

Supplemental Table 6: MUTANT SCREENING RESULTS

MUTANTS WITH MODERATE DEFECTS

6 days

gene name	orf19.#	functions
<i>CPH2</i>	1187	Transcriptional activator of hyphal growth
	4125	putative transcription factor; ortholog ScPzF1
<i>BAS1</i>	3809	similar to <i>S. cerevisiae</i> Bas1p, which is a regulator of purine biosynthetic genes
<i>TEC1</i>	5908	regulates <i>BCR1</i> ; directly transcriptionally regulated by Cph2p under some growth conditions
<i>ECM33</i>	3010.1	Cell wall protein;
	3869	regulated by Tsa1p
<i>ADA2</i>	2331	cell wall integrity role
	9326	ortholog ScMET31
<i>ZPR1</i>	3300	regulated by Gcn4p; repressed in response to amino acid starvation
	2458	ortholog ScSIP5; involved in cellular response to glucose starvation
	6845	no known function
<i>CAS5</i>	3407	ortholog ScRAD18; single stranded DNA binding activity
	4670	regulates cell wall damage response

8 days

gene name	orf19.#	functions	
	4972	ortholog <i>S. cerevisiae</i> CRZ1	
	5026	no known function; ortholog <i>S. cerevisiae</i> YML081W	
<i>CAS1</i>	1135	putative transcription tractor	
<i>CAP1</i>	9191	role in oxidative stress response and resistance	multidrug resistance
<i>WSC4</i>	7251	cell wall organization and biogenesis	
<i>PGA17</i>	893	Putative GPI-anchored protein of unknown function	
	1178	no known function	
	2399	ortholog ScJJJ1	
<i>ZCF14</i>	3434	no known function	
	2647	aerobic respiration	

11 days

gene name	orf19.#	functions
<i>MIG1</i>	4318	regulates genes for utilization of carbon sources; upregulated in biofilm
<i>WOR1</i>	4884	involved in white-opaque phenotypic switching
<i>STB5</i>	3308	response to xenobiotic stimulus
<i>ZCF18</i>	3405	no known function

MUTANTS NO DEFECT

gene name	orf19.#	
<i>FCR1</i>	6817	
<i>RIM101</i>	7247	
	11410	
<i>CPH1</i>	4433	
<i>NRG1</i>	7150	
<i>MSN4</i>	12215	systematic name orf19.4752
	12786	systematic name orf19.5316
<i>LYS143</i>	4776	

ZNC1	3187	
PPR1	3986	
	668	ortholog ScTOS4
CRZ1	7359	
ZCF38	7518	
ZCF39	7583	
FGR17	5729	
UGA3	7570	
CZF1	3127	
ZCF25	4568	
LYS14	5548	
ZCF2	431	
	7318	feature deleted and merged orf19.7317 UGA33
LYS144	5380	
ZCF6	1497	
ZCF5	1255	
ZCF26	4573	
	1007	putative transcription factor, ortholog ScKCS1
ZCF10	2280	
LYS143	4776	
	13396	systematic name orf19.5975
CRZ2	2356	
FGR15	2054	
	2260	ortholog ScBCD1
	798	putative transcription factor, ortholog ScTAF14
THI20	889	
	2393	putative transcription factor
	3088	putative transcription factor
	2674	putative transcription factor
GCN4	1358	
	1496	putative transcription factor
FGR3	3193	
	1565	putative transcript factor; ortholog ScDUS3
	1729	putative transcription facotr possibly spurious orf
	1826	putative transcription factor
	3683	putative transcription facor; ortholog ScGCS1
	3833	originally orf19.3835 and merged with orf19.3833 in Assembly 20
	6781	putative transcription factor
MCM1	7025	
CRH12	3966	
	299	ortholog ScECM14
ECM21	4887	
ZCF12	2623	
ECM3	1563	
ECM4	2613	
	5412	ortholog ScECM9
	4981	
	1277	
MSB2	1490	
	2476	
PGA10	5674	

RBR2	532
PGA44	1714

Based on Assembly 20 from Candida Genome Database
(CGD:<http://www.candidagenome.org/>) April 2007