT	*gal4* knockout
OMM90 (SacI)	acgagctcAACTAACCCAAAAAAAAATCGT	*gal4* knockout
OMM101 (PstI)	ccctgcagGTTCAACTAATGAATAATAAGACAAAAT	p*GDH3-lacZ*
OMM102 (BamHI)	ggggatccTGTGTATATGTGTATTTATGGATAAGTG	p*GDH3-lacZ*
OMM99 (BamHI)	ggggatccGGTATAACTCTTTCTTATAAAAATCGG	p*GAL10-lacZ*
OMM100 (BamHI)	ggggatccGTTTAAGTTTTTATTATTATGAGTTGTATATG	p*GAL10-lacZ*
OMM115 (PstI)	ggctgcagTTGGTTCCTCTTCGTCAATAT	p*GAL10-lacZ*-840Δ176-188
OMM116 (PstI)	ggctgcagCTGAAGAAAACACATAATAAACGG	p*GAL10-lacZ*-840Δ176-188
OMM123 (PstI + BsrGI)	gAGTGTAACGTTACATTGGTTCCTCTTCGTCAATATCAGATCTTCCCTCACt	p*GAL10-lacZ*-188
OMM124 (PstI + BsrGI)	gtacaGTGAGGGAAGATCTGATATTGACGAAGAGGAACCAATGTAACGTTACACTctgca	p*GAL10-lacZ*-188
OMM131 (PstI + BsrGI)	gctgcagTTGGTTCCTCTTCGTCAATATCAGATCTTCCCTCACt	p*GAL10-lacZ*-176
OMM132 (PstI + BsrGI)	gtacaGTGAGGGAAGATCTGATATTGACGAAGAGGAACCAActgcagctgca	p*GAL10-lacZ*-176
OMM133 (PstI)	ggctgcaGGGCCCGTCGACAAG	p*GAL10-lacZ*'s
OMM202 (PstI + BamHI)	gCGGAGGTCGTGTCTCCGTCTACACTCTGGGTGTAGATGTCCCTATATATCAAGGTGGTATTTCCCTGACACAAACGTCGCATAAACCAACAAGAATAATTTTATCACACCTTTATTTCCCCCCACCg	p*TLO-lacZ-126*
OMM203(PstI + BamHI)	gatccGGTGGGGGGAAATAAAGGTGTGATAAAATTATTCTTGTTGGTTTATGCGACGTTTGTGTCAGGGAAATACCACCTTGATATATAGGGACATCTACACCCAGAGTGTAGACGGAGACACGACCTCCGctgca	p*TLO-lacZ-126*
OMM204 (PstI + BamHI)	gTCTACACTCTGGGTGTAGATGTCCCTATATATCAAGGTGGTATTTCCCTGACACAAACGTCGCATAAACCAACAAGAATAATTTTATCACACCTTTATTTCCCCCCACCg	p*TLO-lacZ-114*
OMM205 (PstI + BamHI)	gatccGGTGGGGGGAAATAAAGGTGTGATAAAATTATTCTTGTTGGTTTATGCGACGTTTGTGTCAGGGAAATACCACCTTGATATATAGGGACATCTACACCCAGAGTGTAGActgca	p*TLO-lacZ-114*
OMM244 (PstI)	ggctgcagCGGACAAGATCAATCCATTGA	p*LAT1-lacZ-270*
OMM245 (PstI)	ggctgcagTTGAACACCGCAAAACAACG	p*LAT1-lacZ-253*
OMM246 (BamHI)	ggggatccTATAATTCAATGAATCTGAATAGGTTGATAGTAG	p*LAT1-lacZ*

[a] Lowercase letters in the sequence indicate restriction sites.