Table S1. *C. albicans* Transcription-Factor Mutant Library

	Transcription-Factor Gene (ORF #)	Contig # for ORF	DNA Binding Motif	Closest *S. cerevisiae* Homolog	Isolation of Homozygote	Biofilm Formation by Mutant	Strain Name (Homozygous Mutant)
1	19.1007	19-10083	bZIP	*YDR017C*	yes	normal	CJN609
2	19.10266	19-20158	zinc finger	*ADR1*	triplications only	ND	
3	19.10478	19-20163	zinc finger	*MIG1*	triplications only	ND	
4	19.1135	19-10097	b-barrel	*YMR284W*	yes	normal	CJN523
5	19.11410	19-20194	zinc finger	*AZF1*	yes	normal	CJN299
6	19.1178	19-10099	bZIP	*YGL232W*	yes	normal	CJN866
7	19.1187	19-10099	Myc-like	*YOR032C*	yes	normal	CJN524
8	19.12215	19-20215	zinc finger	*MSN2*	yes	normal	CJN334
9	19.1227	19-10104	zinc cluster	*ECM22*	triplications only	ND	
10	19.1255	19-10104	zinc cluster	*HAP1*	yes	normal	CJN592
11	19.12786	19-20225	zinc finger	*MIG1*	yes	normal	CJN348
12	19.13396	19-20236	zinc finger	*ADR1*	yes	normal	CJN809
13	19.1358	19-10113	bZIP	*GCN4*	yes	normal	CJN913
14	19.1496	19-10119	zinc finger	*YIL130W*	yes	normal	CJN922
15	19.1497	19-10119	zinc cluster	*YIL130*	yes	normal	CJN582
16	19.1565	19-10119	zinc finger	*YLR401C*	yes	normal	CJN941
17	19.1589	19-10119	TATA binding	*YJL025W*	yes	normal	CJN932
18	19.1694	19-10123	zinc finger	*YIL129C*	yes	normal	CJN958
19	19.1729	19-10123	zinc finger	*Unknown*	yes	normal	CJN966
20	19.173	19-10040	zinc finger	*AZF1*	yes	normal	CJN395
21	19.1822	19-10131	zinc cluster	*UME6*	triplications only	ND	
22	19.1826	19-10131	zinc finger	*YGL219C*	yes	normal	CJN975
23	19.2054	19-10139	zinc finger	*YDL020C*	yes	normal	CJN831
24	19.2064	19-10139	zinc finger	*YKL165C*	triplications only	ND	
25	19.2077	19-10139	zinc cluster	*ECM22*	triplications only	ND	
26	19.2260	19-10143	zinc finger	*YHR040W*	yes	normal	CJN854
27	19.2280	19-10143	zinc cluster	*CAT8*	yes	normal	CJN799
28	19.2315	19-10146	bZIP	*RTG3*	yes	normal	CJN864
29	19.2331	19-10146	zinc finger	*ADA2*	yes	normal	CJN863
30	19.2356	19-10147	zinc finger	*CRZ1*	yes	normal	CJN811
31	19.2393	19-10148	zinc finger	*YPR107C*	yes	normal	CJN872
32	19.2399	19-10148	zinc finger	*YNL227C*	yes	normal	CJN874
33	19.2432	19-10150	bZIP	*HAC1*	triplications only	ND	
34	19.2458	19-10150	zinc finger	*YMR140W*	yes	normal	CJN878
35	19.2612	19-10151	zinc finger	*YDR463W*	yes	normal	CJN908
36	19.2623	19-10152	zinc cluster	*ECM22*	triplications only	ND	
37	19.2647	19-10155	zinc cluster	*HAP1*	yes	normal	CJN544
38	19.2674	19-10158	zinc finger	*Unknown*	yes	normal	CJN911
39	19.2745	19-10158	zinc cluster	*UME6*	yes	normal	CJN494
40	19.3088	19-10166	bZIP	*Unknown*	yes	normal	CJN885
41	19.3127	19-10166	zinc cluster	*UME6*	yes	normal	CJN517
42	19.3187	19-10170	zinc cluster	*HAL9*	yes	normal	CJN403
43	19.3193	19-10170	bZIP	*YHL009C*	yes	normal	CJN926
44	19.3300	19-10173	zinc finger	*YGR211W*	yes	normal	CJN928
45	19.3305	19-10173	zinc cluster	*ECM22*	yes	normal	CJN593
46	19.3308	19-10173	zinc cluster	*STB5*	yes	normal	CJN531
47	19.3390	19-10176	zinc finger	*YDR228C*	triplications only	ND	
48	19.3405	19-10176	zinc finger	*YJR087W*	yes	normal	CJN943
49	19.3407	19-10176	zinc finger	*RAD18*	yes	normal	CJN945
50	19.3683	19-10186	zinc finger	*YDL226C*	yes	normal	CJN979

	Transcription-Factor Gene (ORF #)	Contig # for ORF	DNA Binding Motif	Closest *S. cerevisiae* Homolog	Isolation of Homozygote	Biofilm Formation by Mutant	Strain Name (Homozygous Mutant)
51	19.3753	19-10190	zinc cluster	*SEF1*	yes	normal	CJN983
52	19.3809	19-10192	Myc-like	*YKR099W*	yes	normal	CJN256
53	19.3835	19-10192	TFIIC subunit	*YAL001C*	yes	normal	CJN993
54	19.3986	19-10194	zinc cluster	*PPR1*	yes	normal	CJN411
55	19.4125	19-2119	zinc finger	*PZF1*	yes	normal	CJN396
56	19.431	19-10052	zinc cluster	*PUT3*	yes	normal	CJN563
57	19.4318	19-10202	zinc finger	*MIG1*	yes	normal	CJN434
58	19.4433	19-10205	STE12-like	*STE12*	yes	normal	CJN305
59	19.4568	19-10212	zinc cluster	*YIL130*	yes	normal	CJN518
60	19.4573	19-10212	zinc cluster	*YIL130*	yes	normal	CJN598
61	19.4649	19-10212	zinc cluster	*VID31*	triplications only	ND	
62	19.4670	19-10212	zinc finger	*AZF1*	yes	normal	CJN432
63	19.4766	19-10215	zinc cluster	*ARG81*	yes	normal	CJN401
64	19.4767	19-10215	zinc cluster	*ECM22*	yes	normal	CJN803
65	19.4776	19-10215	zinc cluster	*LYS14*	yes	normal	CJN805
66	19.4778	19-10215	zinc cluster	*LYS14*	yes	normal	CJN807
67	19.487	19-10053	suppress Ty	*YPL175W*	triplications only	ND	
68	19.4972	19-10216	zinc finger	*CRZ1*	yes	normal	CJN393
69	19.5026	19-10216	zinc finger	*YML081*	yes	normal	CJN427
70	19.5338	19-10225	zinc cluster	*GAL4*	yes	normal	CJN801
71	19.5380	19-10227	zinc cluster	*LYS14*	yes	normal	CJN577
72	19.5548	19-10230	zinc cluster	*LYS14*	yes	normal	CJN528
73	19.567	19-10057	zinc finger—C3HC4	*YDR460W*	triplications only	ND	
74	19.5729	19-10233	zinc cluster	*CHA4*	yes	normal	CJN506
75	19.5908	19-10236	TEA/ATTS	*YBR083W*	yes	defective	CJN308
76	19.6182	19-2405	zinc cluster	*HAP1*	yes	normal	CJN548
77	19.6680	19-2472	zinc cluster	*YIL130*	yes	normal	CJN419
78	19.6781	19-10254	zinc finger	*Unknown*	yes	normal	CJN997
79	19.6817	19-10254	zinc cluster	*YIL130*	yes	normal	CJN242
80	19.6845	19-10256	bZIP	*YDR249C*	yes	normal	CJN1001
81	19.6850	19-10256	zinc finger—C3HC4	*YDR255C*	yes	normal	CJN1003
82	19.6985	19-2500	zinc cluster	*TEA1*	triplications only	ND	
83	19.7025	19-10262	MADS domain	*YMR043W*	yes	normal	CJN1007
84	19.7150	19-2506	zinc finger	*YBR066C*	yes	normal	CJN322
85	19.718	19-10070	RNA pol I	*YML043C*	triplications only	ND	
86	19.8342	19-10070	zinc finger	*YPL230W*	yes	defective	CJN459
87	19.7247	19-2507	zinc finger	*RIM101*	yes	normal	CJN267
88	19.7318	19-2511	zinc cluster	*UGA3*	yes	normal	CJN571
89	19.735	19-10071	TFIID subunit	*YGR274C*	triplications only	ND	
90	19.7359	19-2513	zinc finger	*CRZ1*	yes	normal	CJN442
91	19.7518	19-2516	zinc cluster	*TEA1*	yes	normal	CJN491
92	19.7570	19-2518	zinc cluster	*UGA3*	yes	normal	CJN511
93	19.7583	19-2518	zinc cluster	*HAL9*	yes	normal	CJN495
94	19.798	19-10076	TFIIF subunit	*YPL129W*	yes	normal	CJN856
95	19.889	19-10076	TENA	*YOL055C*	yes	normal	CJN857
96	19.909	19-10076	zinc finger	*STP4*	yes	normal	CJN817
97	19.9191	19-20123	bZIP	*YML007W*	yes	normal	CJN608
98	19.9326	19-20125	zinc finger	*MET32*	yes	normal	CJN815
99	19.976	19-10080	zinc finger—C3HC4	*YDL074C*	triplications only	ND	

This table lists 99 putative transcription-factor genes for which *UAU1* insertions were constructed in the genome. In 16 cases, no homozygous mutants were isolated. Details are provided in the Supplemental Experimental Procedures section. Strain CJN308 (entry number 75) is the *tec1/tec1* mutant; strain CJN459 (entry number 86) is the *bcr1/bcr1* mutant. ND denotes “not determined.”

Table S2. *C. albicans* Strains Used in This Study

Strain	Genotype	Reference
BWP17	*ura3Δ::λimm434 arg4::hisG his1::hisG* *ura3Δ::λimm434 arg4::hisG his1::hisG*	[S2]
CJN308	*ura3Δ::λimm434 arg4::hisG his1::hisG tec1::Tn7-UAU1* *ura3Δ::λimm434 arg4::hisG his1::hisG tec1::Tn7-URA3*	This study
CJN459	*ura3Δ::λimm434 arg4::hisG his1::hisG bcr1::Tn7-UAU1* *ura3Δ::λimm434 arg4::hisG his1::hisG bcr1::Tn7-URA3*	This study
CJN688	*ura3Δ::λimm434 arg4::hisG his1::hisG bcr1::ARG4* *ura3Δ::λimm434 arg4::hisG his1::hisG bcr1::URA3*	This study
CJN698	*ura3Δ::λimm434 arg4::hisG his1::hisG::pHIS1-BCR1 bcr1::ARG4* *ura3Δ::λimm434 arg4::hisG his1::hisG bcr1::URA3*	This study
CJN702	*ura3Δ::λimm434 arg4::hisG his1::hisG::pHIS1 bcr1::ARG4* *ura3Δ::λimm434 arg4::hisG his1::hisG bcr1::URA3*	This study
CJN750	*ura3Δ::λimm434 arg4::hisG his1::hisG::pHIS1-TEF1-GFP bcr1::ARG4* *ura3Δ::λimm434 arg4::hisG his1::hisG bcr1::URA3*	This study
CJN823	*ura3Δ::λimm434 arg4::hisG his1::hisG::pHIS1-TEF1-GFP tec1::Tn7-UAU1* *ura3Δ::λimm434 arg4::hisG his1::hisG tec1::Tn7-URA3*	This study
CJN896	*ura3Δ::λimm434 arg4::hisG his1::hisG::pHIS1 tec1::Tn7-UAU1* *ura3Δ::λimm434 arg4::hisG his1::hisG tec1::Tn7-URA3*	This study
CJN1023	*ura3Δ::λimm434 arg4::hisG his1::hisG::pHIS1-TEC1 tec1::Tn7-UAU1* *ura3Δ::λimm434 arg4::hisG his1::hisG tec1::Tn7-URA3*	This study
DAY185	*ura3Δ::λimm434 ARG4:URA3::arg4::hisG his1::hisG::pHIS1* *ura3Δ::λimm434 arg4::hisG his1::hisG*	[S4]
DAY286	*ura3Δ::λimm434 ARG4:URA3::arg4::hisG his1::hisG* *ura3Δ::λimm434 arg4::hisG his1::hisG*	[S3]
MLR62	*ura3Δ::λimm434 ARG4:URA3::arg4::hisG his1::hisG::pHIS1-TEF1-GFP* *ura3Δ::λimm434 arg4::hisG his1::hisG*	M. Richard (personal communication)

Table S3. Microarray Comparison of *bcr1Δ/bcr1Δ* and *bcr1Δ/bcr1Δ* +p*BCR1* Strains

log2 Expression Change (Mutant versus Complemented Strain)	t test/ANOVA	Gene ID (ORF19# or Genbank Accession Number)	Gene Symbol	CandidaDB Accession Number	Description
–3.939029783	*1.08001E-09*	*Z50123*	*HYR1*	*CA1576*	*hyphally regulated protein*
–3.432749152	*1.02716E-09*	*U64206*	*HWP1*	*CA2825*	*Hyphal wall protein*
–3.069862068	*1.73622E-07*	*U15800*	*CHT2*	*CA1051*	*chitinase 2 precursor*
–2.654586349	*1.39721E-05*	*L17087*	*ECE1*	*CA1402*	*Cell Elongation Protein*
–2.365453273	*7.06662E-08*	*orf19.5636*	*RBT5*	*CA2558*	*repressed by TUP1 protein 5*
–2.083872288	*5.02087E-05*	*U29369*	*HWP1*	*CA2825*	*Hyphal wall protein*
–1.916229054	0.014986323	orf19.4175	TOK1.3	CA3725	Outward-rectifier potassium channel, 3′ end
–1.900078237	1.10841E-05	orf19.8342	BCR1	CA3685	Transcription factor
–1.734017491	4.1556E-05	orf19.12174			unknown function
–1.68715263	0.000291448	orf19.5637			unknown function
–1.657277837	6.48451E-06	orf19.12173	IPF4450	CA0684	unknown function
–1.53686735	9.98143E-07	orf19.716	IPF15781	CA1238	unknown function
–1.427173926	0.042405365	orf19.214			unknown function
–1.278785862	0.025561718	orf19.6079	IPF14618	CA0286	unknown function
–1.215053246	*0.001888994*	*CAU87956*	*ALS3*		*Agglutinin-like protein*
–1.145474458	0.029837177	orf19.1964	IPF6298	CA2947	unknown function
–1.142758362	*0.000706668*	*orf19.6996*	*IPF4514*	*CA5042*	*putative alpha-1,3-mannosyltransferase*
–1.133155396	0.031900836	orf19.3981	MAL31	CA3404	maltose permease
–1.119200314	0.002042567	orf19.5333	GCN1.5f	CA5493	translational activator, 5′ end
–1.100447115	*0.000356805*	*orf19.6420*	*IPF1341*	*CA5112*	*Similarity to mucin proteins*
–1.04591055	0.025380263	orf19.4622	IPF11090.exon1	CA5183	weak similarity to glutenin, exon 1
–1.044362193	0.000434692	orf19.7199	IPF2138	CA5325	unknown function
–1.037687976	0.03070496	orf19.7392	DED1	CA5691	RNA helicase
–1.008256772	0.004784861	orf19.6078	IPF17652.3	CA0037	reverse transcriptase, 3′ end
–1.003614094	0.000176754	orf19.2943	DIP51.5f	CA2204	dicarboxylic amino acid permease, 5′ end
–1.003514735	0.030328204	orf19.4056	IPF7666	CA1120	unknown function
–0.979694955	0.008672128	orf19.7404	CHA11	CA5704	L-serine/L-threonine deaminase
–0.976667121	0.005571647	orf19.467	IPF10055	CA1624	unknown function
–0.958739173	0.000873426	orf19.7566	GNP1	CA5972	High-affinity glutamine permease
–0.952514768	0.036653387	orf19.1772	IPF16267	CA0634	unknown function
–0.941534551	0.014405507	orf19.5972			unknown function
–0.927984059	0.003336673	orf19.7922	KRE5.3eoc	CA2786	UDP-glucose:glycoprotein glucosyltransferase, 3′ end
–0.922276148	0.003621288	X77589			CDR1
–0.900480565	0.002123512	orf19.7033	PPS1	CA5215	protein tyrosine phosphatase
–0.896635339	0.002500416	orf19.6856	NSP49.3f	CA4459	nucleoporin, 3′ end

log2 Expression Change (Mutant versus Complemented Strain)	t test/ANOVA	Gene ID (ORF19# or Genbank Accession Number)	Gene Symbol	CandidaDB Accession Number	Description
–0.888442628	0.008805893	orf19.139	TRA1.5eoc	CA1814	ATM/Mec1/TOR1+2-related, 5′ end
–0.865217336	0.003613065	orf19.10422	IPF18298	CA3765	unknown function
–0.851045616	0.016223684	orf19.5980	IPF21	CA6080	unknown function
–0.844694238	0.012463017	orf19.1211			unknown function
–0.84131626	0.000835473	orf19.691	GPD2	CA0824	Glycerol 3-phosphate dehydrogenase
–0.81783073	0.011821748	orf19.3446	MOG1	CA4018	Ran-Binding Protein
–0.814452959	0.006988321	orf19.2358			unknown function
–0.812215318	0.00014802	orf19.1473	IPF4386	CA4532	unknown function
–0.80963953	0.000208586	orf19.3159	IPF14693	CA1268	unknown function
–0.790585546	0.016235693	orf19.6834			unknown function
–0.78720998	0.045377083	orf19.24	RTA2	CA3607	unknown function
–0.763954502	0.011791338	orf19.5431	IPF1129	CA5784	unknown function
–0.753693026	0.010540987	orf19.6772	ECM29.exon1	CA5931	Involved in cell wall biogenesis and architecture, exon 1
–0.745342074	0.011936012	orf19.73	IPF17430	CA0011	possible zinc protease
–0.741075542	0.003082786	orf19.4556	ALS12.3f	CA0413	agglutinin-like protein, 3′ end
–0.736229099	0.035670624	orf19.2337	ALP1	CA3334	amino acid permease
–0.72962115	0.012421542	X94753	GFA1	CA4016	glutamine:fructose-6-phosphateamidotransferase
–0.716840548	0.004778704	orf19.575	IFF2	CA2714	unknown function
–0.711361798	0.029155082	orf19.7922	KRE5.5eoc	CA2410	UDP-glucose:glycoprotein glucosyltransferase, 5′ end
–0.709664226	0.001066299	orf19.7590	IPF690.5f	CA5990	NADH dehydrogenase (ubiquinone) 78K chain precursor, 5′ end
–0.70823198	0.020206601	orf19.5912	MAK21	CA6134	Ribosome biogenesis protein
–0.705312096	0.004724159	orf19.3219	IPF14538	CA1616	unknown function
–0.704374341	0.000560623	orf19.11452	IPF8627	CA1309	unknown function
–0.70196241	0.018564115	orf19.6833	IPF12082.5f	CA5876	bumetanide-sensitive Na-K-Cl cotransport protein, 5′ end
–0.701373164	0.000666643	orf19.4645	BEM1	CA0514	bud emergence mediator
–0.698242181	0.011908485	U67192	ERG16	CA1387	cytochrome P450 lanosterol 14a-demethylase
–0.692657374	0.038915975	orf19.9891	ALS10	CA0448	agglutinin-like protein
–0.682426249	0.018743085	orf19.2849	AQY1	CA2873	similarity to plasma membrane and water channel proteins (aquaporin-like)
–0.682022561	0.002220514	orf19.5792	SMP3	CA4149	Protein kinase C pathway protein
–0.678143336	0.020730509	orf19.1021	IPF17520.53eoc	CA0141	unknown function, internal fragment
–0.67749295	0.004113537	orf19.3701	IPF8075	CA1396	unknown function

log2 Expression Change (Mutant versus Complemented Strain)	t test/ANOVA	Gene ID (ORF19# or Genbank Accession Number)	Gene Symbol	CandidaDB Accession Number	Description
–0.675929874	0.005078295	orf19.2248	ARE2	CA3590	acyl-CoA sterol acyltransferase-like
–0.6607759	0.027628907	orf19.30	SPF1	CA3613	P-type ATPase
–0.658685967	0.001922291	orf19.1944	IPF11281	CA3354	similar to *Saccharomyces cerevisiae* Gpr1p G-protein coupled receptor
–0.655113243	0.002294889	orf19.7053	GAC1	CA5641	ser/thr phosphoprotein phosphatase 1, regulatory chain
–0.650743596	1.41809E-05	AF177670	RAS1	CA2261	GTP binding protein
–0.646691509	0.022585323	orf19.5994	IPF4842	CA6070	similar to *Saccharomyces cerevisiae* Rsg1p ras-related GTP binding protein
–0.639041075	0.004753865	orf19.1893	IPF6455	CA4475	unknown function
–0.633296452	0.034775045	orf19.5693	GAA1	CA2612	required for attachment of GPI anchor onto proteins by homology
–0.627442166	0.009605274	orf19.4763	IPF10916	CA2627	unknown function
–0.620794916	0.01293192	orf19.1326	IFA7	CA2829	unknown function
–0.620321173	0.017454707	orf19.815	IPF5806	CA4216	unknown function
–0.618054658	0.004972313	orf19.5281	IPF4697	CA4971	similar to *Saccharomyces cerevisiae* Scp160p required for maintenance of exact ploidy
–0.617411897	0.026355391	orf19.6100	IPF4641	CA3856	similar to *Saccharomyces cerevisiae* Crd1p cardiolipin synthase
–0.614936349	0.01336301	orf19.12212	IPF13919	CA2212	unknown function
–0.614018817	0.001029964	orf19.1317	IPF14554	CA2823	similar to *Saccharomyces cerevisiae* Osh3p oxysterol binding protein
–0.611456962	0.02890197	orf19.2198	IPF5505	CA2438	unknown function
–0.610646382	0.010156729	orf19.6885	IPF9430	CA4574	similar to *Saccharomyces cerevisiae* Spo7p meiotic protein
–0.600187888	0.035362635	orf19.7466	ACC1	CA5816	acetyl-coenzyme-A carboxylase
–0.599271154	0.04519433	orf19.13821	IPF11432	CA3663	unknown function
–0.593010509	0.012940719	orf19.1659	ALG8	CA3463	glucosyltransferase
–0.588641962	0.009061246	orf19.5123	IPF17914.3eoc	CA1760	unknown function
–0.585604526	0.020641513	orf19.10097	MDM1.3	CA0140	intermediate filament protein, 3′ end
–0.582458741	0.012770294	orf19.4966	IPF16755	CA1367	unknown function
–0.581817394	0.033679489	orf19.8270			unknown function
–0.580629037	0.002074794	orf19.1685	IPF6510	CA2306	unknown function

log2 Expression Change (Mutant versus Complemented Strain)	t test/ANOVA	Gene ID (ORF19# or Genbank Accession Number)	Gene Symbol	CandidaDB Accession Number	Description
–0.577443305	0.005908015	orf19.763	IPF3899	CA1953	similar to *Saccharomyces cerevisiae* Cbc2p small subunit of the nuclear cap-binding protein complex CBC
–0.575476218	0.022148142	orf19.657	SAM2	CA0959	S-adenosylmethionine synthetase 2
–0.574103806	0.020618695	orf19.13133	IPF8486	CA2657	unknown function
–0.573879498	0.012012363	orf19.2149	IPF11607	CA3189	unknown function
–0.569598788	0.018695113	orf19.3700	TOM72	CA1397	mitochondrial import receptor
–0.566532958	0.023695875	orf19.11970	KTR2	CA1444	mannosyltransferase
–0.563743792	0.035837401	orf19.4480	IPF13756.5f	CA2413	unknown function, 5′ end
–0.560487838	0.016190431	orf19.6444	IPF1382	CA5097	unknown function
–0.555380734	0.013391456	orf19.4623	IPF11090.exon2	CA5184	weak similarity to glutenin, exon 2
–0.544688873	0.013930387	orf19.11797	DAP2	CA1660	dipeptidyl aminopeptidase B
–0.542191503	0.046063388	orf19.1486	IPF6011	CA1000	unknown function
–0.53578213	0.004320624	orf19.391	IPF7289	CA3878	similar to *Saccharomyces cerevisiae* Upc2p RNA polymerase II transcription factor
–0.533897165	0.032138628	orf19.13064	IFA12	CA2755	unknown function
–0.533642863	0.03909445	orf19.4304	GAP3	CA2638	General amino acid permease
–0.531584613	0.035835388	orf19.3874	IPF13228	CA3550	unknown function
–0.529785795	0.005912985	orf19.3431	IPF19795	CA4033	similar to *Saccharomyces cerevisiae* Mip1p DNA-directed DNA polymerase gamma catalytic subunit, mitochondrial
–0.524623875	0.033801617	orf19.6197	DHH1	CA3217	RNA helicase by homology
–0.524254033	0.039787719	orf19.7710	IPF17790	CA0030	unknown function
–0.521648458	0.039124992	orf19.2272	IPF10298	CA1878	unknown function
–0.517344499	0.00118173	orf19.4000	IPF9385	CA4768	similar to *Saccharomyces cerevisiae* Pho2p homeobox-domain containing transcription factor
–0.51722828	0.047210764	orf19.749	IPF17515	CA0103	unknown function
–0.516496963	0.000564862	AF069763			cell wall synthesis protein Kre9p
–0.513186904	0.041593596	orf19.6806	IPF2379	CA5900	unknown function
–0.512790672	0.011983063	orf19.1352	TIM22	CA0367	Mitochondrial import inner membrane translocase subunit
–0.507290693	0.011464928	orf19.5293	IPF11879	CA2163	unknown function
–0.506539475	0.036469579	orf19.9554	HNM1	CA3939	Choline permease
–0.505922414	0.025397243	orf19.4657	NEM1	CA2705	required for nuclear morphology

log2 Expression Change (Mutant versus Complemented Strain)	t test/ANOVA	Gene ID (ORF19# or Genbank Accession Number)	Gene Symbol	CandidaDB Accession Number	Description
–0.502476165	0.005793237	orf19.6966	IPF11120	CA5014	similar to *Saccharomyces cerevisiae* Cki1p choline kinase
–0.500045687	0.007857129	orf19.6968	IPF7561	CA5016	unknown function
–0.499857459	0.00573335	orf19.3481	IPF15646	CA2898	putative ATP-dependent RNA helicase
–0.498411371	0.025222236	orf19.5641	R2	CA2561	ornithine aminotransferase
–0.497115259	0.001279281	orf19.6003	IPF8311	CA6063	unknown function
–0.47891141	0.001397743	orf19.3706	IPF8619	CA0942	unknown function
–0.47214737	0.003814726	orf19.7610	IPF643	CA6009	similar to *Saccharomyces cerevisiae* Ptp3p protein tyrosine phosphatase
–0.461152696	0.003753944	orf19.5811	MET1	CA4162	siroheme synthase
–0.453185163	0.017858152	orf19.2909	ERG26	CA3760	C-3 sterol dehydrogenase (C-4 decarboxylase)
–0.449134907	0.019213591	orf19.6285	GLC7	CA3224	Ser/thr phosphoprotein phosphatase 1
–0.44899697	0.00652579	orf19.4141	IPF9821.3f	CA3092	unknown function, 3′ end
–0.447014215	0.037710135	Z12822	EFT3	CA3081	translation elongation factor 3
–0.44403773	0.008221358	orf19.2928	IPF14219	CA2042	probable membrane protein
–0.435355846	0.045656736	orf19.10265	IPF16120.5eoc	CA1890	unknown function, 5′ end
–0.435264478	0.013384566	orf19.7051	IPF448	CA5643	unknown function
–0.43012382	0.035087765	orf19.3713	IPF9211.5f	CA3142	unknown function, 3′ end
–0.42970025	0.033818532	orf19.4521	IPF15523	CA2906	unknown function
–0.429623326	0.001878906	orf19.7265	IPF5228.5	CA5379	similar to *Saccharomyces cerevisiae* Sad1p snRNP assembly factor required for pre-mRNA splicing, 5-prime end
–0.421834405	0.016893553	orf19.5777	IPF19961	CA2804	unknown function
–0.42169464	0.027170846	orf19.3220	IPF14536	CA1617	unknown function
–0.420983539	0.018898704	orf19.5258	IPF2039	CA4990	unknown function
–0.419119727	0.024552658	orf19.7860			unknown function
–0.416705661	0.040930361	orf19.1701	RKI1	CA1503	D-ribose-5-phosphate ketol-isomerase
–0.415963569	0.032269378	orf19.5428	IPF1126	CA5781	unknown function
–0.41046585	0.00062559	orf19.7762	IPF19622	CA0484	unknown function
–0.407052206	0.013493109	orf19.5537	IPF9126	CA1924	unknown function
–0.396137712	0.025850774	orf19.1531	RNA14.3eoc	CA0743	component of pre-mRNA 3 -end processing factor CF I, 3′ end
–0.394198047	0.011891815	orf19.2926	PSO2	CA0562	Interstrand crosslink repair protein
–0.392581144	0.049795905	orf19.1956	IPF14757	CA2256	unknown function
–0.39036235	0.029370607	orf19.2290	IPF9987	CA1118	similar to phosphatidylinositol kinase
–0.387364077	0.023637396	orf19.4929	IPF19785	CA3599	unknown function

log2 Expression Change (Mutant versus Complemented Strain)	t test/ANOVA	Gene ID (ORF19# or Genbank Accession Number)	Gene Symbol	CandidaDB Accession Number	Description
–0.384550473	0.012278239	orf19.4278	IPF8744	CA1549	unknown function
–0.378224639	0.027801556	orf19.3311	IFD3	CA4620	OXIDOREDUCTASE
–0.376867013	0.023353071	orf19.10366	RPC82	CA2869	DNA-directed RNA polymerase III, 82 kDa subunit
–0.375525294	0.013651215	orf19.6198			unknown function
–0.369144306	0.015454989	orf19.7238	NPL3	CA5361	nucleolar shuttling protein with an RNA recognition motif
–0.368050234	0.014910827	orf19.1784			unknown function
–0.367735319	0.041787793	orf19.3635	IPF14241	CA1312	unknown function
–0.356723387	0.008133194	orf19.4562			unknown function
–0.350720352	0.039844562	orf19.6531	NUC2	CA4947	NADH-UBIQUINONE OXIDOREDUCTASE
–0.343985936	0.026391782	orf19.1718	IPF19769	CA2799	unknown function
–0.338556694	0.017065919	orf19.2193	PRS5	CA2442	Phosphoribosylpyrophosphate synthetase (ribose-phosphate pyrophosphokinase)
–0.336714463	0.028516001	orf19.10042			unknown function
–0.33359082	0.049468804	orf19.556	IPF15839	CA0056	unknown function
–0.317721893	0.013790022	orf19.10046	IPF19665	CA2140	unknown function
–0.30497992	0.040508967	orf19.12155	IPF10555.5eoc	CA3238	unknown function, 5′ end
–0.29095602	0.012210418	orf19.1634	IPF4258	CA4002	unknown function
–0.252817803	0.034728745	orf19.7066			unknown function
0.186885945	0.045980655	orf19.5073	DPM1	CA3899	dolichol-phosphate (beta-D) mannosyltransferase 1 by homology
0.257003987	0.035766165	orf19.5974	IPF32	CA6085	similar to *Saccharomyces cerevisiae* Apg9p integral membrane protein required for Cvt and autophagy transport
0.262097873	0.039217589	orf19.1975	DIB1	CA0468	Component of the U4/U6.U5 snRNP
0.276381361	0.022818734	orf19.813			unknown function
0.287917364	0.033706011	CAPHERS	FRS1	CA2682	Phenylalanyl-tRNA synthetase
0.289260458	0.031729709	orf19.4617	MAK3	CA5179	N-acetyltransferase
0.305205921	0.008309388	orf19.889	IPF3679	CA4681	similar to *Saccharomyces cerevisiae* Thi20p hydroxymethylpyrimidine phosphate (HMP-P) kinase
0.319629278	0.007229412	orf19.7428	APN1	CA5723	AP endonuclease, exonuclease III homologue
0.322417847	0.046788944	orf19.7583	IPF907	CA5985	unknown function
0.33002543	0.035439108	orf19.5125	IPF14744	CA1759	unknown function

log2 Expression Change (Mutant versus Complemented Strain)	t test/ANOVA	Gene ID (ORF19# or Genbank Accession Number)	Gene Symbol	CandidaDB Accession Number	Description
0.331252544	0.027684208	orf19.884	HSP78.3f	CA4683	heat shock protein of clpb family of ATP-dependent proteases, mitochondrial, 3′ end
0.33416284	0.040667813	orf19.2050	TGL1	CA3658	Triacylglycerol lipase
0.337234069	0.018263418	orf19.7330	PET18	CA5566	Putative transcriptional regulator
0.338880219	0.020302568	orf19.5254	IPF2033	CA4994	unknown function
0.339029519	0.002807519	orf19.1418	IPF11236.3f	CA3959	similar to *Saccharomyces cerevisiae* Sec15p component of the exocyst complex, 3′ end
0.341523957	0.049511325	orf19.1561			unknown function
0.344572076	0.048223252	orf19.6373	PSU1	CA3537	suppressor of petit mutations by homology
0.346556826	0.030519281	orf19.12698	IPF13941	CA5013	Unknown function
0.35119351	0.020944855	AF205716	GCN4	CA3126	transcriptional activator
0.36379115	0.002084557	orf19.4411	HOS1	CA1453	Putative histon deacetylase
0.365721291	0.032688875	orf19.2965	IPF7781	CA4168	putative pump-driving ATPase
0.37700595	0.023939099	orf19.4723	FAD1	CA1603	flavin adenine dinucleotide (FAD) synthetase
0.379560928	0.039283503	orf19.287	IPF3810	CA2784	unknown function
0.382583892	0.034751615	orf19.5260	RPN2	CA4988	Proteasome regulatory subunit
0.402248915	0.044044274	orf19.3737	IPF4721	CA3251	unknown Function
0.404468831	0.032437446	orf19.7421	CYP51	CA5717	Cyclophilin—peptidylprolyl cis-trans isomerase or PPIase
0.407791478	0.022128349	orf19.4979	KNS1	CA1577	Ser/thr protein kinase
0.410698284	0.016234258	orf19.13978	IPF6665	CA4289	unknown function
0.415429011	0.039491578	orf19.2205			unknown function
0.422510786	0.016229793	orf19.3932	IPF16253	CA0782	unknown function
0.42503785	0.013312541	orf19.593	IPF11873	CA3425	similar to *Saccharomyces cerevisiae* Swa2p clathrin-binding protein required for normal clathrin function and for uncoating of clathrin-coated vesicles
0.430891253	0.023732195	orf19.3399	IPF12959	CA2433	unknown function
0.434993774	0.040791088	CASRP54	SRP54	CA5440	54 kDa signal recognition particle subunit
0.43571735	0.041988656	orf19.7656			unknown function
0.437504844	0.039137472	orf19.6773	ECM29.exon2	CA5930	Involved in cell wall biogenesis and architecture, exon 2
0.43838308	0.030413703	orf19.3093	MSH2	CA4413	DNA mismatch repair protein
0.441109532	0.008364058	orf19.1862	IPF4065	CA0386	unknown function
0.448974302	0.037657952	orf19.4125	PZF1	CA1157	TFIIIA (transcription initiation factor)

log2 Expression Change (Mutant versus Complemented Strain)	t test/ANOVA	Gene ID (ORF19# or Genbank Accession Number)	Gene Symbol	CandidaDB Accession Number	Description
0.458208676	0.039993384	orf19.6039	SED5	CA4902	Syntaxin
0.465633797	0.019383406	orf19.7288	IPF2852	CA5529	putative acetyl-coenzyme-A dehydrogenase
0.471166465	0.0328914	orf19.5642	IPF19953	CA2562	unknown function
0.480039711	0.018520637	orf19.5691	CDC11	CA2610	septin by homology
0.485736014	0.047724663	orf19.9218	RNA1	CA1044	GTPase activating protein
0.488331395	0.01157795	orf19.12194	SEC24	CA0958	component of COPII coat of ER-Golgi vesicles
0.490767039	0.031335603	orf19.11227	IPF4728	CA3254	unknown function
0.497445217	0.022670354	M61128	CMD1	CA1451	Calmodulin
0.498219177	0.018399573	orf19.972	IPF1588	CA5422	unknown function
0.500958246	0.046826043	orf19.5367	RDH54	CA5519	helicase required for mitotic diploid-specific recombination and repair
0.509166788	0.036681094	orf19.8850	IPF14959	CA3462	similar to *Saccharomyces cerevisiae* Trs130p TRAPP subunit of 130 kDa involved in targeting and fusion of ER to golgi transport vesicles
0.509392819	0.036260121	orf19.1264	CFL2	CA3461	ferric reductase
0.510447603	0.023001604	orf19.7412	MUB1	CA5711	Regulation of bud site selection
0.513746664	0.046806022	orf19.7527	IPF361	CA5866	unknown function
0.514004678	0.001662098	orf19.7447	JEN1	CA5737	Carboxylic acid transporter protein
0.516646444	0.017843228	orf19.4593	RGA2	CA5154	rho-GTPase activating protein 2
0.517922649	0.003059526	orf19.3839	IPF4089	CA4863	secretory aspartyl proteinase
0.519485166	0.009802479	orf19.4162	MLH1	CA1229	DNA mismatch repair protein
0.525487142	0.006683793	orf19.13058			unknown function
0.553077478	0.024254285	orf19.9881			unknown function
0.55313788	0.017847289	orf19.7564	DPB2	CA5970	DNA-directed DNA polymerase epsilon, subunit B
0.555057717	0.016681048	orf19.7141	UFE1	CA5284	Endoplasmic reticulum t-SNARE
0.556959711	0.003012708	orf19.1694	IPF6521.3eoc	CA1499	similar to *Saccharomyces cerevisiae* Tao3p transcriptional activator, 3′ end
0.569753687	0.002667392	orf19.3123	RPT5	CA4389	26S proteasome regulatory subunit
0.573400127	0.020651976	orf19.5032	SUN42	CA5232	Putative cell wall beta-glucosidase
0.578442253	0.00441487	X62289	SAP2	CA3138	aspartic protease
0.589464888	0.008658891	orf19.5357	AKL1	CA5511	serine/threonine protein kinase
0.595466157	0.019699058	orf19.4369	IPF12368	CA0999	unknown function

log2 Expression Change (Mutant versus Complemented Strain)	t test/ANOVA	Gene ID (ORF19# or Genbank Accession Number)	Gene Symbol	CandidaDB Accession Number	Description
0.605243728	0.018067999	orf19.2341	HNT1	CA2345	similarity to protein kinase C inhibitor-I
0.609186998	0.023731531	orf19.4129			unknown function
0.612372487	0.021630497	orf19.7453	IPF2898	CA5744	unknown function
0.614860069	0.039949077	M94160	CDC25	CA4698	cell division cycle protein
0.635438398	0.03942519	orf19.3021	IPF3701	CA5055	unknown function
0.645306004	0.045083677	orf19.1029	RPP1	CA1630	required for processing of tRNA and 35S rRNA
0.681789733	0.032090318	orf19.9115	IPF6493	CA0193	unknown function
0.699427847	0.010890104	orf19.348	IPF1505	CA4641	similar to *Saccharomyces cerevisiae* Kre6p glucan synthase subunit
0.714282397	0.022847028	AF046872	SOD1.3	CA4120	Cu,Zn-superoxide dismutase, 3′ end
0.717545362	0.02601988	orf19.4930	SPC3	CA3600	signal peptidase subunit
0.727484334	0.000281153	orf19.7085	IPF525	CA5613	unknown function
0.731489416	0.021552505	orf19.2728	IPF10258	CA1162	similar to *Saccharomyces cerevisiae* Rad24p cell cycle checkpoint protein
0.746481424	0.044417756	orf19.3310	IPF5756	CA4619	unknown function
0.781004801	0.013988865	orf19.5992	IPF4835	CA6071	zinc finger protein
0.797085084	4.33876E-05	orf19.944	IFG3.3	CA5402	probable d-amino acid oxidase, 3′ end
0.851591008	0.045502806	orf19.1819			unknown function
0.90156541	0.000249539	orf19.893	IPF3674	CA4679	unknown function
0.915299803	0.000227201	orf19.4934	OPS4	CA3713	opaque—phase-specific protein OP4, precursor
0.950956996	0.024147226	orf19.2105	IPF10632	CA2741	unknown function
1.020916572	0.002018336	orf19.4688	IPF14119	CA0689	unknown function
1.039966844	0.000114147	orf19.3282	IPF300	CA5470	unknown function
1.11374709	0.034690985	orf19.4065			unknown function
1.12972831	6.36571E-05	orf19.1120	IPF13879	CA1812	unknown function
1.131466202	0.006257557	orf19.1239	IPF12540	CA2974	unknown function
1.242885888	0.00311009	orf19.11225	IPF4724	CA3253	unknown function
1.490403906	4.77473E-05	orf19.935	IPF10571	CA5392	unknown function
1.614598423	*1.07841E-05*	*Orf19.4255*	*ECM331*	*CA2181*	*Involved in cell wall biogenesis and architecture*
1.722587101	0.000337052	Z30193			aspartyl protease
1.732300878	*0.002184633*	*Orf19.5557*	*IPF5376*	*CA2288*	*unknown function*
1.871063255	0.035502054	orf19.2766			unknown function
2.068168521	0.000331989	orf19.9486	FRE31	CA0397	Ferric reductase

Results are the average of eight independent array hybridizations with dye swaps, as detailed in the Supplemental Experimental Procedures section. Only expression changes for which ANOVA $p < 0.05$ are listed. Italicized entries represent 11 genes that govern cell wall properties among the 20 most highly Bcr1p-responsive genes.