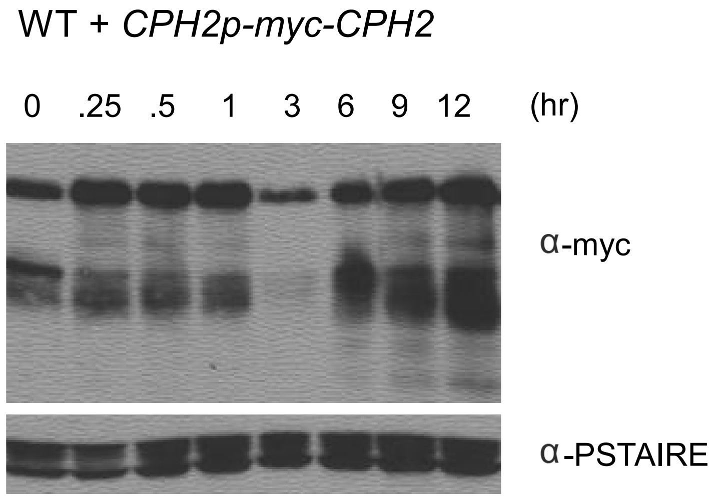

Figure S1. Levels of Cph2N during different phases of growth.
WT cells containing Cph2p-myc-Cph2 (HLY3927) were diluted from an overnight culture to a concentration of 1 X 10^7 cells/ml in YPD at 30°C. Timepoints were taken and cells processed for Western analysis. High levels of the N-terminal Cph2 were present in cells from saturating cultures, where the OD_{600} was around 10.

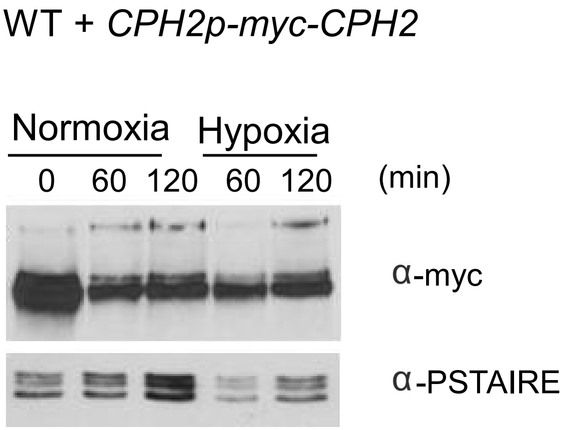

Figure S2. Cph2N level is similar in hypoxia and normoxia
Late log phase cells of Cph2-myc-Cph2 (HLY3927) were washed twice and inoculated 1:50 into prewarmed YPD at 37^{o}C, pretreated in air or hypoxia conditions for 30 minutes. Cells were collected at the times indicated for Western analysis.

Supplemental Table 1. Cph2 bound genes from ChIP-seq

	Systematic Name	**Gene Name**	**Peak Score**	**Description**	**Location**	**Peak Start**	**Peak End**
1	orf19.921	*HMS1*	288.09	Transcriptional regulator required for morphogenesis	UPSTREAM	155374	155825
2	orf19.1048	*IFD6*	199.46	Aldo-keto reductase family member	UPSTREAM	867078	867423
3	orf19.6116	*GLK4*	154.43	Putative glucokinase	UPSTREAM	162567	162594
4	orf19.3867	*RPL7*	66.67	Ribosomal protein L7; genes encoding cytoplasmic ribosomal subunits	DOWNSTREAM	131241	131282
5	orf19.6390	*UNK*	38.53	Ortholog of *Candida albicans WO-1* : CAWG_02114	INTRAGENIC	179141	179226
6	orf19.734	*GLK1*	30.74	Putative glucokinase	UPSTREAM	155874	155902
7	orf19.727	*UNK*	29.32	Predicted ORF in Assemblies 19, 20 and 21	UPSTREAM	135437	135478
8	orf19.673	*TCC1*	25.49	Protein involved in regulation of filamentous growth and virulence	UPSTREAM	172807	172844
9	orf19.4476	*UNK*	22.6	Predicted ORF in Assemblies 19, 20 and 21	UPSTREAM	844014	844360
10	orf19.5191	*FGR6-1*	20.31	Protein lacking an ortholog in S. cerevisiae	UPSTREAM	580906	581283
11	orf19.2023	*HGT7*	18.46	Putative glucose transporter	INTRAGENIC	165886	166175
12	orf19.4450.1	*UNK*	18.19	Protein conserved among the fungal CTG-clade	UPSTREAM	153578	153609
13	orf19.1785	*UNK*	17.84	Hap43p-repressed gene	UPSTREAM	204129	204161
14	orf19.7084	*DFI1*	15.88	Cell-surface associated glycoprotein	UPSTREAM	57453	58163
15	orf19.3682	*CWH8*	14.59	Putative dolichyl pyrophosphate (Dol-P-P) phosphatase	UPSTREAM	473723	473979
16	orf19.6874	*UNK*	12.26	Putative helix-loop-helix (HLH) transcription factor	UPSTREAM	114388	114408
17	orf19.882	*HSP78*	11.92	Putative heat-shock protein	UPSTREAM	709801	710055
18	orf19.7054	*UNK*	11.66	Ortholog of *Candida albicans WO-1* : CAWG_05421	INTRAGENIC	113811	114430
19	orf19.3504	*RPL23A*	11.23	Ribosomal protein	INTRAGENIC	425223	425448
20	orf19.7436	*AAF1*	10.91	Possible regulatory protein	UPSTREAM	147531	147560
21	orf19.3549	*CDC21*	10.89	Putative thymidylate synthase	UPSTREAM	106935	106958
22	orf19.1353	*UNK*	10.37	Biofilm-and planktonic growth-induced gene	INTRAGENIC	167681	167760
23	orf19.3231	*CDC27*	8.9	Putative ubiquitin-protein ligase	UPSTREAM	291026	291260
24	orf19.4961	*STP2*	8.41	Amino-acid-regulated transcription factor	UPSTREAM	291114	291140
25	orf19.5005	*OSM2*	8.32	Putative mitochondrial fumarate reductase	UPSTREAM	300599	300641
26	orf19.2943.5	*UNK*	8.3		UPSTREAM	536492	536756
27	orf19.4805	*UNK*	7.96	Putative membrane protein; Hap43p-induced gene	INTRAGENIC	208010	208034
28	orf19.2809	*CTN3*	7.82	Predicted peroxisomal carnitine acetyl transferase	UPSTREAM	835695	835967
29	orf19.5604	*MDR1*	7.72	Plasma membrane multidrug efflux pump	UPSTREAM	668512	668789
30	orf19.1659	*ALG8*	7.32	Putative glucosyltransferase involved in cell wall mannan biosynthesis	UPSTREAM	412075	412339
31	orf19.88	*ILV5*	7.07	Ketol-acid reductoisomerase	UPSTREAM	171491	171794
32	orf19.5762	*PGA61*	6.76	Putative GPI-anchored protein	UPSTREAM	843223	843466
33	orf19.33	*UNK*	6.7	Predicted ORF from Assembly 19; removed from Assembly 20	UPSTREAM	133313	133375
34	orf19.2529.1	*UNK*	6.24		UPSTREAM	338519	338932
35	orf19.4669	*AAT22*	6.17	Protein similar to S. cerevisiae Aat2p	UPSTREAM	245481	245888
46	orf19.434	*PRD1*	5.84	Putative proteinase	UPSTREAM	111607	111629
37	orf19.6659	*GAP6*	5.45	Broad-specificity amino acid permease	UPSTREAM	784941	785370
38	orf19.251	*UNK*	5.43	ThiJ/PfpI protein	UPSTREAM	566093	566415
39	orf19.5952	*UNK*	5.2	Sef1p-, Sfu1p-, and Hap43p-induced protein of unknown function	UPSTREAM	103898	103924
40	orf19.5079	*CDR4*	5.08	Putative transporter of ATP-binding cassette (ABC) superfamily	UPSTREAM	175711	175789
41	orf19.6869	*UNK*	4.73	Ortholog(s) have role in protein targeting to membrane and cytoplasm	UPSTREAM	113217	113270
42	orf19.542	*HXK2*	4.58	Hexokinase II	UPSTREAM	994880	995199
43	orf19.4679	*AGP2*	4.55	Amino acid permease	UPSTREAM	227679	228124
44	orf19.1313	*CDR3*	4.48	Transporter of the Pdrp/Cdrp family of the ATP-binding cassette	UPSTREAM	780135	780536
45	orf19.3981	*MAL31*	4.48	Putative high-affinity maltose transporter	UPSTREAM	107625	107661
46	orf19.6738	*VAN1*	4.38	Member of Mnn9p family of mannosyltransferases	UPSTREAM	171275	171299
47	orf19.5626	*UNK*	4.32	Biofilm-induced gene	UPSTREAM	707988	708250
48	orf19.460	*CEK2*	4.31	MAP kinase required for wild-type efficiency of mating	UPSTREAM	124368	124391
49	orf19.4702	*UNK*	4	Biofilm-induced gene	UPSTREAM	168104	168411
50	orf19.1826	*MDM34*	3.93	Putative transcription factor with zinc finger DNA-binding motif	UPSTREAM	130314	130351
51	orf19.4081	*UNK*	3.92	Ortholog of *Candida dubliniensis CD36* : CD36_23345	UPSTREAM	188804	188834
52	orf19.3490	*FGR6-4*	3.73	Protein lacking an ortholog in S. cerevisiae	UPSTREAM	214745	214782
53	orf19.822	*HSP21*	3.73	Small heat shock protein involved in stress response and virulence	INTRAGENIC	838509	838780
54	orf19.347	*RSN1*	3.67	Hap43p-repressed gene	UPSTREAM	742403	742794
55	orf19.7077	*UNK*	3.64	Putative ferric reductase	INTRAGENIC	70565	70819

56	orf19.6986	*UNK*	3.57	Has domain(s) with predicted Rab GTPase activator activity	UPSTREAM	123254	123288
57	orf19.2468	*UNK*	3.52	Ortholog(s) have trans-aconitate 3-methyltransferase activity	UPSTREAM	121374	121398
58	orf19.903	*GPM1*	3.32	Phosphoglycerate mutase	INTRAGENIC	675941	676726
59	orf19.2825	*UNK*	3.26	Putative cytosolic Fe-S protein assembly protein	UPSTREAM	611274	611696
60	orf19.5334	*UNK*	3.24	Biofilm- and planktonic growth-induced gene	INTRAGENIC	217980	218046
61	orf19.3405	*ZCF18*	3.1	Putative transcription factor with zinc finger DNA-binding motif	UPSTREAM	378654	378913
62	orf19.1690	*TOS1*	3.1	Protein similar to alpha agglutinin anchor subunit	UPSTREAM	339956	340170
63	orf19.837	*GNA1*	3.03	Glucosamine-6-phosphate acetyltransferase	UPSTREAM	810256	810642
64	orf19.2929	*GSC1*	3.02	Subunit of beta-1,3-glucan synthase	UPSTREAM	513495	513762
65	orf19.542	*HXK2*	2.96	Hexokinase II; antigenic in humans	INTRAGENIC	995409	996312
66	orf19.2529.1	*UNK*	2.94		UPSTREAM	339448	339710
67	orf19.515	*UNK*	2.91	Has domain(s) with predicted nucleic acid binding, zinc ion binding	UPSTREAM	955207	955498
68	orf19.396	*EAF6*	2.87	Subunit of the NuA4 histone acetyltransferase complex	UPSTREAM	186571	186642
69	orf19.7021	*GPH1*	2.74	Putative glycogen phosphorylase with a role in glycogen metabolism	UPSTREAM	193154	193386
70	orf19.4064	*GPI7*	2.37	Protein involved in attachment of GPI-linked proteins to cell wall	UPSTREAM	106254	106281

Supplemental Table 2. Genes regulated by Cph2 in RNA-seq.

	Systematic Name	Gene Name	Description	Mean Wild Type	Mean *cph2*	fold change	p-value
1	**orf19.4450.**		**Protein conserved among the fungal CTG-clade**	**8374.47**	**204.18**	**-41.01**	**1.69E-006**
2	orf19.822	*HSP21*	Small heat shock protein involved in stress response and	3549.29	266.543	-13.31	0.00818
3	orf19.1187	*CPH2*	Myc-bHLH family transcriptional activator of hyphal growth	136.131	11.3625	-11.98	5.83E-005
4	orf19.5308		Predicted ORF in Assemblies 19, 20 and 21	24.8238	4.65898	-5.328	0.00863
5	orf19.823		Ortholog of *C. parapsilosis CDC317* : CPAR2_209270	354.824	72.1822	-4.915	0.000530
6	orf19.6882	*OSM1*	Putative flavoprotein subunit of fumarate reductase	258.922	54.9780	-4.709	0.000363
7	orf19.4035	*PGA4*	GPI-anchored cell surface protein	181.815	38.7474	-4.692	0.000271
8	orf19.2608	*ADH5*	Putative alcohol dehydrogenase	2944.90	628.101	-4.688	0.00417
9	orf19.5288	*IFE2*	Putative alcohol dehydrogenase	291.002	64.3727	-4.520	0.00236
10	orf19.675.1		Putative adhesin-like protein	62.1758	14.1706	-4.387	0.00357
11	**orf19.2529.**			**308.161**	**71.165**	**-4.330**	**0.003700**
12	orf19.2175		Putative mitochondrial cell death effector	364.292	85.2045	-4.275	0.00883
13	**orf19.2023**	***HGT7***	**Putative glucose transporter**	**38.8441**	**9.3978**	**-4.133**	0.000892
14	orf19.2344	*ASR1*	Putative heat shock protein	1226.59	299.269	-4.098	0.00247
15	orf19.7284	*ASR2*	Gene regulated by cAMP and by osmotic stress	1868.84	477.657	-3.912	0.00551
16	orf19.2241	*PST1*	Putative 1,4-benzoquinone reductase	1444.31	392.951	-3.675	0.00285
17	orf19.3548.	*WH11*	Cytoplasmic protein expressed specifically in white phase	65535.4	18317.5	-3.577	3.29E-009
18	orf19.4816		Predicted ORF in Assemblies 19, 20 and 21; induced by	68.876	19.8661	-3.467	0.00497
19	orf19.7283		Ortholog of *C. parapsilosis CDC317* : CPAR2_201190	93.6196	27.6754	-3.382	0.000558
20	orf19.5813		Putative adhesin-like protein	302.097	90.5174	-3.337	0.000630
21	orf19.320		Has domain(s) with predicted nucleotide binding,	152.254	45.8673	-3.319	0.00527
22	orf19.5342.		Protein of unknown function	433.591	130.669	-3.318	0.005047
23	orf19.4044	*MUM2*	Protein similar to *S. cerevisiae* Mum2p	212.756	65.1743	-3.264	0.004214
24	orf19.3822	*SCS7*	Putative ceramide hydroxylase	82.7424	25.4679	-3.248	0.00192
25	orf19.2803	*HEM13*	Coproporphyrinogen III oxidase;	137.405	43.1068	-3.187	0.00558
26	orf19.1395		Ortholog(s) have inorganic phosphate transmembrane	46.507	15.0772	-3.084	0.004478
27	**orf19.88**	***ILV5***	**Ketol-acid reductoisomerase**	**150.131**	**48.779**	**-3.077**	**0.006042**
28	orf19.5158		Protein with similarity to a human gene associated with	370.254	122.215	-3.029	0.00857
29	**orf19.921**	***HMS1***	**Transcriptional regulator required for morphogenesis**	**20.3001**	**6.8038**	**-2.983**	**0.000143**
30	orf19.4943	*PSA2*	Mannose-1-phosphate guanyltransferase	365.304	123.754	-2.951	0.00234
31	orf19.4631	*ERG251*	C-4 sterol methyl oxidase with a role in ergosterol	158.298	53.704	-2.947	0.00314
32	orf19.3932.		Has domain(s) with predicted nucleic acid binding,	148.006	51.689	-2.863	0.00179
33	orf19.3651	*PGK1*	Phosphoglycerate kinase, enzyme of glycolysis	3478.05	1215.47	-2.861	0.00547
34	orf19.5437	*RHR2*	Glycerol 3-phosphatase	148.099	54.124	-2.736	0.00122
35	orf19.5307	*JEN2*	Dicarboxylic acid transporter	102.965	37.660	-2.734	0.000811
36	orf19.4043		Predicted ORF in Assemblies 19, 20 and 21	152.648	56.1162	-2.720	0.00106
37	orf19.5906	*ADE2*	Phosphoribosylaminoimadazole carboxylase	51.5727	18.979	-2.717	0.00193
38	orf19.6321	*PGA48*	Putative GPI-anchored; adhesin-like protein	104.393	40.0591	-2.605	0.00957
39	orf19.3707	*YHB1*	Nitric oxide dioxygenase, acts in nitric oxide	275.450	105.74	-2.604	0.00305
40	orf19.6731		Predicted ORF in Assemblies 19, 20 and 21	43.6092	16.8821	-2.583	0.00247
41	orf19.6770		Ortholog of *Candida dubliniensis CD36* : CD36_87190	84.7933	32.917	-2.575	0.00165
42	orf19.11		Gene transcription regulated by Mig1p and Tup1p	24.2975	9.43942	-2.574	0.000478
43	orf19.1862		Possible stress protein	3859.69	1502.06	-2.569	0.00881
44	orf19.4886		Putative adhesin-like protein	32.3986	12.609	-2.569	0.000223
45	**orf19.1048**	***IFD6***	**Aldo-keto reductase family member**	**41.0022**	**16.012**	**-2.560**	**0.000769**
46	orf19.7027		Ortholog of *C. parapsilosis CDC317* : CPAR2_301430	89.7418	35.095	-2.557	0.00387
47	orf19.2583	*PTR2*	Oligopeptide transporter involved in uptake of di-	78.6124	31.157	-2.523	0.00254
48	orf19.4530.1		Biofilm- and planktonic growth-induced gene	162.565	65.1257	-2.4962	0.008624
49	orf19.3997	*ADH1*	Alcohol dehydrogenase ihuman/mocomplements S.	14698.3	5908.91	-2.4875	0.000547
50	orf19.6387	*HSP104*	Heat-shock protein	368.23	150.035	-2.4543	0.006258
51	orf19.4051	*HTS1*	Putative tRNA-His synthetase	100.889	41.1232	-2.4533	0.006179
52	orf19.238	*CCP1*	Similar to cytochrome-c peroxidase N terminus	1209.8	502.189	-2.409	0.007917
53	orf19.395	*ENO1*	Enolase, enzyme of glycolysis and gluconeogenesis	6041.99	2526.71	-2.3912	0.001792
54	orf19.3612	*PST2*	Putative NADH:quinone oxidoreductase	174.807	73.5279	-2.3774	0.007618
55	orf19.2770		Ortholog of C. parapsilosis CDC317 : CPAR2_500340	49.6368	21.0461	-2.3585	0.000932

56	**orf19.5079**	***CDR4***	**Putative transporter of ATP-binding cassette (ABC)**	**142.547**	**60.5898**	**-2.3527**	0.00179
57	orf19.4040	*ILV3*	Putative dihydroxyacid dehydratase	58.6053	24.9113	-2.3526	0.002409
58	orf19.2691		Planktonic growth-induced gene	133.542	57.467	-2.3238	0.003818
59	orf19.1375	*LEU42*	Putative alpha-isopropylmalate synthase	39.5192	17.051	-2.3177	0.004711
60	orf19.1802	*OFD1*	Putative termination and polyadenylation protein	78.7728	34.2806	-2.2979	0.007733
61	orf19.903	*GPM1*	Phosphoglycerate mutase	4492.86	1978.79	-2.2705	0.007469
62	orf19.6688		Decreased transcription is observed upon benomyl	392.397	173.536	-2.2612	0.007204
63	orf19.6640	*TPS1*	Trehalose-6-phosphate synthase	137.694	61.7288	-2.2306	0.002658
64	orf19.3515		Putative 3-hydroxyanthranilic acid dioxygenase	275.165	125.934	-2.185	0.007145
65	orf19.5446		Putative protein of unknown function	308.353	144.481	-2.1342	0.006577
66	orf19.7053	*GAC1*	Putative regulatory subunit of serine/threonine	69.477	32.6912	-2.1252	0.006993
67	orf19.6472	*CYP1*	Peptidyl-prolyl cis-trans isomerase	5727.28	2699.15	-2.1219	0.006625
68	orf19.7080	*LEU2*	Isopropyl malate dehydrogenase	130.496	62.9254	-2.0738	0.005276
69	**orf19.4476**		**Predicted ORF in Assemblies 19, 20 and 21**	**58.5462**	**28.5623**	**-2.0498**	0.008523
70	orf19.3139		Hap43p-repressed gene	34.3907	17.1416	-2.0063	0.009489
71	orf19.1290	*XKS1*	Putative xylulokinase	62.5369	31.7229	-1.9714	0.005875
72	orf19.1034		Hap43p-repressed gene	110.042	56.6731	-1.9417	0.007308
73	orf19.4032	*RPN5*	Putative COP9 signalosome component	60.7539	31.2904	-1.9416	0.008987
74	orf19.6814	*TDH3*	NAD-linked glyceraldehyde-3-phosphate dehydrogenase	13536	7057.48	-1.918	8.49E-005
75	orf19.4056	*BRG1*	DNA-binding transcription factor involved in control of	148.637	77.5231	-1.9173	0.008672
76	orf19.3150	*GRE2*	Putative reductase; Nrg1p- and Tup1p-regulated	61.1909	32.1308	-1.9044	0.004936
77	orf19.3104	*YDC1*	Protein with Mob2p-dependent hyphal regulation	21.6807	11.4035	-1.9012	0.009673
78	orf19.3859		Putative microsomal beta-keto-reductase	131.331	69.6242	-1.8863	0.009104
79	orf19.6602		Ortholog(s) have role in aerobic respiration	93.122	49.8379	-1.8685	0.009203
80	orf19.801	*TBF1*	Essential transcriptional activator that regulates ribosomal	28.1394	15.1279	-1.8601	0.002751
81	orf19.5205		Hap43p-repressed gene	28.0279	15.1716	-1.8474	0.001643
82	orf19.4953		Ortholog(s) have ATPase activity, role in ER-associated	77.9322	42.5306	-1.8324	0.007376
83	orf19.2219	*ORF298*	Predicted ORF in retrotransposon Tca3 with similarity to	38.2106	20.948	-1.8241	0.003566
84	orf19.904		Ortholog(s) have cytosol, nucleus localization	46.7435	25.8557	-1.8079	0.005568
85	orf19.5206		Ortholog(s) have unfolded protein binding activity	23.1821	12.8312	-1.8067	0.001713
86	orf19.4029		Ortholog(s) have role in ribosomal large subunit assembly	140.732	80.2452	-1.7538	0.009456
87	orf19.4046		Putative transcription factor containing a Zn(2)-Cys(6)	50.7143	29.1152	-1.7418	0.006605
88	orf19.4045	*EST1*	Telomerase subunit; allosteric activator of catalytic activity	50.7908	29.687	-1.7109	0.006727
89	orf19.260	*SLD1*	Sphingolipid delta-8 desaturase	41.8382	24.4719	-1.7096	0.005366
90	orf19.1979	*GIT3*	Putative glycerophosphoinositol permease	46.6121	27.3	-1.7074	0.004603
91	orf19.6891	*RFC1*	Protein similar to S. cerevisiae Rfc1p	47.2491	27.8008	-1.6996	0.009178
92	orf19.5210		Hap43p-repressed gene	28.6134	16.9757	-1.6856	0.004617
93	orf19.4871	*ERO1*	Protein similar to S. cerevisiae Ero1p	27.7984	16.8659	-1.6482	0.008914
94	orf19.5801	*RNR21*	Ribonucleoside-diphosphate reductase	44.3686	26.9703	-1.6451	0.008728
95	orf19.5855	*MBP1*	Putative component of the MBF transcription complex	23.6166	14.5325	-1.6251	0.007366
96	orf19.6800	*POS5*	Protein similar to S. cerevisiae Pos5p	34.2607	21.6371	-1.5834	0.009456
97	orf19.7668	*MAL2*	Alpha-glucosidase that hydrolyzes sucrose	31.0262	20.4803	-1.5149	0.009374
98	orf19.3940.1	*CUP1*	Metallothionein, involved in copper resistance	33223.2	24760.9	-1.3418	2.31E-005
99	orf19.2107.1	*STF2*	Protein involved in ATP biosynthesis	26462.8	22096.5	-1.1976	0.009328
100	orf19.918	*CDR11*	Putative transporter of PDR subfamily of ABC family	26.9966	43.6533	1.61699	0.005554
101	orf19.1617		Protein similar to S. cerevisiae Ydr282cp	28.6718	46.3732	1.61738	0.008994
102	orf19.6923		Ortholog(s) have chromatin binding activity	26.7027	44.1878	1.6548	0.004538
103	orf19.6781	*ZFU2*	Transcriptional regulator of yeast form adherence	23.4062	38.7594	1.65594	0.008013
104	orf19.2974	*YKT6*	Putative protein of the vacuolar SNARE complex	46.456	77.3722	1.6655	0.00726
105	orf19.4988		Predicted ORF in Assemblies 19, 20 and 21	30.09	50.3279	1.67258	0.004992
106	orf19.3167		Ortholog(s) have role in heme a biosynthetic process	52.9198	90.0801	1.7022	0.007225
107	orf19.100		Hap43p-repressed gene; late-stage biofilm-induced	23.4129	39.9023	1.70429	0.004302
108	orf19.1653		Has domain(s) with predicted integral to membrane	100.848	172.332	1.70883	0.006688
109	orf19.5215	*TES15*	Putative acyl-CoA thioesterase; Hap43p-repressed gene	29.5171	51.1599	1.73323	0.005433
110	orf19.2154	*HXK1*	N-acetylglucosamine (GlcNAc) kinase	63.0099	109.472	1.73737	0.006152
111	orf19.5617		Ortholog(s) have methylated histone residue binding	73.6881	128.678	1.74625	0.008064
112	orf19.2215	*GLE1*	Putative nucleoporin; moderately induced at 42 degrees C	71.2031	124.366	1.74664	0.006556
113	orf19.339	*NDE1*	Putative NADH dehydrogenase	44.0523	77.0306	1.74861	0.005229
114	orf19.4811		Putative tricarboxylate carrier family protein	30.9706	54.2066	1.75026	0.006333

115	orf19.5142	*DFR1*	Trimethoprim resistant dihydrofolate reductase (DHFR)	32.1555	56.7851	1.76595	0.006531
116	orf19.5143		Predicted component of the mitochondrial TIM22	66.3276	117.423	1.77035	0.008756
117	orf19.685.1		Ortholog of C. parapsilosis CDC317 : CPAR2_602135	33.6957	59.9614	1.7795	0.004762
118	orf19.4028		Ortholog(s) have dehydrodolichyl diphosphate synthase	42.2892	75.2758	1.78002	0.009542
119	orf19.1738.1		Ortholog(s) have beta-tubulin binding activity	95.9463	171.188	1.78421	0.005627
120	orf19.871		Ortholog(s) have protein transporter activity	27.8127	50.3503	1.81033	0.002447
121	orf19.2671		Predicted ORF in Assemblies 19, 20 and 21	24.9487	45.1834	1.81105	0.004783
122	orf19.1133	*MSB1*	Putative regulator of transcription	43.94	79.5839	1.8112	0.00536
123	orf19.3829	*PHR1*	Glycosidase of cell surface	67.8759	123.138	1.81417	0.009854
124	orf19.1547		Ortholog(s) have polynucleotide 3'-phosphatase activity	28.1037	51.1821	1.82118	0.007989
125	orf19.2463	*PRN2*	Protein similar to pirin; Hap43p-repressed gene	21.7233	39.6704	1.82617	0.004701
126	orf19.3963		Ortholog(s) have mitochondrion localization	27.9693	51.433	1.83891	0.003318
127	orf19.2956	*MGM101*	Putative mitochondrial genome maintenance protein	83.3428	154.657	1.85567	0.003496
128	orf19.685	*YHM1*	Putative mitochondrial carrier protein	100.956	187.36	1.85585	0.004521
129	orf19.7125			59.3591	110.476	1.86115	0.005036
130	orf19.5755		Ortholog(s) have cyclin-dependent protein kinase regulator	37.5667	70.2229	1.86929	0.007902
131	orf19.3516		Hap43p-repressed gene	22.9719	42.9538	1.86984	0.000956
132	orf19.4894		Protein with similarity to S. cerevisiae Yer010cp	50.8737	95.4026	1.87528	0.004591
133	orf19.5026		Putative transcription factor with zinc finger DNA-binding	46.4331	88.2526	1.90064	0.003006
134	orf19.3213		Ortholog of S. cerevisiae : JIP4, C. glabrata CBS138 :	28.6406	54.5311	1.90398	0.00522
135	orf19.372		Putative protein of unknown function; Hap43p-repressed gene	52.62	101.883	1.93619	0.008403
136	orf19.4983		Ortholog of C. parapsilosis CDC317: CPAR2_201720	20.7581	40.1979	1.93649	0.001586
137	orf19.4956	*RPN1*	Putative 19S regulatory particle of the 26S proteasome	93.5421	182.594	1.95199	0.002894
138	**orf19.2809**	***CTN3***	**Predicted peroxisomal carnitine acetyl transferase**	**88.2843**	**172.648**	**1.95559**	0.003617
139	orf19.5650	*PRO3*	Delta 1-pyrroline-5-carboxylate reductase	97.3529	191.489	1.96696	0.006174
140	orf19.4506	*LYS22*	Putative homocitrate synthase	40.9754	81.2707	1.9834	0.001509
141	orf19.73		Ortholog(s) have role in ribosome biogenesis and	20.2609	40.2208	1.98514	0.000905
142	orf19.9		Ortholog of C. parapsilosis CDC317 : CPAR2_204280	24.2302	48.5458	2.00352	0.002819
143	orf19.1866	*VMA10*	Ortholog(s) have cytosol, nucleus, vacuolar proton-	6632.9	13527.8	2.0395	0.004442
144	orf19.1089	*PEX11*	Putative peroxisomal membrane protein	156.423	322.507	2.06176	0.005958
145	orf19.234	*PHA2*	Putative prephenate dehydratase	34.0887	72.1067	2.11527	0.002727
146	orf19.5474		Predicted ORF in Assemblies 19, 20 and 21	102.377	216.643	2.11613	0.006495
147	orf19.6112	*CTA2*	Putative transcriptional activator	180.067	396.758	2.20339	0.002294
148	orf19.376		Hap43p-repressed gene	59.8166	134.124	2.24226	0.005097
149	orf19.6916		Ortholog(s) have unfolded protein binding activity	20.822	47.2336	2.26845	0.000946
150	orf19.7306		Aldo-keto reductase family protein	40.3784	91.9867	2.27811	0.001375
151	orf19.4012	*PCL5*	Protein similar to S. cerevisiae Pcl5p and other cyclins for	35.7162	82.1279	2.29946	0.001162
152	orf19.6724	*FUM12*	Putative fumarate hydratase, enzyme of citric acid cycle	140.139	323.46	2.30815	0.000752
153	orf19.1797		Predicted ORF in Assemblies 19, 20 and 21	30.0966	69.8721	2.3216	0.001892
154	orf19.6163	*CSE4*	Centromeric histone H3 variant	21.9305	51.1511	2.33242	0.002388
155	orf19.5589		Predicted ORF in Assemblies 19, 20 and 21	90.1086	215.168	2.38788	0.002831
156	orf19.7098		Putative protein of unknown function	35.3206	84.8364	2.40189	0.001512
157	orf19.2125		GlcNAc-induced protein	149.214	358.639	2.40351	0.009773
158	orf19.1064	*ACS2*	Acetyl-CoA synthetase	99.9497	240.231	2.40352	0.001332
159	orf19.588		Ortholog(s) have role in aerobic respiration	25.6727	62.6333	2.43969	0.000661
160	orf19.1301		Ortholog(s) have cytoplasm, nucleus, ribosome localization	55.345	135.63	2.45062	0.00078
161	orf19.2269		Putative 3-phosphoserine phosphatase	45.811	112.429	2.45418	0.000611
162	orf19.4324		Has domain(s) with predicted NADH dehydrogenase	35.3669	87.6095	2.47716	0.00022
163	orf19.6509		Ortholog(s) have role in cellular response to zinc ion and	118.189	293.297	2.48159	0.003075
164	orf19.6972	*SMI1B*	Putative cell wall assembly regulatory protein	55.0073	139.784	2.54119	0.004613
165	orf19.7127.1		Putative protein of unknown function	44.6319	113.582	2.54486	0.00182
166	orf19.2752	*ADR1*	Putative transcription factor with zinc finger DNA-binding	20.5526	55.2982	2.69057	0.00034
167	orf19.6114		Predicted ORF in Assemblies 19, 20 and 21	278.3	760.001	2.73087	0.001427
168	orf19.5975	*TRY4*	Putative zinc finger DNA-binding transcription factor	225.715	616.699	2.73221	0.002659
169	orf19.4600		Ortholog(s) have mitochondrion localization	42.8462	125.291	2.92419	0.000152
170	orf19.5806	*ALD5*	NAD-aldehyde dehydrogenase	1707.65	5080.87	2.97536	0.001791
171	orf19.5741	*ALS1*	Adhesin; ALS family of cell-surface glycoproteins	169.607	524.629	3.0932	0.001508
172	orf19.3441	*FRP6*	Putative ammonia transport protein	143.482	447.26	3.11719	0.001477
173	orf19.499		Ortholog(s) have S-adenosylmethionine-dependent	26.8841	84.1157	3.12883	0.000131

174	orf19.183	*HIS3*	Imidazoleglycerol-phosphate dehydratase	24.6584	82.0688	3.32823	0.000363
175	orf19.6169	*ATO1*	Putative fungal-specific transmembrane protein	61.9306	213.287	3.44397	0.002506
176	orf19.4551	*CTN1*	Predicted carnitine acetyl transferase	23.9638	83.3609	3.47862	0.000158
177	orf19.1258		Putative adhesin-like protein	21.9508	78.6629	3.58359	0.000215
178	orf19.7112	*FRP2*	Putative ferric reductase	32.4452	133.272	4.10759	0.000125
179	orf19.1743	*ACS1*	Putative acetyl-CoA synthetase	161.543	681.531	4.21889	0.000871
180	orf19.4773	*AOX2*	Alternative oxidase	164.72	730.437	4.43443	0.000774
181	orf19.4921.1		Ortholog of C. parapsilosis CDC317 : CPAR2_801610	752.891	3392.78	4.50634	0.000623
182	orf19.3934	*CAR1*	Arginase involved in arginine catabolism	266.082	1368.33	5.14249	0.000997
183	orf19.4393	*CIT1*	Citrate synthase	251.299	1302.52	5.18316	0.000233

* The bolded genes are overlapping with the ChIP-Seq Genes.

Supplemental Table 3. qPCR verification of genes differentially regulated in *cph2* versus wild type in RNA-seq

	Systematic	**Gene Name**	**Mean Wild Type**	**Mean *cph2***	**fold change**	**p-value**	**qPCR value**
1	orf19.4450.		8374.5	204.2	-41.0	1.7E-006	-18
2	orf19.822	*HSP21*	3549.3	266.5	-13.3	0.0082	-7.9
3	orf19.6882	*OSM1*	258.9	55.0	-4.7	0.00036	-2.6
4	orf19.2803	*HEM13*	137.4	43.1	-3.2	0.0056	-3.1
5	orf19.921	*HMS1*	20.3	6.8	-3.0	0.00014	-5.7
6	orf19.4631	*ERG251*	158.3	53.7	-2.9	0.0031	-7.6
7	orf19.2583	*PTR2*	78.6	31.2	-2.5	0.0025	-2.5
8	orf19.5079	*CDR4*	142.5	60.6	-2.4	0.0018	-13.7
9	orf19.4056	*BRG1*	148.6	77.5	-1.9	0.0087	-6.5
10	orf19.3940.	*CUP1*	33223.2	24760.9	-1.3	2.3E-005	-1.4
11	orf19.7112	*FRP2*	32.4	133.3	4.1	0.000125	3.8
12	orf19.4393	*CIT1*	251.3	1302.5	5.2	0.00023	6.0

Supplemental Table 4. Gene ontology terms for Cph2-regulated genes from RNA-seq

Gene Ontology term	Cluster frequency	Background frequency	Corrected P-value	False discovery rate	Genes annotated to the term
oxidation-reduction process	35 out of 183 genes, 19.1%	418 out of 6517 background genes, 6.4%	1.79e-06	0.00%	ACS1, ADH1, ADH5, ALD5, AOX2, CCP1, CIT1, CTN1, DFR1, ERG251, ERO1, FRP2, FUM12, GAC1, HEM13, IFE2, ILV5, LEU2, NDE1, OFD1, OSM1, PEX11, PRO3, RNR21, SCS7, TDH3, YHB1, orf19.2175, orf19.2671, orf19.3139, orf19.3515, orf19.5158, orf19.588, orf19.6602, orf19.7098
glycolytic process	6 out of 183 genes, 3.3%	16 out of 6517 background genes, 0.2%	0.00168	0.00%	ADH1, ENO1, GPM1, HXK1, PGK1, TDH3
single-organism metabolic process	74 out of 183 genes, 40.4%	1656 out of 6517 background genes, 25.4%	0.00261	0.00%	ACS1, ACS2, ADE2, ADH1, ADH5, ALD5, AOX2, CAR1, CCP1, CIT1, CTN1, CTN3, CYP1, DFR1, ENO1, ERG251, ERO1, EST1, FRP2, FUM12, GAC1, GPM1, HEM13, HIS3, HSP104, HSP21, HTS1, HXK1, IFE2, ILV3, ILV5, LEU2, LEU42, LYS22, MAL2, MGM101, MUM2, NDE1, OFD1, OSM1, PEX11, PGA4, PGK1, PHA2, POS5, PRO3, RFC1, RHR2, RNR21, SCS7, SLD1, STF2, TBF1, TDH3, TPS1, XKS1, YDC1, YHB1, orf19.100, orf19.1547, orf19.2175, orf19.2671, orf19.3139, orf19.3167, orf19.3515, orf19.372, orf19.3859, orf19.4028, orf19.4988, orf19.5158, orf19.588, orf19.6602, orf19.7098, orf19.7306
generation of precursor metabolites and energy	15 out of 183 genes, 8.2%	135 out of 6517 background genes, 2.1%	0.00284	0.00%	ACS1, ADH1, AOX2, CIT1, CTN1, ENO1, FUM12, GAC1, GPM1, HXK1, NDE1, PGK1, TDH3, orf19.588, orf19.6602
single-organism biosynthetic process	36 out of 183 genes, 19.7%	628 out of 6517 background genes, 9.6%	0.01252	0.00%	ACS1, ACS2, ADE2, ALD5, DFR1, ENO1, ERG251, EST1, GPM1, HEM13, HIS3, HTS1, ILV3, ILV5, LEU2, LEU42, LYS22, MUM2, PGA4, PGK1, PHA2, POS5, PRO3, RHR2, RNR21, SCS7, SLD1, STF2, TPS1, YDC1, orf19.3167, orf19.3515, orf19.3859, orf19.4028, orf19.6602, orf19.7306
cofactor metabolic process	14 out of 183 genes, 7.7%	135 out of 6517 background genes, 2.1%	0.01324	0.00%	ACS1, ACS2, CIT1, CTN1, CTN3, DFR1, HEM13, NDE1, POS5, TES15, orf19.2175, orf19.3167, orf19.3515, orf19.6602
thioester metabolic process	6 out of 183 genes, 3.3%	23 out of 6517 background genes, 0.4%	0.01803	0.00%	ACS1, ACS2, CIT1, CTN1, CTN3, TES15
acyl-CoA metabolic process	6 out of 183 genes, 3.3%	23 out of 6517 background genes, 0.4%	0.01803	0.00%	ACS1, ACS2, CIT1, CTN1, CTN3, TES15

Terms from the Process Ontology

Supplemental Table 5. Plasmids

P866	Mal2p-myc-GFP
P873	Mal2p-GFP-Hgc1
P1021	Mal2-myc-Cph2 #15
P1048	Mal2p-myc-Cph2N plasmid
P1033	Cph2p-myc-Cph2 plasmid
P1085	Cph2p-Cph2-myc plasmid
P1028	Mal2p-GFP-Cph2 plasmid
P1032	Mal2p-GFP-Cph2-myc plasmid
pLC597	Shapiro et al., 2012 (7)

Supplemental Table 6. Primers used in this study

Primer#	Sequence	Purpose
1	CG GGATCC CTTATCGCAGTATGATGAACA	CPH2p-Cph2-myc subcloning
2	GCG ACGCGT CG CTGCTTCATCACTCTCATTAA	
9	5'- AGCTGGTGTGCCACCTCCAC	*BRG1* qPCR
10	5'- TACCACACCTGTGACATCTG	
GFPMluI Forward	GCACGCGTATGTCTAAAGGTGAAGAATTATTC	Mal2p-myc-GFP subcloning
GFPKpnI Reverse	GGGGTACCTTATTTGTACAATTCATCCATACC	
GFPXBaI Forward	GCTCTAGAATGTCTAAAGGTGAAGAATTATTC	Mal2p-GFP-HGC1 subcloning
842	CGACGCGTTTTGTACAATTCATCCATACC	
1086	CCATCGATATTTGTTGGGAGGTATGG	Mal2p-GFP-Cph2-myc subclone
925	CGGGGTACCTCAGTGATTGATTAATTTTTGTTCACCG	
990	TGGAAGCTGCTGGTATTGAC	*ACT1* qPCR
991	TTCAGCAATACCTGGGAACA	
1052	CGACGCGTATGTTATCGCAGTATGATGAAC	Mal2p-myc-Cph2 and Mal2-GFP-Cph2 subcloning
1053	GGGGTACCCTCTTGTCTATACTGTTCCG	
1102	ATAAGAATGCGGCCGCATTGGAGTTTACAGAGGAACG	Cph2p-myc-Cph2 subcloning
1103	GGACTAGTTAGATGGTTGAATTATAATTCG	
1124	CCTCCACCTCCTCAACAAAT	*CPH2* qPCR
1125	GGGTGACATTGAATGATTGG	
1128	GGGGTACCTTATTGAATAGTCAATGGCGATGG	Mal2p-myc-Cph2N subcloning
1475	TGGAGGTGTGTGCTATGGTT	*orf19.4450.1* qPCR
1476	TGCATTGGGTGAACTCTTTC	
1479	TGCAGACAATGTTGTGTTGG	*OSM1* qPCR
1480	TTTGTCCGTCACCAGTTGTT	
1481	GGTCTCTCGTTATGGTGCTG	*HSP21* qPCR
1482	ACATTGTCATCGAAACCAACA	
1501	CCACCACAGCTACATCCTCA	*HMS1* qPCR
1502	TTGGAGCAGAATTGGATGTG	
1511	ATTGCAAACTCCAGGGTCTC	*HEM13* qPCR
1512	GGTTCAGGATGATGGTCGTA	
1513	TGCTTATTTGGCCACAGTTT	*ERG251* qPCR
1514	CCCAAAGTGGGAAGAACTTG	
1515	ATGAGTTGCGGAAATGACAA	*FRP2* qPCR
1516	TTTGGTGCATCTTTAACCCA	
1517	CGGTAAGACCAAGAACCCAT	*CIT1* qPCR
1518	AATTGTGGCAAGACACCAAA	
1519	TCACAATGTGTTTGGCCTTT	*CDR4* qPCR
1520	CACTGACAACATCACCGACA	
1525	TACGCATCTGGCTGCTCTT	*CUP1* qPCR
1526	GAAGCACATTTGCATTCAGTTT	
1543	GGGTATTCCTTGCAATTGGT	*PTR2* qPCR
1544	CCTCTGTTGGCTTCCTCTTC	
1577	TTTTTCAACAAAAGCTGTTGCG	ARG4 Transformation
1578	TCAAAGGACTCTCATTAGAGC	

Supplemental Table 7. Strains used in this study

Strains	Genotype	Source
SC5314	Wild Type	(1)
CAI4	*ura3Δ::imm^{434}/ura3Δ::imm^{434}*	(2)
BWP17	*ura3Δ::imm^{434}/ura3Δ::imm^{434}, his1Δ::hisG/his1Δ::hisG, arg4Δ::hisG/arg4Δ::hisG*	(3)
HLY3927	*ura3Δ::imm^{434}/ura3Δ::imm^{434}, his1Δ::hisG/his1Δ::hisG, arg4Δ::hisG/arg4Δ::hisG, ADE2/ade2Δ::CPH2p-myc-CPH2-URA3*	This Study
HLY3829	*ura3Δ::imm^{434}/ura3Δ::imm^{434}, his1Δ::hisG/his1Δ::hisG, arg4Δ::hisG/arg4Δ::hisG, CPH2/CPH2::CPH2-myc-URA3*	This Study
HLY3918	*ura3Δ::imm^{434}/ura3Δ::imm^{434}, his1Δ::hisG/his1Δ::hisG, arg4Δ::hisG/arg4Δ::hisG, ADE2/ade2Δ::MAL2p-GFP-CPH2-URA3*	This Study
HLY3919	*ura3Δ::imm^{434}/ura3Δ::imm^{434}, his1Δ::hisG/his1Δ::hisG, arg4Δ::hisG/arg4Δ::hisG, ADE2/ade2Δ::MAL2p-GFP-CPH2-myc-URA3*	This Study
HLY3966	*ura3Δ::imm^{434}/ura3Δ::imm^{434}, his1Δ::hisG/his1Δ::hisG, arg4Δ::hisG/arg4Δ::hisG, ADE2/ade2Δ::MALp-myc-CPH2N-URA3*	This Study
HLY3968	*ura3Δ::imm^{434}/ura3Δ::imm^{434}, his1Δ::hisG/his1Δ::hisG, arg4Δ::hisG/arg4Δ::hisG, ADE2/ade2Δ::MALp-myc-CPH2-URA3*	This Study
HLY1928	*cph2Δ::ARG4/cph2Δ::HIS1, ura3Δ::imm^{434}/ura3Δ::imm^{434}, his1Δ::hisG/his1Δ::hisG, arg4Δ::hisG/arg4Δ::hisG, ADE2/ade2Δ::URA3*	(4)
HLY4149	*cph2Δ::ARG4/cph2Δ::HIS1, ura3Δ::imm^{434}/ura3Δ::1 imm^{434}, his1Δ::hisG/his1Δ::hisG, arg4Δ::hisG/arg4Δ::hisG, ADE2/ade2Δ::URA3 ACT1/ACT1p-6xHIS-FLAG-HMS1-NAT* (pLC597)	This Study (5)
hms1	*arg4Δ/arg4Δ leu2Δ/leu2Δ his1Δ/his1Δ URA3/ura3Δ::imm^{434} IRO1/iro1Δ::imm^{434} hms1Δ:: C.dubliniensis HIS1/hms1Δ: C. maltose LEU2*	(6)
SN250	*his1Δ/his1Δ, leu2Δ::C.dubliniensis HIS1/ leu2Δ:: C. maltose LEU2, arg4Δ/arg4Δ, URA3/ura3Δ::imm^{434} IRO1/iro1Δ::imm^{434}*	(7)
cph2	*arg4Δ/arg4Δ leu2Δ/leu2Δ his1Δ/his1Δ URA3/ura3Δ::imm^{434} IRO1/iro1Δ::imm^{434} cph2Δ:: C.dubliniensis HIS1/cph2Δ: C. maltose LEU2*	(7)
HLY4151	*his1Δ/his1Δ, leu2Δ::C.dubliniensis HIS1/ leu2Δ:: C. maltose LEU2, arg4Δ::ARG4/arg4Δ, URA3/ura3Δ::imm^{434} IRO1/iro1Δ::imm^{434}*	This Study
HLY4152	*arg4Δ::ARG4/arg4Δ leu2Δ/leu2Δ his1Δ/his1Δ URA3/ura3Δ::imm^{434} IRO1/iro1Δ::imm^{434} cph2Δ:: C.dubliniensis HIS1/cph2Δ: C. maltose LEU2*	This Study
HLY4153	*arg4Δ::ARG4/arg4Δ leu2Δ/leu2Δ his1Δ/his1Δ URA3/ura3Δ::imm^{434} IRO1/iro1Δ::imm^{434} hms1Δ:: C.dubliniensis HIS1/hms1Δ: C. maltose LEU2*	This Study
upc2	*arg4Δ/arg4Δ leu2Δ/leu2Δ his1Δ/his1Δ URA3/ura3Δ::imm^{434} IRO1/iro1Δ::imm^{434} upc2Δ:: C.dubliniensis HIS1/upc2Δ: C. maltose LEU2*	(6)
HLY4007	*arg4Δ/arg4Δ leu2Δ/leu2Δ his1Δ/his1Δ ura3/ura3Δ::imm^{434} IRO1/iro1Δ::imm^{434} upc2Δ:: C.dubliniensis HIS1/upc2Δ: C. maltose LEU2 cph2Δ::ARG4/cph2Δ::URA3*	This Study
HLY4008	*arg4Δ/arg4Δ leu2Δ/leu2Δ his1Δ/his1Δ ura3/ura3Δ::imm^{434} IRO1/iro1Δ::imm^{434}*	This Study

	upc2Δ:: C.dubliniensis HIS1/upc2Δ: C. maltose LEU2 cph2Δ::ARG4/cph2Δ::URA3	
HLY4113	*ofd1Δ::ARG4/ofd1Δ::URA3/ofd1::HIS1, ura3Δ::imm*^{434}*/ura3Δ::imm*^{434}*, his1Δ::hisG/his1Δ::hisG, arg4Δ::hisG/arg4Δ::hisG*	(8)
HLY4180	*ubr1::ARG4/ubr1Δ::HIS1, ura3Δ::imm*^{434}*/ura3Δ::imm*^{434}*, his1Δ::hisG/his1Δ::hisG, arg4Δ::hisG/arg4Δ::hisG, ADE2/ade2Δ::URA3*	(8)
HLY4208	*ofd1Δ::ARG4/ofd1Δ::URA3/ofd1::HIS1, ura3Δ::imm*^{434}*/ura3Δ::imm*^{434}*, his1Δ::hisG/his1Δ::hisG, arg4Δ::hisG/arg4Δ::hisG, ADE2/ade2Δ::MALp-myc-CPH2-URA3*	This Study
HLY4224	*ubr1::ARG4/ubr1Δ::HIS1, ura3Δ::imm*^{434}*/ura3Δ::imm*^{434}*, his1Δ::hisG/his1Δ::hisG, arg4Δ::hisG/arg4Δ::hisG, ADE2/ade2Δ::MALp-myc-CPH2-URA3*	This Study
HLY4226	*ura3Δ::imm*^{434}*/ura3Δ::imm*^{434}*, his1Δ::hisG/his1Δ::hisG, arg4Δ::hisG/arg4Δ::hisG, ADE2/ade2Δ::MALp-myc-CPH2-URA3 RP10::ACT1p-*$OFD1_{261-617}$*-13MYC-SAT1*	This Study

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